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High Resolution X Chromosome Copy Number Variation in Autism

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High Resolution X Chromosome Copy Number Variation in Autism

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Advisor: Stephen T. Warren, Ph.D.

An abstract of a dissertation submitted to the Faculty of the James T. Laney School of Graduate Studies of Emory University in partial fulfillment of the requirements for the degree of Doctor of Philosophy in the Graduate Division of Biological and Biomedical Sciences Genetics and Molecular Biology

Abstract

High Resolution X Chromosome Copy Number Variation in Autism

By Morna A. Ikeda

The autism spectrum disorders (ASD) are a broadly defined set of developmental disorders that include autism and Asperger syndrome. Individuals with ASD are defined as having impairments in social interaction, deficiencies in communication, as well as restricted and stereotyped behaviors and interests. Leo Kanner first described autism in 1943, and subsequent twin and family studies have demonstrated a substantial genetic component underlying ASD. A marked increase in the prevalence of ASD has been noted in the last decade, and the most recent estimate suggests a prevalence of 1:88. A four- to ten-fold male preponderance of ASD suggests the existence of sex-specific risk alleles and the possibility of a recessive susceptibility locus on the X-chromosome. In the last eight years, copy number variation (CNV) has been appreciated as a rich source of both inherited and *de novo* human genomic variation.

Technological advances in array Comparative Genomic Hybridization (aCGH), the common microarray based assay used to assess copy number state, have enabled detection of increasingly smaller variants. We developed a custom high-density array consisting of 2.1 million oligonucleotide probes dedicated to the X-chromosome. Non-repetitive sequence is probed at a resolution of one probe per 50 bp or 96.8 megabases of unique sequence. Additionally, we further enhanced the stringency and thus rigor with which samples are interrogated by developing a hybridization and wash protocol for the Tecan HSPro 4800. The application of this machine standardized hybridization, wash, and dry conditions across all samples.

Using our custom X-chromosome CGH microarrays, we screened three cohorts for Xchromosome CNV. The first cohort was a series of 100 ASD males from the Autism Genetic Resource Exchange collection. Our second cohort of 64 ASD males was derived from the Simons Simplex Collection. Finally, our third cohort consisted of 100 males from a National Institute of Mental Health control population where individuals were selected as controls for the study of neuropsychiatric disease. In total, 164 ASD males and 100 non-ASD males were evaluated for X-chromosome CNV.

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Acknowledgements

I would like to first thank Stephen Warren, Dave Cutler, Christa Lese Martin, Stephanie Sherman and Mike Zwick for their constant support, guidance and encouragement through all the different stages of my thesis work and scientific growth. Truly, I left every encounter with a sense of forward progression in my experiments and/or critical thinking of the work at hand. With their gentle nudges, my mind and confidence in what I knew grew more than I ever imagined. Furthermore, it was through their efforts that I have learned to move beyond the answer at hand to the question it now posed.

I would also like to thank all those in the Department of Human Genetics. I received a tremendous amount of encouragement and supportive inquiry of my science from faculty, staff and students. But, their efforts to support and nourish me personally made DoHG a genuine resource and community for me. And, I would be completely remiss if I didn't acknowledge the incredible support and guidance from my lab mates: Reid Alisch, Steven Bray, Pankaj Chopra, Brad Coffee, Stephen Collins, Anne Dodd, Krayton Keith, Bryan Lynch, Tamika Malone, Julie Mowrey, Jen Mulle, Leila Myrick, Mika Nakamoto, Mike Sanotoro, Josh Suhl, Tao Wang, and Fuping Zhang. Of course, a special note of thanks to my peers, Adam Locke and Mike Santoro, for their efforts to better my scientific thoughts and work throughout my graduate career.

Finally, I would like to thank my family and friends from both within and outside of the Emory community. While some claim to never have understood how I spent my time and efforts, all were a constant source of encouragement and refuge when I sought balance in my life.

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Chapter 1. Introduction

1. Introduction

a. Background and prevalence of the autism spectrum disorders

Autism is a developmental disorder characterized by deficiencies in verbal communication, impaired social interaction, and restricted or patterned behaviors and interests.[1] Leo Kanner first described autism or an "inborn autistic disturbance of affective contact" in 11 children in 1943.[2] While Kanner notes that there are similarities to childhood schizophrenia, he argues that these children affected with autistic disturbance are a distinct group and necessitate further study. With each update of the Diagnostic and Statistical Manual of Mental Disorders (DSM) put out by the American Psychiatric Association, the criteria for autistic diagnosis has continually expanded and the definition further refined.[1, 3, 4] The fourth edition of the DSM was first released in 1994 and later revised in 2000. In this edition, autism has been considered one end of a larger series of disorders collectively identified as autism spectrum disorder (ASD).[1, 5] Individuals with ASD have a range of verbal, social, and behavioral deficits that can individually define a syndrome but collectively are considered variable presentations of the same disorder. The umbrella designation of ASD includes pervasive developmental disorder, not otherwise specified (PDD-NOS), Asperger Syndrome, as well as autism. Autism is the most predominant and severe of the ASD.

With an expanded and more specific clinical definition for autism and related presentations introduced with the *DSM-III* in 1980, a marked increase in the diagnosis of autism and its related disorders was subsequently observed. [4, 6-8] Gillberg *et al* noted

that the rate of autism nearly doubled from 0.5 in 1000 to 1 in 1000 over a thirty-year period. However, the increase seemed to begin prior to the release of the third edition. Studies conducted from 1970-1997 reported the higher rate (1:1000) as compared to those conducted between 1966 and 1970 (0.5:1000). [7] *DSM-IV* was introduced in 1994 and further clarified and organized autism and ASD under the 'Pervasive Developmental Disorders' along with Childhood Disintegrative Disorder and Rett's Disorder. Despite specific criteria by which autism and ASD are defined, they remain phenotypically heterogeneous in their presentation. While any or all aspects of autism may manifest before the age of three and a diagnosis possible at that time, this disorder is typically diagnosed between four-five years of age. [9] Additionally, despite the *DSM-IV* definitions in place for nearly 20 years, the prevalence of ASD has shown a clear increase in recent years with a majority of studies estimating 1:110 children with ASD and the 2012 release of 2008 data the Autism and Developmental Disabilities Monitoring Network estimating 1:88. [4, 9-12]

A consistent and notable feature of ASD is the preponderance of males affected by these disorders. Despite the increasing prevalence estimates and various studies and populations ascertained, the male to female sex ratio in autism has been repeatedly estimated to be about 4:1. The expansion of diagnosis to include all ASD increases this bias to 10:1. However, when stratified by intellectual disability, for IQ < 70, the male to female ratio in autism approaches 1:1. [9, 13]

b. A strong genetic component underlies ASD

Epidemiologic twin and family studies have demonstrated a strong genetic component to these disorders. Twin studies assessing disease concordance among monozygotic twins (MZ) have estimated rates of 47-96%, while dizygotic (DZ) twins have been found to be concordant at rates of 10-36%.[14-21] Consistent with the DZ concordance rate for ASD, the sibling risk ranges from 3-11% representing an almost ten-fold risk over that of the general population.[19, 22-25] These data suggest a highly heritable component to autism and ASD. In spite of the large number of genetic studies, to date nearly 70-85% of individuals affected with these disorders remain idiopathic.[26]

c. Genes and loci causal and implicated in ASD

Within the ASD, a genetic basis for disease can be identified in 15-27% percent of individuals affected.[27] Fragile X Syndrome has long been the most common diagnosis, accounting for nearly 0-8% of all individuals with ASD. A duplication or triplication event of maternal 15q11-13 has been shown to account for 1-3%, and co-morbidity with tuberous sclerosis has been reported to account for a similar rate of 1-4%. [26, 28] A growing body of literature has identified multiple candidate loci associated with ASD through association and linkage studies.[29-34] A recent review of the literature by Catalina Betancur has identified 103 genes and 44 genomic imbalances located throughout the genome as playing a role in ASD.[35] The distributive nature of these findings further substantiates the significant genetic heterogeneity underlying these disorders. Additionally the representation of multiple loci with structural changes in ASD suggests a significant mutational mechanism in ASD. While monogenic forms of ASD

clearly exist, genomic loci disrupted in ASD often bear multiple genes. This suggests that dosage sensitivity can also be a factor in susceptibility to these disorders.

The current understanding of the molecular basis underlying ASD comes from the accumulated knowledge gathered from linkage and genome wide association studies as well as cellular pathways disrupted by genomic imbalances. However, despite the genes and loci implicated in ASD, the vast majority of individuals affected with autism or ASD remain idiopathic.

2. Known genomic structural changes in ASD

Copy number variants (CNV) are lengths of sequence greater than one kilobase (kb) in size that can vary in copy number from the reference of two copies autosomally, one copy of chromosome X and one copy chromosome Y (males), or two copies chromosome X (females). CNV can be either pathogenic or benign. In the mid 2000s, submicroscopic CNV (less than one Mb in size) in autism was a relatively understudied mutational mechanism. Cytogenetic observations (resolution of five megabase (MB) though two to three Mb is possible) and BAC-based arrays (genome-wide: one Mb resolution, targeted tiling: ~150 kb) accounted for the known structural changes in ASD.[36] Increasing advances in oligonucleotide array technology beginning in the early 2000s enabled researchers to screen target regions at a much greater resolution than that afforded by cytogenetic or BAC-based analysis.

a. Knowledge of CNV as discerned from oligonucleotide-array based studies

Advances in oligonucleotide array technology in the last decade have enabled the remarkable discovery of large-scale copy number changes within normal individual genomes as well as across populations.[37] In 2004, two landmark papers were published characterizing the widespread occurrence of large-scale CNV within individuals as well as across different ethnic populations.[38, 39] These initial descriptions characterized changes 200 kilobases (kb) or larger in 75 individuals and estimated at least 11-12 CNV/person exist in the normal population. The Sebat and Iafrate studies motivated multiple research efforts to more fully characterize normal CNV in many different populations.

Since 2004, the search for copy number changes has undergone further advances in the ability to discriminate smaller sequence changes (increased resolution) as well as an expanded diversity of platforms from which to interrogate individual genomes. More probes per array, single nucleotide polymorphism (SNP) based arrays, paired-end sequencing, and most recently, next-generation sequencing (NGS) technologies have contributed to a greater understanding of genomic structure at greater and greater resolution.

Several characteristics seem to hold true with each new study and advance in technology. Copy number variation exists in normal populations, and copy number variant loci are shared across different ethnic populations.[40-51] Consistent with SNP studies of African populations, a greater diversity of CNV exists in African derived populations than in any other.[38, 40, 44, 46, 47, 50-54] Additionally, the majority of copy number changes identified within the HapMap populations have suggested that the majority of CNV are inherited. [42, 43, 47, 51-53, 55]

While there is growing clarity about the pervasive nature of CNV, several aspects remain to be resolved about these copy number changes. It is unclear at what size distributions CNV exist as well as whether CNV are randomly dispersed or clustered throughout the genome. It has already been demonstrated that a significant set of CNV located genomewide are mediated by non-allelic homologous recombination between flanking segmental duplications.[44, 46, 47, 52, 56-60] However, the full interrogation of CNV not associated with segmental duplications is incomplete. While many studies of genome wide CNV have been conducted throughout the mid-late 2000s, array platform, number and distribution of probes, study population, and CNV identification algorithms have varied greatly from study to study.[54, 61] For example, while one study might identify a locus as altered by a single, large variant another study might later identified the locus as harboring multiple, smaller variants. This example illustrates conflicting results that can arrive when using multiple array platforms and criteria by which CNV are identified. The array resolution (i.e., the number of probes interrogating a fixed length) and probe distribution (e.g., SNP-based arrays initially lacked even coverage throughout the genome and other arrays used a targeted rather than tiling based approach) are two variables that can easily contribute to differing interpretations of the same biological phenomena.[53, 54, 61, 62]

Additionally, characterization of CNV on the sex chromosomes has proceeded more slowly than autosomal loci. Searching for structural changes on the sex chromosomes is difficult due to the comparative nature of the technologies used to identify such changes. Using an array Comparative Genomic Hybridization (aCGH) or SNP-based platform, fluorescent intensity of a given marker in the tested sample is compared to that of a normal reference at the same marker. Where intensity values are the same, the locus is interpreted to have the same copy number in both samples. A relative increase in fluorescence of the tested sample compared to the reference suggests an increase in copy number in the test relative to reference, while a decrease in test fluorescence relative to the reference suggests a decrease in copy number in the test relative to the reference. In a sex-mismatched comparison, much of the entirety of either sex chromosome in the test will appear shifted relative to the reference at a statistically significant level. [63] Mining for additional copy number changes (i.e., identifying segments of the sex chromosome that are deleted or duplicated relative to flanking sequence) in such data is quite difficult, and often, studies will not include the sex chromosomes for this reason. Consistent with this notion, the Database of Genomic Variants has proportionally fewer CNV and indels reported in the sex chromosomes than in the autosomes.

The Database of Genomic Variants (DGV) is a collection of sequences reported as copy number variant. [64] (projects.tcag.ca/variation) CNV and indels (changes in copy number sequence from 100 base pairs to 1 kb) in this database are considered to be polymorphic rather than mutant, although this database is not well curated and therefore prone to some error. In a brief assessment of reported genomic variation, we observed two features specific to the sex chromosomes. First, of the 42 studies reporting CNV and indels in DGV, the proportion of references for all autosomes is quite similar at a mean percentage of 90%, but this rate declines for the sex chromosomes (mean: 55%). (Figure 1.1.a) Second, when we asses the proportion of all calls reported for each chromosome, we observe a similar proportion as the percent of the genome (length of the chromosome) that the chromosome represents for the autosomes. Specifically, the mean difference between the percentage of CNV and indels reported for the autosomes and the percent size of the autosome is 0.15%. However, these similar proportions deviate when accounting for the sex chromosomes. Both chromosome X and Y show a greater mean difference (-1.68%) between CNV reported in the DGV and the percentage of the genome these chromosomes represent. (Figure 1.1.b) Several reasons may explain why there are fewer CNV reported for chromosome X and Y. First, it may be that CNV formation on these chromosomes occurs less frequently than their autosomal counterparts. Second, while the sex chromosomes may be equally susceptible to such rearrangements, these changes may not be well tolerated by the organism and thus more heavily selected against. [52, 53, 55] Finally, a non-biological explanation may simply extend from the fact that fewer studies have evaluated these chromosomes for copy number changes as described above.

b. CNV in the ASD

Large rearrangements identifiable by cytogenetic and FISH based assays have long played a role in the identification of genomic disorders.[26, 65-73] With increasing resolution made possible by technical advances, normal variation is being cataloged and curated in individuals and diverse populations worldwide, and similarly, multiple studies are also being conducted in effort to ascertain a more comprehensive description for the role of genomic structural change in disease as well.[74] Included in these efforts have been multiple exploratory studies of genome wide copy number variation in populations affected with the autism spectrum disorders. Out of these efforts, over 40 loci have been implicated and identified as causal in ASD.[35] Structural changes have been identified on most autosomes as well as the X chromosome. Imbalances can range anywhere in magnitude from cytogenetically visible changes (e.g., five Mb disruptions) to less than 300 kb, and no ethnic/race-specific loci have been identified.

In 2007, Sebat and colleagues were the first to report increased *de novo* rates of CNV in ASD relative to those rates observed in normal populations.[75] Interestingly, a higher proportion of females to males affected with ASD in the *de novo* group (male:female ratio: 1.8:1 *de novo*, 5:1 overall sample) were observed.[75] This reduction in the skewed sex ratio suggested to the authors that these *de novo* CNV were more penetrant than inherited CNV and likely contributed to disease in a sex independent fashion. Since this initial report, additional groups studying other ASD populations have found similar increases in *de novo* rates of CNV in their cases relative to controls.[66, 68, 70, 72, 76, 77]

3. A role for the X chromosome in ASD

As noted previously, a conspicuous feature of autism is the significantly larger proportion of males diagnosed with autism or ASD. Males continually outnumber females four to

one within the autistic diagnosis, while expansion to include all ASD extends this bias to as high as 10 to 1.[5, 10, 11, 78] This extreme skewing of the sex ratio is consistent with a pattern of X-linked inheritance. Under such a model, a genetic lesion on the X chromosome would be unveiled in the male, hemizygous state.

[5]

a. A hemizygous X chromosome as a susceptibility to ASD

Typically, studies of the hemizygous X chromosome occur in affected males. However, women affected with Turner Syndrome (45, X) are similarly susceptible to changes on the X chromosome. One study of women with TS observed distinct behavioral and cognitive differences between women who inherited the paternal versus maternal X chromosome. Specifically, the authors suggested the existence of an imprinted locus on the X chromosome where females with TS who maintained the paternal X chromosome appeared to be more socially adjusted than those who had inherited the maternal, imprinted X chromosome.[79] The authors suggested this locus may help to moderate social adaptability. Additionally, in an unselected sample of women with TS, five of 150 were identified as having autism as well as TS. All individuals with autism also had intact maternal X chromosomes.[80] These data suggest that a locus on the X chromosome may serve to play a role in autism susceptibility.

b. Sex-specific risk loci exist in ASD

Another compelling role for the X chromosome arises from the results of a 2004 linkage study conducted by Stone *et al* suggesting sex-specific risk alleles exist in autism. In this study, multiplex families were stratified by the presence of an affected female child,

thereby splitting the families into 'male only' or 'female containing' groups. Significant linkage peaks were obtained within both sets, but the identified loci did not overlap suggesting different etiologies were responsible for disease in the two different groups. [81] While 17q11 was implicated in the male stratified sample set, their findings do not exclude the X chromosome from playing a role in ASD as well.

Additionally, in 2006, Gauthier *et al* identified two markers (DXS6789 and DXS8043) located at Xq21.33 and Xq27.3 to be significantly associated with males affected with ASD in a French Canadian cohort (FC). This finding is remarkable for the fact that a strong founder effect exists within the FC population. [82] While additional studies of autism susceptibility loci in this population reported in 2010 and 2011 did not identify any further signal at or near DXS6789 and DXS8043, these follow-up studies also included an expanded, non-FC population. This diversified sample population may have diluted the original signal identified by Gauthier and colleagues. [83, 84] In another distinct study, Vincent and colleagues identified a modest signal at Xq27 in multiplex families with autism and related phenotypes.[85] In combination, these data suggest that a subset of individuals affected with ASD may bear a lesion on the X chromosome that underlies their autistic phenotype.

c. Skewed X-inactivation is increased in autistic females

Talebizadeh *et al* found significantly increased skewed X inactivation patterns (> 80:20%) in females with autism (33%) as compared to females unaffected by this disorder. Furthermore, the mothers of daughters affected with autism show an increased

rate of skewed X-inactivation.[86] This is striking in light of analysis conducted by Amos-Landgraf and colleagues. The X inactivation patterns for over 1,000 phenotypically unaffected females were determined. These authors found that only 8.8% of this normal female population showed skewing of greater than 80:20%. [87] Showing a nearly 4 fold increase in skewed X-inactivation, the findings of Talebizadeh and colleagues evidences the potential for a disrupted locus on the active X chromosome.

Additionally, Thomas *et al* identified a possible critical region for autism at Xp22.3. Three of eight females bearing a deletion at this locus were also diagnosed with autism. Skewed inactivation of the intact chromosome led the authors to suggest the loss of genetic material at this loci (including the genes *SS*, *CDPX*, *STS*, *KAL*, and *MLS*) explains the autism in the three affected females.[88] Both studies suggest that those X chromosomes that remain active also harbor a genetic lesion that either significantly contributes to or increases susceptibility to ASD.

4. Conclusion

a. Summary of autism, CNV in disease, and the X chromosome in ASD

ASD are a phenotypically heterogeneous set of developmental disorders and are very common with a prevalence of 1:88. While family and twin studies have firmly established a genetic component underlying susceptibility, monogenic findings as well as genomic imbalances have implicated multiple regions throughout the genome as functioning in ASD etiology. Cytogenetic analysis has long played a role in identifying novel loci involved with disease. Recent technological advances have enabled the detection of genomic imbalance on a finer scale. As CNV discovery in normal populations is progressing, so is the identification of CNV in disease.

b. Identification of novel ASD loci: Hypothesis and Experimental design Given the strong genetic character of the ASD and as well as the striking male bias, we hypothesized that high susceptibility gene(s) to ASD may reside on the X chromosome. When disrupted, an autistic locus on the X chromosome would put a 46, XY male at tremendous risk for disease. To this end, we sought to capitalize on the recent advances in oligonucleotide array technology to explore the nature of fine structural variation on the X chromosome of individuals with autism. In addition, our findings would expand the current description of CNV on chromosome X.

c. Summary of our experiments and samples studied

Our initial experimental strategy was to screen 100 unrelated males with autism from the Autism Genetic Resource Exchange (AGRE, research.agre.org) multiplex cohort by high-resolution array Comparative Genomic Hybridization (aCGH). Those CNV identified and validated from this sample set would then be genotyped in two additional sample sets. First, an additional 200 unrelated males with autism as well as all the presumably unaffected and unrelated fathers (n=300) would be genotyped to assess population frequency. Secondly, because families selected from the AGRE cohort were multiplex, mothers, concordant siblings, and discordant siblings would be genotyped to assess whether a CNV was inherited and/or tracked with autistic disorder within the family.

As the study progressed, two more sample populations became available. The first population to become available was the Simons Simplex Collection (SSC, sfari.org). This is a collection of families with one child affected with autism or ASD (simplex). We screened 64 unrelated males affected with autism from this cohort for CNV on chromosome X. Given that the SSC is a collection of simplex families, we anticipated that probands from this cohort may harbor more *de novo* structural changes involved with ASD than probands from the multiplex families from the AGRE cohort.

The second new population we screened by chromosome X high-resolution aCGH was the National Institute of Mental Health (NIMH) Human Genetics Initiative (HGI) control population. This population is largely comprised of adult males and females who selfreport no known neuropsychiatric disorders (proportion of adults: ~3900/4300). We chose to use this cohort in two ways. First, we selected 100 males over the age of 18 to be used to determine if our autistic samples had a larger burden of CNV than this unaffected population. Secondly, a total number of 1,500 adult males over the age of 18 would be CNV genotyped to estimate general population frequency of any CNV identified.

In total, 164 unrelated males with ASD were selected for fine-scale structural analysis of the X chromosome. Validated CNV were to be re-genotyped in the 164 as well as an additional 200 unrelated males affected with ASD to estimate CNV frequency in an autistic population (total n = 364). One hundred males unaffected with ASD were screened by aCGH (NIMH), and a total of 1,800 unaffected males (300 unrelated fathers

from AGRE and 1,500 males from NIMH) were genotyped to estimate CNV frequency in an unaffected population. (Table 1.1)

High-resolution aCGH analysis of the X chromosome first began with our use of the chromosome X, 385K CGH array from NimbleGen (now Roche NimbleGen). Tiled across the X chromosome, 385,000 oligonucleotide probes targeting repeat masked X chromosome sequence were synthesized in a single array. We processed and ran four samples from the AGRE cohort before the opportunity to use the 2.1M CGH arrays arose. The new 'High Density' CGH arrays were comprised of 2.1 million probes tiled along the X chromosome. By shifting our array platform to the 2.1M CGH arrays, our probe coverage increased from an average of four probes/kb to 20 probes/kb. Fifty samples from the AGRE cohort were run on the 2.1M aCGH arrays.

Concurrent with the sample processing and array hybridization were our early efforts of validating array identified CNV. By the time we had processed the first 50 AGRE samples on the HD aCGH arrays, a high false positive rate prompted us to explore aCGH protocol changes that might increase our capture of true CNV and reduce the false CNV call rate. Once an optimized protocol was established, we processed 100 AGRE samples as well as the 64 SSC samples using the new protocol on the HD CGH arrays.

Array behavior appeared to shift with purchases of new arrays in the latter end of our 2.1M aCGH experiments with the samples from the autistic populations. Discussions with Roche NimbleGen confirmed our suspicions of altered array synthesis chemistry. It was decided that the 100 NIMH control samples for 2.1M aCGH screening would be processed and hybridized following the manufacturer's protocol and not the optimized one we had developed.

In summary, we conducted four independent studies of two populations using two CGH arrays and two different protocols. Three different approaches were taken to interrogate individuals with autism. We first began with a brief analysis of four individuals from the AGRE cohort and screened the X chromosome for CNV using the 385k CGH array and the NimbleGen protocol. Next, we increased our array resolution and screened 50 individuals from AGRE using the 2.1M CGH array and the NimbleGen protocol. Then, our optimized protocol was used to screen 100 individuals from AGRE and 64 individuals from SSC on the 2.1M CGH array. Finally, our studies of the NIMH normal controls were conducted on the 2.1M CGH array using NimbleGen's protocol for the 100 males selected for study.

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	NimbleGen Protocol		Emory Protocol	
Sample	385K aCGH	2.1M aCGH	2.1M aCGH	CNV genotyping
AGRE - autistic proband	4	50	100	300
AGRE - unaffected father	-	-	-	300
SSC - autistic proband	-	-	64	64
NIMH - unaffected control	-	100	-	1,500

Table 1.1 - CNV detection and genotyping in autistic and unaffected populations.

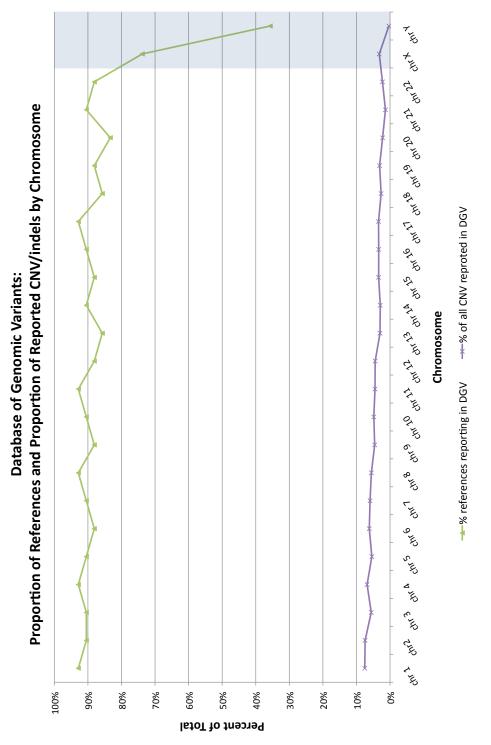


Figure 1.1.a – Proportion of References and CNV or indels reported in the DGV. Proportion of all references reporting CNV or indel in the DGV (Hg18) as well as the proportion of all CNV or indel in the DGV plotted by chromosome.

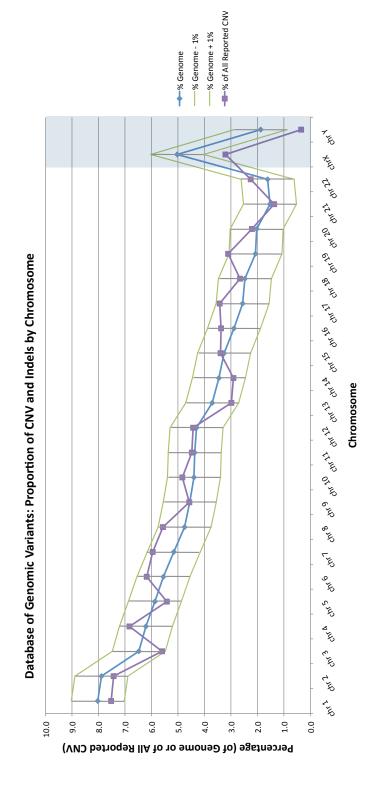


Figure 1.1.b - Proportion of CNV or indels reported in the DGV by chromosome.

Chapter 2. Optimization of the NimbleGen array Comparative Genomic Hybridization (aCGH) Protocol

1. Background

a. Properties of Oligonucleotide Microarray Data

While oligonucleotide CGH arrays enable a higher resolution of copy number variant (CNV) detection than BAC-based arrays, it is recognized that multiple oligonucleotide probes are required to 'call' a CNV with the same confidence as a single BAC probe due to increased noise in oligonucleotide based arrays. [36, 46] BAC-based arrays have a higher signal to noise ratio than oligonucleotide-based arrays enabling CNV detection by fewer probes.[36, 51, 89, 90] Reported false positive rates (or the identification of CNV that fail to validate) for oligonucleotide arrays tend to range from 5-17%, rates have been reported as high as 32-66%. [38, 44, 45, 49, 52, 55, 91-96] Using the genome-wide NimbleGen high-density array (2.1M) with the resolution of one probe/35 kilobases (kb), Itsara and colleagues reported a false call rate of 23%. However, for those variants greater than 100 kb, the false call rate was reduced to 15%. [60]

Additionally, Locke *et al* reported a high false negative call rates (true CNV that fail to be identified) for oligonucleotide-based arrays. Using a BAC-based array to identify CNV in 269 HapMap individuals, the authors employed a custom 385K NimbleGen CGH array dedicated to the same regions as the BAC array to validate their findings in nine individuals. They found that 66% of CNV were identified by both arrays. Forty of 63 calls not made by the oligonucleotide array were called by other platforms in other

studies. The authors concluded the failure to capture all calls by both arrays was due to the high false negative (34%) of the oligonucleotide array. [55]

Our initial analysis of 50 samples hybridized to the 2.1M CGH array, resulted in an unusually high false call rate of 65%. Additionally, our false negative calls (those CNV not called despite being real) were high. We base this evaluation on two validated CNV, a deletion and duplication, in our reference. An 826 bp deletion in the reference (duplication in test samples) failed to be called in 39/48 (81%) individuals, and a 293 bp duplication (deletion in test samples) failed to be called in 21/48 (44%).

A number of strategies exist to identify CNV that are likely real (true calls) rather than a technical artifact. These include stringent probe selection to reduce cross hybridization, dye-swap experiments to identify CNV that are likely real and not random noise-generated, self-vs-self hybridizations to determine a platform specific false call rate, or comparison of CNV calls for one sample across multiple platforms to determine false discovery rate for a given platform again to increase fidelity of calls.[61] While these strategies are all possible, they are also quite labor and resource intensive. Additionally, more difficult to assess are the loss of CNV to false negative calls. However, an ideal platform for CNV identification would be able to accurately call CNV that exist (increase true calls, decrease false negatives) while minimizing noise or other artifacts that result in false calls.

b. Specifications for the CGH arrays (385K, 2.1M)

Our study of the fine scale nature of copy number variation on the X chromosome began with the 385K Comparative Genomic Hybridization array (385K aCGH) from NimbleGen (now Roche NimbleGen). We used a custom design array that tiled 385,000 probes along the X chromosome with an average intermarker distance of 270 bp or four probes/kb. However, early in our screen of the Autism Genetic Resource Exchange (AGRE, research.agre.org) cohort, a high density CGH array (2.1M aCGH) for the X chromosome became available. Again, NimbleGen designed a custom array dedicated to the X chromosome that now tiled 2,100,000 probes among three subarrays (A01, A02, and A03; approximately 714,000 probes each) synthesized on a single glass slide. Our intermarker distance was greatly shortened to 50 bp or 20 probes/kb.

c. General description of the manufacturer's protocol

Oligonucleotide based aCGH sample processing and hybridization are largely similar across different platforms. For different aCGH protocols, sample amplification is often a variation of a randomly primed single-strand displacement reaction[97], and Cy3 or Cy5 fluorophores are conjugated to either the randomer primers or a subset of nucleotides that are then incorporated during extension. Hybridization is mediated during sample agitation over the array area for an extended period of time depending on probe density and at a platform specific temperature. Array washing is either manual or automated.

The NimbleGen protocols for sample processing and array hybridization of the 385K and 2.1M CGH arrays are quite similar. Depending on the density of array, one to two micrograms of DNA are sonicated to 200 - 2,000 bp. This material is then concurrently

amplified and labeled using Cy3 or Cy5 5' fluorinated random nonamers in a two hour Klenow extension reaction. The Klenow polymerase fragment does not have exonuclease activity, and as the polymerase extends along the template, it will displace rather than degrade any double stranded product downstream of its starting position.[97] DNA being tested for CNV is typically labeled with the Cy3 fluorophore, and the reference DNA typically labeled with the Cy5 fluorophore. The amplified and labeled product is then isolated, and a spectrophotometer is used to estimate amount of labeled product as well as the amount of fluorescence per unit DNA (Specific Activity, picomol/microgram).

Equal amounts (15 micrograms (µg) for 385K, 30 µg for 2.1M) of the labeled test and reference samples are then mixed together in a hybridization solution and applied to the microarrays. Disposable 'lids' are applied to each array creating a hybridization chamber over the array area, sample is injected into the chamber, and sealing of the airports at either end of the chamber create a closed system. The lid-array assembly is then loaded onto a BioMicro MAUI mixing station where a preprogrammed setting controls the frequency of agitation by which an internal airbladder shifts the hybridization solution over the array area. Both array and lid assembly sit are held at 42° Celsius during hybridization. The 385K arrays are hybridized for 16-20 hours and the 2.1M arrays for 48-60 hours. Once hybridization is complete, the lid-array assembly is separated, the arrays are manually rinsed in three increasingly stringent washes, and then arrays are spun dry. Scanning for either array is done on the Axon 4000B dual laser scanner at five micron resolution. At this resolution, there are approximately 10 pixels/feature for the

385K array (feature size: 16 um x 16 um), and 7 pixels/feature for the 2.1M array (feature size: 13 um x 13 um).

d. Experimental steps that were altered

In effort to reduce our observed false positive rates and false negative rates, we explored ways to make the NimbleGen protocol more stringent. We hypothesized that a large underlying component to these relatively high rates may be cross hybridization of nonspecific DNA. We considered how we might incorporate a Tecan array hybridization and wash station (HSPro 4800) into NimbleGen's array processing protocol. This instrument was already utilized by the Agilent aCGH platform with great success and would allow a more dynamic hybridization program as well as automated washing and drying. Additionally, rubber gaskets ringing the array area of the hybridization chamber created the closed system as opposed to the BioMicro lids. The lid system is based on an adhesive seal, and, on occasion, this seal would leak during hybridization. Typically, array data was not recoverable from arrays that had 'leaked'. The Tecan hybridization chamber and gasket sealing system could minimize array loss. Additionally, automation would provide more consistent processing conditions across experiments and batches. By minimizing the degree and nature of manual processing, we sought to reduce noise introduced by any manual procedures, and increased stringency in hybridization would reduce signal due to non-specific hybridization.

2. Optimized Steps

a. Experimental Protocol Changes and quality controls instituted

<u>Reference used and Ozone-free space used to process arrays</u>

Our protocol optimization is based on the 2006 version of the manufacturer's protocol. At that time, the original protocol implemented the use of sonication to normalize genomic DNA size across samples; however, the manufacturer no longer considered sonication necessary in subsequent, updated versions of their protocol. Nonetheless, we continued to sonicate all test and reference DNA prior to labeling and amplification to allow for a direct comparison of further downstream changes that we would make to the manufacturer's protocol. Additionally, once sonicated sizes were confirmed by gel electrophoresis, all sonicated reference DNAs were then pooled together before labeling and amplification. Pooling created a normalized reference source of sonicated DNAs for each batch of processed samples.

High ozone and humidity levels have been identified as strong contributors to Cy5 signal degradation. [98, 99] To reduce ambient exposure of labeled samples and hybridized arrays to ozone and humidity, a separate room was retrofitted for sample processing, array hybridization and wash, and array scanning. This room was maintained under positive pressure, a dehumidifier continually operated to reduce humidity, and a continually operated ozone scrubber removed ozone from ambient air. A highly sensitivite ozone detector installed in the room typically registered 8-10 parts per billion (ppb) or less. While this level might seem somewhat elevated, ozone levels inside the room were greatly reduced as compared to those outside of the room (ranging as high as 100+ ppb in peak ozone season), ozone levels were maintained at a constant level throughout high and low ambient ozone season, and the measurement error of the reader

was five ppb suggesting the actual ozone level may have been on the order of three to five ppb. All steps in sample and array processing described below were conducted in this environment.

Labeling and Amplification

Further downstream in the aCGH protocol, the stringency of sample hybridization and washing were increased to minimize non-specific hybridizations. Initial runs indicated that raw fluorescent signal was too close to background noise to make identification of copy number changes possible. While this decrease in signal suggests an increase in the stringency of hybridization kinetics, it was clear that we needed to increase overall sample fluorescence in order to proceed with the more stringent application.

Labeling of the test and reference DNAs with fluorescent molecules Cy3 and Cy5 respectively occurs during the amplification step. Traditional aCGH protocols employ one of two labeling strategies that feature either a 5'-fluorinated primer to end label the amplified material, or a nucleotide conjugated with Cy3 or Cy5 is incorporated during extension. To maximize these labeling potentials, we combined both of these methods. (Figure 2.1) One drawback of backbone labeling with a Cy3 or a Cy5 fluoraphor is that the fluoraphor is bulky. Lee *et al* hypothesized that an observed intensity bias of Cy3 over Cy5 stemmed from the difference in size of the two fluorophors contributed to a bias in the fluorinated nucleotide incorporation.[100] The hypothesis is predicated on the assumption that the Klenow fragment has difficulty incorporating the fluorinated nucleotide. This is substantiated by our own observations that samples labeled with a

fluorinated nucleotide result in a shorter fragment population than those labeled with unmodified nucleotides.

To circumvent any bias in labeling efficiency and to maintain a similar population length of amplified molecules as seen in the manufacturer's protocol, we employed an indirect labeling method that utilizes a uradine base conjugated with an aminohexylacrylamido (aha) tag.[101] Amine reactive Cy3 or Cy5 dyes are then added to the DNA once amplification is complete. The reactive fluors label the backbone of the amplified fragments. The aha tag is considerably smaller than the Cy3 or Cy5 fluoraphor, which improves the Klenow fragment's ability to incorporate the modified nucleotides and allows for larger fragments to be amplified, generating a labeled product similar in size to the manufacturer's protocol 5' end labeled size.[100, 101] Utilizing the same sized tag in both the test and reference DNA enabled a systematic incorporation rate of aha-modified nucleotides for either the sample or reference. Remarkably, by using both the 5' labeled primer and the backbone labeling strategy, we were able to increase the overall fluorescence of the hybridized samples over 2.23 fold with the 5' end labeling strategy yielding an average 30 pmol/ug and the combined strategy yielding an average 67 pmol/ug in initial tests. With this gain in fluorescence per amplified unit, we could continue to hybridize the same amounts of amplified material as recommended by the manufacturer without losing signal in a more stringent hybridization and wash environment.

Array Hybridization and Wash

The manufacturer's hybridization protocol utilizes the BioMicro MAUI hybridization system and a manual wash protocol. The MAUI system uses disposable, one-time use hybridization chambers that result in a low-volume and closed hybridization environment. Airbladders within each chamber mix hybridization liquid over the array surface and frequency of agitation is hard-coded into the hybridization station with four frequency-of-agitation options available on the MAUI 4-bay system (two options on the 12-bay system). Manual washing inherently introduces variation in frequency, force and duration of array exposure to wash solutions and the environment. This design makes it nearly impossible to ensure each array is treated identically.

Thus, we automated the hybridization and wash steps of the protocol by utilizing the Tecan 4800Pro Hybridization station. This stand-alone system uniformly hybridizes, washes, and dries microarrays with constant agitation frequencies, force, and time duration. Additionally, an Active Bubble Suppression system is incorporated into the fluid dynamics of the machine to prevent bubble formation over array areas. Moreover, the Tecan system comes equipped with a program designed specifically for Agilent CGH arrays. With assistance from the technical support staff from Tecan, we custom developed a hybridization, wash, and dry program for the Roche NimbleGen arrays. The hybridization annealing temperature was increased from 42°C to 52°C to select for a decrease in non-specific hybridization and false calls. Hybridization force and frequency were elevated, and hybridization time was increased from 48 hours to 60 hours as Dai *et al* have reported that longer hybridization times reduce noise in array data.[102] Also, additional washes with the least stringent buffer were added in effort to remove any

precipitates that may have formed during the long hybridization time. Sterile nitrogen gas was used to dry arrays. Arrays were then held in the closed, nitrogen filled environment until ready for scanning to protect array signal from possible ozone degradation.

b. Computational Protocol Changes and Quality Control Steps Instituted

<u>Array Scanning</u>

We developed an array scanning protocol meant to maintain as consistent a set of scanning conditions and parameters as possible for all arrays scanned. To start, all arrays were scanned on the same GenePix 4000B scanner with the same resolution setting (five micron). The scanner was calibrated once a month or more depending on overall usage. The GenePix 4000B is a dual laser scanner (532 nanometers (nm) and 635nm) that can scan for both Cy3 and Cy5 fluors using both lasers concurrently.

Using the 'Histogram' function hard coded into the scanner software, pixel intensities are plotted against their log-transformed frequencies. Each channel, 532 nm (green color, Cy3) and 635 nm (red color, Cy5) are plotted together. The 'Count Ratio' measurement is the ratio of the sum of fluorescent signal from each channel with an ideal measurement of one.[103] Scanned images were evaluated by their Count Ratio (CR) value and the final placement of the high-intensity 'tails' of the intensity histogram. The photomultiplier (PMT) gain settings were manually adjusted to generate CR values of 1 +/- 0.15 to provide the greatest overlap of total fluorescence, and the high intensity-tails targeted to the 1e-5 to 1e-4 range. (Figure 2.2)

Evaluation of Probe Quality

We used a Roche NimbleGen custom microarray comprised of approximately two million oligonucleotide probes tiled along the X chromosome. This first step in our computational optimization was the development of a bioinformatic strategy that would determine whether any of the probes behaved inconsistently. We hypothesized that removal of such probes would purge a portion of false positive variants from our data. [104]

Multiple studies of immobilized probe sequence selection and kinetic behavior have been previously conducted in an effort to identify those properties of a probe that enable it to hybridize reliably across experiments. The parameters that have been evaluated and found to play a significant role in the fidelity of specific oligonucleotide hybridization include probe GC content, melting temperature, sequence homopolymers, stem loop structure, self-folding, and sequence similarity.[104-114] In a recent work, Mulle *et al.* found that probe melting temperature, single nucleotide polymorphisms (SNPs), and homocytosine motifs affected oligonucleotide array data quality. [104] These authors identified probes having irregular patterns of hybridization by evaluating individual probe log2 values their variance across nineteen arrays.

Using the data generated by the fifty AGRE samples run by the NimbleGen protocol on the 2.1M arrays, we evaluated the log2 probe variance in this data set. For each of the three subarrays (A01, A02, and A03), the log2 values for the 714,456 experimental probes on each subarray were collected, and variance for each probe determined. As with the findings made by Mulle *et al*, we similarly identified a subset of probes with a relatively high variance as compared to the remainder of probes on the subarray. These probes with the high variance were defined as "poorly" behaving if their variance was greater than 0.175. The value of 0.175 was chosen based on the comparative behavior of probe variance within a subarray. We determined the variance for each probes, sorted the probes by their variance, and plotted all probes from the subarray by their ranking (x-axis) and variance (y-axis). (Figure 2.3a-c) The cutoff value of 0.175 was subjectively chosen because in all three subarrays, this value appeared to remove the majority of high-variance probes. Removal of these increased variance probes resulted in the total loss of 122,544 experimental probes (5.72% of all experimental probes). (Table 2.1)

After deviant probes were removed from analysis, the intensity distribution from each array was assessed using an MA plot ('M' is the intensity ratio or log2(R) - log2(G), and 'A' is the average intensity or 1/2 (log2(R) + log2(G))). An MA plot is an intensity-dependent ratio of raw microarray data plotted against the total average intensities. (Figure 2.4.a) MA plots were evaluated on several parameters. Acceptable plots exhibited an oval shape symmetric about the y=0 line, extended within x=9 to x=16 values, and overall height bounded by y=+/-1. Additionally, a fitted linear regression model was applied to each subarray where the M values were regressed on the A values. The outputted coefficients of intercept and slope were plotted on each MA plot, and the slope recorded as a further assessment of array performance.

Data exhibiting non-symmetric shapes about the y=0 axis, demonstrating a more condensed body (typically, 2-3 units along the x-axis), showing dense scatter beyond +/-1 on the y-axis, and/or having a regressed slope deviating greatly from '0' were removed from further analysis and samples re-run. (Figure 2.4.b-c) Each subarray was evaluated by these criteria, and a passing subarray was then assessed for copy number changes.

Identification and selection of high confidence CNV

The manufacturer's segment analysis software, NimbleScan (v2.4) was used to assess copy number change in subarrays that passed the MA plot quality control step. The output file, 'segtable', is a text report that returns the entire evaluated region (i.e., in our study, the chromosome X from bases 2,709,520 to 154,583,236; Build Hg18) as defined by its log2 values. With a majority of the chromosome near log2=0, this extensive list of segments or potential CNV is quite cumbersome to go filter by hand. In order to extract relevant and plausible segments for further analysis/validation, we developed an automated selection strategy to refine our candidate validation list.

We evaluated segments that had a log2 value greater (more positive or more negative depending on the shift) than one standard deviation (SD) from the mean of all log2 values of the respective subarray. Further inspection of our data showed larger CNV as represented by multiple segments shifted in the same direction. To identify the most parsimonious set of segments for validation, we merged all segments that ended within three kb of each other and shifted in the same direction (i.e., all log2s were either greater than one SD or less than one SD from the mean). These merged variants were then

defined as having the most extreme 5' and 3' boundaries of the originally identified segments, and the log2 value assigned to the merged variant was an average of the original log2s weighted by the number of probes within the original segment. (Figure 2.5) We also developed an exclusionary strategy that removed segments identified by fewer than nine probes per kb. And, we excluded individuals with a number of variants greater than three standard deviations from the mean number of variants called for all individuals. Together, these selection and exclusion strategies provided us with a list of loci that we further analyzed and validated for their contribution to disease status.

3. Results

a. Results from Experimental Changes

While reference selection and sonication contributed to overall experimental strategy and consistency throughout processing of all samples, the development of a labeling protocol that increased Specific Activity (fluorescence per amplified DNA unit) was critical for the implementation of the more stringent hybridization and wash parameters introduced by the use of the Tecan 4800Pro. Using the same samples to label and amplify by the NimbleGen and our optimized protocol, we increased the SA values from 29.7 pmol/ μ g to 67.3 pmol/ μ g.

The Tecan 4800Pro has excelled in its ability to hybridize, wash and dry Agilent arrays. Unfortunately, despite all efforts to refine the final hybridization and wash protocol for the NimbleGen arrays, the hybridization, wash and dry parameters do not have nearly the high degree of performance or reliability as seen for Agilent and other array platforms. Specifically, areas of saturated fluorescence that mimicked a 'streaking' or 'drip' -like pattern from the liquid ports located at the top and bottom of the array slide were frequently observed. (Figure 2.6) We hypothesized that residual hybridization solution and/or sample may be 'sticking' in the capillary tubes of the hybridization chambers. But, despite rigorous purging and washing of the hybridization chambers and liquid handling lines of the machine after hybridizing arrays, the issue persisted. An alternative hypothesis that may explain our observations is that component(s) of the hybridization solution are not compatible with the increased annealing temperature and/or the hybridization chamber and tubing materials used in the Tecan system. While it may be possible to develop a hybridization solution that is compatible with both NimbleGen High Density microarrays and the Tecan HS4800Pro hybridization station, for purposes of time and effort efficiency, we did not pursue such an option.

b. Results from Computational Changes

We identified 122,544 experimental probes (5.72% of all experimental probes) as having a log2 variance > 0.175 across 50 arrays. We evaluated the two probe sets (greater or less than 0.175 log2 variance) by probe length, GC content, AG (purine) content and melting temperature (T_m). Probe length, GC content, Ag content, and T_m were significantly different for those probes having a log2 variance greater than 0.174 versus those less than 0.175. (Table 2.2, Figure 2.7) These findings are consistent with previous reports. [104, 110-112, 114] We then assessed the 'poorly' behaving experimental probes by position across the X chromosome. These probes showed a similar positional distribution as the remaining probes, indicating that they were randomly distributed along the chromosome and interspersed among probes that behave more consistently. Removal of the 'poorly' behaving probes did not result in significant gaps in probe coverage of the X-chromosome, and further analysis without them will remain largely comprehensive.

c. Results from the Sum of All Optimized (Experimental and Computational) Steps We then sought to evaluate how our modifications both experimentally and computationally compared to values generated following NimbleGen's protocol. First, we assessed the overall performance of the arrays by their average log2 values from each protocol. The expected average log2 value for each probe is '0'. We found that the optimized technical protocol produced average log2 values that were closer to the expected value of '0,' irrespective of subarray. However, these optimized data were also 'noisier' as seen in their slightly larger standard deviations. (Table 2.3)

Next, we evaluated the CNV identified by both protocols for the same 30 samples for which there was data on both platforms. Using the Segment Filtering strategy described above, the original protocol identified 302 total variants with an average 10.1 CNV/chrX while the optimized protocol identified 174 total variants with an average 5.8 CNV/chrX. This reduction in number of calls is significantly different with p < 0.001069. The total number of variant bases identified increased with the optimized protocol because the average size of calls made using the optimized protocol were 2.7 times as large as those

made by the original. (Table 2.4, Figure 2.8) Another feature distinguishing the CNV identified from the two protocols was the distribution of deletion and duplication events identified. NimbleGen's protocol resulted in the identification of 184 deletions and 118 duplications (1.6 deletions:duplications) while the optimized protocol identified 44 deletions and 130 duplications (0.34 deletions:duplications). The five-fold decrease in the deletion to duplication ratio was significantly different at $p < 1.36 \times 10^{-13}$.

The average size of calls made by the optimized protocol was nearly three times that of the original. CNV identified by NimbleGen's protocol averaged 2,681 bases (SD = 5,673), while the average size of the optimized protocol was 7,264 bases (SD = 30,914). While the optimized protocol resulted in larger CNV on average, this shift was statistically significant when CNV size was evaluated by all variant (all CNV: p < 0.05). When stratified by nature of the CNV, statistical significance was lost (deletions: p < 0.16, duplications: p < 0.16). (Table 2.5, Figure 2.9)

We also evaluated the probe coverage of CNV identified by each protocol. The entire experimental probe set is comprised of 2,020,823 probes covering base positions 2,709,520 to 154,583,236 (build Hg18) on chromosome X, and after repeat masking, average intermarker distance is 50 basepairs. This translates to about 20 probes/kb, and we were willing tolerate copy number variants called by as low as nine probes/kb. Using the same number of 'good' probes for copy number analysis, the optimized protocol returns a slightly diminished probe coverage per variant than that of the original protocol (18.0 probes/kb and 20.4 probes/kb respectively). This decrease in coverage is significant

for all CNV: $p < 5.24 \times 10^{-10}$, for deletions: $p < 2.23 \times 10^{-12}$, for duplications: $p < 2.23 \times 10^{-12}$. ¹². (Table 2.5, Figure 2.9)

GC content of all variants identified by both protocol was also evaluated and found to be significantly different. Variants identified by the original protocol tended to have a lower GC content than those identified by the optimized strategy (original: 0.45 (SD=0.08), optimized: 0.56 (SD=0.13)). This difference was significant for all CNV, deletions only, and duplications only. (all CNV: $p < 6.97 \times 10^{-21}$, deletions: p < 0.03, duplications: p < 0.03). (Table 2.5, Figure 2.9)

As a final measure of protocol performance, we evaluated by several metrics the true and false call rates for CNV called within the same samples from each protocol. First, the optimized protocol was successful in reducing our false negative call rate. For the 30 samples run on both protocols, 33 CNV are known to be real. The NimbleGen protocol failed to call 11 (33%) of these loci, and the false negative (true CNV that fail to be called) rate for the optimized protocol dropped this number to 7 or 21%. And the true positive call rate (true CNV that are called) increased with implementation of the optimized protocol. The true positive call rate in the NimbleGen protocol was 22/62 (35%) for PCR validated loci, and the optimized protocol rate increased for a different set of 62 loci to 26 (42%). However, these two rates were statistically indistinguishable with p < 0.58). (Table 2.6, Figure 2.10)

We also evaluated what proportion of true and false calls were made as stratified by GC content. Remarkably, for both protocols, we found GC content to be a strong indicator for a variant's true or false call identity within each protocol. All false positives, irrespective of copy number state (deletion or duplication), showed an elevated GC content over those loci that validated. For both the original and optimized protocols, the average GC content was significantly different between true and false calls with the original protocol: p < 5.43E-06 and optimized p < 2.20E-16.

While both protocols showed a significant difference in the GC content of the true and false calls, the optimized protocol enables better discrimination of true calls when evaluated by their GC content. For both protocols, a GC content of 56% or less accounted for all true calls while minimizing the number of false calls. Specifically, in the original protocol, variants with a GC content less than or equal to 56% accounted for 26/26 or 100% of all true calls and 59/68 or 87% of all false calls. While in the optimized protocol, variants with GC content equal to or less than 56% still accounted for 52/52 or 100% of all true calls, but the proportion of false calls dropped tremendously to 59/116 or 51% of all false calls. The proportion of false calls dropped by 41% under this threshold. (Figure 2.11a-b)

Additionally, we evaluated the GC content of the X chromosome by 1,000 bp bins. The increasing proportion of chromosome X is plotted by GC content on these two plots (Fig 2.11.a-b) as well. This feature in addition to our optimized call rate data suggests several conclusions. First, a significant proportion of the X chromosome remains assayable at

both the GC content cut offs of 56% and 47% (98.2% and 88.3% of chromosome X remain). Second, the true calls from the optimized protocol mimic a distribution similar to the chromosome on a whole. This should be expected if we were truly 'sampling' real loci for CNV on the X chromosome. And finally, using our optimized protocol, we can assay nearly all (98.2%) of the X chromosome for CNV with a GC content of 56% while eliminating the majority of false calls.

4. Summary

Overall, much effort was expended to develop an aCGH protocol and analysis strategy that would identify copy number variant calls with greater fidelity than the existing protocol. While issues remain to be resolved, our current version of optimized sample processing and array analysis outperforms the original protocol in its ability to better discriminate false from true calls when using GC content as an indicator.

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Subarray	Variance Cut-Off	# of probes (%)
All	-	122,540 (5.72%)
A01	> 0.175	46,266 (6.48%)
A02	> 0.175	38,865 (5.44%)
A03	> 0.175	37,410 (5.24%)

Table 2.1 – Number of high variance probes.

	Good Probes	Poor Probes	p value
N (% Total)	1,908,871 (94.5%)	122,544 (5.72%)	
Mean Length in bp (SD)	56 (4.6)	55 (4.3)	< 6.97E-49
Mean AG Content (SD)	50.1 (10.0)	50.7 (10.6)	< 2.20E-16
Mean GC Content (SD)	39.0 (8.4)	37.4 (9.0)	< 2.20E-16
Mean Tm in °C (SD)	75.6 (3.0)	74.4 (3.3)	< 2.20E-16

Table 2.2 - 'Poor' and Well Behaving Probes Evaluated Across Four Parameters

	# of probes	n (samples)	Mean Log2 (SD)	Median Log2
Subarray A01	668,189			
NimbleGen		48	0.00116 (0.26)	0.003
Optimized		75	-0.00002 (0.34)	0.002
Subarray A02	675,590			
NimbleGen		48	0.00232 (0.26)	0.005
Optimized		81	-0.00002 (0.34)	0.002
Subarray A03	677,044			
NimbleGen		48	0.00207 (0.28)	0.005
Optimized		80	-0.00001 (0.34)	0.001

Table 2.3 – Probe Behavior by NimbleGen and Optimized Protocols

N (samples)	Total CNV*	Total Variant Bases (% ChrX)	CNVs/ChrX	Mean # Variant Bases/ChrX (% ChrX)
30	302	809,723 (0.52%)	10.1	2,696 (0.0017%)
30	174**	1,271,198 (0.82%)	5.8	11,059 (0.0071%)
n	Total Deletions	Total Deleted Bases (% ChrX)	Deletions / ChrX	Mean # Deleted Bases/ChrX (% ChrX)
30	184	376,981 (0.24%)	6.1	2,161 (0.0014%)
22	44	344,113 (0.22%)	2.0	11,787 (0.0076%)
n	Total Duplications	Total Duplicated Bases (% ChrX)	Duplications / ChrX	Mean # Duplicated Bases/ChrX (% ChrX)
28	118	432,742 (0.28%)	4.2	3,054 (0.0020%)
26	130	925,612 (0.60%)	5.0	6,751 (0.0044%)

*Counts do not include confirmed reference variants.

** Wilcoxon rank sum, p-value < 0.001069

Table 2.4 - CNV identified by the NimbleGen and Optimized protocols. Both protocols were applied to the same thirty samples.

	N (samples)	Total CNV*	Mean Size in bp (SD)	Median Size in bp	Mean # Probes/kb (SD)	% GC (SD)
NimbleGen	30	302	2,681 (5,673)	1,178	20.4 (3.7)	45 (8)
Optimized	30	174**	7,264 (30,914)	1,700	18.0** (4.0)	56** (13)
Deletions	n	Total	Mean Size in bp (SD)	Median Size in bp	Mean # Probes/kb (SD)	% GC (SD)
NimbleGen	30	184	2,049 (3,854)	1,100	21.0 (3.0)	44 (5)
Optimized	22	44	7,821 (26,891)	1,710	15.2** (4.0)	41** (7)
Duplications	n	Total	Mean Size in bp (SD)	Median Size in bp	Mean # Probes/kb (SD)	% GC (SD)
NimbleGen	28	118	3,667 (7,615)	1,532	19.4 (4.3)	47 (11)
Optimized		130	7,120 (32,367)	1,703	18.9** (3.6)	61** (10)

*Counts do not include confirmed reference variants. ** Optimized significantly different from NimbleGen.

Table 2.5 - CNV characteristics by the NimbleGen and Optimized protocols. Both protocols were applied to the same thirty samples.

_	Total CNV (% of Category)	Mean Size in bp Median Size (SD) in bp	Median Size in bp	Mean Probes/kb (SD)	Median Probes/kb	Mean GC Content (SD)	Median GC Content
ALL CNV				i i			
TRUE CALLS							
NimbleGen	22 (35%)	4,884 (7,113)	1,442	19.3 (3.2)	19.8	42% (6)	41%
Optimized		18,392 (67,005)	2,148	15.3 (3.7)*	15.7	41% (5)	39%
FALSE CALLS							
NimbleGen	40 (65%)	2,176 (2,119)	1,293	20.5 (1.8)	21.1	50% (8)	48%
Optimized	36 (58%)	6,852 (29,366)*	1,935	19.5 (2.9)*	20.0	58% (10)	61%
DELEITONS							
TRUE CALLS							
NimbleGen	20 (40%)	3,625 (6,129)	1,272	19.5 (3.1)	20.4	42% (6)	41%
Optimized	23 (79%)	4,302 (6,254)	1,955	15.3 (3.8)	15.5	41% (5)	39%
FALSE CALLS							
NimbleGen	30 (60%)	2,169 (2,429)	1,138	20.6 (2.0)	21.3	47% (5)	48%
Optimized	6 (21%)	31,169 (71,970)	675	17.9 (4.9)	16.9	43% (14)	40%
DUPLICATIONS							
TRUE CALLS							
NimbleGen	2 (17%)	17,471 (508)	17,471	16.9 (3.2)	16.9	41% (3)	41%
Optimized	3 (9%)	126,413 (189,487)	33,261	15.1 (3.7)	15.9	38% (1)	39%
FALSE CALLS							
NimbleGen	10	2,198 (664)	2,140	20.4 (1.2)	20.8	(6) %65	61%
Optimized	30 (90%)	1,988 (943)	2,108	19.8 (2.3)	20.2	61% (4)	61%

Table 2.6 – True and False positive loci by the NimbleGen and Optimized protocols.

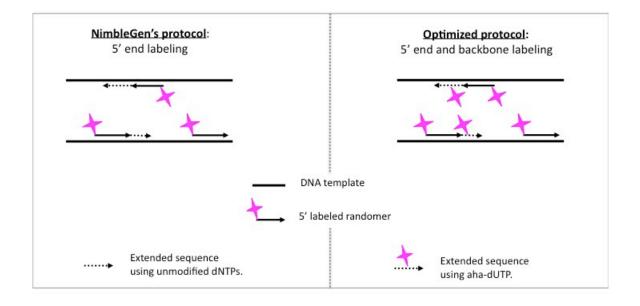


Figure 2.1 – NimbleGen and Optimized DNA labeling strategy.

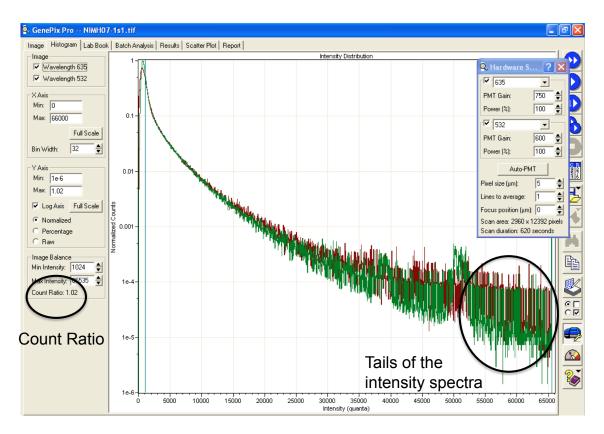
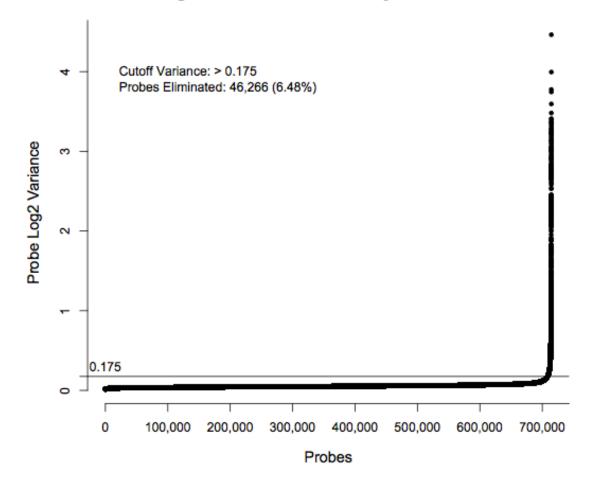
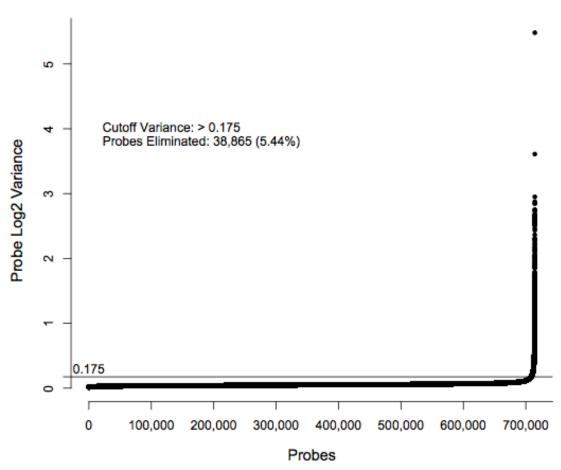


Figure 2.2 - Scanning parameters as informed by the Intensity Distribution Histogram



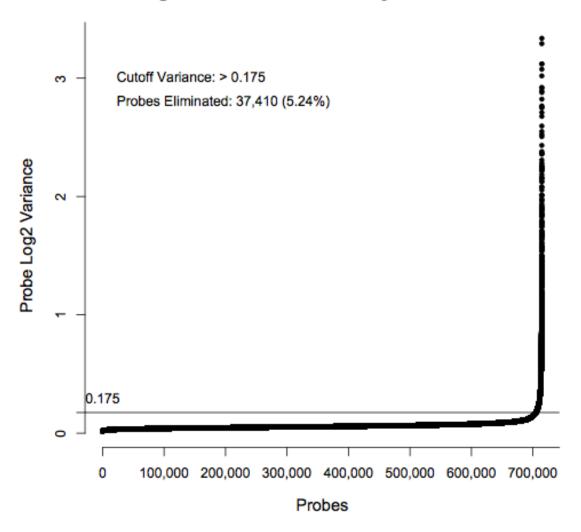
Log2 Variance of Subarray A01 Probes

Figure 2.3.a – Variance Analysis of Subarray A01 Probes



Log2 Variance of Subarray A02 Probes

Figure 2.3.b – Variance Analysis of Subarray A02 Probes



Log2 Variance of Subarray A03 Probes

Figure 2.3.c – Variance Analysis of Subarray A03 Probes

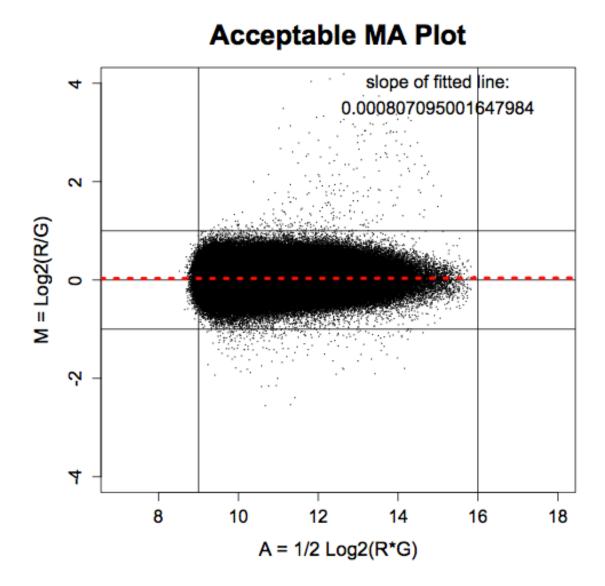


Figure 2.4.a - Acceptable MA Plot

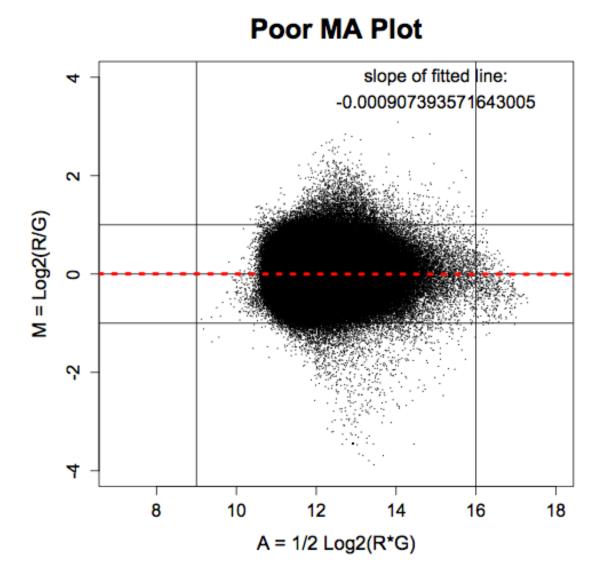


Figure 2.4.b - Poor MA Plot #1

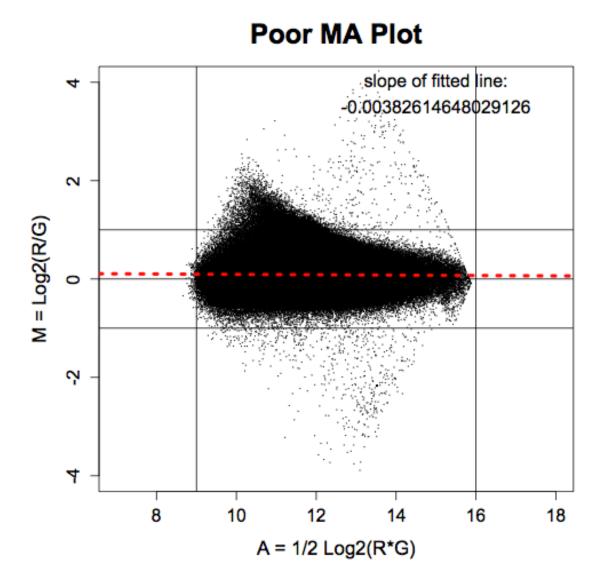


Figure 2.4.c - Poor MA Plot #2

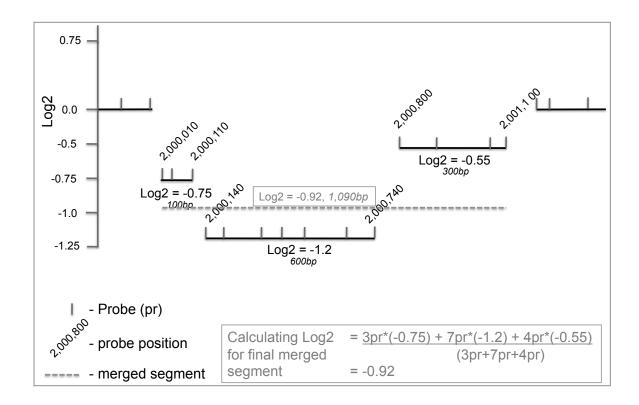


Figure 2.5 - Hypothetical example of merging multiple segments representing a single, deleted locus.

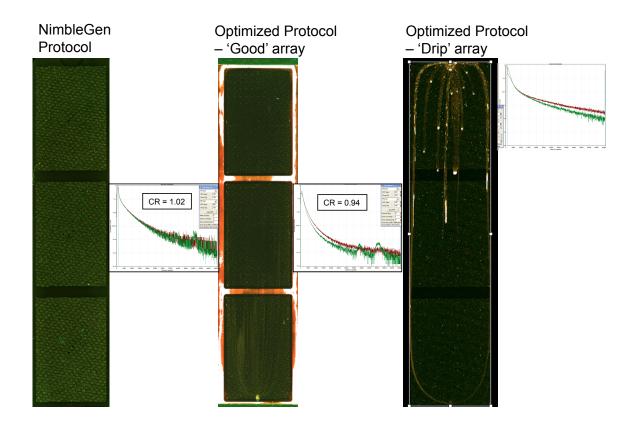
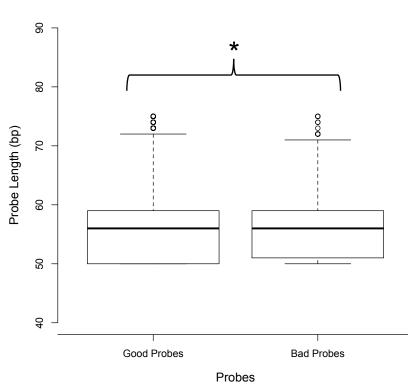


Figure 2.6 – Array performance by NimbleGen and Optimized protocols.



Probe Length: Good and Poor Probes

Figure 2.7.a – Boxplots of Good and Bad probes by Length.

Probe GC Content

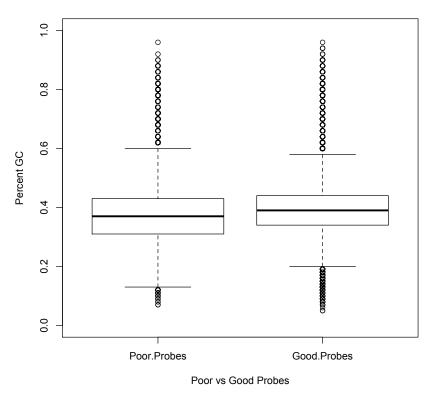


Figure 2.7.b – Boxplots of Good and Bad probes by GC Content.

C. Probe AG Content: Good and Poor Probes

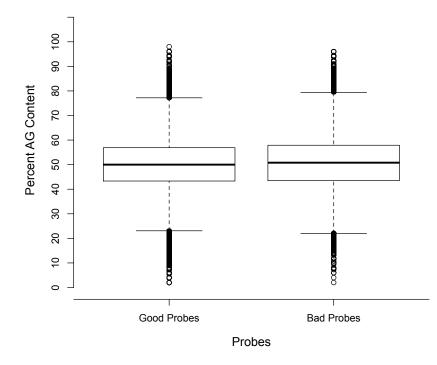
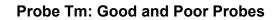


Figure 2.7.c – Boxplots of Good and Bad probes by AG Content.



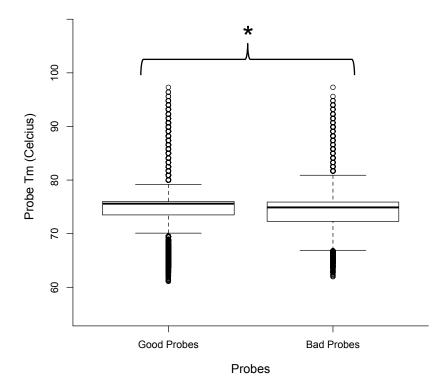


Figure 2.7.d – Boxplots of Good and Bad probes by melting temperature.

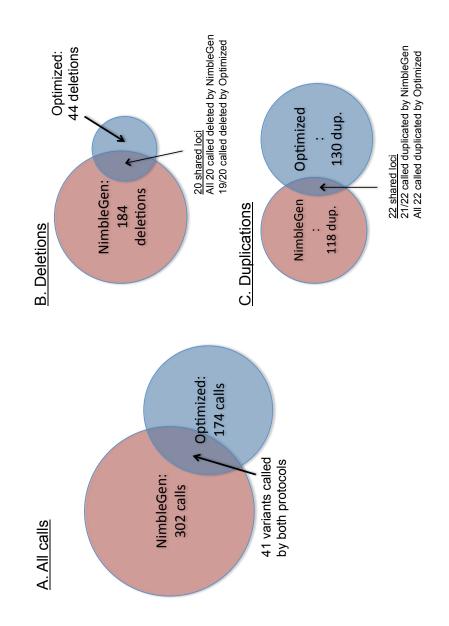


Figure 2.8 – CNV call overlap of NimbleGen and Optimized protocols.

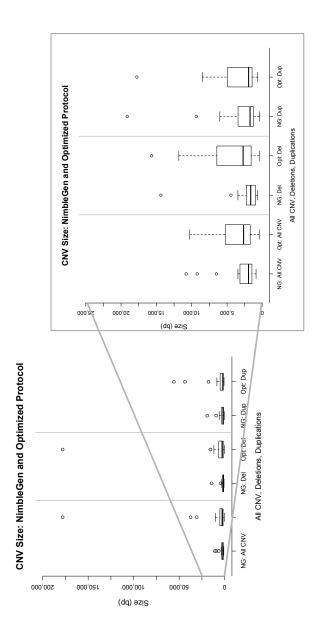


Fig. 2.9.a – CNV size distributions by the NimbleGen and Optimized protocols

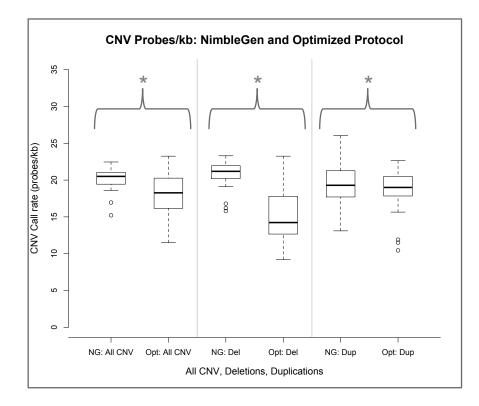


Fig. 2.9.b – CNV Probes/kb by the NimbleGen and Optimized protocols

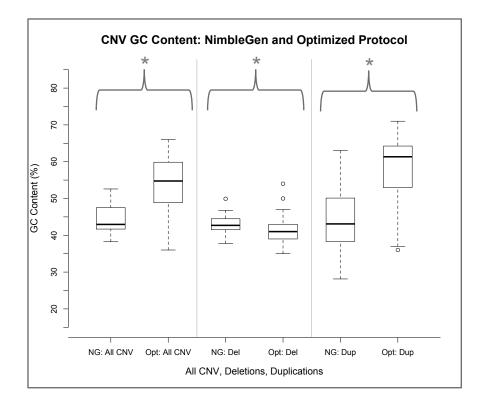


Fig. 2.9.c - CNV GC content by the NimbleGen and Optimized protocols

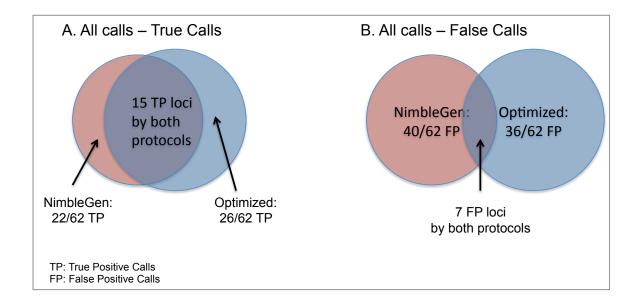


Figure 2.10 – Overlap of true and false CNV calls between protocols

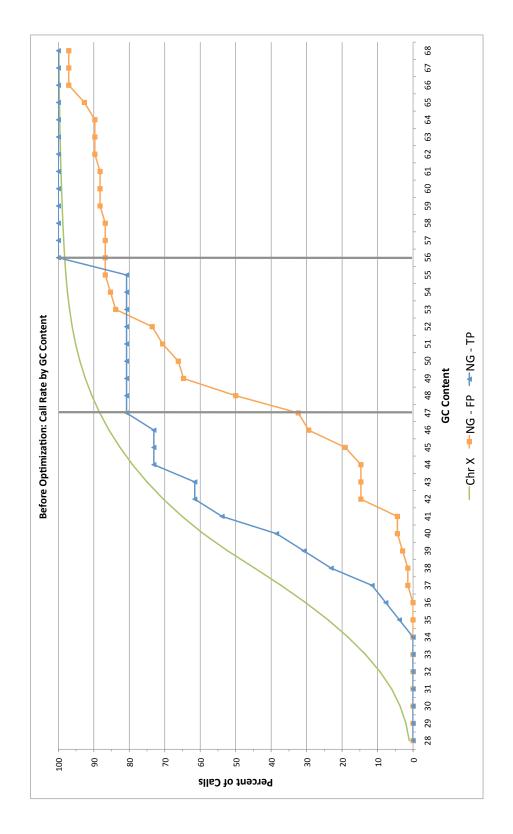


Figure 2.11.a – NimbleGen Protocol: Proportion of true and false calls plotted by GC

Content

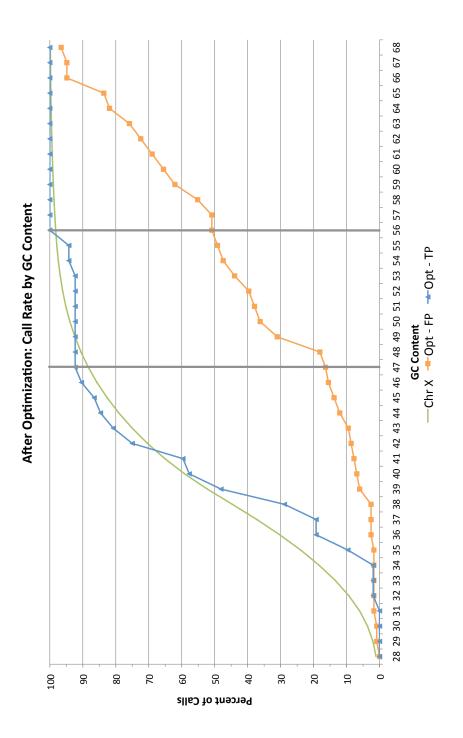


Figure 2.11.b - After Optimization: Proportion of true and false calls plotted by GC Content

Chapter 3. X-Chromsome Copy Number Variation and Breakpoint Analysis

1. Introduction to Copy Number Variation on the X Chromosome

We hypothesized that the X chromosome bears susceptibility loci for the autism spectrum disorders (ASD). With over 40 genomic structural changes located throughout the genome already identified as playing a role in ASD, we speculated that smaller changes (less than one megabase) could similarly disrupt autism susceptibility loci on the X chromosome. Capitalizing on advances in oligonucleotide-array technology that enable identification of fine-scale structural variation (500 base pairs (bp) in size or greater), we developed a study design to screen the X chromosome at high resolution in males with ASD. We studied several populations of samples using two array platforms and two array protocols to identify copy number variation on the X chromosome. This chapter describes our copy number findings, validation efforts, functional studies, and analysis of structural breaks.

Over the course of this project, we generated copy number variant (CNV, sequence that varies in copy number from the reference one kb in size or greater, can be benign or pathogenic) and indel (sequence that varies in copy number from the reference 100bp-1kb in size, can be benign or pathogenic) data from four different combinations of samples, two different array densities, and two different array-processing protocols . The first, and most brief, screened four samples from the Autism Genetic Resource Exchange (AGRE, multiplex families) by the 385K Comparative Genomic Hybridization (CGH) array following the manufacturer's (NimbleGen) protocol. This array probes the X

chromosome with 385,000 oligonucleotide probes resulting in an intermarker distance of approximately one probe ever 200 bp (four probes/kilobase (kb)). Next, the platform was upgraded to the 2.1M CGH array harnessing 2,100,000 million probes to interrogate the X chromosome. Data from 50 AGRE samples were generated. Early validation efforts suggested a high false call rate (65%), so we developed an optimized protocol in effort to reduce our false positive and false negative calls. Our third set of CNV and indel was derived from 100 AGRE samples and 64 samples from the Simons Simplex Collection (SSC, simplex families) screened by the 2.1M CGH array using our optimized protocol. Finally, we assayed 100 male controls from the National Institute of Mental Health (NIMH) control population ascertained for the Human Genetics Initiative by the 2.1M CGH array using NimbleGen's protocol.

2. Copy Number Changes Identified by array CGH

Before discussing the specifics of our findings, there are two characteristics to appreciate about our data. First, we describe our CNV data set in two different ways. The first is a summary of all CNV identified within a group, and the second is a summary of 'distinct' CNV characteristics. Studies of CNV will often make a distinction between 'singletons' (those loci found only in one individual and no others) and 'copy number variant regions' (CNVR, a locus that is found to be variant in more than one individual and if boundaries are not shared, percent overlap is defined by the authors). We identified both singletons and CNVR in our CNV screens of the X chromosome, and we assessed the nature, size, and gene content of those sequences. However, we defined a 'distinct locus' as sequence found to be copy number variant in one or more individuals. This grouping of singleton and CNVR allowed us to describe and characterize all copy number variant loci on the X chromosome as a whole. We defined our CNVR as having upstream and/or downstream breaks ending within three kb of one another or if one variant completely encompasses another; most often, ends were within one kb.

A second item to note is our characterization of CNV size. While the mean and standard deviation (SD) for the size of all and distinct CNV were calculated, this estimate of central tendency can be misleading. The majority of our data are quite small, but the presence of large variants within data sets inflates both the mean and SD estimates. These will be listed in the summary tables, but discussions of CNV or indel size will be based on the median values.

a. Study One: Four individuals from AGRE on the 385K array using the NimbleGen protocol

Using the 385K CGH arrays and following NimbleGen's protocol, we identified 16 CNV in four samples from the AGRE cohort (4.0 variants/person). The median size for these CNV was 3,263 bp. There were half as many deletions as duplications (0.45:1, five deletions, 11 duplications), and only one variant, a 149 kilobase (kb) duplication, involved a gene, *melanoma antigen family A, 8 (MAGEA8)*. (Table 3.1.a, Appendix: Table A.1)

The 16 CNV represented nine distinct loci in these four individuals. The median size of the distinct loci was 4,007 bp. Deletions and duplications were nearly equal in

representation with four deleted-only and four duplicated-only loci. No loci showed both a deletion and a duplication event. All CNV in this data set overlap at least four or more variants from the Database of Genomic Variants (DGV). In fact, 90 reported CNV and indels intersect with our 16 CNV. (Table 3.1.b, Appendix: Table A.1)

b. Study Two: Fifty individuals from AGRE on the 2.1M array using the NimbleGen protocol

Our next effort at screening the X chromosome for CNV and indels utilized the 2.1M CGH array (20 probes/kb) to evaluate 50 AGRE samples. We were able to generate data from 48 of these individuals, and 581 CNV and indels were identified (12.1 variants/person). Deletions accounted for 65% (379 CNV) of all CNV identified and duplications the remaining 35% (202 CNV and indels). The deletion: duplication ratio was 1.88:1. The median size for all CNV and indels was 1,080 bp. Overall, deleted loci were smaller than duplicated loci with the median deleted size being 1,005 bp and the median duplicated size 1,419 bp. Two hundred-sixty CNV and indels overlapped coding or intragenic sequence. Proportional to the number of deletions in the data set overall, deletions in coding or intragenic sequence accounted for 63% of all such CNV and indels and duplications the remaining 37%. Many CNV and indels in our data set overlapped with reported variants in the DGV. Of the 581 CNV and indels we identified, 420 overlapped with 509 previously reported variants while the remaining 161 CNV and indels did not intersect with any reported DGV variants. (Table 3.1.a, Appendix: Table A.2)

The 581 CNV and indel identified in these 50 AGRE samples by the NimbleGen protocol represented 282 distinct loci. There were 153 deleted-only loci (63%), 82 duplicated-only loci (34%), and seven loci showing both deletions and duplications (3%). For all categories of distinct loci, the median size was about 1,000 bp (all distinct: 1,152 bp; deletion-only: 994 bp; duplication-only: 1,443 bp; deleted and duplicated loci: 1,355 bp). A little less than half (112/282 distinct CNV loci, 46%) of the distinct variant loci overlapped coding or intragenic sequence. Fifty deleted-only loci (21%), 50 duplicated-only loci (21%) and 10 deleted and duplicated loci (4% of all distinct) involved a gene structure. (Table 3.1.b, Appendix: Table A.2)

c. Study Three: 100 affected males from AGRE and 64 affected males from SSC on the 2.1M array using the Optimized protocol

Using the more stringent protocol we developed and the 2.1M aCGH, we screened 164 samples from the AGRE (n=100) and SSC (n=64) cohorts for CNV on chromosome X. Of these samples, 149 (91%) passed array and data quality control measures, and 517 CNV were identified (3.5 variants/person). Nearly equal representation of deletions and duplications were observed (deletion:duplication = 0.88:1, 242 deletions (46.8%), 275 duplications (53.2%)). Unlike the CNV and indels identified by the NimbleGen protocol, under the conditions of our altered protocol, most CNV and indels in our data set are nearly the same size irrespective of state (median size all: 1,719 bp: median size deletions: 1,694 bp; median size duplications: 1,724). Sixty-one percent (313 CNV) of all CNV and indels overlapped genes with 108 deletions (21%) and 205 duplications (40%) involving coding or intragenic sequence. (Table 3.1.a, Appendix: Table A.3)

The 517 CNV and indels identified in our 164 individuals represent 244 distinct variant loci. Interestingly, similar rates of deleted-only CNV and duplicated-only CNV were observed. 118 deleted-only variants (48% of distinct), 106 duplicated-only (43% of distinct), and 20 both deleted and duplicated variants (8% of distinct) were found. Median size values suggest all distinct loci are about the same size at about 2,000 bp. The median size for all distinct loci is 1,951 bp, for deletion only: 1,608 bp, for duplication-only: 2,063 bp, and deleted and duplicated: 4,203 bp. About half (128 distinct CNV, 53%) of these distinct CNV intersect coding or intragenic sequence with duplications accounting for the majority (73 distinct CNV, 30%), and deleted-only (41 distinct CNV, 17%) and deleted and duplicated (14 distinct CNV, 6%) the remainder. (Table 3.1.b, Appendix: Table A.3)

d. Study Four: 100 unaffected males from NIMH on the 2.1M array using the NimbleGen protocol

Due to our agreement with Roche NimbleGen, we ran the 100 NIMH control samples following the NimbleGen protocol on the 2.1M arrays. Before running all 100, we first ran two samples in a proof-of-performance in our hands for Roche NimbleGen before proceeding with the remaining samples. Our analysis of 102 male samples yielded data from 101 arrays and identified 1,231 variants (12.2 variants/sample). Distinctly different from the two previous large studies of the AGRE samples, duplications comprised the majority of CNV (775 CNV, 63%) over deletions (456 CNV, 37%), and the deletion:duplication ratio was 0.59. Additionally, the observed CNV sizes in this data set

were larger, on average, than those observed in our earlier findings. The median size of all CNV is 2,015 bp, for deletions 933 bp, and for duplications 4,062 bp. Nearly half (634/1231 or 54%) of the CNV identified overlapped with 272 different genes. Consistent with an increase in observed duplications, 409 duplications overlapped with a gene while 225 deletions intersected a gene. Nearly three-fourths (851 of 1,231 or 69% CNV and indels) overlap with reported variants from the DGV. (Table 3.1.a, Appendix: Table A.4)

The 1,231 CNV identified in the NIMH control population represented 462 distinct regions where 155 distinct regions (34%) were deleted, 285 distinct regions (62%) were duplicated, and 22 distinct loci (5%) were deleted and duplicated. The median sizes for the distinct loci were more similar to those previously observed with 2,221 bp, 1,375 bp, 2,935 bp, and 6,435 bp for all, deleted-only, duplicated-only, and deleted and duplicated only sequences. Again, about half (216 or 49%) of the distinct loci overlapped with coding or intragenic sequence. Duplication-only events comprised most of these loci at 136, 60 deletion-only events and 20 deleted and duplicated loci overlapping gene structures. Of the 426 distinct loci, 241 overlapped with 664 CNV and indels reported in DGV. (Table 3.1.b, Appendix: Table A.4)

Emory CNV Overlap with Reports from the Database of Genomic Variants While the sex chromosomes do not bear similar rates of reported copy number events as compared to the autosomes (Figure 3.1) in the Database of Genomic Variants (DGV, Hg18), 75% of those studies reporting variants in this database have reported structural

changes for the X chromosome. Currently, 3,268 CNV and indels from over 4,600 individuals (male and female) screened have been reported for chromosome X. These data suggest that the X chromosome in the normal population has less than 0.7 copy number changes on chromosome X per person. The exact value is difficult to calculate as not all CNV and indels are identified as having been discovered in a male or female. We observed a five-fold increase (3.5 CNV/chromosome X) among those samples derived from the AGRE and SSC cohorts and a 17-fold increase (12.2 CNV/chromosome X) for those samples derived from the NIMH cohort. The median size of deletions, duplications or inversions reported on chromosome X in DGV is 2,013 bp. These reports are similar to what we observed in the NIMH samples (median size: 2,105bp), but somewhat larger than our observations of the AGRE and SSC cohorts (median size: 1,719 bp). The pattern of size distribution, where a majority of calls are 'small' and larger CNV represent a minority of calls, is similar when we compare the DGV and our own findings. However, the majority of CNV identified among the AGRE and SSC samples, or the NIMH samples are significantly smaller than those reported variants in DGV. Figure 3.2a-e

3. Validated Copy Number Changes

Our first pass selection of CNV for validation studies targeted possible candidate genes. Our strategy was to select structurally altered genes with 1) a known disease association (e.g., X-linked Mental Retardation), 2) a known molecular function that could plausibly be involved with autistic disorder, or 3) found to be expressed in the brain. In our screen of the AGRE and SSC cohorts, we identified 152 genes that intersected our array identified CNV and indels. The most compelling candidates genes were derived from the

disease-associated; we found 16 (ARHGEF9, ARX, CUL4B, DLG3, DMD, FTSJ1, JARID1C/KDM5C, KDM6A/UTX, KIAA2022, MAOA, PAK3, PHF6, RPS6KA3, SLC6A8, SYP, ZNF41) to be disrupted. Eleven of these 16 were selected for their role in nonsyndromic X linked Mental Retardation (ARX, CUL4B, DLG3, FTSJ1, JARID1C/KDM5C, KIAA2022, PAK3, RPS6KA3, SLC6A8, SYP, and ZNF41). We identified seven genes (BCAP31, FRMPD4/KIAA0316, GABRQ, GPR173, TCEAL2, *TMEM47*, *TREX2*, *HAUS7*) with a compelling cellular role such as functioning in neuronal processes (FRMPD4 and GABRQ). And 50 genes (ARHGEF9, ARX, BCOR, BGN, CUL4B, DDX26B, DDX3X, DLG3, DMD, ELK1, F8A1, FAM122B, FGF13, FOXO4, GPRASP2, GPRASP2, GRIPAP1, H2AFB3, HEPH, IDH3G, IQSEC2, KIAA2022, LAMP2, LOC550643, MID1IP1, MTMR1, NAP1L2, OTUD5, PCYT1B, PDZD4, PGRMC1, PHF6, PPP1R3F, PRKX, RBBP7, SH3KBP1, SHROOM2, SLC38A5, SLC6A8, SLITRK4, SSR4, STAG2, STS, SYP, TBL1X, TCEAL2, TMEM164, TMEM47, UBA1, USP9X) were identified as being expressed in the brain. Of these 50, eight were identified from the disease-associated category and two from the cellular-function category.

a. Characteristics of validation assays developed for CNV identified in AGRE and SSC cohorts

Using PCR based strategies to capture deletion and duplication junction breakpoints, we ultimately developed validation assays for 105 distinct loci representing 179 CNV in the AGRE and SSC cohorts. Specifically, for each working assay, an amplicon of an expected variant size would confirm or refute the validity of the array identified copy

number change. For deletions, the expected amplicon would be smaller in size relative to intact sequece (i.e., reference and control DNAs); for duplications, the expected amplicon would be larger in size than single copy, reference or control DNAs, or a junction amplicon generated where no amplicon is expected from a single copy. It is important to note that this PCR based strategy for validation of duplications assumes that the duplicated sequence is located in tandem with the original. While most duplicated sequence to exist elsewhere in the genome.

For these 105 distinct loci, 39 loci (37%) representing 58 CNV validated while the remaining 66 loci (63%) representing 121 CNV proved to be false positive. A majority of the true calls were deletion events (35 or 90%) while a somewhat more even distribution of deletions and duplications were found to be false (26 deleted (39%) and 35 duplicated (53%), the remaining five deleted or duplicated (8%)). The false call rate (failure to validate an array identified variant sequence) for deletions was 26 or 43% and for duplications was 35 or 90%. Additionally, those variants that validated tended to be larger with a median size of 2,343 bp versus 1,370 bp for variants that did not validate. (Table 3.2)

b. Inheritance and Population Data for validated CNV

We assessed 33 of the 39 validated loci for maternal inheritance, the remaining six were not tested for inheritance. Of these, 32 CNV or indel was also identified in the mother. A 14 kb deletion was the only *de novo* structural change identified. This locus does not overlap any genes but has a few semi-conserved sequences and is located 174 kb downstream of *gastrin-releasing peptide receptor* (*GRPR*, found to be disrupted in an individual with autism).

Genotyping in an extended autistic population (200 additional, unrelated AGRE samples) as well normal control populations (300 unrelated fathers from the AGRE cohort, 1500 males from the NIMH cohort) was begun for those CNV that validated. Two CNV, AU016.3 and AU122.1 were completely genotyped on all autistic samples (n = 364, 300AGRE and 64 SSC) and control samples (300 AGRE fathers, 1,500 NIMH males). The first CNV, AU016.3, is a deletion approximately eight kb in size located at chrX: 16,249,363 - 16,266,863 (Hg18); sequencing is not complete and exact coordinates not yet determined. Our observed frequencies are 2/364 (0.5%) in our autistic samples and 2/1800 (0.1%) in our controls. These frequencies are not statistically different with p < 0.2684. Our second CNV, AU122.1, is the *GRIA3* 561 bp promoter deletion at chrX: 122,143,696 – 122,144,257 (Hg18). We observed 6/364 (1.6%) and 20/1799 (1.1%) for our autistic and normal populations. Unfortunately, these frequencies were also not statistically different with p < 0.5531. Additionally, genotyping has begun for seven additional CNV (AU015.2, AU033.95, AU065.4, AU082.1, AU096.5, AU113.2, and AU122.1). (Table 3.3)

c. Candidate genes that have been validated and remain to be validated

As noted previously, we initially identified 17 loci as having compelling molecular and disease related functions that prioritized these loci for validation. Eight of the 17 loci had

validation assays developed for them though seven of the eight proved to be false calls. The remaining nine loci are *ARX*, *GABRQ*, *KDM6A/UTX*, *KIAA2022*, *MAOA*, *SYP*, *TMEM47*, and *ZNF41*. Four genes, *GABRQ*, *MAOA*, *SYP*, and *ZNF41* have the compelling feature of having GC content less than 53%. Based on our validation rates, a greater than 50% chance remains that each will be a false call, but the potential exists that these variants will validate true. (Figure 3.4)

The only validated CNV located in a gene was a deletion event in the first intron of the *FERM and PDZ domain containing 4* gene (*FRMPD4*). This gene was first identified from a large protein cDNA library of human brain. *Lee et* al demonstrated the gene product's involvement with the maintenance of excitatory synaptic transmission as well as its interactions with PSD95, a postsynaptic density protein.[115] Our 2.5 kb deletion lies 277 kb downstream of the first exon and about 80 kb upstream of the second exon within chrX: 12,344,184 – 12,346,734. One hypothesis might suggest that the deletion creates an alternative splice site, and breakpoint sequencing would further substantiate this possibility. While this deletion event could have removed an enhancer or promoter for this gene, the deleted sequence is not significantly conserved but this does not disprove the notion that a human specific modifier could be lost. (Figure 3.4)

Additional candidate CNV for validation were identified by their proximity but to coding or intragenic sequence. While these CNV do not overlap exonic or intronic sequence, they may arise upstream or downstream of gene. These locations might hold modifier

sequence that could affect (enhance or repress) gene expression, and gain or loss of such sequence may perturb expression levels enough to result in an autistic phenotype.

We identified a 560 bp deletion 1,541 bp upstream of the first coding exon of *glutamate receptor, ionotropic, AMPA3 (GRIA3).* Array CGH identified two individuals as being deleted at this locus. This gene is interesting as a candidate for ASD because of its causal role in X-linked Mental Retardation (OMIM: 305915, MRX94) and its molecular role as an AMPA-responsive glutamate receptor, the predominant excitatory neurotransmitter receptors in the human brain.[116] We hypothesized a potential role in ASD as mis-regulation of protein expression for this gene product ultimately disturbs neuronal function. The 560 bp deletion removes relatively un-conserved sequence, but does not negate the possibility of human specific regulatory sequences in and overlapping the deleted sequence. (Figure 3.5) Confirmation PCR validated these deletion events, and breakpoint sequencing revealed the two individuals shared the same breakpoints. The dinucleotides 'AG' and 'GT' are found at the upstream and downstream breakpoints suggesting a non-homologous end joining mechanism mediated a double strand break.

We conducted functional studies of this upstream promoter region by a luciferase assay. The intact and deleted sequences were placed upstream of a luciferase promoter construct, transfected into N2A cells, and luciferase expression from protein lysates was measured. We found an increase in luciferase expression when the reporter was modified by the deleted locus. (Figure 3.6) However, genotyping for the deletion in our expanded autistic cohort (300 AGRE samples) and a normal sample population (1,500 normal

white males and the 300 normal fathers) demonstrated similar frequencies in both populations (p < 0.2247).

4. Analysis of Junction Sequence

a. Validated CNV with breakpoint sequencing

CNV identified and sequenced from the autistic cohorts screened at Emory

We bi-directionally sequenced 27 validated copy number variant loci. These sequenced variants are comprised of 26 deletions and one duplication event. Eight were found to be variant in multiple individuals, and all breaks in these shared loci were the same suggesting that at some point the variant may have been inherited from a common ancestor. We further assessed the sequenced breakpoints for homology at both ends, insertion of sequence, and repeat content at the points of junction. Breakpoints, or the ends of the copy number variant, have been evaluated for the presence of homologous sequence in effort to discern a mechanism by which the structure was resolved. We found 26 junction fragments showing homology at the immediate ends of the upstream and downstream breaks. Seventeen of these homologous sequences were four bp or smaller, and two of the 17 had small insertions (one bp and four bp) at the breakpoint junction. The microhomology of four bp or less as well as the small insertions are suggestive of non-homologous end joining (NHEJ) to repair a double strand break during replication.[117-120] Five of the 27 showed homologies ranging from five to eight bp fall within the range of a non-classical NHEJ (previously known as microhomology mediated end-joining (MMEJ, typified by microhomologies ranging from 5-25 bp).[119-121] Additionally, Alu elements and a 200 bp sequence were found in both the upstream and

downstream breaks of three deletions suggesting non-allelic homologous recombination between the homologous sequences at each end may have mediated the deletion of intervening sequence.[119-122] (Table 3.4)

<u>CNV identified and sequenced from reports in the literature</u>

Microhomologies, repeat elements and other sequence-based motifs have been found at or around breakpoints, and their presence is an indicator for how a structural event may have been resolved.[93, 117-121, 123-128] While much effort went into the identification and collection of our set of sequenced breakpoints, our data set remains relatively small. By using data from other studies, additional sequenced breaks can be used to ask broader questions of the occurrence of microhomology as well as evaluate junctions for the enrichment of motif sequences. We searched the literature for sequenced breakpoints or junctions and identified 12 articles from 2002-2010.[49, 92, 93, 129-137]. (Table 3.5)

We collected 681 deletions or duplications having nucleotide resolution of their junctions. (Appendix: Table A.4) The deletions and duplications were identified by various methods and are distributed throughout the genome from diverse populations. (Figure 3.7.a-b) In all data sets, duplications are much larger than deletions. While most of the data are derived from deletions with only 17 duplications (3%) represented, this is similar to what we identified in our data where our single duplication represented 4% of our set. (Table 3.4, Table 3.6) The data generated by Conrad et al is split out from the rest of the reference as it bears the great similarity to our own data set. Conrad's study utilized high-density arrays from NimbleGen as well. Their study conducted a screen of

fine scale variation of the human genome using the HapMap population. However, no calls were made for the X chromosome from their study.

Nearly 80% (536) of the literature sequences were evaluated for homology at the breakpoints. About one third (200 or 37%) of the evaluated sequences showed no homology at both ends of the variant, and the remaining two thirds (337 or 63%) had some degree of homology. Of the 337 structural changes showing homology at their breaks, 74% (249/337) of the homology was four bp or less suggesting NHEJ as the major mechanism of repair to double strand breaks. The remaining structural changes were largely composed of breakpoints having microhomology ranging with the 5-25 bp in size that is indicative of a MMEJ mechanism (24%) of double strand break resolution. The remaining 2% ranged as high as 200 bp, and such relatively long stretches of homology suggest the non-allelic homologous recombination mechanism of repair. Additionally, 102 of the 563 evaluated breaks (18%) showed an insertion at the breakpoint, and 64% (65/z) of these insertions were seven bp or less in size suggesting some sort of slippage during repair or participating in NHEJ.[54] (Table 3.7, Figure 3.8.a-c)

Using all sequenced breakpoints (the 27 from Emory and 681 from the literature), we evaluated single base insertion and deletion events and found no bias for any particular nucleotide for either (p < 0.61, and p < 0.73 respectively).

b. Analysis of sequence motifs at breakpoint junctions

Various sequence motifs have been previously identified as being significantly associated with structural break resolution. We identified 39 such motifs from six different categories including 1) Chi-like sites, 2) hotspots for deletions, insertions, and indels, 3) DNA polymerase specific sequences, 4) Eukaryotic Transcription Regulation, 5) Mobile Elements, and 6) Recombination sites. [123, 129, 133, 138-148] (Table 3.8) We evaluated the frequency of these motifs at the breakpoints of both the sequenced data set and the randomly generated data sets. The goal was to assess whether these motifs were enriched in the sequenced breakpoint data set over that of the random set.

c. Development and evaluation of randomly chosen breakpoint sequences We wanted to ask the question whether the frequency of previously reported motif sequences were increased at the breakpoints of CNV relative to random spots in the genome. To do so, we first identified a set of 565 'real' CNV with well-characterized breakpoints. Those CNV consisted of the 27 first described here, together with 305 described by Conrad et al, and the remaining from 11 published sources. For each of these 565 'real' CNV, we created 1,000 'random' CNV. Each random CNV was the same size as the corresponding real CNV, and located on the same chromosome, but with its start location uniformly distributed across the chromosome. The percent 'GC' and percent 'N' (undetermined nucleotide composition) of each 'random' set was similar to the 'GC' and 'N' content of the corresponding 'real' CNV. (Figure 3.9.a-b) 98% of the 1,000 random sets differed from the 'real' variants in their mean GC content at the breaks by less than 10%, and all but three data sets had the same mean 'N' content as the 'real'

values. This resulted in 565,000 randomly positioned 'variants' to be used to compare the frequency of observed characteristics versus a randomly selected population.

For each pair of breakpoints (real or random), we defined 50 bp windows on either side of each breakpoint in both the upstream and downstream breaks. (Figure 3.10) We considered all four windows (('A', 'B', 'C' and 'D') as representative of susceptibility to structural resolution. In other words, we hypothesized that the sequences located in A-D were more susceptible/amenable to resolve a structural event (the product being a deletion or duplication) than a randomly chosen sequence. This susceptibility/amenability to structural resolution may occur in windows inside (B, C) or outside (A, D) or all (A-D) of the CNV breakpoints. We evaluated all possibilites (All windows, inside, or outside) in 565 of the sequenced breakpoints ('real' sequences) and 565,000 random windows ('random' sequences) were evaluated for the frequency of the 39 motifs previously ascribed to breakpoint resolution. We identified eight motif sequences that were overrepresented in our data set as compared to the randomly generated data set. These sequences (Human hypervariable minisatellite core sequence, DNA polymerase α frameshift hotspots, DNA polymerase β frameshift hotspots, AT-rich signal, Curved DNA signal, Topoisomerase II consensus cleavage site (Drosophila), Murine LTR recombination hotspot, Nonamer recombination signal) did not cluster in any one category, and only one motif, Topoisomerase II consensus cleavage site (Drosophila), was significant in all three window types (all, inside and outside). Table 9

5. Summary

We conducted four different studies using three different sample populations, two different array platforms, and two different array hybridization protocols. In total, the X chromosome of 302 samples was screened by high-resolution aCGH. We identified 2,300 CNV of which 1,357 (59%) were deletions and 1,263 (55%) were duplications. We attempted to validate 331 loci, and 146 successful genotyping assays were developed. Of these 146 assays, 100 identified falsely called CNV loci, 44 identified truly called CNV loci, and two confirmed CNV in the reference sample. Of the validated loci, a 560 bp deletion 1,541 bp upstream of the *GRIA3* locus was confirmed. Functional studies in Neuro2A cells were developed to assay the effect of this region with and without the deleted sequence on expression of a luciferase gene. Loss of this sequence resulted in an increase in expression. Genotyping for this deletion in 364 individuals with autism and 1,799 normal individuals did not reveal enrichment for this deletion in the autistic population.

We characterized a subset of our confirmed CNV breakpoint junctions. In addition to identifying microhomology, insertions at the breakpoint, and repeats associated at the breaks, we also expanded our analysis to include an assessment of motif occurrence. We identified 39 sequence motifs that have been previously reported as being enriched at breakpoint junctions. We combined our breakpoints with 565 additional breakpoints with nucleotide resolution from the literature. Using our and the literature sequences, we identified eight different sequence motifs that were enriched within 50 bp windows of the breakpoints.

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	# of Samples	# of CNVs (% all CNVs)	# of CNVs/Sample (SD)	Mean size in bp (SD)	Median size in bp	# of CNV which overlap genes (% all CNV)
		A	AGRE - 385K, NimbleGen protocol	Gen protocol		
ALL	4	16	4.0 (2.9)	13,415 (36,584)	3,263	1 (6.3%)
Deletions	1	5 (31%)	1.3 (1.5)	3,961 (4,239)	1,227	0 (%0) 0
Duplications	ı	11 (69%)	2.8 (1.5)	17,712 (43,993)	3,539	1 (6.3%)
		A	AGRE - 2.1M, NimbleGen protocol	eGen protocol		
ALL	48	581	12.1	2,955 (21,279)	1,080	260
Deletions	ı	379 (65.2%)	7.9	1,685 (2,974)	1,005	164 (63.1%)
Duplications	ı	202 (34.8%)	4.2	5,340 (35,795)	1,419	96 (36.9%)
		A	AGRE + SSC - 2.1M, Emory protocol	mory protocol		
ALL	149	517	3.5 (3.8)	7,447 (28,307)	1,719	313 (60.5%)
Deletions	I	242 (46.8%)	1.6	5,347 (16,628)	1,694	108 (20.9%)
Duplications	ı	275 (53.2%)	1.9	9,282 (35,435)	1,724	205 (39.7%)
		Z	NIMH - 2.1M, NimbleGen protocol	eGen protocol		
ALL	101	1186	11.7 (10.1)	26,606 (101,842)	2,104	634 (53.5%)
Deletions	ı	413 (34.8%)	4.1	6,522 (79,825)	1,043	225 (19.0%)
Duplications	·	773 (65.2%)	7.7	37,336 (110,402)	4,091	409 (34.5%)
bp: base pairs, CNV: C	V: Copy Num	opy Number Variant, SD: Standard Deviation	andard Deviation			

Table 3.1.a All Copy Number Variants Identified by high-density aCGH

	# of Samples	# of CNVs (% all CNVs)	# of Distinct CNV loci (% ofAll distinct)	Mean size in bp (SD)	Median size in bp	# of Distinct Loci which overlap genes (% all distinct)
			AGRE - 385K, NimbleGen protocol	Gen protocol		
ALL	4	16	6	21,437 (48,395)	4,007	1 (6.3%)
Deletions		5 (31%)	4 (44%)	4,645 (4,566)	3,514	0 (0%)
Duplications	,	11 (69%)	5 (56%)	34,872 (64,505)	4,007	1 (6.3%)
Deleted & Dupliated		ı	·	I	I	-
			AGRE - 2.1M, NimbleGen protocol	Gen protocol		
ALL	48	581	282	5,073 (32,850)	1,152	112 (46%)
Deletions		379 (65.2%)	153 (63%)	2,171 (4,318)	994	52 (21%)
Duplications		202 (34.8%)	82 (34%)	10,677 (55,916)	1,443	50 (21%)
Deleted & Dupliated	·	I	7 (2.9%)	2,876 (3,538)	1,355	10 (4%)
			AGRE + SSC - 2.1M, Emory protocol	nory protocol		
ALL	149	517	244	10,890 (37,869)	1,951	128 (53%)
Deletions		242 (46.8%)	118 (48%)	4,929 (10,902)	1,608	41 (17%)
Duplications	ı	275 (53.2%)	106 (43%)	13,725 (45,971)	2,063	73 (30%)
Deleted & Dupliated		ı	20 (8.2%)	31,034 (72,368)	4,203	14 (6%)
			NIMH - 2.1M, NimbleGen protocol	Gen protocol		
ALL	101	1186	426	18,900 (107,802)	1,945	206 (48%)
Deletions	ı	413 (34.8%)	151 (35%)	15,351 (131,806)	1,375	58 (14%)
Duplications		773 (65.2%)	252 (59%)	20.910 (96,095)	2,407	128 (30%)
Deleted & Dupliated		ı	23 (5.4%)	20,174 (23,647)	9,118	20 (4.7%)
					1	

Table 3.1.b Distinct Copy Number Variants Identified by high-density aCGH

	# of CNV	# of Unique Loci	Mean Size of All CNV (bp)	Median Size of All CNV (bp)	Mean GC Content of All CNV (%)
True Positive	58	39	11,451	2,343	40.6%
Deletion	54	35	11,778	2,243	40.6%
Duplication	4	4	7,036	7,141	39.9%
False Positive	121	66	3,254	1,370	53.3%
Deletion	59	26	1,481	1,205	54.0%
Duplication	62	35	4,940	1,439	52.6%
Deleted & Duplicated	-	5	3,165	4,114	52.4%

bp: base pairs, CNV: Copy Number Variant

Table 3.2 – Characteristics of validated copy number variants.

Locus	chrX Start	chrX Stop	Size (bp)	State	Autistic Frequency	Control Frequency
AU015.2	15,161,742	15,197,116	35,374	duplication	1/299	0/300
AU033.95	33,952,914	33,982,773	29,859	deletion	2/364	0/300
AU065.4	65,381,486	65,415,746	34,260	duplication	1/300	0/300
AU082.1	82,085,921	82,094,944	9,023	deletion	pooled DNA genotyped	?
AU096.5	96,493,413	96,495,398	1,985	deletion	pooled DNA genotyped	?
AU113.2	113,234,594	113,241,627	7,033	deletion	pooled DNA genotyped	?
AU120.4	120,416,100	120,419,999	3,899	deletion	pooled DNA genotyped	?

Table 3.3 – CNV genotyping in progress for autistic and unaffected populations.

ID	State	Start*	End*	Homology at Junction	Insertions
1	deletion	24,021,195	24,026,627	Alu element	-
2	deletion	30,048,860	30,056,098	ТТ	-
3	deletion	30,257,687	30,258,519	AG	А
4	deletion	33,952,914	33,982,773	AGGT	-
5	deletion	38,271,449	38,272,275	AAAAT	СТ
6	deletion	44,264,761	44,266,313	Alu element	-
7	deletion	58,256,036	58,256,488	AGGCATTCTAATGATAGAGACACCTGTGGTGA	-
8	deletion	64,002,062	64,014,239	ACACT	-
9	duplication	65,381,485	65,415,746	С	-
10	deletion	80,303,149	80,304,088	ATA	-
11	deletion	82,085,921	82,094,944	CAGAG	-
12	deletion	87,545,357	87,547,591	ATTA	-
13	deletion	96,493,413	96,495,398	AG	-
14	deletion	97,842,279	97,843,597	ATT	-
15	deletion	103,289,074	103,289,688	ATTGCCCT	-
16	deletion	103,295,675	103,296,655	CATT	-
17	deletion	111,753,107	111,753,796	AA	-
18	deletion	113,234,594	113,241,627	GGC	-
19	deletion	116,588,176	116,591,267	GCT	CTTC
20	deletion	120,416,100	120,416,999	-	AATCAA
21	deletion	122,143,696	122,144,257	AG	-
22	deletion	131,767,115	131,769,226	GCC	-
23	deletion	133,692,157	133,693,471	AA	-
24	deletion	143,436,372	143,445,447	ATATCC	-
25	deletion	145,207,078	145,208,683	ATTT	-
26**	deletion	149,678,591	149,679,508	TCTG	-
27	deletion	150,457,729	150,462,994	~220 nt	-

*If breaks not clearly identifiable, the average position based on earliest and last possible base is shown. **5 nt deleted 37 bp upstream of break

Table 3.4 - Validated and bidirectionally sequenced CNV breakpoints identified in our

study.

Study	Year	Population Phenotype/Disease	Samples in CNV Analysis	CGH analysis Platform	# of CNVs Identified	Sequence Analysis Platform	# of Sequenced Breaks
Emory	2010	Autistic, male	142	NimbleGen HD aCGH ChrX	517	Sanger sequencing	27
Conrad	2010	Normal, HapMap, male/female	450	NimbleGen HD aCGH genome-wide	11,700	454 sequencing	324
deSmith	2008	Normal, French Caucasian males	50	Agilent aCGH 1) 185K genome-wide 2) 244K targeted	2,208	Sanger sequencing	20
Edamura	2005	Fragile X Syndrome	n/a	various	16	Sanger sequencing	16
Goldman	2010	Familial hypercholesterolemia	1447	Multiple Ligation Probe Amplification	37	Sanger sequencing	8
Kim	2008	Normal	Published Sources	Published Sources: Segmental Duplication Db, Human Copy Variation Consortium, Fosmid Paired-End Sequencing, Genome Comparison	NA	454 sequencing	67
Korbel	2007	Cat-Eye Syndrome, Emanuel syndrome, Dup22 syndrome, 22q11 Deletion syndrome, Digeorge syndrome	10	Nimblegen aCGH 385K, targeted	>400	Sanger sequencing	167
Lam	2010	CEPH male, Published Sources	Published Sources	Published Sources: Sanger sequencing, fosmid-paired-end- sequencing, next-gen sequencing, high-resolution aCGH	NA	Sanger sequencing	12
Nobile	2002	DMD/BMD	22		22	Sanger sequencing	4
Park	2010	Normal, HapMap, female	30	Agilent HD aCGH 1) 24M, genome-wide 2) 185K, targeted	20,099	Sanger sequencing	42
Vissers	2009	Mutiple Congenital Anomalies (MCA), MR with or without MCA, Epilepsy or Autism	38	NimbleGen HD aCGH 1) 385K, 2.1M genome-wide 2) two 385K targeted	38	Sanger sequencing	38
Woodward	2005	Pelizaeus-Merzbacher Disease	59	FISH, multiplex PCR	59	Sanger sequencing	12
Zhang	2010	Charcot-Marie-Tooth disease Type 1A, hereditary neuropathy with liability to pressure palsy	21	Agilent aCGH 15K, targeted	17	Sanger sequencing	9

Table 3.5 – Summary of articles identified in the literature.

