Supplementary Table 1_Sample data and sequencing template
METADATA TEMPLATE

 # High-throughput sequencing metadata template. (Version: April 28, 2020)
 # All fields in this template must be completed.
 # See METADATA EXAMPLES in tabs at the foot of this page.
 # Field names in blue on this sheet should not be edited. Hover over cells containing field names to view field content guidelines.
 # Human data. If there are patient privacy concerns regarding making data fully public through GEO, please submit to NCBI's dbGaP (http://www.ncbi.nlm.nih.gov/gap/) database. dbGaP has controlled access mechanisms and is an appropriate resource for hosting sensitive patient data.

SERIES
This section describes the overall study. Complete all fields.

title	Diverse human astrocyte and microglial transcriptional responses to Alzheimer's pathology
summary	To better define roles that astrocytes and microglia play in Alzheimer's disease (AD), we used single-nuclei RNA sequencing to comprehensively characterize transcriptomes in astrocyte and microglia nuclei isolated post-mortem from neuropathologically-defined AD and control brains with a range of amyloid-beta and phospho-tau (pTau) pathology. Significant differences in glial gene expression (including AD risk genes expressed in astrocytes [CLU, MEF2C, IQCK] and microglia [APOE, MS4A6A, PILRA]) were correlated with tissue amyloid and pTau expression. Astrocytes were enriched for proteostatic, inflammatory and metal ion homeostasis pathways. Pathways for phagocytosis, proteostasis and autophagy were highly enriched in microglia and perivascular macrophages. Gene co-expression analyses revealed potential functional associations of soluble biomarkers of AD in astrocytes (CLU) and microglia (GPNMB). Our work highlights responses of both astrocytes and microglia for pathological protein clearance and inflammation, as well as glial transcriptional diversity in AD.
overall design	Single-nuclei RNA-sequencing of microglia and astrocyte nuclei isolated *post mortem* from non-diseased control and neurodiathological- defined AD brains.
contributor	Amy, M. Smith
contributor	Kanen, Davey
contributor	Skerglos, Tsantsalis
contributor	Combs, Khoozie
contributor	Nunun, Fancy
contributor	See Swee, Tang
contributor	Elvini, Liaptsi
contributor	Maria, Weinert
contributor	Aisling, McGarry
contributor	Robert, C.I. Muirhead
contributor	Steve, Gentleman
contributor	David, R, Owen
contributor	Paul, M, Matthews
supplementary file	

SAMPLES
Thoroughly describe each of the biological Samples under investigation. **Tissue/cell type/cell line** information is required.
 # include all biological and experimental variables in characteristics columns (for example, characteristics: tissue, characteristics: cell type, characteristics: treatment, characteristics: genotype, characteristics: disease state or any clinical variables. etc...)
 # --> KEEP SCROLLING TO THE RIGHT FOR IMPORTANT FIELDS. RAW AND PROCESSED FILES MUST BE LISTED IN THIS SECTION <- #

Sample name	title	source name	organism	characteristics: Disease caterec	characteristics: Braak tangle sta	characteristics: Brain regi	characteristics: Ag	characteristics: Sx	characteristics: RI	characteristics: cTau histosomics	characteristics: Amyloid immuno	molecule	description	processed data file	raw file	raw file
IGF112633	A127/11 SSC	Human post-mortem cortex	Homo sapiens	Non-disease control	0	SSC	73	male	6.3	0.00465811	0.280797	nuclear RNA		IGF112633_filtered_feature_bc_matrix.tar.gz	IGF112633_HISEQ4000_cellranaer_count_HG38_20191005.cram	IGF112633_HISEQ4000_cellranaer_count_HG38_20191005.cram.crai
IGF112634	A053/11 SSC	Human post-mortem cortex	Homo sapiens	Non-disease control	0	SSC	77	male	6.7	0.01438067	0.3253	nuclear RNA		IGF112634_filtered_feature_bc_matrix.tar.gz	IGF112634_HISEQ4000_cellranaer_count_HG38_20191006.cram	IGF112634_HISEQ4000_cellranaer_count_HG38_20191006.cram.crai
IGF112635	A282/14 SSC	Human post-mortem cortex	Homo sapiens	AD	3	SSC	68	female	8.1	0.01427371	0.329722	nuclear RNA		IGF112635_filtered_feature_bc_matrix.tar.gz	IGF112635_HISEQ4000_cellranaer_count_HG38_20191005.cram	IGF112635_HISEQ4000_cellranaer_count_HG38_20191005.cram.crai
IGF112636	A127/11 EC	Human post-mortem cortex	Homo sapiens	Non-disease control	0	EC	73	male	6	0.01023607	0.331774	nuclear RNA		IGF112636_filtered_feature_bc_matrix.tar.gz	IGF112636_HISEQ4000_cellranaer_count_HG38_20191005.cram	IGF112636_HISEQ4000_cellranaer_count_HG38_20191005.cram.crai
IGF112637	A282/14 EC	Human post-mortem cortex	Homo sapiens	AD	3	EC	68	female	8.2	0.2473569	0.995141	nuclear RNA		IGF112637_filtered_feature_bc_matrix.tar.gz	IGF112637_HISEQ4000_cellranaer_count_HG38_20191005.cram	IGF112637_HISEQ4000_cellranaer_count_HG38_20191005.cram.crai
IGF112638	A096/14 SSC	Human post-mortem cortex	Homo sapiens	AD	4	SSC	87	male	6.9	0.176706404	1.52959	nuclear RNA		IGF112638_filtered_feature_bc_matrix.tar.gz	IGF112638_HISEQ4000_cellranaer_count_HG38_20191006.cram	IGF112638_HISEQ4000_cellranaer_count_HG38_20191006.cram.crai
IGF112639	A183/17 SSC	Human post-mortem cortex	Homo sapiens	AD	5	SSC	83	male	7.6	0.081139368	0.357876	nuclear RNA		IGF112639_filtered_feature_bc_matrix.tar.gz	IGF112639_HISEQ4000_cellranaer_count_HG38_20191005.cram	IGF112639_HISEQ4000_cellranaer_count_HG38_20191005.cram.crai
IGF112640	A096/14 EC	Human post-mortem cortex	Homo sapiens	AD	4	EC	87	male	6	0.780064692	0.370786	nuclear RNA		IGF112640_filtered_feature_bc_matrix.tar.gz	IGF112640_HISEQ4000_cellranaer_count_HG38_20191005.cram	IGF112640_HISEQ4000_cellranaer_count_HG38_20191005.cram.crai
IGF112641	A183/17 EC	Human post-mortem cortex	Homo sapiens	AD	5	EC	83	male	7.7	2.597481599	0.821953	nuclear RNA		IGF112641_filtered_feature_bc_matrix.tar.gz	IGF112641_HISEQ4000_cellranaer_count_HG38_20191006.cram	IGF112641_HISEQ4000_cellranaer_count_HG38_20191006.cram.crai
IGF112642	A402/14 SSC	Human post-mortem cortex	Homo sapiens	AD	3	SSC	83	male	6.8	0.052077306	0.717751	nuclear RNA		IGF112642_filtered_feature_bc_matrix.tar.gz	IGF112642_HISEQ4000_cellranaer_count_HG38_20191006.cram	IGF112642_HISEQ4000_cellranaer_count_HG38_20191006.cram.crai
IGF112643	A069/10 SSC	Human post-mortem cortex	Homo sapiens	AD	5	SSC	85	female	7.1	1.559536545	2.58539	nuclear RNA		IGF112643_filtered_feature_bc_matrix.tar.gz	IGF112643_HISEQ4000_cellranaer_count_HG38_20191006.cram	IGF112643_HISEQ4000_cellranaer_count_HG38_20191006.cram.crai
IGF112644	A053/11 EC	Human post-mortem cortex	Homo sapiens	Non-disease control	0	EC	77	male	6.8	0.036788375	0.5444	nuclear RNA		IGF112644_filtered_feature_bc_matrix.tar.gz	IGF112644_HISEQ4000_cellranaer_count_HG38_20191005.cram	IGF112644_HISEQ4000_cellranaer_count_HG38_20191005.cram.crai
IGF112645	A402/14 EC	Human post-mortem cortex	Homo sapiens	AD	3	EC	83	male	6.9	0.1219934	0.987485	nuclear RNA		IGF112645_filtered_feature_bc_matrix.tar.gz	IGF112645_HISEQ4000_cellranaer_count_HG38_20191006.cram	IGF112645_HISEQ4000_cellranaer_count_HG38_20191006.cram.crai
IGF112646	A069/10 EC	Human post-mortem cortex	Homo sapiens	AD	5	EC	85	female	6.6	1.883831427	1.76422	nuclear RNA		IGF112646_filtered_feature_bc_matrix.tar.gz	IGF112646_HISEQ4000_cellranaer_count_HG38_20191006.cram	IGF112646_HISEQ4000_cellranaer_count_HG38_20191006.cram.crai
IGF112647	A297/16 SSC	Human post-mortem cortex	Homo sapiens	Non-disease control	1	SSC	81	male	2.7	0.029022244	0.374616	nuclear RNA		IGF112647_filtered_feature_bc_matrix.tar.gz	IGF112647_HISEQ4000_cellranaer_count_HG38_20191005.cram	IGF112647_HISEQ4000_cellranaer_count_HG38_20191005.cram.crai
IGF112648	A297/16 EC	Human post-mortem cortex	Homo sapiens	Non-disease control	1	EC	81	male	3.4	0.0390994	0.513866	nuclear RNA		IGF112648_filtered_feature_bc_matrix.tar.gz	IGF112648_HISEQ4000_cellranaer_count_HG38_20191005.cram	IGF112648_HISEQ4000_cellranaer_count_HG38_20191005.cram.crai
IGF112649	A159/11 EC	Human post-mortem cortex	Homo sapiens	Non-disease control	1	EC	74	male	4.6	0.0386497	1.38521	nuclear RNA		IGF112649_filtered_feature_bc_matrix.tar.gz	IGF112649_HISEQ4000_cellranaer_count_HG38_20191006.cram	IGF112649_HISEQ4000_cellranaer_count_HG38_20191006.cram.crai
IGF112650	A277/12 SSC	Human post-mortem cortex	Homo sapiens	AD	6	SSC	79	male	7.7	1.70910729	3.65359	nuclear RNA		IGF112650_filtered_feature_bc_matrix.tar.gz	IGF112650_HISEQ4000_cellranaer_count_HG38_20191006.cram	IGF112650_HISEQ4000_cellranaer_count_HG38_20191006.cram.crai
IGF112651	A277/12 EC	Human post-mortem cortex	Homo sapiens	AD	6	EC	79	male	6.3	3.790909878	1.94764	nuclear RNA		IGF112651_filtered_feature_bc_matrix.tar.gz	IGF112651_HISEQ4000_cellranaer_count_HG38_20191006.cram	IGF112651_HISEQ4000_cellranaer_count_HG38_20191006.cram.crai
IGF112652	A159/11 SSC	Human post-mortem cortex	Homo sapiens	Non-disease control	1	SSC	74	male	6.3	0	0.854616	nuclear RNA		IGF112652_filtered_feature_bc_matrix.tar.gz	IGF112652_HISEQ4000_cellranaer_count_HG38_20191006.cram	IGF112652_HISEQ4000_cellranaer_count_HG38_20191006.cram.crai
IGF112653	PDC016 SSC	Human post-mortem cortex	Homo sapiens	Non-disease control	1	EC	91	female	6.6	0.863503	0.821825	nuclear RNA		IGF112653_filtered_feature_bc_matrix.tar.gz	IGF112653_HISEQ4000_cellranaer_count_HG38_20191006.cram	IGF112653_HISEQ4000_cellranaer_count_HG38_20191006.cram.crai
IGF112654	PDC016 SSC	Human post-mortem cortex	Homo sapiens	Non-disease control	1	SSC	91	female	7.9	0.0628815	0.226991	nuclear RNA		IGF112654_filtered_feature_bc_matrix.tar.gz	IGF112654_HISEQ4000_cellranaer_count_HG38_20191007.cram	IGF112654_HISEQ4000_cellranaer_count_HG38_20191007.cram.crai
IGF112655	PDC026 EC	Human post-mortem cortex	Homo sapiens	Non-disease control	1	EC	80	female	4.1	0.457716	0.454358	nuclear RNA		IGF112655_filtered_feature_bc_matrix.tar.gz	IGF112655_HISEQ4000_cellranaer_count_HG38_20191007.cram	IGF112655_HISEQ4000_cellranaer_count_HG38_20191007.cram.crai
IGF112656	PDC026 SSC	Human post-mortem cortex	Homo sapiens	Non-disease control	1	SSC	80	female	5.3	0.040833	0.059688	nuclear RNA		IGF112656_filtered_feature_bc_matrix.tar.gz	IGF112656_HISEQ4000_cellranaer_count_HG38_20191006.cram	IGF112656_HISEQ4000_cellranaer_count_HG38_20191006.cram.crai

PROTOCOLS
Protocols applicable to only a subset of Samples can be included as additional columns of the SAMPLES section above instead.

growth protocol	
treatment protocol	Post-mortem delay < 24hr. Grey matter isolated (white matter removed).
extract protocol	Nuclei were isolated from fresh frozen cortical grey matter from AD and control brains using a protocol based on Krishnaswami et al. (2016). Single-nuclei capture was performed using 10X Genomics Single Cell Gene Expression kit v3
library construction protocol	10X Genomics Single Cell 3' Gene Expression kit v3
library strategy	RNASeq

DATA PROCESSING PIPELINE
Data processing steps include base-calling, alignment, filtering, peak-calling, generation of normalized abundance measurements etc...
For each step provide a description, as well as software name, version, parameters, if applicable.

data processing step	Illumina sequencing files were aligned to the genomic sequence (introns and exons) using GRCh38 (gencode v30) annotation in Cell Ranger v3.0.2
data processing step	
data processing step	
data processing step	
data processing step	
genome build	GRCh38_gencode_v30_pre_mRNA
processed data files format and content	Filtered Feature-Barcode Matrix Generated by Cell Ranger Version 3.0.2

For each file listed in the "processed data file" columns of the SAMPLES section, provide additional information below.

PROCESSED DATA FILES

file name	file type	file checksum
IGF112633_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	b35d913a38dc5e6672f5ac6ae7.3380e8
IGF112634_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	590cea82e65ec758a2.2187d2502.2f3b
IGF112635_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	9fbd50752cd33d7209ab94e9da3ba259
IGF112636_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	3b4924954fdd0f2e03c5543352fd4e41b
IGF112637_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	d9ec55da48a3e1b7453308be6e8d51952
IGF112638_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	728baf30d8e4740a3bbe75d33c4d7b49
IGF112639_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	a2fef305d4090f2f65e2dc908ff72c7c
IGF112640_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	1ec5363a5921f2345da0b90f7f3d7211
IGF112641_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	254416ef1988ba2180561349 1a95fdfa1
IGF112642_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	1d3fe03a27afd5f4479b0e2695c33da76
IGF112643_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	de5ce73954597af9d5f39fc2e74842fc
IGF112644_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	e712378fa4f780b947b459e4f82bf3cb
IGF112645_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	5a86160bac1d7c24e57428f5b21c4a8b
IGF112646_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	5bda611d2e5768735c0ea2e5d8f5914e
IGF112647_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	ecea0ca8d8a3135f0097ec4df5729a34b
IGF112648_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	723675be535c3d826fd03ba68a8c7
IGF112649_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	161d46a1d3365ea5b334398b6db2cf9
IGF112650_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	31d8f85ef0479f05de8556712d48a23d
IGF112651_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	398d8aac663eb61433fbdd25d33f23de9
IGF112652_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	00c6ae2d47c9b1cdf8d3e0f05c1e18
IGF112653_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	39b0a7ecff7f36fcee9abc529463c0b0
IGF112654_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	823507ca1159f97f4d4bf5ec4bb64
IGF112655_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	12470d8f8b7aec37ade1453889d2fe4
IGF112656_filtered_feature_bc_matrix.tar.gz	Filtered Feature-Barcode Matrix	2f206664e6a9464e55bf7223c3dd25e

For each file listed in the "raw file" columns of the SAMPLES section above, provide additional information below.

RAW FILES

file name	file type	file checksum
IGF112633_HISEQ4000_cellranger_count_HG38_20191005.cram.crai	CRAM Index	54c4f7e8071057362f3fdb8f9161ac18
IGF112633_HISEQ4000_cellranger_count_HG38_20191005.cram	CRAM	d76a31793207f03990fe9f0f2a6f20357
IGF112634_HISEQ4000_cellranger_count_HG38_20191006.cram	CRAM	bd7b1777fe4da8e12e8f9fbf5f8f9f4d
IGF112634_HISEQ4000_cellranger_count_HG38_20191006.cram.crai	CRAM Index	407c5c57e82c3e9aa7956f01a0949f7a1d
IGF112635_HISEQ4000_cellranger_count_HG38_20191005.cram.crai	CRAM Index	4375dc9e9ede4ea2f3fd4f08c76be86c
IGF112635_HISEQ4000_cellranger_count_HG38_20191005.cram	CRAM	a0988b72f329a83ae42cea2e46e7e3a
IGF112636_HISEQ4000_cellranger_count_HG38_20191005.cram.crai	CRAM Index	a8e0fe8f0374f17ff667bc3b773a65
IGF112636_HISEQ4000_cellranger_count_HG38_20191005.cram	CRAM	d40ae9d8dbc4e60ae63f297 2f3564f0a1
IGF112637_HISEQ4000_cellranger_count_HG38_20191005.cram.crai	CRAM Index	2958ce616c49f2f2f34e9f61bbe7fde6a
IGF112637_HISEQ4000_cellranger_count_HG38_20191005.cram	CRAM	af497bcc513932c1bbaa05fca9d07dc3
IGF112638_HISEQ4000_cellranger_count_HG38_20191006.cram.crai	CRAM Index	846c4183aea3e5bc35995fab24b4be3
IGF112638_HISEQ4000_cellranger_count_HG38_20191006.cram	CRAM	bb57633fdce97d68f52f17fdfc1d043c
IGF112639_HISEQ4000_cellranger_count_HG38_20191005.cram.crai	CRAM Index	513ffccc5d5f9b7484ff7ee78331deac8
IGF112639_HISEQ4000_cellranger_count_HG38_20191005.cram	CRAM	e47bbd0c4b934faf7a7e94c6f96f55
IGF112640_HISEQ4000_cellranger_count_HG38_20191005.cram.crai	CRAM Index	e94ccc3272f84d9d8302dd6a1f9f28b
IGF112640_HISEQ4000_cellranger_count_HG38_20191005.cram	CRAM	3bb7f295ccc8a9e30e4f3ef3265f3fd5
IGF112641_HISEQ4000_cellranger_count_HG38_20191006.cram.crai	CRAM Index	6d43c5f735d85c27be5b0d5d6b47f3c
IGF112641_HISEQ4000_cellranger_count_HG38_20191006.cram	CRAM	69a879f2f0f253d3093ff582ee0ab75f
IGF112642_HISEQ4000_cellranger_count_HG38_20191006.cram.crai	CRAM Index	5d3667f09e452033ce54d39a6e6e6d
IGF112642_HISEQ4000_cellranger_count_HG38_20191006.cram	CRAM	92b40682683b5daa24c5c94 2fef567fb3
IGF112643_HISEQ4000_cellranger_count_HG38_20191006.cram.crai	CRAM Index	c13bb12d4263be0f9f52ba8a2b6f6917
IGF112643_HISEQ4000_cellranger_count_HG38_20191006.cram	CRAM	13ddb5f4971a8243eed5bcf4deaa9d9
IGF112644_HISEQ4000_cellranger_count_HG38_20191006.cram.crai	CRAM Index	6bf6956464607937bea13ecc6d6fdd5
IGF112644_HISEQ4000_cellranger_count_HG38_20191006.cram	CRAM	13bcd0d1d1bb7e828a4cb07e577 764d8
IGF112645_HISEQ4000_cellranger_count_HG38_20191005.cram.crai	CRAM Index	e5bfd778dc77e419ce3c65e5e54ea37a
IGF112645_HISEQ4000_cellranger_count_HG38_20191005.cram	CRAM	70fd018bff31f025f85e5e6d5a8762.1be
IGF112646_HISEQ4000_cellranger_count_HG38_20191006.cram.crai	CRAM Index	1d57bf7fb3723be2 75e0328 6b6f2b5f85
IGF112646_HISEQ4000_cellranger_count_HG38_20191006.cram	CRAM	997640678851152bfe800ed2ce238b61
IGF112647_HISEQ4000_cellranger_count_HG38_20191005.cram.crai	CRAM Index	d0ca2958f2180f43f6b980f03e8b34e
IGF112647_HISEQ4000_cellranger_count_HG38_20191005.cram	CRAM	52a3c96ea2c3814f98d3e2d4be176154
IGF112648_HISEQ4000_cellranger_count_HG38_20191006.cram.crai	CRAM Index	537 7a3abf5710f04257536ade6d47c7e8
IGF112648_HISEQ4000_cellranger_count_HG38_20191006.cram	CRAM	8857ba86969420fc9420aed6833b9b57b
IGF112649_HISEQ4000_cellranger_count_HG38_20191006.cram.crai	CRAM Index	64d3f3e3dbaf7b577795778e66f24f81
IGF112649_HISEQ4000_cellranger_count_HG38_20191006.cram	CRAM	5765988fde7c470bd7ddd4e06314f5db
IGF112650_HISEQ4000_cellranger_count_HG38_20191006.cram.crai	CRAM Index	bbd993fcee8f1f5118bc0f17aba6f89a
IGF112650_HISEQ4000_cellranger_count_HG38_20191006.cram	CRAM	5000d9fe7837518c7129bba0548de5
IGF112651_HISEQ4000_cellranger_count_HG38_20191006.cram.crai	CRAM Index	942abd3a56593bb0874e4702e45ea1be2
IGF112651_HISEQ4000_cellranger_count_HG38_20191006.cram	CRAM	b1764726b8d0519f37a5aace30038179
IGF112652_HISEQ4000_cellranger_count_HG38_20191006.cram.crai	CRAM Index	74f7f74e4827122f3a88e27ee6a823ae8
IGF112652_HISEQ4000_cellranger_count_HG38_20191006.cram	CRAM	6c3fcabc7b4a6435e4f92b7d92f5129e
IGF112653_HISEQ4000_cellranger_count_HG38_20191006.cram.crai	CRAM Index	11eac98d074618bf4a9a2ae229eaf0a8
IGF112653_HISEQ4000_cellranger_count_HG38_20191006.cram	CRAM	d22629ff5686f07f5f94ec5 710de9d5c3
IGF112654_HISEQ4000_cellranger_count_HG38_20191007.cram.crai	CRAM Index	2b23f9053baa5c3161581d1a2f93f36c
IGF112654_HISEQ4000_cellranger_count_HG38_20191007.cram	CRAM	ec05edeee38c59d5fb2f918d9265f40e1
IGF112655_HISEQ4000_cellranger_count_HG38_20191007.cram.crai	CRAM Index	ba01c05a2c9e5e7107fdfaf4ba8b9d
IGF112655_HISEQ4000_cellranger_count_HG38_20191007.cram	CRAM	029dc92cccfac1f36c1f0f05910f16faf
IGF112656_HISEQ4000_cellranger_count_HG38_20191006.cram.crai	CRAM Index	b27de78fc54fe0d1b17c7727961 4f0eee
IGF112656_HISEQ4000_cellranger_count_HG38_20191006.cram	CRAM	1c10e4a6e42dcbd7cd7aac536a8c3e9

For paired-end experiments, list the 2 (or more) fastq files from the same run. For SOLiD experiments, list the 4 file names (include "file name 3" and "file name 4" columns).

PAIRED-END EXPERIMENTS

file name 1	file name 2

instrument ex: single or paired-end

Supplementary Table 1_Sample data and sequencing template
EXAMPLE 1

 # High-throughput sequencing metadata template.
 # All fields in this template must be completed.
 # See METADATA EXAMPLES in tabs at the foot of this page.
 # Field names (in blue on this page) should not be edited. Hover over cells containing field names to view field content guidelines.
 # Human data. If there are patient privacy concerns regarding making data fully public through GEO, please submit to NCBI's dbGaP (http://www.ncbi.nlm.nih.gov/gap/) database. dbGaP has controlled access mechanisms and is an appropriate resource for hosting sensitive patient data.

SERIES
This section describes the overall study. Complete all fields.

title	Genome-wide maps of chromatin state in pluripotent and lineage-committed cells.
summary	We report the application of single-molecule-based sequencing technology for high-throughput profiling of histone modifications in mammalian cells. By obtaining over four billion bases of sequence from chromatin immunoprecipitated DNA, we generated genome-wide chromatin-state maps of mouse embryonic stem cells, neural progenitor cells and embryonic fibroblasts. We find that lysine 4 and lysine 27 trimethylation effectively discriminates genes that are expressed, poised for expression, or stably repressed, and therefore reflect cell state and lineage potential. Lysine 36 trimethylation marks primary coding and non-coding transcripts, facilitating gene annotation. Trimethylation of lysine 9 and lysine 20 is detected at satellite, telomeric and active long-terminal repeats, and can spread into proximal unique sequences. Lysine 4 and lysine 9 trimethylation marks imprinting control regions. Finally, we show that chromatin state can be read in an allele-specific manner by using single nucleotide polymorphisms. This study provides a framework for the application of comprehensive chromatin profiling towards characterization of diverse mammalian cell populations.
overall design	Examination of 2 different histone modifications in Neural progenitor cells.
contributor	John,B,Goode
contributor	Bradley,Smith
supplementary file	

SAMPLES
Thoroughly describe each of the biological Samples under investigation. **Tissue/cell type/cell line** information is required.
 # Include all biological and experimental variables in characteristics columns (for example, characteristics: tissue, characteristics: cell type, characteristics: treatment, characteristics: genotype, characteristics: disease state or any clinical variables, etc...)
 # -> -> KEEP SCROLLING TO THE RIGHT FOR IMPORTANT FIELDS; RAW AND PROCESSED FILES MUST BE LISTED IN THIS SECTION -> ->

Sample name	title	source name	organism	characteristics: cell type	characteristics: strain	characteristics: ChIP antibody	characteristics: treatment	characteristics: cell line	molecule	description	processed data file	processed data file	raw file	raw file
Sample 1	Neural progenitor cells - H3K4me2_rep1	Neural progenitor cells	Mus musculus	ES-derived neural progenitor cells	C57BL/6	H3K4me2 (Millipore, 07-030, lot 12	untreated		genomic DNA		H3K4me2.peaks_rep1.txt	H3K4me2_rep1.wig	080716_BI-EAS46_0001_209DH_L1.fastq.gz	
Sample 2	Neural progenitor cells - H3K4me2_rep2	Neural progenitor cells	Mus musculus	ES-derived neural progenitor cells	C57BL/6	H3K4me2 (Millipore, 07-030, lot 12	untreated		genomic DNA		H3K4me2.peaks_rep2.txt	H3K4me2_rep2.wig	080716_BI-EAS46_0001_209DH_L4.fastq.gz	
Sample 3	Neural progenitor cells - input DNA	Neural progenitor cells	Mus musculus	ES-derived neural progenitor cells	C57BL/6	none	untreated		genomic DNA			H3K4me2_input.wig	080717_BI-EAS46_0001_20DH_L5.fastq.gz	
Sample 4	Neural progenitor cells - H3K4me2 - ABX-treated	Neural progenitor cells	Mus musculus	ES-derived neural progenitor cells	C57BL/6	H3K4me2 (Millipore, 07-030, lot 12	treated with ABX for 24 hours		genomic DNA		H3K4me2.peaks_ABX.txt	H3K4me2_rABX.wig	080716_BI-EAS46_0001_209DH_L6.fastq.gz	

PROTOCOLS
Protocols applicable to only a subset of Samples can be included as additional columns of the SAMPLES section above instead.

growth protocol	ES cell–derived NS cells were routinely generated by re-plating d 7 adherent neural differentiation cultures (typically 2–3 × 106 cells into a T75 flask) on uncoated plastic in NS-A medium (Euroclone, Milan, Italy) supplemented with modified N2 and 10 ng/ml of both EGF and FGF-2 (NS expansion medium).
treatment protocol	One replicate was ABX treated for 24 hours.
extract protocol	Lysates were clarified from sonicated nuclei and histone-DNA complexes were isolated with antibody.
library construction protocol	Libraries were prepared according to Illumina's instructions accompanying the DNA Sample Kit (Part# 0801-0303). Briefly, DNA was end-repaired using a combination of T4 DNA polymerase, E. coli DNA Pol I large fragment (Klenow polymerase) and T4 polynucleotide kinase. The blunt, phosphorylated ends were treated with Klenow fragment (32 to 52 exo minus) and dATP to yield a protruding 3- 'A' base for ligation of Illumina's adapters which have a single 'T' base overhang at the 3' end. After adapter ligation DNA was PCR amplified with Illumina primers for 15 cycles and library fragments of ~250 bp (insert plus adaptor and PCR primer sequences) were band isolated from an agarose gel. The purified DNA was captured on an Illumina flow cell for cluster generation. Libraries were sequenced on the Illumina HiSeq 2500 following the manufacturer's protocols.
library strategy	ChIP-Seq

DATA PROCESSING PIPELINE
Data processing steps include base-calling, alignment, filtering, peak-calling, generation of normalized abundance measurements etc...
For each step provide a description, as well as software name, version, parameters, if applicable.

data processing step	Basecalls performed using CASAVA version 1.4
data processing step	ChIP-seq reads were aligned to the mm9 genome assembly using EasyAlign version 3.2 with the following configurations...
data processing step	Data were filtered using the following specifications...
data processing step	peaks were called using PeaksFind version 2.2 with the following setting: ChIP threshold (0.2), Enrichment Fold (2.5), Rescue Fold (3).
data processing step	
genome build	mm9
processed data files format and content	wig files were generated using ...; Scores represent ...
processed data files format and content	peak text files

For each file listed in the "processed data file" columns of the SAMPLES section, provide additional information below.
PROCESSED DATA FILES

file name	file type	file checksum
H3K4me2.peaks_rep1.txt	peak files	95cf1d1fa509d871b2ef0bb9fd734c3d
H3K4me2.peaks_rep2.txt	peak files	8ec6ee3cce10b970e5bfea4e35cdb231
H3K4me2.peaks_ABX.txt	peak files	f8fcd650914ff1a733956d6d06e8b543
H3K4me2_rep1.wig	wig	604fbb658413c559511eb6ad2bb1472e
H3K4me2_rep2.wig	wig	57cf1d1fa509d871b2ef0bb9fd734c3c
H3K4me2_input.wig	wig	8ec6ee3cce10b970e5bfea4e35cdb231
H3K4me2_rABX.wig	wig	f8fcd650914ff1a733956d6d06e8b543

For each file listed in the "raw file" columns of the SAMPLES section, provide additional information below.
RAW FILES

file name	file type	file checksum	instrument model	single or paired-end
080716_BI-EAS46_0001_209DH_L1.fastq.gz	fastq	6cc6ee3cce10b970e5bfea4e35cdb	Illumina HiSeq 2500	single
080716_BI-EAS46_0001_209DH_L4.fastq.gz	fastq	88ceb0e0d056dda9208a03acf9073	Illumina HiSeq 2500	single
080717_BI-EAS46_0001_20DH_L5.fastq.gz	fastq	f2786fedc5106789a2af4014a0e74f0	Illumina HiSeq 2500	single
080716_BI-EAS46_0001_209DH_L6.fastq.gz	fastq	9a2af4014a0e74f00f2786fedc5106	Illumina HiSeq 2500	single

For paired-end experiments, list the 2 (or more) fastq files from the same run. For SOLID experiments, list the 4 file names (include "file name 3" and "file name 4" columns).
PAIRED-END EXPERIMENTS

file name 1	file name 2

Supplementary Table 1_Sample data and sequencing template
EXAMPLE 2

High-throughput sequencing metadata template.
All fields in this template must be completed.
See METADATA EXAMPLES in tabs at the foot of this page.
Field names (in blue on this page) should not be edited. Hover over cells containing field names to view field content guidelines.
Human data. If there are patient privacy concerns regarding making data fully public through GEO, please submit to NCBI's dbGaP (http://www.ncbi.nlm.nih.gov/gap/) database. dbGaP has controlled access mechanisms and is an appropriate resource for hosting sensitive patient data.

SERIES

This section describes the overall study. Complete all fields.

title	Next Generation Sequencing Facilitates Quantitative Analysis of Wild Type and Nrl-/- Retinal Transcriptomes
summary	Purpose: Next-generation sequencing (NGS) has revolutionized systems-based analysis of cellular pathways. The goals of this study are to compare NGS-derived retinal transcriptome profiling (RNA-seq) to microarray and quantitative reverse transcription polymerase chain reaction (qRT–PCR) methods and to evaluate protocols for optimal high-throughput data analysis
summary	Methods: Retinal mRNA profiles of 21-day-old wild-type (WT) and neural retina leucine zipper knockout (Nrl−/−) mice were generated by deep sequencing, in triplicate, using Illumina GAIIx. The sequence reads that passed quality filters were analyzed at the transcript isoform level with two methods: Burrows–Wheeler Aligner (BWA) followed by ANOVA (ANOVA) and TopHat followed by Cufflinks. qRT–PCR validation was performed using TaqMan and SYBR Green assays
summary	Results: Using an optimized data analysis workflow, we mapped about 30 million sequence reads per sample to the mouse genome (build mm9) and identified 16,014 transcripts in the retinas of WT and Nrl−/− mice with BWA workflow and 34,115 transcripts with TopHat workflow. RNA-seq data confirmed stable expression of 25 known housekeeping genes, and 12 of these were validated with qRT–PCR. RNA-seq data had a linear relationship with qRT–PCR for more than four orders of magnitude and a goodness of fit (R2) of 0.8798. Approximately 10% of the transcripts showed differential expression between the WT and Nrl−/− retina, with a fold change ≥1.5 and p value <0.05. Altered expression of 25 genes was confirmed with qRT–PCR, demonstrating the high degree of sensitivity of the RNA-seq method. Hierarchical clustering of differentially expressed genes uncovered several as yet uncharacterized genes that may contribute to retinal function. Data analysis with BWA and TopHat workflows revealed a significant overlap yet provided complementary insights in transcriptome profiling.
summary	Conclusions: Our study represents the first detailed analysis of retinal transcriptomes, with biologic replicates, generated by RNA-seq technology. The optimized data analysis workflows reported here should provide a framework for comparative investigations of expression profiles. Our results show that NGS offers a comprehensive and more accurate quantitative and qualitative evaluation of mRNA content within a cell or tissue. We conclude that RNA-seq based transcriptome characterization would expedite genetic network analyses and permit the dissection of complex biologic functions.
overall design	Retinal mRNA profiles of 21-day old wild type (WT) and Nrl-/- mice
contributor	Rebecca,A,Smith
contributor	David,Doe
supplementary file	Raw_gene_counts_matrix.txt

SAMPLES

Thoroughly describe each of the biological Samples under investigation. **Tissue/cell type/cell line** information is required.
Include all biological and experimental variables in characteristics columns (for example, characteristics: tissue, characteristics: cell type, characteristics: treatment, characteristics: genotype, characteristics: disease state or any clinical variables, etc...)
-> -> KEEP SCROLLING TO THE RIGHT FOR IMPORTANT FIELDS; RAW AND PROCESSED FILES MUST BE LISTED IN THIS SECTION -> ->

Sample name	title	source name	organism	characteristics: strain	characteristics: tissue	characteristics: age	characteristics: genotype	characteristics: cell line	characteristics: treatmen	molecule	description	processed data file	raw file	raw file
Sample 1	Retina WT rep1	Retina	Mus musculus	C57BL/6	retina	post natal day 21	wild type			total RNA		WT1.txt	080716_BI-EAS46_0001_2	080716_BI-EAS46_0001_209DH_L1_R1.fastq.gz
Sample 2	Retina WT rep2	Retina	Mus musculus	C57BL/6	retina	post natal day 21	wild type			total RNA		WT2.txt	080716_BI-EAS46_0001_2	080716_BI-EAS46_0001_209DH_L2_R1.fastq.gz
Sample 3	Retina Nrl-KO rep1	Retina	Mus musculus	C57BL/6	retina	post natal day 21	Nrl-/-			total RNA		mutant1.txt	080717_BI-EAS46_1.fastq.	080717_BI-EAS46_2.fastq.gz
Sample 4	Retina Nrl-KO rep2	Retina	Mus musculus	C57BL/6	retina	post natal day 21	Nrl-/-			total RNA		mutant2.txt	080718_BI-EAS49_1.fastq.	080718_BI-EAS49_2.fastq.gz

PROTOCOLS

Protocols applicable to only a subset of Samples can be included as additional columns of the SAMPLES section above instead.

growth protocol	
treatment protocol	
extract protocol	Retinas were removed, flash frozen on dry ice, and RNA was harvested using Trizol reagent. Illumina TruSeq RNA Sample Prep Kit (Cat#FC-122-1001) was used with 1 ug of total RNA for the construction of sequencing libraries.
library construction protocol	RNA libraries were prepared for sequencing using standard Illumina protocols
library strategy	RNA-Seq

DATA PROCESSING PIPELINE

Data processing steps include base-calling, alignment, filtering, peak-calling, generation of normalized abundance measurements etc…
For each step provide a description, as well as software name, version, parameters, if applicable.

data processing step	Illumina Casava1.7 software used for basecalling.
data processing step	Sequenced reads were trimmed for adaptor sequence, and masked for low-complexity or low-quality sequence, then mapped to mm8 whole genome using bowtie v0.12.2 with parameters -q -p 4 -e 100 -y -a -m 10 --best --strata
data processing step	Reads Per Kilobase of exon per Megabase of library size (RPKM) were calculated using a protocol from Chepelev et al., Nucleic Acids Research, 2009. In short, exons from all isoforms of a gene were merged to create one meta-transcript. The number of reads falling in the exons of this meta-transcript were counted and normalized by the size of the meta-transcript and by the size of the library.
data processing step	
data processing step	
genome build	mm9
processed data files format and content	tab-delimited text files include FPKM values for each Sample ...
processed data files format and content	Matrix table with raw gene counts for every gene and every sample

For each file listed in the "processed data file" columns of the SAMPLES section, provide additional information below.

PROCESSED DATA FILES

file name	file type	file checksum
WT.txt	abundance measurements	d8fcd650914ff1a733956d6d06e8b091
WT2.txt	abundance measurements	abcdef123456789abc123456789abc
mutant1.txt	abundance measurements	95cf1d1fa509d871b2ef0bb9fd734c3d
mutant2.txt	abundance measurements	0wd6ee3cce10b970e5bfea4e35cdb987
Raw_gene_counts_matrix.txt	raw counts	57cf1d1fa509d871b2ef0bb9fd734c3c

For each file listed in the "raw file" columns of the SAMPLES section, provide additional information below.

RAW FILES

file name	file type	file checksum	instrument model	single or paired-end
080716_BI-EAS46_0001_209DH_L1_R1.fast	fastq	6cc6ee3cce10b970e5bfea4	Illumina HiSeq 2000	paired-end
080716_BI-EAS46_0001_209DH_L1_R2.fast	fastq	88ceb0e0d056dda9208a03	Illumina HiSeq 2000	paired-end
080716_BI-EAS46_0001_209DH_L2_R1.fast	fastq	f2786fedc5106789a2af401	Illumina HiSeq 2000	paired-end
080716_BI-EAS46_0001_209DH_L2_R2.fast	fastq	d8fcd650914ff1a733956d6	Illumina HiSeq 2000	paired-end
080717_BI-EAS46_1.fastq.gz	fastq	03839cca2e797b28b9f937	Illumina HiSeq 2000	paired-end
080717_BI-EAS46_2.fastq.gz	fastq	604fbb658413c559511eb6	Illumina HiSeq 2000	paired-end
080718_BI-EAS49_1.fastq.gz	fastq	57cf1d1fa509d871b2ef0bbf	Illumina HiSeq 2000	paired-end
080718_BI-EAS49_2.fastq.gz	fastq	e5718e1a97690d410464f2	Illumina HiSeq 2000	paired-end

For paired-end experiments, list the 2 (or more) fastq files from the same run. For SOLiD experiments, list the 4 file names (include "file name 3" and "file name 4" columns).

