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Abstract

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Background: The placenta is the primary means by which fetal growth and development is regulated during pregnancy. Heavy metal exposure has been found to have explicit effects on infant birth weight – among other developmental outcomes – with placental dysfunction potentially playing a role in these effects. LincRNAs expression specific to the placenta may be a possible mediator of this exposure-outcome pathway.

Objectives: Assess the biological plausibility of lincRNA expression within the placenta mediating the effects of maternal exposure to cadmium, mercury and lead on birth weight outcomes.

Methods: Using linear and logistic modeling of lincRNA transcriptional expression in the placenta relative to birth weight, standardized birth weight categories and placental metal concentrations, we assessed associations with lincRNA expression in a subset of the Rhode Island Child Health Study (n = 199) with full RNA-sequencing data and metal-expression and metal-birth weight trends within a portion of this population with placental trace metal data available (n = 85).

Results: Of the 1198 lincRNA transcripts sequenced, 46 demonstrated FDR-significant ($q<0.05$) associations with birth weight when controlling for infant sex and maternal age, BMI, education level, and smoking during pregnancy. Further, we identified 4 of these transcripts associated with placental Cd concentrations, 13 with placental Hg, and 1 with placental Pb, with the majority demonstrating moderate increases in transcript expression with increasing exposure. Finally, logistic regression of transcript levels against large (LGA) and small (SGA) for gestational age birth categories yielded 11 and 19 significant associations, respectively, among the same 46 transcripts; SGA outcomes were also significantly associated with increasing placental cadmium concentrations within the cohort.

Conclusions: In this birth cohort study, we examined the relationship between LincRNA expression and both placental metal concentrations and birth weight (continuous and categorized), finding that differences in metal concentrations were associated with specific lincRNA expression variation, and that those transcripts also significantly associated with birth weight. Our research findings in regards to metal exposure and birth weight were consistent with the literature, and these results present the possibility of lincRNAs mediating causal pathways from these exposures to developmental outcomes.

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1. Introduction

Increasing scientific understanding of the intrauterine environment has highlighted the importance of prenatal conditions in development and lifelong health (Barker, 1995; De Boo & Harding, 2006). While the intrauterine environment is physically isolated from external conditions, maternal exposures, particularly trace metals such as lead, mercury and cadmium, have been explicitly linked to negative fetal newborn and infant health outcomes (Rahbar et al., 2015). The hazard of metals in both developed and undeveloped regions is extremely high, as they are incorporated into daily exposures through a number of explicit and multiple less obvious pathways. Exposure to lead can arise from leaded paint, contaminated soil and particulate matter, dissolved ions from lead piping, industrial emissions or occupational exposures (Tong et al., 2000). Prior to 1980, one of the primary sources of lead exposure in the United States was inhaled lead from use of leaded gasoline in motor vehicles, though blood lead levels have steadily declined since legislation banning lead paint was passed in 1976 and an amendment to the Clean Air Act banning leaded gasoline was put into place in 1990. Mercury exposure occurs primarily through ingestion of fish that have accumulated methyl mercury through contamination of the food chain (Bjornberg et al., 2003). Sources of environmental mercury contamination include industrial or utility facilities whose metal wastes infiltrate fresh and saltwater ecosystems as well as coal-burning power plants (Trasande et al., 2005). Dental amalgams, which utilize an alloy of silver, tin, copper and up to 50% inorganic mercury, are another possible source of maternal mercury exposure (Sanchez-Martin et al., 2000). Cadmium exposure can occur from contact with air and dust contaminated by industrial pollution, phosphate fertilizers, gasoline and diesel combustion and particles released by tire wear (Pan et al., 2010; Sanchez-Martin et al., 2000); the highest levels of exposure, however, result from tobacco smoking and dietary consumption of certain varieties of contaminated mushrooms and shellfish, liver, and plant products (Satarug et al., 2010). Specific trace metals such as copper, iron, zinc, manganese and selenium are essential to proper biologic function, whether by acting as cofactors, expression regulators or signaling factors, but imbalance of these metals or infiltration of toxic metals into maternal or neonatal systems can disrupt homeostasis and result in long term developmental, neurodegenerative in a developing fetus (Mounicou et al., 2009; Punshon et al., 2016).

1.1 Trace Metals and Neonatal Health

Trace metals such as lead, mercury and cadmium have numerous toxic effects on human health. Metal exposures display a broad range of systemic effects on immune (Colombo et al., 2004), neurological (Geier & Geier, 2007; Grandjean & Landrigan, 2006; Rice & Barone, 2000; Rodier, 1995), renal (Reyes et al., 2013), and reproductive health (Caserta et al., 2008; Caserta et al., 2011; Caserta et al., 2013). Lead and cadmium are implicated in oxidative cell stress (Caserta et al., 2011; Reyes et al., 2013) and impaired calcium metabolism (Bhattacharyya, 2009), while both cadmium and mercury can interfere with use of essential elements or their availability to the fetus during via the placenta during pregnancy (Osman et al., 2000). Some metals associated health effects are potentially due to endocrine disruption, with cadmium being a likely candidate (Ribas-Fito et al., 2006). Finally, lead and mercury are explicitly implicated in both adult and child neurological damage, with neonatal exposure particularly developmentally dangerous (Baranowska-Bosiacka et al., 2012; Farina et al., 2011).

Neurotoxicity in the womb is among the most pressing threats to child health, notably because it is widely linked to commonly encountered metals. The most direct route of neurotoxicity is for the metal to directly cross the fetal blood brain barrier (BBB), though not all trace metals can initially cross the placenta to the fetus nor pass through the developing safeguards of the fetal brain (Saunders et al., 2012). Specific metals such as lead and mercury, however, are known to affect BBB permeability (Sharma et al., 2014) and disrupt brain function. Interruption of neuronal development by these two metals are directly associated with mental deficits in childhood, lowered IQ , and subclinical brain disorders (Caserta et al., 2013). For lead, even small blood concentrations – as little as 10 μg/dL according to Bellinger (2008) – have been found to result in reduced IQ, fine-motor control, attention span and academic achievement. Mercury displays similarly detrimental neuronal effects (Axelrad et al., 2007). Despite cadmium's inability to cross the placenta, the metal has also been linked to neurodevelopmental outcomes (Tian et al., 2009); because it has little direct access to the BBB or the brain itself, these neurological outcomes are likely indirectly due to other effects cadmium is known to have on fetal development (Bhattacharyya, 1983) and potentially include alterations to placental function (Everson et al., 2017, 2016). Though the brain continues to develop well after birth, damage to fetal anatomical structures has global developmental effects that are unlikely to be overcome in an individual's lifetime (Rice & Barone, 2000; Rodier, 1995).

Beyond their effects on the nervous system, lead, mercury and cadmium have also been linked to numerous other developmental outcomes. Immediate effects of acute exposures to these metals include spontaneous abortion, stillbirth, low birth weight, preterm birth, reduced fetal growth, impaired neurodevelopment, and congenital malformation (Bellinger, 2005; Kim et al., 2013; Yu et al., 2011). Most exposures to these compounds occur gradually, yet even chronic exposure over the course of nine months can have subtle, yet detrimental effects on the unborn child's health. Rahbar et al. (2015) found cord blood lead concentration to be significantly inversely proportional to head circumference in a Jamaican birth cohort examined for trace metal exposures, and noted that cord blood lead levels have also been associated with changes to birth weight, a key indicator of infant health and development (Bellinger, 2005; Zhang et al., 2004). Mercury's link between cord blood concentrations and birth weight are not quite as firm, with conflicting results for (Foldspang & Hansen, 1990; Sikorski et al., 1986) and against (Grandjean et al., 2001; Lucas et al., 2004) an inverse association between concentration and birth weight. Evidence demonstrating cadmium's distinct potential for decreasing size and birth weight of infants has been found in multiple studies despite cadmium's relative inability to cross the placenta (Gardner et al., 2013; Johnston et al., 2014). Some of the most compelling proof of this was found in a study of non-smoking, healthy women that found cord blood cadmium concentrations were associated with decreased birth weight in their newborns (Salpietro et al., 2002). In absence of primary exposure to cadmium through smoking, fetal development was still affected by the presence of cadmium, demonstrating the importance of cadmium's placental interaction in determining child birth weight.

1.2 The Placenta

The importance of the placenta's role in pregnancy and fetal development cannot be overstated. Representing the interface between the mother and the fetus, the placenta performs the functions of numerous organs for the developing child, including the lung, liver, gastrointestinal tract, kidney and endocrine organs (Burton & Jauniaux, 2015). These critical functions make proper development of the placenta central to fetal health. For example, the hepatic functions of the placenta include disposing of toxic waste materials, expressing protein complexes that efflux potentially dangerous exogenous compounds, and blocking some exposures outright from entering fetal blood in order to maintain a proper growth environment for the fetus (Osman et al., 2000). This occurs simultaneous to necessary nutrients being allowed to pass to the fetal bloodstream (Punshon et al., 2016). Stresses to the intrauterine environment from various sources can alter placental vascularization, growth, transport activity, metabolism and hormone production, consequently impacting the long term development of the fetus (Burton et al., 2016; Jansson & Powell, 2007). Fetal growth restriction (undergrowth) and macrosomia (overgrowth) are commonly reported outcomes linked to placental dysfunction, and children with these conditions are at elevated risk for postnatal morbidities, everything from metabolic syndrome to impaired neurobehavioral and cognitive development (Colman et al., 2012; Grissom & Reyes, 2013; Moore et al., 2012; Van Lieshout & Boyle, 2011)

Trace metals represent either necessary nutrients or dangerous toxicants in placental and fetal development (Gundacker & Hengstschläger, 2012). The placenta actively transports essential elements such as calcium, copper, zinc, and iron to the fetus (Iyengar & Rapp, 2001), yet lead was found to easily cross the placenta via passive diffusion (Goyer, 1990) and organic mercury infiltrates fetal blood by passive transport and amino- acid carriers (Ask et al., 2002). In contrast, cadmium is largely sequestered to the placenta by an uptick in the placental protein metallothionein (Kippler et al., 2010; McAleer & Tuan, 2001), which serves to bind cadmium and limit its access to the fetal bloodstream. However, an increase in metallothionein alters zinc transport across the placenta (Yoshida et al., 2011), posing a threat to the proper development of the fetus in absence of adequate zinc levels. This demonstrates one instance in which adjustment for the presence of exogenous toxicants disrupts the function of the placenta (Osman et al., 2000), and the widespread potential for metal exposures points to numerous threats to fetal development. Conversely, Punshon et al. (2016) found an inverse correlation showing higher maternal concentrations of essential nutrients with lower toxicant metal accumulation, findings supported by Laine et al. (2015). The exact mechanism behind these effects remains unknown however, thus requiring additional investigation of factors regulating placental function and facilitating safe – or aberrant – fetal development.

1.3 Long Non-coding RNAs

Long Non-coding RNAs (lncRNAs) are an emerging field of study that owes much of its recent attention to the advent of new high-throughput sequencing technologies. This new technology led to the discovery that lncRNAs are not simply transcriptional by-products but rather actively synthesized and regulated RNA transcripts that play cellular roles in homeostasis and pathogenesis (Chen & Conn, 2017). Guttman et al. (2009) discovered histone H3 subunits whose K4 and K36 amino acids were trimethylated – hallmarks of active gene regions – in seemingly non-coding regions; 1,600 intergenic, spliced non-coding transcripts were found that displayed coordinated regulation, more than could be argued as transcriptional noise, a previous theory for any seemingly errant transcription of non-coding RNA. Prior to the last ten years, one of the only known examples of active lncRNA was XIST, an RNA transcript implicated in the dosage inactivation of one of the two X chromosome in female cells (Brown et al., 1991, 1992; Heard et al., 1999; Migeon et al., 1999), but now over 100,000 lncRNAs have been described for humans alone (Volders et al., 2015).

Knowledge of lncRNAs is evolving, but we do understand a number of broad trends in terms of their properties and functions. In general, lncRNA transcripts measure greater than 200nt with a median size of 500nt (Mattick & Rinn, 2015), generally smaller than mRNAs. Around 98% are spliced, with 80% having 2-4 exons, and are polyadenylated like some mRNAs, though most show a relative absence of open reading frames greater than 100nt (Guttman et al., 2013). LncRNAs are far more tissue-specific and expressed at lower levels than mRNAs (Cabili et al., 2015; Cabili et al., 2011; Hezroni et al., 2015), though this relationship is still being investigated in various tissue types. The functional capabilities of lncRNA as they are understood are vast, and there is little evidence that lncRNAs broadly act through similar structures (Ulitsky, 2016). In fact, lncRNAs also divide into a number of different subclasses primarily based upon their transcriptional locations within the genome and structure. These classes include intronic lncRNAs, appropriately located within introns of genes and often found to be circular in shape, sense/antisense lncRNAs transcribed from combinations of coding and non-coding regions of genes, and intergenic lncRNAs (LincRNAs), transcripts derived from regions between genes (Ma et al., 2013). Regardless of their structural composition, some lncRNAs bind writers, erasers, and readers of histone modifications, as well as other chromatin regulatory factors (Guttman et al., 2011), and it is known lncRNAs like NEAT1 can assemble with protein complexes at their sites of transcription (Mao et al., 2011), allowing for alternate forms of gene regulation. This list of functions also includes cell-cycle regulation, apoptosis, and establishment of cell identity (Pauli et al., 2011; Ponting et al., 2009), pointing to potential for disease in cases of aberrant expression.

Dysregulation of lncRNAs has been linked to diseases from cancer to immune and neurological disorders (Bhan & Mandal, 2014; Gibb, Brown, & Lam, 2011; Mitra, Mitra, &

Triche, 2012), but these RNA transcripts have also been found to be relevant to developmental function. Whether cardiovascular regulation by Braveheart (Klattenhoff et al., 2013) or neurogenesis controlled by Pnky (Ramos et al., 2015), developmental processes are frequently regulated by lncRNAs, and the placenta is not excluded from this regulation. Data presented by Gao et al. (2012) and Keniry et al. (2012) implicate the lncRNA H19 in placenta formation, specifically as a source of miR-675, a miRNA that directly down-regulates NOMO1 (Nodal modulator 1). This miRNA inhibits NOMO1's ability to stimulate proliferation human trophoblasts. In normal placentae, H19 and its miR-675 repress NOMO1-mediated proliferation, but this pathway is repressed in preeclamptic placentas, causing placental overgrowth. Van Dijk et al. (2012) found that accumulation of HELLP lncRNA rescued the effects of "HELLP" syndrome, characterized by hemolysis, elevated liver enzymes and low platelets, in placental trophoblasts – due to knockdown of the HELLP gene region. Additionally, intrauterine growth restriction (IUGR) was found by Gremlich et al. (2014) to be associated with fourfold enrichment in NEAT1, an lncRNA present in nuclear paraspeckles (Clemson et al., 2009), though the temporality of this association remains unclear.

Relatively few studies to date have focused exclusively on placental expression of lncRNAs, and few to none specifically on placental lncRNA expression in relation to various exposures. However, numerous associations between lncRNAs and placental cellular regulation and pregnancy or developmental pathogenesis have been examined that are worth highlight. H19, mentioned above, has a critical reciprocal relationship with the Insulin-like Growth Factor 2 (IGF2) protein; while H19 suppresses fetal and placental development (Gao et al., 2012; Keniry et al., 2012; Tycko & Morison, 2002), IGF2 was proposed by DeChiara et al. (1991) to promote the opposite. The complex has been associated with fetal and placental growth, trophoblast migration/invasion, Intrauterine Growth Restriction (IUGR) and birth weight (Constancia et al., 2002; Fowden, Sibley, Reik, & Constancial, 2006; Petry et al., 2005, 2011; Zuckerwise et al., 2016), and altered imprinting of chromosome 11p15 – the location of these two genes – is related to growth disorders, such as Beckwith-Wiedeman and Silver-Russel syndrome (Bartholdi et al., 2009; Weksberg et al., 2003). Decreased H19 and increased IGF2 expression have also been observed in relation to gestational diabetes (Su et al., 2016), with the opposite true when comparing placental expression in women with and without assistive reproductive technology (Sakian et al., 2015). Misregulation of each of the lncRNAs LOC391533, LOC284100, CEACAMP8 (He et al., 2013), SPRY4-IT1 (Zou et al., 2013), and MALAT1 (H. Chen et al., 2015) is linked to potential mechanisms underlying preeclampsia. MALAT1 specifically promotes expression of specific genes and cell migration (Tano et al., 2010), where experimental knockdown was found to inhibit trophoblast-like cell invasion *in vitro* (Tseng et al., 2009). Additional lncRNAs, including Air (Lyle et al., 2000; Sleutels, Zwart, & Barlow, 2002; Wutz et al., 1997; Yotova et al., 2008), Kcnq1ot1 (Kanduri, 2011; Mohammad et al., 2010), UCA1 (F. Wang et al., 2008; X.S. Wang et al., 2006), Hoxa11as (Potter & Branford, 1998; Sasaki et al., 2007; Sessa et al., 2007), HOTTIP (Sasaki et al., 2007a, 2007b; Wang et al., 2011), HOXA6as (Sasaki et al., 2007a, 2007b), DIO3OS, (Hernandez et al., 2004), and SAF (Yan et al., 2005) have been found within human placental – and possibly fetal – tissues, with various regulatory roles involved in fetal development. The intimate involvement of these lncRNAs with conditions that endanger maternal and fetal health warrants further investigation of regulators of lncRNA expression, whether endogenous or exogenous.

1.4 Study Objective

Numerous toxic metals have been found to have effects on both placental function and fetal development, with large health and economic consequences around the world. The placenta is an essential organ in the process of fetal growth, and alterations to its function are linked to potentially dire consequences. LincRNAs, a subtype of lncRNAs known as long intergenic non-coding RNAs and the focus of this study, are one possible source of these changes within the placenta, and a great deal of research has gone into identifying and characterizing new transcripts and their native tissues. However, there has been little to no investigation of the factors that regulate lincRNA expression specifically, particularly in terms of exposure to exogenous toxicants and whether these compounds can induce changes in lincRNA locality or transcription. This study will first seek to examine the relationship between lincRNA expression levels and infant birth weight, assessing directionality in these associations and highlighting individual transcripts for further analysis. Birth weight analysis will be followed by testing the relationship between maternal exposure to heavy metals and expression variation in placental lincRNAs. These exposures will be analyzed separately to address specific lead, mercury and cadmium exposures. The implications of any changes found will be examined in relation to newborn growth outcomes – specifically birth weight categories, in order to determine if variation in lincRNA expression may be related to more clinically meaningful extremes of birth weight. These analyses will be performed in a birth cohort drawn from the Rhode Island Child Health Study (Deyssenroth et al., 2017). Use of linear modeling of transcriptional expression relative to birth weight and placental metal levels will allow for investigation of any association between changes in lincRNAs and birth outcomes and whether lincRNA expression is biologically plausible as a mediator in the developmental effects of exposure to trace metals.

2. Methods

2.1 The Study Population

The Rhode Island Child Health Study is a birth cohort of 840 women recruited from the population of Rhode Island and Southeastern Massachusetts. These women were approached following the delivery of their infant at Women and Infants Hospital of Providence, RI, where 63% of those originally eligible agreed to participate (Everson et al., 2017). All subjects provided written informed consent approved by the Institutional Review Boards at Women and Infants Hospital. All of the births occurred between Sept 2008 and June 2014, and eligibility criteria included singleton, term infants born at ≥ 37 weeks gestation and without pregnancy complications and lacking congenital or chromosomal abnormalities and whose mothers were over the age of 18 and spoke English as a language of consent (Deyssenroth et al., 2017; Everson et al., 2016). The cohort was oversampled for small for gestational age (SGA, ≤ 10th percentile of BW) and large for gestational age (LGA, ≥ 90th percentile of BW) infants based on the a priori interest in studying fetal growth and development. These infants were matched to average for gestational age (AGA, 10% < BW percentile < 90%) infants on sex, gestational age (± 3 days), and maternal age (± 2 years) (Everson et al., 2016). Birth weight (BW) percentiles were calculated based on the Fenton charts accounting for gestational age, infant sex, birth weight, head circumference, and length (Fenton & Kim, 2013). Data on gestational weeks, infant sex, birth weight (grams) and intrauterine growth restriction (IUGR) status – determined in utero via ultrasound – were obtained via medical records abstraction (Everson et al., 2017). An interviewer administered questionnaire was used to collect self-reported sociodemographic, lifestyle, and medical history data, followed by structured medical records review to collect anthropometric and clinical data. Of the 840 births, placental RNA sequencing took place for a subset of 199 subjects representative of the parent cohort and placental metal concentrations were taken for a subset of 259 subjects, resulting in an overlap of 85 subjects with both RNA sequencing and metal biomarker measurements (Deyssenroth et al., 2017).

2.2 Placental Sampling

Full-thickness sections of placenta were taken within two hours of birth from the fetal side of the placenta. Sections were chosen 2 cm from the umbilical cord insertion site from each of the four quadrants around the cord insertion (Everson et al., 2016) – free of maternal decidua – and were immediately placed in RNAlater TM (Applied Biosystems, Inc., AM7020) and held at 4° C. After at least 72 h at this temperature, samples were blotted dry and snap-frozen in liquid nitrogen, followed by homogenization and storage at -80° C until analysis. Concentrations of cadmium, mercury and lead were measured in parts per million within these homogenized samples post-storage using mass spectrometry (Punshon et al., 2016).

2.3 RNA Sequencing

Total RNA was isolated from homogenized placental samples using the RNeasy Mini Kit (Qiagen, Valencia, CA) and stored separately in RNAse-free water at -80 °C (Deyssenroth et al., 2017). Yields were quantified using a Quibit Fluorometer (Thermo Scientific, Waltham, MA) and integrity assessed using an Agilent Bioanalyzer (Agilent, Santa Clara, CA). Ribosomal RNA was removed using a Ribo-Zero Kit (Huang et al., 2011), with the remaining RNA converted to cDNA using random hexamers (Thermo Scientific, Waltham, MA). Using the HiSeq 2500 platform (Illumina, San Diego, CA) (Bentley et al., 2008), transcriptome-wide 50 bp single-end RNA sequencing was conducted in three sequencing batches; 10% of samples within each batch were run in triplicate.

2.4 QC Filtering and Normalization

Raw RNA sequencing data were quality assessed for both read length and GC content using the FastQC software, with quality reads mapped to the hg19 human reference genome using the Spliced Transcripts Alignment to a Reference aligner (Dobin et al., 2013). This technique masked SNPs in the reference genome to alignment, where genes with counts less than 1 per million across 30 or more samples were considered unexpressed (Deyssenroth et al., 2017). The EDASeq R package (Risso et al., 2011) was used to adjust for GC content within read counts, with subsequent use of the calcNormFactors function of the edgeR R package (Robinson et al., 2010) for TMM correction of library size differences across samples. The limma R package's voom function (Smyth, 2005) was used to transform the data into logCPM values that accounted for the mean-variance relationship in gene expression among the triplicate samples, eliminating any duplicates. Next, any logCPM normalized counts below 2 on a the log2 scale in a minimum of 30 samples were eliminated. The final filtered, normalized data-set included 12,135 transcripts, of which around 3,000 were unique non-coding transcripts and 1191 classified as lincRNAs.

2.5 Linear Analysis of Differential LincRNA Expression with Birth Weight

Differential placental lincRNA expression was assessed using the limma R package (Smyth, 2005). Limma acts by employing empirical Bayes methods to generate transcript-wise moderated t-statistics across contrasts of interest, where a Benjamini-Hochberg FDR of $q<0.05$ was subsequently applied to limit those considered to be demonstrating statistically significant differences by exposure. Each lincRNA transcript was placed in a unique linear model that associated its log-expression with continuous birth weight in grams – controlling for gestational age, infant sex, maternal age, maternal BMI and maternal smoking during pregnancy. These combinations produced 1191 unique models; any models that demonstrated FDR significant trends were utilized in subsequent analyses. Associated figures were generated using the ggplot2 package within R (Wickham, 2009). All analysis was conducted within R 3.4.1 (R Core Team, 2015).