	# of CNVs (% all CNVs)	Mean size in bp (SD)	Median size in bp
Emory			
ALL	27	5,270 (8,377)	1,605
Deletions	26 (96%)	4,155 (6,169)	1,579
Duplications	1 (4%)	34,261 (n/a)	34,261
Conrad			
ALL	305	6,623 (19,157)	2,534
Deletions	302 (99%)	6,592 (19,245)	2,447
Duplications	3 (1%)	9,707 (5,396)	9,235
11 Other Liter	ature Referenc	es	
ALL	375	202,066 (993,372)	6,049
Deletions	361 (96%)	177,580 (979,610)	6,035
Duplications	14 (4%)	833,461 (1,169,881)	491,597

Table 3.6 – Characteristics of breakpoint sequenced CNV from the literature and our studies.

Α.	Deletion	and D	uplication	Proportions

	# CNV	Deletions (% of set)	Duplications (% of set)
All	708	690 (97%)	18 (3%)
Emory	27	26 (96%)	1 (4%)
Conrad	305	302 (99%)	3 (1%)
Literature*	376	362 (96%)	14 (4%)

* Literature less Conrad data

B. Homology characteristics

	# CNV	No homology at Break (% evaluated)	Microhomology ≤ 4 bp (% evaluted)	Microhomology 5-25 bp (% evaluted)	Homology >25 bp (% evaluted)
All	708	200/563 (36%)	266/563 (47%)	84/563 (15%)	13/563 (2%)
Emory	27	1/27 (4%)	17/27 (63%)	5/27 (19%)	4/27 (15%)
Conrad	305	115 (38%)	161 (53%)	27 (9%)	2 (1%)
Literature*^	376	85/232 (37%)	87/232 (38%)	53/232 (23%)	7/232 (3%)

* Literature less Conrad data

^not all sequences were evaluated for homologies or insertions

C. Insertion characteristics

	# CNV	No insertion at Break* (% evaluated)	Insertion at Break* (% evaluated)	Insertions [*] ≤ 7 bp (% evaluted)
All	708	461/563 (82%)	102/563 (18%)	69/563 (12%)
Emory	27	23/27 (85%)	4/27 (15%)	4/27 (15%)
Conrad	305	215 (70%)	90 (30%)	55 (18%)
Literature*	376	224/232 (97%)	7/232 (3%)	5/232 (2%)

* Literature less Conrad data

^not all sequences were evaluated for homologies or insertions

Table 3.7 - Characteristics of junction breaks from our study and the literature.

Cite Name	Matif Converse(a)	Deference
Site Name	Motif Sequence(s)	Reference
X- and X-like Sites		
Chi-sequence	GCTGGTGG	Abeysinghe, Dohoney
Chi-sequence truncated	TGGTGG	Chuzhanova
Human Fra(X) breakpoint cluster	CGGCGG	Chuzhanova
Human minisatellite conserved sequence/X-like element	GCWGGWGG	Abeysinghe, Kvikstad
Human hypervariable minisatellite core sequence	GGGCAGGANG, GGAGGTGGGCAGGARG	Abeysinghe, Kvikstad
Human hypervariable minisatellite recombination sequence	AGAGGTGGGCAGGTGG	Abeysinghe, Kvikstad
Deletion, Insertion, and Indel Hotspots		
Deletion hotspot consensus sequence	TGRRKM, YYTG	Abeysinghe, Kvikstad
Hamster deletion hotspot	TGGAG	Chuzhanova
Hamster and human APRT deletion hotspot	ПСПТС	Chuzhanova
Indel hotspot	GTAAT	Kvikstad
Indel Super-hotspot motifs	CCCAG, TTCWCCCC, CCACCA, GGGACA,	Chuzhanova
Inder Super-notspot motifs		Chuzhanova
Insertion hotspots	GCCCCG, AGCTG, CCATCT, GGAGAA ATMMGCC, TACCRC	Kvikstad
Insertion notspots	ATMMGCC, TACCRC	KVIKSLOU
DNA Polymerase Pause or Frameshift Hotspots		
DNA polymerase α frameshift hotspots	TCCCCC, CTGGCG	Abeysinghe, Kvikstad
DNA polymerase β frameshift hotspots	ACCCWR, TTTT	Abeysinghe, Kvikstad
DNA polymerase α/β frameshift hotspots	TGGNGT, ACCCCA	Abeysinghe, Kvikstad
DNA polymerase α pause site core sequence	GAG, ACG, GCS	Abeysinghe, Kvikstad
DNA polymerase arrest site	WGGAG	Abeysinghe, Kvikstad
Eukaryotic Transcriptional Regulation	14/14/14/14/14/14/	Circh
AT-rich signal		Singh
Curved DNA signal	ΑΑΑΑΝ7ΑΑΑΝ7ΑΑΑΑ, ΤΤΤΤΝ7ΤΤΤΝ7ΤΤΤΤ, ΤΤΤΑΑΑ	Singh
Kinked DNA signal	TAN3TGN3CA, TAN3CAN3TG, TGN3TAN3CA,	Singh
	TGN3CAN3TA, CAN3TAN3TG, CAN3TGN3TA	
ORI signal		Singh
TG-rich signal	TGTTTTG, TGTTTTTG, TTTTGGGG	Singh
Topoisomerase Cleavage Sites	1000	
Topoisomerase I consensus cleavage site (Vaccinia)	YCCTT	Abeysinghe, Kvikstad
Topoisomerase I consensus cleavage site (vertebrate/plant)	CAT, CTY, GTY, RAT	Abeysinghe, Kvikstad
Topoisomerase II consensus cleavage site (Drosophila)	GTNWAYATTNATNNR	Singh
Topoisomerase II consensus cleavage site (vertebrate)	RNYNNCNNGYNGKTNYNY	Abeysinghe, Kvikstad, Singh
Mobile Elements		
Alu core element	CCTGTAATCCCAGCACTTTGGGAGGC	Abeysinghe, Rudinger
Mariner transposon-like element (3' end)	GAAAATGAAGCTATTTACCCAGGA	Abeysinghe, Kvikstad
Recombination Sites		
Autonomously replicated sequence	WRTTTATTTAW	Chuzhanova
Chinese hamster scaffold attachment site		
Classical meiotic recombination hotspot	AATAAAYAAA	Chuzhanova
Hamster and human APRT deletion hotspot	ССТСССТ	Chuzhanova Chuzhanova
Human hypervariable minisatellite recombination sequence	AGAGGTGGGCAGGTGG	Abeysinghe, Kvikstad Chuzhanova
Indel Super-hotspot motifs	CCCAG, TTCWCCCC, CCACCA, GGGACA, GCCCCG, AGCTG, CCATCT, GGAGAA	Chuzhdhova
Meiotic recombination hotspot	CCTCCCCT	Chuzhanova
Murine LTR recombination hotspot	TGGAAATCC	Abeysinghe, Kvikstad
Murine MHC recombination hotspot	CAGRCAGR	Abeysinghe, Kvikstad
Murine parvovirus recombination hotspot	CTWTTY	Abeysinghe, Kvikstad
Translin target sites	ATGCAG, GCCCWSSW	Abeysinghe, Aoki, Kvikstad
V(D)J Recombination Signals		ADEYSINGNE, ADKI, KVIKSIAA
Heptamer recombination signal	CACAGTG	Abeysinghe, Kvikstad
Nonamer recombination signal	ACAAAAACC	Abeysinghe, Kvikstad
Immunoglobulin heavy chain class switch repeats	GAGCT, GGGCT, GGGGT, TGGGG, TGAGC	Abeysinghe, Kvikstad
minunogiobulin neavy chain class switch repeats		Abeysingile, Kvikstau

Table 3.8. - Motifs previously associated with genomic rearrangement.

Site Name	p-values		
X- and X-like Sites	ALL	INSIDE	OUTSIDE
Chi-sequence	1	1	1
Chi-sequence truncated	1	1	1
Human Fra(X) breakpoint cluster	1	1	1
Human minisatellite conserved sequence/X-like element	1	1	1
Human hypervariable minisatellite core sequence	1	1	8.09E-185
Human hypervariable minisatellite recombination sequence	*	*	*
Deletion, Insertion, and Indel Hotspots			
Deletion hotspot consensus sequence	1	0.25	1
Hamster deletion hotspot	1	1	1
Hamster and human APRT deletion hotspot	1		1
Indel hotspot	1	1	1
Indel Super-hotspot motifs	1	1	1
Insertion hotspots	1	1	1
		-	-
DNA Polymerase Pause or Frameshift Hotspots	-	-	
DNA polymerase α frameshift hotspots	1	1	7.98E-02
DNA polymerase β frameshift hotspots	9.44E-03	2.80E-04	1
DNA polymerase α/β frameshift hotspots	1	1	1
DNA polymerase α pause site core sequence	1	1	1
DNA polymerase arrest site	1	1	1
Eukaryotic Transcriptional Regulation			
AT-rich signal	0.52	2.14E-02	1
Curved DNA signal	0.52	3.85E-02	1
Kinked DNA signal	1	1	1
ORI signal	1	1	1
TG-rich signal	1	1	1
Topoisomerase Cleavage Sites			
Topoisomerase I consensus cleavage site (Vaccinia)	1	1	1
Topoisomerase I consensus cleavage site (vertebrate/plant)	1	1	1
Topoisomerase II consensus cleavage site (Drosophila)	7.43E-280	5.66E-136	1.11E-146
Topoisomerase II consensus cleavage site (vertebrate)	1	0	1
Mobile Elements			
Alu core element	1	1	1
Mariner transposon-like element (3' end)	*	*	*
Recombination Sites			
Autonomously replicated sequence	1	1	1
Chinese hamster scaffold attachment site	1		
			1
Classical meiotic recombination hotspot	1	1	1
Hamster and human APRT deletion hotspot	1	1	1 *
Human hypervariable minisatellite recombination sequence			
Indel Super-hotspot motifs	1	1	1
Meiotic recombination hotspot	1	1	1
Murine LTR recombination hotspot	1	1	5.28E-100
Murine MHC recombination hotspot	1	1	1
Murine parvovirus recombination hotspot	1	1	1
Translin target sites	1	1	1
V(D)J Recombination Signals			
Heptamer recombination signal	1	1	1
Nonamer recombination signal	0	1.79E-274	6.83E-282
Immunoglobulin heavy chain class switch repeats	1	1	1

* motif not observed in literature and random sequences

Table 3.9 – Motifs with literature frequencies significantly different from random.

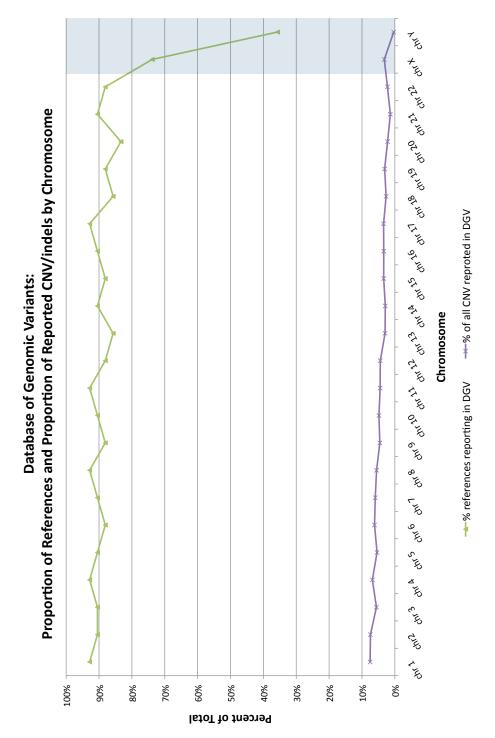


Figure 3.1 - Proportion of References and CNV or indels reported in the DGV.

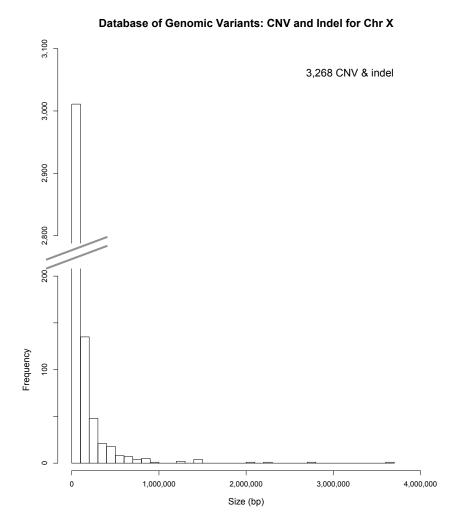


Figure 3.2.a – Size distribution of CNV and Indels from the Database of Genomic Variants.

Conrad (2009): CNV and Indel for all autosomes

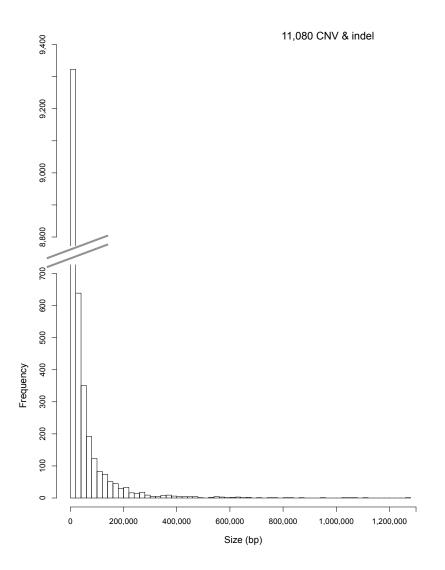


Figure 3.2b – Size distribution of CNV and indels from all autosomes reported by Conrad et al.

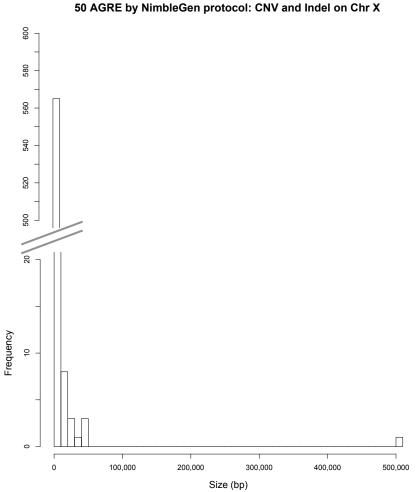


Figure 3.2.c – Size distribution of CNV and indels identified in the AGRE cohort folloing the NimbleGen protocol.

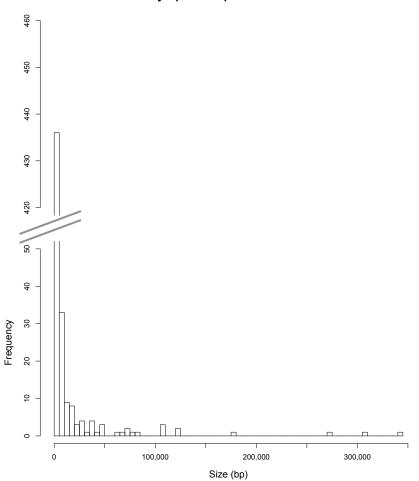


Figure 3.2.d – Size distribution of CNV and indels from the AGRE cohort following the Optimized protocol.

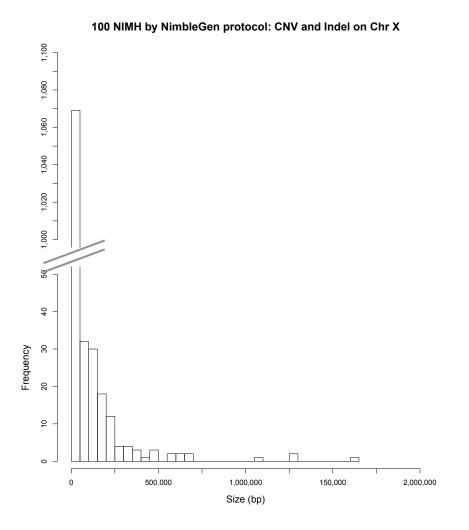


Figure 3.2.e – Size distribution of CNV and indels from the NIMH cohort following the NimbleGen protocol.

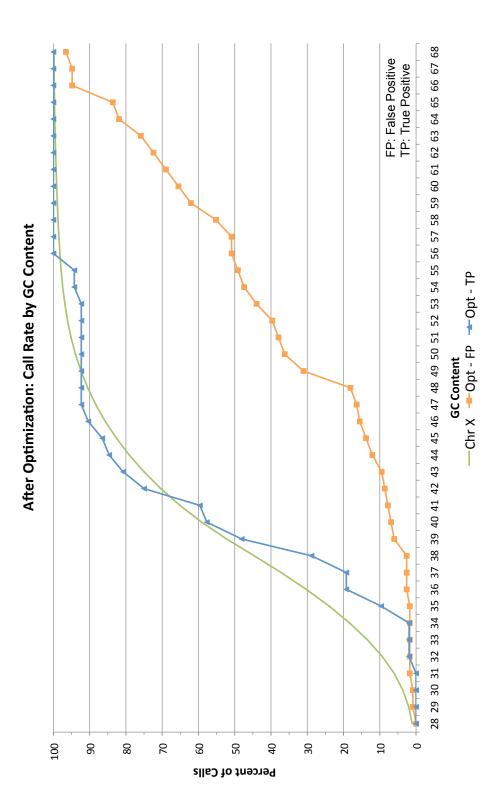


Figure 3.3 - Proportion of true and false calls plotted by GC Content

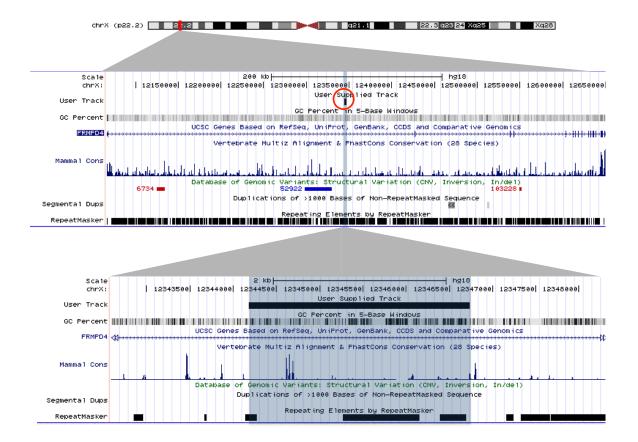


Figure 3.4 – 2.5kb intragenic deletion of FRMPD4.

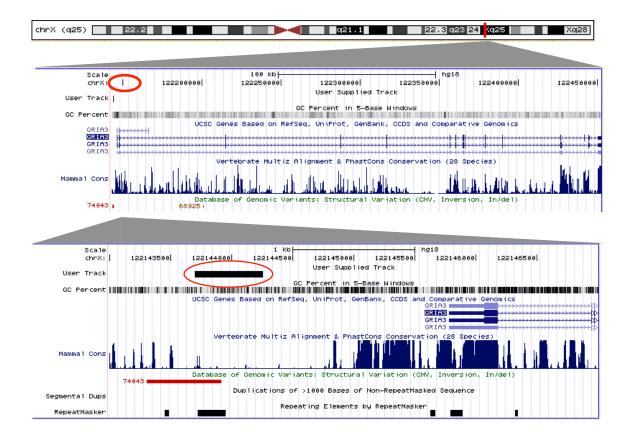


Figure 3.5 – 561 bp deletion 1.5 kb upstream of GRIA3.

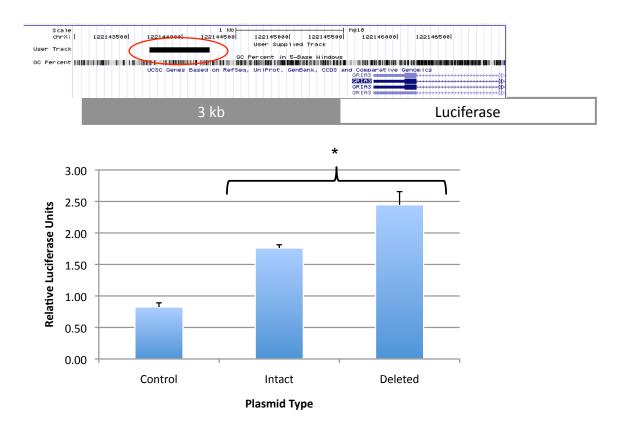


Figure 3.6 – The *GRIA3* promoter deletion has increased activity.

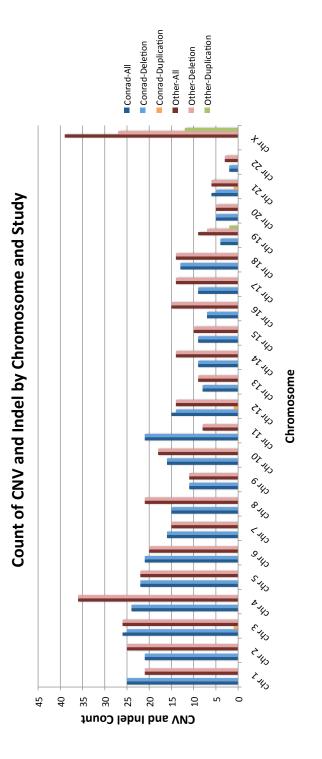


Figure 3.7.a – Literature breakpoint sequence distribution throughout the genome.

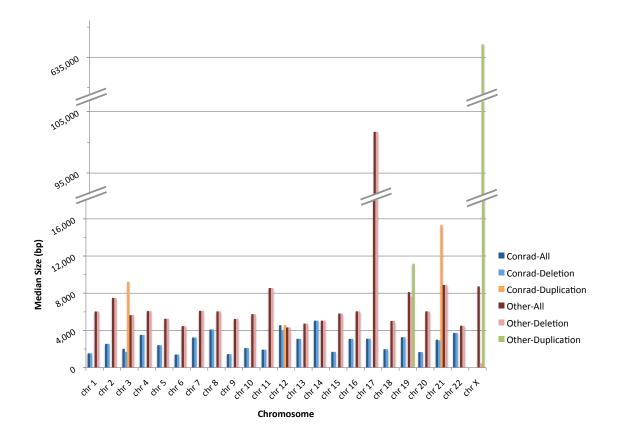
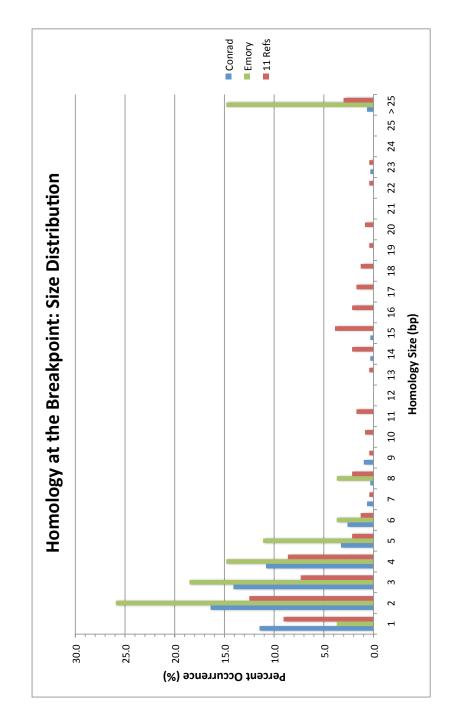


Figure 3.7.b – Median size of literature breakpoint sequence by chromosome.



Figre 3.8.a - Size distribution of homologies at breakpoints.

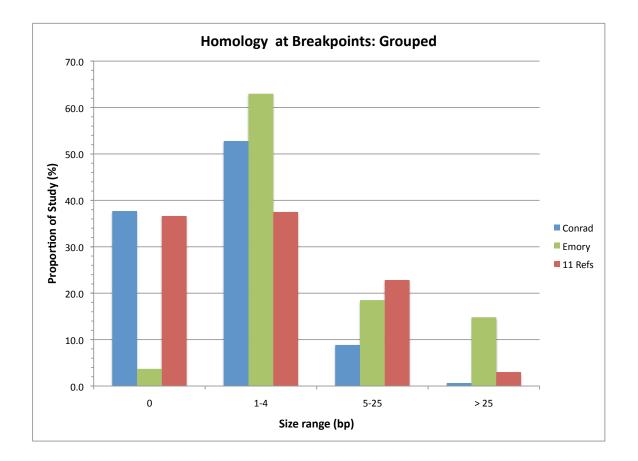


Figure 3.8.b - Grouped size distribution of homologies at breakpoints.

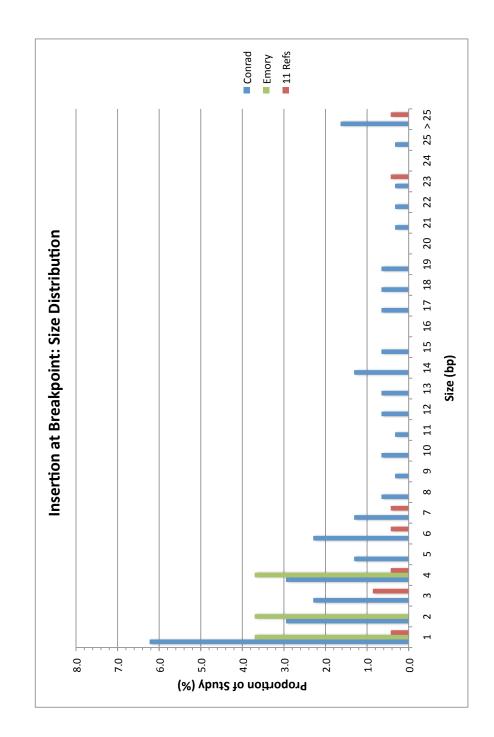
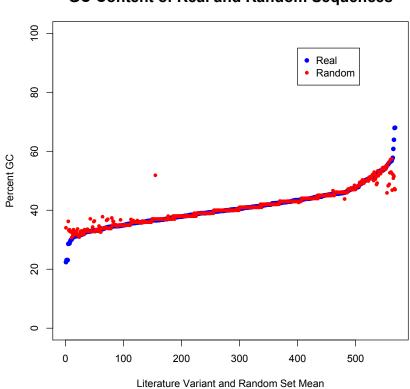


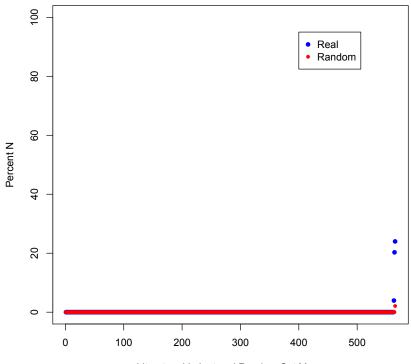
Figure 3.8.c - Size distribution of insertions at breakpoints.



GC Content of Real and Random Sequences

Figure 3.9.a – Average GC content of 1,000 Random Sequences and Real Sequence





Literature Variant and Random Set Mean

Figure 3.9.b – Average N content of 1,000 Random Sequences and Real Sequence.

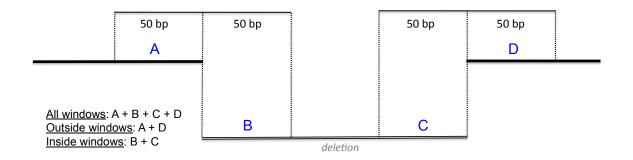


Figure 3.10 – Schematic for breakpoint junction analysis.

Chapter 4. Conclusion

With a prevalence currently estimated as being 1:88 [1], identifying the genetic components underlying the autism spectrum disorders (ASD) would benefit those individuals affected with these disorders as well as their caretakers. While understanding the molecular etiology of ASD can provide incite into unaffected behavior and cognitive functioning, this understanding could also focus the development of future drug and therapeutic strategies in the management of these disorders. A male bias of 4:1 in ASD [2-4] suggests a role for an X-linked susceptibility locus. Furthermore, skewed inactivation in females affected with autism and ASD as well as linkage for sex-specific risk alleles have further implicated the X chromosome.[5-11] These lines of evidence have led us to hypothesize that gene(s) residing on the X chromosome play a causal role in the susceptibility to ASD. To investigate this hypothesis, we developed an experimental strategy to screen copy number variation (CNV) on the X chromosome and assess the role of CNV in these disorders. This chapter discusses the methods and tools that we developed to identify high confidence CNV in autistic and normal cohorts, CNV identification and subsequent validation studies conducted on our findings, and finally conclusions that can be drawn and potential strategies to move forward in the investigation of the genetic underpinnings to autism.

1. The Optimization of array Comparative Genomic Hybridization and CNV Identification

We utilized a custom high density Comparative Genomic Hybridization array (aCGH) dedicated to the X chromosome to interrogate the size and distribution of CNV in our sample populations. During the course of our experiments, we developed a protocol that optimized the quality of the output from these arrays. Our efforts included increasing the fluorescence of labeled sample for greater signal discrimination, increasing the stringency of array hybridization and washing by moving to an automated platform (Tecan HSPro4800), establishing quality control measures of array data (fluorescent Count Ratio limits, MA plot evaluation), removal of unreliable probes, and developing an algorithm for identifying a parsimonious set of array-identified copy number variants (segment filtering). Under the conditions of the new protocol, restricting analysis to CNV with a GC content of less than 56% resulted in a drop from 86.8% of our false calls to 50.9% while still identifying all true calls. A caveat to limiting CNV validation to those CNV less than 56% GC content is reflected in the nature of genes and their elevated GC content. Most of the X chromosome (98%) has a GC content of 56% or less. However, it may be prudent to explore what percentage of genes exist within the remaining 2%. Validation studies require expenditures of effort and resources. However, if the goal is to identify changes in sequence as an underlying cause to disease, it may be warranted to continue efforts of validation for those CNV with a GC content greater than 56% and involving a gene structure.

Additionally, because our PCR based strategy assumes a tandem orientation of duplicated sequence, it is possible that the false call rate is inflated by our inability to confirm non-

tandem duplications. Overall, our optimized protocol reduces the false call rate for deletions from 60% of all deletions to 21% of all deletions irrespective of GC content.

While our false call rate may seem 'high', it is not inconsistent with reports in the literature. [12, 13] Greenway *et al* reported a false call rate of 66% for CNV greater than 20 kilobases (kb). Their validation strategy utilized the multiplex ligation-dependent probe amplification (MLPA), so those duplication events not in tandem would be positively identified.[12] Given our CNV data are much smaller (median size is approximately two kb), we observe a similar false call rate as for larger CNV.

2. Copy Number Variation in Autistic and Normal Populations

In total, four studies of 320 samples on two different aCGH resolutions by two different protocols were conducted. Our autistic populations were derived from the Autism Genetic Resource Exchange (AGRE, multiplex) cohort and the Simons Simplex Collection (SSC, simplex), and our normal DNA came from the National Institute of Mental Health (NIMH) control population ascertained for the Human Genetics Initiative. We used the 385K (385,000 oligonucleotide probes) and the 2.1M (2,100,000 oligonucleotide probes) CGH arrays from Roche NimbleGen, and processed both arrays by the manufacturer's recommended protocol as well as developing an optimized protocol for the 2.1M array.

a. Chromosome X CNV in individuals with autism

We identified 2,300 CNV and developed 146 validation assays. The majority of assays identified a false call (false call: 100 or 68%, true call: 46 or 32%). However, the caveat remains that our validation strategy assumed tandemly duplicated sequence. The possibility remains that a subset of those validation assays that failed to capture a junction fragment from a duplication call may simply be a failure of validation strategy not a failure of the array.

A genotyping assay was developed to characterize the effect of a deletion in identified in two individuals with autism on the immediate downstream gene, *GRIA3*, the gene identified as causing X-linked Mental Retardation (OMIM: 305915, MRX94).[14] While an increase due to loss of sequence was observed, genotyping in an expanded population with autism (n=364) and a normal population (1,799) revealed enrichment for this deletion in the population with autism at a statistically non-significant frequency (p < 0.5531).

Two validated loci remain compelling for further follow-up studies. First, familial and case and control genotyping for a 2.5 kb intronic deletion of the *FERM and PDZ domain containing* 4 gene (*FRMPD4*) remains to be conducted. This gene is highly compelling as a candidate gene due its regulatory function of excitatory synaptic transmission and its demonstrated interaction with postsynaptic density protein, PSD95. Secondly, a *de novo* deletion (AU016.3) about 175 kb downstream of *gastrin-releasing peptide receptor* (*GRPR*) has been identified. *GRPR* has been found to be disrupted in an individual with autism. While this CNV does not overlap with any gene structure its proximity to *GRPR*

and loss of sequence could effect expression. Again, genotyping of this variant locus in families and cases and controls remains to be conducted.

The remainder of our validated set of copy number changes is not immediately suggestive of a role in ASD. However, further research remains that might indeed unveil one or more of the variants identified as a susceptibility locus. Assessment of genotype frequency in both ASD and normal populations would help to prioritize variants for further characterization. Notably, those variants found to be enriched in the population of males with ASD over that of controls may loci involved with the manifestation of ASD.

While further validation and molecular study of our CNV data remains, we can conclude a few points from the data set that we have. Before discussing the specifics of our data, we wish to clarify our understanding and confidence in the larger CNV identified in our data set. Our experience is based on X chromosome CNV studies of two individuals manifesting developmental delay that were consistent with loss or disruption of the *fragile X mental retardation* 1 gene (*FMR1*), the gene underlying Fragile X Syndrome, the most common form of inherited intellectual disability. The first study was of a patient known to have a partial deletion of the *FMR1* gene.[15] This deletion began upstream of the first coding exon and ended before the eighth exon in *FMR1*. The breakpoints had not yet been determined, and this sample served as an ideal positive control for our CGH studies. We successfully identified the deletion boundaries by the 385K CGH array, and breakpoint sequencing determined the full size and location of the deletion (chrX: 146,703,942 - 146,820,448 (Hg18); 116,506 bp). The second study arose from Brad

Coffee's suspicion of a mosaic deletion involving *FMR1*.[16] Using the 2.1M CGH arrays, we identified a 1,013,394 bp deletion that extended from chrX: 147,047,696 - 146,047,696 (Hg18) and included the *FMR1* gene as well as the next downstream gene, *FMR1NB*. We use these two studies of CNV on the X chromosome as a measure of our ability to accurately identify CNV greater 100 kb in size. To further support this confidence threshold, we did identify and validate a 350 kb duplication in an AGRE sample. First pass breakpoint sequencing suggests this duplication event is 345,617 bp in size.

One of the first conclusions we can make from our data is regarding our large CNV. From the CNV data collected from the 164 AGRE and SSC samples, we identified but did not validate three deletions and six duplications greater than 100 kb in size. We believe that these CNV are real and that all variants larger than 100kb in size from all samples successfully screened were identified. We point out several significant observations in relation to testing our original hypothesis. While the large duplication and deletion variants (greater than 100kb) are likely to be real, we did not develop a genotyping assay for these CNV. Thus, we were unable to compare the frequency data for such structural changes among males with ASD and those of normal controls (NIMH neuropsychiatric control samples and unaffected fathers of our autistic cohorts). Due to their size, it is not unreasonable to hypothesize that these structural disruptions (three deletions, six duplications) may contribute to ASD in many ways including but not restricted to altering expression of dosage sensitive genes, altering usage of enhancer or

repressor loci, abrogating or creating species specific loci integral to gene and/or genomic function in cell processes (e.g., Matrix Assembly Regions).[17]

The largest variant identified was a 344 kb, and we can say with high confidence that there were no additional variants as large or larger within our data set. This suggests that large(r) structural changes on the X chromosome do not play a role in males with ASD. In retrospect, this may not be so surprising as one might expect that such changes in a hemizygous context (46, XY) may result in a more extreme phenotype than ASD and thus not be observed in the AGRE or SSC sample set.

A second point of discussion of our data is regarding the other end of the spectrum: the small CNV that comprise the majority of our data set. It is well known that oligonucleotide CGH arrays exhibit 'noisier' log2 values than their BAC-based predecessors and require more probes per variant to make a reliable call.[18-21] As described earlier, the 'streaking' sometimes generated by the optimized protocol likely contributed to more log2-based noise in our data as well. These two factors likely contributed to the high number of calls in the five kb and under range (84% of all calls). Unlike the variants greater than 100kb, we have less confidence in calls of this size.

However, we also found that the GC content of a given variant is a strong indicator for whether an aCGH identified CNV is likely a false or true positive call. Following either NimbleGen's protocol or our own optimized protocol, we found that all true positive calls made thus far had a GC content of 56% or less. While the optimized protocol did improve our overall ability to identify true variants under this threshold, over half of all calls with a GC content less than 56% are still likely to be false positives (i.e., at GC cutoff of 56%: 59 false calls, 52 true calls). However, a GC cutoff of 56% also captures nearly the entirety of the X chromosome (98%). A more stringent percent GC cutoff, 48%, may be warranted. This threshold shifts our true to false call proportion to 21 false calls and 48 true calls while capturing 91% of chromosome X.

With these caveats in mind, 265 CNV less than five kb in size remain to be validated from the AGRE and SSC study, and 121 (46%) of these have a GC content less than or equal to 56%. While there exists a less than random chance that these variants will validate, the possibility still remains that CNV at any or all of these loci may play a role in autism susceptibility. Additionally, three of the 20 genes, *GABRQ, SYP*, and *ZNF4*, overlap with this data set are from our original list of candidates.

Finally, our breakpoint junction analysis suggests that fewer motifs play a role in resolving structural events then previously implicated. We tested 565 breakpoints for an enrichment of 39 motifs previously identified as associating with structural breaks. The eight motifs were found to be enriched in these breaks as compared to a randomly generated data set (Human hypervariable minisatellite core sequence, DNA polymerase α frameshift hotspots, DNA polymerase β frameshift hotspots, AT-rich signal, Curved DNA signal, Topoisomerase II consensus cleavage site (Drosophila), Murine LTR recombination hotspot, Nonamer recombination signal). We expected to identify more motifs associated with the breakpoints as the 39 motifs selected had been previously

implicated in playing a role in resolving structural events. However, after multiple test correction, only these eight continued to remain significant. While it is possible other motifs are also involved in the breakpoint resolution of sequence gains and losses, these appear to play a more prominent role.

b. CNV identification in 102 normal males

Using the X-chromosome 2.1M CGH array and following NimbleGen's protocol, we were able to collect data from 101 of 102 individuals. We identified 1,231 CNV covering (12.2 CNV/person) with a median CNV size of 2,015 bp.

While it is difficult to discern much from the NIMH data without having validated any of these loci, there are a few conclusions that can be drawn. First, the size distribution of CNV identified within the NIMH population is consistent with those reported in the literature (and curated and stored in Database of Genomic Variants (DGV)), as well as the distribution observed in the AGRE samples processed by the NimbleGen. Both the NIMH cohort and the 50 AGRE samples by this method demonstrated a CNV rate of 12.2 and 12.1 CNV/person respectively. The median sizes for both sets were somewhat similar with the NIMH median size of 2, 015 bp and the AGRE median size of 1,080 bp. The NIMH samples had slightly larger median sizes but distributions were quite similar to both the AGRE samples as well as those in the DGV.[22]

Secondly, the NIMH data show a marked increase of duplication events over deletion events as compared to the prior studies in our AGRE cohort by both NimbleGen's protocol and the optimized protocol. Following NimbleGen's protocol, the deletion:duplication ratio has shifted from 1.88 in the AGRE samples (2.1M, NimbleGen) to 0.53 in the NIMH samples (2.1M, NimbleGen). This 3.5 fold change may be a function of biology in that the AGRE samples manifest more deletion events than the NIMH samples, it may be a function of sample source in how cell lines were maintained and DNA extracted, or, this shift may be due to the change in chemistry of array synthesis and processing reagents. While it is not unreasonable to suggest that the genome is more tolerant to increases in copy number rather than loss of sequence, reports in the literature are conflicting over the observed deletion:duplication rates. [23-26] Validation studies of the NIMH CNV data set would greatly increase our understanding of the reliability of CNV called by the NimbleGen protocol. These variants may similarly show stratification of true and false call rates by GC content. This metric would then help in the interpretation of those loci that remain unvalidated, and a more accurate biological understanding of CNV in this sample population might be determined.

3. Why might we have not found loci involved with ASD?

a. The technological limitations of array CGH

Array Comparative Genomic Hybridization (aCGH) has been used with success in multiple studies, on different manufactured platforms, interrogating different regions of the genome, and using different sources of DNA. It thus seemed reasonable to use the X chromosome as our target region of interest to interrogate our cell line derived DNAs from the AGRE and Simons cohorts.

In 2006, NimbleGen, now Roche NimbleGen, developed a novel method in which oligomer probes were synthesized by a photo-mediated chemistry on a glass substrate. This mask-less approach allowed for the dynamic building and synthesis of an array in a more cost-effective fashion. Any oligonucleotide-based array could be synthesized by this method, including arrays for Comparative Genomic Hybridization. As my thesis involved the identification of structural changes on the X chromosome, we chose to use NimbleGen's cost effective and flexible array platform for this purpose. NimbleGen agreed to train me in every step of their aCGH protocol at their labs in Madison, WI. My training started from the first step of assessing sample integrity and proceeded through to array analysis of copy number variation. As our relationship and commitment to the NimbleGen CGH technology progressed, we were also permitted early access to their new custom High Density arrays in which 2.1 million probes could be designed for any region(s) of interest. We shifted my fine scale exploration of X chromosome structural changes to an even finer resolution when we moved our platform design from the 385,000 probes of the 385K platform to the 2.1 million probes dedicated to the X chromosome.

Early validation efforts of our custom 2.1M CGH arrays indicated a high false positive rate (65%) that spurred us on to explore methods by which we could reduce this rate and increase the integrity of calls made by this platform. During the course of our own experimentation with NimbelGen's aCGH protocol, NimbleGen was conducting optimization efforts as well. Within several years time, we observed a shift in array behavior as compared to the earlier arrays we had been using. Specifically, when we

applied the same optimized protocol that we had previously developed to arrays manufactured at a later date (a year or more), we found that the 'newer' arrays underperformed (i.e., overall reduced signal across arrays, reduced call rates, increase in noise) as compared to those on which we had conducted our earlier optimization experiments. Discussions with NimbleGen technical and marketing representatives revealed that they had indeed modified the array synthesis chemistries.

Concurrent with our optimization work, we also observed several revisions of NimbleGen's recommended sample processing protocol. While the newer protocol versions were more streamlined and user friendly, they were also less transparent. NimbleGen may have been using the same chemical component and ratios as in earlier versions, but it was not clear whether the noticeable change in array response was wholly due to the improved array synthesis chemistry, to any changes in the sample processing reagents, or a combination of both.

Our final study of 102 individuals from the NIMH control population used the latest 2.1M CGH arrays and was conducted using the latest reagent formulas following NimbleGen's protocol. As discussed previously, we identified 1,231 variants with a median size of 2,104 bp in size. While some of these variants may validate, we anticipate a great many more are falsely called based on the number and size of variants identified in this population. While these data have not been validated, given our experience with this platform, we are inclined to believe that NimbleGen's improvements to array

manufacture and sample processing have not minimized the false call rates we had previously observed.

One of our first efforts to increase array performance was to evaluate kinetics of the probes on the custom arrays. Using the log2 values as a marker for probe behavior, we identified a small subset of probes on the HD arrays as having an abnormally high variance. Specifically, 5% of all experimental probes on the array showed a variance greater than 0.175 across 50 arrays. While we were able to empirically determine that this subset of probes was likely contributing noise and not signal to our analysis, it is possible that the overall probe selection algorithm utilized by NimbleGen needed further optimization. Perhaps, with less reliance on NimbleGen and increased effort on our part to evaluate probes before array synthesis, we may have been able to develop a set of probes that were better adapted to the unique characteristics of the X chromosome (e.g., overall repeat content, GC rich regions).

In the application of aCGH, oligonucleotide arrays are known to be much noisier than BAC arrays. [18-20] While oligomer based arrays can interrogate regions on a much finer scale than BAC-based arrays, more probes (typically, 10-20 oligonucleotide probes or more versus 1-3 BAC probes) are required to call variants with statistical confidence.[27] Additionally, it is possible that aCGH tiling arrays such as our high-density arrays, irrespective of manufacturer (ex: Agilent, Illumina, Roche NimbleGen), are inherently more noisy (i.e., increased standard deviation of log2 values across all probes) than their reduced coverage predecessors. As probe density increases so does overall 'noise' of the experiment. While it has been noted that genome wide aCGH evaluation has been used with great success, variants identified in such studies were orders of magnitude larger (e.g., 50 kb - 200kb) than the bulk of those loci identified as variant by our custom arrays (less than five kb). Simply said: larger variants were called more often with greater success. A recent study by Sanders *et al* explored *de novo* CNV in autism utilizing two Illumina arrays to assess copy number. In initial attempts to determine their 'de novo prediction thresholds', they found a 47% false call rate for variants identified with 20 or more probes or an average size of 60 kb or greater. A majority (82%) of the failures were false positive. The authors compared their data set where it overlapped with another study that had utilized NimbleGen's 2.1 million arrays for genome wide CNV detection (42 million probes) to validate their findings. Again, a minimum criterion of 20 probes or 60 kb on average was used, and 55/58 (95%) rare, de novo CNV were identified by both platforms. However, analysis of rare, de novo CNV less than 20 probes was not nearly as positive for the 31 CNV called between both studies. Only 4/31 (13%) CNV were identified by both platforms. These data suggest that our efforts to identify fine-scale structural variation, or variants less than even 25 kb in size, would have been plagued with multiple false calls no matter the platform or rigor used.

It appears that aCGH is a promising tool and has been advanced to the level of whole genome analysis with perhaps reliable performance limited to structural variants greater than 60 kb. However, for the purposes of screening a genome for variants smaller than this, alternative technologies such as those offered by next-generation sequencing (NGS) platforms may be the more suitable alternative. Technically, NGS can capture breakpoint or junction sequence, however, mining for those junction sequences captured by the experiment is highly challenging. However, a few recent studies report successful application and identification of breakpoints ranging from large chromosomal breaks to smaller CNV. [28-30] For the purposes of furthering our own work, a NGS platform could be harnessed to identify the sequence breaks of structural changes. Re-evaluating the X chromosome of our sample population could identify insertion/deletion events (less than one kb), nucleotide substitution, inversion events, as well as the structural changes that we had hoped to identify comprehensively. Furthermore, NGS is capable of identifying sequence changes from one base to megabases encompassing the detection range of both BAC- and oligonucleotide-based arrays.

b. Consistency of sample phenotyping in autism

Despite the technical logistics that went into evaluating fine-scale structural variation on the X chromosome, our net findings left few if any compelling loci as being possibly involved with ASD. Our initial hypothesis leading to the screening of chromosome X specifically was based on compelling evidence for such X-linked loci. Further, such loci were hypothesized to confer a highly penetrant contribution to disease. It is possible that the samples used were themselves not appropriate for this type of experimental hypothesis and strategy.

Our sample selection strategy encompassed the entirety of the AGRE collection, and selection was made in a step-wise fashion to select for the most severely affected individuals (e.g., families containing only affected males, transmitted through females in

extended pedigrees, and, diagnosed with ASD by both ADI-R and ADOS). The majority of the pedigrees selected were nuclear in structure. Additionally, extensive prenatal and familial histories were collected. Chromosomal analysis and molecular testing for Fragile X Syndrome were conducted to exclude those pedigrees having individuals with an identifiable chromosomal or molecular alteration that would explain the observed ASD traits. The AGRE collection is primarily comprised of multiplex families and represented the largest portion of our sample population (100/164 samples assessed by the chromosome X CGH arrays with an additional 200 samples for genotype frequency studies); all samples were obtained from unrelated individuals. The multiplex nature of this cohort allowed us to select for pedigrees likely segregating a disease locus on the X chromosome.

For any genetic study, phenotyping of the affected individual(s) as well as their family members is a critical aspect of pedigree selection. As in our two sample populations, AGRE and SSC, we chose those affected individuals identified as autistic, excluding those with "Broad Spectrum" or "Not Quite Autism". We speculated that individuals with a more mild presentation such as Broad Spectrum may have an underlying genetic lesion that is a more subtle change compared with the deletions or duplications for which we were screening. For example, a mis-sense mutation that leaves a gene product intact but with diminished functionality might explain the more modest phenotype. We also excluded families in which notes suggesting autistic-like phenotypes were present in 'unaffected' members as some of these may represent families segregating for autosomal genes instead of X-linked ones. However, we also observed some inconsistencies in the phenotyping of affected individuals. An example comes from the AGRE pedigree AU0983. In this family, the three boys are scored as having 'Autism'. One of the siblings (not the proband we used for our studies) was listed as 'not Spectrum or Autism' in the ADOS category. We understand the 'score' to be derived from the ADI-R test. The other two brothers are listed as having 'Autism' both by score and by ADOS. This is simply an example of an inconsistency that, while not frequent, suggests that phenotyping of individuals for autism is not nearly as straightforward a process one might suspect.

In effort to find a genetic basis for disease, the researcher must first depend on the phenotyping capabilities of clinicians and counselors in the collection of the diseased sample population. The goal is to identify a locus that has been disrupted in some form and shared among individuals with a common disorder. Depending on search strategy, that susceptibility locus is shared more often among cases than controls or segregates with disease within families. This search is based on the assumption that the underlying genetic lesion is responsible for the phenotype observed. However, if a patient's phenotype differs from clinician to clinician, then the underlying genetic contribution to that individual's particular traits might be different than that of another patient having the same diagnosis.

This scenario is not all that unlikely. Our study samples were derived from the AGRE and SSC collections of families affected with ASD. Affected individuals are evaluated by what are currently considered the gold standards for ASD diagnosis, the Autism Diagnostic Interview, Revised (ADI-R) and/or the Autism Diagnostic Observation Schedule (ADOS). [31, 32] Cathy Lord developed both of these autism diagnostic metrics. Earlier this year, Lord reported ASD diagnostic variability across 12 different sites despite clinical training and correct implementation of ADI-R and ADOS. Specifically, children that met both ADI-R and ADOS criteria for ASD did not share the same final diagnostic conclusions. [33]

A second possibility for our failure to clearly identify autism susceptibility loci was that our sample size was not sufficiently powered to identify a locus/loci that may contribute to disease. Because we initially studied multiplex families, we presumed that we would find inherited structural changes within one pedigree and that might be found with some repeat occurrence in others. While such a CNV event could be rare and private to a single family, the locus implicated might be disrupted in additional, different forms (other CNV throughout the gene body, coding sequence changes, or aberrant methylation) in other families affected with ASD. We could then use a normal population to compare genotype frequencies (ASD versus control). For a CNV mediating autistic traits, we might find two possible outcomes to CNV genotyping. First, we might find that a CNV occurs rarely or only in our population with ASD. Or secondly, we might find enrichment or increased frequency of occurrence of the given genotype in our ASD. For example, using our sample of 300 males with ASD and 1,800 controls (1,500 NIMH controls as well as 300 fathers), assuming a minimum frequency of 2% in our control population and 80% power, we would need to observe a frequency of 5.2% or more in our case population in

order to claim a statistically significant difference at a level of 0.05. The minimum frequency observed for our ASD population stays about the same whether we include the fathers as controls or not (5.3% minimum). However, a 5% frequency is quite high and suggests a relatively common genetic change. While a locus may play a role in disease, it does not necessarily have to share the same mechanism of mutation. Our genotyping is based on a copy number change for a given locus, but a gene may be disrupted by changes in coding sequence as well as by other modifiers (e.g., sequence based - enhancers, repressors, post-synthesis alterations - methylation). But, by simply assaying for copy number change, in our study we are requiring that more affected individuals carry the same mutation in order to say with statistical certainty that a given locus is involved with ASD.

An increase in our sample size would benefit our study design on a few different levels. First, the power due to genetic heterogeneity introduced by phenotypic inconsistencies might be minimized, as the greater the pool of individuals studied, the greater the chance of selecting individuals who share the same susceptibility locus. Secondly, an increase of the sample size of males with ASD would increase the power to detect a difference in frequency of an observed structural change in our case/control comparisons. For example, to detect a 1% increase (i.e., a 3% frequency in our ASD sample) as statistically significant over a normal population frequency of 2% with 80% power, we would need 4,000 unrelated males with ASD as well as controls.

4. Alternative hypotheses that may explain our findings

A possible explanation for our lack of identified causal variants might lie in alternative explanations to the assumptions of the underlying genetic lesion(s). We hypothesized that a locus/loci resides on the X chromosome and defects in this locus/loci strongly contribute to ASD in individual carriers as well as the male bias in these disorders. While our hypothesis is based on empirically determined findings, it also presumes that a single locus largely contributes to ASD in the patient (monogenic), is highly penetrant, and is homogenous in its expressivity of the lesion(s). These assumptions are not unreasonable given that the X chromosome was selected to exist in a hemizygous state in our sample set (i.e., no Klinefelter's Syndrome or other sex chromosome anomalies were identified in our study population), and structural lesions on this chromosome would likely confer a more severe molecular and thus phenotypic response.

a. Our cohorts are comprised of a genetically heterogeneous population

We built our experimental design on the assumption that, in at least a subset of our cases, we could identify a highly penetrant, monogenic locus on the X chromosome that had been structurally altered and might therefore molecularly explain ASD. However, we also anticipated more than one locus was likely to play a role in ASD given how genetically heterogeneous ASD has already been demonstrated as being. With as much as 30% of all ASD bearing a known molecular etiology representing a minimum of 44 different genomic loci and 103 different genes, initially, we may have been able to predict or gauge how many loci we might reasonably expect to find on the X chromosome in a given sample size. [34-38]

b. Observed CNV may have reduced penetrance in a normal population

As the body of literature on structural changes in ASD grows, reduced penetrance of structural lesions has been used to explain observed deletion and/or duplication events that occur in both normal and affected populations. Under the model of a reduced penetrant genetic lesion, a structural change identified in an ASD cohort has an enriched frequency of occurrence as compared to the frequency of occurrence in a normal or phenotypically non-ASD control group. Additionally, this change can also be inherited from non-affected parents. One example of such a locus is 16p11 where recurrent microdeletions and microduplications have been identified and implicated as causal in ASD. Since its first identification in 2007, multiple studies of ASD cohorts have found structural changes at this locus to be significantly enriched in cases over controls.[38-42] However, Glessner *et al* found structural variants at this locus to be equally frequent in their ASDcases and controls. [43] While the findings of Glessner et al are valid, as in all studies, frequencies are based on the respective patient and control populations studied. The accumulating reports of structural changes at 16p11 enriched in ASD populations suggest a legitimate role for 16p11 gene(s) in ASD disorder.

If we were to relax our requirement for 'highly penetrant' genetic lesions, several variants identified in our AGRE and SSC studies would now be eligible for further examination. For example, we identified three duplications that overlapped the *synaptophysin (SYP)* gene, but we did not validate because they overlapped with other reported structural changes identified among those with different phenotypes. *SYP* encodes a membrane protein that localizes to small synaptic vesicles in brain and endocrine cells and has been

identified as the gene responsible in X-linked Mental Retardation (OMIM: 300802, MRX96) in four different pedigrees.[14] Currently, a 43kb and a 42kb inversion fully encompass *SYP* and as well as upstream neighboring genes and a 1.3 Mb deletion that includes *SYP* as well as *FTSJ1* (OMIM: 309549, MRX9 and/or MRX44) have been identified in normal populations. While an inversion event might change the genomic context in which a gene lies (*i.e.*, change expression pattern due to altered exposure to local enhancers and repressors), the deletion event might be considered more severe, especially in that it was identified in a supposedly normal male. No karyotypic information was made available for this individual, so this male could possibly be XXY. However the study utilized aCGH arrays with a female reference, and an increased X chromosome dosage should have been readily seen and presumably reported by the authors. Given that two X-linked Mental Retardation genes are encompassed in the deletion, it might not be unreasonable to either suspect this deletion call as a false positive or, at the least, a reduced penetrant lesion.

Our duplications are novel in that they directly involve the *SYP* gene. The three duplications overlap significantly and involve a substantial portion of the 3'UTR on one isoform and the last intron (intron 6) of the second isoform. (Figure 4.1) One could hypothesize that if these duplications validated, they may also introduce a subtle change to the function and expression of this gene product in our males with ASD distinct from that of a complete loss or complete inversion of this locus.

c. CNV identified in our cohorts may require additionally altered loci for a manifestation of autism

Finally, perhaps our assumption of a singe susceptibility locus on the X chromosome needs to be expanded to allow for the broader, multigenic model for ASD etiology.[44-51] Under an oligogenic model, a disruption of a single ASD susceptibility locus on the X chromosome may be required but additional genetic liabilities elsewhere in the genome are necessary for phenotypic expression of ASD. Within the context of a multiplex family, both parents would carry susceptibility alleles that result in ASD when they coexist in a single individual. While a similar genetic set-up may exist in a simplex family, it may be more likely that one parent may carry such a susceptibility allele, and a secondmutation at another critical locus is required for manifestation of autism. Considering a multigenic model, those CNV that do not segregate with autism in our multiplex (or even simplex) families may still play a role in these disorders as the required '2nd hit' is elsewhere in the genome.

d. Partial inactivation of X chromosome loci can act as susceptibility loci to ASD in males.

Skuse et al suggest that there exists on the X chromosome an imprinted locus. When inherited from mothers, women with Turner Syndrome (45, X) display an impaired social and cognitive phenotype distinct from women with TS who inherit their father's chromosome X. Such a locus or loci would inherently cause males to be more susceptible to these social and cognitive phenotypes as males are hemizygous for the X chromosome.[52, 53] Because all males inherit the maternal X chromosome, this fact may place males at an inherently higher risk than females for the ASD. Should a susceptibility locus of the inherited X be inactivated, this might result in an autistic phenotype. The mechanism of mutation is mediated by methylation-based gene silencing. Altered methylation regulation has already been described in a subset of females with autism (OMIM: 300496, autism susceptibility). [14, 54] The alterations and loss of the *methyl-CpG-Binding protein, MECP2* gene are know to cause Rett Syndrome, a regressive form of autism (OMIM: 312750, Rett Syndrome). [14]

5. Final Summary

In conclusion, we found no evidence to support our hypothesis that there are large structural variants on the X chromosome that are highly penetrant and have a causal role in ASD. However, we may very well have found susceptibility loci, but we are currently unable to discern a role for those loci due to difficulty validating CNV, as well as possibly being underpowered to identify susceptibility loci due to genetic heterogeneity and to the rarity of the variant. Additionally, we may not have sufficient molecular understanding of cellular processes to appreciate a role for a given locus and ASD, so a rare CNV found only once in our data set may indeed be causal in ASD. There may be human specific regulatory regions unidentified by conservation that are critical for 'normal' social and behavioral development (e.g., microRNAs, enhancers, repressor).

Despite what CNV we have and have not found, CNV remain to be further interrogated for validity and possibly functional involvement in ASD. Additionally, broadening our genotyping efforts to include all pedigrees from the AGRE (861 multiplex pedigrees) and SSC cohorts would increase our power to detect an autistic locus that has reduced penetrance. Incorporating sequencing for coding changes of these loci would add to our power to identify a new X-linked autistic locus. While our hypothesis remains valid, it may be that search for a CNV based mechanism may not be the best mutational mechanism by which to capture new ASD loci. Identification of such loci may require a more subtle change such decreased or increased expression as those mediated by methylation changes or even subtle coding changes that do not abrogate but change gene product function.

6. References

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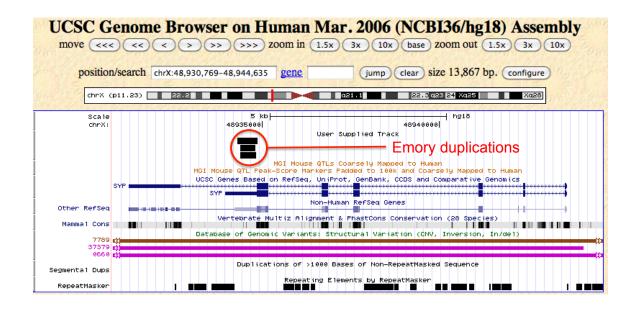


Figure 4.1 – Three duplication calls map to the *SYP* (X-linked Mental Retardation gene) gene.

Bars near bottom of image: Pink - inversion, brown - deletion

Chapter 5. Subjects, Materials, and Methods

1. Sample DNA

a. Autism Genetic Resource Exchange (AGRE)

The Autism Genetic Resource Exchange (AGRE, familyagre.org or research.agre.org) is the product of the Autism Speaks scientific initiative, and houses an extensive collection of biomaterials to be used for the study of autism spectrum disorder (ASD). At the time we began our study, 949 families had been enrolled in their collection. AGRE consists principally of multiplex families where affected individuals have been evaluated by one or both of the current gold-standards for autistic diagnostic evaluation: the autism Diagnostic Interview, Revised (ADI-R) and/or the Autism Diagnostic Observation Schedule (ADOS) prior to enrollment.[1, 2] Extensive medical histories are collected extending as far back as the conception and gestation of affected individuals. The racial content of pedigrees we selected for CNV analysis is largely composed of families selfidentified as white, not Hispanic or Latino (60%), 20% as white Hispanic or Latino, and the remaining 20% were listed as either Asian, African American, more than one race, or unknown. We analyzed 300 pedigrees (300 probands, 300 fathers, and an assortment of full families) from this collection.

DNA used in our studies was derived from immortalized cell lines.

b. Simons Simplex Collection (SSC)

Our second cohort of individuals with autism is derived from the Simons Simplex Collection (SSC, sfari.org). The SSC houses biomaterials, phenotypic and clinical data for families having only one child affected with ASD (simplex). Affected individuals are evaluated by ADI-R and/or ADOS, and extensive family histories are taken. The ethnic breakdown is similar to our first cohort in that a majority of samples are white, not Hispanic (67%). The remaining twenty-one samples are a diverse representation of African-American, Asian, more than one race, Native American, white Hispanic and unknown ethnicities. We analyzed 64 samples from this collection.

DNA used in our studies was derived from immortalized cell lines.

c. National Institute of Mental Health (NIMH) control population

This cohort of Caucasian individuals was identified and collected by the National Institute of Mental Health (NIMH) as part of a Human Genetics Initiative. (nimhgenetics.org/available_data/controls/) The aim of this program was to create a large biological resource of biomaterials and clinical data from individuals affected with severe neuropsychiatric disorders (e.g., autism, schizophrenia, and bipolar are among the disorders being targeted as part of this collection). In addition, a control set for this program was collected for case and control studies. 3,828 individuals are in this group, and they are derived from cord and venous blood. A normal phenotype was determined from an "online, short self-report clinical assessment". We selected 1,500 males over the age of 18 to be used for our studies.

We used DNA housed by this collection.

d. Array Comparative Genomic Hybridization (aCGH) Reference DNA: NA10851 We used the male CEPH sample NA10851 from the Human Genetic Cell Repository at the Coriell Institute (<u>www.coriell.org</u>) for our sex-matched reference in our array comparative genomic hybridization (aCGH) studies. We chose to use a sex-matched reference as this strategy has been previously found to result in a better signal to noise ratio, greater dynamic range of log2 values, and repeat sequences are more grossly matched.[3] This male has been recommended for copy number studies in effort to enable comparison of findings across studies. [4] Additionally, this DNA was used as a 'normal' control for our PCR-based validation studies. It is often annotated as 'NA' in the PCR protocols.

DNA from this individual is derived from a B-Lymphocyte cell line.

e. Validation control DNA

J1 and CM108 are two male DNAs that we used as additional controls for our validation experiments. CM108 may be referred to as 'CM' in our PCR protocols. These DNAs are housed in the Warren Cell Line collection, and DNA was derived from lymphoblasts.

2. AGRE Pedigree Selection

We selected families in a step-wise fashion in effort to identify those families likely segregating an X-linked lesion. Each step or filter removes families because of a single criterion.

<u>Start</u>: All pedigrees in collection (n=949) <u>Filter 1</u>: Remove simplex families (n=861) <u>Filter 2</u>: Remove families with at least one affected female (n=520) <u>Filter 3</u>: Remove families with possible non-idiopathic diagnosis or chromosomal anomalies (n=493) <u>Filter 4</u>: Remove affected individuals prematurely born + other notes (e.g., family reports autism/spectrum diagnosis of father/daughter) (n = 471) <u>Filter 5</u>: Remove families with no parental DNA (n = 418) <u>Filter 6</u>: Select families with \geq two affecteds with first diagnosis by ADOS then ADI-R of 'Autism' or 'Spectrum' (n = 375) <u>Filter 7</u>: Remove remaining families with clinically relevant notes; Remove if pedigree extends through male (i.e., brother-sister have affected children, 9 such pedigrees) (n = 359)

3. Database of Genomic Variants: CNV and indel analysis

Chapter 1. Figure 1A and Figure 1B.

Chapter 3. Figure 1.

We evaluated the Database of Genomic Variants (DGV, projects.tcag.ca/variation, build Hg18) by the number of references reporting in the DGV and the number of copy number variants (CNV, sequence having different copy number, greater than one kilobase (kb), benign or pathogenic) and indels (sequence having different copy number, 100 base pairs (bp) to one kb in size, benign or pathogenic) reported. In total, 42 different reports from the literature have contributed varying amounts of data to the DGV. All reports are assumed to be benign but validation and curation of reported variants is incomplete. There is overlap among sample populations, and various methodologies (e.g., BAC-based, SNP-based, aCGH, paired-end sequencing) were used to identify variants.

First, we categorized CNV and indels by chromosome and originating reference. Using this data, we were able to identify the percentage of references reporting CNV by chromosome ('green' line in Chapter 1, Figure 1A and Chapter 3, Figure 1). Second, we determined what percentage of all CNV and indel reported in DGV were found for each chromosome ('purple' line in Chapter 1, Figure 1A and 1B and Chapter 3, Figure 1).

4. Comparative Genomic Hybridization (CGH) Arrays

We utilized a two custom designed high-density array Comparative Genomic Hybridization microarrays (aCGH) manufactured by Roche NimbleGen. The first was a custom designed array that tiled 385,000 probes along the X chromosome with an average intermarker distance of 270 base pairs (bp) or 4 probes/kilobase (kb). Probes were photolythically synthesized on a glass slide. Probes were randomly distributed by position throughout the array area. This density array is no longer available for CNV detection.

The second custom CGH array we used tiled approximately two million probes (2,143,369 probes total, and 1,979,586 experimental probes) ranging from 50-75 bp in length along the X chromosome. (P/N 05223873001, nimblegen.com/products/cgh) 96.8 megabases (Mb) of unique sequence were targeted, and this resulted in a median spacing of one probe every 50 basepairs (bp). Prior to tiling-probe selection, the chromosomal sequence was first repeat masked, including masking of the PAR1 and PAR2 loci. This array is in fact comprised of three small arrays of photosynthesized probes built on a glass slide. In our custom micorarray, each 'subarray' represents one third of chromosome X in ascending order. Ie, subarry A01 contains probes from 2,709,520-47,369,192 bp, subarray A02 contains probes from 47,369,267-107,160,255 bp, and subarray A03 contains probes from 107,160,305-154,583,236 bp. While each subarray represents one third of the chromosome in sequential order, probes are randomized within the subarray. Ie, probes selected from the first third of the chromosome are physically randomized in (X,Y) position within the first subarray, the second third randomized within the second subarray, and the last third randomized within the third subarray.

5. aCGH Protocol and Scanning

a. NimbleGen's protocol for sample processing, array hybridization and wash, and scanning

Please see Figure 5.1.

- b. Optimized protocol for sample processing, array hybridization and wash Please see Figure 5.2.
- c. Array scanning

Use the Axon 4000B scanner at five micron. Scanner needs to be warmed up 15 minutes prior to use. The scanner was calibrated once a month or more depending on overall usage. The GenePixPro software is used to control the scanner and run scanner diagnostics.

We followed the following steps to scan an array. 1) In the 'Image' tab, preview scan the entire array area. 2) Once preview scan is complete, select the scan area. I scanned each subarray individually. 3) After scan has begun, use the 'Histogram' tab to evaluate the selected PMT settings. Make sure the y-axis is the log-normalized count. The 'Count Ratio' (CR) measurement should be 1 +/- 0.15 to provide the greatest overlap of total fluorescence, and the high intensity-tails targeted to the 1e-5 to 1e-4 range. Adjust PMT settings for 635nm and 532nm lasers to reach these criteria. (635nm is the 'red' plotted data and the numerator in the CR, 532nm is the 'green' plotted data and the denominator in the CR) 4) Once scan is complete, save images as separate .tiff files, uncompressed. Figure 5.3

6. CNV identification

a. Create .pair reports in NimbleScan

Fluorescence intensity data must first be linked to probe information before CNV identification can be conducted. We used the NimbleScan software (NS, v2.40) to create .pair reports, and followed the manufacturer's instructions to create these first report files. In brief, open NS, select the .tiff file to be gridded (532nm or 635nm). Then, select the .ndf or design file for the subarray to be paired (A01: 071108_HG18_MI_CGH01.ndf, A02: 071108_HG18_MI_CGH02.ndf, A03: 071108_HG18_MI_CGH03.ndf). Select auto brightness/contrast; select auto autoalign. Zoom in to the alignment oligo probes to ensure gridding is accurate; otherwise, manually adjust gridding such that all grids are centered over the alignment oligos. At minimum, I reviewed all four corners and the central 'X' features before saving. Under the Analysis menu, the Reports menu allows you to select 'Pair Report'. Reports can be generated singly or by batch. This report option will generate two .pair files (one each for the 532nm and 635nm scans).

b. Remove poorly behaving probes (5% of all experimental)

Using a custom perl script, poorly behaving probes were removed from .pair files prior to segmentation analysis. The perl script used the list of 'poor' probes, searched each .pair file for the 'bad' or 'poor' probe, and wrote a 2nd .pair file less the poor probes (and their associated fluorescent data). The files containing the 'poor' probes are: A01 bad probes 6 5percent.txt, A02 bad probes 5 4percent.txt, A03_bad_probes_5_24percent.txt, chrX_HD_bad_probes.txt. These files list the probes by Probe_ID for each of the subarrays and the 2.1M array in its entirety respectively.

c. Run NimbleScan analysis algorithm (segMNT)

We used the segMNT algorithm as the DNACopy algorithm reportedly generated a tremendous amount of false calls. We followed the manufacturer's instructions for how to analyze our .pair reports with the segMNT algorithm. In brief, under the Analysis menu, the CGH menu allows you to select 'segMNT'. Choose the .pair files to be analyzed, choose the destination folder for analyzed data, choose the .pos file, and hit Run. The .pos files for the arrays with poor probes removed are:

071108_HG18_MI_CGH01.good6.5.pos, 071108_HG18_MI_CGH02.good5.4.pos, 071108_HG18_MI_CGH03.good5.24.pos

We used the default settings for analysis. They are as follows:

<u>Min segment difference</u> (score units): 0.0 <u>Min segment length</u> (number of probes): 2 <u>Acceptance percentile</u> (0.4-0.999): 0.999

Do not include <u>non-unique probes</u> in analysis. Do use <u>'Spatial Correction'</u>. Do <u>'Normalize'</u>.

d. Quality Control

Create MA Plots

Using the _segMNT.txt files generated by the segMNT analysis, we created MA plots for each subarray in R (r-project.org). To automate this procedure, we developed a custom perl script to create a 'source' document to be run in R. The

perl script essentially grabbed the file names of _segMNT.txt files to be analyzed, and the 'source' document was a single file that could be read in R to plot and save the MA plot files for each _segMNT.txt_file.

In brief, the 'source' file read in each _segMNT.txt file with read.table. Four variables were created for each of the probes in the _segMNT.txt file. These variables were then used to make the MA plots: $\underline{M} = EXP_NORM - REF_NORM$, $\underline{A} = 0.5 * (EXP_NORM + REF_NORM)$, $\underline{fit} = lm(M\sim A)$, and $\underline{fit.coef} = coef(fit)$. The variables 'M' versus 'A' were plotted and the linear regression line 'fit' was plotted in red as well. This allowed us to visualize and quantitatively assess overall data performance.

Create file containing mean and standard deviation of each subarray

Additionally, while each file was read into R, we generated a file that collected some basic statistics for the log2 values of the subarray. Using the RATIO_CORRECTED values, we generated a table listing the mean +/- one standard deviation (SD) as well as the mean +/- two SD. These values would be used to select segments or CNV called by the segMNT algorithm in the _segtable_segMNT.txt files.

7. Analysis of CNV identified by the NimbleGen and Optimized protocols

a. All CNV called by the NimbleGen and Optimized protocols

Chapter 2. Table 4 and Table 5.

Using the same number of 'good' probes for copy number analysis, CNV generated by 30 samples run on both protocols resulted in a significantly different call rate between the two protocols. We evaluated the number of CNV called per individual for each protocol. Using the Wilcoxon Signed Rank test, the p-value was less than 0.0011.

This significant difference was similarly reflected in our analysis of all deletions and duplications called by each protocol. By the Pearson's Chi-squared test with Yates' continuity correction, we observed a significant difference between the number of deletions (NimbleGen: 184, Tecan: 44) and duplications (NimbleGen: 118, Tecan: 130) with p < 1.36e-13.

b. CNV characteristics generated by the NimbleGen and Optimized protocols <u>Chapter 2. Table 5 and Figures 9 A-C.</u>

We also compared several characteristics of the CNV called by either protocol. The same number of 'good' probes was used for copy number analysis as well as the same samples. We used the Welch Two Sample t-test with unequal variances to evaluate CNV size, the average number of probes/kb called for CNV by protocol, and the average GC content for all CNV, for deletions and for duplications.

Evaluation of CNV size for each protocol was not statistically different (all CNV: p < 0.0537, deletions: p < 0.1627, duplications: p < 0.1627). However, when we evaluated the probe coverage per variant (number of probes/CNV), we found that the diminished coverage observed in the Optimized protocol (all CNV: NimbleGen: 20.4, Optimized:

18.0; <u>deletions</u>: NimbleGen: 21.0, Optimized: 15.2; <u>duplications</u>: NimbleGen: 19.4, Optimized: 18.9) was statistically different for all categories (<u>all CNV</u>: p < 5.24E-10, <u>deletions</u>: p < 2.23E-12, <u>duplications</u>: p < 2.23E-12). And, GC content for these three categories was also found to be statistically significantly different between the two protocols (<u>all CNV</u>: p < 6.97E-21, <u>deletions</u>: p < 0.0310, <u>duplications</u>: p < 0.0310).

c. Analysis of false positive and true positive calls

Please see Table A.6.a and A.6.b for sample and locus data.

False and True CNV calls

Chapter 2. Table 6 and Figure 10.

For the same individuals and the same 'good' probes, we evaluated the false positive call rates for all CNV identified by the NimbleGen and Optimized protocols. The number of false positive (NimbleGen: 40, Optimized: 36) and true positive calls (NimbleGen: 22, Optimized: 26) was not statistically different between the two protocols by the Fisher's Exact Test for Count Data (p < 0.5804).

Characteristics of falsely and truly called CNV by the NimbleGen and Optimized protocols

Chapter 2. Table 6.

We also assessed the characteristics of all CNV falsely and truly called by size, number of probes/kb, and the average GC content. We found that the size of CNV falsely called was statistically significantly different between the two protocols by the Kolmogrov-Smirnov test (p < 0.0077). Not surprisingly, the truly called loci were not statistically different in size (p < 0.4282).

By the Kolmogrov-Smirnov test, the probe coverage for the true and false calls were statistically different with the number of probes/CNV for false calls p < 8.01E-05 and true calls p < 0.0010.

Chapter 2. Table 6 and Figure 11A and 11B.

Like CNV size, the GC content of true and false calls by each protocol was statistically different for false calls but not truly called CNV. Using the Kolmogrov-Smirnov test, the GC content for false calls was statistically different (p < 7.45E-06) but not for the truly called loci (p < 0.4022). We furthered our analysis by also assessing these call rates as compared to the X chromosome GC content. For this purpose, we binned the X chromosome by 1,000 bp bins and assessed the GC content for each of these bins as distributed across the chromosome. Figure 11 plots the cumulative percentage of the X chromosome 1,000 bp bins, the truly called loci, and the falsely called loci by the percent GC content.

8. Probe Analysis

a. Identification of 'poorly' behaving probes

We modeled our analysis of probe kinetics off of the methods reported by Mulle *et al.* [5] Specifically, we used the data from the 48 AGRE samples run on the 2.1M CGH arrays following the NimbleGen protocol. We used R to evaluate the log2 values for all probes. (r-project.org) For each subarray (714,457 probes), we determined the variance of the log2 value for each probe. We then sorted the probes by variance, and plotted the probes' variance by index number. We chose a variance cutoff of 0.175 for all subarrays. Figure 5.4

b. Evaluation of 'poor' and 'good' probes

Chapter 2. Table 2 and Figures 7 A-D.

With the identification of the 'poor' probe set, we evaluated several properties of the 'poor' and 'good' probes. Specifically, we asked if the probes in the 'poor' probe set had qualities that were statistically different from the probes in the 'good' probe set. We evaluated probe length, purine content, GC content, and T_m (melting temperature) by the Welch t-test with unequal variance. All four parameters were statistically significant with the following pvalues: p < 6.97E-49, p < 2.20E-16, p < 2.20E-16, and p < 2.20E-16.

c. Evaluation of probe log2 values by processing protocol: NimbleGen versus Optimized

Chapter 2. Table 3.

We found that the optimized technical protocol produced average log2 values that were closer to the expected value of '0,' irrespective of subarray. However, when the log2 values for arrays tested by the NimbleGen or Optimized protocol (NimbleGen: 48 arrays, Optimized: 75-81 arrays) were evaluated, this difference was not significant different by the paired Wilcoxon Rank Sum test with Bonferroni correction.

d. Evaluation of probe coverage (probes/kb) by processing protocol: NimbleGen versus Optimized

Chapter 2. Table 5 and Figure 9B

Using the same number of 'good' probes for copy number analysis, the optimized protocol returns a slightly diminished probe coverage per variant than that of the original protocol. This decrease in coverage is significant by the Welch t-test with un-equal variances (all CNV: p < 5.24E-10, deletions: p < 2.23E-12, duplications: p < 2.23E-12).

9. Select high-confidence segments or copy number variants

Using a custom perl script, we selected those segments listed in the _segtable_segMNT.txt files generated by the segMNT algorithm. These segments were more than one SD from the mean of each individual array. Selected segments were sent to two output files. The first was simply another _segtable_segMNT.txt file containing only those segments one SD from the mean, while the second file collected all segments, irrespective of array origin, in one file. This became our working for CNV analysis.

a. Select segments greater than one standard deviation from the mean

b. Identify and merge multiple segments calling a single, variant locus

We found that occasionally, larger copy number variants (CNV) would be identified by more than one 'segment' by the segMNT algorithm. We selected segments for merging into a single call by the following criteria. 1) The 3' end of the 'upstream' segment is within three kilobases (kb) of the 5' end of the next downstream segment. 2) The log2 values are shifted in the same direction. 3) The length of the new segment is determined by the most upstream and downstream probes, the number of probes is the sum of all probes within the original, smaller segments, and the new log2 value is a weighted

average of the number of probes and log2 values of the original segments. Specifically, the number of probes for each original segment is multiplied by the log2 value for the segment, the sum is taken of all these products and the sum divided by the sum of all probes.

c. Select segments which have more than nine probes/kb

The average density of probes is 20 probes/kb. Given the dense nature of our custom array, we believed that half the probes (10 probes/kb) would be sufficient for a call. With this in mind, we purged the remaining segments in the total set of any segments called with less than nine probes/kb. Figure 5.5

d. Remove samples with relatively high call rates

Finally, we determined the number of segments called/individual as well as the mean and SD for the number of calls/individual for the set. For those individuals who had more than two SD from the mean number of calls, we removed their calls from the data set entirely. Figure 5.6

10. Validation of array identified CNV

a. PCR Confirmation

We used a PCR based strategy to validate aCGH identified structural variants. For deletions, primers flanking the outsides of the breakpoints were designed for amplification of the junction fragment. Primers were selected outside of the first probe having a log2 value near '0'. Figure 5.7

One of two types of validations assays were developed to confirm duplications. All 'duplicated' sequence was assumed to be in tandem to the 'original' sequence. The first strategy was implemented for 'relatively' small duplication events (less than three kb) where primers were designed to flank the supposedly duplicated sequence (resulting in an approximate six kb sequence). For those duplications too large to be accommodated by this strategy, we used a PCR-based approach elegantly explained by Arlt *et al.*[6] Essentially two 'outward' facing primers are designed at the internal junction of duplicated sequence. If the duplication is real and in tandem, a junction fragment will be captured by these primers. Figure 5.8

For those duplications screened by the 'outward' facing primers and a junction fragment was not observed, an additional set of primers was designed to confirm that the 'duplication' primers actually worked. These additional primers sat 'outside' of the duplication boundary and would amplify a small region between the 'outside' primer and the internal 'duplication' primer. This assay also confirmed relative orientation of the duplicated sequences relative to flanking, single copy sequence. Figure 5.9

Because of the various sizes and sequence characteristics represented by all CNV, we employed several different Taq polymerases (Invitrogen Platinum Taq, Roche Expand Long taq, Roche High Fidelity Taq, and Takara Ex taq), varying MgCl₂ concentrations, various supplements (betaine (mono) hydrate – for GC rich regions, dimethyl sulfoxide (DMSO) – reduce secondary structure and for GC rich regions, and formamide – increase

specificity and for GC rich regions, tetramethylammonium chloride (TMAC) – reduce non-specific priming), and various annealing temperatures to develop the validation assays.[7-9]

b. Breakpoint sequencing

For those CNV junction fragments that validated, amplicons were gel eluted from sterile, agarose gel and TA-cloned for bidirectional sequencing. We aimed to complete all steps within one day to ensure the integrity of the 'A' overhang found at the ends of our amplicon to increase efficiency of cloned product. For gel elution, we used either the Promega (Wizard® SV Gel and PCR Clean-Up System, P/N A9280, promega.com) or Qiagen (QIAquick® Gel Extraction Kit, P/N 28704, qiagen.com) based systems to extract our PCR products. We followed the manufacturer's instructions to elute amplicons. Both systems utilized a membrane to 'catch' the amplicon, and we used dH₂O to elute.

TA-cloning was conducted using the pCR2.1-TOPO (amplicons up to three kb in size, P/N K4500-01) and pCR-XL-TOPO (amplicons three to ten kb in size, P/N K4700-10) systems from Invitrogen (invitrogen.com). We followed the manufacturer's instructions to clone and transform TOP10 or DH5 α -T1 chemically competent cells. In all cloning reactions, we used the maximum volume of 4 μ L of amplicon (no water), and for the 2.1-TOPO clones, we used the optional one μ L of salt solution to enhance incorporation of our products. Transformed bacteria were grown on agar plates containing ampicillin (2.1-TOPO clones) or kanamycin (XL-TOPO clones). Warm agar plates were spread with 40

 μ L X-gal (20 mg/mL) and 100 μ L SOC half an hour prior to plating 10-50 μ L of transformants.

Typically, five to ten colonies were picked for expansion in two mL of LB containing ampicillin (2.1-TOPO clones) or kanamycin (XL-TOPO clones). Plasmids were extracted using the Promega (PureYield[™] Plasmid Miniprep System, P/N A1223) or Qiagen (Plasmid Mini Kit, P/N 12123) mini-prep systems. Plasmid extraction was conducted following the manufacturer's protocols.

Plasmids were then assayed for amplicon ligation by digestion with Hind III and Xho I enzymes. For each clone, we ran four conditions of no enzyme, only Hind III, only Xho I, and Hind III and Xho I. For a 1x reaction, we used one μ L of BSA (1 mg/mL), one μ L #2 Buffer (10x), 0.3 μ L enzyme #1 (200 U/uL) (optional), 0.3 μ L enzyme #2 (200 U/uL) (optional) and sterile, filtered water for a final volume of five uL. We added this five μ L of enzyme mix to five μ L of 200 ng of vector. Reaction was incubated at 37°C for minimum of one hour and were then run on an agarose gel to visualize cleavage products.

For those plasmids that had ligated our amplicon, first pass sequencing utilized the universal M13 Forward (-20) and M13 Reverse primers. These primers are positioned 100 bp and 292 bp respectively from the ligation site. Depending on length of sequence and size of amplicon product, new primers were designed to ensure bidirectional sequencing of the breakpoint junction. We obtained sequence data for 40 unique loci and bidirectional sequence for 28 of those loci.

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11. Junction analysis

a. Literature breakpoint evaluation

We identified 681 (bidirectionally) sequenced breakpoints from 12 reports in the literature.[10-21] Populations and methods varied by study. For breakpoint/motif analysis, we removed two sets of variants from this data set. The first was based on variant size. In our preliminary analysis of the occurrence of motif frequency at the breakpoint, we evaluated various window sizes at the breaks. Because the window sizes were as large as 500 bp, we removed any indels that were less than one kb in size. This reduced the literature data set to 569 CNV. The second round of removals was based on our inability to match 'GC' content as well as 'N' content during random sequence generation. This reduced the final data set to 565 CNV.

b. Single nucleotide insertion or deletion at the breakpoint

For those CNV and indels that had homology and insertion data available, using Pearson's Chi-squared test, we asked if any one nucleotide was over- or underrepresented at the breakpoint. For 57 CNV or indels showing a deletion of a single nucleotide, no single nucleotide occurred at a frequency statistically different from expected (p < 0.727). Similarly, for 21 CNV or indels showing an insertion of a single nucleotide, no single nucleotide occurred at a frequency statistically different from expected (p < 0.727). Similarly, for 21 CNV or indels showing an insertion of a single nucleotide, no single nucleotide occurred at a frequency statistically different from expected (p < 0.6134).

c. Development of random data set

For each literature CNV or 'Real' CNV that we used (n=565), we selected 1,000 random positions on the Real CNV's chromosome and set those positions as the 'start' for the 'Random' CNV. These 1,000 Random CNV were then assigned the same length as the Real CNV to determine the 'end' of the Random CNV. This process was repeated for all 565 Real CNV to generate 565,000 Random CNV representing 1,000 sets of Random CNV having the same chromosomal and size distribution as the Real CNV data set. Additionally, we ensured that the 'GC' and 'N' content of each Real CNV was matched or closely matched by each of the Random CNV.

d. Evaluation of Real and Random CNV for the frequency of motif occurrence at the breakpoints

First, we identified 39 motifs from the literature that had been previously identified as enriched at the breakpoint junctions. [22-28] Second, we defined windows (defined by A, B, C, and D in the figure) of varying sizes (25 bp, 50 bp, 100 bp, and 500 bp) for each breakpoint, Real or Random. Figure 5.10 Third, for each window in each breakpoint (Real or Random), we determined the frequency of occurrence for each of the 39 motifs in both the forward and reverse strands. Because two motifs were greater than 26 bp in size (Alu core element and Curved DNA signal), we eliminated evaluation of the 25 bp window sizes.

Finally, the observed frequencies were then normalized by motif and window size. Specifically, for each motif frequency, we divided the motif count by [2 * (Window Size – Length of Motif + 1)]. The factor of two in the denominator is to account for searching both the forward and reverse strands.

For each of the motifs, we compared the normalized frequency for All windows (A+B+C+D), Outside windows (A+D) and Inside windows (B+C) in the Real breakpoints and Random breakpoints by the z-test.

12. Assess functional activity of GRIA3 deletion: Luciferase Reporter Assay

a. Ligate region of interest into reporter backbone

We used the Promega luciferase reporter system (luciferase vectors: pGL3-Basic, pGL3-Promoter) to evaluate the region three kb upstream of the *GRIA3* gene. To generate pGL3-Promoter plasmids containing our two promoter sequence, we first PCR amplified our two regions of interest using primers with the Xho I and Hind III digestion sequences tagging the 5' end of the amplification primers. The forward and reverse primers had Xho I and Hind III tags, and the negative control primers (same sequence) had Hind III and Xho I tags (effectively, insert sequence 'backwards'). PCR amplicons and pGL3-Promoter plasmid were Hind III and Xho I digested. Digestion products were agarose gel eluted.

We then used the Takara DNA Ligation Kit v2.1 (Takara, takara-bio.com) and followed the manufacturer's instructions to ligate our amplicons to vector at two different ratios (0.01 pmol vector: 0.05 pmol amplicon, 0.03 pmol vector: 0.09 pmol amplicon). We made two sets of 0.01 pmol vector: 0.05 pmol amplicon; the second set did not receive

ligation agent and served as our negative control. After mixing the appropriate amounts of vector (45.07 ng/uL) and amplicon, we added water to bring the final volume to 10 μ L. Then, 10 μ L of Solution I was added to all combinations (with the exception of the negative control – 10 μ L of sterile, dH₂O was added). All mixes were incubated at 4°C overnight. We ran 30 ng of each on an agarose gel to confirm ligation.

b. Transfect reporter plasmids into Neuro2A cells

The luciferase assay used three 6-well plates of Neuro2A cells, each plate had two rows of three replicates. Plate one contained transfection reagents and pGL3-Basic and pRL-TK (Renilla Luciferase, internal control); plate two contained the negative control plasmids (promoter sequence ligated in 'backwareds') and pRL-TK, and plate three had the plasmid containing the promoter sequence ('forward' orientation) for the intact and deleted allele as well as pRL-TK. Prior to transfection, PBS was incubated at 37°C for five minutes, and 32 mL of Opti-MEM were incubated at room temperature for five minutes.

Transfection was conducted following the Mirus protocol (TransIT-LT1, P/N MIR 2304, mirusbio.com). The luciferase and Renilla vectors were mixed at a 5:1 molar ratio for all plates and incubated at room temperature for 5-20 minutes. Concurrently, the TransIT-LI1 transfection reagent was mixed with the room temperature Opti-MEM and incubated at room temperature for 5-20 minutes (1x/well: 250 uL Opti-MEM and five uL TransIT-LIT1). TransIT-LT1 mixtures was dropped along the sides of the vector mixture tube, the

tube flicked and shaken vigorously (to create micelles), and incubated at room temperature for 5-20 minutes.

Prior to transfection, Neuro2A cells were rinsed twice with two mL of PBS, and 1,250 uL of Opti-MEM were then added to each well. 285 uL of vector/transfection mixture were added to each well (three wells for each vector type) in a drop-wise fashion. Plates were rocked to distribute mixture evenly and then incubated at 37C for 24-72 hours.

c. Assay luciferase activity

We evaluated lucifierase activity following Promega's protocol for the Dual Luciferase Reporter Assay System (P/N E1910). We briefly describe the protocol. For cells grown in 6-well plate, first wash cells with 1 mL PBS – rock to wash. Aspirate PBS with seripipette. Lyse cells using 250 μ L Passive Lysis Buffer (PLB) (1x); rock or shake plate at room temperature for 15 minutes. Collect cells by transferring lysate to 1.5 mL tube. Spin at top speed at 4°C for 5 minutes to clear lysate. Transfer supernatant to new 1.5 mL tube. Can be stored at -20°C.

To assess luciferase activity from the lysed cells, first, prepare Luciferase Assay Reagent II (LAR II). Resuspend LAR II in 10 mL of Luciferase Assay Buffer II. Aliquot to 1.3 mL (enough for 12 assays) to 1.5 mL tubes for future assays. Store -80° C. For a 1x preparation, prepare Stop & Glo Reagent (SG) by mixing 2 µL S&G (50x) + 100 uL S&G Buffer (3.8 mL total) in a glass/polypropylene tube.

Turn on the luminometer (five minutes to warm up). Confirm program is for Single (not Dual) read; MODE: \langle STD> with a two-second pre-measurement delay; 10-second measurement. To assay activity, add 20uL cell lysate (one ug total protein) to luminometer tubes. Add 100 µL LARII reagent to sample. Aspirate up and down three times; do not vortex. Place tube in reader. Hit 'READ'. Do this for all samples. Then, add 100 µL S&G reagent. Aspirate up and down three times; do not vortex. (FLICK well.) Place tube in reader. Hit 'READ'.

d. Evaluate luciferase data

The first and second luminometer readings were for the fluorescence generated by the luciferase vectors (Firely; containing no insert (pGL3-Basic), insert in 'backwards' orientation (Negative Control, pGL3-Promoter), and insert in 'forward' orientation (the test, pGL3-Promoter)) and the Renilla reporter (pRL-TK) respectively. The Firely:Renilla ratio was determined for each replicate and the average of all three replicates was then compared. Using the t-test of equal variance, the deleted allele was found to be significantly increased over that of the intact allele (p < 4.10E-05).

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Figure 5.1 – NimbleGen aCGH Protocol used.

Sample labeling and hybridization for NimbleGen array Comparative Genomic Hybridization

Protocol For:

Processing and hybridization of NimbleGen aCGH by the manufacturer's instructions

Morna Ikeda and Stephen T. Warren Department of Human Genetics, Emory University, Atlanta, GA USA

LEGEND $\Rightarrow_{ATTENTION}$ $*_{HINT}$ $\stackrel{W}{\sim}_{REST}$

REAGENTS AND CONSUMABLES

Deionized, filtered (0.22 um) sterile water Tris-HCl (1M, pH 7.4, any vendor) MgCl2 (1M, any vendor) β-Mercaptoethanol (98%, any vendor) Cy3/Cy5 9mer Wobble (Cy3: P/N N46-0001-50, Cy5: N46-0002-50, Trilink Biotechnologies, San Diego, CA, USA) Ethanol (100%, any vendor) Tris-HCl (1M, any vendor) EDTA (0.5M, any vendor) dNTP Set (100mM dNTP Set, P/N 10297-018, Invitrogen) Klenow Fragment (3' \rightarrow 5' exo-, 50 U/µL, P/N M0212M, New England Biolabs, Ipswich, MA, USA) Sodium Chloride (5 M, any vendor) Isopropanol (100%, any vendor) Alexa Fluor Reactive Dye Decapacks (P/N 10297-018, Invitrogen) Sodium Bicarbonate (any vendor) DMSO (100%, any vendor) Hybridization Kit (P/N 05583683001, Roche NimbleGen, Madison, WI, USA) 2X Hybridization Buffer Hybridization Component A Alignment Oligo Wash Buffer Kit (P/N 05584507001, Roche NimbleGen) Wash Buffer I, II, and III DTT (Use is optional. Follow manufacturer's instructions for amount to add.) CP100 Pipette Tips (P/N F148414, Gilson Inc., Middleton, WI, USA, pipetman.com)

EQUIPMENT

<u>Misonix sonicator with microtip</u> (QSonica, Newton, CT, USA) <u>Thermocycler</u> (any vendor) <u>Benchtop centrifuge</u> (any vendor) <u>Vortex</u> (any vendor) <u>Spectrophotometer</u> (P/N ND-1000, NanoDrop) <u>Heat block</u> (95°C, any vendor) <u>Speed-vac</u> (Thermo Savant) <u>Precision Mixer Alignment Tool</u> (PMAT, P/N 00832, Roche NimbleGen) <u>Positive Displacement Microman (10-100 uL, P/N M100, Gilson)</u> <u>Microarray Dryer</u> (Array-Go-Round, P/N 00898, Roche NimbleGen) <u>Axon 4000B</u> (P/N 4000B, Molecular Devices)

Reduced Ozone environment (optional)

PROCEDURE

USE FILTERED STERILIZED WATER FOR ALL STEPS

RANDOMER PREPATION

- 1. Centrifuge lyophilized primer to collect at the bottom of tube.
- 2. Using fresh Randomer Buffer, add enough Buffer to rehydrate to 1 OD/42 μ L.
- 3. Invert tube several times.
- 4. Centrifuge to collect liquid at bottom of tube.
- 5. Incubate at room temperature for 5-10 minutes protected from light.
- 6. Invert and centrifuge tube once again.
- 7. Aliquot 42 μ L of primer to fresh, sterile thin-walled PCR strip tubes (0.2 mL).



Primers can be stored at -20°C protected from light until ready for sample labeling. Thaw frozen primers protected from light at room temperature. Centrifuge tubes before adding sample.

DNA SONICATION & QC

- 8. In separate 1.5 mL tubes, bring 2 μ g of genomic DNA to a final volume of 80 μ L using dH₂O for both the test sample and a reference sample.
- 9. Flick tubes to mix contents, and centrifuge to collect liquid at bottom.
- 10. Incubate tubes at 55°C for 5-10 minutes to ensure DNA is in solution.
- 11. Flick tubes to mix contents and centrifuge to collect liquid at bottom again.
- 12. Store DNA on ice while preparing for sonication.
- 13. Using a Misonix sonicator, clean tip with 10% bleach followed by 80%-100% ethanol.
- 14. To sonicate DNA, place tip near bottom of tube and follow sonication protocol.

Sonication Protocol:

Total Time	11 sec
on/off	0.5 sec
Amp	1.0

- 15. Return DNA to ice after sonication. Repeat tip cleaning with bleach and ethanol before sonicating next sample.
- 16. Run 5 μ L of sonicated genomic DNA on 1% agarose gel. Confirm a smear between 200-2,000 bp.



DNA can be stored at 4°C (less than one week) or -20°C (long term storage).

DNA AMPLIFICATION & LABELING

- 17. Add 40 μL sonicated DNA to 42 μL pre-aliquoted Cy3/Cy5 randomers. (Test DNA to Cy3, Reference DNA to Cy5)
- 18. Incubate mixture at 98°C for 5-10 min.
- 19. Ice water bath to snap-cool mixture while making master mix for at least 2 min.
- 20. Add 20 μ L master mix to cooled mixture.
- 21. Aspirate up and down 10x using pipette. Centrifuge to collect liquid at bottom of tube.
- 22. Incubate at 37°C for 4 hours.

DNA PRECIPITATION

- 23. Add 10 μ L EDTA (0.5M) to stop reaction.
- 24. Add 11.5 µL NaCL (5 M) to each tube.
- 25. Vortex briefly and centrifuge to collect liquid at bottom of tube.
- 26. Add 110 µL room temperature Isopropanol to 1.5mL tube.
- 27. Transfer stopped reaction (121.5 μ L) to 1.5 mL tube containing Isopropanol.
- 28. Vortex briefly and centrifuge to collect liquid at bottom of tube.
- 29. Incubate at room temperature for 10 minutes shielded from light.
 - *

At this point, I pool the references together to minimize loss.

<u>REFERENCE: 3 references</u>

Add 330 μ L Isopropanol to 1.5 mL tube.

Transfer three stopped reactions to same tube.

Vortex briefly and centrifuge to collect liquid at bottom of tube.

Incubate at room temperature for 10 minutes shielded from light).

- 30. Centrifuge at max speed for 10 min.
- 31. Remove supernatant with pipette (232 μ L).
- 32. Rinse with 500 μ L of ice cold ethanol (80%) be sure to dislodge pellet.
- 33. Centrifuge at max speed for 2 min.
- 34. Remove supernatant with pipette (500 μ L).
- 35. Speedvac-low for 5 min to dry pellet.

NY .

DNA pellet can be stored at -20°C protected from light and in sealed bag with desiccant (optional).

LABELED DNA QUANTIFICATION AND HYBRIDIZATION PREP

48. Rehydrate precipitated DNA in 20 μ L dH₂O water.

- 49. Quantify labeled DNA on Nanodrop.
- *

Use the Microarray Module to quantify Cy3 or Cy5 activity and DNA concentration.

The linear range of this module is 740 ng/ $\mu L.$

To ensure the measured DNA is within the limit of the reader, dilute DNA 1:4 and adjust calculations accordingly.

Specific Activity should be between 10-20 pmol/ μ g.

50. Merge 34 µg of test, reference each.

51. Dry down.



Mixed DNA pellet can be stored at -20°C protected from light and in sealed bag with desiccant (optional).

- 52. Re-hydrate mixed DNA pellet in 12.3 μ L H₂O.
- 53. Incubate at 55°C for 5-10 minutes. Gently tap bottom of tube to mix. Centrifuge.

HYBRIDIZATION PREPARATION

- 54. Make hybridization solution 31.7 μ L/array).
- 55. Add 31.7 µL Hybridization Solution to sample.
- 56. Incubate Blank and Samples at 95°C for five minutes.
- 57. Hold at 42°C until ready.
- 58. Prepare slide and mixer (MAUI disposable lid) assembly using PMAT and place on MAUI bay (42°C) while preparing remaining slides.
- 59. Before adding sample, re-bray adhesive area to ensure complete annealing.
- 60. Using Pipetman, aspirate 41 µL and slowly dispense onto array.
- 61. Using Kim-wipe, wipe residual hybridization solution from each port before applying gel-stickers to enclose array chamber. Be careful not to wick solution from within.
- 62. Place sample and array assembly on MAUI. Once all samples loaded, close lid, and select hybridization program 'B'.
- 63. Hybridize 60 hours or more.

WASH SOLUTION

- 64. Make Wash Solution I, II, III.
- 65. Load jig into Wash I in upturned 1000p lid. Remove MAUI hybridization mixer while submerged. Agitate array 10-15 seconds in Wash I.
- 66. Move array to Wash I in staining dish while removing lids for additional arrays. Process up to eight arrays/batch.
- 67. Once all arrays are in Wash I, agitate vigorously up and down for two minutes. Tranfer to Wash II.
- 68. Agitate vigorously up and down for one minute. Tranfer to Wash III.
- 69. Agitate vigorously up and down for 30 secones. Tap array holder on paper towel to remove excess liquid. Load into balanced Array-Go-Round.
- 70. Dry for two minutes. Wipe residual liquid from edge of each slide. Store in dark dessicator until ready to scan.

71. RECIPES

Randomer Buffer (make fresh every time)

Component		1x (uL)
DI, sterile H2O		861
Tris-HCl (1M) (pH 7.4)		125
MgCl2 (1M)		12.5
B-MercaptoEtOH (98%)		1.75
	TOTAL	1000

Rehydrate 9mers to one OD/42 μ L

Add 1050 μ L of Randomer Buffer to 25 ODs. This gives a final concentration of one OD/42 μ L.

TE (10x) (*store at room temperature*)

Components		1x (mL)
Tris-HCl (1M)		1.5
EDTA (.5M)		0.3
DI, sterile H2O		13.2
	Total	15

dNTP Mix (50x) (*store at -20°C*)

Component	1x (uL)	Final Concentration		
DI, sterile H2O	250			
TE (10x)	50			
dATP (100mM)	50	10 mM		
dGTP (100mM)	50	10 mM		
dTTP (100mM)	50	10 mM		
dCTP (100mM)	50	10 mM		
SUM 500				
Aliquot by 200 uL to minimize freeze-thaws.				

Master Mix (for DNA amplification and labeling)

Component	1x (uL)
DI, sterile H2O	8
dNTPs 50x, (10mM)	10
Klenow (50 U/uL)	2
Total	20

Hybridization Solutions

Component	1x (uL)
Merged labl'd sample	12.3
Hybridization Buffer (2x)	22.0
Hybridization Component A	8.80
Alignment oligo	0.90
MM - total	31.7

Wash Buffers

Follow manufacturer's instructions to make 1x solutions. Use filtered (0.2um), sterile water to dilute. Two sets of 500 mL Wash Buffer I are needed (place one in upturned, 1000p lid, place second in Tissue-Tek dish). In brief, for 25 mL of Wash Buffer (10x), 225 mL of deionized, sterile water, and 25 uL of DTT (1 M).

Figure 5.2 – Optimized aCGH Protocol.

Modified sample labeling and hybridization for NimbleGen array Comparative Genomic Hybridization

PROTOCOL FOR: Increased sample fluorescence labeling and stringency of hybridization using a Tecan HSPro 4800 for NimbleGen aCGH

Morna Ikeda and Stephen T. Warren Department of Human Genetics, Emory University, Atlanta, GA USA

LEGEND $\rightarrow_{ATTENTION}$ $*_{HINT}$ $\stackrel{W}{\sim}_{REST}$

REAGENTS

Deionized, filtered (0.22 um) sterile water Tris-HCl (1M, pH 7.4, any vendor) MgCl2 (1M, any vendor) β-Mercaptoethanol (98%, any vendor) Cy3/Cy5 9mer Wobble (Cy3: P/N N46-0001-50, Cy5: N46-0002-50, Trilink Biotechnologies, San Diego, CA, USA) Ethanol (100%, any vendor) Tris-HCl (1M, any vendor) EDTA (0.5M, any vendor) 5-aminohexylacrylamido-dUTP (aha-dUTP, 50 mM in TE/50 µL, P/N A32761, Invitrogen, Carlsbad, CA, USA) dNTP Set (100mM dNTP Set, P/N 10297-018, Invitrogen) Klenow Fragment (3' \rightarrow 5' exo-, 50 U/µL, P/N M0212M, New England Biolabs, Ipswich, MA, USA) Sodium Chloride (5 M, any vendor) Isopropanol (100%, any vendor) Alexa Fluor Reactive Dye Decapacks (P/N 10297-018, Invitrogen) Sodium Bicarbonate (any vendor) DMSO (100%, any vendor) Hybridization Kit (P/N 05583683001, Roche NimbleGen, Madison, WI, USA) 2X Hybridization Buffer Hybridization Component A Alignment Oligo (I did not use the packaged oligo – I ordered my own.)

<u>Cy3/Cy5 Alignment oligo</u> (5' end - Cy3/Cy5 labeling, TTCCTCTCGCTGTAATGACCTCTATGAATAATCCTATCAAACAACTCA, IDT, Coralville, Iowa, USA) <u>Wash Buffer Kit</u> (P/N 05584507001, Roche NimbleGen) Wash Buffer I, II, and III DTT (Use is optional. Follow manufacturer's instructions for amount to add.)

EQUIPMENT

<u>Misonix sonicator with microtip</u> (QSonica, Newton, CT, USA) <u>Thermocycler</u> (any vendor) <u>Benchtop centrifuge (any vendor)</u> <u>Vortex</u> (any vendor) <u>Spectrophotometer</u> (P/N ND-1000, NanoDrop) <u>Heat block</u> (95°C) (any vendor) <u>Tecan HS4800 Pro</u> (Tecan, Durham, NC, USA) <u>Speed-vac</u> (Thermo Savant) <u>Axon 4000B</u> (P/N 4000B, Molecular Devices)

Reduced Ozone environment (optional)

PROCEDURE

↔ USE FILTERED STERILIZED WATER FOR ALL STEPS

RANDOMER PREPATION

- 36. Centrifuge lyophilized primer to collect at the bottom of tube.
- 37. Using fresh Randomer Buffer, add enough Buffer to rehydrate to 1 OD/42 µL.
- 38. Invert tube several times.
- 39. Centrifuge to collect liquid at bottom of tube.
- 40. Incubate at room temperature for 5-10 minutes protected from light.
- 41. Invert and centrifuge tube once again.
- 42. Aliquot 42 μL of primer to fresh, sterile thin-walled PCR strip tubes (0.2 mL).



Primers can be stored at -20°C protected from light until ready for sample labeling. Thaw frozen primers protected from light at room temperature. Centrifuge tubes before adding sample.

DNA SONICATION & QC

- 43. In separate 1.5 mL tubes, bring 2 μ g of genomic DNA to a final volume of 80 μ L using dH₂O for both the test sample and a reference sample.
- 44. Flick tubes to mix contents, and centrifuge to collect liquid at bottom.
- 45. Incubate tubes at 55°C for 5-10 minutes to ensure DNA is in solution.
- 46. Flick tubes to mix contents and centrifuge to collect liquid at bottom again.
- 47. Store DNA on ice while preparing for sonication.
- 48. Using a Misonix sonicator, clean tip with 10% bleach followed by 80%-100% ethanol.

49. To sonicate DNA, place tip near bottom of tube and follow sonication protocol. Sonication Protocol:

Total Time	11 sec
on/off	0.5 sec
Amp	1.0

- 50. Return DNA to ice after sonication. Repeat tip cleaning with bleach and ethanol before sonicating next sample.
- 51. Run 5 µL of sonicated genomic DNA on 1% agarose gel. Confirm a smear between 200-2,000 bp.



DNA can be stored at 4°C (less than one week) or -20°C (long term storage).

DNA AMPLIFICATION & LABELING

- 52. Add 40 µL sonicated DNA to 42 µL pre-aliquoted Cy3/Cy5 randomers. (Test DNA to Cy3, Reference DNA to Cy5)
- 53. Incubate mixture at 98°C for 5-10 min.
- 54. Ice water bath to snap-cool mixture while making master mix for at least 2 min.
- 55. Add 20 µL master mix to cooled mixture.
- 56. Aspirate up and down 10x using pipette. Centrifuge to collect liquid at bottom of tube
- 57. Incubate at 37°C for 4 hours.
- 58. Incubate at 98°C for 5-10 min. Ice water bath to snap-cool for at least 2 min.
- 59. Add 1 µL Klenow, mix well by flicking bottom of tube. Centrifuge to collect liquid.
- 60. Incubate 37°C over night.

DNA PRECIPITATION

- 61. Add 10 µL EDTA (0.5M) to stop reaction.
- 62. Add 11.5 µL NaCL (5 M) to each tube.
- 63. Vortex briefly and centrifuge to collect liquid at bottom of tube.
- 64. Add 110 µL room temperature Isopropanol to 1.5mL tube.
- 65. Transfer stopped reaction (121.5 μ L) to 1.5 mL tube containing Isopropanol.
- 66. Vortex briefly and centrifuge to collect liquid at bottom of tube.
- 67. Incubate at room temperature for 10 minutes shielded from light.

* At this point, I pool the references together to minimize loss.

REFERENCE: 3 references

Add 330 µL Isopropanol to 1.5 mL tube.

Transfer three stopped reactions to same tube.

Vortex briefly and centrifuge to collect liquid at bottom of tube.

Incubate at room temperature for 10 minutes shielded from light).

- 68. Centrifuge at max speed for 10 min.
- 69. Remove supernatant with pipette (232 μ L).
- 70. Rinse with 500 μ L of ice cold ethanol (80%) be sure to dislodge pellet.
- 71. Centrifuge at max speed for 2 min.
- 72. Remove supernatant with pipette (500 μ L).
- 73. Speedvac-low for 5 min to dry pellet.



DNA pellet can be stored at -20°C protected from light and in sealed bag with desiccant (optional).

CONJUGATE REACTIVE DYES TO AMPLIFIED DNA

- 74. Rehydrate DNA in 10 μ L dH₂O and warm in 52°C heat block for 5 min.
- 75. Add 6 μL of Labeling Buffer to rehydrated DNA. Mix gently and centrifuge to collect liquid at bottom of tube.
- 76. Add 4 μ L of DMSO to reactive dye. Vortex for 10 sec and centrifuge to collect liquid at bottom of tube.
- 77. Add the prepared DNA (16 μ L) to dye. Vortex to ensure well mixed and centrifuge to collect liquid at bottom of tube.
- 78. Incubate for 1 hour at room temperature in the dark.
- 79. Add 90 μ L dH₂O and follow precipitation steps starting with addition of NaCl (Step 27).



Once precipitated, DNA pellet can be stored at -20°C protected from light and in sealed bag with desiccant (optional).

LABELED DNA QUANTIFICATION AND HYBRIDIZATION PREP

- 48. Rehydrate precipitated DNA in 20 μ L dH₂O water.
- 49. Quantify labeled DNA on Nanodrop.
- *

Use the Microarray Module to quantify Cy3 or Cy5 activity and DNA concentration.

The linear range of this module is 740 ng/ μ L.

To ensure the measured DNA is within the limit of the reader, dilute DNA 1:4 and adjust calculations accordingly.

Specific Activity should be > 20 pmol/ μ g, minimum 22 μ g amplified.

- 72. Merge equal amounts of test, reference each.
- 73. Dry down.

Mixed DNA pellet can be stored at -20°C protected from light and in sealed bag with desiccant (optional).

74. Re-hydrate mixed DNA pellet in 26 μ L H₂O.

75. Incubate at 55°C for 5-10 minutes. Gently tap bottom of tube to mix. Centrifuge.

HYBRIDIZATION SOLUTION, WASH SOLUTION, AND MACHINE PREPARATION

76. Make Wash Solution I, II, III.

- 77. De-gas 1x Wash buffers:
 - a. Allow Wash I (1x) to heat to 37°C for at least 30 minutes.
 - b. Place Wash II (1x) and III (1x) under vacuum for at least 20 minutes.
- 78. Make blank hybridization solution (130 µL/array).
- 79. Make hybridization solution (64.0 μ L/array).
- 80. Add 64 µL Hybridization Solution to sample.
- 81. Incubate Blank and Samples at 95°C for five minutes.
- 82. Hold at 52°C until ready.
- 83. Place correct lines to designated Wash Buffer.

- 84. Prime each line for 30 seconds.
- 85. Begin hybridization/wash program: Emory v10.

86. RECIPES

Randomer Buffer (make fresh every time)

Component		1x (uL)
DI, sterile H2O		861
Tris-HCl (1M) (pH 7.4)		125
MgCl2 (1M)		12.5
B-MercaptoEtOH (98%)		1.75
	TOTAL	1000

Rehydrate 9mers to 1 OD/42 µL

Add 1050 μ L of Randomer Buffer to 25 ODs. This gives a final concentration of 1 OD/42 μ L.

TE (10x) (*store at room temperature*)

Components	1x (mL)
Tris-HCl (1M)	1.	.5
EDTA (.5M)	0.	.3
DI, sterile H2O	13	.2
T	otal 1	5

Aha-dNTP Mix (50x) (store at -20°C)

Component	1x (uL)	Final Concentration		
DI, sterile H2O	91			
TE (10x)	21			
dATP (100mM)	21	10 mM		
dGTP (100mM)	21	10 mM		
dTTP (100mM)	7	3.33 mM		
dCTP (100mM)	21	10 mM		
dUPT (50 mM)	28	6.67 mM		
SUM	210			

Master Mix (for DNA amplification and labeling)

Component		1x (uL)
DI, sterile H2O		9
aha-dNTPs (50x)		10
Klenow (50U/uL)		1
Т	otal	20

Labeling Buffer (for reactive dye conjugation to aha-amplified sample)

Component	1x
DI, sterile H2O	1 mL
Sodium Bicarbonate	25 mg

Add 25 mg of Sodium Bicarbonate to 1 mL of deionized water. Vortex to get into solution. Aliquot 200μ L to 1.5mL tubes, store at -20° C.

CPK6 Alignment Oligo Dilutions

Cy3 CPK6 dilutions - w	vant 50 nM	
For 50 uM	50.7nmol/1.014 mL	
	Add 1.014 mL H2O to rehyrdate.	
For 500 nM	10 uL(50 uM) + 990 uL H2O.	
For 50 nM	150 uL(500 nM) + 1350 uL H2O	
	Aliquot out 15 uL to 0.2 mL tubes.	
Cy5 CPK6 dilutions - v	vant 100 nM	
	vant 100 nM 34.9nmol/0.698 mL	
For 50 uM	34.9nmol/0.698 mL	
For 50 uM For 500 nM	34.9nmol/0.698 mL Add 0.698 mL H2O to rehyrdate.	