PAIRED-END EXPERIMENTS

file name 1	file name 2
080716_BI-EAS46_0001_209DH_L1_R1.fast	080716_BI-EAS46_0001_209DH_L1_R1.fastq.gz
080716_BI-EAS46_0001_209DH_L2_R1.fast	080716_BI-EAS46_0001_209DH_L2_R1.fastq.gz
080717_BI-EAS46_1.fastq.gz	080717_BI-EAS46_2.fastq.gz
080718_BI-EAS49_1.fastq.gz	080718_BI-EAS49_2.fastq.gz

Supplementary Table 2_AUCell gene set enrichment
Contents

Sheet name	Description
Gene sets from literature	Gene sets used in the analyses
AUCell enrichment	Enrichment of literature gene lists in microglia clusters
Ext Data Fig 7 AUC values	Raw AUC enrichment values for Ext Data Fig 7

Analyses were performed using AUCell (R package v1.6.1)

Supplementary Table 2_AUCell gene set enrichment
Gene sets from literature

Supplementary Table 2_AUCell gene set enrichment
AUCell enrichment

Gene List	Comparison Group	Test Group	p.adj	Cohen's d eff_size	Eff_size_term	Lower conf interval	Upper conf interval
Core Microglial Genes (Galatro)	Micro_1	Micro_2	2.10E-132	-0.4044782	(small)	-0.4352231	-0.3737334
Core Microglial Genes (Galatro)	Micro_1	Micro_3	0	-1.451992	(large)	-1.487855	-1.416128
Core Microglial Genes (Galatro)	Micro_1	PVM	3.30E-277	-0.8980096	(large)	-0.9394599	-0.8565594
Aging (Olah)	Micro_1	Micro_2	2.10E-57	0.2705161	(small)	0.2399132	0.3011191
Aging (Olah)	Micro_1	Micro_3	3.00E-47	0.2377403	(small)	0.2049114	0.2705692
Aging (Olah)	Micro_1	PVM	1.40E-43	0.3338133	(small)	0.2933249	0.3743017
DAM (Keren-Shaul)	Micro_1	Micro_2	0	0.7091486	(medium)	0.677877	0.7404203
DAM (Keren-Shaul)	Micro_1	Micro_3	0.000028	-0.06944977	(negligible)	-0.10219857	-0.03670096
DAM (Keren-Shaul)	Micro_1	PVM	5.70E-97	0.5059975	(medium)	0.4653071	0.5466879
ARM (Sala Frigerio)	Micro_1	Micro_2	7.10E-278	0.6517729	(medium)	0.6206217	0.6829242
ARM (Sala Frigerio)	Micro_1	Micro_3	1.10E-161	-0.3972333	(small)	-0.4302185	-0.3642481
ARM (Sala Frigerio)	Micro_1	PVM	2.50E-57	0.4119251	(small)	0.3713552	0.452495
IRM (Sala Frigerio)	Micro_1	Micro_2	4.10E-78	0.3127979	(small)	0.2821561	0.3434396
IRM (Sala Frigerio)	Micro_1	Micro_3	0.021	0.03815325	(negligible)	0.005409667	0.070896833
IRM (Sala Frigerio)	Micro_1	PVM	6.90E-68	0.4270782	(small)	0.3864905	0.4676659
PIG (Chen)	Micro_1	Micro_2	2.70E-17	0.1410731	(negligible)	0.1105541	0.1715922
PIG (Chen)	Micro_1	Micro_3	5.90E-69	-0.2689941	(small)	-0.3018475	-0.2361407
PIG (Chen)	Micro_1	PVM	0.022	0.05432948	(negligible)	0.01399327	0.09466569

Supplementary Table 2_AUCell gene set enrichment
Ext data figure 11 AUC values

Gene List	Micro1	Micro2	Micro3	PVM
DAM (Keren-Shaul)	0.1400868	0.15581126	0.13874868	0.1510533
ARM (Sala Frigerio)	0.03799058	0.04800219	0.03285514	0.0440068
Aging (Olah)	0.04465521	0.04894072	0.04802817	0.04979458
Core Microglial Genes (Galatro)	0.10716635	0.09945952	0.08286285	0.08964665

Supplementary Table 3_DGE enrichment in other datasets
Contents

Sheet name	Description
Astrocyte_DGE	Astrocyte DEG enrichment in samples reported in previous studies
Microglia_DGE	Microglia DEG enrichment in samples reported in previous studies

Terms:

DEGs_amyloid_UP	Genes found to be significantly positively associated with amyloid pathology in astrocytes or microglia (see Supplementary Tables 1 and 2 respectively)
DEGs_amyloid_DOWN	Genes found to be significantly negatively associated with amyloid pathology in astrocytes or microglia (see Supplementary Tables 1 and 2 respectively)
DEGs_ptau_UP	Genes found to be significantly positively associated with pTau pathology in astrocytes or microglia (see Supplementary Tables 1 and 2 respectively)
DEGs_ptau_DOWN	Genes found to be significantly negatively associated with pTau pathology in astrocytes or microglia (see Supplementary Tables 1 and 2 respectively)

Analyses were performed using AUCell and limma (see Methods)

Previous studies:

Grubman et al 2019, doi: 10.1038/s41593-019-0539-4
Mathys et al 2019, doi: 10.1038/s41586-019-1195-2
Zhou et al 2020, doi: 10.1038/s41591-019-0695-9
Gerrits et al 2021, doi: 10.1007/s00401-021-02263-w

Supplementary Table 3_DGE enrichment in other datasets
Astrocyte DGE

Grubman et al 2019	**logFC**	**P.Value**	**adj.P.Val**
DEGs_amyloid_UP	0.43864158	5.80E-112	1.1603E-111
DEGs_amyloid_DOWN	-0.6633103	5.75E-213	2.2991E-212
DEGs_ptau_UP	0.33956493	4.91E-74	4.91345E-74
DEGs_ptau_DOWN	-0.5068653	5.07E-101	6.7615E-101

Mathys et al 2019	**logFC**	**P.Value**	**adj.P.Val**
DEGs_amyloid_UP	0.13023331	4.85E-32	9.70988E-32
DEGs_amyloid_DOWN	-0.1007316	3.97E-17	5.29454E-17
DEGs_ptau_UP	0.13588274	4.54E-33	1.8156E-32
DEGs_ptau_DOWN	-0.0955003	4.61E-13	4.61453E-13

Zhou et al 2020	**logFC**	**P.Value**	**adj.P.Val**
DEGs_amyloid_UP	0.20404415	7.52E-195	1.5049E-194
DEGs_amyloid_DOWN	-0.0810627	6.06E-18	6.05788E-18
DEGs_ptau_UP	0.25388578	1.50E-307	6.0061E-307
DEGs_ptau_DOWN	-0.1680302	1.73E-60	2.30681E-60

Gerrits et al 2021	**logFC**	**P.Value**	**adj.P.Val**
DEGs_amyloid_UP	0.01363858	2.09E-14	2.78474E-14
DEGs_amyloid_DOWN	-0.0169866	1.99E-20	7.95435E-20
DEGs_ptau_UP	0.00750133	0.00015475	0.000154753
DEGs_ptau_DOWN	-0.015916	5.28E-15	1.05699E-14

Supplementary Table 3_DGE enrichment in other datasets
Microglia DGE

Grubman et al 2019	**logFC**	**P.Value**	**adj.P.Val**
DEGs_amyloid_UP	0.37751126	2.63E-15	1.05233E-14
DEGs_amyloid_DOWN	-0.2022053	6.76E-05	0.000135176
DEGs_ptau_UP	0.13650833	0.01612692	0.021502553
DEGs_ptau_DOWN	0.15115991	0.02941246	0.029412464

Mathys et al 2019	**logFC**	**P.Value**	**adj.P.Val**
DEGs_amyloid_UP	0.09607165	1.89E-06	3.78594E-06
DEGs_amyloid_DOWN	-0.0535726	0.0347086	0.034708597
DEGs_ptau_UP	0.13853693	5.61E-08	2.24362E-07
DEGs_ptau_DOWN	-0.0595375	0.03117732	0.034708597

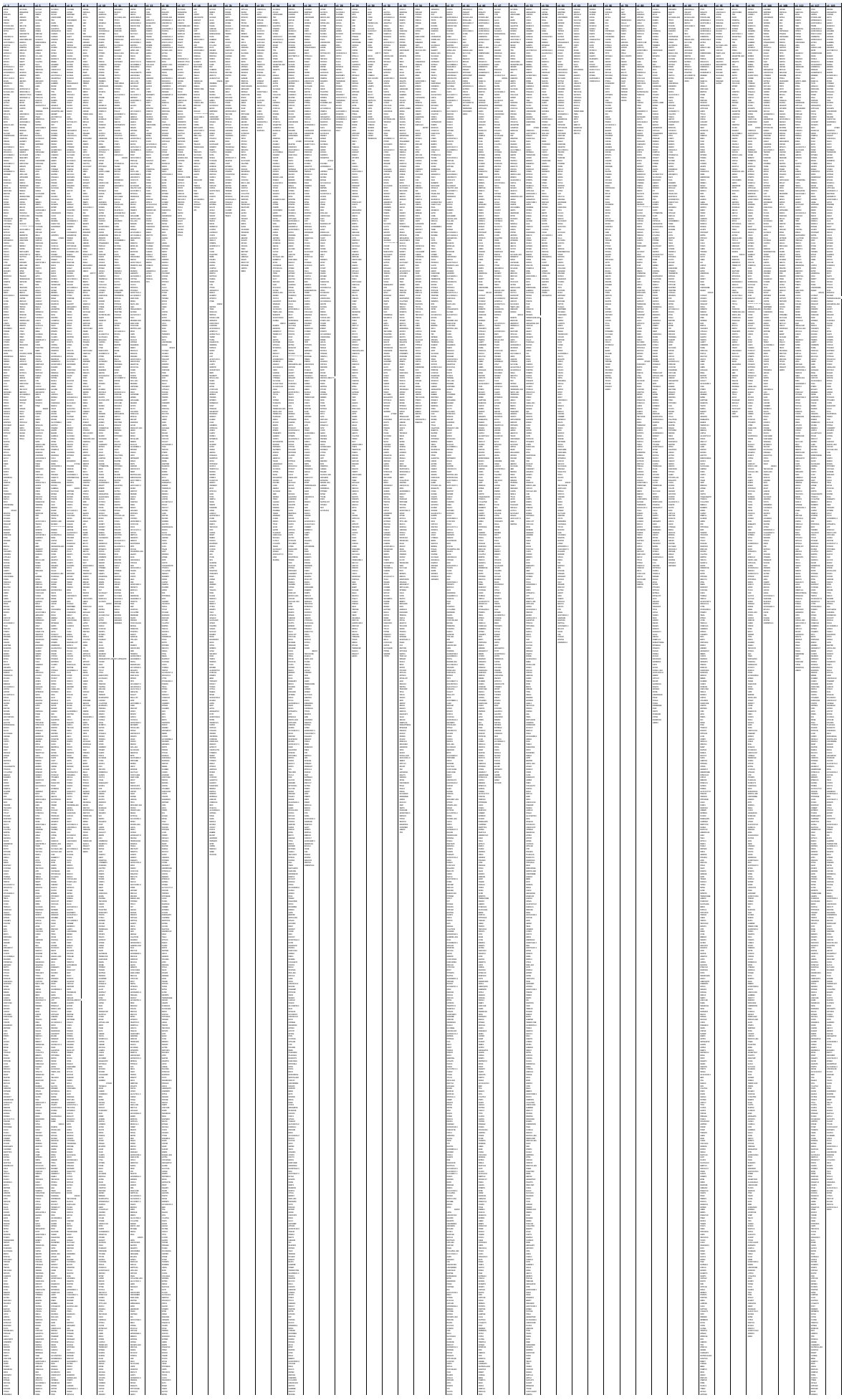
Zhou et al 2020	**logFC**	**P.Value**	**adj.P.Val**
DEGs_amyloid_UP	0.19889297	1.51E-40	2.01207E-40
DEGs_amyloid_DOWN	-0.0590511	0.00393719	0.003937194
DEGs_ptau_UP	0.36264581	4.33E-76	1.73373E-75
DEGs_ptau_DOWN	-0.3735525	4.98E-45	9.95415E-45

Gerrits et al 2021	**logFC**	**P.Value**	**adj.P.Val**
DEGs_amyloid_UP	0.1383819	0	0
DEGs_amyloid_DOWN	0.00788924	0.00012742	0.000127415
DEGs_ptau_UP	0.18163868	0	0
DEGs_ptau_DOWN	-0.028563	1.93E-32	2.56905E-32

Supplementary Table 4_Astrocyte MEGENA modules
Contents

Sheet name	Description
Module_list	MEGENA Gene Co-expression Modules in Astrocytes
Module_description	MEGENA Gene Co-expression Module description
Module 9 FE	Functional enrichment of Module 9 (CLU hub gene) genes by enrichR
Module 30 FE	Functional enrichment of Module 30 (CLU hub gene) genes by enrichR
Module 13 FE	Functional enrichment of Module 13 (APOE hub gene) genes by enrichR
Pathology_enrichment	logFC of the enrichment (AUCell and limma) of modules with amyloid-beta and pTau pathology
Enrichment_other_datasets	logFC of the enrichment (AUCell and limma) of modules in AD samples compared to Control samples from previous studies
MSS	Module specificity scores (MSS) in astrocytic subclusters

Supplementary Table 4_Astrocyte MEGENA modules
Module list



Supplementary Table 4_Astrocyte MEGENA modules

Module description

MEGENA Gene Co-expression Module description

Co-expression module	Module size	Parent module	Hub genes (number of edges in parentheses)
c1_3	1260	c1_1	MALAT1(965),FP236383.1(411),PCDH9-AS2(134),FTH1(129),HEPN1(129),AQP4(98),APOE(93),ZNF518A(89),ZDHHC21(68),PNISR(62),CKB(58),LUC7L3(32),ARGLU1(31),AC079385.1(26),SRSF5(26),AC012404.1(23),ITM2C(17),B4GALNT4(15),AP000462.1(14)
c1_4	157	c1_2	XIST(91),LINGO1(83),UTY(50),SLC26A3(39),RASGEF1B(25)
c1_5	530	c1_2	SLC1A2(213),ATP1A2(101),SLC1A3(87),SLC4A4(47),FGFR3(44),GRIA2(43),C1orf61(39),ANKDD1A(36),DLC1(32),PRODH(30),GLUL(26),MAST4(16),PIK3C2A(16),NAT8L(15),TPCN1(15),SMAD9(14),PLEKHA5(14),TTYH1(14),NRP1(13)
c1_6	907	c1_2	NRXN1(304),CADM2(158),DCLK1(148),GPM6A(93),CD44(74),SLC38A1(68),GPC5(48),LRP1B(47),FLRT2(30),ADGRB3(29),AC092691.1(26),GNA14(25),RORA(25),CABLES1(24),GFAP(24),CADM1(23),NCKAP5(23),ETNPPL(22),ERBB4(21),PLCB1(21),DNAH7(20),CLASP2(20),MAGI2(20),PCDH9(19),GABRB1(19),LSAMP(18),ASPH(18),LINC01088(17),LMO3(17),MEF2C-AS1(17),AC073941.1(16),FAM155A(16),RANBP3L(16),ARHGAP24(15),MAN1C1(15),ADAMTSL3(15),PDE4D(15),NKAIN3(15),KCND3(15),ADGRV1(15),TNC(14),SOX5(14),GPD2(14),EMP1(14)
c1_8	540	c1_2	ZNF98(197),DPP10(196),COL5A3(98),HPSE2(75),CACNB2(66),NDRG2(58),LINC00609(51),HIF3A(32),LINC00299(27),VCAN(23),TRPM3(22),RGS20(22),NR2F2-AS1(21),SLC39A11(21),WDR49(16),OLFM2(16),KCNIP1(16),ADCY2(16),ALDH1A1(15)
c1_9	307	c1_2	CRYAB(107),HSP90AA1(72),MT2A(68),CLU(60),HSPA1A(47),MT3(25),VEGFA(25),GJA1(23),UBC(20),FOS(15),HMGB1(15),GAPDH(15)
c1_10	688	c1_2	F3(252),CHI3L1(216),ITPR2(180),CAMK2G(72),ANGPTL4(69),DTNA(59),ATP1B2(53),CADPS(41),NRCAM(38),PTPRZ1(38),SAMD4A(35),APC(35),BCL6(29),ACOT11(23),PFKFB3(20),LINC02649(16),AHCYL1(14)
c1_11	224	c1_2	TPST1(164),ARHGEF3(72),SLC44A3-AS1(46),DST(30),FAM189A2(23),MACF1(21),BAALC-AS1(21),MAPRE2(20),OSMR(15)
c1_12	517	c1_2	NEAT1(424),HSPB1(109),AC091826.2(83),LINC01748(67),RFX3-AS1(47),NPAS2(39),SLC38A2(24),ZMAT1(24),AC138627.1(22),CRB1(19),AC104596.1(17),CIRBP(16),HSPH1(15),AC002429.2(15)
c1_13	100	c1_3	APOE(87),CKB(58),ITM2C(17),B4GALNT4(15)
c1_16	1127	c1_3	MALAT1(965),FP236383.1(411),PCDH9-AS2(134),HEPN1(128),AQP4(98),FTH1(92),ZNF518A(89),ZDHHC21(68),PNISR(62),LUC7L3(32),ARGLU1(31),AC079385.1(26),SRSF5(26),AC012404.1(23)
c1_17	83	c1_4	LINGO1(79),SLC26A3(36),RASGEF1B(18)
c1_18	74	c1_4	XIST(67),UTY(46)
c1_19	308	c1_5	SLC1A2(209),SLC4A4(47),GRIA2(43),DLC1(32),GLUL(18),PIK3C2A(16),SMAD9(14),PLEKHA5(14),CFAP54(12)
c1_21	76	c1_5	SLC1A3(62),MAST4(16),NRP1(12)
c1_22	96	c1_5	ATP1A2(86),C1orf61(26),FGFR3(15),TPCN1(15),TTYH1(14)
c1_23	45	c1_5	ANKDD1A(35),PRODH(24)
c1_24	201	c1_6	DCLK1(125),SLC38A1(66),GNA14(25),PLCB1(21),CABLES1(18),LINC01088(17),AC073941.1(16),ADAMTSL3(15),KCND3(15),TNC(14)
c1_25	706	c1_6	NRXN1(303),CADM2(158),GPM6A(93),CD44(73),LRP1B(47),GPC5(42),FLRT2(30),ADGRB3(29),AC092691.1(26),RORA(25),GFAP(24),NCKAP5(23),ETNPPL(22),ERBB4(21),CADM1(20),DNAH7(20),CLASP2(20),MAGI2(20),PCDH9(19),GABRB1(19),LSAMP(18),ASPH(18),LMO3(17),MEF2C-AS1(17),FAM155A(16),RANBP3L(16),PDE4D(15),NKAIN3(15),ADGRV1(15),ARHGAP24(14),MAN1C1(14),SOX5(14),GPD2(14),EMP1(14)
c1_26	312	c1_8	DPP10(187),COL5A3(68),LINC00609(51),CACNB2(41),VCAN(23),TRPM3(21),WDR49(16),ADCY2(16),OLFM2(15)
c1_27	183	c1_8	ZNF98(155),HPSE2(28),LINC00299(27),RGS20(22),NR2F2-AS1(21),ALDH1A1(15)
c1_28	45	c1_8	HIF3A(28),NDRG2(27),SLC39A11(21)
c1_29	236	c1_9	CRYAB(106),HSP90AA1(72),MT2A(67),HSPA1A(46),MT3(24),UBC(20),FOS(15),HMGB1(15)
c1_30	48	c1_9	CLU(33),GJA1(23)
c1_32	236	c1_10	F3(185),ATP1B2(53),ANGPTL4(52)
c1_33	300	c1_10	CHI3L1(213),CAMK2G(72),DTNA(39),CADPS(37),SAMD4A(35),ACOT11(23),BCL6(17)
c1_34	151	c1_10	ITPR2(143),NRCAM(37),APC(35),PTPRZ1(31)
c1_36	208	c1_11	TPST1(164),ARHGEF3(61),SLC44A3-AS1(46),DST(26),FAM189A2(22),BAALC-AS1(21),MAPRE2(20),MACF1(17)
c1_37	504	c1_12	NEAT1(424),HSPB1(109),AC091826.2(83),LINC01748(67),RFX3-AS1(47),NPAS2(33),SLC38A2(24),ZMAT1(24),AC138627.1(22),CRB1(19),AC104596.1(17),CIRBP(16),HSPH1(15),AC002429.2(15)
c1_41	39	c1_16	AC012404.1(20),LINC00513(11)
c1_46	1038	c1_16	MALAT1(965),FP236383.1(411),AQP4(98),PCDH9-AS2(96),ZNF518A(89),ZDHHC21(68),HEPN1(66),FTH1(65),PNISR(62),LUC7L3(32),ARGLU1(31),AC079385.1(23),SRSF5(23)
c1_47	282	c1_19	SLC1A2(209),SLC4A4(47),GRIA2(43),DLC1(31),PIK3C2A(16),PLEKHA5(14)
c1_51	188	c1_24	DCLK1(125),SLC38A1(66),PLCB1(21),CABLES1(18),LINC01088(17),AC073941.1(16),ADAMTSL3(15)
c1_53	550	c1_25	NRXN1(301),GPM6A(91),GPC5(41),CD44(30),ADGRB3(27),AC092691.1(25),RORA(25),GFAP(24),NCKAP5(23),ETNPPL(22),CADM1(20),DNAH7(20),PCDH9(19),GABRB1(19),ASPH(18),LMO3(17),MEF2C-AS1(17),RANBP3L(16),PDE4D(15),NKAIN3(15),FAM155A(15),ADGRV1(15),ARHGAP24(14),SOX5(14),GPD2(14),PREX2(13),ATP13A4(13),BMPR1B(13)
c1_54	105	c1_25	CADM2(83),LRP1B(29),FLRT2(29),CLASP2(14)
c1_61	231	c1_26	DPP10(186),CACNB2(40),LINC00609(26),VCAN(23),WDR49(16),ADCY2(15)
c1_62	46	c1_26	COL5A3(45)
c1_65	27	c1_28	HIF3A(26),NDRG2(15)
c1_66	139	c1_29	CRYAB(106),HSP90AA1(53),MT2A(35),HSPA1A(29),UBC(17)
c1_78	34	c1_30	CLU(32)
c1_80	211	c1_32	F3(185),ATP1B2(53),ANGPTL4(29)
c1_83	260	c1_33	CHI3L1(212),DTNA(39),CADPS(36),SAMD4A(35),CAMK2G(35),BCL6(17),CNTN1(13)
c1_86	203	c1_36	TPST1(164),ARHGEF3(61),SLC44A3-AS1(46),DST(26),FAM189A2(22),BAALC-AS1(21),MAPRE2(18),MACF1(17)
c1_89	27	c1_41	AC012404.1(20)
c1_92	1020	c1_46	MALAT1(965),FP236383.1(393),AQP4(98),PCDH9-AS2(96),ZNF518A(89),HEPN1(66),FTH1(65),PNISR(62),ZDHHC21(51),LUC7L3(32),ARGLU1(31),AC079385.1(23),SRSF5(23)
c1_95	28	c1_51	SLC38A1(22),DPP6(9)
c1_96	149	c1_51	DCLK1(121),AC073941.1(16),LINC01088(14),ADAMTSL3(14)
c1_99	483	c1_53	NRXN1(301),GPM6A(69),GPC5(41),CD44(30),ADGRB3(27),GFAP(24),NCKAP5(23),CADM1(20),DNAH7(20),PCDH9(19),GABRB1(19),ASPH(18),RORA(18),LMO3(17),PDE4D(15),NKAIN3(15),FAM155A(15),AC092691.1(15),ADGRV1(15),ARHGAP24(14),SOX5(14),ETNPPL(14),GPD2(14),PREX2(13),ATP13A4(13)
c1_106	224	c1_61	DPP10(186),CACNB2(40),LINC00609(26),VCAN(23),WDR49(16)
c1_108	132	c1_66	CRYAB(106),HSP90AA1(52),MT2A(35),HSPA1A(29)
c1_112	241	c1_83	CHI3L1(212),CADPS(36),CAMK2G(35),SAMD4A(31),DTNA(20),BCL6(17),CNTN1(13)
c1_117	1010	c1_92	MALAT1(965),FP236383.1(393),PCDH9-AS2(96),AQP4(96),ZNF518A(89),HEPN1(66),FTH1(65),PNISR(54),ZDHHC21(51),ARGLU1(31),LUC7L3(24),AC079385.1(23),SRSF5(23)
c1_119	437	c1_99	NRXN1(301),GPM6A(69),GPC5(35),CD44(30),NCKAP5(23),CADM1(20),ADGRB3(18),ASPH(18),GABRB1(17),DNAH7(17),LMO3(17),PDE4D(15),NKAIN3(15),GFAP(15),AC092691.1(15),ADGRV1(15),ARHGAP24(14),SOX5(14),ETNPPL(14),GPD2(14),ATP13A4(13)