2.6 Analysis of Log-linear association of LincRNA Expression and Heavy Metals

Differential placental lincRNA expression was assessed using the limma R package, this time compared against log-transformed levels of placental cadmium, mercury and lead – given generally log-normal distributions of metal within the 85-member metals subset. Transcripts for this analysis were drawn from the significant results of the prior linear analysis of lincRNAs versus birth weight. The contrasts of interest were likewise subjected to Benjamini-Hochberg p-adjustment, with any significant results after FDR application demonstrating statistically significant difference in transcript by metal exposure. Covariates included to adjust for potential confounders of this relationship varied per each metal. Models with cadmium included maternal smoking status – as the primary source of cadmium exposure - during pregnancy and infant sex; while maternal education and infant sex were the covariates included in both lead and mercury models, maternal education was highly correlated with smoking status within the cohort and thus removed from cadmium models due to collinearity issues. Controlling infant sex in all models accounted for consistently larger concentrations of metals in placentas of male infants.

2.7 Logistic Regression Analysis

Transcripts with statistically significant BW-associations were subsequently also selected for logistic regression analysis of their relationship with LGA and SGA birth outcomes. Each transcript was placed in its own model as an independent variable compared against birth weight categories to highlight potential associations between differential lincRNA expression and LGA and SGA births. Two different types of logistic models were constructed, one where SGA children were compared purely against AGA – with LGA excluded – and the other comparing only LGA to AGA children. These restrictions simplified the interpretation of the resulting odds ratios, despite the reduction of the subjects for each analysis. This analysis was performed in the full transcriptional cohort of 199 and adjusted for known factors associated with birth weight outcomes that are not accounted for within the Fenton classifications: maternal age, highest education level as an indicator of SES, BMI and smoking status during pregnancy.

In order to assess the association of metals to these birth weight outcomes directly, logistic regression of LGA and SGA status was also performed against log placental metal concentrations. LGA and SGA comparisons were constructed in the same manner as previously described, with comparisons limited to the single extreme category and AGA children. Six regression models were produced, each controlling for maternal age and BMI. Cadmium models also controlled for maternal smoking status rather than maternal education – used in mercury and lead models – owing to the same collinearity issues mentioned previously.

3. Results

3.1 Study Population

The demographics of the full RNA-Seq population and metal panel subset are shown in Table 1. Based on study design, the population is oversampled for small (SGA), large (LGA) for gestational age births compared to average for gestational age (AGA). Average gestational age was consistent across all weight categories in the full population - around 39 weeks - with similar distributions that differed primarily in interquartile range (median (IQR): LGA = 39.3 (0.85); SGA = 39.3 (1.29); AGA = 39.4 (1.00)). Consistent with existing literature (Di Renzo et al., 2007), a greater percentage of LGA infants in the cohort were male (0.64) and a greater proportion of SGA infants were female (0.77), with AGA infants close to evenly represented across sexes. The majority of the cohort (76%) was born to caucasian mothers, but both black and asian mothers were overrepresented among SGA infants (23 and 17% respectively) despite each group composing 5.5 and 5.0% of the overall cohort respectively. This is consistent with previous literature (Khalil et al., 2013). These demographic characteristics were largely comparable within the 85-member metal panel subset. For continuous measures, slight decreases were present in SGA and AGA mothers for BMI and maternal age. Most other demographic measures did not differ widely in proportions among the three birth weight categories, though the decreased sample size did slightly alter the proportion composed by certain ethnic groupings within the metal panel subset. Overall, the subset was deemed to be representative of the full RNA-Seq. cohort.

3.2 Birth Weight Regression

We initially aimed to identify the lincRNAs associated with birth weight, and found that of the 1198 transcripts, 46 demonstrated an association with birth weight with an FDR $q<0.05$, controlling for infant sex and maternal age, BMI, education level, and smoking during pregnancy, with the majority, 40, demonstrated a positive relationship with birth weight and only 6, a negative association (Figure 1). These transcripts, listed in Table 2, spanned 17 chromosomes, with chromosomes 1, 8, and the X chromosome as the three most common transcriptional locations (5, 5, and 7 transcripts for each respectively). The magnitude of associations varied widely among the 46 transcripts, with a maximal decrease of -462.7 g per log change in MIR22HG expression (chromosome 17) and a maximal increase of 558.7 g per log change in JPX expression (X chromosome). (See Appendix: Table 9 for full regression output)

3.3 Metal-Transcript Regression

The 46 birth weight-associated lincRNAs were subsequently examined for their associations with placental trace metals concentrations amongst a subset of samples with available metals data (n=85). In these models we identified 18 transcripts that were nominally-significantly ($p \leq 0.05$) associated with metal expression: 4 with cadmium, 13 with mercury and 1 with lead. These transcripts were spread across 14 chromosomes, with X, 8 and 12 being the most common (3,2, and 2 transcripts respectively). All ß estimates produced for each metal, including those that were not nominally significant, were negative (Appendix Tables 6 - 8). Estimates for cadmium ranged from -1.54 to 0.47 log fold change expression per log cadmium increase, with MIR22HG (ß= 0.40, P-value = 0.002) as the closest transcript to FDR significance across all three metals (FDR P-value = 0.074) (Table 3). The mercury-associated transcripts, both numerous and next most FDR-significant, demonstrated a much more negative average association, with a mean log fold change of 0.24, as well as two transcripts each from chromosomes 8 and X. The sole borderline-significant association with lead was transcript ACO25031.1 (logFC = -0.63, P-value = 0.050), which was one of only four negative log fold change values across the three metals. These regression results demonstrated the presence of association - though not FDR significant - between metal exposure and placental lincRNA expression within the smaller 85-member metals subset. Full regression results from these analyses are displayed in Appendix Tables 6, 7 and 8 for cadmium, mercury and lead respectively.

3.4 Logistic Birth Outcome Analysis

In addition to examining the linear association between lincRNA expression and birth weight, we also examined how differences in their expression could relate to more extremes of growth, using logistic regression to model the odds for either LGA or SGA status compared to AGA with a log increase in lincRNA expression. LGA status was associated significantly with 11 different transcripts among the full transcription analysis cohort (Table 4), while SGA births were associated significantly with 19 transcripts (Table 5). Of the significant LGA transcripts, 8 were associated with increased odds of LGA status with increased lincRNA expression, with the remaining 3 transcripts protective against LGA status within the cohort. Conversely, only 3 transcripts were associated with increased odds of SGA status; the remaining 16 transcripts were protectively associated against SGA, a trend that mirrored the larger trends within the transcript subset, namely 41 of the 46 transcripts being both positively associated with LGA and protectively associated with SGA outcomes.

Each transcript was uniquely associated with either LGA for SGA births with the exception of AP000766.1 located on chromosome 11, which demonstrated a protective association with SGA birth but a positive association with LGA birth within the cohort (LGA OR = 2.04, 95% CI = (1.23, 3.27); SGA OR = 0.52, 95% CI = (0.30, 0.92)), demonstrating a logical inverse effect for opposite outcomes. Transcript associations with birth outcomes varied in both direction and magnitude. AC008543.1 on chromosome 19 had the strongest significant association with LGA births (OR = 2.34, 95% CI = (1.25, 4.39)), while ERVH48-1 (chromosome 21) had the strongest protective association (OR = 0.38, 95% CI = (0.18, 0.81)), mirrored by its large - though not significant - positive association with SGA birth

(OR = 2.14, 95% CI = (0.86, 5.31)) (Appendix Table 9). The largest significant association with SGA birth came from OSER1-AS1 (chromosome 20; OR = 3.19, 95% CI = (1.30, 7.82)) with the strongest significant protective association being from HCG11 on chromosome 6 (OR = 0.05, 95% CI = (0.01, 0.21)). OSER1-AS1 did not have the strongest association with SGA births however; MIR22HG (chromosome 17) had both SGA odds ratio of 3.59 (95% CI = (0.83, 15.57)) and an LGA odds ratio of 0.36 (95% CI = (0.11, 1.18)). Though neither measure of association was significant, these represented the strongest opposing associations from any transcript.

Having found varying degrees of association across parts of the conceptual pathway - via lincRNA transcript expression - from heavy metals to birth weight outcomes, we conducted introductory steps to a mediation analysis. However, no significant association was found between birth weight and placental metals concentration for cadmium, lead or mercury in the metals cohort subset. Cadmium showed the greatest effect, with a linear regression ß-coefficient of -447.1g per ug/g increase in Cd (P-value = 0.140), and lead was likewise negatively associated with birth weight (ß = -278.7g per ug/g increase, P-value = 0.308). Cadmium was found in logistic regression to be significantly associated with SGA in logistic regression of birth weight categories against metals (OR = 25.00, 95% CI = (1.28,489.5)); this was the only association found. Given a lack of main effect observable in this sub-cohort and the lack of precision in our logistic estimate, we could not complete a formal mediation analysis.

4. Discussion

In this study, we explored a potential molecular mechanism underlying the relationship between in-utero toxic metal exposures and the critical infant outcome of birth weight, despite the function of most of the 1191 transcripts included in this analysis being unknown within the placenta. We found that a number of these transcripts were significantly associated with either increases or decreases in continuous birth weight, with the results of our logistic regression mirroring the directionality of these associations for each of the highlighted transcripts. The initial analysis of transcript expression relative to birth weight revealed that the majority of the significant transcripts - 40 of 46 - were associated with increased growth relative to expression, indicating growth-promotion as the predominant role for placental lincRNAs, with primarily positive ß-coefficients across the 46 FDR-significant transcripts highlighted from the linear regression. While all of these transcripts have been classified based upon their chromosomal locations, only a few have been characterized beyond nomenclature. JPX, which displayed the largest ß estimate associating it with growth (558.7 g/log(JPX)), was found by (D. Tian, Sun, & Lee, 2010) to be an Xist activator involved in X chromosome inactivation, thereby mediating dosage control of X-linked genes; JPX deletion was lethal in X/X-phenotype embryonic stem cells. MIR22HG, the strongest growth-opposing transcript identified, was found to be an early-responding indicator of chemically-induced cell stress in human induced pluripotent stem cells (Tani et al., 2014) as well as appearing to be down-regulated in ovarian cancer tissues when compared to ovarian surface epithelium (Li et al., 2016). These examples present lincRNAs - among their many potential roles - as playing regulatory roles in dosage control for properly-directed cell growth and restricting of growth in conditions that endanger the cell, with clear oncogene potential in cancer development when aberrantly expressed.

Analysis of the metal exposures in relation to transcript expression offered further insight into potential association of lincRNA expression and birth weight outcomes. As previously highlighted, all nominally significant associations showed negative correlation between increasing placental metal levels and lincRNA expression, indicating these metals possess some level of inhibitory relationship with these transcripts. The lack of any FDR-significant associations here can likely be attributed to primarily low sample size within the metal subset cohort. The most significant association found (FDR and nominal) was again MIR22HG, offering a potential mechanism for cadmium-mediated aberrant growth via reduced MIR22HG anti-inflammatory activity. Another cadmium-associated transcript ERVH48-1 - found to be negatively associated with growth in the previous analysis (Table 2) - was identified as a human endogenous retroviral transcript involved in syncytialization (spontaneous cell fusion) repression via binding of the syn1 receptor protein (Okahara et al., 2004; Sugimoto et al., 2013). The localization of most HERV transcripts exclusively to the placenta indicates the importance of this anti-fusion property in controlling placental growth, and their expression was found to be reduced in cases of pregnancy-induced hypertension (Kudaka et al., 2008). The presence of JPX among transcripts linked to Mercury concentrations also presents a possible link to the neurological outcomes possibly attributed to the metal, as JPX is normally expressed in fairly high levels within brain cells (Fagerberg et al., 2014). It should be noted here that the relative activity level of lincRNAs - similar to other lncRNAs but different from translated mRNAs - varies greatly across transcript type; one transcript can potentially perform substantial regulatory activity at concentrations previously undetectable a decade ago, perhaps the same amount of activity as another lincRNA transcript at easily-measured, abundant concentrations. PART1, prostate androgen-regulated transcript 1, is another growth-promoting (Table 2) item on this list with mercury. The transcript is preferentially expressed primarily in the brain, prostate, salivary glands, placenta and bladder (Fagerberg et al., 2014) and is involved in androgen receptor-mediated regulation of the prostate (Lin et al., 2000) as well as cell proliferation in cases of colorectal cancer (Hu et al., 2017). These growth mechanisms could potentially be involved normal cell proliferation and growth during development yet result in deleterious cellular phenotypes if dysregulated during both fetal growth or adulthood.

Logistic regression produced 29 transcripts that were significantly associated with LGA births, SGA births or - in the case of AP000766.1 - both, with the direction of association broadly consistent with the prior linear regression of birth weight. While this overlap is readily apparent, logistic regression of birth weight categories was selected as a way of controlling for variability in both gestational age and birth weight with sex using one variable, and served to highlight the strength and directionality of potential pathologic associations within the cohort. As previously mentioned LGA and SGA births have been explicitly associated with a litany of health outcomes and morbidities within newborn infants, young children and even adults (Colman et al., 2012; Grissom & Reyes, 2013; Moore et al., 2012; Van Lieshout & Boyle, 2011), so each category is treated with the same gravity in our analyses. Within the LGA category PART1 appears again (OR = 1.72, 95% CI = (1.01, 2.92)), indicating its potential role in aberrant cell growth in cases of over-expression. It is important to note that a number of the strong, significant associations highlighted in the previous linear analysis, such as MIR22HG and JPX, are not present among the significant transcripts. This is likely due to the method utilized to code birth weight categories for regression, which excluded SGA children from the SGA regression and LGA children from the SGA regression, meaning the only comparison was between individual extreme phenotypes and AGA children. This reduced sample sizes down to 169 and 140 for LGA and SGA regressions, around a 15% and 30% change for these groups respectively from the 199 subjects with full transcriptional data. Examination of Figure 2 shows that some of the more pronounced odds ratios produced belong to transcripts positively associated with SGA birth outcomes, including MIR22HG, ERVH48-1, LINC00337 and OSER1-AS1, though these transcripts also have the widest (MIR22HG) or among the widest confidence intervals in the entire list of transcripts. This is consistent with increasing data variability due to smaller sample size, though the direction and magnitude of these prominent associations cannot be ignored despite incomplete significance.

The collection of metal samples for 259 subjects in the overall study population greatly surpassed the majority of previous work done in trace metal sampling. Esteban-Vasallo et al. (2012), who reviewed a large number of studies examining cadmium, mercury and lead measurement within the placenta, stated only 19 of the included 74 studies had greater than 100 subjects. This low sample size reduces the statistical robustness of these studies' findings, which in turn varied widely in their associations between environmental exposures and placental trace metal concentrations as well as the presence of birth outcomes relating to these metals (Esteban-Vasallo et al., 2012). Consequently, this is a limitation of this specific analysis within the RICHS cohort study, which was restricted to 85 subjects by the availability of both metal and lncRNA data. Utilizing only 199 subjects for full RNA sequencing analyses also limits study power compared to larger GWAS-style investigations. The cross-sectional design represents the largest hurtle in making temporal conclusions regarding the causal association of trace metals and birth weight outcomes via lincRNAs. The low sample size of our cohort also limited our ability to highlight associations closer to the null within all of our analyses, particularly those involving the smaller metal-subset. However, it cannot be ignored that this was the largest study on placental RNA profiles ever performed, and the data nonetheless does indicate that lincRNA expression may play a role in the placenta's impact on birth weight.

The strengths of our study design should be highlighted, as its methodology accounts for a number of the inconsistencies encountered by previous work in placental metals measurement. These included our assumption of a lack of homogenous metal deposition, which was addressed via homogenization of multiple samples from a single placenta; previous studies frequently would treat a single sample as representative of the entire placenta (Esteban-Vasallo et al., 2012). Additionally, both our metal and transcriptional analyses were preceded by stringent quality control and storage procedures aimed at RNA preservation, increasing the likelihood of accurate metal and transcript measurements and consistency of measurements across samples. Our sample of 199 subjects also represents one of the largest full transcriptome cohorts constructed to date for the purposes of human development investigation, and this cannot be overstated. Further analysis within larger cohorts will be required in the future to further characterization of the various associations highlighted to definitively address the role of lincRNAs in mediating developmental disease phenotypes.

5. Tables and Figures

Table 1: Demographic Characteristics of the Study Population

	RICHS RNA-Seq. Group (n = 199)			Metal Panel Subset (n = 85)		
Variables	SGA[a] (n = 30)	AGA[b] (n = 110)	LGA[c] (n = 59)	SGA[a] (n = 15)	AGA[b] (n = 38)	LGA[c] (n = 32)
	Mean (SD)	Mean (SD)	Mean (SD)	Mean (SD)	Mean (SD)	Mean (SD)
Continuous measures						
Birth weight (g)	2577 (368.1)	3394 (363.0)	4270 (241.2)	2663 (463.3)	3314 (386.6)	4251 (245.8)
Gestational Age (weeks)	39.1 (1.1)	39.4 (1.0)	39.4 (0.8)	39.1 (1.3)	39.2 (1.0)	39.3 (0.8)
Maternal Age (years)	31.5 (5.8)	31.1 (4.7)	31.4 (4.0)	29.3 (6.7)	30.8 (5.5)	30.7 (4.1)
Maternal BMI (Kg/mˆ2)	25.6 (6.9)	25.6 (6.0)	28.2 (6.7)	24.8 (5.5)	24.4 (6.1)	28.8 (6.8)
	N (%)	N (%)	N (%)	N (%)	N (%)	N (%)
Infant gender						
Female	23 (77)	57 (52)	21 (36)	12 (80)	18 (47)	12 (38)
Male	7 (23)	53 (48)	38 (64)	3 (20)	20 (53)	20 (62)
Maternal race						
Caucasian	16 (53)	88 (80)	50 (85)	7 (47)	27 (71)	25 (78)
Black	5 (17)	3 (3)	3 (5)	2 (13)	2 (5)	3 (9)
Asian	2 (7)	2 (2)	0 (0)	1 (7)	0 (0)	0 (0)
Other	5 (17)	17 (15)	5 (8)	3 (20)	9 (24)	4 (13)
Unknown	2 (7)	0 (0)	1 (2)	2 (13)	0 (0)	0 (0)
Maternal education level						
Any post graduate schooling	4 (13)	31 (28)	15 (25)	2 (13)	7 (18)	9 (28)
College graduate	12 (40)	37 (34)	21 (36)	4 (27)	18 (47)	11 (34)
Junior college graduate or equivalent	9 (30)	25 (23)	16 (27)	5 (33)	4 (11)	8 (25)
High school graduate	3 (10)	14 (13)	6 (10)	3 (20)	8 (21)	3 (9)
Less than 11th grade	2 (7)	3 (3)	1 (2)	1 (7)	1 (3)	1 (3)
Smoking during pregnancy						
Yes	3 (10)	7 (6)	7 (12)	1 (7)	4 (11)	3 (9)
No	27 (90)	103 (94)	52 (88)	14 (93)	34 (89)	29 (91)

[a] Small for gestational age

[b] Average for gestational age

[c] Large for gestational age

Table 2: Forty-six lincRNA transripts with FDR significant continuous-birthweight associations

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000237491	AC008543.1	19	285.0	152.8	417.1	<0.001	0.018
ENSG00000177757	AL359851.1	X	144.6	75.9	213.2	<0.001	0.018
ENSG00000225880	LINC00472	6	263.9	138.4	389.4	<0.001	0.018
ENSG00000230368	AL359715.3	6	159.0	82.7	235.3	<0.001	0.018
ENSG00000230699	LINC01355	1	262.0	135.3	388.7	<0.001	0.018
ENSG00000223823	LINC01465	12	272.7	136.6	408.7	<0.001	0.020
ENSG00000260179	MIRLET7DHG	9	289.9	142.1	437.6	<0.001	0.020
ENSG00000225285	AC234772.2	X	211.1	103.5	318.7	<0.001	0.020
ENSG00000236423	LINC00113	21	116.8	56.9	176.7	<0.001	0.020
ENSG00000233304	AC063944.1	3	124.2	59.9	188.6	<0.001	0.020
ENSG00000225077	AP000462.3	11	119.2	57.2	181.2	<0.001	0.020
ENSG00000238290	ERVH48-1	21	-320.9	-487.8	-154.0	<0.001	0.020
ENSG00000228423	AC009812.4	8	216.6	103.4	329.7	<0.001	0.020
ENSG00000228526	AP000766.1	11	213.3	101.3	325.2	<0.001	0.020
ENSG00000228140	AC087857.1	3	-116.1	-178.0	-54.3	<0.001	0.020
ENSG00000226029	LINC00629	X	142.9	66.7	219.0	<0.001	0.020
ENSG00000228549	PART1	5	232.0	108.4	355.6	<0.001	0.020
ENSG00000204362	LINC00337	1	-226.9	-348.6	-105.2	<0.001	0.020
ENSG00000261781	AC114763.2	2	111.3	51.4	171.1	<0.001	0.020
ENSG00000236963	MIR210HG	11	-157.1	-241.6	-72.6	<0.001	0.020
ENSG00000261326	AC119674.1	1	190.3	87.8	292.7	<0.001	0.020
ENSG00000225643	HCG11	6	424.1	191.5	656.7	<0.001	0.023
ENSG00000241169	JPX	X	558.7	251.9	865.6	<0.001	0.023
ENSG00000228634	AL353804.1	X	254.4	111.9	396.9	0.001	0.029
ENSG00000227533	LINC01695	21	125.0	54.1	196.0	0.001	0.032
ENSG00000230615	LINC00106	X	198.5	85.2	311.8	0.001	0.032
ENSG00000225028	AC011287.2	7	136.7	58.6	214.7	0.001	0.032
ENSG00000225675	AC025031.1	12	181.7	77.4	286.1	0.001	0.033
ENSG00000234810	MIR181A1HG	1	192.6	81.8	303.5	0.001	0.033
ENSG00000230250	RAB30-AS1	11	325.5	136.7	514.4	0.001	0.033
ENSG00000233079	AL672032.1	X	121.4	50.7	192.2	0.001	0.033
ENSG00000235612	AC003984.1	7	133.4	55.6	211.1	0.001	0.033
ENSG00000260971	AC097480.1	4	106.2	44.2	168.1	0.001	0.033
ENSG00000223956	AC022087.1	15	157.7	65.4	249.9	0.001	0.033
ENSG00000234807	OSER1-AS1	20	-307.0	-486.5	-127.4	0.001	0.033
ENSG00000226476	LINC00265	7	283.8	113.7	453.9	0.001	0.042
ENSG00000231252	AC079193.2	8	185.2	73.9	296.5	0.001	0.042
ENSG00000230817	MIR22HG	17	-462.7	-741.5	-183.9	0.001	0.042
ENSG00000233008	AP003696.1	8	182.4	72.1	292.7	0.001	0.042
ENSG00000260464	AC022730.3	8	134.7	53.1	216.3	0.001	0.042
ENSG00000225206	LINC01753	1	123.5	48.3	198.7	0.002	0.044
ENSG00000261055	C21orf91-OT1	21	161.5	62.6	260.4	0.002	0.045
ENSG00000259834	AC073530.1	12	146.6	56.8	236.4	0.002	0.045
ENSG00000231346	LINC00470	18	230.8	88.9	372.7	0.002	0.045
ENSG00000215866	AC022973.3	8	120.1	45.9	194.4	0.002	0.047
ENSG00000224167	AL445123.1	6	98.5	37.4	159.7	0.002	0.048

[*] Controlled for gestational age; infant sex; maternal age, BMI, education and smoking status