Combine and dry down 50 uM and 500 nM dilutions for future use.

Hybridization Solutions

Blank Solution (to load onto arrays prior to sample loading)

Component	1x Tecan
H2O	37.73
2X Hybridization Buffer	65.00
Hybridization Component A	26.00
Alignment oligo-Cy3 (50 nM)	1.13
Alignment oligo-Cy5 (100 nM)	0.27
Total	130
	``

Make BLANK hyb solutions (130 uL / array).

Hybridization Solution (to add to re-hydrated sample)

Component	1x (Tecan)
Merged labl'd sample	26.0
2X Hybridization Buffer	45
Hybridization Component A	18
Alignment oligo-Cy3 (50 nM)	0.78
Alignment oligo-Cy5 (100 nM)	0.18
Total	64.0
Hyb mix + sample - total	90.0

Wash Buffers

Follow manufacturer's instructions to make 1x solution. Use filtered (0.2um), sterile water to dilute.

For the Tecan HS4800Pro and Emory wash program v10:

Bottle 1: Wash Buffer 1 Bottle 2: Wash Buffer 2 Bottle 3: Wash Buffer 3 Bottle 5: dH₂0

Volumes estimates (11mL/minute) :

Bottle 1: 580mL + (11mL/minute * 6.5minute * number of arrays)
Bottle 2: 305mL + (11mL/minute * 0.5minute * number of arrays)
Bottle 3: 305mL + (11mL/minute * 0.5minute * number of arrays)
Bottle 5: 380mL + (11mL/minute * 1.0minute * number of arrays)

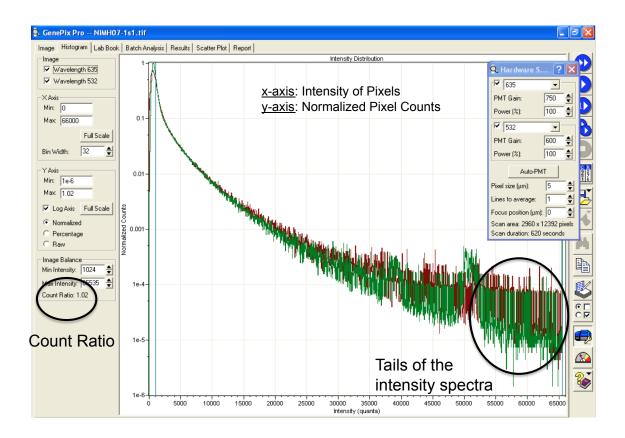


Figure 5.3 – Scanning parameters as informed by the Intensity Distribution Histogram

Log2 Variance of Probes: Subarray A01

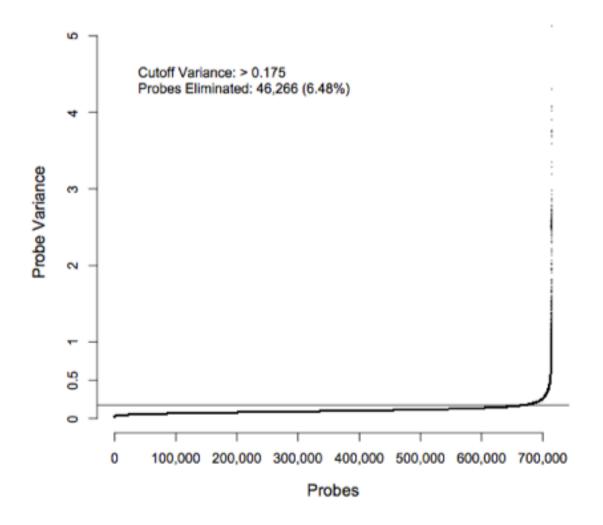


Figure 5.4 – Probe Variance Analysis

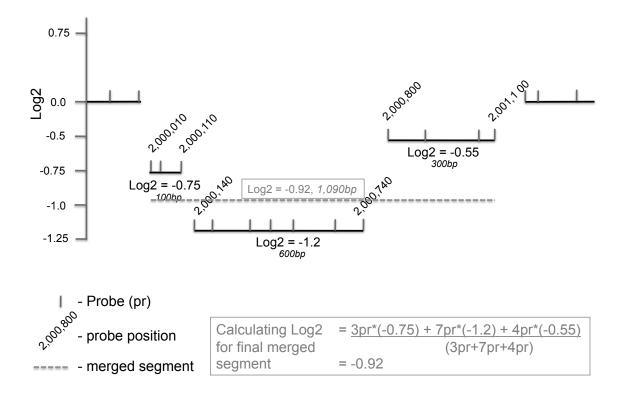


Figure 5.5 - Hypothetical example of merging multiple segments representing a single, deleted locus.

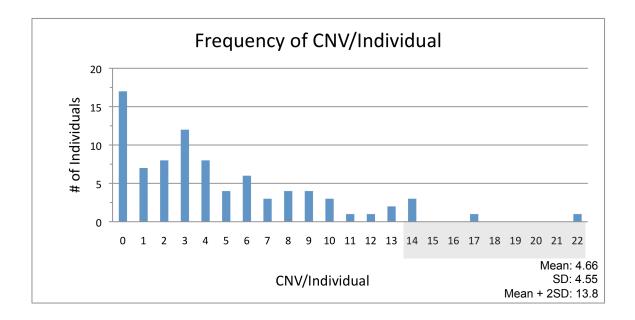
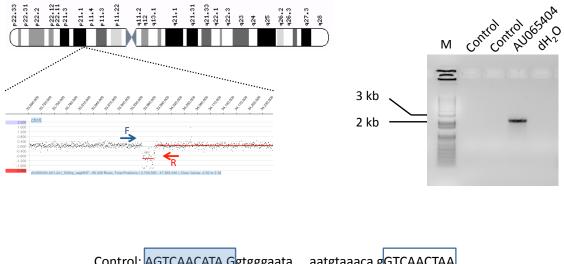


Figure 5.6 – Histogram of the number of CNV calls per individual.



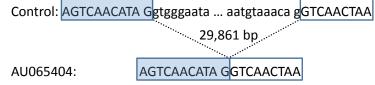


Figure 5.7 - Validation of an array identified deletion.

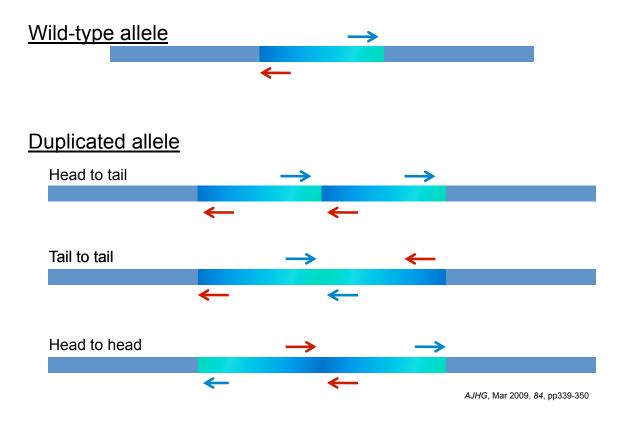


Figure 5.8 – Validation strategy for tandem duplications.

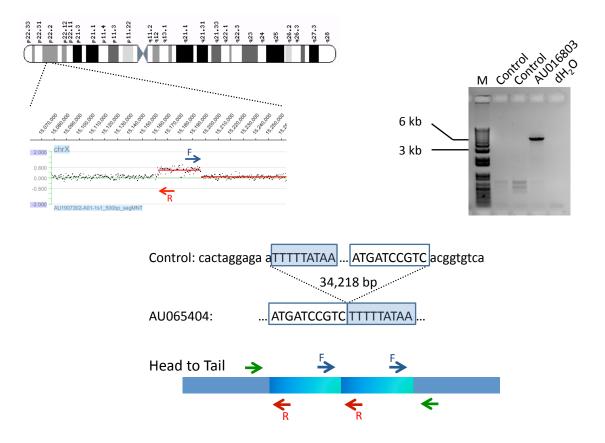


Figure 5.9 - Validation of an array identified duplication.

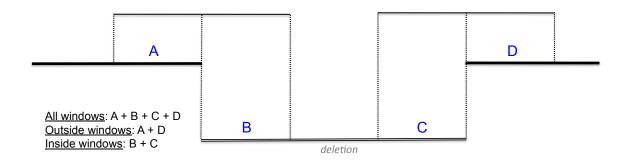


Figure 5.10 – Schematic for breakpoint junction analysis.

Appendix

1. Tables A.1 – A.4

Tables A.1-A.4 list the copy number variants (CNV) identified by the four combinations of array resolution (385,000 (385K) or 2,100,000 probes (2.1M)), array processing protocol (NimbleGen's or our optimized protocol), and sample population (Autism Genetic Resource (AGRE) males with autism, Simons Simplex Collection (SSC) males with autism, or National Institute of Mental Health (NIMH) control population).

CNV shaded in 'grey' indicate CNV or indel grouped together because 1) CNV or indel upstream and/or downstream breaks end within three kilobases of the next segment or 2) CNV or indel are called with complete overlap. 'Yellow' log2 values indicate a minority state (e.g., single deletion among several duplications) within a grouping.

Column headers for these tables are defined as:

<u>ARRAY_ID</u>	Name of original scan file (.tiff)
<u>Sample</u>	Sample ID
CHR	Chromosome
START	Start position (Hg18)
<u>STOP</u>	End position (Hg18)
SIZE	Length of segment in base pairs
<u>Probes</u>	Number of probes that called the segment
Probes/kb	Number of probes per kilobase
<u>LOG2_RATIO</u> The average Log2 ratio of the Cy3 (test) to Cy5 (reference) intensity	
<u>GC</u>	The percent GC content of the segment

2. Table A.5

Table A.5 list CNV and indel identified in the literature with breakpoint sequencing. The data are derived from the following 12 reports:

1 Conrad, D.F., et al., Origins and functional impact of copy number variation in the human genome. Nature, 2010. 464(7289): p. 704-12.

2 de Smith, A.J., et al., Array CGH analysis of copy number variation identifies 1284 new genes variant in healthy white males: implications for association studies of complex diseases. Hum Mol Genet, 2007. 16(23): p. 2783-94.

3 Nichol Edamura, K. and C.E. Pearson, DNA methylation and replication: implications for the "deletion hotspot" region of FMR1. Hum Genet, 2005. 118(2): p. 301-4.

4 Korbel, J.O., et al., Systematic prediction and validation of breakpoints associated with copy-number variants in the human genome. Proc Natl Acad Sci U S A, 2007. 104(24): p. 10110-5.

5 Goldmann, R., et al., Genomic characterization of large rearrangements of the LDLR gene in Czech patients with familial hypercholesterolemia. BMC Med Genet, 2010. 11: p. 115.

6 Kim, P.M., et al., Analysis of copy number variants and segmental duplications in the human genome: Evidence for a change in the process of formation in recent evolutionary history. Genome Res, 2008. 18(12): p. 1865-74.

7 Lam, H.Y., et al., Nucleotide-resolution analysis of structural variants using BreakSeq and a breakpoint library. Nat Biotechnol, 2010. 28(1): p. 47-55.

8 Nobile, C., et al., Analysis of 22 deletion breakpoints in dystrophin intron 49. Hum Genet, 2002. 110(5): p. 418-21.

9 Park, H., et al., Discovery of common Asian copy number variants using integrated high-resolution array CGH and massively parallel DNA sequencing. Nat Genet, 2010. 42(5): p. 400-5.

10 Vissers, L.E., et al., Rare pathogenic microdeletions and tandem duplications are microhomology-mediated and stimulated by local genomic architecture. Hum Mol Genet, 2009. 18(19): p. 3579-93.

11 Woodward, K.J., et al., Heterogeneous duplications in patients with Pelizaeus-Merzbacher disease suggest a mechanism of coupled homologous and nonhomologous recombination. Am J Hum Genet, 2005. 77(6): p. 966-87.

12 Zhang, F., et al., Mechanisms for nonrecurrent genomic rearrangements associated with CMT1A or HNPP: rare CNVs as a cause for missing heritability. Am J Hum Genet, 2010. 86(6): p. 892-903.

13 Emory - CNV and indel identified, validated, and breakpoint sequenced (AGRE and SSC cohorts)

Column headers for this table are defined as:

Ref	The first author of the reference from which the CNV/indel came.
<u>Chr</u>	Chromosome
<u>Start</u>	Start Position (Hg18)
<u>Stop</u>	Stop Position (Hg18)
state	Deletion or duplication or inversion
<u>homology</u>	Any homology noted at the breakpoints. '?' indicates that the original authors/I did not search for homologies

hom. Length
insertionLength of the observed homology
Any insertion sequence found at the breakpointinsertion (remove spaces)Any insertion sequence found at the breakpoint - no spaces
in the sequenceins. LengthLength of the observed insertionIDID the authors may have assigned to the CNV/indel

3. Tables A.6.a-b

These two tables list validated calls by the NimbleGen and Optimized protocols. The

NimbleGen protocol was run on 50 AGRE samples, and the Optimized protocol was run

on 100 AGRE and 64 SSC samples. Both protocols were applied to the 2.1M CCGH

array.

The headers for the true (A.6.a) and falsely (A.6.b) called tables are defined as:

ARRAY_ID	Name of original scan file (.tiff)	
Sample	Sample ID	
<u>CHR</u>	Chromosome	
<u>START</u>	Start position (Hg18)	
<u>STOP</u>	End position (Hg18)	
<u>SIZE (bp)</u>	Length of segment in base pairs (bp)	
Probes	Number of probes that called the segment	
Probes/kb	Number of probes per kilobase (kb)	
Mean_Log2	The average Log2 ratio of the Cy3 (test) to Cy5 (reference) intensity	
<u>GC</u>	The percent GC content of the segment	
Primer Set	The primer set used to validate the locus	
<u>CGH_Protocol</u> Which CGH protocol was used: NG (NimbleGen) or Opt (Optimized)		

Table A.1 – CNV from four AGRE samples run on 385K arrays by the NimbleGen protocol.

ARRAY_ID	Sample	CHR	START	STOP	SIZE	Probes	Probes/kb	LOG2_RATIO	GC
AU028304-1s3	AU028304	chrX	34,063,446	34,065,771	2,325	8	3.4	0.55	34.0
AU004404-1s2	AU004404	chrX	67,040,957	67,046,757	5,800	16	2.8	-0.61	37.2
AU028304-1s3	AU028304	chrX	69,648,398	69,649,328	930	4	4.3	-0.88	45.8
AU004404-1s2	AU004404	chrX	78,808,938	78,811,924	2,986	10	3.3	0.69	34.5
AU028304-1s3	AU028304	chrX	78,809,398	78,811,444	2,046	7	3.4	0.63	36.4
AU015004-1s1	AU015004	chrX	78,809,398	78,811,193	1,795	6	3.3	0.87	38.3
AU028304-1s3	AU028304	chrX	115,051,644	115,066,806	15,162	30	2.0	0.37	38.2
AU004404-1s2	AU004404	chrX	115,051,999	115,057,702	5,703	18	3.2	0.54	36.1
AU002204-1s3	AU002204	chrX	115,052,833	115,057,262	4,429	14	3.2	0.41	34.6
AU015004-1s1	AU015004	chrX	115,053,308	115,056,847	3,539	12	3.4	0.64	33.7
AU004404-1s2	AU004404	chrX	126,425,995	126,430,002	4,007	11	2.7	0.62	31.3
AU028304-1s3	AU028304	chrX	126,425,995	126,428,962	2,967	8	2.7	0.64	32.1
AU004404-1s2	AU004404	chrX	147,317,361	147,318,588	1,227	5	4.1	-0.93	38.9
AU028304-1s3	AU028304	chrX	147,317,361	147,318,588	1,227	5	4.1	-0.85	38.9
AU004404-1s2	AU004404	chrX	148,451,913	148,462,535	10,622	30	2.8	-0.46	42.9
AU004404-1s2	AU004404	chrX	148,686,217	148,836,095	149,878	298	2.0	0.27	40.7

Table A.2 - CNV from 50 AGRE samples run on 2.1M arrays by the NimbleGen protocol.

AU0780301-1s1A01	AU0780301	chrX	34,063,531	34,065,771	2,240	33	14.7	0.43	34.1
AU016803-1s1A01	AU016803	chrX	34,063,631	34,065,771	2,140	31	14.5	0.46	34.4
AU002403-1s1A01	AU002403	chrX	34,063,839	34,065,771	1,932	28	14.5	0.67	35.3
AU009503-1s1A01	AU009503	chrX	34,063,839	34,065,771	1,932	28	14.5	0.69	35.3
AU029303-1s1A01	AU029303	chrX	34,063,839	34,065,846	2,007	29	14.4	0.78	36.1
AU083504-1s1A01	AU083504	chrX	34,063,839	34,065,846	2,007	29	14.4	0.57	36.1
AU0875302-1s2A01	AU0875302	chrX	34,063,839	34,065,771	1,932	28	14.5	0.57	35.3
AU012004-1s2A01	AU012004	chrX	36,652,992	36,653,157	165	5	30.3	-0.78	47.1
AU014505-1s1A01	AU014505	chrX	36,652,992	36,653,217	225	6	26.7	-1.64	46.4
		chrX					26.7		
AU016803-1s1A01	AU016803		36,652,992	36,653,217	225	6		-1.63	46.4
AU080803-1s1A01	AU080803	chrX	36,652,992	36,653,217	225	6	26.7	-1.63	46.4
AU083504-1s1A01	AU083504	chrX	36,652,992	36,653,217	225	6	26.7	-1.91	46.4
AU028903-1s1A01	AU028903	chrX	38,029,782	38,032,254	2,472	38	15.4	-0.26	48.5
AU034904-1s1A01	AU034904	chrX	38,208,962	38,210,787	1,825	39	21.4	-0.34	37.5
AU009503-1s1A01	AU009503	chrX	38,209,627	38,210,842	1,215	26	21.4	-0.50	37.9
AU055503-1s1A01	AU055503	chrX	38,547,627	38,550,411	2,784	59	21.2	0.31	63.0
AU034604-1s1A01	AU034604	chrX	39,525,943	39,549,870	23,927	385	16.1	0.47	45.9
AU009503-1s1A01	AU009503	chrX	39,628,002	39,628,334	332	8	24.1	-0.72	41.5
AU024003-1s1A01	AU024003	chrX	41,096,920	41,097,246	326	8	24.5	-0.69	42.4
AU074704-1s1A01	AU074704	chrX	42,163,664	42,164,864	1,200	26	21.7	-0.31	42.7
AU009503-1s1A01	AU009503	chrX	43,830,073	43,834,898	4,825	81	16.8	-0.32	43.5
					· · · · · · · · · · · · · · · · · · ·				
AU018304-1s1A01	AU018304	chrX	43,844,730	43,845,335	605	14	23.1	-0.55	47.6
AU0852304-1s1A01	AU0852304	chrX	44,265,421	44,265,881	460	11	23.9	-0.52	36.7
AU024003-1s1A01	AU024003	chrX	45,703,426	45,704,121	695	16	23.0	0.44	53.7
AU034604-1s1A01	AU034604	chrX	46,190,999	46,193,830	2,831	53	18.7	0.31	54.1
AU034904-1s1A01	AU034904	chrX	46,580,348	46,581,804	1,456	25	17.2	0.44	56.1
AU024003-1s1A01	AU024003	chrX	46,888,299	46,888,847	548	9	16.4	0.75	52.9
AU034604-1s1A01	AU034604	chrX	46,888,299	46,888,812	513	8	15.6	0.98	53.2
AU030603-1s3A01	AU030603	chrX	46,888,484	46,888,812	328	7	21.3	1.11	54.4
AU062203-1s1A01	AU062203	chrX	46,888,484	46,888,847	363	8	22.0	0.72	53.8
AU083603-1s1A01	AU083603	chrX	46,888,484	46,888,847	363	8	22.0	0.60	53.8
AU032705-1s1A01	AU032705	chrX	46,888,529	46,888,847	318	7	22.0	0.67	54.9
AU065404-1s1A01	AU065404	chrX	46,888,599	46,888,812	213	5	23.5	1.11	60.2
AU038805-1s1A01	AU038805	chrX	46,963,626	46,965,349	1,723	37	21.5	0.29	53.0
AU043803-1s1A01	AU043803	chrX	46,964,064	46,965,589	1,525	33	21.6	-0.35	50.1
AU016803-1s1A01	AU016803	chrX	47,226,156	47,226,756	600	14	23.3	-0.49	46.0
AU058103-1s1A01	AU058103	chrX	47,226,241	47,226,756	515	12	23.3	-0.53	47.9
AU074704-1s1A01	AU074704	chrX	47,226,241	47,226,756	515	12	23.3	-0.56	47.9
AU018003-1s1A01	AU018003	chrX			415	10	24.1	-0.73	48.2
		-	47,226,341	47,226,756					
AU028903-1s1A01	AU028903	chrX	47,322,258	47,322,828	570	13	22.8	-0.58	51.3
AU004803-1s1A02	AU004803	chrX	47,377,313	47,379,754	2,441	39	16.0	-0.28	46.6
AU056603-1s1A02	AU056603	chrX	47,377,313	47,379,754	2,441	39	16.0	-0.40	46.6
AU043803-1s1A02	AU043803	chrX	47,378,054	47,379,930	1,876	39	20.8	-0.47	45.8
AU016803-1s1A02	AU016803	chrX	47,378,074	47,379,704	1,630	35	21.5	-0.35	46.1
AU028903-1s1A02	AU028903	chrX	47,468,996	47,469,816	820	18	22.0	-0.57	55.2
AU038805-1s1A02		chrX				16		0.43	55.6
	AU038805		47,469,046	47,469,741	695		23.0		
AU056003-1s1A02	AU056003	chrX	47,469,046	47,469,741	695	16	23.0	0.46	55.6
AU066103-1s1A02	AU066103	chrX	47,469,071	47,469,866	795	17	21.4	-0.53	55.2
AU008504-1s1A02	AU008504	chrX	47,814,113	47,818,002	3,889	56	14.4	0.28	49.2
AU018003-1s1A02	AU018003	chrX	47,829,938	47,830,368	430	10	23.3	-0.85	44.8
AU058103-1s1A02	AU058103	chrX	48,219,896	48,221,146	1,250	27	21.6	-0.40	47.2
AU066103-1s1A02	AU066103	chrX	48,219,966	48,221,126	1,160	25	21.6	-0.61	45.9
AU009503-1s1A02	AU009503	chrX	48,220,021	48,221,126	1,105	24	21.7	-0.50	45.5
AU028903-1s1A02	AU028903	chrX	48,220,021	48,221,221	1,200	26	21.7	-0.42	46.3
AU034904-1s1A02	AU034904	chrX	48,220,021	48,221,051	1,030	23	22.3	-0.35	45.0
AU038805-1s1A02	AU038805	chrX	48,220,021	48,221,126	1,105	24	21.7	0.30	45.5
AU043803-1s1A02	AU043803	chrX	48,220,021	48,221,126	1,105	24	21.7	-0.59	45.5
AU055503-1s1A02	AU055503	chrX	48,220,021	48,221,146	1,125	25	22.2	-0.41	45.6
AU034904-1s1A02	AU034904	chrX	48,271,876	48,272,356	480	11	22.9	-0.48	48.3
AU018003-1s1A02	AU018003	chrX	48,271,941	48,272,406	465	11	23.7	-0.67	49.4
AU018003-1s1A02	AU018003	chrX	48,276,384	48,278,319	1,935	40	20.7	-0.39	51.0
AU028903-1s1A02	AU028903	chrX	48,276,384	48,278,284	1,900	39	20.5	-0.45	51.1
AU043803-1s1A02	AU043803	chrX	48,276,384	48,278,379	1,995	41	20.6	-0.48	50.6
AU056003-1s1A02	AU056003	chrX	48,276,454	48,278,944	2,490	44	17.7	0.28	50.2
AU058503-1s1A02	AU058503	chrX	48,453,617	48,458,412	4,795	100	20.9	-0.36	44.6
					4,795				
AU034904-1s1A02	AU034904	chrX	48,453,752	48,458,562		100	20.8	-0.34	44.7
AU056803-1s1A02	AU056803	chrX	48,453,917	48,462,698	8,781	162	18.4	-0.23	45.1
AU043803-1s1A02	AU043803	chrX	48,454,787	48,458,412	3,625	76	21.0	-0.59	44.7
AU058103-1s1A02	AU058103	chrX	48,456,222	48,462,698	6,476	114	17.6	-0.30	44.8
AU028903-1s1A02	AU028903	chrX	48,530,120	48,531,142	1,022	22	21.5	-0.56	48.3
AU014803-1s1A02	AU014803	chrX	48,530,197	48,531,062	865	19	22.0	-0.33	47.9
AU014803-1s1A02 AU018003-1s1A02	AU014803 AU018003				865	19	22.0	-0.49	47.9
		chrX	48,530,197	48,531,062					
AU034904-1s1A02	AU034904	chrX	48,530,197	48,531,062	865	19	22.0	-0.44	47.9
AU043803-1s1A02	AU043803	chrX	48,530,197	48,530,987	790	18	22.8	-0.91	47.4
AU055503-1s1A02	AU055503	chrX	48,530,197	48,531,062	865	19	22.0	-0.62	47.9
AU056603-1s1A02	AU056603	chrX	48,530,197	48,531,087	890	20	22.5	-0.55	48.1
AU058103-1s1A02	AU058103	chrX	48,530,197	48,531,087	890	20	22.5	-0.55	48.1
AU058503-1s1A02	AU058503	chrX	48,530,197	48,531,062	865	19	22.0	-0.52	47.9
AU009503-1s1A02	AU009503	chrX	48,530,217	48,530,987	770	17	22.1	-0.61	47.1
		Crit A			,,,,			0.01	-
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AU021503-1s1A02	AU021503	chrX	48,530,217	48,531,062	845	18	21.3	-0.42	47.6
AU066103-1s1A02	AU066103	chrX	48,530,217	48,530,987	770	17	22.1	-0.97	47.1
AU0780301-1s1A02	AU0780301	chrX	48,530,217	48,531,087	870	19	21.8	-0.37	47.8
AU043803-1s1A02	AU043803	chrX	48,788,958	48,799,173	10,215	98	9.6	-0.39	50.3
AU018003-1s1A02	AU018003	chrX	48,794,839	48,795,977	1,138	19	16.7	-0.52	48.0
AU066103-1s1A02	AU066103	chrX	48,794,874	48,797,608	2,734	39	14.3	-0.52	46.7
AU028903-1s1A02	AU028903	chrX	48,798,558	48,799,268	710	16	22.5	-0.53	50.8
AU028903-1s1A02	AU028903	chrX	48,823,450	48,824,287	837	18	21.5	-0.54	53.9
AU008504-1s1A02	AU008504	chrX	48,908,480	48,909,147	667	15	22.5	0.49	56.3
AU028903-1s1A02	AU028903	chrX	48,941,474	48,943,347	1,873	40	21.4	-0.39	55.1
AU043803-1s1A02	AU043803	chrX	48,967,547	48,968,172	625	14	22.4	-0.71	51.7
AU038805-1s1A02									
	AU038805	chrX	48,995,154	48,996,304	1,150	25	21.7	0.39	53.1
AU028903-1s1A02	AU028903	chrX	48,995,264	48,996,414	1,150	25	21.7	-0.60	52.7
AU043803-1s1A02	AU043803	chrX	48,995,294	48,996,284	990	21	21.2	-0.79	52.5
AU055503-1s1A02	AU055503	chrX	48,995,294	48,996,304	1,010	22	21.8	-0.55	52.3
AU066103-1s1A02	AU066103	chrX	48,995,294	48,996,304	1,010	22	21.8	-0.62	52.3
AU058103-1s1A02	AU058103	chrX	48,995,364	48,996,304	940	21	22.3	-0.50	52.1
AU018003-1s1A02	AU018003	chrX	48,995,439	48,996,284	845	18	21.3	-0.47	52.5
	AU080803	chrX			700	16	22.9	0.59	59.2
AU080803-1s1A02			49,012,390	49,013,090					
AU0920301-1s1A02	AU0920301	chrX	49,012,490	49,013,180	690	16	23.2	0.39	59.2
AU066103-1s1A02	AU066103	chrX	49,720,668	49,721,053	385	9	23.4	-0.71	39.3
AU034904-1s1A02	AU034904	chrX	50,145,837	50,146,797	960	21	21.9	-0.64	44.7
AU066103-1s1A02	AU066103	chrX	50,145,837	50,146,797	960	21	21.9	-0.66	44.7
AU017504-1s1A02	AU017504	chrX	50,145,957	50,146,797	840	19	22.6	-0.60	44.4
AU021503-1s1A02	AU021503	chrX	50,145,957		840	19	22.6	-0.52	44.4
				50,146,797					
AU055503-1s1A02	AU055503	chrX	50,145,957	50,146,797	840	19	22.6	-0.57	44.4
AU018003-1s1A02	AU018003	chrX	50,146,172	50,146,797	625	14	22.4	-0.73	44.3
AU030603-1s3A02	AU030603	chrX	50,146,422	50,146,797	375	9	24.0	-0.82	41.8
AU008504-1s1A02	AU008504	chrX	50,146,517	50,146,797	280	7	25.0	-0.80	42.9
AU074704-1s1A02	AU074704	chrX	50,146,517	50,146,797	280	7	25.0	-0.85	42.9
AU083504-1s1A02	AU083504	chrX	50,146,517	50,146,797	280	7	25.0	-0.89	42.9
AU012004-1s2A02	AU012004	chrX	50,146,567	50,146,797	230	6	26.1	-0.85	43.2
AU034904-1s1A02	AU034904	chrX	50,572,385	50,574,411	2,026	42	20.7	0.33	60.1
AU018003-1s1A02	AU018003	chrX	51,627,974	51,629,858	1,884	28	14.9	-0.46	44.4
AU043803-1s1A02	AU043803	chrX	51,628,034	51,629,199	1,165	24	20.6	-0.59	41.8
AU034904-1s1A02	AU034904	chrX	51,628,124	51,629,129	1,005	22	21.9	-0.47	42.1
AU058503-1s1A02	AU058503	chrX	51,628,194	51,629,199	1,005	22	21.9	-0.51	42.0
AU009503-1s1A02	AU009503	chrX	51,628,384	51,629,104	720	16	22.2	-0.61	42.3
AU0780301-1s1A02		chrX	53,081,197	53,082,112	915	20	21.9	-0.35	43.3
AU009503-1s1A02	AU009503	chrX	53,097,412	53,108,214	10,802	158	14.6	-0.35	45.1
AU043803-1s1A02	AU043803	chrX	53,097,412	53,107,174	9,762	140	14.3	-0.38	45.6
AU0920301-1s1A02	AU0920301	chrX	53,099,892	53,102,717	2,825	53	18.8	0.36	48.1
AU008504-1s1A02	AU008504	chrX	53,100,432	53,102,672	2,240	47	21.0	0.42	48.1
AU032705-1s1A02	AU032705	chrX	53,100,432	53,102,212	1,780	38	21.3	0.39	48.7
AU038805-1s1A02	AU038805	chrX	53,100,452	53,102,317	1,865	39	20.9	0.45	48.6
AU014505-1s1A02	AU014505	chrX	53,100,517	53,102,427	1,910	40	20.9	0.39	48.3
AU028903-1s1A02	AU028903	chrX	53,100,517	53,102,747	2,230	47	21.1	-0.63	47.6
AU056003-1s1A02	AU056003	chrX	53,100,517	53,102,557	2,040	43	21.1	0.33	48.3
AU058503-1s1A02	AU058503	chrX	53,100,517	53,107,369	6,852	89	13.0	-0.29	46.2
AU021503-1s1A02	AU021503	chrX	53,126,892	53,127,752	860	17	19.8	-0.43	61.1
AU066103-1s1A02	AU066103	chrX	53,439,228	53,439,718	490	11	22.4	-0.69	45.2
AU034904-1s1A02	AU034904	chrX	53,604,041	53,604,391	350	8	22.9	-0.71	46.9
AU018003-1s1A02	AU018003	chrX	54,524,898	54,525,338	440	10	22.7	-0.56	47.2
AU056803-1s1A02	AU056803	chrX	54,790,338	54,791,943	1,605	33	20.6	-0.35	44.2
AU0050803-151A02 AU004803-1s1A02	AU036803 AU004803	chrX	54,790,538			29	20.8	-0.35	44.2
				54,791,943	1,335				
AU018003-1s1A02	AU018003	chrX	54,790,608	54,791,943	1,335	29	21.7	-0.54	43.8
AU056603-1s1A02	AU056603	chrX	54,790,608	54,791,753	1,145	25	21.8	-0.47	43.7
AU0852304-1s1A02			54,790,608	54,792,093	1,485	32	21.5	-0.35	43.4
AU016803-1s1A02	AU016803	chrX	54,790,693	54,791,943	1,250	27	21.6	-0.44	43.4
AU021503-1s1A02	AU021503	chrX	54,790,693	54,792,008	1,315	28	21.3	-0.43	42.8
AU034904-1s1A02	AU034904	chrX	54,790,693	54,792,033	1,340	29	21.6	-0.46	42.9
AU055503-1s1A02	AU055503	chrX	54,790,693	54,792,008	1,315	28	21.3	-0.47	42.8
AU0780301-1s1A02			54,790,693	54,791,893	1,200	26	21.7	-0.39	43.8
AU009503-1s1A02	AU009503	chrX	54,790,763	54,791,893	1,130	25	22.1	-0.48	43.7
AU043803-1s1A02	AU043803	chrX	54,790,763	54,791,943	1,180	26	22.0	-0.51	43.3
AU066103-1s1A02	AU066103	chrX	54,790,763	54,791,868	1,105	24	21.7	-0.67	43.7
AU058103-1s1A02	AU058103	chrX	54,790,858	54,791,868	1,010	22	21.8	-0.49	44.6
AU083504-1s1A02	AU083504	chrX	54,964,123	54,965,178	1,055	23	21.8	0.41	57.1
AU080803-1s1A02	AU080803	chrX	54,964,213	54,965,519	1,306	28	21.4	0.43	55.6
AU066103-1s1A02	AU066103	chrX	55,043,872	55,044,637	765	17	22.2	-0.48	49.5
						42			
AU030603-1s3A02	AU030603	chrX	55,087,790	55,090,034	2,244		18.7	-1.14	40.3
AU066103-1s1A02	AU066103	chrX	55,790,524	55,790,929	405	9	22.2	-0.94	36.4
AU017504-1s1A02	AU017504	chrX	55,790,644	55,790,929	285	7	24.6	-0.90	35.7
AU029303-1s1A02	AU029303	chrX	55,790,644	55,790,929	285	7	24.6	-1.20	35.7
AU030603-1s3A02	AU030603	chrX	55,790,644	55,790,929	285	7	24.6	-1.16	35.7
AU032705-1s1A02	AU032705	chrX	55,790,644	55,790,929	285	7	24.6	-0.67	35.7
AU034604-1s1A02	AU034604	chrX	55,790,644	55,790,929	285	7	24.6	-1.06	35.7
AU034904-1s1A02	AU034904	chrX	55,790,644	55,790,929	285	7	24.6	-1.07	35.7
AU056603-1s1A02			55,790,644			7		-0.96	
	AU056603	chrX	55,790,644	55,790,929	285	/	24.6	-0.90	35.7
									220

AU065404 1c1402	ALIO65404	chrV	55 700 644	55 700 020	205	7	24.6	0.00	35.7
AU065404-1s1A02 AU017504-1s1A02	AU065404 AU017504	chrX chrX	55,790,644 56,804,741	55,790,929 56,805,726	285 985	19	24.6 19.3	-0.90 -0.52	46.9
AU024003-1s1A02	AU024003	chrX	56,804,741	56,805,631	890	17	19.1	-0.41	47.7
AU1038303-1s1A02	AU1038303	chrX	56,804,741	56,805,081	340	8	23.5	-0.87	48.6
AU008504-1s1A02	AU008504	chrX	56,804,861	56,805,231	370	9	24.3	-0.70	51.4
AU083603-1s1A02	AU083603	chrX	56,804,861	56,805,081	220	6	27.3	-0.99	51.3
AU0920301-1s1A02	AU0920301	chrX	57,617,045	57,634,875	17,830	262	14.7	0.40	43.0
AU050703-1s1A02	AU050703	chrX	57,763,081	57,768,570	5,489	70	12.8	0.79	35.1
AU083504-1s1A02 AU083504-1s1A02	AU083504 AU083504	chrX chrX	58,256,031 62,386,739	58,256,531 62,392,087	500 5,348	11 94	22.0 17.6	-0.59 0.47	46.1 31.6
AU083504-131A02	AU083504	chrX	62,410,230	62,436,937	26,707	343	12.8	0.38	40.6
AU014505-1s1A02	AU014505	chrX	62,410,410	62,415,998	5,588	110	19.7	0.70	43.2
AU0920301-1s1A02	AU0920301	chrX	62,410,410	62,415,948	5,538	109	19.7	0.43	43.1
AU009503-1s1A02	AU009503	chrX	63,363,769	63,364,774	1,005	22	21.9	-0.41	42.0
AU066103-1s1A02	AU066103	chrX	64,685,989	64,688,884	2,895	53	18.3	0.32	61.9
AU034904-1s1A02	AU034904	chrX	65,163,446	65,164,201	755	17	22.5	-1.33	42.0
AU016803-1s1A02	AU016803	chrX	65,382,556	65,399,668	17,112	328	19.2	0.39	38.4
AU034904-1s1A02	AU034904	chrX chrX	66,705,960 66,706,065	66,706,865	905 705	20	22.1 22.7	-0.52 -0.59	41.1 40.4
AU009503-1s1A02 AU018003-1s1A02	AU009503 AU018003	chrX	67,044,882	66,706,770 67,046,967	2,085	16 44	21.1	-0.60	39.0
AU030603-1s1A02	AU030603	chrX	67,045,802	67,046,892	1,090	24	22.0	-1.43	41.6
AU021503-1s1A02	AU021503	chrX	67,045,887	67,046,967	1,080	23	21.3	-0.85	41.2
AU066103-1s1A02	AU066103	chrX	67,879,957	67,880,347	390	8	20.5	-0.66	47.7
AU066103-1s1A02	AU066103	chrX	68,661,986	68,662,690	704	15	21.3	-0.58	44.5
AU009503-1s1A02	AU009503	chrX	68,662,061	68,662,690	629	14	22.3	-0.46	45.1
AU067803-1s2A02	AU067803	chrX	69,201,942	69,203,705	1,763	38	21.6	0.39	58.6
AU080803-1s1A02	AU080803	chrX	69,582,062	69,582,692	630	14	22.2	0.59	61.6
AU066103-1s1A02	AU066103	chrX	69,644,495	69,645,125	630	14	22.2	-0.55	47.4
AU030603-1s3A02	AU030603	chrX	69,648,398	69,650,576	2,178	30 6	13.8	-1.26	43.0
AU014505-1s1A02 AU018304-1s1A02	AU014505 AU018304	chrX chrX	70,057,777 70,057,777	70,057,992 70,057,992	215 215	6	27.9 27.9	1.02 1.04	39.2 39.2
AU018304-191A02 AU056003-191A02	AU018304 AU056003	chrX	70,281,553	70,282,617	1,064	23	27.9	0.32	59.2
AU0920301-1s1A02	AU0920301	chrX	70,281,553	70,282,817	1,282	25	20.3	0.43	58.1
AU080803-1s1A02	AU080803	chrX	70,281,623	70,282,463	840	19	22.6	0.65	58.7
AU043803-1s1A02	AU043803	chrX	70,292,124	70,293,024	900	20	22.2	-0.54	48.3
AU0920301-1s1A02	AU0920301	chrX	70,292,254	70,293,429	1,175	25	21.3	0.44	50.0
AU058103-1s1A02	AU058103	chrX	70,292,319	70,293,024	705	16	22.7	-0.47	48.6
AU018003-1s1A02	AU018003	chrX	70,292,354	70,292,994	640	14	21.9	-0.51	49.2
AU028903-1s1A02	AU028903	chrX	70,292,424	70,293,479	1,055	23	21.8	-0.50	49.7
AU083504-1s1A02	AU083504	chrX	70,714,603	70,716,868	2,265	48	21.2	0.43	60.0
AU008403-1s1A02 AU050703-1s1A02	AU008403 AU050703	chrX chrX	70,714,778 70,714,913	70,716,728 70,716,928	1,950 2,015	41 42	21.0 20.8	0.51 0.30	61.3 61.6
AU008504-1s1A02	AU008504	chrX	70,715,008	70,716,928	1,920	40	20.8	0.36	61.5
AU032705-1s1A02	AU032705	chrX	70,715,008	70,716,868	1,860	39	21.0	0.36	62.3
AU067803-1s2A02	AU067803	chrX	70,715,008	70,716,403	1,395	29	20.8	0.36	63.3
AU009904-1s1A02	AU009904	chrX	70,715,118	70,716,868	1,750	37	21.1	0.37	62.2
AU080803-1s1A02	AU080803	chrX	70,715,118	70,716,773	1,655	35	21.1	0.61	62.1
AU005304-1s1A02	AU005304	chrX	70,715,168	70,716,728	1,560	33	21.2	0.28	62.7
AU014505-1s1A02 AU038805-1s1A02	AU014505 AU038805	chrX chrX	70,715,248 70,715,248	70,716,868 70,716,773	1,620 1,525	34 32	21.0 21.0	0.37 0.33	63.2 63.2
AU014803-1s1A02	AU014803	chrX	71,076,415	71,077,915	1,525	32	21.3	-0.29	45.5
AU034904-1s1A02	AU034904	chrX	71,076,415	71,077,675	1,260	27	21.3	-0.54	45.4
AU066103-1s1A02	AU066103	chrX	71,076,415	71,077,770	1,355	29	21.4	-0.69	45.4
AU1069302-1s1A02		chrX	71,076,415	71,077,525	1,110	24	21.6	-0.46	46.1
AU043803-1s1A02	AU043803	chrX	71,076,460	71,077,675	1,215	26	21.4	-0.67	45.5
AU009503-1s1A02	AU009503	chrX	71,076,500	71,077,710	1,210	26	21.5	-0.47	45.6
AU056603-1s1A02	AU056603	chrX	71,076,500	71,077,770	1,270	27	21.3	-0.53	45.7
AU0780301-1s1A02 AU055503-1s1A02	AU0780301 AU055503	chrX chrX	71,076,500 71,076,560	71,077,605 71,077,710	1,105 1,150	24 25	21.7 21.7	-0.39 -0.49	46.0
AU018003-1s1A02	AU018003	chrX	71,076,620	71,077,770	1,150	25	21.7	-0.53	46.6
AU058503-1s1A02	AU058503	chrX	71,076,620	71,077,710	1,090	24	22.0	-0.56	46.5
AU058103-1s1A02	AU058103	chrX	71,076,650	71,077,770	1,120	24	21.4	-0.55	46.6
AU056603-1s1A02	AU056603	chrX	72,262,655	72,263,025	370	9	24.3	-0.82	38.3
AU1038303-1s1A02	8	chrX	73,082,436	73,084,643	2,207	29	13.1	-0.63	38.8
AU0920301-1s1A02		chrX	75,918,087	75,919,468	1,381	23	16.7	0.50	40.2
AU024003-1s1A02	AU024003	chrX	76,541,200	76,541,585	385	9	23.4	-0.68	41.2
AU002403-1s2A02 AU018304-1s1A02	AU002403 AU018304	chrX chrX	77,008,320 77,008,320	77,010,300 77,010,225	1,980 1,905	29 28	14.6 14.7	0.76 0.86	42.7 43.1
AU018304-191A02 AU021503-191A02	AU018304 AU021503	chrX	77,008,320	77,008,540	220	28 6	27.3	1.13	37.4
AU058103-1s1A02	AU058103	chrX	77,008,320	77,008,540	220	6	27.3	0.94	37.4
AU1038303-1s1A02		chrX	77,008,320	77,010,330	2,010	30	14.9	0.61	42.4
AU083504-1s1A02	AU083504	chrX	77,010,060	77,010,225	165	5	30.3	1.75	40.8
AU034904-1s1A02	AU034904	chrX	77,908,755	77,911,012	2,257	23	10.2	-0.46	37.2
AU018304-1s1A02	AU018304	chrX	78,485,431	78,490,725	5,294	52	9.8	0.37	34.7
AU1038303-1s1A02		chrX	82,086,497	82,094,944	8,447	91	10.8	-0.53	39.0
AU066103-1s1A02 AU065404-1s1A02	AU066103 AU065404	chrX chrX	85,039,398 86,344,937	85,040,403 86,345,922	1,005 985	22 21	21.9 21.3	-0.47 0.51	42.4 48.9
AU055503-1s1A02	AU055503	chrX	88,186,430	88,193,757	7,327	136	18.6	-0.35	33.7
AU004803-1s1A02	AU0033303	chrX	92,682,938	92,688,057	5,119	78	15.2	-0.63	39.8
				,					221

AU014505-1s1A02	AU014505	chrX	92,682,938	92,684,510	1,572	32	20.4	-1.09	35.7
AU014803-1s1A02 AU017504-1s1A02	AU014803 AU017504	chrX chrX	92,682,938 92,682,938	92,683,038 92,684,690	100 1,752	3 33	30.0 18.8	-1.25 -1.04	34.4
AU029303-1s1A02	AU017504 AU029303	chrX	92,682,938	92,684,690	4,856	77	15.9	-0.86	39.8
AU030603-1s3A02	AU029505 AU030603	chrX	92,682,938	92,687,794	4,856	77	15.9	-0.80	39.8
AU055503-1s1A02	AU055503	chrX	92,682,938	92,684,690	1,752	33	18.8	-0.87	36.7
AU0852304-1s1A02		chrX	93,989,084	93,990,989	1,905	39	20.5	0.24	28.1
AU018304-1s1A02	AU018304	chrX	94,346,925	94,347,740	815	18	22.1	-0.38	48.5
AU030603-1s3A02	AU030603	chrX	94,937,476	94,938,101	625	10	22.4	1.99	37.8
AU034904-1s1A02	AU034904	chrX	94,937,476	94,938,101	625	14	22.4	1.95	37.8
AU066103-1s1A02	AU066103	chrX	94,937,476	94,938,026	550	13	23.6	1.37	37.4
AU018003-1s1A02	AU018003	chrX	94,937,506	94,938,026	520	12	23.1	0.85	37.8
AU024003-1s1A02	AU024003	chrX	94,937,506	94,938,101	595	13	21.8	1.58	38.2
AU050703-1s1A02	AU050703	chrX	94,937,506	94,938,026	520	12	23.1	0.93	37.8
AU055303-1s1A02	AU055303	chrX	94,937,506	94,938,026	520	12	23.1	1.22	37.8
AU058503-1s1A02	AU058503	chrX	94,937,506	94,938,026	520	12	23.1	1.44	37.8
AU1038303-1s1A02	AU1038303	chrX	94,937,506	94,938,101	595	13	21.8	1.22	38.2
AU066103-1s1A02	AU066103	chrX	94,940,516	94,942,651	2,135	40	18.7	-0.32	37.4
AU083504-1s1A02	AU083504	chrX	96,493,478	96,493,778	300	7	23.3	-0.74	41.3
AU0875302-1s1A02		chrX	96,985,461	96,986,463	1,002	22	22.0	-0.40	53.4
AU009503-1s1A02	AU009503	chrX	97,054,641	97,054,971	330	8	24.2	-1.44	37.1
AU066103-1s1A02	AU066103	chrX	99,821,471	99,822,616	1,145	24	21.0	-0.50	41.3
AU0852304-1s1A02	AU0852304	chrX	99,863,364	99,864,422	1,058	16	15.1	-0.41	42.1
AU080803-1s1A02	AU080803	chrX		100,361,746	2,184	39	17.9	0.31	44.4
AU024003-1s1A02	AU024003	chrX		100,869,338	614	13	21.2	-0.53	38.4
AU017504-1s1A02	AU017504	chrX		102,918,175	1,493	32	21.4	-0.43	47.4
AU021503-1s1A02	AU021503	chrX	103,062,566	103,110,269	47,703	566	11.9	0.53	40.9
AU021503-1s1A02	AU021503	chrX		103,192,016	44,039	624	14.2	0.71	43.0
		chrX		103,296,615	961	15	15.6	-1.35	40.5
AU012004-1s2A02	AU012004	chrX	103,826,567	103,827,112	545	11	20.2	0.49	38.5
AU004803-1s1A02	AU004803	chrX	105,828,470	105,829,000	530	12	22.6	-0.59	44.3
AU066103-1s1A02	AU066103	chrX	106,045,447	106,047,742	2,295	42	18.3	-0.38	44.5
AU024003-1s1A02	AU024003	chrX	106,918,604	106,919,763	1,159	25	21.6	-0.37	41.0
AU018003-1s1A03	AU018003	chrX	107,366,406	107,367,451	1,045	22	21.1	-0.44	44.0
AU066103-1s1A03	AU066103	chrX	107,366,406	107,367,291	885	19	21.5	-0.74	44.0
AU1069302-1s1A03	AU1069302	chrX	107,366,406	107,367,451	1,045	22	21.1	-0.37	44.0
AU034904-1s1A03	AU034904	chrX	107,864,565	107,866,535	1,970	42	21.3	0.40	62.7
AU021503-1s1A03	AU021503	chrX	109,131,515	109,132,446	931	20	21.5	0.45	58.5
AU043803-1s1A03	AU043803	chrX	110,234,691	110,236,566	1,875	39	20.8	-0.44	40.1
AU056603-1s1A03	AU056603	chrX	111,172,139	111,172,529	390	9	23.1	-1.06	42.0
AU009904-1s1A03	AU009904	chrX	111,683,385	111,683,880	495	11	22.2	0.65	38.2
AU024003-1s1A03	AU024003	chrX	111,683,455	111,683,810	355	9	25.4	0.75	41.6
AU004803-1s1A03	AU004803		113,234,646	113,241,227	6,581	122	18.5	-0.83	37.8
AU066103-1s1A03	AU066103		114,211,054	114,212,014	960	21	21.9	-0.53	39.6
AU056603-1s1A03	AU056603	chrX	114,211,104	114,211,944	840	19	22.6	-0.59	39.7
AU024003-1s1A03	AU024003	chrX	114,211,134	114,212,199	1,065	23	21.6	-0.50	40.4
AU065404-1s1A03	AU065404	chrX	114,330,245	114,333,513	3,268	68	20.8	0.33	64.3
AU021503-1s1A03	AU021503	chrX	114,330,510	114,333,265	2,755	57	20.7	0.31	65.6
AU034604-1s1A03	AU034604	chrX		114,333,225	2,215	46	20.8	0.45	64.6
AU080803-1s1A03	AU080803	chrX	114,331,350	114,333,225	1,875	39	20.8	0.38	65.1
AU018003-1s1A03	AU018003	chrX	114,331,470	114,333,225	1,755	36	20.5	0.47	65.1
AU018304-1s1A03	AU018304		114,449,045	114,452,862	3,817	73	19.1	0.35	36.9
AU014505-1s1A03	AU014505		114,449,640	114,450,305	665	15	22.6	0.98	33.2
AU016803-1s1A03	AU016803	chrX	114,449,740	114,450,445	705	16	22.7	0.91	34.1
AU029303-1s1A03	AU029303		114,449,740	114,450,340	600	14	23.3	1.32	34.3
AU1038303-1s1A03			114,449,740	114,450,405	665	15	22.6	0.72	34.5
AU014803-1s1A03	AU014803	chrX		115,057,412	6,883	125	18.2	0.33	35.5
AU008403-1s1A03			115,051,804	115,054,775	2,971	52	17.5	0.32 0.40	33.6 37.5
	AU008403		115 051 060	115 050 100	7 250				
AU080803-1s1A03	AU080803	chrX	115,051,869	115,059,128	7,259	132	18.2		
AU002403-1s2A03	AU080803 AU002403	chrX chrX	115,051,999	115,066,171	14,172	132 145	10.2	0.39	38.5
AU002403-1s2A03 AU018304-1s1A03	AU080803 AU002403 AU018304	chrX chrX chrX	115,051,999 115,052,163	115,066,171 115,070,463	14,172 18,300	132 145 200	10.2 10.9	0.39 0.41	38.5 37.0
AU002403-1s2A03 AU018304-1s1A03 AU083504-1s1A03	AU080803 AU002403 AU018304 AU083504	chrX chrX chrX chrX chrX	115,051,999 115,052,163 115,066,476	115,066,171 115,070,463 115,066,596	14,172 18,300 120	132 145 200 4	10.2 10.9 33.3	0.39 0.41 1.05	38.5 37.0 32.6
AU002403-1s2A03 AU018304-1s1A03 AU083504-1s1A03 AU018304-1s1A03	AU080803 AU002403 AU018304 AU083504 AU018304	chrX chrX chrX chrX chrX	115,051,999 115,052,163 115,066,476 116,422,024	115,066,171 115,070,463 115,066,596 116,422,614	14,172 18,300 120 590	132 145 200 4 13	10.2 10.9 33.3 22.0	0.39 0.41 1.05 -0.80	38.5 37.0 32.6 36.1
AU002403-1s2A03 AU018304-1s1A03 AU083504-1s1A03 AU018304-1s1A03 AU055303-1s1A03	AU080803 AU002403 AU018304 AU083504 AU018304 AU055303	chrX chrX chrX chrX chrX chrX chrX	115,051,999 115,052,163 115,066,476 116,422,024 116,422,024	115,066,171 115,070,463 115,066,596 116,422,614 116,422,614	14,172 18,300 120 590 590	132 145 200 4 13 13	10.2 10.9 33.3 22.0 22.0	0.39 0.41 1.05 -0.80 -0.54	38.5 37.0 32.6 36.1 36.1
AU002403-1s2A03 AU018304-1s1A03 AU083504-1s1A03 AU018304-1s1A03 AU055303-1s1A03 AU0875302-1s2A03	AU080803 AU002403 AU018304 AU083504 AU018304 AU055303 AU0875302	chrX chrX chrX chrX chrX chrX chrX chrX	115,051,999 115,052,163 115,066,476 116,422,024 116,422,024 116,422,134	115,066,171 115,070,463 115,066,596 116,422,614 116,422,614 116,422,614	14,172 18,300 120 590 590 480	132 145 200 4 13 13 13 11	10.2 10.9 33.3 22.0 22.0 22.9	0.39 0.41 1.05 -0.80 -0.54 -0.68	38.5 37.0 32.6 36.1 36.1 35.0
AU002403-1s2A03 AU018304-1s1A03 AU083504-1s1A03 AU083504-1s1A03 AU055303-1s1A03 AU0855302-1s2A03 AU066103-1s1A03	AU080803 AU002403 AU018304 AU083504 AU018304 AU055303 AU0875302 AU066103	chrX chrX chrX chrX chrX chrX chrX chrX	115,051,999 115,052,163 115,066,476 116,422,024 116,422,024 116,422,134 117,574,923	115,066,171 115,070,463 115,066,596 116,422,614 116,422,614 116,422,614 117,575,298	14,172 18,300 120 590 590 480 375	132 145 200 4 13 13 11 9	10.2 10.9 33.3 22.0 22.0 22.9 24.0	0.39 0.41 1.05 -0.80 -0.54 -0.68 -0.80	38.5 37.0 32.6 36.1 36.1 35.0 39.4
AU002403-1s2A03 AU018304-1s1A03 AU083504-1s1A03 AU018304-1s1A03 AU055303-1s1A03 AU0875302-1s2A03 AU066103-1s1A03 AU038805-1s1A03	AU080803 AU002403 AU018304 AU083504 AU018304 AU055303 AU0875302 AU066103 AU038805	chrX chrX chrX chrX chrX chrX chrX chrX	115,051,999 115,052,163 115,066,476 116,422,024 116,422,024 116,422,134 117,574,923 117,804,762	115,066,171 115,070,463 115,066,596 116,422,614 116,422,614 116,422,614 117,575,298 117,806,258	14,172 18,300 120 590 590 480 375 1,496	132 145 200 4 13 13 11 9 16	10.2 10.9 33.3 22.0 22.0 22.9 24.0 10.7	0.39 0.41 1.05 -0.80 -0.54 -0.68 -0.80 -0.36	38.5 37.0 32.6 36.1 36.1 35.0 39.4 40.4
AU002403-1s2A03 AU018304-1s1A03 AU083504-1s1A03 AU083504-1s1A03 AU055303-1s1A03 AU0875302-1s2A03 AU066103-1s1A03 AU065404-1s1A03	AU080803 AU002403 AU018304 AU018304 AU018304 AU018304 AU055303 AU0875302 AU086103 AU038805 AU065404	chrX chrX chrX chrX chrX chrX chrX chrX	115,051,999 115,052,163 115,066,476 116,422,024 116,422,024 116,422,134 117,574,923 117,804,762 117,845,440	115,066,171 115,070,463 115,066,596 116,422,614 116,422,614 116,422,614 117,575,298 117,806,258 117,846,430	14,172 18,300 120 590 480 375 1,496 990	132 145 200 4 13 13 11 9 16 22	10.2 10.9 33.3 22.0 22.0 22.9 24.0 10.7 22.2	0.39 0.41 1.05 -0.80 -0.54 -0.68 -0.80 -0.36 0.34	38.5 37.0 32.6 36.1 36.1 35.0 39.4 40.4 54.8
AU002403-1s2A03 AU018304-1s1A03 AU083504-1s1A03 AU018304-1s1A03 AU055303-1s1A03 AU055303-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU065404-1s1A03 AU0920301-1s1A03	AU080803 AU002403 AU018304 AU083504 AU018304 AU055303 AU0875302 AU066103 AU066404 AU0920301	chrX chrX chrX chrX chrX chrX chrX chrX	115,051,999 115,052,163 115,066,476 116,422,024 116,422,024 116,422,134 117,574,923 117,804,762 117,845,440 118,254,638	115,066,171 115,070,463 115,066,596 116,422,614 116,422,614 116,422,614 117,575,298 117,866,283 117,846,430 118,255,609	14,172 18,300 120 590 480 375 1,496 990 971	132 145 200 4 13 13 11 9 16 22 20	10.2 10.9 33.3 22.0 22.9 24.0 10.7 22.2 20.6	0.39 0.41 1.05 -0.80 -0.54 -0.68 -0.80 -0.36 0.34 0.50	38.5 37.0 32.6 36.1 35.0 39.4 40.4 54.8 58.8
AU002403-1s2A03 AU018304-1s1A03 AU083504-1s1A03 AU083504-1s1A03 AU055303-1s1A03 AU0875302-1s2A03 AU066103-1s1A03 AU066103-1s1A03 AU065404-1s1A03 AU0920301-1s1A03 AU014803-1s1A03	AU080803 AU002403 AU018304 AU083504 AU018304 AU055303 AU0875302 AU066103 AU065404 AU065404 AU0920301 AU014803	chrX chrX chrX chrX chrX chrX chrX chrX	115,051,999 115,052,163 115,066,476 116,422,024 116,422,024 116,422,134 117,574,923 117,804,762 117,845,440 118,254,638 120,665,480	115,066,171 115,070,463 115,066,596 116,422,614 116,422,614 116,422,614 117,575,298 117,806,258 117,846,430 118,255,609 120,666,390	14,172 18,300 120 590 590 480 375 1,496 990 971 910	132 145 200 4 13 13 11 9 16 22 20 19	10.2 10.9 33.3 22.0 22.9 24.0 10.7 22.2 20.6 20.9	0.39 0.41 1.05 -0.80 -0.54 -0.68 -0.80 -0.36 0.34 0.50 -0.46	38.5 37.0 32.6 36.1 35.0 39.4 40.4 54.8 58.8 36.9
AU002403-1s2A03 AU018304-1s1A03 AU083504-1s1A03 AU083504-1s1A03 AU055303-1s1A03 AU0875302-1s2A03 AU066103-1s1A03 AU065404-1s1A03 AU0920301-1s1A03 AU014803-1s1A03 AU056003-1s1A03	AU080803 AU002403 AU018304 AU018304 AU018304 AU055303 AU0875302 AU066103 AU066103 AU065404 AU065404 AU0920301 AU014803 AU056003	chrX chrX chrX chrX chrX chrX chrX chrX	115,051,999 115,052,163 115,066,476 116,422,024 116,422,024 116,422,134 117,574,923 117,804,762 117,845,440 118,254,638 120,665,480 121,710,758	115,066,171 115,070,463 115,066,596 116,422,614 116,422,614 116,422,614 117,575,298 117,806,258 117,846,430 118,255,609 120,666,390 121,711,793	14,172 18,300 120 590 480 375 1,496 990 971 910 1,035	132 145 200 4 13 13 11 9 16 22 20 20 19 15	10.2 10.9 33.3 22.0 22.9 24.0 10.7 22.2 20.6 20.9 14.5	0.39 0.41 1.05 -0.80 -0.54 -0.68 -0.80 -0.36 0.34 0.50 -0.46 0.41	38.5 37.0 32.6 36.1 35.0 39.4 40.4 54.8 58.8 36.9 39.2
AU002403-1s2A03 AU018304-1s1A03 AU083504-1s1A03 AU055303-1s1A03 AU055303-1s1A03 AU0875302-1s2A03 AU066103-1s1A03 AU065404-1s1A03 AU0920301-1s1A03 AU014803-1s1A03 AU056003-1s1A03 AU065404-1s1A03	AU080803 AU002403 AU018304 AU018304 AU018304 AU05503 AU0875302 AU066103 AU065404 AU065404 AU0920301 AU014803 AU056003 AU065404	chrX chrX chrX chrX chrX chrX chrX chrX	115,051,999 115,052,163 115,066,476 116,422,024 116,422,024 116,422,134 117,574,923 117,804,762 117,845,440 118,254,638 120,665,480 121,710,758 121,906,483	115,066,171 115,070,463 115,066,596 116,422,614 116,422,614 116,422,614 117,575,298 117,806,258 117,846,430 118,255,609 120,666,390 121,711,793 121,907,369	14,172 18,300 120 590 590 480 375 1,496 990 971 910 1,035 886	132 145 200 4 13 13 11 9 16 22 20 20 19 15 15 17	10.2 10.9 33.3 22.0 22.9 24.0 10.7 22.2 20.6 20.9 14.5 19.2	$\begin{array}{c} 0.39\\ 0.41\\ 1.05\\ -0.80\\ -0.54\\ -0.68\\ -0.80\\ -0.36\\ 0.34\\ 0.50\\ -0.46\\ 0.41\\ -0.41\\ \end{array}$	38.5 37.0 32.6 36.1 35.0 39.4 40.4 54.8 58.8 36.9 39.2 37.7
AU002403-1s2A03 AU018304-1s1A03 AU083504-1s1A03 AU083504-1s1A03 AU055303-1s1A03 AU0875302-1s2A03 AU066103-1s1A03 AU065404-1s1A03 AU065404-1s1A03 AU0920301-1s1A03 AU056003-1s1A03 AU065404-1s1A03 AU065404-1s1A03	AU080803 AU002403 AU018304 AU083504 AU018304 AU055303 AU0875302 AU065103 AU065404 AU0920301 AU014803 AU056003 AU065404 AU083504	chrX chrX chrX chrX chrX chrX chrX chrX	115,051,999 115,052,163 115,066,476 116,422,024 116,422,024 116,422,134 117,574,923 117,804,762 117,845,440 118,254,638 120,665,480 121,710,758 121,906,483 122,143,410	115,066,171 115,070,463 115,066,596 116,422,614 116,422,614 116,422,614 117,575,298 117,806,258 117,846,430 118,255,609 120,666,390 121,711,793 121,907,369 122,144,175	14,172 18,300 120 590 590 480 375 1,496 990 971 910 1,035 886 765	132 145 200 4 13 13 11 9 16 22 20 19 15 17 17	10.2 10.9 33.3 22.0 22.0 22.9 24.0 10.7 22.2 20.6 20.9 14.5 19.2 22.2	0.39 0.41 1.05 -0.80 -0.54 -0.68 -0.80 -0.36 0.34 0.50 -0.36 0.41 -0.41 -0.73	38.5 37.0 32.6 36.1 36.1 35.0 39.4 40.4 54.8 58.8 36.9 39.2 37.7 39.8
AU002403-1s2A03 AU018304-1s1A03 AU083504-1s1A03 AU083504-1s1A03 AU055303-1s1A03 AU065103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU065404-1s1A03 AU0920301-1s1A03 AU014803-1s1A03 AU056003-1s1A03 AU065404-1s1A03 AU08504-1s1A03 AU083504-1s1A03	AU080803 AU002403 AU018304 AU083504 AU055303 AU065303 AU066103 AU066404 AU065404 AU0920301 AU014803 AU065404 AU065404 AU083504 AU034904	chrX chrX chrX chrX chrX chrX chrX chrX	115,051,999 115,052,163 115,066,476 116,422,024 116,422,024 116,422,134 117,574,923 117,804,762 117,845,440 118,254,638 120,665,480 121,710,758 121,906,483 122,143,410 122,143,675	115,066,171 115,070,463 115,066,596 116,422,614 116,422,614 117,575,298 117,866,243 117,846,430 118,255,609 120,666,390 121,711,793 121,907,369 122,144,175 122,144,235	14,172 18,300 120 590 480 375 1,496 990 971 910 1,035 886 765 560	132 145 200 4 13 13 11 9 16 22 20 19 15 17 17 17 13	10.2 10.9 33.3 22.0 22.9 24.0 10.7 22.2 20.6 20.9 14.5 19.2 22.2 23.2	$\begin{array}{c} 0.39\\ 0.41\\ 1.05\\ -0.80\\ -0.54\\ -0.68\\ -0.80\\ -0.36\\ 0.34\\ 0.50\\ -0.46\\ 0.41\\ -0.41\\ -0.73\\ -0.95\\ \end{array}$	38.5 37.0 32.6 36.1 35.0 39.4 40.4 54.8 54.8 54.8 36.9 39.2 37.7 39.8 40.5
AU002403-1s2A03 AU018304-1s1A03 AU083504-1s1A03 AU083504-1s1A03 AU05503-1s1A03 AU065103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU065404-1s1A03 AU0920301-1s1A03 AU014803-1s1A03 AU065404-1s1A03 AU08504-1s1A03 AU083504-1s1A03 AU066103-1s1A03	AU080803 AU002403 AU018304 AU083504 AU018304 AU055303 AU0875302 AU066103 AU065404 AU0920301 AU014803 AU065404 AU056003 AU065404 AU083504 AU034904 AU066103	chrX chrX chrX chrX chrX chrX chrX chrX	115,051,999 115,052,163 115,066,476 116,422,024 116,422,024 116,422,134 117,574,923 117,845,440 118,254,638 120,665,480 121,710,758 121,906,483 122,143,410 122,143,675 122,191,374	115,066,171 115,070,463 115,066,596 116,422,614 116,422,614 116,422,614 117,575,298 117,846,430 118,255,609 120,666,390 121,711,793 121,907,369 122,144,175 122,144,235 122,192,284	14,172 18,300 120 590 480 375 1,496 990 971 910 1,035 886 765 560 910	132 145 200 4 13 13 11 9 16 22 20 19 15 17 17 17 13 20	10.2 10.9 33.3 22.0 22.9 24.0 10.7 22.2 20.6 20.9 14.5 19.2 22.2 23.2 23.2 22.0	$\begin{array}{c} 0.39\\ 0.41\\ 1.05\\ -0.80\\ -0.54\\ -0.68\\ -0.80\\ -0.36\\ 0.34\\ 0.50\\ -0.46\\ 0.41\\ -0.41\\ -0.41\\ -0.73\\ -0.95\\ -0.48\end{array}$	38.5 37.0 32.6 36.1 35.0 39.4 40.4 54.8 58.8 36.9 39.2 37.7 39.8 40.5 40.2
AU002403-1s2A03 AU018304-1s1A03 AU083504-1s1A03 AU083504-1s1A03 AU055303-1s1A03 AU055302-1s2A03 AU066103-1s1A03 AU066103-1s1A03 AU065404-1s1A03 AU0920301-1s1A03 AU056003-1s1A03 AU065404-1s1A03 AU083504-1s1A03 AU086103-1s1A03 AU065404-1s1A03 AU065404-1s1A03	AU080803 AU002403 AU018304 AU083504 AU055303 AU0875302 AU066103 AU065404 AU0920301 AU014803 AU056003 AU065404 AU083504 AU083504 AU066103 AU065404	chrX chrX chrX chrX chrX chrX chrX chrX	115,051,999 115,052,163 115,066,476 116,422,024 116,422,024 116,422,134 117,574,923 117,804,762 117,845,440 118,254,638 120,665,480 121,710,758 121,906,483 122,143,410 122,143,415 122,191,374 122,200,279	115,066,171 115,070,463 115,066,596 116,422,614 116,422,614 116,422,614 117,575,298 117,806,258 117,846,430 118,255,609 120,666,390 121,711,793 121,907,369 122,144,235 122,144,235 122,192,284 122,201,069	14,172 18,300 120 590 480 375 1,496 990 971 910 1,035 886 765 560 910 790	132 145 200 4 13 13 11 9 16 22 20 19 15 17 17 17 17 13 20 18	10.2 10.9 33.3 22.0 22.9 24.0 10.7 22.2 20.6 20.9 14.5 19.2 22.2 23.2 23.2 22.0 22.8	0.39 0.41 1.05 -0.80 -0.54 -0.68 -0.80 -0.36 0.34 0.50 -0.46 0.41 -0.41 -0.73 -0.95 -0.48 -1.03	38.5 37.0 32.6 36.1 36.1 35.0 39.4 40.4 54.8 58.8 36.9 39.2 37.7 39.8 40.5 40.2 41.8
AU002403-1s2A03 AU018304-1s1A03 AU083504-1s1A03 AU083504-1s1A03 AU055303-1s1A03 AU0875302-1s2A03 AU066103-1s1A03 AU065404-1s1A03 AU0920301-1s1A03 AU014803-1s1A03 AU056003-1s1A03 AU065404-1s1A03 AU083504-1s1A03 AU063404-1s1A03 AU065404-1s1A03 AU065404-1s1A03 AU0625404-1s1A03 AU032705-1s2A03	AU080803 AU002403 AU018304 AU018304 AU018304 AU05503 AU0875302 AU066103 AU065404 AU0920301 AU014803 AU065404 AU083504 AU083504 AU08304 AU065404 AU065404 AU065404 AU032705	chrX chrX chrX chrX chrX chrX chrX chrX	115,051,999 115,052,163 115,066,476 116,422,024 116,422,024 116,422,134 117,574,923 117,804,762 117,845,440 118,254,638 120,665,480 121,710,758 121,906,483 122,143,410 122,143,410 122,143,475 122,191,374 122,200,279 122,200,614	115,066,171 115,070,463 115,066,596 116,422,614 116,422,614 117,575,298 117,806,258 117,846,430 118,255,609 120,666,390 121,711,793 121,907,369 122,144,175 122,144,235 122,192,284 122,201,069 122,201,069	14,172 18,300 120 590 590 480 375 1,496 990 971 910 1,035 886 765 560 910 790 455	132 145 200 4 13 13 11 9 16 22 20 19 15 17 17 17 17 17 13 20 18 11	10.2 10.9 33.3 22.0 22.9 24.0 10.7 22.2 20.6 20.9 14.5 19.2 22.2 23.2 22.0 22.8 24.2	0.39 0.41 1.05 -0.80 -0.54 -0.68 -0.80 -0.36 0.34 0.50 -0.46 0.41 -0.41 -0.73 -0.95 -0.48 -1.03 -1.00	38.5 37.0 32.6 36.1 35.0 39.4 40.4 54.8 58.8 36.9 39.2 37.7 39.8 40.5 40.5 40.5 41.8
AU002403-1s2A03 AU018304-1s1A03 AU083504-1s1A03 AU083504-1s1A03 AU055303-1s1A03 AU085502-1s2A03 AU066103-1s1A03 AU065404-1s1A03 AU0920301-1s1A03 AU014803-1s1A03 AU056003-1s1A03 AU065404-1s1A03 AU083504-1s1A03 AU083504-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU065404-1s1A03 AU065404-1s1A03 AU025303-1s1A03	AU080803 AU002403 AU018304 AU083504 AU083504 AU0875302 AU065103 AU065404 AU0920301 AU014803 AU056003 AU065404 AU033504 AU034904 AU065103 AU065404 AU032705 AU055303	chrX chrX chrX chrX chrX chrX chrX chrX	115,051,999 115,052,163 115,066,476 116,422,024 116,422,024 116,422,134 117,574,923 117,804,762 117,845,440 118,254,638 120,665,480 121,710,758 121,906,483 122,143,410 122,143,675 122,191,374 122,200,614 122,200,614	115,066,171 115,070,463 115,066,596 116,422,614 116,422,614 117,575,298 117,806,258 117,846,430 118,255,609 120,666,390 121,711,793 121,907,369 122,144,175 122,144,235 122,192,284 122,201,069 122,201,069	14,172 18,300 120 590 480 375 1,496 990 971 910 1,035 886 765 560 910 790 455 455	132 145 200 4 13 13 11 9 16 22 20 19 15 17 17 17 17 13 20 18 11 11	10.2 10.9 33.3 22.0 22.9 24.0 10.7 22.2 20.6 20.9 14.5 19.2 22.2 23.2 22.0 22.8 24.2 22.8 24.2	$\begin{array}{c} 0.39\\ 0.41\\ 1.05\\ -0.80\\ -0.54\\ -0.68\\ -0.80\\ -0.36\\ 0.34\\ 0.50\\ -0.46\\ 0.41\\ -0.41\\ -0.41\\ -0.73\\ -0.95\\ -0.48\\ -1.03\\ -1.00\\ -1.09\\ \end{array}$	38.5 37.0 32.6 36.1 36.1 35.0 39.4 40.4 54.8 58.8 36.9 39.2 37.7 39.8 40.5 40.2 41.8 44.1 44.1
AU002403-1s2A03 AU018304-1s1A03 AU083504-1s1A03 AU083504-1s1A03 AU055303-1s1A03 AU0875302-1s2A03 AU066103-1s1A03 AU065404-1s1A03 AU0920301-1s1A03 AU014803-1s1A03 AU056003-1s1A03 AU065404-1s1A03 AU083504-1s1A03 AU063404-1s1A03 AU065404-1s1A03 AU065404-1s1A03 AU0625404-1s1A03 AU032705-1s2A03	AU080803 AU002403 AU018304 AU018304 AU018304 AU05503 AU0875302 AU066103 AU065404 AU0920301 AU014803 AU065404 AU083504 AU083504 AU08304 AU065404 AU065404 AU065404 AU032705	chrX chrX chrX chrX chrX chrX chrX chrX	115,051,999 115,052,163 115,066,476 116,422,024 116,422,024 116,422,134 117,574,923 117,804,762 117,845,440 118,254,638 120,665,480 121,710,758 121,906,483 122,143,410 122,143,410 122,143,475 122,191,374 122,200,279 122,200,614	115,066,171 115,070,463 115,066,596 116,422,614 116,422,614 117,575,298 117,806,258 117,846,430 118,255,609 120,666,390 121,711,793 121,907,369 122,144,175 122,144,235 122,192,284 122,201,069 122,201,069	14,172 18,300 120 590 590 480 375 1,496 990 971 910 1,035 886 765 560 910 790 455	132 145 200 4 13 13 11 9 16 22 20 19 15 17 17 17 17 17 13 20 18 11	10.2 10.9 33.3 22.0 22.9 24.0 10.7 22.2 20.6 20.9 14.5 19.2 22.2 23.2 22.0 22.8 24.2	0.39 0.41 1.05 -0.80 -0.54 -0.68 -0.80 -0.36 0.34 0.50 -0.46 0.41 -0.41 -0.73 -0.95 -0.48 -1.03 -1.00	38.5 37.0 32.6 36.1 36.1 35.0 39.4 40.4 54.8 58.8 36.9 39.2 37.7 39.8 40.5 40.5 40.5 40.5 41.8

AU034904-1s1A03	AU034904	chrX	124,109,638	124,110,833	1,195	26	21.8	-0.36	38.5
AU032705-1s2A03	AU032705		124,787,689	124,788,214	525	12	22.9	-0.92	43.4
AU034904-1s1A03	AU034904			125,128,920	2,540	51	20.1	0.33	62.9
AU066103-1s1A03	AU066103	chrX		125,434,831	1,474	14	9.5	-1.14	43.9
AU043803-1s1A03	AU043803			125,434,831	1,439	13	9.0	-1.55	43.3
AU058103-1s1A03	AU058103	chrX	125,433,517	125,434,906	1,389	13	9.4	-1.04	43.3
AU034904-1s1A03	AU034904	chrX		126,430,002	9,388	137	14.6	0.30	33.2
AU029303-1s1A03	AU029303	chrX		126,430,052	4,997	83	16.6	0.55	31.4
AU083504-1s1A03	AU083504	chrX	126,425,325	126,430,002	4,677	77	16.5	0.41	31.5
AU066103-1s1A03	AU066103	chrX		128,291,662	596	13	21.8	-0.69	38.5
AU009904-1s1A03	AU009904			128,330,085	1,875	38	20.3	-0.64	40.5
AU083504-1s1A03 AU065404-1s1A03	AU083504 AU065404	chrX chrX		128,330,085 128,330,085	1,875 1,655	38 34	20.3 20.5	-0.77 -0.72	40.5
AU030603-1s3A03	AU030603		128,328,535	128,330,085	1,550	33	21.3	-1.13	39.5
AU034904-1s1A03	AU034904	chrX	128,328,560	128,330,085	1,525	32	21.0	-0.93	39.7
AU034604-1s1A03	AU034604	chrX		128,894,009	1,183	25	21.1	0.57	64.7
AU066103-1s1A03	AU066103		129,306,360	129,306,695	335	8	23.9	-0.78	41.7
AU066103-1s1A03	AU066103	chrX	129,711,202	129,715,287	4,085	78	19.1	-0.45	41.5
AU018003-1s1A03	AU018003	chrX	129,711,252	129,714,877	3,625	68	18.8	-0.37	41.1
AU028903-1s1A03	AU028903	chrX	129,711,302	129,715,197	3,895	74	19.0	-0.32	41.4
AU056803-1s1A03	AU056803	chrX	129,711,402	129,715,172	3,770	71	18.8	-0.33	41.3
AU058103-1s1A03	AU058103			129,715,287	3,845	73	19.0	-0.35	41.3
AU0852304-1s1A03	AU0852304	chrX	· · ·	129,715,267	1,335	27	20.2	-0.44	44.0
AU083603-1s1A03	AU083603	chrX	130,832,459	130,836,198	3,739	62	16.6	-0.49	40.2
AU020003-1s1A03	AU020003	chrX	130,832,744	130,835,768	3,024	47	15.5	-0.28	40.8
AU016803-1s1A03	AU016803		130,832,939	130,836,198	3,259	52	16.0	-0.83	41.3
AU002403-1s2A03	AU002403	chrX		130,836,198	2,919	51	17.5	-1.02	40.4
AU043803-1s1A03	AU043803	chrX	130,833,279 130,833,279	130,836,198	2,919	51	17.5	-1.09	40.4
AU067803-1s2A03 AU083504-1s1A03	AU067803 AU083504	chrX	130,833,279	130,836,198 130,836,198	2,919 2,919	51 51	17.5 17.5	-1.16 -1.05	40.4
AU1069302-1s1A03	AU1069302	chrX	130,833,279	130,836,198	2,919	51	17.5	-0.75	40.4
AU009904-1s1A03	AU009904	chrX	130,833,304	130,836,198	2,894	50	17.3	-0.91	40.6
AU080803-1s1A03	AU080803	chrX	130,833,304	130,836,198	2,894	50	17.3	-0.83	40.6
AU020003-1s1A03	AU020003	chrX	130,835,813	130,836,198	385	9	23.4	-1.07	42.8
AU056803-1s1A03	AU056803	chrX	131,572,555	131,573,010	455	11	24.2	-0.77	42.7
AU0875302-1s2A03	AU0875302	chrX	131,766,925	131,769,270	2,345	47	20.0	-0.79	41.7
AU018304-1s1A03	AU018304	chrX	131,917,783	131,919,816	2,033	43	21.2	0.40	65.1
AU034604-1s1A03	AU034604		133,133,179	133,135,279	2,100	44	21.0	0.33	59.5
AU056003-1s1A03	AU056003	chrX		133,350,722	4,580	83	18.1	-0.37	39.9
AU021503-1s1A03	AU021503		133,692,426		970	21	21.6	-0.86	43.7
AU008504-1s1A03	AU008504		134,119,690	134,159,690	40,000	568	14.2	0.41	40.2
AU034604-1s1A03 AU050703-1s1A03	AU034604 AU050703	chrX chrX	135,056,972 135,057,257	135,058,348 135,058,152	1,376 895	30 20	21.8 22.3	0.53 0.42	71.3
AU080803-1s1A03	AU080803	chrX	135,057,642	135,058,248	606	14	23.1	0.67	65.7
AU066103-1s1A03	AU066103	chrX	135,359,543	135,360,598	1,055	23	21.8	-0.74	42.0
AU018003-1s1A03	AU018003	chrX	135,359,623	135,361,388	1,765	23	13.0	-0.40	39.5
AU034904-1s1A03	AU034904	chrX		135,767,811	705	10	14.2	-0.63	44.6
AU030603-1s3A03	AU030603	chrX	1 1	135,904,947	5,302	85	16.0	-1.02	36.3
AU028903-1s1A03	AU028903		135,941,581		1,250	27	21.6	-0.39	52.1
AU066103-1s1A03	AU066103	chrX	135,941,971	135,943,299	1,328	28	21.1	-0.42	50.3
AU066103-1s1A03	AU066103	chrX	135,943,359	135,944,189	830	18	21.7	0.38	69.3
AU018003-1s1A03	AU018003	chrX	137,810,150	137,810,705	555	12	21.6	-0.57	43.7
AU0852304-1s1A03			138,905,808		295	7	23.7	-0.53	49.3
AU034904-1s1A03	AU034904		139,000,488		1,823	39	21.4	0.33	62.3
AU083603-1s1A03	AU083603		139,410,814		1,182	26	22.0	0.34	54.1
AU028903-1s1A03	AU028903		139,623,380		760	16	21.1	-0.49	49.9
AU009503-1s1A03 AU009503-1s1A03	AU009503		139,640,097 139,814,885	· · · · · · · · · · · · · · · · · · ·	480	11 31	22.9	-0.69	43.6
AU066103-1s1A03	AU009503 AU066103		140,219,706	139,816,340	1,455 2,067	42	21.3 20.3	-0.35	39.0 40.7
AU1038303-1s1A03	AU1038303		142,179,913		1,094	23	21.0	-0.49	37.2
AU083603-1s1A03	AU083603		142,548,496		2,369	49	20.7	0.29	61.4
AU062203-1s1A03	AU062203		142,743,647		2,434	36	14.8	0.25	32.8
AU002403-1s2A03	AU002403		143,111,964		40,402	494	12.2	-0.53	35.4
AU002403-1s2A03	1000021000				12,400	211	17.0	-0.45	36.2
A0002403-132A03	AU002403	chrX	143,163,522	143,173,922					
AU043803-1s1A03		chrX	143,213,032	143,213,462	430	10	23.3	-0.68	37.0
AU043803-1s1A03 AU009904-1s1A03	AU002403 AU043803 AU009904	chrX chrX	143,213,032 143,436,349	143,213,462 143,441,886	430 5,537	10 106	19.1	-0.68 -0.46	38.8
AU043803-1s1A03 AU009904-1s1A03 AU066103-1s1A03	AU002403 AU043803 AU009904 AU066103	chrX chrX chrX	143,213,032 143,436,349 143,818,658	143,213,462 143,441,886 143,818,868	430 5,537 210	10 106 5	19.1 23.8	-0.68 -0.46 -1.23	38.8 37.7
AU043803-1s1A03 AU009904-1s1A03 AU066103-1s1A03 AU055303-1s1A03	AU002403 AU043803 AU009904 AU066103 AU055303	chrX chrX chrX chrX	143,213,032 143,436,349 143,818,658 143,962,926	143,213,462 143,441,886 143,818,868 143,964,923	430 5,537 210 1,997	10 106 5 43	19.1 23.8 21.5	-0.68 -0.46 -1.23 -0.30	38.8 37.7 40.6
AU043803-1s1A03 AU009904-1s1A03 AU066103-1s1A03 AU055303-1s1A03 AU083504-1s1A03	AU002403 AU043803 AU009904 AU066103 AU055303 AU083504	chrX chrX chrX chrX chrX	143,213,032 143,436,349 143,818,658 143,962,926 144,229,903	143,213,462 143,441,886 143,818,868 143,964,923 144,231,198	430 5,537 210 1,997 1,295	10 106 5 43 23	19.1 23.8 21.5 17.8	-0.68 -0.46 -1.23 -0.30 0.54	38.8 37.7 40.6 40.3
AU043803-1s1A03 AU009904-1s1A03 AU066103-1s1A03 AU055303-1s1A03 AU083504-1s1A03 AU065404-1s1A03	AU002403 AU043803 AU009904 AU066103 AU055303 AU083504 AU065404	chrX chrX chrX chrX chrX chrX chrX	143,213,032 143,436,349 143,818,658 143,962,926 144,229,903 145,622,896	143,213,462 143,441,886 143,818,868 143,964,923 144,231,198 145,623,136	430 5,537 210 1,997 1,295 240	10 106 5 43 23 6	19.1 23.8 21.5 17.8 25.0	-0.68 -0.46 -1.23 -0.30 0.54 -0.78	38.8 37.7 40.6 40.3 41.8
AU043803-1s1A03 AU009904-1s1A03 AU066103-1s1A03 AU055303-1s1A03 AU083504-1s1A03 AU065404-1s1A03 AU056003-1s1A03	AU002403 AU043803 AU009904 AU066103 AU055303 AU083504 AU065404 AU056003	chrX chrX chrX chrX chrX chrX chrX chrX	143,213,032 143,436,349 143,818,658 143,962,926 144,229,903 145,622,896 145,658,097	143,213,462 143,441,886 143,818,868 143,964,923 144,231,198 145,623,136 145,658,347	430 5,537 210 1,997 1,295 240 250	10 106 5 43 23 6 6	19.1 23.8 21.5 17.8 25.0 24.0	-0.68 -0.46 -1.23 -0.30 0.54 -0.78 -0.61	38.8 37.7 40.6 40.3 41.8 43.7
AU043803-1s1A03 AU009904-1s1A03 AU066103-1s1A03 AU055303-1s1A03 AU083504-1s1A03 AU065404-1s1A03 AU056003-1s1A03 AU066103-1s1A03	AU002403 AU043803 AU009904 AU066103 AU055303 AU083504 AU065404 AU056003 AU066103	chrX chrX chrX chrX chrX chrX chrX chrX	143,213,032 143,436,349 143,818,658 143,962,926 144,229,903 145,622,896 145,658,097 146,211,155	143,213,462 143,441,886 143,818,868 143,964,923 144,231,198 145,623,136 145,658,347 146,211,895	430 5,537 210 1,997 1,295 240 250 740	10 106 5 43 23 6 6 6 16	19.1 23.8 21.5 17.8 25.0 24.0 21.6	-0.68 -0.46 -1.23 -0.30 0.54 -0.78 -0.61 -0.54	38.8 37.7 40.6 40.3 41.8 43.7 40.7
AU043803-1s1A03 AU009904-1s1A03 AU066103-1s1A03 AU055303-1s1A03 AU083504-1s1A03 AU065404-1s1A03 AU056003-1s1A03 AU066103-1s1A03 AU056803-1s1A03	AU002403 AU043803 AU009904 AU066103 AU055303 AU083504 AU065404 AU056003 AU066103 AU056803	chrX chrX chrX chrX chrX chrX chrX chrX	143,213,032 143,436,349 143,818,658 143,962,926 144,229,903 145,622,896 145,658,097 146,211,155 147,316,191	143,213,462 143,441,886 143,818,868 143,964,923 144,231,198 145,623,136 145,658,347 146,211,895 147,318,913	430 5,537 210 1,997 1,295 240 250 740 2,722	10 106 5 43 23 6 6 6 6 16 56	19.1 23.8 21.5 17.8 25.0 24.0 21.6 20.6	-0.68 -0.46 -1.23 -0.30 0.54 -0.78 -0.61 -0.54 -0.33	38.8 37.7 40.6 40.3 41.8 43.7 40.7 40.7
AU043803-1s1A03 AU009904-1s1A03 AU066103-1s1A03 AU055303-1s1A03 AU083504-1s1A03 AU065404-1s1A03 AU066003-1s1A03 AU056003-1s1A03 AU1069302-1s1A03	AU002403 AU043803 AU009904 AU066103 AU055303 AU083504 AU065404 AU056003 AU066103 AU056803 AU1069302	chrX chrX chrX chrX chrX chrX chrX chrX	143,213,032 143,436,349 143,818,658 143,962,926 144,229,903 145,652,896 145,658,097 146,211,155 147,316,191 147,316,526	143,213,462 143,441,886 143,818,868 143,964,923 144,231,198 145,652,3136 145,658,347 146,211,895 147,318,913 147,318,858	430 5,537 210 1,997 1,295 240 250 740 2,722 2,332	10 106 5 43 23 6 6 6 16 56 48	19.1 23.8 21.5 17.8 25.0 24.0 21.6 20.6 20.6	-0.68 -0.46 -1.23 -0.30 0.54 -0.78 -0.61 -0.54 -0.33 -0.51	38.8 37.7 40.6 40.3 41.8 43.7 40.7 40.7 39.9
AU043803-1s1A03 AU009904-1s1A03 AU065103-1s1A03 AU055303-1s1A03 AU083504-1s1A03 AU065404-1s1A03 AU066003-1s1A03 AU066103-1s1A03 AU056803-1s1A03 AU1069302-1s1A03 AU073003-1s1A03	AU002403 AU043803 AU009004 AU066103 AU055303 AU085504 AU065404 AU066003 AU06603 AU0660302 AU073003	chrX chrX chrX chrX chrX chrX chrX chrX	143,213,032 143,436,349 143,818,658 143,962,926 144,229,903 145,622,896 145,658,097 146,211,155 147,316,191 147,316,526 147,316,601	143,213,462 143,441,886 143,964,923 144,231,198 145,623,136 145,658,347 146,211,895 147,318,913 147,318,858 147,318,858	430 5,537 210 1,997 1,295 240 250 740 2,722 2,332 2,257	10 106 5 43 23 6 6 6 6 16 56 48 47	19.1 23.8 21.5 17.8 25.0 24.0 21.6 20.6 20.6 20.6 20.8	-0.68 -0.46 -1.23 -0.30 0.54 -0.78 -0.61 -0.54 -0.54 -0.33 -0.51 -0.40	38.8 37.7 40.6 40.3 41.8 43.7 40.7 39.9 39.9
AU043803-1s1A03 AU009904-1s1A03 AU066103-1s1A03 AU055303-1s1A03 AU083504-1s1A03 AU065404-1s1A03 AU066003-1s1A03 AU056003-1s1A03 AU1069302-1s1A03	AU002403 AU043803 AU009904 AU066103 AU055303 AU083504 AU065404 AU056003 AU066103 AU056803 AU1069302	chrX chrX chrX chrX chrX chrX chrX chrX	143,213,032 143,436,349 143,818,658 143,962,926 144,229,903 145,652,896 145,658,097 146,211,155 147,316,191 147,316,526	143,213,462 143,441,886 143,964,923 144,231,198 145,623,136 145,658,347 146,211,895 147,318,858 147,318,858 147,318,858	430 5,537 210 1,997 1,295 240 250 740 2,722 2,332	10 106 5 43 23 6 6 6 16 56 48	19.1 23.8 21.5 17.8 25.0 24.0 21.6 20.6 20.6	-0.68 -0.46 -1.23 -0.30 0.54 -0.78 -0.61 -0.54 -0.33 -0.51	38.8 37.7 40.6 40.3 41.8 43.7 40.7 40.7 39.9
AU043803-1s1A03 AU009904-1s1A03 AU065103-1s1A03 AU055303-1s1A03 AU085504-1s1A03 AU065404-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056803-1s1A03 AU1069302-1s1A03 AU073003-1s1A03 AU008504-1s1A03	AU002403 AU043803 AU009904 AU066103 AU05503 AU08504 AU055003 AU066103 AU056003 AU056003 AU056032 AU073003 AU008504	chrX chrX chrX chrX chrX chrX chrX chrX	143,213,032 143,436,349 143,818,658 143,962,926 144,229,903 145,622,896 145,658,097 146,211,155 147,316,191 147,316,601 147,316,601 147,317,016	143,213,462 143,441,886 143,964,923 144,231,198 145,623,136 145,658,347 146,211,895 147,318,858 147,318,858 147,318,858 147,318,858	430 5,537 210 1,997 1,295 240 250 740 2,722 2,332 2,257 1,842	10 106 5 43 23 6 6 6 16 56 48 47 38	19.1 23.8 21.5 17.8 25.0 24.0 21.6 20.6 20.6 20.8 20.6	-0.68 -0.46 -1.23 -0.30 0.54 -0.78 -0.61 -0.54 -0.33 -0.51 -0.40 -0.63	38.8 37.7 40.6 40.3 41.8 43.7 40.7 39.9 39.9 39.1
AU043803-1s1A03 AU009904-1s1A03 AU055103-1s1A03 AU055303-1s1A03 AU085504-1s1A03 AU055003-1s1A03 AU056003-1s1A03 AU066103-1s1A03 AU1069302-1s1A03 AU073003-1s1A03 AU008504-1s1A03 AU002403-1s2A03	AU002403 AU043803 AU009904 AU066103 AU055303 AU085304 AU085404 AU056003 AU066103 AU06603 AU06603 AU1069302 AU073003 AU008504 AU002403	chrX chrX chrX chrX chrX chrX chrX chrX	143,213,032 143,436,349 143,818,658 143,962,926 144,229,903 145,622,896 145,658,097 146,211,155 147,316,191 147,316,526 147,317,016 147,317,016	143,213,462 143,441,886 143,868,923 144,231,198 145,623,136 145,658,347 146,211,895 147,318,913 147,318,858 147,318,858 147,318,913 147,318,913 147,318,958	430 5,537 210 1,997 1,295 240 250 740 2,722 2,332 2,257 1,842 1,752	10 106 5 43 23 6 6 6 6 16 56 48 47 38 36	19.1 23.8 21.5 17.8 25.0 24.0 21.6 20.6 20.6 20.8 20.6 20.5	-0.68 -0.46 -1.23 -0.30 0.54 -0.78 -0.61 -0.54 -0.54 -0.33 -0.51 -0.40 -0.63 -0.98	38.8 37.7 40.6 40.3 41.8 43.7 40.7 40.7 39.9 39.9 39.1 39.1