Supplementary Table 4_Astrocyte MEGENA modules
Module 9 FE

geneset	description	size	overlap	odds_ratio	pval	FDR	database	X.Log10.FDR.	genes
GO:0060050	positive regulation of protein glycosylation	6	3	64.77	0.000069	0.0033	GO	2.4815	GOLGA2,CHORDC1,RAMP1
R-HSA-5660526	Response to metal ions	11	5	54.32	0.00000035	0.000036	Reactome	4.444	MT2A;MT1M;MT1F;MT1G;MT3
R-HSA-5662231	Metallothionein bind metals	11	5	54.32	0.00000035	0.000036	Reactome	4.444	MT2A;MT1M;MT1F;MT1G;MT3
GO:0051131	chaperone-mediated protein complex assembly	17	7	45.93	3.2E-09	0.00000086	GO	6.0655	HSP90AA1;HSPD1B;HSPA4;PTGES3;CLU;HSPD1;HSPA1A
GO:0097201	negative regulation of transcription from RNA polymerase II promoter in response to stress	10	4	43.32	0.00001	0.00091	GO	3.041	DNAJB1;JUN;EGR1;HSPA1A
GO:0051085	chaperone-mediated protein folding requiring cofactor	24	9	39.62	4.5E-11	3.2E-08	GO	7.4949	HSPA8;HSPA8.DNAJB1;HSPA5;DNAJC7;HSPA4;PTGES3;HSPA4L;HSPA1A
GO:0060049	regulation of protein glycosylation	12	4	32.48	0.00004	0.0015	GO	2.8239	GOLGA2;CHORDC1;MT3;RAMP1
GO:0090190	positive regulation of branching involved in ureteric bud morphogenesis	12	4	32.48	0.00004	0.0015	GO	2.8239	SMO;SOX9;AGT;VEGFA
R-HSA-3000484	Scavenging by Class F Receptors	6	2	32.28	0.0034	0.041	Reactome	1.387	HSP90AA1;CALR
R-HSA-5336415	Uptake and function of diphtheria toxin	6	2	32.28	0.0034	0.041	Reactome	1.387	HSP90AA1;HSP90AB1
WP3943	Robo4 and VEGF Signaling Pathways Crosstalk	6	2	32.28	0.0034	0.031	Wikipathway	1.5086	RAC1;VEGFA
R-HSA-3371511	HSF1 activation	29	9	29.71	3.2E-10	6.5E-08	Reactome	7.187	YWHAZ;EIF1AY;DNAJB1;HSPD1A;HSPA8;HSPA1L;HSPA1A
R-HSA-3371568	Attenuation phase	26	8	29.25	3.5E-09	0.00000056	Reactome	6.252	DNAJB1;HSPA8;HSPA8.DNAJB1;HSPA5;DNAJC7;DNAJB6;UBB;PTGES3;HSPA1A
GO:0051084	'de novo' posttranslational protein folding	9	3	28.29	4.5E-10	0.00000019	GO	6.7212	HSPA8;DNAJB1;HSPA8.DNAJB1;HSPA5;DNAJC7;HSPA4;PTGES3;HSPA4L;HSPA1A
GO:0090084	negative regulation of inclusion body assembly	10	3	27.75	0.0004	0.013	GO	1.8861	DNAJB1;DNAJB6;HSPA1A
R-HSA-4513068	Activation of Ca-permeable Kainate Receptor	10	3	27.75	0.0004	0.013	Reactome	1.886	GRIK5;GRIK2;CALM1
R-HSA-451306	Ionotropic activity of Kainate Receptors	10	3	27.75	0.0004	0.013	Reactome	1.886	GRIK5;GRIK2;CALM1
R-HSA-5663084	Diseases of carbohydrate metabolism	10	3	27.75	0.0004	0.013	Reactome	1.886	GYS1;UBB;UBC
R-HSA-3785653	Myoclonic epilepsy of Lafora	10	3	27.75	0.0004	0.013	Reactome	1.886	GYS1;UBB;UBC
R-HSA-3229121	Glycogen storage diseases	10	3	27.75	0.0004	0.013	Reactome	1.886	GYS1;UBB;UBC
R-HSA-390450	Folding of actin by CCT/TriC	10	3	27.75	0.0004	0.013	Reactome	1.886	CCT3;ACTB;CCT4
GO:0071280	cellular response to copper ion	21	6	26.15	0.00000056	0.000092	GO	4.0362	PRNP;MT2A;MT1M;MT1F;MT1G;MT3
GO:0034620	cellular response to unfolded protein	22	6	24.51	0.00000076	0.00012	GO	3.9208	HSPA5;HSPA8;HSPA8.DNAJB1;HSPA4;HSPA4L;HSPA1A
GO:0090083	regulation of inclusion body assembly	11	3	24.28	0.00054	0.016	GO	1.7959	DNAJB1;DNAJB6;HSPA1A
GO:2001044	regulation of integrin-mediated signaling pathway	11	3	24.28	0.00054	0.016	GO	1.7959	CD63;FLNA;PRKD1
GO:0010560	positive regulation of glycoprotein biosynthetic process	11	3	24.28	0.00054	0.016	GO	1.7959	GOLGA2;CHORDC1;RAMP1
GO:0090189	regulation of branching involved in ureteric bud morphogenesis	15	4	23.62	0.00065	0.0032	GO	2.4949	SMO;SOX9;AGT;VEGFA
GO:0061213	positive regulation of mesonephros development	15	4	23.62	0.00065	0.0032	GO	2.4949	SMO;SOX9;AGT;VEGFA
GO:0071294	cellular response to zinc ion	19	5	23.27	0.000068	0.00072	GO	3.1427	MT2A;MT1M;MT1F;MT1G;MT3
GO:0060686	negative regulation of prostatic bud formation	43	11	22.83	3.5E-11	3.2E-08	GO	7.4949	HSPA8;DNAJA1;DNAJB1;HSPA8.DNAJB1;HSPD1A;HSPA1L;HSPA4;HSPD1;HSPA1A
WP1425	Bone Morphogenic Protein (BMP) Signalling and Regulation	12	3	21.58	0.00071	0.011	Wikipathway	1.9586	SMAD1;TOB2;TOB1
GO:0071276	cellular response to cadmium ion	29	7	20.86	0.00000022	0.000047	GO	4.3279	MT2A;JUN;MT1M;MT1F;MT1G;FOS;MT3
GO:0046688	response to copper ion	25	6	20.64	0.0000017	0.00025	GO	3.6021	PRNP;MT2A;MT1M;MT1F;MT1G;MT3
WP1528	Physiological and Pathological Hypertrophy of the Heart	25	6	20.64	0.0000017	0.00016	Wikipathway	3.7959	JUN;RAC1;FOS;CALM1;RHOA;AGT
R-HSA-3371571	HSF1-dependent transactivation	34	8	20.24	1.6E-08	0.0000069	Reactome	5.31	DNAJB1;HSPA8;HSPA8.DNAJB1;HSPA5;DNAJB6;UBB;PTGES3;HSPA1A
GO:0010939	regulation of necrotic cell death	13	3	19.42	0.00091	0.024	GO	1.6198	UBB;UBC;MT3
GO:0046686	response to cadmium ion	31	7	19.12	0.00000036	0.00007	GO	4.1549	MT2A;JUN;MT1M;MT1F;MT1G;FOS;MT3
GO:0035967	cellular response to topologically incorrect protein	27	6	18.67	0.00000028	0.00038	GO	3.4202	HSPA8;HSPA8.DNAJB1;HSPA5;HSPA4;HSPA4L;HSPA1A
GO:1905322	positive regulation of morphogenesis of an epithelium	18	4	18.56	0.00014	0.0058	GO	2.2366	SMO;SOX9;AGT;VEGFA
GO:1903320	regulation of protein modification by small protein conjugation or removal	34	7	17.66	0.0011	0.028	GO	1.5528	HSPA8;HSPA1A;HSPD1A;HSPA1A
R-HSA-1236382	Constitutive Signaling by Ligand-Responsive EGFR Cancer Variants	19	4	17.32	0.00018	0.0095	Reactome	2.022	HSP90AA1;UBB;UBC;SOS1
R-HSA-5673415	Signaling by Ligand-Responsive EGFR Variants in Cancer	19	4	17.32	0.00018	0.0095	Reactome	2.022	HSP90AA1;UBB;UBC;SOS1
R-HSA-1643713	Signaling by EGFR in Cancer	19	4	17.32	0.00018	0.0095	Reactome	2.022	HSP90AA1;UBB;UBC;SOS1
GO:0061620	glycolytic process through glucose-6-phosphate	25	5	16.29	0.00004	0.0019	GO	2.7212	GPI;PKM;PGK1;ENO1;GAPDH
GO:0061621	canonical glycolysis	25	5	16.29	0.00004	0.0019	GO	2.7212	GPI;PKM;PGK1;ENO1;GAPDH
GO:0061718	glucose catabolic process to pyruvate	25	5	16.29	0.00004	0.0019	GO	2.7212	GPI;PKM;PGK1;ENO1;GAPDH
GO:0071384	cellular response to corticosteroid stimulus	35	7	16.9	0.0014	0.033	GO	1.4815	HNRNPU;ZFP36L1;UBE2L3
R-HSA-69298	Association of licensing factors with the pre-replicative complex	15	3	16.19	0.0014	0.028	Reactome	1.553	UBB;UBC;CDT1
R-HSA-2691232	Constitutive Signaling by NOTCH1 HD Domain Mutants	15	3	16.19	0.0014	0.028	Reactome	1.553	UBB;UBC;NRM1
R-HSA-2691230	Signaling by NOTCH1 HD Domain Mutants in Cancer	15	3	16.19	0.0014	0.028	Reactome	1.553	UBB;UBC;NRM1
R-HSA-3322077	Glycogen synthesis	15	3	16.19	0.0014	0.028	Reactome	1.553	GYS1;UBB;UBC
GO:0055069	zinc ion homeostasis	31	6	15.68	0.0000066	0.00065	GO	3.1871	MT2A;MT1M;MT1F;MT1G;SLC30A1;MT3
GO:0006882	cellular zinc ion homeostasis	31	6	15.68	0.0000066	0.00065	GO	3.1871	MT2A;MT1M;MT1F;MT1G;SLC30A1;MT3
R-HSA-3371556	Cellular response to heat stress	96	18	15.66	6.3E-15	5.1E-12	Reactome	11.292	YWHAZ;HSPA8;HSPA8.HSPA8;HSPA8.DNAJB1;HSPA8.DNAJB1;HSPA5;HSPA4;ST13;PTGES3;HSP4AL;EIF1AY;DNAJB1;DNAJC7;DNAJB6;UBB;PDM21C;BAG3;HSPA1A
WP3614	Photodynamic therapy-induced HIF-1 survival signaling	37	7	15.29	0.00000013	0.00016	Wikipathway	3.7959	EGLN1;BNIP3L;PKM;BNIP3;PGK1;MCL1;VEGFA
GO:0010043	response to zinc ion	32	6	15.08	0.0000081	0.00072	GO	3.1427	MT2A;MT1M;MT1F;MT1G;SLC30A1;MT3
GO:1902229	regulation of intrinsic apoptotic signaling pathway in response to DNA damage	16	3	14.94	0.0017	0.038	GO	1.4202	ACIN1;CUL1;TP73
R-HSA-199054	SamulA PAK-dependent Axon repulsion	16	3	14.94	0.0017	0.028	Reactome	1.553	HSP90AA1;HSPD1B;RAC1
R-HSA-5625900	RHO GTPases activate CIT	16	3	14.94	0.0017	0.028	Reactome	1.553	RAC1;RHOA;RHOB
R-HSA-2173791	TGF-beta receptor signaling in EMT (epithelial to mesenchymal transition)	16	3	14.94	0.0017	0.028	Reactome	1.553	UBB;UBC;RHOA
WP1946	Cori Cycle	16	3	14.94	0.0017	0.022	Wikipathway	1.6576	GPI;PGK1;GAPDH
R-HSA-3371453	Regulation of HSF1-mediated heat shock response	80	14	14.21	1.8E-11	4.9E-09	Reactome	8.31	YWHAZ;HSPA8;HSPA8.HSPA8;HSPA5;HSP4;ST13;HSP4AL;DNAJB1;DNAJC7;DNAJB6;UBB;PDM21C;BAG3;HSPA1A
GO:0014074	response to purine-containing compound	17	3	13.87	0.0021	0.042	GO	1.3768	JUN;JUND;JUNB
GO:0071385	cellular response to glucocorticoid stimulus	17	3	13.87	0.0021	0.042	GO	1.3768	HNRNPU;ZFP36L1;UBE2L3
R-HSA-532668	N-glycan trimming in the ER and Calnexin/Calreticulin cycle	17	3	13.87	0.0021	0.03	Reactome	1.523	CANX;MLEC;CALR
GO:0050771	negative regulation of axonogenesis	23	4	13.67	0.00038	0.013	GO	1.8861	GDI1;LRP4;MT3;RHOA
GO:0014605	cellular response to heat	47	8	13.48	0.00000053	0.000092	GO	4.0362	YWHAZ;HSPA8;HSPA8.HSPA8;HSPA5;BAG3;HSPA4;HSPA4L;HSPA1A
GO:1900034	regulation of cellular response to heat	78	13	13.35	1.8E-10	9.9E-08	GO	7.0044	YWHAZ;HSPA8;HSPA8.HSPA8;HSPA5;HSP4;BAG3;HSPA4;HSPA4L;HSPA1A
WP3129	Zinc homeostasis	36	6	13.07	0.000016	0.00076	Wikipathway	3.1192	MT2A;MT1M;MT1F;MT1G;SLC30A1;MT3
GO:0042398	cellular modified amino acid biosynthetic process	24	4	12.99	0.00045	0.015	GO	1.8239	PTDSS2;PLOD3;PLOD2;HAGH
GO:0009250	glucan biosynthetic process	18	3	12.95	0.0025	0.046	GO	1.3372	GYS1;UBB;UBC
GO:0005978	glycogen biosynthetic process	18	3	12.95	0.0025	0.046	GO	1.3372	GYS1;UBB;UBC
GO:0046683	response to organophosphorus	18	3	12.95	0.0025	0.046	GO	1.3372	JUN;JUND;JUNB
GO:0050849	negative regulation of calcium-mediated signaling	18	3	12.95	0.0025	0.046	GO	1.3372	PRNP;CHORDC1;CALM1
R-HSA-1234176	Oxygen-dependent proline hydroxylation of hypoxia-inducible Factor Alpha	18	3	12.95	0.0025	0.033	Reactome	1.481	EGLN1;UBB;UBC
GO:0021762	substantia nigra development	43	7	12.74	0.00000038	0.00047	GO	3.3279	YWHAE;HSPA5;S100A1;LONRF1;CALM1;ACTB;RHOA
R-HSA-983170	Antigen Presentation: Folding, assembly and peptide loading of class I MHC	25	4	12.37	0.00053	0.017	Reactome	1.77	HSPA5;CANX;HLA-A;CALR
GO:0034109	homotypic cell-cell adhesion	38	6	12.25	0.000023	0.0015	GO	2.8239	CSRP1;TYRO3;GNAS;FLNA;PLPP3;ACTB
WP4300	Extracellular vesicles in the crosstalk of cardiac cells	19	3	12.14	0.0029	0.029	Wikipathway	1.5376	CD63;CDH1;SOD1
R-HSA-70171	Glycolysis	32	5	12.06	0.00012	0.0087	Reactome	2.06	GPI;PKM;PGK1;ENO1;GAPDH
GO:0043277	apoptotic cell clearance	26	4	11.8	0.00062	0.018	GO	1.7447	SCARB1;TYRO3;HMGB1;RAC1
R-HSA-1234174	Regulation of Hypoxia-inducible Factor (HIF) by oxygen	26	4	11.8	0.00062	0.017	Reactome	1.77	EGLN1;UBB;UBC;VEGFA
R-HSA-2262749	Cellular response to hypoxia	26	4	11.8	0.00062	0.017	Reactome	1.77	EGLN1;UBB;UBC;VEGFA
GO:0050768	negative regulation of neurogenesis	33	5	11.63	0.00014	0.0058	GO	2.2366	ID2;ID4;ID3;PARK2;CAB
GO:0070527	platelet aggregation	33	5	11.63	0.00014	0.0058	GO	2.2366	CSRP1;TYRO3;GNAS;FLNA;ACTB
GO:0051123	regulation of protein transport	27	4	11.29	0.00072	0.02	GO	1.699	SNX3;DNAJA1;HSPA8;CHORDC1
R-HSA-389957	Prefoldin mediated transfer of substrate to CCT/TriC	27	4	11.29	0.00072	0.02	Reactome	1.699	CCT3;TUBA1A;ACTB;CCT4
GO:0043392	negative regulation of DNA binding	34	5	11.23	0.00014	0.0063	GO	2.2007	JUN;SMO;ID2;ID4;ID3
GO:0046916	cellular transition metal ion homeostasis	93	13	10.84	1.8E-09	0.00000054	GO	6.2676	PRNP;MT1M;CYBRD1;SLC30A1;MT3;SOD1;MT2A;UBB;SLC22A17;UBC;MT1F;MT1G;FTL
R-HSA-2979096	NOTCH2 Activation and Transmission of Signal to the Nucleus	21	3	10.79	0.0039	0.043	Reactome	1.367	UBB;UBC;MIB1
R-HSA-5627123	RHO GTPases activate PAKs	21	3	10.79	0.0039	0.043	Reactome	1.367	RUN;RAC1;CALM1
GO:0080135	regulation of cellular response to stress	104	14	10.41	6.9E-10	0.00000025	GO	6.6021	YWHAE;HSPA8;HSPA8.HSPA8;HSPA8.DNAJB1;HSPA8.DNAJB1;PDM21C;DNAJC7;DNAJB6;BAG3;CHORDC1;CRYAB;MCL1;HSPA1A
GO:0060003	positive regulation of transcription from RNA polymerase II promoter in response to stress	29	4	10.39	0.00096	0.024	GO	1.6198	CSRP1;HSPA1L;MYD88;VEGFA
WP3286	Copper homeostasis	52	7	10.19	0.000014	0.00076	Wikipathway	3.1192	PRNP;MT2A;MT1M;MT1F;MT1G;MT3;SOD1
R-HSA-5620922	BBSome-mediated cargo-targeting to cilium	23	3	9.71	0.0051	0.049	Reactome	1.31	CCT3;SMO;CCT4
WP712	Estrogen signaling pathway	23	3	9.71	0.0051	0.04	Wikipathway	1.3979	JUN;GNAS;FOS
WP2526	PDGF Pathway	39	5	9.57	0.00031	0.0071	Wikipathway	2.1487	JUN;RAC1;FOS;SOS1;RHOA
GO:0010941	regulation of cell death	96	12	9.5	2.7E-08	0.0000065	GO	5.1871	BNIP3L;JUN;JUNB;UBB;BNIP3;CHORDC1;PRKD1;CUL1;UNB;CRYAB;MT3;HSPA1A
GO:0036294	cellular response to decreased oxygen levels	64	8	9.38	0.0000059	0.00065	GO	3.1871	BNIP3L;FAM162A;BNIP3;HIF1BP1;PGK1;MT3;ZFP36L1;VEGFA
R-HSA-70263	Gluconeogenesis	32	4	9.27	0.0014	0.028	Reactome	1.553	GPI;PGK1;ENO1;GAPDH
R-HSA-389958	Cooperation of Prefoldin and TriC/CCT in actin and tubulin folding	32	4	9.27	0.0014	0.028	Reactome	1.553	CCT3;TUBA1A;ACTB;CCT4
WP3612	Photodynamic therapy-induced NFE2L2 (NRF2) survival signaling	24	3	9.24	0.0057	0.043	Wikipathway	1.3665	JUN;EPHX1;FOS
GO:0050821	protein stabilization	152	18	9.09	2.2E-11	3.2E-08	GO	7.4949	CCT3;HSPA5;DNAJA1;HSPA8;UBE2B;PTGES3;CLU;MT3;HSPD1;ANP32B;PPP1CC;PLPP3;CRYAB;GAPDH;CCT4;HSPA1A
GO:0005977	glycogen metabolic process	33	4	8.95	0.0016	0.035	GO	1.4559	GYS1;UBB;UBC;CALM1
WP4290	Metabolic reprogramming in colon cancer	42	5	8.8	0.00044	0.0093	Wikipathway	2.0315	GPI;PKM;PGK1;ENO1;GAPDH
GO:0051248	negative regulation of protein metabolic process	43	5	8.56	0.00049	0.016	GO	1.7959	SNX3;PRNP;FLNA;CLU;CRYAB
GO:0051101	regulation of DNA binding	52	6	8.51	0.00014	0.0058	GO	2.2366	JUN;SMO;ID2;ID4;ID3;HMGB1
GO:0010595	positive regulation of endothelial cell migration	70	8	8.47	0.000012	0.00092	GO	3.0362	SCARB1;HMGB1;PRKD1;CALR;PLPP3;AGT;RHOB;VEGFA
R-HSA-70326	Glucose metabolism	79	9	8.47	0.0000034	0.0003	Reactome	3.523	GPI;SYS1;PKM;UBB;UBC;PGK1;ENO1;CALM1;GAPDH
WP3519	Parkin-Ubiquitin Proteasomal System pathway	70	8	8.47	0.000012	0.00076	Wikipathway	3.1192	HSPA5;HSPA8;TUBA1A;HSPA5;HSPA8.UBA1;UBE2L3;HSPA1A
GO:0051973	positive regulation of telomerase activity	35	4	8.37	0.002	0.041	GO	1.3872	HSP90AA1;HSPD1B;HSPD1;PTGES3;CCT4
GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	62	7	8.33	0.000045	0.0025	GO	2.6021	DNAJA1;ACIN1;ENO1;CLU;TPT1;MCL1;HSPA1A
R-HSA-1227986	Signaling by ERBB2	45	5	8.13	0.00061	0.017	Reactome	1.77	HSP90AA1;UBB;UBC;SOS1;RHOA
WP534	Glycolysis and Gluconeogenesis	45	5	8.13	0.00061	0.011	Wikipathway	1.9586	GPI;PKM;PGK1;ENO1;GAPDH
GO:0050999	regulation of nitric-oxide synthase activity	36	4	8.11	0.0022	0.043	GO	1.3665	SCARB1;HSP90AA1;S100A1;CALM1
WP2873	Aryl Hydrocarbon Receptor Pathway	46	5	7.94	0.00068	0.011	Wikipathway	1.9586	JUN;HSP90AA1;JUND;PTGES3;JUNB
GO:0000879	cellular iron homeostasis	56	6	7.83	0.00021	0.0079	GO	2.1024	UBB;SLC22A17;UBC;TBRG1;FTL;SOD1
GO:0010642	positive regulation of cell death	57	6	7.68	0.00023	0.0084	GO	2.0757	PRNP;BNIP3;DDIT4;FOS;CLU;MT3
GO:1901216	positive regulation of neuron death	38	4	7.63	0.0027	0.049	GO	1.3098	PRNP;DDIT4;FOS;CLU
GO:0001895	retina homeostasis	38	4	7.63	0.0027	0.049	GO	1.3098	WHRN;PRDX1;ACTB;SOD1
WP534	Glycolysis and Gluconeogenesis	39	4	7.41	0.0029	0.029	Wikipathway	1.5376	GNAI1;RAC1;CALM1;RHOA
WP3611	Photodynamic therapy-induced AP-1 survival signaling.	50	5	7.23	0.00099	0.014	Wikipathway	1.8539	HSP90AA1;JUN;FOS;JUNB;MCL1
R-HSA-5620924	Intraflagellar transport	41	4	7.01	0.0035	0.042	Reactome	1.377	IFT140;IFT172;DYNLRB1;DYNLL1
GO:0055072	iron homeostasis	63	6	6.87	0.00041	0.013	GO	1.8861	UBB;SLC22A17;UBC;TBRG1;FTL;SOD1
GO:0010634	positive regulation of epithelial cell migration	74	7	6.83	0.00014	0.0058	GO	2.2366	SCARB1;SOX9;PRKD1;CAV1;AGT;RHOB;VEGFA
WP4018	Pathways in clear cell renal cell carcinoma	85	8	6.82	0.000049	0.0019	Wikipathway	2.7212	GPI;PKM;PGK1;PLOD2;PHGDH;ENO1;GAPDH;VEGFA
R-HSA-917937	Iron uptake and transport	43	4	6.65	0.0042	0.044	Reactome	1.357	ATP6V0E1;SLC22A17;CYBRD1;FTL
WP364	IL-6 signaling pathway	43	4	6.65	0.0042	0.034	Wikipathway	1.4685	RAC1;SOS1;JUNB;AGT
GO:0051129	negative regulation of cellular component organization	54	6	6.64	0.0014	0.033	GO	1.4815	DNAJB1;HSPA8;DNAJB6;PRKD1;HSPA1A
WP2374	Oncostatin M Signaling Pathway	65	6	6.63	0.00048	0.0093	Wikipathway	2.0315	CEBPB;JUND;FOS;SOS1;JUNB;VEGFA
GO:0071248	cellular response to metal ion	100	9	6.51	0.000024	0.0015	GO	2.8239	PRNP;MT2A;JUN;BNIP3;MT1M;MT1F;MT1G;FOS;MT3
GO:0071560	cellular response to transforming growth factor beta stimulus	100	9	6.51	0.000024	0.0015	GO	2.8239	SMAD1;WWOX;JUN;UBB;UBC;SOX9;FOS;RHOA;ZFP36L1
GO:2000573	positive regulation of DNA biosynthetic process	55	5	6.5	0.0015	0.035	GO	1.4559	CSRP1;HSP90AA1;HSPD1B;HSPD1;PTGES3;CCT4
R-HSA-2262752	Cellular responses to stress	367	31	6.47	1.4E-14	5.6E-12	Reactome	11.252	YWHAE;CEBPB;HSP90AB1;HSPA8;HSPA8.;DNAJB1;PDM21C;UBB;DNAJB6;BAG3;PRDX1;UBE2T;EIF1AY;HIST1H2AC;EGLN1;HSPA8;HSPA8.JUN;HSPA8.DNAJA1;HSPA5;ST13;HSP4;PTGES3;ATG10;FOS;DYNLL1;PRDX6;VEGFA;SOD1;EEF1A1;DNAJC7;HSPA1A
WP138	Androgen receptor signaling pathway	90	8	6.4	0.000073	0.0025	Wikipathway	2.6021	JUN;UBE2I;PRDX1;FLNA;RAC1;CALR;RHOA;RHOB
GO:0010594	regulation of endothelial cell migration	69	6	6.21	0.00066	0.019	GO	1.7212	SCARB1;PRKD1;CALR;AGT;RHOB;VEGFA
WP2355	Corticotropin-releasing hormone signaling pathway	93	8	6.17	0.000093	0.0026	Wikipathway	2.585	GNA1;HSP90AA1;JUND;GNAS;FOS;JUNB;RHOA;GNAI2
GO:0004810	vascular endothelial growth factor receptor signaling pathway	70	6	6.11	0.00072	0.02	GO	1.699	HSP90AA1;RAC1;PRKD1;ACTB;RHOA;VEGFA
GO:0051100	negative regulation of binding	82	7	6.1	0.00027	0.0092	GO	2.0362	GOLGA2;JUN;SMO;ID2;ID4;ID3;ACTB
GO:0072001	renal system development	59	5	6.02	0.0021	0.042	GO	1.3768	SMO;ITT140;LRP4;AGT;VEGFA
GO:0034329	cell junction assembly	59	5	6.02	0.0021	0.042	GO	1.3768	CDH1;TJP1;FLNA;ACTB;RHOA
GO:0071456	cellular response to hypoxia	132	11	6.01	0.000062	0.00065	GO	3.1871	EGLN1;BNIP3L;UBB;FAM162A;BNIP3;UBC;HIF1BP1;PGK1;MT3;ZFP36L1;VEGFA
GO:1902214	regulation of neuron death	72	6	5.93	0.00083	0.022	GO	1.6576	PRNP;UBB;CHORDC1;DDIT4;FOS;CLU
R-HSA-168180	TRAF6 Mediated Induction of proinflammatory cytokines	72	6	5.93	0.00083	0.022	Reactome	1.658	JUN;UBC;HNRNPU;FOS;S100B
GO:0000302	response to reactive oxygen species	60	5	5.91	0.0023	0.044	GO	1.3565	EGLN1;JUN;FOS;APTX;SOD1
R-HSA-5625740	RHO GTPases activate PKNs	60	5	5.91	0.0023	0.032	Reactome	1.495	YWHAZ;RAC1;HIST1H2AC;RHOA;RHOB
WP410	Exercise-induced Circadian Regulation	48	4	5.9	0.0062	0.044	Wikipathway	1.3565	DNAJA1;HSPA8;CEBPB;TOB1
GO:0034250	positive regulation of cellular amide metabolic process	61	5	5.81	0.0024	0.046	GO	1.3372	FXR1;RPS27L;VIM;CLU;EIF4A1
R-HSA-206998	Cell death signalling via NRAGE, NRIF and NADE	61	5	5.81	0.0024	0.033	Reactome	1.481	YWHAE;UBB;UBC;RAC1;SOS1
WP3646	Hepatitis C and Hepatocellular Carcinoma	49	4	5.76	0.0067	0.045	Wikipathway	1.3468	JUN;RAC1;SOS1;VEGFA
R-HSA-2565942	Regulation of PLK1 Activity at G2/M Transition	87	7	5.72	0.00038	0.013	Reactome	1.886	YWHAE;HSP90AA1;TUBA1A;UBB;UBC;ALMS1;DYNLL1
WP183	Proteasome Degradation	62	5	5.7	0.0026	0.028	Wikipathway	1.5528	UBB;UBE2B;UBC;UBA1;HLA-A
GO:0034249	negative regulation of cellular amide metabolic process	75	6	5.67	0.001	0.026	GO	1.585	FXR1;PRNP;CALR;CLU;GAPDH;TOB1
GO:0072503	cellular divalent inorganic cation homeostasis	101	8	5.64	0.00017	0.0063	GO	2.2007	MT2A;MT1M;MT1F;MT1G;SLC30A1;CALR;MT3;TPT1
GO:0007179	transforming growth factor beta receptor signaling pathway	76	6	5.59	0.0011	0.028	GO	1.5528	SMAD1;JUN;UBB;UBC;FOS;RHOA
R-HSA-2500362	Senescence-Associated Secretory Phenotype (SASP)	76	6	5.51	0.0012	0.028	Reactome	1.553	CEBPB;JUN;UBB;UBC;FOS;HIST1H2AC
GO:0032270	positive regulation of cellular protein metabolic process	91	7	5.45	0.0005	0.016	GO	1.7959	FXR1;HSP90AA1;ATG10;RPS27L;VIM;ELAVL1;AGT
WP1772	Apoptosis Modulation and Signaling	91	7	5.45	0.0005	0.0093	Wikipathway	2.0315	JUN;BAG3;BNIP3;FOS;PRKD1;MCL1;HSPA1A
WP4-114608	Platelet degranulation	105	8	5.41	0.00022	0.011	Reactome	1.959	CD63;HSPA5;PSAP;FLNA;CALM1;CLU;VEGFA;SOD1
WP2032	Human Thyroid Stimulating Hormone (TSH) signaling pathway	66	5	5.33	0.0034	0.031	Wikipathway	1.5086	GNA11;JUN;GNAS;FOS;GNAI2
GO:0043618	regulation of transcription from RNA polymerase II promoter in response to stress	93	7	5.32	0.00058	0.017	GO	1.7696	EGLN1;DNAJB1;UBB;BAG3;UBC;VEGFA;HSPA1A
GO:0032870	cellular response to hormone stimulus	80	6	5.28	0.0014	0.034	GO	1.4685	JUN;JUND;JUNB;RAMP1;UBE2L3;ZFP36L1
R-HSA-373755	Semaphorin interactions	67	5	5.24	0.0037	0.043	Reactome	1.367	HSP90AA1;HSPD1B;RAC1;RHOA;RHOB
GO:0060548	negative regulation of cell death	81	6	5.21	0.0015	0.035	GO	1.4559	BNIP3L;BNIP3;PRKD1;CLU;MT3;HSPA1A
R-HSA-168142	Toll Like Receptor 10 (TLR10) Cascade	82	6	5.15	0.0016	0.028	Reactome	1.553	JUN;UBB;UBC;HNRNPU;FOS;S100B
R-HSA-168176	Toll Like Receptor 5 (TLR5) Cascade	82	6	5.15	0.0016

Supplementary Table 4_Astrocyte MEGENA modules
Module 30 FE

geneset	description	size	overlap	odds_ratio	pval	FDR	database	X.Log10.FDR.	genes
GO:0035627	ceramide transport	6	2	212.2	0.000088	0.015	GO	1.824	PSAP;PLTP
GO:1902430	negative regulation of amyloid-beta formation	9	2	121.24	0.00021	0.02	GO	1.699	PRNP;CLU
GO:0097104	postsynaptic membrane assembly	9	2	121.24	0.00021	0.02	GO	1.699	NLGN2;LRP4
GO:0097105	presynaptic membrane assembly	10	2	106.08	0.00026	0.02	GO	1.699	NLGN2;LRP4
GO:1902992	negative regulation of amyloid precursor protein catabolic process	11	2	94.29	0.00032	0.02	GO	1.699	PRNP;CLU
GO:0099068	postsynapse assembly	11	2	94.29	0.00032	0.02	GO	1.699	NLGN2;LRP4
GO:0097090	presynaptic membrane organization	11	2	94.29	0.00032	0.02	GO	1.699	NLGN2;LRP4
R-HSA-532668	N-glycan trimming in the ER and Calnexin/Calreticulin cycle	17	3	92.87	0.0000092	0.0017	Reactome	2.77	CANX;MLEC;CALR
GO:0090190	positive regulation of branching involved in ureteric bud morphogenesis	12	2	84.86	0.00038	0.022	GO	1.658	SOX9;AGT
GO:0010470	regulation of gastrulation	14	2	70.71	0.00053	0.024	GO	1.62	CRB2;DAG1
GO:0090189	regulation of branching involved in ureteric bud morphogenesis	15	2	65.26	0.0006	0.024	GO	1.62	SOX9;AGT
GO:0099054	presynapse assembly	15	2	65.26	0.0006	0.024	GO	1.62	NLGN2;LRP4
GO:0061213	positive regulation of mesonephros development	15	2	65.26	0.0006	0.024	GO	1.62	SOX9;AGT
R-HSA-901042	Calnexin/calreticulin cycle	15	2	65.26	0.0006	0.0363	Reactome	1.44	CANX;CALR
GO:0001941	postsynaptic membrane organization	16	2	60.6	0.00069	0.025	GO	1.602	NLGN2;LRP4
GO:1902229	regulation of intrinsic apoptotic signaling pathway in response to DNA damage	16	2	60.6	0.00069	0.025	GO	1.602	ACKR3;CLU
R-HSA-983170	Antigen Presentation: Folding, assembly and peptide loading of class I MHC	25	3	59.08	0.000031	0.0028	Reactome	2.55	CANX;HLA-A;CALR
GO:1902003	regulation of amyloid-beta formation	18	2	53.02	0.00088	0.025	GO	1.602	PRNP;CLU
GO:1905332	positive regulation of morphogenesis of an epithelium	18	2	53.02	0.00088	0.025	GO	1.602	SOX9;AGT
GO:0061098	positive regulation of protein tyrosine kinase activity	28	3	51.98	0.000043	0.013	GO	1.886	PRNP;GPRC5B;AGT
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	28	3	51.98	0.000043	0.013	GO	1.886	CANX;HLA-A;CALR
GO:0051353	positive regulation of oxidoreductase activity	19	2	49.9	0.00098	0.025	GO	1.602	POR;AGT
R-HSA-190861	Gap junction assembly	19	2	49.9	0.00098	0.0441	Reactome	1.36	GJA1;GJB6
GO:0061097	regulation of protein tyrosine kinase activity	31	3	46.4	0.000059	0.013	GO	1.886	PRNP;GPRC5B;AGT
GO:0071709	membrane assembly	23	2	40.39	0.0014	0.029	GO	1.538	NLGN2;LRP4
GO:1902230	negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage	24	2	38.55	0.0016	0.03	GO	1.523	ACKR3;CLU
GO:2001021	negative regulation of response to DNA damage stimulus	28	2	32.61	0.0021	0.039	GO	1.409	ACKR3;CLU
GO:0048488	synaptic vesicle endocytosis	29	2	31.4	0.0023	0.039	GO	1.409	NLGN2;CANX
GO:0045995	regulation of embryonic development	29	2	31.4	0.0023	0.039	GO	1.409	CRB2;DAG1
GO:0036465	synaptic vesicle recycling	29	2	31.4	0.0023	0.039	GO	1.409	NLGN2;CANX
GO:0070527	platelet aggregation	33	2	27.34	0.003	0.048	GO	1.319	CSRP1;TYRO3
GO:0050768	negative regulation of neurogenesis	33	2	27.34	0.003	0.048	GO	1.319	ID4;CALR
GO:0045665	negative regulation of neuron differentiation	64	3	21.27	0.00052	0.024	GO	1.62	ID4;SOX9;CALR
GO:0010634	positive regulation of epithelial cell migration	74	3	18.26	0.00079	0.025	GO	1.602	SOX9;CALR;AGT
GO:0034249	negative regulation of cellular amide metabolic process	75	3	18.01	0.00082	0.025	GO	1.602	PRNP;CALR;CLU
GO:0045664	regulation of neuron differentiation	84	3	16	0.0011	0.025	GO	1.602	GPRC5B;ID4;CALR
GO:0050730	regulation of peptidyl-tyrosine phosphorylation	85	3	15.8	0.0012	0.025	GO	1.602	PRNP;CD81;AGT
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	116	4	15.75	0.00019	0.02	GO	1.699	PRNP;GPRC5B;CD81;AGT
GO:0071702	organic substance transport	87	3	15.42	0.0013	0.026	GO	1.585	SLC22A17;PSAP;PLTP
GO:0046916	cellular transition metal ion homeostasis	93	3	14.39	0.0015	0.03	GO	1.523	PRNP;SLC22A17;CYBRD1
WP536	Calcium Regulation in the Cardiac Cell	149	4	12.14	0.00048	0.028	Wikipathway	1.55	GJA1;GJB6;CALR;GNAI2
GO:0045860	positive regulation of protein kinase activity	172	4	10.47	0.00083	0.025	GO	1.602	PRNP;GPRC5B;CLU;AGT
GO:0006898	receptor-mediated endocytosis	188	4	9.55	0.0012	0.025	GO	1.602	CD81;CANX;ACKR3;CALR
GO:1902533	positive regulation of intracellular signal transduction	479	6	5.75	0.0011	0.025	GO	1.602	GJA1;GPRC5B;SLC44A2;TYRO3;SOX9;AGT
GO:0043312	neutrophil degranulation	479	6	5.75	0.0011	0.025	GO	1.602	CYB5R3;LAMP1;SLC44A2;PSAP;MLEC;METTL7A
GO:0002283	neutrophil activation involved in immune response	483	6	5.7	0.0011	0.025	GO	1.602	CYB5R3;LAMP1;SLC44A2;PSAP;MLEC;METTL7A
GO:0002446	neutrophil mediated immunity	487	6	5.65	0.0012	0.025	GO	1.602	CYB5R3;LAMP1;SLC44A2;PSAP;MLEC;METTL7A

Supplementary Table 4_Astrocyte MEGENA modules
Module 13 FE

geneset	description	size	overlap	odds_ratio	pval	FDR	database	X.Log10.FDR.	genes
R-HSA-3595172	Defective CHST3 causes SEDCJD	7	2	80.38	0.00052	0.042	Reactome	1.377	BCAN;CSPG5
R-HSA-3595177	Defective CHSY1 causes TPBS	7	2	80.38	0.00052	0.042	Reactome	1.377	BCAN;CSPG5
R-HSA-3595174	Defective CHST14 causes EDS, musculocontractural type	7	2	80.38	0.00052	0.042	Reactome	1.377	BCAN;CSPG5
R-HSA-2022923	Dermatan sulfate biosynthesis	11	2	44.65	0.00135	0.078	Reactome	1.108	BCAN;CSPG5
WP4313	Ferroptosis	40	3	16.43	0.0011	0.07	Wikipathway	1.155	SLC3A2;SAT2;ACSL4
WP1591	Heart Development	44	3	14.83	0.0014	0.07	Wikipathway	1.155	NOTCH1;VEGFB;NFATC4
WP268	Notch Signaling	45	3	14.47	0.0015	0.07	Wikipathway	1.155	NOTCH1;DTX3;RFNG
R-HSA-1474244	Extracellular matrix organization	283	7	5.29	0.00058	0.042	Reactome	1.377	DDR1;BCAN;LAMA5;COL16A1;PTPRS;COL6A1;LTBP3

Supplementary Table 4_Astrocyte MEGENA modules
Pathology enrichment

Positive logFC values indicate a higher enrichment with pathology

Amyloid-pathology

Co-expression module	logFC	P.Value	adj.P.Val
c1_3	-0.06859778	0.770659255	0.875925579
c1_4	-0.293860665	0.420888066	0.587028092
c1_5	-0.305587773	0.273096821	0.54196649
c1_6	-0.079824225	0.694585651	0.818067544
c1_8	0.454540874	0.077108067	0.340560628
c1_9	1.559016384	0.000247637	0.003281187
c1_10	-0.396756475	0.07060206	0.34017356
c1_11	-0.400185388	0.313135127	0.54196649
c1_12	-0.641982034	0.022802997	0.151069854
c1_13	1.182116093	0.145035488	0.452169464
c1_16	-0.207024806	0.390488261	0.574885495
c1_17	-0.467720407	0.517766138	0.669307447
c1_18	-0.127940017	0.776764193	0.875925579
c1_19	-0.290918128	0.367318118	0.556224579
c1_21	-0.271745458	0.553188396	0.698071071
c1_22	0.046291632	0.945835147	0.945835147
c1_23	-1.234766179	0.192284314	0.536372033
c1_24	0.328108419	0.49800718	0.659859514
c1_25	-0.13622104	0.569094838	0.701442474
c1_26	0.544847304	0.045101098	0.239035817
c1_27	0.028805576	0.943497552	0.945835147
c1_28	1.866372275	0.037553386	0.22114772
c1_29	1.836336771	0.000131389	0.002573233
c1_30	0.914491167	0.241374039	0.54196649
c1_32	-1.094852605	0.005607146	0.04952979
c1_33	0.025093669	0.923994014	0.945835147
c1_34	-0.595811145	0.104036173	0.399445376
c1_36	-0.430635271	0.296555333	0.54196649
c1_37	-0.681094856	0.016719801	0.126592779
c1_41	1.424539976	0.337524278	0.542084447
c1_46	-0.27568285	0.259877663	0.54196649
c1_47	-0.333128973	0.320578586	0.54196649
c1_51	0.385137827	0.450845351	0.612687272
c1_53	-0.243333831	0.363890385	0.556224579
c1_54	0.309517354	0.32722505	0.54196649
c1_61	0.435492337	0.127393979	0.421992554
c1_62	1.65850416	0.110690437	0.399445376
c1_65	1.453411772	0.182186565	0.536372033
c1_66	2.669025097	0.000145655	0.002573233
c1_78	1.092524906	0.248128164	0.54196649
c1_80	-1.195901964	0.002970513	0.031487435
c1_83	-0.021896459	0.936105395	0.945835147
c1_86	-0.424631693	0.306445098	0.54196649
c1_89	1.077959421	0.589070715	0.709562452
c1_92	-0.271847814	0.271903138	0.54196649
c1_95	0.110383254	0.914865889	0.945835147
c1_96	0.464238962	0.402648742	0.576767117
c1_99	-0.283404927	0.296587568	0.54196649
c1_106	0.459532508	0.113050578	0.399445376
c1_108	2.776922194	8.47E-05	0.002573233
c1_112	0.036996988	0.897509781	0.945835147
c1_117	-0.27405863	0.269141455	0.54196649
c1_119	-0.312564613	0.265138855	0.54196649

pTau pathology

Co-expression module	logFC	P.Value	adj.P.Val
c1_3	0.209969455	0.29858848	0.494537171
c1_4	-0.10412534	0.739709466	0.891013674
c1_5	-0.374587327	0.117581474	0.250112001
c1_6	-0.233831533	0.180281995	0.353886879
c1_8	-0.006399877	0.976869411	0.976869411
c1_9	1.767123627	1.30E-06	1.73E-05
c1_10	-0.450575706	0.016758831	0.080747097
c1_11	-0.675226545	0.047410314	0.167516441
c1_12	-0.654586064	0.006844468	0.051822399
c1_13	1.726224321	0.013171821	0.070538104
c1_16	0.029044349	0.888386781	0.905471142
c1_17	0.279000683	0.653106788	0.821398545
c1_18	-0.260231335	0.501681526	0.699404505
c1_19	-0.477066394	0.085031213	0.204847921
c1_21	-0.488692757	0.214124495	0.391330974
c1_22	0.381131129	0.514656145	0.699404505
c1_23	-0.672258624	0.408266218	0.65570029
c1_24	0.243893344	0.55734765	0.738485636
c1_25	-0.305731317	0.136565391	0.278383298
c1_26	0.173749962	0.456660171	0.691513973
c1_27	-0.621283766	0.07494616	0.204847921
c1_28	1.568771222	0.041710681	0.158372208
c1_29	2.054629163	6.22E-07	1.10E-05
c1_30	1.284860386	0.055166692	0.182739667
c1_32	-0.893856771	0.008429792	0.055847371
c1_33	-0.097328938	0.666417688	0.821398545
c1_34	-0.778808534	0.013309076	0.070538104
c1_36	-0.720942079	0.041771851	0.158372208
c1_37	-0.682142356	0.005242011	0.046304427
c1_41	1.494312166	0.241202516	0.426124445
c1_46	-0.049693107	0.812978419	0.892042551
c1_47	-0.543206289	0.05918544	0.184519313
c1_51	0.307168593	0.483582004	0.699404505
c1_53	-0.375104864	0.102987235	0.237318411
c1_54	-0.050401422	0.85256374	0.892042551
c1_61	0.04375695	0.858380568	0.892042551
c1_62	1.175904721	0.187677162	0.355246057
c1_65	1.462043015	0.117977359	0.250112001
c1_66	3.107801305	2.57E-07	6.81E-06
c1_78	1.414253003	0.081576634	0.204847921
c1_80	-0.977743629	0.004663508	0.046304427
c1_83	-0.153025297	0.513980607	0.699404505
c1_86	-0.725363854	0.041834168	0.158372208
c1_89	1.34206982	0.433354868	0.675523765
c1_92	-0.041206877	0.846169426	0.892042551
c1_95	-0.494808375	0.576672413	0.745454582
c1_96	0.509790776	0.28434592	0.486139798
c1_99	-0.410030284	0.078537451	0.204847921
c1_106	0.053330337	0.830365737	0.892042551
c1_108	3.217133701	1.12E-07	5.96E-06
c1_112	-0.064023202	0.795121006	0.892042551
c1_117	-0.040425998	0.849397095	0.892042551
c1_119	-0.437095093	0.069472986	0.204559349

Supplementary Table 4_Astrocyte MEGENA modules
Enrichment other datasets

Positive logFC values indicate a higher enrichment in AD compared to Control

Grubman et al 2019, doi: 10.1038/s41593-019-0539-4

Co-expression module	logFC	P.Value	adj.P.Val
c1_3	0.049461881	4.00E-07	5.17E-07
c1_4	0.238267601	8.24E-18	1.75E-17
c1_5	-0.142380073	3.40E-22	1.00E-21
c1_6	-0.258733709	2.44E-155	3.23E-154
c1_8	-0.027240801	0.032764228	0.035438858
c1_9	0.253162063	5.01942E-28	1.77353E-27
c1_10	0.100150497	1.63E-17	3.33E-17
c1_11	0.321683462	2.56E-45	2.26E-44
c1_12	-0.08371632	1.60E-07	2.12E-07
c1_13	-0.086340282	0.012933065	0.014280259
c1_16	0.067950687	8.13E-11	1.31E-10
c1_17	0.572760706	3.98E-29	1.51E-28
c1_18	-0.031314602	0.450093306	0.450093306
c1_19	-0.221752679	1.03E-33	4.97E-33
c1_21	-0.099868959	0.001153473	0.001358535
c1_22	-0.124475013	0.001123915	0.001353806
c1_23	0.35381773	1.37E-07	1.86E-07
c1_24	0.040052847	0.181832557	0.19274251
c1_25	-0.292387868	3.10E-154	3.29E-153
c1_26	-0.054823547	0.000196345	0.000242007
c1_27	-0.185056692	2.37E-10	3.69E-10
c1_28	0.692081873	2.04E-32	8.31E-32
c1_29	0.270728909	8.89E-25	2.95E-24
c1_30	0.263092626	3.27318E-09	4.68861E-09
c1_32	0.252232245	5.49E-24	1.71E-23
c1_33	0.125287878	3.11E-14	5.50E-14
c1_34	-0.08239362	0.001265692	0.001458297
c1_36	0.311008328	3.72E-41	2.46E-40
c1_37	-0.089681739	1.89E-08	2.63E-08
c1_41	-0.515878938	4.39E-10	6.47E-10
c1_46	0.099216802	6.77E-20	1.79E-19
c1_47	-0.254638704	4.00E-40	2.36E-39
c1_51	0.03456916	0.266361621	0.276807175
c1_53	-0.348137387	1.03E-183	1.81E-182
c1_54	-0.14748805	6.43E-15	1.26E-14
c1_61	-0.116708848	1.27E-12	2.11E-12
c1_62	0.063607457	0.27574471	0.281047493
c1_65	0.561295942	2.47E-18	5.70E-18
c1_66	0.444145514	4.73E-34	2.51E-33
c1_78	0.428373651	1.24E-14	2.36E-14
c1_80	0.226974949	5.33E-18	1.18E-17
c1_83	0.133241722	1.33E-14	2.43E-14
c1_86	0.316057009	2.17E-41	1.64E-40
c1_89	-0.630317558	2.97E-10	4.50E-10
c1_92	0.099516636	8.29E-20	2.09E-19
c1_95	-0.285967326	1.03E-05	1.30E-05
c1_96	0.105991671	0.003183604	0.003590021
c1_99	-0.367766906	1.25E-194	3.31E-193
c1_106	-0.122860339	1.00E-13	1.71E-13
c1_108	0.439807834	1.28E-33	5.65E-33
c1_112	0.171113616	1.12E-20	3.13E-20
c1_117	0.097768607	4.06E-19	9.78E-19
c1_119	-0.397116145	1.41E-206	7.48E-205

Mathys et al 2019, doi: 10.1038/s41586-019-1195-2

Co-expression module	logFC	P.Value	adj.P.Val
c1_3	-0.006947811	0.283634747	0.37581604
c1_4	0.073123904	7.22E-07	3.83E-06
c1_5	-0.010214001	0.210054451	0.309246831
c1_6	-0.022982624	0.000708684	0.002209427
c1_8	-0.018062078	0.022823257	0.046524332
c1_9	0.085495915	1.59822E-10	2.82351E-09
c1_10	-0.017228138	0.028122846	0.055204105
c1_11	0.024980953	0.05652905	0.099867989
c1_12	-0.011312795	0.254581128	0.345969225
c1_13	0.049784241	0.013091206	0.030166692
c1_16	-0.024173045	0.000630718	0.002089252
c1_17	0.170902212	1.48E-13	7.86E-12
c1_18	-0.000761956	0.971416724	0.980747539
c1_19	-0.008624374	0.374478076	0.461566001
c1_21	-0.041997313	0.009825871	0.023671417
c1_22	0.023261411	0.206356253	0.309246831
c1_23	-0.096075718	0.006100189	0.015395715
c1_24	-0.00586585	0.680176164	0.767007163
c1_25	-0.025683157	0.000384102	0.001454101
c1_26	0.007511351	0.391967613	0.472142807
c1_27	-0.089833808	5.47E-11	1.45E-09
c1_28	0.029876575	0.248790751	0.345969225
c1_29	0.076114846	2.26E-07	2.00E-06
c1_30	0.117870058	5.46598E-07	3.21886E-06
c1_32	-0.009897032	0.450446206	0.530525532
c1_33	-0.010088313	0.300956422	0.389041229
c1_34	-0.04711322	0.00046515	0.001643529
c1_36	0.026865694	0.047919769	0.087577509
c1_37	-0.013258481	0.186213254	0.290273601
c1_41	-0.15860211	0.000276202	0.001219892
c1_46	-0.02046982	0.004924115	0.013048905
c1_47	-0.020347305	0.043543774	0.082422144
c1_51	0.003384027	0.818962345	0.868100085
c1_53	-0.032386483	2.41E-05	0.000115899
c1_54	-0.00478179	0.672464566	0.767007163
c1_61	0.01108666	0.24590283	0.345969225
c1_62	-0.053904452	0.066558467	0.113793508
c1_65	0.007337203	0.811484075	0.868100085
c1_66	0.122515222	2.22E-09	2.94E-08
c1_78	0.10338037	0.000308896	0.001259344
c1_80	0.000331038	0.980747539	0.980747539
c1_83	0.003400177	0.740960268	0.818143629
c1_86	0.022656167	0.09786834	0.162094439
c1_89	-0.119013441	0.016380381	0.034726408
c1_92	-0.020923555	0.004283068	0.011947505
c1_95	0.0848138	0.01614217	0.034726408
c1_96	-0.016589984	0.327237504	0.412942565
c1_99	-0.039291667	4.66E-07	3.14E-06
c1_106	0.014609767	0.13047484	0.209550501
c1_108	0.106191114	4.74E-07	3.14E-06
c1_112	-0.001391519	0.895534214	0.930653203
c1_117	-0.021114616	0.004073622	0.011947505
c1_119	-0.041790322	1.60E-07	1.69E-06