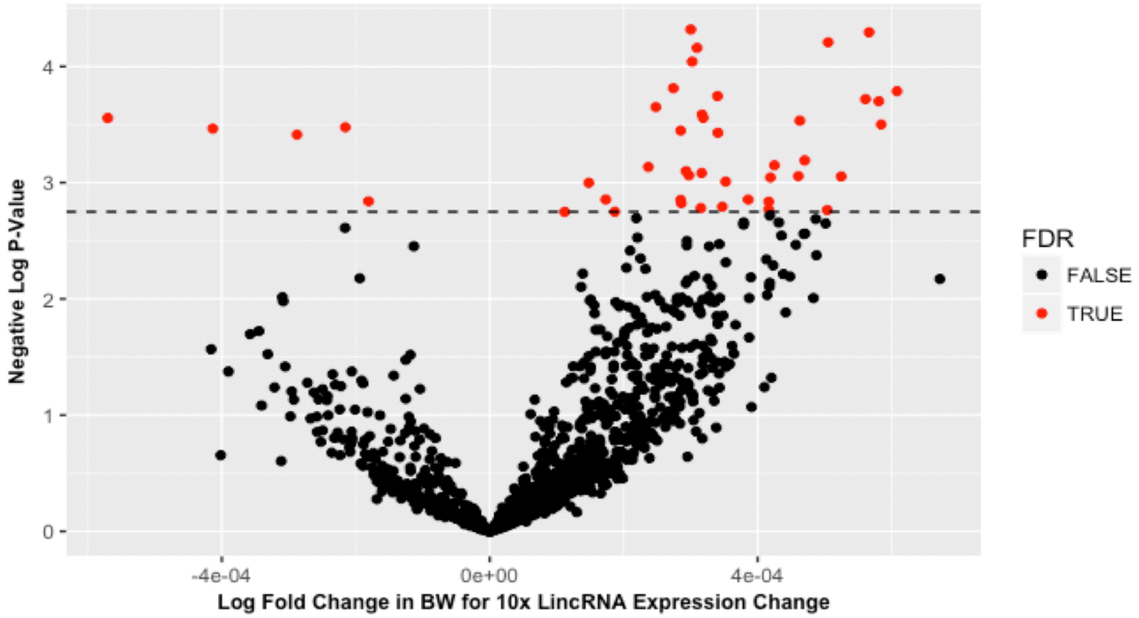


Figure 1: Birth weight-lincRNA expression linear regression results. Individual linear models controlled for gestational age, infant sex, maternal age, maternal BMI, maternal education and smoking status during pregnancy, with an FDR significance threshold based upon Benjamini-Hochberg adjustment

Table 3: Nominal-significant linear associations of lincRNA expression with metals among BW-significant transcripts[*]

	General		Regression Output[†‡§]	Significance	
Ensemble ID	Gene Name	Chromosome	logFC	P.Value	FDR P.Value
Cadmium					
ENSG00000186594	MIR22HG	17	0.40	0.002	0.074
ENSG00000230569	AC114763.2	2	-1.54	0.009	0.202
ENSG00000233056	ERVH48-1	21	0.47	0.029	0.444
ENSG00000231566	AC234772.2	X	-0.65	0.039	0.444
Mercury					
ENSG00000257083	AC073530.1	12	0.39	0.012	0.144
ENSG00000132204	LINC00470	18	0.25	0.012	0.144
ENSG00000237713	AC011287.2	7	0.44	0.015	0.144
ENSG00000247095	MIR210HG	11	-0.45	0.015	0.144
ENSG00000225470	JPX	X	0.13	0.024	0.144
ENSG00000233237	LINC00472	6	0.26	0.026	0.144
ENSG00000152931	PART1	5	0.28	0.027	0.144
ENSG00000261326	LINC01355	1	0.23	0.027	0.144
ENSG00000239828	AC063944.1	3	0.42	0.031	0.144
ENSG00000253385	AP003696.1	8	0.28	0.034	0.144
ENSG00000230262	MIRLET7DHG	9	0.21	0.037	0.144
ENSG00000227060	LINC00629	X	0.38	0.038	0.144
ENSG00000260317	AC009812.4	8	0.26	0.042	0.149
Lead					
ENSG00000257496	AC025031.1	12	-0.63	0.050	0.587

[*] Candidate transcripts limited to 46 BW-significant transcripts identified via linear analysis

[†] Linear models using cadmium control for smoking during pregnancy and infant sex

[‡] Linear models using mercury control for infant sex and maternal education level

[§] Linear models using lead control for infant sex and maternal education level

Table 4: LincRNA transcripts with significant logistic associaton with LGA births*

	General		Regression Output†			Significance
Ensemble ID	Gene Name	Chromosome	Odds Ratio	LL	UL	P.val
ENSG00000260971	AC119674.1	1	2.00	1.23	3.27	0.005
ENSG00000253143	AC022730.3	8	1.86	1.19	2.92	0.006
ENSG00000261098	AP000766.1	11	2.04	1.21	3.43	0.007
ENSG00000230569	AC114763.2	2	1.45	1.11	1.90	0.007
ENSG00000197332	AC008543.1	19	2.34	1.25	4.39	0.008
ENSG00000233056	ERVH48-1	21	0.38	0.18	0.81	0.012
ENSG00000259715	AC022087.1	15	1.65	1.07	2.53	0.023
ENSG00000247095	MIR210HG	11	0.65	0.44	0.94	0.024
ENSG00000132204	LINC00470	18	1.99	1.05	3.78	0.035
ENSG00000235813	AL672032.1	X	1.42	1.02	1.98	0.039
ENSG00000152931	PART1	5	1.72	1.01	2.92	0.046

[*] Candidate transcripts limited to 46 BW-significant transcripts identified via linear analysis

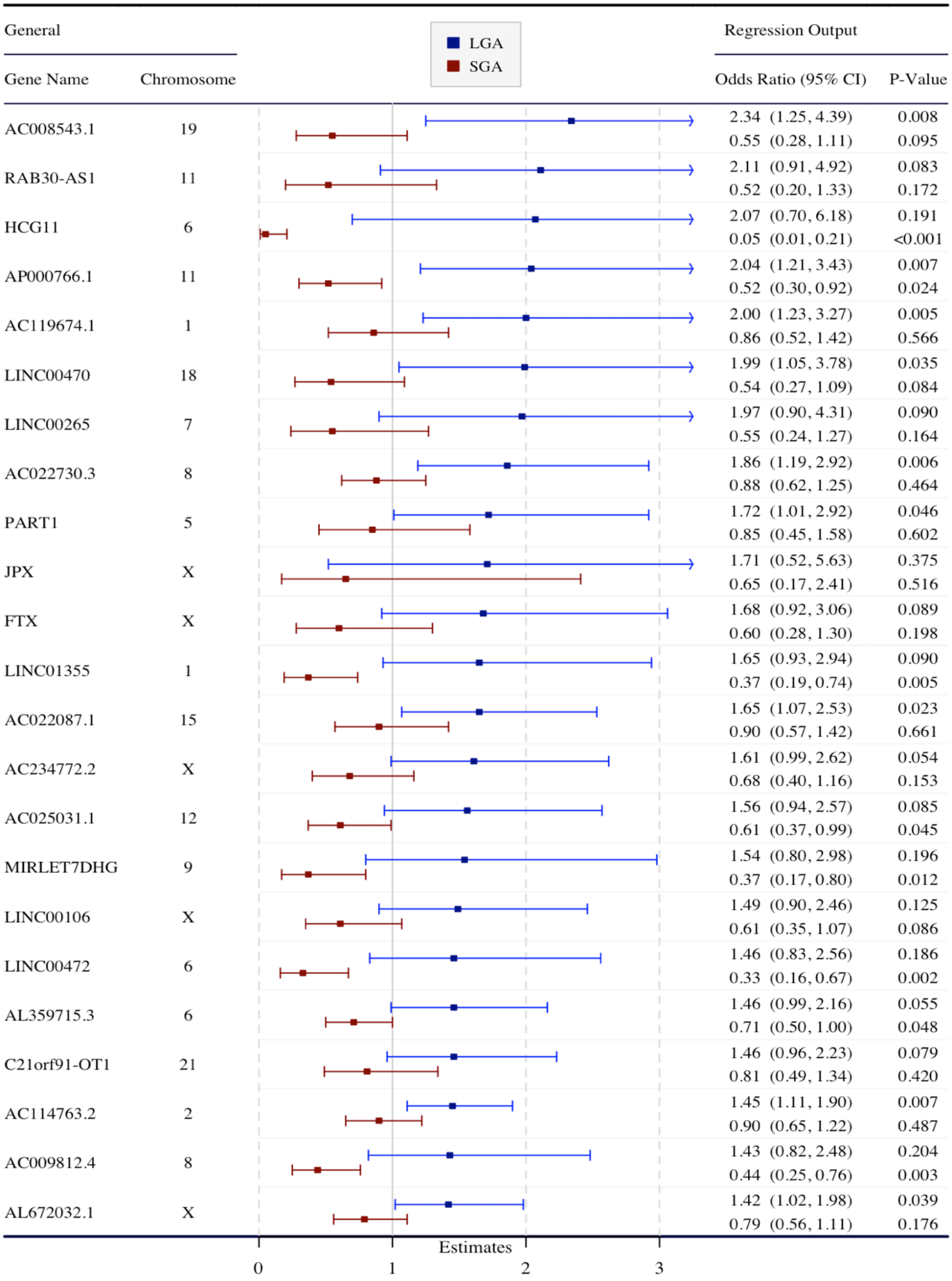
[†] Regression controlled for maternal age, BMI, educational level and smoking status

Table 5: LincRNA transcripts with significant logistic associaton with SGA births*

	General		Regression Output†			Significance
Ensemble ID	Gene Name	Chromosome	Odds Ratio	LL	UL	P.val
ENSG00000228223	HCG11	6	0.05	0.01	0.21	<0.001
ENSG00000229989	MIR181A1HG	1	0.40	0.22	0.72	0.002
ENSG00000233237	LINC00472	6	0.33	0.16	0.67	0.002
ENSG00000235139	AC003984.1	7	0.54	0.36	0.81	0.003
ENSG00000260317	AC009812.4	8	0.44	0.25	0.76	0.003
ENSG00000260585	AL359851.1	X	0.61	0.43	0.86	0.005
ENSG00000261326	LINC01355	1	0.37	0.19	0.74	0.005
ENSG00000227060	LINC00629	X	0.60	0.41	0.86	0.006
ENSG00000225077	LINC00337	1	2.68	1.27	5.67	0.010
ENSG00000236532	LINC01695	21	0.59	0.40	0.88	0.010
ENSG00000229642	AC087857.1	3	1.61	1.12	2.31	0.011
ENSG00000223891	OSER1-AS1	20	3.18	1.30	7.82	0.012
ENSG00000230262	MIRLET7DHG	9	0.37	0.17	0.80	0.012
ENSG00000253385	AP003696.1	8	0.50	0.28	0.90	0.021
ENSG00000256972	AP000462.3	11	0.68	0.49	0.95	0.024
ENSG00000261098	AP000766.1	11	0.52	0.30	0.92	0.024
ENSG00000221949	LINC01465	12	0.49	0.25	0.96	0.039
ENSG00000257496	AC025031.1	12	0.61	0.37	0.99	0.045
ENSG00000260645	AL359715.3	6	0.71	0.50	1.00	0.048

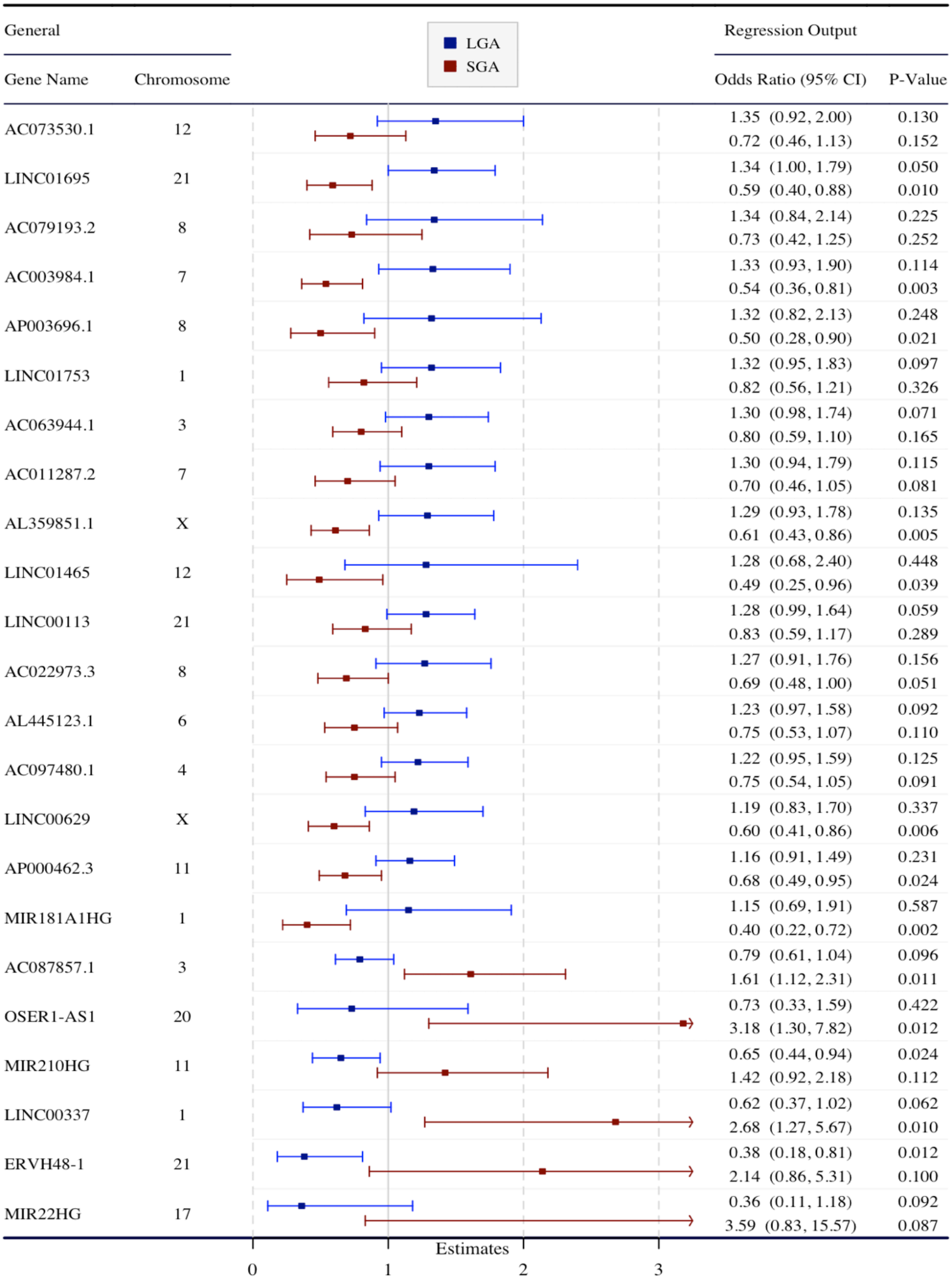
[*] Candidate transcripts limited to 46 BW-significant transcripts identified via linear analysis

[†] Regression controlled for maternal age, BMI, educational level and smoking status



General		Regression Output	
Gene Name	Chromosome	Odds Ratio (95% CI)	P-Value
AC008543.1	19	2.34 (1.25, 4.39)	0.008
		0.55 (0.28, 1.11)	0.095
RAB30-AS1	11	2.11 (0.91, 4.92)	0.083
		0.52 (0.20, 1.33)	0.172
HCG11	6	2.07 (0.70, 6.18)	0.191
		0.05 (0.01, 0.21)	<0.001
AP000766.1	11	2.04 (1.21, 3.43)	0.007
		0.52 (0.30, 0.92)	0.024
AC119674.1	1	2.00 (1.23, 3.27)	0.005
		0.86 (0.52, 1.42)	0.566
LINC00470	18	1.99 (1.05, 3.78)	0.035
		0.54 (0.27, 1.09)	0.084
LINC00265	7	1.97 (0.90, 4.31)	0.090
		0.55 (0.24, 1.27)	0.164
AC022730.3	8	1.86 (1.19, 2.92)	0.006
		0.88 (0.62, 1.25)	0.464
PART1	5	1.72 (1.01, 2.92)	0.046
		0.85 (0.45, 1.58)	0.602
JPX	X	1.71 (0.52, 5.63)	0.375
		0.65 (0.17, 2.41)	0.516
FTX	X	1.68 (0.92, 3.06)	0.089
		0.60 (0.28, 1.30)	0.198
LINC01355	1	1.65 (0.93, 2.94)	0.090
		0.37 (0.19, 0.74)	0.005
AC022087.1	15	1.65 (1.07, 2.53)	0.023
		0.90 (0.57, 1.42)	0.661
AC234772.2	X	1.61 (0.99, 2.62)	0.054
		0.68 (0.40, 1.16)	0.153
AC025031.1	12	1.56 (0.94, 2.57)	0.085
		0.61 (0.37, 0.99)	0.045
MIRLET7DHG	9	1.54 (0.80, 2.98)	0.196
		0.37 (0.17, 0.80)	0.012
LINC00106	X	1.49 (0.90, 2.46)	0.125
		0.61 (0.35, 1.07)	0.086
LINC00472	6	1.46 (0.83, 2.56)	0.186
		0.33 (0.16, 0.67)	0.002
AL359715.3	6	1.46 (0.99, 2.16)	0.055
		0.71 (0.50, 1.00)	0.048
C21orf91-OT1	21	1.46 (0.96, 2.23)	0.079
		0.81 (0.49, 1.34)	0.420
AC114763.2	2	1.45 (1.11, 1.90)	0.007
		0.90 (0.65, 1.22)	0.487
AC009812.4	8	1.43 (0.82, 2.48)	0.204
		0.44 (0.25, 0.76)	0.003
AL672032.1	X	1.42 (1.02, 1.98)	0.039
		0.79 (0.56, 1.11)	0.176

Figure 2 (Part 1): Full results from logistic regression of LGA and SGA outcomes on transcript expression. Logistic models controlled for known factors associated with birth weight outcomes that are not accounted for within the Fenton classifications: maternal age, highest education level – as an indicator of SES – BMI and smoking status during pregnancy.



General		Regression Output	
Gene Name	Chromosome	Odds Ratio (95% CI)	P-Value
AC073530.1	12	1.35 (0.92, 2.00)	0.130
		0.72 (0.46, 1.13)	0.152
LINC01695	21	1.34 (1.00, 1.79)	0.050
		0.59 (0.40, 0.88)	0.010
AC079193.2	8	1.34 (0.84, 2.14)	0.225
		0.73 (0.42, 1.25)	0.252
AC003984.1	7	1.33 (0.93, 1.90)	0.114
		0.54 (0.36, 0.81)	0.003
AP003696.1	8	1.32 (0.82, 2.13)	0.248
		0.50 (0.28, 0.90)	0.021
LINC01753	1	1.32 (0.95, 1.83)	0.097
		0.82 (0.56, 1.21)	0.326
AC063944.1	3	1.30 (0.98, 1.74)	0.071
		0.80 (0.59, 1.10)	0.165
AC011287.2	7	1.30 (0.94, 1.79)	0.115
		0.70 (0.46, 1.05)	0.081
AL359851.1	X	1.29 (0.93, 1.78)	0.135
		0.61 (0.43, 0.86)	0.005
LINC01465	12	1.28 (0.68, 2.40)	0.448
		0.49 (0.25, 0.96)	0.039
LINC00113	21	1.28 (0.99, 1.64)	0.059
		0.83 (0.59, 1.17)	0.289
AC022973.3	8	1.27 (0.91, 1.76)	0.156
		0.69 (0.48, 1.00)	0.051
AL445123.1	6	1.23 (0.97, 1.58)	0.092
		0.75 (0.53, 1.07)	0.110
AC097480.1	4	1.22 (0.95, 1.59)	0.125
		0.75 (0.54, 1.05)	0.091
LINC00629	X	1.19 (0.83, 1.70)	0.337
		0.60 (0.41, 0.86)	0.006
AP000462.3	11	1.16 (0.91, 1.49)	0.231
		0.68 (0.49, 0.95)	0.024
MIR181A1HG	1	1.15 (0.69, 1.91)	0.587
		0.40 (0.22, 0.72)	0.002
AC087857.1	3	0.79 (0.61, 1.04)	0.096
		1.61 (1.12, 2.31)	0.011
OSER1-AS1	20	0.73 (0.33, 1.59)	0.422
		3.18 (1.30, 7.82)	0.012
MIR210HG	11	0.65 (0.44, 0.94)	0.024
		1.42 (0.92, 2.18)	0.112
LINC00337	1	0.62 (0.37, 1.02)	0.062
		2.68 (1.27, 5.67)	0.010
ERVH48-1	21	0.38 (0.18, 0.81)	0.012
		2.14 (0.86, 5.31)	0.100
MIR22HG	17	0.36 (0.11, 1.18)	0.092
		3.59 (0.83, 15.57)	0.087

Figure 2 (Part 2): Full results from logistic regression of LGA and SGA outcomes on transcript expression. Logistic models controlled for known factors associated with birth weight outcomes that are not accounted for within the Fenton classifications: maternal age, highest education level – as an indicator of SES – BMI and smoking status during pregnancy.

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Appendices

Table 6: Linear association of lincRNA expression with cadmium among BW-significant transcripts

	General		Regression Output*	Significance	
Ensemble ID	Gene Name	Chromosome	logFC	P.Value	FDR P.Value
ENSG00000186594	MIR22HG	17	0.40	0.002	0.074
ENSG00000230569	AC114763.2	2	-1.54	0.009	0.202
ENSG00000233056	ERVH48-1	21	0.47	0.029	0.444
ENSG00000231566	AC234772.2	X	-0.65	0.039	0.444
ENSG00000260585	AL359851.1	X	-0.89	0.059	0.500
ENSG00000253143	AC022730.3	8	-0.70	0.079	0.500
ENSG00000250064	AC097480.1	4	-0.98	0.081	0.500
ENSG00000235813	AL672032.1	X	-0.84	0.097	0.500
ENSG00000260971	AC119674.1	1	-0.52	0.115	0.500
ENSG00000247095	MIR210HG	11	0.64	0.118	0.500
ENSG00000260645	AL359715.3	6	-0.55	0.135	0.500
ENSG00000227060	LINC00629	X	-0.61	0.136	0.500
ENSG00000228223	HCG11	6	-0.22	0.142	0.500
ENSG00000229989	MIR181A1HG	1	-0.39	0.158	0.500
ENSG00000223891	OSER1-AS1	20	0.26	0.163	0.500
ENSG00000229642	AC087857.1	3	0.71	0.176	0.507
ENSG00000221949	LINC01465	12	0.25	0.279	0.723
ENSG00000240770	C21orf91-OT1	21	-0.36	0.283	0.723
ENSG00000260317	AC009812.4	8	-0.29	0.307	0.739
ENSG00000225470	JPX	X	-0.12	0.321	0.739
ENSG00000256972	AP000462.3	11	-0.53	0.338	0.741
ENSG00000230590	FTX	X	-0.20	0.372	0.779
ENSG00000230262	MIRLET7DHG	9	-0.19	0.402	0.804
ENSG00000197332	AC008543.1	19	0.18	0.473	0.877
ENSG00000236532	LINC01695	21	-0.32	0.499	0.877
ENSG00000261098	AP000766.1	11	-0.18	0.501	0.877
ENSG00000253385	AP003696.1	8	-0.19	0.515	0.877
ENSG00000235139	AC003984.1	7	-0.22	0.571	0.890
ENSG00000237713	AC011287.2	7	-0.21	0.601	0.890
ENSG00000257083	AC073530.1	12	-0.17	0.617	0.890
ENSG00000233237	LINC00472	6	0.11	0.674	0.890
ENSG00000225298	LINC00113	21	-0.26	0.680	0.890
ENSG00000225077	LINC00337	1	0.10	0.724	0.890
ENSG00000236871	LINC00106	X	-0.08	0.761	0.890
ENSG00000239828	AC063944.1	3	0.13	0.767	0.890
ENSG00000254263	AC022973.3	8	-0.12	0.769	0.890
ENSG00000257496	AC025031.1	12	0.10	0.773	0.890
ENSG00000249258	AC079193.2	8	-0.09	0.775	0.890
ENSG00000246067	RAB30-AS1	11	0.05	0.786	0.890
ENSG00000132204	LINC00470	18	-0.06	0.793	0.890
ENSG00000152931	PART1	5	-0.07	0.793	0.890
ENSG00000234675	AL445123.1	6	0.11	0.843	0.923
ENSG00000230250	LINC01753	1	0.07	0.883	0.939
ENSG00000261326	LINC01355	1	0.02	0.929	0.939
ENSG00000188185	LINC00265	7	-0.02	0.935	0.939
ENSG00000259715	AC022087.1	15	-0.02	0.939	0.939

* Linear models using cadmium control for smoking during pregnancy and infant sex

Table 7: Linear association of lincRNA expression with mercury among BW-significant transcripts