AU1038303-1s1A03	AU1038303	chrX	147,317,206	147,318,858	1,652	34	20.6	-0.69	39.1
AU080803-1s1A03	AU080803	chrX	147,317,251	147,318,858	1,607	33	20.5	-0.80	39.2
AU004803-1s1A03	AU004803	chrX	147,317,311	147,318,858	1,547	32	20.7	-0.92	39.2
			147,317,311			32	20.7		39.2
AU014505-1s1A03	AU014505			147,318,858	1,547			-0.87	
AU029303-1s1A03	AU029303	chrX		147,318,913	1,602	33	20.6	-1.19	38.9
AU030603-1s3A03	AU030603	chrX	147,317,361	147,318,858	1,497	31	20.7	-1.18	39.0
AU0920301-1s1A03	AU0920301	chrX	148,428,696	148,430,108	1,412	28	19.8	0.49	66.2
AU073003-1s1A03	AU073003	chrX	148,452,537	148,453,157	620	14	22.6	-1.91	55.2
AU034904-1s1A03	AU034904		148,543,469	148,543,924	455	9	19.8	-1.05	31.4
								1	
AU056003-1s1A03	AU056003	chrX		149,679,625	1,115	24	21.5	-0.58	55.4
AU029303-1s1A03	AU029303	chrX	149,678,535	149,679,480	945	20	21.2	-0.90	55.2
AU055303-1s1A03	AU055303	chrX	149,678,535	149,679,480	945	20	21.2	-0.67	55.2
AU1038303-1s1A03	AU1038303	chrX	149,678,535	149,679,545	1,010	21	20.8	-0.71	55.3
AU014505-1s1A03	AU014505	chrX	149,678,585	149,679,480	895	19	21.2	-0.71	55.7
AU018003-1s1A03	AU018003		149,766,445		700	14	20.0	-0.43	45.6
								1	
AU016803-1s1A03	AU016803		149,942,828	149,946,773	3,945	83	21.0	-0.31	37.3
AU066103-1s1A03	AU066103	chrX	149,942,828	149,946,773	3,945	83	21.0	-0.45	37.3
AU018003-1s1A03	AU018003	chrX	149,942,873	149,946,743	3,870	81	20.9	-0.36	37.3
AU034904-1s1A03	AU034904	chrX	149,942,873	149,946,958	4,085	86	21.1	-0.38	37.3
AU058103-1s1A03	AU058103	chrX	149,942,898	149,946,868	3,970	83	20.9	-0.34	37.3
						81			
AU0852304-1s1A03	AU0852304	chrX		149,946,833	3,865		21.0	-0.31	37.3
AU058503-1s1A03	AU058503	chrX	149,942,993	149,946,868	3,875	81	20.9	-0.30	37.3
AU024003-1s1A03	AU024003	chrX	150,044,196	150,046,376	2,180	20	9.2	0.98	38.9
AU056003-1s1A03	AU056003	chrX	150,044,246	150,046,534	2,288	21	9.2	0.56	38.5
AU014803-1s1A03	AU014803	chrX	150,045,071	150,046,514	1,443	18	12.5	0.80	38.9
AU017504-1s1A03	AU017504	chrX	150,045,071	150,046,514	1,443	18	12.5	0.85	38.9
AU029303-1s1A03	AU029303	chrX	150,045,071	150,046,514	1,443	18	12.5	0.98	38.9
AU0875302-1s2A03	AU0875302	chrX	150,045,071	150,046,281	1,210	15	12.4	0.88	40.4
AU043803-1s1A03	AU043803	chrX	150,045,266	150,046,281	1,015	14	13.8	0.99	39.6
AU056603-1s1A03	AU056603	chrX	150,045,266	150,046,376	1,110	16	14.4	0.87	39.3
AU012004-1s2A03	AU012004	chrX	150,045,576	150,046,281	705	13	18.4	0.58	39.2
AU018304-1s1A03	AU018304	chrX	150,045,576	150,046,351	775	14	18.1	1.02	39.1
AU020003-1s1A03	AU020003	chrX	150,045,576	150,046,534	958	17	17.7	0.73	37.1
AU050703-1s1A03	AU050703	chrX	150,045,576	150,046,514	938	16	17.1	0.87	37.2
AU073003-1s1A03	AU073003	chrX	150,045,576	150,046,281	705	13	18.4	0.70	39.2
AU1038303-1s1A03	AU1038303	chrX	150,045,576	150,046,534	958	17	17.7	0.77	37.1
AU016803-1s1A03	AU016803	chrX	150,045,626	150,046,376	750	14	18.7	0.99	38.7
AU034904-1s1A03	AU034904	chrX	150,608,758	150,610,143	1,385	29	20.9	-0.33	44.0
					1,330				
AU056603-1s1A03	AU056603	chrX	150,608,758	150,610,088	1.330	28	21.1	-0.43	43.7
AU009503-1s1A03	AU009503	chrX	150,608,963	150,610,618	1,655	36	21.8	-0.35	44.4
AU009503-1s1A03 AU043803-1s1A03	AU009503 AU043803						21.8 22.2	-0.35 -0.39	44.4 44.5
			150,608,963	150,610,618	1,655	36			
AU043803-1s1A03	AU043803	chrX	150,608,963 150,608,963	150,610,618 150,610,088	1,655 1,125	36 25	22.2	-0.39	44.5
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03	AU043803 AU058503 AU066103	chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963	150,610,618 150,610,088 150,610,143 150,610,398	1,655 1,125 1,180 1,435	36 25 26 31	22.2 22.0 21.6	-0.39 -0.43 -0.46	44.5 44.9 44.7
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU018003-1s1A03	AU043803 AU058503 AU066103 AU018003	chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480	1,655 1,125 1,180 1,435 680	36 25 26 31 15	22.2 22.0 21.6 22.1	-0.39 -0.43 -0.46 -0.53	44.5 44.9 44.7 43.0
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU018003-1s1A03 AU0920301-1s1A03	AU043803 AU058503 AU066103 AU018003 AU0920301	chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441	1,655 1,125 1,180 1,435 680 2,185	36 25 26 31 15 46	22.2 22.0 21.6 22.1 21.1	-0.39 -0.43 -0.46 -0.53 0.46	44.5 44.9 44.7 43.0 53.4
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU018003-1s1A03 AU0920301-1s1A03 AU056003-1s1A03	AU043803 AU058503 AU066103 AU018003 AU0920301 AU056003	chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,591	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391	1,655 1,125 1,180 1,435 680 2,185 1,800	36 25 26 31 15 46 38	22.2 22.0 21.6 22.1 21.1 21.1 21.1	-0.39 -0.43 -0.46 -0.53 0.46 0.31	44.5 44.9 44.7 43.0 53.4 54.1
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU018003-1s1A03 AU0920301-1s1A03 AU056003-1s1A03 AU056603-1s1A03	AU043803 AU058503 AU066103 AU018003 AU0920301 AU056003 AU056603	chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,591 152,269,845	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135	1,655 1,125 1,180 1,435 680 2,185 1,800 290	36 25 26 31 15 46 38 7	22.2 22.0 21.6 22.1 21.1 21.1 21.1 24.1	-0.39 -0.43 -0.46 -0.53 0.46 0.31 -1.03	44.5 44.9 44.7 43.0 53.4 54.1 44.1
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU018003-1s1A03 AU0920301-1s1A03 AU056003-1s1A03	AU043803 AU058503 AU066103 AU018003 AU0920301 AU056003	chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,591	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391	1,655 1,125 1,180 1,435 680 2,185 1,800	36 25 26 31 15 46 38	22.2 22.0 21.6 22.1 21.1 21.1 21.1	-0.39 -0.43 -0.46 -0.53 0.46 0.31	44.5 44.9 44.7 43.0 53.4 54.1
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU018003-1s1A03 AU0920301-1s1A03 AU056003-1s1A03 AU056603-1s1A03	AU043803 AU058503 AU066103 AU018003 AU0920301 AU056003 AU056603	chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,591 152,269,845	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135	1,655 1,125 1,180 1,435 680 2,185 1,800 290	36 25 26 31 15 46 38 7	22.2 22.0 21.6 22.1 21.1 21.1 21.1 24.1	-0.39 -0.43 -0.46 -0.53 0.46 0.31 -1.03	44.5 44.9 44.7 43.0 53.4 54.1 44.1
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU018003-1s1A03 AU0920301-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU062203-1s1A03 AU080803-1s1A03	AU043803 AU058503 AU066103 AU018003 AU0920301 AU056003 AU056603 AU062203 AU080803	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,259 152,269,845 152,269,845	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175	1,655 1,125 1,180 1,435 680 2,185 1,800 290 290 330	36 25 26 31 15 46 38 7 7 7 8	22.2 22.0 21.6 22.1 21.1 21.1 24.1 24.1 24.2	-0.39 -0.43 -0.46 -0.53 0.46 0.31 -1.03 -0.85 -0.91	44.5 44.9 44.7 43.0 53.4 54.1 44.1 44.1 44.4
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU018003-1s1A03 AU0920301-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU062203-1s1A03 AU080803-1s1A03 AU014803-1s1A03	AU043803 AU058503 AU066103 AU0920301 AU0920301 AU056003 AU05603 AU062203 AU080803 AU014803	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,591 152,269,845 152,269,845 152,269,845	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,175 152,270,175	1,655 1,125 1,180 1,435 680 2,185 1,800 290 290 330 280	36 25 26 31 15 46 38 7 7 8 7 7	22.2 22.0 21.6 22.1 21.1 21.1 24.1 24.1 24.2 25.0	-0.39 -0.43 -0.46 -0.53 -0.46 0.31 -1.03 -0.85 -0.91 -0.89	44.5 44.9 44.7 43.0 53.4 54.1 44.1 44.1 44.4 43.9
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU018003-1s1A03 AU0920301-1s1A03 AU056003-1s1A03 AU056603-1s1A03 AU05603-1s1A03 AU062203-1s1A03 AU014803-1s1A03 AU014803-1s1A03	AU043803 AU058503 AU06103 AU018003 AU0920301 AU056003 AU056603 AU062203 AU062203 AU080803 AU014803 AU043803	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,259 152,269,845 152,269,845 152,269,895 152,269,895	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,270,175	1,655 1,125 1,180 1,435 680 2,185 1,800 290 290 290 330 280 280 240	36 25 26 31 15 46 38 7 7 8 7 6	22.2 22.0 21.6 22.1 21.1 21.1 24.1 24.1 24.1 24.2 25.0 25.0	-0.39 -0.43 -0.53 0.46 0.31 -1.03 -0.85 -0.91 -0.89 -1.26	44.5 44.9 44.7 43.0 53.4 54.1 44.1 44.1 44.4 43.9 43.4
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU018003-1s1A03 AU0920301-1s1A03 AU056003-1s1A03 AU05603-1s1A03 AU062203-1s1A03 AU080803-1s1A03 AU014803-1s1A03 AU043803-1s1A03 AU055503-1s1A03	AU043803 AU058503 AU06103 AU0920301 AU05003 AU05603 AU05603 AU080803 AU04803 AU04803 AU043803 AU05503	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,259 152,269,845 152,269,845 152,269,845 152,269,895 152,269,895	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,270,135 152,270,135	1,655 1,125 1,180 1,435 680 2,185 1,800 290 290 290 330 280 240 280	36 25 26 31 15 46 38 7 7 8 7 6 7	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.1 24.2 25.0 25.0 25.0	-0.39 -0.43 -0.53 0.46 0.31 -1.03 -0.85 -0.91 -0.89 -1.26 -1.04	44.5 44.9 44.7 53.4 54.1 44.1 44.1 44.4 43.9 43.4 43.9
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU0920301-1s1A03 AU056003-1s1A03 AU056603-1s1A03 AU056603-1s1A03 AU062203-1s1A03 AU0480803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU055503-1s1A03 AU066103-1s1A03	AU043803 AU058503 AU06103 AU0920301 AU0920301 AU056003 AU06603 AU06203 AU080803 AU014803 AU043803 AU05503 AU066103	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,591 152,269,845 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175	1,655 1,125 1,180 1,435 680 2,185 1,800 290 290 330 280 280 280 280 280	36 25 26 31 15 46 38 7 7 8 7 6 7 7 7 7	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0	-0.39 -0.43 -0.46 -0.53 0.46 0.31 -1.03 -0.85 -0.91 -0.89 -1.26 -1.04 -1.08	44.5 44.9 44.7 43.0 53.4 54.1 44.1 44.1 44.1 44.4 43.9 43.4 43.9 43.9
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU056003-1s1A03 AU050603-1s1A03 AU056003-1s1A03 AU056603-1s1A03 AU062203-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU066103-1s1A03 AU066103-1s1A03	AU043803 AU058503 AU066103 AU0920301 AU0920301 AU056603 AU056603 AU06203 AU080803 AU04803 AU044803 AU044803 AU04503 AU06103 AU0920301	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,608,963 151,742,256 151,742,591 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175	1,655 1,125 1,180 1,435 680 2,185 1,800 290 330 290 330 280 240 280 280 280 280 280	36 25 26 31 15 46 38 7 7 8 7 7 6 7 7 7 35	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 17.9	-0.39 -0.43 -0.46 -0.53 0.46 0.31 -1.03 -0.85 -0.91 -0.89 -1.26 -1.04 -1.08 0.49	44.5 44.9 44.7 43.0 53.4 54.1 44.1 44.1 44.4 43.9 43.4 43.9 43.4 43.9 51.8
AU043803-1s1A03 AU058503-1s1A03 AU06103-1s1A03 AU0920301-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU062003-1s1A03 AU04803-1s1A03 AU043803-1s1A03 AU043803-1s1A03 AU06103-1s1A03 AU0920301-1s1A03 AU080803-1s1A03	AU043803 AU058503 AU06103 AU0920301 AU0920301 AU056003 AU06603 AU06203 AU080803 AU014803 AU043803 AU05503 AU066103	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,591 152,269,845 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175	1,655 1,125 1,180 1,435 680 2,185 1,800 290 290 330 280 280 280 280 280	36 25 26 31 15 46 38 7 7 8 7 8 7 6 7 7 7 35 27	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0	$\begin{array}{c} -0.39\\ -0.43\\ -0.46\\ 0.53\\ 0.46\\ 0.31\\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ 0.49\\ 0.60\\ \end{array}$	44.5 44.9 44.7 43.0 53.4 54.1 44.1 44.1 44.1 44.4 43.9 43.4 43.9 43.9
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU056003-1s1A03 AU050603-1s1A03 AU056003-1s1A03 AU056603-1s1A03 AU062203-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU066103-1s1A03 AU066103-1s1A03	AU043803 AU058503 AU066103 AU0920301 AU0920301 AU056603 AU056603 AU06203 AU080803 AU04803 AU044803 AU044803 AU04503 AU06103 AU0920301	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,608,963 151,742,256 151,742,591 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,209,895	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175	1,655 1,125 1,180 1,435 680 2,185 1,800 290 330 290 330 280 240 280 280 280 280 280	36 25 26 31 15 46 38 7 7 8 7 7 6 7 7 7 35	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 17.9	-0.39 -0.43 -0.46 -0.53 0.46 0.31 -1.03 -0.85 -0.91 -0.89 -1.26 -1.04 -1.08 0.49	44.5 44.9 44.7 43.0 53.4 54.1 44.1 44.1 44.4 43.9 43.4 43.9 43.4 43.9 51.8
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU0920301-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU05603-1s1A03 AU062203-1s1A03 AU043803-1s1A03 AU043803-1s1A03 AU055503-1s1A03 AU066103-1s1A03 AU06920301-1s1A03 AU055503-1s1A03 AU055503-1s1A03	AU043803 AU058503 AU06103 AU0920301 AU056003 AU056003 AU06203 AU06203 AU04803 AU04803 AU043803 AU043803 AU05503 AU06103 AU0920301 AU080803	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,256 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,301,264 152,465,584 152,649,628	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175	1,655 1,125 1,180 1,435 680 2,185 1,800 290 290 330 280 240 280 280 280 1,950 1,250 1,193	36 25 26 31 15 46 38 7 7 8 7 6 7 7 6 7 7 35 27 23	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.46\\ 0.53\\ 0.46\\ 0.31\\ \hline \\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ 0.49\\ 0.60\\ -0.35\\ \end{array}$	$\begin{array}{c} 44.5\\ 44.9\\ 44.7\\ 43.0\\ 53.4\\ 54.1\\ 44.1\\ 44.1\\ 44.4\\ 43.9\\ 43.4\\ 43.9\\ 43.4\\ 43.9\\ 51.8\\ 61.4\\ 41.4\\ \end{array}$
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU0920301-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU05603-1s1A03 AU062203-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU080803-1s1A03 AU055503-1s1A03 AU014803-1s1A03	AU043803 AU058503 AU06103 AU0920301 AU056003 AU056003 AU05603 AU062203 AU08803 AU04803 AU04803 AU045503 AU066103 AU0920301 AU08003 AU055503 AU014803	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,256 152,269,845 152,269,845 152,269,895 152,301,264 152,465,584 152,469,628	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175	1,655 1,125 1,180 1,435 680 2,185 1,800 290 290 290 290 290 290 290 290 290 2	36 25 26 31 15 46 38 7 7 8 7 7 8 7 6 7 7 7 35 27 23 11	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.46\\ 0.31\\ \hline \\ -0.53\\ 0.46\\ 0.31\\ \hline \\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ \hline \\ 0.49\\ 0.60\\ -0.35\\ 0.86\\ \end{array}$	44.5 44.9 44.7 33.0 53.4 54.1 44.1 44.1 44.1 44.1 43.9 43.4 43.9 43.9 51.8 61.4 41.4 48.6
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU0920301-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU062203-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU066103-1s1A03 AU0920301-1s1A03 AU0920301-1s1A03 AU0920301-1s1A03 AU055503-1s1A03 AU055503-1s1A03 AU014803-1s1A03 AU014803-1s1A03 AU034904-1s1A03	AU043803 AU058503 AU06103 AU0920301 AU0920301 AU056003 AU06203 AU080803 AU04803 AU04803 AU04803 AU04920301 AU080803 AU055503 AU04803 AU04803 AU04803 AU04803	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 152,269,845 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,301,264 152,465,584 152,465,584 153,157,712	150,610,618 150,610,483 150,610,483 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,230,3,214 152,466,834 152,650,821 153,158,914	1,655 1,125 1,180 1,435 680 2,185 1,800 290 290 290 290 290 290 290 290 280 240 280 280 280 1,950 1,250 1,193 1,202 7,000	36 25 26 31 15 46 38 7 7 7 8 7 6 6 7 7 7 35 27 23 11 109	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.46\\ \hline 0.53\\ \hline 0.46\\ 0.31\\ \hline -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ \hline 0.49\\ \hline 0.60\\ -0.35\\ \hline 0.86\\ -0.60\\ \end{array}$	$\begin{array}{r} 44.5\\ 44.9\\ 44.7\\ 33.0\\ 53.4\\ 54.1\\ 44.1\\ 44.1\\ 44.1\\ 44.4\\ 43.9\\ 43.4\\ 43.9\\ 43.9\\ 51.8\\ 61.4\\ 41.4\\ 48.6\\ 48.2\\ \end{array}$
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU060103-1s1A03 AU0920301-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU062203-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU0920301-1s1A03 AU0920301-1s1A03 AU0920301-1s1A03 AU05503-1s1A03 AU05503-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03	AU043803 AU058503 AU066103 AU0920301 AU0920301 AU056003 AU06203 AU06203 AU04803 AU04803 AU04803 AU045503 AU0920301 AU080803 AU055503 AU04803 AU04803 AU04803	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,591 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,465,584 152,464,528 153,157,712 153,473,214	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,31,158,914 153,158,914 153,541,207	1,655 1,125 1,180 1,435 680 2,185 1,800 290 290 330 280 240 280 240 280 280 1,950 1,250 1,250 1,193 1,202 7,000 705	36 25 26 31 15 46 38 7 7 8 8 7 7 6 7 7 7 7 35 27 23 11 109 16	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 17.9 21.6 19.3 9.2 15.6 22.7	$\begin{array}{c} -0.39\\ -0.43\\ -0.46\\ \hline 0.53\\ \hline 0.46\\ 0.31\\ \hline -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ \hline 0.49\\ \hline 0.60\\ -0.35\\ \hline 0.86\\ -0.60\\ \hline 0.52\\ \end{array}$	44.5 44.9 44.7 43.0 53.4 54.1 44.1 44.1 44.1 44.4 43.9 43.9 43.9 43.9 51.8 61.4 41.4 48.6 48.2 54.9
AU043803-1s1A03 AU058503-1s1A03 AU06103-1s1A03 AU0920301-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU062003-1s1A03 AU04803-1s1A03 AU043803-1s1A03 AU043803-1s1A03 AU06103-1s1A03 AU0920301-1s1A03 AU055503-1s1A03 AU055503-1s1A03 AU055503-1s1A03 AU055503-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU083504-1s1A03	AU043803 AU058503 AU06103 AU0920301 AU056003 AU05603 AU05603 AU062203 AU04803 AU044803 AU044803 AU045503 AU055503 AU055503 AU055503 AU014803 AU04803 AU04803 AU080803 AU04803 AU083504	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,551 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,301,264 153,157,712 153,473,214 153,540,502 154,047,451	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,303,214 153,450,8214 153,450,140 153,541,207 154,056,710	1,655 1,125 1,180 1,435 680 2,185 1,800 290 290 330 280 240 280 240 280 280 1,950 1,250 1,250 1,193 1,202 7,000 705 9,259	36 25 26 31 15 46 38 7 7 8 7 7 8 7 7 6 7 7 7 35 27 23 11 109 16 152	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 17.9 21.6 19.3 9.2 15.6 22.7 16.4	$\begin{array}{c} -0.39\\ -0.43\\ -0.46\\ 0.53\\ 0.46\\ 0.31\\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ 0.49\\ 0.60\\ -0.35\\ 0.86\\ -0.60\\ 0.52\\ -0.64\\ \end{array}$	$\begin{array}{r} 44.5\\ 44.9\\ 44.7\\ 43.0\\ 53.4\\ 54.1\\ 44.1\\ 44.1\\ 44.4\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.4\\ 43.9\\ 43.4\\ 43.9\\ 43.4\\ 43.9\\ 43.4\\ 43.9\\ 43.4\\ 43.9\\ 43.4\\ 43.9\\ 43.4\\ 43.9\\ 43.4\\ 43.9\\ 43.4\\$
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU018003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU062203-1s1A03 AU062203-1s1A03 AU043803-1s1A03 AU043803-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU065503-1s1A03 AU055503-1s1A03 AU014803-1s1A03 AU014803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU085504-1s1A03 AU09503-1s1A03	AU043803 AU058503 AU06103 AU0920301 AU056003 AU056003 AU05603 AU062203 AU08803 AU04803 AU04803 AU055503 AU06103 AU0920301 AU0920301 AU0920301 AU092030 AU04803 AU04803 AU04803 AU04803 AU08504 AU09503	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,591 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,301,264 152,445,584 152,649,628 153,157,712 153,473,214 153,540,502 154,047,451 154,139,152	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,303,214 152,466,834 152,650,821 153,158,914 153,480,214 153,480,214 153,541,207 154,056,710 154,139,992	1,655 1,125 1,180 1,435 680 2,185 1,800 290 290 330 280 240 280 240 280 280 1,950 1,250 1,250 1,193 1,202 7,000 705 9,259 840	36 25 26 31 15 46 38 7 7 8 7 8 7 6 7 7 35 27 23 11 109 16 152 19	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.46\\ 0.31\\ \hline \\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ 0.49\\ 0.60\\ -0.35\\ 0.86\\ -0.60\\ 0.52\\ -0.64\\ -1.25\\ \end{array}$	44.5 44.9 44.7 43.0 53.4 54.1 44.1 44.1 44.1 43.9 43.9 43.9 43.9 43.9 43.9 43.9 43.9
AU043803-1s1A03 AU058503-1s1A03 AU06103-1s1A03 AU0920301-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU062003-1s1A03 AU04803-1s1A03 AU043803-1s1A03 AU043803-1s1A03 AU06103-1s1A03 AU0920301-1s1A03 AU055503-1s1A03 AU055503-1s1A03 AU055503-1s1A03 AU055503-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU083504-1s1A03	AU043803 AU058503 AU06103 AU0920301 AU056003 AU05603 AU05603 AU062203 AU04803 AU044803 AU044803 AU045503 AU055503 AU055503 AU055503 AU014803 AU04803 AU04803 AU080803 AU04803 AU083504	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,591 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,301,264 152,445,584 152,649,628 153,157,712 153,473,214 153,540,502 154,047,451 154,139,152	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,303,214 153,450,8214 153,450,140 153,541,207 154,056,710	1,655 1,125 1,180 1,435 680 2,185 1,800 290 290 330 280 240 280 240 280 280 1,950 1,250 1,250 1,193 1,202 7,000 705 9,259	36 25 26 31 15 46 38 7 7 8 7 7 8 7 7 6 7 7 7 35 27 23 11 109 16 152	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 17.9 21.6 19.3 9.2 15.6 22.7 16.4	$\begin{array}{c} -0.39\\ -0.43\\ -0.46\\ 0.53\\ 0.46\\ 0.31\\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ 0.49\\ 0.60\\ -0.35\\ 0.86\\ -0.60\\ 0.52\\ -0.64\\ \end{array}$	$\begin{array}{r} 44.5\\ 44.9\\ 44.7\\ 43.0\\ 53.4\\ 54.1\\ 44.1\\ 44.1\\ 44.4\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.4\\ 43.9\\ 43.4\\ 43.9\\ 43.4\\ 43.9\\ 43.4\\ 43.9\\ 43.4\\ 43.9\\ 43.4\\ 43.9\\ 43.4\\ 43.9\\ 43.4\\$
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU018003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU062203-1s1A03 AU062203-1s1A03 AU043803-1s1A03 AU043803-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU065503-1s1A03 AU055503-1s1A03 AU014803-1s1A03 AU014803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU085504-1s1A03 AU09503-1s1A03	AU043803 AU058503 AU06103 AU0920301 AU056003 AU056003 AU05603 AU062203 AU08803 AU04803 AU04803 AU055503 AU06103 AU0920301 AU0920301 AU0920301 AU092030 AU04803 AU04803 AU04803 AU04803 AU08504 AU09503	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,591 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,301,264 152,445,584 152,649,628 153,157,712 153,473,214 153,540,502 154,047,451 154,139,152	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,303,214 153,450,821 153,158,914 153,541,207 154,056,710 154,139,992	1,655 1,125 1,180 1,435 680 2,185 1,800 290 290 330 280 240 280 240 280 280 1,950 1,250 1,250 1,193 1,202 7,000 705 9,259 840	36 25 26 31 15 46 38 7 7 8 7 8 7 6 7 7 35 27 23 11 109 16 152 19	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.46\\ 0.31\\ \hline \\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ 0.49\\ 0.60\\ -0.35\\ 0.86\\ -0.60\\ 0.52\\ -0.64\\ -1.25\\ \end{array}$	44.5 44.9 44.7 43.0 53.4 54.1 44.1 44.1 44.1 43.9 43.9 43.9 43.9 43.9 43.9 43.9 43.9
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU0660103-1s1A03 AU0920301-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU062203-1s1A03 AU062203-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU066103-1s1A03 AU0920301-1s1A03 AU0920301-1s1A03 AU0920301-1s1A03 AU092031-1s1A03 AU092031-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU004803-1s1A03 AU09503-1s1A03 AU09503-1s1A03 AU09503-1s1A03 AU09503-1s1A03 AU09503-1s1A03 AU014803-1s1A03 AU024003-1s1A03	AU043803 AU058503 AU06103 AU0920301 AU056003 AU05603 AU06203 AU080803 AU04803 AU04803 AU04803 AU0920301 AU0920301 AU0920301 AU0920301 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,591 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,301,264 152,465,584 153,157,712 153,473,214 153,540,502 154,139,152	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,180,214 153,180,214 153,180,214 153,41207 154,139,952 154,140,052	1,655 1,125 1,180 1,435 680 2,185 1,800 290 330 280 240 280 280 280 1,950 1,250 1,193 1,202 7,000 705 9,259 840 800 900	36 25 26 31 15 46 38 7 7 7 8 8 7 7 7 8 7 7 35 27 23 11 1 109 16 152 19 18 20	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.46\\ 0.31\\ \hline \\ -0.53\\ 0.46\\ 0.31\\ \hline \\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ \hline \\ 0.49\\ 0.60\\ 0.49\\ \hline \\ 0.60\\ -0.35\\ 0.86\\ \hline \\ -0.60\\ 0.52\\ \hline \\ -0.60\\ 0.52\\ \hline \\ -0.64\\ \hline \\ -1.25\\ -1.09\\ -1.06\\ \hline \end{array}$	$\begin{array}{r} 44.5\\ 44.9\\ 44.7\\ 43.0\\ 53.4\\ 54.1\\ 44.1\\ 44.1\\ 44.1\\ 44.4\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 51.8\\ 61.4\\ 43.9\\ 43.9\\ 43.9\\ 34.4\\ 41.1\\ 41.7\\ 40.8\\ \end{array}$
AU043803-1s1A03 AU058503-1s1A03 AU06103-1s1A03 AU0920301-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU062003-1s1A03 AU062003-1s1A03 AU043803-1s1A03 AU043803-1s1A03 AU043803-1s1A03 AU055503-1s1A03 AU055503-1s1A03 AU055503-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU09503-1s1A03 AU024003-1s1A03 AU067803-1s2A03	AU043803 AU058503 AU06103 AU0920301 AU056003 AU056003 AU05603 AU06203 AU04803 AU04803 AU04803 AU04803 AU05503 AU05503 AU05503 AU05503 AU04803 AU05503 AU04803 AU080803 AU080803 AU080803 AU09503 AU083504 AU09503 AU014803 AU09503 AU0480 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,259 152,269,845 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,264,895 152,465,584 152,464,528 153,157,712 153,473,214 153,540,502 154,037,152 154,139,152 154,139,152	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,33,214 153,480,214 153,480,214 153,541,207 154,056,710 154,139,992 154,140,052	1,655 1,125 1,180 1,435 680 2,185 1,800 290 290 330 280 240 280 240 280 240 280 240 280 240 280 240 280 240 280 240 280 290 290 30 290 290 30 290 290 30 290 290 30 290 290 290 30 290 290 290 30 290 290 290 290 290 290 290 290 290 29	36 25 26 31 15 46 38 7 7 8 7 7 8 7 7 7 7 35 27 23 11 109 16 152 19 18 20 20	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.46\\ 0.53\\ 0.46\\ 0.31\\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ 0.49\\ 0.60\\ -0.35\\ 0.86\\ -0.60\\ 0.52\\ -0.64\\ -1.25\\ -1.09\\ -1.06\\ -1.37\end{array}$	$\begin{array}{r} 44.5\\ 44.9\\ 44.7\\ 43.0\\ 53.4\\ 54.1\\ 44.1\\ 44.1\\ 44.4\\ 43.9\\ 43.4\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 51.8\\ 61.4\\ 41.4\\ 48.6\\ 54.9\\ 34.4\\ 41.1\\ 41.7\\ 40.8\\ 40.8\\ 40.8\\ \end{array}$
AU043803-1s1A03 AU058503-1s1A03 AU06103-1s1A03 AU0920301-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU05503-1s1A03 AU014803-1s1A03 AU043803-1s1A03 AU055503-1s1A03 AU06103-1s1A03 AU06103-1s1A03 AU06103-1s1A03 AU06103-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU09503-1s1A03 AU009503-1s1A03 AU014803-1s1A03 AU014803-1s1A03 AU014803-1s1A03 AU014803-1s1A03 AU014803-1s1A03 AU014803-1s1A03 AU014803-1s1A03 AU014803-1s1A03 AU014803-1s1A03 AU014803-1s1A03 AU014803-1s1A03 AU063803-1s1A03 AU063803-1s1A03 AU063803-1s1A03 AU063803-1s1A03 AU063803-1s1A03 AU063803-1s1A03 AU063803-1s1A03 AU063803-1s1A03 AU063803-1s1A03	AU043803 AU058503 AU06103 AU0920301 AU056003 AU056003 AU05603 AU062203 AU08803 AU04803 AU04803 AU04803 AU0920301 AU0920301 AU08033 AU055503 AU014803 AU04803 AU04803 AU04803 AU09503 AU04803 AU09503 AU014803 AU02903 AU04803 AU02903 AU024003 AU02803 AU04803 AU02803 AU02803 AU02803 AU02803 AU02803 AU02803 AU02803 AU02803 AU02803 AU083504	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,256 151,742,591 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,301,264 152,465,584 152,465,584 153,473,214 153,473,214 154,139,152 154,139,152 154,139,152	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,33,214 153,450,821 153,450,821 153,450,100 154,139,992 154,140,052 154,140,052	1,655 1,125 1,180 1,435 680 2,185 1,800 290 290 330 280 240 280 240 280 280 1,950 1,250 1,193 1,250 1,193 1,250 1,193 1,202 7,000 705 9,259 840 800 900 900	36 25 26 31 15 46 38 7 7 8 7 7 8 7 7 6 7 7 7 35 27 23 11 109 16 152 19 18 20 20 20	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.43\\ -0.53\\ 0.46\\ 0.31\\ \hline \\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ 0.49\\ 0.60\\ -0.35\\ 0.86\\ -0.60\\ 0.52\\ -0.64\\ \hline \\ -1.25\\ -1.09\\ -1.06\\ -1.37\\ -1.34\\ \end{array}$	$\begin{array}{r} 44.5\\ 44.9\\ 44.7\\ 43.0\\ 53.4\\ 54.1\\ 44.1\\ 44.1\\ 44.4\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 51.8\\ 61.4\\ 41.4\\ 48.6\\ 61.4\\ 41.4\\ 48.6\\ 48.2\\ 54.9\\ 34.4\\ 41.1\\ 41.7\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ \end{array}$
AU043803-1s1A03 AU058503-1s1A03 AU06103-1s1A03 AU06103-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU05603-1s1A03 AU062203-1s1A03 AU04803-1s1A03 AU043803-1s1A03 AU043803-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU065503-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU09503-1s1A03 AU014803-1s1A03 AU014803-1s1A03 AU04803-1s1A03 AU047803-1s1A03 AU067803-1s2A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU0920301-1s1A03	AU043803 AU058503 AU066103 AU0920301 AU056003 AU056003 AU05603 AU062203 AU08803 AU04803 AU04803 AU045503 AU06103 AU0920301 AU0920301 AU09503 AU04803 AU04803 AU04803 AU04803 AU04803 AU09503 AU04803 AU08804 AU08804 AU0820301	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,608,963 151,742,256 151,742,256 151,742,591 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,301,264 152,455,584 152,649,628 153,157,712 153,473,214 153,473,214 153,473,214 153,473,214 154,139,152 154,139,152 154,139,152 154,139,152	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,303,214 153,480,214 153,480,214 153,480,214 153,480,210 154,139,952 154,139,952 154,140,052 154,140,052	1,655 1,125 1,180 1,435 680 2,185 1,800 290 290 290 290 290 290 290 290 290 2	36 25 26 31 15 46 38 7 7 8 7 7 8 7 7 7 35 27 23 11 109 16 152 19 18 20 20 20 20	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.43\\ -0.53\\ 0.46\\ 0.31\\ \hline \\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ 0.49\\ 0.60\\ -0.35\\ 0.86\\ -0.60\\ 0.52\\ -0.64\\ \hline \\ -1.25\\ -1.09\\ -1.06\\ -1.37\\ -1.34\\ -0.72\\ \end{array}$	$\begin{array}{r} 44.5\\ 44.9\\ 44.7\\ 43.0\\ 53.4\\ 54.1\\ 44.1\\ 44.1\\ 44.1\\ 44.1\\ 44.4\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 51.8\\ 61.4\\ 41.4\\ 48.6\\ 48.2\\ 54.9\\ 34.4\\ 41.1\\ 41.7\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ \end{array}$
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU0920301-1s1A03 AU056603-1s1A03 AU056603-1s1A03 AU062203-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU06403-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU067803-1s2A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU0920301-1s1A03 AU0920301-1s1A03 AU0920301-1s1A03 AU09303-1s1A03 AU03803-1s1A03	AU043803 AU058503 AU06103 AU05003 AU05603 AU05603 AU05603 AU062203 AU08803 AU04803 AU04803 AU045503 AU06403 AU0920301 AU0920301 AU03803 AU034904 AU034904 AU004803 AU034904 AU004803 AU08803 AU014803 AU0880 A	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,256 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,301,264 152,455,584 153,157,712 153,473,214 153,540,502 154,139,152 154,139,152 154,139,152 154,139,152	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,303,214 153,450,821 153,158,914 153,450,6710 154,139,992 154,140,052 154,140,052 154,140,052	1,655 1,125 1,180 2,185 1,800 290 290 290 290 290 290 290 290 280 280 280 1,950 1,250 1,193 1,202 7,000 705 9,259 840 800 900 900 900 900 900 1,016	36 25 26 31 15 46 38 7 7 8 7 7 8 7 7 8 7 7 35 27 23 11 109 16 152 19 18 20 20 20 20 20 20 20 22	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.43\\ -0.53\\ 0.46\\ 0.31\\ \hline \\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ \hline \\ 0.49\\ 0.60\\ -0.35\\ 0.86\\ -0.60\\ 0.52\\ -0.64\\ \hline \\ -1.25\\ -1.09\\ -1.37\\ -1.34\\ -0.72\\ -0.93\\ \end{array}$	$\begin{array}{r} 44.5\\ 44.9\\ 44.7\\ 43.0\\ 53.4\\ 54.1\\ 44.1\\ 44.1\\ 44.1\\ 44.1\\ 44.4\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 51.8\\ 61.4\\ 43.9\\$
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU062203-1s1A03 AU062203-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU0920301-1s1A03 AU0920301-1s1A03 AU0920301-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU067803-1s2A03 AU067803-1s2A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU0920301-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03	AU043803 AU058503 AU06103 AU0920301 AU056003 AU05603 AU080803 AU06203 AU080803 AU04803 AU04803 AU055503 AU06103 AU0920301 AU0920301 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU027803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU08304 AU0920301 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,608,963 151,742,256 151,742,256 151,742,591 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,301,264 152,455,584 152,649,628 153,157,712 153,473,214 153,473,214 153,473,214 153,473,214 154,139,152 154,139,152 154,139,152 154,139,152	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 154,140,052 154,140,052 154,140,052	1,655 1,125 1,180 1,435 680 2,185 1,800 290 330 280 240 280 240 280 280 1,950 1,250 2,59 9,259 1,000 9,0000 9,0000 9,0000 9,0000 9,00000000	36 25 26 31 15 46 38 7 7 8 8 7 7 7 8 7 7 7 35 27 23 11 109 16 152 19 18 20 20 20 20 20 20 22 14	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.46\\ 0.31\\ \hline \\ -0.53\\ 0.46\\ 0.31\\ \hline \\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ \hline \\ 0.49\\ 0.60\\ 0.49\\ \hline \\ 0.60\\ 0.52\\ \hline \\ -0.60\\ 0.52\\ \hline \\ -0.60\\ 0.52\\ \hline \\ -0.60\\ 0.52\\ \hline \\ -1.09\\ -1.26\\ -1.25\\ -1.09\\ -1.37\\ -1.34\\ -0.72\\ -0.93\\ -1.17\end{array}$	$\begin{array}{r} 44.5\\ 44.9\\ 44.7\\ 43.0\\ 53.4\\ 54.1\\ 44.1\\ 44.1\\ 44.1\\ 44.4\\ 43.9\\$
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU0920301-1s1A03 AU056603-1s1A03 AU056603-1s1A03 AU062203-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU06403-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU067803-1s2A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU0920301-1s1A03 AU0920301-1s1A03 AU0920301-1s1A03 AU09303-1s1A03 AU03803-1s1A03	AU043803 AU058503 AU06103 AU05003 AU05603 AU05603 AU05603 AU062203 AU08803 AU04803 AU04803 AU045503 AU06403 AU0920301 AU0920301 AU03803 AU034904 AU034904 AU004803 AU034904 AU004803 AU08803 AU014803 AU0880 A	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,256 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,301,264 152,455,584 153,157,712 153,473,214 153,540,502 154,139,152 154,139,152 154,139,152 154,139,152	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,303,214 153,450,821 153,158,914 153,450,6710 154,139,992 154,140,052 154,140,052 154,140,052	1,655 1,125 1,180 2,185 1,800 290 290 290 290 290 290 290 290 280 280 280 1,950 1,250 1,193 1,202 7,000 705 9,259 840 800 900 900 900 900 900 1,016	36 25 26 31 15 46 38 7 7 8 7 7 8 7 7 8 7 7 35 27 23 11 109 16 152 19 18 20 20 20 20 20 20 20 22	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.43\\ -0.53\\ 0.46\\ 0.31\\ \hline \\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ \hline \\ -1.04\\ -1.08\\ \hline \\ 0.49\\ 0.60\\ -0.35\\ 0.86\\ -0.60\\ 0.52\\ \hline \\ -0.64\\ \hline \\ -1.25\\ -1.09\\ -1.37\\ -1.34\\ -0.72\\ -0.93\\ \hline \end{array}$	$\begin{array}{r} 44.5\\ 44.9\\ 44.7\\ 43.0\\ 53.4\\ 54.1\\ 44.1\\ 44.1\\ 44.1\\ 44.1\\ 44.4\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 51.8\\ 61.4\\ 43.9\\$
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU062203-1s1A03 AU062203-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU0920301-1s1A03 AU0920301-1s1A03 AU0920301-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU067803-1s2A03 AU067803-1s2A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU0920301-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU004803-1s1A03	AU043803 AU058503 AU06103 AU0920301 AU056003 AU05603 AU080803 AU06203 AU080803 AU04803 AU04803 AU055503 AU06103 AU0920301 AU0920301 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU027803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU08304 AU0920301 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803	chrX chrX chrX chrX chrX chrX chrX chrX chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,591 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,301,264 152,465,584 153,157,712 153,473,214 153,540,502 154,139,152 154,139,152 154,139,152 154,139,152	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,33,214 153,480,214 153,480,214 153,480,214 153,541,207 154,139,992 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052	1,655 1,125 1,180 1,435 680 2,185 1,800 290 290 330 280 240 280 240 280 240 280 1,950 1,250 1,00 2,59 9,259 840 800 900 900 900 900 900 900 900 900 90	36 25 26 31 15 46 38 7 7 8 8 7 7 7 8 7 7 7 35 27 23 11 109 16 152 19 18 20 20 20 20 20 20 22 14	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.46\\ 0.31\\ \hline \\ -0.53\\ 0.46\\ 0.31\\ \hline \\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ \hline \\ 0.49\\ 0.60\\ 0.49\\ \hline \\ 0.60\\ 0.52\\ \hline \\ -0.60\\ 0.52\\ \hline \\ -0.60\\ 0.52\\ \hline \\ -0.60\\ 0.52\\ \hline \\ -1.09\\ -1.26\\ -1.25\\ -1.09\\ -1.37\\ -1.34\\ -0.72\\ -0.93\\ -1.17\end{array}$	$\begin{array}{r} 44.5\\ 44.9\\ 44.7\\ 43.0\\ 53.4\\ 54.1\\ 44.1\\ 44.1\\ 44.4\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.4\\ 44.4\\ 48.6\\ 48.6\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.0\\ 41.8\\ 41.0\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.8\\ 41.0\\ 41.0\\ 41.8\\ 41.0\\ 41.0\\ 41.8\\ 41.0\\ 41.0\\ 41.8\\ 41.0\\ 41.0\\ 41.8\\ 41.0\\ 41.0\\ 41.0\\ 41.0\\ 41.8\\ 41.0\\$
AU043803-1s1A03 AU058503-1s1A03 AU06103-1s1A03 AU0920301-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU05503-1s1A03 AU043803-1s1A03 AU043803-1s1A03 AU043803-1s1A03 AU055503-1s1A03 AU055503-1s1A03 AU06103-1s1A03 AU06103-1s1A03 AU08031-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU09503-1s1A03 AU04803-1s1A03 AU024003-1s1A03 AU024003-1s1A03 AU024003-1s1A03 AU0920301-1s1A03 AU0920301-1s1A03 AU0920301-1s1A03 AU0920301-1s1A03 AU028903-1s1A03 AU028903-1s1A03 AU028903-1s1A03 AU028903-1s1A03 AU028903-1s1A03 AU028903-1s1A03 AU028903-1s1A03	AU043803 AU058503 AU06103 AU0520301 AU056003 AU05603 AU05603 AU062203 AU08803 AU04803 AU04803 AU04803 AU0920301 AU0920301 AU08803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU08504 AU0920301 AU08304 AU0920301 AU08304 AU08304 AU08304 AU08304 AU08304 AU08303 AU04803 AU028503 AU028503	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,591 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,301,264 153,473,214 153,473,214 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,332 154,139,332	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,33,124 153,158,914 153,158,914 153,450,710 154,139,992 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052	1,655 1,125 1,180 2,185 1,800 290 290 290 290 290 290 290 280 240 280 280 1,950 1,250 1,193 1,250 1,193 1,250 1,193 1,250 1,193 1,250 1,193 1,250 1,193 1,250 1,193 1,250 1,250 1,250 1,100 705 9,259 840 800 900 900 900 900 900 900 900 900 90	36 25 26 31 15 46 38 7 7 8 7 7 8 7 7 6 7 7 7 35 27 23 11 109 16 152 19 16 152 19 18 20 20 20 20 20 20 20 20 20 20 20 20 20	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.43\\ -0.53\\ 0.46\\ 0.31\\ \hline \\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ 0.49\\ 0.60\\ -0.35\\ 0.86\\ -0.60\\ 0.52\\ -0.64\\ \hline \\ -1.25\\ -1.09\\ -1.06\\ -1.37\\ -1.34\\ -0.72\\ -0.93\\ -1.17\\ -0.60\\ \hline \\ -1.31\\ \end{array}$	$\begin{array}{r} 44.5\\ 44.9\\ 44.7\\ 43.0\\ 53.4\\ 54.1\\ 44.1\\ 44.1\\ 44.1\\ 44.1\\ 44.4\\ 3.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 51.8\\ 61.4\\ 41.4\\ 48.6\\ 61.4\\ 41.4\\ 48.6\\ 48.2\\ 54.9\\ 34.4\\ 41.1\\ 41.7\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 41.0\\ 38.2\\ \end{array}$
AU043803-1s1A03 AU058503-1s1A03 AU06103-1s1A03 AU06103-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU05603-1s1A03 AU062203-1s1A03 AU043803-1s1A03 AU043803-1s1A03 AU043803-1s1A03 AU055503-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU065503-1s1A03 AU065503-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU063504-1s1A03 AU063504-1s1A03 AU063503-1s1A03 AU063803-1s1A03 AU063803-1s1A03 AU063803-1s1A03 AU063803-1s1A03 AU063803-1s1A03 AU025803-1s1A03 AU058503-1s1A03 AU058503-1s1A03 AU058503-1s1A03	AU043803 AU058503 AU06103 AU0520301 AU056003 AU05603 AU05603 AU062203 AU08803 AU04803 AU04803 AU045503 AU06103 AU05503 AU05503 AU05503 AU014803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU024003 AU024003 AU024003 AU028503 AU028503 AU028503 AU058503 AU09503	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,608,963 151,742,256 151,742,256 151,742,591 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,301,264 152,465,584 152,445,584 153,157,712 153,473,212 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,332	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,303,214 153,466,834 152,466,834 153,466,834 153,480,214 153,480,214 153,480,214 153,480,214 153,480,214 154,139,952 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,139,992	1,655 1,125 1,180 2,185 1,800 290 290 290 290 290 290 290 290 290 2	36 25 26 31 15 46 38 7 7 8 7 7 8 7 7 7 35 27 23 11 109 16 152 19 16 152 19 18 20 20 20 20 20 20 20 20 20 20 20 20 20	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.43\\ -0.53\\ 0.46\\ 0.31\\ \hline \\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ 0.49\\ 0.60\\ -0.35\\ 0.86\\ -0.60\\ 0.52\\ -0.64\\ \hline \\ -1.25\\ -1.09\\ -1.06\\ -1.37\\ -1.34\\ -0.72\\ -0.93\\ -1.17\\ -0.60\\ \hline \\ -1.31\\ 0.67\\ \end{array}$	$\begin{array}{r} 44.5\\ 44.9\\ 44.7\\ 43.9\\ 53.4\\ 54.1\\ 44.1\\ 44.1\\ 44.1\\ 44.1\\ 44.1\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 51.8\\ 61.4\\ 43.9\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 41.0\\ 38.2\\ 42.3\\$
AU043803-1s1A03 AU058503-1s1A03 AU058503-1s1A03 AU06103-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU05603-1s1A03 AU062203-1s1A03 AU04803-1s1A03 AU043803-1s1A03 AU043803-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU064803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU024003-1s1A03 AU024003-1s1A03 AU024003-1s1A03 AU02803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03	AU043803 AU058503 AU06103 AU05003 AU056003 AU056003 AU05603 AU05603 AU062203 AU08803 AU04803 AU04803 AU05503 AU0920301 AU0920301 AU0803 AU05503 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU024003 AU04803 AU08504 AU0920301 AU1038304 AU028503 AU04803 AU04803 AU04803 AU028503 AU04803 AU028503 AU067803	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,608,963 151,742,256 151,742,259 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,464,855 153,157,712 153,473,214 153,540,502 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,332 154,139,332 154,428,778	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,175 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,952 154,140,952 154,140,952 154,140,952 154,140,952	1,655 1,125 1,180 2,185 1,800 290 290 330 280 240 280 280 280 1,950 1,250 1,250 1,250 1,250 1,250 1,250 1,250 1,250 1,250 1,250 1,250 1,250 1,250 1,250 1,00 705 9,259 840 800 900 900 900 900 900 900 900 900 90	36 25 26 31 15 46 38 7 7 8 7 7 8 7 7 35 27 23 11 109 16 152 19 18 20 20 20 20 20 20 20 20 20 20 20 20 20	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.53\\ 0.46\\ 0.31\\ \hline \\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ \hline \\ -1.04\\ -1.08\\ \hline \\ 0.60\\ -0.35\\ \hline \\ 0.60\\ -0.35\\ \hline \\ 0.60\\ -0.52\\ \hline \\ -0.64\\ \hline \\ -1.25\\ -1.09\\ -1.06\\ -1.37\\ -1.37\\ -1.34\\ -0.72\\ -0.93\\ -1.17\\ -0.60\\ \hline \\ -1.31\\ \hline \\ 0.67\\ 1.11\\ \end{array}$	$\begin{array}{r} 44.5\\ 44.9\\ 44.7\\ 43.0\\ 53.4\\ 54.1\\ 44.1\\ 44.1\\ 44.1\\ 44.1\\ 44.1\\ 44.1\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 51.8\\ 61.4\\ 43.9\\ 40.8\\ 40.8\\ 40.8\\ 40.6\\ 41.8\\ 43.2\\ 38.2\\ 42.3\\ 41.1\\ 41.7\\ 42.3\\ 41.1\\ 41.7\\ 42.2\\ 42.3\\ 41.1\\ 41.7\\ 42.3\\ 41.1\\ 43.9\\$
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU050503-1s1A03 AU050603-1s1A03 AU056603-1s1A03 AU056603-1s1A03 AU062203-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU067803-1s2A03 AU004803-1s1A03 AU0920301-1s1A03 AU0920301-1s1A03 AU004803-1s1A03 AU004803-1s1A03 AU004803-1s1A03 AU004803-1s1A03 AU004803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s2A03 AU067803-1s2A03 AU07803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03	AU043803 AU058503 AU05603 AU05003 AU05603 AU05603 AU08030 AU08030 AU08030 AU04803 AU04803 AU05503 AU06103 AU05503 AU06403 AU05503 AU04803 AU05503 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU02803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU02803 AU04803 AU028503 AU08503 AU08503 AU07803 AU038303	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,591 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,301,264 152,465,584 152,443,712 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,332 154,428,778 154,443,339 154,443,339	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,210,175 152,210,175 152,210,175 152,189,100 154,19,952 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,168 154,139,992 154,429,578 154,446,9670 154,450,670	1,655 1,125 1,180 2,185 1,800 290 290 330 280 240 280 280 280 1,950 1,250 1,00 2,59 9,059 9,00 900 900 900 900 900 1,016 620 660 7,031	36 25 26 31 15 46 38 7 7 8 8 7 7 8 7 7 7 35 27 23 11 109 16 152 19 18 20 20 20 20 20 20 20 20 20 20 20 20 20	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.46\\ 0.31\\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ -1.04\\ -1.08\\ 0.49\\ 0.60\\ -0.35\\ 0.86\\ -0.60\\ 0.52\\ -0.64\\ -1.25\\ -1.09\\ -1.06\\ -1.37\\ -1.34\\ -0.72\\ -0.93\\ -1.17\\ -0.60\\ -1.31\\ 0.67\\ 1.11\\ 0.79\\ \end{array}$	$\begin{array}{r} 44.5\\ 44.9\\ 44.7\\ 43.0\\ 53.4\\ 54.1\\ 44.1\\ 44.1\\ 44.1\\ 44.1\\ 44.4\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 51.8\\ 61.4\\ 43.9\\ 43.9\\ 43.9\\ 51.8\\ 61.4\\ 43.9\\ 44.1\\ 41.1\\$
AU043803-1s1A03 AU058503-1s1A03 AU058503-1s1A03 AU06103-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU05603-1s1A03 AU062203-1s1A03 AU04803-1s1A03 AU043803-1s1A03 AU043803-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU064803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU024003-1s1A03 AU024003-1s1A03 AU024003-1s1A03 AU02803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03	AU043803 AU058503 AU06103 AU05003 AU056003 AU056003 AU05603 AU05603 AU062203 AU08803 AU04803 AU04803 AU05503 AU0920301 AU0920301 AU0803 AU05503 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU024003 AU04803 AU08504 AU0920301 AU1038304 AU028503 AU04803 AU04803 AU04803 AU028503 AU04803 AU028503 AU067803	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,608,963 151,742,256 151,742,259 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,464,855 153,157,712 153,473,214 153,540,502 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,332 154,139,332 154,428,778	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,210,175 152,210,175 152,210,175 152,189,100 154,19,952 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,168 154,139,992 154,429,578 154,446,9670 154,450,670	1,655 1,125 1,180 2,185 1,800 290 290 330 280 240 280 280 280 1,950 1,250 1,250 1,250 1,250 1,250 1,250 1,250 1,250 1,250 1,250 1,250 1,250 1,250 1,250 1,00 705 9,259 840 800 900 900 900 900 900 900 900 900 90	36 25 26 31 15 46 38 7 7 8 7 7 8 7 7 35 27 23 11 109 16 152 19 18 20 20 20 20 20 20 20 20 20 20 20 20 20	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.53\\ 0.46\\ 0.31\\ \hline \\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ \hline \\ -1.04\\ -1.08\\ \hline \\ 0.60\\ -0.35\\ \hline \\ 0.60\\ -0.35\\ \hline \\ 0.60\\ -0.52\\ \hline \\ -0.64\\ \hline \\ -1.25\\ -1.09\\ -1.06\\ -1.37\\ -1.37\\ -1.34\\ -0.72\\ -0.93\\ -1.17\\ -0.60\\ \hline \\ -1.31\\ \hline \\ 0.67\\ 1.11\\ \end{array}$	$\begin{array}{r} 44.5\\ 44.9\\ 44.7\\ 43.0\\ 53.4\\ 54.1\\ 44.1\\ 44.1\\ 44.1\\ 44.1\\ 44.1\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 51.8\\ 61.4\\ 43.9\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 41.1\\ 43.9\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 41.8\\ 41.1\\ 41.7\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 41.8\\ 41.1\\ 41.7\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 41.8\\ 41.1\\ 41.7\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 41.8\\ 41.1\\ 41.7\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 41.1\\ 41.7\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 41.1\\ 41.1\\ 41.7\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 41.1\\ 41.1\\ 41.7\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 41.1\\ 41.1\\ 41.1\\ 41.2\\ 42.3\\ 41.1\\ 41.1\\ 41.1\\ 41.1\\ 41.2\\ 42.3\\ 41.1\\ 41.1\\ 41.1\\ 41.2\\ 42.3\\ 41.1\\ 41.1\\ 41.1\\ 41.1\\ 41.2\\ 42.3\\ 41.1\\ 41.1\\ 41.1\\ 41.1\\ 41.1\\ 41.2\\ 42.3\\ 41.1\\$
AU043803-1s1A03 AU058503-1s1A03 AU066103-1s1A03 AU050503-1s1A03 AU050603-1s1A03 AU056603-1s1A03 AU056603-1s1A03 AU062203-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU067803-1s2A03 AU004803-1s1A03 AU0920301-1s1A03 AU0920301-1s1A03 AU004803-1s1A03 AU004803-1s1A03 AU004803-1s1A03 AU004803-1s1A03 AU004803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s2A03 AU067803-1s2A03 AU07803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03	AU043803 AU058503 AU05603 AU05003 AU05603 AU05603 AU08030 AU08030 AU04803 AU04803 AU04803 AU05503 AU06103 AU05503 AU06403 AU05503 AU04803 AU05503 AU04803 AU028503 AU028503 AU00503 AU07803 AU038303	chrX chrX chrX chrX chrX chrX chrX chrX chrX chrX chrX chrX chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,591 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,301,264 152,465,584 152,443,712 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,332 154,428,778 154,443,339 154,443,339	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,210,175 152,210,175 152,210,175 152,189,100 154,19,952 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,168 154,139,992 154,429,578 154,446,9670 154,450,670	1,655 1,125 1,180 2,185 1,800 290 290 330 280 240 280 280 280 1,950 1,250 1,00 2,59 9,059 9,00 900 900 900 900 900 1,016 620 660 7,031	36 25 26 31 15 46 38 7 7 8 8 7 7 8 7 7 7 35 27 23 11 109 16 152 19 18 20 20 20 20 20 20 20 20 20 20 20 20 20	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.46\\ 0.31\\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ -1.04\\ -1.08\\ 0.49\\ 0.60\\ -0.35\\ 0.86\\ -0.60\\ 0.52\\ -0.64\\ -1.25\\ -1.09\\ -1.06\\ -1.37\\ -1.34\\ -0.72\\ -0.93\\ -1.17\\ -0.60\\ -1.31\\ 0.67\\ 1.11\\ 0.79\\ \end{array}$	$\begin{array}{r} 44.5\\ 44.9\\ 44.7\\ 43.0\\ 53.4\\ 54.1\\ 44.1\\ 44.1\\ 44.1\\ 44.1\\ 44.4\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 51.8\\ 61.4\\ 43.9\\ 44.1\\ 41.1\\$
AU043803-1s1A03 AU058503-1s1A03 AU06103-1s1A03 AU05003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU05503-1s1A03 AU043803-1s1A03 AU043803-1s1A03 AU043803-1s1A03 AU055503-1s1A03 AU055503-1s1A03 AU06103-1s1A03 AU06103-1s1A03 AU06103-1s1A03 AU06403-1s1A03 AU014803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU024003-1s1A03 AU024003-1s1A03 AU024003-1s1A03 AU024003-1s1A03 AU028503-1s1A03 AU02803-1s1A03 AU02803-1s1A03 AU02803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU058503-1s1A03 AU058503-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03	AU043803 AU058503 AU06103 AU0520301 AU056003 AU05603 AU05603 AU062203 AU08803 AU04803 AU04803 AU045503 AU05503 AU05503 AU014803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU02503 AU04803 AU04803 AU04803 AU02503 AU04803 AU02503 AU04803 AU02503 AU04803 AU02503 AU02503 AU02503 AU02503 AU02503 AU02503 AU02503 AU02503 AU02503 AU02503 AU02503 AU02503 AU02503 AU02503 AU02503 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803	chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,256 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,301,264 153,473,214 153,473,214 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,332 154,439,332 154,443,339 154,443,339 154,446,165	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,33,214 153,480,214 153,480,214 153,480,214 153,4120,70 154,139,992 154,140,052 154,140,140,14010 154,150,16010 154,150,16010 154,15	1,655 1,125 1,180 2,185 1,800 290 290 290 330 280 240 280 280 1,950 1,250 1,193 1,202 7,000 705 9,259 840 800 900 900 900 900 900 900 900 900 90	36 25 26 31 15 46 38 7 7 8 7 7 8 7 7 6 7 7 7 35 27 23 11 109 16 152 19 16 152 19 16 152 20 20 20 20 20 20 20 20 20 20 20 20 20	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.43\\ -0.53\\ 0.46\\ 0.31\\ \hline \\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ 0.49\\ 0.60\\ -0.35\\ 0.86\\ -0.60\\ 0.52\\ -0.64\\ \hline \\ -1.25\\ -1.09\\ -1.06\\ -1.37\\ -1.34\\ -0.72\\ -0.93\\ -1.17\\ -0.60\\ \hline \\ -1.31\\ \hline \\ 0.67\\ 1.11\\ 0.79\\ 0.96\\ 1.01\\ \end{array}$	$\begin{array}{r} 44.5\\ 44.9\\ 44.7\\ 43.9\\ 44.7\\ 43.4\\ 54.1\\ 44.1\\ 44.1\\ 44.1\\ 44.1\\ 44.1\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 51.8\\ 61.4\\ 43.9\\ 44.1\\ 41.1\\ 41.1\\ 41.1\\ 41.7\\ 40.8\\$
AU043803-1s1A03 AU058503-1s1A03 AU058503-1s1A03 AU06103-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU062203-1s1A03 AU062203-1s1A03 AU04803-1s1A03 AU043803-1s1A03 AU043803-1s1A03 AU055503-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU06403-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU067803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03	AU043803 AU058503 AU06103 AU0520301 AU056003 AU056003 AU05603 AU062203 AU080803 AU04803 AU04803 AU05503 AU06103 AU05503 AU05503 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU024003 AU024003 AU02803 AU04803 AU05803 AU04803 AU05803 AU05803 AU05803 AU067803 AU07803 AU07803 AU07803 AU07803 AU07803 AU07803 AU07803 AU07803 AU07803 AU07803 AU07803 AU07803 AU07803 AU07803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU024003	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,608,963 151,742,256 151,742,256 151,742,591 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,301,264 152,45,584 152,445,584 153,473,214 153,473,214 153,473,214 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,332 154,443,339 154,443,339 154,446,755 154,446,755	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,303,214 153,450,821 153,158,914 153,466,834 153,466,834 153,466,834 153,466,834 153,480,214 153,480,214 154,139,952 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,139,992 154,429,538 154,446,900 154,450,670 154,446,925 154,450,670	1,655 1,125 1,180 2,185 1,800 290 290 290 290 290 290 290 290 290 2	36 25 26 31 15 46 38 7 7 8 7 7 8 7 7 35 27 23 11 109 16 152 27 23 11 109 16 152 20 20 20 20 20 20 20 20 20 20 20 20 20	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.43\\ -0.53\\ 0.46\\ 0.31\\ \hline \\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ \hline \\ 0.49\\ 0.60\\ -0.35\\ 0.86\\ -0.60\\ \hline \\ 0.52\\ -0.64\\ \hline \\ -1.25\\ -1.09\\ -1.36\\ \hline \\ -1.37\\ -1.34\\ -0.72\\ -0.93\\ -1.17\\ -0.60\\ \hline \\ -1.31\\ \hline \\ 0.67\\ 1.11\\ 0.79\\ 0.96\\ 1.01\\ 1.09\\ \hline \end{array}$	$\begin{array}{r} 44.5\\ 44.9\\ 44.7\\ 43.0\\ 53.4\\ 54.1\\ 44.1\\ 44.1\\ 44.1\\ 44.1\\ 44.4\\ 3.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 51.8\\ 61.4\\ 43.9\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 41.1\\ $
AU043803-1s1A03 AU058503-1s1A03 AU06103-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU062203-1s1A03 AU062203-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU024003-1s1A03 AU028503-1s1A03 AU004803-1s1A03 AU004803-1s1A03 AU004803-1s1A03 AU004803-1s1A03 AU004803-1s1A03 AU004803-1s1A03 AU004803-1s1A03 AU004803-1s1A03 AU067803-1s2A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03	AU043803 AU058503 AU06103 AU05003 AU056003 AU056003 AU05603 AU062203 AU08030 AU04803 AU04803 AU04803 AU055503 AU0920301 AU0920301 AU0803 AU05503 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU024003 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU028503 AU0480 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,608,963 150,815,800 151,742,256 151,742,591 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,465,584 152,465,584 153,473,214 153,540,502 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,132 154,433,339 154,443,339 154,443,339 154,445,755 154,446,755	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,468,834 152,466,834 153,450,670 154,139,952 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,139,952 154,450,670 154,450,670 154,450,670 154,450,670	1,655 1,125 1,180 2,185 1,800 290 290 330 280 240 280 280 280 280 1,950 1,250	36 25 26 31 15 46 38 7 7 8 8 7 7 8 7 7 35 27 23 11 109 16 152 19 109 16 152 19 19 18 20 20 20 20 20 20 20 20 20 20 20 20 20	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.43\\ -0.53\\ 0.46\\ 0.31\\ \hline \\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ \hline \\ -1.04\\ -1.08\\ \hline \\ 0.60\\ -0.35\\ \hline \\ 0.60\\ -0.35\\ \hline \\ 0.60\\ -0.35\\ \hline \\ 0.60\\ -0.52\\ -0.64\\ \hline \\ -1.25\\ -1.09\\ -1.06\\ -1.37\\ -0.60\\ -1.01\\ -1.09\\ -0.57\\ -1.01\\ -0.57\\ -0.57\\ -0.55\\ -$	$\begin{array}{r} 44.5\\ 44.9\\ 44.7\\ 43.9\\ 53.4\\ 54.1\\ 44.1\\ 44.1\\ 44.1\\ 44.1\\ 44.1\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 51.8\\ 61.4\\ 43.9\\$
AU043803-1s1A03 AU058503-1s1A03 AU058503-1s1A03 AU06103-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU056003-1s1A03 AU062203-1s1A03 AU062203-1s1A03 AU04803-1s1A03 AU043803-1s1A03 AU043803-1s1A03 AU055503-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU066103-1s1A03 AU06403-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU067803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU067803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03 AU04803-1s1A03	AU043803 AU058503 AU06103 AU0520301 AU056003 AU056003 AU05603 AU062203 AU080803 AU04803 AU04803 AU05503 AU06103 AU05503 AU05503 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU024003 AU024003 AU02803 AU04803 AU05803 AU04803 AU05803 AU05803 AU05803 AU067803 AU07803 AU07803 AU07803 AU07803 AU07803 AU07803 AU07803 AU07803 AU07803 AU07803 AU07803 AU07803 AU07803 AU07803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU04803 AU024003	chrX chrX chrX chrX chrX chrX chrX chrX	150,608,963 150,608,963 150,608,963 150,608,963 150,608,963 151,742,256 151,742,256 151,742,591 152,269,845 152,269,845 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,269,895 152,301,264 152,45,584 152,445,584 153,473,214 153,473,214 153,473,214 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,152 154,139,332 154,443,339 154,443,339 154,446,755 154,446,755	150,610,618 150,610,088 150,610,143 150,610,398 150,816,480 151,744,441 151,744,391 152,270,135 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,270,175 152,303,214 153,450,821 153,158,914 153,466,834 153,466,834 153,466,834 153,466,834 153,480,214 153,480,214 154,139,952 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,140,052 154,139,992 154,429,538 154,446,900 154,450,670 154,446,925 154,450,670	1,655 1,125 1,180 2,185 1,800 290 290 290 290 290 290 290 290 290 2	36 25 26 31 15 46 38 7 7 8 7 7 8 7 7 35 27 23 11 109 16 152 27 23 11 109 16 152 20 20 20 20 20 20 20 20 20 20 20 20 20	22.2 22.0 21.6 22.1 21.1 24.1 24.1 24.2 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	$\begin{array}{c} -0.39\\ -0.43\\ -0.43\\ -0.53\\ 0.46\\ 0.31\\ \hline \\ -1.03\\ -0.85\\ -0.91\\ -0.89\\ -1.26\\ -1.04\\ -1.08\\ \hline \\ 0.49\\ 0.60\\ -0.35\\ 0.86\\ -0.60\\ \hline \\ 0.52\\ -0.64\\ \hline \\ -1.25\\ -1.09\\ -1.36\\ \hline \\ -1.37\\ -1.34\\ -0.72\\ -0.93\\ -1.17\\ -0.60\\ \hline \\ -1.31\\ \hline \\ 0.67\\ 1.11\\ 0.79\\ 0.96\\ 1.01\\ 1.09\\ \hline \end{array}$	$\begin{array}{r} 44.5\\ 44.9\\ 44.7\\ 43.9\\ 53.4\\ 54.1\\ 44.1\\ 44.1\\ 44.1\\ 44.1\\ 44.4\\ 3.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 43.9\\ 51.8\\ 61.4\\ 43.9\\ 40.8\\ 40.8\\ 40.8\\ 40.8\\ 41.0\\ 38.2\\ 42.3\\ 41.1\\ 41.1\\ 41.1\\ 39.5\\ 55.6\\ 39.9\\ 9\end{array}$

Table A.3 - CNV from 100 AGRE and 64 SSC samples run on 2.1M arrays by the Optimized protocol.

AU1953303-A01-1s1	AU1953303 chrX	23,694,128	23,695,658	1,530	31	20.3	0.44	61.05
AU0976303-1s1A01	AU0976303 chrX	23,952,568	23,954,076	1,508	26	17.2	-0.49	69.16
AU021203-1s1A01	AU021203 chrX	24,021,215	24,026,159	4,944	43	8.7	-0.72	41.67
AU056803-A01-2s1 SSC00460-A01-1s1	AU056803 chrX SSC00460 chrX	24,022,009 24,203,022	24,026,159 24,205,262	4,150	41 30	9.9 13.4	-0.74 -1.12	38.96 44.1
SSC00264-A01-3s1	SSC00400 chrX SSC00264 chrX	24,508,719	24,510,099	1,380	28	20.3	-1.46	45.3
AU1038303-A01-2s1		24,933,183	24,933,900	717	14	19.5	0.67	68.76
AU1898303-A01-1s2		26,273,052	26,276,195	3,143	54	17.2	-1.34	38.53
AU1534302-1s1A01	AU1534302 chrX	26,375,390	26,375,975	585	13	22.2	-0.97	43.08
AU1534302-1s1A01 AU1054302-1s1A01	AU1534302 chrX AU1054302 chrX	26,390,763 26,432,577	26,391,753 26,433,232	990 655	21 15	21.2 22.9	-0.72 0.51	38.18 59.08
AU1056304-1s1A01	AU1056304 chrX	26,432,602	26,433,322	720	16	22.3	0.51	59.86
SSC00549-A01-1s1	SSC00549 chrX	26,720,715	26,731,591	10,876	195	17.9	0.58	32.9
AU080803-A01-2s1	AU080803 chrX	30,048,831	30,055,680	6,849	122	17.8	-0.71	35.99
AU1953303-A01-1s1		30,236,143	30,237,705	1,562	28	17.9	0.45	65.81
AU1069302-A01-2s1		30,236,575	30,237,705	1,130	22	19.5	0.48	67.17
AU1378304-2s1A01 SSC00461-A01-2s1	AU1378304 chrX SSC00461 chrX	30,257,653 30,716,521	30,258,043 30,734,701	390 18,180	8 322	20.5	-1.18 0.74	31.03 52.1
AU065404-A01-2s1	AU065404 chrX	30,716,581	30,734,646	18,065	320	17.7	0.34	52.37
SSC00392-A01-2s1	SSC00392 chrX	30,716,696	30,734,701	18,005	320	17.8	0.45	52.1
A01AU1327305-1s3	AU1327305 chrX	30,716,811	30,734,701	17,890	318	17.8	-0.34	52.35
AU1211303-1s2A01	AU1211303 chrX	30,721,066	30,734,701	13,635	244	17.9	-0.62	52.12
AU032701-A01-3s1	AU032701 chrX	32,363,198	32,364,497	1,299	24	18.5	-0.59	37.18 31.14
AU1054302-1s1A01 SSC00549-A01-1s1	AU1054302 chrX SSC00549 chrX	32,897,210 32,897,851	32,898,212 32,898,716	1,002 865	19 10	19.0 11.6	-0.83 -1.20	36.0
AU0875302-A01-2s1		33,749,081	33,756,552	7,471	69	9.2	-0.53	35.02
SSC00510-A01-2s1	SSC00510 chrX	33,952,881	33,980,077	27,196	451	16.6	-0.94	35.0
AU065404-A01-2s1	AU065404 chrX	33,952,911	33,982,646	29,735	497	16.7	-1.06	35.44
AU021203-1s1A01	AU021203 chrX	34,062,085	34,066,166	4,081	30	7.4	0.51	35.73
AU004803-A01-3s1	AU004803 chrX	34,063,446	34,065,846	2,400	21	8.8	0.73	35.00
AU0452303-A01-2s1 AU1038303-A01-2s1		34,063,446 34,063,446	34,066,116 34,066,661	2,670 3,215	25 30	9.4 9.3	0.61 0.55	35.36 33.56
AU1159302-2s1A01		34,063,446	34,065,466	2,020	20	9.9	0.66	33.51
AU065404-A01-2s1	AU065404 chrX	34,063,531	34,065,466	1,935	18	9.3	0.88	33.54
AU016803-A01-2s1	AU016803 chrX	34,063,576	34,065,846	2,270	18	7.9	0.65	35.24
AU0875302-A01-2s1		34,063,739	34,065,466	1,727	14	8.1	0.85	34.51
AU056803-A01-2s1 AU1134303-A01-2s1		34,064,509 34,064,509	34,065,916 34,065,466	1,407 957	13 11	9.2 11.5	1.03 1.02	37.03 34.48
AU1947303-A01-1s1		34,349,231	34,351,198	1,967	19	9.7	-0.72	34.42
AU1953303-A01-1s1		34,349,231	34,351,378	2,147	20	9.3	-0.81	34.75
AU1267302-1s1A01		34,349,301	34,351,378	2,077	19	9.1	-0.56	34.81
AU1069302-A01-2s1		34,584,572	34,585,553	981	19	19.4	0.48	74.31
AU1069302-A01-2s1 SSC00518-A01-1s1	SSC00518 chrX	34,870,749 35,622,301	34,871,874 35,625,671	1,125 3,370	18 56	16.0 16.6	0.43	60.80 38.8
AU1631303-1s1A01	AU1631303 chrX	36,516,858	36,540,028	23,170	295	12.7	-0.45	35.68
AU1953303-A01-1s1		36,885,407	36,886,107	700	11	15.7	0.62	72.57
AU1134303-A01-2s1		36,936,692	36,938,657	1,965	24	12.2	0.47	62.09
AU0852304-A01-2s1		36,936,957	36,938,657	1,700	20	11.8	0.69	63.00
SSC00452-A01-2s2 AU1631303-1s1A01	SSC00452 chrX	36,941,242	36,944,207 37,004,231	2,965	39 116	13.2 13.4	-0.72 -0.44	45.2 37.33
SSC00592-A01-3s1		36,995,555 37,285,506	37,288,191	8,676 2,685	53	19.7	0.44	57.7
AU1953303-A01-1s1		37,286,201	37,287,886	1,685	32	19.0	0.53	61.78
AU056803-A01-2s1		38,547,557	38,549,428	1,871	39	20.8	0.59	65.15
AU1397313-A01-2s1		38,547,677	38,549,955	2,278	48	21.1	0.35	65.06
AU028903-A01-2s1		38,547,707	38,550,411	2,704	55	20.3	0.46	63.76
AU1953303-A01-1s1		38,547,752	38,551,610	3,858	75	19.4	0.35	55.29
A01AU1799302-1s4 AU0976303-1s1A01	AU0976303 chrX	39,208,803 39,853,069	39,209,233 39,854,158	430 1,089	9 18	20.9 16.5	0.66	48.14 73.74
AU1953303-A01-1s1		40,828,639	40,831,205	2,566	50	19.5	0.51	66.21
AU1947303-A01-1s1	AU1947303 chrX	40,828,679	40,830,870	2,191	43	19.6	0.42	69.97
AU065404-A01-2s1		40,828,724	40,830,725	2,001	39	19.5	0.38	70.81
AU083504-A01-3s1		40,828,724	40,830,965	2,241	44	19.6	0.52	69.79
AU1069302-A01-2s1 AU1397313-A01-2s1		40,828,799 40,828,839	40,830,522 40,830,870	1,723 2,031	34 40	19.7 19.7	0.49 0.45	70.75
AU1038303-A01-2s1		40,828,889	40,830,925	2,031	40	19.6	0.61	69.89
AU014803-A01-2s1		40,828,919	40,830,407	1,488	29	19.5	0.53	69.49
AU1038303-A01-2s1		41,077,342	41,079,467	2,125	40	18.8	0.43	63.39
AU1267302-1s1A01		41,077,342	41,079,437	2,095	39	18.6	0.36	63.44
AU1346302-1s1A01 AU016803-A01-2s1	AU1346302 chrX AU016803 chrX	41,228,399	41,230,584	2,185	26 24	11.9 14.2	-0.87 -1.20	44.35 42.44
SSC00137-A01-2s1	SSC00137 chrX	41,228,827 41,228,827	41,230,514 41,230,514	1,687 1,687	24 24	14.2	-0.90	42.44
SSC00379-A01-3s1	SSC00379 chrX	43,457,535	43,465,245	7,710	88	20.4	-0.35	49.9
E	· · · · · · · · · · · · · · · · · · ·	· · · · · ·	· · · · · · · · · · · · · · · · · · ·					

SSC00035-3s1A01	SSC00035 chrX	43,829,768	43,831,743	1,975	37	18.7	-1.16	45.2
AU0852304-A01-2s1		44,264,996 44,617,076	44,266,216 44,618,261	1,220	20 24	16.4	-1.31 0.46	41.6 69.4
AU1397313-A01-2s1 SSC00461-A01-2s1	SSC00461 chrX	46,955,606	46,956,590	1,185 984	24	20.3 20.3	0.40	47.9
AU028903-A01-2s1	AU028903 chrX	46,962,238	46,964,449	2,211	44	19.9	0.48	62.7
	· · · · · · · · · · · · · · · · · · ·	47,226,241	47,226,731	490	11	22.4	-0.85	48.6
	AU1211303 chrX	47,226,291	47,226,731	440	10	22.7	-0.97	49.8
AU0939304-1s1A02		47,394,069	47,395,282	1,213	26	21.4	0.44	61.3
AU056803-A02-2s1	AU056803 chrX	47,394,397	47,395,422	1,025	22	21.5	0.53	64.5
AU1069302-A02-2s1	AU1069302 chrX	47,394,397	47,395,552	1,155	25	21.6	0.54	63.6
AU1001202-1s1A02	AU1001202 chrX	47,758,088	47,878,128	120,040	1147	9.6	0.56	45.0
SSC00317-A02-2s1	SSC00317 chrX	47,765,076	47,870,767	105,691	1139	10.8	-1.26	44.6
AU1573302-1s2A02	AU1573302 chrX	47,778,068	47,887,478	109,410	987	9.0	-0.39	44.8
AU014803-A02-2s1	AU014803 chrX	48,208,660	48,211,205	2,545	54	21.2	0.39	58.9
AU1953303-A02-1s1		48,220,111	48,221,051	940	21	22.3	-0.42	44.5
AU1592301-1s2A02		48,276,454	48,278,154	1,700	33	19.4	-0.47	51.4
AU1622302-1s2A02		48,530,120	48,531,087	967	21 19	21.7	-0.52	48.6
AU1592301-1s2A02 AU1953303-A02-1s1		48,530,197 48,530,197	48,531,062 48,531,087	865 890	20	22.0 22.5	-0.49 -0.50	48.2 48.4
AU1424304-1s2A02		48,530,217	48,531,087	870	19	22.5	-0.54	48.3
AU1791303-1s2A02		48,530,217	48,531,142	925	20	21.6	-0.50	48.1
AU056003-A02-2s1	AU056003 chrX	48,533,289	48,534,370	1,081	17	15.7	0.74	53.7
AU056803-A02-2s1	AU056803 chrX	48,698,770	48,700,805	2,035	41	20.1	0.54	64.6
AU1953303-A02-1s1	AU1953303 chrX	48,714,198	48,714,773	575	13	22.6	-0.55	45.7
AU1592301-1s2A02	AU1592301 chrX	48,714,353	48,714,843	490	11	22.4	-0.75	44.7
AU0983302-1s1A02	AU0983302 chrX	48,738,809	48,739,434	625	13	20.8	-0.54	45.9
AU004803-A02-3s1	AU004803 chrX	48,934,299	48,934,869	570	12	21.1	0.78	53.3
AU1069302-A02-2s1		48,934,364	48,934,799	435	9	20.7	1.08	51.7
AU1134303-A02-2s1		48,934,364	48,934,824	460	10	21.7	0.84	52.4
AU1211303-1s2A02		48,967,547	48,967,942	395	9	22.8	-0.56	52.2
AU1791303-1s2A02		48,995,264	48,996,414	1,150	24	20.9	-0.48	53.2
AU1211303-1s2A02		48,995,294	48,996,414	1,120	23	20.5	-0.39	53.1
AU1346302-1s1A02 AU1573302-1s2A02		48,995,294	48,996,284	990	20	20.2	-0.50	52.8
AU1953303-A02-1s1		48,995,294 48,995,294	48,996,304 48,996,359	1,010 1,065	21 22	20.8 20.7	-0.46 -0.43	52.7 52.7
AU1424304-1s2A02		48,995,594	48,996,284	690	14	20.3	-0.60	52.7
AU065404-A02-2s1	AU065404 chrX	49,012,185	49,013,180	995	22	22.1	0.65	58.3
AU0939304-1s1A02		49,012,240	49,014,323	2,083	41	19.7	0.37	67.1
AU0983302-1s1A02	AU0983302 chrX	49,012,240	49,013,180	940	21	22.3	0.51	58.7
AU1338304-1s1A02	AU1338304 chrX	49,012,295	49,013,135	840	19	22.6	0.51	58.8
AU1056304-1s1A02		49,012,330	49,013,180	850	19	22.4	0.55	59.1
AU004803-A02-3s1	AU004803 chrX	49,012,390	49,013,180	790	18	22.8	0.63	59.4
AU055303-A02-2s1	AU055303 chrX	49,012,390	49,013,180	790 790	18 18	22.8 22.8	0.63 0.63	59.4 59.4
AU1001202-1s1A02 A02AU1143303-1s2		49,012,390 49,012,390	49,013,180 49,013,180	790	18	22.8	0.60	59.4
A02A01145505 132 A02AU1327305-1s3		49,012,390	49,013,180	790	18	22.8	0.43	59.4
AU1397313-A02-2s2		49,012,390	49,013,615	1,225	25	20.4	0.58	66.3
AU1134303-A02-2s1		49,012,415	49,013,180	765	17	22.2	0.67	59.5
AU014803-A02-2s1	AU014803 chrX	49,012,490	49,014,388	1,898	37	19.5	0.50	68.4
AU018304-A02-2s1		49,012,490	49,013,180	690	16	23.2	0.98	59.7
AU055503-A02-2s1		49,012,490	49,013,180	690	16	23.2	0.75	59.7
AU083504-A02-3s1		49,012,490	49,013,270	780	17	21.8	0.69	62.1
AU0875302-A02-2s1		49,012,490 49,012,490	49,013,180 49,013,180	690	16 16	23.2	0.87	59.7
AU0920301-A02-2s1 AU0780301-A02-2s1		49,012,490 49,012,510	49,013,180	690 670	16 15	23.2 22.4	0.78 0.77	59.7 59.4
AU083603-A02-2s1		49,012,510	49,013,180	670	15	22.4	0.63	59.4
	AU056003 chrX	49,012,575	49,013,180	605	14	23.1	0.77	60.2
AU063303-A02-1s1	AU063303 chrX	49,012,575	49,013,270	695	15	21.6	0.76	62.7
AU1054302-1s1A02		49,012,575	49,013,180	605	14	23.1	0.72	60.2
AU1344302-1s1A02	AU1344302 chrX	49,012,575	49,013,135	560	13	23.2	0.58	60.5
SSC00035-3s1A02	SSC00035 chrX	49,265,935	49,271,538	5,603	83	14.8	-0.45	44.0
	AU1211303 chrX	49,529,973	49,531,486	1,513	29	19.2	0.41	67.5
AU1069302-A02-2s1		50,229,081	50,231,210	2,129	41	19.3	0.45	62.8
AU056803-A02-2s1	AU056803 chrX	50,229,416	50,231,140	1,724	34	19.7	0.46	61.8
SSC00379-A02-3s1	SSC00379 chrX	52,065,715	52,066,910	1,195	25	20.9	-1.04	37.8
AU056803-A02-2s1	AU056803 chrX	52,966,038	52,967,318	1,280 265	22	17.2	0.50	60.5 63.8
AU1134303-A02-2s1 SSC00098-A02-3s1	SSC00098 chrX	52,966,813 53,099,842	52,967,078 53,102,277	265	7 44	26.4 18.1	0.80	48.5
AU008504-A02-2s1	AU008504 chrX	53,099,842	53,102,277	2,435 2,510	44 45	17.9	0.35	48.5
AU1346302-1s1A02		53,100,087	53,102,557	2,310	45	18.2	-0.50	49.5
A02AU1143303-1s2		53,100,432	53,102,672	2,240	46	20.5	-0.47	48.5
SSC00181-A02-2s1	SSC00181 chrX	53,100,432	53,102,317	1,885	39	20.7	-0.46	48.6
AU1054302-1s1A02	AU1054302 chrX	53,100,452	53,101,922	1,470	30	20.4	-0.39	49.7
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AU1056304-1s1A02	AU1056304 chrX	53,100,452	53,102,672	2,220	45	20.3	-0.41	48.5
AU1324303-1s2A02		53,100,452	53,102,472	2,020	41	20.3	-0.36	49.2
AU1334303-1s1A02					37		-0.39	
		53,100,452	53,102,277	1,825		20.3		49.0
AU1953303-A02-1s1		53,100,452	53,102,622	2,170	44	20.3	-0.48	48.6
AU1073302-A02-2s1	AU1073302 chrX	53,100,517	53,102,317	1,800	37	20.6	-0.59	48.7
AU1267302-1s1A02	AU1267302 chrX	53,100,517	53,102,672	2,155	44	20.4	-0.44	48.2
A02AU1327305-1s3		53,100,517	53,102,717	2,200	45	20.5	-0.42	48.1
AU1344302-1s1A02		53,100,517	53,102,622	2,105	43	20.4	-0.46	48.3
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AU1592301-1s2A02		53,100,517	53,103,956	3,439	57	16.6	-0.44	47.2
SSC00093-A02-1s1	SSC00093 chrX	53,100,517	53,102,472	1,955	40	20.5	-0.55	48.5
SSC00317-A02-2s1	SSC00317 chrX	53,100,517	53,102,882	2,365	49	20.7	-0.47	47.4
AU1414305-1s2A02	AU1414305 chrX	53,100,552	53,102,502	1,950	40	20.5	-0.44	48.9
AU004803-A02-3s1	AU004803 chrX	53,127,122	53,127,609	487	8	16.4	-0.99	68.0
			, ,	1			1	
AU1397313-A02-2s2		53,238,467	53,241,061	2,594	51	19.7	0.36	61.5
AU0939304-1s1A02	AU0939304 chrX	53,238,692	53,242,246	3,554	71	20.0	0.32	59.2
AU1344302-1s1A02	AU1344302 chrX	53,800,995	53,801,260	265	7	26.4	-1.35	53.2
AU1791303-1s2A02	AU1791303 chrX	54,573,144	54,573,631	487	8	16.4	0.75	62.6
AU056803-A02-2s1	AU056803 chrX	54,591,828	54,593,323	1,495	25	16.7	-0.45	48.4
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AU1267302-1s1A02		54,863,979	54,868,109	4,130	52	12.6	0.32	54.6
AU021203-1s1A02	AU021203 chrX	54,867,594	54,868,109	515	11	21.4	0.57	59.4
A02AU1143303-1s2	AU1143303 chrX	55,069,357	55,070,762	1,405	30	21.4	-0.43	43.9
AU1134303-A02-2s1		56,826,211	56,827,896	1,685	35	20.8	0.37	55.8
AU1592301-1s2A02								54.4
		56,845,230	56,846,164	934	18	19.3	0.63	
AU0920301-A02-2s1		57,615,600	57,960,046	344,446	3789	11.0	0.47	38.6
AU050703-A02-2s1	AU050703 chrX	57,763,046	57,767,996	4,950	57	11.5	1.07	36.0
AU1324303-1s2A02	AU1324303 chrX	57,763,081	57,768,570	5,489	66	12.0	1.09	35.4
AU083504-A02-3s1	AU083504 chrX	58,256,056	58,256,496	440	8	18.2	-1.33	46.8
SSC00440-A02-2s1	SSC00440 chrX	62,386,739	62,422,538	35,799	443	12.4	0.67	38.5
AU0920301-A02-2s1	AU0920301 chrX	62,386,914	62,422,378	35,464	441	12.4	0.59	38.9
SSC00180-A02-2s1	SSC00180 chrX	62,386,914	62,422,378	35,464	441	12.4	0.58	38.5
SSC00460-A02-1s1	SSC00460 chrX	62,386,914	62,426,622	39,708	444	11.2	0.50	38.6
AU1038303-A02-2s1		62,494,361				1	1	38.7
			62,520,001	25,640	294	11.5	-0.41	
AU1134303-A02-2s1		62,921,207	62,922,007	800	18	22.5	0.51	62.4
AU1159302-2s1A02	AU1159303 chrX	64,002,046	64,013,621	11,575	201	17.4	-1.04	35.3
AU016803-A02-2s1	AU016803 chrX	65,382,441	65,415,702	33,261	530	15.9	0.51	38.9
AU014803-A02-2s1	AU014803 chrX	67,040,517	67,046,967	6,450	84	13.0	-0.48	38.7
AU1585301-1s2A02		67,040,517	67,047,042	6,525	85	13.0	-0.38	38.6
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SSC00314-A02-2s1	SSC00314 chrX	67,040,517	67,046,967	6,450	84	13.0	-0.89	38.3
SSC00366-A02-2s1	SSC00366 chrX	67,040,517	67,047,042	6,525	85	13.0	-0.71	38.2
AU0983302-1s1A02	AU0983302 chrX	67,040,582	67,046,967	6,385	83	13.0	-1.13	38.6
AU018003-A02-2s1	AU018003 chrX	67,045,802	67,046,892	1,090	19	17.4	-0.74	41.8
AU0920301-A02-2s1		67,761,197	67,761,872	675	9	13.3	-0.75	28.9
								40.9
AU0983302-1s1A02	AU0983302 chrX	67,879,047	67,880,967	1,920	26	13.5	-1.87	
AU0983302-1s1A02		68,073,913	68,074,543	630	14	22.2	-0.42	39.5
AU1069302-A02-2s1	. AU1069302 chrX	68,752,123	68,753,594	1,471	30	20.4	0.45	65.1
AU067803-A02-2s1	AU067803 chrX	69,201,902	69,205,364	3,462	72	20.8	0.48	57.9
AU0920301-A02-2s1	AU0920301 chrX	69,202,002	69,204,994	2,992	62	20.7	0.51	58.4
AU014803-A02-2s1	AU014803 chrX	69,202,022	69,205,124	3,102	64	20.6	0.39	58.6
AU1038303-A02-2s1		69,202,132	69,204,769	2,637	55	20.9	0.57	58.8
AU055503-A02-2s1	AU055503 chrX	69,588,687	69,592,509	3,822	75	19.6	0.39	59.0
SSC00505-A02-1s1	SSC00505 chrX	70,039,798	70,040,318	520	12	23.1	-1.47	35.2
AU020003-A02-2s1	AU020003 chrX	70,039,948	70,040,318	370	9	24.3	-1.18	37.0
AU0983302-1s1A02	AU0983302 chrX	70,039,948	70,040,318	370	9	24.3	-1.61	37.0
SSC00357-A02-2s1				420	10			
	SSC00357 chrX	70,039,948	70,040,368			23.8	-1.60	36.3
AU1378304-2s1A02	AU1378304 chrX	70,237,266	70,238,316	1,050	23	21.9	0.48	59.0
AU0939304-1s1A02	AU0939304 chrX	70,714,508	70,715,873	1,365	30	22.0	0.40	61.2
AU056803-A02-2s1	AU056803 chrX	70,714,913	70,716,073	1,160	25	21.6	0.56	64.2
AU1211303-1s2A02		70,714,913	70,715,873	960	21	21.9	0.42	64.3
AU067803-A02-2s1	AU067803 chrX	70,714,983	70,717,347	2,364	43	18.2	0.58	59.3
AU008504-A02-2s1	AU008504 chrX	70,715,008	70,716,773	1,765	37	21.0	0.41	62.4
AU1069302-A02-2s1		70,715,008	70,715,928	920	20	21.7	0.60	64.0
AU080803-A02-2s1	AU080803 chrX	70,715,118	70,716,773	1,655	35	21.1	0.47	62.4
AU0920301-A02-2s1	AU0920301 chrX	70,715,118	70,716,928	1,810	38	21.0	0.49	61.8
AU065404-A02-2s1	AU065404 chrX	70,715,168	70,716,838	1,670	35	21.0	0.55	62.9
AU083603-A02-2s1	AU083603 chrX	70,715,198	70,716,868	1,670	35	21.0	0.46	63.5
A02AU1327305-1s3	AU1327305 chrX	70,715,978	70,716,773	795	17	21.4	-0.45	60.3
AU1871302-1s1A02		70,740,201	70,740,796	595	6	10.1	0.90	50.8
AU1953303-A02-1s1	AU1953303 chrX	70,796,602	70,803,737	7,135	116	16.3	0.36	58.3
AU1346302-1s1A02		72,249,888	72,523,656	273,768	2927	10.7	0.39	38.2
AU1069302-A02-2s1		73,672,126	73,674,216	2,090	43	20.6	0.42	61.6
AU0939304-1s1A02		74,060,721	74,062,672	1,951	37	19.0	0.32	65.6
AU020003-A02-2s1	AU020003 chrX	75,282,723	75,283,263	540	12	22.2	-1.38	46.3
AU0920301-A02-2s1	AU0920301 chrX	75,917,772	75,919,918	2,146	35	16.3	0.64	41.0
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AU093304-161/02 AU093304 chrx 77,406,460 77,410,491 6,181 74 12.0 0.75 45.5 AU162302 1.62/02 1.62/02 AU	8								-
AulteG 202 - 152/A02 AulteG 202 - chrX B0.302,657 B0.304,067 1,410 22 15.6 -0.61 SSC00035 - 31AU2 SSC00055 - 30AU2 SSC00052 - 30AU2 SSC00152 - 30AU2 SSC00053 - 30AU2 SSC00054 - 30AU2 SSSC00054 - 30AU2 SSSC00054 - 30AU2<								-0.75	45.4
Sec0003-3:BL02 SEC00035 chrX B0.303,147 B0.304,212 L, 1065 20 18.8 0.97 37.9 SSC00035-BL02 SSC00035 chrX SL, 004,228 ALU025303-A02-21 AU1038303-A02-21 AU1038303-A02-21 AU1038303-A02-21 AU103503-A02-21 AU1055031-A02 AU1055031-A02 AU SSC00035-BL02-21 AU305503-A02-21 AU1055031-A02 AU1055031-A02 AU1055031-A02 AU1055031-A02 AU10150501-A02 AU10150501-A02 AU101502-A02 AU10150				· · ·	•				
SCC0003-3:IA02 SSC00035 chr. 81.060.422 81.062.537 c.115 45 cl.13 0.93 35.7 AU08303-A02-251 AU085204 chr. 82.668.283 87.547.547 1.264 12 9.5 0.95 36.0 AU085203-A22-21 AU085204 chr. 89.548 81.945.27 2.673 34 16.1 1.26 35.5 AU085204-A22-242 SSC00452 chr. 89.649.77 92.610.562 1.965 35 1.7.8 -1.073 37.2 AU08304-A02-341 AU083054 66.453.478 96.495.167 1.7.14 26 15.1 -0.7.3 37.2 AU09403-A02-341 AU0180354 67.673 1.477 26 17.6 0.50 67.1 AU0933-A02-241 AU021503 chr. 10.3.0.127 10.3.10.309 46.528 553 11.4 0.79 41.4 SSC00131-402-241 AU1021503 chr. 10.3.16.327 10.3.10.309 46.528 553 0.52 43.55 AU162230-1									
AU102803-002-281 AU02503 chrx 82,086,071 82,096,074 8,843 92 10.4 -1.04 93.0 AU05530-A02-281 AU055503 chrx 88,191,554 88,194,527 2,673 43 16.1 -1.26 36.3 SCCO0452-A02-281 AU05503 chrx 86,493,478 96,495,107 1.719 26 15.1 -0.73 37.2 AU106304-L012-181 AU001A02 chrx 97,442,228 97,443,302 1.064 18 16.9 -1.06 45.5 SC00035-A02-251 AU105303 chrx 10.064,516 100,613,616 860 14 20.0 -0.88 53.4 AU105303-A02-151 AU195303 chrx 10.064,1727 10.31,450,473 14,77 26 17.6 0.50 64.1 SC00013-402-251 AU021503 chrx 10.32,91,727 10.32,91,04 46,689 646 13.8 0.64 43.5 5 SC00013-402-251 AU021503 chrx 10.32,91,928 53.591 9.2 43.6 41.62332 43.6 43.6 43.6 43.6 43.6 43.6 43.6 43.6 43.6 43.6 43.6 43.6					· · · · · · · · · · · · · · · · · · ·				
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SSC00317-A02-2s1 SSC00317 Antik 103,999,466 103,999,425 359 9 9 25.1 -1.45 36.5 AU092031-b2203 AU0952031-chx 107,866,6975 2,310 43 18.6 0.34 63.5 SSC00073-A03-315 SSC00073 Anx 108,183,989 108,184,388 399 6 15.0 -1.63 55.3 SSC00092-A03-315 SSC00097 Anx 108,183,989 108,184,388 399 6 15.0 -1.81 55.3 SSC00092-A03-321 SSC00097 Anx 108,183,989 108,184,388 399 6 15.0 -1.81 55.3 SSC000316-A03-2s1 SSC00316 Chx 108,183,989 108,184,388 399 6 15.0 -1.81 55.3 SSC00316-A03-2s1 SSC00316 Chx 109,131,645 109,133,610 38 21.0 -0.75 40.3 SSC00316-A03-2s1 SSC00326 HX 111,561,566 1,810 38 21.0 -0.61 37.4 55.0 <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>									
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SSC00077-A03-3s1 SSC0007 hrx 108,183,989 108,184,388 399 6 15.0 -1.63 55.3 SSC00097-A03-1s2 SSC00093 hrx 108,183,989 108,184,388 399 6 15.0 -1.81 55.3 SSC00097-A03-1s1 SSC00098 hrx 108,183,989 108,184,388 399 6 15.0 -1.87 55.3 SSC00036-A03-2s1 SSC00260 hrx 108,183,989 108,184,388 399 6 15.0 -1.92 55.3 SSC00316-A03-2s1 SSC00316 hrx 109,131,565 109,133,410 1,665 32 10.2 0.56 64.8 AU014803-A03-2s1 SSC00316 hrx 111,521,12 111,628,128 29,466 18.00 38 21.0 0.075 40.3 SSC00240-A03-2s1 SSC00332 hrx 111,598,162 111,628,128 29,466 18.0 0.6.2 6 14.6 0.61 37.4 0.91 36.0 SSC00240-A03-2s1 AU169302-ArX 112,2					· · · · · · · · · · · · · · · · · · ·				
SSC00093-A03-1s1 SSC00097 chrX 108,183,989 108,184,388 399 6 15.0 -2.00 55.3 SSC00098-A03-3s1 SSC00097 chrX 108,183,989 108,184,388 399 6 15.0 -1.87 55.3 SSC00316-A03-2s1 SSC00316 chrX 108,183,989 108,184,388 399 6 15.0 -2.40 55.3 AU01803-A03-2s1 SSC00316 chrX 109,131,65 109,134,047 2,482 48 19.3 0.37 64.8 AU01803-A03-2s1 SSC00316 chrX 110,234,756 110,235,566 1,810 38 21.0 -0.75 40.3 SSC00316-A03-2s1 SSC00246 chrX 111,501,112 111,523,128 29,466 378 12.8 -0.91 36.6 SSC0032-A03-2s1 SSC00264 chrX 111,970,302 111,971,664 1,362 28 20.6 0.39 63.8 SC00264-A03-3s1 SSC00264 chrX 112,047,857 112,052,442 4,585	SSC00077-A03-3s1	SSC00077 chrX	108,183,989						
SSC00097-A03-1s1 SSC00097-A03-1s1 SSC00098 ANX 108,183,989 108,184,388 399 6 15.0 -1.81 55.3 SSC000360-A03-2s1 SSC000360 ANX 108,183,989 108,184,388 399 6 15.0 -1.92 55.3 SSC00316-A03-2s1 SSC00316 AnX 109,131,565 109,134,047 2,482 48 19.3 0.37 64.8 AU014803-A03-2s1 AU014803 AnX-2s1 SSC00316 AnX 110,234,756 110,234,756 101,33,310 1,665 32 19.2 0.61 37.4 0.0.61 37.4 0.0.61 37.4 0.0.61 37.4 0.0.61 37.6 0.80 55.00316 AnX 111,529,142 11,529,142 2,42 2.1 0.50 66.2 6 100.01 10.6 0.61 37.6 0.90 65.2 6.38 4 10.939304 111,970,302 111,971,474 1,127 2.2 2.1.4 0.50 6.38 4 0.0444303 0.91 1.4.5 <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>									
SSC00098-A03-3c1 SSC00096 A03-3c1 SSC00260 chrx 108,183,989 108,184,388 399 6 15.0 -1.87 55.3 SSC00316-A03-2c1 SSC00260 chrx 108,183,399 108,184,388 399 6 15.0 -2.40 55.3 AU0852304-A03-2c1 AU0682304 chrx 109,131,655 109,134,047 2,482 48 19.3 0.37 64.8 AU01803-A03-2c1 SSC00316 chrx 110,234,756 110,235,566 1,810 38 21.0 -0.75 40.3 SSC00316-A03-2c1 SSC002264 chrx 111,751,411 111,753,134 10.03 14.6 -0.61 37.4 SSC00264-A03-3c1 SSC00269 chrx 111,970,302 111,971,664 1,362 28 20.6 0.39 65.2 SSC00269-A03-2c1 SSC00269 chrx 112,047,857 112,052,442 4,585 68 14.8 -0.84 38.4 AU04803-A03-321 AU04803-Arx 111,271,477 6,986 1									55.3
S5C00316-A03-2s1 SSC00316 chrx 109,131,645 109,131,047 2,482 48 19.3 0.37 64.8 AU0852304-A03-2s1 AU014803 chrx 109,131,645 109,133,101 1,665 32 19.2 0.59 67.6 SSC00316-A03-2s1 SSC0017 chrx 110,234,756 110,236,556 1,810 38 21.0 -0.75 40.3 SSC00316-A03-2s1 SSC0032 chrx 111,753,1579 13 22.5 -0.90 28.2 AU0939304-151A03 AU0939304 chrX 111,970,302 111,971,424 1,122 24 21.4 0.50 63.8 SSC00259-A03-2s1 SSC00269 chrX 112,024,257 112,054,242 4,585 68 14.8 -0.86 38.4 AU004803-A03-3s1 AU004803 chrX 114,330,335 114,333,305 2,625 50 19.0 0.45 65.8 AU1631303-1s1A03 AU1631303 chrX 114,333,010 114,333,305 2,215 45 20.0 0.39 6	SSC00098-A03-3s1	SSC00098 chrX	108,183,989	108,184,388	399	6	15.0	-1.87	55.3
AU0852304-A03-2s1 AU018052304 chrX 109,131,655 109,133,10 1,665 32 19.2 0.59 67.6 SSC00316-A03-2s1 SSC00316 chrX 110,234,756 110,235,566 1,810 38 21.0 -0.75 40.3 SSC00417-A03-s1 SSC00264 chrX 111,599,650 68,478 1003 14.6 -0.61 37.4 SSC00332-A03-s21 SSC00264 chrX 111,753,154 111,753,733 579 13 22.5 -0.90 28.2 AU0939304-151A03 AU039304 chrX 111,970,302 111,971,464 1,362 28 20.6 0.39 62.6 AU1069302-A03-251 SSC00269 chrX 112,247,857 113,241,577 6,966 101 14.5 -0.86 38.4 AU040403-A03-361 AU004003 chrX 114,333,052 114,333,350 2,625 50 19.0 0.45 65.8 AU0169302-A03-251 AU069303 chrX 114,333,052 144,333,350 2,625 50 19.0 0.45 65.9 AU016303 chrX 114,333,052 144,333,350 2,625 50 </td <td>SSC00260-A03-2s1</td> <td>SSC00260 chrX</td> <td>108,183,989</td> <td>108,184,388</td> <td>399</td> <td>6</td> <td>15.0</td> <td>-1.92</td> <td>55.3</td>	SSC00260-A03-2s1	SSC00260 chrX	108,183,989	108,184,388	399	6	15.0	-1.92	55.3
Au014803-A03-2s1 Au014803 chrx 110,213,4756 110,213,510 1.665 32 19.2 0.59 67.6 SSC00316-A03-2s1 SSC00316 chrx 111,524,556 110,236,566 1,810 38 21.0 -0.75 40.3 SSC00264-A03-3s1 SSC00322 chrx 111,559,566 111,657,373 579 13 22.5 -0.90 28.2 AU0939304-ts1A03 AU0939304 chrx 111,970,302 111,971,644 1,362 28 20.6 0.39 63.8 SSC00269-A03-2s1 SSC00269 chrx 111,270,302 111,971,424 1,122 24 21.4 0.50 63.8 SSC00269-A03-2s1 SSC00269 chrx 113,224,686 113,241,182 6,469 94 14.5 -0.48 38.1 AU163103 chrx 114,330,255 144,333,350 2,970 56 18.9 0.35 65.2 AU163103 chrx 114,331,010 114,333,350 2,215 44 19.9 0.44 65.2	SSC00316-A03-2s1	SSC00316 chrX	108,183,989	108,184,388	399	6	15.0	-2.40	55.3
SSC00316-A03-2s1 SSC00417 ChrX 110,234,756 110,236,566 1,810 38 21.0 -0.75 40.3 SSC00417-A03-1s1 SSC00264 ChrX 111,595,950 68,478 1003 14.6 -0.61 37.4 SSC00322-A03-2s1 SSC00323 ChrX 111,753,154 111,753,733 579 13 22.5 -0.90 28.2 AU0093030-AN3-2s1 SSC00269 A01344302 chrX 111,970,302 111,971,644 1,122 24 21.4 0.50 63.8 SSC00269-A03-2s1 SSC00269 chrX 113,224,691 113,241,577 6,966 101 14.5 -0.46 38.4 AU04803-A03-3s1 AU004803 chrX 114,330,725 114,333,305 2,625 50 9.0 0.45 65.8 AU13803-1s2A03 AU161303 chrX 114,331,010 114,333,325 2,215 44 19.9 0.52 64.9 AU1069302-A03-2s1 AU069503 chrX 114,331,010 114,333,325 2,130 42 19.7 0.59 65.0 AU1069302-A03-2s1 AU069503 ch	AU0852304-A03-2s1	AU0852304 chrX	109,131,565	109,134,047	2,482	48	19.3	0.37	64.8
SSC00417-A03-Is1 SSC00417 chrx 111,590,112 111,591,5950 68,478 1003 14.6 -0.61 37.4 SSC00264-A03-3s1 SSC0032 chrX 111,598,662 111,1753,73 579 13 22.5 -0.90 28.2 AU0939304-1s1A03 AU0939304 chrX 111,970,302 111,971,644 1,362 28 20.6 0.99 62.6 6.38 SSC00269-A03-2s1 SSC00269 chrX 112,047,857 112,052,442 4,585 68 14.8 -0.84 36.5 AU04803-A03-3s1 AU004803 chrX 113,224,691 113,241,827 6,986 101 14.5 -0.40 38.1 AU163103-1s1A03 AU131303 chrX 114,330,035 114,333,350 2,275 56 18.9 0.35 65.2 AU169302-A03-2s2 AU0895303 chrX 114,331,010 114,333,255 2,215 44 19.9 0.44 65.0 AU0895303-1s2A03 AU0895303 chrX 114,331,010 114,333,350 2,215 44 19.9 0.44 65.1	AU014803-A03-2s1		109,131,645	109,133,310	1,665	32	19.2	0.59	67.6
SSC00264-A03-3s1 SSC0032 chrX 111,598,662 111,628,128 29,466 378 12.8 -0.91 36.0 SSC00332-A03-2s1 SSC00332 chrX 111,770,302 111,971,664 1,362 28 20.6 0.39 62.6 AU0939304-ISLA03 AU0939302 chrX 111,970,302 111,971,424 1,122 24 21.4 0.50 63.8 SSC00269-A03-2s1 SSC00269 chrX 113,244,957 16,986 101 14.5 -0.40 38.1 AU104803-A03-3s1 SAC00269 chrX 113,234,691 113,241,182 6,496 94 14.5 -0.40 38.1 AU1211303 chrX 114,330,335 114,333,350 2,625 50 19.0 0.45 65.8 AU160302-A03-2s2 AU08030 chrX 114,331,010 114,333,350 2,215 44 19.9 0.52 64.9 AU08932-31-S2A03 AU085303 chrX 114,331,095 114,333,350 2,210 44 19.9 0.44 65.2 AU065404-A03-2s1 AU085403 chrX 114,33	SSC00316-A03-2s1	SSC00316 chrX	110,234,756	110,236,566	1,810	38	21.0	-0.75	40.3
SSC00332-A03-2s1 SSC00332 chrX 111,753,154 111,753,733 579 13 22.5 -0.90 28.2 AU0939304-Is1A03 AU0939304 chrX 111,970,302 111,971,664 1,362 28 20.6 0.39 62.6 AU1069302-A03-2s1 AU1069302 chrX 111,970,302 111,971,424 1,122 24 21.4 0.50 63.8 AU1344302-Ls1A03 AU1211303-arb2A03 AU1211303 chrX 113,244,591 113,241,182 6,496 94 14.5 -0.60 38.1 AU1631303 chrX 114,330,375 114,333,350 2,970 56 18.9 0.35 65.2 AU16803-A03-2s2 AU018003 chrX 114,331,010 114,333,350 2,215 44 19.9 0.52 64.9 AU1069302-chr32s1 AU0652304 chrX 114,331,010 114,333,250 2,340 47 20.1 0.54 65.0 AU065204-A03-2s1 AU065303 chrX 114,331,095 114,333,250 2,130 42 19.7 0.59 65.1 AU065203 chrX	SSC00417-A03-1s1	SSC00417 chrX	111,501,112	111,569,590	68,478	1003	14.6	-0.61	
AU039304-1s1A03 AU039304 chrX 111,970,302 111,971,664 1,362 28 20.6 0.39 62.6 AU1069302-A03-2s1 SC00269 chrX 111,970,302 111,971,424 1,122 24 21.4 0.50 63.8 SC00269-A03-2s1 SC00269 chrX 112,047,857 112,047,857 112,047,857 116,052,442 4,585 68 14.8 0.84 36.5 AU134302-1s1A03 AU134302 chrX 113,234,651 113,241,577 6,986 101 14.5 -0.86 38.4 AU004803-A03-3s1 AU004803 chrX 114,330,335 114,333,305 2,970 56 18.9 0.35 65.2 AU131303-1s1A03 AU1631303 chrX 114,330,725 114,333,350 2,970 56 18.9 0.35 65.2 AU1631303-1s1A03 AU1631303 chrX 114,331,010 114,333,255 2,215 44 19.9 0.52 64.9 AU0089302-A03-2s1 AU1069302 chrX 114,331,010 114,333,350 2,210 44 19.9 0.52 64.9 AU065404-A03-2s1 AU065404 chrX 114,331,010 114,333,350 2,210 44 19.9 0.54 65.2 AU065404-A03-2s1 AU065404 chrX 114,331,095 114,333,350 2,210 44 19.9 0.54 65.2 AU195303-403-2s1 AU0055404 chrX 114,331,095 114,333,350 2,210 44 19.9 0.44 65.2 AU195303-A03-1s1 AU1953303 chrX 114,331,095 114,333,265 2,170 43 19.8 0.43 65.2 SC00292-A03-2s1 SC00592 chrX 114,331,095 114,333,265 2,170 41 19.8 0.60 65.1 AU1947303-A03-1s1 AU1953303 chrX 114,331,095 114,333,265 2,170 41 19.8 0.60 65.1 SC00592-0403-2s1 SC00592 chrX 114,331,095 114,333,265 2,170 41 19.8 0.60 65.1 SC00592-0403-2s1 SC00592 chrX 114,331,095 114,333,265 2,170 41 19.8 0.60 65.1 SC00592-0403-2s1 SC00592 chrX 114,331,095 114,333,265 2,170 41 19.8 0.60 65.1 AU195303-A03-1s1 AU1953303 chrX 114,331,375 114,333,305 2,070 41 19.8 0.642 65.2 SC00592-11A03 AU185303 chrX 114,331,375 114,333,305 1,915 38 19.8 0.642 65.2 SC00592-11A03 AU1875302 chrX 114,484,155 114,433,265 1,915 38 19.8 0.642 65.1 AU195302-11A03 AU1975302 chrX 114,484,155 114,450,696 2,281 28 12.3 0.55 33.7 SC00426-A03-2s1 AU042203 chrX 114,484,150 114,450,696 2,281 28 12.3 0.55 33.7 SC00426-A03-2s1 AU0425303 chrX 114,480,514 114,450,696 2,281 28 12.3 0.55 33.7 SC00426-A03-2s1 AU0425303 chrX 114,480,5101 115,539,553 4,652 81 17.4 0.966 34.2 AU105302-21A03 AU153903 chrX 114,480,5102 114,450,696 2,281 28 12.3 0.55 33.7 SC00426-A03-2s1 AU048523	SSC00264-A03-3s1	SSC00264 chrX	111,598,662	111,628,128				-0.91	
AU1069302-A03-2s1 AU1069302 chrX 111,970,302 111,971,424 1,122 24 21.4 0.50 63.8 SSC00269-A03-2s1 SSC00269 chrX 112,047,857 112,052,442 4,855 68 14.8 -0.84 36.5 AU1344302-1s1A03 AU1344302-1k1A03 AU1344302-1k1A03 AU1211303 chrX 113,241,577 6,986 101 14.5 -0.86 38.4 AU04803-A03-3s1 AU004803 chrX 114,330,355 114,333,350 2,625 50 19.0 0.45 65.8 AU1631303-1s2A03 AU1631030 chrX 114,331,010 114,333,255 2,255 45 20.0 0.39 65.0 AU069302-A03-2s1 AU1065404 chrX 114,331,010 114,333,255 2,340 47 20.1 0.54 65.0 AU0852304-A03-2s1 AU065404 chrX 114,331,095 114,333,265 2,170 43 19.7 0.59 65.1 AU195303-A03-1s1 AU195303 chrX 114,31,095 114,333,265 2,170 43 19.8 0.43	SSC00332_A03_2c1	CCC00222 abyV	111 753 154	111 753 733	579	13	22.5	-0.90	28.2
SSC00269-A03-2s1 SSC00269 chrX 112,047,857 112,052,442 4,585 68 14.8 -0.84 36.5 AU1344302-ts1A03 AU1344302 chrX 113,234,591 113,241,182 6,496 94 14.5 -0.86 38.4 AU04803-stA03-3s1 AU004803 chrX 114,330,355 114,333,305 2,970 56 18.9 0.35 65.2 AU1303-1s2A03 AU1211303 chrX 114,330,725 114,333,305 2,970 56 18.9 0.35 65.2 AU18030-A03-2s2 AU018003 chrX 114,331,010 114,333,255 2,215 44 19.9 0.52 64.9 AU169302-A03-2s1 AU065404 chrX 114,331,095 114,333,255 2,210 44 19.9 0.44 65.2 AU0852304-A03-2s1 AU085204 chrX 114,331,095 114,333,140 2,045 41 20.0 0.57 65.2 SC00292-A03-3s1 SC00592 chrX 114,331,250 114,333,140 2,045 41 20.0 0.57 65.2 <t< td=""><td>33C00332-A03-231</td><td>55C00332 CIIIX</td><td>111,755,154</td><td>111,755,755</td><td>575</td><td>15</td><td>22.0</td><td></td><td></td></t<>	33C00332-A03-231	55C00332 CIIIX	111,755,154	111,755,755	575	15	22.0		
AU1344302-1s1A03 AU1344302 chrX 113,234,591 113,241,577 6,986 101 14.5 -0.86 38.4 AU004803-A03-3s1 AU004803 chrX 113,234,686 113,241,182 6,986 94 14.5 -0.40 38.1 AU1211303-1s2A03 AU1211303 chrX 114,330,335 114,333,305 2,970 56 18.9 0.35 65.2 AU1631303-1s1A03 AU1211303 chrX 114,331,010 114,333,255 2,215 45 20.0 0.39 65.0 AU0895303-1s2A03 AU0895303 chrX 114,331,010 114,333,225 2,215 44 19.9 0.52 64.9 AU1069302-A03-2s1 AU1069302 chrX 114,331,005 114,333,305 2,340 47 20.1 0.54 65.2 AU0852304-A03-2s1 AU065404 chrX 114,331,095 114,333,350 2,340 47 20.1 0.54 65.2 AU195303-A03-1s1 AU852304 chrX 114,331,095 114,333,265 2,170 43 19.8 0.43 65.2 AU195303-A03-1s1 AU195303 chrX 114,331,095 114,333,265 2,170 43 19.8 0.43 65.2 AU195303-A03-1s1 AU1953303 chrX 114,331,095 114,333,265 2,170 43 19.8 0.60 65.1 SSC00292-A03-2s1 SSC00296 chrX 114,331,350 114,333,265 1,915 38 19.8 0.62 65.1 AU198303-1s1A03 AU1898303 chrX 114,331,350 114,333,265 1,915 38 19.8 0.62 65.1 AU1898303-1s1A03 AU1898303 chrX 114,331,375 114,333,300 1,265 3 19.7 0.59 65.7 AU1895301-A03-2s1 AU0920301 chrX 114,331,350 114,333,265 1,915 38 19.8 0.62 65.1 AU1898303-1s1A03 AU1898303 chrX 114,331,350 114,333,300 1,285 25 19.5 0.70 65.7 AU1875302-1s1A03 AU1898303 chrX 114,331,805 114,333,300 1,285 25 19.5 0.70 65.7 AU1875302-1s1A03 AU1898303 chrX 114,331,805 114,333,300 1,285 25 19.5 0.70 65.7 AU195302-2s1A03 AU1939303 chrX 114,431,805 114,433,300 1,285 25 19.5 0.70 65.4 AU093303-4s15A03 AU1898303 chrX 114,438,415 114,450,696 2,281 28 12.3 -0.69 33.4 AU021203-1s1A03 AU021203 chrX 114,448,415 114,450,696 2,281 28 12.3 -0.69 33.4 AU1069302-2s1A03 AU0159303 chrX 114,448,701 114,59,742 2,487 44 17.7 -1.64 38.6 AU018304-A03-2s1 AU069303 chrX 114,638,655 117,130 24 21.2 0.47 65.0 AU0129303-A03-2s1 AU085303 chrX 116,538,748 114,551,948 114,591,745 24 19.8 0.455 65.5 AU1069302-A03-2s1 AU085303 chrX 116,538,748 114,450,696 2,281 28 12.3 -0.69 33.4 AU021203-1s1A03 AU021203 chrX 116,538,783 118,255,949 1,706 22 20.4 0.50 70.7 AU021803-A03-2s1 AU0189303 chrX 118,253,848 118,255,5	AU0939304-1s1A03	AU0939304 chrX	111,970,302	111,971,664	1,362	28	20.6	0.39	62.6
AU004803-A03-3s1 AU004803 chr 113,234,686 113,241,182 6,496 94 14.5 -0.40 38.1 AU1211303-1s2A03 AU1211303 chrX 114,330,325 114,333,305 2,970 56 18.9 0.35 65.2 AU1631303-1s1A03 AU1631303 chrX 114,331,010 114,333,255 2,255 45 20.0 0.39 65.0 AU0895303-A03-2s2 AU0169302 chrX 114,331,010 114,333,350 2,215 44 19.9 0.52 64.9 AU065404-A03-2s1 AU065404 chrX 114,331,095 114,333,305 2,210 44 19.9 0.44 65.2 AU0852304-A03-2s1 AU0852304 chrX 114,331,095 114,333,265 2,170 43 19.8 0.43 65.2 SC00296-A03-2s1 SC00296 chrX 114,331,255 114,333,265 1,170 43 19.8 0.62 65.1 SC00296-A03-2s1 SC00296 chrX 114,331,255 1,41,333,305 2,070 41 19.8 0.66 65.1	AU0939304-1s1A03	AU0939304 chrX	111,970,302	111,971,664 111,971,424	1,362 1,122	28 24	20.6 21.4	0.39 0.50	62.6 63.8
AU1211303-1s2A03 AU1211303 chrX 114,330,335 114,333,305 2,970 56 18.9 0.35 65.2 AU1631303-1s1A03 AU1631303 chrX 114,331,010 114,333,255 2,255 55 25 20.0 0.39 65.0 AU0895303-1s2A03 AU0895303 chrX 114,331,010 114,333,255 2,215 44 19.9 0.52 64.9 AU1069302-A03-2s1 AU1069302 chrX 114,331,010 114,333,305 2,340 47 20.1 0.54 65.0 AU0852304-A03-2s1 AU065404 chrX 114,331,095 114,333,305 2,104 44 19.9 0.444 65.2 AU0852304-A03-2s1 AU0852304 chrX 114,331,095 114,333,255 2,130 42 19.7 0.59 65.1 AU197303-A03-1s1 AU197303 chrX 114,331,095 114,333,255 2,170 43 19.8 0.43 65.2 SSC00296-A03-2s1 SSC00296 chrX 114,331,255 114,333,265 4,170 43 19.8 0.63 65.1 SSC00296-A03-2s1 SSC00296 chrX 114,331,350 114,333,255 1,915 38 19.8 0.62 65.1 AU198303-1s1A03 AU1898303 chrX 114,331,351 114,333,255 1,915 38 19.8 0.62 65.1 AU198303-1s1A03 AU1898303 chrX 114,331,455 114,333,255 1,915 38 19.8 0.62 65.7 AU1975302-1s1A03 AU1898303 chrX 114,331,455 114,333,255 1,915 38 19.8 0.62 65.7 AU1975302-1s1A03 AU1898303 chrX 114,331,455 114,333,255 1,915 38 19.8 0.62 65.7 AU0452303-A03-2s1 AU0922301 chrX 114,331,455 114,333,090 1,285 25 19.5 0.70 65.7 AU0452303-A03-2s1 AU092303 chrX 114,431,455 114,433,090 1,285 25 19.5 0.70 65.4 AU0939304-1s1A03 AU1895302 chrX 114,431,455 114,433,090 1,285 25 19.5 0.70 65.4 AU0939304-1s1A03 AU03939304 chrX 114,484,15 114,450,696 2,281 28 12.3 0.55 33.7 SSC00426-A03-2s1 SSC00426 chrX 114,448,415 114,450,696 2,281 28 12.3 0.55 33.7 AU169302-2s1A03 AU159303 chrX 114,448,415 114,450,696 1,916 26 13.6 0.45 30.6 AU159302-2s1A03 AU0452303 chrX 114,448,415 114,450,696 1,916 26 13.6 0.45 30.6 AU1059302-2s1A03 AU0452303 chrX 114,450,895 1,130 2,487 44 17.7 -1.64 38.6 AU0852304-A03-2s1 AU0852304 chrX 114,530,825 116,590,742 2,487 44 17.7 -1.64 38.6 AU0852304-A03-2s1 AU0852304 chrX 116,588,255 116,590,742 2,487 44 17.7 -1.64 38.6 AU0852304-A03-2s1 AU0852304 chrX 116,588,255 116,590,742 2,487 44 17.7 -1.64 38.6 AU0852304-A03-2s1 AU0852304 chrX 118,253,882 118,255,199 2,137 45 21.1 0.41 61.6 AU014803-A03-2s1 AU028903 chrX 118,253,848 118	AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1	AU0939304 chrX AU1069302 chrX SSC00269 chrX	111,970,302 111,970,302 112,047,857	111,971,664 111,971,424 112,052,442	1,362 1,122 4,585	28 24 68	20.6 21.4 14.8	0.39 0.50 -0.84	62.6 63.8
AU1631303-1s1A03 AU1631303 chrX 114,330,725 114,333,350 2,625 50 19.0 0.45 65.8 AU018003-A03-2s2 AU018003 chrX 114,331,010 114,333,255 2,255 45 20.0 0.39 65.0 AU0895303-1s2A03 AU0895303 chrX 114,331,010 114,333,255 2,215 44 19.9 0.52 64.9 AU065404-A03-2s1 AU065404 chrX 114,331,095 114,333,255 2,210 44 19.9 0.44 65.2 AU065204-A03-2s1 AU065204 chrX 114,331,095 114,333,255 2,170 43 19.8 0.43 65.2 AU1947303-A03-1s1 AU1947303 chrX 114,331,095 114,333,265 2,170 43 19.8 0.62 65.1 SC00292-A03-2s1 SSC00296 chrX 114,331,305 114,333,265 1,915 38 19.8 0.62 65.1 AU1989303-1s1A03 AU1989303 chrX 114,331,405 1,765 35 19.8 0.51 65.4 AU0920301-A03-2s1 AU0920301 chrX 114,331,405 1,430 28 19.6 0.42 65.2<	AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03	AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX	111,970,302 111,970,302 112,047,857 113,234,591	111,971,664 111,971,424 112,052,442 113,241,577	1,362 1,122 4,585 6,986	28 24 68 101	20.6 21.4 14.8 14.5	0.39 0.50 -0.84 -0.86	62.6 63.8 36.5 38.4
AU018003-A03-2s2 AU018003 chrX 114,331,010 114,333,265 2,255 45 20.0 0.39 65.0 AU0895303-1s2A03 AU0895303 chrX 114,331,010 114,333,225 2,215 44 19.9 0.52 64.9 AU1069302-A03-2s1 AU1065404 chrX 114,331,095 114,333,305 2,210 44 19.9 0.44 65.2 AU0852304-A03-2s1 AU065404 chrX 114,331,095 114,333,265 2,170 43 19.8 0.43 65.2 AU1953303-A03-1s1 AU1953303 chrX 114,331,235 114,333,265 2,070 41 19.8 0.43 65.2 SC00296-A03-2s1 SC00296 chrX 114,331,235 114,333,265 1,915 38 19.8 0.62 65.1 AU1898303-1s1A03 AU1898303 chrX 114,331,455 114,333,306 1,765 35 19.8 0.51 65.4 AU0892031-A03-2s1 AU0452303 chrX 114,331,450 114,433,090 1,285 25 19.5 0.70 65.4 AU087303-chrX 114,331,805 <t< td=""><td>AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1</td><td>AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU004803 chrX</td><td>111,970,302 111,970,302 112,047,857 113,234,591 113,234,686</td><td>111,971,664 111,971,424 112,052,442 113,241,577 113,241,182</td><td>1,362 1,122 4,585 6,986 6,496</td><td>28 24 68 101 94</td><td>20.6 21.4 14.8 14.5 14.5</td><td>0.39 0.50 -0.84 -0.86 -0.40</td><td>62.6 63.8 36.5 38.4 38.1</td></t<>	AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1	AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU004803 chrX	111,970,302 111,970,302 112,047,857 113,234,591 113,234,686	111,971,664 111,971,424 112,052,442 113,241,577 113,241,182	1,362 1,122 4,585 6,986 6,496	28 24 68 101 94	20.6 21.4 14.8 14.5 14.5	0.39 0.50 -0.84 -0.86 -0.40	62.6 63.8 36.5 38.4 38.1
AU0895303-1s2A03 AU0895303 chrX 114,331,010 114,333,225 2,215 44 19.9 0.52 64.9 AU1069302-A03-2s1 AU065404 chrX 114,331,010 114,333,350 2,340 47 20.1 0.54 65.0 AU0852304-A03-2s1 AU0852304 chrX 114,331,095 114,333,225 2,110 42 19.7 0.59 65.1 AU1953303-A03-1s1 AU1947303 chrX 114,331,095 114,333,225 2,170 43 19.8 0.43 65.2 SC00296-A03-2s1 SC00296 chrX 114,331,250 114,333,305 2,045 41 20.0 0.57 65.2 SSC00296-A03-2s1 SSC00292 chrX 114,331,250 114,333,255 1,915 38 19.8 0.62 65.1 AU1898303-1s1A03 AU1898030 chrX 114,331,450 114,333,225 1,780 35 19.7 0.59 65.7 AU1875302-1s1A03 AU1875302 chrX 114,331,450 114,333,400 1,430 28 19.6 0.42 65.2 AU1875302-1s1A03 AU1875302 chrX 114,331,805 114,433,3090 1,430 28	AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1 AU1211303-1s2A03	AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU004803 chrX AU1211303 chrX	111,970,302 111,970,302 112,047,857 113,234,591 113,234,686 114,330,335	111,971,664 111,971,424 112,052,442 113,241,577 113,241,182 114,333,305	1,362 1,122 4,585 6,986 6,496 2,970	28 24 68 101 94 56	20.6 21.4 14.8 14.5 14.5 18.9	0.39 0.50 -0.84 -0.86 -0.40 0.35	62.6 63.8 36.5 38.4 38.1 65.2
AU1069302-A03-2s1 AU1069302 chrX 114,331,010 114,333,350 2,340 47 20.1 0.54 65.0 AU065404-A03-2s1 AU065404 chrX 114,331,095 114,333,225 2,110 42 19.7 0.59 65.1 AU0852304-A03-2s1 AU0852304 chrX 114,331,095 114,333,265 2,170 43 19.8 0.43 65.2 AU1953303-A03-1s1 AU1953303 chrX 114,331,095 114,333,265 2,170 41 20.0 0.57 65.2 SC00296-A03-2s1 SC00296 chrX 114,331,305 114,333,265 1,915 38 19.8 0.62 65.1 AU1898303-1s1A03 AU1898303 chrX 114,331,475 114,333,265 1,915 38 19.8 0.62 65.7 AU1898303-1s1A03 AU1898303 chrX 114,331,475 114,333,090 1,285 19.5 0.70 65.4 AU0920301-A03-2s1 AU0452303 chrX 114,433,2135 114,333,090 1,285 19.5 0.70 65.4 AU0452303-A03-2s1 AU045303 chrX 114,433,160 114,430,696 2,281 28 12.3 0.5	AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1 AU1211303-1s2A03 AU1631303-1s1A03	AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU004803 chrX AU1211303 chrX AU1631303 chrX	111,970,302 111,970,302 112,047,857 113,234,591 113,234,686 114,330,335 114,330,725	111,971,664 111,971,424 112,052,442 113,241,577 113,241,182 114,333,305 114,333,350	1,362 1,122 4,585 6,986 6,496 2,970 2,625	28 24 68 101 94 56 50	20.6 21.4 14.8 14.5 14.5 18.9 19.0	0.39 0.50 -0.84 -0.86 -0.40 0.35 0.45	62.6 63.8 36.5 38.4 38.1 65.2 65.8
AU065404-A03-2s1 AU065404 chrX 114,331,095 114,333,305 2,210 44 19.9 0.44 65.2 AU0852304-A03-2s1 AU0852304 chrX 114,331,095 114,333,225 2,130 42 19.7 0.59 65.1 AU1947303-A03-1s1 AU1947303 chrX 114,331,095 114,333,265 2,170 43 19.8 0.43 65.2 SSC00296-A03-2s1 SSC00296 chrX 114,331,255 114,333,305 2,070 41 19.8 0.60 65.1 SSC00296-A03-2s1 SSC00592 chrX 114,331,375 114,333,140 1,765 35 19.8 0.62 65.1 AU08920301-A03-2s1 AU0920301 chrX 114,331,600 114,333,090 1,430 28 19.6 0.42 65.2 AU0452303-A03-2s1 AU0452303 chrX 114,331,805 114,333,090 1,430 28 19.6 0.42 65.5 AU189802-2s1A03 AU189303 chrX 114,431,805 114,433,3090 1,285 25 19.5 0.70 65.4 AU045203-A03-2s1 AU045203 chrX 114,448,415	AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1 AU1211303-1s2A03 AU1631303-1s1A03 AU018003-A03-2s2	AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU004803 chrX AU1211303 chrX AU1631303 chrX AU018003 chrX	111,970,302 111,970,302 112,047,857 113,234,591 113,234,686 114,330,335 114,330,725 114,331,010	111,971,664 111,971,424 112,052,442 113,241,577 113,241,182 114,333,305 114,333,350 114,333,265	1,362 1,122 4,585 6,986 6,496 2,970 2,625 2,255	28 24 68 101 94 56 50 45	20.6 21.4 14.8 14.5 14.5 18.9 19.0 20.0	0.39 0.50 -0.84 -0.86 -0.40 0.35 0.45 0.39	62.6 63.8 36.5 38.4 38.1 65.2 65.8 65.0
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AU1947303-A03-1s1 AU1947303 chrX 114,331,095 114,333,265 2,170 43 19.8 0.43 65.2 AU1953303-A03-1s1 AU1953303 chrX 114,331,095 114,333,140 2,045 41 20.0 0.57 65.2 SSC00296-A03-2s1 SSC00592 chrX 114,331,350 114,333,265 1,915 38 19.8 0.62 65.1 SSC00592-A03-3s1 SSC00592 chrX 114,331,350 114,333,265 1,915 38 19.8 0.62 65.1 AU1898303-1s1A03 AU1898303 chrX 114,331,455 114,333,225 1,780 35 19.7 0.59 65.7 AU1875302-1s1A03 AU1875302 chrX 114,331,465 114,333,900 1,285 25 19.5 0.70 65.4 AU0452303-A03-2s1 AU0452303 chrX 114,433,21,35 114,333,350 1,215 24 19.8 0.45 65.5 AU1159302-2s1A03 AU1159303 chrX 114,448,415 114,450,696 2,281 28 12.3 -0.69 33.4 AU021203-1s1A03 AU021203 chrX 114,448,780 114,450,696 2,281 28 </td <td>AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1 AU1211303-1s2A03 AU1631303-1s1A03 AU018003-A03-2s2 AU0895303-1s2A03 AU1069302-A03-2s1</td> <td>AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU04803 chrX AU1211303 chrX AU1631303 chrX AU0895303 chrX AU0895303 chrX AU1069302 chrX</td> <td>111,970,302 111,970,302 112,047,857 113,234,591 113,234,686 114,330,335 114,330,725 114,331,010 114,331,010</td> <td>111,971,664 111,971,424 112,052,442 113,241,577 113,241,182 114,333,350 114,333,265 114,333,225 114,333,350</td> <td>1,362 1,122 4,585 6,986 6,496 2,970 2,625 2,255 2,255 2,215 2,340</td> <td>28 24 68 101 94 56 50 45 44 47</td> <td>20.6 21.4 14.8 14.5 14.5 18.9 19.0 20.0 19.9 20.1</td> <td>0.39 0.50 -0.84 -0.86 -0.40 0.35 0.45 0.39 0.52 0.54</td> <td>62.6 63.8 36.5 38.4 38.1 65.2 65.8 65.0 64.9 65.0</td>	AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1 AU1211303-1s2A03 AU1631303-1s1A03 AU018003-A03-2s2 AU0895303-1s2A03 AU1069302-A03-2s1	AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU04803 chrX AU1211303 chrX AU1631303 chrX AU0895303 chrX AU0895303 chrX AU1069302 chrX	111,970,302 111,970,302 112,047,857 113,234,591 113,234,686 114,330,335 114,330,725 114,331,010 114,331,010	111,971,664 111,971,424 112,052,442 113,241,577 113,241,182 114,333,350 114,333,265 114,333,225 114,333,350	1,362 1,122 4,585 6,986 6,496 2,970 2,625 2,255 2,255 2,215 2,340	28 24 68 101 94 56 50 45 44 47	20.6 21.4 14.8 14.5 14.5 18.9 19.0 20.0 19.9 20.1	0.39 0.50 -0.84 -0.86 -0.40 0.35 0.45 0.39 0.52 0.54	62.6 63.8 36.5 38.4 38.1 65.2 65.8 65.0 64.9 65.0
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SSC00296-A03-2s1 SSC00296 chrX 114,331,235 114,333,305 2,070 41 19.8 0.60 65.1 SSC00592-A03-3s1 SSC00592 chrX 114,331,350 114,333,265 1,915 38 19.8 0.62 65.1 AU1898303-1s1A03 AU1898030 chrX 114,331,475 114,333,140 1,765 35 19.8 0.51 65.7 AU1875302-1s1A03 AU1875302 chrX 114,331,445 114,333,090 1,430 28 19.6 0.42 65.2 AU092303-A03-2s1 AU0452303 chrX 114,331,805 114,333,090 1,285 25 19.5 0.70 65.4 AU0939304-1s1A03 AU0329304 chrX 114,432,135 114,433,350 1,215 24 19.8 0.45 65.5 AU1159302-2s1A03 AU1159303 chrX 114,448,415 114,450,696 2,281 28 12.3 -0.69 33.4 AU1069302-A03-2s1 SSC00426 chrX 114,448,780 114,450,696 1,916 26 13.6 0.45 30.6 AU1159302-2s1A03 AU1159303 chrX 115,635,001	AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1 AU1211303-1s2A03 AU1631303-1s1A03 AU018003-A03-2s2 AU0895303-1s2A03 AU1069302-A03-2s1 AU065404-A03-2s1 AU0852304-A03-2s1	AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU004803 chrX AU1211303 chrX AU1631303 chrX AU018003 chrX AU0895303 chrX AU1069302 chrX AU065404 chrX AU0852304 chrX	111,970,302 111,970,302 112,047,857 113,234,591 113,234,686 114,330,335 114,330,725 114,331,010 114,331,010 114,331,015 114,331,095	111,971,664 111,971,424 112,052,442 113,241,577 113,241,182 114,333,305 114,333,265 114,333,265 114,333,350 114,333,350 114,333,305 114,333,225	1,362 1,122 4,585 6,986 6,496 2,970 2,625 2,255 2,215 2,215 2,340 2,210 2,130	28 24 68 101 94 56 50 45 44 47 44 42	20.6 21.4 14.8 14.5 14.5 18.9 19.0 20.0 19.9 20.1 19.9 20.1 19.9 19.7	0.39 0.50 -0.84 -0.86 -0.40 0.35 0.45 0.39 0.52 0.54 0.44 0.59	62.6 63.8 36.5 38.4 38.1 65.2 65.8 65.0 64.9 65.0 65.2 65.1
SSC00592-A03-3s1 SSC00592 chrX 114,331,350 114,333,265 1,915 38 19.8 0.62 65.1 AU1898303-1s1A03 AU1898303 chrX 114,331,375 114,333,140 1,765 35 19.8 0.51 65.4 AU0920301-A03-2s1 AU0920301 chrX 114,331,405 114,333,090 1,430 28 19.6 0.42 65.2 AU1875302-1s1A03 AU1875302 chrX 114,331,805 114,333,090 1,430 28 19.6 0.42 65.2 AU0452303-A03-2s1 AU0452303 chrX 114,331,805 114,333,090 1,285 25 19.5 0.70 65.4 AU0939304-1s1A03 AU159303 chrX 114,484,415 114,450,696 2,281 28 12.3 0.55 33.7 SSC00426-A03-2s1 SSC00426 chrX 114,448,415 114,450,696 1,916 26 13.6 0.45 30.6 AU1159302-2s1A03 AU12033 chrX 115,635,001 115,639,653 4,652 81 17.4 -0.96 34.2 AU069302-A03-2s1 AU0652304 chrX 116,588,255	AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1 AU1211303-1s2A03 AU1631303-1s1A03 AU018003-A03-2s2 AU0895303-1s2A03 AU1069302-A03-2s1 AU065404-A03-2s1 AU0852304-A03-2s1 AU1947303-A03-1s1	AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU04803 chrX AU1211303 chrX AU1631303 chrX AU018003 chrX AU0895303 chrX AU1069302 chrX AU065404 chrX AU0652304 chrX AU1947303 chrX	111,970,302 111,970,302 112,047,857 113,234,591 113,234,686 114,330,335 114,330,725 114,331,010 114,331,010 114,331,015 114,331,095	$\begin{array}{c} 111,971,664\\ 111,971,424\\ 112,052,442\\ 113,241,577\\ 113,241,182\\ 114,333,305\\ 114,333,350\\ 114,333,265\\ 114,333,350\\ 114,333,350\\ 114,333,305\\ 114,333,305\\ 114,333,225\\ 114,333,225\\ 114,333,265\\ \end{array}$	1,362 1,122 4,585 6,986 6,496 2,970 2,625 2,255 2,255 2,215 2,340 2,210 2,130 2,170	28 24 68 101 94 56 50 45 45 44 47 44 42 43	20.6 21.4 14.8 14.5 14.5 18.9 19.0 20.0 19.9 20.1 19.9 20.1 19.9 19.7 19.8	0.39 0.50 -0.84 -0.86 -0.40 0.35 0.45 0.39 0.52 0.54 0.54 0.59 0.43	62.6 63.8 36.5 38.4 38.1 65.2 65.8 65.0 64.9 65.0 65.2 65.1 65.2
AU1898303-1s1A03 AU1898303 chrX 114,331,375 114,333,140 1,765 35 19.8 0.51 65.4 AU0920301-A03-2s1 AU0920301 chrX 114,331,445 114,333,225 1,780 35 19.7 0.59 65.7 AU1875302-1s1A03 AU1875302 chrX 114,331,660 114,333,090 1,430 28 19.6 0.42 65.2 AU0452303-A03-2s1 AU0452303 chrX 114,331,805 114,333,090 1,285 25 19.5 0.70 65.4 AU0939304-1s1A03 AU0939304 chrX 114,432,135 114,333,350 1,215 24 19.8 0.45 65.5 AU1159302-2s1A03 AU1159303 chrX 114,448,415 114,450,696 2,281 28 12.3 -0.69 33.4 AU021203-1s1A03 AU021203 chrX 115,635,001 115,639,653 4,652 81 17.4 -0.96 34.2 AU1069302 chrX 116,588,255 116,590,742 2,487 44 17.7 -1.64 38.6 AU0852304-A03-2s1 AU0852304 chrX 116,588,255 117,155,095 1,130 24 21.2	AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1 AU1211303-1s2A03 AU1631303-1s1A03 AU018003-A03-2s2 AU0895303-1s2A03 AU1069302-A03-2s1 AU065404-A03-2s1 AU0852304-A03-2s1 AU1947303-A03-1s1	AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU004803 chrX AU1211303 chrX AU1631303 chrX AU0805303 chrX AU1069302 chrX AU065404 chrX AU0852304 chrX AU1947303 chrX	111,970,302 111,970,302 112,047,857 113,234,591 113,234,686 114,330,335 114,330,725 114,331,010 114,331,010 114,331,095 114,331,095 114,331,095	$\begin{array}{c} 111,971,664\\ 111,971,424\\ 112,052,442\\ 113,241,577\\ 113,241,182\\ 114,333,305\\ 114,333,305\\ 114,333,265\\ 114,333,225\\ 114,333,305\\ 114,333,205\\ 114,333,225\\ 114,333,225\\ 114,333,265\\ 114,333,265\\ 114,333,140\\ \end{array}$	1,362 1,122 4,585 6,986 6,496 2,970 2,625 2,255 2,255 2,215 2,340 2,210 2,130 2,170 2,045	28 24 68 101 94 56 50 45 44 47 44 42 43 41	20.6 21.4 14.8 14.5 14.5 18.9 19.0 20.0 19.9 20.1 19.9 19.7 19.8 20.0	0.39 0.50 -0.84 -0.86 -0.40 0.35 0.45 0.39 0.52 0.54 0.44 0.59 0.43 0.57	62.6 63.8 36.5 38.4 38.1 65.2 65.8 65.0 64.9 65.0 64.9 65.2 65.1 65.2 65.1 65.2
AU0920301-A03-2s1 AU0920301 chrX 114,331,445 114,333,225 1,780 35 19.7 0.59 65.7 AU1875302-1s1A03 AU1875302 chrX 114,331,660 114,333,090 1,430 28 19.6 0.42 65.2 AU0452303-A03-2s1 AU0452303 chrX 114,331,805 114,333,090 1,285 25 19.5 0.70 65.4 AU0939304-1s1A03 AU0939304 chrX 114,432,135 114,433,350 1,215 24 19.8 0.45 65.5 AU1159302-2s1A03 AU1159303 chrX 114,448,415 114,450,696 2,281 28 12.3 -0.69 33.4 AU021203-1s1A03 AU021203 chrX 114,448,415 114,450,696 1,916 26 13.6 0.45 30.6 AU159302-2s1A03 AU1159303 chrX 115,635,001 115,639,653 4,652 81 17.4 -0.96 34.2 AU1069302-A03-2s1 AU069302 chrX 115,832,448 115,931,741 108,293 1603 14.8 0.38 36.6 AU0852304-A03-2s1 AU0852304 chrX 117,133,965 117	AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1 AU1211303-1s2A03 AU1631303-1s1A03 AU018003-A03-2s2 AU0895303-1s2A03 AU1069302-A03-2s1 AU065404-A03-2s1 AU1947303-A03-1s1 AU1953303-A03-1s1 SSC00296-A03-2s1	AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU104803 chrX AU1211303 chrX AU1631303 chrX AU0895303 chrX AU069302 chrX AU065404 chrX AU065404 chrX AU065204 chrX AU1947303 chrX AU1953303 chrX SSC00296 chrX	111,970,302 111,970,302 112,047,857 113,234,591 113,234,686 114,330,335 114,330,725 114,331,010 114,331,010 114,331,095 114,331,095 114,331,095 114,331,095 114,331,235	$\begin{array}{c} 111,971,664\\ 111,971,424\\ 112,052,442\\ 113,241,577\\ 113,241,182\\ 114,333,305\\ 114,333,350\\ 114,333,265\\ 114,333,255\\ 114,333,350\\ 114,333,205\\ 114,333,225\\ 114,333,225\\ 114,333,265\\ 114,333,265\\ 114,333,265\\ 114,333,265\\ 114,333,305\\ 114,332,305$	1,362 1,122 4,585 6,986 6,496 2,970 2,625 2,255 2,215 2,340 2,210 2,130 2,170 2,045 2,070	28 24 68 101 94 56 50 45 44 47 44 42 43 41 41	20.6 21.4 14.8 14.5 14.5 18.9 19.0 20.0 19.9 20.1 19.9 20.1 19.7 19.7 19.8 20.0 19.8	0.39 0.50 -0.86 -0.40 0.35 0.45 0.39 0.52 0.54 0.44 0.59 0.43 0.57 0.60	62.6 63.8 36.5 38.4 38.1 65.2 65.8 65.0 64.9 65.0 65.2 65.1 65.2 65.1 65.2 65.1
AU1875302-1s1A03 AU1875302 chrX 114,331,660 114,333,090 1,430 28 19.6 0.42 65.2 AU0452303-A03-2s1 AU0452303 chrX 114,331,805 114,333,090 1,285 25 19.5 0.70 65.4 AU0939304-1s1A03 AU0939304 chrX 114,332,135 114,333,350 1,215 24 19.8 0.45 65.5 AU1159302-2s1A03 AU1159303 chrX 114,448,415 114,450,696 2,281 28 12.3 0.55 33.7 SSC00426-A03-2s1 SSC00426 chrX 114,448,415 114,450,696 2,281 28 12.3 -0.69 33.4 AU021203-1s1A03 AU159303 chrX 115,635,001 115,639,653 4,652 81 17.4 -0.96 34.2 AU1069302-A03-2s1 AU069302 chrX 115,823,448 115,931,741 108,293 1603 14.8 0.38 36.6 AU0852304-A03-2s1 AU0852304 chrX 116,588,255 116,590,742 2,487 44 17.7 -1.64 38.6 AU0895303-1s2A03 AU0895303 chrX 117,1991,249 117,1994,889 65 1	AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1 AU1211303-1s2A03 AU1631303-1s1A03 AU018003-A03-2s2 AU0895303-1s2A03 AU1069302-A03-2s1 AU065404-A03-2s1 AU0852304-A03-2s1 AU1947303-A03-1s1 AU1953303-A03-1s1 SSC00296-A03-2s1 SSC00592-A03-3s1	AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU1344302 chrX AU1211303 chrX AU1631303 chrX AU0895303 chrX AU069302 chrX AU065404 chrX AU065404 chrX AU0852303 chrX AU1947303 chrX AU1947303 chrX SSC00296 chrX	111,970,302 111,970,302 112,047,857 113,234,591 113,234,686 114,330,335 114,330,725 114,331,010 114,331,010 114,331,095 114,331,095 114,331,095 114,331,095 114,331,235	$\begin{array}{c} 111,971,664\\ 111,971,424\\ 112,052,442\\ 113,241,577\\ 113,241,182\\ 114,333,350\\ 114,333,265\\ 114,333,265\\ 114,333,255\\ 114,333,305\\ 114,333,225\\ 114,333,265\\ 114,333,265\\ 114,333,140\\ 114,333,305\\ 114,333,265\\ \end{array}$	1,362 1,122 4,585 6,986 6,496 2,970 2,625 2,255 2,215 2,340 2,210 2,130 2,170 2,045 2,070 1,915	28 24 68 101 94 56 50 45 44 47 44 42 43 41 41 38	20.6 21.4 14.8 14.5 14.5 18.9 19.0 20.0 19.9 20.1 19.9 20.1 19.7 19.8 20.0 19.8 20.0 19.8 19.8	0.39 0.50 -0.86 -0.40 0.35 0.45 0.39 0.52 0.54 0.44 0.59 0.43 0.57 0.60 0.62	62.6 63.8 36.5 38.4 38.1 65.2 65.0 65.0 65.0 65.0 65.2 65.1 65.2 65.1 65.2 65.1 65.1
AU0452303-A03-2s1 AU0452303 chrX 114,331,805 114,333,090 1,285 25 19.5 0.70 65.4 AU0939304-1s1A03 AU0939304 chrX 114,332,135 114,333,350 1,215 24 19.8 0.45 65.5 AU1159302-2s1A03 AU1159303 chrX 114,448,415 114,450,696 2,281 28 12.3 0.55 33.7 SSC00426-A03-2s1 SSC00426 chrX 114,448,415 114,450,696 2,281 28 12.3 -0.69 33.4 AU021203-1s1A03 AU021203 chrX 114,448,780 114,450,696 1,916 26 13.6 0.45 30.6 AU1159302-2s1A03 AU1069302 chrX 115,639,653 4,652 81 17.4 -0.96 34.2 AU1069302-A03-2s1 AU0852304 chrX 115,823,448 115,931,741 108,293 1603 14.8 0.38 36.6 AU0852304-A03-2s1 AU0852304 chrX 116,588,255 116,590,742 2,487 44 17.7 -1.64 38.6 AU0895303-1s2A03 AU0895303 chrX 117,1994,289 117,1994,889 65 17.9 0.31 <td>AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1 AU1211303-1s2A03 AU1631303-1s1A03 AU018003-A03-2s2 AU0895303-1s2A03 AU1069302-A03-2s1 AU065404-A03-2s1 AU0852304-A03-2s1 AU1947303-A03-1s1 SSC00296-A03-2s1 SSC00592-A03-3s1 AU1898303-1s1A03</td> <td>AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU1344302 chrX AU1211303 chrX AU1631303 chrX AU0895303 chrX AU0895303 chrX AU065404 chrX AU0852304 chrX AU0852304 chrX AU1947303 chrX AU1953303 chrX SSC00296 chrX SSC00592 chrX AU1898303 chrX</td> <td>111,970,302 111,970,302 112,047,857 113,234,591 113,234,686 114,330,335 114,330,725 114,331,010 114,331,010 114,331,095 114,331,095 114,331,095 114,331,095 114,331,235 114,331,350 114,331,375</td> <td>$\begin{array}{c} 111,971,664\\ 111,971,424\\ 112,052,442\\ 113,241,577\\ 113,241,182\\ 114,333,305\\ 114,333,350\\ 114,333,265\\ 114,333,265\\ 114,333,305\\ 114,333,205\\ 114,333,265\\ 114,333,265\\ 114,333,140\\ 114,333,140\\ \end{array}$</td> <td>1,362 1,122 4,585 6,986 6,496 2,970 2,625 2,255 2,215 2,340 2,210 2,130 2,170 2,045 2,070 1,915 1,765</td> <td>28 24 68 101 94 56 50 45 44 47 44 42 43 41 41 38 35</td> <td>20.6 21.4 14.8 14.5 18.9 19.0 20.0 19.9 20.1 19.9 20.1 19.9 19.7 19.8 20.0 19.8 19.8 19.8</td> <td>0.39 0.50 -0.84 -0.86 -0.40 0.35 0.45 0.52 0.54 0.44 0.59 0.43 0.57 0.60 0.62 0.51</td> <td>62.6 63.8 36.5 38.4 38.1 65.2 65.8 65.0 64.9 65.0 65.2 65.1 65.2 65.1 65.2 65.1 65.1 65.4</td>	AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1 AU1211303-1s2A03 AU1631303-1s1A03 AU018003-A03-2s2 AU0895303-1s2A03 AU1069302-A03-2s1 AU065404-A03-2s1 AU0852304-A03-2s1 AU1947303-A03-1s1 SSC00296-A03-2s1 SSC00592-A03-3s1 AU1898303-1s1A03	AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU1344302 chrX AU1211303 chrX AU1631303 chrX AU0895303 chrX AU0895303 chrX AU065404 chrX AU0852304 chrX AU0852304 chrX AU1947303 chrX AU1953303 chrX SSC00296 chrX SSC00592 chrX AU1898303 chrX	111,970,302 111,970,302 112,047,857 113,234,591 113,234,686 114,330,335 114,330,725 114,331,010 114,331,010 114,331,095 114,331,095 114,331,095 114,331,095 114,331,235 114,331,350 114,331,375	$\begin{array}{c} 111,971,664\\ 111,971,424\\ 112,052,442\\ 113,241,577\\ 113,241,182\\ 114,333,305\\ 114,333,350\\ 114,333,265\\ 114,333,265\\ 114,333,305\\ 114,333,205\\ 114,333,265\\ 114,333,265\\ 114,333,140\\ 114,333,140\\ \end{array}$	1,362 1,122 4,585 6,986 6,496 2,970 2,625 2,255 2,215 2,340 2,210 2,130 2,170 2,045 2,070 1,915 1,765	28 24 68 101 94 56 50 45 44 47 44 42 43 41 41 38 35	20.6 21.4 14.8 14.5 18.9 19.0 20.0 19.9 20.1 19.9 20.1 19.9 19.7 19.8 20.0 19.8 19.8 19.8	0.39 0.50 -0.84 -0.86 -0.40 0.35 0.45 0.52 0.54 0.44 0.59 0.43 0.57 0.60 0.62 0.51	62.6 63.8 36.5 38.4 38.1 65.2 65.8 65.0 64.9 65.0 65.2 65.1 65.2 65.1 65.2 65.1 65.1 65.4
AU0939304-1s1A03AU0939304 chrX114,332,135114,333,3501,2152419.80.4565.5AU1159302-2s1A03AU1159303 chrX114,448,415114,450,6962,2812812.30.5533.7SSC00426-A03-2s1SSC00426 chrX114,448,415114,450,6962,2812812.3-0.6933.4AU021203-1s1A03AU021203 chrX114,448,780114,450,6961,9162613.60.4530.6AU1159302-2s1A03AU159303 chrX115,635,001115,639,6534,6528117.4-0.9634.2AU1069302-A03-2s1AU0852304 chrX115,638,255116,590,7422,4874417.7-1.6438.6AU018304-A03-2s1AU0852304 chrX117,133,965117,135,0951,1302421.20.4765.0AU0895303-1s2A03AU0895303 chrX117,991,249117,994,8896517.90.3163.9AU028903-A03-2s1AU028903 chrX118,253,082118,255,2192,1374521.10.4161.6AU014803-A03-2s1AU028903 chrX118,253,873118,255,1441,2962720.80.5168.8AU028903-1s2A03AU0895303 chrX118,253,873118,254,9491,0762220.40.5070.7AU021203-1s1A03AU021203 chrX118,941,966118,948,3326,3667011.00.5142.3AU1378304-2s1A01AU1378304 chrX119,486,893119,487,273380923.7 <td>AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1 AU1211303-1s2A03 AU1631303-1s1A03 AU018003-A03-2s2 AU0895303-1s2A03 AU1069302-A03-2s1 AU065404-A03-2s1 AU0852304-A03-2s1 AU1947303-A03-1s1 SSC00296-A03-2s1 SSC00592-A03-3s1 AU1898303-1s1A03 AU0920301-A03-2s1</td> <td>AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU004803 chrX AU1211303 chrX AU1631303 chrX AU018003 chrX AU0895303 chrX AU069302 chrX AU065404 chrX AU0852304 chrX AU1947303 chrX AU1947303 chrX SSC00296 chrX SSC00592 chrX AU1898303 chrX AU1898303 chrX</td> <td>$\begin{array}{c} 111,970,302\\ 111,970,302\\ 112,047,857\\ 113,234,591\\ 113,234,686\\ 114,330,335\\ 114,330,725\\ 114,331,010\\ 114,331,010\\ 114,331,005\\ 114,331,095\\ 114,331,095\\ 114,331,095\\ 114,331,095\\ 114,331,235\\ 114,331,350\\ 114,331,375\\ 114,331,375\\ 114,331,445\\ \end{array}$</td> <td>$\begin{array}{c} 111,971,664\\ 111,971,424\\ 112,052,442\\ 113,241,577\\ 113,241,182\\ 114,333,350\\ 114,333,350\\ 114,333,265\\ 114,333,350\\ 114,333,305\\ 114,333,305\\ 114,333,265\\ 114,333,265\\ 114,333,140\\ 114,333,265\\ 114,333,140\\ 114,333,225\\ \end{array}$</td> <td>1,362 1,122 4,585 6,986 6,496 2,970 2,625 2,255 2,215 2,340 2,210 2,130 2,170 2,130 2,170 2,045 2,070 1,915 1,765 1,780</td> <td>28 24 68 101 94 56 50 45 44 47 44 42 43 41 41 38 35 35</td> <td>20.6 21.4 14.8 14.5 18.9 19.0 20.0 19.9 20.1 19.9 20.1 19.9 19.7 19.8 20.0 19.8 19.8 19.8 19.8 19.7</td> <td>0.39 0.50 -0.84 -0.86 -0.40 0.35 0.45 0.39 0.52 0.54 0.44 0.59 0.43 0.57 0.60 0.62 0.51 0.59</td> <td>62.6 63.8 36.5 38.4 38.1 65.2 65.8 65.0 64.9 65.0 65.2 65.1 65.1 65.4 65.7</td>	AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1 AU1211303-1s2A03 AU1631303-1s1A03 AU018003-A03-2s2 AU0895303-1s2A03 AU1069302-A03-2s1 AU065404-A03-2s1 AU0852304-A03-2s1 AU1947303-A03-1s1 SSC00296-A03-2s1 SSC00592-A03-3s1 AU1898303-1s1A03 AU0920301-A03-2s1	AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU004803 chrX AU1211303 chrX AU1631303 chrX AU018003 chrX AU0895303 chrX AU069302 chrX AU065404 chrX AU0852304 chrX AU1947303 chrX AU1947303 chrX SSC00296 chrX SSC00592 chrX AU1898303 chrX AU1898303 chrX	$\begin{array}{c} 111,970,302\\ 111,970,302\\ 112,047,857\\ 113,234,591\\ 113,234,686\\ 114,330,335\\ 114,330,725\\ 114,331,010\\ 114,331,010\\ 114,331,005\\ 114,331,095\\ 114,331,095\\ 114,331,095\\ 114,331,095\\ 114,331,235\\ 114,331,350\\ 114,331,375\\ 114,331,375\\ 114,331,445\\ \end{array}$	$\begin{array}{c} 111,971,664\\ 111,971,424\\ 112,052,442\\ 113,241,577\\ 113,241,182\\ 114,333,350\\ 114,333,350\\ 114,333,265\\ 114,333,350\\ 114,333,305\\ 114,333,305\\ 114,333,265\\ 114,333,265\\ 114,333,140\\ 114,333,265\\ 114,333,140\\ 114,333,225\\ \end{array}$	1,362 1,122 4,585 6,986 6,496 2,970 2,625 2,255 2,215 2,340 2,210 2,130 2,170 2,130 2,170 2,045 2,070 1,915 1,765 1,780	28 24 68 101 94 56 50 45 44 47 44 42 43 41 41 38 35 35	20.6 21.4 14.8 14.5 18.9 19.0 20.0 19.9 20.1 19.9 20.1 19.9 19.7 19.8 20.0 19.8 19.8 19.8 19.8 19.7	0.39 0.50 -0.84 -0.86 -0.40 0.35 0.45 0.39 0.52 0.54 0.44 0.59 0.43 0.57 0.60 0.62 0.51 0.59	62.6 63.8 36.5 38.4 38.1 65.2 65.8 65.0 64.9 65.0 65.2 65.1 65.1 65.4 65.7
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SSC00426-A03-2s1 SSC00426 chrX 114,449,415 114,450,696 2,281 28 12.3 -0.69 33.4 AU021203-1s1A03 AU021203 chrX 114,448,780 114,450,696 1,916 26 13.6 0.45 30.6 AU1159302-2s1A03 AU1159303 chrX 115,635,001 115,639,653 4,652 81 17.4 -0.96 34.2 AU1069302-A03-2s1 AU1069302 chrX 115,823,448 115,931,741 108,293 1603 14.8 0.38 36.6 AU0852304-A03-2s1 AU0852304 chrX 116,588,255 116,590,742 2,487 44 17.7 -1.64 38.6 AU018304-A03-2s1 AU0852303 chrX 117,133,965 117,135,095 1,130 24 21.2 0.47 65.0 AU0895303-1s2A03 AU0895303 chrX 118,253,082 118,255,119 2,137 45 21.1 0.41 61.6 AU014803-A03-2s1 AU014803 chrX 118,253,848 118,255,144 1,296 27 20.8 0.51 68.8 AU021203-1s1A03 <td>AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1 AU1211303-1s2A03 AU1631303-1s1A03 AU018003-A03-2s2 AU0895303-1s2A03 AU1069302-A03-2s1 AU065404-A03-2s1 AU065404-A03-2s1 AU1947303-A03-1s1 SSC00296-A03-2s1 SSC00296-A03-2s1 SSC00592-A03-3s1 AU1898303-1s1A03 AU0920301-A03-2s1 AU1875302-1s1A03 AU0452303-A03-2s1</td> <td>AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU004803 chrX AU1211303 chrX AU1631303 chrX AU0895303 chrX AU069302 chrX AU065404 chrX AU065404 chrX AU1947303 chrX AU1947303 chrX SSC00296 chrX SSC00296 chrX SSC00592 chrX AU1898303 chrX AU1898303 chrX AU1875302 chrX AU1875302 chrX</td> <td>$\begin{array}{c} 111,970,302\\ 111,970,302\\ 112,047,857\\ 113,234,591\\ 113,234,686\\ 114,330,335\\ 114,330,325\\ 114,331,010\\ 114,331,010\\ 114,331,005\\ 114,331,095\\ 114,331,095\\ 114,331,095\\ 114,331,095\\ 114,331,375\\ 114,331,375\\ 114,331,375\\ 114,331,345\\ 114,331,460\\ 114,331,805\\ \end{array}$</td> <td>111,971,664 111,971,424 112,052,442 113,241,577 113,241,182 114,333,305 114,333,265 114,333,350 114,333,350 114,333,350 114,333,305 114,333,265 114,333,265 114,333,265 114,333,265 114,333,265 114,333,265 114,333,265 114,333,209 114,333,090</td> <td>1,362 1,122 4,585 6,986 6,496 2,970 2,625 2,255 2,215 2,340 2,210 2,130 2,170 2,045 2,070 1,915 1,765 1,780 1,430 1,285</td> <td>28 24 68 101 94 56 50 45 44 47 44 42 43 41 41 38 35 35 28 25</td> <td>$\begin{array}{c} 20.6\\ 21.4\\ 14.8\\ 14.5\\ 14.5\\ 19.0\\ 20.0\\ 19.9\\ 20.1\\ 19.9\\ 20.1\\ 19.9\\ 20.1\\ 19.8\\ 20.0\\ 19.8\\ 19.8\\ 19.8\\ 19.8\\ 19.8\\ 19.8\\ 19.7\\ 19.6\\ 19.5\\ \end{array}$</td> <td>0.39 0.50 -0.84 -0.86 -0.40 0.35 0.45 0.39 0.52 0.54 0.44 0.59 0.43 0.57 0.60 0.62 0.51 0.59 0.42 0.70</td> <td>62.6 63.8 36.5 38.4 38.1 65.2 65.8 65.0 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.7 65.2 65.4</td>	AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1 AU1211303-1s2A03 AU1631303-1s1A03 AU018003-A03-2s2 AU0895303-1s2A03 AU1069302-A03-2s1 AU065404-A03-2s1 AU065404-A03-2s1 AU1947303-A03-1s1 SSC00296-A03-2s1 SSC00296-A03-2s1 SSC00592-A03-3s1 AU1898303-1s1A03 AU0920301-A03-2s1 AU1875302-1s1A03 AU0452303-A03-2s1	AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU004803 chrX AU1211303 chrX AU1631303 chrX AU0895303 chrX AU069302 chrX AU065404 chrX AU065404 chrX AU1947303 chrX AU1947303 chrX SSC00296 chrX SSC00296 chrX SSC00592 chrX AU1898303 chrX AU1898303 chrX AU1875302 chrX AU1875302 chrX	$\begin{array}{c} 111,970,302\\ 111,970,302\\ 112,047,857\\ 113,234,591\\ 113,234,686\\ 114,330,335\\ 114,330,325\\ 114,331,010\\ 114,331,010\\ 114,331,005\\ 114,331,095\\ 114,331,095\\ 114,331,095\\ 114,331,095\\ 114,331,375\\ 114,331,375\\ 114,331,375\\ 114,331,345\\ 114,331,460\\ 114,331,805\\ \end{array}$	111,971,664 111,971,424 112,052,442 113,241,577 113,241,182 114,333,305 114,333,265 114,333,350 114,333,350 114,333,350 114,333,305 114,333,265 114,333,265 114,333,265 114,333,265 114,333,265 114,333,265 114,333,265 114,333,209 114,333,090	1,362 1,122 4,585 6,986 6,496 2,970 2,625 2,255 2,215 2,340 2,210 2,130 2,170 2,045 2,070 1,915 1,765 1,780 1,430 1,285	28 24 68 101 94 56 50 45 44 47 44 42 43 41 41 38 35 35 28 25	$\begin{array}{c} 20.6\\ 21.4\\ 14.8\\ 14.5\\ 14.5\\ 19.0\\ 20.0\\ 19.9\\ 20.1\\ 19.9\\ 20.1\\ 19.9\\ 20.1\\ 19.8\\ 20.0\\ 19.8\\ 19.8\\ 19.8\\ 19.8\\ 19.8\\ 19.8\\ 19.7\\ 19.6\\ 19.5\\ \end{array}$	0.39 0.50 -0.84 -0.86 -0.40 0.35 0.45 0.39 0.52 0.54 0.44 0.59 0.43 0.57 0.60 0.62 0.51 0.59 0.42 0.70	62.6 63.8 36.5 38.4 38.1 65.2 65.8 65.0 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.7 65.2 65.4
AU021203-1s1A03 AU021203 chrX 114,448,780 114,450,696 1,916 26 13.6 0.45 30.6 AU1159302-2s1A03 AU1159303 chrX 115,635,001 115,639,653 4,652 81 17.4 -0.96 34.2 AU1069302-A03-2s1 AU1069302 chrX 115,823,448 115,931,741 108,293 1603 14.8 0.38 36.6 AU0852304-A03-2s1 AU0852304 chrX 116,588,255 116,590,742 2,487 44 17.7 -1.64 38.6 AU08304-A03-2s1 AU0852304 chrX 117,133,965 117,135,095 1,130 24 21.2 0.47 65.0 AU0895303-1s2A03 AU0895303 chrX 117,991,249 117,994,889 65 17.9 0.31 63.9 AU028903-A03-2s1 AU028903 chrX 118,253,082 118,255,144 1,296 27 20.8 0.51 68.8 AU0895303-1s2A03 AU0895303 chrX 118,253,873 118,254,949 1,076 22 20.4 0.50 70.7 AU021203-1s1A03 AU0895303	AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1 AU1631303-1s2A03 AU1631303-1s1A03 AU018003-A03-2s2 AU0895303-1s2A03 AU1069302-A03-2s1 AU065404-A03-2s1 AU065204-A03-2s1 AU1947303-A03-1s1 SSC00296-A03-2s1 SSC00296-A03-2s1 SSC00592-A03-3s1 AU198303-1s1A03 AU0920301-A03-2s1 AU1875302-1s1A03 AU0452303-A03-2s1 AU0452303-A03-2s1 AU0939304-1s1A03	AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU104803 chrX AU1211303 chrX AU1631303 chrX AU0895303 chrX AU065404 chrX AU065404 chrX AU065204 chrX AU1947303 chrX AU1953303 chrX SSC00296 chrX SSC00296 chrX SSC00592 chrX AU1988303 chrX AU1982303 chrX AU1975302 chrX AU1898303 chrX AU1875302 chrX AU1875302 chrX AU1452303 chrX AU0452303 chrX	$\begin{array}{c} 111,970,302\\ 111,970,302\\ 112,047,857\\ 113,234,591\\ 113,234,686\\ 114,330,335\\ 114,330,325\\ 114,331,010\\ 114,331,010\\ 114,331,010\\ 114,331,095\\ 114,331,095\\ 114,331,095\\ 114,331,095\\ 114,331,235\\ 114,331,350\\ 114,331,350\\ 114,331,375\\ 114,331,345\\ 114,331,455\\ 114,331,460\\ 114,331,805\\ 114,332,135\\ \end{array}$	$\begin{array}{c} 111,971,664\\ 111,971,424\\ 112,052,442\\ 113,241,577\\ 113,241,182\\ 114,333,305\\ 114,333,305\\ 114,333,205\\ 114,333,350\\ 114,350\\ 114,350\\ 114,350\\ 114,350\\ 114,350\\ 114,350\\ 114,350\\ 114,350\\ 114,350\\ 114,350\\$	1,362 1,122 4,585 6,986 6,496 2,970 2,625 2,255 2,215 2,340 2,210 2,130 2,170 2,045 2,070 1,915 1,765 1,780 1,430 1,285 1,215	28 24 68 101 94 56 50 45 44 47 44 42 43 41 41 38 35 35 28 25 24	$\begin{array}{c} 20.6\\ 21.4\\ 14.8\\ 14.5\\ 14.5\\ 19.0\\ 20.0\\ 19.9\\ 20.1\\ 19.9\\ 20.1\\ 19.9\\ 20.1\\ 19.9\\ 20.0\\ 19.8\\ 19.7\\ 19.8\\ 19.8\\ 19.8\\ 19.8\\ 19.7\\ 19.6\\ 19.5\\ 19.8\\ 19.8\\ 19.5\\ 19.8\\ 19.5\\ 19.8\\ 19.8\\ 19.5\\ 19.8\\ 19.8\\ 19.5\\ 19.8\\ 19.8\\ 19.5\\ 19.8\\ 19.8\\ 19.5\\ 19.8\\ 19.8\\ 19.5\\ 19.8\\ 19.8\\ 19.5\\ 19.8\\ 19.8\\ 19.8\\ 19.5\\ 19.8\\ 19.8\\ 19.8\\ 19.5\\ 19.8\\ 19.8\\ 19.8\\ 19.8\\ 19.5\\ 19.8\\ 19.8\\ 19.8\\ 19.5\\ 19.8\\ 19.8\\ 19.8\\ 19.8\\ 19.5\\ 19.8\\$	0.39 0.50 -0.86 -0.40 0.35 0.45 0.39 0.52 0.54 0.44 0.59 0.43 0.57 0.60 0.62 0.51 0.59 0.42 0.70 0.45	62.6 63.8 36.5 38.4 38.1 65.2 65.8 65.0 64.9 65.0 65.2 65.1 65.2 65.1 65.1 65.1 65.4 65.2 65.2 65.4 65.2
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AU021203-1s1A03AU021203chrX118,940,776118,948,4727,6968110.50.5941.9AU1073302-A03-2s1AU1073302chrX118,941,966118,948,3326,3667011.00.5142.3AU1378304-2s1A03AU1378304chrX119,486,893119,487,273380923.70.5862.4AU074704chrX119,578,099119,579,5721,4732919.70.4959.5	AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1 AU1211303-1s2A03 AU1631303-1s1A03 AU018003-A03-2s2 AU0895303-1s2A03 AU1069302-A03-2s1 AU065404-A03-2s1 AU065404-A03-2s1 AU0652304-A03-2s1 SSC00296-A03-2s1 SSC00296-A03-2s1 SSC00592-A03-3s1 AU1898303-1s1A03 AU0920301-A03-2s1 AU1875302-1s1A03 AU0452303-A03-2s1 AU0939304-1s1A03 AU1159302-2s1A03 SSC00426-A03-2s1 AU1159302-2s1A03 AU1159302-2s1A03 AU1159302-2s1A03 AU1159302-2s1A03 AU1159302-2s1A03 AU1159302-2s1A03 AU1159302-2s1A03 AU1159302-2s1A03 AU1159302-2s1A03 AU1159302-2s1A03 AU1069302-A03-2s1 AU0852304-A03-2s1 AU0852304-A03-2s1 AU085303-1s2A03	AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU1344302 chrX AU1631303 chrX AU1631303 chrX AU0895303 chrX AU065404 chrX AU065404 chrX AU065404 chrX AU065404 chrX AU1947303 chrX AU1947303 chrX SSC00296 chrX SSC00296 chrX SSC00592 chrX AU1993303 chrX AU195303 chrX AU195303 chrX AU195303 chrX AU159303 chrX AU159303 chrX SSC00426 chrX AU159303 chrX AU159303 chrX AU159303 chrX AU159303 chrX AU159303 chrX AU159303 chrX AU169302 chrX AU169302 chrX AU0852304 chrX AU0852304 chrX	$\begin{array}{c} 111,970,302\\ 111,970,302\\ 112,047,857\\ 113,234,591\\ 113,234,686\\ 114,330,335\\ 114,330,725\\ 114,331,010\\ 114,331,010\\ 114,331,010\\ 114,331,095\\ 114,331,095\\ 114,331,095\\ 114,331,095\\ 114,331,095\\ 114,331,095\\ 114,331,350\\ 114,331,350\\ 114,331,350\\ 114,331,375\\ 114,331,375\\ 114,331,375\\ 114,331,375\\ 114,331,375\\ 114,331,445\\ 114,331,445\\ 114,331,405\\ 114,331,405\\ 114,331,405\\ 114,331,405\\ 114,331,405\\ 114,331,405\\ 114,331,405\\ 114,331,405\\ 114,331,405\\ 114,331,405\\ 114,331,405\\ 114,332,135\\ 114,448,415\\ 114,448,415\\ 114,448,415\\ 114,448,415\\ 115,635,001\\ 115,632,448\\ 116,588,255\\ 117,133,965\\ 117,991,249\\ \end{array}$	111,971,664 111,971,424 112,052,442 113,241,577 113,241,182 114,333,305 114,333,350 114,333,265 114,333,265 114,333,265 114,333,265 114,333,265 114,333,265 114,333,140 114,333,265 114,333,140 114,333,265 114,333,200 114,333,200 114,333,200 114,333,090 114,333,090 114,333,350 114,450,696 114,450,696 114,450,696 114,450,696 115,639,653 115,931,741 116,590,742 117,135,095 117,994,889	1,362 1,122 4,585 6,986 6,496 2,970 2,625 2,255 2,215 2,340 2,210 2,130 2,170 2,045 2,070 1,915 1,765 1,780 1,285 1,215 2,281 2,281 2,281 1,916 4,652 108,293 2,487 1,130	28 24 68 101 94 56 50 45 44 47 44 47 44 47 44 42 43 41 41 38 35 35 28 25 24 28 28 28 28 26 81 1603 44 42 45	20.6 21.4 14.8 14.5 18.9 19.0 20.0 19.9 20.1 19.9 20.1 19.9 20.1 19.9 19.7 19.8 20.0 19.8 19.8 19.8 19.8 19.5 19.8 19.5 19.8 12.3 12.3 12.3 13.6 17.4 14.8 17.7 21.2 17.9	0.39 0.50 -0.84 -0.86 -0.40 0.35 0.45 0.39 0.52 0.54 0.44 0.59 0.43 0.57 0.60 0.62 0.51 0.59 0.42 0.70 0.45 -0.69 0.45 -0.60 0.38 -1.64 0.47 0.31	62.6 63.8 36.5 38.4 38.1 65.2 65.0 64.9 65.0 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.3 33.7 33.4 30.6 34.2 36.6 65.0 63.8
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AU1378304-2s1A03AU1378304 chrX119,486,893119,487,273380923.70.5862.4AU074704chrX119,578,099119,579,5721,4732919.70.4959.5	AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1 AU1211303-1s2A03 AU1631303-1s1A03 AU018003-A03-2s2 AU0895303-1s2A03 AU1069302-A03-2s1 AU065404-A03-2s1 AU065404-A03-2s1 AU0852304-A03-2s1 AU1947303-A03-1s1 SSC00296-A03-2s1 SSC00296-A03-2s1 AU1875302-1s1A03 AU0452303-A03-2s1 AU0939304-1s1A03 AU1159302-2s1A03 SSC00426-A03-2s1 AU0159302-2s1A03 AU1159302-2s1A03 AU1159302-2s1A03 AU1159302-2s1A03 AU1159302-2s1A03 AU1159302-2s1A03 AU1159302-2s1A03 AU1159302-2s1A03 AU1159302-2s1A03 AU1159302-2s1A03 AU1169302-A03-2s1 AU0852304-A03-2s1 AU0895303-1s2A03 AU028903-A03-2s1 AU028903-A03-2s1 AU028903-A03-2s1	AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU1344302 chrX AU1211303 chrX AU1631303 chrX AU169302 chrX AU065404 chrX AU065404 chrX AU065404 chrX AU065204 chrX AU1947303 chrX AU1953303 chrX SSC00296 chrX SSC00296 chrX SSC00296 chrX SSC00296 chrX AU1898303 chrX AU1898303 chrX AU1875302 chrX AU092301 chrX AU092301 chrX AU0939304 chrX AU0939304 chrX AU159303 chrX AU1159303 chrX AU1159303 chrX AU1159303 chrX AU1159303 chrX AU1159303 chrX AU1159303 chrX AU1159303 chrX AU1159303 chrX AU0852304 chrX AU0852304 chrX AU0852304 chrX AU0852304 chrX AU085303 chrX AU085303 chrX AU028903 chrX AU028903 chrX	111,970,302 111,970,302 112,047,857 113,234,591 113,234,686 114,330,335 114,330,725 114,331,010 114,331,010 114,331,005 114,331,095 114,331,095 114,331,095 114,331,095 114,331,095 114,331,375 114,331,350 114,331,375 114,331,350 114,331,375 114,331,445 114,332,135 114,432,135 114,448,415 114,448,415 114,448,415 114,448,415 114,448,415 114,448,415 114,448,415 114,448,415 114,448,415 114,448,415 114,448,415 114,448,415 114,448,415 114,448,415 114,448,415 114,582,55 117,133,965 117,991,249 118,253,082 118,253,848	111,971,664 111,971,424 112,052,442 113,241,577 113,241,182 114,333,305 114,333,305 114,333,265 114,333,265 114,333,205 114,333,205 114,333,205 114,333,205 114,333,205 114,333,400 114,333,205 114,333,140 114,333,205 114,333,140 114,333,205 114,333,900 114,333,900 114,333,900 114,450,696 115,639,653 115,931,741 116,590,742 117,135,095 117,994,889 118,255,219 118,255,114	1,362 1,122 4,585 6,986 6,496 2,970 2,625 2,255 2,215 2,340 2,130 2,170 2,045 2,070 1,915 1,765 1,780 1,430 1,430 1,430 1,285 1,215 2,281 2,281 1,916 4,652 108,293 2,487 1,130	28 24 68 101 94 56 50 45 44 47 44 47 44 42 43 41 41 38 35 35 28 25 24 28 28 28 28 28 28 26 81 1603 44 24 65 527	$\begin{array}{c} 20.6\\ 21.4\\ 14.8\\ 14.5\\ 14.5\\ 19.0\\ 20.0\\ 19.9\\ 20.1\\ 19.9\\ 20.1\\ 19.9\\ 20.1\\ 19.9\\ 20.1\\ 19.9\\ 19.7\\ 19.8\\ 19.7\\ 19.8\\ 19.8\\ 19.8\\ 19.7\\ 19.8\\ 19.8\\ 19.8\\ 19.7\\ 19.6\\ 19.5\\ 19.8\\ 19.7\\ 19.6\\ 19.5\\ 19.8\\ 12.3\\ 12.3\\ 13.6\\ 17.4\\ 14.8\\ 17.7\\ 21.2\\ 17.9\\ 21.1\\ 20.8\\ \end{array}$	0.39 0.50 -0.84 -0.86 -0.40 0.35 0.45 0.52 0.54 0.44 0.59 0.43 0.57 0.60 0.62 0.51 0.59 0.42 0.70 0.45 -0.69 0.45 -0.96 0.38 -1.64 0.47 0.31 0.41 0.51	62.6 63.8 36.5 38.4 38.1 65.2 65.0 65.2 65.1 65.2 65.1 65.2 65.1 65.4 65.5 33.7 33.4 30.6 34.2 36.6 38.7 33.4 30.6 34.2 36.6 38.9 61.6 68.8
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AU1001202-1s1A03 AU1001202 chr 119,892,291 119,893,176 885 15 16.9 -0.97 59.9	AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1 AU1631303-1s1A03 AU018003-A03-2s2 AU0895303-1s2A03 AU1069302-A03-2s1 AU065404-A03-2s1 AU065404-A03-2s1 AU0652304-A03-2s1 AU197303-A03-1s1 SSC00296-A03-2s1 SSC00296-A03-2s1 SSC00296-A03-2s1 AU1898303-1s1A03 AU0920301-A03-2s1 AU1898303-1s1A03 AU0452303-A03-2s1 AU0939304-1s1A03 AU1159302-2s1A03 AU1159302-2s1A03 AU1069302-A03-2s1 AU0852304-A03-2s1 AU0852304-A03-2s1 AU0852304-A03-2s1 AU085303-1s2A03 AU028903-A03-2s1 AU0895303-1s2A03 AU028903-A03-2s1 AU04803-A03-2s1 AU0895303-1s2A03 AU021203-1s1A03 AU021203-1s1A03 AU021203-1s1A03 AU021203-1s1A03 AU021203-1s1A03 AU021203-1s1A03 AU021203-1s1A03 AU021203-1s1A03 AU021203-1s1A03 AU021203-1s1A03 AU021203-1s1A03	AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU1344302 chrX AU1631303 chrX AU1631303 chrX AU0895303 chrX AU065404 chrX AU065404 chrX AU065404 chrX AU065204 chrX AU1947303 chrX AU1947303 chrX SSC00296 chrX SSC00296 chrX SSC00296 chrX SSC00592 chrX AU1953003 chrX AU195303 chrX AU0452303 chrX AU0452303 chrX AU159303 chrX AU159303 chrX AU159303 chrX AU159303 chrX AU159303 chrX AU159303 chrX AU169302 chrX AU0852304 chrX AU169303 chrX AU0852304 chrX AU085303 chrX AU085303 chrX AU04895303 chrX AU04895303 chrX AU04895303 chrX AU04895303 chrX AU04895303 chrX AU014803 chrX AU021203 chrX AU021203 chrX AU021203 chrX AU021203 chrX AU014803 chrX AU021203 chrX AU021203 chrX AU021203 chrX	111,970,302 111,970,302 112,047,857 113,234,591 113,234,686 114,330,335 114,331,010 114,331,010 114,331,010 114,331,095 114,331,095 114,331,095 114,331,095 114,331,095 114,331,350 114,331,350 114,331,455 114,331,445 114,331,445 114,331,460 114,331,485 114,331,485 114,331,485 114,331,485 114,448,415 114,448,415 114,448,415 114,448,415 114,448,415 114,448,415 114,448,415 114,448,415 114,448,780 115,635,001 115,635,855 117,991,249 118,253,873 118,940,776 118,941,966 119,486,893	111,971,664 111,971,424 112,052,442 113,241,577 113,241,182 114,333,305 114,333,350 114,333,225 114,333,225 114,333,225 114,333,225 114,333,225 114,333,225 114,333,225 114,333,265 114,333,140 114,333,265 114,333,265 114,333,265 114,333,265 114,333,209 114,333,209 114,333,209 114,333,350 114,450,696 115,639,653 115,639,653 115,639,653 115,639,653 115,639,653 115,639,653 115,639,742 117,135,095 117,994,889 118,255,144 118,255,219 118,255,144 118,254,949 118,948,472 118,948,472	1,362 1,122 4,585 6,986 6,496 2,970 2,625 2,255 2,215 2,340 2,210 2,130 2,170 2,045 2,070 1,915 1,765 1,780 1,285 1,215 2,281 2,281 2,281 2,281 2,281 2,281 1,916 4,652 108,293 2,487 1,130 2,137 1,296 1,076 7,696 6,366 380	28 24 68 101 94 56 50 45 44 47 44 42 43 41 41 38 35 35 28 25 24 28 28 26 81 1603 44 24 65 45 27 22 81 70 9	$\begin{array}{c} 20.6\\ 21.4\\ 14.8\\ 14.5\\ 14.5\\ 19.0\\ 20.0\\ 19.9\\ 20.1\\ 19.9\\ 20.1\\ 19.9\\ 20.1\\ 19.9\\ 20.0\\ 19.8\\ 19.7\\ 19.7\\ 19.8\\ 20.0\\ 19.8\\ 19.7\\ 19.8\\ 10.5\\ 11.0\\ 23.7\\ 10.5\\ 11.0\\ 23.7\\ 10.5\\ 11.0\\ 23.7\\ 10.5\\$	0.39 0.50 -0.84 -0.86 -0.40 0.35 0.45 0.39 0.52 0.54 0.44 0.59 0.43 0.57 0.60 0.62 0.51 0.59 0.42 0.70 0.45 -0.69 0.45 -0.69 0.45 -0.96 0.38 -1.64 0.47 0.31 0.51 0.50 0.59 0.51 0.59 0.51 0.55 -0.59 0.51 0.55 -0.59 0.51 0.55 -0.59 0.51 0.55 -0.55 -0.56 0.55 -0.55 -0.56 0.55 -0.55	62.6 63.8 36.5 38.4 38.1 65.2 65.0 64.9 65.0 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.4 65.5 33.7 33.4 30.6 34.2 38.6 65.0 63.9 61.6 68.8 70.1 41.9 42.3 62.4
	AU0939304-1s1A03 AU1069302-A03-2s1 SSC00269-A03-2s1 AU1344302-1s1A03 AU004803-A03-3s1 AU1211303-1s2A03 AU1631303-1s1A03 AU018003-A03-2s2 AU0895303-1s2A03 AU1069302-A03-2s1 AU065404-A03-2s1 AU065404-A03-2s1 AU0652304-A03-2s1 AU1947303-A03-1s1 AU1953303-A03-1s1 SSC00296-A03-2s1 SSC00296-A03-2s1 AU1898303-1s1A03 AU0920301-A03-2s1 AU1875302-1s1A03 AU0159302-2s1A03 SSC00426-A03-2s1 AU0159302-2s1A03 SSC00426-A03-2s1 AU0159302-2s1A03 AU1159302-2s1A03 AU1069302-A03-2s1 AU0852304-A03-2s1 AU08803-A03-2s1 AU0895303-1s2A03 AU021203-1s1A03 AU021203-1s1A03 AU012303-1s2A03 AU021203-1s1A03 AU012303-1s2A03 AU0123-1s1A03 AU0123-1s1A03 AU1073302-A03-2s1 AU03803-A03-2s1 AU014803-A	AU0939304 chrX AU1069302 chrX SSC00269 chrX AU1344302 chrX AU1344302 chrX AU1631303 chrX AU1631303 chrX AU0895303 chrX AU065404 chrX AU065404 chrX AU065404 chrX AU065404 chrX AU1947303 chrX AU1947303 chrX SSC00296 chrX SSC00296 chrX SSC00296 chrX SSC00296 chrX AU1993303 chrX AU1923031 chrX AU0920301 chrX AU0920301 chrX AU0939304 chrX AU159303 chrX SSC00426 chrX AU159303 chrX AU159303 chrX AU159303 chrX AU169302 chrX AU0652304 chrX AU0852304 chrX AU0852304 chrX AU0895303 chrX AU04803 chrX AU04895303 chrX AU04895303 chrX AU04895303 chrX AU014803 chrX	111,970,302 111,970,302 112,047,857 113,234,591 113,234,686 114,330,335 114,330,725 114,331,010 114,331,010 114,331,095 114,331,095 114,331,095 114,331,095 114,331,095 114,331,350 114,331,350 114,331,350 114,331,355 114,331,455 114,331,445 114,448,415 114,448,415 114,448,415 114,448,415 114,448,415 114,448,415 114,448,415 114,448,415 114,448,415 114,448,415 114,448,415 115,635,001 115,635,001 115,635,001 115,633,488 116,588,255 117,133,965 117,991,249 118,253,888 118,253,873 118,941,966 119,486,893 119,578,099	111,971,664 111,971,424 112,052,442 113,241,577 113,241,182 114,333,305 114,333,350 114,333,205 114,333,090 114,333,090 114,333,090 114,450,696 115,639,653 115,931,741 116,590,742 117,135,095 117,994,889 118,255,219 118,2	1,362 1,122 4,585 6,986 6,496 2,970 2,625 2,255 2,215 2,340 2,210 2,130 2,170 2,045 2,070 1,915 1,765 1,780 1,285 1,215 2,281 2,281 2,281 1,916 4,652 108,293 2,487 1,130 2,137 1,296 1,076 7,696 6,366 380 1,473	28 24 68 101 94 56 50 45 44 47 44 42 43 41 41 38 35 35 28 25 24 28 28 28 28 26 81 1603 44 24 65 45 45 27 22 81 70 9 9 29	20.6 21.4 14.8 14.5 18.9 19.0 20.0 19.9 20.1 19.9 20.1 19.9 20.1 19.9 19.7 19.8 20.0 19.8 19.8 19.8 19.8 19.5 19.8 19.5 19.8 19.5 19.8 12.3 12.3 12.3 13.6 17.4 14.8 17.7 21.2 17.9 21.1 20.8 20.4 10.5 11.0 23.7 19.7	0.39 0.50 -0.84 -0.86 -0.40 0.35 0.45 0.39 0.52 0.54 0.44 0.59 0.43 0.57 0.60 0.62 0.51 0.59 0.42 0.70 0.45 -0.69 0.45 -0.69 0.45 -0.96 0.38 -1.64 0.47 0.31 0.51 0.59 0.55 -0.59 0.54 0.45 -0.69 0.45 -0.69 0.45 -0.96 0.38 -1.64 0.41 0.51 0.55 -0.50 0.55 -0.55 -0.56 0.38 -1.64 0.41 0.51 0.55 -0.55	62.6 63.8 36.5 38.4 38.1 65.2 65.0 64.9 65.0 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.1 65.2 65.3 33.7 33.4 30.6 34.2 36.6 65.0 63.9 61.6 68.8 70.7 42.3 62.4 59.5