Zhou et al 2020, doi: 10.1038/s41591-019-0695-9

Co-expression module	logFC	P.Value	adj.P.Val
c1_3	0.045780677	9.97E-28	1.82E-27
c1_4	0.103627858	1.93E-20	3.29E-20
c1_5	0.143620904	3.00E-94	7.56E-94
c1_6	0.119473594	2.29E-83	5.52E-83
c1_8	0.164210011	8.78E-109	2.58E-108
c1_9	0.041606692	1.35769E-07	1.99882E-07
c1_10	-0.216313508	1.91E-268	2.53E-267
c1_11	-0.405628331	0	0
c1_12	0.064063064	2.46E-19	4.08E-19
c1_13	0.292242852	2.01E-166	9.70E-166
c1_16	0.007532299	0.129067951	0.159083753
c1_17	0.181272053	4.29E-31	8.12E-31
c1_18	0.000523756	0.972802243	0.972802243
c1_19	0.11083771	6.86E-47	1.45E-46
c1_21	-0.055436335	3.44E-05	4.68E-05
c1_22	0.372170104	1.03E-187	6.06E-187
c1_23	0.005893917	0.784486182	0.822245386
c1_24	-0.057942939	3.10E-07	4.32E-07
c1_25	0.147415696	7.60E-98	2.01E-97
c1_26	0.176093603	2.29E-101	6.37E-101
c1_27	-0.003155673	0.791217258	0.822245386
c1_28	0.508773306	3.00E-130	1.22E-129
c1_29	-0.001503693	0.871898548	0.888665827
c1_30	0.203383984	3.19236E-55	7.04981E-55
c1_32	-0.283850747	1.03E-254	1.09E-253
c1_33	-0.218015901	1.26E-163	5.58E-163
c1_34	-0.075782955	1.25E-13	1.96E-13
c1_36	-0.415588048	0	0
c1_37	0.063842304	8.49E-19	1.36E-18
c1_41	0.083872189	0.006284511	0.008326977
c1_46	-0.003667788	0.477957222	0.527744433
c1_47	0.131544926	2.83E-58	6.52E-58
c1_51	-0.025298488	0.031786282	0.04011126
c1_53	0.18474917	1.58E-125	5.99E-125
c1_54	0.116805472	4.89E-23	8.63E-23
c1_61	0.107475927	1.14E-34	2.24E-34
c1_62	0.561498226	2.11E-168	1.12E-167
c1_65	0.538029007	1.94E-115	6.43E-115
c1_66	0.01274467	0.241413692	0.284354636
c1_78	0.097858526	6.97E-13	1.06E-12
c1_80	-0.282075227	1.96E-234	1.73E-233
c1_83	-0.277714002	1.27E-221	9.65E-221
c1_86	-0.418538673	0	0
c1_89	0.191940738	1.40E-07	2.01E-07
c1_92	-0.004276834	0.408735148	0.460914103
c1_95	0.038785696	0.257723555	0.296942357
c1_96	-0.031324077	0.013993182	0.018088748
c1_99	0.178435848	3.77E-115	1.17E-114
c1_106	0.109012072	4.66E-35	9.51E-35
c1_108	0.005734277	0.604738863	0.654105301
c1_112	-0.284627632	7.38E-219	4.89E-218
c1_117	-0.0060824	0.241433181	0.284354636
c1_119	0.186579028	9.38E-120	3.32E-119

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Co-expression module	logFC	P.Value	adj.P.Val
c1_3	0.075916706	0	0
c1_4	0.016337584	2.26E-14	2.73E-14
c1_5	-0.058606949	0	0
c1_6	-0.04730356	0	0
c1_8	-0.09745998	0	0
c1_9	0.078383121	1.41547102464818e-313	3.00079857227589e-313
c1_10	0.034590295	1.45E-215	2.55E-215
c1_11	0.131502765	0	0
c1_12	-0.011737617	2.90E-18	3.75E-18
c1_13	0.003548397	0.416187693	0.424191303
c1_16	0.078699044	0	0
c1_17	-0.012018728	0.010078055	0.011127853
c1_18	0.030931929	1.53E-32	2.13E-32
c1_19	-0.04900626	1.66E-187	2.76E-187
c1_21	-0.017264937	1.65E-12	1.90E-12
c1_22	-0.196589443	0	0
c1_23	-0.078857166	5.68E-48	8.60E-48
c1_24	0.006095102	0.023645017	0.025063718
c1_25	-0.055292338	0	0
c1_26	-0.098517151	0	0
c1_27	-0.060445824	9.57E-162	1.54E-161
c1_28	-0.346598217	0	0
c1_29	0.106274546	0	0
c1_30	0.039346668	6.6953E-14	7.88558E-14
c1_32	0.085027649	2.10E-269	4.27E-269
c1_33	-0.001170824	0.394023522	0.409475425
c1_34	0.061686408	3.69E-253	6.99E-253
c1_36	0.142860632	0	0
c1_37	-0.011574435	1.95E-17	2.45E-17
c1_41	-0.030204861	3.65E-06	4.12E-06
c1_46	0.081521428	0	0
c1_47	-0.059693744	1.82E-251	3.33E-251
c1_51	0.000659386	0.815515666	0.815515666
c1_53	-0.073998199	0	0
c1_54	-0.023484961	2.67E-36	3.82E-36
c1_61	-0.076555442	0	0
c1_62	-0.283321687	0	0
c1_65	-0.350149602	0	0
c1_66	0.163116448	0	0
c1_78	0.069036167	4.01E-25	5.45E-25
c1_80	0.075848097	4.28E-199	7.31E-199
c1_83	0.018520326	6.30E-37	9.27E-37
c1_86	0.14167171	0	0
c1_89	0.025665927	0.020423319	0.022090528
c1_92	0.083949835	0	0
c1_95	-0.102079457	5.35E-58	8.35E-58
c1_96	0.024653859	3.41E-17	4.20E-17
c1_99	-0.074716093	0	0
c1_106	-0.080577714	0	0
c1_108	0.129076471	1.72E-253	3.38E-253
c1_112	0.014702304	1.67E-21	2.21E-21
c1_117	0.084609327	0	0
c1_119	-0.078920261	0	0

Supplementary Table 4_Astrocyte MEGENA modules
Module specificity scores

Module specificity scores (MSS) in astrocytic subclusters

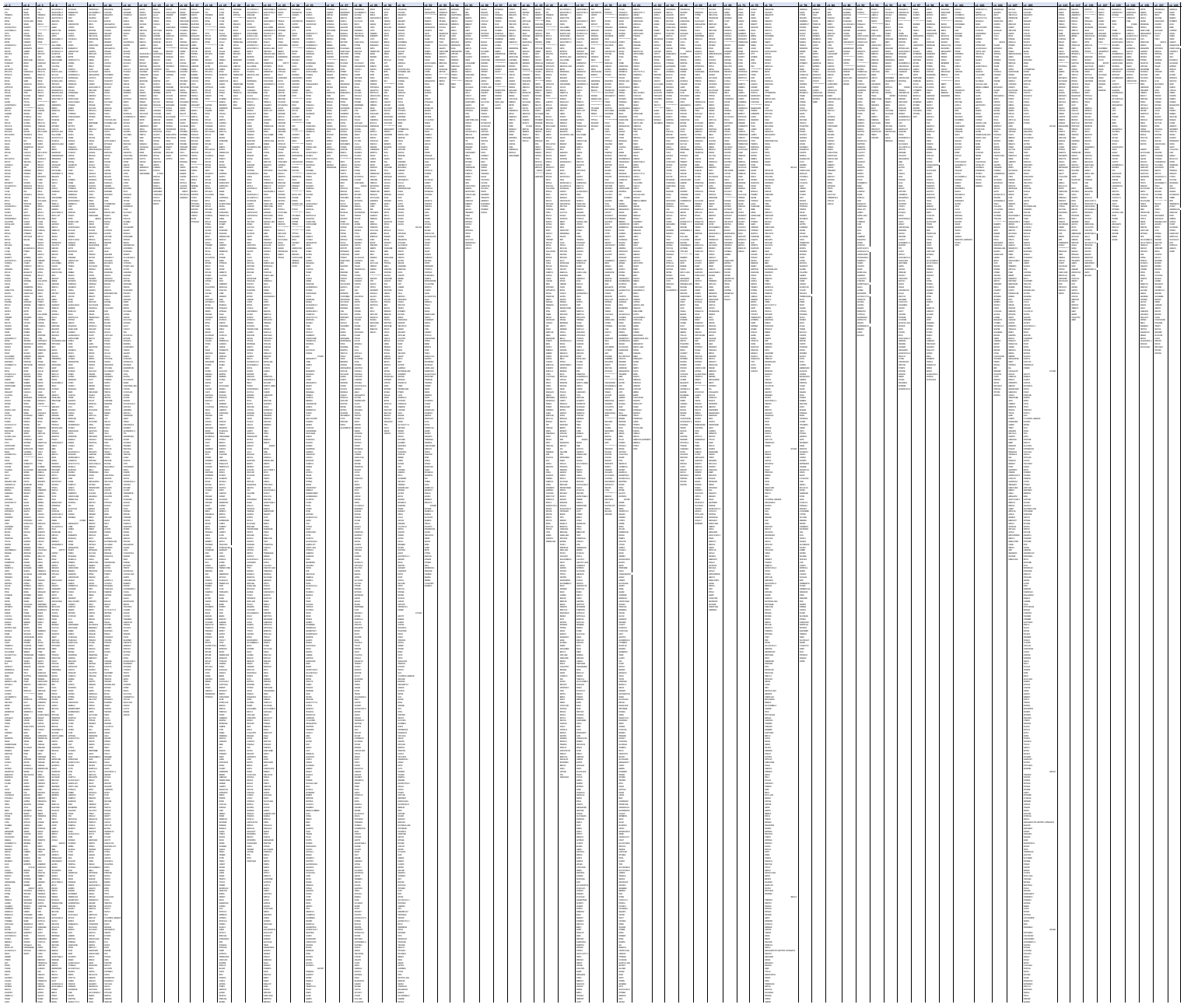
A high module specificity score indicates a relatively specific enrichment of this module for a particular subcluster

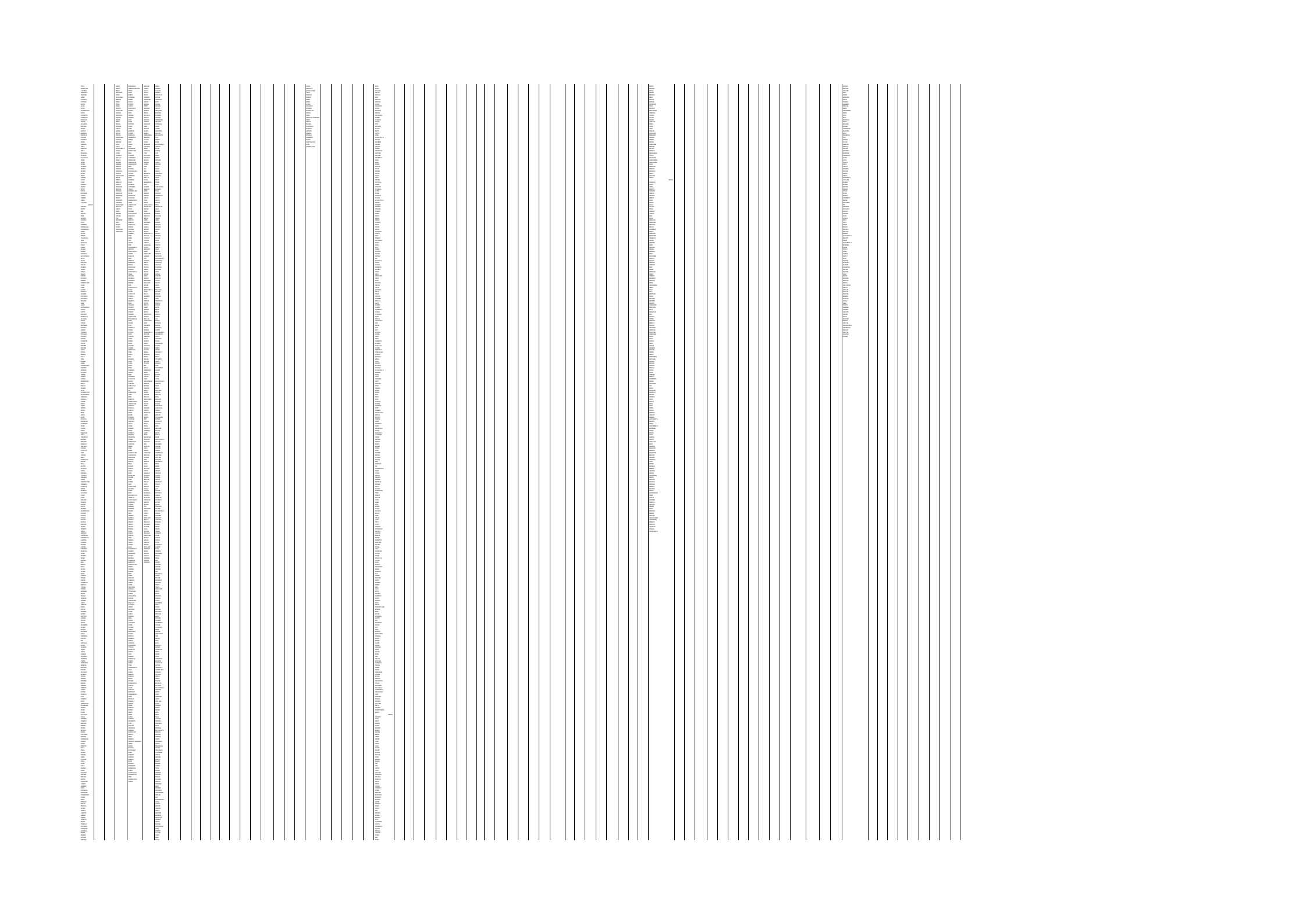
Co-express	Astro1	Astro2	Astro3	Astro4	Astro5	Astro6
c1_3	0.399	0.374	0.329	0.316	0.297	0.215
c1_4	0.400	0.374	0.329	0.312	0.298	0.214
c1_5	0.407	0.388	0.326	0.315	0.279	0.211
c1_6	0.407	0.383	0.328	0.311	0.286	0.211
c1_8	0.403	0.385	0.326	0.313	0.288	0.211
c1_9	0.392	0.369	0.326	0.313	0.308	0.218
c1_10	0.399	0.377	0.325	0.324	0.290	0.212
c1_11	0.393	0.369	0.323	0.331	0.296	0.211
c1_12	0.403	0.375	0.332	0.310	0.295	0.213
c1_13	0.394	0.377	0.321	0.309	0.286	0.215
c1_16	0.399	0.373	0.329	0.316	0.297	0.215
c1_17	0.389	0.363	0.325	0.311	0.303	0.214
c1_18	0.402	0.376	0.329	0.310	0.293	0.213
c1_19	0.407	0.389	0.325	0.315	0.277	0.210
c1_21	0.406	0.382	0.327	0.318	0.278	0.210
c1_22	0.401	0.386	0.323	0.308	0.280	0.212
c1_23	0.395	0.374	0.323	0.311	0.290	0.212
c1_24	0.389	0.364	0.325	0.308	0.329	0.216
c1_25	0.409	0.385	0.329	0.311	0.280	0.210
c1_26	0.402	0.381	0.327	0.313	0.293	0.212
c1_27	0.405	0.391	0.322	0.316	0.279	0.209
c1_28	0.400	0.378	0.326	0.299	0.290	0.213
c1_29	0.389	0.363	0.326	0.311	0.315	0.219
c1_30	0.399	0.380	0.324	0.307	0.284	0.216
c1_32	0.395	0.375	0.323	0.329	0.289	0.212
c1_33	0.400	0.377	0.325	0.323	0.292	0.212
c1_34	0.401	0.378	0.326	0.320	0.286	0.212
c1_36	0.393	0.368	0.323	0.332	0.295	0.211
c1_37	0.403	0.375	0.332	0.309	0.294	0.213
c1_41	0.392	0.382	0.317	0.308	0.274	0.208
c1_46	0.399	0.373	0.329	0.316	0.298	0.215
c1_47	0.408	0.390	0.325	0.315	0.276	0.210
c1_51	0.388	0.363	0.325	0.306	0.333	0.216
c1_53	0.410	0.386	0.329	0.310	0.278	0.210
c1_54	0.408	0.384	0.327	0.312	0.282	0.210
c1_61	0.402	0.382	0.327	0.314	0.291	0.212
c1_62	0.397	0.387	0.317	0.311	0.274	0.211
c1_65	0.400	0.378	0.326	0.296	0.289	0.212
c1_66	0.379	0.354	0.323	0.309	0.325	0.221
c1_78	0.392	0.373	0.322	0.310	0.294	0.218
c1_80	0.397	0.377	0.323	0.328	0.287	0.212
c1_83	0.399	0.376	0.325	0.324	0.291	0.212
c1_86	0.392	0.368	0.323	0.332	0.295	0.211
c1_89	0.384	0.379	0.312	0.300	0.268	0.208
c1_92	0.399	0.373	0.329	0.316	0.298	0.215
c1_95	0.392	0.371	0.318	0.296	0.316	0.220
c1_96	0.385	0.359	0.326	0.308	0.338	0.216
c1_99	0.410	0.386	0.329	0.310	0.278	0.210
c1_106	0.402	0.382	0.326	0.314	0.290	0.212
c1_108	0.380	0.355	0.322	0.308	0.324	0.220
c1_112	0.398	0.376	0.325	0.324	0.293	0.212
c1_117	0.399	0.373	0.329	0.316	0.298	0.215
c1_119	0.410	0.387	0.329	0.310	0.277	0.210

Supplementary Table 5_Microglia MEGENA Modules
Contents

Sheet name	Description
Module_list	MEGENA Gene Co-expression Modules in Microglia
Module_description	MEGENA Gene Co-expression Module description
Module 11 FE	Functional enrichment of Module 11 (GPNMB hub gene) genes by enrichR
Module 34 FE	Functional enrichment of Module 34 (GPNMB hub gene) genes by enrichR
Module 19 FE	Functional enrichment of Module 19 (APOE hub gene) genes by enrichR
Pathology_enrichment	logFC of the enrichment (AUCell and limma) of modules with amyloid-beta and pTau pathology
Enrichment_other_datasets	logFC of the enrichment (AUCell and limma) of modules in AD samples compared to Control samples from previous studies
MSS	Module specificity scores (MSS) in microglial subclusters

Supplementary Table 5_Microglia MEGENA Modules
Module list





Supplementary Table 5_Microglia MEGENA Modules
Module description

MEGENA Gene Co-expression Module description

Co-expression module	Module size	Parent module	Hub genes (number of edges in parentheses)
c1_2	1664	c1_1	DLEU7(342),AC220159.1(265),CSGC(264),DDX5(211),AC044781.1(184),FTL(170),AP003086.2(170),CD74(120),TMSB4X(83),PSAP(66),C1QB(65),RAPGEF1(65),APOE(65),RPL19(63),IFI27(63),RGS1(60),SRGN(60),MALAT1(52),HIF1A-AS2(50),PFKFB3(49),ACTB(46),B2M(42),ABHD15-AS1(38),CTSB(31),TTC7A(31),FTH1(28),ANKUB1(28),HSPA5(28),SAT1(27),HIST2H2BE(26),NABP1L2(25),PGK1(25),TUBA1B(24),HSP90B1(24),DNAJC3(24),WSB1(24),AC016739.1(22),HNRNPA2B1(22),FAM177B(21),ITGB2(21),FKBP1A(21),STX7(21),NEAT1(20),FRG1H(20),TPT1(19),CPED1(18),PPP6R3(18),RAB11A(17),AC073861.1(16),ENTPD1-AS1(16),PDE8A(16),C1QA(15),AC079793.1(15),HDAC9(15),ANKRD10(14)
c1_4	317	c1_2	BAIAP2(105),RGS1(59),HIF1A(59),SRGN(56),MALAT1(52),HIF1A-AS2(50),PFKFB3(49),TTC7A(31),SAT1(27),PGK1(25),NEAT1(20),CPED1(19),PDE8A(16),HDAC9(15)
c1_5	610	c1_2	C1QC(284),FTL(168),CD74(99),TMSB4X(83),PSAP(66),C1QB(65),APOE(65),RPL19(63),ACTB(46),B2M(42),CTSB(31),HSPA5(28),TUBA1B(24),HSP90B1(24),DNAJC3(24),IFITM1(23),AC016739.1(22),FCGR3A(21),TPT1(19),AC073861.1(16),C1QA(15)
c1_6	737	c1_2	DLEU7(341),AC220159.1(284),DDX5(211),AC044781.1(184),APOD(086.2)(170),ABHD15-AS1(38),ANKUB1(28),HIST2H2BE(26),NABP1L2(25),WSB1(24),HNRNPA2B1(22),FAM177B(21),ITGB2(21),FKBP1A(20),PPP6R3(18),RAB11A(17),ENTPD1-AS1(16),AC079793.1(15),ANKRD10(14)
c1_7	983	c1_3	HSPA1(103),DPYD(92),PICALM(88),APOD(977.1(87),P2RY12(78),BASGEF1C(73),NAV3(63),ANKRD44(60),CD163(57),FRMD4A(51),SORL1(46),IPCEF1(43),XIST(42),KCNQ3(39),PALD1(38),MGAT4A(36),LSAMP(33),UNGO1(32),F13A1(32),SYNDIG1(28),ACSL1(27),IFI44L(26),HSP90AA1(25),A2M(25),CHORDC1(24),ACO08691.1(24),SOCS6(24),TLN2(24),EPST1(24),FRMD4B(23),UTY(22),ABCC4(22),JAZF1(22),LRRK2(21),CTNNA2(20),NTM(19),DOCK8(19),LINC02232(18),TGFBI(18),C3(18),OLR1(18),AC007262.2(18),LINC00278(16),AC011586.2(15),ZNFBD4A(15),SLC26A3(14),HSPB1(14),DOCK4(14)
c1_9	885	c1_3	DENND3(172),SLC11A1(158),GRB2(140),SND1(117),TMEM163(108),PTPN2(100),TGFBR1(79),SH3RF3(76),TBC1D14(67),SCFD2(62),NCK2(58),PVT1(50),PRKCA(46),EIF2(35),SUSD6(28),JARS(26),ZFAND3(26),BIRC6(26),LYN(25),RNF149(22),HIVEP3(20),WDFY3(19),GNAQ(18),A1034397.3(17),BACH1(17),MAPKAP1(16),PAG1(15),ETV6(15),IL4R(15),SLC2A3(14),AC011933.4(14)
c1_10	1362	c1_3	SRGAP2(674),SRGAP2-2(94),SRGAP2(147),CSGALNACT1(166),IL6ST(127),HNRNPC(97),TCF12(92),ITM2B(83),FGD2(79),MED13L(75),CX3CR1(37),HIS1T6(27),ARHGAP24(34),TENT2(33),ELMO2(31),PTPRJ(30),CCND2(27),SWAP22(7),KANSL1(25),ATP2C1(25),ANKS1A(21),ANKRD17(19),CSF1R(18),APBB1IP(17),CAB39(16),ZMAT3(15),MGAT5(15),BHLHE41(15),RASA1(15),ACTR2(14)
c1_11	237	c1_3	ASAH1(73),GPNMB(68),ATG7(65),KCNMA1(64),STARD13(61),NPL(28),IQGAP2(21),CPVL(18),TANC2(18),MERTK(17),MITF(16),SNX29(15)
c1_12	58	c1_4	MALAT1(42),CPED1(17),HDAC9(15)
c1_13	66	c1_4	PFKFB3(44),TTC7A(31),RGS1(29)
c1_15	51	c1_4	HIF1A-AS2(49),PGK1(25)
c1_16	64	c1_4	SRGN(50),SAT1(21)
c1_17	72	c1_4	RAPGEF1(64),HIF1A(28),NEAT1(20)
c1_18	231	c1_5	FTL(146),TMSB4X(80),RPL19(63),ACTB(46),TUBA1B(24),FTH1(23),AC016739.1(22),TPT1(19),AC073861.1(16)
c1_19	344	c1_5	C1QC(283),CD74(86),PSAP(66),APOE(65),C1QB(64),B2M(35),CTSB(27),FCGR3A(21),C1QA(14)
c1_20	34	c1_5	DNAJC3(23),HSPB8(19)
c1_21	286	c1_6	AC220159.1(203),AC044781.1(116),ABHD15-AS1(38),FAM177B(21),ANKUB1(18),RAB11A(17),ENTPD1-AS1(16),HIST2H2BE(14),WSB1(14)
c1_22	366	c1_6	DLEU7(336),AP003086.2(78),AC079793.1(13),DLEU1(13)
c1_23	84	c1_6	DDX5(75),HNRNPA2B1(21),NABP1(21,20),PPP6R3(17),STX7(16)
c1_24	87	c1_7	XIST(37),LINGO1(32),IFI44L(26),EPST1(24),UTY(22)
c1_25	699	c1_7	HSPA1(103),DPYD(92),APOD1977.1(87),P2RY12(78),BASGEF1C(73),NAV3(62),CD163(57),IPCEF1(43),FRMD4A(42),KCNQ3(39),PALD1(38),MGAT4A(36),F13A1(32),ACSL1(27),SYNDIG1(26),HSP90AA1(25),A2M(25),CHORDC1(24),AC008691.1(24),SOCS6(24),TLN2(24),FRMD4B(23),JAZF1(22),LRRK2(21),DOCK8(19),TGFBI(18),C3(18),OLR1(18),AC007262.2(18),LINC02232(16),AC011586.2(15),ZNFBD4A(15),HSPB1(14)
c1_26	54	c1_7	LSAMP(33),NTM(19),CTNNA2(18)
c1_27	141	c1_7	PICALM(88),ANKRD44(57),SORL1(40)
c1_28	633	c1_9	DENND3(172),SLC11A1(158),GRB2(140),PTPN2(100),TMEM163(98),TBC1D14(67),SH3RF3(65),PRKCA(46),EIF2(33),SUSD6(28),ZFAND3(26),LYN(25),RNF149(22),HIVEP3(20),WDFY3(19),BACH1(16),ETV6(15),IL4R(15),SLC2A3(14),AC011933.4(14)
c1_29	109	c1_9	TGFBR1(76),NCK2(25),GNAQ(18),PAG1(15)
c1_30	143	c1_9	SND1(117),SCFD2(46),PVT1(29),BIRC6(26),JARS(20),MAPKAP1(16)
c1_31	1168	c1_10	SRGAP2(674),SRGAP2-2(94),SRGAP2(147),IL6ST(127),HNRNPC(97),TCF12(92),FGD2(79),MED13L(75),CX3CR1(37),TENT2(33),PTPRJ(30),KANSL1(25),ANKS1A(21),ANKRD17(19),CSF1R(18),APBB1IP(17),ATP2C1(17),CAB39(16),ZMAT3(15),MGAT5(15),BHLHE41(15),RASA1(15),ACTR2(14)
c1_32	194	c1_10	CSGALNACT1(147),TMEM163(65),ARHGAP24(14),ELMO2(11),HIS1T6(2B),CCND2(27),SWAP22(22)
c1_33	26	c1_11	STARD13(20),IQGAP2(16)
c1_34	27	c1_11	GPNMB(23)
c1_35	81	c1_11	ATG7(62),NPL(24),MERTK(17)
c1_36	69	c1_11	ASAH1(67)
c1_37	34	c1_11	KCNMA1(25),CPVL(12)
c1_39	50	c1_12	MALAT1(42),CPED1(17)
c1_41	45	c1_13	PFKFB3(43),RGS1(20),TTC7A(20)
c1_43	57	c1_16	SRGN(49),SAT1(14)
c1_45	179	c1_18	FTL(144),RPL19(63),TMSB4X(42),FTH1(23),AC016739.1(22),TPT1(19),AC073861.1(16)
c1_49	258	c1_21	AC220159.1(203),AC044781.1(85),ABHD15-AS1(38),FAM177B(21),ANKUB1(18),RAB11A(17),ENTPD1-AS1(16),WSB1(14)
c1_55	345	c1_22	DLEU7(336),AP003086.2(57),AC079793.1(13),DLEU1(13)
c1_57	41	c1_24	XIST(30),UTY(20),LINC02278(14)
c1_59	170	c1_25	P2RY12(72),IPCEF1(38),AZM(25),SOCS6(24),JAZF1(22),OLR1(18),DOCK8(15),AC011586.2(13),CD83(13)
c1_60	381	c1_25	DPYD(92),BASGEF1C(68),CD163(57),NAV3(55),FRMD4A(42),PALD1(38),MGAT4A(36),KCNQ3(33),F13A1(32),ACSL1(27),SYNDIG1(26),TLN2(24),FRMD4B(23),LRRK2(21),TGFBI(18),C3(18),LINC02232(16),ZNFBD4A(15)
c1_61	148	c1_25	HSPA1(103),AP003077.1(84),CHORDC1(24),HSP90AA1(22),AC007262.2(18)
c1_62	39	c1_27	SORL1(28),FMN1(12),RASAL2(11)
c1_64	95	c1_27	PICALM(87),ANKRD44(38)
c1_65	160	c1_28	TMEM163(90),SH3RF3(40),PRKCA(28),EIRC2(23),HIVEP3(20),BACH1(15)
c1_66	173	c1_28	DENND3(148),EIF4G3(12)
c1_67	202	c1_28	SLC11A1(147),TBC1D14(45),RNF149(22),WDFY3(19),ETV6(15),SLC2A3(14)
c1_68	96	c1_28	GRB2(85),PTPN2(13),ZFAND3(20),SUSD6(18)
c1_71	82	c1_29	TGFBR1(76),NCK2(29),GNAQ(18),PAG1(15)
c1_75	122	c1_30	SND1(117),SCFD2(27),BIRC6(26),MAPKAP1(16)
c1_76	871	c1_31	SRGAP2(674),SRGAP2(246),SRGAP2(199),IL6ST(127),HNRNPC(97),MED13L(75),CX3CR1(36),TENT2(33),KANSL1(25),ATP2C1(17),RASA1(15),CAB39(15),BHLHE41(14),ACTR2(14)
c1_78	219	c1_31	TCF12(90),FGD2(77),PTPRJ(25),ANKS1A(19),ANKRD17(18),MGAT5(14),PIK3R1(11)
c1_80	32	c1_31	()
c1_84	66	c1_35	ATG7(61)
c1_86	28	c1_37	KCNMA1(22)
c1_92	110	c1_59	P2RY12(71),AZM(24),SOCS6(23),DOCK8(14),ACD11586.2(13)
c1_93	44	c1_59	IPCEF1(30),SKAP2(9)
c1_95	45	c1_60	CD163(30),F13A1(28)
c1_96	128	c1_60	RASGEF1C(60),FRMD4A(36),KCNQ3(30),SYNDIG1(19),PALD1(18),C3(16)
c1_97	32	c1_60	NAV3(31)
c1_98	125	c1_60	DPYD(89),ACSL1(24),FRMD4B(23),LRRK2(21),TGFBI(17)
c1_99	30	c1_60	MGAT4A(27)
c1_101	80	c1_61	HSPA1(70),CHORDC1(21),HSP90AA1(17)
c1_102	60	c1_61	AP003977.1(54),AC007262.2(15)
c1_104	130	c1_65	TMEM163(90),PRKCA(28),EIRC2(23),HIVEP3(20),SH3RF3(18),BACH1(15)
c1_107	185	c1_67	SLC11A1(147),TBC1D14(32),RNF149(22),WDFY3(19),ETV6(15),SLC2A3(14)
c1_109	784	c1_76	SRGAP2(674),SRGAP2(246),SRGAP2C(199),HNRNPC(97),MED13L(75),IL6ST(48),TENT2(33),CX3CR1(29),KANSL1(25),RASA1(15),CAB39(15)
c1_115	98	c1_78	FGD2(77),PTPRJ(25),ANKS1A(11)
c1_117	105	c1_78	TCF12(89),ANKRD17(18),MGAT5(13)
c1_123	90	c1_92	P2RY12(71),AZM(18),DOCK8(14)
c1_127	28	c1_95	F13A1(24)
c1_129	78	c1_96	RASGEF1C(58),KCNQ3(20),SYNDIG1(15)
c1_130	26	c1_96	FRMD4A(23)
c1_133	114	c1_98	DPYD(89),FRMD4B(23),LRRK2(21),TGFBI(17)
c1_137	116	c1_104	TMEM163(90),EIRC2(23),SH3RF3(18),PRKCA(16),BACH1(15)
c1_145	82	c1_115	FGD2(77)

Supplementary Table 5_Microglia MEGENA Modules
Module 11 FE

geneset	description	size	overlap	odds_ratio	pval	FDR	database	X.Log10.FDR.	genes
GO:0010885	regulation of cholesterol storage	12	4	42.21	0.000009	0.012	GO	1.92082	ABCA1;SCARB1;PPARG;ABCG1
GO:0010887	negative regulation of cholesterol storage	6	3	84.08	0.000032	0.022	GO	1.65758	ABCA1;PPARG;ABCG1

Supplementary Table 5_Microglia MEGENA Modules
Module 34 FE

geneset	description	size	overlap	odds_ratio	pval	FDR	database	X.Log10.FDR.	genes
GO:0010887	negative regulation of cholesterol storage	6	2	384	0.000028	0.0051	GO	2.29	ABCA1;ABCG1
GO:0032366	intracellular sterol transport	7	2	307.18	0.00004	0.0051	GO	2.29	ABCA1;ABCG1
GO:0055091	phospholipid homeostasis	8	2	255.97	0.000053	0.0051	GO	2.29	ABCA1;ABCG1
GO:0032367	intracellular cholesterol transport	10	2	191.96	0.000084	0.006	GO	2.22	ABCA1;ABCG1
GO:0010885	regulation of cholesterol storage	12	2	153.55	0.00012	0.006	GO	2.22	ABCA1;ABCG1
GO:0033700	phospholipid efflux	12	2	153.55	0.00012	0.006	GO	2.22	ABCA1;ABCG1
GO:0010745	negative regulation of macrophage derived foam cell differentiation	13	2	139.59	0.00015	0.0061	GO	2.21	ABCA1;ABCG1
GO:0010888	negative regulation of lipid storage	16	2	109.66	0.00022	0.0082	GO	2.09	ABCA1;ABCG1
GO:0043691	reverse cholesterol transport	17	2	102.34	0.00025	0.0083	GO	2.08	ABCA1;ABCG1
GO:0055081	anion homeostasis	18	2	95.94	0.00029	0.0084	GO	2.08	ABCA1;ABCG1
R-HSA-194223	HDL-mediated lipid transport	19	2	90.29	0.00032	0.00653	Reactome	2.185	ABCA1;ABCG1
GO:0033344	cholesterol efflux	23	2	73.08	0.00047	0.0125	GO	1.9	ABCA1;ABCG1
GO:0010743	regulation of macrophage derived foam cell differentiation	29	2	56.82	0.00075	0.0183	GO	1.74	ABCA1;ABCG1
GO:1902652	secondary alcohol metabolic process	31	2	52.9	0.00086	0.0193	GO	1.71	ABCA1;ABCG1
R-HSA-73923	Lipid digestion, mobilization, and transport	71	4	49.51	0.0000028	0.00011	Reactome	3.959	ABCA1;NCEH1;MGLL;ABCG1
WP299	Nuclear Receptors in Lipid Metabolism and Toxicity	33	2	49.48	0.00097	0.022	Wikipathway	1.66	ABCA1;ABCG1
R-HSA-174824	Lipoprotein metabolism	34	2	47.93	0.001	0.01409	Reactome	1.851	ABCA1;ABCG1
GO:0030301	cholesterol transport	44	2	36.5	0.0017	0.0361	GO	1.44	ABCA1;ABCG1
GO:0006690	icosanoid metabolic process	46	2	34.84	0.0019	0.0368	GO	1.43	LTA4H;MGLL
GO:0055088	lipid homeostasis	49	2	32.61	0.0021	0.0391	GO	1.41	ABCA1;ABCG1
GO:0015914	phospholipid transport	58	2	27.36	0.003	0.0451	GO	1.35	ABCA1;ABCG1
GO:0042632	cholesterol homeostasis	58	2	27.36	0.003	0.0451	GO	1.35	ABCA1;ABCG1
GO:0055092	sterol homeostasis	58	2	27.36	0.003	0.0451	GO	1.35	ABCA1;ABCG1
GO:0016125	sterol metabolic process	59	2	26.88	0.0031	0.0451	GO	1.35	ABCA1;ABCG1
R-HSA-556833	Metabolism of lipids and lipoproteins	659	5	6.42	0.002	0.02053	Reactome	1.688	ABCA1;NCEH1;LTA4H;MGLL;ABCG1

