

**Supplementary Materials for  
Gene expression in the dorsolateral and ventromedial prefrontal cortices  
implicates immune-related gene networks in PTSD.  
by Logue et al.**

**Supplementary Methods**

**Methods and Materials**

**Tissue and RNA extraction:** The VA National PTSD Brain Bank collection and clinical assessment methods have been described in detail previously<sup>1</sup>. In brief, this study used VA National PTSD Brain Bank tissue from donors who were assessed for PTSD, depression, and other conditions by way of post-mortem medical record reviews and clinical interviews with next-of-kin. The analyses reported were based on comparisons of samples from three groups: (a) a PTSD group composed of individuals with a history of PTSD with or without comorbid depression; (b) a depression group composed of individuals with a history of depression but no PTSD; and (c) a control group of individuals with no history of either condition. Individuals with a history of bipolar disorder were excluded from the analyses. The dlPFC analyses were based on tissue from 94 donors, 50 (53.19%) of whom were also in the Girgenti et al. study, from a region adjacent to that extracted for that study. Of the 87 donors in our vmPFC analysis, 46 (52.87%) were in Girgenti et al.'s cohort. Approximately 25mg of tissue was extracted from frozen blocks of vmPFC (Brodmann areas 12/32) and dlPFC (Brodmann area 9/46) tissue taken at the level of the genu of the corpus callosum. The Girgenti et al. region is superior to the one examined here and primarily consists of BA 9 with a small portion of BA 46, is very dorsal, and involves the superior frontal sulcus. The block examined here consists of BA 46 and a proportionally smaller amount of BA9 and is more lateral. Both regions are considered part of the dorsolateral frontal cortex.

**RNA-sequencing and Quality Control:** RIN numbers were generated for a subset of the data indicating modest sample quality, but at a level sufficient that library prep would succeed for a large proportion of the samples. Library preparation was performed using the Illumina TruSeq Stranded total RNA kit with globin depletion. The libraries were sequenced using a Hiseq 2500, which generated paired-end 75 bp reads. The Hiseq was run in two different run modes to avoid empty lanes: "high output" mode which runs a flow cell over 8 lanes which each contain a unique pool of libraries and "rapid" mode in which a single cell which was run over two lanes. Trimmomatic<sup>2</sup> removed adapters and filtered short/low quality reads followed by alignment against the hg38 human reference genome using STAR<sup>3</sup> and transcriptome quantification was performed with Kallisto<sup>4,5</sup>. Quality metrics for the assigned reads were computed with FastQC, RSeQC, and MultiQC<sup>6</sup>. Samples with lower than 50% uniquely mapped reads were dropped.

Kallisto transcript abundance estimates were collapsed to the gene level using the tximport Bioconductor package and log-transformed using the regularized log transformation (rLog) method implemented in DEseq2<sup>7</sup>. PCs were computed from the rLog transformed expression values. Any samples more than 6 SDs away from the group mean on any of the first 10 PCs were considered outliers and removed.

For samples passing QC, self-report sex was confirmed by examining brain expressed X and Y chromosome genes<sup>8</sup>. Correspondence between genotype data and RNA-seq data was confirmed by comparing the chip-based genotypes to genotypes generated from RNA-seq data using the GATK HaplotypeCaller (software.broadinstitute.org/gatk/documentation/tooldocs/4.0.8.0/org\_broadinstitute\_hellbender\_tools\_walkers\_haplotypecaller\_HaplotypeCaller.php).

**Cell-type Proportion Analyses:** Weightings of different cell proportions present in neural tissue was estimated using BrainInABlender<sup>9</sup>. To confirm cell type weightings estimated with BrainInABlender, the proportion of different cell types was estimated using CIBERSORTx<sup>10</sup> based on single-cell RNAseq data from PsychENCODE, specifically DER-22\_Single\_cell\_expression\_raw\_UMI.tsv from <http://resource.psychencode.org/>. For the purpose of CIBERSORTx estimation, cell type proportions for the different layers of excitatory neurons were collapsed into a single excitatory neuron cell type. Similarly, the different populations of inhibitory neurons were collapsed into a single cell type. We tested for association between indicators of the relative proportion of different types of cells and PTSD in the dlPFC, vmPFC, and in sex-stratified analyses of each brain region based on both the BrainInABlender weights and the logit of the cell type proportions as estimated by CIBERSORTx. R's standard linear regression package (lm) was used with the cell proportion variable as the response, and with PTSD, age, sex, PMI, and sequencing-run ID as covariates. As RIN values were not available for all RNA-seq samples, quality surrogate variables, which summarize RNA degradation in degradation sensitive regions,<sup>11</sup> were calculated using the sva R package. The first 3 QSVAs were included in the model. One of these QSVAs was highly correlated with RIN value in the subset of samples for which RIN values were available ( $r=0.69$ ,  $p=0.0016$ ).

**Transcriptome-wide Differential Expression:** Within each brain region, single-gene association analysis was performed on genes with sufficient expression levels (read count >1 in at least 30 samples). Case-control analyses were performed in DEseq2. Age, sex, PMI, cell type weights from BrainInABlender (astrocytes, endothelial cells, microglia, mural, neurons, oligodendrocytes and red blood cells), three QSVAs, and sequencing-run ID were included as covariates.

Within each brain region, PTSD cases were compared with controls in the whole cohort, then in males and females separately. Analyses within sex were similarly performed in DEseq2. Our expression-level criterion for analyzing a gene was adapted to the lower sample size within each sex ( $\geq 1$  read in 16 subjects in males, and  $\geq 1$  read in 14 subjects in the females). Covariates for the sex-stratified analyses included age, PMI, indicators of the relative proportion of different types of cells, sequencing-run ID, and 3 qSVAs.

A Benjamini-Hochburg false discovery rate corrected p-value ( $p_{cor}$ ), sometimes called a Q value, was used for multiple testing correction across all these analyses, including the 2 regions examined in the full cohort, and in males and females separately. This p-value correction is very conservative for several reasons, including that expression values for many genes are correlated, the joint and sex-stratified analyses are correlated, and gene expression levels for the vmPFC/dlPFC are correlated for many genes. For our experiment-wide significant genes ( $p_{cor} < 0.05$  corrected for six transcriptome-wide analyses), we also performed a case-control analysis of depression cases (comparing depression and depression NOS subjects to controls). This was

performed in DEseq2 as described above with identical covariates as the PTSD analyses and using the same set of controls. To ensure that these analyses were properly normalized, the analyses were run transcriptome-wide, and the genes of interest were extracted from the results.

The overlap between associated genes in different regions and in different subgroups was visualized using VENN diagrams. Significance of the level of overlap was estimated using a null simulation which adjusted for the fact that larger genes and genes with higher levels of expression were more likely to be significant, similar to the adjustments performed in goSEQ enrichment analysis<sup>12</sup>. First, a logistic regression model estimated the probability that each gene would be significant ( $p < 0.05$ ) based on the gene length and the mean expression level for the gene. Note that both variables were very significantly associated with a gene expression difference ( $p < 2 \times 10^{-16}$  for length and  $p = 0.0095$  for mean expression level). Then, we performed a Monte Carlo simulation to estimate the distribution of overlap given these probabilities. The significance of the observed overlap under the null was estimated by taking one minus the percentile of the observed overlap in this estimated null distribution.

**Ancestry Association Analysis:** As ancestry was confounded with PTSD and depression status in women (Supplementary Table 2), we could not simply perform a sensitivity analysis for ancestry as we performed for the other potential confounders, as it would eliminate associations observed in the female stratified analyses, whether or not the association was due to PTSD. Therefore, we instead looked within our top (Table 3) genes to explore whether there was evidence of association with ancestry within the different diagnosis groups. We used a linear model to test whether log-normalized expression levels of table 3 genes were associated with non-white non-Hispanic (WNH) ancestry within each brain region x diagnosis group combination (PTSD, depression, controls), controlling for age, sex, PMI, cell types, and qSVAs. Then, we meta-analyzed across the three diagnosis groups within each brain region using a mixed effect meta-analysis model using the R metafor package<sup>13</sup>. We used an FDR correction to adjust for the 21 Table 3 genes that were examined.

**Overrepresentation Analyses:** We examined the relationship between our RNA-seq results and GO terms using GOseq, which performed an over-representation analysis of the top 200 differentially expressed genes<sup>12</sup>. We also examined enrichment of associations in different cell types by examining the association with PTSD of a set of representative cell type markers from PsychENCODE, specifically DER-21\_Single\_cell\_markergenes\_UMI file from <http://resource.psychencode.org/>. Enrichment for different cell type markers in the dlPFC and vmPFC results was evaluated in two ways. First, we tested for an enrichment of smaller (more significant) p-values for each of the cell types and in males/females using the GSEA method<sup>14,15</sup>. We looked for cell type enrichment in all of the genes, and then in up and downregulated genes separately. Next, similar to the analysis performed for GO terms, we tested for enrichment of the top 200 genes using GOseq in both the dlPFC and vmPFC and in the sex-stratified analyses. For the GOseq cell-type analysis, we also examined the top 200 upregulated and top 200 downregulated genes.

**PTSD Candidate Gene Analyses:** We also examined association for a previously published list of 143 PTSD implicated candidate genes (Huckins et al 2019<sup>16</sup>, in Supplementary Table 5 of that paper). To ensure that these targeted analyses were properly normalized, analyses were run transcriptome-wide, and the results from the candidate PTSD-associated genes were extracted. In

order to avoid being too conservative when evaluating the significance of genes with prior evidence of PTSD involvement, our multiple testing correction for candidate genes was only adjusted for the number of tests within each cohort and region ( $p_{\text{cor-candidate}}$ ).

**Gene-Network Analyses:** Within each brain region, we evaluated association with PTSD within gene networks identified using a weighted gene co-expression networks (WGCNA) analysis<sup>17</sup>. We calculated networks first in the whole cohort and then in men and women separately. Gene correlations were computed from the rlog transformed values of highly expressed genes:  $\geq 10$  reads in 30 samples. The filter for gene expression in the sex-specific WGCNA runs was  $\geq 10$  reads in 16 subjects for the male cohort, and  $\geq 10$  reads in 14 subjects for the female cohort. Within each of the identified networks, which are labeled with arbitrary color names, we tested for association between PTSD and a PC summarizing network activity. The putative function of each pathway was examined using an overrepresentation analysis performed in DAVID, using the set of all highly expressed genes as a background gene set. The reported p-values for the DAVID analyses are corrected for the number of pathways examined ( $p_{\text{cor}}$ ) using the Benjamini method. We also tested for overrepresentation of cell-type markers in the PTSD associated networks, using the background of expressed genes which were also cell-type markers. Significance was judged using a hypergeometric distribution. A FDR multiple testing correction was used, correcting for the number of cell type markers tested within each network. As a follow-up investigation, association was tested with depression in networks which achieved at least a nominally significant association with PTSD.

**Upstream Regulator Analyses:** *Upstream regulator analysis (URA)*<sup>18</sup> was performed as described previously<sup>19</sup> on overall differential gene expression signatures and PTSD-associated modules' differential gene expression signatures. In brief, this analysis: i) infers the enrichment of target genes for each regulator and; ii) uses the differential gene expression effects (i.e., group fold changes) to estimate a z-score, which represents whether the upstream transcription factor is statistically predicted to be “activated” or “inhibited” ( $z > 0$  or  $z < 0$ , respectively). Criteria for detecting the activity of an upstream regulator were: (a) absolute bias-corrected z-score more or equal to 2.0; (b) enrichment Benjamini-Hochberg adjusted p-value  $< .05$ . Upstream regulators that weren't expressed in the tissues examined and for which PTSD associations were not available were discarded.

**Comparison to Prior Results:** Finally, we compare our association results to those presented in Girgenti et al. The Girgenti et al. cohort represent a combined study of two different cohorts: the VA National PTSD brain bank cohort and the UPMC cohort. A subset of the VA National PTSD Brain Bank cohort overlaps with the cohort examined here. The UPMC cohort is completely independent of the current study cohort. We compared our dlPFC results first to the non-independent complete Girgenti et al. published dlPFC results (VA Brain Bank+UPMC) and then to the results of the completely UPMC cohort, which allowed us the possibility of independently replicating our dlPFC results. In addition, we compared our PTSD association results with those obtained by Morrison et al., a qPCR candidate gene study of immune response genes in the dlPFC in a subset ( $n = 50$ ) of the VA National PTSD Brain Bank cohort<sup>20</sup>.

## Supplementary Results

**RNA Sequencing and Quality Control:** One sample was an outlier and dropped. For vmPFC, two samples were dropped due to a low proportion of mapped reads (<50%) and two samples were dropped as outliers, including the subject excluded from the dlPFC data. From the remaining cohort, subjects with bipolar disorder (n=4) were excluded from both the dlPFC and vmPFC, leaving 94 dlPFC and 90 vmPFC samples for analysis.

**WGCNA Network analysis:** The following networks were associated with PTSD at the  $p < 0.05$  level. See the main text for a description of the dlPFC-orange and the vmPFC-sienna-3 network.

**dlPFC-brown4 (p=0.046).** There were 69 at least nominally significant PTSD-associated genes in the dlPFC-brown4 network, 68 of which were upregulated in PTSD cases. None of these genes were associated with PTSD at an experiment-wide level. Only one gene from our PTSD candidate list, *PPP1R8*, was in the dlPFC-brown4 network, which was not significantly associated with PTSD in the dlPFC ( $\log_{2}fc=0.078$ ,  $p=0.077$ ). Overrepresentation analysis indicated dlPFC-brown4 is involved in cellular processes such as protein targeting and mRNA decay (GO:0006614 and GO:0000184).

**vmPFC-mediumpurple3 (p=0.036):** This is a small network of only 35 genes. There are no significant GO term associations for this network (Table 6). It does not contain any of the PTSD candidate genes. It does not contain any genes that achieved corrected significant associations with PTSD, but it does contain 7 genes that were nominally (or better) significantly associated with PTSD, all of which were downregulated in the vmPFC of PTSD cases. The most significant of these was the gene *REGL* ( $\log_{2}fc=-1.20$ ,  $p=0.0037$ ), which has been implicated educational attainment, specifically for mathematics<sup>21</sup>. Both *REGL* and *NAV2* have been implicated in a GWAS of white matter micro-structure<sup>22</sup>. Follow-up analyses indicated that vmPFC-sienna3 was downregulated in both PTSD and depression cases.

**dlPFC-Female-lightgreen (p=0.019).** This network was down regulated in women with PTSD. This network contains 27 genes that were nominally associated with PTSD in the dlPFC female sex-stratified analysis, 24 of which were downregulated in the dlPFC of women with PTSD. One of these, *NOTCH1* ( $\log_{2}fc=-0.88$ ,  $p=0.0086$ ), was a prior PTSD candidate locus. Two other PTSD candidate loci, *COMT* and *SLC6A9*, were in dlPFC-Female-lightgreen, but were not significant in the dlPFC analysis of women with PTSD ( $p > 0.30$ ). One of the experiment-wide significant genes, *PIRT*, is a member of this network, but this gene was upregulated in the vmPFC analyses ( $\log_{2}fc=2.1$ ,  $p=4.90 \times 10^{-7}$ ), and not the dlPFC or the female dlPFC analyses ( $p > 0.50$ ). The function of this network is unclear, as there were no significant GO terms for this network.

**vmPFC-Male-orange (p=0.037).** This network was nominally significantly enriched for GO:0009897~external side of plasma membrane, and may be associated with immune response

as GO:0051607: defense response to virus and GO:0009615:response to virus were nominally significantly enriched in this network. There were 20 nominally significant PTSD-associated genes in vmPFC-Male-orange, all of which are downregulated in the vmPFC of men with PTSD. The most significant of these is the GTPase, IMAP FAMILY, MEMBER 8 gene (*GIMAP8*, logfc=-1.01, p=8.78x10<sup>-5</sup>). The GIMAP family of genes modulate the immune response by regulating apoptosis of lymphocytes<sup>23</sup>. The GIMAP2 gene was also a vmPFC-male-orange gene that was associated with PTSD (logfc=-1.04, p=0.029). While these associations and the overrepresentation analysis indicated some immune response role for vmPFC-Male-orange, this network does not share genes with the vmPFC-sienna3 network which was an immune-related network in the vmPFC which was also downregulated in PTSD cases.

**Comparison to qPCR data from Morrison et al.:** Many of the dlPFC samples were also used by our group in a candidate gene study by Morrison et al. that was based on qPCR assessment of immune-related gene expression based on n=12 PTSD cases, 13 controls, and 25 depressed cases that were also included in this study. The association with *IL1B* was at the trend level (p=0.082) in that paper, which is perhaps unsurprising given the smaller sample size, with the same direction of effect as we noted here ( $\Delta\Delta\text{CT}$  logfc estimated to be -0.92, which indicates higher expression in PTSD cases relative to controls). We reexamined the individual-level qPCR data for *IL1B* generated from that paper and found that the correlation between the individual qPCR and RNA-seq expression values was r=0.74 (after adjustment for  $\Delta\Delta\text{CT}$ , which would make associations negative, p=1.61x10<sup>-8</sup>). This validates the RNA-seq assessment of *IL1B* expression.

## Supplementary Tables

**Supplementary Table 1:** Descriptive Statistics for the analyzed PTSD cases, depression cases, and controls in the dlPFC A) and vmPFC cohorts B), stratified by sex.