AU1378304-2s1A03	AU1378304 chrX	120,416,082	120,416,943	861	8	9.3	-1.09	39.6
AU083504-A03-3s1	AU083504 chrX	122,143,675	122,144,235	560	11	19.6	-0.77	41.1
AU0983302-1s1A03	AU0983302 chrX	122,143,675	122,144,235	560	11	19.6	-1.47	41.1
AU1875302-1s1A03	AU1875302 chrX	122,778,683	122,780,424	1,741	19	10.9	-0.73	45.8
SSC00129-3s1A03	SSC00129 chrX	122,779,743	122,780,189	446	5	11.2	-1.65	44.1
SSC00346-A03-2s1	SSC00346 chrX	122,779,768	122,780,279	511	6	11.7	-1.20	43.4
AU0983302-1s1A03	AU0983302 chrX	122,815,537	122,819,376	3,839	59	15.4	0.72	44.9
AU083504-A03-3s1	AU083504 chrX	122,920,791	122,923,535	2,744	52	19.0	0.34	59.2
AU032701-A03-3s1	AU032701 chrX	124,787,664	124,788,414	750	16	21.3	-1.14	46.5
AU0895303-1s2A03	AU0895303 chrX	125,126,235	125,128,490	2,255	44	19.5	0.37	64.8
AU028903-A03-2s1 AU1953303-A03-1s1	AU028903 chrX	125,126,325 125,126,380	125,128,380 125,128,380	2,055 2,000	40 39	19.5 19.5	0.41 0.47	65.8 66.1
AU0895303-1s2A03	AU0895303 chrX	125,513,144	125,514,709	1,565	32	20.4	0.47	67.0
SSC00093-A03-1s2	SSC00093 chrX	125,514,204	125,515,019	815	18	22.1	-0.72	62.9
SSC00180-A03-2s1	SSC00180 chrX	125,687,154	125,687,444	290	7	24.1	-0.88	28.8
SSC00549-A03-1s1	SSC00549 chrX	126,158,051	126,158,891	840	19	22.6	-1.22	41.1
AU1334303-1s1A03	AU1334303 chrX	126,425,325	126,430,262	4,937	50	10.1	0.35	31.9
SSC00468-A03-2s1	SSC00468 chrX	128,327,945	128,329,860	1,915	25	13.1	-1.11	39.6
AU058103-A03-2s1	AU058103 chrX	128,328,110	128,329,810	1,700	21	12.4	-0.65	40.5
AU065404-A03-2s1	AU065404 chrX	128,328,110	128,329,710	1,600	20	12.5	-0.90	41.8
AU083504-A03-3s1	AU083504 chrX	128,328,110	128,329,860	1,750	22	12.6	-0.57	40.2
AU0920301-A03-2s1		128,328,110	128,329,625	1,515	18	11.9	-0.80	42.5
AU1054302-1s1A03		128,328,110	128,329,625	1,515	18	11.9	-0.99	42.5
AU1069302-A03-2s1 AU1327305-1s2A03		128,328,110	128,329,710	1,600 1,515	20 18	12.5 11.9	-0.91 -0.53	41.8 42.5
	AU1327305 CHIX AU1338304 chrX	128,328,110 128,328,110	128,329,625 128,329,590	1,480	17	11.9	-0.55	42.5
SSC00331-A03-2s1	SSC00331 chrX	128,328,110	128,329,710	1,600	20	12.5	-0.76	41.2
SSC00391-A03-3s1	SSC00391 chrX	128,328,110	128,329,675	1,565	19	12.5	-1.05	41.5
SSC00460-A03-1s1	SSC00460 chrX	128,328,110	128,329,860	1,750	22	12.6	-0.80	39.7
SSC00549-A03-1s1	SSC00549 chrX	128,328,110	128,329,860	1,750	22	12.6	-1.27	39.7
SSC00035-3s1A03	SSC00035 chrX	128,328,160	128,329,625	1,465	17	11.6	-0.98	41.9
AU062203-A03-2s1	AU062203 chrX	128,328,360	128,329,625	1,265	15	11.9	-0.88	42.3
AU1211303-1s2A03	AU1211303 chrX	128,328,360	128,329,625	1,265	15	11.9	-0.91	42.3
SSC00518-A03-1s1	SSC00518 chrX	128,328,430	128,329,625	1,195	13	10.9	-1.54	42.1
AU0895303-1s2A03	AU0895303 chrX	128,483,910	128,485,657	1,747	35	20.0	0.33	62.6
AU1073302-A03-2s1	AU1073302 chrX	128,609,906	128,610,211	305	7	23.0	1.10	57.0
AU065404-A03-2s1	AU065404 chrX	128,893,016	128,894,561	1,545	29	18.8	0.57	71.8
AU083504-A03-3s1	AU083504 chrX	128,893,016	128,894,009	993	21	21.1	0.57	66.5
AU083504-A03-3s1 AU1056304-1s1A03	AU083504 chrX AU1056304 chrX	128,893,016 128,893,104	128,894,009 128,894,009	993 905	21 20	21.1 22.1	0.57 0.52	66.5 67.7
AU083504-A03-3s1 AU1056304-1s1A03 AU1143303-1s1A03	AU083504 chrX AU1056304 chrX AU1143303 chrX	128,893,016 128,893,104 128,893,104	128,894,009 128,894,009 128,894,105	993 905 1,001	21 20 22	21.1 22.1 22.0	0.57 0.52 0.67	66.5 67.7 68.8
AU083504-A03-3s1 AU1056304-1s1A03 AU1143303-1s1A03 AU1378304-2s1A03	AU083504 chrX AU1056304 chrX AU1143303 chrX AU1378304 chrX	128,893,016 128,893,104 128,893,104 128,893,104	128,894,009 128,894,009 128,894,105 128,895,462	993 905 1,001 2,358	21 20 22 41	21.1 22.1 22.0 17.4	0.57 0.52 0.67 0.46	66.5 67.7 68.8 67.0
AU083504-A03-3s1 AU1056304-1s1A03 AU1143303-1s1A03 AU1378304-2s1A03 AU1159302-2s1A03	AU083504 chrX AU1056304 chrX AU1143303 chrX AU1378304 chrX AU1159303 chrX	128,893,016 128,893,104 128,893,104 128,893,104 128,893,104 128,893,169	128,894,009 128,894,009 128,894,105 128,895,462 128,894,105	993 905 1,001 2,358 936	21 20 22 41 21	21.1 22.1 22.0 17.4 22.4	0.57 0.52 0.67 0.46 0.52	66.5 67.7 68.8 67.0 69.9
AU083504-A03-3s1 AU1056304-1s1A03 AU1143303-1s1A03 AU1378304-2s1A03 AU159302-2s1A03 AU056803-A03-2s1	AU083504 chrX AU1056304 chrX AU1143303 chrX AU1378304 chrX AU1159303 chrX AU056803 chrX	128,893,016 128,893,104 128,893,104 128,893,104 128,893,169 128,941,017	128,894,009 128,894,009 128,894,105 128,895,462 128,894,105 128,946,320	993 905 1,001 2,358 936 5,303	21 20 22 41 21 93	21.1 22.1 22.0 17.4 22.4 17.5	0.57 0.52 0.67 0.46 0.52 0.40	66.5 67.7 68.8 67.0 69.9 67.4
AU083504-A03-3s1 AU1056304-1s1A03 AU1143303-1s1A03 AU1378304-2s1A03 AU159302-2s1A03 AU056803-A03-2s1 AU014803-A03-2s1	AU083504 chrX AU1056304 chrX AU1143303 chrX AU1378304 chrX AU1159303 chrX	128,893,016 128,893,104 128,893,104 128,893,104 128,893,104 128,993,169 128,941,017 128,941,142	128,894,009 128,894,009 128,894,105 128,895,462 128,894,105 128,946,320 128,946,290	993 905 1,001 2,358 936 5,303 5,148	21 20 22 41 21 93 89	21.1 22.1 22.0 17.4 22.4 17.5 17.3	0.57 0.52 0.67 0.46 0.52 0.40 0.40	66.5 67.7 68.8 67.0 69.9
AU083504-A03-3s1 AU1056304-1s1A03 AU1143303-1s1A03 AU1378304-2s1A03 AU159302-2s1A03 AU056803-A03-2s1	AU083504 chrX AU1056304 chrX AU1143303 chrX AU1378304 chrX AU1159303 chrX AU056803 chrX AU056803 chrX AU014803 chrX	128,893,016 128,893,104 128,893,104 128,893,104 128,893,169 128,941,017	128,894,009 128,894,009 128,894,105 128,895,462 128,894,105 128,946,320	993 905 1,001 2,358 936 5,303	21 20 22 41 21 93	21.1 22.1 22.0 17.4 22.4 17.5	0.57 0.52 0.67 0.46 0.52 0.40	66.5 67.7 68.8 67.0 69.9 67.4 67.8
AU083504-A03-3s1 AU1056304-1s1A03 AU114303-1s1A03 AU1378304-2s1A03 AU159302-2s1A03 AU056803-A03-2s1 AU014803-A03-2s1 AU080803-A03-2s1	AU083504 chrX AU1056304 chrX AU1143303 chrX AU1159303 chrX AU1596803 chrX AU056803 chrX AU014803 chrX AU01803 chrX	128,893,016 128,893,104 128,893,104 128,893,104 128,893,104 128,993,169 128,941,017 128,941,142 128,942,154	128,894,009 128,894,009 128,894,105 128,895,462 128,894,105 128,946,320 128,946,290 128,945,257	993 905 1,001 2,358 936 5,303 5,148 3,103	21 20 22 41 21 93 89 59	21.1 22.1 22.0 17.4 22.4 17.5 17.3 19.0	0.57 0.52 0.67 0.46 0.52 0.40 0.40 0.40 0.39	66.5 67.7 68.8 67.0 69.9 67.4 67.8 65.1
AU083504-A03-3s1 AU1056304-1s1A03 AU114303-1s1A03 AU1378304-2s1A03 AU159302-2s1A03 AU056803-A03-2s1 AU014803-A03-2s1 AU018304-A03-2s1	AU083504 chrX AU1056304 chrX AU1143303 chrX AU1178304 chrX AU159303 chrX AU056803 chrX AU014803 chrX AU080803 chrX AU018304 chrX	128,893,016 128,893,104 128,893,104 128,893,104 128,893,169 128,941,017 128,941,142 128,942,154 128,943,153	128,894,009 128,894,009 128,894,105 128,895,462 128,894,105 128,946,220 128,946,220 128,945,257 128,946,320	993 905 1,001 2,358 936 5,303 5,148 3,103 3,167	21 20 22 41 21 93 89 59 58	21.1 22.1 22.0 17.4 22.4 17.5 17.3 19.0 18.3	0.57 0.52 0.67 0.46 0.52 0.40 0.40 0.39 0.46	66.5 67.7 68.8 67.0 69.9 67.4 67.8 65.1 67.1
AU083504-A03-3s1 AU1056304-1s1A03 AU1143303-1s1A03 AU1378304-2s1A03 AU159302-2s1A03 AU056803-A03-2s1 AU014803-A03-2s1 AU088080-A03-2s1 AU018304-A03-2s1 AU0976303-1s1A03	AU083504 chrX AU1056304 chrX AU1143303 chrX AU1378304 chrX AU159303 chrX AU056803 chrX AU04803 chrX AU04803 chrX AU018304 chrX AU0976303 chrX	128,893,016 128,893,104 128,893,104 128,893,104 128,893,169 128,941,017 128,941,142 128,942,154 128,943,153 128,945,088	128,894,009 128,894,009 128,894,105 128,895,462 128,946,105 128,946,290 128,946,290 128,945,257 128,946,320 128,946,380	993 905 1,001 2,358 936 5,303 5,148 3,103 3,167 1,292	21 20 22 41 21 93 89 59 58 22	21.1 22.1 22.0 17.4 22.4 17.5 17.3 19.0 18.3 17.0	0.57 0.52 0.67 0.46 0.52 0.40 0.40 0.39 0.46 -0.49	66.5 67.7 68.8 67.0 69.9 67.4 67.8 65.1 67.1 72.7
AU083504-A03-3s1 AU1056304-1s1A03 AU1143303-1s1A03 AU1378304-2s1A03 AU159302-2s1A03 AU056803-A03-2s1 AU014803-A03-2s1 AU08803-A03-2s1 AU018304-A03-2s1 AU0976303-1s1A03 SSC00391-A03-3s1	AU083504 chrX AU1056304 chrX AU1143303 chrX AU1378304 chrX AU159303 chrX AU056803 chrX AU04803 chrX AU018003 chrX AU018304 chrX AU018304 chrX AU018304 chrX AU018304 chrX AU018304 chrX AU0976303 chrX SSC00391 chrX	128,893,016 128,893,104 128,893,104 128,893,104 128,893,104 128,941,017 128,941,142 128,942,154 128,942,154 128,945,088 128,963,185	128,894,009 128,894,009 128,894,105 128,895,462 128,946,320 128,946,320 128,945,257 128,946,320 128,946,320 128,946,380 128,964,555	993 905 1,001 2,358 936 5,303 5,148 3,103 3,167 1,292 1,370	21 20 22 41 21 93 89 59 58 22 30	21.1 22.1 22.0 17.4 22.4 17.5 17.3 19.0 18.3 17.0 21.9	0.57 0.52 0.67 0.46 0.52 0.40 0.40 0.40 0.39 0.46 -0.49 -0.41	66.5 67.7 68.8 67.0 69.9 67.4 67.8 65.1 67.1 72.7 52.8
AU083504-A03-3s1 AU1056304-1s1A03 AU1143303-1s1A03 AU1378304-2s1A03 AU159302-2s1A03 AU056803-A03-2s1 AU014803-A03-2s1 AU018304-A03-2s1 AU018304-A03-2s1 AU0976303-1s1A03 SSC00391-A03-3s1 AU056003-A03-2s1 AU014803-A03-2s1 SSC00093-A03-1s2	AU083504 chrX AU1056304 chrX AU1143303 chrX AU1378304 chrX AU1159303 chrX AU056803 chrX AU056803 chrX AU014803 chrX AU018304 chrX AU0976303 chrX AU0976303 chrX AU0976303 chrX AU056003 chrX AU056003 chrX AU056003 chrX AU014803 chrX AU056003 chrX AU014803 chrX AU014803 chrX AU014803 chrX	128,893,016 128,893,104 128,893,104 128,893,104 128,893,104 128,941,017 128,941,017 128,942,154 128,943,153 128,943,153 128,945,088 128,963,185 128,964,095 129,070,418 129,491,300	128,894,009 128,894,009 128,894,105 128,895,462 128,946,320 128,946,320 128,946,290 128,946,290 128,946,320 128,946,380 128,946,380 128,964,555 128,964,615 129,073,992 129,493,100	993 905 1,001 2,358 936 5,303 5,148 3,103 3,167 1,292 1,370 520 3,574 1,800	21 20 22 41 21 93 89 59 58 22 30 12 65 34	21.1 22.1 22.0 17.4 22.4 17.5 17.3 19.0 18.3 17.0 21.9 23.1 18.2 18.9	0.57 0.52 0.67 0.46 0.52 0.40 0.40 0.40 0.39 0.46 -0.49 -0.41 0.98 0.40 0.60	66.5 67.7 68.8 67.0 69.9 67.4 67.8 65.1 67.1 72.7 52.8 55.6 65.2 62.4
AU083504-A03-3s1 AU1056304-1s1A03 AU114303-1s1A03 AU1378304-2s1A03 AU159302-2s1A03 AU056803-A03-2s1 AU014803-A03-2s1 AU018304-A03-2s1 AU0976303-1s1A03 SSC00391-A03-2s1 AU056003-A03-2s1 AU014803-A03-2s1 SSC00093-A03-1s2 SSC00035-3s1A03	AU083504 chrX AU1056304 chrX AU1143303 chrX AU1178304 chrX AU159303 chrX AU056803 chrX AU014803 chrX AU014803 chrX AU018304 chrX AU0976303 chrX AU0976303 chrX AU0976303 chrX AU0976303 chrX SSC00391 chrX AU014803 chrX SSC00093 chrX SSC00035 chrX	128,893,016 128,893,104 128,893,104 128,893,104 128,893,104 128,941,017 128,941,017 128,941,142 128,942,154 128,943,153 128,945,088 128,963,185 128,964,095 129,070,418 129,491,300 129,495,427	128,894,009 128,894,009 128,894,105 128,895,462 128,894,105 128,946,320 128,946,290 128,945,257 128,946,320 128,946,320 128,946,320 128,964,555 128,964,615 129,073,992 129,493,100 129,496,564	993 905 1,001 2,358 936 5,303 5,148 3,103 3,167 1,292 1,370 520 3,574 1,800 1,137	21 20 22 41 21 93 89 59 59 58 22 30 12 65 34 25	21.1 22.1 22.0 17.4 22.4 17.5 17.3 19.0 18.3 17.0 21.9 23.1 18.2 18.9 22.0	0.57 0.52 0.67 0.46 0.52 0.40 0.40 0.39 0.46 -0.49 -0.41 0.98 0.40 0.60 -1.05	66.5 67.7 68.8 67.0 69.9 67.4 67.8 65.1 67.1 72.7 52.8 55.6 55.2 62.4 49.4
AU083504-A03-3s1 AU1056304-1s1A03 AU114303-1s1A03 AU1378304-2s1A03 AU159302-2s1A03 AU056803-A03-2s1 AU014803-A03-2s1 AU018304-A03-2s1 AU0976303-1s1A03 SSC00391-A03-3s1 AU014803-A03-2s1 AU014803-A03-2s1 SSC00093-A03-1s2 SSC00035-3s1A03 SSC00518-A03-1s1	AU083504 chrX AU1056304 chrX AU1143303 chrX AU1143003 chrX AU1159303 chrX AU156803 chrX AU056803 chrX AU018304 chrX AU018304 chrX AU0976303 chrX AU0976303 chrX AU0976303 chrX AU056003 chrX AU056003 chrX SSC00391 chrX SSC0032 chrX SSC0035 chrX SSC0035 chrX	128,893,016 128,893,104 128,893,104 128,893,104 128,893,109 128,941,017 128,941,017 128,941,142 128,942,154 128,943,153 128,945,088 128,963,185 128,964,095 129,070,418 129,491,300 129,495,427 129,495,549	128,894,009 128,894,009 128,894,105 128,895,462 128,894,105 128,946,290 128,946,290 128,945,257 128,946,320 128,946,320 128,946,380 128,964,555 128,964,615 129,073,992 129,493,100 129,496,564 129,496,504	993 905 1,001 2,358 936 5,303 5,148 3,103 3,167 1,292 1,370 520 3,574 1,800 1,137 955	21 20 22 41 21 93 89 59 59 58 22 30 12 65 34 25 21	21.1 22.0 17.4 22.4 17.5 17.3 19.0 18.3 17.0 23.1 18.2 23.1 18.2 18.9 22.0 22.0	0.57 0.52 0.67 0.46 0.52 0.40 0.40 0.39 0.46 -0.49 -0.41 0.98 0.40 0.60 -1.05 -1.10	66.5 67.7 68.8 67.0 69.9 67.4 67.8 65.1 67.1 72.7 52.8 55.6 62.4 49.4
AU083504-A03-3s1 AU1056304-1s1A03 AU114303-1s1A03 AU1378304-2s1A03 AU159302-2s1A03 AU056803-A03-2s1 AU014803-A03-2s1 AU080803-A03-2s1 AU018304-A03-2s1 AU0976303-1s1A03 SSC00391-A03-3s1 AU056003-A03-2s1 SSC00093-A03-2s1 SSC00093-A03-1s2 SSC000518-A03-1s1 AU1327305-1s2A03	AU083504 chrX AU1056304 chrX AU1143303 chrX AU1178304 chrX AU1159303 chrX AU056803 chrX AU056803 chrX AU080803 chrX AU018304 chrX AU0976303 chrX AU0976303 chrX AU0976303 chrX AU0976303 chrX SSC00391 chrX AU014803 chrX SSC00035 chrX SSC00035 chrX SSC0035 chrX SSC0035 chrX SSC0035 chrX SSC0035 chrX SSC0035 chrX SSC00518 chrX	128,893,016 128,893,104 128,893,104 128,893,104 128,893,109 128,941,017 128,941,142 128,942,154 128,943,153 128,945,088 128,963,185 128,964,095 129,070,418 129,491,300 129,495,427 129,495,549 129,711,402	128,894,009 128,894,009 128,894,105 128,895,462 128,946,320 128,946,290 128,945,257 128,946,320 128,945,380 128,946,380 128,964,615 129,073,992 129,493,100 129,496,564 129,496,504 129,712,522	993 905 1,001 2,358 936 5,303 5,148 3,103 3,167 1,292 1,370 520 3,574 1,800 1,137 955 1,120	21 20 22 41 21 93 89 59 58 22 30 12 65 34 25 21 24	21.1 22.1 22.0 17.4 22.4 17.5 17.3 19.0 18.3 17.0 21.9 23.1 18.2 18.9 22.0 22.0 22.0 21.4	0.57 0.52 0.67 0.46 0.52 0.40 0.40 0.39 0.46 -0.49 -0.41 0.98 0.40 0.60 -1.05 -1.10 -0.40	66.5 67.7 68.8 67.0 69.9 67.4 67.8 65.1 67.1 72.7 52.8 55.6 65.2 49.4 49.4 43.8
AU083504-A03-3s1 AU1056304-1s1A03 AU114303-1s1A03 AU1378304-2s1A03 AU159302-2s1A03 AU056803-A03-2s1 AU014803-A03-2s1 AU088003-A03-2s1 AU08304-A03-2s1 AU0976303-1s1A03 SSC00391-A03-3s1 AU056003-A03-2s1 AU014803-A03-2s1 SSC00035-3s1A03 SSC00518-A03-1s1 AU1327305-1s2A03 SSC00048-A03-1s1	AU083504 chrX AU1056304 chrX AU1143303 chrX AU1178304 chrX AU1159303 chrX AU056803 chrX AU018003 chrX AU080803 chrX AU0976303 chrX AU0976303 chrX AU0976303 chrX AU056003 chrX AU0976303 chrX SSC00391 chrX SSC00035 chrX SSC00035 chrX SSC00518 chrX SSC00518 chrX SSC00518 chrX SSC00048 chrX	128,893,016 128,893,104 128,893,104 128,893,104 128,893,109 128,941,017 128,941,142 128,942,154 128,942,154 128,943,153 128,945,088 128,963,185 128,964,095 129,070,418 129,491,300 129,495,427 129,495,549 129,711,402 129,711,402	128,894,009 128,894,009 128,894,105 128,895,462 128,894,105 128,946,220 128,946,220 128,946,320 128,946,320 128,946,380 128,946,380 128,964,615 129,073,992 129,493,100 129,496,564 129,496,504 129,712,522 129,715,197	993 905 1,001 2,358 936 5,303 5,148 3,103 3,167 1,292 1,370 520 3,574 1,800 1,137 955 1,120 3,755	21 20 22 41 93 89 59 58 22 30 12 65 34 25 21 24 68	21.1 22.1 22.0 17.4 22.4 17.5 17.3 19.0 18.3 17.0 21.9 23.1 18.2 18.9 22.0 22.0 22.0 21.4 18.1	0.57 0.52 0.67 0.46 0.52 0.40 0.39 0.46 -0.49 -0.41 0.98 0.40 0.60 -1.05 -1.10 -0.40 0.50	66.5 67.7 68.8 67.0 69.9 67.4 67.8 65.1 67.8 65.1 67.8 65.1 67.4 65.1 67.4 62.4 49.4 43.8 41.3
AU083504-A03-3s1 AU1056304-1s1A03 AU1143303-1s1A03 AU1378304-2s1A03 AU159302-2s1A03 AU056803-A03-2s1 AU014803-A03-2s1 AU018304-A03-2s1 AU0976303-1s1A03 SSC00391-A03-3s1 AU014803-A03-2s1 AU014803-A03-2s1 SSC00093-A03-1s2 SSC00093-A03-1s2 SSC00035-3s1A03 SSC00518-A03-1s1 AU1327305-1s2A03 SSC0048-A03-1s1 SSC00366-A03-2s1	AU083504 chrX AU1056304 chrX AU1143303 chrX AU1178304 chrX AU159303 chrX AU159303 chrX AU056803 chrX AU080803 chrX AU018304 chrX AU0976303 chrX AU0976303 chrX AU056003 chrX AU014803 chrX SSC00931 chrX SSC00935 chrX SSC00035 chrX SSC00518 chrX AU1327305 chrX SSC00048 chrX	128,893,016 128,893,104 128,893,104 128,893,104 128,893,109 128,941,017 128,941,142 128,942,154 128,942,154 128,942,154 128,943,153 128,945,088 128,963,185 129,070,418 129,491,300 129,495,549 129,711,402 129,711,442	128,894,009 128,894,009 128,894,105 128,895,462 128,894,105 128,946,320 128,946,290 128,946,320 128,946,320 128,946,380 128,946,380 128,964,615 129,073,992 129,493,100 129,496,564 129,712,522 129,715,197 129,715,557	993 905 1,001 2,358 936 5,303 5,148 3,103 3,167 1,292 1,370 520 3,574 1,800 1,137 955 1,120 3,755 4,115	21 20 22 41 93 89 59 58 22 30 12 65 34 25 21 24 68 71	21.1 22.1 22.0 17.4 22.4 17.5 17.3 19.0 18.3 17.0 21.9 23.1 18.2 18.9 22.0 22.0 22.0 21.4 18.1 17.3	0.57 0.52 0.67 0.46 0.52 0.40 0.39 0.46 -0.49 -0.41 0.98 0.40 -0.40 0.60 -1.05 -1.10 -0.40 0.50 0.58	66.5 67.7 68.8 67.0 69.9 67.4 67.8 65.1 67.1 72.7 52.8 55.6 65.2 62.4 49.4 43.8 41.3 41.0
AU083504-A03-3s1 AU1056304-1s1A03 AU1143303-1s1A03 AU1378304-2s1A03 AU159302-2s1A03 AU056803-A03-2s1 AU014803-A03-2s1 AU018304-A03-2s1 AU018304-A03-2s1 AU0976303-1s1A03 SSC00391-A03-3s1 AU056003-A03-2s1 SSC00093-A03-1s2 SSC00093-A03-1s2 SSC00018-A03-1s1 SSC00048-A03-1s1 SSC000417-A03-1s1	AU083504 chrX AU1056304 chrX AU1143303 chrX AU1378304 chrX AU159303 chrX AU056803 chrX AU04803 chrX AU014803 chrX AU018304 chrX AU0976303 chrX AU0976303 chrX AU056003 chrX AU056003 chrX SSC00931 chrX SSC00933 chrX SSC00935 chrX SSC00518 chrX AU1327305 chrX SSC00448 chrX SSC00445 chrX	128,893,016 128,893,104 128,893,104 128,893,104 128,893,109 128,941,017 128,941,017 128,942,154 128,942,154 128,942,154 128,943,153 128,945,088 128,963,185 129,070,418 129,491,300 129,495,549 129,711,402 129,711,402 129,711,442 130,029,230	128,894,009 128,894,009 128,894,105 128,895,462 128,894,105 128,946,320 128,946,290 128,946,290 128,945,257 128,946,320 128,946,380 128,946,380 128,964,555 128,964,615 129,073,992 129,493,100 129,496,564 129,496,504 129,712,522 129,715,197 129,715,557 130,030,433	993 905 1,001 2,358 936 5,303 5,148 3,103 3,167 1,292 1,370 520 3,574 1,800 1,137 955 1,120 3,755 4,115 1,203	21 20 22 41 93 89 59 58 22 30 12 65 34 25 21 24 68 71 25	21.1 22.1 22.0 17.4 22.4 17.5 17.3 19.0 18.3 17.0 21.9 23.1 18.2 18.9 22.0 22.0 22.0 21.4 18.1 17.3 20.8	0.57 0.52 0.67 0.46 0.52 0.40 0.39 0.46 -0.49 -0.41 0.98 0.40 0.60 -1.05 -1.05 -1.10 -0.40 0.50 0.58 0.74	66.5 67.7 68.8 67.0 69.9 67.4 67.5 65.1 67.1 72.7 52.8 55.6 65.2 62.4 49.4 43.8 41.3 41.0 55.4
AU083504-A03-3s1 AU1056304-1s1A03 AU1143303-1s1A03 AU1378304-2s1A03 AU159302-2s1A03 AU056803-A03-2s1 AU014803-A03-2s1 AU018304-A03-2s1 AU018304-A03-2s1 AU0976303-1s1A03 SSC00391-A03-3s1 AU056003-A03-2s1 SSC00093-A03-1s2 SSC00035-3s1A03 SSC00518-A03-1s1 AU1327305-1s2A03 SSC00048-A03-1s1 SSC00417-A03-1s1 AU0939304-1s1A03	AU083504 chrX AU1056304 chrX AU1143303 chrX AU1378304 chrX AU159303 chrX AU056803 chrX AU056803 chrX AU014803 chrX AU018304 chrX AU0976303 chrX AU0976303 chrX AU0976303 chrX SSC00391 chrX SSC0093 chrX SSC0035 chrX SSC00518 chrX SSC00366 chrX SSC00417 chrX SSC00417 chrX	128,893,016 128,893,104 128,893,104 128,893,104 128,893,104 128,943,107 128,941,017 128,942,154 128,942,154 128,942,154 128,943,153 128,945,088 128,963,185 129,070,418 129,491,300 129,495,427 129,495,549 129,711,402 129,711,402 129,711,442 130,029,230 130,640,034	128,894,009 128,894,009 128,894,105 128,895,462 128,946,320 128,946,320 128,945,257 128,946,320 128,945,257 128,946,320 128,946,380 128,946,380 128,964,555 128,964,615 129,073,992 129,493,100 129,496,504 129,496,504 129,712,522 129,715,197 129,715,557 130,030,433 130,641,821	993 905 1,001 2,358 936 5,303 5,148 3,103 3,167 1,292 1,370 520 3,574 1,800 1,137 955 1,120 3,755 4,115 1,203 1,787	21 20 22 41 93 89 59 58 22 30 12 65 34 25 21 24 68 71 25 16	21.1 22.1 22.0 17.4 22.4 17.5 17.3 19.0 18.3 17.0 21.9 23.1 18.2 18.9 22.0 22.0 22.0 21.4 18.1 17.3 20.8 9.0	0.57 0.52 0.67 0.46 0.52 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.4	66.5 67.7 68.8 67.0 69.9 67.4 67.5 65.1 67.1 72.7 52.8 55.6 65.2 62.4 49.4 43.8 41.3 41.0 55.4 48.6
AU083504-A03-3s1 AU1056304-1s1A03 AU114303-1s1A03 AU1378304-2s1A03 AU159302-2s1A03 AU056803-A03-2s1 AU014803-A03-2s1 AU018304-A03-2s1 AU01803-A03-2s1 AU0976303-1s1A03 SSC00391-A03-2s1 AU056003-A03-2s1 SSC00035-3s1A03 SSC00035-3s1A03 SSC0035-3s1A03 SSC0035-1s2A03 SSC0048-A03-1s1 SSC0048-A03-1s1 SSC00417-A03-1s1 AU0939304-1s1A03 AU028903-A03-2s1	AU083504 chrX AU1056304 chrX AU1143303 chrX AU1178304 chrX AU1159303 chrX AU056803 chrX AU014803 chrX AU014803 chrX AU018304 chrX AU0976303 chrX AU0976303 chrX AU0976303 chrX SSC00391 chrX SSC00093 chrX SSC00035 chrX SSC00518 chrX SSC005518 chrX SSC00417 chrX AU0328903 chrX	128,893,016 128,893,104 128,893,104 128,893,104 128,893,104 128,941,017 128,941,017 128,941,142 128,942,154 128,943,153 128,943,153 128,963,185 128,964,095 129,070,418 129,491,300 129,495,549 129,711,442 129,711,442 129,711,442 130,029,230 130,640,034 131,178,818	128,894,009 128,894,009 128,894,009 128,894,105 128,894,105 128,946,320 128,946,320 128,946,320 128,946,320 128,946,320 128,946,320 128,946,355 128,964,615 129,073,992 129,493,100 129,496,564 129,712,522 129,715,197 129,715,557 130,030,433 130,641,821	993 905 1,001 2,358 936 5,303 5,148 3,103 3,167 1,292 1,370 520 3,574 1,800 1,137 955 1,120 3,755 4,115 1,203 1,787 1,162	21 20 22 41 93 89 59 58 22 30 12 65 34 25 21 24 68 71 25 16 22	21.1 22.1 22.0 17.4 22.4 17.5 17.3 19.0 18.3 17.0 21.9 23.1 18.2 18.9 22.0 22.0 21.4 18.1 17.3 20.8 9.0 18.9	0.57 0.52 0.67 0.46 0.52 0.40 0.40 0.39 0.46 -0.49 -0.41 0.98 0.40 0.60 -1.05 -1.10 -0.40 0.50 0.58 0.74 0.55 0.55	66.5 67.7 68.8 67.0 69.9 67.4 67.8 65.1 67.1 72.7 52.8 65.2 62.4 49.4 49.4 49.4 43.8 41.3 55.4 48.6 67.6
AU083504-A03-3s1 AU1056304-1s1A03 AU114303-1s1A03 AU1178304-2s1A03 AU159302-2s1A03 AU056803-A03-2s1 AU014803-A03-2s1 AU01803-A03-2s1 AU01803-A03-2s1 AU0976303-1s1A03 SSC00391-A03-3s1 AU014803-A03-2s1 SSC00035-A03-2s1 SSC00048-A03-1s1 SSC00417-A03-1s1 SSC00417-A03-1s1 AU028903-A03-2s1 AU014803-A03-2s1	AU083504 chrX AU1056304 chrX AU1143303 chrX AU1143003 chrX AU1159303 chrX AU056803 chrX AU056803 chrX AU018304 chrX AU018304 chrX AU0976303 chrX AU0976303 chrX AU0976303 chrX AU014803 chrX SSC00391 chrX SSC00303 chrX SSC0035 chrX SSC0035 chrX SSC0035 chrX SSC00416 chrX SSC00417 chrX SSC00417 chrX AU028903 chrX	128,893,016 128,893,104 128,893,104 128,893,104 128,893,104 128,993,109 128,941,017 128,941,017 128,941,017 128,941,017 128,942,154 128,943,153 128,945,088 128,963,185 129,495,088 129,491,300 129,495,427 129,491,300 129,495,549 129,711,442 129,711,442 130,029,230 130,640,034 131,178,818 131,178,818	128,894,009 128,894,009 128,894,105 128,895,462 128,894,105 128,946,290 128,946,290 128,945,257 128,946,320 128,946,320 128,946,380 128,964,555 128,964,615 129,073,992 129,493,100 129,496,564 129,712,522 129,715,197 129,715,557 130,030,433 130,641,821 131,179,980 131,180,176	993 905 1,001 2,358 936 5,303 5,148 3,103 3,167 1,292 1,370 520 3,574 1,800 1,137 955 1,120 3,755 4,115 1,203 1,787 1,162 1,288	21 20 22 41 93 89 59 58 22 30 12 65 34 25 21 24 68 71 25 16 22 24	21.1 22.0 17.4 22.4 17.5 17.3 19.0 18.3 17.0 23.1 18.2 18.9 22.0 22.0 22.0 22.0 21.4 18.1 17.3 20.8 9.0 18.9 18.6	0.57 0.52 0.67 0.46 0.52 0.40 0.40 0.39 0.46 -0.49 -0.41 0.98 0.40 0.60 -1.05 -1.10 -0.40 0.50 0.58 0.74 0.55 0.55 0.55	66.5 67.7 68.8 67.0 69.9 67.1 67.8 65.1 67.1 72.7 52.8 65.2 62.4 49.4 49.4 43.8 41.3 45.4 48.6 67.6 69.9
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AU083504-A03-3s1 AU1056304-1s1A03 AU1143303-1s1A03 AU1378304-2s1A03 AU159302-2s1A03 AU056803-A03-2s1 AU014803-A03-2s1 AU018003-A03-2s1 AU018003-A03-2s1 AU017403-A03-2s1 AU014803-A03-2s1 AU014803-A03-2s1 AU014803-A03-2s1 SSC0003-A03-1s2 SSC00035-3s1A03 SSC00048-A03-1s1 SSC00366-A03-2s1 SSC00417-A03-1s1 AU028903-A03-2s1 AU014803-A03-2s1 AU014803-A03-2s1 AU014803-A03-2s1 AU014803-A03-2s1 AU014803-A03-2s1 AU134302-1s1A03 SSC0012-3s1A03 SSC0012-3s1A03 SSC00366-A03-2s1 AU137305-1s2A03 SSC00366-A03-2s1 AU137305-1s2A03 SSC00366-A03-2s1 AU137304-2s1A03 AU028903-A03-2s1 AU137304-2s1A03 AU028903-A03-2s1 AU137304-2s1A03 AU028903-A03-2s1 AU137304-2s1A03 AU028903-A03-2s1 AU137304-2s1A03 AU028903-A03-2s1 AU137304-2s1A03 AU028903-A03-2s1	AU083504 chrX AU1056304 chrX AU1143303 chrX AU1178304 chrX AU1178303 chrX AU159303 chrX AU018304 chrX AU014803 chrX AU018304 chrX AU0976303 chrX AU0976303 chrX AU0976303 chrX SSC00391 chrX SSC00093 chrX SSC00035 chrX SSC00036 chrX SSC003705 chrX SSC00366 chrX SSC00417 chrX AU028903 chrX AU028903 chrX AU014803 chrX AU014803 chrX AU014803 chrX AU014803 chrX AU014803 chrX AU014803 chrX SSC00510 chrX SSC00510 chrX SSC00510 chrX AU028	128,893,016 128,893,104 128,893,104 128,893,104 128,893,104 128,893,104 128,941,017 128,941,017 128,941,142 128,943,153 128,943,153 128,963,185 128,963,185 128,963,185 129,070,418 129,491,300 129,495,549 129,711,442 129,711,442 130,029,230 130,640,034 131,178,818 131,178,818 131,178,818 131,767,075	128,894,009 128,894,009 128,894,005 128,894,105 128,894,105 128,946,320 128,946,320 128,946,320 128,946,320 128,946,320 128,946,320 128,946,320 128,946,355 129,073,992 129,493,100 129,496,564 129,712,527 130,030,433 130,641,821 131,179,980 131,180,176 131,768,880 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220	993 905 1,001 2,358 936 5,303 5,148 3,103 3,167 1,292 1,370 520 3,574 1,800 1,137 955 1,120 3,575 4,115 1,203 1,787 1,162 1,288 1,955 2,345 2,145 2,145 2,145 2,145 2,145 2,145 2,145 2,145 2,145 2,145	21 20 22 41 93 89 59 58 22 30 12 65 34 25 21 24 68 71 25 16 22 24 25 31 27 27 27 27 27 27 27 27 27 27 27 27 27	21.1 22.0 17.4 22.4 17.5 17.3 19.0 18.3 17.0 21.9 23.1 18.2 18.9 22.0 22.0 21.4 18.1 17.3 20.8 9.0 18.9 18.6 12.8 13.2 12.6 12.6 12.6 12.6 12.6 12.6 12.6 12	0.57 0.52 0.67 0.46 0.52 0.40 0.40 0.39 0.40 -0.49 -0.49 -0.41 0.98 0.40 -1.05 -1.10 -0.40 0.50 0.55 0.50 0.55 0.54 0.73 0.73 0.73 0.73 0.73 0.75 0	66.5 67.7 68.8 67.0 69.9 67.4 67.8 65.1 67.1 72.7 525.6 65.2 62.4 49.4 49.4 49.4 43.8 41.0 55.4 42.2 42.1 41.4 41.4 41.4 41.4 43.3 60.5
AU083504-A03-3s1 AU1056304-1s1A03 AU1143303-1s1A03 AU1378304-2s1A03 AU159302-2s1A03 AU056803-A03-2s1 AU014803-A03-2s1 AU01803-A03-2s1 AU01803-A03-2s1 AU0976303-1s1A03 SSC00391-A03-2s1 AU056003-A03-2s1 AU014803-A03-2s1 SSC00035-3s1A03 SSC00048-A03-1s1 SSC0048-A03-1s1 SSC0048-A03-1s1 AU1327305-1s2A03 SSC00417-A03-1s1 AU028903-A03-2s1 AU014803-A03-2s1 AU014803-A03-2s1 AU014803-A03-2s1 AU134302-1s1A03 AU1327305-1s2A03 SSC00129-3s1A03 SSC00129-3s1A03 SSC00129-3s1A03 SSC00129-3s1A03 SSC00129-3s1A03 AU1378304-2s1A03 AU1378304-2s1A03 AU028903-A03-2s1 AU1378304-2s1A03 AU021503-A03-2s1 AU137302-1s1A03 AU021503-A03-2s1 AU1875302-1s1A03	AU083504 chrX AU1056304 chrX AU1143303 chrX AU1178304 chrX AU1178303 chrX AU1159303 chrX AU018003 chrX AU018003 chrX AU018004 chrX AU0976303 chrX AU0976303 chrX AU0976303 chrX SSC00391 chrX AU014803 chrX SSC00035 chrX SSC000518 chrX SSC00055 chrX SSC00047 chrX SSC00417 chrX AU028903 chrX AU028903 chrX AU028903 chrX AU014803 chrX AU028903 chrX AU014803 chrX AU014803 chrX AU014803 chrX AU014803 chrX SSC0012 chrX AU01378304 chrX AU0	128,893,016 128,893,104 128,893,104 128,893,104 128,893,104 128,893,104 128,941,017 128,941,017 128,941,142 128,942,154 128,943,153 128,943,153 128,963,185 128,964,095 129,070,418 129,491,300 129,495,549 129,711,442 129,711,442 129,711,442 130,029,230 130,640,034 131,178,818 131,178,818 131,766,925 131,767,075	128,894,009 128,894,009 128,894,009 128,894,005 128,894,005 128,946,320 128,946,320 128,946,320 128,946,320 128,946,320 128,946,320 128,946,320 128,946,355 128,964,615 129,073,992 129,493,100 129,496,564 129,712,527 130,030,433 130,641,821 131,179,980 131,180,176 131,768,880 131,769,220 133,758,910 133,758,910	993 905 1,001 2,358 936 5,303 5,148 3,103 3,167 1,292 1,370 520 3,574 1,800 1,137 955 1,120 3,575 4,115 1,203 1,787 1,162 1,288 1,955 2,345 2,14	21 20 22 41 93 89 59 58 22 30 12 65 31 25 21 24 68 71 25 16 22 24 25 31 27 27 27 27 27 27 27 27 27 27 27 27 27	21.1 22.0 17.4 22.4 17.5 17.3 19.0 18.3 17.0 23.1 18.2 18.9 22.0 22.0 21.4 18.1 17.3 20.8 9.0 18.9 18.6 12.8 13.2 12.6 12.6 12.6 12.6 12.6 12.6 12.6 12	0.57 0.52 0.67 0.46 0.52 0.40 0.40 0.39 0.46 -0.49 -0.41 0.98 0.40 0.60 -1.05 -1.10 -0.40 0.50 0.58 0.74 0.55 0.57 0	66.5 67.7 68.8 67.0 69.7 67.8 65.1 67.4 67.8 65.1 67.4 67.8 65.1 67.4 67.8 65.1 67.4 67.6 65.2 62.4 49.4 49.4 43.8 41.3 67.6 69.2 42.1 41.4 41.4 41.4 41.4 43.3 60.5 57.7
AU083504-A03-3s1 AU1056304-1s1A03 AU1143303-1s1A03 AU1378304-2s1A03 AU159302-2s1A03 AU056803-A03-2s1 AU014803-A03-2s1 AU018003-A03-2s1 AU018003-A03-2s1 AU017403-A03-2s1 AU014803-A03-2s1 AU014803-A03-2s1 AU014803-A03-2s1 SSC0003-A03-1s2 SSC00035-3s1A03 SSC00048-A03-1s1 SSC00366-A03-2s1 SSC00417-A03-1s1 AU028903-A03-2s1 AU014803-A03-2s1 AU014803-A03-2s1 AU014803-A03-2s1 AU014803-A03-2s1 AU014803-A03-2s1 AU134302-1s1A03 SSC0012-3s1A03 SSC0012-3s1A03 SSC00366-A03-2s1 AU137305-1s2A03 SSC00366-A03-2s1 AU137304-1s1A03 AU137305-1s2A03 SSC00366-A03-2s1 AU1378304-2s1A03 AU028903-A03-2s1 AU1378304-2s1A03 AU028903-A03-2s1 AU1372301-1s2A03 AU028903-A03-2s1 AU137304-2s1A03 AU028903-A03-2s1 AU137304-2s1A03 AU028903-A03-2s1 AU137304-2s1A03 AU028903-A03-2s1	AU083504 chrX AU1056304 chrX AU1143303 chrX AU1178304 chrX AU1178303 chrX AU159303 chrX AU018304 chrX AU014803 chrX AU018304 chrX AU0976303 chrX AU0976303 chrX AU0976303 chrX SSC00391 chrX SSC00093 chrX SSC00035 chrX SSC00036 chrX SSC003705 chrX SSC00366 chrX SSC00417 chrX AU028903 chrX AU028903 chrX AU014803 chrX AU014803 chrX AU014803 chrX AU014803 chrX AU014803 chrX AU014803 chrX SSC00510 chrX SSC00510 chrX SSC00510 chrX AU028	128,893,016 128,893,104 128,893,104 128,893,104 128,893,104 128,893,104 128,941,017 128,941,017 128,941,142 128,943,153 128,943,153 128,963,185 128,963,185 128,963,185 129,070,418 129,491,300 129,495,549 129,711,442 129,711,442 130,029,230 130,640,034 131,178,818 131,178,818 131,178,818 131,767,075	128,894,009 128,894,009 128,894,005 128,894,105 128,894,105 128,946,320 128,946,320 128,946,320 128,946,320 128,946,320 128,946,320 128,946,320 128,946,355 129,073,992 129,493,100 129,496,564 129,712,527 130,030,433 130,641,821 131,179,980 131,180,176 131,768,880 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220 131,769,220	993 905 1,001 2,358 936 5,303 5,148 3,103 3,167 1,292 1,370 520 3,574 1,800 1,137 955 1,120 3,575 4,115 1,203 1,787 1,162 1,288 1,955 2,345 2,145 2,145 2,145 2,145 2,145 2,145 2,145 2,145 2,145 2,145	21 20 22 41 93 89 59 58 22 30 12 65 34 25 21 24 68 71 25 16 22 24 25 31 27 27 27 27 27 27 27 27 27 27 27 27 27	21.1 22.0 17.4 22.4 17.5 17.3 19.0 18.3 17.0 21.9 23.1 18.2 18.9 22.0 22.0 21.4 18.1 17.3 20.8 9.0 18.9 18.6 12.8 13.2 12.6 12.6 12.6 12.6 12.6 12.6 12.6 12	0.57 0.52 0.67 0.46 0.52 0.40 0.40 0.39 0.40 -0.49 -0.49 -0.41 0.98 0.40 -1.05 -1.10 -0.40 0.50 0.55 0.50 0.55 0.54 0.73 0.73 0.73 0.73 0.73 0.75 0	66.5 67.7 68.8 67.0 69.9 67.4 67.8 65.1 67.1 72.7 525.6 65.2 62.4 49.4 49.4 49.4 43.8 41.0 55.4 42.2 42.1 41.4 41.4 41.4 41.4 43.3 60.5

SSC00592-A03-3s1	SSC00592 chrX	134,393,837	134,400,858	7,021	118	16.8	0.40	63.4
AU0976303-1s1A03 AU028903-A03-2s1	AU0976303 chrX AU028903 chrX	134,394,595 134,482,494	134,400,410 134,483,554	5,815 1,060	96 23	16.5 21.7	-0.43 0.54	65.7 68.6
SSC00093-A03-1s2	SSC00093 chrX	134,883,591	134,884,816	1,225	27	22.0	-0.77	62.5
SSC00097-A03-1s1	SSC00097 chrX	134,883,591	134,884,721	1,130	25	22.1	-0.88	64.3
SSC00077-A03-3s1	SSC00077 chrX	134,883,761	134,884,721	960	21	21.9	-0.91	65.7
AU0920301-A03-2s1	AU0920301 chrX	135,126,873	135,129,790	2,917	47	16.1	-0.97	43.6
SSC00129-3s1A03	SSC00129 chrX	135,126,908	135,129,790	2,882	46	16.0	-1.15	43.3
	AU1592301 chrX	135,767,231	135,767,911	680	8	11.8	-0.78	46.0
SSC00417-A03-1s1 AU055303-A03-2s1	SSC00417 chrX AU055303 chrX	135,819,528 135,819,673	135,820,308 135,820,148	780 475	17 11	21.8 23.2	0.86 0.68	56.2
AU028903-A03-2s1	AU028903 chrX	135,940,186	135,941,906	1,720	36	20.9	0.00	58.4
SSC00460-A03-1s1	SSC00460 chrX	135,941,711	135,943,359	1,648	34	20.6	0.35	50.5
AU1953303-A03-1s1	AU1953303 chrX	137,620,314	137,621,972	1,658	32	19.3	0.41	65.0
SSC00331-A03-2s1	SSC00331 chrX	139,323,442	139,328,934	5,492	87	15.8	-0.85	37.3
SSC00316-A03-2s1	SSC00316 chrX	139,623,340	139,638,648	15,308	219	14.3	-0.70	44.8
AU1378304-2s1A03	AU1378304 chrX	140,302,728	140,307,726	4,998	47	9.4	-0.61	34.6 33.2
AU1159302-2s1A03 SSC00505-A03-1s1	AU1159303 chrX SSC00505 chrX	140,304,158 140,519,717	140,306,721 140,592,330	2,563 72,613	29 1200	11.3 16.5	-0.79 0.54	37.3
AU1334303-1s1A03	AU1334303 chrX	141,159,633	141,160,783	1,150	22	19.1	0.49	58.2
SSC00093-A03-1s2	SSC00093 chrX	142,550,345	142,551,155	810	17	21.0	-0.89	61.4
SSC00097-A03-1s1	SSC00097 chrX	142,550,405	142,551,155	750	16	21.3	-0.89	61.0
AU002403-A03-2s1	AU002403 chrX	143,165,878	143,166,968	178,000	23	21.1	-1.01	49.9
SSC00426-A03-2s1	SSC00426 chrX	143,289,593	143,290,073	480	11	22.9	-1.70	51.9
SSC00426-A03-2s1 AU1159302-2s1A03	SSC00426 chrX AU1159303 chrX	143,429,179 143,436,414	143,445,368 143,445,418	16,189 9,004	253 132	15.6 14.7	0.46 -0.83	35.2 38.0
AU1159302-251AU3 AU062203-A03-2s1	AU1159303 chrX AU062203 chrX	143,436,414	143,445,418 143,445,418	9,004 8,624	132	14.7	-0.83	38.0
AU032701-A03-3s1	AU032701 chrX	144,229,938	144,231,343	1,405	21	14.9	0.51	39.6
AU0852304-A03-2s1	AU0852304 chrX	145,207,069	145,208,670	1,601	22	13.7	-0.85	44.8
AU1862302-1s1A03	AU1862302 chrX	145,928,240	145,938,424	10,184	141	13.8	0.67	37.7
SSC00366-A03-2s1	SSC00366 chrX	146,880,046	146,883,212	3,166	31	9.8	0.89	54.4
SSC00417-A03-1s1	SSC00417 chrX AU1001202 chrX	146,880,076	146,883,237	3,161	31	9.8	0.61	54.3 57.9
AU1001202-1s1A03 SSC00417-A03-1s1	SSC00417 chrX	148,424,029 148,424,029	148,430,302 148,430,028	6,273 5,999	69 63	11.0 10.5	0.38 0.50	57.9
AU1143303-1s1A03	AU1143303 chrX	148,424,584	148,425,204	620	10	16.1	0.79	55.0
SSC00225-A03-2s1	SSC00225 chrX	148,451,773	148,464,425	12,652	149	11.8	-1.23	42.8
SSC00098-A03-3s1	SSC00098 chrX	148,452,512	148,462,190	9,678	129	13.3	-1.33	43.0
SSC00225-A03-2s1	SSC00225 chrX	148,683,832	148,701,373	17,541	273	15.6	0.59	46.6
AU058503-A03-2s1	AU058503 chrX	148,856,643	148,859,450	2,807	58	20.7	0.37	66.8 59.8
AU067803-A03-2s1 AU014803-A03-2s1	AU067803 chrX AU014803 chrX	148,857,223 148,857,413	148,863,113 148,864,793	5,890 7,380	66 76	11.2 10.3	0.44 0.46	59.8
AU018304-A03-2s1	AU018304 chrX	148,857,493	148,859,665	2,172	44	20.3	0.60	67.4
SSC00417-A03-1s1	SSC00417 chrX	148,857,722	148,859,420	1,698	34	20.0	0.74	69.1
AU028903-A03-2s1	AU028903 chrX	148,992,605	148,992,915	310	8	25.8	-0.74	30.3
AU1338304-1s1A03	AU1338304 chrX	149,280,368	149,281,173	805	16	19.9	-0.53	67.1
AU028903-A03-2s1 AU055303-A03-2s1	AU028903 chrX AU055303 chrX	149,678,535	149,679,160	625 1,559	11 19	17.6 12.2	-1.15	55.5 53.9
AU0939304-1s1A03	AU0939304 chrX	149,678,535 149,678,535	149,680,094 149,679,160	625	19	17.6	-0.52 -1.32	55.5
AU1875302-1s1A03	AU1875302 chrX	149,678,535	149,679,545	1,010	14	13.9	-1.07	55.7
SSC00366-A03-2s1	SSC00366 chrX	149,942,968	149,946,773	3,805	80	21.0	0.54	37.3
AU1378304-2s1A03	AU1378304 chrX	149,943,088	149,946,648	3,560	74	20.8	-0.35	37.8
AU1001202-1s1A03	AU1001202 chrX	150,457,842	150,462,001	4,159	49	11.8	-0.85	38.7
AU1159302-2s1A03	AU1159303 chrX AU058503 chrX	150,457,902	150,462,690	4,788	53	21.5	-1.04	39.0
AU058503-A03-2s1 AU1211303-1s2A03	AU058503 chrX AU1211303 chrX	150,608,963 150,614,032	150,610,913 150,614,924	1,950 892	42 15	21.5 16.8	-0.45 0.47	45.3 75.4
AU1585301-1s2A03	AU1585301 chrX	150,627,527	150,629,067	1,540	27	17.5	-0.92	51.8
SSC00035-3s1A03	SSC00035 chrX	150,627,527	150,629,137	1,610	28	17.4	-1.90	50.9
AU1953303-A03-1s1	AU1953303 chrX	150,779,751	150,783,476	3,725	76	20.4	-0.74	43.0
SSC00316-A03-2s1	SSC00316 chrX	151,562,641	151,564,146	1,505	32	21.3	-0.94	41.7
SSC00316-A03-2s1	SSC00316 chrX	151,742,321	151,744,296	1,975	42	21.3	-0.76	53.3
SSC00417-A03-1s1	SSC00417 chrX SSC00035 chrX	151,742,456	151,743,651	1,195	26 62	21.8 20.4	0.82 -1.24	54.3
SSC00035-3s1A03 AU1073302-A03-2s1		151,854,912 151,979,999	151,857,952 151,980,324	3,040 325	8	20.4	-1.24	53.0 38.5
AU0939304-1s1A03	AU0939304 chrX	152,120,424	152,192,189	71,765	807	11.2	0.46	43.4
AU1143303-1s1A03	AU1143303 chrX	152,238,877	152,240,102	1,225	17	13.9	0.59	60.0
SSC00093-A03-1s2	SSC00093 chrX	152,264,330	152,265,430	1,100	23	20.9	0.74	55.8
SSC00097-A03-1s1	SSC00097 chrX	152,264,330	152,265,335	1,005	21	20.9	0.75	55.8
SSC00316-A03-2s1	SSC00316 chrX	152,301,264	152,303,154	1,890	34	18.0	-0.75	51.7
AU1344302-1s1A03 AU0895303-1s2A03	AU1344302 chrX AU0895303 chrX	152,363,112 152,372,416	152,364,047 152,494,466	935 122,050	17 2291	18.2 18.8	-0.50 0.26	67.8 59.6
AU014803-A03-2s1	AU0895505 ClirX AU014803 chrX	152,372,416	152,389,570	494	10	20.2	0.26	72.9
AU0895303-1s2A03		152,546,991	152,562,004	15,013	282	18.8	0.27	58.7
								221

SSC00316-A03-2s1	SSC00316 chrX	152,560,776	152,561,914	1,138	24	21.1	-0.96	70.4
AU1622302-1s2A03	AU1622302 chrX	152,573,639	152,576,282	2,643	24	9.1	-0.65	47.6
SSC00093-A03-1s2	SSC00093 chrX	152,606,438	152,608,370	1,932	26	13.5	-0.56	75.9
AU0895303-1s2A03	AU0895303 chrX	152,642,042	152,724,158	82,116	1266	15.4	0.25	58.1
AU028903-A03-2s1	AU028903 chrX	152,690,489	152,730,588	40,099	726	18.1	0.33	61.6
SSC00077-A03-3s1	SSC00077 chrX	152,695,235	152,695,665	430	10	23.3	-0.98	74.6
SSC00093-A03-1s2	SSC00093 chrX	152,890,765	152,892,370	1,605	25	15.6	-0.59	62.7
SSC00549-A03-1s1	SSC00549 chrX	154,039,041	154,063,752	24,711	276	11.2	-1.30	36.7
AU0983302-1s1A03	AU0983302 chrX	154,044,880	154,057,130	12,250	179	14.6	-1.07	35.0
AU083504-A03-3s1	AU083504 chrX	154,047,946	154,057,440	9,494	147	15.5	-0.68	34.8
AU083504-A03-3s1	AU083504 chrX	154,067,596	154,071,868	4,272	60	14.0	-0.77	36.1
AU0983302-1s1A03	AU0983302 chrX	154,067,596	154,071,023	3,427	59	17.2	-1.12	35.3
AU1001202-1s1A03	AU1001202 chrX	154,278,014	154,583,237	305,223	2995	9.8	0.51	38.1
AU058103-A03-2s1	AU058103 chrX	154,431,718	154,434,720	3,002	33	11.0	-0.63	36.1
SSC00260-A03-2s1	SSC00260 chrX	154,582,223	154,583,237	1,014	12	11.8	-1.54	37.5

Table A.4 – CNV from 102 NIMH samples run on 2.1M arrays by NimbleGen protocol.