Supplementary Table 5_Microglia MEGENA Modules
Module 19 FE

geneset	description	size	overlap	odds_ratio	pval	FDR	database	X.Log10.FDR.	genes
GO:0002480	antigen processing and presentation of exogenous p	9	5	72.46	0.00000017	0.000043	GO	4.3665	HLA-B;HLA-C;HLA-A;B2M;HLA-E
R-HSA-12369	Endosomal/Vacuolar pathway	12	6	58.14	2.1E-08	0.0000027	Reactome	5.5686	HLA-B;HLA-C;HLA-A;B2M;CTSS;HLA-E
R-HSA-98317	Antigen Presentation: Folding, assembly and peptide	25	11	46.35	1.2E-13	9.3E-11	Reactome	10.0315	PDIA3;SEC13;HSPA5;SAR1B;HLA-B;HLA-C;HLA-A;CALR;B2M;TAPBP;HLA-E
GO:0050686	negative regulation of mRNA processing	15	6	38.75	0.00000011	0.000031	GO	4.5086	PTBP1;RNPS1;TMBIM6;SRSF6;RBMX;SRSF10
GO:0048025	negative regulation of mRNA splicing, via spliceosom	13	5	36.22	0.0000017	0.00034	GO	3.4685	PTBP1;RNPS1;SRSF6;RBMX;SRSF10
GO:1904871	positive regulation of protein localization to Cajal bo	8	3	34.58	0.00026	0.016	GO	1.7959	CCT6A;CCT8;CCT5
GO:1904869	regulation of protein localization to Cajal body	8	3	34.58	0.00026	0.016	GO	1.7959	CCT6A;CCT8;CCT5
GO:0002474	antigen processing and presentation of peptide antig	28	10	32.66	2E-11	0.00000004	GO	7.3979	PDIA3;SEC13;SAR1B;HLA-B;HLA-C;HLA-A;CALR;B2M;TAPBP;HLA-E
GO:0033119	negative regulation of RNA splicing	18	6	29.06	0.00000039	0.000086	GO	4.0655	PTBP1;RNPS1;TMBIM6;SRSF6;RBMX;SRSF10
GO:0036500	ATF6-mediated unfolded protein response	9	3	28.81	0.00039	0.018	GO	1.7447	XBP1;HSPA5;CALR
GO:0035437	maintenance of protein localization in endoplasmic r	9	3	28.81	0.00039	0.018	GO	1.7447	PDIA3;HSPA5;OS9
GO:1904851	positive regulation of establishment of protein locali	9	3	28.81	0.00039	0.018	GO	1.7447	CCT6A;CCT8;CCT5
R-HSA-16791	Trafficking and processing of endosomal TLR	13	4	25.68	0.000054	0.002	Reactome	2.699	UNC93B1;CNPY3;CTSS;CTSB
GO:0070203	regulation of establishment of protein localization to	10	3	24.7	0.00055	0.022	GO	1.6576	CCT6A;CCT8;CCT5
R-HSA-38118	ATF6-alpha activates chaperone genes	10	3	24.7	0.00055	0.012	Reactome	1.9208	XBP1;HSPA5;CALR
R-HSA-39045	Folding of actin by CCT/TriC	10	3	24.7	0.00055	0.012	Reactome	1.9208	CCT6A;CCT8;CCT5
GO:1904816	positive regulation of protein localization to chromo	11	3	21.61	0.00075	0.025	GO	1.6021	CCT6A;CCT8;CCT5
R-HSA-90104	Calnexin/calreticulin cycle	15	4	21.01	0.0001	0.0036	Reactome	2.4437	PDIA3;GANAB;OS9;CALR
GO:1903513	endoplasmic reticulum to cytosol transport	16	4	19.26	0.00013	0.011	GO	1.9586	VCP;OS9;AUP1;HERPUD1
GO:1904951	positive regulation of establishment of protein locali	12	3	19.21	0.00099	0.032	GO	1.4949	CCT6A;CCT8;CCT5
GO:0002183	cytoplasmic translational initiation	12	3	19.21	0.00099	0.032	GO	1.4949	EIF3M;EIF2S3;EIF4H
R-HSA-38102	ATF6-alpha activates chaperones	12	3	19.21	0.00099	0.019	Reactome	1.7212	XBP1;HSPA5;CALR
R-HSA-53266	N-glycan trimming in the ER and Calnexin/Calreticuli	17	4	17.78	0.00017	0.0053	Reactome	2.2757	PDIA3;GANAB;OS9;CALR
GO:0071404	cellular response to low-density lipoprotein particle	13	3	17.28	0.0013	0.035	GO	1.4559	ITGB1;CD81;ITGB2
GO:0046641	positive regulation of alpha-beta T cell proliferation	13	3	17.28	0.0013	0.035	GO	1.4559	EBI3;RASAL3;HLA-E
GO:0030970	retrograde protein transport, ER to cytosol	18	4	16.51	0.00022	0.016	GO	1.7959	VCP;OS9;AUP1;HERPUD1
GO:1902236	negative regulation of endoplasmic reticulum stress-	14	3	15.71	0.0016	0.04	GO	1.3979	XBP1;TMBIM6;HERPUD1
GO:0032527	protein exit from endoplasmic reticulum	19	4	15.4	0.00027	0.016	GO	1.7959	VCP;OS9;AUP1;HERPUD1
GO:1904874	positive regulation of telomerase RNA localization to	15	3	14.4	0.002	0.045	GO	1.3468	CCT6A;CCT8;CCT5
GO:1901797	negative regulation of signal transduction by p53 cla	15	3	14.4	0.002	0.045	GO	1.3468	CD74;RNF34;PTTG1IP
GO:0010955	negative regulation of protein processing	15	3	14.4	0.002	0.045	GO	1.3468	PRNP;TMEM59;CTSZ
R-HSA-16493	Nef-mediates down modulation of cell surface recep	21	4	13.59	0.00041	0.0097	Reactome	2.0132	ARF1;CD4;HLA-A;B2M
GO:0019079	viral genome replication	22	4	12.84	0.00049	0.02	GO	1.699	CDC42;VCP;GRK2;CTBP1
R-HSA-12225	ROS, RNS production in response to bacteria	34	6	12.44	0.000022	0.001	Reactome	3	ATP6V1A;ATP6V0B;ATP6V0E1;NCF4;CYBA;ATP6V0D1
WP3937	Microglia Pathogen Phagocytosis Pathway	40	7	12.35	0.0000048	0.00056	Wikipathway	3.252	C1QB;C1QA;TGB2;NCF4;TREM2;CYBA;C1QC
R-HSA-12369	Antigen processing-Cross presentation	82	13	11.15	1.4E-09	0.00000028	Reactome	6.5528	PDIA3;NCF4;HLA-B;HLA-C;CYBA;HLA-A;CTSS;TAPBP;HLA-E;SEC61A1;PSMC6;CALR;B2M
R-HSA-12369	ER-Phagosome pathway	65	10	10.67	0.00000015	0.000012	Reactome	4.9208	PDIA3;SEC61A1;PSMC6;HLA-B;HLA-C;HLA-A;CALR;B2M;TAPBP;HLA-E
R-HSA-68035	FGFR2 alternative splicing	26	4	10.5	0.00095	0.019	Reactome	1.7212	PTBP1;HNRNPM;POLR2A;HNRNPF
R-HSA-77387	Insulin receptor recycling	26	4	10.5	0.00095	0.019	Reactome	1.7212	ATP6V1A;ATP6V0B;ATP6V0E1;ATP6V0D1
WP3941	Oxidative Damage	40	6	10.24	0.000058	0.0045	Wikipathway	2.347	C1QB;CDC42;C1QA;BAG4;C3AR1;C1QC
GO:0002479	antigen processing and presentation of exogenous p	75	11	10.11	6.1E-08	0.000024	GO	4.6198	PDIA3;PSMC6;NCF4;HLA-B;HLA-C;CYBA;HLA-A;CALR;B2M;TAPBP;HLA-E
GO:0090383	phagosome acidification	27	4	10.04	0.0011	0.032	GO	1.4949	ATP6V1A;ATP6V0B;ATP6V0E1;ATP6V0D1
R-HSA-38995	Prefoldin mediated transfer of substrate to CCT/TriC	27	4	10.04	0.0011	0.02	Reactome	1.699	CCT6A;PFDN1;CCT8;CCT5
GO:0007029	endoplasmic reticulum organization	34	5	9.98	0.00027	0.016	GO	1.7959	LMAN1;SEC61A1;ATL3;TMEM33;ATL2
GO:0042590	antigen processing and presentation of exogenous p	78	11	9.66	9.2E-08	0.000031	GO	4.5086	PDIA3;PSMC6;NCF4;HLA-B;HLA-C;CYBA;HLA-A;CALR;B2M;TAPBP;HLA-E
R-HSA-43272	Lysosome Vesicle Biogenesis	35	5	9.65	0.00031	0.0084	Reactome	2.0757	ARF1;CTSZ;M6PR;CLTA;GNS
R-HSA-16495	The role of Nef in HIV-1 replication and disease path	28	4	9.62	0.0013	0.022	Reactome	1.6576	ARF1;CD4;HLA-A;B2M
R-HSA-91797	Transferrin endocytosis and recycling	29	4	9.24	0.0015	0.024	Reactome	1.6198	ATP6V1A;ATP6V0B;ATP6V0E1;ATP6V0D1
GO:1903902	positive regulation of viral life cycle	44	6	9.16	0.0001	0.0084	GO	2.0757	DDB1;CD74;CD4;DDX3X;CNOT7;ADAR
GO:0072384	organelle transport along microtubule	31	4	8.55	0.0019	0.045	GO	1.3468	CDC42;RAB1A;MAP1S;PEX14
GO:0045070	positive regulation of viral genome replication	31	4	8.55	0.0019	0.045	GO	1.3468	DDB1;DDX3X;CNOT7;ADAR
GO:0000381	regulation of alternative mRNA splicing, via spliceosc	39	5	8.51	0.00052	0.021	GO	1.6778	PTBP1;WTAP;RNPS1;SRSF6;RBMX
R-HSA-38107	IRE1alpha activates chaperones	55	7	8.49	0.000042	0.0016	Reactome	2.7959	SEC61A1;XBP1;HSPA5;GFPT1;SSR1;TLN1;ATP6V0D1
GO:0090382	phagosome maturation	32	4	8.25	0.0021	0.047	GO	1.3279	ATP6V1A;ATP6V0B;ATP6V0E1;ATP6V0D1
R-HSA-38995	Cooperation of Prefoldin and TriC/CCT in actin and t	32	4	8.25	0.0021	0.033	Reactome	1.4815	CCT6A;PFDN1;CCT8;CCT5
GO:0071357	cellular response to type I interferon	65	8	8.19	0.0000015	0.0017	GO	2.7696	BST2;STAT2;HLA-B;HLA-C;ADAR;TYK2;HLA-A;HLA-E
GO:0060337	type I interferon signaling pathway	65	8	8.19	0.0000015	0.0017	GO	2.7696	BST2;STAT2;HLA-B;HLA-C;ADAR;TYK2;HLA-A;HLA-E
GO:0036498	IRE1-mediated unfolded protein response	57	7	8.14	0.000053	0.005	GO	2.301	SEC61A1;XBP1;HSPA5;GFPT1;SSR1;TLN1;ATP6V0D1
R-HSA-56945	Cargo concentration in the ER	33	4	7.96	0.0024	0.036	Reactome	1.4437	LMAN1;TMED10;SAR1B;CTSZ
R-HSA-68141	Cooperation of PDCL (PhLP1) and TRiC/CCT in G-prot	42	5	7.82	0.00074	0.016	Reactome	1.7959	CCT6A;CSNK2A2;CCT8;CCT5;GNAI2
R-HSA-90973	Interferon alpha/beta signaling	68	8	7.78	0.000021	0.001	Reactome	3	BST2;STAT2;HLA-B;HLA-C;ADAR;TYK2;HLA-A;HLA-E
R-HSA-38113	Unfolded Protein Response (UPR)	86	10	7.71	0.0000022	0.00013	Reactome	3.8861	SEC61A1;XBP1;HSPA5;DI53;GFPT1;SSR1;CALR;TLN1;ATP6V0D1;HERPUD1
GO:0018279	protein N-linked glycosylation via asparagine	44	5	7.42	0.00092	0.03	GO	1.5229	LMAN1;VCP;RPN2;ST3GAL5;UBE2G2
GO:0090304	nucleic acid metabolic process	80	9	7.41	0.0000094	0.0013	GO	2.8861	PTBP1;HNRNPM;POLR2A;WTAP;ERI1;HNRNPF;HNRNPD;CASC3;RBMX
R-HSA-38103	XBP1(S) activates chaperone genes	53	6	7.41	0.00029	0.0083	Reactome	2.0809	SEC61A1;XBP1;GFPT1;SSR1;TLN1;ATP6V0D1
GO:0044257	cellular protein catabolic process	62	7	7.4	0.0000991	0.0079	GO	2.1024	CTSZ;CLTA;YME1L1;IDE;UBE2G2;CTSS;CTSB
WP183	Proteasome Degradation	62	7	7.4	0.0000991	0.0054	Wikipathway	2.268	PSMC6;RPN2;HLA-B;HLA-C;UBA1;HLA-A;HLA-E
GO:0018196	peptidyl-asparagine modification	45	5	7.23	0.001	0.032	GO	1.4949	LMAN1;VCP;RPN2;ST3GAL5;UBE2G2
GO:0035722	interleukin-12-mediated signaling pathway	46	5	7.06	0.0011	0.032	GO	1.4949	CDC42;ARF1;CAPZA1;HNRNPF;TYK2
GO:0071349	cellular response to interleukin-12	46	5	7.06	0.0011	0.032	GO	1.4949	CDC42;ARF1;CAPZA1;HNRNPF;TYK2
GO:0017038	protein import	56	6	6.96	0.00039	0.018	GO	1.7447	RPAIN;PDIA3;LAMP2;NUP88;PTTG1IP;APOE
R-HSA-72163	mRNA Splicing - Major Pathway	134	14	6.91	8.1E-08	0.0000079	Reactome	5.1024	SF3B2;CASC3;USP39;PRPF8;ELAVL1;HNRNPM;PTBP1;SNRNP40;POLR2A;HNRNPF;HNRNPD;RNPS1;SRSF6;RBMX
GO:0034976	response to endoplasmic reticulum stress	106	11	6.8	0.0000022	0.00039	GO	3.4089	PDIA3;VCP;CEBPB;UFM1;TMX3;HSPA5;OS9;TMEM259;TMX1;TMEM33;HERPUD1
WP411	mRNA Processing	126	13	6.79	0.00000027	0.000064	Wikipathway	4.194	SF3B2;TMED10;SMC1A;PRPF8;HNRNPM;PTBP1;SNRNP40;POLR2A;HNRNPD;RNPS1;SRSF6;SRSF10;RBMX
GO:0002221	pattern recognition receptor signaling pathway	48	5	6.73	0.0014	0.035	GO	1.4559	UNC93B1;CD14;CNPY3;CTSS;CTSB
GO:0030433	ubiquitin-dependent ERAD pathway	58	6	6.69	0.00047	0.02	GO	1.699	VCP;PSMC6;OS9;HSPA5;AUP1;UBE2G2
R-HSA-20400	COPII (Coat Protein 2) Mediated Vesicle Transport	68	7	6.67	0.00017	0.0053	Reactome	2.2757	RAB1A;LMAN1;SEC13;TMED10;SAR1B;CTSZ;NAPG
GO:0048024	regulation of mRNA splicing, via spliceosome	60	6	6.44	0.00057	0.022	GO	1.6576	PTBP1;WTAP;RNPS1;SRSF6;SRSF10;RBMX
R-HSA-72172	mRNA Splicing	144	14	6.37	0.0000002	0.000014	Reactome	4.8539	SF3B2;CASC3;USP39;PRPF8;ELAVL1;HNRNPM;PTBP1;SNRNP40;POLR2A;HNRNPF;HNRNPD;RNPS1;SRSF6;RBMX
WP3945	TYROBP Causal Network	61	6	6.33	0.00062	0.021	Wikipathway	1.678	CD4;ITGB2;PPP1R18;TMEM106A;CXCL16;C1QC
GO:2001243	negative regulation of intrinsic apoptotic signaling pa	62	6	6.21	0.00068	0.025	GO	1.6021	URI1;XBP1;DDX3X;TMBIM6;PTTG1IP;HERPUD1
R-HSA-72203	Processing of Capped Intron-Containing Pre-mRNA	193	18	6.15	6.9E-09	0.0000011	Reactome	5.9586	FYTTD1;SF3B2;WTAP;CASC3;USP39;PRPF8;ELAVL1;HNRNPM;PTBP1;SNRNP40;POLR2A;HNRNPF;HNRNPD;NUP88;RNPS1;NUP54;SRSF6;RBMX
R-HSA-72165	mRNA Splicing - Minor Pathway	52	5	6.15	0.002	0.031	Reactome	1.5086	SF3B2;SNRNP40;POLR2A;SRSF6;PRPF8
GO:0006901	vesicle coating	63	6	6.1	0.00074	0.025	GO	1.6021	RAB1A;LMAN1;SEC13;TMED10;SAR1B;CTSZ
GO:0048208	COPII vesicle coating	63	6	6.1	0.00074	0.025	GO	1.6021	RAB1A;LMAN1;SEC13;TMED10;SAR1B;CTSZ
GO:0048207	vesicle targeting, rough ER to cis-Golgi	63	6	6.1	0.00074	0.025	GO	1.6021	RAB1A;LMAN1;SEC13;TMED10;SAR1B;CTSZ
GO:0045069	regulation of viral genome replication	63	6	6.1	0.00074	0.025	GO	1.6021	DDB1;BST2;ILF3;DDX3X;CNOT7;ADAR
GO:0036503	ERAD pathway	77	7	5.81	0.00036	0.018	GO	1.7447	VCP;PSMC6;OS9;HSPA5;AUP1;UBE2G2;HERPUD1
WP2328	Allograft Rejection	89	8	5.75	0.00015	0.007	Wikipathway	2.155	C1QB;C1QA;CSNK2A2;HLA-B;HLA-C;HLA-A;HLA-E;C1QC
R-HSA-68078	COPI-mediated anterograde transport	78	7	5.73	0.00039	0.0097	Reactome	2.0132	RAB1A;COPB2;ARF1;DYNC1LI2;TMED10;COPB1;NAPG
GO:0032091	negative regulation of protein binding	67	6	5.7	0.001	0.032	GO	1.4949	HSPA5;CTSZ;PRKCD;TMBIM6;B2M;PEX14
GO:0090114	COPII-coated vesicle budding	68	6	5.61	0.0011	0.032	GO	1.4949	RAB1A;LMAN1;SEC13;TMED10;SAR1B;CTSZ
R-HSA-15923	Transport of Mature mRNA derived from an Intron-C	68	6	5.61	0.0011	0.02	Reactome	1.699	FYTTD1;NUP54;NUP88;RNPS1;CASC3;SRSF6
GO:0060333	interferon-gamma-mediated signaling pathway	70	6	5.43	0.0013	0.035	GO	1.4559	PRKCD;HLA-B;HLA-C;HLA-A;B2M;HLA-E
R-HSA-19999	trans-Golgi Network Vesicle Budding	70	6	5.43	0.0013	0.022	Reactome	1.6576	TGOLN2;ARF1;CTSZ;M6PR;CLTA;GNS
R-HSA-42183	Clathrin derived vesicle budding	70	6	5.43	0.0013	0.022	Reactome	1.6576	TGOLN2;ARF1;CTSZ;M6PR;CLTA;GNS
R-HSA-19997	ER to Golgi Anterograde Transport	131	11	5.38	0.0000017	0.00094	Reactome	3.0269	COPB2;RAB1A;LMAN1;DYNC1LI2;ARF1;SEC13;TMED10;SAR1B;COPB1;CTSZ;NAPG
GO:0019886	antigen processing and presentation of exogenous p	97	8	5.23	0.00027	0.016	GO	1.7959	CD74;DYNC1LI2;ARF1;SEC13;SAR1B;CAPZA1;CLTA;CTSS
GO:0002478	antigen processing and presentation of exogenous p	97	8	5.23	0.00027	0.016	GO	1.7959	CD74;DYNC1LI2;ARF1;SEC13;SAR1B;CAPZA1;CLTA;CTSS
GO:0050730	regulation of peptidyl-tyrosine phosphorylation	85	7	5.21	0.00066	0.025	GO	1.6021	CD74;PRNP;CNOT7;CD81;ITGB2;PRKCD;TREM2
GO:0006487	protein N-linked glycosylation	73	6	5.19	0.0016	0.04	GO	1.3979	LMAN1;VCP;RPN2;GFPT1;ST3GAL5;UBE2G2
GO:0002495	antigen processing and presentation of peptide antig	98	8	5.18	0.00029	0.016	GO	1.7959	CD74;DYNC1LI2;ARF1;SEC13;SAR1B;CAPZA1;CLTA;CTSS
R-HSA-72202	Transport of Mature Transcript to Cytoplasm	74	6	5.11	0.0017	0.028	Reactome	1.5528	FYTTD1;NUP54;NUP88;RNPS1;CASC3;SRSF6
GO:0034249	negative regulation of cellular amide metabolic proc	75	6	5.04	0.0018	0.045	GO	1.3468	PRNP;ILF3;DDX3X;CNOT7;APOE;CALR
R-HSA-21322	MHC class II antigen presentation	103	8	4.9	0.00041	0.0097	Reactome	2.0132	CD74;DYNC1LI2;ARF1;SEC13;SAR1B;CLTA;CTSS;CTSB
R-HSA-19893	Immunoregulatory interactions between a Lymphoid	157	12	4.86	0.000018	0.00094	Reactome	3.0269	ITGB1;FCGR3A;CD81;SIGLEC10;ITGB2;HLA-B;HLA-C;TREM2;HLA-A;B2M;LAIR1;HLA-E
GO:0051603	proteolysis involved in cellular protein catabolic proc	93	7	4.73	0.0011	0.032	GO	1.4949	DDB1;VCP;CTSZ;YME1L1;IDE;CTSS;CTSB
R-HSA-44620	Asparagine N-linked glycosylation	259	19	4.73	0.0000013	0.000011	Reactome	4.9586	PDIA3;COPB2;RAB1A;ARF1;SEC13;TMED10;RPN2;SAR1B;COPB1;CTSZ;GFPT1;NAPG;LMAN1;DYNC1LI2;GANAB;NAGK;OS9;ST3GAL5;CALR
GO:0045055	regulated exocytosis	148	11	4.71	0.000052	0.005	GO	2.301	TMX3;TMED10;SYNGR2;APOOL;APLP2;LAMP2;PSAP;ANXA5;QSOX1;TLN1;FERMT3
GO:0019058	viral life cycle	107	8	4.7	0.00053	0.021	GO	1.6778	RAB1A;VCP;GRK2;CD81;CTBP1;NUP88;NUP54;APOE
GO:0016070	RNA metabolic process	191	14	4.67	0.000006	0.00091	GO	3.041	EIF4A2;DDX18;DDX3X;WTAP;DI53;CASC3;HNRNPM;PTBP1;SNRNP40;POLR2A;HNRNPF;HNRNPD;DHX29;RBMX
R-HSA-68114	COPI-dependent Golgi-to-ER retrograde traffic	81	6	4.63	0.0027	0.039	Reactome	1.4089	RAB1A;COPB2;ARF1;TMED10;COPB1;NAPG
GO:0050821	protein stabilization	152	11	4.57	0.0000066	0.006	GO	2.2218	CCT6A;TBRG1;CRTAP;LAMP1;CDC37;LAMP2;PRKCD;CALR;CCT8;NAPG;CCT5
GO:0002576	platelet degranulation	124	9	4.57	0.0003	0.016	GO	1.7959	TMX3;APOO;APLP2;LAMP2;PSAP;ANXA5;QSOX1;TLN1;FERMT3
GO:0051247	positive regulation of protein metabolic process	96	7	4.57	0.0013	0.035	GO	1.4559	DDB1;NFKBIA;RAB1A;VCP;SCAP;IDE;APOE
GO:0034504	protein localization to nucleus	96	7	4.57	0.0013	0.035	GO	1.4559	RPAIN;PDIA3;TBRG1;NUP88;PTTG1IP;CALR;TOR1AIP1
R-HSA-73857	RNA Polymerase II Transcription	124	9	4.57	0.0003	0.003	Reactome	2.0809	FYTTD1;SUPT16H;POLR2A;TAF11;RNPS1;GTF2H1;CASC3;SRSF6;TAF2
WP2806	Human Complement System	97	7	4.52	0.0014	0.042	Wikipathway	1.377	PRNP;FCGR3A;SELPLG;ITGB2;C3AR1;CALR;GNAI2
GO:0019941	modification-dependent protein catabolic process	141	10	4.46	0.00017	0.013	GO	1.8861	DDB1;RNF146;XBP1;RNF34;PSMC6;OS9;UBA6;UBA1;UBE2G2;FBXO7
GO:0071427	mRNA-containing ribonucleoprotein complex export	100	7	4.37	0.0017	0.042	GO	1.3768	FYTTD1;NUP88;RNPS1;NUP54;CASC3;SRSF6;SRSF10
WP4217	Ebola Virus Pathway on Host	129	9	4.37	0.0004	0.016	Wikipathway	1.796	BST2;ITGB1;CDC42;HLA-B;HLA-C;CLTA;HLA-A;HLA-E;CTSB
GO:0000377	RNA splicing, via transesterification reactions with bu	236	16	4.31	0.0000036	0.00059	GO	3.2291	SF3B2;CASC3;USP39;PRPF8;ELAVL1;HNRNPM;PTBP1;SNRNP40;POLR2A;HNRNPF;HNRNPD;RNPS1;SRSF6;SRSF10;RBMX;SF1
R-HSA-94802	Transport to the Golgi and subsequent modification	162	11	4.27	0.00012	0.004	Reactome	2.3979	COPB2;RAB1A;LMAN1;DYNC1LI2;ARF1;SEC13;TMED10;SAR1B;COPB1;CTSZ;NAPG
R-HSA-98316	Class I MHC mediated antigen processing & presenta	305	20	4.2	0.00000037	0.000024	Reactome	4.6198	PDIA3;SEC13;RNF34;HSPA5;SAR1B;UBA6;NCF4;HLA-B;HLA-C;CYBA;HLA-A;UBE2G2;CTSS;HLA-E;TAPBP;SEC61A1;PSMC6;UBA1;CALR;B2M
GO:0006405	RNA export from nucleus	119	8	4.19	0.0011	0.032	GO	1.4949	FYTTD1;SSB;NUP88;RNPS1;NUP54;CASC3;SRSF6;SRSF10
GO:0051028	mRNA transport	104	7	4.19	0.0021	0.047	GO	1.3279	FYTTD1;NUP88;RNPS1;NUP54;CASC3;SRSF6;SRSF10
R-HSA-91353	Interferon Signaling	196	13	4.18	0.000037	0.0016	Reactome	2.7959	EIF4A2;STAT2;PRKCD;HLA-B;HLA-C;ADAR;HLA-A;TYK2;HLA-E;BST2;NUP88;NUP54;B2M
GO:0006406	mRNA export from nucleus	105	7	4.15	0.0023	0.049	GO	1.3098	FYTTD1;NUP88;RNPS1;NUP54;CASC3;SRSF6;SRSF10
R-HSA-11460	Platelet degranulation	105	7	4.15	0.0023	0.035	Reactome	1.4559	TMX3;HSPA5;APLP2;LAMP2;PSAP;QSOX1;TLN1
GO:0007030	Golgi organization	121	8	4.12	0.0012	0.033	GO	1.4815	CDC42;NSFL1C;RAB1A;LMAN1;TMED10;ATL3;UBXN2A;ATL2
GO:0043312	neutrophil degranulation	479	30	4.09	1.2E-09	0.00000089	GO	6.0506	GRN;VCP;DDX3X;COPB1;CTSZ;ITGB2;FGL2;GNS;CTSS;DPP7;LAMP1;LAMP2;PSAP;C3AR1;SIRPA;STOM;QSOX1;CD14;CCT8;B2M;LAIR1;CTSB;TMEM30A;PRKCD;AP1B1;CMTM6;CYBA;ARPC5;UNC13D;BST2
GO:0002283	neutrophil activation involved in immune response	483	30	4.05	1.5E-09	0.00000089	GO	6.0506	GRN;VCP;DDX3X;COPB1;CTSZ;ITGB2;FGL2;GNS;CTSS;DPP7;LAMP1;LAMP2;PSAP;C3AR1;SIRPA;STOM;QSOX1;CD14;CCT8;B2M;LAIR1;CTSB;TMEM30A;PRKCD;AP1B1;CMTM6;CYBA;ARPC5;UNC13D;BST2
GO:0002446	neutrophil mediated immunity	487	30	4.01	1.8E-09	0.00000089	GO	6.0506	GRN;VCP;DDX3X;COPB1;CTSZ;ITGB2;FGL2;GNS;CTSS;DPP7;LAMP1;LAMP2;PSAP;C3AR1;SIRPA;STOM;QSOX1;CD14;CCT8;B2M;LAIR1;CTSB;TMEM30A;PRKCD;AP1B1;CMTM6;CYBA;ARPC5;UNC13D;BST2
R-HSA-88566	Golgi-to-ER retrograde transport	110	7	3.94	0.0029	0.039	Reactome	1.4089	COPB2;RAB1A;DYNC1LI2;ARF1;TMED10;COPB1;NAPG
R-HSA-76005	Response to elevated platelet cytosolic Ca2+	110	7	3.94	0.0029	0.039	Reactome	1.4089	TMX3;HSPA5;APLP2;LAMP2;PSAP;QSOX1;TLN1
GO:0000398	mRNA splicing, via spliceosome	261	16	3.86	0.0000013	0.0016	GO	2.7959	SF3B2;CASC3;USP39;PRPF8;ELAVL1;HNRNPM;PTBP1;SNRNP40;POLR2A;HNRNPF;HNRNPD;RNPS1;SRSF6;SRSF10;RBMX;SF1
GO:0006397	mRNA processing	283	17	3.79	0.0000089	0.0013	GO	2.8861	SF3B2;GTF2H1;CASC3;USP39;PRPF8;ELAVL1;HNRNPM;PTBP1;SNRNP40;POLR2A;HNRNPF;HNRNPD;RNPS1;SRSF6;SRSF10;RBMX;SF1
GO:0006605	protein targeting	133	8	3.72	0.0022	0.047	GO	1.3279	TOMM70;SEC61A1;SPCS3;CDC37;LAMP2;ATG4B;ZDHHC7;FBXO7
GO:0006461	protein complex assembly	189	11	3.61	0.00045	0.02	GO	1.699	RAB1A;LMAN1;SEC13;CDC123;TMED10;SAR1B;CTSZ;AKR1B1;RBMX;FERMT3;TNFRSF1A
R-HSA-16889	Toll-Like Receptors Cascades	140	8	3.52	0.003	0.039	Reactome	1.4089	NFKBIA;PPP2CB;UNC93B1;ITGB2;CNPY3;CD14;CTSS;CTSB
GO:0006417	regulation of translation	213	12	3.5	0.00034	0.018	GO	1.7447	EIF4A2;CDC123;ILF3;CNOT7;DDX3X;POLR2A;HNRNPD;EIF4H;NUP88;NUP54;CALR;ELAVL1
R-HSA-16258	HIV Life Cycle	141	8	3.49	0.0031	0.04	Reactome	1.3979	SUPT16H;CD4;POLR2A;TAF11;NUP88;NUP54;GTF2H1;TAF2
GO:0016032	viral process	220	12	3.38	0.00045	0.02	GO	1.699	PTBP1;RAB1A;ARF1;VCP;CD4;GRK2;SSB;CTBP1;NUP88;NUP54;APOE;B2M
R-HSA-16290	HIV Infection	222	12	3.35	0.00049	0.011	Reactome	1.9586	ARF1;SUPT16H;CDK9;SMC6;POLR2A;TAF11;NUP88;GTF2H1;NUP54;HLA-A;B2M;TAF2
GO:0048193	Golgi vesicle transport	271	14	3.2	0.00027	0.016	GO	1.7959	COPB2;RAB1A;ARF1;TMED10;SAR1B;COPB1;CTSZ;NAPG;SCAMP2;TAPBP;GOLGA3;LMAN1;DYNC1LI2;CAPZA1
R-HSA-68114	Intra-Golgi and retrograde Golgi-to-ER traffic	179	9	3.08	0.0039	0.049	Reactome	1.3098	TGOLN2;COPB2;RAB1A;DYNC1LI2;ARF1;TMED10;COPB1;M6PR;NAPG
R-HSA-12802	Adaptive Immune System	762	36	3.05	4.5E-08	0.000005	Reactome	5.301	ITGB1;ARF1;RNF34;SAR1B;CD81;UBA6;NCF4;ITGB2;CLTA;TREM2;CTSS;CDC42;PPP2CB;SEC61A1;FCGR3A;B2M;LAIR1;CTSB;PDIA3;CD74;SEC13;HSPA5;SIGLEC10;HLA-B;HLA-C;CYBA;HLA-A;UBE2G2;HLA-E
GO:0015031	protein transport	326	16

Supplementary Table 5_Microglia MEGENA Modules
Pathology enrichment

Positive logFC values indicate a higher enrichment with pathology

Amyloid-pathology

Co-expression moduli	logFC	P.Value	adj.P.Val
c1_2	0.2862	0.17193163	0.350524
c1_4	-0.0089	0.97167591	0.971676
c1_5	0.4025	0.37583873	0.615736
c1_6	0.4504	0.04977189	0.174202
c1_7	0.0574	0.75412301	0.855844
c1_9	-0.5935	0.01037905	0.049949
c1_10	0.1586	0.45077098	0.708354
c1_11	1.2345	0.00091194	0.007022
c1_12	0.0763	0.7940627	0.886128
c1_13	-0.7658	0.14624212	0.325059
c1_15	-0.7443	0.2690202	0.493204
c1_16	0.3291	0.56365235	0.789113
c1_17	0.5396	0.18209055	0.350524
c1_18	0.3157	0.67061233	0.849967
c1_19	0.5602	0.13789563	0.321756
c1_20	-0.4173	0.68899939	0.855544
c1_21	-0.0231	0.94032824	0.952701
c1_22	0.7117	0.01122234	0.050831
c1_23	0.8038	0.04326356	0.158633
c1_24	-1.0214	0.03473101	0.133714
c1_25	0.1946	0.32095102	0.545958
c1_26	-0.4033	0.73332301	0.855544
c1_27	0.0521	0.8534151	0.931046
c1_28	-0.7079	0.00280927	0.018026
c1_29	-0.1807	0.62973347	0.822396
c1_30	-0.2539	0.52163634	0.757849
c1_31	0.0386	0.85849742	0.931046
c1_32	0.712	0.02438046	0.098805
c1_33	2.3441	0.00808842	0.044486
c1_34	2.3215	0.05585215	0.186983
c1_35	0.7214	0.11630047	0.289663
c1_36	1.5864	0.00684973	0.040571
c1_37	1.0893	0.08093223	0.23333
c1_39	0.1268	0.6733502	0.849967
c1_41	-1.2076	0.06539507	0.201417
c1_43	0.3191	0.5933357	0.806371
c1_45	0.6445	0.47385214	0.715424
c1_49	-0.0356	0.91131458	0.94826
c1_55	0.7458	0.00886303	0.045497
c1_57	0.4382	0.53609073	0.764426
c1_59	-0.4567	0.13216366	0.318019
c1_60	-0.0835	0.70371253	0.855544
c1_61	2.22	1.05E-09	8.05E-08
c1_62	0.4326	0.32204191	0.545958
c1_64	-0.045	0.88798889	0.942329
c1_65	-1.1863	0.00030499	0.002936
c1_66	-0.6879	0.02315288	0.098805
c1_67	-0.4753	0.14775389	0.325059
c1_68	-0.4701	0.18128153	0.350524
c1_71	-0.1417	0.72050787	0.855544
c1_75	-0.272	0.50224359	0.743707
c1_76	0.12	0.59692436	0.806371
c1_78	-0.2823	0.32324416	0.545958
c1_80	-0.0459	0.94025148	0.952701
c1_84	0.9416	0.0599406	0.192309
c1_86	0.7017	0.32615653	0.545958
c1_92	-0.4899	0.16406002	0.350524
c1_93	-0.4911	0.25106085	0.471505
c1_95	0.4459	0.43798114	0.702595
c1_96	-1.0804	0.0027764	0.018026
c1_97	-0.8052	0.11661777	0.289663
c1_98	1.853	0.00015178	0.002337
c1_99	-0.4459	0.47297835	0.715424
c1_101	2.3098	2.74E-06	9.74E-05
c1_102	2.5592	3.80E-06	9.74E-05
c1_104	-1.2367	0.00028977	0.002936
c1_107	-0.4539	0.17627398	0.350524
c1_109	0.0783	0.73139242	0.855544
c1_115	-0.7152	0.08181691	0.23333
c1_117	-0.0454	0.89337692	0.942329
c1_123	-0.6332	0.09310672	0.247214
c1_127	0.2557	0.75581052	0.855844
c1_129	-1.7946	0.00012563	0.002337
c1_130	-0.1855	0.63014776	0.822396
c1_133	1.9017	0.0001845	0.002368
c1_137	-1.2536	0.00038373	0.003283
c1_145	-0.7661	0.08839628	0.24309

pTau pathology

Co-expression moduli	logFC	P.Value	adj.P.Val
c1_2	0.38893	0.032	0.090824
c1_4	0.05243	0.809516	0.86403
c1_5	0.55452	0.158678	0.341184
c1_6	0.55676	0.005086	0.021755
c1_7	0.08567	0.589495	0.709236
c1_9	-0.6772	0.000729	0.00569
c1_10	0.26525	0.145133	0.338645
c1_11	1.26264	8.90E-05	0.001143
c1_12	0.11667	0.644889	0.741141
c1_13	-0.5553	0.223577	0.407647
c1_15	-0.4126	0.479068	0.636004
c1_16	0.31712	0.520437	0.664656
c1_17	0.49279	0.159245	0.341184
c1_18	0.63238	0.324997	0.532442
c1_19	0.68045	0.037343	0.099153
c1_20	-0.7045	0.435139	0.619661
c1_21	0.2054	0.442615	0.619661
c1_22	0.79207	0.001115	0.007152
c1_23	0.7339	0.033027	0.090824
c1_24	-0.9515	0.023068	0.070872
c1_25	0.17612	0.299553	0.501426
c1_26	-0.8815	0.389629	0.593074
c1_27	0.22199	0.363258	0.570834
c1_28	-0.7951	0.000106	0.001163
c1_29	-0.1884	0.561543	0.6974
c1_30	-0.4233	0.217166	0.407647
c1_31	0.15484	0.409317	0.601477
c1_32	0.8105	0.003075	0.015783
c1_33	1.91678	0.01236	0.047586
c1_34	2.37326	0.023931	0.070872
c1_35	0.90438	0.022932	0.070872
c1_36	1.67806	0.000952	0.006666
c1_37	0.92906	0.085496	0.21944
c1_39	0.11239	0.665917	0.743125
c1_41	-0.8579	0.130501	0.314018
c1_43	0.29317	0.570875	0.697737
c1_45	0.94652	0.224308	0.407647
c1_49	0.22599	0.414004	0.601477
c1_55	0.83237	0.000739	0.00569
c1_57	-0.4401	0.472831	0.636004
c1_59	-0.1236	0.6378	0.741141
c1_60	-0.1204	0.526546	0.664656
c1_61	1.70182	6.55E-08	5.04E-06
c1_62	0.6121	0.10551	0.262072
c1_64	0.12271	0.657034	0.743125
c1_65	-1.224	1.68E-05	0.000258
c1_66	-0.7553	0.003973	0.017994
c1_67	-0.6786	0.016957	0.059351
c1_68	-0.4282	0.159515	0.341184
c1_71	-0.1308	0.702829	0.773112
c1_75	-0.4162	0.235648	0.412384
c1_76	0.25411	0.195673	0.38633
c1_78	-0.2114	0.392815	0.593074
c1_80	0.04683	0.929668	0.95446
c1_84	1.05435	0.014951	0.054821
c1_86	0.74635	0.227647	0.407647
c1_92	-0.0697	0.819145	0.86403
c1_93	-0.3531	0.340375	0.546018
c1_95	0.00439	0.992964	0.996924
c1_96	-0.7983	0.010664	0.043217
c1_97	-0.3016	0.497226	0.648922
c1_98	1.22306	0.003875	0.017994
c1_99	-0.3982	0.45912	0.631289
c1_101	1.84425	1.52E-05	0.000258
c1_102	1.84132	0.000122	0.001177
c1_104	-1.3203	7.83E-06	0.000254
c1_107	-0.67	0.021118	0.070698
c1_109	0.20674	0.295319	0.501426
c1_115	-0.4888	0.169473	0.348666
c1_117	-0.0671	0.819061	0.86403
c1_123	-0.1638	0.615798	0.729483
c1_127	-0.0027	0.996924	0.996924
c1_129	-1.3101	0.001221	0.007234
c1_130	-0.0613	0.854066	0.88869
c1_133	1.31132	0.002896	0.015783
c1_137	-1.3504	9.91E-06	0.000254
c1_145	-0.5315	0.172069	0.348666

Supplementary Table 5_Microglia MEGENA Modules Enrichment other datasets

Positive logFC values indicate a higher enrichment in AD compared to Control

Grubman et al 2019, doi: 10.1038/s41593-019-0539-4

Co-expressio	logFC	P.Value	adj.P.Val
c1_2	-0.005767339	0.790952536	0.89563743
c1_4	-0.064816457	0.038244412	0.070114755
c1_5	0.104387362	0.049020284	0.083879152
c1_6	-0.05208393	0.040215433	0.070377008
c1_7	-0.155915153	1.35E-14	1.74E-13
c1_9	0.245963279	8.83E-18	1.70E-16
c1_10	-0.110149651	7.70E-08	3.30E-07
c1_11	0.120821508	0.01450547	0.029392663
c1_12	-0.0861973	0.050599635	0.08469939
c1_13	0.05151979	0.579293114	0.696962027
c1_15	0.041333687	0.744958882	0.856146775
c1_16	-0.365746243	0.000316928	0.000787209
c1_17	0.107822586	0.10118333	0.155822328
c1_18	0.120005636	0.12546088	0.189421329
c1_19	0.116401155	0.006973477	0.014512372
c1_20	0.612058699	6.55E-05	0.000180245
c1_21	0.015432659	0.685402111	0.811937885
c1_22	-0.121560444	0.000821298	0.001859998
c1_23	-0.069355147	0.356404903	0.473158234
c1_24	0.482708741	3.74E-07	1.37E-06
c1_25	-0.141230137	3.19E-09	1.53E-08
c1_26	-0.642954401	3.58E-09	1.62E-08
c1_27	-0.261819569	1.58E-11	1.22E-10
c1_28	0.26828931	5.63E-17	8.68E-16
c1_29	0.150026472	0.019174711	0.036911319
c1_30	0.161672438	0.01697926	0.033523153
c1_31	-0.098534694	1.44E-05	4.62E-05
c1_32	-0.159459084	1.12E-05	3.75E-05
c1_33	0.246656348	0.08471518	0.133123854
c1_34	0.033233276	0.856191377	0.915837372
c1_35	0.050615058	0.532743976	0.661633647
c1_36	0.143383095	0.152406321	0.221420505
c1_37	0.011944635	0.928710285	0.928710285
c1_39	-0.082903787	0.072530853	0.116351577
c1_41	0.01552144	0.891205286	0.915837372
c1_43	-0.425369363	5.22E-05	0.000148979
c1_45	0.161076096	0.059967785	0.098245094
c1_49	0.014964528	0.701160527	0.818020615
c1_55	-0.139283005	0.000214913	0.000570631
c1_57	0.121297994	0.368210079	0.480545357
c1_59	-0.550935346	4.60E-34	3.54E-32
c1_60	-0.004203644	0.891340507	0.915837372
c1_61	0.010808106	0.892049388	0.915837372
c1_62	-0.444795653	4.04E-12	3.45E-11
c1_64	-0.116429165	0.023210496	0.043590444
c1_65	0.166239759	0.003455266	0.007390429
c1_66	0.316727514	3.21E-10	2.06E-09
c1_67	0.350195974	1.64E-12	1.58E-11
c1_68	0.198747477	0.001674059	0.003682931
c1_71	0.101431872	0.145222163	0.215040511
c1_75	0.14171791	0.040201309	0.070377008
c1_76	-0.132192804	1.02E-07	4.13E-07
c1_78	0.006057765	0.87134735	0.915837372
c1_80	0.125545415	0.277040396	0.394669176
c1_84	0.09084341	0.309686479	0.425818908
c1_86	0.084981603	0.553380824	0.676354341
c1_92	-0.675703929	2.83E-33	1.09E-31
c1_93	-0.059911658	0.3332668	0.45020252
c1_95	0.676572803	1.50E-09	8.23E-09
c1_96	-0.400344022	6.04E-11	4.23E-10
c1_97	-0.270740811	0.000789999	0.001843331
c1_98	0.44527301	1.62E-09	8.32E-09
c1_99	-0.023409304	0.845324545	0.915837372
c1_101	0.087537347	0.419536889	0.529841828
c1_102	-0.106984099	0.419744825	0.529841828
c1_104	0.224948545	0.000281407	0.000722279
c1_107	0.361471296	7.94E-13	8.73E-12
c1_109	-0.104048887	4.66E-05	0.000137893
c1_115	0.008021808	0.910316447	0.922294295
c1_117	-0.053558997	0.281906554	0.394669176
c1_123	-0.709839841	5.67E-30	1.46E-28
c1_127	0.54498186	3.00E-05	9.25E-05
c1_129	-0.405534311	2.61E-07	1.01E-06
c1_130	-0.314652796	0.000692732	0.001666887
c1_133	0.494822105	1.00E-09	5.95E-09
c1_137	0.29034071	9.87E-06	3.45E-05
c1_145	0.018718522	0.804568686	0.897852011