	General		Regression Output	Significance	
Ensemble ID	Gene Name	Chromosome	logFC	P.Value	FDR P.Value
ENSG00000257083	AC073530.1	12	0.39	0.012	0.144
ENSG00000132204	LINC00470	18	0.25	0.012	0.144
ENSG00000237713	AC011287.2	7	0.44	0.015	0.144
ENSG00000247095	MIR210HG	11	-0.45	0.015	0.144
ENSG00000225470	JPX	X	0.13	0.024	0.144
ENSG00000233237	LINC00472	6	0.26	0.026	0.144
ENSG00000152931	PART1	5	0.28	0.027	0.144
ENSG00000261326	LINC01355	1	0.23	0.027	0.144
ENSG00000239828	AC063944.1	3	0.42	0.031	0.144
ENSG00000253385	AP003696.1	8	0.28	0.034	0.144
ENSG00000230262	MIRLET7DHG	9	0.21	0.037	0.144
ENSG00000227060	LINC00629	X	0.38	0.038	0.144
ENSG00000260317	AC009812.4	8	0.26	0.042	0.149
ENSG00000261098	AP000766.1	11	0.24	0.053	0.163
ENSG00000260971	AC119674.1	1	0.29	0.053	0.163
ENSG00000223891	OSER1-AS1	20	-0.16	0.058	0.167
ENSG00000246067	RAB30-AS1	11	0.16	0.081	0.220
ENSG00000235813	AL672032.1	X	0.38	0.099	0.252
ENSG00000249258	AC079193.2	8	0.23	0.120	0.291
ENSG00000257496	AC025031.1	12	0.23	0.150	0.329
ENSG00000240770	C21orf91-OT1	21	0.22	0.150	0.329
ENSG00000230590	FTX	X	0.14	0.177	0.355
ENSG00000188185	LINC00265	7	0.13	0.178	0.355
ENSG00000253143	AC022730.3	8	0.23	0.210	0.403
ENSG00000228223	HCG11	6	0.08	0.225	0.413
ENSG00000197332	AC008543.1	19	0.13	0.238	0.420
ENSG00000186594	MIR22HG	17	0.07	0.273	0.454
ENSG00000230250	LINC01753	1	0.23	0.276	0.454
ENSG00000225077	LINC00337	1	0.13	0.314	0.473
ENSG00000260645	AL359715.3	6	0.17	0.318	0.473
ENSG00000225298	LINC00113	21	-0.28	0.319	0.473
ENSG00000229989	MIR181A1HG	1	0.12	0.352	0.493
ENSG00000229642	AC087857.1	3	-0.22	0.353	0.493
ENSG00000259715	AC022087.1	15	0.13	0.366	0.496
ENSG00000256972	AP000462.3	11	0.20	0.415	0.545
ENSG00000221949	LINC01465	12	0.08	0.457	0.583
ENSG00000250064	AC097480.1	4	0.17	0.505	0.628
ENSG00000234675	AL445123.1	6	-0.15	0.565	0.684
ENSG00000254263	AC022973.3	8	0.10	0.594	0.701
ENSG00000235139	AC003984.1	7	0.08	0.635	0.730
ENSG00000231566	AC234772.2	X	0.06	0.672	0.754
ENSG00000236532	LINC01695	21	-0.06	0.795	0.871
ENSG00000260585	AL359851.1	X	0.05	0.826	0.884
ENSG00000230569	AC114763.2	2	0.03	0.909	0.921
ENSG00000233056	ERVH48-1	21	0.01	0.914	0.921
ENSG00000236871	LINC00106	X	-0.01	0.921	0.921

[*] Linear models using mercury control for infant sex and maternal education level

Table 8: Linear association of lincRNA expression with lead among BW-significant transcripts

	General		Regression Output	Significance	
Ensemble ID	Gene Name	Chromosome	logFC	P.Value	FDR P.Value
ENSG00000257496	AC025031.1	12	-0.63	0.050	0.587
ENSG00000235813	AL672032.1	X	-0.84	0.066	0.587
ENSG00000186594	MIR22HG	17	0.21	0.082	0.587
ENSG00000260971	AC119674.1	1	-0.48	0.111	0.587
ENSG00000257083	AC073530.1	12	-0.49	0.117	0.587
ENSG00000231566	AC234772.2	X	-0.44	0.121	0.587
ENSG00000188185	LINC00265	7	-0.30	0.122	0.587
ENSG00000249258	AC079193.2	8	-0.43	0.146	0.587
ENSG00000223891	OSER1-AS1	20	0.25	0.152	0.587
ENSG00000132204	LINC00470	18	-0.29	0.159	0.587
ENSG00000260645	AL359715.3	6	-0.47	0.162	0.587
ENSG00000240770	C21orf91-OT1	21	-0.41	0.183	0.587
ENSG00000227060	LINC00629	X	-0.49	0.187	0.587
ENSG00000197332	AC008543.1	19	-0.30	0.190	0.587
ENSG00000152931	PART1	5	-0.32	0.200	0.587
ENSG00000253385	AP003696.1	8	-0.34	0.204	0.587
ENSG00000229989	MIR181A1HG	1	0.31	0.226	0.611
ENSG00000234675	AL445123.1	6	-0.54	0.282	0.657
ENSG00000260585	AL359851.1	X	-0.45	0.296	0.657
ENSG00000228223	HCG11	6	-0.14	0.299	0.657
ENSG00000253143	AC022730.3	8	-0.37	0.313	0.657
ENSG00000236871	LINC00106	X	-0.23	0.337	0.657
ENSG00000225298	LINC00113	21	0.53	0.346	0.657
ENSG00000230590	FTX	X	-0.19	0.347	0.657
ENSG00000261326	LINC01355	1	-0.19	0.364	0.657
ENSG00000233056	ERVH48-1	21	-0.18	0.371	0.657
ENSG00000221949	LINC01465	12	-0.18	0.402	0.675
ENSG00000225470	JPX	X	-0.09	0.411	0.675
ENSG00000254263	AC022973.3	8	-0.29	0.440	0.698
ENSG00000236532	LINC01695	21	0.31	0.474	0.705
ENSG00000250064	AC097480.1	4	0.36	0.488	0.705
ENSG00000239828	AC063944.1	3	-0.26	0.503	0.705
ENSG00000247095	MIR210HG	11	0.24	0.519	0.705
ENSG00000235139	AC003984.1	7	0.22	0.521	0.705
ENSG00000259715	AC022087.1	15	0.13	0.650	0.855
ENSG00000225077	LINC00337	1	-0.10	0.699	0.863
ENSG00000237713	AC011287.2	7	-0.14	0.706	0.863
ENSG00000256972	AP000462.3	11	-0.18	0.713	0.863
ENSG00000230250	LINC01753	1	0.09	0.830	0.918
ENSG00000260317	AC009812.4	8	0.06	0.833	0.918
ENSG00000229642	AC087857.1	3	0.09	0.845	0.918
ENSG00000261098	AP000766.1	11	0.05	0.856	0.918
ENSG00000230262	MIRLET7DHG	9	-0.03	0.866	0.918
ENSG00000246067	RAB30-AS1	11	0.03	0.878	0.918
ENSG00000230569	AC114763.2	2	-0.05	0.920	0.941
ENSG00000233237	LINC00472	6	0.00	0.987	0.987

[*] Linear models using lead control for infant sex and maternal education level

Table 9: Full results of linear lincRNA-BW regression

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000197332	AC008543.1	19	285.0	152.8	417.1	<0.001	0.018
ENSG00000260585	AL359851.1	X	144.6	75.9	213.2	<0.001	0.018
ENSG00000233237	LINC00472	6	263.9	138.4	389.4	<0.001	0.018
ENSG00000260645	AL359715.3	6	159.0	82.7	235.3	<0.001	0.018
ENSG00000261326	LINC01355	1	262.0	135.3	388.7	<0.001	0.018
ENSG00000221949	LINC01465	12	272.7	136.6	408.7	<0.001	0.020
ENSG00000230262	MIRLET7DHG	9	289.9	142.1	437.6	<0.001	0.020
ENSG00000231566	AC234772.2	X	211.1	103.5	318.7	<0.001	0.020
ENSG00000225298	LINC00113	21	116.8	56.9	176.7	<0.001	0.020
ENSG00000239828	AC063944.1	3	124.2	59.9	188.6	<0.001	0.020
ENSG00000256972	AP000462.3	11	119.2	57.2	181.2	<0.001	0.020
ENSG00000233056	ERVH48-1	21	-320.9	-487.8	-154.0	<0.001	0.020
ENSG00000260317	AC009812.4	8	216.6	103.4	329.7	<0.001	0.020
ENSG00000261098	AP000766.1	11	213.3	101.3	325.2	<0.001	0.020
ENSG00000229642	AC087857.1	3	-116.1	-178.0	-54.3	<0.001	0.020
ENSG00000227060	LINC00629	X	142.9	66.7	219.0	<0.001	0.020
ENSG00000152931	PART1	5	232.0	108.4	355.6	<0.001	0.020
ENSG00000225077	LINC00337	1	-226.9	-348.6	-105.2	<0.001	0.020
ENSG00000230569	AC114763.2	2	111.3	51.4	171.1	<0.001	0.020
ENSG00000247095	MIR210HG	11	-157.1	-241.6	-72.6	<0.001	0.020
ENSG00000260971	AC119674.1	1	190.3	87.8	292.7	<0.001	0.020
ENSG00000228223	HCG11	6	424.1	191.5	656.7	<0.001	0.023
ENSG00000225470	JPX	X	558.7	251.9	865.6	<0.001	0.023
ENSG00000230590	AL353804.1	X	254.4	111.9	396.9	0.001	0.029
ENSG00000236532	LINC01695	21	125.0	54.1	196.0	0.001	0.032
ENSG00000236871	LINC00106	X	198.5	85.2	311.8	0.001	0.032
ENSG00000237713	AC011287.2	7	136.7	58.6	214.7	0.001	0.032
ENSG00000257496	AC025031.1	12	181.7	77.4	286.1	0.001	0.033
ENSG00000229989	MIR181A1HG	1	192.6	81.8	303.5	0.001	0.033
ENSG00000246067	RAB30-AS1	11	325.5	136.7	514.4	0.001	0.033
ENSG00000235813	AL672032.1	X	121.4	50.7	192.2	0.001	0.033
ENSG00000235139	AC003984.1	7	133.4	55.6	211.1	0.001	0.033
ENSG00000250064	AC097480.1	4	106.2	44.2	168.1	0.001	0.033
ENSG00000259715	AC022087.1	15	157.7	65.4	249.9	0.001	0.033
ENSG00000223891	OSER1-AS1	20	-307.0	-486.5	-127.4	0.001	0.033
ENSG00000188185	LINC00265	7	283.8	113.7	453.9	0.001	0.042
ENSG00000249258	AC079193.2	8	185.2	73.9	296.5	0.001	0.042
ENSG00000186594	MIR22HG	17	-462.7	-741.5	-183.9	0.001	0.042
ENSG00000253385	AP003696.1	8	182.4	72.1	292.7	0.001	0.042
ENSG00000253143	AC022730.3	8	134.7	53.1	216.3	0.001	0.042
ENSG00000230250	LINC01753	1	123.5	48.3	198.7	0.002	0.044
ENSG00000240770	C21orf91-OT1	21	161.5	62.6	260.4	0.002	0.045
ENSG00000257083	AC073530.1	12	146.6	56.8	236.4	0.002	0.045
ENSG00000132204	LINC00470	18	230.8	88.9	372.7	0.002	0.045
ENSG00000254263	AC022973.3	8	120.1	45.9	194.4	0.002	0.047
ENSG00000234675	AL445123.1	6	98.5	37.4	159.7	0.002	0.048
ENSG00000228886	AL138963.1	13	116.9	43.8	190.0	0.002	0.051
ENSG00000231713	AF064860.2	21	-225.1	-366.3	-83.9	0.002	0.051
ENSG00000256155	AC022075.2	12	98.7	36.4	161.1	0.002	0.053
ENSG00000258733	LINC02328	14	126.1	46.3	205.9	0.002	0.054
ENSG00000256287	LINC02398	12	110.2	40.3	180.2	0.002	0.054
ENSG00000232986	AL139081.1	13	125.1	45.6	204.7	0.002	0.054
ENSG00000255580	AP000462.1	11	94.2	34.2	154.2	0.002	0.054
ENSG00000259820	AC083843.2	8	211.2	75.7	346.7	0.003	0.057

Table 9: Full results of linear lincRNA-BW regression *(continued)*

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000225877	PSG8-AS1	19	96.5	33.8	159.3	0.003	0.062
ENSG00000249413	AC116049.2	4	96.9	33.9	159.9	0.003	0.062
ENSG00000254060	AC022778.1	8	103.7	36.1	171.4	0.003	0.063
ENSG00000224074	LINC00691	3	152.6	52.8	252.4	0.003	0.063
ENSG00000215866	LINC01356	1	211.3	72.1	350.5	0.003	0.067
ENSG00000237243	AC022173.1	7	149.8	50.8	248.7	0.003	0.067
ENSG00000260979	AC022167.3	16	128.4	43.5	213.2	0.003	0.067
ENSG00000228697	AL023755.1	1	133.2	44.8	221.6	0.004	0.068
ENSG00000235570	LINC00533	6	95.1	31.8	158.4	0.004	0.068
ENSG00000242622	AC092910.3	3	306.9	100.6	513.3	0.004	0.074
ENSG00000230490	AL139383.1	13	188.6	61.6	315.7	0.004	0.074
ENSG00000227681	AL033504.1	6	85.1	27.1	143.1	0.004	0.081
ENSG00000251562	MALAT1	11	201.1	63.3	338.9	0.005	0.084
ENSG00000256146	AC006206.1	12	99.1	31.0	167.1	0.005	0.084
ENSG00000227502	LINC01268	6	115.1	35.7	194.5	0.005	0.086
ENSG00000227606	AC005392.1	19	173.4	53.4	293.4	0.005	0.087
ENSG00000241316	SUCLG2-AS1	3	292.2	88.7	495.6	0.005	0.089
ENSG00000224000	Z97198.1	1	94.1	28.6	159.6	0.005	0.089
ENSG00000260868	LINC01960	2	-202.0	-343.9	-60.2	0.006	0.094
ENSG00000230542	LINC00102	X	125.3	36.3	214.3	0.006	0.102
ENSG00000260930	LINC01416	18	87.2	25.2	149.2	0.006	0.102
ENSG00000178457	LINC00314	21	84.3	23.9	144.6	0.007	0.104
ENSG00000239513	LINC01210	3	96.8	27.5	166.1	0.007	0.104
ENSG00000227082	LINC00623	1	115.9	32.9	198.9	0.007	0.104
ENSG00000256115	LINC02443	12	127.3	36.0	218.6	0.007	0.104
ENSG00000249877	AC105924.1	4	55.2	15.3	95.0	0.007	0.108
ENSG00000251526	LINC02435	4	126.6	35.1	218.1	0.007	0.108
ENSG00000196758	AC079612.1	2	87.7	24.0	151.5	0.008	0.111
ENSG00000197813	AC011450.1	19	109.9	29.7	190.0	0.008	0.112
ENSG00000258038	LINC02327	14	240.8	64.9	416.7	0.008	0.112
ENSG00000212694	LINC01089	12	241.9	64.8	419.1	0.008	0.113
ENSG00000241169	FO393419.2	1	86.2	22.9	149.4	0.008	0.114
ENSG00000257097	CLIP1-AS1	12	142.6	36.8	248.4	0.009	0.118
ENSG00000197291	RAMP2-AS1	17	149.1	38.0	260.2	0.009	0.118
ENSG00000254162	AC009812.3	8	224.2	57.2	391.3	0.009	0.118
ENSG00000259345	AC013652.1	15	184.4	46.4	322.5	0.01	0.118
ENSG00000228906	FTX	X	105.5	26.4	184.6	0.01	0.118
ENSG00000254177	AC079209.2	8	83.3	20.8	145.8	0.01	0.118
ENSG00000228634	AL136115.1	1	120.1	29.9	210.2	0.01	0.118
ENSG00000255864	AC069208.1	12	123.0	30.6	215.4	0.01	0.118
ENSG00000183674	LINC00518	6	-111.2	-194.7	-27.7	0.01	0.118
ENSG00000253364	AL928742.1	14	99.5	24.5	174.5	0.01	0.118
ENSG00000229236	TTTY10	Y	133.9	32.7	235.0	0.01	0.118
ENSG00000261019	AC010132.4	7	87.8	21.4	154.1	0.01	0.118
ENSG00000246145	RRS1-AS1	8	173.1	42.2	304.0	0.01	0.118
ENSG00000259129	LINC00648	14	121.8	29.7	213.9	0.01	0.118
ENSG00000251363	LINC02315	14	106.8	26.0	187.6	0.01	0.118
ENSG00000230233	AF240627.1	21	70.1	17.0	123.1	0.01	0.118
ENSG00000236453	AC003092.1	7	114.3	27.6	201.0	0.01	0.118
ENSG00000204148	LINC00474	9	174.6	42.1	307.2	0.011	0.118
ENSG00000227676	LINC01068	13	-109.2	-192.2	-26.3	0.011	0.118
ENSG00000203721	LINC00862	1	119.5	28.7	210.3	0.011	0.118
ENSG00000248187	AC078850.1	4	101.6	24.2	179.0	0.011	0.118

Table 9: Full results of linear lincRNA-BW regression *(continued)*

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000224959	AC017002.1	2	112.8	26.9	198.8	0.011	0.118
ENSG00000242282	AC108488.1	2	161.3	38.3	284.3	0.011	0.118
ENSG00000254054	AC087273.2	8	99.5	23.6	175.4	0.011	0.118
ENSG00000242759	LINC00882	3	212.3	50.0	374.6	0.011	0.119
ENSG00000232104	RFX3-AS1	9	151.2	34.7	267.7	0.012	0.124
ENSG00000227542	AC092614.1	2	105.3	24.1	186.5	0.012	0.124
ENSG00000223842	AL360093.1	1	124.7	28.5	220.9	0.012	0.124
ENSG00000206129	AC006305.1	18	118.6	26.6	210.7	0.012	0.127
ENSG00000229807	XIST	X	103.4	23.0	183.8	0.013	0.129
ENSG00000214870	AC004540.1	7	146.1	31.9	260.2	0.013	0.130
ENSG00000250790	AC127070.3	12	101.6	22.2	181.0	0.013	0.130
ENSG00000229618	AC011287.1	7	115.1	25.1	205.2	0.013	0.130
ENSG00000228386	AL031668.1	20	99.9	21.3	178.5	0.014	0.135
ENSG00000235244	DANT2	X	70.9	15.0	126.9	0.014	0.135
ENSG00000189229	AC069277.1	3	139.0	29.4	248.7	0.014	0.135
ENSG00000228980	LINC01205	3	109.6	23.0	196.3	0.014	0.136
ENSG00000257151	PWAR6	15	88.9	18.4	159.4	0.014	0.138
ENSG00000260761	AC106754.1	5	91.1	18.7	163.5	0.014	0.138
ENSG00000231755	CHODL-AS1	21	131.7	25.7	237.6	0.016	0.149
ENSG00000233828	LINC01949	5	189.2	36.5	342.0	0.016	0.150
ENSG00000245694	CRNDE	16	136.3	26.3	246.2	0.016	0.150
ENSG00000261423	TMEM202-AS1	15	180.4	34.4	326.4	0.016	0.151
ENSG00000250303	AP002884.3	11	141.7	26.5	256.9	0.017	0.154
ENSG00000261159	AC112484.4	3	86.5	16.1	157.0	0.017	0.154
ENSG00000235021	AL591848.2	1	111.2	20.4	202.0	0.017	0.155
ENSG00000259450	AC113146.2	15	79.8	14.6	144.9	0.017	0.155
ENSG00000234509	AP000253.1	21	120.9	22.1	219.7	0.017	0.155
ENSG00000228106	AL392172.1	1	143.8	25.9	261.8	0.018	0.157
ENSG00000254211	LINC01485	5	116.0	20.8	211.2	0.018	0.157
ENSG00000233008	LINC01725	1	141.6	24.4	258.8	0.019	0.165
ENSG00000259306	AC020891.2	15	120.6	20.5	220.7	0.019	0.166
ENSG00000248874	C5orf17	5	161.2	27.3	295.1	0.019	0.166
ENSG00000234948	LINC01524	20	-81.9	-150.1	-13.8	0.02	0.166
ENSG00000249476	AC008467.1	5	139.0	22.5	255.5	0.02	0.172
ENSG00000230317	LINC01284	X	-77.2	-142.2	-12.3	0.021	0.175
ENSG00000247157	LINC01252	12	69.7	10.4	129.1	0.022	0.186
ENSG00000228933	AC107419.1	X	81.7	12.1	151.4	0.023	0.186
ENSG00000242553	AP001432.1	21	141.1	20.7	261.4	0.023	0.186
ENSG00000258768	AL356019.2	14	79.5	11.0	148.0	0.024	0.196
ENSG00000213468	FIRRE	X	-221.7	-413.2	-30.3	0.024	0.197
ENSG00000226149	AL356124.1	6	127.6	17.1	238.0	0.025	0.199
ENSG00000258548	LINC00645	14	84.6	11.2	158.1	0.025	0.201
ENSG00000261220	AC103706.1	8	162.4	20.6	304.1	0.026	0.203
ENSG00000231401	AC023481.1	3	80.7	10.2	151.2	0.026	0.203
ENSG00000226751	AF127936.1	21	94.4	11.9	176.9	0.026	0.203
ENSG00000229108	MEOX2-AS1	7	110.5	13.9	207.0	0.026	0.203
ENSG00000242781	LINC02050	3	70.7	8.8	132.6	0.026	0.203
ENSG00000227517	LINC01483	17	146.6	18.0	275.1	0.027	0.203
ENSG00000234535	AL161719.1	13	104.0	12.8	195.2	0.027	0.203
ENSG00000226258	GRM7-AS3	3	84.9	10.4	159.3	0.027	0.203
ENSG00000261795	AC093627.7	7	88.3	10.7	166.0	0.027	0.203
ENSG00000238198	AL357055.3	1	135.9	16.3	255.4	0.027	0.203
ENSG00000249464	LINC01091	4	169.6	19.6	319.7	0.028	0.207