NIMH54-1s1	NIMH54	chrX	31,773,231	31,773,887	656	14	21.3	-0.48	40.5
NIMH53-A01-2s2	NIMH53	chrX	33,558,581	33,559,556	975	20	20.5	0.47	55.2
NIMH95-1s1	NIMH95	chrX	33,558,581	33,559,556	975	20 473	20.5	0.42	55.2
NIMH36-1s1 NIMH40-1s1	NIMH36 NIMH40	chrX chrX	33,952,881 33,952,911	33,981,250 33,964,182	28,369 11,271	473	16.7 16.2	-0.79 -0.99	34.8
NIMH01-1s1	NIMH01	chrX	34,063,446	34,065,466	2,020	20	9.9	0.58	33.1
NIMH04-1s1	NIMH04	chrX	34,063,446	34,065,466	2,020	20	9.9	0.81	33.1
NIMH07-1s1 NIMH08-1s1	NIMH07 NIMH08	chrX chrX	34,063,446	34,065,466	2,020 2,020	20 20	9.9 9.9	0.75 0.60	33.1 33.1
NIMH100-1s1	NIMH100		34,063,446 34,063,446	34,065,466 34,065,466	2,020	20	9.9 9.9	0.88	33.1
NIMH16-1s1	NIMH16	chrX	34,063,446	34,065,401	1,955	19	9.7	0.79	32.9
NIMH19-1s1	NIMH19	chrX	34,063,446	34,065,466	2,020	20	9.9	0.81	33.1
NIMH20-1s1	NIMH20	chrX	34,063,446	34,065,401	1,955	19	9.7	0.72	32.9
NIMH30-1s2 NIMH35-1s1	NIMH30 NIMH35	chrX chrX	34,063,446 34,063,446	34,065,401 34,065,466	1,955 2,020	19 20	9.7 9.9	0.69 0.66	32.9 33.1
NIMH43-1s1	NIMH43	chrX	34,063,446	34,065,401	1,955	19	9.9	0.83	32.9
NIMH49-1s1	NIMH49	chrX	34,063,446	34,065,401	1,955	19	9.7	1.04	32.9
NIMH50-1s1	NIMH50	chrX	34,063,446	34,065,401	1,955	19	9.7	0.99	32.9
NIMH51-1s1	NIMH51	chrX	34,063,446	34,065,466	2,020	20	9.9	0.85	33.1
NIMH53-A01-2s2	NIMH53	chrX	34,063,446	34,065,401	1,955	19	9.7	0.86	32.9
NIMH55-1s1 NIMH56-1s1	NIMH55 NIMH56	chrX chrX	34,063,446 34,063,446	34,065,274 34,065,466	1,828 2,020	18 20	9.8 9.9	0.74 0.74	32.5 33.1
NIMH57-1s1	NIMH57	chrX	34,063,446	34,065,401	1,955	19	9.7	0.92	32.9
NIMH63-1s1	NIMH63	chrX	34,063,446	34,065,401	1,955	19	9.7	0.90	32.9
NIMH66-1s1	NIMH66	chrX	34,063,446	34,065,401	1,955	19	9.7	0.69	32.9
NIMH67-1s1	NIMH67	chrX	34,063,446	34,065,466	2,020	20	9.9	0.82	33.1
NIMH69-2s1 NIMH75-1s1	NIMH69 NIMH75	chrX chrX	34,063,446 34,063,446	34,065,401 34.065.401	1,955 1,955	19 19	9.7 9.7	0.77 1.03	32.9 32.9
NIMH76-1s1	NIMH76	chrX	34,063,446	34,065,401	1,955	19	9.7	1.05	32.9
NIMH80-1s1	NIMH80	chrX	34,063,446	34,065,466	2,020	20	9.9	0.81	33.1
NIMH81-1s1	NIMH81	chrX	34,063,446	34,066,116	2,670	25	9.4	0.61	35.0
NIMH82-1s1	NIMH82	chrX	34,063,446	34,065,401	1,955	19	9.7	0.67	32.9
NIMH84-1s1	NIMH84	chrX	34,063,446	34,066,116	2,670	25	9.4	0.72	35.0
NIMH88-1s1 NIMH90-1s1	NIMH88 NIMH90	chrX chrX	34,063,446 34,063,446	34,065,401 34,065,401	1,955 1,955	19 19	9.7 9.7	1.02 0.86	32.9 32.9
NIMH93-1s1	NIMH93	chrX	34,063,446	34,065,466	2,020	20	9.9	0.90	33.1
NIMH94-1s1	NIMH94	chrX	34,063,446	34,065,466	2,020	20	9.9	0.73	33.1
NIMH96-1s1	NIMH96	chrX	34,063,446	34,065,466	2,020	20	9.9	0.81	33.1
NIMH99-A01-1s2	NIMH99	chrX	34,063,446	34,066,116	2,670	25	9.4	0.66	35.0
NIMH24-1s1	NIMH24	chrX	34,063,466	34,065,401	1,935	18	9.3	0.77	32.8
NIMH64-1s1 NIMH69-2s1	NIMH64 NIMH69	chrX chrX	35,624,856 35,689,759	35,625,766 35,690,664	910 905	19 17	20.9 18.8	-1.11 0.38	37.8 50.6
NIMH68-1s1	NIMH68	chrX	35.921.767	36,190,195	268.428	3,995	14.9	0.66	34.9
NIMH32-1s1	NIMH32	chrX	36,361,872	36,363,155	1,283	22	17.1	-0.52	41.7
NIMH67-1s1	NIMH67	chrX	36,560,109	36,561,739	1,630	32	19.6	0.28	48.0
NIMH75-1s1	NIMH75	chrX	37,998,850	37,999,025	175	5	28.6	0.73	41.9
NIMH69-2s1	NIMH69	chrX	38,283,541	38,283,926	385	8	20.8	0.64	33.8
NIMH37-A01-2s2 NIMH75-1s1	NIMH37 NIMH75	chrX chrX	38,283,561 38,305,103	38,283,926 38,306,959	365 1,856	7	19.2 19.9	0.81	34.6 61.2
NIMH84-1s1	NIMH84	chrX	39,494,577	39,502,493	7,916	128	16.2	0.63	49.6
NIMH17-1s1	NIMH17	chrX	39,810,721	39,864,432	53,711	972	18.1	0.34	53.7
NIMH19-1s1	NIMH19	chrX	39,823,805	39,853,234	29,429	560	19.0	0.36	57.5
NIMH21-1s1	NIMH21	chrX	39,833,606	39,848,822	15,216	291	19.1	0.28	57.8
NIMH32-1s1	NIMH32	chrX	39,834,985	39,835,866	881	19	21.6	-0.59	47.3
NIMH30-1s2 NIMH28-1s1	NIMH30 NIMH28	chrX chrX	39,835,100 39,848,822	39,839,101 39,854,158	4,001 5,336	82 96	20.5 18.0	-0.25 0.63	55.0 68.5
NIMH44-1s1	NIMH44	chrX	39,913,004	39,913,864	860	17	19.8	-0.59	50.2
NIMH66-1s1	NIMH66	chrX	40,006,882	40,008,277	1,395	29	20.8	0.34	52.4
NIMH37-A01-2s2	NIMH37	chrX	40,324,376	40,325,651	1,275	20	15.7	0.37	60.1
NIMH96-1s1	NIMH96	chrX	40,828,639	40,831,205	2,566	50	19.5	0.31	65.8
NIMH37-A01-2s2 NIMH28-1s1	NIMH37 NIMH28	chrX chrX	41,084,397 41,217,647	41,085,107 41,218,957	710 1,310	16 24	22.5 18.3	0.57	36.1
NIMH28-151 NIMH53-A01-2s2	NIMH28	chrX	41,217,647 43,398,261	43,398,971	710	15	21.1	-0.48	53.2
NIMH28-1s1	NIMH28	chrX	43,458,110	43,464,890	6,780	139	20.5	0.56	49.8
NIMH53-A01-2s2	NIMH53	chrX	43,499,243	43,501,120	1,877	39	20.8	0.27	48.3
NIMH74-A01-1s2	NIMH74	chrX	44,616,456	44,618,401	1,945	36	18.5	0.25	68.7
NIMH44-1s1	NIMH44	chrX	45,354,014	45,355,254	1,240	26	21.0	0.31	55.2
NIMH02-1s1 NIMH28-1s1	NIMH02 NIMH28	chrX	45,671,748 46,317,849	45,674,192 46,319,871	2,444 2,022	45 40	18.4 19.8	-1.02	33.7 69.6
NIMH28-151 NIMH37-A01-2s2	NIMH28 NIMH37	chrX chrX	46,317,849 46,317,985	46,320,612	2,022 2,627	40 51	19.8 19.4	0.76	69.6
		Sin X	,011,000	,010,012	2,021			0.00	224

NIMH89-1s1	NIMH89	chrX	46,318,765	46,320,346	1,581	31	19.6	0.32	64.3
NIMH95-1s1	NIMH95	chrX	46,407,337	46,412,560	5,223	73	14.0	0.55	41.6
NIMH92-1s1	NIMH92	chrX	46,408,444	46,412,560	4,116	69	16.8	0.50	39.7
NIMH20-1s1	NIMH20	chrX	46,892,390	46,991,488	99,098	1,596	16.1	0.30	50.0
NIMH21-1s1	NIMH21	chrX	46,913,091	46,935,978	22,887	406	17.7	0.29	54.9
NIMH24-1s1	NIMH24 NIMH46	chrX	46,913,091	46,947,729	34,638 5,815	622 97	18.0 16.7	0.27 0.24	54.0 54.6
NIMH46-1s1 NIMH17-1s1	NIMH46 NIMH17	chrX chrX	46,925,929 46,940,817	46,931,744 46,974,251	33,434	609	18.2	0.24	54.6 51.9
NIMH23-1s1	NIMH23	chrX	46,962,695	46,965,814	3,119	63	20.2	-0.33	56.5
NIMH44-1s1	NIMH44	chrX	46,963,535	46,965,744	2,209	47	21.3	-0.41	52.0
R085B11-A01-1s1	R085B11	chrX	46,963,756	46,965,524	1,768	38	21.5	-0.31	51.9
NIMH94-1s1	NIMH94	chrX	46,965,794	46,972,101	6,307	122	19.3	0.19	54.3
NIMH32-1s1	NIMH32	chrX	46,966,104	46,974,361	8,257	157	19.0	0.30	53.0
NIMH79-1s1 NIMH39-1s1	NIMH79 NIMH39	chrX chrX	47,213,816 47,214,228	47,227,191 47,227,451	13,375 13,223	149 151	11.1 11.4	-0.25 -0.37	41.5 42.0
R085B11-A01-1s1	R085B11	chrX	47,225,263	47,226,731	1,468	21	14.3	-0.51	42.0
NIMH23-1s1	NIMH23	chrX	47,226,291	47,228,673	2,382	47	19.7	-0.33	52.4
NIMH19-1s1	NIMH19	chrX	47,361,748	47,373,433	11,685	230	19.7	0.34	52.9
NIMH01-1s1	NIMH01	chrX	47,364,422	47,371,993	7,571	150	19.8	0.23	52.4
NIMH33-1s1	NIMH33	chrX	47,369,703	47,376,220	6,517	120	18.4	0.30	54.3
NIMH31-1s2	NIMH31	chrX	47,465,711	47,468,996	3,285	67	20.4	0.32	55.5
NIMH24-1s1	NIMH24	chrX	47,465,856	47,471,201	5,345	103	19.3	0.25	55.1
NIMH05-2s1 NIMH92-1s1	NIMH05 NIMH92	chrX chrX	48,202,382 48,201,697	48,208,560 48,208,745	6,178 7,048	97 113	15.7 16.0	0.40 0.27	51.7 52.2
NIMH17-1s1	NIMH192	chrX	48,201,887	48,267,211	65,324	1,050	16.1	0.27	52.2
R085B11-A02-1s1	R085B11	chrX	48,220,111	48,221,146	1,035	23	22.2	-0.50	45.3
NIMH05-2s1	NIMH05	chrX	48,251,623	48,257,519	5,896	117	19.8	0.37	54.3
NIMH23-1s1	NIMH23	chrX	48,282,983	48,284,033	1,050	23	21.9	-0.71	59.5
NIMH33-1s1	NIMH33	chrX	48,283,123	48,283,993	870	19	21.8	-0.72	57.3
NIMH24-1s1	NIMH24	chrX	48,283,188	48,283,888	700	16	22.9	-0.52	56.1
NIMH25-1s1 NIMH38-1s1	NIMH25 NIMH38	chrX chrX	48,283,188 48,283,188	48,283,888 48,284,033	700 845	16 19	22.9 22.5	-0.59 -0.59	56.1 55.4
NIMH34-1s1	NIMH34	chrX	48,283,223	48,284,033	810	18	22.3	-0.61	54.4
R085B11-A02-1s1	R085B11	chrX	48,283,338	48,283,993	655	15	22.9	-0.57	52.1
NIMH08-1s1	NIMH08	chrX	48,341,265	48,345,123	3,858	71	18.4	0.38	57.7
NIMH40-1s1	NIMH40	chrX	48,342,305	48,345,558	3,253	59	18.1	0.37	57.2
NIMH24-1s1	NIMH24	chrX	48,426,969	48,452,477	25,508	471	18.5	0.23	52.0
NIMH08-1s1	NIMH08	chrX	48,435,103	48,449,215	14,112	256	18.1	0.20	51.4
NIMH23-1s1 NIMH23-1s1	NIMH23 NIMH23	chrX chrX	48,439,518 48,441,198	48,441,098 48,453,617	1,580 12,419	29 245	18.4 19.7	-0.49 0.25	63.0 52.6
NIMH33-1s1	NIMH23	chrX	48,443,238	48,454,022	10,784	245	19.7	0.23	53.5
NIMH67-1s1	NIMH67	chrX	48,447,204	48,452,902	5,698	110	19.3	0.32	56.1
R085B10-1s1	R085B10		48,454,022	48,471,467	17,445	298	17.1	-0.34	43.3
NIMH28-1s1	NIMH28	chrX	48,456,967	48,464,854	7,887	137	17.4	0.34	43.4
NIMH17-1s1	NIMH17	chrX	48,528,440	49,005,879	477,439	6,344	13.3	0.27	50.4
R085B11-A02-1s1	R085B11	chrX	48,530,197	48,531,062	865	19	22.0	-0.58	47.9
NIMH13-1s1	NIMH13	chrX	48,557,175	48,571,137	13,962 12,112	234	16.8	0.29	55.8
NIMH10-1s1 NIMH96-1s1	NIMH10 NIMH96	chrX chrX	48,557,395 48,566,205	48,569,507 48,571,232	5,027	199 97	16.4 19.3	0.36 0.23	53.9 59.8
NIMH25-1s1	NIMH25	chrX	48,575,220	48,578,431	3,211	54	16.8	-0.39	48.9
NIMH31-1s2	NIMH31	chrX	48,575,721	48,578,381	2,660	46	17.3	-0.36	43.9
NIMH38-1s1	NIMH38	chrX	48,575,721	48,578,431	2,710	47	17.3	-0.40	44.0
NIMH34-1s1	NIMH34	chrX	48,576,846	48,578,431	1,585	31	19.6	-0.40	45.5
R085B11-A02-1s1	R085B11	chrX	48,577,861	48,578,431	570	12	21.1	-0.57	50.2
NIMH08-1s1 NIMH04-1s1		chrX	48,631,753 48,632,601	48,668,438 48,653,495	36,685 20,894	613 341	16.7	0.21	52.9 52.9
NIMH04-151 NIMH44-1s1	NIMH04 NIMH44	chrX chrX	48,698,440	48,653,495	20,894	341 18	16.3 22.5	0.18 -0.55	52.9 52.4
NIMH33-1s1	NIMH44 NIMH33	chrX	48,698,580	48,699,240	660	15	22.5	-0.55	53.4
NIMH25-1s1	NIMH25	chrX	48,698,635	48,699,240	605	14	23.1	-0.66	53.5
NIMH34-1s1	NIMH34	chrX	48,698,635	48,699,240	605	14	23.1	-0.66	53.5
NIMH32-1s1	NIMH32	chrX	48,698,660	48,699,240	580	13	22.4	-0.81	53.3
NIMH21-1s1	NIMH21	chrX	48,782,705	48,847,113	64,408	854	13.3	0.26	52.2
NIMH20-1s1	NIMH20	chrX	48,788,428	49,031,490	243,062	3,470	14.3	0.29	51.3
NIMH16-1s1 R085B11-A02-1s1	NIMH16 R085B11	chrX chrX	48,796,167 48,797,828	48,827,185 48,798,448	31,018 620	512 13	16.5 21.0	0.27 0.39	54.7 73.8
NIMH30-1s2	NIMH30	chrX	48,798,448	48,799,503	1,055	22	20.9	-0.37	52.1
NIMH31-1s2	NIMH31	chrX	48,798,448	48,799,503	1,055	22	20.9	-0.33	52.1
NIMH32-1s1	NIMH32	chrX	48,798,448	48,799,243	795	16	20.1	-0.60	51.7
NIMH33-1s1	NIMH33	chrX	48,798,448	48,799,433	985	20	20.3	-0.56	52.1
									225

NIMH34-1s1	NIMH34	chrX	48,798,448	48,799,433	985	20	20.3	-0.46	52.1
NIMH38-1s1	NIMH38	chrX	48,798,448	48,799,458	1,010	21	20.8	-0.43	52.3
NIMH40-1s1	NIMH40	chrX	48,798,448	48,799,368	920	19	20.7	-0.57	52.2
NIMH23-1s1	NIMH23	chrX	48,798,523	48,799,503	980	21	21.4	-0.62	51.8
NIMH25-1s1	NIMH25	chrX	48,798,523	48,799,503	980	21	21.4	-0.45	51.8
R085B11-A02-1s1	R085B11	chrX	48,798,523	48,799,268	745	16	21.5	-0.50	51.4
NIMH23-1s1	NIMH23	chrX	48,799,563	48,816,512	16,949	284	16.8	0.24	54.3
NIMH31-1s2	NIMH31	chrX	48,799,563	48,822,720	23,157	331	14.3	0.31	55.3
					· ·		14.3		
NIMH19-1s1	NIMH19	chrX	48,806,232	48,821,770	15,538	265		0.37	57.0
NIMH05-2s1	NIMH05	chrX	48,809,147	48,813,283	4,136	80	19.3	0.48	58.3
NIMH23-1s1	NIMH23	chrX	48,816,537	48,818,120	1,583	33	20.8	-0.46	61.5
NIMH23-1s1	NIMH23	chrX	48,818,195	48,823,690	5,495	99	18.0	0.29	56.0
NIMH19-1s1	NIMH19	chrX	48,898,879	48,937,479	38,600	595	15.4	0.30	54.0
NIMH05-2s1	NIMH05	chrX	48,898,899	49,018,033	119,134	1,979	16.6	0.25	52.9
NIMH21-1s1	NIMH21	chrX	48,899,204	48,936,714	37,510	575	15.3	0.30	54.1
NIMH04-1s1	NIMH04	chrX	48,899,359	48,935,279	35,920	549	15.3	0.19	54.4
NIMH16-1s1	NIMH16	chrX	48,899,404	49,005,129	105,725	1,719	16.3	0.22	53.3
NIMH23-1s1	NIMH23	chrX	48,906,630	48,907,975	1,345	26	19.3	-0.66	60.8
NIMH30-1s2	NIMH30	chrX	48,907,145	48,907,975	830	18	21.7	-0.56	57.2
NIMH44-1s1	NIMH44	chrX	48,907,145	48,907,975	830	18	21.7	-0.62	57.2
NIMH40-1s1	NIMH40	chrX	48,907,230	48,908,005	775	17	21.9	-0.72	55.3
NIMH25-1s1	NIMH25	chrX	48,907,350	48,908,070	720	16	22.2	-0.66	53.1
NIMH26-1s1	NIMH26	chrX	48,907,350	48,907,975	625	14	22.4	-0.61	52.8
NIMH31-1s2	NIMH31	chrX	48,907,350	48,907,755	405	10	24.7	-0.69	55.2
NIMH32-1s1	NIMH32	chrX	48,907,350	48,908,005	655	15	22.9	-0.67	52.6
NIMH33-1s1	NIMH33	chrX	48,907,350	48,907,975	625	14	22.4	-0.70	52.8
NIMH34-1s1	NIMH34	chrX	48,907,350	48,908,070	720	16	22.2	-0.66	53.1
					720		22.2		53.1
NIMH38-1s1	NIMH38	chrX	48,907,350	48,908,070		16		-0.67	
NIMH31-1s2	NIMH31	chrX	48,948,311	48,956,342	8,031	140	17.4	0.37	53.4
NIMH75-1s1	NIMH75	chrX	48,973,682	48,975,270	1,588	33	20.8	0.27	60.6
NIMH63-1s1	NIMH63	chrX	48,987,490	48,988,715	1,225	21	17.1	-0.26	50.2
NIMH92-1s1	NIMH92	chrX	48,988,570	48,999,259	10,689	192	18.0	0.24	56.3
NIMH63-1s1	NIMH63	chrX	48,989,090	49,005,464	16,374	309	18.9	0.23	56.4
NIMH48-1s1	NIMH48	chrX	48,989,869	49,005,184	15,315	293	19.1	0.23	57.3
NIMH50-1s1	NIMH50	chrX	48,989,869	48,996,304	6,435	130	20.2	0.37	59.5
R085B11-A02-1s1	R085B11	chrX	48,989,869	48,995,154	5,285	107	20.2	0.28	60.9
NIMH10-1s1	NIMH10	chrX	48,989,894	48,995,546	5,652	114	20.2	0.47	60.5
						107	20.2		59.2
NIMH31-1s2	NIMH31	chrX	48,991,049	48,996,304	5,255			0.38	
NIMH33-1s1	NIMH33	chrX	48,991,699	48,995,104	3,405	70	20.6	0.37	60.7
NIMH35-1s1	NIMH35	chrX	48,991,699	48,995,419	3,720	76	20.4	0.30	60.2
R085B11-A02-1s1	R085B11	chrX	48,995,219	48,996,359	1,140	24	21.1	-0.35	52.8
NIMH44-1s1	NIMH44	chrX	48,995,364	48,996,414	1,050	22	21.0	-0.28	52.6
NIMH92-1s1	NIMH92	chrX	48,999,329	48,999,754	425	9	21.2	-0.60	53.9
NIMH26-1s1	NIMH26	chrX	48,999,379	48,999,834	455	9	19.8	-0.58	53.6
NIMH32-1s1	NIMH32	chrX	48,999,379	48,999,834	455	9	19.8	-0.73	53.6
NIMH94-1s1	NIMH94	chrX	48,999,379	48,999,834	455	9	19.8	-0.65	53.6
NIMH95-1s1	NIMH95	chrX	48,999,379	48,999,754	375	8	21.3	-0.59	53.7
		chrX			475	9	18.9	-0.62	52.2
NIMH38-1s1	NIMH38		48,999,424	48,999,899					
NIMH53-2s1	NIMH53	chrX	48,999,424	48,999,754	330	7	21.2	-0.72	53.2
NIMH96-1s1	NIMH96	chrX	48,999,424	48,999,754	330	7	21.2	-0.82	53.2
NIMH38-1s1	NIMH38	chrX	48,999,924	49,005,224	5,300	105	19.8	0.24	56.4
NIMH32-1s1	NIMH32	chrX	49,012,855	49,013,180	325	8	24.6	-0.89	58.7
NIMH34-1s1	NIMH34	chrX	49,012,920	49,013,270	350	8	22.9	-0.82	63.9
NIMH38-1s1	NIMH38	chrX	49,012,920	49,013,135	215	6	27.9	-0.85	58.2
NIMH96-1s1	NIMH96	chrX	49,029,180	49,030,525	1,345	28	20.8	0.32	62.2
NIMH57-1s1	NIMH57	chrX	49,438,765	49,450,241	11,476	219	19.1	0.23	43.0
NIMH90-1s1	NIMH90	chrX	49,443,375	49,448,387	5,012	219 96	19.1	0.23	43.0
					, .				
NIMH04-1s1	NIMH04	chrX	50,145,957	50,146,797	840	19	22.6	-0.59	44.4
NIMH21-1s1	NIMH21	chrX	50,228,557	50,232,495	3,938	78	19.8	0.32	56.5
NIMH67-1s1	NIMH67	chrX	51,069,986	51,070,966	980	22	22.4	0.38	55.4
	NIMH60	chrX	51,166,273	51,167,998	1,725	37	21.4	0.35	64.1
NIMH60-1s1				51,629,289	1,350	27	20.0	0.96	41.5
	NIMH28	chrX	51,627,939						
NIMH28-1s1	NIMH28 R085B11	chrX chrX	51,627,939 51 628 194			18	22.2	-0.60	42 2
NIMH28-1s1 R085B11-A02-1s1	R085B11	chrX	51,628,194	51,629,004	810	18	22.2	-0.60	42.2
NIMH28-1s1 R085B11-A02-1s1 NIMH05-2s1	R085B11 NIMH05	chrX chrX	51,628,194 51,654,500	51,629,004 51,656,155	810 1,655	35	21.1	0.36	52.2
NIMH28-1s1 R085B11-A02-1s1 NIMH05-2s1 NIMH06-1s1	R085B11 NIMH05 NIMH06	chrX chrX chrX	51,628,194 51,654,500 52,966,578	51,629,004 51,656,155 52,967,078	810 1,655 500	35 12	21.1 24.0	0.36 0.77	52.2 63.7
NIMH28-1s1 R085B11-A02-1s1 NIMH05-2s1 NIMH06-1s1 NIMH07-1s1	R085B11 NIMH05 NIMH06 NIMH07	chrX chrX chrX chrX	51,628,194 51,654,500 52,966,578 53,099,962	51,629,004 51,656,155 52,967,078 53,102,357	810 1,655 500 2,395	35 12 43	21.1 24.0 18.0	0.36 0.77 -0.33	52.2 63.7 48.7
NIMH28-1s1 R085B11-A02-1s1 NIMH05-2s1 NIMH06-1s1	R085B11 NIMH05 NIMH06	chrX chrX chrX	51,628,194 51,654,500 52,966,578	51,629,004 51,656,155 52,967,078	810 1,655 500	35 12	21.1 24.0	0.36 0.77	52.2 63.7
NIMH28-1s1 R085B11-A02-1s1 NIMH05-2s1 NIMH06-1s1 NIMH07-1s1	R085B11 NIMH05 NIMH06 NIMH07	chrX chrX chrX chrX	51,628,194 51,654,500 52,966,578 53,099,962	51,629,004 51,656,155 52,967,078 53,102,357	810 1,655 500 2,395	35 12 43	21.1 24.0 18.0	0.36 0.77 -0.33	52.2 63.7 48.7
NIMH28-1s1 R085B11-A02-1s1 NIMH05-2s1 NIMH06-1s1 NIMH07-1s1 NIMH79-1s1	R085B11 NIMH05 NIMH06 NIMH07 NIMH79	chrX chrX chrX chrX chrX chrX	51,628,194 51,654,500 52,966,578 53,099,962 53,100,517	51,629,004 51,656,155 52,967,078 53,102,357 53,102,747	810 1,655 500 2,395 2,230	35 12 43 46	21.1 24.0 18.0 20.6	0.36 0.77 -0.33 0.33	52.2 63.7 48.7 47.6

NIMH26-1s1	NIMH26	chrX	53,238,248	53,243,646	5,398	107	19.8	0.30	57.2
NIMH35-1s1	NIMH35	chrX	53,238,268	53,242,691	4,423	88	19.9	0.31	57.7
NIMH33-1s1	NIMH33	chrX	53,367,506	53,368,361	855	19	22.2	-0.42	55.7
NIMH21-1s1	NIMH21	chrX	53,726,483	53,731,155	4,672	96	20.5	0.26	49.6
NIMH75-1s1	NIMH75	chrX	53,801,385	53,803,940	2,555	36	14.1	0.28	55.3
NIMH67-1s1	NIMH67	chrX	53,801,995	53,804,775	2,780	35	12.6	0.47	56.3
NIMH08-1s1	NIMH08	chrX	54,400,369	54,403,940	3,571	70	19.6	0.28	52.7
NIMH33-1s1	NIMH33	chrX	54,539,576	54,540,066	490	11	22.4	-0.69	49.5
NIMH20-1s1	NIMH20	chrX	54,572,044	54,576,106	4,062	74	18.2	0.41	51.7
NIMH31-1s2	NIMH31	chrX	54,790,608	54,792,468	1,860	39	21.0	-0.22	42.6
NIMH33-1s1	NIMH33	chrX	54,790,608	54,791,893	1,285	28	21.8	-0.38	44.2
NIMH44-1s1	NIMH44	chrX	54,790,608	54,792,193	1,585	33	20.8	-0.36	43.5
R085B11-A02-1s1	R085B11	chrX	54,790,693	54,791,893	1,200	26	21.7	-0.47	43.8
NIMH63-1s1	NIMH63	chrX	54,862,794	54,868,184	5,390	59	10.9	0.37	54.4
NIMH94-1s1	NIMH94	chrX	54,863,029	54,870,904	7,875	106	13.5	0.25	53.3
NIMH13-1s1	NIMH13	chrX	54,864,114	54,865,024	910	20	22.0	0.60	56.4
NIMH46-1s1	NIMH46	chrX	54,864,114	54,868,374	4,260	53	12.4	0.37	53.8
NIMH66-1s1	NIMH66	chrX	54,864,114	54,874,190	10,076	102	10.1	0.30	48.1
NIMH56-1s1	NIMH56	chrX	54,864,159	54,865,024	865	19	22.0	0.50	56.1
NIMH57-1s1	NIMH57	chrX	54,964,293	54,968,774	4,481	92	20.5	0.24	51.0
NIMH31-1s2	NIMH31	chrX	54,976,064	54,979,453	3,389	67	19.8	0.37	54.4
NIMH33-1s1	NIMH33	chrX	55,011,721	55,012,228	507	10	19.7	-1.23	29.5
NIMH33-1s1	NIMH33	chrX	56,605,975	56,607,060	1,085	21	19.4	-0.63	50.1
NIMH23-1s1	NIMH23	chrX	56,606,070	56,607,155	1,085	22	20.3	-0.62	53.3
NIMH30-1s2	NIMH30	chrX	56,606,070	56,607,060	990	20	20.2	-0.46	52.0
NIMH34-1s1	NIMH34	chrX	56,606,070	56,606,755	685	14	20.4	-0.63	43.3
NIMH40-1s1	NIMH40	chrX	56,606,070	56,607,155	1,085	22	20.3	-0.55	53.3
NIMH69-2s1	NIMH69	chrX	56,801,592	56,839,447	37,855	448	11.8	0.24	52.6
NIMH75-1s1	NIMH75	chrX	56,845,230	56,846,209	979	19	19.4	0.95	53.7
NIMH67-1s1	NIMH67	chrX	57,558,981	57,560,926	1,945	37	19.0	0.41	49.7
NIMH92-1s1	NIMH92	chrX	57,559,476	57,560,426	950	21	22.1	0.55	55.0
NIMH96-1s1	NIMH96	chrX	57,783,495	57,784,695	1,200	26	21.7	0.32	52.8
NIMH10-1s1	NIMH10	chrX	58,292,047	58,310,299	18,252	353	19.3	0.27	57.0
NIMH15-1s1	NIMH15	chrX	58,292,647	58,358,518	65,871	1,126	17.1	0.23	51.4
NIMH84-1s1	NIMH84	chrX	58,293,082	58,336,004	42,922	839	19.5	0.33	59.3
NIMH29-1s1	NIMH29	chrX	58,296,252	58,323,045	26,793	527	19.7	0.20	60.7
NIMH38-1s1	NIMH38	chrX	58,296,252	58,310,189	13,937	271	19.4	0.22	60.0
NIMH41-1s1	NIMH41	chrX	58,296,282	58,340,997	44,715	828	18.5	0.26	57.6
NIMH42-1s1	NIMH42	chrX	58,301,112	58,336,004	34,892	681	19.5	0.28	60.4
NIMH51-1s1	NIMH51	chrX	58,304,375	58,333,665	29,290	573	19.6	0.31	60.8
NIMH36-1s1	NIMH36	chrX	58,307,292	58,329,969	22,677	446	19.7	0.27	61.1
NIMH89-1s1	NIMH89	chrX	58,309,851	58,330,259	20,408	404	19.8	0.26	61.2
NIMH19-1s1	NIMH19	chrX	58,312,070	58,344,028	31,958	564	17.6	0.27	54.3
NIMH50-1s1	NIMH50	chrX	58,312,690	58,363,350	50,660	795	15.7	0.26	47.3
NIMH88-1s1	NIMH88	chrX	61,905,249	61,916,897	11,648	144	12.4	-0.60	36.6
NIMH17-1s1	NIMH17	chrX	62,386,739	62,413,236	26,497	272	10.3	0.45	36.9
NIMH53-2s1	NIMH53	chrX	62,386,739	62,415,948	29,209	322	11.0	0.61	37.5
NIMH56-1s1	NIMH56	chrX	62,386,739	62,415,998	29,259	323	11.0	0.66	37.5
NIMH59-1s1	NIMH59	chrX	62,386,739	62,422,378	35,639	442	12.4	0.78	38.6
NIMH38-1s1	NIMH38	chrX	63,169,441	63,171,216	1,775	36	20.3	0.28	52.1
NIMH67-1s1	NIMH67	chrX	63,169,541	63,171,216	1,675	34	20.3	0.37	52.3
NIMH53-2s1	NIMH53	chrX	63,568,900	63,571,275	2,375	48	20.2	0.33	54.9
NIMH94-1s1	NIMH94	chrX	63,568,900	63,571,350	2,450	49	20.0	0.27	54.9
NIMH95-1s1	NIMH95	chrX	63,568,900	63,571,350	2,450	49	20.0	0.26	54.9
NIMH89-1s1	NIMH89	chrX	63,568,975	63,570,395	1,420	31	21.8	0.34	56.1
NIMH44-1s1	NIMH44	chrX	64,389,740	64,390,835	1,095	24	21.9	0.47	56.8
NIMH30-1s2	NIMH30	chrX	64,803,458	64,804,533	1,075	21	19.5	-0.34	59.7
NIMH73-2s1	NIMH73	chrX	64,939,637	64,941,872	2,235	40	17.9	-1.38	32.4
NIMH75-1s1	NIMH75	chrX	65,190,638	65,191,913	1,275	27	21.2	0.34	55.0
NIMH26-1s1	NIMH26	chrX	65,634,335	65,635,710	1,375	30	21.8	0.35	52.3
NIMH67-1s1	NIMH67	chrX	66,413,571	66,414,941	1,370	28	20.4	0.41	52.3
NIMH57-1s1	NIMH57	chrX	66,574,116	66,645,439	71,323	768	10.8	0.47	35.9
NIMH21-1s1	NIMH21	chrX	66,682,160	66,685,094	2,934	58	19.8	0.25	51.1
NIMH34-1s1	NIMH34	chrX	66,682,595	66,684,030	1,435	28	19.5	-0.46	59.0
NIMH44-1s1	NIMH44	chrX	66,682,595	66,684,070	1,475	29	19.7	-0.46	58.6
NIMH35-1s1	NIMH35	chrX	66,682,765	66,684,070	1,305	26	19.9	-0.48	58.7
NIMH25-1s1	NIMH25	chrX	66,682,945	66,683,935	990	20	20.2	-0.52	58.9
NIMH26-1s1	NIMH26	chrX	66,682,945	66,684,070	1,125	22	19.6	-0.65	57.1
NIMH33-1s1	NIMH33	chrX	66,683,180	66,683,935	755	17	22.5	-0.71	54.1
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NIMH69-2s1	NIMH69	chrX	66,893,410	66,894,459	1,049	16	15.3	0.48	39.3
NIMH100-1s1	NIMH100	chrX	67,040,582	67,046,892	6,310	82	13.0	-1.17	38.2
NIMH18-2s1	NIMH18	chrX	67,040,582	67,046,967	6,385	83	13.0	-1.00	38.2
NIMH50-1s1	NIMH50	chrX	67,040,582	67,046,967	6,385	83	13.0	-1.22	38.2
NIMH53-2s1	NIMH53	chrX	67,040,582	67,046,967	6,385	83	13.0	-1.04	38.2
NIMH75-1s1	NIMH75	chrX	67,040,582	67,046,967	6,385	83	13.0	-1.32	38.2
NIMH49-1s1	NIMH49	chrX	67,045,497	67,046,967	1,470	25	17.0	-1.83	41.0
NIMH79-1s1	NIMH79	chrX	67,046,867	67,046,967	100	3 27	30.0	-1.33	38.5
NIMH31-1s2 NIMH53-2s1	NIMH31 NIMH53	chrX chrX	67,168,843 67,168,878	67,170,063 67,169,728	1,220 850	19	22.1 22.4	0.52 0.45	56.0 55.7
NIMH95-1s1	NIMH95	chrX	67,168,913	67,169,693	780	17	21.8	0.38	55.8
NIMH32-1s1	NIMH32	chrX	67,853,287	67,860,578	7,291	148	20.3	0.27	56.5
NIMH10-1s1	NIMH10	chrX	67,879,927	67,880,997	1,070	23	21.5	-0.35	46.8
NIMH44-1s1	NIMH44	chrX	67,879,927	67,880,467	540	12	22.2	-0.41	47.1
NIMH05-2s1	NIMH05	chrX	67,959,824	67,977,396	17,572	349	19.9	0.30	55.6
NIMH20-1s1	NIMH20	chrX	68,027,878	68,051,613	23,735	426	17.9	0.34	52.1
R085B11-A02-1s1	R085B11	chrX	68,073,913	68,074,853	940	19	20.2	-0.57	37.6
NIMH95-1s1 NIMH20-1s1	NIMH95 NIMH20	chrX chrX	68,085,373 68,750,193	68,085,698 68,753,924	325 3,731	7	21.5 19.8	-0.56 0.30	46.8
NIMH120-151	NIMH120	chrX	69,333,412	69,334,482	1,070	23	21.5	-0.46	37.8
NIMH08-1s1	NIMH08	chrX	69,394,171	69,397,236	3,065	63	20.6	0.25	53.3
NIMH40-1s1	NIMH40	chrX	69,559,670	69,564,248	4,578	94	20.5	0.36	57.1
NIMH05-2s1	NIMH05	chrX	69,580,254	69,587,357	7,103	141	19.9	0.38	57.2
NIMH01-1s1	NIMH01	chrX	69,582,097	69,587,522	5,425	110	20.3	0.22	56.6
NIMH53-2s1	NIMH53	chrX	69,582,247	69,587,132	4,885	99	20.3	0.29	56.6
NIMH24-1s1	NIMH24	chrX	69,582,502	69,587,322	4,820	98	20.3	0.42	56.3
NIMH23-1s1 NIMH44-1s1	NIMH23 NIMH44	chrX chrX	69,582,882 69,582,957	69,588,307 69,586,782	5,425 3.825	104 78	19.2 20.4	0.30 0.35	55.2 56.9
NIMH34-151	NIMH44 NIMH34	chrX	69,583,177	69,587,322	3,825 4,145	85	20.4	0.35	56.0
NIMH10-1s1	NIMH10	chrX	69,583,392	69,591,799	8,407	159	18.9	0.40	55.6
NIMH23-1s1	NIMH23	chrX	69,588,342	69,589,644	1,302	25	19.2	-0.41	61.0
NIMH26-1s1	NIMH26	chrX	69,771,733	69,773,308	1,575	34	21.6	0.36	58.1
NIMH96-1s1	NIMH96	chrX	69,771,793	69,773,378	1,585	34	21.5	0.26	58.7
NIMH57-1s1	NIMH57	chrX	70,064,599	70,065,219	620	13	21.0	0.57	51.2
NIMH40-1s1	NIMH40	chrX	70,232,943	70,240,470	7,527	152	20.2	0.24	52.4
NIMH56-1s1	NIMH56	chrX	70,237,391	70,241,239	3,848	78	20.3	0.28	53.1
NIMH01-1s1 NIMH57-1s1	NIMH01 NIMH57	chrX chrX	70,240,695 70,240,695	70,241,094 70,241,094	399 399	8 8	20.1 20.1	0.67 0.73	49.3 49.3
NIMH93-1s1	NIMH93	chrX	70,268,884	70,269,809	925	19	20.1	-0.42	49.6
NIMH53-2s1	NIMH53	chrX	70,268,989	70,269,809	820	17	20.7	-0.41	48.4
NIMH66-1s1	NIMH66	chrX	70,269,054	70,269,809	755	16	21.2	-0.37	48.3
NIMH67-1s1	NIMH67	chrX	70,269,054	70,269,809	755	16	21.2	-0.38	48.3
NIMH95-1s1	NIMH95	chrX	70,269,054	70,269,809	755	16	21.2	-0.36	48.3
NIMH05-2s1	NIMH05	chrX	70,269,139	70,308,820	39,681	650	16.4	0.25	51.4
NIMH60-1s1	NIMH60	chrX	70,269,194	70,269,809	615	13	21.1	-0.44	47.3
NIMH06-1s1 NIMH24-1s1	NIMH06 NIMH24	chrX chrX	70,270,335 70,270,933	70,292,614 70,308,748	22,279 37,815	387 625	17.4 16.5	0.26 0.22	53.0 51.5
NIMH08-1s1	NIMH08	chrX	70,281,273	70,282,333	1,060	21	19.8	0.22	61.4
NIMH67-1s1	NIMH67	chrX	70,281,428	70,292,354	10,926	208	19.0	0.28	55.1
NIMH07-1s1	NIMH07	chrX	70,283,385	70,291,824	8,439	158	18.7	0.23	55.3
NIMH34-1s1	NIMH34	chrX	70,283,780	70,291,824	8,044	150	18.6	0.22	55.3
NIMH06-1s1	NIMH06	chrX	70,351,393	70,395,754	44,361	644	14.5	0.21	50.4
NIMH47-1s1	NIMH47	chrX	70,380,938	70,392,200	11,262	226	20.1	0.20	54.7
NIMH35-1s1	NIMH35	chrX	70,556,721	70,558,233	1,512	24	15.9	-0.53	49.6
NIMH23-1s1 NIMH34-1s1	NIMH23 NIMH34	chrX chrX	70,714,076 70,714,076	70,714,868 70,714,868	792 792	18 18	22.7 22.7	-1.05 -0.65	49.3 49.3
NIMH32-1s1	NIMH34	chrX	70,714,078	70,714,868	792	10	22.7	-0.05	49.3
NIMH33-1s1	NIMH33	chrX	70,714,111	70,714,868	757	17	22.5	-0.92	49.8
NIMH40-1s1	NIMH40	chrX	70,714,111	70,714,868	757	17	22.5	-1.02	49.8
NIMH24-1s1	NIMH24	chrX	70,751,857	70,755,120	3,263	66	20.2	0.37	59.4
NIMH01-1s1	NIMH01	chrX	70,753,802	70,754,720	918	20	21.8	0.37	59.2
NIMH05-2s1	NIMH05	chrX	70,753,927	70,755,005	1,078	23	21.3	0.54	58.8
NIMH05-2s1	NIMH05	chrX	70,795,042	70,809,426	14,384	234	16.3	0.31	56.0
NIMH30-1s2 NIMH45-1s1	NIMH30 NIMH45	chrX chrX	70,796,237 70,796,237	70,807,097 70,804,362	10,860 8,125	176 136	16.2 16.7	0.41 0.30	58.4 57.8
NIMH45-181 NIMH32-1s1	NIMH45 NIMH32	chrX	70,796,237	70,804,362	6,370	136	15.9	0.30	57.8
NIMH61-1s1	NIMH61	chrX	70,796,287	70,802,037	7,250	118	16.3	0.29	57.1
NIMH90-1s1	NIMH90	chrX	70,796,467	70,816,402	19,935	269	13.5	0.19	54.4
NIMH60-1s1	NIMH60	chrX	70,796,602	70,803,697	7,095	115	16.2	0.31	58.0
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		ohrV.	70 706 600	70 000 507	6.025	110	16.1	0.22	57.0
NIMH76-1s1 NIMH21-1s1	NIMH76 NIMH21	chrX chrX	70,796,602 70,796,687	70,803,537 70,817,797	6,935 21,110	112 290	16.1 13.7	0.33 0.28	57.9 54.4
NIMH23-1s1	NIMH23	chrX	71,002,886	71,012,160	9,274	167	18.0	0.32	56.1
NIMH44-1s1	NIMH44	chrX	71,002,886	71,010,435	7,549	132	17.5	0.34	57.8
NIMH47-1s1	NIMH47	chrX	71,002,886	71,010,575	7,689	135	17.6	0.30	57.7
NIMH38-1s1	NIMH38	chrX	71,002,956	71,010,500	7,544	132	17.5	0.26	57.8
NIMH31-1s2	NIMH31	chrX	71,002,991	71,010,550	7,559	132	17.5	0.39	57.7
NIMH29-1s1	NIMH29	chrX	71,003,031	71,010,550	7,519	131	17.4	0.30	57.8
NIMH75-1s1 NIMH76-1s1	NIMH75 NIMH76	chrX chrX	71,003,106 71,003,251	71,010,575 71,010,550	7,469 7,299	131 127	17.5 17.4	0.25 0.33	57.7 57.9
NIMH96-1s1	NIMH96	chrX	71,003,251	71,010,390	7,299	127	17.4	0.33	58.0
NIMH07-1s1	NIMH07	chrX	71,076,155	71,077,815	1,660	34	20.5	-0.31	44.3
NIMH23-1s1	NIMH23	chrX	71,076,275	71,077,710	1,435	30	20.9	-0.49	43.7
NIMH25-1s1	NIMH25	chrX	71,076,415	71,077,605	1,190	25	21.0	-0.37	45.7
R085B11-A02-1s1	R085B11	chrX	71,076,415	71,077,845	1,430	30	21.0	-0.47	45.4
NIMH45-1s1	NIMH45	chrX	71,263,902	71,277,588	13,686	253	18.5	0.20	52.6
NIMH95-1s1	NIMH95	chrX	72,508,629	72,509,617	988	21	21.3	0.30	51.6
NIMH26-1s1	NIMH26	chrX	73,241,432	73,242,800	1,368	25	18.3	-0.52	48.8
NIMH35-1s1	NIMH35	chrX	73,241,532	73,242,770	1,238	22	17.8	-0.52	49.4
NIMH26-1s1	NIMH26	chrX	73,490,299	73,492,409	2,110	43	20.4	0.34	57.4
NIMH08-1s1 NIMH92-1s1	NIMH08 NIMH92	chrX chrX	73,556,087 74,894,569	73,559,230 74,897,094	3,143 2,525	60 51	19.1 20.2	0.29	61.9 52.9
NIMH53-2s1	NIMH53	chrX	75,056,185	75,058,000	1,815	38	20.2	0.27	50.6
NIMH32-1s1	NIMH32	chrX	76,094,002	76,095,172	1,170	24	20.5	0.44	54.0
NIMH30-1s2	NIMH30	chrX	77,382,294	77,383,534	1,240	27	21.8	0.41	54.5
NIMH95-1s1	NIMH95	chrX	77,408,661	77,410,671	2,010	36	17.9	-1.40	34.7
NIMH96-1s1	NIMH96	chrX	77,418,594	77,419,609	1,015	22	21.7	0.38	47.4
NIMH02-1s1	NIMH02	chrX	77,670,756	77,674,677	3,921	76	19.4	-0.96	39.5
NIMH38-1s1	NIMH38	chrX	79,023,200	79,024,210	1,010	19	18.8	0.36	53.3
NIMH96-1s1	NIMH96	chrX	79,023,200	79,024,165	965	18	18.7	0.33	53.1
NIMH20-1s1 NIMH44-1s1	NIMH20 NIMH44	chrX chrX	79,950,500	79,952,087	1,587 1,230	31 25	19.5 20.3	0.54	57.6 51.8
NIMH66-1s1	NIMH44	chrX	80,090,638 80,709,705	80,091,868 80,710,600	895	20	20.3	0.41	52.5
NIMH66-1s1	NIMH66	chrX	80,800,442	80,801,117	675	13	19.3	0.48	51.0
NIMH63-1s1	NIMH63	chrX	81,593,858	81,595,213	1,355	29	21.4	0.36	55.3
NIMH40-1s1	NIMH40	chrX	81,594,003	81,595,038	1,035	22	21.3	0.45	55.4
NIMH92-1s1	NIMH92	chrX	81,594,218	81,595,038	820	18	22.0	0.43	55.1
NIMH17-1s1	NIMH17	chrX	82,010,041	82,038,392	28,351	437	15.4	-0.93	35.6
NIMH18-2s1	NIMH18	chrX	82,086,347	82,094,874	8,527	86	10.1	-1.04	39.0
NIMH92-1s1	NIMH92	chrX	82,772,373	82,773,418	1,045	23	22.0	0.38	54.3
NIMH67-1s1	NIMH67	chrX	83,538,054	83,539,144	1,090	23	21.1	0.50	51.7
NIMH44-1s1 NIMH92-1s1	NIMH44 NIMH92	chrX chrX	83,932,043 84,249,035	83,933,368 84,250,590	1,325 1,555	28 26	21.1 16.7	0.40	54.6 51.7
NIMH51-1s1	NIMH92 NIMH51	chrX	84,249,035	84,250,590	1,340	20	15.7	0.39	51.7
NIMH40-1s1	NIMH40	chrX	85,289,146	85,291,026	1,880	37	19.7	0.00	55.8
NIMH75-1s1	NIMH75	chrX	86,344,982	86,345,757	775	17	21.9	0.48	47.8
NIMH100-1s1	NIMH100	chrX	87,546,038	87,547,547	1,509	14	9.3	-0.68	35.5
NIMH55-1s1	NIMH55	chrX	87,546,038	87,547,547	1,509	14	9.3	-0.44	35.5
NIMH54-1s1	NIMH54	chrX	87,546,283	87,547,547	1,264	12	9.5	-0.68	35.6
NIMH100-1s1	NIMH100	chrX	88,187,301	88,194,167	6,866	108	15.7	-1.43	34.5
NIMH53-2s1	NIMH53	chrX	90,605,772	90,614,285	8,513	115	13.5	0.40	35.5
NIMH78-1s1	NIMH78	chrX	93,105,619	93,113,214	7,595	135	17.8	-1.00	36.9
NIMH48-1s1 NIMH82-1s1	NIMH48 NIMH82	chrX chrX	93,851,036 94,957,598	93,859,017 94,970,430	7,981 12,832	90 221	11.3 17.2	-0.71 0.39	37.2 33.9
NIMH95-1s1	NIMH95	chrX	96,879,072	96,993,242	114,170	1,823	16.0	0.59	39.2
NIMH75-1s1	NIMH75	chrX	97,793,406	97,794,315	909	1,023	18.7	0.31	40.4
NIMH92-1s1	NIMH92	chrX	97,856,161	97,857,221	1,060	22	20.8	0.36	52.8
NIMH31-1s2	NIMH31	chrX	98,858,607	98,859,887	1,280	27	21.1	0.47	56.8
NIMH66-1s1	NIMH66	chrX	98,858,777	98,859,887	1,110	23	20.7	0.33	57.1
NIMH92-1s1	NIMH92	chrX	98,858,852	98,859,887	1,035	22	21.3	0.37	57.1
NIMH75-1s1	NIMH75	chrX	99,629,579	99,630,514	935	18	19.3	-0.33	42.6
NIMH33-1s1	NIMH33	chrX	100,112,514	100,118,106	5,592	54	9.7	-0.26	49.3
NIMH30-1s2 NIMH75-1s1	NIMH30	chrX chrX	100,374,228	100,377,275	3,047 315	62 7	20.3 22.2	0.33	52.7
NIMH75-151 NIMH10-1s1	NIMH75 NIMH10	chrX	100,491,293 100,627,528	100,491,608 100,633,446	5,918	113	19.1	0.61	44.1 50.0
NIMH05-2s1	NIMH10	chrX	100,627,528	100,636,096	7,441	148	19.1	0.30	53.8
NIMH24-1s1	NIMH24	chrX	100,630,171	100,634,981	4,810	99	20.6	0.36	55.0
NIMH53-2s1	NIMH53	chrX	100,633,491	100,636,131	2,640	53	20.1	0.29	57.9
NIMH25-1s1	NIMH25	chrX	100,635,456	100,636,646	1,190	25	21.0	-0.50	48.7
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NUMH23-151 NIMH23 chrX 100,635,466 100,363,131 645 13 20.2 -0.98 54.2 NIMH33 chrX 100,635,481 100,363,131 645 13 20.2 -0.83 54.2 NIMH33 chrX 100,635,481 100,353,131 645 13 20.2 -0.83 54.2 NIMH33 chrX 100,635,485 100,353,131 645 13 20.2 -0.83 54.2 NIMH35 chrX 100,635,485 100,353,131 645 13 20.2 -0.83 54.2 NIMH35 chrX 100,635,485 100,353,131 645 13 20.2 -0.83 54.2 NIMH35 chrX 100,635,485 100,353,131 645 13 20.2 -0.83 54.2 NIMH35 chrX 101,000,534,185 100,535,185 10,595										
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NIMH21-1s1 NIMH21 chrX 107,862,375 107,867,535 5,160 100 19.4 0.40 56.6 NIMH63-1s1 NIMH63 chrX 108,023,544 108,024,794 1,250 27 21.6 0.36 54.7 NIMH32-1s1 NIMH35 chrX 108,859,590 108,864,517 4,927 90 18.3 -0.25 43.8 NIMH30-1s2 NIMH30 chrX 108,863,302 108,863,917 615 13 21.1 -0.72 54.1 NIMH33-1s1 NIMH33 chrX 108,863,302 108,863,997 550 13 23.6 -0.65 47.0 NIMH73-1s1 NIMH73 chrX 109,944,8175 109,449,226 1,051 22 20.9 -0.60 43.5 NIMH24-1s1 NIMH20 chrX 110,226,483 10,228,547 3,064 62 20.2 0.35 52.4 NIMH28-1s1 NIMH28 chrX 110,236,771 110,236,786 1,615 35 21.7 0.43<	NIMH34-1s1	NIMH34	chrX	106,956,814	106,957,394	580	13	22.4	-0.71	47.8
NIMH63-1s1 NIMH63 chrX 108,023,544 108,024,794 1,250 27 21.6 0.36 54.7 NIMH32-1s1 NIMH32 chrX 108,859,431 108,864,197 4,766 86 18.0 -0.26 43.8 NIMH30-1s2 NIMH30 chrX 108,863,302 108,863,997 550 13 21.1 -0.75 54.1 NIMH33-1s1 NIMH33 chrX 109,863,447 108,863,997 550 13 23.6 -0.65 47.0 NIMH43-1s1 NIMH73 chrX 109,907,243 109,110,882 13,639 224 16.4 -1.60 39.0 NIMH44-1s1 NIMH44 chrX 109,448,175 109,449,226 1,051 22 20.9 -0.60 43.5 NIMH20-1s1 NIMH20 chrX 109,235,171 110,226,763 2,710 56 20.7 0.27 52.0 NIMH22-1s1 NIMH28 chrX 110,236,761 1,615 35 21.7 0.43 40.0	NIMH35-1s1	NIMH35	chrX	106,956,814	106,957,289	475	11	23.2	-0.61	47.8
NIMH32-1s1 NIMH32 chrX 108,859,431 108,864,517 4,766 86 18.0 -0.26 43.8 NIMH35-1s1 NIMH36 chrX 108,863,302 108,864,517 4,927 90 18.3 -0.26 43.7 NIMH30-1s2 NIMH30 chrX 108,863,302 108,863,917 615 13 21.1 -0.72 54.1 NIMH33-1s1 NIMH73 chrX 108,863,447 108,863,997 550 13 23.6 -0.66 47.0 NIMH44-1s1 NIMH44 chrX 109,907,243 109,910,882 13,639 224 16.4 -1.60 39.0 NIMH08-1s1 NIMH42 chrX 109,924,373 109,927,083 2,710 56 20.7 0.27 52.0 NIMH29-1s1 NIMH20 chrX 110,235,171 110,236,751 1,580 34 21.5 0.82 40.4 NIMH419-1s1 NIMH44 chrX 111,210,953 111,213,888 2,935 55 18.7 0.	NIMH21-1s1	NIMH21	chrX	107,862,375	107,867,535	5,160	100	19.4	0.40	56.6
NIMH35-1s1 NIMH35 chrX 100,859,590 108,864,517 4,927 90 18.3 -0.25 43.7 NIMH30-1s2 NIMH30 chrX 108,863,302 108,863,917 615 13 21.1 -0.72 54.1 NIMH33-1s1 NIMH33 chrX 108,863,447 108,863,997 550 13 23.6 -0.65 47.0 NIMH73-1s1 NIMH44 chrX 109,097,243 109,110,882 13,639 224 16.4 -1.60 39.0 NIMH20-1s1 NIMH20 chrX 109,924,373 109,927,083 2,710 56 20.7 0.27 52.0 NIMH20-1s1 NIMH20 chrX 110,235,171 110,236,786 1,615 35 21.7 0.43 40.0 NIMH44-1s1 NIMH13 chrX 111,210,953 111,213,888 2,935 55 18.7 0.31 56.0 NIMH19-1s1 NIMH13 chrX 111,253,733 111,213,888 2,935 55 18.7 0.31	NIMH63-1s1	NIMH63	chrX	108,023,544	108,024,794	1,250	27	21.6	0.36	54.7
NIMH30-1s2 NIMH30 chrx 108,863,302 108,863,917 615 13 21.1 -0.72 54.1 NIMH33-1s1 NIMH33 chrx 109,907,243 109,110,882 13,639 224 16.4 -1.60 39.0 NIMH44-1s1 NIMH44 chrx 109,924,373 109,927,083 2,710 56 20.7 0.27 52.0 NIMH20-1s1 NIMH20 chrx 110,225,483 110,228,547 3,064 62 20.2 0.35 52.4 NIMH28-1s1 NIMH28 chrx 110,235,171 110,236,751 1,580 34 21.5 0.82 40.4 NIMH29-2s1 NIMH29 chrx 111,71,799 111,72,864 1,065 17 16.0 -0.45 38.8 NIMH13-1s1 NIMH4 chrX 111,210,953 111,213,728 2,295 43 18.7 0.37 57.9 NIMH42-1s1 NIMH42 chrX 111,753,733 114 23.2 -0.85 36.4	NIMH32-1s1	NIMH32	chrX	108,859,431	108,864,197	4,766	86	18.0	-0.26	43.8
NIMH33-1s1 NIMH33 chrX 108,863,447 108,863,997 550 13 23.6 -0.65 47.0 NIMH73-1s1 NIMH73 chrX 109,097,243 109,110,882 13,639 224 16.4 -1.60 39.0 NIMH84-1s1 NIMH44 chrX 109,448,175 109,449,226 1,051 22 20.9 -0.60 43.5 NIMH85-1s1 NIMH08 chrX 109,924,373 109,927,083 2,710 56 20.7 0.27 52.0 NIMH20-1s1 NIMH28 chrX 110,235,171 110,236,751 1,580 34 21.5 0.82 40.4 NIMH29-2s1 NIMH29 chrX 111,210,953 111,213,888 2,935 55 18.7 0.31 56.0 NIMH33-1s1 NIMH13 chrX 111,210,953 111,213,888 2,935 55 18.7 0.31 56.0 NIMH42-1s1 NIMH55 chrX 111,753,7119 111,753,733 614 14 22.8 -0.9	NIMH35-1s1	NIMH35	chrX	108,859,590	108,864,517	4,927	90	18.3	-0.25	43.7
NIMH73-1s1 NIMH73 chrX 109,097,243 109,110,882 13,639 224 16.4 -1.60 39.0 NIMH44-1s1 NIMH44 chrX 109,448,175 109,449,226 1,051 22 20.9 -0.60 43.5 NIMH08-1s1 NIMH08 chrX 109,924,373 109,927,083 2,710 56 20.7 0.27 52.0 NIMH20-1s1 NIMH28 chrX 110,225,483 110,226,751 1,580 34 21.5 0.82 40.4 NIMH29-2s1 NIMH29 chrX 110,235,171 110,236,786 1,615 35 21.7 0.43 40.0 NIMH44-1s1 NIMH13 chrX 111,717,799 111,172,864 1,065 17 16.0 -0.45 38.8 NIMH13-1s1 NIMH13 chrX 111,213,888 2,935 55 18.7 0.37 57.9 NIMH22-1s1 NIMH22 chrX 111,553,753 614 14 22.8 -0.90 27.8 <		NIMH30								
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	14101123-151	NIIVI120	UIIX	114,211,004	114,211,044	510	12	20.0	-0.74	

		- h- nV	444 044 404	44.4.040.04.4	500	40	00.4	0.00	20.0
NIMH69-2s1		chrX	114,211,434	114,212,014 114,212,014	580	13	22.4 22.4	-0.96	39.2 39.2
NIMH80-1s1 NIMH89-1s1	NIMH80 NIMH89	chrX chrX	114,211,434 114,211,434	114,212,014	580 580	13 13	22.4 22.4	-0.74 -0.81	39.2
NIMH100-1s1	NIMH109	chrX	114,211,569	114,211,944	375	9	24.0	-0.83	38.5
NIMH84-1s1	NIMH84	chrX	114,330,245	114,332,885	2,640	50	18.9	0.44	64.6
NIMH76-1s1	NIMH76	chrX	114,330,280	114,333,090	2,810	53	18.9	0.38	64.6
NIMH89-1s1	NIMH89	chrX	114,330,280	114,332,800	2,520	47	18.7	0.35	64.6
NIMH60-1s1	NIMH60	chrX	114,330,390	114,333,225	2,835	53	18.7	0.46	65.3
NIMH90-1s1	NIMH90	chrX	114,330,460	114,333,305	2,845	53	18.6	0.33	65.4
NIMH80-1s1	NIMH80	chrX	114,331,095	114,333,140	2,045	41	20.0	0.36	64.9
NIMH94-1s1	NIMH94	chrX	114,331,095	114,333,140	2,045	41	20.0	0.41	64.9
NIMH33-1s1	NIMH33	chrX	114,331,515	114,333,225	1,710	33	19.3	0.48	65.4
NIMH40-1s1	NIMH40	chrX	114,331,515	114,333,090	1,575	31	19.7	0.57	65.3
NIMH64-1s1	NIMH64	chrX	114,447,000	114,450,751	3,751	56	14.9	0.78	35.7
NIMH38-1s1	NIMH38	chrX	114,448,445	114,455,800	7,355	96	13.1	0.28	38.4
NIMH43-1s1	NIMH43	chrX	114,448,445	114,450,485	2,040	24	11.8	0.90	34.5
NIMH01-1s1	NIMH01	chrX	114,448,780	114,450,485	1,705	23	13.5	0.68	31.2
NIMH08-1s1	NIMH08	chrX	114,448,780	114,450,485	1,705	23	13.5	0.71	31.2
NIMH17-1s1	NIMH17	chrX	114,448,780	114,450,751	1,971	27	13.7	0.77	30.6
NIMH24-1s1	NIMH24	chrX	114,448,780	114,450,485	1,705	23	13.5	0.82	31.2
NIMH27-A03-2s2	NIMH27	chrX	114,448,780	114,450,485	1,705	23	13.5	0.82	31.2
NIMH29-2s1	NIMH29	chrX	114,448,780	114,450,485	1,705	23	13.5	0.93	31.2
NIMH32-1s1	NIMH32	chrX	114,448,780	114,450,485	1,705	23	13.5	0.70	31.2
NIMH34-1s1	NIMH34	chrX	114,448,780	114,450,751	1,971	27	13.7	0.64	30.6
NIMH44-1s1	NIMH44	chrX	114,448,780	114,450,485	1,705	23	13.7	1.01	31.2
NIMH48-1s1	NIMH44	chrX	114,448,780	114,450,485	1,705	23	13.5	1.20	31.2
NIMH50-1s1	NIMH50	chrX	114,448,780	114,450,751	1,971	27	13.7	0.95	30.6
NIMH51-1s1	NIMH51	chrX	114,448,780	114,450,836	2,056	28	13.6	0.78	30.6
NIMH53-2s1	NIMH53	chrX	114,448,780	114,450,485	1,705	23	13.5	1.02	31.2
NIMH54-1s1	NIMH54	chrX	114,448,780	114,450,751	1,971	27	13.7	0.81	30.6
NIMH55-1s1	NIMH55	chrX	114,448,780	114,450,485	1,705	23	13.5	0.84	31.2
NIMH57-1s1	NIMH57	chrX	114,448,780	114,450,485	1,705	23	13.5	0.98	31.2
NIMH60-1s1	NIMH60	chrX	114,448,780	114,450,485	1,705	23	13.5	0.90	31.2
NIMH63-1s1	NIMH63	chrX	114,448,780	114,450,751	1,971	27	13.7	1.06	30.6
NIMH67-1s1	NIMH67	chrX	114,448,780	114,450,485	1,705	23	13.5	0.86	31.2
NIMH69-2s1	NIMH69	chrX	114,448,780	114,450,485	1,705	23	13.5	1.20	31.2
NIMH75-1s1	NIMH75	chrX	114,448,780	114,450,445	1,665	23	13.2	1.04	31.1
NIMH76-1s1	NIMH76	chrX	114,448,780	114,450,485	1,705	23	13.5	1.04	31.2
NIMH80-1s1	NIMH80	chrX	114,448,780	114,450,485	1,705	23	13.5	1.11	31.2
NIMH86-1s2	NIMH86	chrX	114,448,780	114,450,485	1,705	23	13.5	0.73	31.2
NIMH87-A03-2s2	NIMH87	chrX	114,448,780	114,450,696	1,916	26	13.6	0.52	30.3
NIMH88-1s1	NIMH88	chrX	114,448,780	114,450,485	1,705	23	13.5	1.11	31.2
NIMH89-1s1	NIMH89	chrX	114,448,780	114,450,445	1,665	22	13.2	1.09	31.1
NIMH92-1s1	NIMH92	chrX	114,448,780	114,450,485	1,705	23	13.5	0.70	31.2
NIMH04-1s1	NIMH04	chrX	114,448,850	114,450,751	1,901	26	13.7	0.78	30.6
NIMH100-1s1	NIMH100	chrX	114,448,850	114,450,445	1,595	20	13.2	1.17	31.0
NIMH42-1s1	NIMH42	chrX	114,448,850	114,450,485	1,635	22	13.5	0.94	31.1
NIMH42-151 NIMH61-1s1	NIMH61	chrX	114,448,850	114,450,485	1,635	22	13.5	1.00	31.1
NIMH81-1s1	NIMH81	chrX	114,448,850	114,450,485	1,635	22	13.5	0.91	31.1
NIMH82-1s1	NIMH82	chrX	114,448,850	114,450,485	1,635	22	13.5	0.97	31.1
NIMH84-1s1	NIMH84	chrX	114,448,850	114,450,751	1,901	26	13.7	0.76	30.6
NIMH85-1s1	NIMH85	chrX	114,448,850	114,450,445	1,595	20	13.2	0.96	31.0
NIMH90-1s1	NIMH90	chrX	114,448,850	114,450,445	1,635	21	13.2	1.00	31.1
NIMH93-1s1	NIMH93	chrX	114,448,850	114,450,485	1,635	22	13.5	1.15	31.1
NIMH96-1s1	NIMH96	chrX	114,448,850	114,450,445	1,595	21	13.2	1.13	31.0
NIMH35-1s1	NIMH35	chrX	114,542,598	114,542,714	116	4	34.5	-1.10	29.7
NIMH35-191	NIMH35	chrX	114,925,429	114,937,770	12,341	248	20.1	0.24	29.7 51.8
NIMH31-181 NIMH39-1s1	NIMH31	chrX	114,925,594	114,937,685	12,341 12,091	248 243	20.1	0.24	51.8
NIMH39-1s1	NIMH39	chrX	114,925,594	114,937,715	9,531	243 191	20.1	0.25	52.2
			114,928,184						
NIMH27-A03-2s2	NIMH27	chrX		114,937,715	625	14	22.4	0.63	48.3
NIMH93-1s1	NIMH93	chrX	114,937,090	114,937,685	595 505	13	21.8	0.59	48.7
NIMH95-1s1	NIMH95	chrX	114,937,090	114,937,685	595	13	21.8	0.49	48.7
NIMH96-1s1	NIMH96	chrX	115,051,924	115,052,093	169	4	23.7	0.75	33.7
NIMH87-A03-2s2	NIMH87	chrX	115,103,362	115,104,537	1,175	25	21.3	0.31	53.1
NIMH53-2s1	NIMH53	chrX	115,623,901	115,624,841	940	21	22.3	0.39	53.1
NIMH96-1s1	NIMH96	chrX	116,022,711	116,023,328	617	11	17.8	-0.44	34.4
NIMH05-2s1	NIMH05	chrX	116,022,771	116,023,121	350	8	22.9	-0.65	35.6
NIMH40-1s1	NIMH40	chrX	116,087,691	116,089,407	1,716	29	16.9	0.45	54.7
NIMH44-1s1	NIMH44	chrX	116,266,983	116,267,663	680	13	19.1	-0.47	36.1
NIMH87-A03-2s2	NIMH87	chrX	116,322,669	116,323,804	1,135	24	21.1	0.33	54.7
									241

NIMHES INIMHES Chr. T16, 675, 035 T17, 85, 58 Z Z D D44 S5, 55 S S5, 57 T17, 70, 34 G2, 14 S5, 77 D3, 98 Z L17, 70, 34 G2, 14 T17, 70, 34 G2, 17 D3, 88 S5, 78										
NIMH01-Isit NIMH12-Isit	NIMH56-1s1	NIMH56	chrX	116,675,035	116,675,610	575	12	20.9	0.57	39.6
NIMH12-1s1 NIMH12 OrtX NIMH20-1s1										
NIMME20-Isit NIMME20 chrX 117.841.298 117.847.010 5,712 108 20.0 45 52.2 NIMME7-Sits NIMM16 chrX 117.846.201 117.846.201 330.0 8 24.2 0.44 50.3 NIMM12-51st NIMM127 chrX 117.993.789 117.994.019 330.0 8 24.2 0.44 50.3 NIMM12-Sits NIMM122 chrX 11.293.789 117.994.019 330.0 8 24.2 0.44 50.3 NIMM122-Isits NIMM122 chrX 118.241.004 118.241.509 505 8 15.8 -1.37 85.5 R085811 IAX 118.220.584 118.291.309 90 22.31 -0.78 85.9 NIMM465-1st NIMM462 NIM1122 IS.41 118.290.584 118.291.309 90 22.21 0.36 80.44 6 NIMM422-1st NIMM42 NIM122 IS.4118.416.189 118.417.149 960 20 20.8 0.68 <				, ,	,,					
NIMH87-003-282 NIMH87 OTX T17.8845.710 T17.8847.10 330 8 24.2 0.44 55.2 NIMH76-1st NIMH76-1st NIMH76-1st NIMH76-1st NIMH76-1st NIMH76-1st NIMH76-1st NIMH76-1st NIMH27-003-2st NIMH27-003-2st NIMH22 NIMH22 <td></td>										
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NIMH161 Chr.X 117.991.019 117.994.644 3.625 64 17.7 0.34 62.1 NIMH22.3161 NIMH23 Chr.X 118.241.004 118.242.158 1.164 21 18.2 7.7 47.1 NIMH23.161 NIMH23.0 Chr.X 118.241.004 118.241.509 505 8 15.8 -1.23 555.5 NIMH30.162 NIMH30.0 Chr.X 118.241.004 118.241.509 505 8 15.8 -1.23 555.5 NIMH661.61 NIMH66.0 Chr.X 118.290.604 118.291.809 785 17 0.49 635 17 0.49 635 17 1.9 0.40 639 16.14 118.161.81 118.291.409 200 20.8 -0.62 44.6 NIMH23-161 NIMH24.118.290.404 885 19 21.5 -0.54 44.6 NIMH24.114.149 960 20 20.8 -0.62 44.6 NIMH24.114.149 118.201.604 118.417.149 960 21.5 -0.64 45					, ,					
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NIMH20-isi NIMH20 chrX 118.241.004 118.241.009 505 8 15.8 -1.37 55.5 R0585111-003-1si R0585111 chrX 118.255.534 300 9 2.3.1 -0.78 51.8 R0585111-003-1si R0585111 chrX 118.290.364 118.291.369 785 17 21.7 0.36 58.9 NIMH463-1si NIMH463 chrX 118.290.364 118.291.369 785 17 21.7 0.40 53.9 NIMH22-isi NIMH26 chrX 118.416.189 118.417.149 960 20 20.8 -0.64 46.6 NIMH32-isi NIMH34 chrX 118.416.264 118.417.149 985 19 21.5 -0.66 45.3 NIMH35-isi NIMH36 chrX 118.416.359 118.417.149 185 19 21.5 -0.66 45.4 NIMH36-isi NIMH40-isi NIMH40-isi 118.416.359 118.417.149 180 17.2 0.54 45.7 <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>-</td>										-
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NIMH-BG-Is1 NIMH-BG chrx 118,290,749 118,291,604 855 17 19.9 0.40 63.9 NIMH20-Is1 NIMH23 chrx 118,416,189 118,417,149 960 20.8 0.64 44.6 NIMH24-Is1 NIMH30 chrx 118,416,189 118,417,149 960 20.2 0.8 0.63 44.6 NIMH20-Is2 NIMH30 chrx 118,416,264 118,417,149 865 19 21.5 0.66 45.3 NIMH25-Is1 NIMH26-Is1 NIMH27 NIME6-Is1 NIMH2										
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NIMH30-1s2 NIMH30 chrx 118,416,264 118,417,149 885 19 21.5 -0.68 45.3 NIMH40-1s1 NIMH40 chrx 118,416,264 118,417,149 885 19 21.5 -0.66 45.3 NIMH25-1s1 NIMH31 chrx 118,416,359 118,417,149 790 17 21.5 -0.66 46.4 NIMH35-1s1 NIMH08 chrx 118,463,037 118,483,522 3.316 57 17.2 -0.84 46.3 NIMH55-1s1 NIMH64 chrx 118,643,287 5,647 70 12.4 0.68 46.3 NIMH51-1s1 NIMH54 chrx 118,537,664 118,542,287 5,647 70 12.4 0.69 46.3 NIMH30-1s2 NIMH30 chrx 118,577,664 118,542,287 5,647 70 12.4 0.69 65.0 NIMH30-1s2 NIMH30 chrx 118,709,537 118,711,117 1.35 24 19.4 -0.35 65.0										
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NIMH40-1s1 NIMH40 chrx 118,416,264 118,417,149 885 19 21.5 -0.60 45.3 NIMH25-1s1 NIMH31 chrx 118,416,359 118,417,149 790 17 21.5 -0.61 46.4 NIMH35-1s1 NIMH35 chrx 118,446,359 118,417,149 790 17 21.5 -0.61 46.4 NIMH45-1s1 NIMH54 chrx 118,450,357 118,482,352 3,315 57 17.2 0.34 64.7 NIMH54-1s1 NIMH55 chrx 118,537,640 118,542,287 5,647 70 12.4 0.69 46.3 NIMH30-1s2 NIMH30 chrx 118,537,650 118,543,287 5,647 70 12.4 0.69 46.3 NIMH30-1s2 NIMH30 chrx 118,709,537 118,711,121 1,575 30 19.0 -0.38 66.0 NIMH30-1s2 NIMH37 118,711,182 118,711,423 3,180 63 19.8 0.316 63.9 <td></td>										
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NIMH27-A03-2s2 NIMH27 chrx 120,476,406 120,477,601 1,195 26 21.8 0.49 42.8 NIMH21-1s1 NIMH21 chrX 120,816,694 1,800 37 20.6 0.35 55.0 NIMH53-2s1 NIMH67 chrX 121,132,578 121,142,362 9,784 162 16.6 -1.16 33.0 NIMH51-1s1 NIMH67 chrX 121,400,522 121,403,442 2,990 57 19.3 0.26 52.4 NIMH51 chrX 121,400,547 121,403,567 2,770 53 19.1 0.33 52.3 NIMH66-1s1 NIMH66 chrX 121,400,547 121,403,582 740 14 18.9 0.39 51.6 NIMH96-1s1 NIMH96 chrX 121,400,842 121,403,582 2,740 53 19.3 0.31 51.9 NIMH96-1s1 NIMH96 chrX 121,400,841 121,907,519 1,176 23 19.6 -0.35 38.3	NIMH57-1s1	NIMH57	chrX	120,476,163	120,477,746	1,583	34	21.5	0.34	41.5
NIMH21-1s1 NIMH21 chrX 120,814,894 120,816,694 1,800 37 20.6 0.35 55.0 NIMH53-2s1 NIMH53 chrX 121,132,578 121,142,362 9,784 162 16.6 -1.16 33.0 NIMH31 chrX 121,400,522 121,403,442 2,895 56 19.3 0.26 52.4 NIMH31 chrX 121,400,547 121,403,367 2,770 53 19.1 0.33 52.3 NIMH66-1s1 NIMH66 chrX 121,400,842 121,403,367 2,770 53 19.1 0.33 51.6 NIMH66-1s1 NIMH66 chrX 121,400,842 121,403,562 2,740 53 19.3 0.31 51.9 NIMH92-1s1 NIMH92 chrX 121,400,842 121,907,369 966 19 19.7 -0.43 38.3 NIMH53-chrX 121,906,443 121,907,7149 666 12 18.0 -0.52 37.9 NIMH454-1s1 NIMH54	NIMH29-2s1	NIMH29	chrX	120,476,188	120,477,406	1,218	26	21.3	0.39	43.1
NIMH53-2s1 NIMH53 chrX 121,132,578 121,142,362 9,784 162 16.6 -1.16 33.0 NIMH67-1s1 NIMH67 chrX 121,400,522 121,403,442 2,920 57 19.5 0.35 52.3 NIMH31-1s1 NIMH31 chrX 121,400,547 121,403,442 2,985 56 19.3 0.26 52.4 NIMH45-1s1 NIMH66 chrX 121,400,547 121,403,367 2,770 53 19.1 0.33 52.3 NIMH66-1s1 NIMH66 chrX 121,400,842 121,401,582 740 14 18.9 0.31 51.6 NIMH96 chrX 121,400,842 121,401,582 2,740 53 19.3 0.31 51.6 NIMH92.1s1 NIMH92 chrX 121,400,343 121,907,519 1,176 23 19.6 -0.35 38.8 NIMH53-2s1 NIMH69 chrX 121,906,343 121,907,349 966 19 19.7 -0.43 38.3	NIMH27-A03-2s2	NIMH27	chrX	120,476,406	120,477,601	1,195	26	21.8	0.49	42.8
NIMH67-1s1 NIMH67 chrX 121,400,522 121,403,442 2,920 57 19.5 0.35 52.3 NIMH31-1s1 NIMH31 chrX 121,400,547 121,403,342 2,955 57 19.3 0.26 52.4 NIMH76-1s1 NIMH76 chrX 121,400,547 121,403,367 2,770 53 19.1 0.33 52.3 NIMH66-1s1 NIMH66 chrX 121,400,842 121,403,367 2,770 53 19.1 0.33 51.6 NIMH96-1s1 NIMH06 chrX 121,400,842 121,403,502 2,225 42 18.9 0.30 51.6 NIMH92-1s1 NIMH92 chrX 121,906,343 121,907,369 966 19 19.7 -0.43 38.8 NIMH53-2s1 NIMH53 chrX 121,906,443 121,907,149 666 12 18.0 -0.50 37.2 NIMH454 chrX 121,906,448 121,907,434 886 17 19.2 -0.52 37.9	NIMH21-1s1	NIMH21	chrX	120,814,894	120,816,694	1,800	37	20.6	0.35	55.0
NIMH31-1s1 NIMH31 chrX 121,400,547 121,403,442 2,895 56 19.3 0.26 52.4 NIMH45-1s1 NIMH45 chrX 121,400,547 121,403,502 2,955 57 19.3 0.26 52.1 NIMH66-1s1 NIMH66 chrX 121,400,597 121,403,582 2,740 14 18.9 0.39 51.6 NIMH96-1s1 NIMH66 chrX 121,400,842 121,401,582 2,740 53 19.3 0.31 51.9 NIMH92-1s1 NIMH92 chrX 121,400,947 121,403,502 2,225 42 18.9 0.30 51.6 NIMH92-1s1 NIMH92 chrX 121,906,433 121,907,369 966 19 19.7 -0.43 38.3 NIMH53-2s1 NIMH54 chrX 121,906,483 121,907,349 866 17 19.2 -0.52 37.9 NIMH440 chrX 121,906,483 121,907,434 886 17 19.2 -0.52 37.9	NIMH53-2s1	NIMH53	chrX	121,132,578	121,142,362	9,784	162	16.6	-1.16	33.0
NIMH45-1s1 NIMH45 chrX 121,400,547 121,403,502 2,955 57 19.3 0.26 52.1 NIMH76-1s1 NIMH66 chrX 121,400,597 121,403,367 2,770 53 19.1 0.33 52.3 NIMH66-1s1 NIMH66 chrX 121,400,842 121,403,582 740 14 18.9 0.39 51.6 NIMH96-1s1 NIMH66 chrX 121,400,842 121,403,582 2,740 53 19.3 0.31 51.9 NIMH92-1s1 NIMH92 chrX 121,400,947 121,401,881 934 16 17.1 0.36 46.3 NIMH53-st1 NIMH53 chrX 121,906,343 121,907,519 1,76 23 19.6 -0.35 38.8 NIMH53-st1 NIMH54 chrX 121,906,443 121,907,149 666 12 18.0 -0.50 37.2 NIMH40-1s1 NIMH17 chrX 122,523,174 122,525,259 3,144 48 15.3 0.41	NIMH67-1s1	NIMH67	chrX	121,400,522	121,403,442	2,920	57	19.5	0.35	52.3
NIMH76-1s1 NIMH76 chrX 121,400,597 121,403,367 2,770 53 19.1 0.33 52.3 NIMH66-1s1 NIMH66 chrX 121,400,842 121,401,582 740 14 18.9 0.39 51.6 NIMH96-1s1 NIMH96 chrX 121,400,842 121,401,582 740 14 18.9 0.39 51.6 NIMH92-1s1 NIMH92 chrX 121,400,947 121,401,881 934 16 17.1 0.36 46.3 NIMH92-1s1 NIMH92 chrX 121,906,343 121,907,519 1,176 23 19.6 -0.35 38.8 NIMH53-2s1 NIMH53 chrX 121,906,443 121,907,149 666 12 18.0 -0.50 37.2 NIMH40-1s1 NIMH40 chrX 121,906,548 121,907,149 666 12 18.0 -0.52 37.9 NIMH411s1 NIMH40 chrX 122,523,174 122,525,559 3,144 48 15.3 0.41	NIMH31-1s1	NIMH31	chrX	121,400,547	121,403,442	2,895	56	19.3	0.26	52.4
NIMH66-1s1 NIMH66 chrX 121,400,842 121,401,582 740 14 18.9 0.39 51.6 NIMH96-1s1 NIMH96 chrX 121,400,842 121,403,582 2,740 53 19.3 0.31 51.9 NIMH91 chrX 121,400,947 121,401,881 934 16 17.1 0.36 46.3 NIMH92-1s1 NIMH92 chrX 121,401,277 121,403,502 2,225 42 18.9 0.30 51.6 NIMH53-2s1 NIMH69 chrX 121,906,343 121,907,369 966 19 19.7 -0.43 38.3 NIMH54-1s1 NIMH54 chrX 121,906,483 121,907,434 886 17 19.2 -0.52 37.9 NIMH21-1s1 NIMH21 chrX 122,523,174 122,525,529 2,075 42 20.2 0.46 57.2 NIMH20-1s1 NIMH20 chrX 122,778,683 122,780,279 1,596 16 10.0 -0.66 45.9 <td>NIMH45-1s1</td> <td>NIMH45</td> <td>chrX</td> <td>121,400,547</td> <td>121,403,502</td> <td>2,955</td> <td>57</td> <td>19.3</td> <td>0.26</td> <td></td>	NIMH45-1s1	NIMH45	chrX	121,400,547	121,403,502	2,955	57	19.3	0.26	
NIMH66-1s1 NIMH66 chrx 121,400,842 121,401,582 740 14 18.9 0.39 51.6 NIMH96-1s1 NIMH96 chrx 121,400,842 121,403,582 2,740 53 19.3 0.31 51.9 NIMH92-1s1 NIMH92 chrx 121,401,277 121,403,502 2,225 42 18.9 0.30 51.6 NIMH69-2s1 NIMH69 chrx 121,906,343 121,907,519 1,176 23 19.6 -0.35 38.8 NIMH53-2s1 NIMH53 chrx 121,906,403 121,907,369 966 19 19.7 -0.43 38.3 NIMH54-1s1 NIMH54 chrx 121,906,483 121,907,149 6666 12 18.0 -0.50 37.2 NIMH40-1s1 NIMH40 chrx 122,521,915 122,525,955 2,781 48 15.3 0.41 50.8 NIMH21-1s1 NIMH21 chrx 122,778,633 122,780,279 1,556 16 10.0 -0.66 <td></td>										
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NIMH17-1s1 NIMH17 chx1 128,425,325 126,428,852 4,527 46 10.2 0.72 31.4 NIMH00-1s1 NIMH00 chx1 128,425,570 128,428,852 4,282 45 10.5 0.58 31.6 NIMH05-1s1 NIMH43 chx1 128,425,570 128,428,852 4,282 45 10.5 0.81 31.6 NIMH43-1s1 NIMH46 chx1 128,425,570 128,428,852 4,282 45 10.5 0.84 31.6 NIMH66-1s1 NIMH66 chx1 128,425,570 128,428,852 4,282 45 10.5 0.93 31.6 NIMH66-1s1 NIMH66 chx1 128,425,570 128,428,852 4,282 45 10.5 0.93 31.6 NIMH47 NIMH47 128,426,740 128,428,852 3,727 43 11.5 0.80 31.2 NIMH46 ntx1 128,426,862 3,112 40 12.9 0.94 30.6 NIMH47 10.8 <td< td=""><td>NIMH10-1s1</td><td>NIMH10</td><td>chrX</td><td>126,420,769</td><td>126,429,852</td><td>9,083</td><td>100</td><td>11.0</td><td>0.29</td><td>33.3</td></td<>	NIMH10-1s1	NIMH10	chrX	126,420,769	126,429,852	9,083	100	11.0	0.29	33.3
NIMH21-1s1 NIMH21 chX 128,425,520 126,429,852 4,267 46 10.2 0.72 31.4 NIMH405-s1 NIMH405 chX 128,425,570 126,428,852 4,282 45 10.5 0.78 31.6 NIMH43-1s1 NIMH445 thX 128,425,570 126,428,852 4,282 45 10.5 0.94 31.6 NIMH45-1s1 NIMH46 thX 128,425,570 128,428,852 4,282 45 10.5 0.93 31.6 NIMH61-1s1 NIMH46 thX 128,425,570 128,428,852 4,282 45 10.5 0.75 31.6 NIMH49-1s1 NIMH49 thX 128,426,570 128,428,852 3,722 44 11.7 0.97 31.1 NIMH49-1s1 NIMH49 thX 128,426,740 126,428,852 3,722 44 11.7 0.97 33.0 NIMH49-1s1 NIMH49 thX 128,426,740 126,428,852 3,112 40 12.9 0.80	NIMH08-1s1	NIMH08	chrX	126,425,325	126,429,852	4,527	46	10.2	0.66	
NIMH01-1s1 NIMH01 chX 126,425,570 126,429,852 4,282 45 10.5 0.58 31.6 NIMH43-1s1 NIMH43 chX 126,425,570 126,429,852 4,282 45 10.5 0.81 31.6 NIMH45-1s1 NIMH46 thX 126,429,852 4,282 45 10.5 0.94 31.6 NIMH61-1s1 NIMH46 thX 126,429,852 4,282 45 10.5 0.75 31.6 NIMH46-1s1 NIMH46 thX 126,425,570 126,429,852 4,282 45 10.5 0.75 31.6 NIMH472-1s1 NIMH472 thX 128,425,570 128,429,852 4,282 45 10.5 0.75 31.6 NIMH472-1s1 NIMH472 thX 128,426,125 128,429,852 3,122 45 10.5 0.75 31.6 NIMH472-1s1 NIMH474 128,426,812 128,428,852 3,112 40 129 0.96 30.6 NIM446-1s1 NIM447	NIMH17-1s1	NIMH17	chrX	126,425,325	126,429,852	4,527	46	10.2	0.64	31.4
NIMH05-bit NIMH405 chr.X 126,425,570 126,429,852 4,282 45 10.5 0.78 31.6 NIMH44-bits NIMH445 chr.X 126,429,852 4,282 45 10.5 0.84 31.6 NIMH46-bits NIMH46 chr.X 126,429,852 4,282 45 10.5 0.84 31.6 NIMH46-bits NIMH46 chr.X 126,429,852 4,282 45 10.5 0.97 31.6 NIMH47-bits NIMH47 chr.X 126,429,852 4,282 45 10.5 0.97 31.6 NIMH47-bits NIMH47 126,425,570 126,429,852 4,282 45 10.5 0.97 31.1 NIMH49-bits NIMH47 124,426,120 124,428,822 3,727 42 11.7 0.95 31.0 NIMH49-bits NIMH47 124,428,120 124,428,822 3,112 40 12.9 0.96 30.6 NIMH49-bits NIMH47 124,428,482 3.022 31.12<	NIMH21-1s1	NIMH21	chrX	126,425,325	126,429,852	4,527		10.2	0.72	31.4
NIMH43-ist NIMH43 ohr 26.425,570 12.6.429,852 4.282 4.55 10.5 1.02 NIMH60-ist NIMH60 hr/k 12.6.425,570 12.6.429,852 4.282 45 10.5 0.59 31.6 NIMH60-ist NIMH61 12.6.425,570 12.6.429,852 4.282 45 10.5 0.59 31.6 NIMH60-ist NIMH76-ist NIMH76-ist 12.6.425,570 12.6.428,852 4.282 45 10.5 0.92 31.6 NIMH92-ist NIMH96-ist 12.6.426,570 12.6.428,852 3.752 44 11.7 0.97 31.1 NIMH65-ist NIMH96-ist 12.6.426,757 12.6.428,852 3.752 44 11.7 0.80 30.5 NIMH55-ist NIMH66 17X 12.6.426,740 12.6.428,852 3.112 40 12.9 0.86 30.6 NIMH75-ist NIMH76 12.8.426,740 12.6.428,852 3.112 40 12.9 0.86 30.6 30.6 <td< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></td<>										
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NIMH75-1s1 NIMH75 chrX 126.426,740 126.429.852 3,112 40 12.9 0.96 30.6 NIMH89-3s1 NIMH89 chrX 126.426,830 126.429.852 3,022 39 12.9 0.89 30.3 NIMH9-1s1 NIMH04 chrX 126.426,830 126.429.852 2,956 38 12.9 0.84 30.2 NIMH100-1s1 NIMH04 chrX 126.426,866 126.429.852 2,956 38 12.9 0.89 30.2 NIMH27-1s1 NIMH24 chrX 126.427.236 126.429.852 2,616 37 14.1 0.88 30.3 NIMH44-1s1 NIMH46 chrX 126.427.236 126.429.852 2,616 37 14.1 0.88 30.3 NIMH46-1s1 NIMH46 chrX 126.427.236 126.429.852 2,616 37 14.1 0.48 30.3 NIMH46-1s1 NIMH46 chrX 126.427.236 126.429.852 2,616 37 14.1 0.14 </td <td>NIMH54-1s1</td> <td>NIMH54</td> <td>chrX</td> <td>126,426,630</td> <td>126,429,852</td> <td>3,222</td> <td>41</td> <td>12.7</td> <td>0.78</td> <td>30.5</td>	NIMH54-1s1	NIMH54	chrX	126,426,630	126,429,852	3,222	41	12.7	0.78	30.5
NIMHB6-1s2 NIMHB6 chrX 126,267,40 126,428,852 3,112 40 12.9 0.60 NIMH95-1s1 NIMH95 chrX 126,428,852 3,022 39 12.9 0.89 33.3 NIMH55-1s1 NIMH95 chrX 126,428,852 2,956 38 12.9 0.89 30.2 NIMH10-1s1 NIMH10 chrX 126,426,896 126,428,852 2,956 38 12.9 0.98 30.2 NIMH2-1s1 NIMH24 chrX 126,426,896 126,428,852 2,616 37 14.1 0.88 30.3 NIMH46-1s1 NIMH46 chrX 126,427,236 126,428,852 2,616 37 14.1 1.03 30.3 NIMH46-1s1 NIMH46 chrX 126,427,236 126,428,852 2,616 37 14.1 1.03 30.3 NIMH46-1s1 NIMH46 chrX 126,427,236 126,428,852 2,616 37 14.1 1.03 30.3 NIMH46-1s1 <	NIMH53-2s1	NIMH53	chrX	126,426,740	126,429,852	3,112	40	12.9	0.94	30.6
NIMHe9-2s1 NIMHe6 chrx 126.426.830 126.429.852 3.022 39 12.9 1.17 30.3 NIMH04-1s1 NIMH04 chrx 126.426.830 126.429.852 2.956 38 12.9 0.84 30.2 NIMH100-1s1 NIMH100 chrx 126.426.896 126.429.852 2.956 38 12.9 0.98 30.2 NIMH24-1s1 NIMH457 chrx 126.426.896 126.429.852 2.916 37 14.1 0.83 30.3 NIMH24-1s1 NIMH44 chrx 126.427.236 126.429.852 2.616 37 14.1 0.84 30.3 NIMH46-1s1 NIMH46 chrx 126.427.236 126.429.852 2.616 37 14.1 0.83 30.3 NIMH46-1s1 NIMH46 chrx 127.479.117 127.480.277 1.160 23 18.8 30.3 NIMH46-1s1 NIMH46 chrx 127.479.117 127.480.277 1.160 23 10.8 33.2 <	NIMH75-1s1	NIMH75	chrX	126,426,740	126,429,852	3,112	40	12.9	0.96	30.6
NIMH96-1s1 NIMH95 chrx 126.426,852 3.022 39 12.9 0.84 30.2 NIMH04-1s1 NIMH00 chrx 126.426,896 22.429.852 2.956 38 12.9 0.84 30.2 NIMH27-1s1 NIMH27 chrx 126.427.366 126.429.852 2.956 38 12.9 0.84 30.2 NIMH24-1s1 NIMH24 chrx 126.427.366 126.429.852 2.616 37 14.1 0.88 30.3 NIMH46-1s1 NIMH46 chrx 126.427.366 126.429.852 2.616 37 14.1 0.83 30.3 NIMH46-1s1 NIMH46 chrx 126.427.236 126.429.852 2.616 37 14.1 0.83 30.3 NIMH25-1s1 NIMH67 chrx 127.47.9117 127.480.277 1.160 23 19.8 0.38 53.0 NIMH25-1s1 NIMH27 chrx 127.47.9117 127.486.965 1.960 34 20.2 0.32 40.0					-, -,	· ·				
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NIMH06-1s1 NIMH06 chrX 128,148,360 128,155,102 6,742 123 18.2 -1.22 39.5 NIMH05-2s1 NIMH05 chrX 128,328,110 128,329,810 1,700 21 12.4 -1.09 40.2 NIMH50-1s1 NIMH55 chrX 128,328,110 128,329,810 1,700 21 12.4 -1.08 40.2 NIMH55-1s1 NIMH55 chrX 128,328,110 128,329,810 1,700 21 12.4 -0.91 40.2 NIMH60-1s1 NIMH66 chrX 128,328,110 128,329,810 1,700 21 12.4 -1.25 40.2 NIMH64-1s1 NIMH66 chrX 128,328,110 128,329,860 1,750 22 12.6 -1.28 39.7 NIMH66-1s1 NIMH66 chrX 128,328,110 128,329,860 1,750 22 12.6 -1.28 39.7 NIMH90-1s1 NIMH67 chrX 128,328,410 128,329,860 1,455 18 12.4 <t< td=""><td>R085B11-A03-1s1</td><td>R085B11</td><td>chrX</td><td>128,065,929</td><td></td><td>709</td><td>16</td><td>22.6</td><td>-0.42</td><td>38.5</td></t<>	R085B11-A03-1s1	R085B11	chrX	128,065,929		709	16	22.6	-0.42	38.5
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NIMH26-1s1NIMH26chrX129,134,946129,135,5816351422.0-0.3742.6NIMH44-1s1NIMH44chrX129,135,191129,135,7115201223.1-0.4839.2NIMH66-1s1NIMH66chrX129,490,335129,494,1353,8006717.60.2257.0NIMH07-1s1NIMH07chrX129,711,077129,715,2674,1907718.4-0.2741.5NIMH29-2s1NIMH29chrX129,711,302129,715,1973,8957118.20.3341.4NIMH27-A03-2s2NIMH27chrX129,711,347129,715,2873,9407218.3-0.2941.4	NIMH38-1s1	NIMH38	chrX	128,974,008	128,978,163	4,155		20.7	0.29	58.8
NIMH44-1s1NIMH44chrX129,135,191129,135,7115201223.1-0.4839.2NIMH66-1s1NIMH66chrX129,490,335129,494,1353,8006717.60.2257.0NIMH07-1s1NIMH07chrX129,711,077129,715,2674,1907718.4-0.2741.5NIMH29-2s1NIMH29chrX129,711,302129,715,1973,8957118.20.3341.4NIMH27-A03-2s2NIMH27chrX129,711,347129,715,2873,9407218.3-0.2941.4				, ,		1,729				
NIMH66-1s1 NIMH66 chrX 129,490,335 129,494,135 3,800 67 17.6 0.22 57.0 NIMH07-1s1 NIMH07 chrX 129,711,077 129,715,267 4,190 77 18.4 -0.27 41.5 NIMH29-2s1 NIMH29 chrX 129,711,302 129,715,197 3,895 71 18.2 0.33 41.4 NIMH27-A03-2s2 NIMH27 chrX 129,711,347 129,715,677 4,330 75 17.3 0.39 41.0 NIMH44-1s1 NIMH44 chrX 129,711,347 129,715,287 3,940 72 18.3 -0.29 41.4		NIMH26								
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NIMH29-2s1NIMH29chrX129,711,302129,715,1973,8957118.20.3341.4NIMH27-A03-2s2NIMH27chrX129,711,347129,715,6774,3307517.30.3941.0NIMH44-1s1NIMH44chrX129,711,347129,715,2873,9407218.3-0.2941.4										
NIMH27-A03-2s2 NIMH27 chrX 129,711,347 129,715,677 4,330 75 17.3 0.39 41.0 NIMH44-1s1 NIMH44 chrX 129,711,347 129,715,287 3,940 72 18.3 -0.29 41.4										
NIMH44-1s1 NIMH44 chrX 129,711,347 129,715,287 3,940 72 18.3 -0.29 41.4										
	NIMH44-1S1	NIMH44	chrX	129,711,347	129,715,287	3,940	72	18.3	-0.29	