Mathys et al 2019, doi: 10.1038/s41586-019-1195-2

Co-expressio	logFC	P.Value	adj.P.Val
c1_2	0.034646734	0.000185429	0.000751477
c1_4	-0.070372111	2.16E-06	1.11E-05
c1_5	0.128391242	1.70E-09	2.62E-08
c1_6	-0.01210198	0.304486437	0.450874148
c1_7	0.004645706	0.698390314	0.853588162
c1_9	-0.070620646	4.70E-08	3.62E-07
c1_10	0.008565222	0.418849043	0.56581362
c1_11	-0.022629207	0.300062582	0.450874148
c1_12	0.149158121	3.40E-08	3.46E-07
c1_13	-0.133169994	0.000264633	0.00097032
c1_15	-0.043944892	0.315930226	0.45899297
c1_16	-0.276923421	1.58E-12	1.22E-10
c1_17	-0.176174113	3.95E-08	3.46E-07
c1_18	0.160628462	2.42E-06	1.16E-05
c1_19	0.114056681	8.96E-10	1.85E-08
c1_20	0.145069845	0.016705924	0.045941292
c1_21	-0.042348602	0.01767002	0.04691695
c1_22	-0.00472834	0.771238734	0.899778523
c1_23	0.035581088	0.243381637	0.398731618
c1_24	-0.127409919	0.00144378	0.005053229
c1_25	0.025762297	0.051948787	0.118157051
c1_26	-0.33965159	9.61E-10	1.85E-08
c1_27	0.01056291	0.59230227	0.735601153
c1_28	-0.085924864	2.32E-09	2.98E-08
c1_29	0.000540952	0.983257889	0.983257889
c1_30	-0.050793137	0.052173243	0.118157051
c1_31	0.00620163	0.567176795	0.715944479
c1_32	0.023561881	0.220816357	0.377841321
c1_33	0.036752242	0.51905938	0.689096074
c1_34	0.151833243	0.011374381	0.032438048
c1_35	-0.019438734	0.542867257	0.696679647
c1_36	-0.045447175	0.264057892	0.414358
c1_37	-0.088444625	0.06499161	0.139009832
c1_39	0.138107866	1.20E-06	7.13E-06
c1_41	-0.195839086	1.73E-05	7.39E-05
c1_43	-0.282382685	6.04E-12	2.33E-10
c1_45	0.192592266	1.32E-06	7.27E-06
c1_49	-0.042673526	0.020297025	0.052095697
c1_55	-0.000515284	0.957286818	0.983257889
c1_57	0.082596939	0.182042443	0.32598298
c1_59	0.095829638	0.000235443	0.000906457
c1_60	-0.0031721	0.837837064	0.92162077
c1_61	0.030836698	0.269063636	0.414358
c1_62	0.061323309	0.111683058	0.226305144
c1_64	-0.0198519	0.357513902	0.499123761
c1_65	-0.042842429	0.067984807	0.141481896
c1_66	-0.064543183	0.002328762	0.007471445
c1_67	-0.118576779	4.04E-08	3.46E-07
c1_68	-0.129310581	3.52E-07	2.26E-06
c1_71	-0.006517818	0.820308469	0.92162077
c1_75	-0.072887107	0.007818197	0.023153892
c1_76	0.001638724	0.887554305	0.945401163
c1_78	-0.00353528	0.834759031	0.92162077
c1_80	-0.005846716	0.896289414	0.945401163
c1_84	0.010217062	0.784047756	0.901069809
c1_86	-0.062255065	0.230941519	0.386576021
c1_92	0.09092184	0.007355517	0.022654994
c1_93	0.163153721	3.72E-06	1.69E-05
c1_95	0.040804025	0.332372109	0.473938007
c1_96	-0.035347246	0.25743752	0.412972688
c1_97	0.054778338	0.193656871	0.338899524
c1_98	0.009187413	0.763603958	0.899778523
c1_99	0.044818021	0.362999099	0.499123761
c1_101	0.0135618	0.773617691	0.882633785
c1_102	0.102127748	0.041577872	0.100046754
c1_104	-0.049381803	0.057614198	0.126751236
c1_107	-0.12036072	6.30E-08	4.41E-07
c1_109	-0.00199335	0.86252598	0.935415499
c1_115	0.037783622	0.163808074	0.300314802
c1_117	-0.046622284	0.034119227	0.084747756
c1_123	0.120666658	0.00158214	0.005296729
c1_127	-0.002165025	0.9672635	0.983257889
c1_129	-0.02485596	0.528231664	0.689387087
c1_130	-0.057856063	0.138302255	0.259738382
c1_133	0.045142639	0.13044124	0.251099387
c1_137	-0.042051351	0.129393603	0.251099387
c1_145	0.001280324	0.96559324	0.983257889

Zhou et al 2020, doi: 10.1038/s41591-019-0695-9

Co-expressio	logFC	P.Value	adj.P.Val
c1_2	-0.006566331	0.444712429	0.450563909
c1_4	-0.044988423	6.33E-05	7.86E-05
c1_5	-0.073994888	3.94E-06	5.23E-06
c1_6	0.127993267	1.31E-32	4.04E-32
c1_7	0.126246789	2.95E-47	1.52E-46
c1_9	-0.251048286	1.53E-102	2.95E-101
c1_10	0.179513971	7.75E-74	6.63E-73
c1_11	0.156941605	8.90344E-19	2.07747E-18
c1_12	0.140085123	1.24E-18	2.73E-18
c1_13	-0.164385815	1.42E-10	2.37E-10
c1_15	-0.186013484	1.33E-07	1.89E-07
c1_16	-0.230360676	1.99E-21	5.27E-21
c1_17	0.060721063	0.003953731	0.004756832
c1_18	-0.204495839	7.86E-18	1.64E-17
c1_19	0.062268768	6.32E-06	8.11E-06
c1_20	-0.12568446	0.006650915	0.007759401
c1_21	0.079026606	9.44E-08	1.40E-07
c1_22	0.168721592	2.63E-38	9.64E-38
c1_23	0.154292099	1.88E-18	4.02E-18
c1_24	-0.363700586	3.12E-35	1.09E-34
c1_25	0.15654579	7.31E-58	4.33E-57
c1_26	-0.518252586	4.32E-19	1.04E-18
c1_27	0.297614661	4.31E-58	2.76E-57
c1_28	-0.283213983	3.57E-111	9.17E-110
c1_29	-0.098284928	2.80E-06	3.79E-06
c1_30	-0.207975984	1.05E-20	2.69E-20
c1_31	0.148682203	6.62E-50	3.64E-49
c1_32	0.360983289	9.58E-95	1.48E-93
c1_33	0.233937111	1.01E-05	1.28E-05
c1_34	-0.053473199	0.292606112	0.304468522
c1_35	0.135123023	1.06E-06	1.48E-06
c1_36	0.247202529	1.95E-14	3.57E-14
c1_37	0.119912092	0.011639016	0.012988467
c1_39	0.130977956	3.16E-15	5.93E-15
c1_41	-0.256902045	2.95E-16	5.67E-16
c1_43	-0.253942891	8.29E-23	2.36E-22
c1_45	-0.223111368	5.94E-17	1.20E-16
c1_49	0.083860359	5.72E-08	8.81E-08
c1_55	0.175719758	2.15E-39	8.29E-39
c1_57	-0.215186978	7.55E-09	1.21E-08
c1_59	0.407245131	1.01E-92	1.29E-91
c1_60	0.069221517	9.06E-09	1.42E-08
c1_61	0.040724268	0.019632122	0.021595334
c1_62	0.611050175	7.13E-62	4.99E-61
c1_64	0.2042953	1.58E-21	4.33E-21
c1_65	-0.269312409	5.36E-40	2.17E-39
c1_66	-0.207469907	5.64E-33	1.81E-32
c1_67	-0.446242346	7.13E-137	5.49E-135
c1_68	-0.193198319	1.81E-19	4.49E-19
c1_71	-0.121439778	1.23E-07	1.79E-07
c1_75	-0.18545602	1.27E-13	2.28E-13
c1_76	0.178776422	3.85E-64	2.97E-63
c1_78	-0.023697368	0.116672701	0.123065726
c1_80	0.14678083	8.04E-05	9.82E-05
c1_84	0.138430782	4.20E-06	5.48E-06
c1_86	0.111202045	0.032194457	0.034915115
c1_92	0.480117527	1.22E-86	1.18E-85
c1_93	0.353060834	8.72E-24	2.58E-23
c1_95	-0.186236705	2.07E-06	2.85E-06
c1_96	0.310020275	5.23E-33	1.75E-32
c1_97	0.276158661	1.48E-12	2.59E-12
c1_98	-0.156767073	1.80E-11	3.08E-11
c1_99	0.09126166	0.037971605	0.040608522
c1_101	0.005831176	0.792017321	0.792017321
c1_102	0.187645714	6.41E-08	9.68E-08
c1_104	-0.305917278	7.39E-43	3.16E-42
c1_107	-0.455183627	1.24E-133	4.78E-132
c1_109	0.148430927	2.45E-45	1.18E-44
c1_115	-0.01952669	0.377834544	0.387910132
c1_117	-0.059792988	0.004680369	0.005544437
c1_123	0.522014052	1.20E-87	1.32E-86
c1_127	-0.118454006	0.009124926	0.010486855
c1_129	0.247848864	1.40E-16	2.77E-16
c1_130	0.379589453	1.23E-18	2.73E-18
c1_133	-0.148593179	5.62E-09	9.20E-09
c1_137	-0.330954778	3.89E-45	1.76E-44
c1_145	-0.065732675	0.009471578	0.010725169

Gerrits et al 2021, doi: 10.1007/s00401-021-02263-w

Co-expressio	logFC	P.Value	adj.P.Val
c1_2	0.05628638	0	0
c1_4	0.030767446	6.93E-124	2.22E-123
c1_5	0.121359031	0	0
c1_6	0.045463605	0	0
c1_7	0.008090544	7.97E-19	1.12E-18
c1_9	0.001376427	0.285108383	0.296666831
c1_10	0.010444227	5.07E-27	8.48E-27
c1_11	0.110396665	0	0
c1_12	0.036018093	2.72E-81	6.76E-81
c1_13	-0.002397504	0.451902749	0.457848838
c1_15	0.070677079	2.37E-76	5.52E-76
c1_16	0.050093958	8.92E-38	1.60E-37
c1_17	0.012567914	5.02E-08	5.86E-08
c1_18	0.180331183	0	0
c1_19	0.105848757	0	0
c1_20	-0.033494497	1.38E-07	1.58E-07
c1_21	0.034536138	1.74E-106	4.79E-106
c1_22	0.051514347	6.48E-259	2.93E-258
c1_23	0.065193203	3.63E-126	1.22E-125
c1_24	0.142493557	0	0
c1_25	-0.000878743	0.39854517	0.409173042
c1_26	-0.026136557	2.80E-08	3.32E-08
c1_27	0.038995619	5.79E-122	1.78E-121
c1_28	-0.012388297	3.98E-18	5.37E-18
c1_29	0.058783947	8.77E-140	3.38E-139
c1_30	0.048204608	1.66E-96	4.41E-96
c1_31	0.015114906	2.61E-53	5.58E-53
c1_32	-0.012723637	5.80E-14	7.44E-14
c1_33	0.137428889	6.85E-128	2.40E-127
c1_34	0.321395381	0	0
c1_35	0.108200863	0	0
c1_36	0.115838987	9.97E-234	4.27E-233
c1_37	0.021136877	1.11E-08	1.34E-08
c1_39	0.014610627	6.88E-14	8.69E-14
c1_41	-0.032163005	1.22E-16	1.62E-16
c1_43	0.041315916	2.63E-22	3.97E-22
c1_45	0.242334366	0	0
c1_49	0.037066705	9.13E-113	2.70E-112
c1_55	0.053304873	1.77E-263	8.50E-263
c1_57	0.040078362	1.53E-18	2.10E-18
c1_59	0.030481173	3.36E-53	7.00E-53
c1_60	-0.009984274	7.22E-19	1.03E-18
c1_61	-0.026449958	1.87E-26	3.07E-26
c1_62	0.054663248	4.80E-77	1.15E-76
c1_64	0.029254606	1.95E-52	3.94E-52
c1_65	0.003071168	0.145473681	0.155468255
c1_66	-0.049863142	5.60E-139	2.05E-138
c1_67	0.026535418	2.90E-33	4.96E-33
c1_68	0.000767514	0.720496618	0.720496618
c1_71	0.066555582	3.21E-148	1.30E-147
c1_75	0.053873847	5.83E-108	1.66E-107
c1_76	0.015922531	2.74E-49	5.42E-49
c1_78	0.020144575	1.53E-42	2.81E-42
c1_80	-0.059438482	1.07E-55	2.42E-55
c1_84	0.173814837	0	0
c1_86	0.039723738	1.04E-20	1.54E-20
c1_92	0.033725394	1.85E-43	3.47E-43
c1_93	0.01789485	1.13E-09	1.38E-09
c1_95	0.057836775	8.14E-48	1.57E-47
c1_96	-0.113971866	0	0
c1_97	-0.053514003	2.07E-54	4.56E-54
c1_98	0.235505956	0	0
c1_99	-0.017212794	6.17E-05	6.98E-05
c1_101	-0.034050919	3.02E-19	4.39E-19
c1_102	-0.027253898	4.11E-11	5.10E-11
c1_104	-0.003311822	0.147391982	0.155468255
c1_107	0.0286692	1.57E-36	2.74E-36
c1_109	0.020692093	1.23E-83	3.15E-83
c1_115	0.017441959	9.32E-15	1.22E-14
c1_117	0.020893328	2.28E-25	3.66E-25
c1_123	0.02567295	9.36E-23	1.47E-22
c1_127	0.013508553	0.011719535	0.012891489
c1_129	-0.161834996	0	0
c1_130	-0.025459258	2.39E-22	3.68E-22
c1_133	0.259320304	0	0
c1_137	-0.006032744	0.013272173	0.014393765
c1_145	0.006817056	0.005291388	0.005904882

Module specificity scores (MSS) in microglial subclusters

A high module specificity score indicates a relatively specific enrichment of this module for a particular subcluster

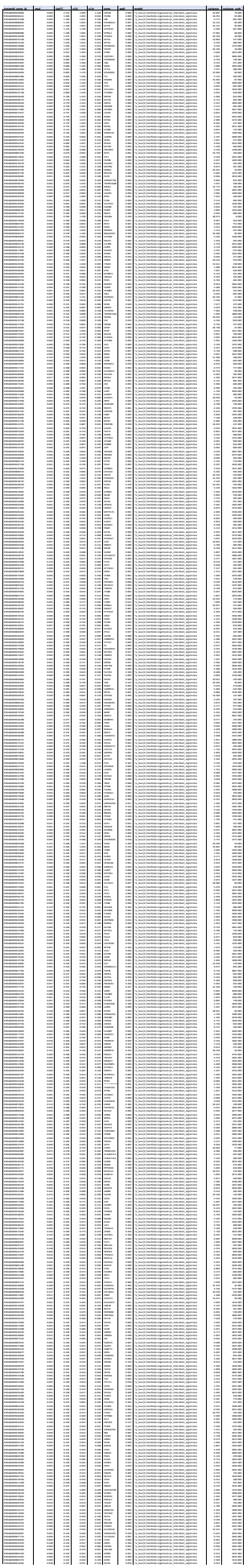
Co-expres	Micro1	Micro2	Micro3	PVM
c1_2	0.549	0.370	0.303	0.282
c1_4	0.548	0.369	0.303	0.282
c1_5	0.535	0.373	0.299	0.284
c1_6	0.553	0.364	0.304	0.280
c1_7	0.559	0.359	0.308	0.276
c1_9	0.557	0.361	0.303	0.277
c1_10	0.563	0.360	0.299	0.277
c1_11	0.530	0.384	0.292	0.293
c1_12	0.555	0.357	0.314	0.273
c1_13	0.544	0.362	0.307	0.272
c1_15	0.534	0.368	0.295	0.277
c1_16	0.528	0.372	0.291	0.297
c1_17	0.541	0.376	0.293	0.285
c1_18	0.513	0.374	0.291	0.281
c1_19	0.542	0.370	0.302	0.284
c1_20	0.519	0.350	0.304	0.279
c1_21	0.555	0.362	0.304	0.277
c1_22	0.549	0.365	0.307	0.279
c1_23	0.552	0.364	0.295	0.284
c1_24	0.542	0.353	0.314	0.279
c1_25	0.559	0.360	0.307	0.276
c1_26	0.457	0.321	0.378	0.262
c1_27	0.563	0.360	0.298	0.275
c1_28	0.557	0.360	0.303	0.277
c1_29	0.556	0.365	0.298	0.274
c1_30	0.549	0.361	0.302	0.281
c1_31	0.563	0.361	0.299	0.276
c1_32	0.557	0.357	0.301	0.281
c1_33	0.506	0.377	0.284	0.307
c1_34	0.460	0.413	0.282	0.299
c1_35	0.533	0.382	0.289	0.291
c1_36	0.523	0.384	0.291	0.289
c1_37	0.541	0.363	0.298	0.283
c1_39	0.555	0.354	0.316	0.275
c1_41	0.540	0.359	0.306	0.268
c1_43	0.527	0.372	0.289	0.298
c1_45	0.497	0.374	0.284	0.282
c1_49	0.555	0.361	0.303	0.277
c1_55	0.549	0.365	0.307	0.279
c1_57	0.545	0.352	0.305	0.278
c1_59	0.565	0.361	0.305	0.263
c1_60	0.557	0.357	0.309	0.279
c1_61	0.542	0.360	0.300	0.286
c1_62	0.558	0.362	0.302	0.269
c1_64	0.563	0.361	0.294	0.277
c1_65	0.560	0.350	0.310	0.272
c1_66	0.565	0.355	0.302	0.272
c1_67	0.543	0.368	0.300	0.283
c1_68	0.552	0.365	0.298	0.279
c1_71	0.555	0.367	0.295	0.275
c1_75	0.549	0.361	0.300	0.281
c1_76	0.564	0.361	0.298	0.276
c1_78	0.558	0.362	0.299	0.279
c1_80	0.557	0.359	0.294	0.274
c1_84	0.530	0.382	0.290	0.293
c1_86	0.538	0.359	0.303	0.280
c1_92	0.567	0.357	0.306	0.260
c1_93	0.561	0.357	0.304	0.267
c1_95	0.530	0.356	0.292	0.317
c1_96	0.569	0.350	0.315	0.256
c1_97	0.572	0.349	0.312	0.253
c1_98	0.519	0.371	0.296	0.312
c1_99	0.559	0.350	0.303	0.272
c1_101	0.534	0.361	0.299	0.286
c1_102	0.540	0.354	0.300	0.284
c1_104	0.560	0.348	0.311	0.272
c1_107	0.543	0.368	0.299	0.283
c1_109	0.563	0.361	0.297	0.276
c1_115	0.558	0.360	0.301	0.274
c1_117	0.555	0.363	0.298	0.281
c1_123	0.569	0.355	0.306	0.257
c1_127	0.519	0.351	0.296	0.318
c1_129	0.571	0.345	0.316	0.249
c1_130	0.563	0.354	0.311	0.264
c1_133	0.517	0.371	0.296	0.313
c1_137	0.560	0.348	0.311	0.272
c1_145	0.557	0.358	0.301	0.275

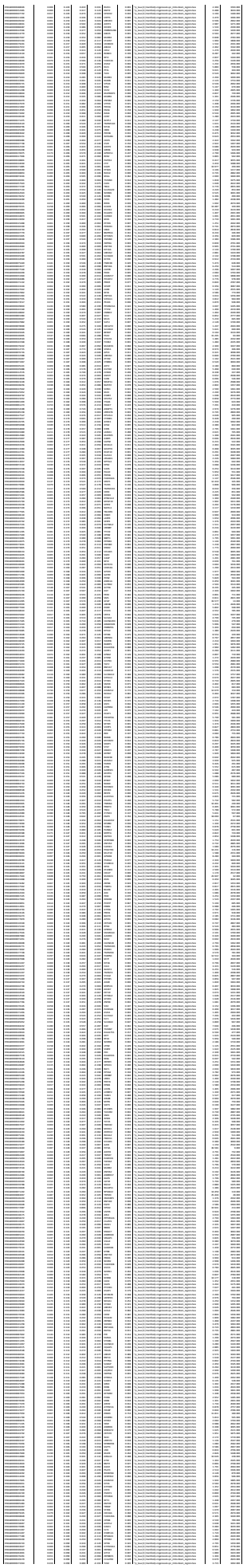
Supplementary Table 6_Astrocyte DGE
Contents

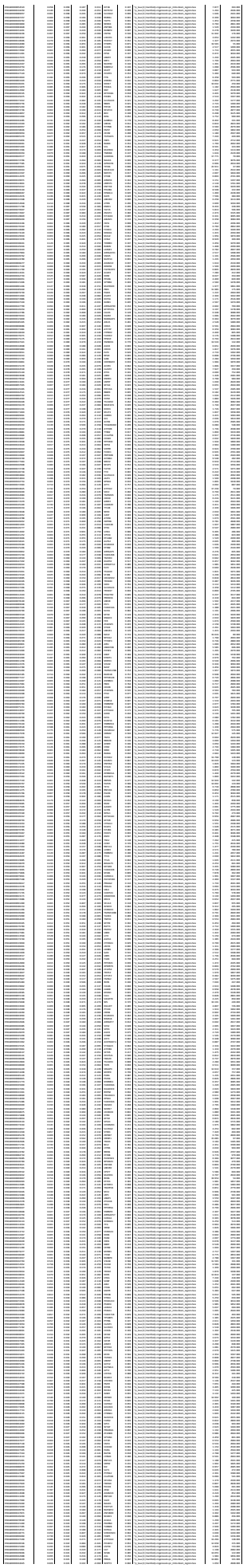
Sheet name	Description
Astrocytes_pTau	DGE analysis in Total Astrocytes using MAST and p_tau as contrast
Astrocytes_beta_amyloid	DGE analysis in Total Astrocytes using MAST and beta_amyloid as contrast

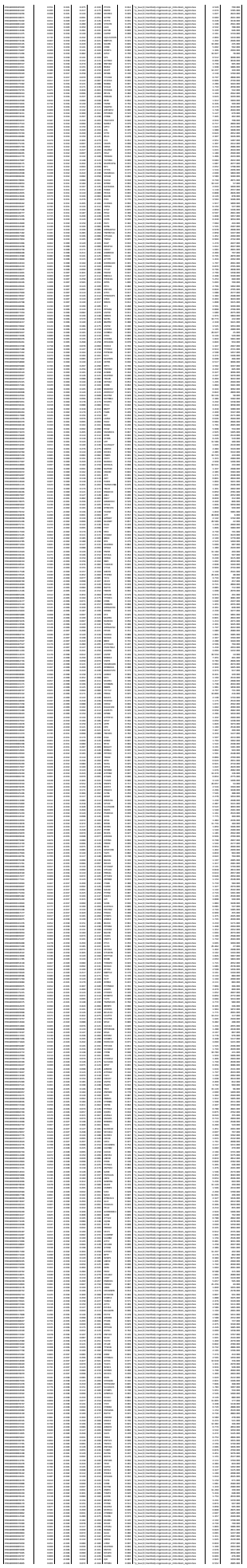
ci.hi/lo: higher and lower confidence intervals of the logFC value, respectively

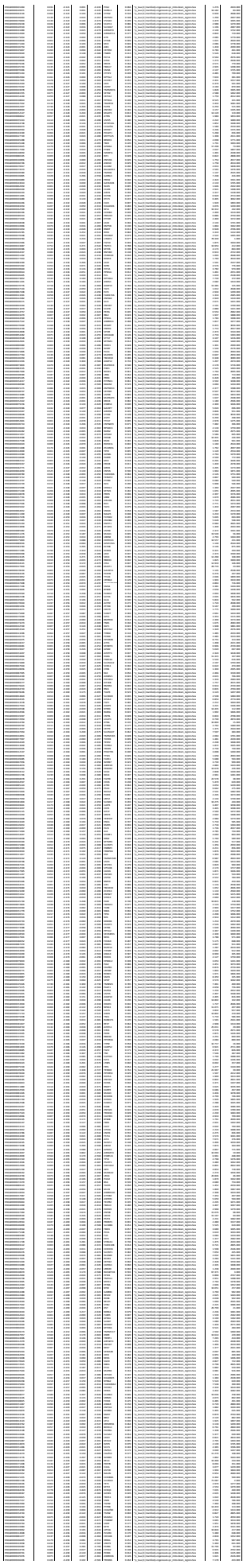
Supplementary Table 6_Astrocyte DGE
Astrocytes pTau

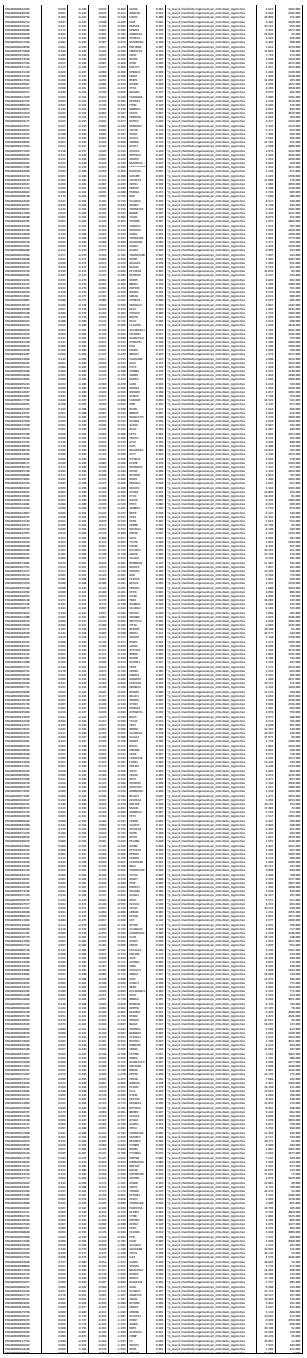






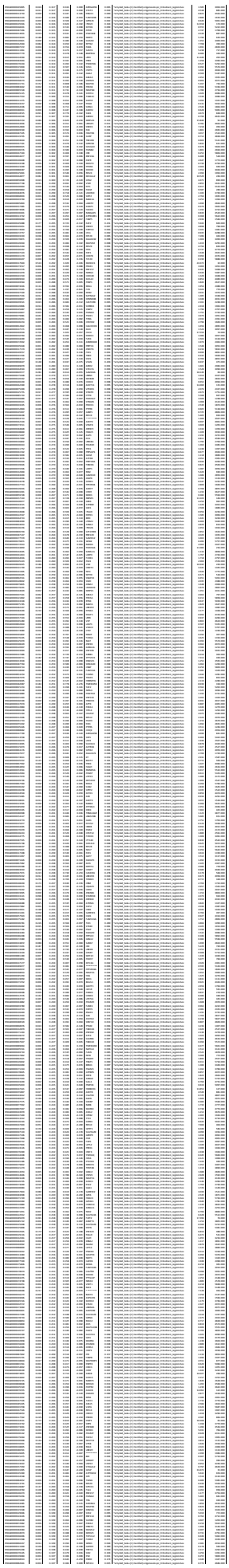


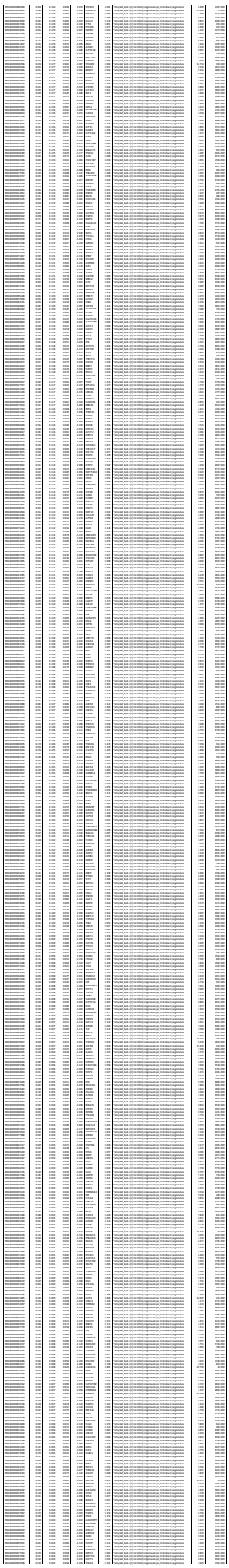


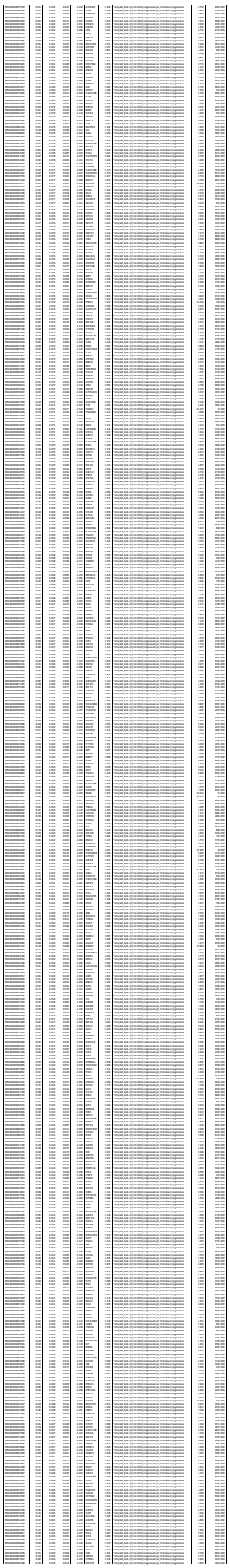


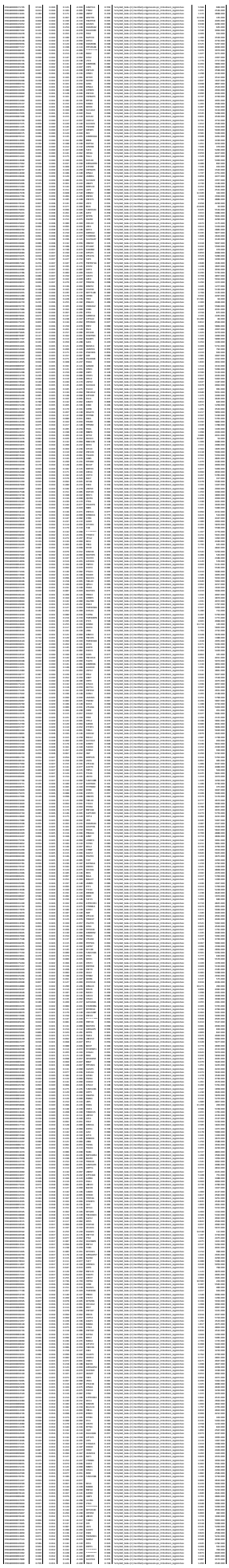
Supplementary Table 6_Astrocyte DGE
Astrocytes beta amyloid

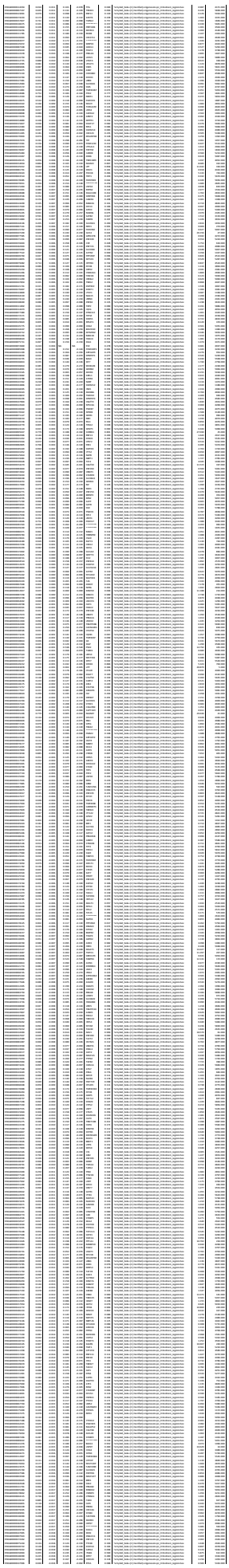
DGE analysis in Total Astrocytes using MAST and beta_amyloid as contrast

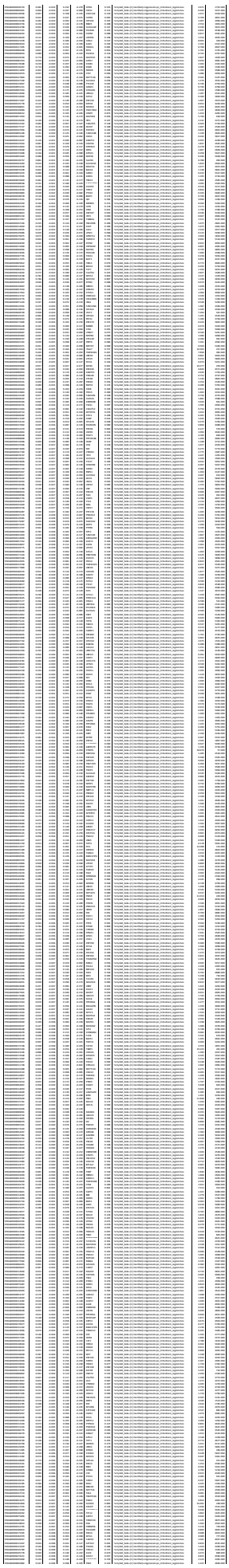


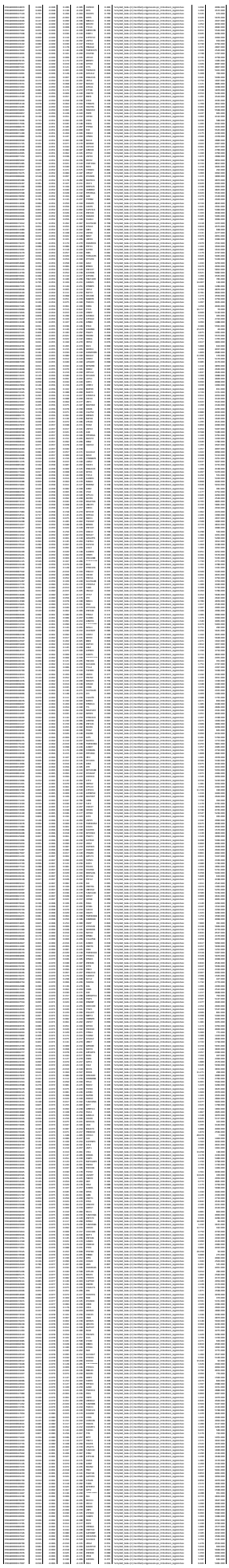


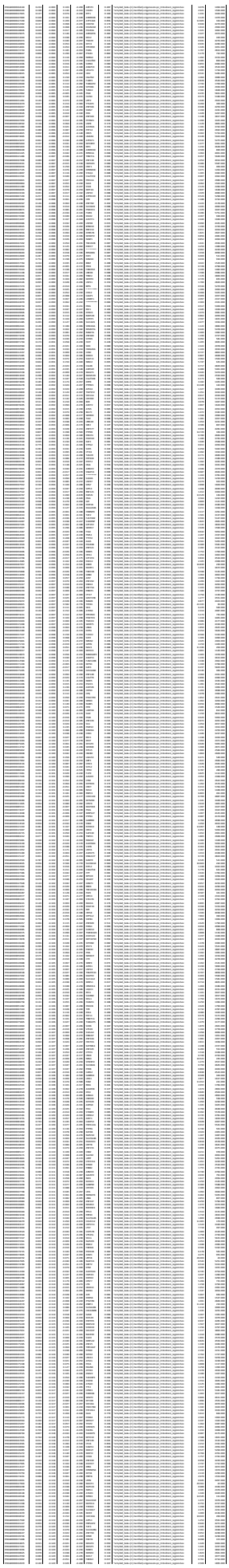


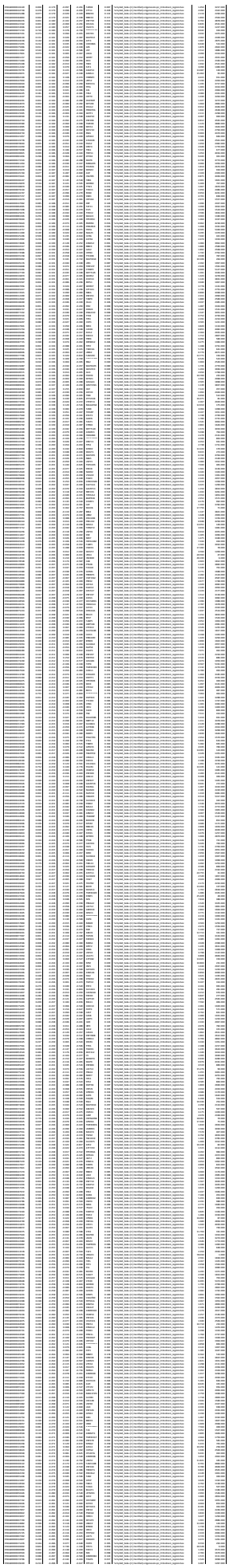


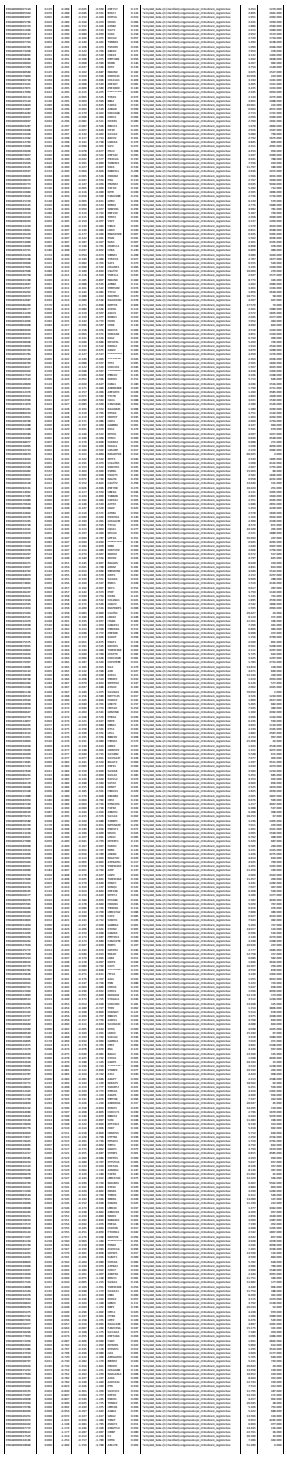










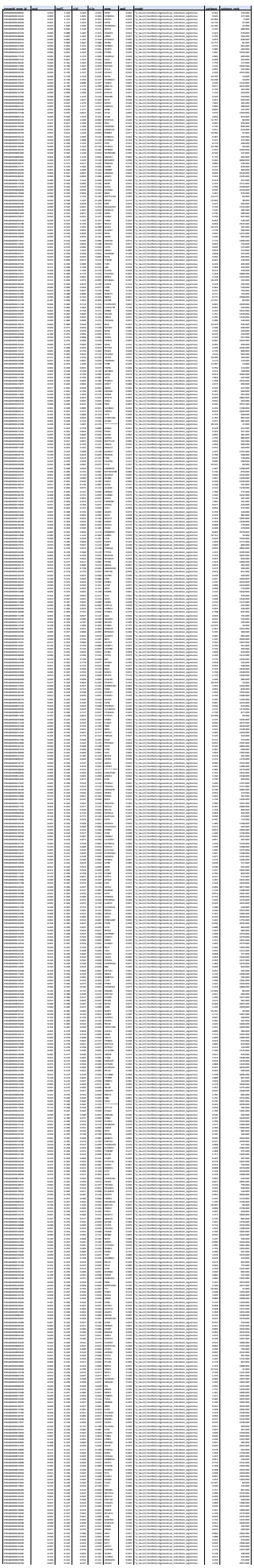


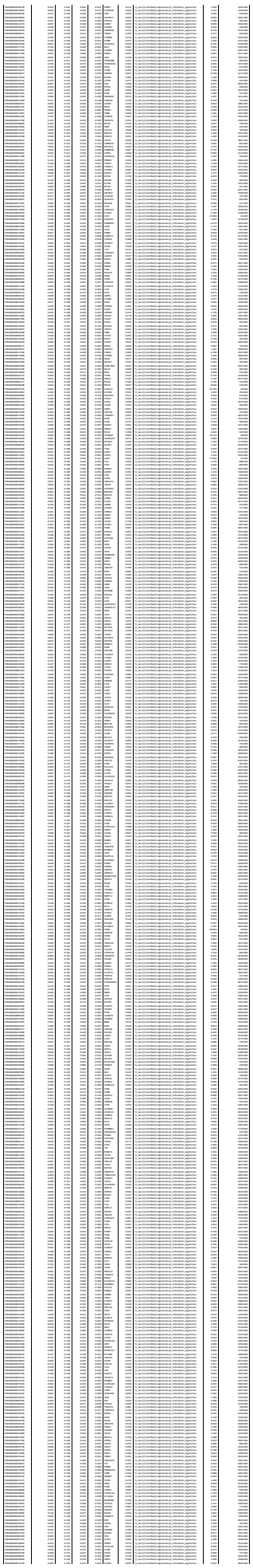
Supplementary Table 7_Microglia and PVMs DGE
Contents