Table 9: Full results of linear lincRNA-BW regression *(continued)*

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000185168	LINC00482	17	-199.2	-375.7	-22.7	0.028	0.207
ENSG00000228261	AL162742.1	10	144.4	16.4	272.4	0.028	0.207
ENSG00000232294	AL031674.1	20	-59.9	-113.1	-6.8	0.028	0.207
ENSG00000249797	LINC02147	5	76.0	8.2	143.7	0.029	0.212
ENSG00000260468	LINC01290	16	119.4	12.6	226.2	0.03	0.214
ENSG00000232855	AF165147.1	21	102.5	10.7	194.3	0.03	0.214
ENSG00000255933	AC117500.3	12	104.3	10.4	198.1	0.031	0.216
ENSG00000260209	AP000842.3	11	66.4	6.6	126.1	0.031	0.216
ENSG00000248599	FLJ42969	8	-72.9	-138.6	-7.2	0.031	0.216
ENSG00000248100	AC087257.1	12	91.5	9.0	174.0	0.031	0.216
ENSG00000234432	AC092171.3	7	170.6	16.5	324.7	0.031	0.218
ENSG00000261087	AP003469.4	8	190.0	17.0	362.9	0.033	0.226
ENSG00000255660	RERG-AS1	12	74.1	6.5	141.7	0.033	0.226
ENSG00000242767	ZBTB20-AS4	3	71.3	6.2	136.4	0.033	0.227
ENSG00000250903	GMDS-AS1	6	173.4	14.5	332.4	0.034	0.230
ENSG00000250508	AP000808.1	11	109.5	8.9	210.1	0.034	0.231
ENSG00000248866	USP46-AS1	4	152.4	11.5	293.4	0.035	0.238
ENSG00000225746	MEG8	14	123.6	9.0	238.1	0.036	0.238
ENSG00000251138	AC090502.1	12	65.1	4.7	125.5	0.036	0.238
ENSG00000259423	AC113146.1	15	67.1	4.8	129.5	0.036	0.238
ENSG00000259240	MIR4713HG	15	87.3	6.1	168.5	0.036	0.238
ENSG00000254998	AP003181.1	11	105.4	7.2	203.5	0.037	0.238
ENSG00000185904	LINC00839	10	80.1	5.5	154.8	0.037	0.238
ENSG00000240050	AL590542.1	6	103.1	6.9	199.3	0.037	0.238
ENSG00000228043	AC114763.1	2	110.7	7.4	214.0	0.037	0.238
ENSG00000257474	AC027288.1	12	70.7	4.6	136.8	0.037	0.239
ENSG00000255980	AP000439.3	11	84.2	5.4	163.1	0.038	0.239
ENSG00000228423	AL357552.2	1	62.6	4.0	121.2	0.038	0.239
ENSG00000259692	AC104041.1	15	120.6	7.3	234.0	0.038	0.241
ENSG00000203709	C1orf132	1	148.2	8.8	287.5	0.038	0.241
ENSG00000227544	AC018647.1	7	79.3	4.5	154.0	0.039	0.241
ENSG00000255565	AC073651.1	12	79.8	4.5	155.1	0.039	0.241
ENSG00000260558	AC018557.2	16	89.2	5.0	173.5	0.039	0.241
ENSG00000234378	AC098828.3	2	-72.2	-140.4	-4.0	0.039	0.241
ENSG00000253733	LZTS1-AS1	8	62.2	3.3	121.1	0.04	0.244
ENSG00000259336	AC021231.1	15	73.6	3.7	143.6	0.04	0.244
ENSG00000230817	LINC01362	1	65.7	3.3	128.0	0.04	0.244
ENSG00000242268	LINC02082	3	85.8	4.2	167.4	0.041	0.244
ENSG00000235180	LINC00601	10	-104.6	-204.6	-4.6	0.042	0.249
ENSG00000225791	TRAM2-AS1	6	-149.5	-292.8	-6.3	0.042	0.249
ENSG00000254233	LINC02365	4	172.6	7.2	338.0	0.042	0.249
ENSG00000250889	LINC01336	5	177.1	7.3	346.9	0.042	0.249
ENSG00000230563	AL121757.1	20	-54.1	-106.3	-1.9	0.044	0.256
ENSG00000254653	AC024475.1	11	84.6	2.8	166.3	0.044	0.256
ENSG00000237484	LINC01684	21	66.0	2.1	129.8	0.044	0.256
ENSG00000251273	LINC02228	5	82.0	2.6	161.5	0.044	0.256
ENSG00000250072	AC091940.1	5	148.7	4.5	292.8	0.045	0.256
ENSG00000203999	LINC01270	20	-89.2	-175.7	-2.6	0.045	0.256
ENSG00000236204	LINC01376	2	182.2	5.1	359.3	0.045	0.256
ENSG00000255910	AC024901.1	12	94.4	2.6	186.1	0.045	0.256
ENSG00000226935	LINC00161	21	60.7	1.6	119.8	0.045	0.256
ENSG00000236892	AL357833.2	10	96.8	2.3	191.4	0.046	0.259
ENSG00000259359	AC012409.1	15	65.8	1.5	130.0	0.046	0.259

Table 9: Full results of linear lincRNA-BW regression *(continued)*

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000238113	LINC01410	9	73.9	1.4	146.3	0.047	0.261
ENSG00000223546	LINC00630	X	303.6	5.3	601.9	0.047	0.261
ENSG00000203809	LIN28B-AS1	6	85.1	1.4	168.8	0.048	0.261
ENSG00000259365	AC019254.2	15	76.2	1.2	151.3	0.048	0.261
ENSG00000254266	PKIA-AS1	8	79.2	1.3	157.1	0.048	0.261
ENSG00000245532	NEAT1	11	111.6	1.7	221.4	0.048	0.261
ENSG00000245060	LINC00847	5	-104.8	-208.8	-0.9	0.05	0.265
ENSG00000214691	LINC01913	2	47.6	0.4	94.9	0.05	0.265
ENSG00000257556	LINC02298	14	90.8	0.7	180.9	0.05	0.265
ENSG00000251504	LINC01099	4	81.5	0.6	162.3	0.05	0.265
ENSG00000255142	AP006621.2	11	81.6	0.6	162.7	0.05	0.265
ENSG00000237523	LINC00857	10	-191.2	-381.6	-0.9	0.05	0.267
ENSG00000258526	AL049875.1	14	69.8	0.3	139.3	0.051	0.267
ENSG00000256973	AC053513.1	12	73.9	0.1	147.6	0.051	0.268
ENSG00000260955	AC100821.2	8	76.4	-0.2	153.0	0.052	0.271
ENSG00000260418	AL023284.4	6	-103.3	-207.1	0.5	0.052	0.273
ENSG00000250241	AC105383.1	4	71.9	-0.5	144.3	0.053	0.275
ENSG00000259915	AC017071.1	2	75.3	-0.7	151.3	0.054	0.275
ENSG00000230105	AL354793.1	X	-71.0	-142.8	0.7	0.054	0.275
ENSG00000261770	AC006504.1	19	65.5	-0.7	131.7	0.054	0.275
ENSG00000232316	LINC02518	6	-82.8	-166.9	1.4	0.055	0.281
ENSG00000223387	LINC02068	3	63.8	-1.3	128.9	0.056	0.281
ENSG00000224957	LINC01266	3	64.3	-1.3	129.9	0.056	0.281
ENSG00000214548	MEG3	14	83.4	-1.7	168.5	0.056	0.281
ENSG00000238039	AC244197.2	X	74.3	-1.6	150.2	0.056	0.281
ENSG00000258028	AL138974.1	14	120.1	-2.6	242.8	0.056	0.281
ENSG00000234292	AC123595.1	5	-85.0	-171.9	1.9	0.057	0.282
ENSG00000258100	AC025035.1	12	64.6	-1.8	131.1	0.058	0.287
ENSG00000249628	LINC00942	12	-57.4	-116.8	2.0	0.06	0.292
ENSG00000248685	LINC02484	4	45.0	-1.6	91.5	0.06	0.292
ENSG00000248605	AC022140.1	5	53.6	-1.9	109.2	0.06	0.293
ENSG00000241449	AC092666.1	7	62.3	-2.4	127.0	0.061	0.293
ENSG00000233208	LINC00642	14	-73.3	-149.4	2.9	0.061	0.293
ENSG00000250658	AC097652.1	4	79.5	-3.1	162.1	0.061	0.293
ENSG00000232229	LINC00865	10	101.1	-4.2	206.4	0.061	0.294
ENSG00000240219	AL512306.2	1	82.3	-3.5	168.1	0.061	0.294
ENSG00000223956	LINC01767	1	73.3	-3.3	149.9	0.062	0.297
ENSG00000226674	TEX41	2	55.2	-2.7	113.0	0.063	0.299
ENSG00000259543	AC060809.1	15	62.8	-3.1	128.7	0.064	0.300
ENSG00000259685	AC092769.1	15	-60.3	-123.8	3.2	0.064	0.302
ENSG00000228044	AL160408.1	1	-67.5	-138.8	3.8	0.065	0.305
ENSG00000179523	EIF3J-AS1	15	289.4	-16.7	595.5	0.065	0.305
ENSG00000251654	AC099499.1	5	53.0	-3.1	109.2	0.066	0.305
ENSG00000256443	AP003559.1	11	95.3	-5.9	196.5	0.066	0.307
ENSG00000259230	LINC02323	14	58.3	-3.6	120.1	0.067	0.307
ENSG00000260025	AC009414.2	2	-139.1	-287.2	9.0	0.067	0.309
ENSG00000259518	LINC01583	15	57.5	-3.8	118.7	0.068	0.310
ENSG00000261008	LINC01572	16	86.5	-6.3	179.2	0.069	0.315
ENSG00000248762	AC012339.1	8	69.6	-5.1	144.3	0.069	0.315
ENSG00000231742	LINC01273	20	-70.6	-146.5	5.3	0.07	0.315
ENSG00000259834	AL365361.1	1	56.5	-4.2	117.1	0.07	0.315
ENSG00000235612	AL353681.1	1	78.7	-6.0	163.5	0.07	0.316
ENSG00000231010	AL121672.1	22	61.1	-4.7	127.0	0.071	0.316

Table 9: Full results of linear lincRNA-BW regression *(continued)*

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000234111	LINC02433	4	62.3	-5.0	129.6	0.071	0.317
ENSG00000260179	AL162741.1	1	63.2	-5.1	131.6	0.071	0.317
ENSG00000253508	AC004080.2	7	78.9	-6.4	164.2	0.072	0.317
ENSG00000259594	AC023034.1	15	81.2	-6.7	169.2	0.072	0.317
ENSG00000227306	AP006285.1	11	55.6	-4.7	115.9	0.072	0.317
ENSG00000256540	AC007406.3	12	67.9	-5.8	141.7	0.073	0.318
ENSG00000244041	LINC01011	6	116.9	-10.2	244.0	0.073	0.319
ENSG00000215386	MIR99AHG	21	81.3	-7.2	169.8	0.073	0.319
ENSG00000241219	AC078785.2	3	-64.8	-135.5	6.0	0.075	0.322
ENSG00000261542	AC011978.2	8	101.4	-9.5	212.3	0.075	0.322
ENSG00000227619	AL391056.1	9	-56.2	-117.9	5.4	0.076	0.324
ENSG00000259005	AC005479.2	14	-67.6	-141.7	6.6	0.076	0.324
ENSG00000256422	LINC02552	11	48.3	-5.1	101.7	0.078	0.331
ENSG00000260509	AL590787.1	13	56.9	-6.0	119.8	0.078	0.331
ENSG00000251370	SEMA5A-AS1	5	53.1	-5.7	111.9	0.078	0.332
ENSG00000256433	AC005840.3	12	94.7	-10.3	199.7	0.079	0.332
ENSG00000253270	AC090541.1	8	105.2	-11.5	221.9	0.079	0.332
ENSG00000248174	LINC02268	4	58.2	-6.4	122.8	0.079	0.332
ENSG00000236318	AC019117.2	7	83.9	-9.3	177.0	0.079	0.332
ENSG00000231028	LINC00271	6	76.0	-8.6	160.7	0.08	0.333
ENSG00000260710	AC120498.4	16	99.3	-11.6	210.3	0.081	0.336
ENSG00000260423	LINC02367	12	56.2	-6.8	119.1	0.082	0.338
ENSG00000247400	DNAJC3-AS1	13	163.9	-19.9	347.8	0.082	0.338
ENSG00000245156	AP001107.1	11	93.3	-11.5	198.1	0.082	0.338
ENSG00000233321	AL357833.1	10	81.3	-10.0	172.7	0.083	0.338
ENSG00000253773	C8orf37-AS1	8	105.0	-13.6	223.6	0.084	0.344
ENSG00000224271	AL117329.1	22	-45.3	-96.6	6.0	0.085	0.346
ENSG00000231595	AC005224.1	17	106.2	-14.2	226.7	0.086	0.346
ENSG00000253686	LINC01484	5	69.4	-9.3	148.2	0.086	0.346
ENSG00000231236	AP001605.1	21	54.0	-7.4	115.4	0.086	0.347
ENSG00000204446	C9orf170	9	90.6	-12.6	193.8	0.087	0.349
ENSG00000247765	AC068446.2	15	59.8	-8.4	128.0	0.087	0.349
ENSG00000227292	AC009229.1	2	85.7	-12.3	183.7	0.088	0.350
ENSG00000234449	FAM239A	X	38.8	-5.6	83.1	0.088	0.350
ENSG00000237877	LINC01473	2	89.0	-12.9	190.9	0.088	0.350
ENSG00000228784	LINC00954	2	83.4	-12.3	179.1	0.089	0.352
ENSG00000251497	PITPNM2-AS1	12	74.1	-11.1	159.3	0.09	0.353
ENSG00000232774	FLJ22447	14	-74.3	-159.9	11.2	0.09	0.353
ENSG00000259687	LINC01220	14	-66.7	-143.6	10.1	0.09	0.353
ENSG00000258399	AL117190.1	14	70.5	-10.9	151.8	0.091	0.355
ENSG00000259532	AC009269.3	15	54.0	-8.6	116.6	0.093	0.359
ENSG00000233895	AL121761.1	20	194.9	-31.2	421.0	0.093	0.359
ENSG00000249740	OSMR-AS1	5	98.6	-16.2	213.4	0.094	0.362
ENSG00000233903	Z83851.1	22	-80.1	-173.4	13.2	0.094	0.362
ENSG00000215244	AL137145.2	10	54.5	-9.2	118.2	0.095	0.365
ENSG00000224934	AL391684.1	10	87.7	-15.2	190.6	0.096	0.367
ENSG00000254538	AC027018.1	8	59.0	-10.4	128.4	0.097	0.367
ENSG00000251136	AF117829.1	8	152.0	-27.0	331.1	0.098	0.367
ENSG00000256218	AC007848.2	12	51.7	-9.2	112.7	0.098	0.367
ENSG00000226756	AC007365.1	2	82.9	-14.9	180.7	0.098	0.367
ENSG00000197182	MIRLET7BHG	22	97.2	-17.5	212.0	0.098	0.367
ENSG00000257084	MIR200CHG	12	-118.0	-257.1	21.2	0.098	0.367
ENSG00000258171	LINC02412	12	45.5	-8.2	99.2	0.098	0.367
ENSG00000259153	AC004816.1	14	-86.2	-188.3	15.9	0.1	0.371

Table 9: Full results of linear lincRNA-BW regression *(continued)*

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000251432	AC108062.1	4	162.1	-30.1	354.3	0.1	0.371
ENSG00000260855	AL591848.4	1	84.0	-15.8	183.7	0.101	0.372
ENSG00000228340	MIR646HG	20	77.0	-14.7	168.7	0.101	0.374
ENSG00000237989	LINC01679	21	-57.7	-126.6	11.2	0.102	0.375
ENSG00000255670	AC007619.1	12	73.7	-14.4	161.7	0.103	0.376
ENSG00000226383	LINC01876	2	64.2	-12.6	141.1	0.103	0.376
ENSG00000226197	AL583785.1	9	90.3	-17.8	198.4	0.103	0.376
ENSG00000235731	LINC02250	15	61.3	-12.3	134.8	0.104	0.376
ENSG00000250230	AP002754.1	11	90.1	-18.2	198.3	0.105	0.376
ENSG00000237940	LINC01238	2	52.5	-10.6	115.5	0.105	0.376
ENSG00000222030	LINC01793	2	63.4	-12.9	139.6	0.105	0.376
ENSG00000248432	AC139718.1	4	-46.0	-101.4	9.4	0.105	0.376
ENSG00000227885	AL590652.1	6	97.6	-19.9	215.1	0.105	0.376
ENSG00000256204	AC073862.1	12	-53.0	-116.7	10.8	0.105	0.376
ENSG00000257817	AC026765.2	12	92.7	-19.3	204.7	0.106	0.378
ENSG00000227630	LINC01132	1	-114.3	-253.0	24.4	0.108	0.382
ENSG00000254367	AC087269.1	8	51.8	-11.2	114.9	0.109	0.384
ENSG00000230615	AL139220.2	1	-50.0	-111.0	10.9	0.109	0.384
ENSG00000250786	SNHG18	5	77.4	-16.9	171.6	0.109	0.384
ENSG00000234083	AJ006995.1	21	50.0	-11.1	111.1	0.11	0.386
ENSG00000245937	LINC01184	5	162.6	-36.3	361.5	0.111	0.387
ENSG00000228707	AL691426.1	9	147.9	-33.6	329.4	0.112	0.389
ENSG00000225879	AL109924.1	6	47.4	-10.8	105.5	0.112	0.389
ENSG00000226380	AC016831.1	7	96.4	-22.2	215.1	0.113	0.391
ENSG00000225206	MIR137HG	1	42.9	-10.0	95.8	0.114	0.392
ENSG00000261734	AC116096.1	3	47.6	-11.2	106.3	0.114	0.393
ENSG00000237604	AP001056.1	21	54.1	-12.8	120.9	0.114	0.393
ENSG00000236008	LINC01814	2	73.2	-17.5	163.9	0.115	0.395
ENSG00000235823	OLMALINC	10	119.6	-28.8	267.9	0.116	0.395
ENSG00000237560	LINC01497	17	58.2	-14.1	130.6	0.116	0.395
ENSG00000175746	C15orf54	15	53.8	-13.1	120.7	0.117	0.395
ENSG00000251676	SNHG27	4	51.4	-12.7	115.6	0.118	0.399
ENSG00000255284	AP006621.3	11	115.3	-29.6	260.2	0.12	0.403
ENSG00000260777	AC061975.1	17	54.9	-14.2	124.0	0.121	0.403
ENSG00000253821	AC090796.1	8	44.1	-11.4	99.6	0.121	0.403
ENSG00000238097	LINC02037	3	-104.4	-236.0	27.1	0.121	0.403
ENSG00000247982	LINC00926	15	93.0	-24.2	210.2	0.122	0.403
ENSG00000254290	AC124067.4	8	-127.2	-287.6	33.2	0.122	0.403
ENSG00000260988	AC090260.1	15	71.8	-18.8	162.4	0.122	0.403
ENSG00000230454	U73166.1	3	107.6	-28.1	243.3	0.122	0.403
ENSG00000181798	LINC00471	2	57.3	-15.5	130.2	0.125	0.411
ENSG00000261842	AC073314.1	7	59.7	-16.7	136.2	0.127	0.419
ENSG00000251442	LINC01094	4	87.8	-24.9	200.6	0.128	0.421
ENSG00000249857	AC027338.2	5	45.8	-13.1	104.6	0.129	0.423
ENSG00000241163	LINC00877	3	-80.7	-184.9	23.4	0.13	0.425
ENSG00000253138	LINC00967	8	-106.9	-245.1	31.3	0.131	0.426
ENSG00000227946	AC007383.2	2	173.3	-51.0	397.7	0.132	0.426
ENSG00000224141	MIR548XHG	21	35.1	-10.3	80.5	0.132	0.426
ENSG00000225399	AC121247.1	3	52.7	-15.6	121.0	0.132	0.426
ENSG00000173862	AC008080.1	7	54.6	-16.2	125.5	0.132	0.426
ENSG00000248131	LINC01194	5	130.8	-39.3	301.0	0.133	0.427
ENSG00000226599	AL450344.2	6	50.3	-15.1	115.8	0.133	0.427
ENSG00000256073	URB1-AS1	21	-130.5	-300.7	39.7	0.135	0.430

Table 9: Full results of linear lincRNA-BW regression *(continued)*

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000245468	LINC02447	4	55.1	-16.9	127.1	0.135	0.430
ENSG00000198685	LINC01565	3	53.3	-16.7	123.2	0.137	0.434
ENSG00000255247	AP003390.2	11	50.6	-15.8	117.1	0.137	0.434
ENSG00000227467	LINC01537	11	-46.0	-106.6	14.5	0.138	0.435
ENSG00000235641	LINC00484	9	52.2	-16.5	121.0	0.138	0.435
ENSG00000197180	CH17-340M24.3	X	-90.5	-209.9	29.0	0.139	0.438
ENSG00000259610	AC023034.2	15	60.7	-19.6	141.1	0.14	0.438
ENSG00000259070	LINC00639	14	60.7	-19.6	141.1	0.14	0.438
ENSG00000259995	AC106729.1	16	-54.9	-127.7	17.8	0.141	0.438
ENSG00000261177	AC135012.1	16	36.7	-12.0	85.3	0.141	0.439
ENSG00000237166	LINC01792	2	-43.6	-101.6	14.4	0.142	0.441
ENSG00000260259	LINC02166	16	50.6	-16.8	117.9	0.143	0.441
ENSG00000231826	LINC01819	2	-49.2	-114.9	16.4	0.143	0.441
ENSG00000245832	MIR4300HG	11	58.6	-19.6	136.8	0.144	0.441
ENSG00000254197	AC011676.3	8	46.3	-15.5	108.1	0.144	0.441
ENSG00000234390	USP27X-AS1	X	-137.6	-321.5	46.2	0.144	0.441
ENSG00000179082	C9orf106	9	58.8	-19.8	137.4	0.145	0.441
ENSG00000249685	AC079921.2	4	100.8	-35.1	236.6	0.148	0.449
ENSG00000250620	LINC02515	4	45.3	-15.9	106.4	0.148	0.451
ENSG00000227244	LINC00845	10	50.7	-17.9	119.2	0.149	0.451
ENSG00000224914	LINC00863	10	71.8	-25.4	169.0	0.149	0.451
ENSG00000250748	AC025419.1	12	45.4	-16.1	107.0	0.15	0.452
ENSG00000243701	DUBR	3	130.4	-46.6	307.4	0.15	0.452
ENSG00000256120	SOX5-AS1	12	48.1	-17.5	113.6	0.152	0.455
ENSG00000224286	LINC01142	1	43.9	-16.0	103.7	0.152	0.455
ENSG00000260193	AL138781.1	9	-59.6	-141.0	21.7	0.152	0.455
ENSG00000182165	TP53TG1	7	95.5	-35.0	226.0	0.153	0.456
ENSG00000237525	AC012668.3	2	45.7	-17.1	108.5	0.155	0.461
ENSG00000223685	LINC00571	13	98.9	-37.1	235.0	0.156	0.461
ENSG00000245975	AC090515.2	15	-100.2	-238.3	37.9	0.157	0.461
ENSG00000122548	KIAA0087	7	54.5	-20.6	129.7	0.157	0.461
ENSG00000235947	EGOT	3	51.4	-19.5	122.4	0.157	0.461
ENSG00000236120	AC110995.1	X	56.3	-21.5	134.2	0.158	0.461
ENSG00000251164	HULC	6	48.8	-18.8	116.3	0.159	0.461
ENSG00000224939	LINC00184	1	-50.5	-120.3	19.4	0.159	0.461
ENSG00000258169	LINC00485	12	43.1	-16.6	102.7	0.159	0.461
ENSG00000224310	LINC01567	16	-44.9	-107.1	17.4	0.159	0.461
ENSG00000189419	SPATA41	15	-44.6	-106.4	17.3	0.159	0.461
ENSG00000249267	LINC00939	12	44.3	-17.1	105.7	0.159	0.461
ENSG00000198221	AFDN-AS1	6	52.1	-20.5	124.6	0.161	0.463
ENSG00000258537	FRMD6-AS2	14	62.4	-24.6	149.5	0.161	0.463
ENSG00000260805	AC092803.2	1	124.1	-48.9	297.1	0.161	0.463
ENSG00000257612	MIR4307HG	14	32.0	-12.8	76.9	0.163	0.465
ENSG00000260388	LINC00562	13	45.6	-18.2	109.5	0.163	0.465
ENSG00000253776	AC099520.2	5	44.5	-17.9	106.9	0.164	0.465
ENSG00000225675	LINC01771	1	-75.8	-182.1	30.5	0.164	0.465
ENSG00000219159	AC011298.1	2	-46.2	-111.1	18.6	0.164	0.465
ENSG00000259786	LINC02109	5	51.9	-21.1	125.0	0.165	0.467
ENSG00000253428	LINC01942	5	40.4	-16.5	97.3	0.166	0.468
ENSG00000217825	AC099552.1	7	-53.6	-129.2	22.0	0.166	0.468
ENSG00000226548	AC016722.1	2	74.2	-30.6	179.1	0.167	0.468
ENSG00000212766	EWSAT1	15	65.1	-27.1	157.4	0.168	0.469
ENSG00000233079	LINC01755	1	53.1	-22.2	128.4	0.168	0.469