NIMH57-1s1	NIMH57	chrX	129,711,402	129,715,047	3,645	67	18.4	0.27	41.3
NIMH28-1s1	NIMH28	chrX	129,711,442	129,715,197	3,755	68	18.1	0.87	41.3
NIMH23-1s1	NIMH23	chrX	129,713,742	129,715,267	1,525	30	19.7	-0.53	44.0
R085B11-A03-1s1	R085B11	chrX	129,771,750	129,773,040	1,290	26	20.2	0.31	58.2
NIMH30-1s2	NIMH30	chrX	130,139,847	130,140,407	560	12	21.4	-0.65	48.5
NIMH60-1s1	NIMH60	chrX	130,239,122	130,240,995	1,873	35	18.7	0.31	53.9
NIMH29-2s1	NIMH29	chrX	130,239,507	130,243,140	3,633	68	18.7	0.26	50.9
NIMH30-1s2	NIMH30	chrX	130,473,430	130,476,783	3,353	46	13.7	0.28	48.6
NIMH76-1s1	NIMH76	chrX	130,640,914	130,641,821	907	12	13.2	-1.81	45.3
NIMH46-1s1	NIMH46	chrX	130,724,611	130,725,466	855	13	15.2	0.42	51.4
NIMH24-1s1	NIMH24	chrX	130,985,386	130,986,591	1,205	25	20.7	-1.10	48.0
R085B10-1s2		chrX	, ,		39,096	649	16.6	-0.49	40.8
	R085B10		131,757,779	131,796,875					
NIMH38-1s1	NIMH38	chrX	131,766,925	131,769,220	2,295	30	13.1	-0.93	41.7
NIMH90-1s1	NIMH90	chrX	131,766,925	131,769,220	2,295	30	13.1	-1.25	41.7
NIMH05-2s1	NIMH05	chrX	131,766,995	131,769,220	2,225	29	13.0	-1.27	41.4
NIMH38-1s1	NIMH38	chrX	132,514,136	132,515,072	936	20	21.4	-0.40	38.9
R085B11-A03-1s1	R085B11	chrX	132,514,136	132,514,761	625	14	22.4	-0.61	39.8
NIMH35-1s1	NIMH35	chrX	132,840,193	132,841,109	916	18	19.7	-1.86	38.7
NIMH26-1s1	NIMH26	chrX	133,421,463	133,423,144	1,681	31	18.4	-0.58	58.3
NIMH23-1s1	NIMH23	chrX	133,421,538	133,423,144	1,606	30	18.7	-0.67	58.7
NIMH30-1s2	NIMH30	chrX	133,421,538	133,423,144	1,606	30	18.7	-0.61	58.7
NIMH35-1s1	NIMH35	chrX	133,422,003	133,423,144	1,000	24	21.0	-0.55	54.4
NIMH38-1s1		chrX	133,422,003	133,423,144	980	24 22	21.0		54.4
	NIMH38							-0.66	
NIMH44-1s1	NIMH44	chrX	133,422,164	133,423,529	1,365	29	21.2	-0.57	48.1
NIMH01-1s1	NIMH01	chrX	133,904,983	133,906,470	1,487	24	16.1	0.54	42.2
NIMH23-1s1	NIMH23	chrX	134,055,097	134,059,687	4,590	75	16.3	0.32	57.9
NIMH95-1s1	NIMH95	chrX	134,055,317	134,058,122	2,805	51	18.2	0.25	57.0
NIMH21-1s1	NIMH21	chrX	134,057,817	134,060,683	2,866	42	14.7	0.44	64.5
NIMH50-1s1	NIMH50	chrX	134,119,690	134,160,090	40,400	552	13.7	0.62	40.3
NIMH32-1s1	NIMH32	chrX	134,305,630	134,306,235	605	14	23.1	-0.50	52.6
NIMH89-1s1	NIMH89	chrX	134,382,794	134,388,717	5,923	98	16.5	0.27	60.1
NIMH87-A03-2s2	NIMH87	chrX	134,384,099	134,388,897	4,798	81	16.9	0.27	58.5
NIMH34-1s1	NIMH34	chrX	134,882,626	134,885,031	2,405	50	20.8	-0.54	56.4
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NIMH33-1s1	NIMH33	chrX	134,883,591	134,885,031	1,440	31	21.5	-0.79	59.9
NIMH24-1s1	NIMH24	chrX	134,883,641	134,884,781	1,140	25	21.9	-0.65	63.7
NIMH25-1s1	NIMH25	chrX	134,883,641	134,885,031	1,390	30	21.6	-0.80	60.1
NIMH23-1s1	NIMH23	chrX	134,883,686	134,884,816	1,130	25	22.1	-1.06	63.4
NIMH30-1s2	NIMH30	chrX	134,883,686	134,884,966	1,280	28	21.9	-0.95	61.6
NIMH42-1s1	NIMH42	chrX	134,883,686	134,884,966	1,280	28	21.9	-0.76	61.6
NIMH43-1s1	NIMH43	chrX	134,883,686	134,885,031	1,345	29	21.6	-0.64	60.4
NIMH44-1s1	NIMH44	chrX	134,883,731	134,884,966	1,235	27	21.9	-0.83	61.7
NIMH40-1s1	NIMH40	chrX	134,883,761	134,884,966	1,205	26	21.6	-0.82	61.5
NIMH31-1s1	NIMH31	chrX	134,884,431	134,884,966	535	12	22.4	-0.98	45.8
NIMH46-1s1	NIMH46	chrX	134,987,293	134,990,779	3,486	54	15.5	0.56	42.9
NIMH45-1s1	NIMH45	chrX	135,129,255	135,129,790	535	12	22.4	-1.53	43.0
NIMH29-2s1	NIMH29	chrX	135,382,010	135,382,385	375	8	21.3	0.81	49.2
NIMH45-1s1	NIMH45	chrX	135,939,306		2,175	45	20.7	0.30	51.7
NIMH17-1s1	NIMH45 NIMH17	chrX	135,939,756	135,941,481 135,944,189	4,433	45 88	19.9	0.30	56.1
	NIMH17 NIMH20		· · ·						
NIMH20-1s1		chrX	135,939,856	135,944,189	4,333	86	19.8	0.39	56.4
NIMH67-1s1	NIMH67	chrX	135,939,906	135,941,751	1,845	39	21.1	0.33	56.2
NIMH35-1s1	NIMH35	chrX	135,941,811	135,944,899	3,088	61	19.8	-0.33	54.1
NIMH40-1s1	NIMH40	chrX	135,941,811	135,945,219	3,408	67	19.7	-0.34	53.3
NIMH44-1s1	NIMH44	chrX	135,941,811	135,945,219	3,408	67	19.7	-0.46	53.3
NIMH23-1s1	NIMH23	chrX	135,941,971	135,945,219	3,248	64	19.7	-0.45	53.3
R085B11-A03-1s1	R085B11	chrX	135,941,971	135,943,419	1,448	30	20.7	-0.46	49.6
NIMH34-1s1	NIMH34	chrX	135,941,996	135,943,419	1,423	29	20.4	-0.55	49.7
NIMH25-1s1	NIMH25	chrX	135,942,056	135,943,419	1,363	28	20.5	-0.57	50.0
NIMH30-1s2	NIMH30	chrX	135,942,056	135,945,084	3,028	60	19.8	-0.46	53.7
NIMH32-1s1	NIMH32	chrX	135,942,096	135,943,419	1,323	27	20.4	-0.57	49.9
NIMH33-1s1	NIMH33	chrX	135,942,096	135,943,419	1,323	27	20.4	-0.56	49.9
R085B11-A03-1s1	R085B11	chrX	135,943,464	135,944,189	725	13	17.9	0.36	72.1
R085B11-A03-1s1	R085B11	chrX	135,944,214	135,945,469	1,255	26	20.7	-0.32	45.9
NIMH47-1s1	NIMH47	chrX	136,336,931	136,339,448	2,517	48	19.1	0.38	61.3
NIMH60-1s1	NIMH60	chrX	136,337,136	136,339,239	2,103	43	20.4	0.35	59.5
NIMH25-1s1	NIMH25	chrX	136,351,701	136,352,176	475	11	23.2	-0.94	51.1
NIMH26-1s1	NIMH26	chrX	136,351,736	136,352,176	440	10	22.7	-1.02	48.4
NIMH30-1s2	NIMH30	chrX	136,351,736	136,352,176	440	10	22.7	-0.95	48.4
NIMH31-1s1	NIMH31	chrX	136,351,796	136,352,711	915	18	19.7	-0.59	44.8
NIMH34-1s1	NIMH34	chrX	136,351,796	136,352,176	380	9	23.7	-1.02	43.9
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NMM35:1s1 NMM35 chtX 13.83,17.96 136,352,176 380 9 23.7 -0.90 43.9 NMM40-1s1 NMM40 chtX 136,352,176 380 9 23.7 -1.03 43.9 NMM40-1s1 NMM40 chtX 136,352,176 380 9 23.7 -1.03 43.9 NMM42-1s1 NMM42 136,352,176 380 9 23.7 -1.03 43.9 NMM42-1s1 NMM42 136,352,876 418,378,883 4.417 401 16.6 0.22 50.7 7.3 NMM423-1s1 NMM423 chtX 136,767,771 136,788,686 860 02 2.0.8 0.8 37.1 NMM423-1s1 NMM475 136,787,471 136,788,611 840 18 21.3 0.53 57.3 NMM475-1s1 NMM476 thX1<30,572,671 136,788,611 840 18 20.6 0.52 57.5 NMM475-1s1 NMM476 thX1<30,352,621 136,353,631 4.										
NIMH40-1st NIMH40 chr.X 133,317,76 138,322,176 380 9 23.7 -1.03 439 NIMH32-1st NIMH32 chr.X 133,351,946 138,352,176 330 8 24.2 -1.13 439 NIMH20-1st NIMH21 rkx 136,472,889 136,473,988 6,509 128 19.7 0.28 5.74 NIMH32-1st NIMH32 rkx 136,787,726 136,786,666 960 20.2 0.80 3.73 NIMH32-1st NIMH32 rkx 136,787,721 136,786,666 915 19 2.08 -0.82 3.74 NIMH47-1st NIMH47 rkx 136,787,777 136,786,666 915 19 2.08 -0.63 3.74 NIMH47-1st NIMH47 rkx 136,351,320 139,352,421 136,353,420 139,352,431 70 18,3 0.32 4.11 NIMH47-1st NIMH47 rkx 136,352,320 139,352,431 773 3.31 70 18,34 </td <td></td>										
NIMH44- Is1 NIMH44- Is1 NIMH42- Is1 NIMH47- Is1										
NIMH22 rtx 138,351,846 138,352,175 330 8 24.2 -1.13 40.8 NIMH27-1s1 NIMH17 chxx 136,472,889 138,479,898 6,509 128 19.7 0.28 -0.78 37.3 NIMH32-1s1 NIMH32 chrx 135,787,728 136,788,886 960 20 20.8 -0.80 37.3 NIMH32-1s1 NIMH32 chrx 136,787,771 136,788,686 915 19 20.8 -0.82 37.4 NIMH27-1s1 NIMH47 thxx 136,787,771 136,786,686 915 19 20.8 -0.82 37.4 NIMH27-1s1 NIMH47 thxx 138,787,728 138,789,281 4,313 18.842,22 24.07 45 18.7 0.43 55.8 NIMH470-1s1 NIMH47 thxx 138,797,728 138,793,228 24,417 45 13.43 0.43 55.8 NIMH47-1s1 NIMH47 thxx 138,797,728 138,797,728 14.9 14.9 </td <td></td> <td></td> <td></td> <td></td> <td>· · ·</td> <td></td> <td></td> <td></td> <td></td> <td></td>					· · ·					
NIMH20-Ist NIMH17 NIMH17 NIMH17 NIMH17 NIMH17 NIMH17 NIMH12 NIM										
NIMH30-152 NIMH30 chr.X 136,787,771 136,787,771 136,787,771 136,787,771 136,786,771 136,787,771 136,786,866 950 20 20.8 -0.80 37.3 NIMH23-1s1 NIMH72 chr.X 136,787,771 136,786,866 915 19 20.8 -0.85 37.4 NIMH27-1s1 NIMH67 chr.X 136,787,771 136,786,866 915 19 20.8 -0.85 37.4 NIMH20-1s1 NIMH67 chr.X 136,787,741 136,786,482 136,554,471 145 18 21.3 0.53 55.8 NIMH20-1s1 NIMH67 chr.X 139,352,402 139,329,434 57.5 10 12.3 023 39.3 NIMH20-1s1 NIMH67 chr.X 139,636,233 4,313 79 18.3 022 44.1 NIMH40-1s1 NIMH40 chr.X 140,073,630 2,277 43 18.9 -0.83 53.3 NIMH40-1s1 NIMH40 chr.X 141,169,										
NIMH22-is1 NIMH22 htt NIMH23-is1 NIMH23-is1 NIMH27-is1 NIMH27-	NIMH17-1s1	NIMH17	chrX	136,472,889	136,479,398	6,509	128	19.7	0.28	57.4
NIMH23-is1 NIMH23 chr.X 138, 787, 771 136, 788, 680 915 19 20.2 -0.085 37.4 NIMH67-is1 NIMH67 chr.X 138, 787, 711 136, 788, 680 915 19 20.8 -0.85 37.4 NIMH20-is1 NIMH67 chr.X 138, 840, 822 24.07 45 18.2 -0.85 55.8 NIMH20-is1 NIMH20 chr.X 138, 840, 822 24.07 45 18.7 -0.48 66.0 NIMH67-is1 NIMH67 rh.X 139, 935, 730 139, 372, 71 13.6 75.7 15 11.9 -0.63 42.6 R055011-03-is1 R056511 chr.X 140, 007, 337 2.277 43 18.9 -0.78 31.3 NIMH40-is1 NIMH40-is1 NIMH40 rh.X 140, 007, 31.755 15 19.9 0.34 656 NIMH40-is1 NIMH40-is1 NIMH40-is1 NIMH40-is1 141, 169, 323 14.66 30 11.8 0.43 576	NIMH30-1s2		chrX			1,460	30	20.5	-0.78	37.3
NIMMP7-Is1 NIMMP7 chr.X 136,787,771 136,786,686 915 19 20.8 -0.82 37.7 NIMMP7-Is1 NIMMP67 chr.X 136,786,686 87.7 18 20.8 37.7 NIMMP0-Is1 NIMMP67 chr.X 136,986,842 136,959,492 24.07 45 18 21.3 0.53 55.8 NIMMP0-Is1 NIMMP67 chr.X 139,323,202 139,330,303 4,313 79 18.3 0.32 44.1 NIMMP67-Is1 11.09,335 14.10,03,37 2.277 13 19.9 0.56 76.6 NIMMP67-Is1 NIMMP67-Is1 NIMMP67-Is1 NIMMP67-Is1 11.09,356 14.1160,328 1.585 30 19.9 0.55 76.6 NIMMP67-Is1 NIMMP67-Is1 NIMMP67 14.119,358 14.160,623 1.55 30 19.9										
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NIMH67 Interest 18 213 0.53 65.8 NIMH20-1s1 NIMH20 chr.X 138,408.8 138,432.92 2.407 45 18.7 0.48 66.0 NIMH67-1s1 NIMH67 chr.X 139,323,202 139,328,934 5,732 92 16.1 1.47 366.6 66.0 NIMH66-1s1 NIMH66 chr.X 139,375,780 139,375,780 139,375,780 139,375,780 139,375,780 139,375,780 139,375,780 139,375,780 139,375,780 139,375,780 139,375,780 139,876,215 1,755 26 14,8 -0.78 39,33 39,33 NIMH0-1s1 NIMH0-1s1 NIMH0-1s1 NIMH0-1s1 NIMH0-1s1 NIMH0-1s1 NIMH0-1s1 NIMH0-1s2 141,169,384 141,160,282 1,565 30 18,9 0.32 56,4 NIMH0-1s1					, ,					
NIM-P20-1s1 NIM-P20 chr.X 138,840,885 138,842,292 2,407 45 18.7 0.48 66 NIM-P57-1s1 NIM-P67 chr.X 139,635,320 139,639,633 4,313 79 18.3 0.32 44,1 NIM-P67-1s1 NIM-P67 chr.X 139,635,320 139,630,633 4,313 79 18.8 0.72 0.23 0.63 42.6 R085B11-A03-1s1 NIM-P67 chr.X 140,073,060 140,075,027 17,55 26 14.8 0.76 31.3 NIM-P67-1s1 NIM-P67 chr.X 140,082,33 141,106,223 1556 30 18.9 0.32 56.4 NIM-P67-1s1 NIM-P67 chr.X 141,169,338 141,160,823 1570 30 18.9 0.32 56.4 NIM-P63-1s1 NIM-P13 chr.X 141,159,388 141,160,823 1.275 23 18.0 0.43 57.6 NIMH40-1s1 NIM-P140 chr.X 141,159,343 141,160,823 1.27										
NIM-H90-1s1 NIM-H90 chr.X 139,323,202 139,232,924 5,732 92 16.1 1.47 36.8 NIM-H66-1s1 NIM-H66 chr.X 139,875,780 139,876,215 433 10 23.0 0.83 42.6 NIM-H60-1s1 NIM-H60 chr.X 140,304,966 44.0 43.5 10 23.0 39.3 NIM-H60-1s1 NIM-H60 chr.X 140,304,966 44.0 17.55 15 15 19.9 0.55 57.6 NIM-H60-1s1 NIM-H67 chr.X 140,867,429 44.16,93.2 1,555 30 18.9 0.32 65.4 NIM-H67-1s1 NIM-H67 chr.X 141,159,38 141,160,823 1,570 30 18.1 0.43 57.6 NIM-H36-1s1 NIM-H67 chr.X 141,159,38 141,160,623 1,225 24.6 14.1 163.3 1,42,10.0 1,41.0 14.5 14.1 14.141,160,133 1,41.00 14.141,10.0 14.141,10.13 14.14.10.13 14				, ,	, ,					
NIMH67-1s1 NIMH67 chx 139,635,320 139,636,633 4,313 79 18,3 0.32 44,1 R085B11-A03-1s1 N08461 chx 139,636,621 2,277 43 18,9 0.32 39,33 NIMH40-1s1 NIMH40 chx 140,073,060 140,075,037 2,277 43 18,9 0.34 55,6 NIMH40-1s1 NIMH40 chx 140,024,424 140,068,641 1,215 23 18,9 0.34 55,6 56 18,9 0.34 55,6 56 18,9 0.34 55,6 56 18,9 0.34 56,4 18,8 0.43 57,8 18,9 0.34 56,4 18,6 0.44 57,3 141,159,389 141,169,389 141,169,389 141,169,389 141,169,389 141,169,389 12,275 23 18,0 0.43 57,6 NIMH43,11 NIMH40,151 NIMH41,11 141,159,473 141,169,389 142,175,773 142,289,080 141,275,73 142,289,080 142,179,778 <td></td> <td></td> <td></td> <td></td> <td>, ,</td> <td>, -</td> <td></td> <td></td> <td></td> <td></td>					, ,	, -				
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NIMHe0-1s1 NIMHe0-2 NIMHe0-1s1 NIMHe0-2	NIMH66-1s1	NIMH66	chrX	139,875,780	139,876,215		10	23.0	-0.63	42.6
NIMH40-1s1 NIMH40 chrx 140.324.648 140.325.403 755 15 19.9 0.55 57.6 NIMH67-1s1 NIMH67-1s1 NIMH67-1s1 NIMH67-1s1 0.33 55.3 NIMH67-1s1 NIMH67-1s1 NIMH67-1s1 NIMH67-1s1 0.33 55.3 NIMH57-1s1 NIMH67-1s1 NIMH67-1s1 0.43 57.6 NIMH57-1s1 NIMH67-1s1 NIMH67-1s1 NIMH67-1s1 0.43 57.6 NIMH53-1s1 NIMH67-1s1 NIMH67-1s1 NIMH57-1s2 23 18.0 0.47 57.3 NIMH50-1s2 NIMH50-1s1 NIMH50-1s1 NIMH57-703-282 NIMH57-73 141.160.253 1,160.252 18.4 0.42 58.4 NIMH57-203-252 NIMH57 chr1 141.159.743 141.160.252 1,060 21 19.4 0.42 58.4 NIMH57-203-252 NIMH57 chr1 141.159.7473 975 20 20.5 1-147 98.9 NIMH57-203-252 NIMH57 chr1 141.159.7473 <td></td>										
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NIMH87-A03-2s2 NIMH87 chrx 141,159,743 141,160,823 1,080 21 19.4 0.42 58.4 NIMH30-1s2 NIMH30 chrx 141,242,03 141,244,103 1,900 35 18.4 0.26 52.8 NIMH25-1s1 NIMH87 chrx 141,191,282 673 14 20.8 -0.53 36.2 NIMH87-0.322 NIMH87 chrx 141,197,978 142,180,887 1,109 21 18.9 -0.50 37.6 NIMH87-181 NIMH89 chrx 142,179,853 142,180,952 1,099 20 18.2 -0.34 37.4 NIMH82-151 NIMH82 chrx 142,550,345 142,515,290 1,405 28 19.9 -0.51 60.9 NIMH23-151 NIMH23 chrx 142,550,405 142,551,155 810 17 21.0 -0.72 61.4 NIMH23-151 NIMH33 chrX 142,550,405 142,551,155 750 16 21.3 -0.93 61.0 <td></td> <td></td> <td></td> <td>141,159,598</td> <td>141,160,753</td> <td></td> <td></td> <td></td> <td>0.43</td> <td></td>				141,159,598	141,160,753				0.43	
NIMH30-152 NIMH30 chr.X 141,242,203 141,244,103 1,900 35 18.4 0.26 52.8 NIMH100-1s1 NIMH125 chr.X 141,151,202 673 14 20.8 -0.63 36.2 NIMH487-A03-2s2 NIMH487 chr.X 142,179,778 142,181,007 1.494 28 18.7 -0.49 36.9 NIMH487-A03-2s2 NIMH466 chr.X 142,179,778 142,180,952 1.099 20 18.2 -0.55 37.4 NIMH49-1s1 NIMH49-chr.X 142,179,758 142,180,952 1.099 20 18.2 -0.55 60.9 NIMH32-thX NIMH32,607X 142,550,345 142,551,155 810 17 21.0 -0.76 61.4 NIMH22-ts1 NIMH23 chr.X 142,550,405 142,551,155 750 16 21.3 -0.71 61.0 NIMH23-ts1 NIMH33 chr.X 142,550,405 142,551,155 750 16 21.3 -0.71 61.0 0.43<										
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NIMH33-1s1 NIMH33 chrX 142,550,405 142,551,155 810 17 21.0 -0.78 61.4 NIMH23-1s1 NIMH23 chrX 142,550,405 142,551,155 750 16 21.3 -0.93 61.0 NIMH30-1s2 NIMH30 chrX 142,550,405 142,551,260 885 18 20.3 -0.64 559.9 NIMH31 nrX 142,550,405 142,551,260 825 16 19.4 -0.55 57.4 NIMH33-1s1 NIMH33 chrX 142,667,231 142,669,186 1,955 40 20.5 -0.41 47.3 NIMH23-1s1 NIMH33 chrX 142,667,271 142,669,116 1,845 37 20.1 -0.53 48.0 NIMH23-1s1 NIMH23 chrX 143,63,349 143,441,766 5,417 98 18.1 -0.67 38.9 NIMH42-1s1 NIMH42 chrX 143,436,349 143,441,866 5,537 100 18.1 -1.09 38.8					, ,					
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NIMH30-1s2	NIMH30	chrX	148,520,312	148,522,185	1,873	34	18.2	-0.38	59.3
NIMH53-2s1	NIMH53	chrX	148,540,884	148,542,429	1,545	34	20.7	0.32	58.5
NIMH19-1s1	NIMH19	chrX	148,543,514	148,543,959	445	6	13.5	-1.21	31.0
NIMH31-1s1	NIMH31	chrX	148,646,679	148,653,039	6,360	81	12.7	0.31	56.9
NIMH05-2s1	NIMH05	chrX	148,649,444	148,652,699	3,255	47	14.4	0.46	57.5
NIMH96-1s1	NIMH96	chrX	148,649,544	148,653,299	3,755	57	15.2	0.29	56.5
NIMH53-2s1	NIMH53	chrX	148,650,624	148,652,969	2,345	38	16.2	0.32	59.0
NIMH18-2s1	NIMH18	chrX	148,686,097	148,852,282	166,185	1,578	9.5	-1.10	41.4
NIMH67-1s1 NIMH67-1s1	NIMH67 NIMH67	chrX chrX	148,693,656 148,747,339	148,698,741 148,748,844	5,085	101 31	19.9 20.6	0.32	55.6 54.8
NIMH31-1s1	NIMH07	chrX	148,747,539	148,748,844	1,505 1,305	28	20.6	0.44	55.5
NIMH32-1s1	NIMH32	chrX	148,747,739	148,748,789	1,050	23	21.9	0.53	55.2
NIMH93-1s1	NIMH93	chrX	148,857,878	148,859,520	1,642	33	20.1	-0.28	68.2
NIMH10-1s1	NIMH10	chrX	149,276,358	149,285,385	9,027	173	19.2	0.22	59.1
NIMH05-2s1	NIMH05	chrX	149,281,173	149,285,941	4,768	88	18.5	0.32	62.3
NIMH17-1s1	NIMH17	chrX	149,281,238	149,285,605	4,367	81	18.5	0.40	63.4
NIMH30-1s2	NIMH30	chrX	149,421,904	149,428,571	6,667	128	19.2	0.22	53.6
NIMH38-1s1 NIMH05-2s1	NIMH38 NIMH05	chrX chrX	149,433,561 149,678,535	149,435,156 149,679,445	1,595 910	33 13	20.7 14.3	0.41	55.5 54.8
NIMH100-1s1	NIMH05		149,678,535	149,679,445	910 910	13	14.3	-1.03	54.8
NIMH25-1s1	NIMH25	chrX	149,678,535	149,679,160	625	10	17.6	-1.31	55.2
NIMH33-1s1	NIMH33	chrX	149,678,535	149,679,160	625	11	17.6	-1.69	55.2
NIMH35-1s1	NIMH35	chrX	149,678,535	149,679,160	625	11	17.6	-1.18	55.2
NIMH88-1s1	NIMH88	chrX	149,678,535	149,679,625	1,090	16	14.7	-1.56	55.3
NIMH93-1s1	NIMH93	chrX chrX	149,678,535	149,679,325	790 740	12	15.2	-1.70	53.8
NIMH69-2s1 NIMH80-1s1	NIMH69 NIMH80	chrX chrX	149,678,585 149,678,585	149,679,325 149,679,445	740 860	11 12	14.9 14.0	-1.60 -1.77	54.4 55.3
NIMH89-1s1	NIMH89	chrX	149,678,585	149,679,160	575	10	17.4	-1.75	56.0
NIMH19-1s1	NIMH19	chrX	149,678,940	149,693,844	14,904	280	18.8	0.26	53.7
NIMH27-A03-2s2	NIMH27	chrX	149,772,205	149,773,310	1,105	24	21.7	0.43	47.6
NIMH21-1s1	NIMH21	chrX	149,817,013	149,818,719	1,706	34	19.9	0.48	66.7
R085B11-A03-1s1	R085B11	chrX	149,942,898	149,946,958	4,060	85	20.9	-0.41	37.3
NIMH01-1s1	NIMH01	chrX	150,033,568	150,035,033	1,465	31	21.2	0.43	48.6
NIMH38-1s1 NIMH81-1s1	NIMH38 NIMH81	chrX chrX	150,089,543 150,147,769	150,090,288 150,155,706	745 7,937	15 148	20.1 18.6	-0.46	43.3 42.2
NIMH57-1s1	NIMH57	chrX	150,166,784	150,167,314	530	11	20.8	0.69	44.6
NIMH27-A03-2s2	NIMH27	chrX	150,187,985	150,190,496	2,511	51	20.3	0.31	44.3
NIMH07-1s1	NIMH07	chrX	150,458,117	150,459,512	1,395	18	12.9	-1.63	43.9
NIMH69-2s1	NIMH69	chrX	150,598,190	150,598,655	465	11	23.7	0.55	50.6
NIMH82-1s1	NIMH82	chrX	150,598,270	150,598,655	385	9	23.4	0.62	49.2
NIMH57-1s1	NIMH57	chrX	150,598,330	150,598,655	325	8	24.6	0.77	48.8
NIMH19-1s1 NIMH23-1s1	NIMH19 NIMH23	chrX chrX	150,612,380 150,614,684	150,623,387 150,615,759	11,007 1,075	196 24	17.8 22.3	-0.53	53.2 51.5
NIMH25-1s1	NIMH25	chrX	150,614,684	150,615,974	1,075	24	22.3	-0.33	49.8
NIMH26-1s1	NIMH26	chrX	150,614,684	150,616,680	1,996	33	16.5	-0.40	48.6
NIMH34-1s1	NIMH34	chrX	150,614,684	150,615,614	930	21	22.6	-0.58	54.1
NIMH35-1s1	NIMH35	chrX	150,614,684	150,615,669	985	22	22.3	-0.43	53.9
NIMH38-1s1	NIMH38	chrX	150,623,822	150,624,692	870	18	20.7	-0.38	41.9
NIMH53-2s1	NIMH53	chrX	150,831,076	150,843,793	12,717	137	10.8	0.34	59.8
NIMH67-1s1 NIMH84-1s1	NIMH67 NIMH84	chrX chrX	150,831,076 150,831,076	150,843,873 150,843,498	12,797 12,422	139 132	10.9 10.6	0.37 0.40	59.7 59.9
NIMH40-1s1	NIMH64 NIMH40	chrX	150,831,076	150,845,088	12,422	161	10.6	0.40	59.9 58.2
NIMH89-1s1	NIMH89	chrX	150,831,146	150,843,473	12,327	130	10.5	0.29	59.9
NIMH31-1s1	NIMH31	chrX	150,831,221	150,843,908	12,687	138	10.9	0.37	59.8
NIMH12-1s1	NIMH12	chrX	150,831,296	150,843,873	12,577	136	10.8	0.39	59.8
NIMH38-1s1	NIMH38	chrX	150,831,296	150,845,533	14,237	168	11.8	0.25	57.8
NIMH81-1s1		chrX	150,831,296 150,831,316	150,843,123 150,843,873	11,827	121 135	10.2 10.8	0.48	60.2 59.8
NIMH43-1s1 NIMH17-1s1	NIMH43 NIMH17	chrX chrX	150,831,316	150,843,873	12,557 12,087	135	10.8	0.34 0.39	59.8 59.9
NIMH08-1s1	NIMH08	chrX	150,892,265	150,896,392	4,127	77	18.7	0.33	55.1
NIMH63-1s1	NIMH63	chrX	151,033,250	151,040,081	6,831	129	18.9	0.31	56.7
NIMH87-A03-2s2	NIMH87	chrX	151,033,620	151,039,981	6,361	124	19.5	0.27	58.2
NIMH94-1s1	NIMH94	chrX	151,034,600	151,040,231	5,631	111	19.7	0.26	57.9
NIMH66-1s1	NIMH66	chrX	151,034,960	151,039,481	4,521	90	19.9	0.27	58.8
NIMH84-1s1	NIMH84	chrX	151,050,291	151,058,378	8,087	149	18.4	0.21	50.6
NIMH24-1s1 NIMH13-1s1	NIMH24 NIMH13	chrX chrX	151,053,858 151,054,058	151,058,268 151,058,223	4,410 4,165	89 84	20.2 20.2	0.30 0.33	57.0 57.3
NIMH19-1s1	NIMH13	chrX	151,054,203	151,058,418	4,105	85	20.2	0.33	57.5
NIMH60-1s1	NIMH60	chrX	151,055,933	151,058,268	2,335	47	20.2	0.34	59.2
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NIMH05-2s1	NIMH05	chrX	151,057,189	151,058,143	954	21	22.0	0.53	62.6
NIMH44-1s1	NIMH44	chrX	151,370,560	151,371,784	1,224	26	21.2	-0.45	40.5
NIMH27-A03-2s2	NIMH27	chrX	151,562,411	151,564,426	2,015	42	20.8	0.32	42.5
NIMH23-1s1	NIMH23	chrX	151,571,158	151,572,213	1,055	23	21.8	0.53	56.1
NIMH81-1s1	NIMH81	chrX	151,650,913	151,654,360	3,447	53	15.4	0.43	58.1
NIMH100-1s1	NIMH100	chrX	151,651,103	151,653,980	2,877	46	16.0	0.24	58.6
NIMH19-1s1	NIMH19	chrX	151,651,128	151,653,980	2,852	45	15.8	0.43	58.7
NIMH05-2s1 NIMH89-1s1	NIMH05 NIMH89	chrX chrX	151,651,538 151,652,083	151,653,980 151,654,615	2,442 2,532	38 34	15.6 13.4	0.45 0.33	58.5 58.0
NIMH49-1s1	NIMH49	chrX	151,789,191	151,854,852	65,661	1,208	18.4	0.33	53.1
NIMH10-1s1	NIMH10	chrX	151,790,486	151,857,907	67,421	1,244	18.5	0.22	53.1
NIMH76-1s1	NIMH76	chrX	151,810,012	151,849,216	39,204	729	18.6	0.21	56.1
NIMH16-1s1	NIMH16	chrX	151,813,088	151,829,025	15,937	303	19.0	0.30	57.1
NIMH23-1s1	NIMH23	chrX	151,821,209	151,857,952	36,743	671	18.3	0.29	55.1
NIMH40-1s1	NIMH40	chrX	151,829,400	151,857,907	28,507	525	18.4	0.29	54.6
NIMH32-1s1	NIMH32	chrX	151,830,490	151,840,416	9,926	193	19.4	0.30	57.7
R085B11-A03-1s1	R085B11	chrX	151,831,735	151,838,976	7,241	143	19.7	0.29	58.5
NIMH87-A03-2s2 NIMH05-2s1	NIMH87	chrX	151,846,351	151,849,096	2,745 410	57 8	20.8 19.5	0.35	58.7 51.7
NIMH05-251	NIMH05 NIMH06	chrX chrX	151,868,084 151,902,891	151,868,494 151,913,415	10,524	123	19.5	0.30	57.3
NIMH69-2s1	NIMH69	chrX	151,946,060	151,952,575	6,515	114	17.5	0.30	59.1
NIMH100-1s1	NIMH109	chrX	151,949,465	151,952,325	2,860	53	18.5	0.23	60.5
NIMH60-1s1	NIMH60	chrX	151,974,280	151,979,944	5,664	104	18.4	0.32	60.7
NIMH76-1s1	NIMH76	chrX	152,129,668	152,140,580	10,912	207	19.0	0.20	52.5
NIMH17-1s1	NIMH17	chrX	152,136,403	152,140,580	4,177	83	19.9	0.46	59.7
NIMH82-1s1	NIMH82	chrX	152,262,390	152,265,335	2,945	57	19.4	0.26	52.9
NIMH53-2s1	NIMH53	chrX	152,262,600	152,265,525	2,925	57	19.5	0.32	53.1
NIMH95-1s1	NIMH95	chrX	152,263,015	152,265,560	2,545	50	19.6	0.38	53.0
NIMH80-1s1	NIMH80	chrX	152,263,130	152,265,270	2,140	42	19.6	0.40	52.5
NIMH56-1s1	NIMH56	chrX	152,264,255	152,265,270	1,015	21 9	20.7	0.40	55.0
NIMH92-1s1 NIMH96-1s1	NIMH92 NIMH96	chrX chrX	152,269,585 152,269,730	152,270,080 152,270,175	495 445	9	18.2 15.7	-0.54 -0.72	45.1 43.6
NIMH26-1s1	NIMH26	chrX	152,271,504	152,278,265	6,761	87	12.9	0.24	50.7
NIMH14-1s1	NIMH120	chrX	152,291,280	153,544,603	1,253,323	16,299	13.0	0.24	53.6
NIMH09-1s1	NIMH09	chrX	152,293,929	153,553,301	1,259,372	16,292	12.9	0.23	53.6
NIMH15-1s1	NIMH15	chrX	152,293,929	152,942,034	648,105	10,427	16.1	0.29	55.4
NIMH05-2s1	NIMH05	chrX	152,302,579	153,371,776	1,069,197	10,190	9.5	0.31	54.0
NIMH22-1s1	NIMH22	chrX	152,305,682	152,899,701	594,019	9,678	16.3	0.27	55.7
NIMH70-2s1	NIMH70	chrX	152,305,857	152,893,525	587,668	9,650	16.4	0.17	55.7
NIMH12-1s1 NIMH04-1s1	NIMH12 NIMH04	chrX chrX	152,305,917 152,306,027	152,948,952	643,035	10,362 10,683	16.1 16.1	0.27 0.25	55.4 55.2
NIMH19-1s1	NIMH04 NIMH19	chrX	152,310,872	152,969,114 152,982,600	663,087 671,728	10,885	16.1	0.25	55.2
NIMH17-1s1	NIMH17	chrX	152,358,146	152,664,254	306,108	5,139	16.8	0.30	56.4
NIMH16-1s1	NIMH16	chrX	152,379,378	152,742,303	362,925	5,983	16.5	0.31	56.6
NIMH10-1s1	NIMH10	chrX	152,384,882	152,807,186	422,304	6,894	16.3	0.26	56.1
NIMH20-1s1	NIMH20	chrX	152,541,535	153,018,526	476,991	7,238	15.2	0.33	53.9
NIMH21-1s1	NIMH21	chrX	152,541,770	153,014,725	472,955	7,167	15.2	0.30	53.9
NIMH84-1s1	NIMH84	chrX	152,551,110	152,941,984	390,874	5,935	15.2	0.21	55.3
NIMH26-1s1 NIMH24-1s1	NIMH26	chrX chrX	152,306,027 152,306,027	152,312,552	6,525 11,874	74 167	11.3 14 1	0.32 0.29	57.2 57.3
NIMH24-151 NIMH57-1s1	NIMH24 NIMH57	chrX chrX	152,306,027	152,317,901 152,357,672	2,015	167 27	14.1 13.4	-0.32	45.0
NIMH60-1s1	NIMH57	chrX	152,355,657	152,357,672	190,555	3,413	13.4	0.32	45.0 57.0
NIMH20-1s1	NIMH20	chrX	152,320,275	152,531,936	211,661	3,790	17.9	0.27	56.2
NIMH26-1s1	NIMH26	chrX	152,358,806	152,502,824	144,018	2,683	18.6	0.25	58.4
NIMH08-1s1	NIMH08	chrX	152,358,926	152,478,463	119,537	2,216	18.5	0.29	58.9
NIMH45-1s1	NIMH45	chrX	152,359,306	152,510,297	150,991	2,774	18.4	0.25	58.1
NIMH67-1s1	NIMH67	chrX	152,363,927	152,522,269	158,342	2,902	18.3	0.26	58.0
NIMH23-1s1	NIMH23	chrX	152,364,082	152,561,864	197,782	3,562	18.0	0.27	57.0
NIMH39-1s1 NIMH50-1s1	NIMH39 NIMH50	chrX chrX	152,366,252 152,369,801	152,500,629 152,486,224	134,377 116,423	2,515 2,177	18.7 18.7	0.28 0.26	58.6 59.0
NIMH21-1s1	NIMH50 NIMH21	chrX	152,372,679	152,533,266	160,587	2,177	18.3	0.20	59.0
NIMH53-2s1	NIMH53	chrX	152,373,314	152,428,828	55,514	1,039	18.7	0.30	60.4
NIMH61-1s1	NIMH61	chrX	152,373,524	152,463,286	89,762	1,675	18.7	0.32	59.9
NIMH32-1s1	NIMH32	chrX	152,376,007	152,467,389	91,382	1,701	18.6	0.28	59.9
NIMH84-1s1	NIMH84	chrX	152,376,252	152,496,312	120,060	2,255	18.8	0.27	59.2
NIMH48-1s1	NIMH48	chrX	152,379,378	152,500,774	121,396	2,291	18.9	0.29	59.3
NIMH81-1s1	NIMH81	chrX chrX	152,380,470 152,380,945	152,505,239	124,769 107,579	2,331	18.7	0.30	59.0
		TTTT X	172 3811 945	152,488,524	10/ 5/9	2,019	18.8	0.27	59.8
NIMH76-1s1 NIMH24-1s1	NIMH76 NIMH24	chrX	152,381,015	152,512,517	131,502	2,441	18.6	0.33	58.8

NIMH49-1s1	NIMH49	chrX	152,382,595	152,487,429	104,834	1,968	18.8	0.34	59.8
NIMH01-1s1	NIMH01	chrX	152,384,707	152,488,750	104,043	1,948	18.7	0.24	59.9
NIMH90-1s1	NIMH90	chrX	152,386,817	152,435,018	48,201	881	18.3	0.24	61.5
NIMH89-1s1	NIMH89	chrX	152,388,662	152,468,759	80,097	1,492	18.6	0.27	60.8
NIMH40-1s1	NIMH40	chrX	152,389,076	152,505,239	116,163	2,163	18.6	0.31	59.1
NIMH33-1s1	NIMH33	chrX	152,389,525	152,518,694	129,169	2,376	18.4	0.26	58.7
NIMH31-1s1	NIMH31	chrX	152,390,050	152,420,552	30,502	565	18.5	0.30	61.8
NIMH06-1s1	NIMH06	chrX	152,390,120	152,500,544	110,424	2,077	18.8	0.28	59.5
NIMH96-1s1	NIMH96	chrX	152,391,499	152,495,352	103,853	1,951	18.8	0.25	59.8
NIMH95-1s1	NIMH95	chrX	152,391,739	152,467,389	75,650	1,406	18.6	0.23	60.8
NIMH30-1s2	NIMH30	chrX	152,394,634	152,518,184	123,550	2,270	18.4	0.22	58.6
NIMH47-1s1	NIMH47	chrX	152,408,136	152,477,348	69,212	1,291	18.7	0.32	59.8
NIMH63-1s1	NIMH63	chrX	152,409,671	152,500,774	91,103	1,712	18.8	0.27	58.9
NIMH69-2s1	NIMH69	chrX	152,415,276	152,452,150	36,874	672	18.2	0.23	59.1
NIMH33-1s1	NIMH33	chrX	152,389,076	152,389,476	400	8	20.0	-0.51	72.4
NIMH30-1s2	NIMH30	chrX	152,518,279	152,518,739	460	11	23.9	-0.47	48.0
NIMH66-1s1	NIMH66	chrX	152,531,936	152,532,326	390	9	23.1	-0.69	48.2
NIMH94-1s1	NIMH94	chrX	152,541,600	152,560,721	19,121	346	18.1	0.24	58.3
NIMH95-1s1	NIMH95	chrX	152,541,600	152,560,721	19,121	346	18.1	0.22	58.3
NIMH31-1s1	NIMH31	chrX	152,541,600	152,564,158	22,558	409	18.1	0.22	59.8
NIMH24-1s1	NIMH24	chrX	152,541,655	152,560,721	19,066	345	18.1	0.32	58.2
NIMH26-1s1	NIMH26	chrX	152,541,770	152,560,776	19,006	343	18.0	0.27	58.3
NIMH90-1s1	NIMH90	chrX	152,541,770	152,560,776	19,006	343	18.0	0.24	58.3
NIMH60-1s1	NIMH60	chrX	152,541,840	152,572,226	30,386	547	18.0	0.30	59.3
NIMH38-1s1	NIMH38	chrX	152,557,416	152,560,721	3,305	69	20.9	0.31	60.4
NIMH33-1s1	NIMH33	chrX	152,560,776	152,561,819	1,043	22	21.1	-0.42	70.9
NIMH26-1s1	NIMH26	chrX	152,560,851	152,561,479	628	14	22.3	-0.51	74.5
NIMH08-1s1	NIMH08	chrX	152,572,081	152,572,894	813	14	17.2	-0.35	33.2
NIMH44-1s1	NIMH44	chrX	152,572,081	152,572,999	918	16	17.4	-0.47	35.0
NIMH47-1s1	NIMH47	chrX	152,585,682	152,952,822	367,140	5.581	15.2	0.26	55.4
NIMH24-1s1	NIMH24	chrX	152,602,949	152,934,894	331,945	4,996	15.1	0.26	55.4
NIMH39-1s1	NIMH39	chrX	152,603,044	152,735,519	132,475	1,992	15.0	0.24	57.5
NIMH67-1s1	NIMH67	chrX	152,605,699	152,742,303	136,604	2,035	14.9	0.27	57.1
NIMH56-1s1	NIMH56	chrX	152,585,515	152,591,432	5,917	114	19.3	0.23	61.3
	111111100	011170	102,000,010	102,001,102			10.0	0.20	01.0
NIMH90-1s1	NIMH90	chrX	152 585 515	152 591 897	6 382	123	19.3	0.26	61.5
NIMH90-1s1 NIMH33-1s1	NIMH90 NIMH33	chrX chrX	152,585,515 152 585 682	152,591,897 152 591 432	6,382 5 750	123 112	19.3 19.5	0.26 0.36	61.5 62.0
NIMH33-1s1	NIMH33	chrX	152,585,682	152,591,432	5,750	112	19.5	0.36	62.0
NIMH33-1s1 NIMH34-1s1	NIMH33 NIMH34	chrX chrX	152,585,682 152,592,813	152,591,432 152,593,488	5,750 675	112 15	19.5 22.2	0.36 -0.49	62.0 58.3
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1	NIMH33 NIMH34 NIMH40	chrX chrX chrX	152,585,682 152,592,813 152,602,949	152,591,432 152,593,488 152,627,475	5,750 675 24,526	112 15 333	19.5 22.2 13.6	0.36 -0.49 0.41	62.0 58.3 61.4
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1	NIMH33 NIMH34 NIMH40 NIMH96	chrX chrX chrX chrX	152,585,682 152,592,813 152,602,949 152,603,044	152,591,432 152,593,488 152,627,475 152,613,915	5,750 675 24,526 10,871	112 15 333 159	19.5 22.2 13.6 14.6	0.36 -0.49 0.41 0.28	62.0 58.3 61.4 65.9
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH95-1s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95	chrX chrX chrX chrX chrX	152,585,682 152,592,813 152,602,949 152,603,044 152,603,434	152,591,432 152,593,488 152,627,475 152,613,915 152,629,535	5,750 675 24,526 10,871 26,101	112 15 333 159 355	19.5 22.2 13.6 14.6 13.6	0.36 -0.49 0.41 0.28 0.31	62.0 58.3 61.4 65.9 61.1
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH95-1s1 NIMH54-1s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54	chrX chrX chrX chrX chrX chrX	152,585,682 152,592,813 152,602,949 152,603,044 152,603,434 152,604,004	152,591,432 152,593,488 152,627,475 152,613,915 152,629,535 152,616,167	5,750 675 24,526 10,871 26,101 12,163	112 15 333 159 355 164	19.5 22.2 13.6 14.6 13.6 13.5	0.36 -0.49 0.41 0.28 0.31 0.21	62.0 58.3 61.4 65.9 61.1 64.2
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH95-1s1 NIMH54-1s1 NIMH54-1s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH26	chrX chrX chrX chrX chrX chrX chrX chrX	152,585,682 152,592,813 152,602,949 152,603,044 152,603,434 152,604,004 152,608,390	152,591,432 152,593,488 152,627,475 152,613,915 152,629,535 152,616,167 152,633,215	5,750 675 24,526 10,871 26,101 12,163 24,825	112 15 333 159 355 164 324	19.5 22.2 13.6 14.6 13.6 13.5 13.1	0.36 -0.49 0.41 0.28 0.31 0.21 0.37	62.0 58.3 61.4 65.9 61.1 64.2 57.8
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH95-1s1 NIMH54-1s1 NIMH54-1s1 NIMH26-1s1 NIMH32-1s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH26 NIMH32	chrX chrX chrX chrX chrX chrX chrX chrX	152,585,682 152,592,813 152,602,949 152,603,044 152,603,434 152,604,004 152,608,390 152,616,167	152,591,432 152,593,488 152,627,475 152,613,915 152,629,535 152,616,167 152,633,215 152,633,215	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048	112 15 333 159 355 164 324 223	19.5 22.2 13.6 14.6 13.6 13.5 13.1 13.1	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH95-1s1 NIMH54-1s1 NIMH26-1s1 NIMH32-1s1 NIMH96-1s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH26 NIMH32 NIMH96	chrX chrX chrX chrX chrX chrX chrX chrX	152,585,682 152,592,813 152,602,949 152,603,044 152,603,434 152,604,004 152,608,390 152,616,167 152,648,483	152,591,432 152,593,488 152,627,475 152,613,915 152,629,535 152,616,167 152,633,215 152,633,215 152,650,876	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393	112 15 333 159 355 164 324 223 32	19.5 22.2 13.6 14.6 13.6 13.5 13.1 13.1 13.1	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH95-1s1 NIMH54-1s1 NIMH26-1s1 NIMH32-1s1 NIMH96-1s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH26 NIMH26 NIMH32 NIMH96 NIMH94	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,585,682\\ \hline 152,592,813\\ \hline 152,602,949\\ 152,603,044\\ 152,603,434\\ 152,604,004\\ 152,608,390\\ 152,616,167\\ \hline 152,648,483\\ 152,648,880\\ \end{array}$	$\begin{array}{r} 152,591,432\\ \hline 152,593,488\\ 152,627,475\\ 152,613,915\\ 152,629,535\\ 152,616,167\\ 152,633,215\\ 152,633,215\\ 152,650,876\\ 152,650,761\\ \end{array}$	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881	112 15 333 159 355 164 324 223 32 28	19.5 22.2 13.6 14.6 13.5 13.1 13.1 13.4 14.9	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 43.5
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH95-1s1 NIMH54-1s1 NIMH26-1s1 NIMH32-1s1 NIMH96-1s1 NIMH94-1s1 NIMH53-2s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH26 NIMH26 NIMH32 NIMH96 NIMH94 NIMH53	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,585,682\\ \hline 152,592,813\\ \hline 152,602,949\\ 152,603,044\\ 152,603,434\\ 152,604,004\\ 152,608,390\\ 152,616,167\\ \hline 152,648,483\\ 152,648,880\\ 152,649,628\\ \end{array}$	$\begin{array}{r} 152,591,432\\ \hline 152,593,488\\ 152,627,475\\ 152,613,915\\ 152,629,535\\ 152,616,167\\ 152,633,215\\ 152,633,215\\ 152,650,876\\ 152,650,761\\ 152,650,761\\ \end{array}$	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133	112 15 333 159 355 164 324 223 32 28 19	19.5 22.2 13.6 14.6 13.5 13.1 13.1 13.4 14.9 16.8	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 43.5 40.8
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH95-1s1 NIMH54-1s1 NIMH54-1s1 NIMH56-1s1 NIMH56-1s1 NIMH56-1s1 NIMH56-1s1 NIMH96-1s1 NIMH96-1s1 NIMH94-1s1 NIMH53-2s1 NIMH53-1s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH26 NIMH32 NIMH96 NIMH94 NIMH53 NIMH31	chrX chrX chrX chrX chrX chrX chrX chrX	152,585,682 152,592,813 152,602,949 152,603,044 152,603,434 152,604,004 152,608,390 152,616,167 152,648,483 152,648,483 152,648,880 152,649,628	152,591,432 152,593,488 152,627,475 152,613,915 152,629,535 152,616,167 152,633,215 152,633,215 152,650,876 152,650,761 152,650,761 152,731,368	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652	112 15 333 159 355 164 324 223 32 28 19 1,252	19.5 22.2 13.6 14.6 13.5 13.1 13.1 13.1 13.4 14.9 16.8 15.5	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30 0.22	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 43.5 40.8 57.5
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH95-1s1 NIMH54-1s1 NIMH54-1s1 NIMH56-1s1 NIMH56-1s1 NIMH56-1s1 NIMH96-1s1 NIMH94-1s1 NIMH53-2s1 NIMH31-1s1 NIMH96-1s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH26 NIMH32 NIMH96 NIMH94 NIMH931 NIMH96	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,585,682\\ 152,592,813\\ 152,602,949\\ 152,603,044\\ 152,603,434\\ 152,604,004\\ 152,608,390\\ 152,616,167\\ 152,648,483\\ 152,648,483\\ 152,648,880\\ 152,649,628\\ 152,650,716\\ 152,650,901\\ \end{array}$	152,591,432 152,593,488 152,627,475 152,613,915 152,629,535 152,616,167 152,633,215 152,650,876 152,650,876 152,650,761 152,650,761 152,731,368 152,723,248	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652 72,347	112 15 333 159 355 164 324 223 32 28 19 1,252 1,106	19.5 22.2 13.6 14.6 13.5 13.1 13.1 13.1 13.4 14.9 16.8 15.5 15.3	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30 0.22 0.23	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 43.5 40.8 57.5 57.5
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH95-1s1 NIMH54-1s1 NIMH54-1s1 NIMH56-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH93-2s1 NIMH93-1s1 NIMH31-1s1 NIMH45-1s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH26 NIMH32 NIMH96 NIMH94 NIMH53 NIMH31	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,585,682\\ 152,592,813\\ 152,602,949\\ 152,603,044\\ 152,603,434\\ 152,604,004\\ 152,608,390\\ 152,616,167\\ 152,648,483\\ 152,648,480\\ 152,648,480\\ 152,649,628\\ 152,650,716\\ 152,650,901\\ 152,650,971\\ \end{array}$	152,591,432 152,593,488 152,627,475 152,613,915 152,629,535 152,616,167 152,633,215 152,633,215 152,650,876 152,650,761 152,650,761 152,731,368	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652 72,347 86,246	112 15 333 159 355 164 324 223 32 28 19 1,252 1,106 1,333	19.5 22.2 13.6 14.6 13.5 13.1 13.1 13.4 14.9 16.8 15.5 15.3 15.5	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30 0.22 0.23 0.25	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 43.5 40.8 57.5 57.5 57.5
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH95-1s1 NIMH54-1s1 NIMH54-1s1 NIMH96-1s1 NIMH45-1s1 NIMH96-1s1 NIMH63-1s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH32 NIMH32 NIMH96 NIMH45 NIMH31 NIMH96 NIMH45	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,585,682\\ 152,592,813\\ 152,602,949\\ 152,603,044\\ 152,603,434\\ 152,604,004\\ 152,608,390\\ 152,616,167\\ 152,648,483\\ 152,648,480\\ 152,648,880\\ 152,648,628\\ 152,650,716\\ 152,650,901\\ 152,650,971\\ 152,651,021\\ \end{array}$	$\begin{array}{r} 152,591,432\\ 152,593,488\\ 152,627,475\\ 152,613,915\\ 152,629,535\\ 152,616,167\\ 152,633,215\\ 152,650,876\\ 152,650,761\\ 152,650,761\\ 152,731,368\\ 152,723,248\\ 152,737,217\\ 152,664,159\\ \end{array}$	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652 72,347 86,246 13,138	112 15 333 159 355 164 324 223 32 28 19 1,252 1,106 1,333 183	19.5 22.2 13.6 14.6 13.5 13.1 13.4 14.9 16.8 15.5 13.9	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30 0.22 0.23 0.25 0.28	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 43.5 40.8 57.5 57.5 57.5 57.2 58.8
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH96-1s1 NIMH54-1s1 NIMH54-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH53-2s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH26 NIMH26 NIMH96 NIMH94 NIMH31 NIMH96 NIMH45 NIMH63 NIMH60	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,585,682\\ 152,592,813\\ 152,602,949\\ 152,603,044\\ 152,603,434\\ 152,604,004\\ 152,608,390\\ 152,616,167\\ 152,648,483\\ 152,648,480\\ 152,649,628\\ 152,650,716\\ 152,650,901\\ 152,650,971\\ 152,651,021\\ 152,651,161\\ \end{array}$	$\begin{array}{r} 152,591,432\\ 152,593,488\\ 152,627,475\\ 152,613,915\\ 152,629,535\\ 152,616,167\\ 152,633,215\\ 152,650,876\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,731,368\\ 152,723,248\\ 152,723,248\\ 152,737,217\\ 152,664,159\\ 152,731,743\\ \end{array}$	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652 72,347 86,246 13,138 80,582	112 15 333 159 355 164 324 223 28 19 1,252 1,106 1,333 183 1,252	19.5 22.2 13.6 14.6 13.5 13.1 13.4 14.9 16.8 15.5 13.9 15.5	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30 0.22 0.23 0.25 0.28 0.31	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 43.5 57.5 57.5 57.5 57.5 57.2 58.8 57.5
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH96-1s1 NIMH54-1s1 NIMH54-1s1 NIMH96-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH26 NIMH32 NIMH96 NIMH31 NIMH96 NIMH45 NIMH63 NIMH60 NIMH43	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,585,682\\ \hline 152,592,813\\ \hline 152,602,949\\ 152,603,044\\ \hline 152,603,434\\ \hline 152,604,004\\ \hline 152,608,390\\ \hline 152,616,167\\ \hline 152,648,483\\ \hline 152,648,483\\ \hline 152,648,480\\ \hline 152,649,628\\ \hline 152,650,716\\ \hline 152,650,901\\ \hline 152,651,021\\ \hline 152,651,161\\ \hline 152,652,826\\ \end{array}$	152,591,432 152,593,488 152,627,475 152,613,915 152,629,535 152,616,167 152,633,215 152,650,876 152,650,761 152,650,761 152,731,368 152,723,248 152,737,217 152,664,159 152,731,743 152,731,188	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652 72,347 86,246 13,138 80,582 78,362	112 15 333 159 355 164 324 223 32 28 19 1,252 1,106 1,333 183	19.5 22.2 13.6 14.6 13.6 13.5 13.1 13.4 14.9 16.8 15.5 13.9 15.5 13.9 15.5 15.5 15.5	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30 0.22 0.23 0.25 0.28 0.31 0.28	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 43.5 40.8 57.5 57.5 57.5 57.2 58.8 57.5 57.5
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH96-1s1 NIMH54-1s1 NIMH54-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH53-2s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH26 NIMH26 NIMH96 NIMH94 NIMH31 NIMH96 NIMH45 NIMH63 NIMH60	chrX chrX chrX chrX chrX chrX chrX chrX	152,585,682 152,592,813 152,602,949 152,603,044 152,603,434 152,604,004 152,608,390 152,616,167 152,648,483 152,648,483 152,649,628 152,650,716 152,650,971 152,651,021 152,651,021 152,651,161 152,652,826 152,654,809	152,591,432 152,593,488 152,627,475 152,613,915 152,629,535 152,616,167 152,633,215 152,650,761 152,650,761 152,650,761 152,731,368 152,737,217 152,664,159 152,731,743 152,731,188 152,731,188	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652 72,347 86,246 13,138 80,582	112 15 333 159 355 164 324 223 32 28 19 1,252 1,106 1,333 183 1,252 1,211	19.5 22.2 13.6 14.6 13.5 13.1 13.4 14.9 16.8 15.5 13.9 15.5	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30 0.22 0.23 0.25 0.28 0.31	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 43.5 57.5 57.5 57.5 57.5 57.2 58.8 57.5
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH96-1s1 NIMH54-1s1 NIMH54-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH63-1s1 NIMH96-1s1 NIMH96-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH45-1s1 NIMH45-1s1 NIMH45-1s1 NIMH45-1s1 NIMH45-1s1 NIMH40-1s1 R085B11-A03-1s1	NIMH33 NIMH40 NIMH96 NIMH95 NIMH54 NIMH26 NIMH32 NIMH96 NIMH95 NIMH53 NIMH53 NIMH53 NIMH60 NIMH45 NIMH60 NIMH45 NIMH60 NIMH43 NIMH40 R085B11	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,585,682\\ \hline 152,592,813\\ \hline 152,602,949\\ 152,603,044\\ 152,603,434\\ 152,604,004\\ 152,608,390\\ \hline 152,616,167\\ \hline 152,648,483\\ 152,648,480\\ \hline 152,649,628\\ \hline 152,650,716\\ 152,650,971\\ \hline 152,651,021\\ 152,651,021\\ 152,651,161\\ 152,652,826\\ 152,654,809\\ 152,655,094\\ \end{array}$	$\begin{array}{r} 152,591,432\\ \hline 152,593,488\\ \hline 152,627,475\\ \hline 152,613,915\\ \hline 152,629,535\\ \hline 152,616,167\\ \hline 152,633,215\\ \hline 152,650,761\\ \hline 152,650,761\\ \hline 152,650,761\\ \hline 152,731,368\\ \hline 152,731,368\\ \hline 152,731,217\\ \hline 152,664,159\\ \hline 152,731,188\\ \hline 152,731,188\\ \hline 152,663,549\\ \hline 152,664,254\\ \end{array}$	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652 72,347 86,246 13,138 80,582 78,362 8,740 9,160	112 15 333 159 355 164 324 223 32 28 19 1,252 1,106 1,333 1,252 1,211 118 114	19.5 22.2 13.6 14.6 13.5 13.1 13.4 14.9 16.8 15.5 13.9 15.5 13.5 13.4	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30 0.22 0.23 0.25 0.28 0.31 0.28 0.31 0.28 0.46 0.33	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 43.5 40.8 57.5 57.5 57.5 57.5 57.5 57.5 57.5 61.3 61.2
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH96-1s1 NIMH54-1s1 NIMH54-1s1 NIMH96-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH45-1s1 NIMH63-1s1 NIMH40-1s1	NIMH33 NIMH40 NIMH96 NIMH95 NIMH54 NIMH26 NIMH32 NIMH96 NIMH45 NIMH45 NIMH45 NIMH45 NIMH40	chrX chrX chrX chrX chrX chrX chrX chrX	152,585,682 152,592,813 152,602,949 152,603,044 152,603,434 152,604,004 152,608,390 152,616,167 152,648,483 152,648,483 152,649,628 152,650,716 152,650,971 152,651,021 152,651,021 152,651,161 152,652,826 152,654,809	152,591,432 152,593,488 152,627,475 152,613,915 152,629,535 152,616,167 152,633,215 152,650,761 152,650,761 152,650,761 152,731,368 152,737,217 152,664,159 152,731,743 152,731,188 152,731,188	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652 72,347 86,246 13,138 80,582 78,362 8,740	112 15 333 159 355 164 324 223 32 28 19 1,252 1,106 1,333 183 1,252 1,211 118	19.5 22.2 13.6 14.6 13.5 13.1 13.4 14.9 16.8 15.5 13.9 15.5 15.5 15.5 15.5 15.5 15.5 15.5 15.5 15.5 15.5 15.5 13.5	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30 0.22 0.23 0.25 0.28 0.31 0.28 0.31 0.28 0.46	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 43.5 40.8 57.5 57.5 57.5 57.2 58.8 57.5 57.5 61.3
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH96-1s1 NIMH54-1s1 NIMH52-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH94-1s1 NIMH94-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH60-1s1 NIMH63-1s1 NIMH45-1s1 NIMH45-1s1 NIMH45-1s1 NIMH40-1s1 R085B11-A03-1s1 NIMH32-1s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH26 NIMH32 NIMH32 NIMH96 NIMH45 NIMH45 NIMH60 NIMH43 NIMH40 R085B11 NIMH32	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,585,682\\ 152,592,813\\ 152,602,949\\ 152,603,044\\ 152,603,044\\ 152,603,044\\ 152,604,004\\ 152,608,390\\ 152,616,167\\ 152,648,483\\ 152,648,483\\ 152,648,880\\ 152,649,628\\ 152,650,901\\ 152,650,901\\ 152,650,971\\ 152,651,021\\ 152,651,161\\ 152,652,826\\ 152,654,809\\ 152,655,094\\ 152,655,094\\ 152,656,484\\ \end{array}$	$\begin{array}{r} 152,591,432\\ 152,593,488\\ 152,627,475\\ 152,613,915\\ 152,629,535\\ 152,616,167\\ 152,633,215\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,731,368\\ 152,732,248\\ 152,737,217\\ 152,664,159\\ 152,731,743\\ 152,731,743\\ 152,731,743\\ 152,731,788\\ 152,663,549\\ 152,664,254\\ 152,664,792\\ \end{array}$	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652 72,347 86,246 13,138 80,582 78,362 8,740 9,160 8,308	112 15 333 159 355 164 324 223 32 28 19 1,252 1,106 1,333 1,252 1,211 118 114 88	19.5 22.2 13.6 14.6 13.5 13.1 13.1 13.1 13.4 14.9 16.8 15.5 13.9 15.5 13.5 13.5 15.5 13.5 13.5 12.4 10.6	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30 0.22 0.23 0.25 0.28 0.31 0.28 0.46 0.33 0.38	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 43.5 40.8 57.5 57.5 57.5 57.5 57.5 57.5 57.5 57
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH54-1s1 NIMH54-1s1 NIMH96-1s1 NIMH94-1s1 NIMH45-1s1 NIMH60-1s1 NIMH40-1s1 R085B11-A03-1s1 NIMH32-1s1 NIMH32-1s1 NIMH32-1s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH26 NIMH32 NIMH96 NIMH94 NIMH53 NIMH45 NIMH63 NIMH63 NIMH63 NIMH43 NIMH40 R085B11 NIMH32 NIMH32 NIMH50	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,585,682\\ 152,592,813\\ 152,602,949\\ 152,603,044\\ 152,603,044\\ 152,603,434\\ 152,604,004\\ 152,608,390\\ 152,616,167\\ 152,648,483\\ 152,648,483\\ 152,648,880\\ 152,649,628\\ 152,650,901\\ 152,650,901\\ 152,651,021\\ 152,651,021\\ 152,651,161\\ 152,651,161\\ 152,652,826\\ 152,654,809\\ 152,655,094\\ 152,655,094\\ 152,656,484\\ 152,664,887\\ \end{array}$	$\begin{array}{r} 152,591,432\\ 152,593,488\\ 152,627,475\\ 152,613,915\\ 152,629,535\\ 152,616,167\\ 152,633,215\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,731,368\\ 152,732,248\\ 152,737,217\\ 152,664,159\\ 152,731,743\\ 152,731,743\\ 152,731,743\\ 152,663,549\\ 152,664,254\\ 152,664,792\\ 152,724,158\\ \end{array}$	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652 72,347 86,246 13,138 80,582 78,362 8,740 9,160 8,308 59,271	112 15 333 159 355 164 324 223 32 28 19 1,252 1,106 1,333 1,252 1,211 118 114 88 936	19.5 22.2 13.6 14.6 13.5 13.1 13.1 13.1 13.4 14.9 16.8 15.5 13.9 15.5 13.5 13.5 15.5 13.5 15.5 13.5 15.5 13.5 12.4 10.6 15.8	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30 0.22 0.23 0.25 0.28 0.28 0.31 0.28 0.46 0.33 0.38 0.28	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 43.5 40.8 57.5 57.5 57.5 57.5 57.5 57.5 57.5 57
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH95-1s1 NIMH54-1s1 NIMH54-1s1 NIMH52-1s1 NIMH95-1s1 NIMH54-1s1 NIMH94-1s1 NIMH94-1s1 NIMH94-1s1 NIMH94-1s1 NIMH95-1s1 NIMH94-1s1 NIMH45-1s1 NIMH45-1s1 NIMH45-1s1 NIMH63-1s1 NIMH63-1s1 NIMH40-1s1 NIMH40-1s1 R085B11-A03-1s1 NIMH32-1s1 NIMH32-1s1 NIMH32-1s1 NIMH32-1s1 NIMH32-1s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH54 NIMH32 NIMH94 NIMH53 NIMH94 NIMH53 NIMH45 NIMH45 NIMH63 NIMH40 R085B11 NIMH32 NIMH50 NIMH63 NIMH63 NIMH66	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,585,682\\ 152,592,813\\ 152,602,949\\ 152,603,044\\ 152,603,044\\ 152,603,434\\ 152,604,004\\ 152,608,390\\ 152,616,167\\ 152,648,483\\ 152,648,483\\ 152,648,480\\ 152,649,628\\ 152,650,901\\ 152,650,901\\ 152,650,901\\ 152,650,901\\ 152,651,021\\ 152,651,021\\ 152,651,021\\ 152,651,021\\ 152,655,094\\ 152,655,094\\ 152,656,484\\ 152,664,487\\ 152,664,487\\ 152,676,387\\ 152,680,498\\ \end{array}$	$\begin{array}{r} 152,591,432\\ 152,593,488\\ 152,627,475\\ 152,613,915\\ 152,629,535\\ 152,616,167\\ 152,633,215\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,731,368\\ 152,732,248\\ 152,737,217\\ 152,664,159\\ 152,731,743\\ 152,731,188\\ 152,731,188\\ 152,664,254\\ 152,664,254\\ 152,664,792\\ 152,724,158\\ 152,750,355\\ \end{array}$	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652 72,347 86,246 13,138 80,582 78,362 8,740 9,160 8,308 59,271 73,968	112 15 333 159 355 164 324 223 32 28 19 1,252 1,106 1,333 183 1,252 1,211 118 114 88 936 1,250	19.5 22.2 13.6 14.6 13.5 13.1 13.1 13.4 14.9 16.8 15.5 13.5 15.5 13.5 15.5 13.5 15.5 13.5 15.5 13.5 15.5 13.5 15.5 13.5 15.5 13.5 15.5 13.5 15.5 13.5 12.4 10.6 15.8 16.9	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30 0.22 0.23 0.25 0.28 0.31 0.28 0.46 0.33 0.38 0.28 0.27	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 43.5 40.8 57.5 57.5 57.5 57.5 57.5 57.5 57.5 57
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH95-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH63-1s1 NIMH63-1s1 NIMH60-1s1 NIMH45-1s1 NIMH45-1s1 NIMH45-1s1 NIMH40-1s1 R085B11-A03-1s1 NIMH32-1s1 NIMH50-1s1 NIMH40-1s1 R085B11-A03-1s1 NIMH50-1s1 NIMH50-1s1 NIMH60-1s1 NIMH50-1s1 NIMH60-1s1 NIMH60-1s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH54 NIMH32 NIMH96 NIMH94 NIMH93 NIMH94 NIMH45 NIMH63 NIMH63 NIMH40 R085B11 NIMH32 NIMH32 NIMH50 NIMH63	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,585,682\\ 152,592,813\\ 152,602,949\\ 152,603,044\\ 152,603,434\\ 152,603,434\\ 152,604,004\\ 152,608,390\\ 152,616,167\\ 152,648,483\\ 152,648,483\\ 152,648,483\\ 152,648,483\\ 152,650,901\\ 152,650,901\\ 152,650,901\\ 152,651,161\\ 152,652,826\\ 152,654,809\\ 152,655,094\\ 152,655,094\\ 152,655,094\\ 152,655,094\\ 152,656,484\\ 152,664,887\\ 152,676,387\\ \end{array}$	$\begin{array}{r} 152,591,432\\ 152,593,488\\ 152,627,475\\ 152,613,915\\ 152,629,535\\ 152,616,167\\ 152,633,215\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,731,368\\ 152,723,248\\ 152,737,217\\ 152,664,159\\ 152,731,188\\ 152,663,549\\ 152,664,254\\ 152,664,254\\ 152,664,792\\ 152,724,158\\ 152,750,355\\ 152,720,628\\ \end{array}$	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652 72,347 86,246 13,138 80,582 78,362 8,740 9,160 8,308 59,271 73,968 40,130	112 15 333 159 355 164 324 223 32 28 19 1,252 1,106 1,333 1,83 1,252 1,211 118 114 88 936 1,250 738	$\begin{array}{r} 19.5\\ \hline 22.2\\ 13.6\\ 14.6\\ 13.5\\ 13.1\\ 13.1\\ 13.1\\ 13.4\\ 14.9\\ 16.8\\ 15.5\\ 15.5\\ 15.5\\ 15.5\\ 13.9\\ 15.5\\ 13.5\\ 12.4\\ 10.6\\ 15.8\\ 16.9\\ 18.4\\ \end{array}$	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30 0.22 0.23 0.25 0.28 0.31 0.28 0.31 0.28 0.31 0.28 0.33 0.38 0.28 0.27 0.22	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 43.5 40.8 57.5 57.5 57.5 57.5 57.5 57.5 61.3 61.3 61.3 60.3 57.4 57.7 58.2
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH54-1s1 NIMH54-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH63-1s1 NIMH63-1s1 NIMH45-1s1 NIMH45-1s1 NIMH60-1s1 NIMH45-1s1 NIMH45-1s1 NIMH45-1s1 NIMH45-1s1 NIMH45-1s1 NIMH45-1s1 NIMH60-1s1 NIMH50-1s1 NIMH50-1s1 NIMH50-1s1 NIMH60-1s1 NIMH60-1s1 NIMH50-1s1 NIMH60-1s1 NI	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH54 NIMH32 NIMH96 NIMH94 NIMH53 NIMH45 NIMH45 NIMH40 R085B11 NIMH40 NIMH40 R085B11 NIMH50 NIMH66 NIMH66 NIMH66 NIMH76	chrX chrX chrX chrX chrX chrX chrX chrX	152,585,682 152,592,813 152,602,949 152,603,044 152,603,044 152,603,044 152,603,390 152,616,167 152,648,483 152,648,483 152,648,483 152,649,628 152,650,901 152,650,901 152,651,021 152,651,021 152,651,021 152,651,021 152,651,021 152,652,826 152,655,094 152,655,094 152,656,484 152,664,487 152,664,487 152,680,498 152,680,733 152,680,733 152,680,733	$\begin{array}{r} 152,591,432\\ 152,593,488\\ 152,627,475\\ 152,613,915\\ 152,629,535\\ 152,616,167\\ 152,633,215\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,731,368\\ 152,723,248\\ 152,737,217\\ 152,664,159\\ 152,731,188\\ 152,663,549\\ 152,664,254\\ 152,750,355\\ 152,720,628\\ 152,735,519\\ 152,750,355\\ 152,750,35\\$	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652 72,347 86,246 13,138 80,582 78,362 8,740 9,160 8,308 59,271 73,968 40,130 54,786	112 15 333 159 355 164 324 223 32 28 19 1,252 1,106 1,333 1,252 1,211 118 1,251 1,211 118 1,44 88 936 1,250 738 984	19.5 22.2 13.6 14.6 13.5 13.1 13.4 14.9 16.8 15.5 13.9 15.5 13.5 13.4 14.9 16.8 15.5 13.5 15.5 13.5 15.5 13.5 16.9 18.4 18.0	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30 0.22 0.23 0.25 0.28 0.31 0.28 0.31 0.28 0.31 0.22 0.23 0.25 0.28 0.31 0.22 0.23 0.25 0.28 0.31 0.22 0.28 0.31 0.22 0.28 0.31 0.22 0.23 0.25 0.28 0.31 0.22 0.23 0.25 0.28 0.31 0.22 0.23 0.25 0.28 0.31 0.22 0.23 0.25 0.28 0.31 0.22 0.23 0.25 0.28 0.31 0.22 0.28 0.25 0.28 0.31 0.22 0.28 0.25 0.28 0.31 0.28 0.25 0.28 0.31 0.28 0.28 0.27 0.22 0.28 0.31 0.28 0.31 0.28 0.28 0.38 0.28 0.28 0.38 0.28 0.28 0.38 0.28 0.28 0.38 0.28 0.	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 43.5 40.8 57.5 57.5 57.5 57.5 57.5 57.5 61.3 61.2 60.3 57.4 57.7 58.2 58.5
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH63-1s1 NIMH45-1s1 NIMH45-1s1 NIMH45-1s1 NIMH63-1s1 NIMH45-1s1 NIMH45-1s1 NIMH60-1s1 NIMH43-1s1 NIMH43-1s1 NIMH40-1s1 R085B11-A03-1s1 NIMH60-1s1 NIMH50-1s1 NIMH50-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH66-1s1 NIMH76-1s1 NIMH76-1s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH32 NIMH32 NIMH94 NIMH53 NIMH94 NIMH53 NIMH63 NIMH63 NIMH40 R085B11 NIMH32 NIMH30 NIMH40 R085B11 NIMH30 NIMH60 NIMH63 NIMH60 NIMH63 NIMH66 NIMH66 NIMH76 NIMH76	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,585,682\\ 152,592,813\\ 152,602,949\\ 152,603,044\\ 152,603,044\\ 152,603,434\\ 152,604,004\\ 152,608,390\\ 152,616,167\\ 152,648,483\\ 152,648,483\\ 152,649,628\\ 152,650,716\\ 152,650,901\\ 152,650,901\\ 152,650,901\\ 152,650,901\\ 152,651,021\\ 152,651,021\\ 152,651,021\\ 152,655,094\\ 152,655,094\\ 152,655,094\\ 152,656,484\\ 152,656,484\\ 152,664,887\\ 152,676,387\\ 152,680,733\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,73\\$	$\begin{array}{r} 152,591,432\\ 152,593,488\\ 152,627,475\\ 152,613,915\\ 152,629,535\\ 152,616,167\\ 152,633,215\\ 152,650,876\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,731,368\\ 152,723,248\\ 152,731,743\\ 152,731,743\\ 152,731,743\\ 152,664,159\\ 152,664,254\\ 152,664,254\\ 152,664,792\\ 152,724,158\\ 152,750,355\\ 152,720,628\\ 152,735,519\\ 152,937,261\\ \end{array}$	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652 72,347 86,246 13,138 80,582 78,362 8,740 9,160 8,308 59,271 73,968 40,130 54,786 256,528	112 15 333 159 355 164 324 223 28 19 1,252 1,106 1,333 1,252 1,211 118 114 88 936 1,250 738 984 4,026	19.5 22.2 13.6 14.6 13.5 13.1 13.4 14.9 16.8 15.5 13.9 15.5 13.5 13.4 14.9 16.8 15.5 13.9 15.5 13.5 14.9 15.5 15.5 13.5 12.4 10.6 15.8 16.9 18.4 18.0 15.7	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30 0.22 0.23 0.25 0.28 0.31 0.28 0.46 0.33 0.38 0.28 0.27 0.22 0.28 0.31	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 43.5 40.8 57.5 57.5 57.5 57.5 57.5 57.5 61.3 61.2 60.3 57.4 57.7 58.2 58.5 59.3
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH96-1s1 NIMH54-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH45-1s1 NIMH45-1s1 NIMH45-1s1 NIMH45-1s1 NIMH40-1s1 R085B11-A03-1s1 NIMH32-1s1 NIMH40-1s1 R085B11-A03-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH76-1s1 NIMH76-1s1 R085B11-A03-1s1	NIMH33 NIMH40 NIMH96 NIMH95 NIMH54 NIMH26 NIMH26 NIMH32 NIMH94 NIMH53 NIMH96 NIMH45 NIMH63 NIMH40 R085B11 NIMH60 NIMH50 NIMH63 NIMH66 NIMH76 NIMH77 R085B11	chrX chrX chrX chrX chrX chrX chrX chrX	152,585,682 152,592,813 152,602,949 152,603,044 152,603,044 152,603,044 152,603,390 152,616,167 152,648,483 152,648,483 152,648,483 152,649,628 152,650,901 152,650,901 152,651,021 152,651,021 152,651,021 152,651,021 152,651,021 152,652,826 152,655,094 152,655,094 152,656,484 152,664,487 152,664,487 152,680,498 152,680,733 152,680,733 152,680,733	$\begin{array}{r} 152,591,432\\ 152,593,488\\ 152,627,475\\ 152,613,915\\ 152,629,535\\ 152,616,167\\ 152,633,215\\ 152,650,876\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,731,368\\ 152,723,248\\ 152,737,217\\ 152,664,159\\ 152,731,743\\ 152,731,188\\ 152,663,549\\ 152,664,524\\ 152,664,792\\ 152,664,792\\ 152,664,792\\ 152,724,158\\ 152,720,628\\ 152,735,519\\ 152,937,261\\ 152,731,333\\ \end{array}$	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652 72,347 86,246 13,138 80,582 78,362 8,740 9,160 8,308 59,271 73,968 40,130 54,786 256,528 45,674	112 15 333 159 355 164 324 223 28 19 1,252 1,106 1,333 1,252 1,211 118 114 88 936 1,250 738 984 4,026 830	19.5 22.2 13.6 14.6 13.5 13.1 13.4 14.9 16.8 15.5 15.5 13.5 15.5 15.5 13.5 15.5 15.5 15.5 15.5 15.5 15.5 15.5 15.5 15.7 18.0 15.7 18.2	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.23 0.22 0.23 0.25 0.28 0.31 0.28 0.46 0.33 0.38 0.28 0.27 0.22 0.22 0.23 0.31 0.28 0.31 0.29 0.31 0.29	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 43.5 40.8 57.5 57.5 57.5 57.5 57.5 57.5 57.5 57
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH96-1s1 NIMH54-1s1 NIMH54-1s1 NIMH54-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH53-2s1 NIMH45-1s1 NIMH63-1s1 NIMH45-1s1 NIMH45-1s1 NIMH45-1s1 NIMH45-1s1 NIMH63-1s1 NIMH40-1s1 R085B11-A03-1s1 NIMH30-1s1 NIMH40-1s1 R085B11-A03-1s1 NIMH66-1s1 NIMH66-1s1 NIMH76-1s1 NIMH76-1s1 NIMH76-1s1 NIMH76-1s1 NIMH51-1s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH26 NIMH32 NIMH96 NIMH94 NIMH53 NIMH45 NIMH45 NIMH40 R085B11 NIMH32 NIMH40 R085B11 NIMH53 NIMH63 NIMH63 NIMH76 NIMH76 NIMH76 NIMH76	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,585,682\\ 152,592,813\\ 152,602,949\\ 152,603,044\\ 152,603,044\\ 152,603,044\\ 152,604,004\\ 152,604,004\\ 152,604,004\\ 152,604,004\\ 152,604,004\\ 152,604,004\\ 152,604,004\\ 152,604,004\\ 152,604,004\\ 152,604,004\\ 152,605,001\\ 152,651,021\\ 152,651,021\\ 152,651,021\\ 152,651,021\\ 152,651,021\\ 152,651,021\\ 152,651,021\\ 152,651,021\\ 152,651,021\\ 152,652,826\\ 152,650,901\\ 152,650,901\\ 152,650,901\\ 152,650,901\\ 152,650,901\\ 152,650,901\\ 152,650,901\\ 152,650,901\\ 152,650,903\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,732\\ 152,680,732$	152,591,432 152,593,488 152,627,475 152,613,915 152,629,535 152,616,167 152,633,215 152,650,761 152,650,761 152,650,761 152,731,368 152,731,368 152,731,368 152,731,188 152,664,159 152,664,159 152,664,254 152,664,254 152,664,254 152,664,254 152,664,792 152,724,158 152,750,355 152,720,628 152,735,519 152,937,261 152,731,333 152,727,618	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652 72,347 86,246 13,138 80,582 78,362 8,740 9,160 8,308 59,271 73,968 40,130 54,786 256,528 45,674 37,249	112 15 333 159 355 164 324 223 32 28 19 1,252 1,106 1,333 1,252 1,211 118 114 88 936 1,250 738 984 4,026 830 684	19.5 22.2 13.6 14.6 13.5 13.1 13.4 14.9 16.8 15.5 15.5 13.5 15.5 13.5 15.5 13.5 15.5 13.5 15.5 13.5 15.5 13.5 15.5 13.5 15.5 13.5 15.7 18.4 18.0 15.7 18.2 18.4	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30 0.22 0.23 0.25 0.28 0.31 0.28 0.46 0.33 0.38 0.28 0.27 0.22 0.28 0.31 0.28 0.31 0.29 0.25	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 43.5 40.8 57.5 57.5 57.5 57.5 57.5 57.5 57.5 61.3 61.2 60.3 57.4 57.7 58.2 58.8 59.3 55.4 56.6
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH96-1s1 NIMH54-1s1 NIMH54-1s1 NIMH52-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH45-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH32-1s1 NIMH60-1s1 NIMH60-1s1 NIMH50-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH63-1s1 NIMH63-1s1 NIMH65-1s1 NIMH7-1s1 NIMH51-1s1 NIMH49-1s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH26 NIMH32 NIMH32 NIMH96 NIMH45 NIMH45 NIMH45 NIMH40 R085B11 NIMH60 NIMH43 NIMH60 NIMH32 NIMH60 NIMH32 NIMH60 NIMH50 NIMH63 NIMH64 NIMH63 NIMH64 NIMH63 NIMH64 N	chrX chrX chrX chrX chrX chrX chrX chrX	152,585,682 152,592,813 152,602,949 152,603,044 152,603,434 152,603,434 152,608,390 152,616,167 152,648,483 152,648,483 152,648,483 152,648,483 152,650,971 152,650,971 152,651,021 152,651,021 152,652,826 152,654,809 152,655,094 152,655,094 152,655,094 152,655,094 152,655,094 152,656,484 152,664,887 152,664,887 152,664,887 152,660,733 152,680,733 152,680,733 152,680,733	$\begin{array}{r} 152,591,432\\ 152,593,488\\ 152,627,475\\ 152,613,915\\ 152,629,535\\ 152,616,167\\ 152,633,215\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,731,368\\ 152,732,248\\ 152,737,217\\ 152,664,159\\ 152,731,743\\ 152,731,333\\ 152,727,618\\ 152,923,505\\ \end{array}$	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652 72,347 86,246 13,138 80,582 78,362 8,740 9,160 8,308 59,271 73,968 40,130 54,786 256,528 45,674 37,249 151,257	112 15 333 159 355 164 324 223 32 28 19 1,252 1,106 1,333 1,252 1,211 118 114 88 936 1,250 738 984 4,026 830 684 2,352	19.5 22.2 13.6 14.6 13.5 13.1 13.1 13.1 13.4 14.9 16.8 15.5 13.9 15.5 13.5 12.4 10.6 15.8 16.9 18.4 18.0 15.7 18.2 18.4 15.5	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30 0.22 0.23 0.25 0.28 0.31 0.28 0.46 0.33 0.38 0.28 0.27 0.22 0.28 0.31 0.28 0.46 0.33 0.38 0.28 0.27 0.22 0.28 0.31 0.29 0.25 0.30	62.0 58.3 61.4 65.9 61.1 64.2 57.8 57.5 57.5 57.5 57.5 57.5 57.5 57.5
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH54-1s1 NIMH54-1s1 NIMH96-1s1 NIMH94-1s1 NIMH45-1s1 NIMH45-1s1 NIMH60-1s1 NIMH40-1s1 R085B11-A03-1s1 NIMH63-1s1 NIMH60-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH65-1s1 NIMH65-1s1 NIMH65-1s1 NIMH76-1s1 NIMH51-1s1 NIMH49-1s1 NIMH69-2s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH26 NIMH32 NIMH32 NIMH96 NIMH43 NIMH45 NIMH45 NIMH63 NIMH40 R085B11 NIMH32 NIMH63 NIMH66 NIMH76 NIMH76 NIMH71 R085B11 NIMH51 NIMH51 NIMH51 NIMH51 NIMH69	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,585,682\\ 152,592,813\\ 152,602,949\\ 152,603,044\\ 152,603,044\\ 152,603,044\\ 152,603,004\\ 152,608,390\\ 152,616,167\\ 152,648,483\\ 152,648,483\\ 152,648,483\\ 152,649,628\\ 152,650,901\\ 152,650,901\\ 152,651,021\\ 152,651,021\\ 152,651,021\\ 152,651,161\\ 152,652,826\\ 152,654,809\\ 152,655,094\\ 152,655,094\\ 152,655,094\\ 152,656,484\\ 152,664,887\\ 152,664,887\\ 152,664,887\\ 152,664,887\\ 152,664,887\\ 152,660,733\\ 152,680,732\\ 152,680,732\\ 152,680,733\\ 152,680,732\\ 152,680,732\\ 152,680,732$	$\begin{array}{r} 152,591,432\\ 152,593,488\\ 152,627,475\\ 152,613,915\\ 152,629,535\\ 152,616,167\\ 152,633,215\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,731,368\\ 152,723,248\\ 152,737,217\\ 152,664,159\\ 152,731,743\\ 152,731,743\\ 152,731,743\\ 152,663,549\\ 152,664,254\\ 152,664,254\\ 152,664,792\\ 152,724,158\\ 152,750,355\\ 152,720,628\\ 152,735,519\\ 152,937,261\\ 152,731,333\\ 152,727,618\\ 152,923,505\\ 152,807,296\\ \end{array}$	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652 72,347 86,246 13,138 80,582 78,362 8,740 9,160 8,308 59,271 73,968 40,130 54,786 256,528 45,674 37,249 151,257 33,818	112 15 333 159 355 164 324 223 32 28 19 1,252 1,106 1,333 1,252 1,211 118 114 88 936 1,250 738 984 4,026 830 684 2,352 596	19.5 22.2 13.6 14.6 13.5 13.1 13.1 13.1 13.4 14.9 16.8 15.5 13.5 15.5 13.5 15.5 13.5 15.5 13.5 12.4 10.6 15.8 16.9 18.4 15.5 18.2 18.4 15.5 17.6	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30 0.22 0.23 0.25 0.28 0.31 0.28 0.46 0.33 0.38 0.28 0.27 0.22 0.28 0.31 0.28 0.46 0.33 0.38 0.28 0.27 0.22 0.28 0.31 0.29 0.25 0.30 0.29	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 43.5 40.8 57.5 57.5 57.5 57.5 57.5 57.5 61.3 61.2 60.3 57.4 58.5 59.3 55.4 56.6 55.5 57.7
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH95-1s1 NIMH54-1s1 NIMH54-1s1 NIMH52-1s1 NIMH95-1s1 NIMH54-1s1 NIMH94-1s1 NIMH94-1s1 NIMH94-1s1 NIMH94-1s1 NIMH94-1s1 NIMH94-1s1 NIMH94-1s1 NIMH45-1s1 NIMH45-1s1 NIMH45-1s1 NIMH63-1s1 NIMH63-1s1 NIMH45-1s1 NIMH66-1s1 NIMH66-1s1 NIMH66-1s1 NIMH66-1s1 NIMH66-1s1 NIMH66-1s1 NIMH76-1s1 NIMH76-1s1 NIMH71-1s1 NIMH51-403-1s1 NIMH49-1s1 NIMH69-2s1 NIMH63-1s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH26 NIMH32 NIMH96 NIMH94 NIMH93 NIMH40 R085B11 NIMH40 R085B11 NIMH60 NIMH66 NIMH66 NIMH76 NIMH71 R085B11 NIMH71 R085B11 NIMH51 NIMH51 NIMH69 NIMH69 NIMH63	chrX chrX chrX chrX chrX chrX chrX chrX	152,585,682 152,592,813 152,602,949 152,603,044 152,603,434 152,603,434 152,604,004 152,608,390 152,616,167 152,648,483 152,648,483 152,648,483 152,648,483 152,650,971 152,650,971 152,651,021 152,651,021 152,655,094 152,655,094 152,655,094 152,656,484 152,656,484 152,664,887 152,664,887 152,664,887 152,664,887 152,660,498 152,660,733 152,680,733 152,680,733 152,680,733 152,680,734 152,772,248 152,772,478	$\begin{array}{r} 152,591,432\\ 152,693,488\\ 152,627,475\\ 152,613,915\\ 152,629,535\\ 152,616,167\\ 152,633,215\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,650,761\\ 152,731,368\\ 152,732,248\\ 152,737,217\\ 152,664,159\\ 152,731,743\\ 152,731,188\\ 152,663,549\\ 152,664,254\\ 152,664,254\\ 152,664,254\\ 152,664,792\\ 152,724,158\\ 152,750,355\\ 152,720,628\\ 152,735,519\\ 152,937,261\\ 152,731,333\\ 152,727,618\\ 152,923,505\\ 152,807,296\\ 152,805,016\\ \end{array}$	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652 72,347 86,246 13,138 80,582 78,362 8,740 9,160 8,308 59,271 73,968 40,130 54,786 256,528 45,674 37,249 151,257 33,818 30,668	112 15 333 159 355 164 324 223 32 28 19 1,252 1,106 1,333 183 1,252 1,211 118 114 88 936 1,250 738 984 4,026 830 684 2,352 596 546	19.5 22.2 13.6 14.6 13.5 13.1 13.4 14.9 16.8 15.5 15.5 13.5 13.4 14.9 16.8 15.5 13.9 15.5 13.5 15.5 13.5 15.5 15.5 15.5 15.7 18.4 18.0 15.7 18.2 18.4 15.5 17.6 17.8	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30 0.22 0.23 0.25 0.28 0.31 0.28 0.46 0.33 0.38 0.28 0.27 0.22 0.28 0.31 0.28 0.31 0.25 0.28 0.31 0.25 0.28 0.31 0.25 0.28 0.31 0.25 0.28 0.31 0.25 0.28 0.31 0.25 0.28 0.31 0.25 0.28 0.31 0.25 0.28 0.31 0.25 0.28 0.31 0.25 0.28 0.31 0.25 0.28 0.31 0.25 0.28 0.31 0.25 0.28 0.31 0.25 0.28 0.31 0.25 0.28 0.31 0.25 0.28 0.31 0.25 0.28 0.31 0.25 0.28 0.27 0.22 0.23 0.25 0.30 0.25 0.30 0.25 0.28 0.31 0.27 0.22 0.23 0.25 0.28 0.31 0.25 0.28 0.31 0.27 0.22 0.22 0.23 0.25 0.28 0.27 0.22 0.22 0.23 0.25 0.28 0.31 0.27 0.22 0.22 0.23 0.25 0.28 0.27 0.22 0.22 0.22 0.23 0.25 0.28 0.27 0.22 0.22 0.22 0.28 0.27 0.22 0.28 0.27 0.22 0.28 0.31 0.29 0.25 0.28 0.30 0.29 0.29 0.29 0.29 0.29 0.29 0.29 0.29 0.29 0.29	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 43.5 40.8 57.5 57.7 58.5 59.3 55.5 57.7 58.0
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH95-1s1 NIMH54-1s1 NIMH54-1s1 NIMH54-1s1 NIMH95-1s1 NIMH54-1s1 NIMH94-1s1 NIMH94-1s1 NIMH94-1s1 NIMH94-1s1 NIMH94-1s1 NIMH94-1s1 NIMH45-1s1 NIMH45-1s1 NIMH45-1s1 NIMH45-1s1 NIMH60-1s1 NIMH45-1s1 NIMH60-1s1 NIMH45-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH76-1s1 NIMH51-1s1 NIMH51-1s1 NIMH69-2s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH54 NIMH32 NIMH96 NIMH96 NIMH94 NIMH53 NIMH63 NIMH63 NIMH40 R085B11 NIMH32 NIMH66 NIMH76 NIMH76 NIMH76 NIMH76	chrX chrX chrX chrX chrX chrX chrX chrX	152,585,682 152,592,813 152,602,949 152,603,044 152,603,434 152,603,434 152,608,390 152,616,167 152,648,483 152,648,483 152,648,483 152,648,483 152,650,971 152,650,971 152,651,161 152,652,826 152,654,809 152,655,094 152,655,094 152,655,094 152,655,094 152,655,094 152,656,484 152,664,887 152,664,887 152,664,887 152,660,733 152,680,733 152,680,733 152,680,733 152,680,733 152,680,733 152,680,733 152,680,733 152,680,498 152,772,248 152,772,478 152,774,918	152,591,432 152,593,488 152,627,475 152,613,915 152,629,535 152,616,167 152,633,215 152,650,761 152,650,761 152,650,761 152,731,368 152,732,248 152,737,217 152,664,159 152,731,743 152,731,188 152,664,254 152,664,254 152,664,254 152,764,792 152,724,158 152,750,355 152,720,628 152,735,519 152,937,261 152,937,261 152,937,261 152,935,05 152,807,296 152,807,296 152,805,016 152,809,606	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652 72,347 86,246 13,138 80,582 78,362 8,740 9,160 8,308 59,271 73,968 40,130 54,786 256,528 45,674 37,249 151,257 33,818 30,668 124,688	112 15 333 159 355 164 324 223 32 19 1,252 1,106 1,333 1,83 1,252 1,211 118 114 88 936 1,250 738 984 4,026 830 684 2,352 596 546 2,032	19.5 22.2 13.6 14.6 13.5 13.1 13.4 14.9 16.8 15.5 15.5 13.5 15.5 13.5 15.5 13.5 15.5 13.5 15.5 13.5 15.5 13.5 15.7 18.4 18.2 18.4 15.5 17.6 17.8 16.3	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30 0.22 0.23 0.25 0.28 0.31 0.28 0.46 0.33 0.38 0.28 0.27 0.22 0.28 0.31 0.28 0.31 0.29 0.29 0.29 0.24	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 43.5 40.8 57.5 57.4 57.7 58.0 55.5 57.7 58.0 57.7 58.0 57.4
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH54-1s1 NIMH54-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH45-1s1 NIMH45-1s1 NIMH45-1s1 NIMH60-1s1 NIMH60-1s1 NIMH45-1s1 NIMH60-1s1 NIMH61-1s1 NIMH51-1s1 NIMH51-1s1 NIMH69-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NI	NIMH33 NIMH34 NIMH40 NIMH96 NIMH95 NIMH54 NIMH54 NIMH32 NIMH96 NIMH96 NIMH93 NIMH45 NIMH45 NIMH63 NIMH40 NIMH40 NIMH50 NIMH66 NIMH76 NIMH51 NIM51 NIM51 NIM51 NIM51 NIM51 NIM51 NIM51 NI	chrX chrX chrX chrX chrX chrX chrX chrX	152,585,682 152,592,813 152,602,949 152,603,044 152,603,044 152,603,434 152,604,004 152,608,390 152,616,167 152,648,483 152,648,483 152,648,483 152,648,483 152,650,901 152,650,901 152,650,901 152,650,901 152,651,161 152,652,826 152,654,809 152,655,094 152,656,484 152,656,484 152,664,887 152,664,887 152,664,887 152,664,887 152,664,887 152,664,887 152,660,733 152,680,733 152,680,733 152,680,733 152,680,733 152,680,733 152,680,733 152,680,733 152,680,733 152,680,733 152,680,733 152,680,733 152,680,733 152,680,733 152,680,733 152,680,733 152,680,733 152,677,2,248 152,774,348 152,774,348	152,591,432 152,593,488 152,627,475 152,613,915 152,629,535 152,616,167 152,633,215 152,650,761 152,650,761 152,650,761 152,650,761 152,731,368 152,732,248 152,737,217 152,664,159 152,731,188 152,731,188 152,664,549 152,664,549 152,664,792 152,724,158 152,750,355 152,720,628 152,735,519 152,937,261 152,937,261 152,731,333 152,727,618 152,923,505 152,807,296 152,807,296 152,805,016 152,809,606 152,800,959	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652 72,347 86,246 13,138 80,582 78,362 8,740 9,160 8,308 59,271 73,968 40,130 54,786 256,528 45,674 37,249 151,257 33,818 30,668 124,688 25,941	112 15 333 159 355 164 324 223 32 19 1,252 1,106 1,333 1,252 1,211 118 114 88 936 1,250 738 984 4,026 830 684 2,352 596 546 2,032 457	$\begin{array}{r} 19.5\\ \hline 22.2\\ 13.6\\ 14.6\\ 13.5\\ 13.1\\ 13.1\\ 13.1\\ 13.4\\ 14.9\\ 16.8\\ 15.5\\ 15.$	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30 0.22 0.23 0.25 0.28 0.31 0.28 0.46 0.33 0.38 0.28 0.27 0.22 0.28 0.31 0.28 0.31 0.28 0.31 0.29 0.29 0.29 0.24 0.40	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 40.8 57.5 57.7 58.2 58.5 57.7 58.0 57.4 57.4 57.4 57.4 57.4
NIMH33-1s1 NIMH34-1s1 NIMH40-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH54-1s1 NIMH54-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH96-1s1 NIMH63-1s1 NIMH63-1s1 NIMH45-1s1 NIMH63-1s1 NIMH60-1s1 NIMH45-1s1 NIMH60-1s1 NIMH40-1s1 R085B11-A03-1s1 NIMH60-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH76-1s1 NIMH40-1s1 NIMH40-1s1 NIMH45-1s1	NIMH33 NIMH40 NIMH96 NIMH95 NIMH54 NIMH54 NIMH52 NIMH96 NIMH94 NIMH53 NIMH96 NIMH45 NIMH63 NIMH40 NIMH50 NIMH66 NIMH76 NIMH51 NIMH51 NIMH51 NIMH51 NIMH50 NIMH63 NIMH66 NIMH76 NIMH51 NI	chrX chrX chrX chrX chrX chrX chrX chrX	152,585,682 152,592,813 152,602,949 152,603,044 152,603,044 152,603,434 152,604,004 152,608,390 152,616,167 152,648,483 152,648,483 152,648,483 152,648,483 152,650,901 152,650,901 152,650,901 152,650,901 152,651,161 152,652,826 152,654,809 152,655,094 152,656,484 152,656,484 152,656,484 152,664,887 152,664,887 152,664,887 152,664,887 152,664,887 152,664,887 152,664,887 152,664,887 152,664,887 152,664,887 152,664,887 152,664,887 152,664,887 152,664,887 152,664,887 152,664,887 152,660,733 152,680,733 152,680,733 152,680,733 152,680,733 152,680,733 152,680,733 152,680,733 152,677,3478 152,774,918 152,774,918 152,775,018	152,591,432 152,593,488 152,627,475 152,613,915 152,629,535 152,616,167 152,633,215 152,650,876 152,650,761 152,650,761 152,731,368 152,723,248 152,737,217 152,664,159 152,731,188 152,731,188 152,663,549 152,664,254 152,664,254 152,664,254 152,664,254 152,664,254 152,664,255 152,720,628 152,720,628 152,735,519 152,937,261 152,937,261 152,937,261 152,935,055 152,807,296 152,805,016 152,809,606 152,800,959 152,926,334	5,750 675 24,526 10,871 26,101 12,163 24,825 17,048 2,393 1,881 1,133 80,652 72,347 86,246 13,138 80,582 78,362 8,740 9,160 8,308 59,271 73,968 40,130 54,786 256,528 45,674 37,249 151,257 33,818 30,668 124,688 25,941 151,246	112 15 333 159 355 164 324 223 28 19 1,252 1,106 1,333 1,252 1,211 118 1,251 1,251 1,211 118 1,252 1,211 118 1,250 738 984 4,026 830 684 2,352 596 546 2,032 457 2,337	$\begin{array}{r} 19.5\\ \hline 22.2\\ \hline 13.6\\ \hline 14.6\\ \hline 13.5\\ \hline 13.1\\ \hline 13.1\\ \hline 13.1\\ \hline 13.4\\ \hline 14.9\\ \hline 16.8\\ \hline 15.5\\ \hline 15.5\\ \hline 15.5\\ \hline 15.5\\ \hline 15.5\\ \hline 13.5\\ \hline 15.5\\ \hline$	0.36 -0.49 0.41 0.28 0.31 0.21 0.37 0.31 -0.23 -0.21 -0.30 0.22 0.23 0.25 0.28 0.31 0.28 0.46 0.33 0.38 0.28 0.27 0.22 0.28 0.31 0.28 0.31 0.29 0.25 0.30 0.29 0.29 0.24 0.40 0.25 0.28	62.0 58.3 61.4 65.9 61.1 64.2 57.8 56.2 44.9 40.8 57.5 57.5 57.5 57.5 57.5 61.3 61.2 60.3 57.4 57.5 59.3 55.4 56.6 55.7 58.0 57.7 58.0 57.4 57.4 57.4 57.4 57.7 58.0 57.7 58.0 57.7 58.0 57.4 57.4 57.4 57.4 57.4 57.4