Male dlPFC					
	Control	PTSD	p (PTSD vs Control)	MDD	p (MDD vs Control)
N	16	18		21	
AgeDeath (mean (SD))	47.43 (8.26)	39.39 (10.89)	0.022	39.96 (11.42)	0.034
PMI (mean (SD))	30.34 (8.35)	27.50 (8.76)	0.341	27.52 (7.33)	0.28
White, non-Hispanic (%)	12 (75.00)	13 (72.20)	> 0.99	17 (81.00)	0.97
Smoking (%)	6 (37.50)	13 (72.20)	0.091	16 (76.20)	0.042
Military Service (%)	1 (6.20)	14 (77.80)	0.00011	4 (19.00)	0.52
Suicide Death (%)	0 (0.00)	3 (16.70)	0.269	3 (14.30)	0.33
Alcohol or drug death (%)	0 (0.00)	11 (61.10)	0.0010	10 (47.60)	0.0040

Female dlPFC					
	Control	PTSD	p (PTSD vs Control)	MDD	p (MDD vs Control)
N	8	20		11	
AgeDeath (mean (SD))	44.72 (13.23)	42.42 (12.37)	0.67	43.69 (9.85)	0.068
PMI (mean (SD))	28.00 (2.90)	29.15 (7.90)	0.69	26.91 (8.18)	0.26
White, non-Hispanic (%)	3 (37.50)	18 (90.00)	0.016	10 (90.90)	0.049
Smoking (%)	1 (12.50)	15 (75.00)	0.0090	6 (54.50)	0.0077
Military Service (%)	0 (0.00)	1 (5.00)	1.00	0 (0.00)	--
Suicide Death (%)	0 (0.00)	5 (25.00)	0.31	2 (18.20)	0.60
Alcohol or drug death (%)	0 (0.00)	14 (70.00)	0.0030	19 (59.36)	0.0020

Male vmPFC					
	Control	PTSD	p (PTSD vs Control)	MDD	p (MDD vs Control)
N	13	16		21	
AgeDeath (mean (SD))	48.54 (7.97)	39.36 (10.99)	0.018	39.96 (11.42)	0.024
PMI (mean (SD))	31.08 (8.66)	27.25 (9.27)	0.27	27.52 (7.33)	0.21
White, non-Hispanic (%)	11 (84.60)	11 (68.8)	0.58	81.00)	> 0.99
Smoking (%)	4 (30.80)	12 (75.00)	0.045	16 (76.20)	0.024
Military Service (%)	1 (7.70)	12 (75.00)	0.0012	4 (19.00)	0.68
Suicide Death (%)	0 (0.00)	2 (12.50)	0.56	3 (14.30)	0.42
Alcohol or drug death (%)	0 (0.00)	10 (62.50)	0.0018	10 (47.60)	0.010

Female vmPFC					
	Control	PTSD	p (PTSD vs Control)	MDD	p (MDD vs Control)
N	7	19		11	
AgeDeath (mean (SD))	44.86 (14.28)	42.59 (12.68)	0.70	43.69 (9.85)	0.84
PMI (mean (SD))	28.29 (3.01)	28.82 (7.97)	0.87	26.91 (8.18)	0.68
White, non-Hispanic (%)	3 (42.90)	17 (89.5)	0.048	10 (90.90)	0.093
Smoking (%)	1 (14.30)	14 (73.7)	0.023	6 (54.50)	0.23
Military Service (%)	0 (0.00)	1 (5.30)	> 0.99	11 (100.0)	--
Suicide Death (%)	0 (0.00)	5 (26.30)	0.34	2 (18.20)	0.67
Alcohol or drug death (%)	0 (0.00)	14 (73.70)	0.0037	9 (81.80)	0.0037



**Supplementary Table 2:** The summary of RIN values and qSVAs for PTSD and depression cases/controls. Not all samples had RIN values available, so n for RIN values per group is summarized in the table.

Region	Quality Score	PTSD	MDD	Controls	p	p
		mean and (SD) or [n, min, max]	mean and (SD) or [n, min, max]	mean and (SD), or [n, min, max]	PTSD vs Controls	MDD vs Controls
dlPFC	RIN	5.97 [7, 4.4, 7.7]	5.77 [3, 4.7, 7.8]	5.77 [6, 3.3, 6.9]	0.78	1
	qSVA1	-1.36 (13.65)	1.80 (16.02)	0.98 (19.72)	0.58	0.87
	qSVA2	0.87 (6.74)	-2.44 (6.30)	1.65 (12.43)	0.75	0.11
	qSVA3	-0.54 (5.42)	0.62 (7.98)	-0.13 (6.62)	0.79	0.71
vmPFC	RIN	6.03 [6, 3.6, 7.3]	5.05 [2, 5.0, 5.1]	5.74 [8, 3.6, 7.2]	0.71	0.56
	qSVA1	-2.77 (16.46)	-0.01 (17.34)	4.35 (16.86)	0.13	0.38
	qSVA2	-1.25 (6.05)	-0.33 (10.55)	2.49 (12.74)	0.15	0.39
	qSVA3	-0.46 (5.45)	-0.15 (9.09)	-0.54 (9.87)	0.97	0.88

**Supplementary Table 3:** The summary of the QC statistics for RNA-seq mapping.

Regions	N of Samples	Mean N of Reads (SD) *10 <sup>6</sup>	N of Passing QC Filters	Ave Uniquely Mapped Percentage (SD)
dlPFC	99	18.99 (8.16)	98	75.84 (6.07)
vmPFC	95	18.39 (8.40)	93	73.24 (7.32)

**Supplementary Table 4:** Correlation between logit transformed BrainInABlender cell type scores and CIBERSORTx. Data pooled across both brain regions. Significant correlations are in bold.

		<u>BrainInABlender Estimates</u>									
		Astro	Endo	Microglia	Mural	Neuron All	Neuron Inter	Neuron Proj	Oligo.	Oligo. Immature	RBC
<u>CIBERSORTx Estimates</u>	Ex Neuron	<b>-0.63</b>	<b>-0.55</b>	<b>-0.51</b>	<b>-0.50</b>	<b>0.87</b>	<b>0.50</b>	<b>0.81</b>	<b>-0.61</b>	-0.07	<b>-0.31</b>
	In Neuron	-0.11	<b>-0.15</b>	0.068	<b>-0.19</b>	<b>0.36</b>	<b>0.79</b>	<b>0.24</b>	<b>-0.51</b>	<b>-0.27</b>	<b>-0.17</b>
	Oligo	-0.021	-0.013	<b>0.14</b>	-0.067	<b>-0.46</b>	<b>-0.52</b>	<b>-0.51</b>	<b>0.95</b>	-0.064	<b>0.20</b>
	Astro	<b>0.93</b>	<b>0.40</b>	<b>0.23</b>	<b>0.47</b>	<b>-0.68</b>	<b>-0.46</b>	<b>-0.61</b>	0.031	<b>0.16</b>	<b>0.25</b>
	OPC	<b>0.28</b>	0.048	0.040	0.14	<b>-0.24</b>	<b>-0.23</b>	-0.10	0.0049	<b>0.31</b>	0.07
	Endo	<b>0.21</b>	<b>0.74</b>	<b>0.46</b>	<b>0.59</b>	<b>-0.29</b>	-0.077	<b>-0.29</b>	0.013	0.027	<b>0.16</b>
	Microglia	0.092	<b>0.39</b>	<b>0.45</b>	<b>0.30</b>	<b>-0.21</b>	-0.040	<b>-0.18</b>	0.060	0.046	<b>0.20</b>
	Per	<b>0.48</b>	<b>0.52</b>	<b>0.18</b>	<b>0.64</b>	<b>-0.48</b>	<b>-0.32</b>	<b>-0.29</b>	-0.07	<b>0.23</b>	<b>0.15</b>

**Supplementary Table 5:** Test of association between PTSD and BrainInABlender cell proportion Z scores in the dlPFC and vmPFC and in sex-stratified analyses.

Cohort	Cell Type	dlPFC			vmPFC		
		Estimate	Std. Error	p	Estimate	Std. Error	p
All subjects	Astrocyte	0.079	0.14	0.59	-0.011	0.11	0.92
	Endothelial	0.16	0.15	0.30	<b>-0.26</b>	<b>0.12</b>	<b>0.039</b>
	Microglia	0.00015	0.17	1.00	-0.17	0.12	0.17
	Mural	0.12	0.13	0.37	-0.18	0.12	0.13
	Neuron: All	0.071	0.091	0.44	0.054	0.11	0.63
	Neuron: Interneuron	0.0079	0.053	0.88	-0.020	0.075	0.79
	Neuron: Projection	0.059	0.070	0.40	0.077	0.10	0.42
	Oligodendrocyte	-0.061	0.14	0.66	-0.070	0.22	0.75
	Oligodendrocyte: Immature	0.011	0.059	0.85	0.026	0.060	0.66
	RBC	-0.0081	0.075	0.91	0.12	0.09	0.20
male	Astrocyte	0.16	0.26	0.53	0.15	0.13	0.28
	Endothelial	0.21	0.28	0.46	-0.49	0.21	0.032
	Microglia	0.28	0.28	0.32	0.086	0.15	0.57
	Mural	0.17	0.23	0.47	-0.31	0.17	0.083
	Neuron: All	0.035	0.15	0.82	-0.060	0.15	0.69
	Neuron: Interneuron	-0.029	0.055	0.60	0.031	0.10	0.75
	Neuron: Projection	0.039	0.10	0.70	-0.005	0.12	0.97
	Oligodendrocyte	-0.072	0.12	0.56	-0.14	0.28	0.62
	Oligodendrocyte: Immature	0.10	0.086	0.25	0.014	0.090	0.88
	RBC	0.044	0.10	0.67	0.16	0.13	0.21
female	Astrocyte	0.033	0.15	0.82	-0.026	0.31	0.93
	Endothelial	-0.0046	0.073	0.95	-0.016	0.23	0.95
	Microglia	<b>-0.49</b>	<b>0.12</b>	<b>0.0014</b>	-0.69	0.32	0.052
	Mural	0.052	0.11	0.64	-0.066	0.30	0.83
	Neuron: All	0.20	0.14	0.17	0.31	0.31	0.33
	Neuron: Interneuron	0.10	0.12	0.43	-0.038	0.16	0.82
	Neuron: Projection	0.21	0.14	0.14	0.32	0.27	0.25
	Oligodendrocyte	-0.21	0.35	0.55	-0.28	0.46	0.55
	Oligodendrocyte: Immature	-0.0041	0.10	0.97	0.049	0.14	0.74
	RBC	-0.15	0.14	0.32	0.033	0.25	0.90

**Supplementary Table 6:** Test of association between PTSD and CIBERSORTx estimated cell proportion scores in the dlPFC and vmPFC and in sex-stratified analyses.

Cohort	cell type	dlPFC			vmPFC		
		Estimate	Std. Error	p	Estimate	Std. Error	p
All subjects	Excitatory Neurons	0.012	0.68	0.99	0.20	0.77	0.79
	Inhibitory Neurons	-0.027	1.20	0.98	-0.14	1.30	0.91
	Oligodendrocyte	-0.31	1.40	0.82	-0.31	1.40	0.83
	Astrocyte	0.087	0.95	0.93	0.14	1.10	0.90
	Oligodendrocyte Precursor Cells	-0.58	19.00	0.98	0.85	19.00	0.96
	Endothelial	1.30	3.20	0.69	-2.00	4.30	0.64
	Microglia	1.60	30.00	0.96	3.20E-16	35.00	1.00
	Pericytes	-0.018	2.30	0.99	-0.25	2.60	0.92
male	Excitatory Neurons	-0.060	0.96	0.95	-0.45	1.10	0.69
	Inhibitory Neurons	-0.029	1.60	0.99	-0.031	2.10	0.99
	Oligodendrocyte	-0.088	2.10	0.97	0.93	2.10	0.65
	Astrocyte	0.19	1.40	0.89	0.58	1.60	0.72
	Oligodendrocyte Precursor Cells	2.00	41.00	0.96	1.90	33.00	0.96
	Endothelial	1.80	6.10	0.77	-3.20	8.00	0.68
	Microglia	0.79	63.00	0.99	-7.40E-17	51.00	1.00
	Pericytes	-0.13	3.20	0.97	-0.15	4.20	0.97
female	Excitatory Neurons	0.26	1.30	0.83	0.65	1.50	0.67
	Inhibitory Neurons	0.092	2.50	0.97	0.29	2.70	0.91
	Oligodendrocyte	-0.62	2.70	0.82	-3.30	6.70	0.62
	Astrocyte	0.009	1.70	1.00	-0.03	2.10	0.99
	Oligodendrocyte Precursor Cells	-1.10	44.00	0.98	1.70	69.00	0.98
	Endothelial	0.17	6.70	0.98	-0.37	13.00	0.98
	Microglia	-5.10E-16	56.00	1.00	-1.00E-16	69.00	1.00
	Pericytes	-0.071	4.70	0.99	-0.017	5.90	1.00

**Supplementary Table 7: dlPFC PTSD associations (n=38 PTSD cases vs. n=24 controls) for top genes. Results presented are for all of the genes in Table 2, in that order, regardless of whether or not they were corrected significant in the dlPFC.**

Gene	Overall			Male			Female		
	l2fc	p	p <sub>cor</sub>	l2fc	p	p <sub>cor</sub>	l2fc	p	p <sub>cor</sub>
<i>GLP2R</i>	0.50	0.042	1	0.74	0.06	1	-0.23	0.65	1
<i>MBP</i>	0.084	0.37	1	0.14	0.17	1	-0.11	0.78	1
<i>OTOGL</i>	-0.3	0.00033	0.42	-0.55	6.72E-09	0.00043	-0.28	0.49	1
<i>MOBP</i>	0.065	0.57	1	0.23	0.046	1	-0.26	0.69	1
<i>MAFF</i>	0.79	0.015	1	0.33	0.21	1	0.95	0.49	1
<i>PAIP2B</i>	0.1	0.27	1	0.26	0.031	1	-0.033	0.93	1
<i>PIRT</i>	0.19	0.56	1	0.089	0.81	1	0.58	0.52	1
<i>LPAR1</i>	0.12	0.1	1	0.24	0.053	1	-0.13	0.64	1
<i>KPNA1</i>	0.17	5.95E-07	0.013	0.1	0.031	1	0.21	0.39	1
<i>CFH</i>	-0.12	0.38	1	-0.08	0.63	1	-0.023	0.97	1
<i>SLC2A14</i>	-0.83	0.24	1	-2.88	9.71E-07	0.017	-4.6	0.067	1
<i>PCDH8</i>	-0.05	0.78	1	0.0028	0.99	1	-0.4	0.63	1
<i>FOS</i>	0.16	0.64	1	0.23	0.5	1	-0.91	0.51	1
<i>BCAS1</i>	0.14	0.16	1	0.29	0.019	1	-0.27	0.47	1
<i>ZDHHC11B</i>	-0.2	0.33	1	-0.24	0.31	1	-2.1	0.0088	1
<i>ERMN</i>	-0.045	0.6	1	0.088	0.4	1	-0.4	0.28	1
<i>NR4A1</i>	-0.23	0.43	1	-0.22	0.47	1	-1.1	0.43	1
<i>EDN1</i>	1.25	4.44E-06	0.046	0.82	0.03	1	2.9	7.20E-06	0.062
<i>KIF5A</i>	0.049	0.54	1	0.21	0.04	1	0.031	0.92	1
<i>RBM3</i>	0.25	0.059	1	0.12	0.56	1	1.88	4.98E-06	0.046
<i>EMP1</i>	0.84	0.017	1	0.53	0.25	1	0.025	0.99	1

**Supplementary Table 8:** vmPFC PTSD associations (n=35 PTSD cases vs. n=20 controls) for top genes. Results presented are for all of the genes in Table 2, in that order, regardless of whether or not they were corrected significant in the vmPFC.

Gene	Overall			Male			Female		
	l2fc	p	p <sub>cor</sub>	l2fc	p	p <sub>cor</sub>	l2fc	p	p <sub>cor</sub>
<i>GLP2R</i>	0.67	0.033	1	0.11	0.72	1	3.92	5.12E-10	9.80E-05
<i>MBP</i>	0.17	0.31	1	0.41	0.15	1	-1.46	1.72E-09	0.00016
<i>OTOGL</i>	-0.027	0.84	1	-0.027	0.89	1	-0.76	0.031	1
<i>MOBP</i>	0.025	0.88	1	0.067	0.83	1	-1.49	4.80E-08	0.0021
<i>MAFF</i>	1.2	0.0016	0.72	1.89	5.58E-08	0.0021	1.1	0.15	1
<i>PAIP2B</i>	0.051	0.75	1	0.16	0.42	1	-1.55	1.56E-07	0.005
<i>PIRT</i>	2.11	4.87E-07	0.013	1.1	0.012	1	2.6	0.015	1
<i>LPAR1</i>	0.1	0.51	1	0.26	0.23	1	-1.48	5.75E-07	0.013
<i>KPNA1</i>	0.015	0.83	1	-0.076	0.55	1	0.24	0.47	1
<i>CFH</i>	-0.63	0.00079	0.57	-1.11	8.93E-07	0.017	-0.7	0.21	1
<i>SLC2A14</i>	-1.9	0.0006	0.51	-3.1	0.026	1	-1.9	0.24	1
<i>PCDH8</i>	0.18	0.39	1	0.28	0.39	1	2.08	1.07E-06	0.017
<i>FOS</i>	0.73	0.034	1	1.2	0.0069	1	2.14	1.76E-06	0.026
<i>BCAS1</i>	0.086	0.61	1	0.31	0.3	1	-1.42	2.11E-06	0.028
<i>ZDHC11B</i>	0.018	0.94	1	-0.31	0.36	1	-1.81	2.20E-06	0.028
<i>ERMN</i>	-0.31	0.04	1	-0.2	0.57	1	-1.21	2.75E-06	0.033
<i>NR4A1</i>	0.13	0.7	1	0.36	0.35	1	2.64	4.31E-06	0.046
<i>EDN1</i>	0.91	0.01	1	1.1	0.044	1	-0.038	0.95	1
<i>KIF5A</i>	0.057	0.65	1	0.13	0.35	1	-1.13	4.58E-06	0.046
<i>RBM3</i>	0.17	0.41	1	0.21	0.58	1	0.63	0.2	1
<i>EMP1</i>	1.4	0.00046	0.48	1.56	5.03E-06	0.046	1.2	0.45	1

**Supplementary Table 9:** Associations for the top (Table 3) genes after inclusion of potential confounders in the analysis.