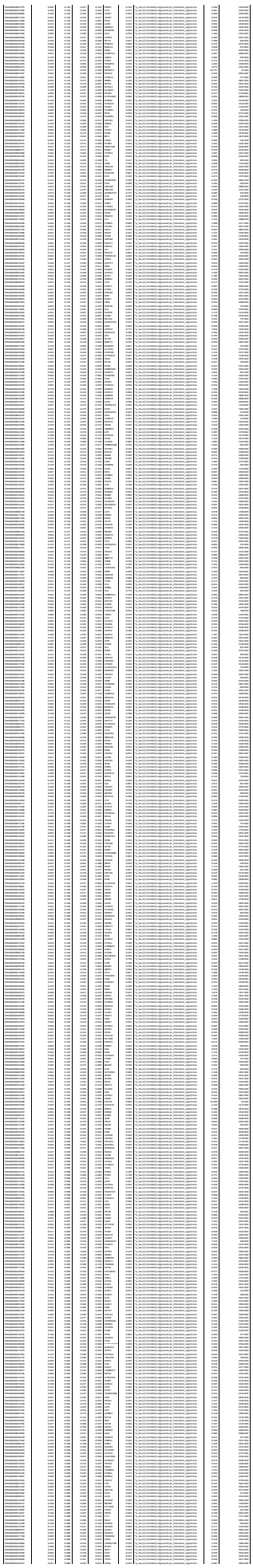
Sheet name	Description
Microglia_pTau	DGE analysis in Microglia using MAST and p_tau as contrast
PVM_pTau	DGE analysis in PVM using MAST and p_tau as contrast
Microglia_beta_amyloi	DGE analysis in Microglia using MAST and beta_amyloid as contrast
PVM_beta_amyloid	DGE analysis in PVM using MAST and beta_amyloid as contrast

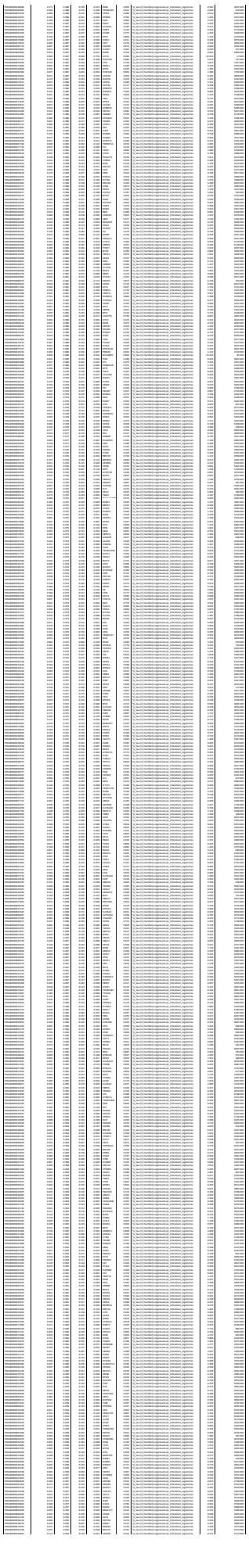
ci.hi/lo: higher and lower confidence intervals of the logFC value, respectively

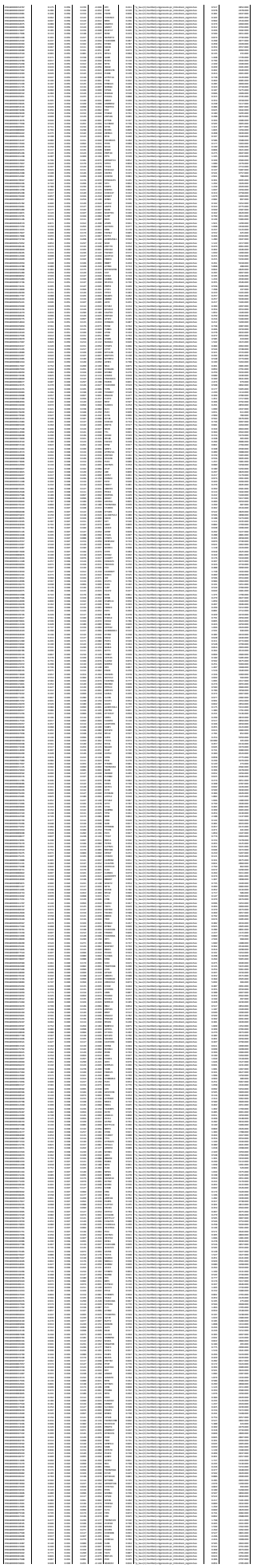
Supplementary Table 7_Microglia and PVMs DGE
Microglia pTau

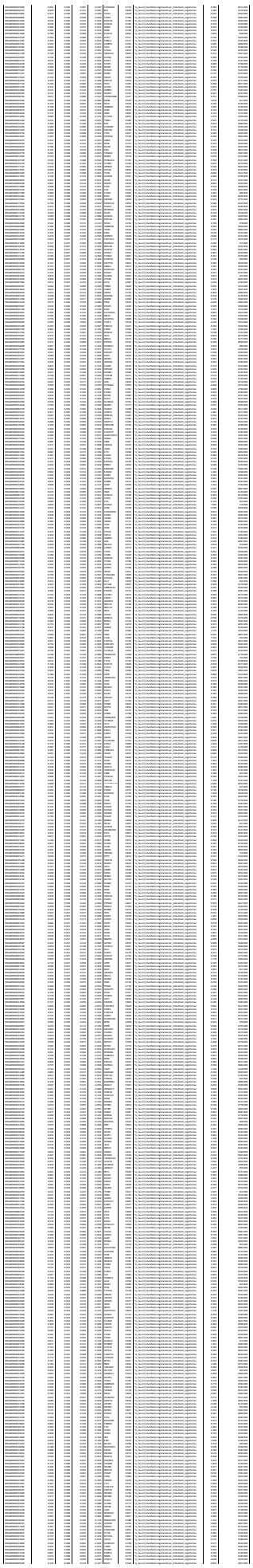


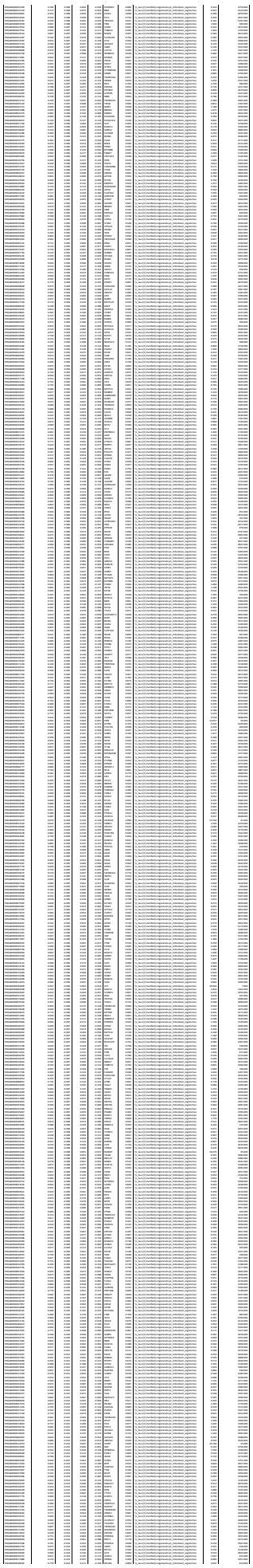


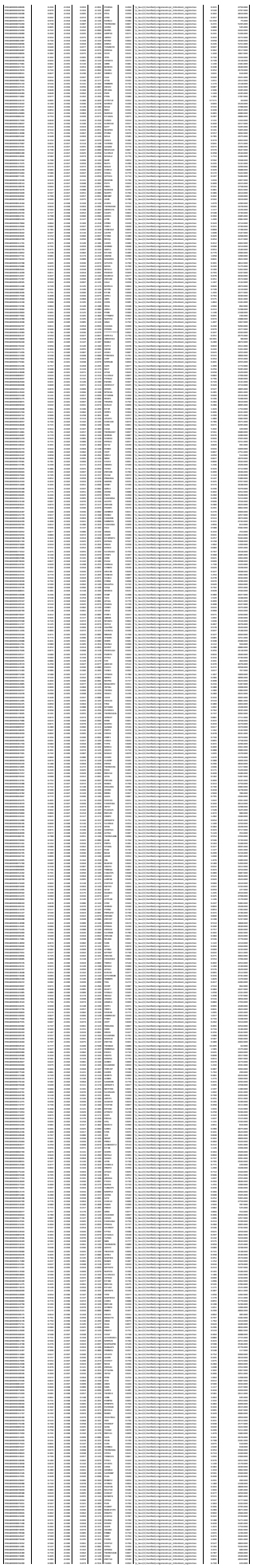


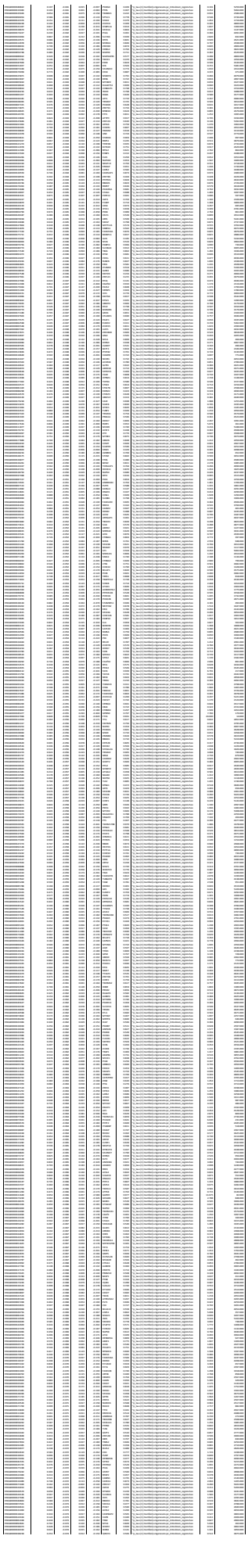


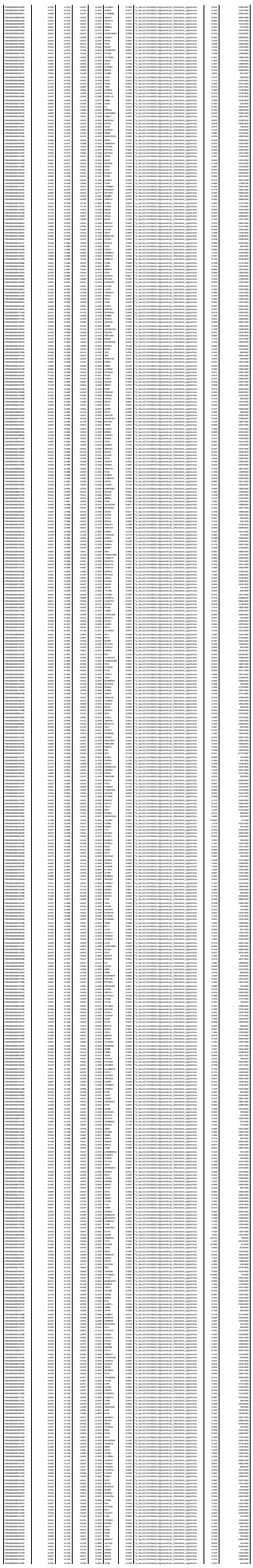


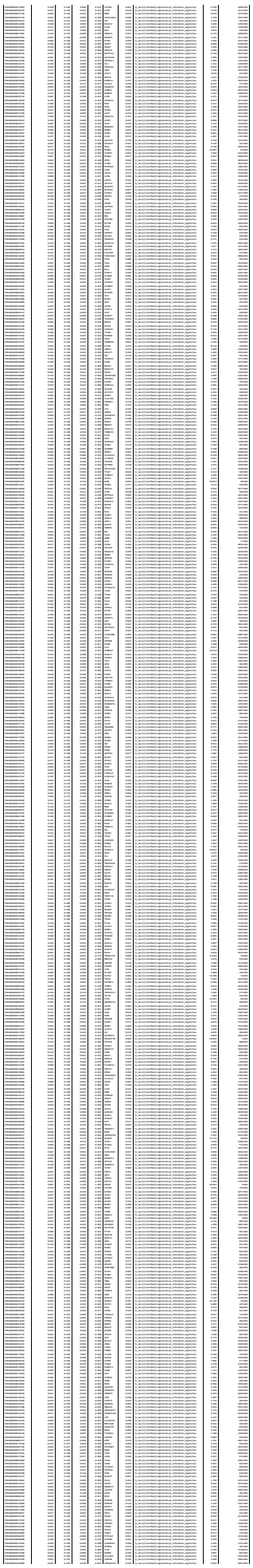


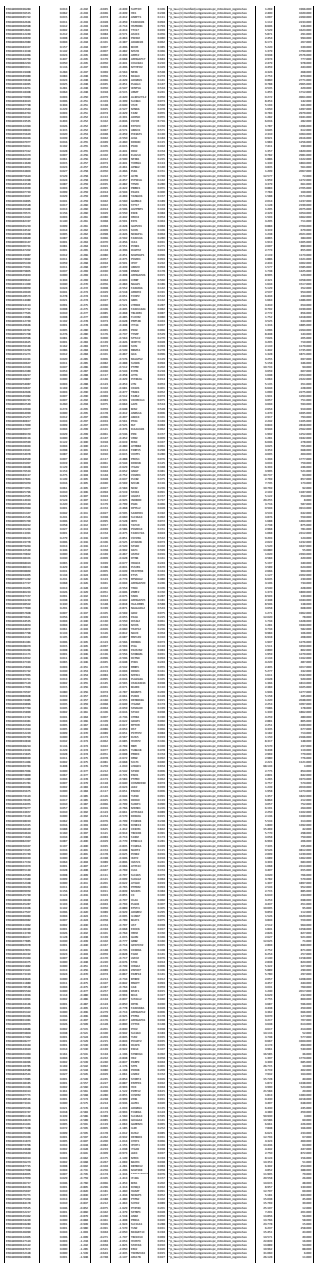








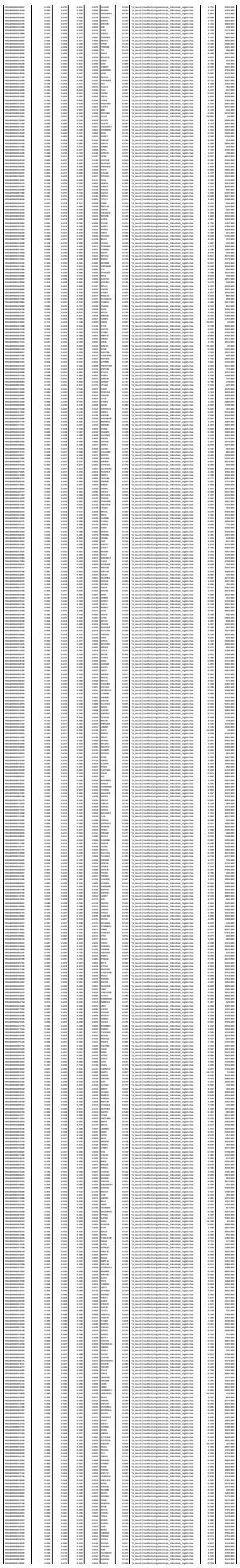


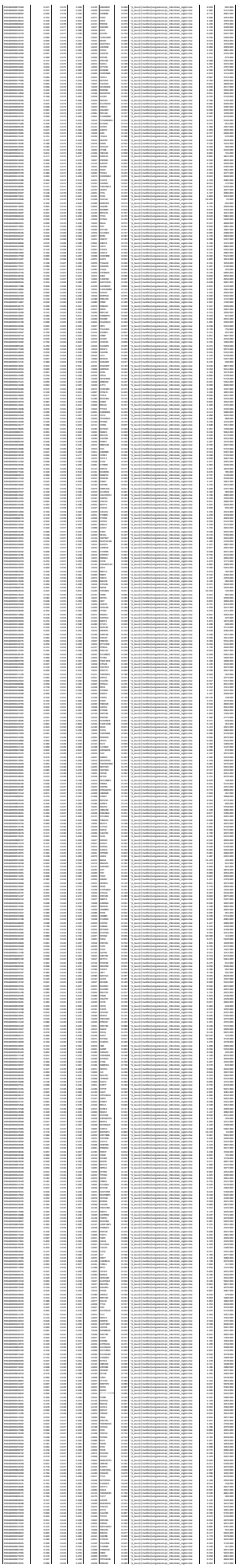


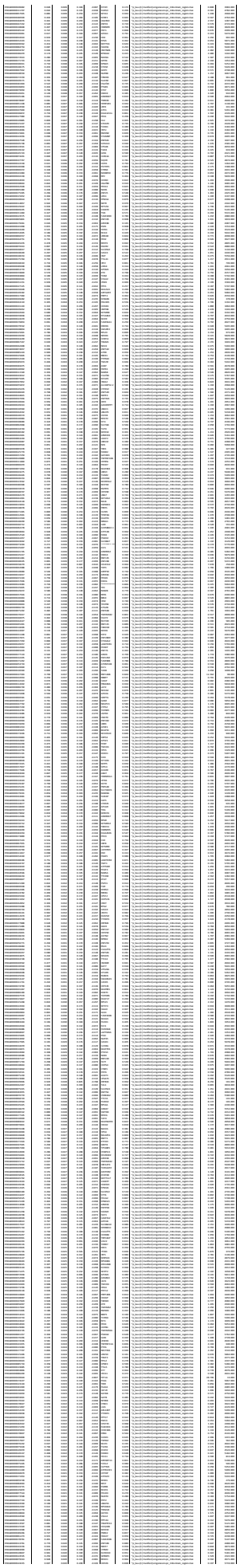
Supplementary Table 7_Microglia and PVMs DGE
PVM pTau

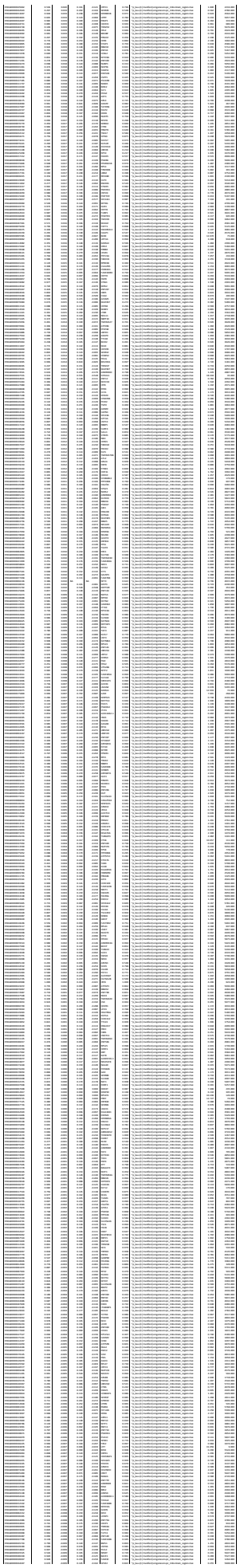
DGE analysis in the PVM subcluster using MAST and g_tsne centroid

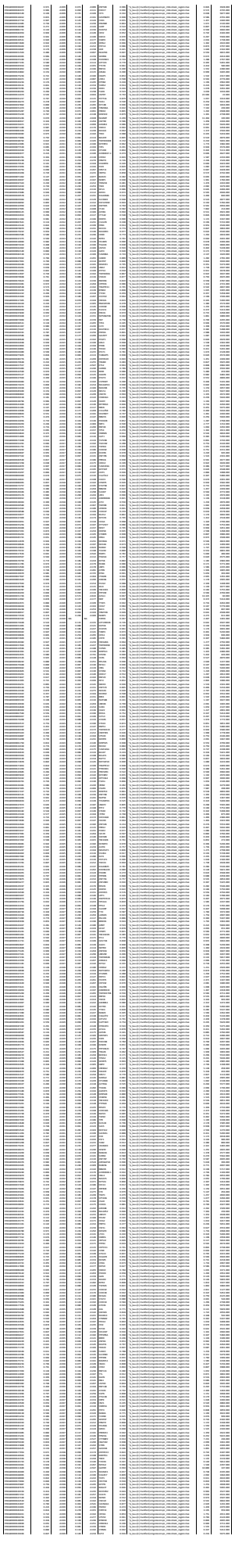
ensembl_exons_id	base	se(x)	z.prob	adj.p	gene	p.val	contrast	numbers_cells1	numbers_cells2
ENSG00000225256	0.2588	0.0276	9.3806	0.0000	ENSG00000225256	0.0000	7_tsne.pTau60.Ctrl.pTau.tsne.pTau_vs_tsne.Ctrl_cluster_7	5,116	500,000

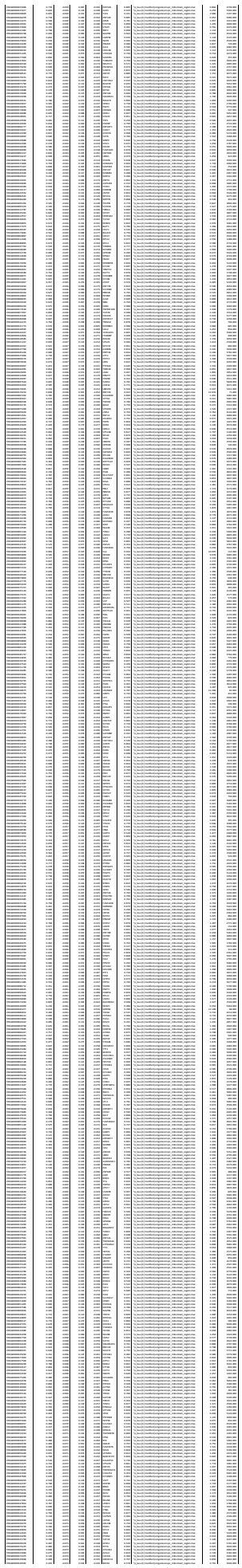


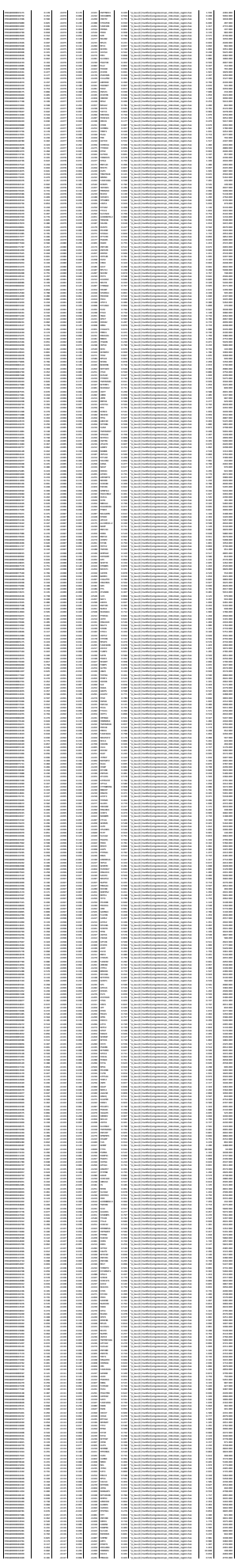


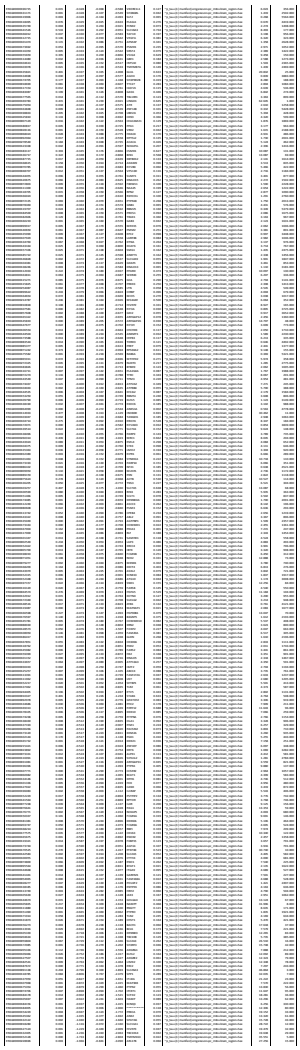












Supplementary Table 7_Microglia and PVMs DGE
Microglia beta amyloid

DGE analysis in Total Microglia using MAST wrathems_amyloid:an contrast

ensembl_gene_id	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	rownames	variance	variance_scaled
ENSMUSG00000000001	0.1197	0.1496	0.1765	0.8477	0.3967	0.5000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.7455	0.01490
ENSMUSG00000000003	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000028	0.1197	0.1496	0.1765	0.8477	0.3967	0.5000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.7455	0.01490
ENSMUSG00000000031	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000037	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000049	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000056	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000058	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000078	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000085	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000086	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000088	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000094	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000097	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000098	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000099	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000100	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000101	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000102	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000103	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000104	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000105	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000106	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000107	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000108	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000109	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000110	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000111	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000112	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000113	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000114	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000115	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000116	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000117	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000118	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000119	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000120	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000121	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000122	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000123	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000124	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000125	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000126	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000127	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000128	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000129	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000130	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000131	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000132	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000133	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000134	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000135	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000136	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000137	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000138	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000139	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000140	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000141	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000142	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000143	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000144	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000145	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000146	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000147	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000148	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000149	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000150	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000151	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000152	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000153	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000154	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000155	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000156	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000157	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000158	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000159	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000160	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000161	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000162	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000163	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000164	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000165	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000166	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000167	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000168	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
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ENSMUSG00000000170	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000171	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000172	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000173	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000174	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
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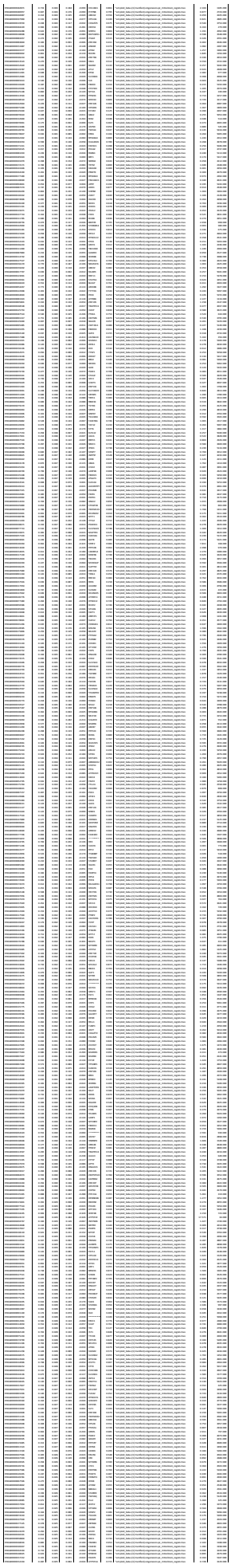
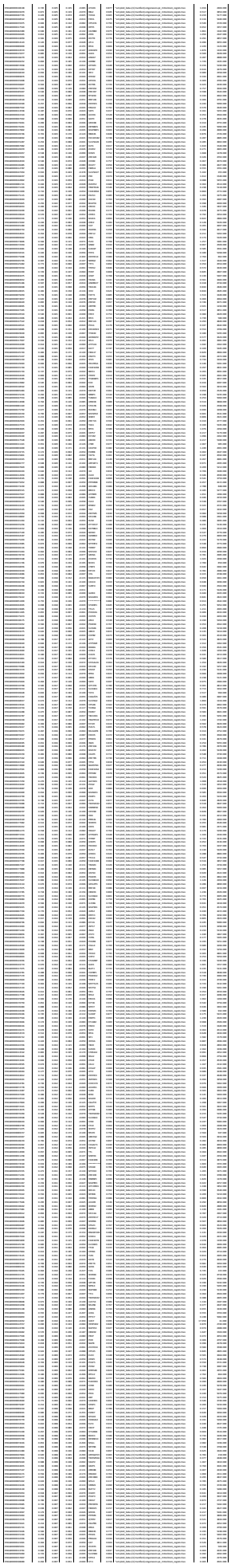
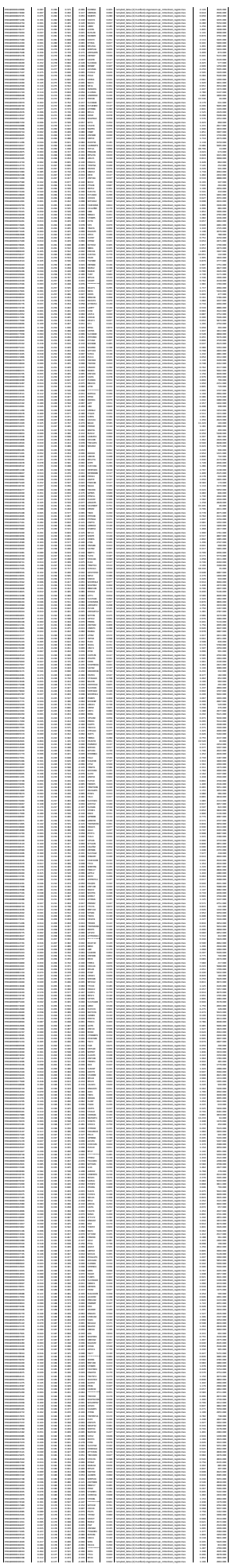
ENSMUSG00000000176	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000177	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000178	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000179	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000180	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000181	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000182	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000183	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000184	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000185	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000186	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000187	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000188	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000189	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000190	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000191	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000192	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000193	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000194	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000195	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000196	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000197	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000198	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000199	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000
ENSMUSG00000000200	0.0000	0.0000	0.0000	0.0000	1.0000	1.0000	Total_Mglia_DGE/results/diagnostics/ad_interactions_mglia.rds	0.0000	0.00000

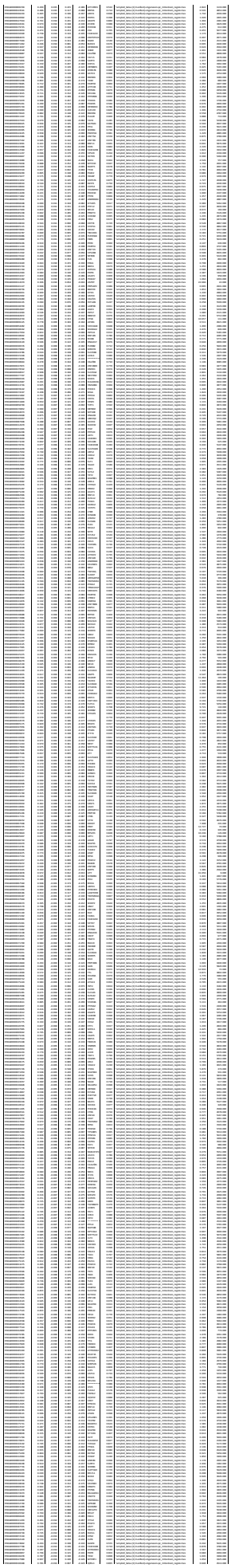


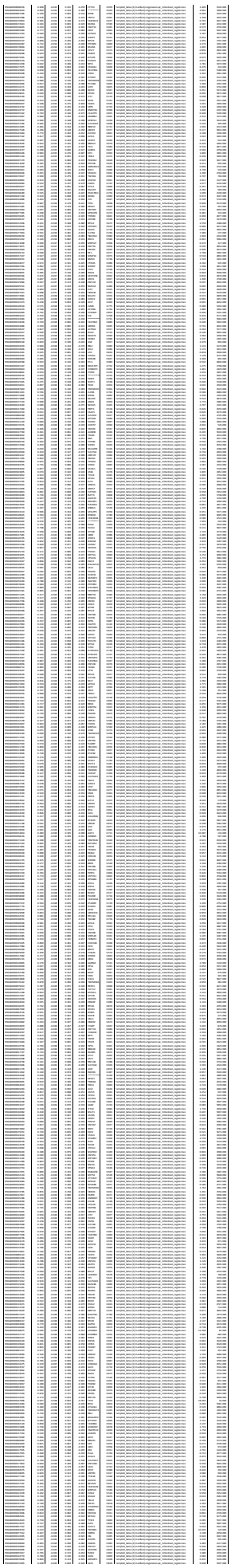


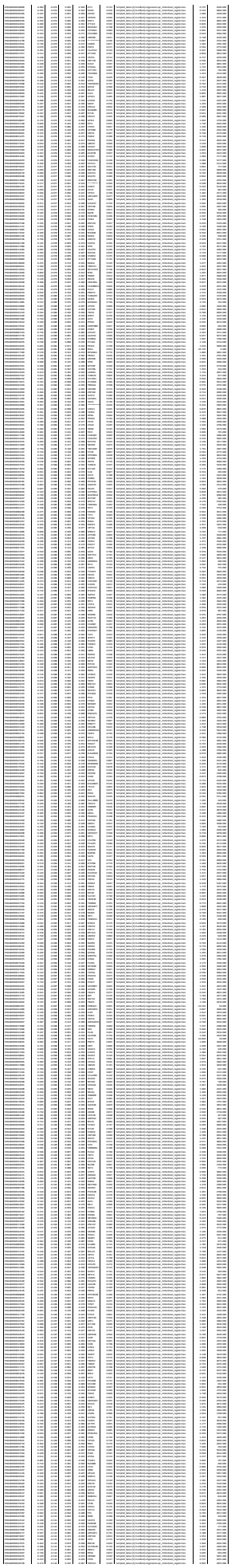
Supplementary Table 7_Microglia and PVMs DGE
PVM beta amyloid

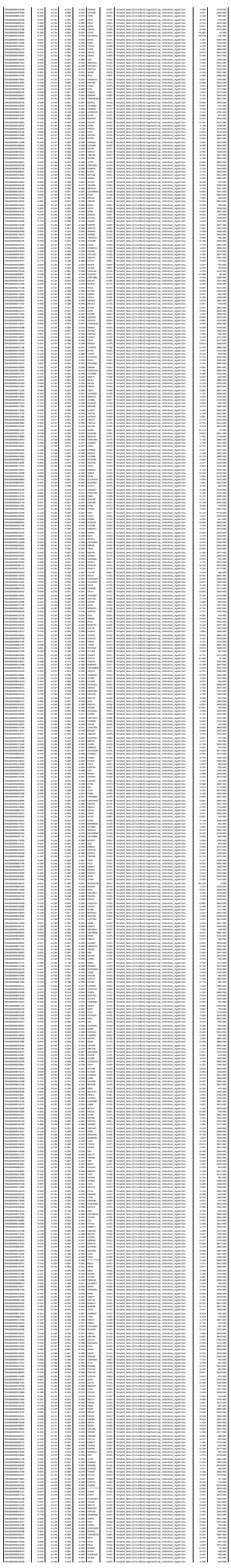
DGE analysis in the PVM subcluster using MAST and beta_amyloid as contrast

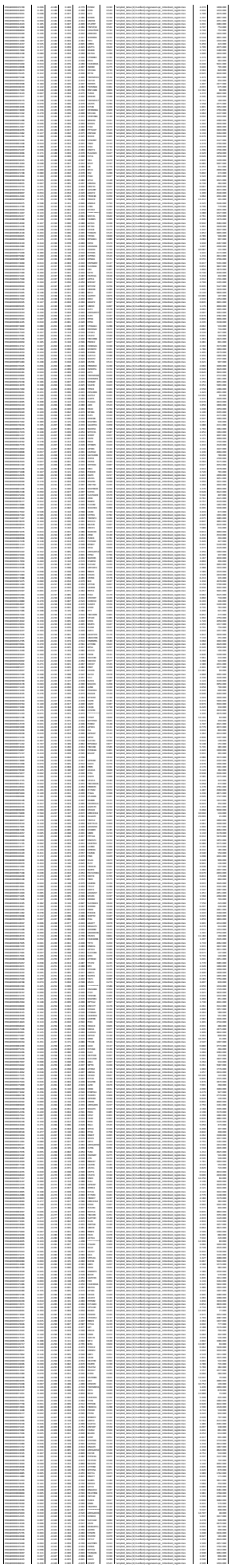


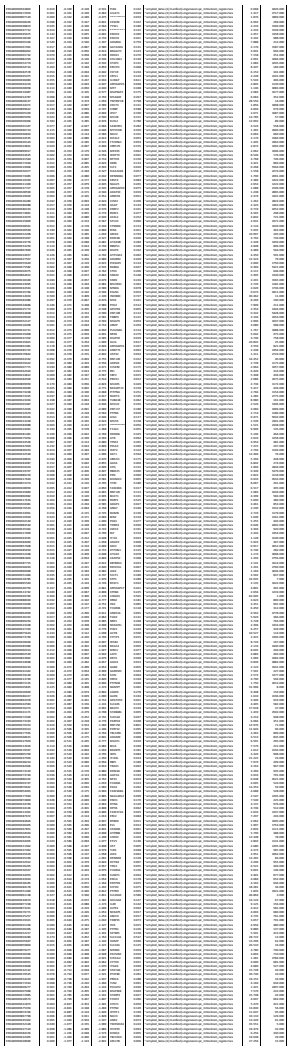












Supplementary Table 8 Enrichment Astrocyte DGE
Contents

Sheet name	Description
Astrocytes_amyloid	Gene ontology and pathway enrichment analysis for Astrocyte genes significantly differentially expressed with amyloid-beta pathology
Astrocytes_pTau	Gene ontology and pathway enrichment analysis for Astrocyte genes significantly differentially expressed with pTau pathology

Analysis performed using enrichR (v 3.0)

