Supplementary Figures and Tables

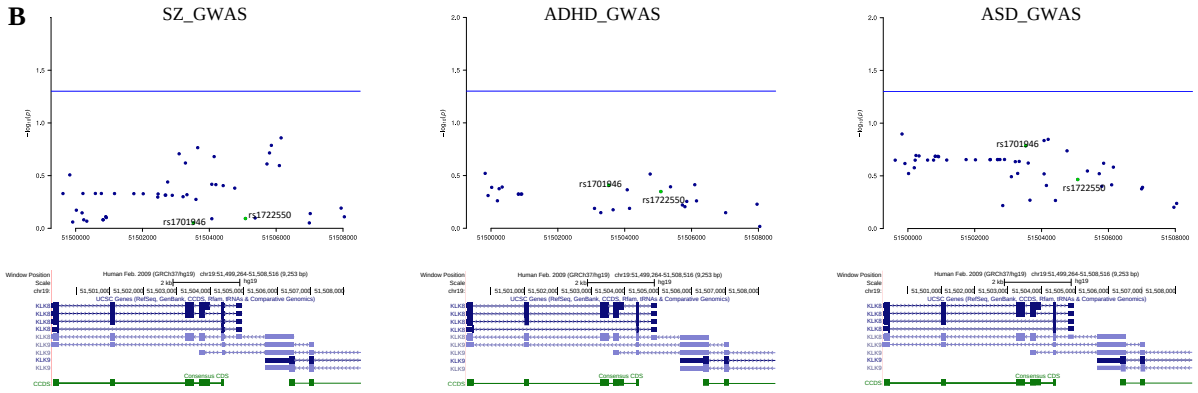
Supplementary Table A.1: *KLK8* expression in human brain single cells. Summarized are *KLK8* expression data from several studies [1-4] and databases [5-7]. Shown are fractions of cells with *KLK8* expression counts (in ‰) in neuronal as well as non-neuronal cells in several tissues and developmental stages.

	Tissue	Developmental stage of donors	Number of nuclei	Fraction of cells with *KLK8* counts (‰)			
				Neuronal		Non-neuronal	Unclassified
				Excitatory	Inhibitory		
Allen Brain Atlas	Primary visual cortex	Adult	8998	4 /8063 (0.50)		0/935	-
	Anterior Cingulate Cortex	Adult	7283	-	-	-	-
	Middle temporal gyros	Adult	15928	37/10525 (3.52)	8/4164 (1.92)	1/914 (1.09)	-
GTEX	Prefrontal cortex	Adult	5932	-	-	-	-
	Hippocampus	Adult	9036	0/3501	0/1061	0/3773	6/701 (8.56)
Linnarsson et al.	Ventral midbrain	Embryo	1977	-	-	-	-
	Middle temporal gyrus cortex	Adult	2028	-	-	-	-
Zhong et al.	Prefrontal cortex	Embryo	2309	-	-	-	-
Darmanis et al.	Temporal lobe	Adult and fetal	466	5/122 (40.98)		1/206 (4.85)	0/138
PsychEncode	Neocortex	Fetal	115	1/40 (25)	0/28	0/47	-
	Frontal cortex	Fetal	249	0/69	2/38 (52.63)	1/142 (7.04)	-
	Pallium	Fetal	398	0/0	2/143 (13.98)	2/255 (7.84)	-
	Frontal cortex	Adult	17093	0/8957	0/3721	0/4415	-