Gene	Region	Cohort	Original Association		With Smoking covariate		With SRI as a covariate		With suicide as a covariate		With Opiates as a covariate		With likely concussion/TBI as a covariate	
			l2fc	p	l2fc	p	l2fc	p	l2fc	p	l2fc	p	l2fc	p
<i>GLP2R</i>	vmPFC	Female	3.9	5.10E-10	5.5	1.50E-14	3.9	4.80E-12	4.1	3.10E-11	3	6.20E-05	4	4.40E-10
<i>MBP</i>	vmPFC	Female	-1.5	1.70E-09	-1.5	1.30E-05	-1.5	1.80E-08	-1.5	9.60E-10	-1.4	1.50E-05	-1.5	6.30E-10
<i>OTOGL</i>	dIPFC	Male	-0.55	6.70E-09	-0.57	2.10E-08	-0.6	1.00E-10	-0.53	4.40E-07	-0.62	1.40E-08	-0.56	1.80E-08
<i>MOBP</i>	vmPFC	Female	-1.5	4.80E-08	-1.8	1.50E-06	-1.5	4.20E-07	-1.5	1.80E-08	-1.4	0.00013	-1.6	1.80E-09
<i>MAFF</i>	vmPFC	Male	1.9	5.60E-08	1.7	7.30E-06	1.8	2.80E-07	1.9	1.50E-07	1.2	0.00099	1.9	1.30E-07
<i>PAIP2B</i>	vmPFC	Female	-1.5	1.60E-07	-1.3	0.0015	-1.6	7.50E-08	-1.5	1.80E-07	-1.5	9.10E-05	-1.5	8.00E-07
<i>PIRT</i>	vmPFC	Complete	2.1	4.90E-07	1.7	0.00037	2	2.50E-06	2.2	7.50E-07	2.4	2.30E-09	2.1	8.20E-07
<i>LPAR1</i>	vmPFC	Female	-1.5	5.70E-07	-1.5	0.0003	-1.5	1.70E-06	-1.5	7.60E-07	-1.3	0.00077	-1.5	4.30E-07
<i>KPNA1</i>	dIPFC	Complete	0.17	5.90E-07	0.15	1.70E-05	0.15	4.00E-05	0.17	4.60E-07	0.15	7.30E-05	0.17	8.80E-07
<i>CFH</i>	vmPFC	Male	-1.1	8.90E-07	-1.1	3.00E-05	-1.1	1.40E-06	-1.1	1.80E-06	-1	0.00017	-1.1	3.00E-06
<i>SLC2A14</i>	dIPFC	Male	-2.9	9.70E-07	-3	5.90E-06	-2.8	1.60E-05	-3.1	3.10E-07	-2.9	1.50E-05	-2.8	4.60E-06
<i>PCDH8</i>	vmPFC	Female	2.1	1.10E-06	2	0.00091	2.1	2.50E-06	1.9	2.40E-07	2.4	1.30E-05	2.1	1.70E-06
<i>FOS</i>	vmPFC	Female	2.1	1.80E-06	2.5	4.90E-05	2.1	5.80E-06	2.2	1.10E-06	1.8	0.0014	2.2	1.70E-06
<i>BCAS1</i>	vmPFC	Female	-1.4	2.10E-06	-1.4	0.0014	-1.4	2.10E-06	-1.4	3.50E-07	-1.3	0.00074	-1.5	2.70E-07
<i>ZDHHC11B</i>	vmPFC	Female	-1.8	2.20E-06	-1.9	0.00043	-1.8	9.80E-06	-1.8	5.20E-06	-1.2	0.005	-1.9	4.70E-06
<i>ERMN</i>	vmPFC	Female	-1.2	2.80E-06	-1.4	0.0002	-1.2	1.50E-05	-1.2	2.70E-06	-1.2	0.00099	-1.3	8.10E-07
<i>NR4A1</i>	vmPFC	Female	2.6	4.30E-06	<b>1.2</b>	<b>0.077</b>	2.6	1.10E-05	2.5	3.50E-06	2.9	8.70E-05	2.4	1.40E-05
<i>EDN1</i>	dIPFC	Complete	1.3	4.40E-06	1.2	2.80E-05	1.1	0.00012	1.4	1.20E-06	1.2	0.0002	1.2	4.70E-06
<i>KIF5A</i>	vmPFC	Female	-1.1	4.60E-06	-1.1	0.0015	-1.1	2.30E-05	-1.1	2.20E-06	-1.2	0.00047	-1.1	1.70E-05
<i>RBM3</i>	dIPFC	Female	1.9	5.00E-06	1.9	1.10E-05	1.6	0.0038	1.8	3.00E-07	1.9	7.60E-05	1.9	1.30E-05
<i>EMP1</i>	vmPFC	Male	1.6	5.00E-06	1.4	0.00029	1.5	1.60E-05	1.6	7.20E-06	0.99	0.0096	1.6	0.00071

**Supplementary Table 10:** Associations for the top (Table 3) genes and non-WNH ancestry. For each brain region, analyses performed within each of the three diagnosis groups (PTSD, depression, and controls) and then meta-analyzed across groups.

Gene	dlPFC			vmPFC		
	l2fc	p	p <sub>cor</sub>	l2fc	p	p <sub>cor</sub>
<i>GLP2R</i>	-0.12	0.55	0.95	-0.18	0.40	0.91
<i>MBP</i>	0.16	0.14	0.37	0.16	0.42	0.91
<i>OTOGL</i>	-0.03	0.68	0.95	0.11	0.29	0.91
<i>MOBP</i>	0.17	0.14	0.37	0.14	0.49	0.91
<i>MAFF</i>	0.01	0.94	0.99	0.05	0.83	0.91
<i>PAIP2B</i>	0.16	<b>0.023</b>	0.12	0.05	0.76	0.91
<i>PIRT</i>	0.00	0.99	0.99	0.02	0.92	0.92
<i>LPAR1</i>	0.23	<b>0.00082</b>	<b>0.011</b>	0.07	0.65	0.91
<i>KPNA1</i>	0.04	0.16	0.37	-0.02	0.70	0.91
<i>CFH</i>	0.04	0.71	0.95	-0.06	0.66	0.91
<i>SLC2A14</i>	-0.08	0.69	0.95	-0.39	0.079	0.91
<i>PCDH8</i>	-0.03	0.80	0.95	0.08	0.53	0.91
<i>FOS</i>	-0.08	0.75	0.95	0.18	0.51	0.91
<i>BCAS1</i>	0.29	<b>0.0010</b>	<b>0.011</b>	0.24	0.18	0.91
<i>ZDHHC11B</i>	-0.03	0.81	0.95	-0.03	0.85	0.91
<i>ERMN</i>	0.20	<b>0.015</b>	0.10	0.03	0.85	0.91
<i>NR4A1</i>	0.03	0.87	0.96	0.33	0.12	0.91
<i>EDN1</i>	0.16	0.14	0.37	-0.33	0.15	0.91
<i>KIF5A</i>	0.11	0.10	0.37	-0.01	0.87	0.91
<i>RBM3</i>	-0.05	0.64	0.95	-0.16	0.26	0.91
<i>EMP1</i>	0.10	0.49	0.95	-0.08	0.65	0.91



**Supplementary Table 11:** dlPFC depression associations (n=32 Depression cases vs. n=24 controls) for top PTSD genes. Results presented are for all of the genes in Table 2, in that order.

Gene	Overall		Male		Female	
	l2fc	p	l2fc	p	l2fc	p
GLP2R	0.38	0.21	0.17	0.63	1.3	0.17
MBP	0.17	0.25	0.2	0.25	-0.058	0.86
OTOGL	-0.46	1.20E-05	-0.31	0.0072	-0.62	0.0085
MOBP	0.11	0.56	0.26	0.22	-0.082	0.84
MAFF	0.47	0.073	0.34	0.14	0.67	0.36
PAIP2B	0.14	0.24	0.31	0.027	0.15	0.51
PIRT	0.56	0.057	0.6	0.043	0.88	0.14
LPAR1	0.044	0.71	0.017	0.91	-0.064	0.66
KPNA1	0.077	0.079	0.063	0.24	0.077	0.62
CFH	-0.23	0.14	-0.12	0.39	-1	0.0019
SLC2A14	0.5	0.46	-0.22	0.76	1.5	0.17
PCDH8	-0.015	0.93	-0.078	0.61	-0.4	0.54
FOS	0.63	0.07	0.34	0.33	-0.14	0.85
BCAS1	0.16	0.27	0.33	0.079	-0.011	0.96
ZDHHC11B	0.21	0.38	0.33	0.21	0.24	0.44
ERMN	-0.14	0.19	-0.031	0.79	-0.12	0.48
NR4A1	-0.042	0.88	-0.36	0.28	-0.96	0.15
EDN1	0.98	0.0024	0.85	0.031	1.8	0.01
KIF5A	0.21	0.027	0.2	0.057	0.21	0.25
RBM3	0.22	0.16	-0.029	0.88	0.72	0.0036
EMP1	0.53	0.15	0.6	0.14	0.76	0.34

**Supplementary Table 12:** vmPFC depression associations (n=32 Depression cases vs. n=20 controls) for top PTSD genes. Results presented are for all of the genes in Table 2, in that order.

Gene	Overall		Male		Female	
	l2fc	p	l2fc	p	l2fc	p
GLP2R	0.0064	0.98	0.23	0.54	1.9	0.0022
MBP	0.32	0.036	0.41	0.01	0.091	0.75
OTOGL	-0.067	0.67	-0.24	0.1	0.22	0.51
MOBP	0.095	0.64	0.34	0.066	0.031	0.93
MAFF	0.85	0.021	0.74	0.07	1	0.24
PAIP2B	0.17	0.26	0.19	0.25	-0.083	0.72
PIRT	1.5	9.60E-06	1.4	3.50E-05	1.4	0.069
LPAR1	0.16	0.28	0.19	0.26	-0.25	0.35
KPNA1	0.0047	0.94	-0.053	0.38	-0.17	0.5
CFH	-0.27	0.13	-0.45	0.021	-1.3	0.0014
SLC2A14	-0.034	0.96	-0.26	0.79	-2.2	0.095
PCDH8	0.35	0.021	0.39	0.018	0.6	0.063
FOS	0.52	0.16	0.51	0.12	0.82	0.26
BCAS1	0.23	0.12	0.36	0.031	0.045	0.87
ZDHHC11B	0.14	0.55	0.0044	0.99	0.35	0.35
ERMN	-0.23	0.12	-0.22	0.21	-0.11	0.68
NR4A1	-0.048	0.89	-0.21	0.52	-0.34	0.7
EDN1	0.63	0.13	0.43	0.41	2.1	0.012
KIF5A	0.035	0.78	-0.0071	0.95	0.16	0.49
RBM3	0.44	0.062	0.43	0.13	0.62	0.3
EMP1	1.3	0.0033	1.3	0.0085	0.65	0.49

**Supplementary Table 13:** Top 5 PTSD candidate gene associations in the dlPFC analysis and sex-stratified analyses.

Sample	Gene	Overall			Male			Female		
		l2fc	p	p <sub>cor</sub>	l2fc	p	p <sub>cor</sub>	l2fc	p	p <sub>cor</sub>
Overall	IL1B	<b>1.4</b>	<b>0.0003</b>	<b>0.033</b>	0.9	0.074	0.86	1.5	0.26	0.83
	VCL	<b>0.19</b>	<b>0.0018</b>	<b>0.098</b>	0.13	0.11	0.86	0.4	0.22	0.83
	NLGN1	<b>0.11</b>	<b>0.0064</b>	<b>0.19</b>	0.022	0.72	0.94	0.28	0.27	0.83
	SNCA	<b>0.2</b>	<b>0.007</b>	<b>0.19</b>	0.085	0.4	0.94	0.32	0.34	0.83
	TPH2	<b>0.39</b>	<b>0.0098</b>	<b>0.2</b>	0.24	0.25	0.94	0.6	0.49	0.83
Male	ADCYAP1R1	0.054	0.36	0.85	<b>0.2</b>	<b>0.0059</b>	<b>0.62</b>	-0.19	0.46	0.83
	VAMP2	0.073	0.26	0.79	<b>0.17</b>	<b>0.022</b>	<b>0.86</b>	0.016	0.95	0.98
	HTR3A	-0.55	0.097	0.57	<b>-1</b>	<b>0.054</b>	<b>0.86</b>	-0.5	0.74	0.95
	OPRL1	-0.11	0.44	0.85	<b>-0.32</b>	<b>0.054</b>	<b>0.86</b>	0.42	0.39	0.83
	CRH	-0.43	0.041	0.48	-0.41	0.062	0.86	-1.1	0.35	0.83
Female	NOTCH1	-0.023	0.81	0.95	0.05	0.61	0.94	<b>-0.88</b>	<b>0.0086</b>	<b>0.83</b>
	SPRY2	-0.1	0.48	0.85	-0.12	0.33	0.94	<b>-1.2</b>	<b>0.018</b>	<b>0.83</b>
	DNMT1	-0.054	0.26	0.79	-0.022	0.77	0.94	<b>-0.54</b>	<b>0.032</b>	<b>0.83</b>
	GLO1	0.11	0.049	0.49	0.021	0.75	0.94	0.55	0.091	0.83
	GRIN2A	-0.01	0.81	0.95	-0.069	0.23	0.94	0.37	0.099	0.83

**Supplementary Table 14:** Top 5 PTSD candidate gene associations in the vmPFC analysis and sex-stratified analyses.

Sample	Gene	Overall			Male			Female		
		l2fc	p	p <sub>cor</sub>	l2fc	p	p <sub>cor</sub>	l2fc	p	p <sub>cor</sub>
Overall	GJA1	<b>-0.31</b>	<b>1.80E-05</b>	<b>0.0019</b>	-0.36	0.0068	0.36	-0.57	0.026	0.51
	VCL	<b>0.21</b>	<b>0.0057</b>	<b>0.31</b>	0.29	0.05	0.65	0.61	0.037	0.54
	FKBP5	<b>0.92</b>	<b>0.02</b>	<b>0.71</b>	0.84	0.14	0.75	-0.27	0.84	0.92
	PRTFDC1	<b>-0.19</b>	<b>0.033</b>	<b>0.72</b>	-0.32	0.095	0.74	-0.31	0.38	0.84
	FOS	<b>0.73</b>	<b>0.034</b>	<b>0.72</b>	1.2	0.0069	0.36	2.1	1.80E-06	0.00019
Male	GJA1	-0.31	1.80E-05	0.0019	<b>-0.36</b>	<b>0.0068</b>	<b>0.36</b>	-0.57	0.026	0.51
	FOS	0.73	0.034	0.72	<b>1.2</b>	<b>0.0069</b>	<b>0.36</b>	2.1	1.80E-06	0.00019
	DBH	0.33	0.069	0.72	<b>1</b>	<b>0.017</b>	<b>0.59</b>	-0.04	0.95	0.96
	COMT	0.095	0.21	0.77	<b>0.29</b>	<b>0.037</b>	<b>0.65</b>	0.1	0.73	0.89
	ALOX12	-0.32	0.12	0.73	<b>-0.91</b>	<b>0.043</b>	<b>0.65</b>	-0.4	0.63	0.84
Female	FOS	0.73	0.034	0.72	1.2	0.0069	0.36	<b>2.1</b>	<b>1.80E-06</b>	<b>0.00019</b>
	NPY1R	-0.25	0.072	0.72	-0.11	0.65	0.92	<b>-1.2</b>	<b>0.00032</b>	<b>0.017</b>
	HTR3A	0.23	0.55	0.96	0.18	0.79	0.98	<b>3.4</b>	<b>0.017</b>	<b>0.51</b>
	GJA1	-0.31	1.80E-05	0.0019	-0.36	0.0068	0.36	<b>-0.57</b>	<b>0.026</b>	<b>0.51</b>
	PER1	0.3	0.2	0.76	0.51	0.16	0.81	<b>0.85</b>	<b>0.028</b>	<b>0.51</b>

**Supplementary Table 15:** Gene Ontology (GO) overrepresentation analysis of the top 200 genes in each group/region. The top 5 GO terms for each analysis are listed along with the PTSD associated genes in each GO term. Genes from Table 2 (significantly associated with PTSD after a multiple testing correction) are in bold.

