**Supplementary Information**

Identification of psychoneuroimmune drug targets in hiPSC-derived astrocytes

**Supplementary Table S1. Differentially expressed genes in hiPSC-derived astrocytes versus parental hiPSCs.** A table containing gene names, base mean expression, log2 fold change, standard error of log fold change (lfcSE), statistical value (stat), raw p-values (pvalue), and adjusted p-values (padj) for differentially expressed genes (DEGs) between hiPSC-derived astrocytes and parental hiPSCs.

**Supplementary Table S2. Differentially expressed genes in non-responders versus healthy controls.** A table containing gene names, base mean expression, log2 fold change, lfcSE, statistical value (stat), raw p-values (pvalue), and adjusted p-values (padj) for DEGs between responders (R) and healthy controls (HC).

**Supplementary Table S3. Differentially expressed genes in non-responders versus healthy controls.** A table containing gene names, base mean expression, log2 fold change, lfcSE, statistical value (stat), raw p-values (pvalue), and adjusted p-values (padj) for DEGs between non-responders (NR) and healthy controls (HC).

**Supplementary Table S4. Differentially expressed genes in non-responders versus responders.** A table containing gene names, base mean expression, log2 fold change, lfcSE, statistical value (stat), raw p-values (pvalue), and adjusted p-values (padj) for DEGs between non-responders (NR) and responders (R).

**Supplementary Table S5. Over-representation analysis in responders versus healthy controls.** A tablelisting Gene Ontology (GO) pathway ID, pathway description, gene ratio, background ratio, p-value (pvalue), adjusted p-value (p.adjust), q-value (qvalue), gene IDs, count of genes in the pathway, direction (up/down), and ontology category (BP, MF, CC) for significantly enriched pathways in responders (R) versus healthy controls (HC).

**Supplementary Table S6. Over-representation analysis in non-responders versus healthy controls.** A table containing GO pathway ID, pathway description, gene ratio, background ratio, p-value (pvalue), adjusted p-value (p.adjust), q-value (qvalue), gene IDs, count of genes in the pathway, direction (up/down), and ontology category (BP, MF, CC) for significantly enriched pathways in non-responders (NR) versus healthy controls (HC).

**Supplementary Table S7. Over-representation analysis in non-responders versus responders.** A table containing GO pathway ID, pathway description, gene ratio, background ratio, p-value (pvalue), adjusted p-value (p.adjust), q-value (qvalue), gene IDs, count of genes in the pathway, direction (up/down), and ontology category (BP, MF, CC) for significantly enriched pathways in non-responders (NR) versus responders (R).

**Supplementary Table S8. Weighted Gene Co-Expression Network Analysis (WGCNA) results.** A table containing module names, module annotation, mean expression values in healthy controls (Mean\_HC), responders (Mean\_R), and non-responders (Mean\_NR), p-values for R vs. HC (p\_value\_R\_vs\_HC), mean expression differences for R vs. HC (mean\_diff\_R\_vs\_HC), p-values for NR vs. HC (p\_value\_NR\_vs\_HC), and mean expression differences for NR vs. HC (mean\_diff\_NR\_vs\_HC).

**Supplementary Table S9. Transcription factors in responders versus healthy controls.** A table showing the transcription factor (TF) name, statistic type, source, experimental condition, TF score, and p-value (p\_value) for significantly differentially active transcription factors in responders (R) versus healthy controls (HC).

**Supplementary Table S10. Transcription factors in non-responders versus healthy controls**. A table containing the transcription factor (TF) name, statistic type, source, experimental condition, TF score, and p-value (p\_value) for significantly differentially active transcription factors in non-responders (NR) versus healthy controls (HC).

**Supplementary Table S11. iLINCS drug perturbation analysis in responders versus healthy controls.** A table listing the source, target drug compound, similarity score, source signature, source cell line, source time, target signature, target cell line, target concentration, target time, tissue, integrated mechanisms of action (MoAs), gene targets, canonical InChI key, canonical InChI, perturbagen ID, canonical SMILES, and maximum FDA approval phase for drug perturbations associated with responders (R) versus healthy controls (HC).

**Supplementary Table S12. iLINCS drug perturbation analysis in non-responders versus healthy controls.** A table containing the source, target drug compound, similarity score, source signature, source cell line, source time, target signature, target cell line, target concentration, target time, tissue, integrated mechanisms of action (MoAs), gene targets, canonical InChI key, canonical InChI, perturbagen ID, canonical SMILES, and maximum FDA approval phase for drug perturbations associated with non-responders (NR) versus healthy controls (HC).

**Supplementary Table S13. Core network nodes in responders versus healthy controls.** A table providing the node name, degree (number of connections), betweenness centrality (node's role in shortest paths), coreness (node's position in network layers), strength (weighted degree), and transitivity (local clustering coefficient) for core nodes in the comparison between responders (R) and healthy controls (HC).

**Supplementary Table S14. Core network nodes in non-responders versus healthy controls.** A table containing the node name, degree, betweenness centrality, coreness, strength, and transitivity for core nodes in the comparison between non-responders (NR) and healthy controls (HC).

**Supplementary Table S15. Protein-protein interaction network centrality analysis of differentially active transcription factors.** A table containing transcription factor (TF) name, degree centrality (number of direct connections), betweenness centrality (frequency of a node in shortest paths), closeness centrality (average shortest path length to all other nodes), eigenvector centrality (influence of a node based on its connections), PageRank (importance based on quantity and quality of connections), composite score (average of normalized centrality values), and composite rank (average ranking across all metrics) for TFs showing differential activity between non-responders (NR) and responders (R) relative to healthy controls (HC).