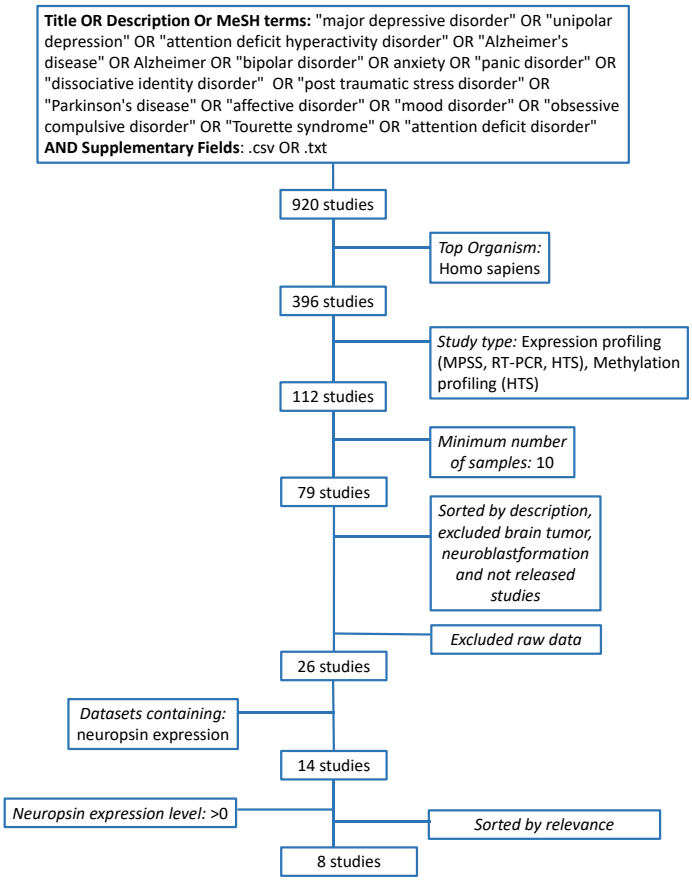
A

	MDD PGC + UKB		BD PGC		SZ PGC		ASD iPSYCH		ADHD iPSYCH	
SNP	OR	P	OR	P	OR	P	OR	P	OR	P
rs1722550	0.985	0.065	0.998	0.868	1.005	0.653	0.984	0.343	0.988	0.449
rs1701946	0.986	0.074	1.009	0.498	1.002	0.889	0.977	0.163	0.986	0.391
rs1612902*	0.986	0.086	1.006	0.678	1.003	0.807	0.984	0.306	0.987	0.407