Analysis	Ontology/GO Term	Term	Count	p <sub>cor</sub>	Significant Genes
PTSD dIPFC Complete (0 sig. out of 7968 terms)	<b>GO:0051051</b>	negative regulation of transport	18	0.054	<b>EDN1</b> PKIA DERL2 YRDC IL1B CABP1 ADA BAG4 PID1 FERMT1 TNFRSF1A SYT11 GNAI2 TRIM27 CAMK2D RAC1 MMP9 KCNE3
	GO:0090317	negative regulation of intracellular protein transport	5	0.28	PKIA DERL2 CABP1 BAG4 FERMT1
	GO:0006665	sphingolipid metabolic process	8	0.28	SAMD8 CREM SGPP1 TNFRSF1A SERINC1 CLN6 SPTSSA PSAP
PTSD dIPFC Female (167 sig. out of 7872 terms)	<b>GO:0072359</b>	<b>circulatory system development</b>	33	0.00013	<b>EDN1</b> NPY2R HEXIM1 ADRA1A GLUL CDH5 EMP2 EPN2 DDIT3 PTPRB LRP5 COL1A2 NOTCH1 FZD8 MSX1 GPNMB FN1 WNT7A FMNL3 RGCC ADM EPHB3 PPARA ID3 MEF2C ID1 RXRA SPRY2 ELN TRIP11 PTCH1 FZD4 ACVR1
	<b>GO:0009888</b>	<b>tissue development</b>	45	0.00013	<b>EDN1</b> MYORG ZBTB40 GSTM3 PODXL ADRA1A CDH5 FERMT1 ETV5 P2RX7 CELSR1 APCDD1 LRP5 COL1A2 NOTCH1 SOX21 MSX1 TMEM119 LRP4 GPNMB FN1 WNT7A LGR6 RGCC NUP210L ADM SCRIB NKX2-2 MET KRT83 RDH10 FAM83H PPARA TUFT1 ICAM1 ID3 MEF2C ID1 RXRA SPRY2 ELN TRIP11 PTCH1 FZD4 ACVR1
	<b>GO:0032501</b>	<b>multicellular organismal process</b>	110	0.00013	<b>EDN1</b> ANLN CROCC MYORG POLR3H MDGA1 SOX13 CACNG4 PAQR8 ZBTB40 SALL3 NPY2R CD177 GSTM3 OLIG1 HEXIM1 PODXL SOX12 ADRA1A GLUL SLC26A2 CDH5 EMP2 CIART EPN2 NPAS4 FERMT1 DDIT3 EID2B PTPRB ETV5 P2RX7 IRF1 SPNS2 KCNMB1 CELSR1 SLC5A3 SDK2 APCDD1 SLC11A1 LRP5 COL1A2 LRFN5 KCNIP3 NOTCH1 KCNN4 LSR EZH1 SOX21 LZTS1 FZD8 TSHR MSX1 TMEM119 LRP4 GPNMB FN1 GLDN WNT7A FMNL3 HMGB2 NEGR1 HMGB3 GNL3 RGCC NUP210L ALB ADM HILPDA NAMPT KCTD15 BCAN SCRIB LMOD1 EPHB3 NKX2-2 LYPD1 RYR3 MET KRT83 ISLR2 IQCB1 RDH10 LIMS2 FAM83H PPARA TUFT1 ICAM1 ID3 CNTFR EPS8 ZFH2 MYBPC2 MEF2C ID1 RXRA SPRY2 ANKS1A DDX11 ELN SHISA6 TRIP11 PTCH1 FZD4 BIRC3 SLC2A5 ACVR1 AKAP12 COL5A3 NR4A2
PTSD dIPFC Male (0 sig. out of 7863 terms)	GO:0000188	inactivation of MAPK activity	4	0.64	DUSP7 DUSP10 RGS4 DUSP16
	GO:0032879	regulation of localization	47	0.64	PKIA CHGA PID1 SCIN SIAH3 SELE ATP2B4 CCL8 KCNH4 TACR2 JUN SYTL2 PAX8 SYT10 KCNJ11 KCNJ16 FKBP1B PEA15 ADCYAP1R1 LPAR3 CLU EDNRB HYAL2 EHD2 MDFIC FOXC2 DUSP10 RGS4 CDT1 NSFL1C MCOLN1 TCAF1 INHA RAB27A HK2 UQCC2 EPHA3 KCNJ4 MCC INSM1 IRS2 YRDC EMILIN1 FTO AKAP12 FBXW7 SSH1
	GO:0051049	regulation of transport	35	0.64	PKIA CHGA PID1 SCIN SIAH3 SELE ATP2B4 KCNH4 TACR2 SYTL2 PAX8 SYT10 KCNJ11 KCNJ16 FKBP1B PEA15 ADCYAP1R1 LPAR3 CLU EDNRB HYAL2 EHD2 MDFIC RGS4 TCAF1 INHA RAB27A HK2 UQCC2 EPHA3 KCNJ4 IRS2 YRDC AKAP12 FBXW7

PTSD vmPFC Complete (57 sig. out of 7961 terms)	<b>GO:0080134</b>	<b>regulation of response to stress</b>	39	0.0026	GJA1 HYAL2 TNFRSF12A CDKN1A SOCS3 CDH5 ADCY8 BAG3 TICAM1 BMP7 CRYAB <b>CFH</b> SEMA4C MAP3K6 ICAM2 THBD SLC7A2 NPY5R LTBR PPARG IFIT1 TNFRSF1A SERPINE1 SESN2 GADD45B GADD45G HSPB8 NOS3 ZBTB7B MCL1 DDIT3 UBAC2 PLA2R1 HSPA1B IRAK2 PKN1 MYH9 HSPA1A NT5E
	<b>GO:0071310</b>	<b>cellular response to organic substance</b>	54	0.0032	GJA1 HYAL2 SHC1 TNFRSF12A IL21R CDKN1A SOCS3 CDH5 ADCY8 CACNA1S BAG3 TICAM1 BMP7 CAPN2 IL27RA PAQR8 COL16A1 IL18R1 LTBR CITED1 PPARG EPOR BHLHA15 IFIT1 HAP1 TNFRSF1A SERPINE1 SESN2 GPAM GLDC HSPB8 NFIL3 SLC25A33 TESC NOS3 LIF ZBTB7B MCL1 DDIT3 MT2A DLL1 CXCL10 ENPP1 B2M HSPA1B IRAK2 MYOCD TGIF1 FOSB GJB6 RXRB MT1X HSPA1A TNFRSF19
	<b>GO:0006950</b>	<b>response to stress</b>	68	0.0043	<b>PIRT</b> GJA1 HYAL2 SHC1 TNFRSF12A CDKN1A SOCS3 CDH5 TNFRSF10B ADCY8 BAG3 TICAM1 SOD3 BMP7 CAPN2 IL27RA CRYAB <b>CFH</b> SEMA4C MAP3K6 ICAM2 TPST1 THBD SLC7A2 <b>MAFF</b> NPY5R IL18R1 LTBR CITED1 PADI4 PPARG BHLHA15 IFIT1 TNFRSF1A SERPINE1 SESN2 APOLD1 SELENOP EPHA2 GADD45B GADD45G ADM HSPB8 DDR1 SFN NOS3 ZBTB7B SLC12A6 MCL1 RBM24 DDIT3 MT2A GNA14 CXCL10 B2M VCL UBAC2 PLA2R1 HSPA1B IRAK2 IGHM MYOCD PKN1 MYH9 HSPA1A MAFK NT5E TNFRSF19
PTSD vmPFC Female (134 sig. out of 7883 terms)	<b>GO:0042611</b>	<b>MHC protein complex</b>	9	4.90E-08	B2M HLA-B HLA-C HLA-DQA1 HLA-A HLA-DRB1 HLA-DRB5 HLA-E HLA-DOA
	<b>GO:0071944</b>	<b>cell periphery</b>	95	2.23E-05	<b>GLP2R MBP LPAR1 PCDH8 ERMN</b> FGF1 LAMP5 SYT2 B2M SLC24A2 PLXNA3 NECAB2 HLA-B LYVE1 HS3ST3B1 TGFB1 KCNK13 NPY1R ICAM5 RASAL1 SCN1A PLCH2 HLA-C CPNE6 CAVIN2 SCIN CXCL10 GRIK4 LRRCS5 CHRNA6 HLA-DQA1 SNAP25 FLNC MRC1 DIRAS2 DGKA FMN1 GPR26 KCNA2 SLC01A2 BTN3A2 PTPRF DCHS2 SLC32A1 HLA-A PCLO IPCEF1 PDGFB NECTIN3 GALR1 PDYN PCDH11X VAMP1 LMBR1L FSHR HLA-DRB1 FOLR2 HLA-DRB5 TPO EPHA6 MFG8 GNB1L KCNG1 MCHR1 GAD1 ADCY8 TESC PPL DNAL4 TAC1 HLA-E CXCR4 FZD1 UNC5C WNT7B PTGER3 HLA-DOA NRP2 C4A EPCAM GPR83 RELN BTN3A3 AMIGO2 GRASP MMP16 BTN3A1 TUB ADRA2A
	<b>GO:0042605</b>	<b>peptide antigen binding</b>	7	2.23E-05	HLA-B HLA-C HLA-DQA1 HLA-A HLA-DRB1 HLA-DRB5 HLA-E
PTSD vmPFC Male (5 sig. out of 7810 terms)	<b>GO:0006950</b>	<b>response to stress</b>	67	0.019	<b>MAFF CFH</b> BAG3 CDKN1A NAPRT MAP3K6 TNFRSF10B SYTL4 THBD LGALS1 CREBBP APOLD1 SOCS3 STAB1 CHI3L1 SHC1 KLF4 EXOSC4 TPST1 ADCY8 GNA14 STC2 MASP1 GADD45A THOC1 HYAL2 CD14 SOD3 CHST2 CCL2 CDH5 EPHA2 ACTG1 CERS2 LILRB3 VASN OSMR GADD45B SHMT2 IFI44L APOBEC3C EPAS1 GADD45G STC1 CLIC1 GPR4 PKD2 GPRC5B FUT10 GJA1 <b>FOS</b> MPEG1 SERPINH1 MAP3K1 SELENOP MARS TNFRSF12A SERINC5 SLC52A3 BLNK HILPDA EXOSC5 ICOSLG MARCO DRD1 MAPK11 GLP1R
	<b>GO:0044421</b>	<b>extracellular region part</b>	57	0.019	<b>CFH</b> ITIH5 NAPRT THBD LIPG COL4A1 MTHFD2 LGALS1 CHI3L1 COL4A2 SNCG GLRX GNA14 OGN COL5A2 STC2 MASP1 ADAMTS9 TUBA4A FRZB THOC1 TUBB6 SNORC AKR1C1 CD14 SOD3 CYP2J2 ACTG1 SLC2A5 BMP5 VASN SCR2N2 SHMT2 SCIN LCP1 ITIH2 IGF2 ABI3BP TNFSF10 STC1 CLIC1 PKD2 GPRC5B EPS8L2 HMCN2 ECM2 RPS2 SERPINH1 SELENOP MARS POP1 PHPT1 TKT SERINC5 SDCBP2 HILPDA ICOSLG
	<b>GO:0001890</b>	<b>placenta development</b>	10	0.019	SOCS3 JUNB STC2 BMP5 IGF2 EPAS1 STC1 PKD2 GJA1 HES1

**Supplementary Table 16:** GSEA-based overrepresentation analysis of different cell type markers in the top 500 PTSD associated genes, including upregulated and downregulated genes. Corrected significant associations.

<b>Analysis</b>	<b>Cell Type</b>	<b>p</b>	<b>p<sub>cor</sub></b>
dIPFC	EX3E	0.0000	0.00
vmPFC	ENDO	0.0000	0.00
vmPFC	PER	0.0000	0.00
vmPFC-down	ENDO	0.0000	0.00
vmPFC-down	PER	0.0000	0.00
dIPFC	EX9	0.0000	0.00
dIPFC	ENDO	0.0040	0.01
dIPFC-up	EX3E	0.0000	0.01
vmPFC -Male-down	OPC	0.0010	0.02
vmPFC -Male-down	OLIGO	0.0000	0.02
vmPFC-Male	OLIGO	0.0010	0.03
dIPFC-up	ENDO	0.017	0.03
dIPFC-up	EX9	0.001	0.03
vmPFC-Male	ENDO	0.016	0.03
vmPFC-Male	OPC	0.0070	0.03
dIPFC -Male-up	OPC	0.031	0.74

**Supplementary Table 17:** Goseq-based overrepresentation analysis of different cell type markers in PTSD-associated genes. All  $p > 0.05$  significant associations.

Analysis	Cell type	num DE In Cat	num In Cat	p	p <sub>cor</sub>	Significant Genes
vmPFC-down	Per	4	39	4.16E-05	0.0010	ITIH5 SLC6A12 NR2F2-AS1 B2M
vmPFC-Female-down	Ex4	20	179	0.00032	0.0081	RORB POU6F2 TOX KCNH5 IPCEF1 SNAP25 ATP2B2 TSHZ3 HS3ST4 PCLO SCN1B GCC2 CCNI FMN1 RIMS3 ZNF385B ELAVL4 SCN1A PCDH11X PRDM2
dIPFC-F	OPC	5	137	0.0086	0.22	BCAN EPN2 FERMT1 HIP1 OLIG1
vmPFC	Endo	3	81	0.0104	0.26	CAVIN2 ITIH5 SLC9A3R2
vmPFC-Male	Per	4	62	0.012	0.30	ITIH5 EPAS1 ADAMTS9-AS2 TJP1
dIPFC	In4a	7	205	0.012	0.31	MACROD2 PRNP SERINC1 PID1 USP11 COG5 ACTG1
dIPFC-Female-down	Endo	4	45	0.015	0.38	HIGD1B ID1 ID3 PTPRB
vmPFC-Female	Ex4	14	279	0.015	0.29	RORB POU6F2 TOX IPCEF1 SNAP25 TSHZ3 HS3ST4 PCLO GCC2 CCNI FMN1 ZNF385B SCN1A PCDH11X
vmPFC-Female-up	In1a	10	143	0.018	0.45	GALNTL6 RELN NECAB2 GAD1 SCG2 COL16A1 EPHA6 CDH13 TUBA1A PLPPR4
vmPFC-Female	Endo	6	81	0.023	0.29	B2M CAVIN2 HLA-B HLA-E RPL3P4 RPS28P7
vmPFC-down	Endo	2	40	0.027	0.34	B2M ITIH5
dIPFC	In1a	7	247	0.030	0.37	PID1 CAMK2D PRNP SERINC1 ACTG1 SYT11 USP11
dIPFC-Female-down	OPC	6	94	0.033	0.42	BCAN EPN2 FERMT1 HIP1 OLIG1 ZNF462
vmPFC-Male	Oligo	6	175	0.035	0.43	ARHGAP21 FMNL2 FRYL GPRC5B TCF12 TJP1
dIPFC-Female-up	Ex4	12	188	0.035	0.53	KCNH5 MEF2C NELL2 LRFN5 KCNQ5 NEGR1 ENO2 NELL1 DDX24 ATP6V1B2 TRIM37 INPP5F
dIPFC-Female-up	Ex2	9	132	0.042	0.53	KCNH7 KCNQ5 NEGR1 CDH8 NELL2 KCNH5 MEF2C LRFN5 PAK1
vmPFC-Male-up	Per	2	20	0.044	1.00	EPAS1 ADAMTS9-AS2
vmPFC-Female-down	Endo	5	39	0.044	0.55	B2M HLA-B HLA-E RPL3P4 RPS28P7
dIPFC-F	Endo	3	81	0.047	0.59	MYRIP PODXL PTPRB
vmPFC-Male-down	Oligo	7	136	0.048	0.83	ARHGAP21 FMNL2 FRYL GPRC5B MAP4K5 TCF12 TJP1
dIPFC-Male-down	Ex3e	7	126	0.048	0.93	RGS4 CRYM CHGA FBXW7 CABP1 NGEF UNC13A



**Supplementary Table 18:** Association Results for Networks which are  $p < 0.05$  significantly associated with PTSD and follow-up analyses in relevant subgroups and depression.

Response	Network (n Genes)	Overall		Male		Female	
		coefficient	p	coefficient	p	coef.	p
PTSD	dIPFC-brown4 (354)	<b>0.02</b>	<b>0.046</b>	0.012	0.26	-0.006	0.82
	dIPFC-orange (450)	<b>0.034</b>	<b>0.04</b>	0.022	0.15	<b>0.1</b>	<b>0.025</b>
	dIPFC-Female-lightgreen (539)	--	--	--	--	<b>-0.11</b>	<b>0.019</b>
	vmPFC-sienna3 (101)	<b>-0.017</b>	<b>0.024</b>	-0.0091	0.31	-0.03	0.073
	vmPFC-mediumpurple3 (34)	<b>-0.06</b>	<b>0.036</b>	-0.064	0.11	-0.05	0.33
	vmPFC-Male-orange (102)	--	--	<b>-0.099</b>	<b>0.037</b>	--	--
	Depression	dIPFC-brown4 (354)	0.024	0.11	0.018	0.26	-0.043
dIPFC-orange (450)		<b>0.04</b>	<b>0.0043</b>	0.043	0.012	0.032	0.35
dIPFC-Female-lightgreen (539)		--	--	--	--	0.015	0.84
vmPFC-sienna3 (101)		-0.014	0.12	-0.015	0.094	-0.046	0.087
vmPFC-mediumpurple3 (34)		<b>-0.087</b>	<b>0.0015</b>	<b>-0.071</b>	<b>0.023</b>	-0.078	0.29
vmPFC-Male-orange (102)		--	--	-0.086	0.026	--	--

**Supplementary Table 19** Gene ontology (GO) overrepresentation analysis of genes in the PTSD-associated WGCNA networks. Genes from Table 2 (significantly associated with PTSD after a multiple testing correction) are in bold.