Table 9: Full results of linear lincRNA-BW regression *(continued)*

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000223783	LINC01983	3	-48.0	-116.2	20.1	0.169	0.469
ENSG00000261222	AC064805.1	17	39.5	-16.6	95.5	0.169	0.469
ENSG00000260476	AC104794.3	2	-65.1	-157.6	27.3	0.169	0.469
ENSG00000226476	LINC01748	1	65.2	-27.7	158.1	0.171	0.473
ENSG00000234492	RPL34-AS1	4	47.9	-20.5	116.4	0.171	0.473
ENSG00000224950	AL390066.1	1	59.1	-25.4	143.6	0.172	0.474
ENSG00000231106	LINC01436	21	-38.5	-93.6	16.6	0.173	0.475
ENSG00000257086	AP001453.3	11	99.2	-43.4	241.9	0.174	0.479
ENSG00000250509	AC034213.1	5	-46.2	-112.9	20.5	0.176	0.483
ENSG00000230401	LINC01972	3	43.6	-19.5	106.6	0.177	0.484
ENSG00000249669	CARMN	5	61.7	-27.7	151.1	0.178	0.485
ENSG00000254039	AC027801.4	17	-83.4	-205.1	38.3	0.181	0.491
ENSG00000230647	AC022816.1	17	-49.6	-122.0	22.8	0.181	0.491
ENSG00000227911	LINC02344	13	41.2	-19.6	102.0	0.186	0.503
ENSG00000228918	LINC01344	1	38.9	-19.1	96.8	0.19	0.514
ENSG00000233154	LINC01762	1	68.5	-33.7	170.8	0.191	0.514
ENSG00000260884	AC009120.4	16	59.8	-29.5	149.1	0.191	0.514
ENSG00000197308	GATA3-AS1	10	61.1	-30.5	152.8	0.192	0.515
ENSG00000212743	AL137145.1	10	-42.4	-105.9	21.1	0.192	0.515
ENSG00000228265	RALY-AS1	20	-101.9	-255.3	51.5	0.195	0.519
ENSG00000258593	AL583810.1	14	38.0	-19.3	95.3	0.195	0.519
ENSG00000244625	MIATNB	22	94.4	-48.3	237.1	0.196	0.521
ENSG00000261229	AC021483.2	15	71.1	-36.4	178.5	0.197	0.521
ENSG00000230733	AC092171.2	7	110.2	-57.0	277.3	0.198	0.524
ENSG00000176659	C20orf197	20	51.7	-26.9	130.3	0.199	0.525
ENSG00000247373	AC055713.1	12	105.7	-55.2	266.6	0.199	0.525
ENSG00000254973	AC105219.4	8	61.5	-32.9	156.0	0.203	0.535
ENSG00000260633	AC010207.1	3	-52.0	-132.6	28.6	0.208	0.545
ENSG00000249816	LINC00964	8	43.7	-24.1	111.5	0.208	0.545
ENSG00000259447	AC013652.2	15	42.1	-23.3	107.4	0.208	0.545
ENSG00000214900	LINC01588	14	113.9	-63.6	291.5	0.21	0.547
ENSG00000234308	LINC01878	2	-39.4	-100.7	22.0	0.21	0.547
ENSG00000245685	AF250324.1	4	42.1	-23.7	108.0	0.211	0.547
ENSG00000248510	LINC02267	4	48.0	-27.1	123.0	0.212	0.547
ENSG00000236924	AL162411.1	9	52.7	-29.8	135.1	0.212	0.547
ENSG00000225493	LINC01107	2	37.9	-21.4	97.2	0.212	0.547
ENSG00000226308	AL122058.1	20	-46.4	-119.3	26.5	0.214	0.549
ENSG00000254235	AC022784.6	8	-34.2	-88.0	19.6	0.214	0.549
ENSG00000225860	LINC02072	17	41.8	-24.4	107.9	0.217	0.555
ENSG00000250635	CXXC5-AS1	5	57.3	-33.4	148.0	0.217	0.555
ENSG00000245750	DRAIC	15	-42.7	-110.4	25.0	0.218	0.555
ENSG00000248508	SRP14-AS1	15	94.2	-55.2	243.5	0.218	0.555
ENSG00000203801	LINC00222	6	54.3	-32.0	140.6	0.219	0.556
ENSG00000234630	AC245060.2	22	38.2	-22.7	99.1	0.22	0.557
ENSG00000255557	AP001266.2	11	47.1	-28.1	122.4	0.221	0.557
ENSG00000251615	AC104825.2	4	87.4	-52.1	226.9	0.221	0.557
ENSG00000258935	AL096869.1	14	56.8	-33.9	147.4	0.221	0.557
ENSG00000245522	AC026250.1	11	-106.9	-277.9	64.1	0.222	0.558
ENSG00000248370	LINC02434	4	81.2	-49.1	211.4	0.223	0.559
ENSG00000233821	ENOX1-AS1	13	36.5	-22.1	95.0	0.223	0.559
ENSG00000189275	LINC01164	10	-34.6	-90.2	21.0	0.224	0.559
ENSG00000246898	LINC00920	16	65.4	-40.0	170.9	0.225	0.559
ENSG00000224750	AL391704.1	10	-41.9	-109.4	25.7	0.226	0.559
ENSG00000227012	LINC02527	6	-19.1	-49.9	11.7	0.226	0.559

Table 9: Full results of linear lincRNA-BW regression *(continued)*

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000236393	AC091806.1	X	-69.3	-181.1	42.6	0.226	0.559
ENSG00000232416	BPESC1	3	35.9	-22.1	93.9	0.227	0.559
ENSG00000261320	AC009061.1	16	40.0	-24.7	104.7	0.227	0.559
ENSG00000233393	AP000688.2	21	48.8	-30.1	127.7	0.227	0.559
ENSG00000260257	AL035071.1	20	-149.3	-391.0	92.4	0.227	0.559
ENSG00000233891	AC007179.2	2	39.7	-24.7	104.0	0.229	0.560
ENSG00000251359	WWC2-AS2	4	51.1	-31.9	134.2	0.229	0.560
ENSG00000259485	LINC02253	15	-55.9	-147.1	35.2	0.23	0.562
ENSG00000246526	LINC002481	4	84.2	-53.4	221.8	0.232	0.565
ENSG00000251310	AC107391.1	4	25.2	-16.1	66.5	0.232	0.565
ENSG00000250490	LINC02145	5	-40.9	-108.0	26.1	0.233	0.565
ENSG00000227486	AL445472.1	X	-82.9	-218.9	53.1	0.234	0.565
ENSG00000231252	AC099792.1	1	38.0	-24.4	100.5	0.234	0.566
ENSG00000226137	BAIAP2-AS1	17	-116.9	-309.3	75.6	0.235	0.567
ENSG00000260672	AC100827.4	15	45.2	-29.3	119.7	0.236	0.567
ENSG00000255198	SNHG9	16	-42.7	-113.2	27.8	0.236	0.567
ENSG00000258498	DIO3OS	14	56.1	-36.7	148.9	0.237	0.567
ENSG00000226782	AC117465.1	3	30.5	-20.0	81.1	0.238	0.567
ENSG00000261489	AC025271.3	15	38.9	-25.5	103.4	0.238	0.567
ENSG00000259705	AC084757.3	15	79.3	-52.0	210.6	0.238	0.567
ENSG00000233987	AC106706.1	3	-41.8	-111.8	28.1	0.243	0.574
ENSG00000250564	AC109454.3	5	48.6	-32.7	129.9	0.243	0.574
ENSG00000257354	AC048341.2	12	74.9	-50.4	200.3	0.243	0.574
ENSG00000254111	AC124067.3	8	49.2	-33.1	131.5	0.243	0.574
ENSG00000214145	LINC00887	3	33.1	-22.6	88.9	0.246	0.579
ENSG00000260597	AC012531.1	12	34.4	-23.5	92.3	0.246	0.579
ENSG00000233967	AL359715.2	6	49.4	-33.9	132.7	0.247	0.579
ENSG00000259673	IQCH-AS1	15	139.2	-96.2	374.5	0.248	0.581
ENSG00000230724	LINC01001	11	41.5	-29.0	112.0	0.25	0.584
ENSG00000223855	HRAT92	7	52.2	-36.8	141.2	0.252	0.585
ENSG00000232611	AL683813.1	X	44.6	-31.5	120.7	0.252	0.585
ENSG00000224794	AL022326.1	22	58.7	-41.5	158.9	0.252	0.585
ENSG00000250994	AC005355.1	5	43.2	-30.6	117.0	0.252	0.585
ENSG00000188660	LINC00319	21	67.2	-47.6	181.9	0.253	0.585
ENSG00000203645	LINC00501	3	-21.9	-59.5	15.6	0.253	0.585
ENSG00000260737	LINC01227	16	68.4	-48.7	185.6	0.254	0.586
ENSG00000230943	LINC02541	6	43.6	-31.5	118.6	0.256	0.591
ENSG00000232931	LINC00342	2	35.3	-25.8	96.4	0.259	0.595
ENSG00000228484	AL137025.1	10	37.4	-27.4	102.2	0.259	0.595
ENSG00000257261	AC008014.1	12	87.2	-64.3	238.8	0.261	0.597
ENSG00000243081	AC092894.1	3	50.0	-37.1	137.2	0.262	0.598
ENSG00000249328	AC036214.1	8	35.1	-26.2	96.5	0.263	0.598
ENSG00000235499	AC073046.1	2	84.6	-63.3	232.5	0.264	0.598
ENSG00000226954	AL023802.1	22	-33.9	-93.2	25.4	0.264	0.598
ENSG00000261146	AC007159.1	3	36.4	-27.3	100.2	0.264	0.598
ENSG00000250256	AC108112.1	5	60.4	-45.4	166.3	0.265	0.598
ENSG00000223749	MIR503HG	X	83.8	-63.1	230.7	0.265	0.598
ENSG00000213373	LINC00671	17	39.0	-29.4	107.4	0.265	0.598
ENSG00000236255	AC009404.1	2	79.4	-60.0	218.7	0.266	0.598
ENSG00000226091	LINC00937	12	60.9	-46.3	168.1	0.267	0.599
ENSG00000259925	AC130456.2	16	51.6	-39.3	142.5	0.267	0.599
ENSG00000237851	AL023584.2	6	40.5	-31.4	112.5	0.271	0.607
ENSG00000237594	AP000251.1	21	43.3	-33.8	120.4	0.272	0.608

Table 9: Full results of linear lincRNA-BW regression *(continued)*

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000239482	AC112487.1	3	-83.6	-232.8	65.7	0.274	0.610
ENSG00000261187	AC079322.1	15	45.2	-35.6	126.0	0.275	0.610
ENSG00000234817	AL136309.2	6	-38.9	-108.5	30.7	0.275	0.610
ENSG00000230368	FAM41C	1	38.6	-30.6	107.9	0.276	0.610
ENSG00000254531	FLJ20021	4	-76.2	-212.9	60.5	0.276	0.610
ENSG00000261104	AC093904.4	2	45.8	-36.5	128.0	0.277	0.612
ENSG00000234880	LINC00163	21	-32.6	-91.3	26.1	0.278	0.612
ENSG00000249526	AC008667.1	5	37.5	-30.1	105.0	0.278	0.613
ENSG00000261742	LINC00922	16	32.0	-26.0	90.1	0.281	0.618
ENSG00000231966	AL359853.2	1	-51.0	-143.8	41.7	0.282	0.618
ENSG00000240859	AC093627.4	7	34.2	-28.2	96.5	0.284	0.618
ENSG00000260417	AC092127.1	16	45.0	-37.1	127.1	0.284	0.618
ENSG00000258592	AL391152.1	14	48.5	-40.0	137.0	0.285	0.618
ENSG00000189238	LINC00943	12	31.4	-26.0	88.7	0.285	0.618
ENSG00000231426	AL050338.2	6	40.6	-33.7	115.0	0.286	0.618
ENSG00000249574	AC226118.1	7	-33.9	-96.0	28.2	0.286	0.618
ENSG00000236013	AL138737.1	6	81.8	-68.0	231.5	0.286	0.618
ENSG00000226237	GAS1RR	9	46.0	-38.3	130.3	0.286	0.618
ENSG00000261265	AC025271.2	15	37.8	-31.7	107.3	0.288	0.621
ENSG00000247970	AL160313.1	14	45.4	-38.9	129.8	0.293	0.629
ENSG00000248809	LINC01095	4	38.2	-32.8	109.3	0.293	0.629
ENSG00000255008	AP000442.1	11	42.4	-36.5	121.3	0.294	0.629
ENSG00000253704	AC023632.2	8	-38.0	-108.6	32.7	0.294	0.629
ENSG00000246640	PICART1	17	-59.7	-171.2	51.7	0.295	0.630
ENSG00000224559	LINC01087	2	31.6	-27.6	90.8	0.297	0.633
ENSG00000249859	PVT1	8	81.3	-72.3	235.0	0.301	0.639
ENSG00000260763	AC106799.3	5	32.0	-28.5	92.5	0.301	0.639
ENSG00000260604	AL590004.4	6	46.4	-41.5	134.3	0.302	0.639
ENSG00000249790	AC092490.1	12	34.7	-31.1	100.6	0.303	0.639
ENSG00000238290	AL034417.2	1	-46.9	-136.1	42.2	0.303	0.639
ENSG00000226965	AC092167.1	7	49.6	-44.7	143.9	0.303	0.639
ENSG00000259572	LINC01491	15	-38.5	-111.6	34.6	0.304	0.639
ENSG00000243629	LINC00880	3	-35.1	-101.9	31.6	0.304	0.639
ENSG00000259865	AL390728.6	1	35.6	-32.1	103.4	0.304	0.639
ENSG00000187013	C17orf82	17	38.7	-35.8	113.1	0.31	0.647
ENSG00000233725	LINC00284	13	47.1	-43.6	137.7	0.31	0.647
ENSG00000226686	LINC01535	19	-32.5	-95.0	30.1	0.31	0.647
ENSG00000253641	LINCR-0001	8	35.7	-33.2	104.6	0.311	0.647
ENSG00000227403	LINC01806	2	63.3	-58.8	185.4	0.311	0.647
ENSG00000223704	LINC01422	22	37.1	-34.5	108.8	0.311	0.647
ENSG00000233396	AC244021.1	1	54.9	-51.2	161.0	0.312	0.647
ENSG00000261683	LINC00838	10	31.9	-30.2	94.0	0.315	0.653
ENSG00000225546	LINC02476	7	27.8	-26.4	81.9	0.317	0.654
ENSG00000228862	AC068389.1	8	29.0	-27.7	85.8	0.317	0.654
ENSG00000254119	AC025524.2	8	32.7	-31.4	96.8	0.318	0.654
ENSG00000124915	DKFZP434K028	11	32.0	-30.6	94.5	0.318	0.654
ENSG00000261670	AC012213.2	8	-31.9	-94.5	30.6	0.318	0.654
ENSG00000255693	LINC02389	12	41.9	-40.4	124.1	0.32	0.655
ENSG00000236914	LINC01852	15	42.6	-41.1	126.2	0.32	0.655
ENSG00000230699	AL645608.3	1	28.4	-27.6	84.4	0.322	0.657
ENSG00000238107	LINC01719	1	-67.1	-199.7	65.5	0.323	0.658
ENSG00000223414	LINC00473	6	26.3	-25.8	78.5	0.323	0.658
ENSG00000237359	AL354977.2	9	37.7	-37.1	112.5	0.324	0.658

Table 9: Full results of linear lincRNA-BW regression *(continued)*

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000255666	AP000943.2	11	43.0	-42.3	128.3	0.324	0.658
ENSG00000230597	AL136164.1	6	32.4	-32.0	96.8	0.325	0.658
ENSG00000251339	AC017091.1	4	32.7	-32.2	97.6	0.325	0.658
ENSG00000253522	MIR3142HG	5	34.2	-34.0	102.3	0.327	0.660
ENSG00000225434	LINC01504	9	50.0	-49.9	149.9	0.328	0.661
ENSG00000183250	LINC01547	21	58.0	-58.1	174.2	0.329	0.661
ENSG00000205959	AC105345.1	4	70.2	-70.8	211.1	0.33	0.663
ENSG00000261182	AL596211.1	1	-28.6	-86.1	28.9	0.331	0.663
ENSG00000205786	LINC01531	19	28.6	-29.1	86.3	0.332	0.663
ENSG00000259182	AC019254.1	15	55.7	-56.7	168.1	0.332	0.663
ENSG00000229494	AC012494.1	2	33.4	-34.0	100.9	0.333	0.663
ENSG00000261526	AC012615.1	19	91.1	-92.9	275.1	0.333	0.663
ENSG00000259071	AL359397.2	14	58.7	-60.2	177.6	0.334	0.664
ENSG00000236682	AC068282.1	2	28.3	-29.0	85.7	0.334	0.664
ENSG00000225174	OSTM1-AS1	6	29.9	-30.9	90.7	0.336	0.665
ENSG00000226067	AC245100.1	1	36.2	-37.4	109.7	0.336	0.665
ENSG00000203684	IBA57-AS1	1	-47.6	-144.4	49.3	0.337	0.666
ENSG00000237513	AC007384.1	7	42.2	-43.9	128.2	0.338	0.667
ENSG00000256248	AC134511.1	12	95.0	-100.1	290.2	0.341	0.671
ENSG00000236908	AC005865.1	12	29.0	-30.6	88.5	0.342	0.671
ENSG00000260578	AC110597.1	18	29.8	-31.6	91.3	0.342	0.671
ENSG00000223403	MEG9	14	40.3	-42.8	123.4	0.343	0.671
ENSG00000163009	C2orf48	2	-32.3	-99.0	34.4	0.343	0.671
ENSG00000229160	AC009229.2	2	41.0	-43.9	125.8	0.345	0.673
ENSG00000233559	LINC00513	7	44.7	-48.1	137.5	0.346	0.674
ENSG00000226578	AL132657.1	10	33.9	-36.5	104.3	0.346	0.674
ENSG00000261615	LINC01858	19	29.0	-31.3	89.4	0.347	0.674
ENSG00000226180	AC010536.1	16	-50.8	-156.7	55.1	0.348	0.675
ENSG00000242086	LINC00969	3	53.3	-58.2	164.9	0.35	0.677
ENSG00000224413	AP001476.1	21	29.5	-32.3	91.3	0.35	0.677
ENSG00000178977	LINC00324	17	-71.0	-220.8	78.8	0.354	0.682
ENSG00000212939	Z97192.1	22	22.6	-25.1	70.3	0.354	0.682
ENSG00000251218	AC103764.1	8	30.1	-33.4	93.6	0.354	0.682
ENSG00000236039	AC019117.1	7	50.1	-56.0	156.2	0.356	0.683
ENSG00000260254	AP000997.2	11	23.4	-26.2	72.9	0.356	0.683
ENSG00000258779	LINC01568	16	26.8	-30.3	83.9	0.359	0.686
ENSG00000250406	AC109811.1	4	31.1	-35.3	97.5	0.36	0.687
ENSG00000235931	LINC01553	10	-28.6	-89.8	32.5	0.36	0.687
ENSG00000229660	AC004975.2	7	36.4	-41.5	114.3	0.361	0.688
ENSG00000246379	AC007495.1	16	-28.1	-88.4	32.2	0.363	0.688
ENSG00000238062	SPATA3-AS1	2	-27.3	-86.1	31.4	0.363	0.688
ENSG00000226206	BX470209.1	9	-54.7	-172.3	63.0	0.364	0.688
ENSG00000258861	MIR381HG	14	31.0	-35.7	97.7	0.364	0.688
ENSG00000259225	LINC02345	15	29.2	-33.7	92.1	0.364	0.688
ENSG00000230487	PSMG3-AS1	7	81.4	-94.6	257.4	0.366	0.690
ENSG00000260555	AC092681.2	7	-30.7	-97.6	36.2	0.369	0.696
ENSG00000245149	RNF139-AS1	8	82.8	-97.8	263.3	0.37	0.696
ENSG00000251216	AC106895.2	4	27.9	-33.2	88.9	0.372	0.698
ENSG00000227330	AF130417.1	21	45.1	-54.0	144.2	0.373	0.698
ENSG00000253872	AC083836.1	8	32.7	-39.2	104.7	0.374	0.698
ENSG00000226644	AL121899.1	20	-24.6	-78.7	29.5	0.374	0.698
ENSG00000196741	LINC01560	X	79.5	-95.8	254.8	0.375	0.698
ENSG00000260464	AL049796.1	1	-62.7	-201.1	75.7	0.376	0.698
ENSG00000255970	LINC02421	12	31.5	-38.0	100.9	0.376	0.698

Table 9: Full results of linear lincRNA-BW regression *(continued)*

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000259439	LINC01833	2	24.2	-29.2	77.7	0.376	0.698
ENSG00000235159	AL121672.2	22	34.2	-41.6	110.1	0.377	0.699
ENSG00000256151	ADGRD1-AS1	12	27.7	-33.7	89.2	0.377	0.699
ENSG00000261786	AC006058.1	3	-25.4	-82.7	31.8	0.385	0.711
ENSG00000260136	AC008915.2	16	53.5	-67.3	174.4	0.386	0.712
ENSG00000228308	LINC01209	3	33.3	-42.0	108.6	0.387	0.712
ENSG00000180066	C10orf91	10	-36.1	-117.8	45.6	0.387	0.712
ENSG00000226673	LINC01108	6	-23.7	-77.5	30.0	0.388	0.712
ENSG00000206567	AC022007.1	3	33.8	-42.8	110.4	0.388	0.712
ENSG00000237753	AC079922.2	2	-46.4	-151.6	58.9	0.389	0.712
ENSG00000228714	AL731897.1	9	-34.4	-112.8	44.0	0.391	0.712
ENSG00000250986	AC141928.1	4	-31.1	-102.0	39.8	0.391	0.712
ENSG00000231535	LINC00278	Y	-40.7	-133.7	52.3	0.392	0.712
ENSG00000231705	AL451069.2	10	33.5	-43.0	109.9	0.392	0.712
ENSG00000228889	UBAC2-AS1	13	-65.5	-215.3	84.3	0.393	0.712
ENSG00000250340	LINC02494	4	-24.1	-79.4	31.1	0.393	0.712
ENSG00000254101	LINC02055	8	50.7	-65.4	166.8	0.393	0.712
ENSG00000253679	AP001330.2	8	-25.3	-83.5	32.8	0.394	0.713
ENSG00000260448	LCMT1-AS1	16	42.5	-55.6	140.6	0.397	0.717
ENSG00000239407	Z68871.1	X	101.3	-133.3	336.0	0.398	0.717
ENSG00000253190	AC084082.1	8	-32.3	-107.3	42.7	0.399	0.717
ENSG00000260807	AC009041.2	16	31.8	-41.9	105.4	0.399	0.717
ENSG00000247624	CPEB2-AS1	4	35.1	-46.4	116.7	0.399	0.717
ENSG00000204261	PSMB8-AS1	6	-55.1	-183.1	73.0	0.4	0.718
ENSG00000235450	AC079760.1	7	21.2	-28.2	70.5	0.401	0.719
ENSG00000260563	AC132872.1	17	40.3	-53.7	134.2	0.402	0.719
ENSG00000251574	AC099520.1	5	53.8	-72.3	180.0	0.404	0.721
ENSG00000213279	Z97192.2	22	21.2	-28.9	71.3	0.408	0.727
ENSG00000250514	LINC02125	16	-30.8	-103.9	42.3	0.41	0.729
ENSG00000253263	AP003354.1	8	48.3	-66.7	163.2	0.411	0.729
ENSG00000260197	AC010889.1	Y	34.9	-48.2	118.0	0.412	0.729
ENSG00000248307	LINC00616	4	25.6	-35.4	86.6	0.412	0.729
ENSG00000225975	LINC01534	19	57.6	-79.8	195.0	0.412	0.729
ENSG00000242641	LINC00971	3	-22.8	-77.1	31.6	0.413	0.730
ENSG00000258742	AL117192.1	14	26.7	-37.1	90.5	0.414	0.730
ENSG00000230552	AC092162.2	2	23.3	-32.5	79.0	0.415	0.730
ENSG00000249332	AC016651.1	5	-30.3	-103.0	42.4	0.415	0.730
ENSG00000248319	LINC02275	4	26.7	-37.6	91.1	0.416	0.731
ENSG00000254153	AC103957.2	8	-27.8	-94.9	39.4	0.419	0.734
ENSG00000226029	LINC01772	1	41.8	-59.5	143.1	0.42	0.734
ENSG00000258815	AC131532.1	12	49.3	-70.3	168.9	0.42	0.734
ENSG00000255135	AP002360.2	11	55.9	-79.9	191.7	0.42	0.734
ENSG00000243694	LINC02027	3	28.0	-40.2	96.3	0.422	0.736
ENSG00000226913	BSN-AS2	3	-29.3	-101.0	42.3	0.423	0.736
ENSG00000257410	AC089984.1	12	48.1	-69.4	165.6	0.423	0.736
ENSG00000224652	LINC00885	3	87.3	-126.5	301.0	0.425	0.737
ENSG00000258819	LINC02289	14	41.6	-60.6	143.8	0.426	0.738
ENSG00000205037	AC134312.1	16	39.8	-58.2	137.7	0.427	0.738
ENSG00000232386	AC015712.1	15	-30.5	-105.6	44.6	0.427	0.738
ENSG00000257056	LINC02282	14	25.7	-37.7	89.2	0.427	0.738
ENSG00000236882	LINC01554	5	-53.9	-186.9	79.1	0.428	0.738
ENSG00000248550	OTX2-AS1	14	-24.4	-85.0	36.1	0.43	0.740
ENSG00000254226	LINC01933	5	-24.5	-85.3	36.3	0.431	0.740