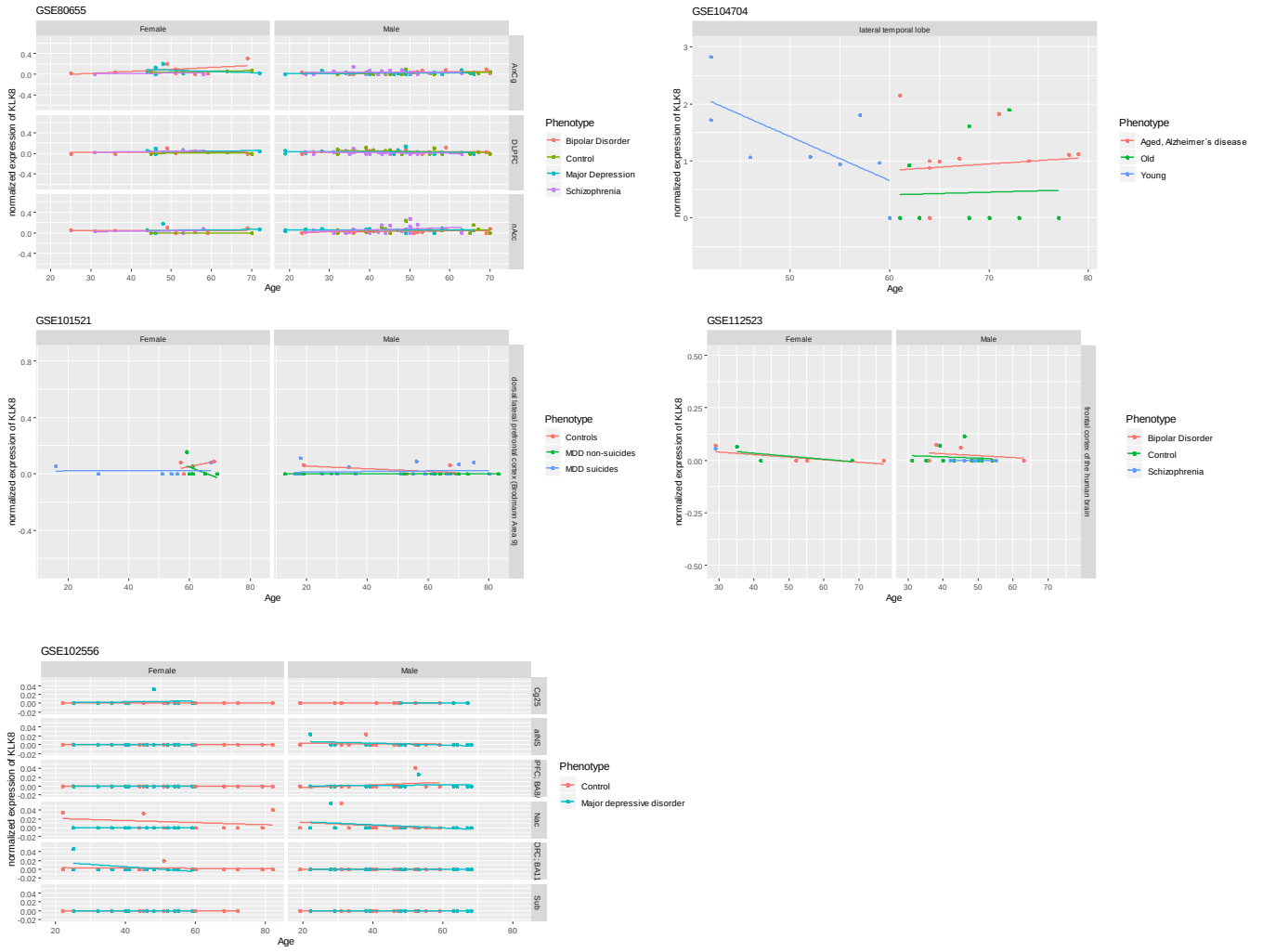
B



Supplementary Figure A.1: Single nucleotide polymorphisms (SNPs) associated with mental disorders. **A)** In the currently largest genome-wide association studies (GWASs) no significant association has been found between variants in the *KLK8* locus and the mental disorders major Schizophrenia (SZ), autism spectrum disorder (ASD) or attention deficit hyperactivity disorder (ADHD) [8-10]. However, three SNPs identified in a genotyping assay [11] show an association with BD and are depicted here in the context of GWAS data. **B)** Shown are SNPs identified in GWASs in relation to the UCSC genomic sequences of *KLK8* splice variants in blue. Blue line: nominal significant threshold of $p < 0.05$. Asterix indicate SNP located 3' to *KLK8.*



Supplementary Figure A.2: Flowchart describing the dataset search in MEDLINE and GEO. The last three steps in the flowchart describe the downstream workflow in R for identifying studies reporting *KLK8* expression levels in mental disorders.



Supplementary Figure A.3: *KLK8* expression in mental disorders. Shown are *KLK8* expression levels by age in several brain tissues and several mental disorder phenotypes as well as healthy controls from selected studies identified as described in Supplementary Figure A.2. In GSE80655 the transcriptome in 281 clinically annotated human post-mortem brain tissues has been measured. GSE104704 compared the genome-wide enrichment of H4K16ac in the lateral temporal lobe of AD individuals against both younger and elderly cognitively normal controls. GSE101521 conducted whole-transcriptome brain expression profiling in MDD and suicide. GSE112523 studied DNA methylation in neurons from post-mortem brains in SZ and BD and GSE102556 combined differential expression and gene co-expression network analyses to provide a comprehensive characterization of male and female transcriptional profiles associated with MDD across six brain regions. Screening of the data from those studies did not reveal significant differences in *KLK8* expression levels between MDD, BD or SZ patients and healthy controls.

References:

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