Network	Term	Fold Enrichment	P <sub>cor</sub>	
dlPFC-orange	GO:0006954 inflammatory response	5.93	6.38E-18	FPR1 SLC11A1 RELA SELE MAPKAPK2 CCL2 S100A9 TNFRSF10A CEBPB MYD88 C5AR1 NOD1 TNFRSF10D ZC3H12A TNFRSF10B C4B NFKBIZ C4A IL1B LTBR ADGRE2 F11R S100A8 ANXA1 EPHA2 CASP4 S1PR3 TNFRSF1B TNIP2 TNFRSF11B TNFRSF1A SELP GGT5 NMI TNFAIP3 SP100 NFKB2 IFI16 TLR2 <b>FOS</b> SMAD1 THBS1 ACKR1 LYZ
	GO:0005615 extracellular space	3.05	4.13E-15	ALOX5 CLIC1 MTHFD2 B4GALT1 CCL2 HAPLN3 ANGPT2 ICAM1 IGF2R C1QTNF1 NAMPT PLAT CMTM3 F3 IRAK4 SERPINA1 C1RL APOL1 MMRN2 TFPI ANXA2 ANXA1 PECAM1 APOL4 FLT1 TINAGL1 ADAMTS9 TNFRSF11B <b>EDN1</b> TNFRSF1A SRGN SELP IGFBP7 SEMA3F NRP1 ANGPTL4 LAMC1 SERPINB8 TIMP1 ENG SERPINH1 LGALS3 ADM CD59 SELE FSTL3 IL15RA S100A9 S100A11 SERPINB1 C4B C4A IL1B PODXL CFB LOX STOM IL6R S100A8 TWSG1 SERPINE1 VASN MSN HMOX1 FSTL1 HILPDA HBEGF IL4R SERPING1 CP THBS1 THBD LYZ
	GO:0005886 plasma membrane	1.82	6.04E-14	CDH5 CDH3 VAMP5 CLIC1 STAT3 LSP1 SLC11A1 OXTR SYTL3 SLC39A14 STEAP4 ANGPT2 MYD88 FZD4 ITGA5 <b>EMP1</b> SWAP70 FLVCR2 DSC2 F3 ADGRE2 RAB8A EMP2 EMP3 ADGRL4 PECAM1 ITPR3 FLT1 P2RY6 VASP S1PR3 PIK3IP1 SELP PLSCR1 ITGB1 CR1 PYGL LPP RIT1 NFKBIA MR1 SELE VCL PLP2 SIGLEC9 CD93 FGR S100A9 LDLR C5AR1 C4B C4A PODXL ANO6 HLA-E PXN JPH2 RGS16 CFB ARAP3 IFITM3 ACVRL1 GBP1 S100A8 TCIRG1 STXBP2 APLNR ADAM15 MYO1G SERPINE1 APOLD1 OSMR TGM2 SLC04A1 MYH9 GPR4 ITPRIP TES HBEGF NECTIN2 SLC26A2 THBD RELL1 EPHB4 SHC1 ICAM2 B4GALT1 IFITM2 SCARF1 CLDN5 ICAM1 SLC2A1 RHOC RHOB ZC3H12A IRAK4 PLAUR CLEC2B F11R CD151 TFP1 NOS3 ANXA2 DLL4 ANXA1 PLIN2 ANXA3 SLC39A1 TNFRSF1B RASSF1 TNFRSF11B EFNA1 TNFRSF1A CD99 PERP <b>PIRT</b> NRP1 GABRE LGALS3 RAB13 BAG3 FPR1 IFITM1 ECE1 CD59 IL15RA CD44 HYAL2 SLC16A3 TNFRSF10A PDPN TNFRSF10D TNFRSF10B LIMS1 MLKL EHD4 IL1R1 SLC50A1 LTBR NRP1 IL6R ITGA1 RAP1B EPHA2 PRX MYOF VASN MSN RGS1 PIM1 HMOX1 GGT5 IL17RA CD163 SLC52A3 TLR2 ACKR3 ATP11C IL18R1 ACKR1
	GO:0001525 angiogenesis	5.17	7.22E-10	JUN EPHB4 ROBO4 SHC1 EPAS1 CCL2 ANGPT2 PRKX TYMP RHOB ZC3H12A ITGA5 MMRN2 NOS3 ANXA2 ACVRL1 DLL4 COL4A2 PECAM1 FLT1 ADAM15 SERPINE1 EFNA1 HMOX1 APOLD1 ANGPTL4 NRP1 SAT1 MYH9 ACKR3
	GO:0006955 immune response	5.12	6.39E-10	SLC11A1 IFITM2 CCL2 TNFRSF10A CEBPB C5AR1 TNFRSF10D TNFRSF10B PNP NFIL3 IL1B IL1R1 HLA-E LTBR SMAD6 IFITM3 GBP2 TINAGL1 TNFRSF1B TNFRSF11B TNFRSF1A RGS1 GEM C1R IL4R TLR2 C7 THBS1 MR1 IL18R1
	...	...	...	...
	GO:0045087 innate immune response	3.93	5.86E-07	FGR S100A9 MYD88 NOD1 C4B C4A IRAK4 HLA-E C1RL APOL1 S100A8 ANXA1 TRIM21 ADAM15 CASP4 TRIM5 JAK3 C1S CR1 C1R IFI16 NFKB2 NLRC5 SERPING1 TLR2 LGALS3 IRF7 ELF4 MR1
	dlPFC-brown4	GO:0006614 SRP-dependent cotranslational protein targeting to membrane	43.50	2.53E-110

	GO:0000184 nuclear-transcribed mRNA catabolic process nonsense-mediated decay	35.28	6.44E-102	RPL35 RPL23 RPL3 RPL31 RPL4 RPL5 RPL32 RPS10 RPL34 RPS11 RPS12 RPS13 RPL35A RPS14 RPL37A RPS15 RPL37 RPL38 RPS15A FAU RPSA RPS16 RPL27 RPS17 RPL26 RPL24 RPL29 RPL28 RPL27A UBA52 RPL30 RPL36 RPS20 RPS19 RPS18 RPS4X RPS5 RPS6 RPLP2 RPL23A RPL18 RPL18A RPL19 RPL21 RPS3A RPL10A RPS3 RPS2 EIF4A3 RPL12 RPL36A RBM8A RPL13 RPL10 RPL41 RPL11 RPL39 RPL8 RPL13A RPL9 RPL7A RPS26 RPS27 RPS25 RPS29 RPLP1 RPS27A RPLP0 RPS28 RPS24 RPS9 RPS23 RPS8 RPS21 RPS7 RPL7 RPL6
	GO:0019083 viral transcription	36.51	5.52E-101	RPL35 RPL23 RPL3 RPL31 RPL4 RPL5 RPL32 RPS10 RPL34 RPS11 RPS12 RPS13 RPL35A RPS14 RPL37A RPS15 RPL37 RPL38 RPS15A FAU RPSA RPS16 RPL27 RPS17 RPL26 RPL24 RPL29 RPL28 RPL27A UBA52 RPL30 RPL36 RPS20 RPS19 RPS18 RPS4X RPS5 RPS6 RPLP2 RPL23A RPL18 RPL18A RPL19 RPL21 RPS3A RPL10A RPS3 RPS2 RPL12 RPL36A RPL13 RPL10 RPL41 RPL11 RPL39 RPL8 RPL13A RPL9 RPL7A RPS26 RPS27 RPS25 RPS29 RPLP1 RPS27A RPLP0 RPS28 RPS24 RPS9 RPS23 RPS8 RPS21 RPS7 RPL7 RPL6
	GO:0006413 translational initiation	31.04	2.99E-97	RPL35 RPL23 RPL3 RPL31 RPL4 RPL5 RPL32 RPS10 RPL34 RPS11 RPS12 RPS13 RPL35A RPS14 RPL37A RPS15 RPL37 RPL38 RPS15A FAU RPSA RPS16 RPL27 RPS17 RPL26 RPL24 RPL29 RPL28 RPL27A UBA52 RPL30 RPL36 RPS20 RPS19 RPS18 RPS4X RPS5 RPS6 RPLP2 RPL23A RPL18 RPL18A RPL19 RPL21 RPS3A RPL10A RPS3 RPS2 RPL12 RPL36A RPL13 RPL10 RPL41 RPL11 RPL39 RPL8 RPL13A RPL9 RPL7A RPS26 RPS27 RPS25 RPS29 EIF3H RPLP1 EIF3G RPS27A RPLP0 RPS28 EIF3D RPS24 RPS9 RPS23 RPS8 RPS21 RPS7 RPL7 RPL6
	GO:0006364 rRNA processing	20.13	1.44E-79	RPL35 RPL23 RPL3 FBL RPL31 RPL4 DDX49 RPL5 RPL32 RPS10 RPL34 RPS11 RPS12 RPS13 RPL35A RPS14 RPL37A RPS15 RPL37 EXOSC4 RPL38 RPS15A FAU RPSA RPS16 RPL27 RPS17 RPL26 RPL24 RPL29 RPL28 RPL27A UBA52 RPL30 RPL36 RPS20 RPS19 RPS18 RPS4X RPS5 RPS6 RPLP2 RPL23A RPL18 RPL18A RPL19 RPL21 RPS3A RPL10A RPS3 RPS2 EIF4A3 RPL12 RPL36A RPL13 RPL10 RPL41 RPL11 RPL39 RPL8 RPL13A RPL9 RPL7A RPS26 RPS27 RPS25 RPS29 RPLP1 RPS27A RPLP0 RPS28 RPS24 RPS9 RPS23 RPS8 RPS21 RPS7 RPL7 RPL6
vmPFC-mediumpurple3	GO:0005525 GTP binding	9.46	0.0060	GIMAP6 GBP4 GIMAP4 RERGL GIMAP1 GIMAP7 GIMAP8
	GO:0002576 platelet degranulation	18.90	0.88	A2M F13A1 CLEC3B
	GO:0016010 dystrophin-associated glycoprotein complex	62.00	0.87	UTRN PGM5
	GO:0045216 cell-cell junction organization	74.03	0.93	OCLN MARVELD2
	GO:0009897 external side of plasma membrane	8.45	0.78	CXCL12 CLEC14A TGFB2
vmPFC-sienna3	GO:0045087 innate immune response	9.47	2.74E-13	TLR6 BTK CSF1R TLR10 NCF2 CLEC7A CD84 LY86 C2 TNFAIP8L2 CD14 TYROBP SYK C1QB C1QA TREM2 C1QC FCER1G HAVCR2 TLR1 CD180 TLR7 CYBA CYBB
	GO:0006954 inflammatory response	9.85	1.64E-12	TLR6 CSF1R TLR10 FPR1 PTGS1 CCR1 CLEC7A PTAFR LY86 CD14 C3AR1 C3 SYK ITGB2 AIF1 HAVCR2 TLR1 CD180 TLR7 CYBA CYBB HCK
	GO:0006955 immune response	8.06	9.89E-10	TLR6 HLA-DPA1 CD4 HLA-DOA TLR10 CD86 CCR1 LST1 CD74 IRF8 PTAFR C3 FCGR1A C1QC CTSS HLA-DMB TLR1 FCGR3A FYB1 HLA-DRA
	GO:0005886 plasma membrane	2.28	6.60E-08	HLA-DOA SIGLEC10 CD86 SLC2A5 CLEC7A ITGAM LY86 FCGR1A FCER1G TLR6 CD84 CD74 CD14 LILRB4 TYROBP SLC1A5 ITGB2 FCGR2A TMEM119 FCGR3A PTPRC CD4 CSF1R TLR10 FPR1

				LAIR1 CD53 CCR1 CSF2RA SYK RGS10 TGFBR1 HLA-DPA1 BTK PIK3AP1 MSR1 PTAFR LAT2 CD300A LCP1 HMOX1 C3AR1 C3 PLCG2 TREM2 TLR1 TLR7 CYBA ADORA3 CYBB FYB1 HLA-DRA
	GO:0042102 positive regulation of T cell proliferation	22.62	1.14E-05	HLA-DPA1 NCKAP1L CD4 AIF1 HLA-DMB HAVCR2 SASH3 PTPRC
dIPFC-Female-lightgreen	GO:0051015 actin filament binding	3.68	0.12	MYH3 USH1C MYO18A SHROOM1 SYNE3 HIP1R TLN1 TRIOBP ANTXR1 MYH14 ABL1 LIMA1 ITPRID2
	GO:0030514 negative regulation of BMP signaling pathway	6.50	0.73	LEMD2 HIPK2 NOTCH1 FSTL3 ABL1 TWSG1 SFRP2
	GO:0016459 myosin complex	6.12	0.27	MYL3 MYO9B MYH3 MYH7B MYO18A MYH14 CGN
	GO:0003774 motor activity	4.73	0.34	MYL3 MYO9B MYH3 MYH7B MYO18A MYH14 KIF1C CGN
	GO:0005737 cytoplasm	1.22	0.24	CLK1 TRIP6 EML3 AKAP17A FOXO4 SCRIB HES1 CHD4 STAT2 RNF213 CPQ NRBP2 TYK2 JUP ACADVL CRYL1 CAVIN1 NUMA1 SMOX SLC2A4RG TRIM56 RIPK1 INVS TSC22D4 DHODH USP40 NRIP2 ZFP36L2 ZFP36L1 SALL1 TRIM62 CFTR ZHX2 CDK5RAP2 TTC7A NCBP3 MAP3K11 FUBP3 ABL1 NADSYN1 TULP3 DOCK1 MVB12A P2RX7 TIA1 ATM CARD14 HSPB8 SRCIN1 TRIM4 GSTM2 PABPC1 PHF2 CDC14B CAPN2 S100A13 PTK6 S100A16 RAI14 SLC9A3R1 RELA FLNB KIAA1958 ARHGAP17 USH1C GNAI2 HIPK2 STARD3 HIP1R HDAC6 LHPP TRAF1 SMAD9 ITPRID2 OAS3 UACA NTN1 PSAT1 FOXO1 ARHGAP6 DDIT4 HEY2 KANK1 WNK1 TP53TG5 RTTN DMTF1 PLEKH81 BPTF RILPL1 PLCD1 EIF2D ENGASE LRCH3 SH3PXD2B TJP2 SNAP23 TCF3 CFLAR WHAMM WHRN CMTM3 INPPL1 CAPN9 MYO9B CDK5RAP3 SERPINB6 DVL2 CRT3 VASH1 GFAP LZTS2 BGN RECQL5 ALDH7A1 MAP4K5 DPYSL5 DPF2 SSH3 RPS6KA2 GEMIN8 TOB2 SHROOM1 MTR DIS3L2 ASAP3 MTSS1 ARHGEF40 DAPK2 LIMA1 PKD2 SMURF2 TNS1 CASKIN2 TTL9 PRPF3 FARP2 MAP4 TRIOBP NASP SNX1 SNTB1 LIX1L TJP1 NKD1 CNTRL PPP1R13L NUAKE2 TEP1 SNRNP70 AAAS HEPACAM RASA3 TP53 NACAD ZFH3 STEAP3 ARHGEF1 TLN1 HDAC1 ZNF274 IRF7
	GO:0009897 external side of plasma membrane	9.52	0.0025	CXCL12 CLEC14A HEG1 TGFBR2 ANXA5 B2M EMCN ITGA6
vmPFC-Male-orange	GO:0005525 GTP binding	4.96	0.014	GIMAP6 GIMAP2 GBP4 GIMAP4 RASL11A RERGL GIMAP1 ARL13B GIMAP7 IFI44L GIMAP8
	GO:0001570 vasculogenesis	15.09	0.22	TIE1 HEG1 TGFBR2 HEY2 SOX17
	GO:0051607 defense response to virus	7.53	0.36	OAS2 TLR3 DDX60 HERC5 IFI44L FAM111A
	GO:0009615 response to virus	8.98	0.44	CXCL12 IFIH1 OAS2 IFI44 DDX60

**Supplementary Table 20** Enrichment analysis of cell type markers in WGCNA network genes. Nominally significantly enriched cell types are presented.