Table 9: Full results of linear lincRNA-BW regression *(continued)*

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000233864	TTTY15	Y	-25.4	-88.9	38.1	0.434	0.744
ENSG00000251259	AC004069.1	4	31.6	-47.5	110.6	0.434	0.745
ENSG00000232347	AL390728.5	1	61.3	-92.5	215.0	0.436	0.746
ENSG00000188511	C22orf34	22	40.6	-62.0	143.3	0.439	0.750
ENSG00000246863	AC012377.1	15	-24.2	-85.6	37.1	0.44	0.751
ENSG00000259124	AC008050.1	14	-28.3	-100.2	43.6	0.442	0.751
ENSG00000256417	AC006206.2	12	32.7	-50.4	115.7	0.442	0.751
ENSG00000248783	AC106771.1	5	-55.6	-197.3	86.0	0.442	0.752
ENSG00000225511	LINC00475	9	-49.7	-176.8	77.3	0.444	0.752
ENSG00000253301	LINC01606	8	21.1	-32.9	75.1	0.444	0.752
ENSG00000261824	LINC00662	19	28.0	-43.7	99.7	0.445	0.753
ENSG00000234460	AL772337.3	9	22.4	-35.0	79.9	0.446	0.753
ENSG00000237588	AL590666.3	1	-20.9	-74.5	32.7	0.446	0.753
ENSG00000241475	AL160408.4	1	-24.8	-88.9	39.3	0.449	0.756
ENSG00000226249	AL365271.1	6	24.0	-38.2	86.3	0.45	0.757
ENSG00000227533	SLC2A1-AS1	1	56.5	-90.1	203.1	0.451	0.757
ENSG00000235538	AL137005.1	6	21.9	-35.0	78.7	0.452	0.758
ENSG00000233304	LINC01346	1	-21.8	-78.4	34.9	0.452	0.758
ENSG00000259737	AC087516.2	15	24.0	-38.6	86.5	0.453	0.758
ENSG00000233124	LINC00456	13	-57.4	-207.6	92.8	0.455	0.759
ENSG00000245556	SCAMP1-AS1	5	-69.3	-251.0	112.5	0.456	0.761
ENSG00000249815	AC004704.1	4	-18.0	-65.3	29.3	0.457	0.761
ENSG00000163364	LINC01116	2	32.8	-53.6	119.3	0.458	0.761
ENSG00000260876	LINC01229	16	24.9	-40.7	90.4	0.458	0.761
ENSG00000257345	LINC02413	12	24.4	-40.1	88.8	0.459	0.762
ENSG00000255366	AC120036.5	8	-23.8	-86.7	39.2	0.46	0.762
ENSG00000225783	MIAT	22	35.1	-58.1	128.3	0.462	0.764
ENSG00000229671	LINC01150	11	26.3	-43.7	96.3	0.463	0.764
ENSG00000230438	SERPINB9P1	6	-30.9	-113.7	51.9	0.465	0.765
ENSG00000261275	AC092447.8	7	-19.2	-70.7	32.3	0.466	0.765
ENSG00000258081	AL110292.1	14	18.2	-30.6	66.9	0.466	0.765
ENSG00000234807	LINC01135	1	23.5	-39.6	86.7	0.466	0.765
ENSG00000231114	AC078842.2	7	26.3	-44.4	97.1	0.467	0.765
ENSG00000205628	LINC01446	7	34.3	-57.9	126.5	0.467	0.765
ENSG00000258909	AC091078.3	15	22.3	-37.8	82.4	0.468	0.766
ENSG00000228434	AC004951.1	7	23.0	-39.8	85.8	0.474	0.774
ENSG00000228100	LINC01820	2	-62.1	-232.3	108.0	0.475	0.774
ENSG00000235385	LINC02154	X	16.1	-28.0	60.2	0.475	0.774
ENSG00000182057	OGFRP1	22	40.5	-70.7	151.6	0.477	0.775
ENSG00000227479	AC124861.1	2	30.9	-54.2	116.1	0.478	0.775
ENSG00000146521	LINC01558	6	-23.7	-88.9	41.5	0.478	0.775
ENSG00000245059	AC092718.1	16	22.1	-38.9	83.2	0.478	0.775
ENSG00000258702	AL137786.1	14	22.4	-39.5	84.3	0.479	0.775
ENSG00000227036	LINC00511	17	22.7	-40.7	86.1	0.484	0.782
ENSG00000227456	LINC00310	21	33.2	-59.6	126.0	0.485	0.782
ENSG00000261126	RBFADN	18	28.0	-50.8	106.8	0.487	0.783
ENSG00000260778	AC009065.4	16	32.8	-59.5	125.1	0.487	0.783
ENSG00000256001	AC079949.1	12	-19.5	-74.5	35.5	0.487	0.783
ENSG00000239921	LINC01471	3	-21.2	-81.0	38.6	0.488	0.784
ENSG00000228566	AC022387.1	10	44.4	-81.5	170.4	0.49	0.785
ENSG00000234210	AC006372.3	7	-20.2	-77.6	37.2	0.491	0.785
ENSG00000234229	LINC01505	9	-22.0	-84.6	40.6	0.492	0.785
ENSG00000250421	AC106798.1	5	-23.3	-89.7	43.1	0.492	0.785

Table 9: Full results of linear lincRNA-BW regression *(continued)*

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000245662	LINC02211	5	29.3	-54.5	113.0	0.494	0.788
ENSG00000251632	LINC02172	4	23.3	-43.4	90.0	0.495	0.788
ENSG00000250015	AC018752.1	5	31.5	-59.0	122.0	0.496	0.789
ENSG00000251209	LINC00923	15	-20.1	-78.0	37.8	0.497	0.790
ENSG00000259445	AC025219.1	15	34.9	-66.3	136.1	0.5	0.793
ENSG00000248540	AC010931.2	15	-19.7	-77.1	37.6	0.501	0.793
ENSG00000251637	AP003716.1	11	-20.3	-79.4	38.8	0.502	0.793
ENSG00000203585	LINC02408	12	-21.9	-85.6	41.9	0.502	0.794
ENSG00000255015	AP000755.1	11	47.5	-91.6	186.5	0.504	0.794
ENSG00000253205	AC011124.1	8	20.6	-39.8	81.0	0.505	0.794
ENSG00000223930	AC109779.1	3	21.4	-41.3	84.1	0.505	0.794
ENSG00000235824	LINC00837	10	-19.6	-77.3	38.0	0.506	0.794
ENSG00000261754	AC008555.1	19	30.0	-58.2	118.2	0.506	0.794
ENSG00000258903	AL390816.2	14	30.6	-59.7	120.9	0.507	0.794
ENSG00000204241	AP000911.1	11	20.8	-40.5	82.0	0.507	0.794
ENSG00000225637	AP001046.1	21	-19.8	-78.4	38.8	0.508	0.794
ENSG00000196273	LINC00523	14	21.9	-42.8	86.5	0.508	0.794
ENSG00000205325	AC005863.1	17	-31.3	-124.0	61.4	0.509	0.794
ENSG00000240875	LINC00886	3	-32.5	-129.2	64.1	0.51	0.794
ENSG00000230658	KLHL7-AS1	7	20.7	-40.8	82.1	0.511	0.794
ENSG00000245164	LINC00861	8	24.1	-47.8	96.0	0.512	0.795
ENSG00000235415	AC005808.1	20	23.0	-45.8	91.8	0.513	0.795
ENSG00000239332	LINC01119	2	51.5	-103.0	206.0	0.515	0.796
ENSG00000260896	LINC02170	16	-25.6	-102.5	51.3	0.515	0.796
ENSG00000205664	BX890604.1	X	61.7	-123.9	247.3	0.515	0.796
ENSG00000260517	AC009093.2	16	23.0	-46.6	92.6	0.517	0.798
ENSG00000224429	LINC00539	13	37.0	-75.4	149.3	0.52	0.801
ENSG00000260771	AL138918.1	6	22.3	-45.6	90.2	0.52	0.801
ENSG00000259252	AC026583.1	15	22.2	-45.6	90.1	0.522	0.801
ENSG00000249395	CASC9	8	30.0	-61.6	121.6	0.522	0.801
ENSG00000259863	SH3RF3-AS1	2	-31.6	-128.1	65.0	0.522	0.801
ENSG00000259959	AC107068.1	4	69.7	-144.9	284.3	0.525	0.803
ENSG00000240707	LINC01168	10	-16.0	-65.2	33.3	0.526	0.803
ENSG00000236497	LINC01744	1	-21.4	-87.4	44.6	0.526	0.803
ENSG00000258667	HIF1A-AS2	14	28.0	-58.6	114.6	0.527	0.804
ENSG00000246430	LINC00968	8	30.1	-63.5	123.6	0.53	0.806
ENSG00000251576	LINC01267	3	26.6	-56.2	109.4	0.53	0.806
ENSG00000215808	LINC01139	1	22.0	-46.7	90.8	0.531	0.807
ENSG00000233379	AL139002.1	13	33.7	-71.9	139.3	0.532	0.807
ENSG00000226434	AC135371.1	X	-12.1	-50.1	25.9	0.533	0.807
ENSG00000237087	AC068134.2	2	23.1	-49.4	95.7	0.533	0.807
ENSG00000235475	LINC01372	7	27.0	-58.2	112.2	0.535	0.809
ENSG00000238121	LINC00426	13	-18.1	-75.3	39.1	0.536	0.809
ENSG00000254615	AC027031.2	8	44.4	-96.2	185.0	0.537	0.809
ENSG00000250337	LINC01021	5	18.8	-41.0	78.6	0.538	0.809
ENSG00000224565	LINC01754	20	-22.9	-95.5	49.7	0.538	0.809
ENSG00000251350	LINC02475	4	19.6	-42.7	81.9	0.538	0.809
ENSG00000254872	AC139749.1	11	18.6	-41.2	78.4	0.543	0.815
ENSG00000261617	LINC02177	16	-17.5	-73.9	38.9	0.544	0.815
ENSG00000249647	C5orf66-AS2	5	-17.6	-74.5	39.3	0.545	0.815
ENSG00000237222	LINC01968	3	23.2	-53.1	99.6	0.551	0.823
ENSG00000261807	LINC02141	16	16.6	-38.0	71.1	0.552	0.823
ENSG00000245812	LINC02202	5	27.6	-63.2	118.4	0.552	0.823
ENSG00000234722	LINC01287	7	-16.4	-70.7	37.9	0.554	0.825

Table 9: Full results of linear lincRNA-BW regression *(continued)*

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000261121	LINC02473	4	18.0	-41.7	77.7	0.555	0.825
ENSG00000226629	LINC00974	17	19.5	-45.3	84.4	0.556	0.825
ENSG00000229433	LINC02069	3	-17.3	-74.7	40.1	0.556	0.825
ENSG00000240893	LINC02042	3	20.9	-48.8	90.7	0.557	0.825
ENSG00000248261	AC008948.1	5	17.6	-41.6	76.8	0.56	0.828
ENSG00000258301	VASH1-AS1	14	-34.1	-148.6	80.5	0.561	0.828
ENSG00000235665	LINC00298	2	19.7	-46.5	85.9	0.561	0.828
ENSG00000260260	SNHG19	16	33.6	-80.2	147.3	0.564	0.830
ENSG00000256092	AC137767.1	12	26.2	-62.7	115.2	0.564	0.830
ENSG00000184274	LINC00315	21	-19.4	-85.4	46.5	0.564	0.830
ENSG00000235621	LINC00494	20	-18.0	-79.2	43.3	0.566	0.831
ENSG00000230923	LINC00309	2	-17.9	-79.4	43.6	0.568	0.833
ENSG00000260676	LINC01541	18	-15.0	-66.5	36.6	0.57	0.834
ENSG00000233817	AL162727.1	9	18.0	-44.0	79.9	0.57	0.834
ENSG00000246777	AC044802.1	16	-19.3	-86.0	47.4	0.571	0.834
ENSG00000226808	LINC00840	10	-19.0	-84.8	46.8	0.572	0.834
ENSG00000224228	AL031599.1	1	-21.5	-96.1	53.2	0.574	0.834
ENSG00000254518	AC109635.2	11	17.7	-44.0	79.5	0.574	0.834
ENSG00000235597	LINC01102	2	-15.6	-69.9	38.7	0.574	0.834
ENSG00000234754	C1orf140	1	18.0	-44.6	80.5	0.574	0.834
ENSG00000226051	ZNF503-AS1	10	37.3	-93.0	167.5	0.575	0.835
ENSG00000224397	SMIM25	20	-30.8	-138.6	77.1	0.577	0.835
ENSG00000226328	NUP50-AS1	22	49.7	-125.4	224.8	0.579	0.837
ENSG00000232677	LINC00665	19	-42.5	-192.8	107.8	0.58	0.837
ENSG00000259831	LINC00567	13	17.0	-43.1	77.0	0.58	0.837
ENSG00000259776	AC093426.1	1	-16.7	-76.0	42.5	0.58	0.837
ENSG00000250453	AC008825.1	5	18.6	-47.3	84.4	0.581	0.837
ENSG00000232118	BACH1-AS1	21	-25.6	-116.7	65.5	0.582	0.837
ENSG00000205632	LINC01310	22	15.0	-39.0	69.0	0.587	0.841
ENSG00000260032	NORAD	20	83.2	-217.2	383.7	0.588	0.841
ENSG00000225331	LINC01678	21	19.8	-51.6	91.2	0.588	0.841
ENSG00000213888	LINC01521	22	41.8	-109.1	192.7	0.588	0.841
ENSG00000260810	AL135818.2	14	-26.9	-124.3	70.5	0.589	0.841
ENSG00000223811	AL589684.1	6	-17.6	-81.2	46.1	0.589	0.841
ENSG00000254810	AP001189.3	11	20.5	-53.8	94.7	0.59	0.841
ENSG00000229404	LINC00858	10	34.0	-89.9	157.9	0.592	0.843
ENSG00000259362	AC046168.1	15	23.2	-62.0	108.4	0.594	0.845
ENSG00000260470	AC023794.5	12	-16.3	-76.4	43.7	0.594	0.845
ENSG00000245317	AC008393.1	5	25.2	-67.7	118.2	0.595	0.845
ENSG00000232098	AC012313.1	19	-47.1	-221.2	126.9	0.596	0.845
ENSG00000228919	AC097381.1	4	16.1	-43.5	75.7	0.597	0.845
ENSG00000259548	AC021483.1	15	18.1	-49.4	85.6	0.6	0.848
ENSG00000223617	LINC00370	13	16.1	-44.5	76.8	0.603	0.851
ENSG00000260947	AL356489.2	9	15.6	-43.4	74.6	0.604	0.851
ENSG00000233067	PTCHD1-AS	X	16.1	-44.8	77.0	0.604	0.851
ENSG00000248339	LINC02504	4	16.0	-44.4	76.3	0.605	0.851
ENSG00000205653	AL035696.1	6	17.3	-48.2	82.8	0.606	0.852
ENSG00000214797	AP002358.1	11	15.5	-43.3	74.3	0.607	0.852
ENSG00000179219	LINC00311	16	14.9	-41.9	71.8	0.607	0.852
ENSG00000205634	LINC00898	22	13.7	-38.6	66.1	0.608	0.852
ENSG00000251533	LINC00605	14	-18.0	-86.7	50.7	0.609	0.852
ENSG00000237643	AL365226.2	6	-18.8	-91.2	53.6	0.611	0.854
ENSG00000253972	MAL2	8	20.0	-57.3	97.4	0.612	0.854

Table 9: Full results of linear lincRNA-BW regression *(continued)*

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000235097	LINC00330	13	11.1	-32.0	54.2	0.613	0.854
ENSG00000259284	LINC02349	15	14.7	-42.2	71.6	0.614	0.854
ENSG00000231680	AP003774.3	11	18.2	-52.4	88.8	0.614	0.854
ENSG00000253669	AP003356.1	8	53.9	-155.9	263.8	0.615	0.854
ENSG00000253490	LINC02099	8	19.8	-57.3	96.9	0.615	0.854
ENSG00000172965	MIR4435-2HG	2	51.4	-150.9	253.6	0.619	0.857
ENSG00000248441	LINC01197	15	-15.4	-75.9	45.1	0.619	0.857
ENSG00000255455	AP003486.1	11	-53.4	-264.1	157.2	0.62	0.857
ENSG00000225489	AL354707.1	9	22.5	-66.5	111.6	0.62	0.857
ENSG00000258711	AL358334.2	14	14.5	-43.2	72.2	0.623	0.859
ENSG00000234647	AL606970.3	6	14.1	-42.2	70.5	0.623	0.859
ENSG00000260814	AC073657.1	15	22.1	-66.2	110.4	0.624	0.860
ENSG00000250284	AC109439.2	5	17.9	-53.8	89.6	0.625	0.860
ENSG00000227964	LINC01429	20	-15.3	-76.9	46.3	0.626	0.860
ENSG00000260077	AC104794.2	2	29.2	-88.9	147.3	0.628	0.862
ENSG00000230725	AL035252.2	20	-14.6	-73.9	44.7	0.63	0.863
ENSG00000226861	AL390835.1	10	17.6	-54.5	89.7	0.633	0.866
ENSG00000258998	LINC02302	14	15.8	-49.1	80.7	0.634	0.866
ENSG00000258609	LINC-ROR	18	17.2	-53.4	87.8	0.634	0.866
ENSG00000176728	TTTY14	Y	20.8	-64.7	106.2	0.635	0.866
ENSG00000246465	AC138904.1	16	15.3	-48.2	78.7	0.638	0.869
ENSG00000260588	AC027702.1	8	22.0	-69.7	113.6	0.639	0.870
ENSG00000206344	HCG27	6	16.5	-52.6	85.6	0.64	0.870
ENSG00000260528	FAM157C	16	-15.6	-81.2	49.9	0.641	0.870
ENSG00000242512	LINC01206	3	-10.5	-54.8	33.8	0.642	0.870
ENSG00000258927	AL133467.2	14	-15.0	-78.2	48.2	0.642	0.870
ENSG00000233515	LINC01518	10	12.0	-38.8	62.7	0.644	0.871
ENSG00000214650	AC073592.1	12	-15.6	-82.0	50.7	0.645	0.871
ENSG00000221953	C1orf229	1	15.8	-51.4	83.0	0.646	0.871
ENSG00000233183	AL138889.1	6	-10.2	-53.5	33.2	0.646	0.871
ENSG00000230400	LINC01747	20	14.2	-46.5	74.8	0.648	0.871
ENSG00000237638	LINC02245	2	-14.7	-77.5	48.2	0.648	0.871
ENSG00000232527	AC245100.6	1	33.8	-111.2	178.9	0.648	0.871
ENSG00000260422	Z97205.2	6	-14.3	-75.8	47.3	0.65	0.872
ENSG00000245719	AC009292.1	15	14.0	-46.6	74.6	0.651	0.872
ENSG00000234883	MIR155HG	21	18.9	-62.9	100.7	0.651	0.872
ENSG00000213062	AL021068.1	1	-42.3	-228.0	143.4	0.656	0.877
ENSG00000225785	AL109610.1	20	-12.8	-69.2	43.6	0.656	0.877
ENSG00000205622	AP001043.1	21	-14.3	-77.3	48.7	0.657	0.878
ENSG00000260239	LINC02533	6	34.0	-116.5	184.6	0.658	0.878
ENSG00000233539	AC011294.1	7	14.1	-48.9	77.1	0.661	0.879
ENSG00000245571	AP001258.1	11	-48.6	-265.6	168.4	0.661	0.879
ENSG00000226762	AL451164.1	10	-15.7	-86.1	54.6	0.662	0.879
ENSG00000230628	AL160408.3	1	-13.4	-73.4	46.6	0.662	0.879
ENSG00000259113	AL118556.1	14	16.2	-56.8	89.3	0.663	0.879
ENSG00000248844	AP003555.1	11	-17.5	-96.5	61.5	0.665	0.879
ENSG00000229214	LINC00242	6	-13.8	-76.1	48.6	0.665	0.879
ENSG00000251381	LINC00958	11	-18.6	-103.2	65.9	0.666	0.879
ENSG00000226777	FAM30A	14	12.5	-44.4	69.4	0.667	0.879
ENSG00000258390	LINC02318	14	16.6	-58.9	92.1	0.667	0.879
ENSG00000238266	LINC00707	10	-11.0	-61.1	39.1	0.667	0.879
ENSG00000229719	MIR194-2HG	11	16.7	-60.3	93.8	0.671	0.883
ENSG00000251226	AP001999.1	11	13.6	-49.3	76.5	0.672	0.884

Table 9: Full results of linear lincRNA-BW regression *(continued)*

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000233901	LINC01503	9	-37.5	-211.4	136.4	0.673	0.884
ENSG00000241135	LINC00881	3	-17.6	-99.8	64.7	0.676	0.886
ENSG00000261402	AL591222.1	9	-13.0	-73.8	47.9	0.677	0.886
ENSG00000234584	AC019186.1	2	18.4	-68.2	105.0	0.678	0.886
ENSG00000259478	AC024651.1	15	14.3	-53.1	81.7	0.678	0.886
ENSG00000229308	AC010737.1	Y	16.8	-63.5	97.1	0.682	0.890
ENSG00000234810	AL603840.1	1	13.9	-52.6	80.3	0.683	0.890
ENSG00000253967	AC022730.4	8	35.8	-137.0	208.5	0.685	0.890
ENSG00000205056	LINC02397	12	11.7	-44.6	67.9	0.685	0.890
ENSG00000232956	SNHG15	7	-37.6	-219.2	144.0	0.685	0.890
ENSG00000261757	AC005592.1	5	12.0	-45.9	69.9	0.686	0.890
ENSG00000226985	LINC01203	X	6.6	-25.3	38.4	0.687	0.891
ENSG00000229373	LINC00452	13	11.7	-45.4	68.8	0.688	0.891
ENSG00000205181	LINC00654	20	21.7	-84.5	128.0	0.689	0.891
ENSG00000226266	AC009961.1	2	36.7	-143.1	216.6	0.689	0.891
ENSG00000223768	LINC00205	21	29.3	-114.6	173.3	0.69	0.891
ENSG00000224848	AL589843.1	9	15.2	-60.2	90.6	0.693	0.894
ENSG00000230013	AL359182.2	9	-19.4	-115.8	77.1	0.695	0.895
ENSG00000225156	AC012354.1	2	11.6	-46.5	69.7	0.696	0.895
ENSG00000179136	LINC00670	17	13.0	-52.0	78.0	0.696	0.895
ENSG00000251584	AC096751.2	4	22.8	-91.9	137.6	0.697	0.895
ENSG00000261467	AC099398.1	7	-11.5	-69.2	46.3	0.698	0.895
ENSG00000232063	AL691447.2	9	13.2	-53.7	80.1	0.699	0.896
ENSG00000170846	AC093323.1	4	54.9	-223.1	332.9	0.699	0.896
ENSG00000153363	LINC00467	1	-35.6	-216.6	145.4	0.7	0.896
ENSG00000204110	LINC02520	6	-10.8	-65.8	44.3	0.702	0.897
ENSG00000204362	AL590644.1	1	9.3	-38.4	57.0	0.703	0.897
ENSG00000224247	AJ009632.1	21	-12.4	-76.2	51.4	0.703	0.897
ENSG00000188825	LINC00910	17	-25.0	-153.6	103.7	0.704	0.897
ENSG00000260910	LINC00565	13	12.9	-54.2	80.0	0.707	0.899
ENSG00000261600	AC233266.2	2	12.2	-51.5	75.8	0.708	0.900
ENSG00000260118	AL157700.1	X	13.3	-56.5	83.2	0.708	0.900
ENSG00000258811	AL583810.2	14	10.4	-45.0	65.7	0.714	0.904
ENSG00000225742	LINC02036	3	17.7	-76.8	112.2	0.714	0.904
ENSG00000260808	AP003096.1	11	15.1	-65.7	95.9	0.715	0.904
ENSG00000253438	PCAT1	8	13.6	-59.6	86.9	0.716	0.904
ENSG00000259641	PCAT29	15	-10.8	-69.4	47.7	0.718	0.904
ENSG00000246100	LINC00900	11	14.9	-65.6	95.4	0.718	0.904
ENSG00000235158	AC087430.1	3	10.2	-45.3	65.8	0.718	0.904
ENSG00000234608	MAPKAPK5-AS1	12	-32.3	-207.6	143.0	0.718	0.904
ENSG00000249125	AC093821.1	4	-26.4	-170.5	117.7	0.72	0.905
ENSG00000253734	LINC01289	8	11.3	-50.6	73.1	0.721	0.906
ENSG00000261781	LINC01654	1	12.8	-57.6	83.1	0.722	0.906
ENSG00000189196	LINC00994	3	-11.5	-74.7	51.8	0.723	0.906
ENSG00000258413	AL158801.2	14	17.4	-79.4	114.1	0.725	0.908
ENSG00000223823	LINC01342	1	-11.1	-73.9	51.6	0.728	0.910
ENSG00000253584	AC091987.1	5	18.7	-86.5	123.8	0.729	0.910
ENSG00000230676	AL353803.2	9	10.4	-48.4	69.2	0.729	0.910
ENSG00000242258	LINC00996	7	10.4	-48.7	69.5	0.73	0.911
ENSG00000228221	LINC00578	3	-8.0	-53.5	37.6	0.733	0.913
ENSG00000260911	AC135050.3	16	18.4	-88.3	125.2	0.736	0.915
ENSG00000260072	AC008938.1	16	-11.6	-79.2	56.0	0.736	0.915
ENSG00000180422	LINC00304	16	-10.3	-70.5	49.9	0.738	0.915
ENSG00000235997	LINC01936	2	10.8	-52.4	73.9	0.739	0.915