NIMH31-1s1	NIMH31	chrX	152,779,722	152,893,525	113,803	1,944	17.1	0.24	55.5
NIMH60-1s1	NIMH60	chrX	152,779,832	152,807,186	27,354	503	18.4	0.38	59.7
NIMH61-1s1	NIMH61	chrX	152,780,012	152,892,600	112,588	1,921	17.1	0.30	56.7
NIMH81-1s1	NIMH81	chrX	152,780,976	152,793,310	12,334	242	19.6	0.36	60.3
NIMH39-1s1	NIMH39	chrX	152,780,996	152,807,131	26,135	480	18.4	0.34	59.8
NIMH94-1s1	NIMH94	chrX	152,783,267	152,804,384	21,117	389	18.4	0.31	59.1
NIMH16-1s1	NIMH16	chrX	152,784,002	152,926,134	142,132	2,187	15.4	0.32	55.8
NIMH23-1s1	NIMH23	chrX	152,784,287	152,809,202	24,915	435	17.5	0.38	58.4
NIMH95-1s1	NIMH95	chrX	152,786,155	152,800,002	13,847	254	18.3	0.28	58.8
NIMH01-1s1	NIMH01	chrX	152,787,180	152,807,046	19,866	359	18.1	0.27	59.9
NIMH53-2s1	NIMH53	chrX	152,789,320	152,800,142	10,822	197	18.2	0.24	58.0
NIMH92-1s1	NIMH92	chrX	152,793,215	152,811,737	18,522	299	16.1	0.23	56.6
NIMH67-1s1	NIMH67	chrX	152,793,290	152,884,425	91,135	1,518	16.7	0.27	55.0
NIMH75-1s1	NIMH75	chrX	152,793,385	152,804,454	11,069	195	17.6	0.25	58.5
NIMH96-1s1	NIMH96	chrX	152,793,460	152,811,642	18,182	292	16.1	0.25	56.6
			· · ·						
NIMH87-A03-2s2	NIMH87	chrX	152,794,560	152,807,321	12,761	222	17.4	0.25	59.4
NIMH01-1s1	NIMH01	chrX	152,820,455	152,889,681	69,226	1,204	17.4	0.24	58.9
NIMH96-1s1	NIMH96	chrX	152,820,495	152,829,786	9,291	179	19.3	0.33	63.5
NIMH10-1s1	NIMH10	chrX	152,820,570	152,951,167	130,597	2,024	15.5	0.28	62.3
					65,584	1,136	17.3	0.33	61.1
NIMH60-1s1	NIMH60	chrX	152,820,570	152,886,154					
NIMH07-1s1	NIMH07	chrX	152,820,570	152,890,330	69,760	1,213	17.4	0.26	61.6
NIMH40-1s1	NIMH40	chrX	152,820,650	152,886,199	65,549	1,136	17.3	0.30	62.0
NIMH63-1s1	NIMH63	chrX	152,820,650	152,830,174	9,524	182	19.1	0.35	63.0
NIMH48-1s1	NIMH48	chrX	152,820,810	152,829,761	8,951	173	19.3	0.39	63.6
NIMH50-1s1	NIMH50	chrX	152,820,885	152,829,786	8,901	172	19.3	0.40	63.7
NIMH69-2s1	NIMH69	chrX	152,821,820	152,890,200	68,380	1,187	17.4	0.25	58.3
NIMH06-1s1	NIMH06	chrX	152,828,921	152,959,283	130,362	1,979	15.2	0.27	58.4
NIMH30-1s2	NIMH30	chrX	152,848,103	152,889,925	41,822	737	17.6	0.26	58.4
NIMH26-1s1	NIMH26	chrX	152,848,128	152,892,035	43,907	772	17.6	0.26	58.4
NIMH90-1s1	NIMH90	chrX			33,290	568	17.1	0.24	58.4
			152,864,867	152,898,157					
NIMH23-1s1	NIMH23	chrX	152,866,352	152,890,445	24,093	467	19.4	0.38	55.7
NIMH30-1s2	NIMH30	chrX	152,889,950	152,892,060	2,110	37	17.5	-0.41	65.5
NIMH23-1s1	NIMH23	chrX	152,890,475	152,891,960	1,485	27	18.2	-0.59	67.3
NIMH33-1s1	NIMH33	chrX	153,014,407	153,017,466	3,059	58	19.0	-0.29	57.1
NIMH44-1s1	NIMH44	chrX	153,016,546	153,017,436	890	19	21.3	-0.53	50.6
NIMH53-2s1	NIMH53	chrX	152,826,496	152,826,811	315	8	25.4	0.77	59.7
									59.7 59.3
NIMH53-2s1	NIMH53	chrX	152,826,496	152,826,811	315	8	25.4	0.77	59.7
NIMH53-2s1 NIMH33-1s1	NIMH53 NIMH33	chrX chrX	152,826,496 152,848,413 153,210,565	152,826,811 152,851,298 153,365,011	315 2,885	8 58 2,150	25.4 20.1	0.77 0.41	59.7 59.3
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1	NIMH53 NIMH33 NIMH69 NIMH19	chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532	152,826,811 152,851,298 153,365,011 153,537,538	315 2,885 154,446 326,006	8 58 2,150 3,471	25.4 20.1 13.9 10.6	0.77 0.41 0.23 0.29	59.7 59.3 57.6 54.8
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21	chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307	152,826,811 152,851,298 153,365,011 153,537,538 153,417,824	315 2,885 154,446 326,006 204,517	8 58 2,150 3,471 2,807	25.4 20.1 13.9 10.6 13.7	0.77 0.41 0.23 0.29 0.37	59.7 59.3 57.6 54.8 56.6
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22	chrX chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307 153,213,307	152,826,811 152,851,298 153,365,011 153,537,538 153,417,824 153,429,930	315 2,885 154,446 326,006 204,517 216,623	8 58 2,150 3,471 2,807 2,973	25.4 20.1 13.9 10.6 13.7 13.7	0.77 0.41 0.23 0.29 0.37 0.30	59.7 59.3 57.6 54.8 56.6 56.5
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH22-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH08	chrX chrX chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307 153,213,307 153,213,447	152,826,811 152,851,298 153,365,011 153,537,538 153,417,824 153,429,930 153,354,185	315 2,885 154,446 326,006 204,517 216,623 140,738	8 58 2,150 3,471 2,807 2,973 1,947	25.4 20.1 13.9 10.6 13.7 13.7 13.8	0.77 0.41 0.23 0.29 0.37 0.30 0.29	59.7 59.3 57.6 54.8 56.6 56.5 58.2
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22	chrX chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307 153,213,307	152,826,811 152,851,298 153,365,011 153,537,538 153,417,824 153,429,930	315 2,885 154,446 326,006 204,517 216,623	8 58 2,150 3,471 2,807 2,973	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6	0.77 0.41 0.23 0.29 0.37 0.30	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH22-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH08	chrX chrX chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307 153,213,307 153,213,447	152,826,811 152,851,298 153,365,011 153,537,538 153,417,824 153,429,930 153,354,185	315 2,885 154,446 326,006 204,517 216,623 140,738	8 58 2,150 3,471 2,807 2,973 1,947	25.4 20.1 13.9 10.6 13.7 13.7 13.8	0.77 0.41 0.23 0.29 0.37 0.30 0.29	59.7 59.3 57.6 54.8 56.6 56.5 58.2
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH22-1s1 NIMH08-1s1 NIMH20-1s1 NIMH43-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH08 NIMH20 NIMH43	chrX chrX chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307 153,213,307 153,213,447 153,213,572 153,213,597	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,537,638\\ 153,354,435\\ \end{array}$	315 2,885 154,446 326,006 204,517 216,623 140,738 324,066 140,838	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6 13.8	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH08-1s1 NIMH08-1s1 NIMH43-1s1 NIMH12-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH08 NIMH20 NIMH43 NIMH12	chrX chrX chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307 153,213,307 153,213,447 153,213,572 153,213,597 153,213,597	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,537,638\\ 153,354,435\\ 153,354,435\\ 153,369,728\\ \end{array}$	315 2,885 154,446 326,006 204,517 216,623 140,738 324,066 140,838 156,131	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6 13.8 14.0	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH20-1s1 NIMH20-1s1 NIMH43-1s1 NIMH43-1s1 NIMH12-1s1 NIMH50-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH08 NIMH20 NIMH43 NIMH12 NIMH50	chrX chrX chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307 153,213,307 153,213,447 153,213,572 153,213,597 153,213,597	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,537,638\\ 153,354,435\\ 153,354,435\\ 153,369,728\\ 153,416,769\\ \end{array}$	315 2,885 154,446 326,006 204,517 216,623 140,738 324,066 140,838 156,131 203,172	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6 13.8 14.0 13.7	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH08-1s1 NIMH08-1s1 NIMH20-1s1 NIMH43-1s1 NIMH12-1s1 NIMH50-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH08 NIMH20 NIMH43 NIMH12 NIMH50 NIMH51	chrX chrX chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307 153,213,307 153,213,447 153,213,597 153,213,597 153,213,597 153,213,597	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,537,638\\ 153,354,435\\ 153,354,435\\ 153,369,728\\ 153,369,728\\ 153,416,769\\ 153,257,756\end{array}$	315 2,885 154,446 326,006 204,517 216,623 140,738 324,066 140,838 156,131 203,172 44,159	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6 13.8 14.0 13.7 13.7	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.5
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH08-1s1 NIMH08-1s1 NIMH43-1s1 NIMH12-1s1 NIMH50-1s1 NIMH50-1s1 NIMH51-1s1 NIMH95-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH20 NIMH20 NIMH43 NIMH12 NIMH50 NIMH51 NIMH55	chrX chrX chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307 153,213,307 153,213,572 153,213,597 153,213,597 153,213,597 153,213,597	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,537,638\\ 153,354,435\\ 153,354,435\\ 153,369,728\\ 153,369,728\\ 153,257,756\\ 153,266,406\\ \end{array}$	315 2,885 154,446 326,006 204,517 216,623 140,738 324,066 140,838 156,131 203,172 44,159 52,809	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6 13.8 14.0 13.7 13.7 14.4	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.5 60.1
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH08-1s1 NIMH08-1s1 NIMH20-1s1 NIMH43-1s1 NIMH12-1s1 NIMH50-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH08 NIMH20 NIMH43 NIMH12 NIMH50 NIMH51	chrX chrX chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307 153,213,307 153,213,447 153,213,597 153,213,597 153,213,597 153,213,597	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,537,638\\ 153,354,435\\ 153,354,435\\ 153,369,728\\ 153,369,728\\ 153,416,769\\ 153,257,756\end{array}$	315 2,885 154,446 326,006 204,517 216,623 140,738 324,066 140,838 156,131 203,172 44,159	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6 13.8 14.0 13.7 13.7	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.5
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH08-1s1 NIMH08-1s1 NIMH43-1s1 NIMH43-1s1 NIMH50-1s1 NIMH50-1s1 NIMH51-1s1 NIMH51-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH20 NIMH20 NIMH43 NIMH12 NIMH50 NIMH51 NIMH55	chrX chrX chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307 153,213,307 153,213,447 153,213,572 153,213,597 153,213,597 153,213,597 153,213,597 153,213,597 153,213,597	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,537,638\\ 153,354,435\\ 153,354,435\\ 153,369,728\\ 153,369,728\\ 153,257,756\\ 153,266,406\\ \end{array}$	315 2,885 154,446 326,006 204,517 216,623 140,738 324,066 140,838 156,131 203,172 44,159 52,809	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6 13.8 14.0 13.7 13.7 14.4	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.31	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.5 60.1
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH08-1s1 NIMH08-1s1 NIMH43-1s1 NIMH50-1s1 NIMH50-1s1 NIMH51-1s1 NIMH95-1s1 NIMH61-1s1 NIMH61-2s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH08 NIMH20 NIMH43 NIMH12 NIMH50 NIMH51 NIMH51 NIMH51 NIMH51 NIMH51	chrX chrX chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307 153,213,307 153,213,507 153,213,597 153,213,597 153,213,597 153,213,597 153,213,597 153,213,597 153,213,597 153,213,642 153,213,642	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,537,638\\ 153,537,638\\ 153,354,435\\ 153,369,728\\ 153,369,728\\ 153,416,769\\ 153,257,756\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ \end{array}$	315 2,885 154,446 326,006 204,517 216,623 140,738 324,066 140,838 156,131 203,172 44,159 52,809 150,699 204,042	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6 13.8 14.0 13.7 13.7 14.4 13.8 13.7	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.23	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.5 60.1 57.9 56.6
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH08-1s1 NIMH08-1s1 NIMH43-1s1 NIMH43-1s1 NIMH51-1s1 NIMH51-1s1 NIMH95-1s1 NIMH61-1s1 NIMH61-1s1 NIMH70-2s1 NIMH47-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH08 NIMH20 NIMH43 NIMH12 NIMH50 NIMH51 NIMH51 NIMH51 NIMH51 NIMH51 NIMH61 NIMH70 NIMH47	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,826,496\\ 152,848,413\\ 153,210,565\\ 153,211,532\\ 153,213,307\\ 153,213,307\\ 153,213,447\\ 153,213,577\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ \end{array}$	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,537,638\\ 153,354,435\\ 153,354,435\\ 153,369,728\\ 153,369,728\\ 153,257,756\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ \end{array}$	315 2,885 154,446 326,006 204,517 216,623 140,738 324,066 140,838 156,131 203,172 44,159 52,809 150,699 204,042 214,009	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,922	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6 13.8 14.0 13.7 13.7 14.4 13.8 13.7 13.7	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.23 0.29	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.5 60.1 57.9 56.6 56.4
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH08-1s1 NIMH08-1s1 NIMH20-1s1 NIMH43-1s1 NIMH50-1s1 NIMH51-1s1 NIMH51-1s1 NIMH61-1s1 NIMH61-1s1 NIMH70-2s1 NIMH47-1s1 NIMH49-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH20 NIMH20 NIMH43 NIMH50 NIMH51 NIMH61 NIMH70 NIMH43	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,826,496\\ 152,848,413\\ 153,210,565\\ 153,211,532\\ 153,213,307\\ 153,213,307\\ 153,213,447\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,642$	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,537,638\\ 153,354,435\\ 153,354,435\\ 153,369,728\\ 153,369,728\\ 153,257,756\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ 153,429,785\\ \end{array}$	315 2,885 154,446 326,006 204,517 216,623 140,738 324,066 140,838 156,131 203,172 44,159 52,809 150,699 204,042 214,009 216,143	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,922 2,963	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6 13.8 14.0 13.7 13.7 14.4 13.8 13.7 13.7 13.7 13.7	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.31 0.23 0.29 0.31	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.1 57.9 56.6 56.4 56.4 56.5
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH08-1s1 NIMH20-1s1 NIMH20-1s1 NIMH50-1s1 NIMH51-1s1 NIMH51-1s1 NIMH51-1s1 NIMH70-2s1 NIMH41-1s1 NIMH49-1s1 NIMH49-1s1 NIMH76-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH20 NIMH20 NIMH43 NIMH20 NIMH51 NIMH51 NIMH51 NIMH51 NIMH51 NIMH70 NIMH47 NIMH49 NIMH76	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,826,496\\ 152,848,413\\ 153,210,565\\ 153,211,532\\ 153,213,307\\ 153,213,307\\ 153,213,447\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,642$	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,537,638\\ 153,354,435\\ 153,354,435\\ 153,369,728\\ 153,416,769\\ 153,257,756\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ 153,429,785\\ 153,394,781\\ \end{array}$	315 2,885 154,446 326,006 204,517 216,623 140,738 324,066 140,838 156,131 203,172 44,159 52,809 150,699 204,042 214,009 216,143 181,084	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,922 2,963 2,511	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6 13.8 14.0 13.7 13.7 14.4 13.8 13.7 13.7 13.7 13.7 13.7	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.31 0.23 0.29 0.31 0.23	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.1 57.9 56.6 56.4 56.5 57.1
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH08-1s1 NIMH08-1s1 NIMH20-1s1 NIMH43-1s1 NIMH50-1s1 NIMH51-1s1 NIMH51-1s1 NIMH61-1s1 NIMH61-1s1 NIMH70-2s1 NIMH47-1s1 NIMH49-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH20 NIMH20 NIMH43 NIMH50 NIMH51 NIMH61 NIMH70 NIMH43	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,826,496\\ 152,848,413\\ 153,210,565\\ 153,211,532\\ 153,213,307\\ 153,213,307\\ 153,213,447\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,642$	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,537,638\\ 153,354,435\\ 153,354,435\\ 153,369,728\\ 153,369,728\\ 153,257,756\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ 153,429,785\\ \end{array}$	315 2,885 154,446 326,006 204,517 216,623 140,738 324,066 140,838 156,131 203,172 44,159 52,809 150,699 204,042 214,009 216,143	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,922 2,963	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6 13.8 14.0 13.7 13.7 14.4 13.8 13.7 13.7 13.7 13.7	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.31 0.23 0.29 0.31	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.1 57.9 56.6 56.4 56.4 56.5
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH08-1s1 NIMH20-1s1 NIMH20-1s1 NIMH50-1s1 NIMH51-1s1 NIMH51-1s1 NIMH51-1s1 NIMH70-2s1 NIMH41-1s1 NIMH49-1s1 NIMH49-1s1 NIMH76-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH20 NIMH20 NIMH43 NIMH20 NIMH51 NIMH51 NIMH51 NIMH51 NIMH51 NIMH70 NIMH47 NIMH49 NIMH76	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,826,496\\ 152,848,413\\ 153,210,565\\ 153,211,532\\ 153,213,307\\ 153,213,307\\ 153,213,447\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,642$	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,537,638\\ 153,354,435\\ 153,354,435\\ 153,369,728\\ 153,416,769\\ 153,257,756\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ 153,429,785\\ 153,394,781\\ \end{array}$	315 2,885 154,446 326,006 204,517 216,623 140,738 324,066 140,838 156,131 203,172 44,159 52,809 150,699 204,042 214,009 216,143 181,084	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,922 2,963 2,511	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6 13.8 14.0 13.7 13.7 14.4 13.8 13.7 13.7 13.7 13.7 13.7	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.31 0.23 0.29 0.31 0.23	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.1 57.9 56.6 56.4 56.5 57.1
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH08-1s1 NIMH08-1s1 NIMH20-1s1 NIMH43-1s1 NIMH51-1s1 NIMH51-1s1 NIMH61-1s1 NIMH61-1s1 NIMH61-1s1 NIMH49-1s1 NIMH49-1s1 NIMH49-1s1 NIMH60-1s1 NIMH26-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH22 NIMH20 NIMH20 NIMH43 NIMH20 NIMH50 NIMH51 NIMH50 NIMH51 NIMH55 NIMH61 NIMH49 NIMH76 NIMH60 NIMH26	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,826,496\\ 152,848,413\\ 153,210,565\\ 153,211,532\\ 153,213,307\\ 153,213,307\\ 153,213,307\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ \end{array}$	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,354,185\\ 153,354,435\\ 153,354,435\\ 153,369,728\\ 153,416,769\\ 153,257,756\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ 153,429,785\\ 153,394,781\\ 153,426,460\\ 153,259,031\\ \end{array}$	315 2,885 154,446 326,006 204,517 216,623 140,738 324,066 140,838 156,131 203,172 44,159 52,809 150,699 204,042 214,009 216,143 181,084 212,763 45,334	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,922 2,963 2,511 2,903 632	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6 13.8 14.0 13.7 13.7 13.7 13.7 13.7 13.7 13.7 13.7	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.24 0.23 0.29 0.31 0.23 0.31 0.31	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.5 60.1 57.9 56.6 56.4 56.4 56.4 56.4 56.4 60.3
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH22-1s1 NIMH20-1s1 NIMH43-1s1 NIMH43-1s1 NIMH50-1s1 NIMH51-1s1 NIMH51-1s1 NIMH61-1s1 NIMH76-1s1 NIMH49-1s1 NIMH40-1s1 NIMH40-1s1 NIMH26-1s1 NIMH26-1s1 NIMH26-1s1 NIMH89-1s1	NIMH53 NIMH33 NIMH69 NIMH21 NIMH21 NIMH22 NIMH20 NIMH20 NIMH20 NIMH20 NIMH20 NIMH20 NIMH51 NIMH51 NIMH51 NIMH61 NIMH47 NIMH476 NIMH26 NIMH26 NIMH26	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,826,496\\ 152,848,413\\ 153,210,565\\ 153,211,532\\ 153,213,307\\ 153,213,307\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,697$	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,354,185\\ 153,354,435\\ 153,369,728\\ 153,416,769\\ 153,257,756\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ 153,429,785\\ 153,394,781\\ 153,429,785\\ 153,394,781\\ 153,426,460\\ 153,259,031\\ 153,266,361\\ \end{array}$	$\begin{array}{r} 315\\ 2,885\\ 154,446\\ 326,006\\ 204,517\\ 216,623\\ 140,738\\ 324,066\\ 140,838\\ 156,131\\ 203,172\\ 44,159\\ 52,809\\ 150,699\\ 204,042\\ 214,009\\ 216,143\\ 181,084\\ 212,763\\ 45,334\\ 52,664\\ \end{array}$	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,922 2,963 2,511 2,903 632 760	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6 13.8 14.0 13.7 13.7 13.7 13.7 13.7 13.7 13.7 13.7	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.24 0.23 0.29 0.31 0.23 0.31 0.27	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.0 56.6 60.5 60.1 57.9 56.6 56.4 56.4 56.5 57.1 56.4 60.3 60.2
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH22-1s1 NIMH20-1s1 NIMH43-1s1 NIMH50-1s1 NIMH51-1s1 NIMH51-1s1 NIMH61-1s1 NIMH61-1s1 NIMH49-1s1 NIMH49-1s1 NIMH40-1s1 NIMH26-1s1 NIMH26-1s1 NIMH26-1s1 NIMH26-1s1 NIMH26-1s1 NIMH20-1s1	NIMH53 NIMH33 NIMH69 NIMH21 NIMH21 NIMH22 NIMH20 NIMH20 NIMH20 NIMH20 NIMH20 NIMH20 NIMH51 NIMH50 NIMH51 NIMH50 NIMH51 NIMH50 NIMH476 NIMH26 NIMH26 NIMH20	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,826,496\\ 152,848,413\\ 153,210,565\\ 153,211,532\\ 153,213,307\\ 153,213,307\\ 153,213,572\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,697\\ 153,215,322\\ 153,215\\ 1$	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,354,185\\ 153,354,435\\ 153,369,728\\ 153,369,728\\ 153,257,756\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ 153,429,785\\ 153,394,781\\ 153,429,785\\ 153,394,781\\ 153,426,460\\ 153,259,031\\ 153,266,361\\ 153,247,589\\ \end{array}$	$\begin{array}{r} 315\\ 2,885\\ 154,446\\ 326,006\\ 204,517\\ 216,623\\ 140,738\\ 324,066\\ 140,838\\ 156,131\\ 203,172\\ 44,159\\ 52,809\\ 150,699\\ 204,042\\ 214,009\\ 204,042\\ 214,009\\ 216,143\\ 181,084\\ 212,763\\ 45,334\\ 52,664\\ 262,267\\ \end{array}$	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,922 2,963 2,511 2,903 632 760 3,094	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6 13.8 14.0 13.7 13.7 13.7 13.7 13.7 13.7 13.7 13.7	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.24 0.23 0.29 0.31 0.23 0.31 0.23 0.31 0.27 0.28	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.5 60.1 57.9 56.6 56.4 56.5 57.1 56.4 60.3 60.2 55.7
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH08-1s1 NIMH08-1s1 NIMH43-1s1 NIMH50-1s1 NIMH50-1s1 NIMH51-1s1 NIMH61-1s1 NIMH61-1s1 NIMH49-1s1 NIMH49-1s1 NIMH40-1s1 NIMH26-1s1 NIMH26-1s1 NIMH26-1s1 NIMH00-1s1 NIMH00-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH20 NIMH20 NIMH43 NIMH12 NIMH50 NIMH51 NIMH50 NIMH51 NIMH55 NIMH61 NIMH76 NIMH47 NIMH47 NIMH47 NIMH460 NIMH26 NIMH26	chrX chrX chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307 153,213,307 153,213,572 153,213,597 153,213,597 153,213,597 153,213,597 153,213,597 153,213,642 153,213,642 153,213,642 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,357,638\\ 153,354,185\\ 153,369,728\\ 153,369,728\\ 153,257,756\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ 153,429,785\\ 153,394,781\\ 153,429,785\\ 153,394,781\\ 153,429,785\\ 153,326,361\\ 153,259,031\\ 153,266,361\\ 153,477,589\\ 153,429,835\\ \end{array}$	$\begin{array}{r} 315\\ 2,885\\ 154,446\\ 326,006\\ 204,517\\ 216,623\\ 140,738\\ 324,066\\ 140,838\\ 156,131\\ 203,172\\ 44,159\\ 52,809\\ 150,699\\ 204,042\\ 214,009\\ 204,042\\ 214,009\\ 216,143\\ 181,084\\ 212,763\\ 45,334\\ 52,664\\ 262,267\\ 214,018\\ \end{array}$	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,922 2,963 2,511 2,903 632 760 3,094 2,919	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6 13.8 14.0 13.7 13.7 13.7 13.7 13.7 13.7 13.7 13.7	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.24 0.23 0.29 0.31 0.23 0.31 0.31 0.27 0.28 0.27	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.5 60.1 57.9 56.6 56.4 56.5 57.1 56.5 57.1 56.3 60.2 55.7 56.5
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH22-1s1 NIMH20-1s1 NIMH43-1s1 NIMH50-1s1 NIMH51-1s1 NIMH51-1s1 NIMH61-1s1 NIMH61-1s1 NIMH49-1s1 NIMH49-1s1 NIMH40-1s1 NIMH26-1s1 NIMH26-1s1 NIMH26-1s1 NIMH26-1s1 NIMH26-1s1 NIMH20-1s1	NIMH53 NIMH33 NIMH69 NIMH21 NIMH21 NIMH22 NIMH20 NIMH20 NIMH20 NIMH20 NIMH20 NIMH20 NIMH51 NIMH50 NIMH51 NIMH50 NIMH51 NIMH50 NIMH476 NIMH26 NIMH26 NIMH20	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,826,496\\ 152,848,413\\ 153,210,565\\ 153,211,532\\ 153,213,307\\ 153,213,307\\ 153,213,572\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,697\\ 153,215,322\\ 153,215\\ 1$	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,354,185\\ 153,354,435\\ 153,369,728\\ 153,257,756\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ 153,429,785\\ 153,394,781\\ 153,426,460\\ 153,259,031\\ 153,266,361\\ 153,266,361\\ 153,477,589\\ 153,429,835\\ 153,364,636\\ \end{array}$	$\begin{array}{r} 315\\ 2,885\\ 154,446\\ 326,006\\ 204,517\\ 216,623\\ 140,738\\ 324,066\\ 140,838\\ 156,131\\ 203,172\\ 44,159\\ 52,809\\ 150,699\\ 204,042\\ 214,009\\ 216,143\\ 181,084\\ 212,763\\ 45,334\\ 52,664\\ 262,267\\ 214,018\\ 148,789\\ \end{array}$	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,922 2,963 2,511 2,903 632 760 3,094 2,919 2,041	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6 13.8 14.0 13.7 13.7 13.7 13.7 13.7 13.7 13.7 13.7	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.24 0.23 0.29 0.31 0.23 0.31 0.23 0.31 0.27 0.28	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.5 60.1 57.9 56.6 56.4 56.5 57.1 56.4 60.2 55.7 56.5 57.9
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH08-1s1 NIMH08-1s1 NIMH43-1s1 NIMH50-1s1 NIMH50-1s1 NIMH51-1s1 NIMH61-1s1 NIMH61-1s1 NIMH49-1s1 NIMH49-1s1 NIMH40-1s1 NIMH26-1s1 NIMH26-1s1 NIMH26-1s1 NIMH00-1s1 NIMH00-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH20 NIMH20 NIMH43 NIMH12 NIMH50 NIMH51 NIMH50 NIMH51 NIMH55 NIMH61 NIMH76 NIMH47 NIMH47 NIMH47 NIMH460 NIMH26 NIMH26	chrX chrX chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307 153,213,307 153,213,572 153,213,597 153,213,597 153,213,597 153,213,597 153,213,597 153,213,642 153,213,642 153,213,642 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,357,638\\ 153,354,185\\ 153,369,728\\ 153,369,728\\ 153,257,756\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ 153,429,785\\ 153,394,781\\ 153,429,785\\ 153,394,781\\ 153,429,785\\ 153,326,361\\ 153,259,031\\ 153,266,361\\ 153,477,589\\ 153,429,835\\ \end{array}$	$\begin{array}{r} 315\\ 2,885\\ 154,446\\ 326,006\\ 204,517\\ 216,623\\ 140,738\\ 324,066\\ 140,838\\ 156,131\\ 203,172\\ 44,159\\ 52,809\\ 150,699\\ 204,042\\ 214,009\\ 204,042\\ 214,009\\ 216,143\\ 181,084\\ 212,763\\ 45,334\\ 52,664\\ 262,267\\ 214,018\\ \end{array}$	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,922 2,963 2,511 2,903 632 760 3,094 2,919	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6 13.8 14.0 13.7 13.7 13.7 13.7 13.7 13.7 13.7 13.7	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.24 0.23 0.29 0.31 0.23 0.31 0.31 0.27 0.28 0.27	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.5 60.1 57.9 56.6 56.4 56.5 57.1 56.5 57.1 56.3 60.2 55.7 56.5
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH08-1s1 NIMH08-1s1 NIMH43-1s1 NIMH50-1s1 NIMH50-1s1 NIMH51-1s1 NIMH61-1s1 NIMH61-1s1 NIMH49-1s1 NIMH49-1s1 NIMH49-1s1 NIMH26-1s1 NIMH26-1s1 NIMH10-1s1 NIMH06-1s1 NIMH63-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH21 NIMH21 NIMH21 NIMH21 NIMH21 NIMH21 NIMH20 NIMH50 NIMH51 NIMH51 NIMH51 NIMH51 NIMH51 NIMH51 NIMH51 NIMH50 NIMH47 NIMH47 NIMH48 NIMH26 NIMH10 NIMH60 NIMH60 NIMH60 NIMH60 NIMH60	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,826,496\\ 152,848,413\\ 153,210,565\\ 153,211,532\\ 153,213,307\\ 153,213,307\\ 153,213,307\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,215,817\\ 153,215,817\\ 153,216,327\\ \end{array}$	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,354,185\\ 153,537,638\\ 153,354,435\\ 153,369,728\\ 153,266,406\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ 153,429,785\\ 153,394,781\\ 153,426,460\\ 153,259,031\\ 153,266,361\\ 153,266,361\\ 153,477,589\\ 153,364,636\\ 153,364,636\\ 153,424,866\\ \end{array}$	$\begin{array}{r} 315\\ 2,885\\ 154,446\\ 326,006\\ 204,517\\ 216,623\\ 140,738\\ 324,066\\ 140,838\\ 156,131\\ 203,172\\ 44,159\\ 52,809\\ 150,699\\ 204,042\\ 214,009\\ 216,143\\ 181,084\\ 212,763\\ 45,334\\ 52,664\\ 262,267\\ 214,018\\ 148,789\\ 208,539\\ \end{array}$	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,922 2,963 2,511 2,903 632 760 3,094 2,919 2,041 2,835	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6 13.8 14.0 13.7 13.7 13.7 13.7 13.7 13.7 13.7 13.7	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.24 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.22 0.24 0.24 0.24 0.24 0.24 0.24 0.24 0.25 0.26 0.27 0.26 0.27 0.26 0.27 0.36 0.29 0.37 0.29 0.37 0.29 0.37 0.29 0.37 0.29 0.37 0.29 0.34 0.26 0.24 0.24 0.23 0.29 0.31 0.26 0.24 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.27 0.32 0.29 0.31 0.27 0.32 0.27 0.32 0.29 0.31 0.27 0.32 0.29 0.31 0.27 0.31 0.27 0.32 0.29 0.31 0.27 0.32 0.29 0.31 0.27 0.31 0.27 0.32 0.29 0.31 0.27 0.31 0.27 0.31 0.27 0.31 0.27 0.32 0.27 0.31 0.27 0.32 0.27 0.31 0.27 0.28 0.27 0.26 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.26 0.27 0.28 0.27 0.27 0.27 0.28 0.27 0.26 0.27 0.26 0.27 0.27 0.26 0.27 0.26 0.27 0.27 0.26 0.27 0.26 0.27 0.27 0.26 0.27 0.26 0.27 0.26 0.27 0.26 0.27 0.26 0.27 0.26	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.5 60.1 57.9 56.6 56.5 57.1 56.4 60.3 60.3 60.3 56.5 57.1 56.4 56.5 57.1 56.4 56.5 57.1 56.5 57.7 56.5 57.9 56.5 57.9 56.5
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH22-1s1 NIMH08-1s1 NIMH43-1s1 NIMH50-1s1 NIMH51-1s1 NIMH51-1s1 NIMH61-1s1 NIMH61-1s1 NIMH70-2s1 NIMH49-1s1 NIMH70-1s1 NIMH60-1s1 NIMH26-1s1 NIMH06-1s1 NIMH06-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH22 NIMH08 NIMH43 NIMH20 NIMH50 NIMH51 NIMH50 NIMH51 NIMH51 NIMH51 NIMH51 NIMH51 NIMH51 NIMH51 NIMH51 NIMH50 NIMH76 NIMH76 NIMH76 NIMH76 NIMH76 NIMH76 NIMH70 NIMH70 NIMH77 NIMH76 NIMH77 NIM77 NIM77 NIM77 NIM77 NIM77 NIM77 NIM77 NIM77 NIM77 NIM7	chrX chrX chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307 153,213,307 153,213,507 153,213,597 153,213,597 153,213,597 153,213,597 153,213,597 153,213,697 153,213,642 153,213,642 153,213,642 153,213,642 153,213,642 153,213,642 153,213,642 153,213,642 153,213,647 153,215,322 153,215,847 153,216,327 153,230,615	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,537,638\\ 153,354,435\\ 153,354,435\\ 153,369,728\\ 153,266,406\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ 153,429,785\\ 153,394,781\\ 153,429,785\\ 153,394,781\\ 153,259,031\\ 153,259,031\\ 153,266,361\\ 153,429,835\\ 153,364,636\\ 153,429,835\\ 153,364,636\\ 153,424,866\\ 153,417,579\\ \end{array}$	$\begin{array}{r} 315\\ 2,885\\ 154,446\\ 326,006\\ 204,517\\ 216,623\\ 140,738\\ 324,066\\ 140,838\\ 156,131\\ 203,172\\ 44,159\\ 52,809\\ 150,699\\ 204,042\\ 214,009\\ 216,143\\ 181,084\\ 212,763\\ 45,334\\ 52,664\\ 262,267\\ 214,018\\ 148,789\\ 208,539\\ 186,964\\ \end{array}$	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,922 2,963 2,511 2,903 632 760 3,094 2,919 2,041 2,835 2,682	$\begin{array}{c} 25.4\\ 20.1\\ 13.9\\ 10.6\\ 13.7\\ 13.8\\ 10.6\\ 13.8\\ 14.0\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.6\\ 13.9\\ 14.4\\ 11.8\\ 13.6\\ 13.7\\ 13.6\\ 14.3\\ \end{array}$	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.24 0.23 0.29 0.31 0.23 0.31 0.23 0.31 0.27 0.28 0.27 0.26 0.27 0.26 0.27	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.5 60.1 57.9 56.6 56.4 56.5 57.1 56.4 60.3 60.2 55.7 56.5 57.9 56.5 56.5
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH21-1s1 NIMH21-1s1 NIMH21-1s1 NIMH20-1s1 NIMH20-1s1 NIMH20-1s1 NIMH43-1s1 NIMH51-1s1 NIMH51-1s1 NIMH51-1s1 NIMH61-1s1 NIMH61-1s1 NIMH61-1s1 NIMH61-1s1 NIMH61-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH06-1s1 NIMH06-1s1 NIMH06-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH13-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH22 NIMH20 NIMH20 NIMH43 NIMH20 NIMH51 NIMH51 NIMH51 NIMH51 NIMH51 NIMH61 NIMH70 NIMH47 NIMH49 NIMH76 NIMH60 NIMH60 NIMH63 NIMH13 NIMH24	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,826,496\\ 152,848,413\\ 153,210,565\\ 153,211,532\\ 153,213,307\\ 153,213,307\\ 153,213,507\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,647\\ 153,215,847\\ 153,215,847\\ 153,215,847\\ 153,215,847\\ 153,215,847\\ 153,230,615\\ 153,231,380\\ \end{array}$	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,537,638\\ 153,354,435\\ 153,354,435\\ 153,354,435\\ 153,369,728\\ 153,416,769\\ 153,257,756\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ 153,429,785\\ 153,394,781\\ 153,426,460\\ 153,259,031\\ 153,266,361\\ 153,429,835\\ 153,364,636\\ 153,429,835\\ 153,364,636\\ 153,429,835\\ 153,364,636\\ 153,424,866\\ 153,417,579\\ 153,481,115\\ \end{array}$	$\begin{array}{r} 315\\ 2,885\\ 154,446\\ 326,006\\ 204,517\\ 216,623\\ 140,738\\ 324,066\\ 140,838\\ 156,131\\ 203,172\\ 44,159\\ 52,809\\ 150,699\\ 204,042\\ 214,009\\ 216,143\\ 181,084\\ 212,763\\ 45,334\\ 52,664\\ 262,267\\ 214,018\\ 148,789\\ 208,539\\ 186,964\\ 249,735\\ \end{array}$	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,922 2,963 2,511 2,903 632 760 3,094 2,919 2,041 2,835 2,682 3,050	$\begin{array}{c} 25.4\\ 20.1\\ 13.9\\ 10.6\\ 13.7\\ 13.7\\ 13.8\\ 10.6\\ 13.8\\ 14.0\\ 13.7\\ 13.7\\ 13.7\\ 14.4\\ 13.8\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.6\\ 13.9\\ 14.4\\ 11.8\\ 13.6\\ 13.7\\ 13.6\\ 14.3\\ 12.2\\ \end{array}$	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.24 0.23 0.29 0.31 0.23 0.31 0.23 0.31 0.27 0.28 0.27 0.26 0.27 0.26 0.27 0.26 0.27 0.27 0.28 0.27 0.26 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.23 0.29 0.31 0.29 0.37 0.29 0.34 0.24 0.24 0.24 0.24 0.24 0.24 0.23 0.29 0.31 0.29 0.31 0.29 0.31 0.29 0.31 0.29 0.31 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.27 0.26 0.24 0.24 0.24 0.23 0.29 0.31 0.23 0.27 0.28 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.27 0.28 0.27 0.27 0.27 0.28 0.27 0.27 0.27 0.28 0.27 0.27 0.27 0.28 0.27 0.27 0.27 0.27 0.28 0.27 0.27 0.27 0.27 0.27 0.28 0.27 0.27 0.27 0.27 0.27 0.27 0.27 0.26 0.27 0.27 0.27 0.27 0.27 0.26 0.27 0.27 0.27 0.27 0.27 0.26 0.27	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.5 60.1 57.9 56.6 56.5 57.1 56.4 60.3 60.2 57.7 56.5 57.7 56.5 57.9 56.5 57.9 56.5 57.5 57.9 56.5 57.5 57.9 56.5 57.5
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH20-1s1 NIMH20-1s1 NIMH20-1s1 NIMH20-1s1 NIMH20-1s1 NIMH20-1s1 NIMH50-1s1 NIMH51-1s1 NIMH51-1s1 NIMH61-1s1 NIMH61-1s1 NIMH61-1s1 NIMH61-1s1 NIMH70-2s1 NIMH70-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH061-1s1 NIMH061-1s1 NIMH061-1s1 NIMH061-1s1 NIMH061-1s1 NIMH03-1s1 NIMH03-1s1 NIMH39-1s1	NIMH53 NIMH33 NIMH69 NIMH21 NIMH21 NIMH22 NIMH20 NIMH20 NIMH20 NIMH20 NIMH20 NIMH20 NIMH20 NIMH20 NIMH20 NIMH51 NIMH51 NIMH51 NIMH51 NIMH51 NIMH51 NIMH70 NIMH47 NIMH60 NIMH76 NIMH60 NIMH60 NIMH60 NIMH60 NIMH60 NIMH61 NIMH67 NIMH13 NIMH24	chrX chrX chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307 153,213,307 153,213,507 153,213,597 153,213,597 153,213,597 153,213,597 153,213,697 153,213,642	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,354,185\\ 153,354,435\\ 153,354,435\\ 153,354,435\\ 153,369,728\\ 153,416,769\\ 153,257,756\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ 153,429,785\\ 153,394,781\\ 153,426,460\\ 153,259,031\\ 153,266,361\\ 153,429,785\\ 153,364,636\\ 153,429,835\\ 153,364,636\\ 153,427,286\\ 153,417,579\\ 153,481,115\\ 153,427,286\\ \end{array}$	$\begin{array}{r} 315\\ 2,885\\ 154,446\\ 326,006\\ 204,517\\ 216,623\\ 140,738\\ 324,066\\ 140,838\\ 156,131\\ 203,172\\ 44,159\\ 52,809\\ 150,699\\ 204,042\\ 214,009\\ 216,143\\ 181,084\\ 212,763\\ 45,334\\ 52,664\\ 262,267\\ 214,018\\ 148,789\\ 208,539\\ 186,964\\ 249,735\\ 192,316\\ \end{array}$	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,963 2,511 2,903 632 760 3,094 2,919 2,041 2,835 2,682 3,050 2,715	$\begin{array}{c} 25.4\\ 20.1\\ 13.9\\ 10.6\\ 13.7\\ 13.7\\ 13.8\\ 10.6\\ 13.8\\ 14.0\\ 13.7\\ 13.7\\ 14.4\\ 13.8\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.9\\ 13.6\\ 13.9\\ 14.4\\ 11.8\\ 13.6\\ 13.7\\ 13.6\\ 14.3\\ 12.2\\ 14.1\\ \end{array}$	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.24 0.23 0.29 0.31 0.23 0.31 0.23 0.31 0.27 0.28 0.27 0.26 0.27 0.26 0.27 0.27 0.26 0.27 0.27 0.26 0.27 0.27 0.28 0.27 0.27 0.26 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.24 0.27 0.24 0.24 0.24 0.24 0.24 0.24 0.24 0.24 0.24 0.24 0.24 0.25 0.27 0.26 0.23 0.27 0.26 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.28 0.27 0.27 0.28 0.27 0.24	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.5 60.1 57.9 56.6 56.5 57.1 56.4 60.3 60.2 57.7 56.5 57.7 56.5 57.9 56.5 57.5 57.5 57.5 57.5 57.5 55.3 56.5 55.3 56.1
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH21-1s1 NIMH21-1s1 NIMH21-1s1 NIMH20-1s1 NIMH20-1s1 NIMH20-1s1 NIMH43-1s1 NIMH51-1s1 NIMH51-1s1 NIMH51-1s1 NIMH61-1s1 NIMH61-1s1 NIMH61-1s1 NIMH61-1s1 NIMH61-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH06-1s1 NIMH06-1s1 NIMH06-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH13-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH22 NIMH20 NIMH20 NIMH43 NIMH20 NIMH51 NIMH51 NIMH51 NIMH51 NIMH51 NIMH61 NIMH70 NIMH47 NIMH49 NIMH76 NIMH60 NIMH60 NIMH63 NIMH13 NIMH24	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,826,496\\ 152,848,413\\ 153,210,565\\ 153,211,532\\ 153,213,307\\ 153,213,307\\ 153,213,507\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,647\\ 153,215,847\\ 153,215,847\\ 153,215,847\\ 153,215,847\\ 153,215,847\\ 153,215,847\\ 153,230,615\\ 153,231,380\\ \end{array}$	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,537,638\\ 153,354,435\\ 153,354,435\\ 153,354,435\\ 153,369,728\\ 153,416,769\\ 153,257,756\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ 153,429,785\\ 153,394,781\\ 153,426,460\\ 153,259,031\\ 153,266,361\\ 153,429,835\\ 153,364,636\\ 153,429,835\\ 153,364,636\\ 153,429,835\\ 153,364,636\\ 153,424,866\\ 153,417,579\\ 153,481,115\\ \end{array}$	$\begin{array}{r} 315\\ 2,885\\ 154,446\\ 326,006\\ 204,517\\ 216,623\\ 140,738\\ 324,066\\ 140,838\\ 156,131\\ 203,172\\ 44,159\\ 52,809\\ 150,699\\ 204,042\\ 214,009\\ 216,143\\ 181,084\\ 212,763\\ 45,334\\ 52,664\\ 262,267\\ 214,018\\ 148,789\\ 208,539\\ 186,964\\ 249,735\\ 192,316\\ 196,590\\ \end{array}$	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,922 2,963 2,511 2,903 632 760 3,094 2,919 2,041 2,835 2,682 3,050	$\begin{array}{c} 25.4\\ 20.1\\ 13.9\\ 10.6\\ 13.7\\ 13.7\\ 13.8\\ 10.6\\ 13.8\\ 14.0\\ 13.7\\ 13.7\\ 13.7\\ 14.4\\ 13.8\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.6\\ 13.9\\ 14.4\\ 11.8\\ 13.6\\ 13.7\\ 13.6\\ 14.3\\ 12.2\\ \end{array}$	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.24 0.23 0.23 0.23 0.31 0.23 0.31 0.27 0.28 0.27 0.26 0.27 0.26 0.27 0.26 0.27 0.26 0.27 0.26 0.27 0.28 0.27 0.27 0.28 0.27 0.22 0.27 0.22 0.27 0.22 0.27 0.24 0.22 0.27 0.24 0.22 0.27 0.24 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.27 0.24 0.24 0.24 0.24 0.23 0.27 0.23 0.29 0.31 0.23 0.27 0.26 0.27 0.24 0.24 0.24 0.27 0.23 0.27 0.22 0.27 0.22	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.5 60.1 57.9 56.6 56.5 57.1 56.4 60.3 60.2 57.7 56.5 57.7 56.5 57.5 57.9 56.5 57.5
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH20-1s1 NIMH20-1s1 NIMH20-1s1 NIMH20-1s1 NIMH20-1s1 NIMH20-1s1 NIMH50-1s1 NIMH51-1s1 NIMH51-1s1 NIMH61-1s1 NIMH61-1s1 NIMH61-1s1 NIMH61-1s1 NIMH70-2s1 NIMH70-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH061-1s1 NIMH061-1s1 NIMH061-1s1 NIMH061-1s1 NIMH061-1s1 NIMH03-1s1 NIMH03-1s1 NIMH39-1s1	NIMH53 NIMH33 NIMH69 NIMH21 NIMH21 NIMH22 NIMH20 NIMH20 NIMH20 NIMH20 NIMH20 NIMH20 NIMH20 NIMH20 NIMH20 NIMH51 NIMH51 NIMH51 NIMH51 NIMH51 NIMH51 NIMH70 NIMH47 NIMH60 NIMH76 NIMH60 NIMH60 NIMH60 NIMH60 NIMH60 NIMH61 NIMH67 NIMH13 NIMH24	chrX chrX chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307 153,213,307 153,213,507 153,213,597 153,213,597 153,213,597 153,213,597 153,213,697 153,213,642	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,354,185\\ 153,354,435\\ 153,354,435\\ 153,354,435\\ 153,369,728\\ 153,416,769\\ 153,257,756\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ 153,429,785\\ 153,394,781\\ 153,426,460\\ 153,259,031\\ 153,266,361\\ 153,429,785\\ 153,364,636\\ 153,429,835\\ 153,364,636\\ 153,427,286\\ 153,417,579\\ 153,481,115\\ 153,427,286\\ \end{array}$	$\begin{array}{r} 315\\ 2,885\\ 154,446\\ 326,006\\ 204,517\\ 216,623\\ 140,738\\ 324,066\\ 140,838\\ 156,131\\ 203,172\\ 44,159\\ 52,809\\ 150,699\\ 204,042\\ 214,009\\ 216,143\\ 181,084\\ 212,763\\ 45,334\\ 52,664\\ 262,267\\ 214,018\\ 148,789\\ 208,539\\ 186,964\\ 249,735\\ 192,316\\ \end{array}$	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,963 2,511 2,903 632 760 3,094 2,919 2,041 2,835 2,682 3,050 2,715	$\begin{array}{c} 25.4\\ 20.1\\ 13.9\\ 10.6\\ 13.7\\ 13.7\\ 13.8\\ 10.6\\ 13.8\\ 14.0\\ 13.7\\ 13.7\\ 14.4\\ 13.8\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.9\\ 13.6\\ 13.9\\ 14.4\\ 11.8\\ 13.6\\ 13.7\\ 13.6\\ 14.3\\ 12.2\\ 14.1\\ \end{array}$	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.24 0.23 0.29 0.31 0.23 0.31 0.23 0.31 0.27 0.28 0.27 0.26 0.27 0.26 0.27 0.27 0.26 0.27 0.27 0.26 0.27 0.27 0.28 0.27 0.27 0.26 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.24 0.27 0.24 0.24 0.24 0.24 0.24 0.24 0.24 0.24 0.24 0.24 0.24 0.25 0.27 0.26 0.23 0.27 0.26 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.28 0.27 0.27 0.28 0.27 0.27 0.28 0.27 0.28 0.27 0.27 0.28 0.27 0.24	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.5 60.1 57.9 56.6 56.5 57.1 56.4 60.3 60.2 57.7 56.5 57.7 56.5 57.9 56.5 57.5 57.5 57.5 57.5 57.5 55.3 56.5 55.3 56.1
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH22-1s1 NIMH20-1s1 NIMH20-1s1 NIMH20-1s1 NIMH20-1s1 NIMH20-1s1 NIMH50-1s1 NIMH51-1s1 NIMH51-1s1 NIMH51-1s1 NIMH61-1s1 NIMH70-2s1 NIMH76-1s1 NIMH49-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH63-1s1 NIMH39-1s1 NIMH39-1s1 NIMH84-1s1 NIMH23-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH22 NIMH20 NIMH20 NIMH43 NIMH12 NIMH50 NIMH51 NIMH50 NIMH51 NIMH51 NIMH51 NIMH51 NIMH61 NIMH60 NIMH66 NIMH66 NIMH66 NIMH66 NIMH67 NIMH63 NIMH63 NIMH13 NIMH24 NIMH39 NIMH84 NIMH23	chrX chrX chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307 153,213,307 153,213,597 153,213,597 153,213,597 153,213,597 153,213,597 153,213,697 153,213,642 153,213,642 153,213,642 153,213,642 153,213,642 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,215,322 153,215,322 153,215,817 153,215,817 153,215,847 153,216,327 153,230,615 153,230,615 153,234,970 153,236,245	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,354,185\\ 153,354,185\\ 153,369,728\\ 153,369,728\\ 153,416,769\\ 153,257,756\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ 153,429,785\\ 153,394,781\\ 153,429,785\\ 153,394,781\\ 153,429,785\\ 153,394,781\\ 153,429,785\\ 153,394,781\\ 153,429,785\\ 153,394,781\\ 153,429,835\\ 153,259,031\\ 153,429,835\\ 153,364,636\\ 153,429,835\\ 153,424,866\\ 153,417,579\\ 153,481,115\\ 153,427,286\\ 153,432,835\\ 153,259,076\\ \end{array}$	$\begin{array}{r} 315\\ 2,885\\ 154,446\\ 326,006\\ 204,517\\ 216,623\\ 140,738\\ 324,066\\ 140,838\\ 156,131\\ 203,172\\ 44,159\\ 52,809\\ 150,699\\ 204,042\\ 214,009\\ 216,143\\ 181,084\\ 212,763\\ 45,334\\ 52,664\\ 262,267\\ 214,018\\ 148,789\\ 208,539\\ 186,964\\ 249,735\\ 192,316\\ 196,590\\ 22,831\\ \end{array}$	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,922 2,963 2,963 2,963 2,963 2,963 2,919 2,041 2,835 2,682 3,050 2,715 2,766 408	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6 13.8 14.0 13.7 13.7 13.7 13.7 13.7 13.7 13.7 13.7	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.24 0.23 0.29 0.31 0.23 0.31 0.23 0.31 0.27 0.28 0.27 0.26 0.27 0.28 0.27 0.26 0.27 0.28 0.28	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.0 56.6 60.5 60.1 57.9 56.6 56.4 56.5 57.1 56.5 57.9 56.5 57.9 56.5 57.9 56.5 55.5
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH22-1s1 NIMH22-1s1 NIMH22-1s1 NIMH20-1s1 NIMH20-1s1 NIMH20-1s1 NIMH50-1s1 NIMH51-1s1 NIMH51-1s1 NIMH51-1s1 NIMH51-1s1 NIMH51-1s1 NIMH61-1s1 NIMH61-1s1 NIMH70-2s1 NIMH49-1s1 NIMH60-1s1 NIMH26-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH89-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH39-1s1 NIMH24-1s1 NIMH23-1s1 NIMH23-1s1 NIMH23-1s1 NI	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH22 NIMH20 NIMH20 NIMH43 NIMH12 NIMH50 NIMH50 NIMH51 NIMH50 NIMH51 NIMH51 NIMH51 NIMH51 NIMH51 NIMH76 NIMH61 NIMH76 NIMH60 NIMH60 NIMH66 NIMH66 NIMH66 NIMH67 NIMH63 NIMH63 NIMH13 NIMH24 NIMH39 NIMH17	chrX chrX chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307 153,213,307 153,213,572 153,213,597 153,213,597 153,213,597 153,213,597 153,213,597 153,213,642 153,213,642 153,213,642 153,213,642 153,213,642 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,215,322 153,215,817 153,215,817 153,215,847 153,216,327 153,231,380 153,234,970 153,234,970 153,236,245 153,236,245	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,354,185\\ 153,354,185\\ 153,369,728\\ 153,369,728\\ 153,369,728\\ 153,369,728\\ 153,257,756\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ 153,429,785\\ 153,394,781\\ 153,429,785\\ 153,394,781\\ 153,429,785\\ 153,394,781\\ 153,429,835\\ 153,364,636\\ 153,429,835\\ 153,364,636\\ 153,427,286\\ 153,417,579\\ 153,432,835\\ 153,259,076\\ 153,429,933\\ \end{array}$	$\begin{array}{r} 315\\ 2,885\\ 154,446\\ 326,006\\ 204,517\\ 216,623\\ 140,738\\ 324,066\\ 140,838\\ 156,131\\ 203,172\\ 44,159\\ 52,809\\ 150,699\\ 204,042\\ 214,009\\ 204,042\\ 214,009\\ 204,042\\ 214,009\\ 216,143\\ 181,084\\ 212,763\\ 45,334\\ 52,664\\ 262,267\\ 214,018\\ 148,789\\ 208,539\\ 186,964\\ 249,735\\ 192,316\\ 196,590\\ 22,831\\ 256,273\\ \end{array}$	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,922 2,963 2,511 2,903 632 760 3,094 2,919 2,041 2,835 2,682 3,050 2,715 2,766 408 3,093	$\begin{array}{c} 25.4\\ 20.1\\ 13.9\\ 10.6\\ 13.7\\ 13.7\\ 13.8\\ 10.6\\ 13.8\\ 14.0\\ 13.7\\ 13.7\\ 14.4\\ 13.8\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.6\\ 13.9\\ 14.4\\ 11.8\\ 13.6\\ 13.9\\ 14.4\\ 11.8\\ 13.6\\ 13.7\\ 13.6\\ 14.3\\ 12.2\\ 14.1\\ 14.1\\ 17.9\\ 12.1\\ \end{array}$	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.24 0.23 0.29 0.31 0.23 0.31 0.23 0.31 0.23 0.31 0.27 0.28 0.27 0.26 0.27 0.28 0.27 0.26 0.27 0.28 0.27 0.26 0.27 0.28 0.27 0.28 0.27 0.26 0.23 0.29 0.31 0.23 0.29 0.34 0.24 0.24 0.24 0.23 0.29 0.34 0.26 0.24 0.24 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.27 0.28 0.27 0.26 0.23 0.27 0.28 0.27 0.28 0.27 0.28 0.27 0.28 0.27 0.28 0.27 0.28 0.27 0.28 0.27 0.28 0.27 0.28 0.27 0.28 0.27 0.28 0.27 0.28 0.27 0.28 0.27 0.28 0.27 0.28 0.27 0.28 0.227 0.28 0.32	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.0 56.6 60.5 60.1 57.9 56.6 56.4 56.4 56.5 57.9 56.5 57.9 56.5 55.7 56.5 55.3 56.5 55.3 56.1 56.0 61.2 54.7
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH22-1s1 NIMH22-1s1 NIMH22-1s1 NIMH20-1s1 NIMH20-1s1 NIMH20-1s1 NIMH43-1s1 NIMH50-1s1 NIMH51-1s1 NIMH51-1s1 NIMH51-1s1 NIMH61-1s1 NIMH61-1s1 NIMH61-1s1 NIMH76-1s1 NIMH49-1s1 NIMH60-1s1 NIMH63-1s1 NIMH63-1s1 NIMH39-1s1 NIMH23-1s1 NIMH23-1s1 NIMH23-1s1 NIMH23-1s1 NIMH46-1s1	NIMH53 NIMH53 NIMH69 NIMH21 NIMH21 NIMH22 NIMH20 NIMH20 NIMH50 NIMH50 NIMH50 NIMH51 NIMH50 NIMH51 NIMH50 NIMH50 NIMH51 NIMH50 NIMH51 NIMH50 NIMH50 NIMH51 NIMH50 NIMH51 NIMH50 NIMH61 NIMH76 NIMH42 NIMH60 NIMH60 NIMH61 NIMH63 NIMH13 NIMH39 NIMH24 NIMH23 NIMH17 NIMH46	chrX chrX chrX chrX chrX chrX chrX chrX	$\begin{array}{r} 152,826,496\\ 152,848,413\\ 153,210,565\\ 153,211,532\\ 153,213,307\\ 153,213,307\\ 153,213,307\\ 153,213,572\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,597\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,642\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,213,697\\ 153,23,624\\ 153,230,615\\ 153,234,970\\ 153,236,245\\ 153,236,245\\ 153,237,660\\ 153,237,730\\ \end{array}$	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,357,638\\ 153,354,185\\ 153,369,728\\ 153,369,728\\ 153,257,756\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ 153,429,785\\ 153,394,781\\ 153,429,785\\ 153,394,781\\ 153,429,785\\ 153,394,781\\ 153,259,031\\ 153,266,361\\ 153,429,835\\ 153,364,636\\ 153,429,835\\ 153,364,636\\ 153,427,886\\ 153,417,579\\ 153,481,115\\ 153,427,286\\ 153,432,835\\ 153,259,076\\ 153,493,933\\ 153,247,253\\ \end{array}$	$\begin{array}{r} 315\\ 2,885\\ 154,446\\ 326,006\\ 204,517\\ 216,623\\ 140,738\\ 324,066\\ 140,838\\ 156,131\\ 203,172\\ 44,159\\ 52,809\\ 150,699\\ 204,042\\ 214,009\\ 204,042\\ 214,009\\ 204,042\\ 214,009\\ 216,143\\ 181,084\\ 212,763\\ 45,334\\ 52,664\\ 262,267\\ 214,018\\ 148,789\\ 208,539\\ 186,964\\ 249,735\\ 192,316\\ 196,590\\ 22,831\\ 256,273\\ 9,523\\ \end{array}$	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,922 2,963 2,511 2,903 632 760 3,094 2,919 2,041 2,835 2,682 3,050 2,715 2,766 408 3,093 170	25.4 20.1 13.9 10.6 13.7 13.7 13.8 10.6 13.8 14.0 13.7 13.7 13.7 13.7 13.7 13.7 13.7 13.7	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.24 0.24 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.26 0.24 0.22 0.23 0.29 0.31 0.26 0.24 0.22 0.23 0.29 0.31 0.26 0.24 0.22 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.27 0.26 0.27 0.24 0.22 0.23 0.27 0.22 0.22 0.31 0.23 0.27 0.26 0.27 0.23 0.27 0.28 0.27 0.26 0.27 0.28 0.27 0.26 0.27 0.28 0.27 0.26 0.27 0.28 0.27 0.26 0.22 0.31 0.31 0.27 0.28 0.27 0.28 0.27 0.26 0.22 0.22 0.22 0.31 0.27 0.28 0.27 0.26 0.22 0.27 0.28 0.27 0.26 0.23 0.27 0.26 0.27 0.26 0.27 0.26 0.27 0.26 0.27 0.26 0.23 0.27 0.26 0.23 0.27 0.26 0.23 0.27 0.26 0.23 0.27 0.26 0.23 0.27 0.26 0.23 0.27 0.26 0.23 0.27 0.26 0.23 0.27 0.26 0.23 0.27 0.26 0.23 0.27 0.26 0.23 0.27 0.26 0.28 0.32 0.29 0.27 0.26 0.23 0.27 0.26 0.28 0.32 0.28 0.32 0.28 0.32 0.28 0.32 0.28 0.32 0.32 0.32	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.5 60.1 57.9 56.6 56.4 56.5 57.1 56.4 60.2 55.7 56.5 57.9 56.5 57.9 56.5 57.9 56.5 57.9 56.5 55.3 56.5 55.3 56.0 61.2 54.7 60.3
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH9-1s1 NIMH21-1s1 NIMH22-1s1 NIMH08-1s1 NIMH20-1s1 NIMH20-1s1 NIMH20-1s1 NIMH50-1s1 NIMH50-1s1 NIMH50-1s1 NIMH50-1s1 NIMH50-1s1 NIMH50-1s1 NIMH50-1s1 NIMH61-1s1 NIMH60-1s1 NIMH47-1s1 NIMH40-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH24-1s1 NIMH23-1s1 NIMH23-1s1 NIMH23-1s1 NIMH46-1s1 NIMH46-1s1 NIMH46-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH22 NIMH22 NIMH20 NIMH43 NIMH12 NIMH50 NIMH50 NIMH51 NIMH50 NIMH51 NIMH50 NIMH51 NIMH50 NIMH51 NIMH76 NIMH61 NIMH76 NIMH76 NIMH76 NIMH76 NIMH76 NIMH76 NIMH76 NIMH76 NIMH76 NIMH76 NIMH76 NIMH76 NIMH76 NIMH76 NIMH76 NIMH76 NIMH77 NIMH76 NIMH73 NIMH73 NIMH77 NIMH73 NIMH77 NIMH746 NIMH746 NIMH746 NIMH746 NIMH746	chrX chrX chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307 153,213,307 153,213,572 153,213,597 153,213,597 153,213,597 153,213,597 153,213,597 153,213,642 153,213,642 153,213,642 153,213,642 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,215,817 153,215,817 153,215,817 153,215,817 153,23,1380 153,234,970 153,236,245 153,237,660 153,237,730	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,357,638\\ 153,354,185\\ 153,369,728\\ 153,369,728\\ 153,257,756\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ 153,429,785\\ 153,394,781\\ 153,429,785\\ 153,394,781\\ 153,429,785\\ 153,394,781\\ 153,429,785\\ 153,394,781\\ 153,429,835\\ 153,364,636\\ 153,429,835\\ 153,364,636\\ 153,424,866\\ 153,417,579\\ 153,427,286\\ 153,432,835\\ 153,427,286\\ 153,432,835\\ 153,259,076\\ 153,493,933\\ 153,247,253\\ 153,429,565\\ \end{array}$	315 2,885 154,446 326,006 204,517 216,623 140,738 324,066 140,838 156,131 203,172 44,159 52,809 150,699 204,042 214,009 216,143 181,084 212,763 45,334 52,664 262,267 214,018 148,789 208,539 186,964 249,735 192,316 196,590 22,831 256,273 9,523 182,502	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,922 2,963 2,511 2,903 632 760 3,094 2,919 2,041 2,835 2,682 3,050 2,715 2,766 408 3,093 170 2,535	$\begin{array}{c} 25.4\\ 20.1\\ 13.9\\ 10.6\\ 13.7\\ 13.7\\ 13.8\\ 10.6\\ 13.8\\ 14.0\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.6\\ 13.6\\ 13.6\\ 13.7\\ 13.6\\ 14.4\\ 11.8\\ 13.6\\ 13.7\\ 13.6\\ 14.4\\ 11.8\\ 13.6\\ 14.3\\ 12.2\\ 14.1\\ 17.9\\ 12.1\\ 17.9\\ 13.9\end{array}$	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.24 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.21 0.23 0.27 0.26 0.23 0.27 0.26 0.27 0.26 0.23 0.27 0.26 0.23 0.27 0.26 0.23 0.29 0.31 0.23 0.29 0.31 0.29 0.34 0.26 0.24 0.24 0.24 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.27 0.26 0.24 0.24 0.24 0.27 0.27 0.26 0.23 0.27 0.27 0.28 0.27 0.26 0.27 0.27 0.28 0.27 0.27 0.26 0.21 0.31 0.23 0.29 0.31 0.23 0.27 0.28 0.27 0.26 0.27 0.28 0.27 0.26 0.27 0.28 0.27 0.27 0.28 0.27 0.26 0.27 0.28 0.27 0.27 0.26 0.27 0.27 0.28 0.27 0.26 0.27 0.27 0.26 0.27 0.27 0.27 0.26 0.23 0.27 0.27 0.26 0.23 0.27 0.27 0.26 0.23 0.27 0.26 0.27 0.26 0.23 0.27 0.26 0.27 0.26 0.27 0.26 0.27 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.32 0.27 0.27 0.27 0.26 0.32 0.27 0.27 0.26 0.32 0.27 0.27 0.27 0.26 0.32 0.27 0.27 0.27 0.27 0.26 0.32 0.27 0.27 0.27 0.27 0.26 0.32 0.27 0.27 0.27 0.27 0.27 0.28 0.32 0.27	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.5 60.1 57.9 56.6 56.4 56.5 57.1 56.5 57.1 56.5 57.5 57.5 56.5 55.3 56.5 55.3 56.5 55.3 56.1 56.5 55.3 55.9
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH19-1s1 NIMH21-1s1 NIMH21-1s1 NIMH22-1s1 NIMH08-1s1 NIMH20-1s1 NIMH20-1s1 NIMH43-1s1 NIMH50-1s1 NIMH50-1s1 NIMH50-1s1 NIMH50-1s1 NIMH50-1s1 NIMH50-1s1 NIMH61-1s1 NIMH61-1s1 NIMH61-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH39-1s1 NIMH24-1s1 NIMH23-1s1 NIMH23-1s1 NIMH23-1s1 NIMH423-1s1 NIMH46-1s1 NIMH46-1s1 NIMH46-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH21 NIMH21 NIMH21 NIMH21 NIMH21 NIMH21 NIMH50 NIMH50 NIMH51 NIMH51 NIMH51 NIMH51 NIMH51 NIMH51 NIMH50 NIMH51 NIMH50 NIMH51 NIMH50 NIMH47 NIMH40 NIMH40 NIMH26 NIMH10 NIMH26 NIMH13 NIMH24 NIMH23 NIMH23 NIMH46 NIMH46 NIMH46 NIMH46	chrX chrX chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307 153,213,307 153,213,507 153,213,597 153,213,597 153,213,597 153,213,597 153,213,597 153,213,642 153,213,642 153,213,642 153,213,642 153,213,642 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,215,817 153,215,827 153,230,615 153,234,970 153,236,245 153,236,245 153,237,730 153,247,063 153,250,328	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,354,185\\ 153,354,435\\ 153,369,728\\ 153,257,756\\ 153,266,406\\ 153,257,756\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ 153,429,785\\ 153,394,781\\ 153,429,785\\ 153,394,781\\ 153,426,460\\ 153,259,031\\ 153,429,835\\ 153,364,636\\ 153,477,589\\ 153,429,835\\ 153,364,636\\ 153,477,589\\ 153,429,835\\ 153,364,636\\ 153,477,589\\ 153,429,835\\ 153,364,636\\ 153,427,286\\ 153,417,579\\ 153,481,115\\ 153,427,286\\ 153,432,835\\ 153,259,076\\ 153,493,933\\ 153,247,253\\ 153,247,253\\ 153,249,565\\ 153,417,774\\ \end{array}$	315 2,885 154,446 326,006 204,517 216,623 140,738 324,066 140,838 156,131 203,172 44,159 52,809 150,699 204,042 214,009 216,143 181,084 212,763 45,334 52,664 262,267 214,018 148,789 208,539 186,964 249,735 192,316 196,590 22,831 256,273 9,523 182,502 167,446	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,922 2,963 2,511 2,903 632 760 3,094 2,919 2,041 2,835 2,682 3,050 2,715 2,766 408 3,093 170 2,535 2,313	$\begin{array}{c} 25.4\\ 20.1\\ 13.9\\ 10.6\\ 13.7\\ 13.7\\ 13.8\\ 10.6\\ 13.8\\ 14.0\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.6\\ 13.9\\ 14.4\\ 11.8\\ 13.6\\ 13.7\\ 13.6\\ 14.3\\ 12.2\\ 14.1\\ 14.1\\ 17.9\\ 12.1\\ 17.9\\ 13.9\\ 13.8\\ \end{array}$	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.24 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.27 0.26 0.23 0.27 0.26 0.27 0.26 0.23 0.27 0.26 0.23 0.27 0.28 0.27 0.26 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.27 0.24 0.24 0.24 0.24 0.24 0.24 0.23 0.29 0.31 0.23 0.27 0.26 0.22 0.27 0.26 0.22 0.22 0.23 0.27 0.26 0.27 0.28 0.27 0.26 0.27 0.28 0.27 0.26 0.27 0.28 0.27 0.26 0.27 0.28 0.27 0.26 0.27 0.28 0.27 0.26 0.27 0.28 0.27 0.26 0.27 0.26 0.27 0.28 0.27 0.26 0.27 0.26 0.27 0.27 0.26 0.27 0.27 0.26 0.27 0.27 0.26 0.27 0.27 0.26 0.27 0.27 0.26 0.27 0.27 0.26 0.27 0.26 0.27 0.27 0.26 0.23 0.27 0.26 0.27 0.26 0.27 0.26 0.27 0.28 0.32 0.32 0.32 0.32 0.32 0.33 0.31	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.5 60.1 57.9 56.6 56.4 56.5 57.1 56.4 56.5 57.1 56.5 57.1 56.5 57.7 56.5 57.7 56.5 57.3 56.5 55.3 56.5 55.3 56.1 56.5 55.3 56.5 55.3 56.1 56.5 55.3 55.5 55.3 55.5 55.3 55.5 55.3 55.5 55.3 55.5 55.5 55.5 55.3 55.5
NIMH53-2s1 NIMH33-1s1 NIMH69-2s1 NIMH9-1s1 NIMH21-1s1 NIMH22-1s1 NIMH08-1s1 NIMH20-1s1 NIMH20-1s1 NIMH20-1s1 NIMH50-1s1 NIMH50-1s1 NIMH50-1s1 NIMH50-1s1 NIMH50-1s1 NIMH50-1s1 NIMH50-1s1 NIMH61-1s1 NIMH60-1s1 NIMH47-1s1 NIMH40-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH60-1s1 NIMH63-1s1 NIMH63-1s1 NIMH63-1s1 NIMH24-1s1 NIMH23-1s1 NIMH23-1s1 NIMH23-1s1 NIMH46-1s1 NIMH46-1s1 NIMH46-1s1	NIMH53 NIMH33 NIMH69 NIMH19 NIMH21 NIMH21 NIMH21 NIMH20 NIMH33 NIMH21 NIMH20 NIMH50 NIMH50 NIMH51 NIMH50 NIMH51 NIMH50 NIMH51 NIMH50 NIMH51 NIMH50 NIMH47 NIMH47 NIMH47 NIMH46 NIMH60 NIMH60 NIMH10 NIMH61 NIMH60 NIMH10 NIMH61 NIMH10 NIMH13 NIMH13 NIMH13 NIMH13 NIMH144 NIMH17 NIMH44 NIMH17 NIMH46 NIMH04	chrX chrX chrX chrX chrX chrX chrX chrX	152,826,496 152,848,413 153,210,565 153,211,532 153,213,307 153,213,307 153,213,572 153,213,597 153,213,597 153,213,597 153,213,597 153,213,597 153,213,642 153,213,642 153,213,642 153,213,642 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,213,697 153,215,817 153,215,817 153,215,817 153,215,817 153,23,1380 153,234,970 153,236,245 153,237,660 153,237,730	$\begin{array}{r} 152,826,811\\ 152,851,298\\ 153,365,011\\ 153,537,538\\ 153,417,824\\ 153,429,930\\ 153,354,185\\ 153,357,638\\ 153,354,185\\ 153,369,728\\ 153,369,728\\ 153,257,756\\ 153,266,406\\ 153,364,341\\ 153,417,684\\ 153,427,651\\ 153,429,785\\ 153,394,781\\ 153,429,785\\ 153,394,781\\ 153,429,785\\ 153,394,781\\ 153,429,785\\ 153,394,781\\ 153,429,835\\ 153,364,636\\ 153,429,835\\ 153,364,636\\ 153,424,866\\ 153,417,579\\ 153,427,286\\ 153,432,835\\ 153,427,286\\ 153,432,835\\ 153,259,076\\ 153,493,933\\ 153,247,253\\ 153,429,565\\ \end{array}$	315 2,885 154,446 326,006 204,517 216,623 140,738 324,066 140,838 156,131 203,172 44,159 52,809 150,699 204,042 214,009 216,143 181,084 212,763 45,334 52,664 262,267 214,018 148,789 208,539 186,964 249,735 192,316 196,590 22,831 256,273 9,523 182,502	8 58 2,150 3,471 2,807 2,973 1,947 3,439 1,949 2,185 2,781 607 763 2,081 2,797 2,922 2,963 2,511 2,903 632 760 3,094 2,919 2,041 2,835 2,682 3,050 2,715 2,766 408 3,093 170 2,535	$\begin{array}{c} 25.4\\ 20.1\\ 13.9\\ 10.6\\ 13.7\\ 13.7\\ 13.8\\ 10.6\\ 13.8\\ 14.0\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.7\\ 13.6\\ 13.6\\ 13.6\\ 13.7\\ 13.6\\ 14.4\\ 11.8\\ 13.6\\ 13.7\\ 13.6\\ 14.4\\ 11.8\\ 13.6\\ 14.3\\ 12.2\\ 14.1\\ 17.9\\ 12.1\\ 17.9\\ 13.9\end{array}$	0.77 0.41 0.23 0.29 0.37 0.30 0.29 0.40 0.27 0.34 0.26 0.24 0.24 0.24 0.24 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.21 0.23 0.27 0.26 0.23 0.27 0.26 0.27 0.26 0.23 0.27 0.26 0.23 0.27 0.26 0.23 0.29 0.31 0.23 0.29 0.31 0.29 0.34 0.26 0.24 0.24 0.24 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.29 0.31 0.23 0.27 0.26 0.24 0.24 0.24 0.27 0.27 0.26 0.23 0.27 0.27 0.28 0.27 0.26 0.27 0.27 0.28 0.27 0.27 0.26 0.21 0.31 0.23 0.29 0.31 0.23 0.27 0.28 0.27 0.26 0.27 0.28 0.27 0.26 0.27 0.28 0.27 0.27 0.28 0.27 0.26 0.27 0.28 0.27 0.27 0.26 0.27 0.27 0.28 0.27 0.26 0.27 0.27 0.26 0.27 0.27 0.27 0.26 0.23 0.27 0.27 0.26 0.23 0.27 0.27 0.26 0.23 0.27 0.26 0.27 0.26 0.23 0.27 0.26 0.27 0.26 0.27 0.26 0.27 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.22 0.27 0.26 0.32 0.27 0.27 0.27 0.26 0.32 0.27 0.27 0.26 0.32 0.27 0.27 0.27 0.26 0.32 0.27 0.27 0.27 0.27 0.26 0.32 0.27 0.27 0.27 0.27 0.26 0.32 0.27 0.27 0.27 0.27 0.27 0.28 0.32 0.27	59.7 59.3 57.6 54.8 56.6 56.5 58.2 54.9 58.3 58.0 56.6 60.5 60.1 57.9 56.6 56.4 56.5 57.1 56.5 57.1 56.5 57.5 57.5 56.5 55.3 56.5 55.3 56.5 55.3 56.1 56.5 55.3 55.9

NIMH26-1s1	NIMH26	chrX	153,311,958	153,324,825	12,867	245	19.0	0.30	58.8
NIMH30-1s2	NIMH30	chrX	153,312,068	153,317,608	5,540	113	20.4	0.35	57.4
NIMH53-2s1	NIMH53	chrX	153,312,758	153,317,588	4,830	98	20.3	0.27	57.9
NIMH53-2s1	NIMH53	chrX	153,317,608	153,318,088	480	10	20.8	-0.34	51.0
NIMH30-1s2	NIMH30	chrX	153,317,723	153,318,774	1,051	18	17.1	-0.33	69.7
NIMH92-1s1	NIMH92	chrX	153,407,872	153,417,404	9,532	145	15.2	0.26	57.5
NIMH45-1s1	NIMH45	chrX	153,430,316	153,431,955	1,639	20	12.2	-0.23	42.3
NIMH57-1s1	NIMH57	chrX	154,044,835	154,056,820	11,985	177	14.8	-1.32	34.5
NIMH77-1s1	NIMH77	chrX	154,044,835	154,057,130	12,295	180	14.6	-1.30	34.6
NIMH09-1s1	NIMH09	chrX	154,051,356	154,071,868	20,512	234	11.4	-0.59	36.6
NIMH77-1s1	NIMH77	chrX	154,067,596	154,071,023	3,427	59	17.2	-1.27	35.0
NIMH83-1s1	NIMH83	chrX	154,208,939	154,219,124	10,185	144	14.1	0.51	35.5
NIMH46-1s1	NIMH46	chrX	154,425,197	154,431,258	6,061	91	15.0	-1.19	36.6
NIMH57-1s1	NIMH57	chrX	154,573,654	154,574,880	1,226	16	13.1	-0.59	30.6
NIMH90-1s1	NIMH90	chrX	154,573,654	154,574,880	1,226	16	13.1	-0.69	30.6

Table A.5 - Sequenced Breakpoints Identified in the Literature

Conrad	3	14,153,187	14,153,863	del	gcccag		CNVR1301.1
Conrad Korbel	3	15,820,177 22,067,362	15,821,743 22,072,811	del del	ATG AAAAATTCAATGTG		CNVR1306.1 NA18505_del 498
Conrad	3	25,005,891	25,007,254	del	AAAATCAATGTG	GGTGTAC	CNVR1326.1
ark	3	26,425,973	26,427,303	del	?		5_AK8
Conrad	3	26,425,974	26,427,303	del	t		CNVR1329.1
onrad	3	28,162,038	28,172,790	del		CTGA	CNVR1334.1
issers orbel	3	29176135(62)	30008810(37)	del	GTGGCTCACGCCTGTAATCCCAGCACT		del 27
orbel	3	32,077,056 32,077,056	32,082,888 32,082,888	del del	G		NA15510_del 281 NA18505_del 518
onrad	3	32,077,056	32,082,888	del	CC		CNVR1341.1
im	3	47,465,673	47,468,445	del	?		000001041.1
onrad	3	47,465,673	47,468,447	del	gc		CNVR1375.1
orbel	3	56,582,769	56,596,625	del			NA15510_del 294
im	3	62,639,438	62,670,706	del	?		
orbel	3	68,822,372	68,830,549	del			NA18505_del 489
orbel	3	68,822,372	68,830,549	del	СТСТ		NA15510_del 283 NA18505 del 500
orbel ark	3	74,230,279 78,862,108	74,237,488 78,862,409	del del	?		6 NA18968
am	3	81,008,005	81,009,297	del	?		Wheeler
onrad	3	84,187,632	84,190,074	del	•		CNVR1447.1
orbel	3	89,592,654	89,598,697	del	AAAAAAGAGAGACAG		NA15510_del 296
onrad	3	100,690,114	100,699,349	dup	AC		CNVR1468
onrad	3	101,111,472	101,112,321	del		t	CNVR1469.1
onrad	3	105,760,890	105,761,737	del	А		CNVR1480.1
onrad	3	105,760,890	105,761,737	del	a		CNVR1480.1
onrad	3	108,520,647	108,523,025	del	gat		CNVR1485.1
orbel im	3	109,202,507 121,644,332	109,223,395 121,647,642	del del	?		NA15510_inv 525
onrad	3	131,614,714	131,615,594	del	ť		CNVR1540.1
ark	3	133,190,943	133,196,075	del	?		7_AK18
onrad	3	142,027,098	142,029,737	del	ccact		CNVR1562.1
onrad	3	147,867,880	147,877,553	del	ca		CNVR1576.1
onrad	3	150,751,166	150,752,841	del	aggga		CNVR1583.1
ark	3	153,247,620	153,248,061	del	?		8_NA18542
onrad	3	157,574,864	157,576,385	del		TTAAA	CNVR1591.1
onrad	3	163,994,828	164,109,029	del	c		CNVR1608.1
issers	3	165,316,928	165,701,172	del	?		del 2
ark onrad	3	167,470,179 180,032,827	167,470,516 180,033,568	del del	GCC		9_NA18968 CNVR1648.2
eSmith	3	181137034(6)	181137500(2)	del	TC		500001000.2
im	3	188,063,727	188,068,042	del	?		
ark	3	191,220,038	191,223,219	del	?		10 AK12
onrad	3	191,220,042	191,223,222	del	ctca		CNVR1669.1
onrad	3	192,547,379	192,554,361	del		TATCCAGA	CNVR1675.1
orbel	3	192,547,379	192,554,362	del			NA15510_del 293
orbel	3	193,420,025	193,471,341	del	TCA		NA15510_del 284
onrad	3	194,358,026	194,368,102	del	TCT	CACACT	CNVR1685.1
onrad	3	198,418,970	198,423,652	del	T	CAGACT	CNVR1716.1
orbel orbel	4	33,805	39,019	del del	Т		NA18505_del 569 NA15510_del 335
orbel	4	3,583,174 3,883,363	3,588,419 3,964,476	del			NA15510_del 330
onrad	4	6,733,297	6,736,765	del	GAA		CNVR1791.1
orbel	4	9,820,365	9,843,671	del	Т		NA18505_del 541
orbel	4	9,820,365	9,843,671	del	T		NA15510_del 311
orbel	4	16,553,336	16,559,843	del			NA18505_del 551
onrad	4	18,666,569	18,667,067	del		ACAGTTAATTCAGTTACAGTTAA-	CNVR1838.1
						TACAGTTAA	
orbel	4	20,769,760	20,776,557	del	TITAGTATAATTITCT		NA15510_del 345
orbel	4	20,769,760	20,776,557	del	TTTAGTATAATTTTCT		NA18505_del 548
orbel onrad	4	20,978,066 28,030,631	20,986,741 28,031,142	del del	Т		NA18505_del 552 CNVR1859.1
ark	4	30,623,047	30,624,073	del	?		11_AK18
orbel	4	39,911,421	39,913,454	del	•		NA15510_inv A
im	4	42,457,435	42,464,300	del	?		
ark	4	43,446,564	43,446,887	del	?		12_NA18949
onrad	4	45,897,554	45,899,785	del	TC		CNVR1904.1
im	4	58,180,961	58,185,488	del	?		
onrad	4	58,506,644	58,513,191	del	CC		CNVR1928.1
onrad	4	61,621,786	61,624,840	del	AA		CNVR1937.1
orbel	4	70,502,047	70,507,392	del	CCA		NA18505_del 559
orbel orbel	4	70,502,047 79,488,148	70,507,392 79,494,224	del del	CCA AAAGCTTCAAGATA		NA15510_del 347 NA18505_del 543
orbel	4	79,488,148	79,494,224	del	AAAGCTTCAAGATA		NA15510 del 327
im	4	79,488,158	79,494,220	del	?		
orbel	4	81,107,078	81,113,124	del	AAGAATAGGGCGTCCG		NA15510_del 325
onrad	4	87,195,401	87,198,978	del	CTA		CNVR1991.1
onrad	4	92,150,579	92,154,859	del			CNVR2000.1
onrad	4	98,573,314	98,578,237	del	g		CNVR2013.1
eSmith	4	98573314(5)	98578237(8)	del	G		
im 	4	106,926,782	106,936,575	del	?	<u></u>	CNIV/D2020_1
onrad	4	107,276,027	107,282,811	del	A ATA	CA	CNVR2030.1
onrad orbel	4	107,823,749 108,347,262	107,828,706 108,351,169	del del	AATA AAAACATTAGGATTCTCTTT		CNVR2032.1 NA18505_del 588
m	4	108,347,262	108,351,109	del	?		
orbel	4	116,148,168	116,151,323	del	GTGA		NA15510_del 344
onrad	4	117,587,246	117,587,942	del	CTC		CNVR2055.1
onrad	4	135,652,452	135,655,151	del		GTACAT	CNVR2080.1
m	4	142,450,233	142,452,513	del	?		
onrad	4	162,098,484	162,104,398	del	AATTT		CNVR2137.1
onrad	4	163,613,455	163,615,872	del	GA		CNVR2141.1
im an and	4	165,024,355	165,039,560	del	?		CNV/D2147.1
onrad	4	165,422,493	165,425,669	del	aaat		CNVR2147.1
ark	4	165,422,493	165,425,670	del	?	TTACCAC	13_NA18942
onrad	4	167,223,766	167,224,369	del	Π	TTAGCAC	CNVR2152.1 NA18505 del 555
orbel orbel	4	168,129,302 168,345,738	168,260,424	del			NA18505_del 555 NA18505_del 589
orbel	4	168,345,738	168,351,840 169,229,628	del del	cttc		CNVR2161.1
onrad	4	172,610,983	172,616,000	del	uu	СП	CNVR2161.1 CNVR2168.1
onrad	4	173,225,214	173,229,506	del		C	CNVR2108.1 CNVR2171.1
onrad	4	173,661,607	173,670,095	del		A	CNVR2172.1
	4	173,661,607	173,670,096	del		••	NA18505_del 576
orbel							

Conrad	4	175,861,744	175,863,548	del	TGG		CNVR2174.1
Korbel Conrad	4	178,704,201 182,293,555	178,725,490 182,294,125	del del	GT		NA18505_del 546 CNVR2196.1
Conrad	4	185,395,045	185,406,164	del	AAAG		CNVR2209.1
Korbel	4	190,630,172	190,634,918	del	ттт		NA18505_del 574
Korbel	4	190,822,807	190,850,110	del			NA18505_inv 931
Korbel Kim	4	190,822,807 71,386	190,850,110 76,029	del del	?		NA15510_inv 527
Conrad	5	2,926,819	2,927,967	del	r		CNVR2318.1
Kim	5	10,579,961	10,585,291	del	?		
Conrad	5	16,177,808	16,178,491	del		aatagaa	CNVR2371.1
Conrad Conrad	5	19,411,028	19,412,156	del	TOOTOTOTOTTATICTICATOTOTO	atgg	CNVR2388.1
Conrad	5	21,485,956 26,832,458	21,488,250 26,837,656	del del	TGGTCTCTGCTTCTTATTCTTCATGTGCTC TTT		CNVR2395.1 CNVR2407.1
Conrad	5	28,526,758	28,531,365	del	TGT		CNVR2412.1
Korbel	5	40,004,665	40,012,423	del			NA18505_del 622
Korbel	5 5	46,306,413	46,311,594	del	TTCT		NA18505_del 632
Korbel Kim	5	46,306,413 49,471,345	46,311,594 49,476,325	del del	TTCT ?		NA15510_del 363
Korbel	5	57,359,234	57,369,537	del	GA		NA15510_del 373
Korbel	5	57,359,234	57,369,537	del	GA		NA18505_del 640
Kim	5	57,715,747	57,721,855	del	?		
Korbel Conrad	5	57,715,755 63,734,102	57,721,865 63,737,115	del del	AAAAAACAC GGC		NA18505_del 605 CNVR2483.1
deSmith	5	65479417(40)	65479953(75)	del	ATTGTATAGTGCTATCATTATGT		CIVIN2403.1
deSmith	5	78,145,556	78,147,626	del			
Vissers	5	78514996(8)	79167040(2)	del	GC		del 11
Conrad Park	5	86,281,760	86,282,899 97,428,518	del del	?	tat	CNVR2522.1 14 NA18997
Conrad	5	97,427,318 97,961,018	97,428,518 97,967,734	del	ŕ	ATGTAGGAAAAT	14_NA18997 CNVR2533.1
Korbel	5	99,541,738	99,548,258	del	A		NA18505_del 625
Conrad	5	106,352,650	106,354,342	del		Т	CNVR2554.1
Korbel	5	108,622,427	108,629,161 111,972,239	del	CCATTCTTATTTCTT	ctaactaataatataactaataatataac-	NA18505_del 608
Conrad	5	111,967,481	111,972,239	del		taatataataatataactaataatataac-	CNVR2566.1
Conrad	5	119,408,045	119,410,579	del		GAG	CNVR2587.1
Conrad	5	121,160,505	121,163,855	del	gaca		CNVR2590.1
Park	5	127,363,899	127,364,827	del	?		15_AK6
Conrad Conrad	5	127,435,338 133,162,590	127,438,815 133,164,387	del del		ggatggaggaagag	CNVR2600.1 CNVR2610.1
Conrad	5	140,202,321	140,219,115	del		сса	CNVR2622.1
Conrad	5	150,157,856	150,161,793	del	Α		CNVR2646.1
Conrad	5	150,183,353	150,203,456	del		AAATAGA	CNVR2647.1
Korbel Korbel	5	151,436,615 151,436,623	151,442,650 151,442,641	del del	CAAAATTACATGGTGGA CAAAATTACATGGTGGA		NA18505_del 606 NA15510 del 362
Conrad	5	155,244,367	155,245,159	del	TAATCT		CNVR2658.1
Conrad	5	162,794,351	162,795,869	del		aacaagatgattcac	CNVR2669.1
Park	5	162,794,351	162,795,870	del	?		16_AK6
Conrad	5 5	166,335,344	166,336,212	del	ACTG		CNVR2676.1
Park Kim	5	170,062,496 177,754,281	170,063,968 177,756,656	del del	?		17_NA18542
Conrad	5	180,501,840	180,502,585	del	Å		CNVR2723.1
Conrad	6	16,992,947	16,994,075	del	а		CNVR2789.1
Park	6	22,158,817	22,162,220	del	?		18_AK6
Conrad deSmith	6	23,851,238 24433341(6)	23,853,924 24435791(6)	del del	тстсс		CNVR2811.1
Conrad	6	31,464,139	31,561,087	del	tttctt		CNVR2842.1
Conrad	6	32,667,951	32,668,369	del	A		CNVR2845.3
Kim	6	34,045,807	34,050,676	del	?		
deSmith Conrad	6 6	34425086(9) 35,734,365	34427582(5) 35,737,724	del del	AGA		CNVR2859.1
Korbel	6	49,038,905	49,046,493	del	?		NA18505_del 675
Conrad	6	51,307,435	51,308,085	del	TTTC		CNVR2899.1
Conrad	6	51,844,070	51,844,767	del	ATT		CNVR2901.1
Conrad	6	55,933,916	55,954,671	del		TACT	CNVR2912.1
Korbel Korbel	6	57,405,149 57,531,030	57,409,206 57,537,083	del del	TAAAAGACTATATACATC		NA15510_del 394 NA15510_del 382
Conrad	6	67,097,521	67,099,910	del		AATTAATACATGCCAGATT	CNVR2946.2
Conrad	6	69,195,308	69,196,113	del		C	CNVR2951.1
Korbel	6	74,648,523	74,659,593	del	AA		NA18505_del 645
Conrad Korbel	6	77,073,432 85,374,868	77,085,882 85,380,946	del del	GG ACATTTCT		CNVR2971.1 NA18505_del 660
Korbel	6	85,374,868	85,380,946	del	ACATTICT		NA15510_del 381
Conrad	6	89,978,472	89,978,896	del			CNVR2996.1
Conrad	6	95,250,045	95,251,059	del	ТА		CNVR3004.1
Conrad Conrad	6 6	96,494,322 100,141,223	96,496,142 100,142,043	del del		AA ATTGC	CNVR3006.1 CNVR3009.1
Conrad	6	100,141,223	100,142,043	del	CAA	ALLOC	CNVR3009.1 CNVR3010.1
Conrad	6	103,844,156	103,869,582	del		tgcca	CNVR3020.1
Korbel	6	107,277,574	107,277,728	del			NA15510_inv 558
Korbel Korbel	6	130,890,026 133,383,515	130,893,988 133,389,581	del del	AGGTGTGATGTTTT		NA18505_inv 972
Korbel	6	133,383,515	133,389,581	del	AGGTGTGATGTTTT		NA18505_del 670 NA15510_del 389
Conrad	6	134,310,673	134,311,422	del	AGAG		CNVR3074.1
Conrad	6	141,590,317	141,591,727	del	TTTC		CNVR3083.1
Conrad	6	154,000,064 155746035(65)	154,003,221	del			CNVR3112.1 del 28
Vissers deSmith	6	162,645,085	157307963(93) 162,645,903	del del	TGTTAGCCAGGATGGTCTTGATCTCCTGAC	ттт	uel 20
Conrad	6	164,463,437	164,467,181	del	С		CNVR3150.1
Korbel	6	164,463,437	164,467,182	del	G		NA15510_del 384
Kim	6	165,644,659	165,652,123	del	?		NA10505 100 070
Korbel Korbel	6	168,836,086 168,836,086	168,836,577 168,836,577	del del			NA18505_inv 973 NA15510_inv 556
Conrad	7	1,822,569	1,830,102	del			CNVR3242.1
Korbel	7	6,866,324	6,889,694	del			NA18505_del 731
Conrad	7	13,244,637	13,247,240	del	с		CNVR3295.1
Conrad	7	16,138,298	16,140,597	del			CNVR3304.1
Conrad Conrad	7	20,715,311 22,401,328	20,720,104 22,403,288	del del	GC CAC		CNVR3311.1 CNVR3314.1
Conrad	7	52,930,697	52,932,410	del	ACAG		CNVR3314.1 CNVR3389.2
Conrad	7	54,563,980	54,564,927	del			CNVR3394.1
Conrad	7	69,834,135	69,840,971	del			CNVR3443.1
deSmith	7	82856583(4)	82857509(10)	del	А		CINVR3443.1

Conrad	7	89,648,345	89,650,537	del	gc		CNVR3485.1
orbel	7	90,869,019	90,880,521 96,319,935	del	G		NA15510_del 405 NA18505_del 722
orbel	7	96,313,826 96,313,826	96,319,935	del del	GCAACTGGAACTTTC GCAACTGGAACTTTC		NA15510 del 401
onrad	7	98,066,481	98,068,689	del	ttg		CNVR3503.1
orbel	7	106,847,671	106,850,014	del			NA18505_inv 936
orbel	7	106,847,671	106,850,014	del			NA15510_inv 559
rbel rbel	7	113,203,397	113,209,444	del	CATAATGGCATTTTT CATAATGGCATTTTT		NA18505_del 694 NA15510 del 408
m	7	113,203,397 113,203,412	113,209,444 113,209,444	del del	?		NA15510_del 408
rbel	7	113,439,881	113,446,502	del	TTGT		NA18505 del 714
nrad	7	115,718,878	115,728,486	del	ag		CNVR3539.1
nrad	7	125,833,125	125,838,686	del	TAC		CNVR3559.1
nrad	7	127,002,204	127,005,218	del	?	ACAC	CNVR3563.1
nrk nrad	7	131,923,553 133,435,543	131,924,090 133,448,872	del del	TGC		19_NA18526 CNVR3573.1
ssers	7	145,936,946	146,244,399	del	160	A	del 3
onrad	7	147,703,799	147,707,262	del	TGGATC		CNVR3609.1
orbel	7	151,620,490	151,704,326	del	TTTG		NA18505_del 696
orbel	7	151,620,490	151,704,326	del	TTTG		NA15510_del 397
onrad	7	158,810,205	158,815,487 589,415	del	?	аа	CNVR3683.1
im orbel	8	584,397 584,453	589,415	del del	f		NA18505_del 762
im	8	2,116,965	2,122,377	del	?		14410505_001702
onrad	8	5,582,924	5,593,187	del		ас	CNVR3760.1
onrad	8	11,282,971	11,284,620	del	aag		CNVR3781.1
orbel	8	13,658,494	13,696,112	del	AA		NA18505_del 759
orbel	8	16,245,681	16,251,905	del	0070		NA18505_del 763
issers onrad	8	24447284(5) 25,028,351	31302615(6) 25,046,862	del del	GGTG		del 5 CNVR3830.1
orbel	8	25,122,595	25,126,570	del			NA18505 del 743
im	8	25,122,602	25,126,570	del	?		
onrad	8	25,122,602	25,126,576	del	GGCTCAG		CNVR3831.1
onrad	8	39,351,231	39,506,385	del		Т	CNVR3859.1
onrad	8	40,004,842	40,009,998	del		tgaccagc	CNVR3860.1
orbel orbel	8	40,893,763 42,309,595	40,898,989 42,313,559	del del			NA15510_del 421 NA18505 del 754
onrad	8	49,255,939	42,313,559	del	G		CNVR3878.1
onrad	8	51,193,644	51,200,882	del		GTGTTTCCTAAGTGCTTA	CNVR3882.1
onrad	8	51,387,538	51,390,870	del	CTA		CNVR3884.1
issers	8	60249086(147)	62195805(66)	del	GGGGTCAGGGACCCACTTGAGGAGGCAGT-		del 29
	-	(17004/0/71)	(1000(05/7)		CTGCCCGTTCTCAGATCTCCAGCTGCGTGCTG		44112
issers ark	8	61798469(71) 62,197,914	61889695(7) 62,198,447	del del	Π ?		del 12 20 NA18552
orbel	8	73,950,326	73,956,385	del	TGCAAATCTT		NA18505_del 768
im	8	73,950,329	73,956,378	del	?		1410505_001700
onrad	8	75,525,426	75,529,531	del		С	CNVR3935.1
onrad	8	82,207,573	82,209,183	del		ttacgtgtac	CNVR3946.2
Conrad	8	85,423,525	85,431,728	del	CAAC		CNVR3952.1
orbel	8	120,223,723	120,230,397	del	AT		NA18505_del 770
Conrad Corbel	8	120,223,725 126,664,303	120,230,432 126,670,317	del del	ta TGTGAGTG		CNVR4031.1 NA15510 del 434
Corbel	8	126,664,303	126,670,317	del	AAACACTCACA		NA18505_del 748
Conrad	8	131,919,931	131,921,920	del		A	CNVR4052.1
Corbel	8	135,152,106	135,158,209	del	CATTCTTCAACATTTT		NA18505_del 773
orbel	8	135,152,106	135,158,209	del	CATTCTTCAACATTTT		NA15510_del 425
Conrad	8	137,229,379	137,233,082	del	GC		CNVR4067.1
orbel Conrad	8	144,771,577 4,366,421	144,785,836 4,367,644	del del	tat		NA15510_del 427 CNVR4153.2
Conrad	9	8,630,851	8,631,666	del	AAGA		CNVR4155.2 CNVR4174.1
Conrad	9	9,506,969	9,507,964	del	701071	GTTTTTCTGTA	CNVR4177.1
Conrad	9	10,394,564	10,395,094	del	CCA		CNVR4181.1
issers	9	14,196,884	16,342,939	del	GT		del 1
Conrad	9	23,352,801	23,367,685	del		GA	CNVR4213.1
Conrad Cim	9	31,281,356	31,282,673 70,933,175	del del	C		CNVR4234.1
lim lorbel	9	70,927,942 70,927,942	70,933,175	del	GT		NA18505_del 788
orbel	9	70,927,942	70,933,177	del	GT		NA15510 del 439
lim	9	73,446,481	73,449,953	del	?		
orbel	9	80,627,751	80,660,989	del	Т		NA18505_del 807
lim	9	84,854,269	84,860,328	del	?		
orbel	9	85,698,412	87,640,324	del	haba-		NA18505_inv 980
im	9 9	100,348,869 112,516,996	100,351,490 112,519,927	del del	tctca ?		CNVR4414.1
issers	9	117097067(8)	117798935(6)	del	r A		del 6
onrad	9	117,235,735	117,237,188	del	T		CNVR4452.1
onrad	9	129,221,443	129,225,901	del	gatc		CNVR4479.1
onrad	9	137,333,959	137,336,077	del	ag		CNVR4527.3
orbel	9	137,353,885	137,357,426	del	TGA		NA15510_del 451
onrad	9 10	137,353,887 4,280,063	137,357,424 4,281,683	del del	tga C		CNVR4527.1 CNVR4594.1
im	10	4,427,701	4,431,391	del	?		CINVIC+394.1
onrad	10	4,698,520	4,700,525	del	•	ATAG	CNVR4596.1
orbel	10	5,277,305	5,283,355	del	AAAAAAATAGTGTAAAGT dup		NA15510_del 64
orbel	10	5,627,107	5,677,112	del			NA18505_del 119
orbel	10	5,627,107	5,677,112	del			NA15510_del 67
im orbel	10 10	5,627,110	5,677,111	del	?		NA18505 dol 00
orbel	10	6,451,584 6,694,413	6,457,651 6,704,196	del del	CAGCAAATCATTTTCCT AC		NA18505_del 99 CNVR4606.1
onrad	10	7,117,046	7,118,307	del		A	CNVR4609.1
am	10	7,117,046	7,118,307	del	?		Wheeler
onrad	10	17,350,717	17,355,515	del		TATACTATGTGTAT	CNVR4634.1
ark	10	20,036,712	20,038,183	del	?		21_AK14
onrad	10	58,879,793	58,881,859	del		gttaaagatcaatc	CNVR4760.1
onrad	10	61,031,970	61,035,014	del	AATCA		CNVR4767.1
onrad onrad	10	65,179,256	65,181,407	del	AC GATA		CNVR4773.1
onrad	10	66,068,780 66,976,938	66,070,754 66,985,301	del del	AC		CNVR4776.1 NA15510_del 82
ark	10	66,976,938	66,985,301	del	?		22_AK6
	10	66,976,940	66,985,302	del	GT		CNVR4779.1
onrad	10						
	10	77,925,582 84,117,799	77,931,030 84,120,345	del del	TTCAGT ?		NA15510_del 72

(orbel	10	96,857,182	96,864,933	del	TCAA		NA18505_del 106
orbel onrad	10 10	102,342,367 107,940,672	102,354,417 107,941,586	del del	TCAA T		NA18505_del 120 CNVR4884.1
rk	10	107,940,672	107,941,586	del	?		23 AK10
nrad	10	107,985,984	107,987,724	del			CNVR4885.1
nrad	10	108,020,308	108,022,533	del	2	A	CNVR4886.1
n	10	114,102,173	114,106,649 114,106,650	del del	? GG		CNVR4893.1
nrad n	10	114,102,173 128,578,838	128,582,206	del	?		CNVR4893.1
'k	10	130,726,861	130,727,265	del	?		24 NA18537
nrad	10	132,799,052	132,802,769	del	TTCA		CNVR4949.1
rbel	11	4,924,739	4,933,353	del			NA18505_del 158
rbel	11	4,924,739	4,933,353	del			NA15510_del 103
nrad	11	5,478,208 5,716,663	5,479,749	del	gt	Т	CNVR5044.1
onrad orbel	11	5,741,150	5,718,941 5,765,860	del del	AC	I	CNVR5048.1 NA15510 del 96
onrad	11	5,741,151	5,765,860	del	AC		CNVR5049.1
onrad	11	7,091,294	7,093,075	del	ccag acTTTAAGAC		CNVR5056.1
onrad	11	11,336,197	11,337,606	del	gcc		CNVR5072.1
onrad	11	22,427,462	22,429,349	del	CAAATA TG		CNVR5103.1
onrad onrad	11	24,399,728 29,924,149	24,408,863 29,925,042	del del	t	AGCAGA	CNVR5109.1 CNVR5125.1
onrad	11	45,386,425	45,388,192	del	GCC		CNVR5125.1 CNVR5158.1
onrad	11	47,014,165	47,020,283	del	000	AAAGTGGGATAGTGGAA	CNVR5162.1
onrad	11	48,557,434	48,560,860	del	TC		CNVR5165.1
onrad	11	58,388,350	58,393,131	del	GC		CNVR5189.1
orbel	11	58,388,350	58,393,132	del	С		NA15510_del 98
onrad	11	59,984,740	59,985,962	del	t		CNVR5192.1
onrad onrad	11	69,660,203 81,534,058	69,662,138 81,540,993	del del	CTC	CAGTTACAAATATGTCTGTTTCT	CNVR5218.1 CNVR5250.1
onrad	11	85,981,878	85,984,206	del		CAGINGAAAAAGICIGIIICI	CNVR5255.1
orbel	11	92,791,149	92,800,594	del			NA18505_del 149
onrad	11	95,641,573	95,643,043	del	С		CNVR5278.1
orbel	11	101,071,002	101,079,503	del			NA15510_del 90
onrad	11	103,772,961	103,778,439	del	ATA		CNVR5294.1
orbel	11	103,772,961	103,778,440	del	ATA		NA18505_del 159
orbel onrad	11	104,798,682 128,187,926	104,804,116 128,188,620	del del		С	NA18505_del 153 CNVR5351.1
onrad onrad	11	134,107,192	128,188,620	del	gtgt	<u>ر</u>	CNVR5351.1 CNVR5372.1
onrad	11	134,238,110	134,239,324	del	GT		CNVR5372.1 CNVR5375.1
onrad	12	247,761	255,094	del	agca		CNVR5382.1
onrad	12	5,092,083	5,093,713	del	-		CNVR5408.1
onrad	12	6,111,699	6,118,340	del	ag		CNVR5412.1
im	12	11,075,858	11,142,017	del	?		011/05/04/
onrad im	12 12	11,917,682	11,918,420	del	?		CNVR5436.1
eSmith	12	15,909,933 20,859,912	15,912,931 20,859,936	del del	AATA	TAG	
onrad	12	22,310,208	22,315,497	del	0010	CCA	CNVR5456.1
orbel	12	22,310,232	22,315,498	del			NA15510_del 111
onrad	12	23,830,789	23,831,356	del	t		CNVR5458.1
onrad	12	33,606,390	33,608,237	del	AACAA		CNVR5492.1
onrad	12	36,294,988	36,304,145	del	2		CNVR5501.2
im ark	12 12	38,587,965 49,259,982	38,602,082	del del	?		25_AK4
im	12	55,618,220	49,261,778 55,663,208	del	?		23_AK4
orbel	12	57,008,350	57,016,840	del	•		NA18505_del 173
orbel	12	57,008,350	57,016,840	del			NA15510_del 108
onrad	12	58,808,112	58,811,308	del	TGTCTA		CNVR5559.1
onrad	12	66,213,619	66,214,389	del	AGA		CNVR5577.1
orbel onrad	12 12	68,881,119	68,883,851 69,164,484	del del	GAAGTGTCATACTTTTT	С	NA15510_del 112 CNVR5582.1
orbel	12	69,158,533 79,379,862	79,380,365	del		C	NA15510_inv 548
onrad	12	83,117,245	83,120,148	del	gcctca		CNVR5607.1
onrad	12	85,128,811	85,133,374	dup	AG		CNVR5595
im	12	94,757,723	94,760,459	del	?		
onrad	12	98,318,079	98,326,901	del	G		CNVR5639.1
onrad	12	100,626,541	100,631,221	del	ACAG		CNVR5644.1
orbel im	12 12	100,626,541 128,624,266	100,631,222 128,628,228	del del	CTGT ?		NA15510_del 109
issers	12	31154817(20)	37648937(40)	del	TGC		del 14
onrad	13	33,033,730	33,042,821	del			CNVR5837.1
im	13	33,033,730	33,042,822	del	?		
onrad	13	37,955,319	37,958,205	del	GGAA		CNVR5850.1
ark	13	38,832,183	38,833,482	del	?		26_AK18
onrad	13	49,411,121	49,412,891	del	gt		CNVR5870.1
im onrad	13 13	56,650,541 69,633,730	56,686,865 69,673,451	del del	? tc		CNVR5918.1
onrad	13	71,375,261	71,378,578	del	c		CNVR5918.1 CNVR5920.1
im	13	71,705,623	71,710,360	del	?		
orbel	13	71,741,038	71,744,926	del	Т		NA15510_del 122
orbel	13	80,703,808	80,712,934	del	Wimpy polyA		NA18505_del 206
onrad	13	82,063,937	82,070,208	del	TG		CNVR5946.1
onrad onrad	13 13	88,219,968	88,220,938 89,662,812	del	АААТ	cattattagcagc	CNVR5960.1 CNVR5962.1
am	13	89,660,856 103,695,322	103,695,323	del del	?		Levy
irk	13	108,159,746	108,160,439	del	?		27 NA18942
ark	14	21,951,506	21,952,100	del	?		28_AK10
onrad	14	21,951,507	21,952,100	del	G		CNVR6084.1
m	14	34,184,839	34,192,011	del	?		
ark .	14	38,074,269	38,074,779	del	?		29_NA18542
onrad	14	39,679,566	39,687,423	del	A A CT	caggctcctttgtaaataa	CNVR6133.1
orbel onrad	14 14	40,883,961	40,929,395 42,062,684	del del	AACT CT		NA18505_del 219 CNVR6140.1
onrad	14	42,057,278 53,780,099	53,783,438	del	TGA		CNVR6140.1 CNVR6158.1
onrad	14	69,086,749	69,092,243	del	gtgt		CNVR6178.1
Smith	14	72402705(7)	72403561(3)	del	GT		
Smith	14	72615517(24)	72616685(92)	del	ттттт		
im	14	73,076,457	73,108,631	del	?		
onrad	14	79,176,043	79,184,853	del	tg	CACACITA 404711001	CNVR6203.1
onrad	14	80,947,966	80,950,367	del		CAGAGTTAAGATAAGCA	CNVR6209.1
onrad im	14 14	81,568,863 81,568,863	81,573,083 81,573,084	del del	?	AACATAAATC	CNVR6211.1
	1.17	01,000,000	81,573,084	del	?		30_AK18

Korbel	14	84,366,861	84,371,909	del	TTAGAAAC		NA15510_del 126
Park Conrad	14 14	84,366,861 84,366,869	84,371,909 84,371,916	del del	? GTTTCTAA		31_NA18973 CNVR6220.1
Corbel	14	105,282,153	105,397,046	del	AGC		NA18505 del 225
im	14	105,282,154	105,397,044	del	?		
orbel	14	105,311,003	105,398,170	del			NA15510_del 133
orbel	15	18,841,481	18,849,632	del			NA18505_del 241
orbel	15	18,841,481	18,849,632	del			NA15510_del 135
onrad im	15 15	21,606,470 22,009,161	21,612,738 22,111,478	del del	?	ac	CNVR6306.1
orbel	15	25,589,686	25,602,096	del			NA18505_del 233
onrad	15	33,947,426	33,949,511	del	ttat		CNVR6355.1
ark	15	37,531,682	37,532,152	del	?		32_NA18592
onrad	15	37,531,683	37,532,239	del	Α		CNVR6357.1
orbel	15	42,941,408	42,947,386	del			NA18505_del 247
ark .	15	44,647,999	44,648,461	del	?		33_AK10
onrad im	15 15	60,493,387	60,495,087	del	ATT ?		CNVR6418.1
onrad	15	68,808,907 69,495,663	68,814,563 69,500,744	del del	I	acc	CNVR6438.1
onrad	15	69,668,624	69,670,021	del		T	CNVR6439.1
onrad	15	82,332,438	82,334,852	del		tttc	CNVR6484.1
Smith	15	83858012(6)	83860206(10)	del	ттт		
onrad	15	97,474,127	97,474,924	del	ctg		CNVR6543.1
ark	15	99,159,012	99,159,896	del	?		34_AK10
onrad	15	99,159,013	99,159,896	del	TGC		CNVR6552.1
onrad orbel	16 16	13,201,968 14,407,231	13,203,997 14,412,704	del del	ct		CNVR6642.1 NA18505_del 277
orbel	16	16,841,867	16,847,919	del	AAGCTTAATTCTTTT		NA18505_del 277
onrad	16	22,955,276	22,957,032	del		GATTCT	CNVR6670.1
Smith	16	22,955,277	22,957,032	del		GATTCT	
orbel	16	25,247,611	25,250,630	del	GG		NA15510_del 160
m	16	29,167,046	86,811,700	del	?		
orbel	16	44,955,510	44,985,518	del		т	NA18505_inv 922 CNVR6737.1
onrad Smith	16 16	55,923,812 56282299(301)	55,924,619 56285908(10)	del del	AAT	1	CINVR0/3/.1
onrad	16	61,101,835	61,108,169	del		GT	CNVR6752.1
onrad	16	75,096,634	75,101,526	del		C	CNVR6782.1
im	16	75,096,634	75,101,526	del	?	_	Wheeler
Smith	16	76115170(4)	76115184(8)	del	GGGG		
onrad	16	76,929,139	76,942,399	del	· · · · · · · · · · · · · · · · · · ·		CNVR6791.2
m	16	76,929,139	76,942,400	del	?		dol 17
ssers ssers	16 16	84275151(5)	86275753(7)	del del	AGCC GAGACCAGCCTGGCCAAC		del 17 del 25
ssers	16	84374208(26) 84402571(9)	85277007(25) 85435712(20)	del	TGAGCCAC		del 20
ssers	16	85157840(3)	85288901(4)	del	GCC		del 15
nrad	16	86,385,864	86,388,966	del	сса		CNVR6850.1
ssers	16	87676976(96)	88037131(51)	del	CCAAAGTGCTGGGATTACAG		del 26
Smith	16	88,089,521	88,095,227	del			
onrad	17	193,767	197,056	del		aaatggttattaatt	CNVR6908.1
onrad	17	5,536,431	5,538,222	del	TCC		CNVR6961.1
onrad onrad	17 17	11,190,428 11,352,392	11,200,650 11,353,062	del del	tctgc	acacaggtccataaagaaagaa	CNVR6988.1 CNVR6990.1
nang	17	14215232(59)	15509173(200)	del	AGCCTCCCAAAGTGCTGGGATTACAGG	acacaggiccataaagaaagaa	C1292 and C2405
nang	17	14,553,352	15,089,591	del			A26
nang	17	14,890,749	15,328,218	del		TAAAATTATCTTTTAGTCATTAA	SP951
nang	17	15057049(59)	15468624(34)	del	GTTTCACCAT		SP54C
nang	17	15079030(1)	15096344(5)	del	T	CAT	SPR2
hang	17 17	15096987(9)	15110285(7)	del	TC A		A29 A23
hang hang	17	15,101,735 15118189(94)	15,106,908 15311614(9)	del del	TCTCT		SPR1
hang	17	15143662(3)	15329785(6)	del	A		SP3672 and SP3840
onrad	17	15,730,280	15,734,511	del		TAGTT	CNVR7004.1
orbel	17	15,730,283	15,734,503	del	т		NA15510_del 181
onrad	17	22,560,680	22,564,522	del	aaattcacatggca		CNVR7043.1
onrad	17	23,804,514	23,807,620	del	ct		CNVR7047.1
ark	17	27,130,737	27,131,657	del	?		35_NA18582
orbel onrad	17 17	49,513,662 53,042,810	49,523,001 53,044,915	del del	ct		NA15510_del 185 CNVR7144.1
orbel	17	63,284,492	63,722,780	del	u		NA18505 del 312
orbel	17	65,966,692	65,972,772	del	CACAAAATCTT		NA15510_del 179
onrad	17	71,873,832	71,876,903	del	GGA		CNVR7201.1
onrad	18	5,314,645	5,316,244	del	CA		CNVR7241.1
orbel	18	14,541,533	14,559,237	del	TGGAAC		NA18505_del 320
m	18	14,542,177	14,558,726	del	?		CNIV/D7292_1
onrad onrad	18 18	22,825,618 28,142,161	22,826,339 28,143,489	del del	022		CNVR7283.1 CNVR7292.3
onrad	18	28,142,161 28,749,691	28,143,489 28,755,259	del	gaatggag		CNVR7292.3 CNVR7293.1
orbel	18	32,507,071	32,513,858	del			NA18505_del 322
ark	18	33,560,058	33,560,631	del	?		36_AK10
onrad	18	36,513,891	36,520,748	del	Т		CNVR7307.1
onrad	18	40,230,705	40,236,072	del		G	CNVR7312.1
ssers	18	44917833(6)	45160155(8)	del	ТАА		del 16
m irk	18 18	45,948,971 45,948,975	45,952,385 45,952,385	del del	?		37_AK4
orbel	18	46,124,317	46,130,364	del	ſ		NA18505 del 323
rk	18	48,716,563	48,717,029	del	?		38_NA18564
nrad	18	49,390,403	49,391,772	del	СТ		CNVR7336.1
nrad	18	49,459,967	49,464,573	del		GAATAGGTGGCTATCTTCTAGGTGGC-	CNVR7337.1
						TAAACACCT	
rbel	18	50,206,961	50,210,958	del	AGCCA		NA18505_del 325
onrad	18	53,097,735	53,099,715	del	2		CNVR7344.1
irk orbel	18	53,097,735	53,099,716	del	?		39_NA18564
orbei onrad	18 18	56,067,879 61,874,818	56,076,109 61,883,348	del del	agattgc		NA18505_del 324 CNVR7364.1
nrad	18	61,917,853	61,920,186	del	ttgg		CNVR7365.1
rbel	18	63,109,994	63,118,242	del	G		NA18505_del 328
rk	18	72,476,184	72,476,990	del	?		40_NA18552
onrad	18	73,395,986	73,397,148	del	t		CNVR7401.1
onrad	18	75,158,734	75,159,972	del			CNVR7428.1
	19	11,059,401	11,072,587	del	CTCCTGCCTCAGCCTCCCGAGTAGCTGG-		Fig1A
oldman					GACTACAGGCACC		1
oldman	19	11065247(58)	11079476(87)	dup	TTTAGTAGAGA		Fig1B

Goldman Goldman	19 19	11078170(4) 110847(53)85	11085805(9) 11098862(95)	del del	AAAA CCTCAGCCTCCCAAAGTGCTGGGATTACAGGT		Fig2A Fig2C
Goldman	19	11093997(4002)	11098862(95)	del	CTCCT		Fig2B
onrad	19	14,907,392	14,910,477	del	t		CNVR7551.1
eSmith	19	35979321(08)	35981593(606)	del	TGCACTCCAGCCT		
onrad orbel	19 19	39,419,441 46,047,867	39,422,452 46,079,914	del		tctagcatgtctactcagcatgcag	CNVR7620.1 NA15510_del 202
onrad	19	51,314,576	51,320,153	del			CNVR7673.1
ark	19	59,548,033	59,548,601	del	?		41_NA18999
onrad	19	61,558,270	61,561,735	del	а		CNVR7740.1
onrad	20	1,337,143	1,338,817	del	ACA		CNVR7762.1
orbel	20	4,393,321	4,397,531	del	2		NA18505_del 429
im orbel	20 20	7,044,793 14,719,512	7,050,847 14,887,609	del del	GT		NA15510_del 265
onrad	20	14,719,512	14,887,611	del	са		CNVR7793.1
onrad	20	15,249,734	15,251,771	del	TT		CNVR7794.1
im	20	28,122,727	28,149,711	del	?		
onrad	20	36,488,476	36,489,226	del	cc		CNVR7842.1
im onrad	20	42,760,727	42,762,938	del	?		CNIV/D7027.1
orbel	20 21	61,195,144 10,118,922	61,196,043 10,130,309	del del	C		CNVR7927.1 NA18505 del 465
orbel	21	10,118,922	10,130,309	del			NA15510_del 267
onrad	21	15,510,251	15,513,325	del	at		CNVR7956.2
im	21	19,758,801	19,765,198	del	?		
orbel	21	20,722,534	20,767,095	del	A		NA18505_del 463
orbel	21	26,942,867	26,943,597	del	?		NA18505_inv 928
ark onrad	21 21	28,634,908 42,223,191	28,635,998 42,226,560	del del	GAGGAA		42_AK8 CNVR8021.1
onrad	21	43,647,128	43,662,451	dup	TCCCACCCA		CNVR8000
onrad	21	43,794,796	43,797,732	del	GAGA		CNVR8030.1
onrad	21	43,983,814	43,985,302	del	CAGG		CNVR8032.1
onrad	21	44,443,627	44,445,149	del	TGAAC		CNVR8037.1
im oSmith	22	27,963,089	27,965,391	del	?		
eSmith onrad	22 22	32085555(72) 32,110,447	32090063(80) 32,113,338	del	TTTTTTTTTTGAGA	AGAT	CNVR8140 1
onrad Conrad	22	37,624,054	37,628,634	del del	taaa	AGAI	CNVR8140.1 CNVR8163.1
orbel	22	47,355,685	47,366,304	del			NA18505 del 486
'issers	X	18297583(94)	18454991(5002)	del	TTTTGTATTTT		del 21
issers	Х	18360769(71)	18498469(71)	del	TC		del 13
issers	Х	18367759(74)	18442628(43)	del	TCCCAGCTACTCGGG		del 23
damura	X	146,801,147	146,801,336	del	?		Mila
damura damura	X X	146,801,175 146,801,176	146,809,912 146,801,333	del del	?		Quan deGraaff
damura	X	146,801,185	146,801,399	del	?		Petek
damura	X	146,801,187	146,801,332	del	?		deGraaff
damura	Х	146,801,187	146,801,752	del	?		deGraaff
damura	Х	146,801,207	146,801,487	del	?		deVries
damura	X	146,801,208	146,801,486	del	?		deGraaff
damura	X X	146,801,213	146,801,322	del del	?		Snow Mannermaa
damura damura	X	146,801,229 146,801,255	146,801,370 146,801,338	del	r ?		deGraaff
damura	X	146801090/92	146801565/67	del	?		Schmucker
damura	X	146801150/54	146801475/79	del	?		Grasso
damura	Х	146801176+7	146,801,333	del	?		Grasso
damura	Х	146801193/95	146801339/43	del	?		Gronskov
damura	Х	146801195/97	146801395/97	del	?		Fan
mory	X	24,021,195	24,026,627	del	Alu element		AU120.4
mory mory	X X	30,257,687 33,952,914	30,258,519 33,982,773	del del	AG AGGT	Α	AU065.4 AU030.3
mory	X	38,271,449	38,272,275	del	AAAAT	СТ	AU087.5
mory	X	44,264,761	44,266,313	del	Alu element, ~90 bp		AU096.5
mory	Х	58,256,036	58,256,488	del	AGGCATTCTAATGATAGAGACACctgtggtga		AU111.8
mory	Х	64,002,062	64,014,239	del	ACACT		AU122.1
mory	Х	65,381,485	65,415,746	dup	C, pyrimidine track		AU133.7
mory	X	80,303,149	80,304,088	del	ATA		AU030.1
mory mory	X X	82,085,921 87,545,357	82,094,944 87,547,591	del del	GCCTCCC, CAGAG ATTA, AT		AU080.3 AU097.8
mory	X	96,493,413	96,495,398	del	ALIA, AL		AU113.2
mory	X	97,842,279	97,843,597	del	ATT		AU116.6
mory	X	103,289,074	103,289,688	del	ATTGCCCT		AU131.8
mory	Х	103,295,675	103,296,655	del	CATT		AU033.95
mory	X	111,753,107	111,753,796	del	AA, poly T		AU103.3
mory	X X	113,234,594	113,241,627	del	GGC GCT	CTTC	AU145.2
mory mory	X	116,588,176 120,416,100	116,591,267 120,416,999	del del	001	AATCAA	AU149.7 AU038.3
mory	x	122,143,696	122,144,257	del	AG, GT	- ANDAA	AU058.5 AU064.0B
mory	Х	131,767,115	131,769,226	del	GCC		AU082.1
mory	Х	133,692,157	133,693,471	del	AA		AU143.4
mory	Х	143,436,372	143,445,447	del	ATATCC		AU103.29
mory	X	145,207,078	145,208,683	del	ATTT		AU058.3
mory mory	X X	149,678,591 150,457,729	149,679,508 150,462,994	del del	TCTG ~220 nt		AU024.0 AU044.3
mory	x	30,048,859(61)	30,056,096(98)	del	TT		AU150.5
im	X	92,682,955	92,688,161	del	?		
orbel	Х	35,537,365	35,544,320	del	Π		NA18505_del 829
orbel	Х	48,902,127	48,906,009	del			NA15510_inv 564
orbel	X	154,570,791	154,574,920	del	~		NA18505_del 833
obile obile	X X	31,750,900	31,832,080	del	CT CA	GCACATATCTCAGCACATATCAGCACA	Junct 2
obile	X	31,753,361 31,640,226(9)	31,810,985 31762772(5)	del del	GCG	GCACATATCTCAGCACATATCAGCACA	Junct 3 Junct 5
obile	x	31,752,508(10)	31,823,801(4)	del	AGC		Junct 1
loodward	X	102,082,641	103,009,563	dup	?		P026
loodward	X	102,259,865	106,837,041	dup	?		P110
loodward	Х	102,362,654	103,127,653	dup	?		PMD9
/oodward	Х	102,435,939	102,945,236	dup	?		P116
loodward	X	102,490,121	103,444,951	dup	?		P114
loodward	X	102,491,424	103,296,881	dup	?		PMD24
loodward loodward	X X	102,537,145 102,602,533	103,011,041 102,994,508	dup dup	?		P134 P224
loodward loodward	X	102,682,198	102,994,508	dup dup	?		P224 P176/PMD7
/oodward	X	102,816,004	102,992,894	dup	?		P015
Voodward	Х	102,830,045	103,110,073	dup	?		P255
Voodward		102,831,298	102,942,004	dup	?		P348

Table A.6.a – Truly called CNV by the NimbleGen and Optimized protocols.

ARRAY_ID	Sample	CHR	START	STOP	SIZE(bp)	Probes	Probes/kb	Mean_Log2	GC	Primer	Platform
AU0780301.1s1A01	AU0780301	chrX	8,746,518	8,746,898	380	8	21.1	-1.68	43.6	AU008.7	NG
AU1038303.1s1A02	AU1038303	chrX	103,295,654	103,296,615	961	15	15.6	-1.35	40.5	AU103.3	NG
AU021503.1s1A03	AU021503	chrX	133,692,426	133,693,396	970	21	21.6	-0.86	43.7	AU133.7	NG
AU004803.1s1A03	AU004803	chrX	113,234,646	113,241,227	6,581	122	18.5	-0.83	37.8	AU113.2	NG
AU016803.1s1A01	AU016803	chrX	19,376,031	19,378,453	2,422	47	19.4	-0.82	40.6	AU019.38	NG
AU080803.1s1A01	AU080803	chrX	30,054,252	30,055,680	1,428	30	21.0	-0.81	37.6	AU030.1	NG
AU0875302.1s2A03	AU0875302	chrX	131,766,925	131,769,270	2,345	47	20.0	-0.79	41.7	AU131.8	NG
AU083504.1s1A02	AU083504	chrX	96,493,478	96,493,778	300	7	23.3	-0.74	41.3	AU096.5	NG
AU083504.1s1A03	AU083504	chrX	122,143,410	122,144,175	765	17	22.2	-0.73	39.8	AU122.1	NG
AU018003.1s1A01	AU018003	chrX	19,375,946	19,378,453	2,507	49	19.5	-0.72	40.7	AU019.38	NG
AU1038303.1s1A03	AU1038303	chrX	149,678,535	149,679,545	1,010	21	20.8	-0.71	55.3	AU149.7	NG
AU050703.1s1A03	AU050703	chrX	122,778,733	122,780,189	1,456	23	15.8	-0.70	46.3	AU122.78	NG
AU055303.1s1A03	AU055303	chrX	149,678,535	149,679,480	945	20	21.2	-0.67	55.2	AU149.7	NG
AU083504.1s1A03	AU083504		154,047,451	154,056,710	9,259	152	16.4	-0.64	34.4	AU154.0A	NG
AU083504.1s1A02	AU083504	chrX	58,256,031	58,256,531	500	11	22.0	-0.59	46.1	AU058.3	NG
AU056003.1s1A03	AU056003		149,678,510	149,679,625	1,115	24	21.5	-0.58	55.4	AU149.7	NG
AU1038303.1s1A02	AU1038303	chrX	· · · · · · · · · · · · · · · · · · ·	82,094,944	8,447	91	10.8	-0.53	39.0	AU082.1	NG
AU0852304.1s1A01	AU0852304	chrX		44,265,881	460	11	23.9	-0.52	36.7	AU044.3	NG
AU065404.1s1A01	AU065404	chrX		33,980,127	27,121	482	17.8	-0.52	35.0	AU033.95	NG
AU056003.1s1A01	AU056003	chrX	8,746,203	8,749,728	3,525	63	17.9	-0.26	37.9	AU008.7	NG
AU016803.1s1A02	AU016803	chrX		65,399,668	17,112	328	19.2	0.39	38.4	AU065.4	NG
AU0920301.1s1A02	AU0920301	chrX	57,617,045	57,634,875	17,830	262	14.7	0.40	43.0	AU057.6	NG
AU0852304-A03-2s1	AU0852304	chrX	116,588,255	116,590,742	2,487	44	17.7	-1.64	38.6	AU116.6	Opt
AU1038303-A02-2s1		chrX	103,295,654	103,296,645	991	16	16.1	-1.40	40.9	AU103.3	Opt
AU083504-A02-3s1	AU083504	chrX	58,256,056	58,256,496	440	8	18.2	-1.33	46.8	AU058.3	Opt
AU0852304-A01-2s1		chrX	44,264,996	44,266,216	1,220	20	16.4	-1.31	41.6	AU044.3	Opt
AU020003-A02-2s1	AU020003	chrX	70,039,948	70,040,318	370	9	24.3	-1.18	37.0	AU070.0	Opt
AU028903-A03-2s1	AU028903	chrX	149,678,535	149,679,160	625	11	17.6	-1.15	55.5	AU149.7	Opt
AU065404-A01-2s1	AU065404	chrX	33,952,911	33,982,646	29,735	497	16.7	-1.06	35.4	AU033.95	Opt
AU1038303-A02-2s1		chrX	82,086,031	82,094,874	8,843	92	10.4	-1.04	39.0	AU082.1	Opt
AU021503-A03-2s1	AU021503	chrX	133,692,526	133,693,326	800	17	21.3	-0.98	43.3	AU133.7	Opt
AU0920301-A03-2s1	AU0920301	chrX	135,126,873	135,129,790	2,917	47	16.1	-0.97	43.6	AU135.1	Opt
AU0852304-A02-2s1		chrX	87,546,283	87,547,547	1,264	12	9.5	-0.95	36.0	AU0135.1	Opt
AU0920301-A03-2s1	AU0920301	chrX	131,766,925	131,768,880	1,204	25	12.8	-0.89	42.2	AU131.8	Opt
AU0852304-A03-2s1		chrX	145,207,069	145,208,670	1,601	22	13.7	-0.85	44.8	AU145.2	Opt
AU083504-A03-3s1	AU083504	chrX	122,143,675	122,144,235	560	11	19.6	-0.77	41.1	AU143.2	Opt
AU056803-A01-2s1	AU056803	chrX	24,022,009	24,026,159	4,150	41	9.9	-0.74	39.0	AU0122.1 AU024.0	Opt
AU016803-A01-2s1	AU016803	chrX	19,375,516	19,379,418	3,902	41	10.5	-0.74	42.3	AU019.38	Opt
AU004803-A01-251	AU010803	chrX	8,746,458	8,748,798	2,340	27	10.5	-0.73	35.3	AU019.38 AU008.7	Opt
AU083504-A02-3s1	AU083504	chrX	96,493,478		1,719	27	11.5	-0.73	37.2	AU008.7 AU096.5	Opt
				96,495,197		122	15.1	-0.73	36.0		· · · · · · · · · · · · · · · · · · ·
AU080803-A01-2s1 AU083504-A03-3s1	AU080803 AU083504	chrX chrX	30,048,831	30,055,680	6,849 9,494	122	17.8	-0.71	36.0	AU030.1 AU154.0A	Opt Opt
			154,047,946	154,057,440		147					· · · · · · · · · · · · · · · · · · ·
AU062203-A03-2s1	AU062203	chrX	143,436,794	143,445,418	8,624	125	14.5	-0.65	38.2 53.9	AU143.4	Opt
AU055303-A03-2s1	AU055303	chrX	149,678,535	149,680,094	1,559		12.2	-0.52		AU149.7	Opt
AU004803-A03-3s1	AU004803	chrX	113,234,686	113,241,182	6,496	94	14.5	-0.40	38.1	AU113.2	Opt
AU0920301-A02-2s1	AU0920301	chrX	57,615,600	57,960,046	344,446	3789	11.0	0.47	38.6	AU057.6	Opt
AU016803-A02-2s1	AU016803	chrX	65,382,441	65,415,702	33,261	530	15.9	0.51	38.9	AU065.4	Opt
AU0920301-A02-2s1	AU0920301	chrX	105,379,514	105,381,047	1,533	28	18.3	0.64	37.8	AU105.4	Opt

Table A.6.b – Falsely cal	lled CNV by the Nin	nbleGen and Or	ptimized i	protocols.

ARRAY_ID	Sample	CHR	START	STOP			Probes/kb			Primer Set	CGH_Protoc
AU021503.1s1A02	AU021503	chrX	67,045,887	67,046,967	1,080	23	21.3	-0.85	41.2	AU067.0	NG
AU028903.1s1A02	AU028903	chrX		53,102,747	2,230	47	21.1	-0.63	47.6	AU053.10	NG
AU055503.1s1A02	AU055503	chrX	48,530,197	48,531,062	865	19	22.0	-0.62	47.9	AU048.5/AU048.533	NG
AU028903.1s1A02	AU028903	chrX	48,995,264	48,996,414	1,150	25	21.7	-0.60	52.7	AU048.995	NG
AU018003.1s1A02	AU018003	chrX	67,044,882	67,046,967	2,085	44	21.1	-0.60	39.0	AU067.0	NG
AU028903.1s1A02	AU028903	chrX	48,530,120	48,531,142	1,022	22	21.5	-0.56	48.3	AU048.5/AU048.533	NG
AU055503.1s1A02	AU055503	chrX	48,995,294	48,996,304	1,010	22	21.8	-0.55	52.3	AU048.995	NG
AU058103.1s1A02	AU058103	chrX	48,530,197	48,531,087	890	20	22.5	-0.55	48.1	AU048.5/AU048.533	NG
AU058503.1s1A02	AU058503	chrX	48,530,197	48,531,062	865	19	22.0	-0.52	47.9	AU048.5/AU048.533	NG
AU058103.1s1A02	AU058103	chrX	48,995,364	48,996,304	940	21	22.3	-0.50	52.1	AU048.995	NG
AU018003.1s1A02	AU018003	chrX	48,530,197	48,531,062	865	19	22.0	-0.49	47.9	AU048.5/AU048.533	NG
AU028903.1s1A02	AU028903		139,623,380	139,624,140	760	16	21.1	-0.49	49.9	AU139.6A	NG
AU018003.1s1A02	AU018003	chrX		48,996,284	845	18	21.3	-0.47	52.5	AU048.995	NG
AU002403.1s2A03	AU0010003		143,163,522		12,400	211	17.0	-0.45	36.2	AU143.2	NG
AU028903.1s2A03				143,175,922							
	AU028903	chrX	48,276,384	48,278,284	1,900	39	20.5	-0.45	51.1	AU048.28	NG
AU0852304.1s1A03	AU0852304		129,713,932	129,715,267	1,335	27	20.2	-0.44	44.0	AU129.7	NG
AU021503.1s1A02	AU021503	chrX	53,126,892	53,127,752	860	17	19.8	-0.43	61.1	AU053.127	NG
AU021503.1s1A02	AU021503	chrX		48,531,062	845	18	21.3	-0.42	47.6	AU048.5/AU048.533	NG
AU028903.1s1A02	AU028903	chrX	48,220,021	48,221,221	1,200	26	21.7	-0.42	46.3	FTSJ1	NG
AU055503.1s1A02	AU055503	chrX	48,220,021	48,221,146	1,125	25	22.2	-0.41	45.6	FTSJ1	NG
AU058103.1s1A02	AU058103	chrX	48,219,896	48,221,146	1,250	27	21.6	-0.40	47.2	FTSJ1	NG
AU028903.1s1A03	AU028903	chrX	135,941,581	135,942,831	1,250	27	21.6	-0.39	52.1	AU135.94	NG
AU018003.1s1A03	AU018003		129,711,252	129,714,877	3,625	68	18.8	-0.37	41.1	AU129.7	NG
AU056003.1s1A03	AU056003		133,346,142	133,350,722	4,580	83	18.1	-0.37	39.9	AU133.3	NG
AU0780301.1s1A02	AU0780301	chrX	48,530,217	48,531,087	870	19	21.8	-0.37	47.8	AU048.5/AU048.533	NG
AU058103.1s1A03	AU058103		129,711,442	129,715,287	3,845	73	19.0	-0.35	41.3	AU129.7	NG
AU056803.1s1A03	AU056803		129,711,402	129,715,172	3,770	71	18.8	-0.33	41.3	AU129.7	NG
AU014803.1s1A02	AU036803 AU014803		48,530,197	48,531,062	865	19	22.0	-0.33	41.5	AU129.7 AU048.5/AU048.533	NG
AU014803.151A02 AU028903.1s1A03	AU014803 AU028903	chrX	129,711,302		3,895	74	19.0	-0.33	47.9	AU048.5/AU048.533 AU129.7	NG
				129,715,197							
AU058503.1s1A02	AU058503	chrX	53,100,517	53,107,369	6,852	89	13.0	-0.29	46.2	AU053.10	NG
AU056003.1s1A02	AU056003	chrX	48,276,454	48,278,944	2,490	44	17.7	0.28	50.2	AU048.28	NG
AU021503.1s1A03	AU021503		114,330,510	114,333,265	2,755	57	20.7	0.31	65.6	AU114.3	NG
AU065404.1s1A03	AU065404	chrX	114,330,245	114,333,513	3,268	68	20.8	0.33	64.3	AU114.3	NG
AU056003.1s1A02	AU056003	chrX	53,100,517	53,102,557	2,040	43	21.1	0.33	48.3	AU053.10	NG
AU058103.1s1A01	AU058103	chrX	20,194,030	20,194,994	964	20	20.7	0.34	72.6	AU020.2	NG
AU0920301.1s1A02	AU0920301	chrX	53,099,892	53,102,717	2,825	53	18.8	0.36	48.1	AU053.10	NG
AU080803.1s1A03	AU080803	chrX	114,331,350	114,333,225	1,875	39	20.8	0.38	65.1	AU114.3	NG
AU067803.1s2A02	AU067803	chrX	69,201,942	69,203,705	1,763	38	21.6	0.39	58.6	AU069.2	NG
AU008504.1s1A02	AU008504	chrX	53,100,432	53,102,672	2,240	47	21.0	0.42	48.1	AU053.10	NG
AU018003.1s1A03	AU018003		114,331,470	114,333,225	1,755	36	20.5	0.47	65.1	AU114.3	NG
		-	,,	,,	,						
AU002403-A03-2s1	AU002403	chrX	143,165,878	143,166,968	178,000	23	21.1	-1.01	49.9	AU143.2	Opt
AU004803-A02-3s1	AU004803	chrX	53,127,122	53,127,609	487	8	16.4	-0.99	68.0	AU053.127	Opt
AU0920301-A02-2s1	AU0920301	chrX	67,761,197	67,761,872	675	9	13.3	-0.75	28.9	AU067.76	Opt
AU028903-A03-2s1	AU028903	chrX	148,992,605	148,992,915	310	8	25.8	-0.74	30.3	AU148.99	Opt
AU018003-A02-2s1	AU018003	chrX	67,045,802	67,046,892	1,090	19	17.4	-0.74	41.8	AU067.0	Opt
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AU014803-A02-2s1	AU014803	chrX	67,040,517	67,046,967	6,450	84	13.0	-0.48	38.7	AU067.0	Opt
AU083504-A03-3s1	AU083504	chrX	122,920,791	122,923,535	2,744	52	19.0	0.34	59.2	AU122.9	Opt
AU008504-A02-2s1	AU008504	chrX	53,099,962	53,102,472	2,510	45	17.9	0.35	49.2	AU053.10	Opt
AU083603-A01-2s1	AU083603	chrX	19,300,606	19,302,311	1,705	34	19.9	0.37	61.6	AU019.3	Opt
AU014803-A02-2s1	AU014803	chrX	48,208,660	48,211,205	2,545	54	21.2	0.39	58.9	AU048.21	Opt
AU014803-A02-2s1	AU014803	chrX	69,202,022	69,205,124	3,102	64	20.6	0.39	58.6	AU069.2	Opt
AU055503-A02-2s1	AU055503	chrX	69,588,687	69,592,509	3,822	75	19.6	0.39	59.0	AU069.6	Opt
AU028903-A03-2s1	AU028903	chrX	135,940,186	135,941,906	1,720	36	20.9	0.41	58.4	AU135.94	Opt
AU1069302-A02-2s1	AU1069302	chrX	73,672,126	73,674,216	2,090	43	20.6	0.42	61.6	AU073.7	Opt
AU1038303-A01-2s1		chrX	41,077,342	41,079,467	2,125	40	18.8	0.43	63.4	AU041.1	Opt
AU1069302-A01-2s1	AU1069302	chrX	34,870,749	34,871,874	1,125	18	16.0	0.43	60.8	AU034.9	Opt
AU065404-A03-2s1	AU065404	chrX	114,331,095	114,333,305	2,210	44	19.9	0.44	65.2	AU114.3	Opt
AU018304-A01-2s1	AU018304	chrX	20,193,739	20,196,889	3,150	64	20.3	0.44	65.2	AU020.2	Opt
AU018304-A01-2s1	AU018304	chrX	117,133,965	117,135,095	1,130	24	20.3	0.43	65.0	AU020.2 AU117.1	Opt
AU018304-A03-251 AU067803-A02-2s1							21.2				
	AU067803	chrX	69,201,902	69,205,364	3,462	72		0.48	57.9	AU069.2	Opt
AU056803-A01-2s1	AU056803	chrX	20,193,659	20,197,128	3,469	71	20.5	0.48	63.0	AU020.2	Opt
AU018003-A01-2s1	AU018003	chrX	20,194,318	20,194,994	676	13	19.2	0.48	73.4	AU020.2	Opt
AU056803-A02-2s1	AU056803	chrX	52,966,038	52,967,318	1,280	22	17.2	0.50	60.5	AU052.97	Opt
AU1069302-A03-2s1	AU1069302	chrX	111,970,302	111,971,424	1,122	24	21.4	0.50	63.8	AU111.97	Opt
AU0920301-A02-2s1	AU0920301	chrX	69,202,002	69,204,994	2,992	62	20.7	0.51	58.4	AU069.2	Opt
U1069302-A01-2s1	AU1069302	chrX	20,193,474	20,194,599	1,125	25	22.2	0.53	61.2	AU020.2	Opt
U1069302-A03-2s1	AU1069302	chrX	114,331,010	114,333,350	2,340	47	20.1	0.54	65.0	AU114.3	Opt
AU1038303-A02-2s1			69,202,132	69,204,769	2,637	55	20.9	0.57	58.8	AU069.2	Opt
U0920301-A03-2s1	AU0920301	chrX	114,331,445	114,333,225	1,780	35	19.7	0.59	65.7	AU114.3	Opt
U0852304-A03-2s1			114,331,095	114,333,225	2,130	42	19.7	0.59	65.1	AU114.3	Opt
AU055303-A03-2s1	AU055303	chrX		135,820,148		11		0.59			
			135,819,673		475		23.2		57.1	AU135.82	Opt
AU0852304-A01-2s1			36,936,957	36,938,657	1,700	20	11.8	0.69	63.0	AU036.93	Opt
AU018304-A03-2s1	AU018304	chrX	133,757,887	133,758,510	623	14	22.5	0.73	60.5	AU133.8	Opt
AU056003-A02-2s1	AU056003	chrX	48,533,289	48,534,370	1,081	17	15.7	0.74	53.7	AU048.533	Opt
AU056003-A03-2s1	AU056003	chrX	128,964,095	128,964,615	520	12	23.1	0.98	55.6	AU128.96	Opt
AU018003-A03-2s2	AU018003	chrX	114,331,010	114,333,265	2,255	45	20.0	0.39	65.0	AU114.3	Opt