Network	N Network Genes	Marker Cell Type	N Markers in Network	Fold Enrichment	p	p <sub>cor</sub>	Cell-type Marker Genes in the Network
dlPFC-brown4	354	Excitatory Neurons 3e	18	2.39	9.12E-05	0.0011	ENO1, GUK1, PFDN5, RPL21, RPL23, RPL3, RPL31, RPL32, RPL34, RPL35, RPL38, RPLP1, RPS14, RPS15, RPS27, RPS27A, RPS28, TMSB4X
		Excitatory Neurons 8	26	4.30	2.00E-13	5.01E-12	GUK1, RPL13, RPL13A, RPL21, RPL23, RPL27, RPL3, RPL31, RPL32, RPL34, RPL35, RPL37, RPL37A, RPL38, RPLP1, RPLP2, RPS12, RPS14, RPS15, RPS18, RPS19, RPS24, RPS27A, RPS4X, RPS6, RPS8
		Excitatory Neurons 9	8	1.93	0.048	0.40	BAD, FTL, GUK1, RPL41, RPS15, SERF2, TMA7, TMSB4X
dlPFC-orange	450	Endothelial cells	12	16.26	6.42E-14	1.60E-12	CAVIN2, CLDN5, EPAS1, FLT1, HLA-E, IFITM3, IGFBP7, NEAT1, PODXL, SLC2A1, TAGLN2, TGM2
		Pericytes	4	7.08	0.0019	0.023	EPAS1, IGFBP7, LPP, NEAT1
dlPFC-Female-lightgreen	539	Astro	8	2.37	0.016	0.10	BAZ2B, FNBP1, MAML2, NCKAP5, NEAT1, PHLPP1, PTGDS, RPS6KA2
		Microglia	5	2.50	0.046	0.23	ATM, FCHSD2, MAML2, NEAT1, PRPF38B
		Oligo	18	4.62	4.04E-09	1.01E-07	BAZ2B, CCDC88A, CDK18, CERCAM, DDX17, DSCAML1, FMNL2, FNBP1, HIPK2, MAP4K5, NCKAP5, NEAT1, PHLPP1, PTGDS, SH3D19, SLCO3A1, SRCIN1, TJP1
		Oligo Precursor Cells	11	3.66	9.73E-05	0.0012	CTTNBP2, DSCAML1, EPN2, FCHSD2, KIF13A, MAML2, MTSS1, NCKAP5, OLIG1, PHLPP1, SH3D19
		Pericytes	5	3.62	0.011	0.089	DDX17, NEAT1, PTGDS, TJP1, UACA
vmPFC-mediumpurple 3	34	Endothelial Cells	5	21.68	1.85E-07	4.63E-06	A2M, ABCG2, ITM2A, SLC38A5, UTRN
vmPFC-sienna3	101	Microglia	22	19.51	2.85E-30	7.13E-29	APBB1IP, C1QA, C1QB, C1QC, C3, CD53, CD74, CD86, CSF1R, CYFIP1, DOCK8, FYB1, HLA-DRA, LAPTMS5, LST1, PTPRC, SAMS1N1, ST6GAL1, SYK, TBXAS1, TREM2, TYROBP
vmPFC-Male-orange	102	Endothelial Cells	14	18.95	7.16E-18	1.79E-16	A2M, ABCB1, ABCG2, B2M, COBLL1, EBF1, GNG11, ID1, ITIH5, ITM2A, LEF1, PTPRB, SLC38A5, UTRN
		Pericytes	5	8.84	0.00015	0.0019	B2M, COBLL1, EBF1, ITIH5, UTRN

**Supplementary Table 21: Significant Upstream Regulators in the dlPFC, vmPFC, and the dlPFC-orange network.** Genes from Table 2 (significantly associated with PTSD after a multiple testing correction) are in bold. TABLE STARTS ON THE FOLLOWING PAGE.

dIPFC Upstream Regulators	Gene	Exp. Log Ratio	Predicted Direction	p	p <sub>cor</sub>	Target Molecules in Dataset
	MYCN	0.026	Activated	2.11E-10	0.000000284	ACTG1 CCND1 CDC42 CDH5 CDKN1A CHPF2 CITED2 CLU COL4A1 COL8A1 CRIM1 DUSP7 EEF1A1 FBN1 FRMD6 HSP90AB1 ITGA2 MYH9 NACA NPM1 RBBP7 RNF11 RPL10 RPL11 RPL17 RPL21 RPL22 RPL23 RPL24 RPL26 RPL27A RPL29 RPL31 RPL4 RPL41 RPL5 RPL7 RPL9 RPS12 RPS23 RPS24 RPS25 RPS3 RPS3A RPS4X RPS6 RPS7 RPS8 SLC2A1 TERC TIMP2 TNFRSF1A TUBB
	TP53	0.20	Activated	7.28E-10	8.06E-07	A2M ACADS ACER2 ACTA2 ADA ADH5 AGTR1 AIFM2 AKAP12 ALB ANLN ANXA3 API5 AR ARHGEF4 ARL6IP1 ATF3 ATG4A BCL6B BDKRB2 BIRC2 BTG1 BTK CAMK2D CAP1 CARD11 CAV2 CCNA2 CCND1 CD82 CDH3 CDK2 CDKN1A CDT1 CEBPD CELSR1 CITED2 CLIC4 CLU CMBL CNN3 COL4A1 COL4A2 CPSF1 CYP26B1 DCLRE1A DDIT3 DPYSL4 DRAM1 DUSP5 DUT ECM1 EDIL3 <b>EDN1</b> EEF1A1 EFNA1 EPAS1 EPHA2 EYA4 F11R FAT1 FBL FERMT2 FGF13 FHL1 FKBP1B FOXO3 FUBP1 GADD45A GADD45B GNAI2 GPM6A GPR17 GPR4 GSTP1 H2AZ1 HBEGF HMGB2 HMGCS1 HMG2 HS3ST1 HSP90AB1 HSPA1L ICAM1 ID3 IGDCC4 IGFBP4 IL16 IL1A IL1B IL4R ITGA2 JUN KCNB1 KCNJ4 KPNA2 KPNB1 LAMP2 LGR5 LHX1 LIAS LIF LIMA1 LIN28B MAP2K3 MB MCL1 MCM6 MEF2A MKI67 MMP9 MT1L MYH9 MYL9 MYO10 MYOCD NAMPT NFKBIA NINJ1 NOLC1 NPM1 NPNT OTX1 PAFAH1B2 PAK3 PAPP A PDE4B PEA15 PECAM1 PEG10 PGR PLAAT3 PLAUR PODXL POSTN PPARGC1B PPP2CA PPP4R2 PRKAB2 PRKG1 PRNP PSAP PSMD1 PTEN PTPRE PYCARD RAN RAP2B RBBP7 RCHY1 RECQL4 RELA RHOA RHOB RLIM RPL10 RPL5 RPL7 RPN1 RPS12 RPS18 RPS25 RPS3 RRM1 SAT1 SCP2 SEL1L SELE SERPINA3 SHC1 SHROOM3 SLC2A1 SLC2A12 SLC2A4 SLC6A6 SMC4 SMURF2 SNRPC SON SPATA18 SRSF3 STAT3 SUCLG1 TCEA3 TET1 TFDP1 TGFBR1 THBD TIMM10 TIMM44 TIMP2 TMED7 TNFRSF10D TNFRSF1A TNFSF10 TPX2 TRAP1 TTN TUBB UBC UIMC1 USP28 VAMP4 VAPA VCL VMP1 WNT3 XBP1 XRCC5 YWHAH ZFP36
	MLXIPL	0.10	Activated	1.87E-09	0.0000018	RPL10 RPL10A RPL11 RPL17 RPL21 RPL22 RPL23 RPL24 RPL26 RPL27A RPL31 RPL36AL RPL4 RPL41 RPL5 RPL7 RPL9 RPS12 RPS14 RPS15A RPS18 RPS23 RPS24 RPS25 RPS27A RPS29 RPS3 RPS6 RPS7 RPS8
	TNF	0.031	Activated	9.58E-09	5.79E-06	A2M ACADS ACTA2 AGTR1 AKAP12 ALB ANGPTL4 AQP7 AR ARF4 ARHGAP22 ARID5B ARL6IP5 ARRDC3 ATF3 ATP2B4 BCYRN1 BDKRB2 BIRC2 BTG1 BTG3 CABP1 CCND1 CCR1 CD200 CD4 CD55 CD69 CD82 CD83 CDC42 CDH3 CDH5 CDK2 CDKN1A CEBPD CEBPG CITED2 CLIC4 CLU CMBL COL4A3 CREM CRH CRISPLD2 CTSS CXCL11 CYP26B1 CYR1 DDIT3 DEPP1 DLEU1 DLL4 DUSP5 EDIL3 <b>EDN1</b> EFNA1 EGLN3 ELK1 ELOVL7 <b>EMP1</b> EPHA2 F11R F2RL1 FBL FERMT1 FLT4 FOXC2 FOXF2 FPR1 FRMD6 GABRA2 GADD45A GADD45B GASK1B GBP4 GCH1 GEM GKAP1 GNAI2 GSTP1 HBEGF HIPK3 HPGDS HSP90AB1 HSP90B1 ICAM1 ICAM2 ID3 IFI6 IFIT5 IGFBP4 IL16 IL1A IL1B IL4R IL7R INPP5D IRAK2 IRAK3 ITGA2 JAG2 JUN KCNJ1 KMO LAMA4 LGR5 LIF LITAF LTBP2 LXN LY6D <b>MAFF</b> MAN1A2 MAP2K3 MAP3K20 MCL1 MEF2C MEOX1 MGP MICA MMP9 MT1A MT1L MT2A MUC5AC MYH9 NAMPT NCR3LG1 NEAT1 NFKBIA NINJ1 NKD2 NTN1 OLR1 OSM PAPP A PDCD1 PDE4B PECAM1 PIM2 PLAAT3 PLAUR PLIN2 PLSCR1 POSTN POU2AF1 PPARGC1B PRKCD PRNP PRSS23 PTEN PTGES PYCARD RAC1 RANBP9 RBP1 RELA RHOA RHOB RPS3 RRM1 SAMD9 SAT1 SDC4 SEC22B SELE SERPINA3 SERPINB8 SLC11A1 SLC2A1 SLC2A4 SLC40A1 SMAD1 SMURF2 SOCS3 STAT3 STEAP4 TCHH TERC TERF2IP TGFBR1 TGIF1 THBD TIMP2 TM4SF1 TNFRSF10D TNFRSF1A TNFSF10 TNFSF8 TPST1 TRAF3 TREM1 TRPC1 TRPC3 TYK2 UGCG VCL VMP1 ZFP36 ZNF267

						<p>ABLIM3 ACTA2 ADI1 ADRA1D ALB ANGPTL4 AP3S1 ARF4 ARID5B ARL4A B4GAT1 BDKRB2 BMP7 BNIP3L BTG1 CADM1 CAP1 CAPN15 CAV2 CAVIN2 CBFBC CDC28A CCL8 CCNA2 CCND1 CCR1 CCT5 CCT6A CD4 CD55 CD69 CD83 CDH5 CDHR1 CDK17 CDK2 CDKN1A CDT1 CEMIP CHST3 CITED2 CLIC4 CLU CNN3 COL11A1 COL4A1 COL4A2 COL8A1 CTSS CXADR DDB1 DDX21 DES DTX4 ECM1 <b>EDN1</b> EEF1A1 ENO2 EPHA2 F12 F2RL1 FAM53B FBLN5 FBN1 FCGR3A/FCGR3B FERMT1 FERMT2 FHL1 FOXC2 FOXO3 FUBP1 GABARAP GADD45A GADD45B GEM GNAI2 GNG7 GNRH1 GTPBP1 HAMP HBEGF HEBP1 HEXIM1 HMGN2 HNRNPC HSPB2 ICAM1 ICAM2 ID3 IGFBP4 IL1A IL1B IL2RB IL4R INHBB INPP5D IRAK2 IRAK3 ITGA2 JAG2 JUN KCNMB1 KPNA3 L1CAM LAMP2 LIF LIMS1 LITAF LSR LTBP2 MAP2K3 MAP3K1 MAVS MEF2C MGAT4A MGP mir-154 MKI67 MMP9 MPP6 MSN MUC5AC MXD4 MYH9 MYO10 MYOCD NAMPT NDUFS4 NFKBIA NT5E OGA OLR1 OSM OSTF1 PAK3 PAPP A PDCD1 PDE7A PDLIM4 PECAM1 PGK1 PGRMC1 PLAUR PLS3 PLSCR1 PLXNC1 PODXL POSTN PPP2CA PPP2R2A PSAT1 PSMD1 PTEN PTGES RAB18 RAC1 RAD21 RAD51C RASSF1 RELA RHOA RHOB RHOC RHOU ROBO3 S100A6 SBNO2 SDC4 SELE SEMA3B SERPINA3 SERPINF2 SERTAD1 SLC2A1 SLC2A3 SMAD4 SMC4 SMURF2 SOCS3 SRSF3 STAT3 STRAP TARDBP TGFBR1 TGIF1 THBD TIMP2 TMOD3 TNFRSF12A TRPC1 TUBA1A UBE2J1 VCL XBP1 ZBTB14 ZFP36</p>
TGFB1	0.0030	Activated	3.26E-08	1.34E-05		
GPER1	0.0020	Activated	0.0000024	0.00051	<p>ACTA2 ATF3 CCND1 CDKN1A CEBPD DDIT3 DUSP5 <b>EDN1</b> ITPRIP JUN MT1A MT1X MT2A NFKBIA TUFT1 ZFP36</p>	
XBP1	0.20	Activated	0.000017	0.0027	<p>ARCN1 ARFGAP3 ATF6 BFAR BHLHA15 COPZ1 DDIT3 DNAJB9 DNAJC1 DOLPP1 ERLEC1 FKBP14 FKBP1B GALK2 HSP90B1 HSPA13 ICAM1 MAP1LC3B PIGA POU2AF1 PRNP RAB33B RELA RPN1 S100A6 SEC22B SEC23A SEC24C SEC63 SRP9 SSR1 TFDP1 VAMP4 XBP1 XRC6 YIPF5</p>	
RICTOR	0.067	Inhibited	0.000037	0.0043	<p>AR ATP6V0A2 ATP6V0E2 ATP6V1H CD4 CD69 COX7A2L IL7R LHPP MCL1 NDUFB8 NDUFS4 NDUFV2 POMP PPA1 PSMA6 PSMD1 PTEN RAC1 RPL10 RPL10A RPL11 RPL17 RPL21 RPL22 RPL23 RPL26 RPL4 RPL41 RPL7 RPL9 RPS18 RPS23 RPS24 RPS27A RPS29 RPS3 RPS6 RPS8</p>	
EIF2AK3	-0.055	Activated	0.00011	0.0099	<p>ATF3 ATF6 BIRC2 CCND1 CEBPG CYB5R1 DDIT3 DNAJB9 GADD45A GCH1 IL1B JUN MAP1LC3B NFIL3 SEL1L SIAH2 TARS1 UIMC1 XBP1 ZFP36</p>	
HIF1A	0.067	Activated	1.23E-04	1.07E-02	<p>ACTA2 AKAP12 ANGPTL4 BIRC2 BNIP3L CCND1 CDCP1 CDKN1A CEMIP CHKB-DT CITED2 DLL4 <b>EDN1</b> EGLN3 ENO2 EPAS1 FHL1 GADD45B HAMP HILPDA IL1A IL1B INHBB JUN L1CAM <b>MAFF</b> MB MCL1 MEF2C MMP9 NPM1 NT5E NUCKS1 P4HA2 PGK1 PHLPP1 PIM2 PLAUR PTEN RAB20 RASSF1 RELA SDC4 SLC2A1 SLC2A3 SLC2A4 SLC40A1 SOCS3 STAT3 TERC TTN ZDHHC9 ZNF267</p>	
OSM	1.46	Activated	0.00016	0.012	<p>A2M ACTA2 ADH5 ALB AMACR ANXA3 AQP7 ARL4A ARTN ATF3 ATP2B4 CBX3 CCND1 CDH3 CDK17 CDKN1A CEBPD COL8A1 CXADR DHRS7 ECM1 EXOSC10 FLG GNRH1 HAMP HBEGF HIPK3 ICAM1 IL1B IL4R ITPKB JUN LIF LITAF LY6D MICA MMP9 MT1X MT2A NAMPT NELL2 NOMO1 (includes others) NRAS OSM PGK1 PTEN PTGES RASL11A RELA SBNO2 SEL1L SELE SERPINA3 SERPINB8 SLC16A6 SMAD4 SOCS3 SON SOST STAT3 TM4SF1 TPX2 TUBA1A ZFP36 ZHX2</p>	



