

Public Transcriptomic Data Meta-Analysis Demonstrates TAAR6 Expression in the Mental Disorder-Related Brain Areas in Human and Mouse Brain

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Table S1. Human transcriptomic GEO datasets meeting the inclusion criteria and included in the analysis.

Accession Number	Title	Samples	Link
GSE53239	RNA-sequencing of the brain transcriptome implicates dysregulation of neuroplasticity, circadian rhythms, and GTPase binding in bipolar disorder	Dorsolateral prefrontal cortex	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE53239
GSE53697	RNAseq in Alzheimer's Disease patients	Dorsolateral prefrontal cortex	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE53697
GSE110727	Characterization of the nuclear and cytosolic transcriptomes in human brain tissue	Frontal cortex	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE110727
GSE123496	Human brain tissues from healthy controls and multiple sclerosis patients	Parietal cortex	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE123496
		Frontal cortex	
		Corpus callosum	
		Internal capsule	
		Hippocampus	
GSE124439	Postmortem Cortex Samples Identify Distinct Molecular Subtypes of ALS: Retrotransposon Activation, Oxidative Stress, and Activated Glia	Frontal cortex	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE124439
		Motor cortex	
GSE160521	Diurnal rhythms across the human dorsal and ventral striatum	Nucleus accumbens	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE160521
		Nucleus caudatus	
		Putamen	

Table S2. Mouse transcriptomic GEO datasets meeting the inclusion criteria and included in the analysis.

Accession Number	Title	Samples	Study Groups
GSE107183	RNA changes in hippocampus of transgenic murine model of tauopathy (rTg4510 mice) compared to controls at asymptomatic stage (2 months) of neurodegeneration as determined by mRNA deep sequencing.	Hippocampus	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE107183
GSE112575	Frontal cortex transcriptomic analysis of a TDP-43 Q331K knock-in mouse [20month]	Frontal cortex	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE112575
GSE116752	Striatal transcriptome of a mouse model of ADHD reveals a pattern of synaptic remodeling	Striatum	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE116752
GSE126814	Quantitative Analysis of Wild Type and Neat1 -/- Cerebral Frontal Cortex Transcriptomes	Frontal cortex	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE126814
GSE130254	Regional Analysis of The Brain Transcriptome In Mice Bred For High And Low Methamphetamine Consumption	Prefrontal cortex	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE130254
		Nucleus accumbens	
		Ventral Midbrain	

GSE136869	Transcriptome analysis using RNA sequencing of the hippocampus of aged LPAR2-/- versus wildtype control mice	Hippocampus	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE136869
GSE146628	Identification of Natural Antisense Transcripts in Mouse Brain and Their Association with Autism Spectrum Disorder Risk Genes	Prefrontal cortex Striatum	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE146628
GSE147842	Adult mouse hippocampal transcriptome changes associated with long-term behavioral and metabolic effects of gestational air pollution toxicity	Hippocampus	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE147842
GSE148075	Wild mice with different social network sizes vary in brain gene expression	Prefrontal cortex Hippocampus Hypothalamus	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE148075
GSE166831	Altered hippocampal transcriptome dynamics following sleep deprivation	Hippocampus	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE166831
GSE170997	Transcriptomics data of blood and brain from the YAC128 Huntington's disease mouse model [brain]	Cerebellum Striatum	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE170997
GSE99353	Frontal cortex transcriptomic analysis of a TDP-43 Q331K knock-in mouse [5month]	Frontal cortex	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE99353

Table S3. Datasets for the specific cellular or subcellular fractions included in the review.

Accession Number	Title	Samples	Link
GSE110727	Characterization of the nuclear and cytosolic transcriptomes in human brain tissue	Frontal cortex (human)	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE110727
GSE121199	Biology and Bias in Cell Type-Specific RNAseq of Nucleus Accumbens Medium Spiny Neurons	Nucleus accumbens (mouse)	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE121199
GSE130376	Next-generation sequencing of cholinergic interneurons in the nucleus accumbens of cocaine-addicted and non-addicted mice	Nucleus accumbens (mouse)	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE130376

Figure S1. Full-length agarose gel: reverse transcription-polymerase chain reaction (RT-PCR) with mouse TAAR6 and GAPDH (housekeeping gene) specific primers using RNA isolated from the prefrontal cortex (lanes 1-6 for TAAR6, 7-12 for GAPDH) and olfactory bulb (lanes 15-20 for TAAR6, and 21-26 for GAPDH) of 6 male animals confirmed TAAR6 mRNA expression. Amplicons from olfactory epithelium cDNA (lane 13) and plasmid containing mouse Taar6 gene sequence (lane 14) were included as primer specificity controls. Negative control is K-, DNA ladder is M (Evrogen, #NL003). Red is a source of cropped image. Gel Doc XR+ Documentation System (Bio-Rad) was used for agarose EtBr-stained gel analysis. Time of imaging exposure was 0.936 sec.