Table 9: Full results of linear lincRNA-BW regression *(continued)*

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000251408	AC113615.1	4	-10.1	-69.1	48.9	0.739	0.915
ENSG00000254416	AP000924.1	11	22.3	-109.1	153.6	0.74	0.916
ENSG00000232190	LINC02181	16	9.3	-45.8	64.4	0.741	0.916
ENSG00000256642	LINC00273	16	10.1	-49.9	70.0	0.743	0.916
ENSG00000230844	ZNF674-AS1	X	37.4	-186.1	260.8	0.744	0.916
ENSG00000261079	AC009053.2	16	15.3	-76.4	107.0	0.744	0.916
ENSG00000203688	LINC02487	6	10.2	-51.2	71.6	0.745	0.916
ENSG00000185186	LINC00313	21	11.2	-56.2	78.6	0.746	0.916
ENSG00000228526	MIR34AHG	1	13.4	-67.9	94.6	0.747	0.916
ENSG00000258499	LINC02287	14	10.4	-53.0	73.9	0.748	0.916
ENSG00000251417	AC145285.2	16	18.6	-95.2	132.5	0.749	0.916
ENSG00000225880	LINC00115	1	-18.9	-134.5	96.7	0.749	0.916
ENSG00000260664	AC004158.1	16	10.9	-55.8	77.6	0.749	0.916
ENSG00000255121	AP003392.4	11	21.9	-112.9	156.8	0.75	0.916
ENSG00000249584	LINC02225	5	9.7	-50.2	69.7	0.751	0.916
ENSG00000248489	LINC02062	5	19.6	-101.3	140.5	0.751	0.916
ENSG00000261200	AC136944.2	16	-9.6	-68.9	49.7	0.751	0.916
ENSG00000255458	AC108471.2	4	-13.3	-95.5	69.0	0.753	0.916
ENSG00000237476	LINC01637	22	-12.5	-90.9	65.9	0.755	0.918
ENSG00000258876	TGFB3-AS1	14	-9.3	-67.8	49.2	0.755	0.918
ENSG00000232504	ST3GAL5-AS1	2	11.1	-59.1	81.3	0.757	0.918
ENSG00000232117	LINC00384	13	-7.5	-55.1	40.1	0.758	0.918
ENSG00000166770	ZNF667-AS1	19	15.0	-80.3	110.2	0.759	0.918
ENSG00000253161	LINC01605	8	17.9	-95.9	131.6	0.759	0.918
ENSG00000177757	FAM87B	1	-13.4	-99.2	72.4	0.759	0.918
ENSG00000222033	LINC01124	2	10.5	-56.9	77.9	0.761	0.919
ENSG00000261586	AC068987.4	12	-13.7	-102.8	75.4	0.763	0.921
ENSG00000224167	AL390729.1	1	20.3	-112.7	153.3	0.766	0.922
ENSG00000249364	AC112206.2	5	-9.5	-72.0	53.0	0.766	0.922
ENSG00000255258	AP001979.2	11	8.7	-48.7	66.1	0.767	0.922
ENSG00000237361	TUSC8	13	9.5	-53.4	72.5	0.767	0.922
ENSG00000204277	LINC01993	17	9.4	-53.5	72.3	0.769	0.923
ENSG00000238284	LINC01448	7	9.6	-54.7	73.9	0.769	0.923
ENSG00000233723	LINC01122	2	8.0	-46.3	62.3	0.773	0.926
ENSG00000226828	AL591885.1	1	-9.9	-77.5	57.7	0.774	0.926
ENSG00000253894	AC011124.2	8	-8.6	-67.7	50.4	0.775	0.926
ENSG00000235770	LINC00607	2	16.1	-94.4	126.7	0.775	0.926
ENSG00000233117	LINC00702	10	-13.7	-108.5	81.0	0.777	0.927
ENSG00000260759	AP001120.1	18	-8.4	-66.6	49.8	0.778	0.927
ENSG00000247317	AC105202.1	8	-12.8	-102.4	76.7	0.779	0.928
ENSG00000234350	AC007405.1	2	11.1	-66.7	88.8	0.781	0.929
ENSG00000231031	LINC01804	2	7.8	-47.4	63.1	0.781	0.929
ENSG00000255983	AC007848.1	12	-9.6	-77.7	58.5	0.783	0.929
ENSG00000224687	RASAL2-AS1	1	31.4	-196.5	259.3	0.787	0.933
ENSG00000205611	LINC01597	20	7.9	-50.2	66.0	0.789	0.933
ENSG00000236790	LINC00299	2	8.8	-55.8	73.3	0.79	0.933
ENSG00000236740	AL033384.1	6	-8.6	-72.0	54.8	0.79	0.933
ENSG00000232896	AL592463.1	9	11.1	-71.0	93.2	0.791	0.933
ENSG00000261211	AL031123.2	6	10.9	-70.3	92.2	0.792	0.933
ENSG00000230010	AL049646.1	20	8.7	-56.2	73.6	0.793	0.933
ENSG00000251396	LINC01301	8	20.1	-130.1	170.3	0.794	0.933
ENSG00000260698	AL591848.3	1	11.4	-74.2	97.1	0.794	0.933
ENSG00000236028	AL354766.2	20	14.6	-95.0	124.3	0.794	0.933

Table 9: Full results of linear lincRNA-BW regression *(continued)*

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000235142	LINC02532	6	-13.1	-112.5	86.3	0.796	0.935
ENSG00000231689	LINC01090	2	21.3	-140.2	182.8	0.796	0.935
ENSG00000254349	MIR2052HG	8	8.7	-58.7	76.1	0.801	0.937
ENSG00000261193	AC134312.4	16	8.2	-55.5	71.9	0.801	0.937
ENSG00000214293	APTR	7	-27.2	-238.8	184.4	0.801	0.937
ENSG00000197176	LINC02291	14	-15.5	-136.7	105.6	0.802	0.937
ENSG00000261623	LINC02179	16	7.3	-50.2	64.8	0.803	0.937
ENSG00000236423	LINC01134	1	12.1	-83.3	107.6	0.803	0.937
ENSG00000198547	C20orf203	20	10.2	-71.3	91.8	0.806	0.939
ENSG00000237491	AL669831.5	1	9.4	-66.2	85.0	0.807	0.940
ENSG00000230131	AL160290.2	10	8.2	-58.5	74.9	0.809	0.940
ENSG00000253379	AC099805.1	8	-7.2	-65.4	51.1	0.809	0.940
ENSG00000205334	LINC01460	2	-7.0	-64.8	50.8	0.812	0.943
ENSG00000228262	LINC01320	2	5.4	-39.8	50.7	0.814	0.944
ENSG00000249550	LINC01234	12	-6.9	-64.7	50.8	0.814	0.944
ENSG00000260792	LINC02280	14	6.7	-50.3	63.8	0.817	0.945
ENSG00000248538	AC022784.1	8	-22.3	-211.8	167.2	0.818	0.945
ENSG00000196366	C9orf163	9	-16.8	-161.7	128.0	0.82	0.945
ENSG00000233746	LINC00656	20	15.6	-118.6	149.7	0.82	0.945
ENSG00000253395	AP003469.2	8	10.1	-77.0	97.1	0.821	0.945
ENSG00000237232	ZNF295-AS1	21	-12.7	-122.8	97.4	0.821	0.945
ENSG00000260440	LINC01544	18	-6.6	-64.2	50.9	0.822	0.945
ENSG00000254874	AP003171.1	11	8.8	-67.5	85.0	0.822	0.945
ENSG00000145063	AC062028.1	2	-6.7	-64.8	51.5	0.823	0.945
ENSG00000205663	FAM239B	X	4.7	-36.9	46.3	0.825	0.947
ENSG00000223850	MYCNUT	2	8.0	-64.4	80.5	0.828	0.949
ENSG00000229425	AJ009632.2	21	9.5	-76.4	95.3	0.829	0.949
ENSG00000178412	AC068473.1	18	8.6	-70.2	87.4	0.831	0.951
ENSG00000259998	AL133279.3	14	7.1	-59.0	73.3	0.833	0.952
ENSG00000242828	AC068756.1	3	11.0	-92.5	114.6	0.835	0.953
ENSG00000235645	AL450311.1	10	6.0	-50.4	62.3	0.836	0.953
ENSG00000251026	LINC02163	5	6.1	-52.4	64.7	0.838	0.955
ENSG00000255874	LINC00346	13	12.9	-111.1	136.8	0.839	0.956
ENSG00000206532	AC117402.1	3	15.8	-137.4	169.0	0.84	0.956
ENSG00000230417	LINC00595	10	5.6	-49.3	60.6	0.841	0.956
ENSG00000225028	AC096541.1	1	-6.2	-68.2	55.8	0.844	0.959
ENSG00000251391	AC113378.1	5	-9.3	-103.9	85.4	0.848	0.961
ENSG00000236494	AC008080.4	7	6.0	-55.7	67.7	0.848	0.961
ENSG00000235532	LINC00402	13	5.8	-54.9	66.6	0.851	0.962
ENSG00000246820	AC091013.1	11	-5.9	-67.2	55.4	0.851	0.962
ENSG00000260059	AC092620.3	2	-7.0	-80.7	66.6	0.852	0.962
ENSG00000261455	LINC01003	7	15.8	-150.0	181.6	0.852	0.962
ENSG00000214894	LINC00243	6	-9.2	-107.1	88.7	0.854	0.963
ENSG00000242021	AC112493.1	X	6.8	-66.4	79.9	0.856	0.964
ENSG00000243083	LINC00870	3	-6.4	-77.9	65.0	0.86	0.968
ENSG00000253182	AC084026.1	8	-10.5	-127.2	106.3	0.861	0.968
ENSG00000258654	AC026495.1	15	4.8	-49.5	59.1	0.862	0.968
ENSG00000250198	LINC02199	5	5.5	-57.2	68.1	0.865	0.968
ENSG00000181908	AP003774.1	11	-7.4	-92.3	77.5	0.865	0.968
ENSG00000260390	AL360014.1	9	7.1	-75.1	89.4	0.865	0.968
ENSG00000246548	LINC02288	14	6.8	-72.0	85.6	0.866	0.968
ENSG00000260902	LINC02011	3	5.0	-53.6	63.6	0.868	0.968
ENSG00000184856	LINC00308	21	-3.7	-48.4	40.9	0.87	0.968

Table 9: Full results of linear lincRNA-BW regression *(continued)*

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000261069	AC124312.3	15	-7.8	-101.4	85.8	0.871	0.968
ENSG00000248112	AC108174.1	5	4.6	-50.4	59.6	0.871	0.968
ENSG00000222041	CYTOR	2	10.8	-120.2	141.8	0.871	0.968
ENSG00000228126	FALEC	1	6.1	-67.4	79.5	0.871	0.968
ENSG00000261334	AL353803.4	9	10.6	-118.9	140.2	0.872	0.968
ENSG00000235625	AL138957.1	13	-4.8	-63.8	54.2	0.873	0.968
ENSG00000196979	AL360004.1	9	-4.4	-58.3	49.5	0.873	0.968
ENSG00000251152	AC025539.1	4	5.0	-56.9	67.0	0.874	0.968
ENSG00000228521	AC099552.3	7	-6.7	-90.6	77.1	0.875	0.968
ENSG00000224032	EPB41L4A-AS1	5	18.6	-213.1	250.3	0.875	0.968
ENSG00000258479	LINC00640	14	5.4	-62.1	72.9	0.875	0.968
ENSG00000250742	LINC02381	12	6.9	-82.6	96.5	0.879	0.969
ENSG00000224715	Z82186.1	22	4.2	-50.4	58.8	0.88	0.969
ENSG00000242753	AL445430.2	6	-4.2	-59.2	50.7	0.88	0.969
ENSG00000258701	LINC00638	14	9.6	-115.0	134.1	0.881	0.969
ENSG00000236347	AL513123.1	6	7.5	-90.3	105.2	0.881	0.969
ENSG00000229921	KIF25-AS1	6	-4.0	-56.1	48.2	0.881	0.969
ENSG00000250548	AL355916.1	14	6.8	-84.1	97.6	0.884	0.970
ENSG00000248677	LINC02102	5	4.9	-60.8	70.5	0.884	0.970
ENSG00000260804	LINC01963	2	12.7	-160.8	186.2	0.886	0.970
ENSG00000233123	LINC01007	7	8.7	-110.1	127.4	0.887	0.970
ENSG00000225285	LINC01770	1	11.6	-148.1	171.4	0.887	0.970
ENSG00000257698	AC084033.3	12	8.1	-103.9	120.1	0.887	0.970
ENSG00000260670	AC134508.1	3	-4.2	-63.2	54.9	0.89	0.972
ENSG00000222005	LINC01118	2	-10.5	-160.3	139.3	0.891	0.973
ENSG00000241933	AC114480.1	3	4.2	-56.8	65.3	0.892	0.973
ENSG00000248954	AC027801.2	17	-7.1	-112.3	98.2	0.895	0.973
ENSG00000245526	LINC00461	5	3.4	-47.7	54.6	0.896	0.973
ENSG00000234283	AC245595.1	1	-5.7	-91.4	80.1	0.897	0.973
ENSG00000251191	LINC00589	8	-4.8	-77.7	68.1	0.897	0.973
ENSG00000235314	LINC00957	7	-7.1	-114.3	100.2	0.898	0.973
ENSG00000261055	AL450468.2	1	-4.3	-69.3	60.8	0.898	0.973
ENSG00000237339	LINC01502	9	-2.9	-47.5	41.7	0.898	0.973
ENSG00000236963	LINC01141	1	3.6	-51.3	58.4	0.899	0.973
ENSG00000260343	LINC01043	13	-3.3	-56.0	49.3	0.901	0.973
ENSG00000224635	AL391095.1	20	4.2	-61.6	70.0	0.901	0.973
ENSG00000220256	AC093802.1	2	3.6	-53.3	60.5	0.901	0.973
ENSG00000236384	LINC00479	21	-3.9	-66.2	58.4	0.902	0.973
ENSG00000198468	FLVCR1-AS1	1	-4.3	-74.8	66.2	0.905	0.976
ENSG00000225411	CR786580.1	9	-3.3	-58.4	51.8	0.906	0.976
ENSG00000224307	AL161785.1	9	4.9	-77.9	87.7	0.908	0.977
ENSG00000255465	AP001995.1	11	3.7	-58.6	65.9	0.909	0.977
ENSG00000248323	LUCAT1	5	-5.7	-105.9	94.5	0.912	0.979
ENSG00000204283	LINC01973	17	3.2	-53.8	60.2	0.913	0.979
ENSG00000244260	AC082651.4	2	3.7	-62.9	70.2	0.914	0.980
ENSG00000260066	AC112176.1	5	3.3	-57.0	63.5	0.916	0.981
ENSG00000236507	BX470209.2	9	5.1	-90.1	100.4	0.916	0.981
ENSG00000255394	C8orf49	8	3.2	-58.5	64.9	0.919	0.981
ENSG00000244578	LINC01391	3	-2.8	-56.6	51.0	0.919	0.981
ENSG00000228140	AL031283.1	1	5.7	-105.9	117.3	0.92	0.981
ENSG00000203711	C6orf99	6	-6.3	-130.2	117.6	0.921	0.981
ENSG00000229066	AC093459.1	2	3.0	-57.3	63.4	0.921	0.981
ENSG00000187185	AC092118.1	16	-5.8	-122.0	110.3	0.922	0.981
ENSG00000250974	LINC02196	5	2.6	-49.4	54.6	0.923	0.982

Table 9: Full results of linear lincRNA-BW regression *(continued)*

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000249375	CASC11	8	-2.6	-57.5	52.2	0.925	0.982
ENSG00000261474	AC026471.4	16	-5.9	-130.8	118.9	0.926	0.982
ENSG00000238033	AC002480.4	7	-2.7	-61.5	56.0	0.928	0.982
ENSG00000236714	LINC01844	5	-3.0	-68.6	62.5	0.928	0.982
ENSG00000175728	C11orf44	11	-2.3	-52.6	48.0	0.928	0.982
ENSG00000253230	LINC00599	8	2.6	-54.0	59.1	0.928	0.982
ENSG00000233858	AC026904.1	8	2.3	-50.6	55.3	0.931	0.982
ENSG00000246223	LINC01550	14	-2.6	-61.2	56.1	0.932	0.982
ENSG00000235609	AF127577.4	21	3.5	-76.7	83.7	0.932	0.982
ENSG00000250682	LINC00491	5	-5.9	-143.4	131.6	0.933	0.982
ENSG00000260977	AC016722.3	2	3.0	-65.6	71.5	0.933	0.982
ENSG00000231453	LINC01305	2	2.8	-64.5	70.1	0.935	0.983
ENSG00000175773	AP002986.1	11	-3.6	-92.6	85.3	0.936	0.983
ENSG00000239467	AC007405.3	2	-4.1	-105.9	97.7	0.937	0.983
ENSG00000248810	LINC02432	4	-2.3	-60.0	55.4	0.938	0.983
ENSG00000232053	AC078845.1	7	2.3	-56.2	60.9	0.938	0.983
ENSG00000226194	LINC02519	6	-2.5	-65.0	60.1	0.939	0.983
ENSG00000224259	LINC01133	1	2.6	-64.5	69.6	0.941	0.984
ENSG00000226741	LINC02554	22	-2.0	-54.4	50.4	0.941	0.984
ENSG00000248238	LINC02438	4	-2.4	-68.3	63.4	0.942	0.984
ENSG00000233760	AC004947.1	7	2.3	-59.5	64.1	0.942	0.984
ENSG00000249346	LINC01016	6	-1.9	-56.9	53.1	0.945	0.985
ENSG00000231918	AC007402.1	2	2.1	-58.9	63.1	0.946	0.985
ENSG00000250899	AC125807.2	12	-4.8	-146.7	137.2	0.947	0.985
ENSG00000248663	LINC00992	5	3.3	-98.0	104.6	0.95	0.985
ENSG00000255375	AL078612.2	11	-2.0	-62.8	58.9	0.95	0.985
ENSG00000256276	AC005186.1	12	-2.0	-64.4	60.4	0.95	0.985
ENSG00000237248	LINC00987	12	3.1	-95.8	102.1	0.951	0.985
ENSG00000224481	LINC01731	1	-2.3	-76.4	71.8	0.951	0.985
ENSG00000228251	AC012442.1	2	4.2	-132.2	140.6	0.952	0.985
ENSG00000227477	STK4-AS1	20	-2.3	-77.8	73.2	0.952	0.985
ENSG00000205682	AC020741.1	4	2.6	-84.3	89.6	0.953	0.985
ENSG00000229323	DLEU1-AS1	13	-2.0	-69.3	65.3	0.954	0.985
ENSG00000225882	LINC01456	X	3.3	-114.3	121.0	0.956	0.985
ENSG00000239572	AC117513.1	3	-1.3	-48.7	46.1	0.957	0.985
ENSG00000251301	LINC02384	12	-1.6	-59.6	56.5	0.957	0.985
ENSG00000245651	AC083805.1	12	1.6	-55.3	58.4	0.957	0.985
ENSG00000204792	LINC01291	2	-1.0	-40.2	38.1	0.959	0.986
ENSG00000231346	LINC01160	1	-1.7	-66.6	63.2	0.96	0.987
ENSG00000233215	LINC01687	21	1.0	-47.9	50.0	0.967	0.992
ENSG00000227744	LINC01940	2	-1.1	-56.1	53.8	0.967	0.992
ENSG00000257771	LINC02395	12	1.1	-51.9	54.0	0.969	0.992
ENSG00000180712	LINC02363	4	-1.3	-66.1	63.5	0.969	0.992
ENSG00000255571	MIR9-3HG	15	2.0	-100.5	104.5	0.969	0.992
ENSG00000229401	MIR5689HG	6	1.4	-72.7	75.6	0.97	0.992
ENSG00000232987	LINC01219	11	1.3	-67.4	69.9	0.971	0.992
ENSG00000261584	AL513548.1	6	-1.2	-69.6	67.2	0.973	0.992
ENSG00000225643	AL606491.1	1	-1.5	-86.2	83.3	0.973	0.992
ENSG00000241593	AC099542.1	3	-0.8	-53.0	51.5	0.977	0.993
ENSG00000234663	LINC01934	2	0.9	-61.1	62.9	0.978	0.993
ENSG00000205293	LINC01602	8	0.7	-50.6	52.1	0.978	0.993
ENSG00000228709	AP001065.1	21	0.8	-59.9	61.6	0.978	0.993
ENSG00000231533	AL078601.2	6	1.2	-87.0	89.5	0.978	0.993

Table 9: Full results of linear lincRNA-BW regression *(continued)*

	General		Regression Output*			Significance	
Ensemble ID	Gene Name	Chromosome	ß Estimate	LL	UL	P.val	FDR P.val
ENSG00000228549	BX284668.2	1	-0.8	-63.1	61.4	0.979	0.993
ENSG00000224511	LINC00365	13	-0.8	-60.8	59.3	0.98	0.993
ENSG00000260274	AC068338.2	15	1.4	-122.0	124.7	0.983	0.994
ENSG00000257894	AC027288.3	12	-0.6	-62.9	61.6	0.984	0.994
ENSG00000248515	AC024230.1	4	0.7	-64.9	66.2	0.985	0.994
ENSG00000228817	BACH1-IT2	21	0.7	-71.4	72.8	0.985	0.994
ENSG00000224184	MIR3681HG	2	0.5	-53.8	54.8	0.985	0.994
ENSG00000248103	AC008443.3	5	-0.7	-81.6	80.1	0.986	0.994
ENSG00000235523	AL135924.2	9	-0.7	-90.3	88.9	0.988	0.994
ENSG00000233791	LINC01136	1	0.5	-71.2	72.2	0.989	0.994
ENSG00000261400	AC011525.1	19	-0.4	-57.4	56.6	0.989	0.994
ENSG00000258754	LINC01579	15	-0.4	-54.1	53.4	0.99	0.994
ENSG00000214039	LINC02418	12	0.4	-57.4	58.1	0.99	0.994
ENSG00000237548	TTLL11-IT1	9	-0.4	-65.8	65.0	0.99	0.994
ENSG00000229205	LINC00200	10	-0.2	-41.1	40.7	0.993	0.995
ENSG00000250075	AC104806.2	4	0.3	-66.0	66.6	0.993	0.995
ENSG00000260430	AC099518.1	16	0.3	-71.2	71.8	0.994	0.995
ENSG00000237390	AL139130.1	1	0.1	-50.8	51.0	0.997	0.997

[*] Linear models ontrolled for gestational age; infant sex; maternal age, BMI, education and smoking status