	IL4	0.64	Activated	0.00023	0.014	ACSL4 ACTA2 ACTG1 ADAP1 APOLD1 BCL11A BIRC2 BNIP3L CBF3 CBX3 CCL8 CCND1 CD200 CD33 CD55 CD58 CD69 CD83 CDK2 CDKN1A CHST3 CITED2 CLDN2 CXCL11 DARS2 DUOX1 EPAS1 EPHA2 F2RL1 FBL FCGR3A/FCGR3B GALK2 GBP5 HBEGF HLA-DMB ICAM1 ID3 IGFBP4 IL16 IL1A IL1B IL2RB IL4R IL7R ITGA2 JUN KMO LACC1 LAMP2 LGALS1 LIF LIG4 LY6D MARCO MATK MCL1 MICA MKI67 MMP9 MYH9 NCR3LG1 NFIL3 NFKBIA NOMO1 (includes others) OSM PDCD1 PDE4B PIM2 PKIB PLIN2 PLSCR1 POSTN POU2AF1 PPARGC1B PPP6C PRKCD PRNP PSMA6 PTGDR2 RELA RHOA RNF213 RNPEP RPS6 SELE SLAMF7 SLC2A1 SNX8 SOCS3 SON TES TGFBR1 THBD TIMP2 TMED5 TNFSF8 TOP3B TRAF3 VPS35 XBP1 XRCC5 XRCC6 ZFP36
	HSF1	-0.020	Inhibited	0.00056	0.024	BMP7 CBX3 CCNA2 CCT5 CCT6A CELSR1 CLU HERC4 HSP90AB1 HSPB2 ICAM1 IL1B IL7R INHBB JUN LAMA4 LIF MCL1 MICA PGK1 POSTN PPP3CB RELA RPL22 SHC1 SNCAIP SPR TRAF3 UBC WNT3
	RASSF1	0.33	Activated	0.00072	0.028	CAV2 CCNA2 CCND1 CDKN1A CLU COL4A1 COL4A2 CPE DPEP3 <b>EMP1</b> H2BC4 HBEGF LIF LITAF MYL9 TUBB
	EGF	0.12	Activated	0.00073	0.028	ACSL4 ADA ANGPTL4 AR ARTN ATF3 BIRC2 CAVIN2 CCND1 CDK2 CDKN1A CEBPD CLDN2 CLU CREM DDIT3 DUSP5 <b>EDN1</b> EEF1A1 ELK1 EPAS1 EPHA2 GAB2 GADD45A GSTP1 HBEGF HMGCS1 HNRNPK ICAM1 IGFBP4 IL1B IL7R ITGA2 JAG2 JUN MAP3K20 MB MCL1 MMP9 MUC5AC PGR PLAUR PLSCR1 PTGES RAC1 RHOA RHOB RRM1 SERPINA3 SHC1 SLC2A4 SMAD1 SOCS3 TFDP1 TGIF1 TNFRSF12A VCL XRCC6 ZBTB33 ZFP36
	IL1B	1.41	Activated	8.15E-04	3.05E-02	A2M ACTA2 AGTR1 ANGPTL4 ARL6IP5 ATF3 BCYRN1 BIRC2 CABP1 CAV2 CCL8 CCR1 CD4 CD55 CD69 CD82 CD83 CDKN1A CEBPD CEBPG CHST6 CREM CRH CTSS CXCL11 DDIT3 DLL4 DUSP5 <b>EDN1</b> EFNA1 EGLN3 EPAS1 F2RL1 GADD45A GADD45B GCH1 GEM GNRH1 HAMP HBEGF HELZ2 HPGDS HSPA1L ICAM1 ID3 IGFBP4 IL16 IL1A IL1B IRAK2 IRAK3 ITPKB JUN KCNJ1 LIF MCL1 MEF2C MMP9 MT2A MUC5AC NAMPT NEAT1 NFIL3 NFKBIA OLR1 OSM PAPP A PDCD1 PDE4B PGR PLSCR1 POSTN PPARGC1B PRKCD PTGES RAN RELA RHOB S100A6 SDC4 SELE SERPINA3 SERPINF2 SFTPA1 SLC2A1 SLC2A4 SNCA SOCS3 SRGN STAT3 TERC THBD TIMP2 TNFSF10 TREM1 UGCG ZFP36
	FGF2	0.28	Activated	8.49E-04	3.12E-02	ACER2 ACTA2 ALB ANGPTL4 AR ASCL1 C1QL1 CBF3 CCND1 CDK2 CDKN1A CNMD CYGB DDIT3 DLL1 DLL4 EGLN3 ELK1 EPAS1 EPHA4 FBN1 FOXO3 GADD45A GCH1 GNRH1 HBEGF ICAM1 ID3 IGFBP4 IL1B JUN MGP MKI67 MMP9 MUC5AC PGK1 PLAUR PRKCD PTPRE SELE SLC2A1 SOCS3 SOST TNFRSF12A TNFSF10 XRCC5 XRCC6 YWHAZ ZFP57
	NFE2L2	-0.010	Activated	0.0017	0.045	ACTG1 ATF3 CBR1 CDKN1A COL4A2 DDIT3 EPAS1 ESD FGF13 FOXO3 GABRA2 GNAI2 GSTO1 GSTP1 HAX1 HSP90AB1 HSP90B1 ICAM1 IL1A IL1B L1CAM <b>MAFF</b> MAP1LC3B MATK MEF2C MMP9 MORF4L2 NGEF PKIA PLIN2 POMP PSAT1 PSMA6 PSMD1 RAN RBBP7 RELA SAT1 SEC23A SERPINA3 SHC1 SLC2A1 SOCS3 SRGN SYN2 TMED2 UBC VCP XBP1
vmPFC	TNF	0.19	Activated	6.14E-18	3.43E-14	A2M ACADVL ADAMTS4 ADGRG6 ADM AGFG2 AKAP12 ALCAM ALDH2 ALOX5 ANGPTL4 ARHGDIB ARRDC3 ATF4 B2M BCL2L2 BCL6 BIRC5 BMPR1A BTG2 BUD23 C1QTNF1 C1QTNF12 CA12 CAVIN3 CDH5 CDKN1A CEBPB CISH CLEC2D COL16A1 CRYAB CXCL10 CYP7B1 CYR1 DDIT3 <b>EDN1</b> EDNRB EGFL7 <b>EMP1</b> EPHA2 FGF2 FGFRL1 FLT4 FN1 <b>FOS</b> FOSB FPR2

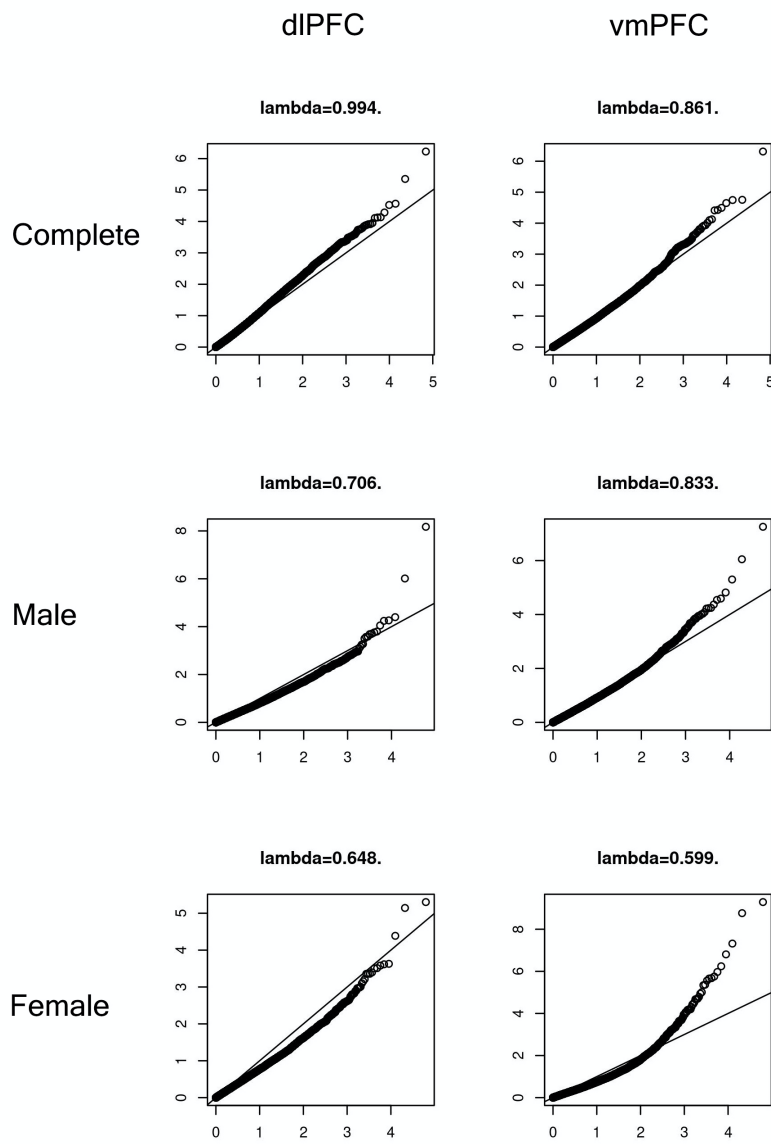
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IL1B	0.76	Activated	6.78E-14	1.89E-10	A2M ADAMTS1 ADAMTS4 ADM ANGPTL4 ATF4 B2M BCL6 BTG2 CDKN1A CEBPB CHST6 CISH CRYAB CSRN1 CXCL10 CYSLTR1 DDIT3 <b>EDN1</b> ENPP1 ERFF1 FGF2 FGFRL1 FKBP5 FN1 <b>FOS</b> FOSB FPR2 GADD45A GADD45B GCH1 GCHFR GCK GEM GJA1 HELZ2 HSPA1A/HSPA1B HSPB1 IFIT1 IGFBP4 IL16 IL18 IL18R1 IL1R1 IL1RL1 IL6R IRAK2 ITGA5 ITPKB JUN LCP1 LIF LUCAT1 MCL1 METRNL MT2A NEAT1 NFATC2 NFIL3 NOCT NOS3 NR2F2-AS1 NRP1 ODC1 PBRM1 PDGFB PLAA PPARG PRDM1 PTENP1-AS PTGIS RARA RGS16 RSAD2 RXRB SELENOP SERPINA3 SERPINE1 SERPINH1 SLC25A25 SOCS3 SOD2 TGFB3 THBD THBS1 TINCRTJP1 TK1 TLR2 TLR3 TNFRSF10A TNFSF10 TRAF2 TREM1 TUNAR ZFP36
NR3C1	-0.034	Activated	7.85E-12	8.77E-09	A2M ADM ANGPTL4 ARRB2 B2M BAG3 BCL2L2 BCL6 C1QTNF1 CAPN2 CARD14 CAVIN2 CDKN1A CEBPB CRYAB CSRN1 CXCL10 DAPK3 DDC DEAF1 DNAJC15 DPP7 DUT <b>EDN1</b> ELMO2 <b>EMP1</b> ERFF1 FKBP5 FN1 <b>FOS</b> GADD45A GADD45B GEM <b>GLP2R</b> GPR65 IDH1 IL18 JMJD6 JUN LIF MCL1 MKNK2 MT1L MT2A NFIL3 NGFR NOS3 NTF3 PC PDGFA PDPN PFKFB3 PLIN2 PPARG PPP1R15A RELT SELENOP SERPINE1 SERTAD2 SLC19A2 SLC25A33 SLC2A3 THBD THBS1 TIPARP TK1 TLE3 TLR2 TNFRSF10A TNFRSF10B TNFRSF12A TNFRSF1A ZNF48
EPAS1	0.16	Activated	1.63E-10	0.000000101	ADM AKAP12 ANGPTL4 CA12 CDCP1 CDKN1A CEBPB DDIT3 <b>EDN1</b> FGF2 FN1 <b>FOS</b> GADD45B GCHFR GJA1 ITIH5 KDM4B <b>MAFF</b> NDRG1 NEAT1 NFIL3 NOS3 NT5E PDGFB PFKFB3 PLIN2 PPARG PTK6 RASSF1 SERPINE1 SLC2A3 SOD2 STC2 TGFB3 ZNF423
ATF4	0.24	Activated	3.17E-09	0.0000014	ATF4 CAR1 CDKN1A CEBPB DDIT3 <b>EDN1</b> FN1 GADD45A GCH1 JUN KLF4 MARS1 MCL1 MITF MT2A MTHFD2 NDRG1 PPARG PPP1R15A PYCR1 SHMT2 SLC39A14 SOD2 STC2 TNFRSF10B TNFRSF12A WNT11
TFRC	-0.006	Inhibited	5.85E-09	0.0000020	ATF4 CDC20 CDKN1A DDIT3 FAM20C <b>FOS</b> GADD45A JUN PFKFB3 PPARG PPP1R15A RGS1 SLC26A11 <b>SLC2A14</b> STC2 TGFB3 TNFRSF12A TNFSF10 XBP1
TGFB1	-0.028	Activated	9.52E-09	2.66E-06	AASS ADAMTS4 ADM ADRA2A AKR1C1/AKR1C2 ALDH2 ALOX5 AMER2 ANGPTL4 ASPN ATF4 B2M BCL6 BIRC5 BMP1 BMP7 CALD1 CAR1 CAVIN2 CDC20 CDC42SE1 CDH5 CDKN1A CEBPB <b>CFH</b> CHST3 CLEC2D COL16A1 CRHR2 CTPS1 CTSX CXCL10 <b>EDN1</b> EDNRB ENPP1 EPHA2 FCGR3A/FCGR3B FGF2 FN1 <b>FOS</b> FOSB FOXC1 FPR2 FUBP1 GADD45A GADD45B GEM GJA1 GNA14 HLA-DQA1 HLA-DRB5 HSD17B6 HSF2BP HSPA1A/HSPA1B HSPB1 ICAM2 ID4 IGFBP4 IGHM IL18 IL1R1 IL1RL1 IL6R IRAK2 ITGA5 ITGA7 ITIH5 JUN KDM6B KLF4 LIF MAP3K1 MARK3 MET METRNL MITF

						MSN MTHFD2 MVD MYH9 MYOCD NCF2 NFATC2 NOS3 NRP1 NT5E P2RX6 PDGFA PDGFB PDLIM4 PDPN PECAM1 PFKL PPARG PRDM1 PRIM1 RARA RASSF1 RHOC RSAD2 RUNX3 SERPINA3 SERPINE1 SERPINH1 SERTAD1 SHMT2 SLC16A3 SLC26A11 SLC2A3 SLC39A14 SMC2 SMTN SOCS3 SOD2 SOD3 STC2 TGFB3 TGIF1 THBD THBS1 TJP1 TJP2 TLR2 TMEM17 TNFRSF10A TNFRSF12A TOP2A VCL WNT11 WNT5B XBP1 ZFP36 ZFPM2
TP53	0.27	Activated	4.19E-08	9.75E-06		A2M AATF ACADVL ACO2 ADA AKAP12 ALDH1A2 ALOX5 ANXA3 ARRB2 ATF4 BCL6B BIRC5 BMP1 BTG2 CARD11 CARS1 CDC20 CDC34 CDKN1A CEBPB CHMP4C CRACR2B CRYAB CSNK1D CTSB CXCL10 CYSLTR1 DAPK3 DCK DDIT3 DDIT4L DDR1 DDX56 DNAJB2 DNAJC15 DUT <b>EDN1</b> EPHA2 FGF2 FKBP5 FN1 <b>FOS</b> FUBP1 GADD45A GADD45B GADD45G GJA1 GLRX GNA14 GPR162 GPR176 GPR4 HLA-DQA1 HSPA1A/HSPA1B HSPB1 IDH1 IGDC4 IGF2BP2 IGFBP4 IL16 IL21R IL27RA INSYN2A IQCB1 JUN KLF4 KPNA2 LAMP3 LATS2 LIF LSS MCL1 MET MICALL1 MST1 MT1L MVD MYH9 MYOCD NDRG1 NOS3 NPNT NRP1 PABPC4 PADI4 PALLD PDGFA PDGFB PDIA5 PECAM1 PFKFB3 PHLDA3 PPARG PPP1R15A PRDM1 PRIM1 PSRC1 PVT1 RALY RGS16 RPS5 SAT1 SERPINA3 SERPINE1 SERPINH1 SESN2 SFN SHC1 SLC19A2 SMC2 SMC3 SOD2 TCEA3 TET1 TGFB3 THBD THBS1 TJP1 TLR3 TNFRSF10A TNFRSF10B TNFRSF18 TNFRSF1A TNFSF10 TOP2A TPD52L1 TRAP1 TTK VCL WNT5B WNT8A XBP1 ZFP36 ZFP36L1
IL6	-0.072	Activated	4.58E-08	0.00001		A2M ADAMTS1 ADAMTS4 ADM BCL6 BIRC5 BTG2 C1QL1 CDC20 CDKN1A CEBPB <b>CFH</b> CISH CRYAB CXCL10 ERFF1 ETV4 FGF2 FN1 <b>FOS</b> FPR2 GADD45A GADD45B GADD45G GCH1 GLRX HLA-DQA1 HLA-DRB5 IFIT1 IGFBP4 IGFN1 IGHM IL1R1 IL1RL1 IL6R JUN KIF11 LAG3 LIF LIN28A MCL1 MET NCF2 NOS3 PDGFA PDGFB PECAM1 PPARG PPP1R15A RASSF1 SERPINA3 SERPINE1 SLC39A14 SOCS3 SOCS5 SOD2 STEAP4 THBS1 TK1 TLR2 TLR3 TNFRSF10B TNFRSF12A TNFRSF1A TNFSF10 TOP2A TRAF7 TTK XBP1
FGF2	0.36	Activated	4.66E-08	1.00E-05		ADM ANGPTL4 ATF4 BCL6 BIRC5 BTG2 C1QL1 CDKN1A CNMD CRYAB DDIT3 DLL1 EDNRB ENPP1 EPOR ERFF1 ETV4 FGF2 FN1 <b>FOS</b> GADD45A GCH1 GJA1 IGFBP4 ITGA5 JUN LMNA MET MITF NES NGFR NOS3 NTF3 ODC1 PDGFA PDGFB PPARG SERPINE1 SOCS3 ST3GAL1 TEAD4 THBS1 TNFRSF12A TNFSF10 TOP2A
CSF3	1.09	Activated	6.14E-08	0.000013		ARHGEF10 BIRC5 CEBPB CISH <b>EDN1</b> FGF2 <b>FOS</b> GADD45A GADD45B GADD45G GJA1 HLA-DPA1 HLA-DQA1 JUN MCL1 MET NFIL3 NOS3 ODC1 PPARG RARA RGS1 SOCS3 TLR2 TNFRSF1A TNFSF10
GPER1	-0.024	Activated	0.000000155	0.000027		CDKN1A DDIT3 <b>EDN1</b> ERFF1 <b>FOS</b> FOSB ITPRIP JUN MT1A MT1X MT2A PPP1R15A RGS16 ZFP36
EGF	0.27	Activated	0.000000288	0.000047		ADA ALCAM ANGPTL4 BIRC5 BTG2 CAVIN2 CDC34 CDC42EP1 CDKN1A CEBPB CHGB CISH DDIT3 E2F3 <b>EDN1</b> EPHA2 ERFF1 FGF2 FN1 <b>FOS</b> FOSB GADD45A GJA1 IDH1 IGFBP4 IL1R1 JUN LIN28A MAPK11 MCL1 MET MST1 MT3 NES NRP1 ODC1 PDPN PPARG SERPINA3 SERPINE1 SHC1 SOCS3 ST3GAL1 TGFB3 TGIF1 THBS1 TJP1 TNFRSF12A TRAF2 VCL ZFP36
TGFB2	-0.18	Activated	0.000000795	0.00011		ALOX5 ANGPTL4 ATF4 BIRC5 CDKN1A CRYAB FGF2 FN1 GADD45B GJA1 GJB6 JUN NOS3 NRP1 PDGFB PDPN PTGIS SERPINE1 SLC2A3 SOCS3 TGFB3 TGIF1 THBD THBS1 TNFRSF12A VCL

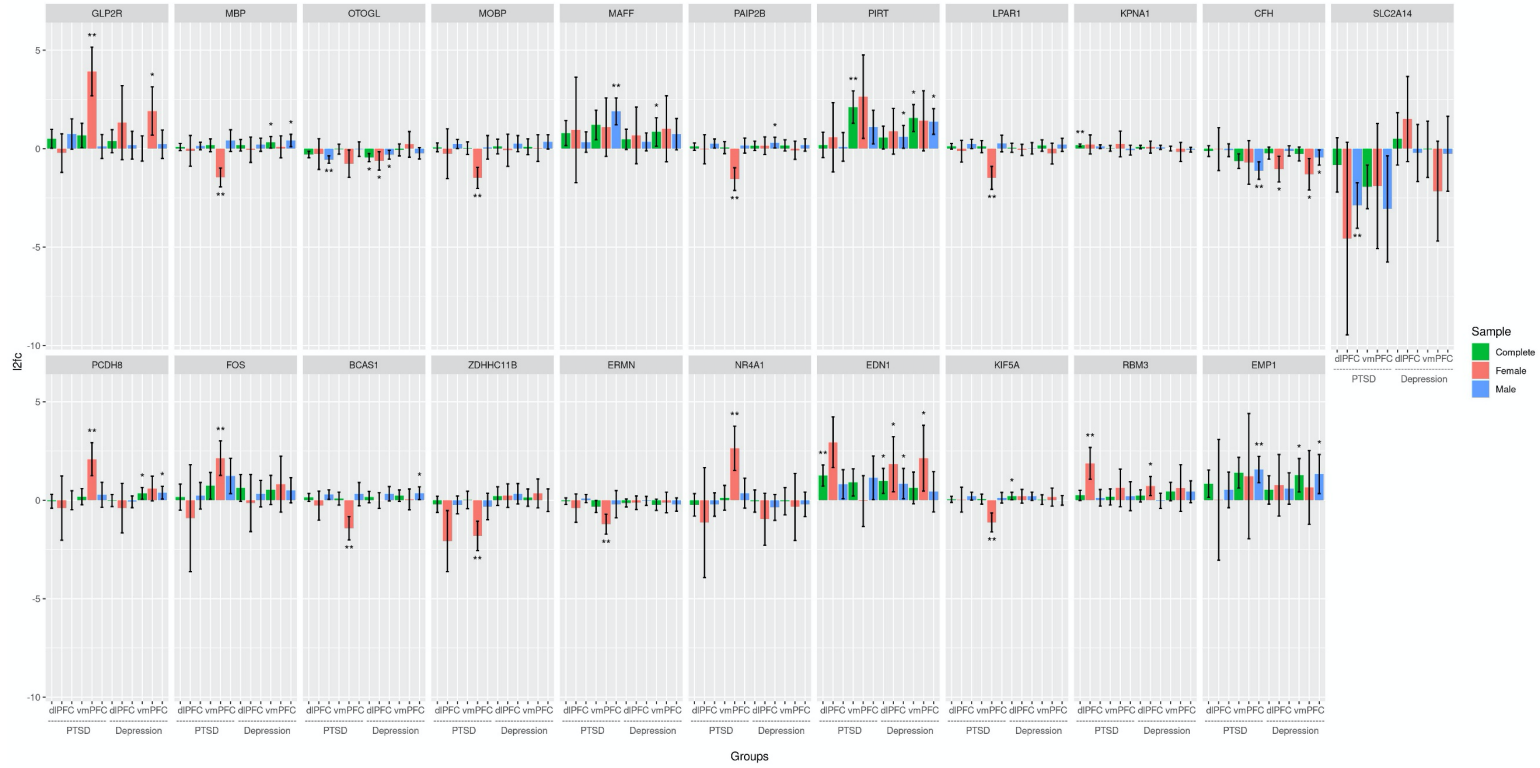
EIF2AK3	-0.0090	Activated	0.0000013	0.00015	ATF4 BTG2 CAR51 CEBPB DDIT3 FGF2 GADD45A GCH1 JUN KLF4 NDRG1 NFIL3 PPP1R15A PRDM1 SHMT2 XBP1 YARS1 ZFP36
ELK1	0.16	Activated	0.0000020	0.00021	ARRB2 CDKN1A <b>FOS</b> FOSB JAM2 JUN MCL1 MTHFD2 THBS1 TIPARP TNFRSF10B TPDS5L1 ZFP36
SS18	0.019	Activated	0.0000023	0.00023	C11orf96 DLL1 GADD45B GCH1 METRNL NGFR PDGFB SLC16A3 SOCS3 TLE3
CSF1	0.23	Activated	0.0000030	0.00027	BIRC5 CAPN2 CDKN1A CTSB FCGR3A/FCGR3B FN1 <b>FOS</b> GPR68 IL11RA IL18 IL1RL1 ITGA5 JUN LAG3 LSS MVD NCF2 PFKFB3 PFKL PMVK PPARG SLC16A3 SLFN12L STAB1 THBS1 TLR2 TNFRSF1A TRAF2 XBP1
NUPR1	0.24	Activated	6.36E-06	4.33E-04	ADM AKAP12 ANGEL1 ATAD5 B3GAT3 CCDC9 CDCA2 CEBPB DDIT3 GADD45A GCH1 IL6R JOSD1 KBTBD7 KIF11 KIF20A KLF4 LIF MKKS MT1X NDRG1 NFIL3 NGFR OSGEPL1 P4HA2 PFKFB3 PMPCA PPP1R15A PXDC1 RNF122 RNU11 SAMD4A SAT1 SERPINE1 SERTAD2 SESN2 SH2D5 SHCBP1 SIK1/SIK1B SIX4 SLC16A6 TNS3 WASHC5 XBP1 ZFP36L1
CEBPA	-0.10	Activated	0.000011	0.00063	A2M AGPAT2 AKAP12 AKR1C1/AKR1C2 ATF4 BTG2 CDKN1A CEBPB <b>FOS</b> GADD45A GCH1 GJA1 GLRX ICAM2 IGFBP4 IL6R JUN KLF4 LIN28A MNDA MT2A NFATC2 NFIL3 NRP1 PLIN2 PPARG PRDM1 PTPN3 RUNX3 SEXTM1 SERPINE1 SOCS3 SOD2 STEAP4 THBD THBS1 TNFRSF10A TNFRSF19 TNFRSF1A TNFSF10 VCL
IL4	0.037	Activated	0.000018	0.00092	ACTG1 AGFG2 ALDH1A2 ALDH2 ALOX5 APOLD1 BCL6 BIRC5 CCDC86 CDKN1A CHST3 CISH CLEC4G CXCL10 CYSLTR1 CYSLTR2 EPHA2 FCGR3A/FCGR3B FKBP5 FN1 <b>FOS</b> FOSB FPR2 GADD45G GJA1 GNA14 HSPA1A/HSPA1B IGFBP4 IL16 IL18 IL18R1 IL1R1 IL1RL1 IL27RA JUN KDM6B LIF LIPG LMO7 MCL1 METRNL MICA MYH9 NDRG1 NEDD1 NFATC2 NFIL3 NKX3-1 NOCT NRP1 OAS3 PFKL PLIN2 PMVK PPARG PRDM1 RNF213 SAMD4A SDF2L1 SERPINE1 SKA1 SLC25A25 SLC7A2 SMC3 SOCS3 STAB1 SWAP70 TGFB3 THBD TICAM1 TLR2 XBP1 ZFP36
BCL6	0.38	Inhibited	0.00010	0.0038	A2M ALCAM BCL6 BLNK C1QTNF12 CDKN1A CGAS CISH CXCL10 FGF2 GADD45A IL18 IL21R IL6R ITPRIP LMNA MITF PRDM1 SERPINE1 SH3PXD2B SMC3 SOCS3 TNFRSF18 XBP1
CREB1	-0.014	Activated	1.36E-04	0.0045	ADM APOLD1 BAG3 BIRC5 BRD9 BTG2 CAR51 CDKN1A CEBPB CHGB CSRNP1 <b>EDN1</b> ERRF1 FN1 <b>FOS</b> FOSB GADD45A GADD45B GADD45G GEM JUN KLF4 KYAT1 LSS MCL1 MIDN MKNK2 MVD NFIL3 NOX5 NRP1 OMG PLPPR1 PPARG PPP1R15A RELT SAT1 SERTAD1 SLC17A6 SLC2A3 SOD2 TGIF1 TIPARP ZFP36 ZFPM2
ATF3	0.63	Activated	0.00019	0.00544	ATF4 BHLHA15 CDKN1A DDIT3 GBP4 HSPB1 JUN MT2A PPP1R15A RSAD2 SERPINE1 TLR2 TNFRSF10B XBP1
CREM	0.18	Activated	0.00049	0.011	APOLD1 BTG2 CEBPB CSRNP1 ERRF1 <b>FOS</b> GADD45B LSS MCL1 MIDN MKNK2 NFIL3 PPP1R15A SERTAD1 SIK1/SIK1B THBS1 TIPARP
RAF1	0.066	Activated	0.00063	0.013	AKAP12 BCL6 CDC42EP1 CDKN1A CRYAB CTSB <b>EMP1</b> <b>FOS</b> HMGB3 HSPB1 IL1R1 JUN LIF MET MT1L MT3 PC PPP1R10 PRDM1 RGS1 RPS2
RNY3	0.10		0.00096	0.018	CXCL10 DDX60 IFIT1 LAMP3 OAS3 RSAD2
TIMP3	-0.13	Inhibited	0.0016	0.025	CEBPB <b>FOS</b> JUN KLF4 MET SERPINE1 THBS1 WNT11
DICER1	-0.034	Inhibited	0.0016	0.025	ANGPTL4 CDKN1A CXCL10 ELOVL2 <b>FOS</b> IGF2BP2 IL18R1 ITGA5 JUN KLRG1 LCP1 LIPG MICA MITF MT2A NGFR NOS3 PELI2 PROCR RGS5 SERPINE1 SERTAD4 SLC4A4 SOCS3 THBS1
BTK	-0.30	Activated	1.79E-03	0.026	C1D CDKN1A CEBPB CISH CXCL10 <b>EMP1</b> IFIT1 IL18 IL21R JUN MTHFD2 OAS3 SLC2A3

	TP63	-0.99	Activated	0.0022	0.029	ADA ADAMTS1 ADM ARAF BMP7 CAVIN2 CDKN1A DLL1 <b>EMP1</b> EPHA2 FN1 <b>FOS</b> FOXD4L3/FOXD4L6 FUBP1 GADD45A HAGH HESS ITGA7 LIN28A <b>MAFF</b> MLPH NT5E P2RY2 SERPINE1 SFN SLC2A3 TGFB3 THBS1 TNFRSF10A TNFRSF10B TNFRSF1A TNFSF10 TOP2A TRAF2 UBE2H
	TGFA	0.027	Activated	0.0032	0.0356	BIRC5 CDKN1A CEBPB CXCL10 ERRF1 <b>FOS</b> IGFBP4 NES PECAM1 SERPINE1
	CAV1	-0.034	Activated	0.0046	0.0445	ADAMTS4 CDKN1A CRNKL1 FGF2 <b>FOS</b> NOS3 SERPINE1 SLC2A3 SLC7A2 THBS1 TJP1 TJP2 TNFRSF1A TRAF2
	SCD	-0.10	Inhibited	0.0051	0.0483	ACADVL ANGPTL4 CEBPB CXCL10 DDIT3 GADD45A GPAM XBP1
	IFNB1	-0.76	Inhibited	0.0058	0.0497	CAPN2 CDKN1A CRYAB CXCL10 DLL1 FGF2 <b>FOS</b> GBP4 GLIS2 <b>GLP2R</b> IFIT1 IL18 IL1R1 NOCT PRDM1 RASSF1 RSAD2 SLC39A14 THBS1 TLR3 TNFRSF10A TNFSF10 VCL
dIPFC-orange Regulators	IL1B	1.41	Activated	1.05E-17	7.35E-15	ANGPTL4 ATF3 CDKN1A CEBPD DLL4 <b>EDN1</b> EFNA1 EPAS1 GADD45A GADD45B GEM HBEGF HELZ2 ICAM1 IL1B IRAK3 JUN MCL1 MT2A NAMPT NEAT1 NFIL3 NFKBIA PLSCR1 RELA RHOB SELE SLC2A1 SOCS3 SRGN STAT3 THBD ZFP36
	MYC	0.0060		3.06E-10	2.00E-08	CDK2 CDKN1A CEBPD COL4A1 COL4A2 <b>EDN1</b> <b>EMP1</b> EPHA2 GADD45A GADD45B ICAM1 JUN LIMS1 MCL1 MSN NFKBIA PECAM1 PLAUR PLSCR1 RHOB SAT1 SLC11A1 SLC2A1 SMAD1 STAT3 TES ZFP36
	TNFRSF1A	0.42	Activated	2.09E-08	0.000000729	CDKN1A EFNA1 ICAM1 IL1B JUN RELA SELE SOCS3 THBD TNFRSF1A
	NUPR1	-0.19	Activated	7.00E-07	1.29E-05	ATF3 BTG1 CDK2 GADD45A HBEGF HILPDA LMNB1 MT1X NFIL3 PXDC1 RAB20 RNF122 SAT1 SLC2A1

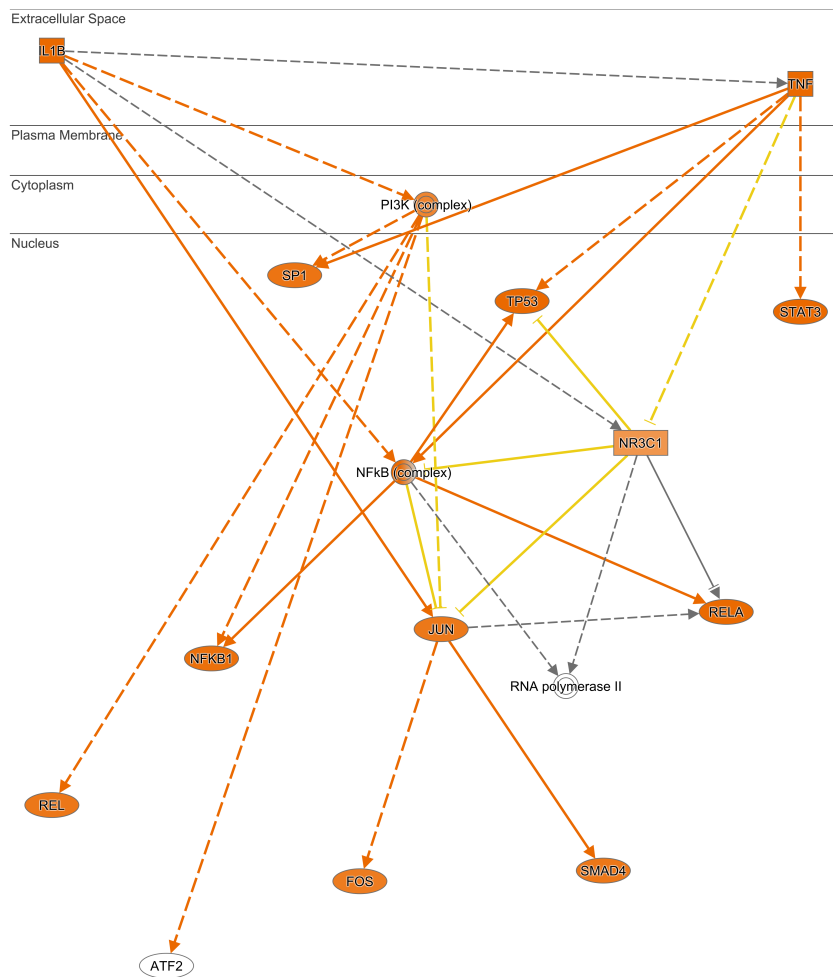
**Supplementary Figure 1:** QQ Plots of the PTSD associations in the dlPFC and vmPFC and in the full cohort and in the stratified analyses.



**Supplementary Figure 2:** Association with PTSD and depression in both brain regions and in stratified analyses for all Genes with corrected significant associations with PTSD (Table 3).



**Supplementary Figure 3.** The dIPFC-orange Upstream Regulator Analysis: *IL1B* as an activated upstream regulator in dIPFC-orange module interacting with other regulators such *NR3C1* (GR gene).





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