Supplementary Table 8 Enrichment Astrocyte DGE
Astrocytes amyloid

geneset	description	size	overlap	odds ratio	pval	FDR	database	X.Log10.FDR.	genes	clusters
R-HSA-5660526	Response to metal ions	11	5	23.17	2.08E-05	0.00067	Reactome	3.1	MT2A;MT1M;MT1F;MT1G;MT1E	20
R-HSA-5661231	Metallothionein bind metals	11	5	23.17	2.08E-05	8.75E-04	Reactome	3.1	MT2A;MT1M;MT1F;MT1G;MT1E	20
R-HSA-844856	The NLRP3 inflammasome	12	4	13.88	5.90E-04	0.01484	Reactome	1.8	APP;HSPB8;MLTK;TNNP1;SUGT1	21
GO:0071294	cellular response to zinc ion	19	6	12.81	3.30E-05	0.007	GO	2.1549	MT2A;HIVEP2;MT1M;MT1F;MT1G;MT1E	4
R-HSA-9375151	HSF1 activation	29	9	12.57	6.00E-07	1.00E-04	Reactome	4	EEF1A1;DNAJB1;VCP;HSPB8;DNAJA1;HSPB6;HSPH1;DNAJB6;UBB;PTGES3	14
R-HSA-209560	NF-kB is activated and signals survival	13	4	12.34	8.20E-04	0.01935	Reactome	1.7	NFKBIA;UBB;UBC;SQSTM1	8
R-HSA-190873	Gap junction degradation	10	3	11.88	4.20E-03	0.05496	Reactome	1.2	MYO6;AP2M1;DNM2	3
R-HSA-451308	Activation of Ca-permeable Kainate Receptor	10	3	11.88	4.20E-03	0.05496	Reactome	1.2	GRM6;GRM2;CACNA1	12
R-HSA-451306	Ionotropic activity of Kainate Receptors	10	3	11.88	4.20E-03	0.05496	Reactome	1.2	GRM6;GRM2;CACNA1	12
R-HSA-5682068	Diseases of carbohydrate metabolism	10	3	11.88	4.20E-03	0.05496	Reactome	1.2	EPN2A;UBB;UBC	8
R-HSA-8786613	Myoclonic epilepsy of Lafora	10	3	11.88	4.20E-03	0.05496	Reactome	1.2	EPN2A;UBB;UBC	8
R-HSA-4129121	Glycogen storage diseases	10	3	11.88	4.20E-03	0.05496	Reactome	1.2	EPN2A;UBB;UBC	8
R-HSA-209615	eNOS activation	10	3	11.88	4.20E-03	0.05496	Reactome	1.2	HSPB8;DAZL;DDAH1;CALM1	12
GO:0051131	chaperone-mediated protein complex assembly	17	5	11.58	2.20E-04	0.028	GO	1.5528	HSPB8;DAZL;HSPB6;HSPH1;HSPA1A;PTGES3;HSPD1	5
GO:0006120	mitochondrial electron transport, cytochrome c to oxygen	6	3	11.13	6.20E-05	0.011	GO	1.9586	COX7B;NDUFA4;CCDC47;CCDC;COX7C;COX6B1	3
R-HSA-5223891	Uptake and function of anthrax toxins	11	3	10.39	0.0057	0.07303	Reactome	1.1	MAPK3;PIDD1;AP2M1;CALM1	17
R-HSA-9717168	Attenuation phase	26	7	10.27	2.30E-05	0.00307	Reactome	3.1	DNAJB1;HSPB8;DAZL;HSPB6;HSPH1;DNAJB6;UBB;PTGES3	14
R-HSA-8122077	Glycogen synthesis	15	4	10.09	1.50E-03	0.03241	Reactome	1.5	EPN2A;USP13;UBB;UBC	8
WP9	Phychemical activity on NRF2 transcriptional activation	15	4	10.09	0.0015	0.04106	WikiPathway	1.4	NQO1;CSRP1;NMY;GCLM	2
R-HSA-1236382	Constitutive Signaling by Ligand-Responsive EGFR Cancer Variants	19	5	9.93	6.00E-04	0.01562	Reactome	2	HSPB8;DAZL;UBB;UBC;SQSTM1	4
R-HSA-5637815	Signaling by Ligand-Responsive EGFR Variants in Cancer	19	5	9.93	6.00E-04	0.01562	Reactome	2	HSPB8;DAZL;UBB;UBC;SQSTM1	4
R-HSA-1643713	Signaling by EGFR in Cancer	19	5	9.93	6.00E-04	0.01562	Reactome	2	HSPB8;DAZL;UBB;UBC;SQSTM1	4
R-HSA-191639	p75NTR signals via NF-kB	16	4	9.25	0.0019	0.0366	Reactome	1.6	NFKBIA;UBB;UBC;SQSTM1	8
R-HSA-399954	Sumoylation of transcription cofactors	16	4	9.25	1.90E-03	0.0366	Reactome	1.6	HSPB8;DAZL;HSPB6;RIC1;PLXNA3	15
WP67	Hedgehog Signaling Pathway	16	4	9.25	0.0019	0.04143	WikiPathway	1.3	GRK2;SMO;PTCH2;ARNTL	5
R-HSA-113501	Inhibition of replication initiation of damaged DNA by RB1/E2F1	12	3	8.91	0.0074	0.08776	Reactome	1.1	RB1;PPP2CB;PPP2R1B	2
GO:0071280	cellular response to copper ion	21	5	8.68	0.00966	0.052	GO	1.284	MT2A;MT1M;MT1F;MT1G;MT1E	4
R-HSA-422012	Inflammasomes	17	4	8.54	0.0024	0.04164	Reactome	1.4	APP;HSPB8;MLTK;TNNP1;SUGT1	21
GO:0006986	response to unfolded protein	43	10	8.47	1.70E-06	7.80E-04	GO	3.1079	DNAJB1;HSPA9;DNAJA1;DNAJB1;HSPB8;HSPA1A;HSPB6;HSPH1;HSPA1L;HSPB1;HSPD1	5
R-HSA-68884	Mitotic Telophase/Cytokinesis	13	3	8.32	0.0094	0.09616	Reactome	1	NUDC;PDS5B;PDS5A	22
R-HSA-209543	p75NTR recruits signalling complexes	13	3	8.32	0.0094	0.09616	Reactome	1	UBB;UBC;SQSTM1	4
R-HSA-174474	Assembly Of The HIV Virion	13	3	8.32	0.0094	0.09616	Reactome	1	UBB;UBC;PPIA	8
R-HSA-879415	Advanced glycosylation endproduct receptor signaling	13	3	8.32	0.0094	0.09616	Reactome	1	APP;PRKCSH;CANX;KX1	21
GO:0010043	response to zinc ion	32	7	7.8	9.70E-05	0.016	GO	1.7959	MT2A;HIVEP2;MT1M;MT1F;MT1G;SLC30A1;MT1E	4
WP4380	Extracellular vesicles in the crosstalk of cardiac cells	19	4	7.6	0.0038	0.07824	WikiPathway	1.1	CD63;STAT3;HSPB1;SOD1	2
GO:0051085	chaperone-mediated protein folding requiring cofactor	24	5	7.51	1.30E-03	0.088	GO	1.0565	HSPB8;DNAJB1;HSPH1;HSPA1E;PTGES3	5
R-HSA-9717571	HSF1-dependent transactivation	34	7	7.22	0.00015	0.00451	Reactome	2.3	DNAJB1;HSPB8;DAZL;HSPB6;DNAJB1;UBB;PTGES3	14
GO:0051188	'de novo' posttranslational protein folding	30	6	6.95	0.00052	0.012	GO	1.286	HSPA8;DNAJB1;HSPH1;HSPA1E;PTGES3;UGGT2	5
GO:0006488	response to copper ion	25	5	6.95	0.0031	0.094	GO	1.0269	MT2A;MT1M;MT1F;MT1G;MT1E	4
R-HSA-202763	eNOS activation and regulation	20	4	6.94	0.0046	0.06297	Reactome	1.2	HSPB8;DAZL;DDAH1;CALM1;DNM2	12
R-HSA-421191	Metabolism of nitric oxide	20	4	6.94	0.0046	0.06297	Reactome	1.2	HSPB8;DAZL;DDAH1;CALM1;DNM2	12
WP5129	Zinc homeostasis	36	7	6.72	0.00021	0.01414	WikiPathway	1.8	MT2A;MT1M;SLC39A11;MT1F;MT1G;SLC30A1;MT1E	5
GO:0055069	zinc ion homeostasis	33	7	6.68	6.20E-05	0.012	GO	1.286	MT2A;MT1M;MT1F;MT1G;SLC30A1;MT1E	4
GO:0006882	cellular zinc ion homeostasis	31	6	6.68	0.00062	0.012	GO	1.286	MT2A;MT1M;MT1F;MT1G;SLC30A1;MT1E	4
WP581	EPO Receptor Signaling	26	5	6.61	0.0018	0.04143	WikiPathway	1.3	NMYC;STAT3;HSPB1;SOD1;EPOR	3
R-HSA-70171	Glycolysis	32	6	6.42	7.40E-04	0.01792	Reactome	1.7	PFKFB2;PPP2CB;PPP3R1B;ENO2;ENO2;PFKP	23
GO:0051085	cytoplasmic translation	54	10	6.35	1.50E-05	0.0042	GO	2.1768	RPL30;RPL22;RPL9;RPL27A;RPL11;RPS27;RPL35A;RPL38;RPS20;RPL19	1
R-HSA-5339562	Uptake and actions of bacterial toxins	27	5	6.31	0.0022	0.03937	Reactome	1.4	HSPB8;DAZL;HSPB6;RIC1;MAPK3K2;PDCD6IP;CALM1	17
R-HSA-1368082	RORA activates gene expression	27	5	6.31	2.20E-03	0.03937	Reactome	1.4	SMARCD1;RORA;NR1D1;HIPK2;ARNTL	5
GO:0030477	glycogen metabolic process	33	6	6.19	0.00088	0.046	GO	1.3805	USP13;PHKG1;UBB;UBC;NR1D1;CALM1	2
R-HSA-5250485	Pink/Parkin Mediated Mitophagy	22	4	6.17	0.0061	0.08097	Reactome	1.1	UBB;UBC;TOMM7;SQSTM1	8
R-HSA-5358487	Mitophagy	22	4	6.17	0.0061	0.08097	Reactome	1.1	UBB;UBC;TOMM7;SQSTM1	8
R-HSA-156902	Peptide chain elongation	84	15	6.11	1.90E-07	0.00058	GO	6	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;EEF1A1;RPL27A;RPL27A;RPS27;RPL38;RPS20;RPL19	7
R-HSA-202765	eNOS activation and regulation	20	4	6.94	0.0046	0.06297	Reactome	1	ZFP36L1;NR4A1;DNAJB1;DNAJB1;MAPK14	11
R-HSA-611105	Respiratory electron transport	88	15	5.78	3.40E-07	1.00E-04	Reactome	4	COX5B;COX7B;NDUFA4;2;NDUFA4;COX6B1;ETFDH;NDUFB2;ETFA;NDUFC1;CCDC;COX7C;UQCRH;CCNA81;NDUFS7;NDUFS2	6
GO:0006414	SKP-dependent ubiquitinated protein targeting to membrane	89	15	5.7	4.20E-07	0.00058	GO	3.2366	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;SNRPG;RPL27A;RPL27A;RPL38;RPS20;RPL19	1
R-HSA-156842	Eukaryotic Translation Elongation	89	15	5.7	4.20E-07	1.00E-04	Reactome	4	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;EEF1A1;RPL27A;RPL27A;RPS27;RPL38;RPS20;RPL19	7
R-HSA-192823	Viral mRNA Translation	84	14	5.61	1.20E-06	0.00023	Reactome	3.6	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;RPL27A;RPL27A;RPS27;RPL38;RPS20;RPL19	7
GO:0050998	regulation of nitric-oxide synthase activity	36	6	5.56	0.0014	0.089	GO	1.8106	NLS1;HSPB8;DAZL;DDAH1;SGSM3;CALM1;DNM2	10
GO:0016575	histone deacetylation	36	6	5.56	0.0014	0.089	GO	1.8106	HDAC1;SPR;UMORF4;ZFP69;MSL3;WRT;SIRT2	7
R-HSA-2129379	Molecules associated with elastic fibres	30	5	5.56	0.0035	0.05346	Reactome	1.3	EFEMP1;MFAP2;ITGB8;FBLN5;LTBP3	13
R-HSA-210500	Glutamate Neurotransmitter Release Cycle	24	4	5.55	0.009	0.09636	Reactome	1	RIMS1;SLC1A2;SLC1A3;SLC1B2	1
R-HSA-70326	Glucose metabolism	79	13	5.52	3.30E-06	0.00035	Reactome	3.5	EPN2A;PFKFB2;ENO1;ENO2;PPP2CB;USP2;PC;PPP3R1B;PKM;G1BB;UBC;CALM1;PFKP	23
GO:0006613	cotranslational protein targeting to membrane	93	15	5.4	7.40E-07	7.02E-04	GO	3.1549	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;SNRPG;RPL27A;RPL27A;RPL38;RPS20;RPL19	1
R-HSA-2408557	Selenocysteine synthesis	87	14	5.38	1.80E-06	0.00016	Reactome	3.6	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;RPL27A;RPL27A;RPS27;RPL38;RPS20;RPL19	7
R-HSA-72764	Eukaryotic Translation Termination	87	14	5.38	1.80E-06	0.00016	Reactome	3.6	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;RPL27A;RPL27A;RPS27;RPL38;RPS20;RPL19	7
R-HSA-975956	Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	89	14	5.24	2.40E-06	1.00E-04	Reactome	3.5	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;RPL27A;RPL27A;RPS27;RPL38;RPS20;RPL19	7
WP477	Cytoplasmic Ribosomal Proteins	89	14	5.24	2.40E-06	0.00102	WikiPathway	3.6	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;RPL27A;RPL27A;RPS27;RPL38;RPS20;RPL19	4
R-HSA-69236	G1 Phase	38	6	5.21	1.90E-03	0.0366	Reactome	1.4	RB1;PPP2CB;PPP3R1B;UBB;TFDP2;UBC	2
R-HSA-69231	Cyclin D associated events in G1	38	6	5.21	1.90E-03	0.0366	Reactome	1.4	RB1;PPP2CB;PPP3R1B;UBB;TFDP2;UBC	2
GO:0045047	protein targeting to ER	97	15	5.19	1.30E-06	0.00078	GO	3.1079	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;SRP14;RPL27A;RPL27A;RPL38;RPS20;RPL19	1
R-HSA-4085001	Sialic acid metabolism	33	5	4.96	0.0054	0.07145	Reactome	1.1	ST6GAL1;GLB1;SLC17A5;ST3GAL1;ST6GALNAC5	16
WP544	Alpha 6-beta 4 signaling pathway	33	5	4.96	0.0054	0.09494	WikiPathway	1	LAMB2;GAS1;RSU1;LAMC1;SOS1	3
GO:0022904	respiratory electron transport chain	94	14	4.91	4.70E-06	0.0016	GO	2.7959	COX7B;NDUFA12;NDUFA4;COX6B1;ETFDH;NDUFB2;ETFA;NDUFC1;CCDC;COX7C;UQCRH;COX6B1;NDUFS7;NDUFS2	3
R-HSA-5173214	Negative regulation of NMDA pathway	40	6	4.81	0.0025	0.06164	Reactome	1.6	PPP2CB;NMYO2;PPP3R1B;UBB;UBC;PSEN1	2
R-HSA-72689	Formation of a pool of free 40S subunits	96	14	4.79	6.00E-06	4.00E-04	Reactome	3.4	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;RPL27A;RPL27A;RPS27;RPL38;RPS20;RPL19	7
WP111	Electron Transport Chain (OXPHOS system in mitochondria)	103	15	4.79	2.90E-06	0.00032	WikiPathway	3.5	ATP5PF;COX7B;NDUFA12;NDUFA4;COX6B1;NDUFB2;NDUFC1;CCDC;COX7C;ATP5F1D;UQCRH;ATP5F1E;COX6B1;NDUFS7;NDUFS2	1
GO:0030770	regulation of lactogenesis	55	8	4.74	0.00061	0.012	GO	1.286	PLXNB1;PLXNB3;LRRC4C;ABHD4;NPDC;ROBO1;ZBND6Z;PLXNA3;SSH1	10
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	112	16	4.69	1.80E-06	0.00078	GO	3.1079	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;SMG8;RPRC1;RPL27A;RPL27A;RPS27;RPL38;RPS20;RPL19	1
GO:0019083	viral transcription	113	16	4.66	2.00E-06	0.00078	GO	3.1079	RPL30;RPL22;NUP188;RPL9;RPL27A;RPL11;RPL35A;SNRPG;RPL27A;RPL27A;RPL38;RPS20;RPL19	1
R-HSA-927802	Nonsense-Mediated Decay (NMD)	106	15	4.63	4.10E-06	1.52E-04	Reactome	3.5	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;SMG8;RPL27A;RPL27A;RPS27;RPL38;RPS20;RPL19	7
R-HSA-975957	Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	106	15	4.63	4.10E-06	0.00035	Reactome	3.5	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;SMG8;RPL27A;RPL27A;RPS27;RPL38;RPS20;RPL19	7
R-HSA-1368108	BMAL1:CLOCK,NPAS2 activates circadian gene expression	42	6	4.63	0.0032	0.05106	Reactome	1	SMARCD1;RORA;NR1D1;ARNTL;NR1D2;ARNTL	5
GO:0006775	mitochondrial ATP synthesis coupled electron transport	85	12	4.6	3.80E-05	0.0076	GO	2.1192	COX7B;NDUFS7;NDUFA12;NDUFA4;COX6B1;NDUFB2;NDUFC1;CCDC;COX7C;UQCRH;COX6B1	3
R-HSA-1799339	SRP-dependent cotranslational protein targeting to membrane	107	15	4.58	4.70E-06	1.52E-04	Reactome	3.5	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;SRP14;RPL27A;RPL27A;RPL38;RPS20;RPL19	7
R-HSA-72706	GTP hydrolysis and joining of the 60S ribosomal subunit	107	15	4.58	4.70E-06	0.00035	Reactome	3.5	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;EEF1A1;RPL27A;RPL27A;RPS27;RPL38;RPS20;RPL19	7
GO:0006614	cellular translation nerve cell homeostasis	93	13	4.53	2.10E-05	0.0052	GO	2.288	APP;CD63;SMT3A;SLC38A1;SOD1;MT3A;UBB;SLC25A17;UBC;MT1F;MT1G;MT1E;FTL	4
GO:0031397	negative regulation of protein ubiquitination	50	7	4.53	0.0017	0.098	GO	1.0088	DNAJA1;UFL1;RPL22;CHD3;CBX1;RPL11;PARK7;DOT	6
R-HSA-163200	Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	109	15	4.48	5.90E-06	4.00E-04	Reactome	3.4	COX5B;COX7B;NDUFA4;2;NDUFA4;COX6B1;ETFDH;NDUFB2;ETFA;NDUFC1;CCDC;COX7C;UQCRH;COX6B1;NDUFS7;NDUFS2	6
GO:0010480	viral gene expression	110	15	4.43	6.40E-06	0.002	GO	2.6699	RPL30;RPL22;NUP188;RPL9;RPL27A;RPL11;RPL35A;SRP72;RPL27A;RPL27A;RPL38;RPS20;RPL19	1
R-HSA-3371556	Cellular response to heat stress	96	13	4.39	2.90E-05	0.00103	Reactome	3	HSPA8;HSPB8;DAZL;VCP;HSPD8A01;NUP188;HSPA4;ST13;PTGES3;KIF1A;LONA81;HSPH1;DNAJB6;UBB	4
WP4286	Copper homeostasis	52	7	4.33	0.0021	0.04642	WikiPathway	1.3	APP;SMT3A;MT2A;MT1F;MT1G;MT1E;SOD1	1
WP623	Oxidative phosphorylation	60	8	4.29	0.0011	0.05148	WikiPathway	1.5	ATP5PF;NDUFS7;NDUFA12;NDUFA4;NDUFB2;NDUFC1;ATP5F1D;ATP5F1E	1
R-HSA-158827	L13a-mediated translational silencing of Ceruloplasmin expression	127	17	4.27	1.90E-05	8.73E-04	Reactome	3.1	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;RPL27A;RPL27A;RPS27;RPL38;RPS20;RPL19	7
R-HSA-113279	3' -UTR-mediated translational regulation	106	14	4.27	1.90E-05	0.00087	Reactome	3.1	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;RPL27A;RPL27A;RPS27;RPL38;RPS20;RPL19	7
R-HSA-72737	Cap-dependent Translation Initiation	114	15	4.25	1.00E-05	0.00056	Reactome	3.3	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;EIF3L;RPL27A;RPL27A;RPS27;RPL38;RPS20;RPL19	7
R-HSA-72613	Eukaryotic Translation Initiation	114	15	4.25	1.00E-05	0.00056	Reactome	3.3	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;EIF3L;RPL27A;RPL27A;RPS27;RPL38;RPS20;RPL19	7
GO:1900034	regulation of cellular response to heat	78	10	4.11	3.90E-04	0.043	GO	1.3665	DNAJB1;HSPB8;DAZL;HSPB6;HSPH1;TAOP308;DNAJB6;HSPB8;PTGES3;ECCHROC5;CRYAB	5
R-HSA-2408522	Selenoamino acid metabolism	111	15	4.05	1.30E-05	0.00111	Reactome	3	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;RPL27A;RPL27A;RPS27;RPL38;RPS20;RPL19	7
R-HSA-400253	Circadian Clock	63	8	4.05	1.50E-03	0.03244	Reactome	1.5	SMARCD1;RORA;UBB;UBC;BHLHE41;NR1D1;NPAS2;ARNTL	5
R-HSA-168273	Influenza Viral RNA Transcription and Replication	128	16	4.01	1.00E-05	0.00056	Reactome	3.3	RPL30;HSPB8;RPL22;NUP188;RPL9;RPL27A;RPL11;RPL35A;RPL27A;RPL27A;RPL38;RPS20;RPL19	7
GO:0080135	regulation of cellular response to stress	104	13	4	6.80E-05	0.012	GO	1.9208	HSPB8;DAZL;HSPD8A01;NUP188;HSPB8;PTGES3;INPP4Z;ARNTL;DNAJB1;CHCHD2;HSPH1;DNAJB6;CHCHD2CC;CRYAB	5
GO:0016032	viral process	220	27	3.98	1.50E-08	4.23E-05	GO	4.3768	RPL30;VCP;RPL32;TBK1;NUP188;RPL36;RPL9;RPL11;BCCIP;RANBP2;UBB;UBC;RPL27A;RPL38;HSPD8A01;RPL19;PDCD6IP;RPL23;RPL35A;PACS1;RPL27A;RPL27A;RPS20;PAN;RPS28;RAB7A	6
R-HSA-73755	Semaphorin interactions	67	8	3.78	2.30E-03	0.03944	Reactome	1.4	HSPB8;DAZL;NR1L4;HSPB8;RIC1;PLXNB3;CRL1;PLXNB1;ARHGAP45;PLXNA3	15
GO:0031396	regulation of protein ubiquitination	101	12	3.77	2.10E-04	0.028	GO	1.5528	DNAJB2;DNAJA1;UFL1;HSPD8A01;HSPB8;RIC1;CBX1;CHCHD2;C1;UBE3A;PARK7;DOT;SASH1	9
R-HSA-168255	Influenza Life Cycle	136	17	3.74	2.20E-05	0.00097	Reactome	3.1	RPL30;HSPB8;RPL22;NUP188;RPL9;RPL27A;RPL11;RPL35A;RPL27A;RPL27A;RPL38;RPS20;RPL19	7
WP635	MET in type 1 papillary renal cell carcinoma	59	7	3.74	0.0041	0.08509	WikiPathway	1.1	MAPK3;TFE3;RPL11;STAT3;GAB1;SOS1;CBX	3
R-HSA-5620920	Cargo trafficking to the periciliary membrane	51	6	3.7	0.0084	0.09174	Reactome	1	CCT3;SMO;PDE4D;PKD1;EXOC1;CCT6	19
WP3984	NRF2 pathway	146	17	3.67	1.40E-05	0.00118	WikiPathway	2.9	ABCC3;NQO1;HSPB8;KX1;HSPB8;B1;TXNRD3;MGST3;SLC39A11;PSD;DNAJB1;SLC4A8;RXRA;PRDX5;MAFG;GCLM;SOST;M1;FTL;GSTM1	7
R-HSA-209908	Cell death signalling via NRAGE, NRIF and NADE	63	7	3.61	5.20E-03	0.07322	Reactome	1.2	TRAF6;UBB;ARHGEF17;UBC;ARHGEF4;SOS1;SOST4S	4
R-HSA-72766	Translation	151	17	3.57	2.20E-05	0.00097	Reactome	3.1	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;SRP14;EEF1A1;RPL27A;RPL27A;RPL38;RPS20;RPL19	7
GO:0006620	protein stabilization	152	17	3.54	2.40E-05	0.0055	GO	2.2596	CCT3;HSPB8;HA1;HSPB;HSPB8;B1;PTGES3;RPL11;CCT6;B1;PARK7;HSPA9;-CHCHD2CC;LAMP2;FUN;SUOT;CRYBA1;CCT4	5
R-HSA-5358537	The citric acid (TCA) cycle and respiratory electron transport	153	17	3.51	2.60E-05	0.00096	Reactome	3	COX5B;COX7B;NDUFA4;2;NDUFA4;COX6B1;ETFDH;NDUFB2;ETFA;NDUFC1;CCDC;COX7C;UQCRH;COX6B1;NDRA;NDUFS7;SUC;UQ;NDUFS2	6
WP138	Androgen receptor signaling pathway	90	10	3.49	0.0012	0.05148	WikiPathway	1.5	RB1;PKA50;PKD51;STAT3;FUN;UBE3A;PARK7;EIF2AB;PLPP1;RADSA	2
R-HSA-446219	Synthesis of substrates in N-glycan biosynthesis	73	8	3.48	0.0063	0.07946	Reactome	1.1	NUS1;ST6GAL 1;GLB1;EGFF2;SLC35A;ST6GAL1;ST6GALNAC5	16
R-HSA-168254	Influenza Infection	147	16	3.43	5.80E-05	1.86E-03	Reactome	2.7	RPL30;HSPB8;RPL22;RPL9;NUP188;RPL36;RPL27A;RPL11;RPL35A;RPL27A;RPL27A;RPL38;RPS20;RPL19	7
R-HSA-5628897	TP53 Regulates Metabolic Genes	84	9	3.39	2.60E-03	0.04169	Reactome	1.4	CDK19;CCNT8;NDUFA4;COX6B1;SESN1;PRDX1;CCDC;COX7C;COX6B1	6
R-HSA-114608	Platelet degranulation	105	11	3.27	0.0011	0.02516	Reactome	1.6	APP;ABCC4;CD63;LAMP2;CTL1;VEGFB;FUN;ACTN1;CALM1;PPIA;SOD1	2
R-HSA-8848021	Signaling by PTK6	67	7	3.24	0.0087	0.09419	Reactome	1	SPID;UBB;UBC;STAT3;ARAP1;CKK;ARHGAP35	8
GO:0019058	viral life cycle	107	11	3.2	0.0013	0.08	GO	1.0555	VCP;ISR42;HSPD8A01;PDCD6IP;NUP188;UBC;TSG101;UBB;NPC1;UBC;PPIA;RAB7A	4
GO:0051256	regulation of small GTPase mediated signal transduction	140	14	3.11	4.00E-04	0.044	GO	1.3545	ARHGEF17;MYO9B;ARAP1;ARHGAP24;ARHGAP31;ARHGAP29;GNAL1;TRAM;ARHGAP45;RHOT1;ARHGEF4;SOS1;SOST4S1;RHOD	11
R-HSA-76005	Response to elevated platelet cytosolic Ca2+	113	11	3.1	1.60E-03	0.03422	Reactome	1.5	APP;ABCC4;CD63;LAMP2;CTL1;VEGFB;FUN;ACTN1;CALM1;PPIA;SOD1	2
R-HSA-3371453	Regulation of HSF1-mediated heat shock response	80	8	3.09	0.0068	0.08186	Reactome	1.1	HSPA9;DNAJB1;HSPH1;TAOP308;DNAJB6;UBB;HSPA4;ST13	14
R-HSA-196843	Rho GTPase cycle	122	12	3.05	1.20E-03	2.43E-02	Reactome	1.6	TRAM1;ARHGAP32;-RHOT1;-ARHGEF17;ARHGEF4;MYO9B;ARAP1;ARHGAP29;SOS1;-ARHGAP45;-ARHGAP24;RHOD	10
GO:0000956	nuclear-transcribed mRNA catabolic process	174	17	3.04	0.00013	0.03	GO	1.7212	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;SMG8;RPRC1;PAN2;RPL27A;RPL27A;RPS27;RPL38;RPS20;RPL19	1
GO:0018105	peptidyl-serine phosphorylation	145	14	2.99	0.00057	0.02	GO	1.288	MAPK3K2;CAMK1D;DMPK;MAST4;PRKCE;STK39;PRKCH;PKD1;STK11;STK33;GRK2;PHKG1;MKNK2;ULK1	3
R-HSA-193704	p75 NTR receptor-mediated signalling	83	8	2.97	0.0084	0.09174	Reactome	1	NFKBIA;TRAF6;UBB;ARHGEF17;UBC;ARHGEF4;SOS1;SOST4S	8
WP2857	Mesodermal Commitment Pathway	147	14	2.91	0.0066	0.05148	WikiPathway	1.5	CTBP2;ATP8B2;PHACS;CC2;DDAH1;SESN3;MT2;RPL35;PLCH1;WDFY2;ASC;CS;TEAD1;FGFR3;BMPR1A	4
WP51	Regulation of Actin Cytoskeleton	150	14	2.88	0.0068	0.05148	WikiPathway	1.5	MYH9;ZCD3N;NWASP;ARHGAP35;SGK1;ENAH;GNA13;MRAS;CYC1;ARHGEF4;SOS1;CRK;FGFR2;FGFR1	3
GO:0043543	peptide biosynthetic process	174	16	2.84	0.00031	0.046	GO	1.3545	RPL30;RPL22;RPL9;RPL27A;RPL11;RPL35A;SNRPG;EIF1AD;RPL27A;RPL27A;RPL38;RPS20;RPL19;RPL19	1
WP2882	Nuclear Receptors Meta-Pathway	218	20	2.81	2.80E-06	0.0002	WikiPathway	3.1	SLC27A4;HSPB8;B1;MGST3;ABHD2;NR1D2;DNAJB6;RORA;ZIC2;PRDX1;STOM;CAP2;NQO1;-ABCC4;HSPB8;RXRA;-FABP7;TOMM20;PTGES3;STAT3;SLC39A11;PSD;TGFBR3;SLC4A8;NMYG;ACER3;GCLM;SOST4S;-GSTM4;-FTL	7
R-HSA-6791226	Major pathway of rRNA processing in the nucleolus	166	15	2.76	7.40E-04	0.

Supplementary Table 8 Enrichment Astrocyte DGE
Astrocytes pTau

geneset	description	size	overlap	odds_ratio	pval	FDR	database	X.Log10.FDR	genes	clusters
R-HSA-5660526	Response to metal ions	11	5	37.02	2.20E-06	0.00098	Reactome	3.009	MT2A;MT1M;MT1G;MT3;MT1E	3
R-HSA-5661231	Metallothioneins bind metals	11	5	37.02	2.20E-06	0.00098	Reactome	3.009	MT2A;MT1M;MT1G;MT3;MT1E	3
R-HSA-844456	The NLRP3 inflammasome	12	4	22.16	1.00E-04	0.01156	Reactome	1.937	APP;HSP90AB1;TXNIP;SUGT1	5
GO:1900274	regulation of phospholipase C activity	10	3	18.95	0.0012	0.0825	GO	1.08355	PDGFRB;BICD1;FGFR1	7
GO:0006878	cellular copper ion homeostasis	10	3	18.95	0.0012	0.0825	GO	1.08355	APP;PRNP;MT2A	3
GO:0071280	cellular response to copper ion	21	6	17.8	4.80E-06	0.0059	GO	2.22915	PRNP;MT2A;MT1M;MT1G;MT3;MT1E	4
GO:0090083	regulation of inclusion body assembly	11	3	16.58	0.0016	0.0968	GO	1.01412	DNAJB1;DNAJB6;SNCAIP	6
GO:0048169	regulation of long-term neuronal synaptic plasticity	11	3	16.58	0.0016	0.0968	GO	1.01412	CAMK2B;APP;NPTN	3
GO:0071294	cellular response to zinc ion	19	5	15.86	4.80E-05	0.0168	GO	1.77469	MT2A;MT1M;MT1G;MT3;MT1E	4
R-HSA-264870	Caspase-mediated cleavage of cytoskeletal proteins	12	3	14.74	0.0021	0.0854	Reactome	1.069	GSN;VIM;PLEC	3
GO:0046688	response to copper ion	25	6	14.05	1.50E-05	0.0071	GO	2.14874	PRNP;MT2A;MT1M;MT1G;MT3;MT1E	4
GO:1903364	positive regulation of cellular protein catabolic process	17	4	13.63	4.60E-04	0.0531	GO	1.27491	HSP90AA1;CD81;PTTG1IP;EZR	9
GO:0051131	chaperone-mediated protein complex assembly	17	4	13.63	0.00046	0.0531	GO	1.27491	HSP90AA1;HSP90AB1;PTGES3;CLU	2
GO:0048008	platelet-derived growth factor receptor signaling pathway	17	4	13.63	0.00046	0.0531	GO	1.27491	PDGFRB;NRP1;PDGFC;PTPRJ	7
R-HSA-622312	Inflammasomes	17	4	13.63	0.00046	0.04069	Reactome	1.391	APP;HSP90AB1;TXNIP;SUGT1	5
R-HSA-3371568	Attenuation phase	26	6	13.35	1.90E-05	0.00412	Reactome	2.385	DNAJB1;HSP90AA1;HSP90AB1;HSPH1;DNAJB6;PTGES3	5
GO:0006622	protein targeting to lysosome	19	4	11.82	0.00072	0.0607	GO	1.21681	ZFYVE16;LAMP2;GCC2;CLU	2
R-HSA-1236382	Constitutive Signaling by Ligand-Responsive EGFR Cancer Variants	19	4	11.82	0.00072	0.04265	Reactome	1.37	HSP90AA1;UBC;GAB1;SOS1	1
R-HSA-5637815	Signaling by Ligand-Responsive EGFR Variants in Cancer	19	4	11.82	0.00072	0.04265	Reactome	1.37	HSP90AA1;UBC;GAB1;SOS1	1
R-HSA-1643713	Signaling by EGFR in Cancer	19	4	11.82	0.00072	0.04265	Reactome	1.37	HSP90AA1;UBC;GAB1;SOS1	1
R-HSA-3371511	HSF1 activation	29	6	11.61	3.60E-05	0.00642	Reactome	2.192	DNAJB1;HSP90AA1;HSP90AB1;HSPH1;DNAJB6;PTGES3	5
R-HSA-3371571	HSF1-dependent transactivation	34	7	11.56	8.20E-06	0.00244	Reactome	2.613	CAMK2B;DNAJB1;HSP90AA1;HSP90AB1;HSPH1;DNAJB6;PTGES3	5
R-HSA-70171	Glycolysis	32	6	10.27	6.50E-05	0.00827	Reactome	2.082	PFKFB2;PPP2CB;PPP2R1B;ENO1;GAPDH;PFKP	6
WP2197	Endothelin Pathways	33	6	9.89	7.80E-05	0.014	Wikipathway	1.8539	EDNRB;GNAS;PLCB1;CALM1;ADRA1A;RAMP1	1
GO:0010922	positive regulation of phosphatase activity	22	4	9.84	0.0013	0.0876	GO	1.0575	PDGFRB;MEF2C;HSP90AB1;CALM1	7
GO:0071276	cellular response to cadmium ion	29	5	9.25	0.00041	0.0531	GO	1.27491	MT2A;MT1M;MT1G;MT3;MT1E	4
WP3529	Zinc homeostasis	36	6	8.9	0.00013	0.014	Wikipathway	1.8539	MT2A;MT1M;SLC39A11;MT1G;MT3;MT1E	1
GO:0051084	'de novo' posttranslational protein folding	30	5	8.88	0.00048	0.0531	GO	1.27491	HSPA9;DNAJB1;HSPH1;PTGES3;UGGT2	6
GO:0055069	zinc ion homeostasis	31	5	8.54	0.00056	0.0531	GO	1.27491	MT2A;MT1M;MT1G;MT3;MT1E	4
GO:0006882	cellular zinc ion homeostasis	31	5	8.54	5.60E-04	0.0531	GO	1.27491	MT2A;MT1M;MT1G;MT3;MT1E	4
GO:0046686	response to cadmium ion	31	5	8.54	5.60E-04	0.0531	GO	1.27491	MT2A;MT1M;MT1G;MT3;MT1E	4
R-HSA-1855204	Synthesis of IP3 and IP4 in the cytosol	25	4	8.44	0.0021	0.0854	Reactome	1.069	INPPL1;PLCH1;PLCB1;CALM1	2
GO:0010043	response to zinc ion	32	5	8.22	0.00065	0.0572	GO	1.2426	MT2A;MT1M;MT1G;MT3;MT1E	4
GO:0048017	inositol lipid-mediated signaling	39	6	8.09	0.00021	0.0439	GO	1.35754	PDGFRB;IRS2;PLCH1;EZR;OGT;FGFR1	7
GO:0070527	platelet aggregation	33	5	7.92	0.00076	0.0618	GO	1.20901	CSRP1;GNAS;HSPB1;FLNA;ACTB	1
GO:0051248	negative regulation of protein metabolic process	43	6	7.21	0.00036	0.0531	GO	1.27491	SNX3;PRNP;EDNRB;FLNA;CLU;CRYAB	2
GO:0006986	response to unfolded protein	43	6	7.21	0.00036	0.0531	GO	1.27491	HSPA9;DNAJB1;HSP90AA1;HSP90AB1;HSPH1;HSPB1	6
WP3286	Copper homeostasis	52	7	6.93	0.00015	0.014	Wikipathway	1.8539	APP;PRNP;MT2A;CCS;MT1G;MT3;MT1E	1
GO:0034109	homotypic cell-cell adhesion	38	5	6.72	0.0015	0.0942	GO	1.02595	CSRP1;GNAS;HSPB1;FLNA;ACTB	1
GO:0045739	positive regulation of DNA repair	38	5	6.72	0.0015	0.0942	GO	1.02595	BABAM2;FAM168A;SLF2;EYA2;NPAS2	8
GO:0051252	regulation of RNA metabolic process	39	5	6.52	0.0016	0.0983	GO	1.00745	CLK1;MBNL2;SON;AHNAK;HNRNPH1	3
GO:0048015	phosphatidylinositol-mediated signaling	56	7	6.36	0.00023	0.0439	GO	1.35754	PDGFRB;IRS2;PLCH1;EZR;OGT;ZFP36L1;FGFR1	7
R-HSA-5578775	Ion homeostasis	51	6	5.93	0.00091	0.05037	Reactome	1.298	RYR1;CAMK2B;TRPC1;ATP2B4;ATP1B3;CALM1	2
GO:1900034	regulation of cellular response to heat	78	9	5.83	5.80E-05	0.0174	GO	1.75945	CAMK2B;DNAJB1;HSP90AA1;HSP90AB1;HSPH1;DNAJB6;HSPB8;PTGES3;CRYAB	6
R-HSA-70326	Glucose metabolism	79	9	5.75	6.40E-05	0.00827	Reactome	2.082	PFKFB2;PPP2CB;PC;PPP2R1B;UBC;ENO1;CALM1;GAPDH;PFKP	6
GO:0019216	regulation of lipid metabolic process	100	11	5.54	1.40E-05	0.0071	GO	2.14874	SLC27A1;SMARCD3;RXRA;ID2;PSAP;IRS2;NR1D2;RGL1;PLPP1;NPAS2;FDFT1	8
R-HSA-3000178	ECM proteoglycans	55	6	5.44	0.0014	0.06347	Reactome	1.197	BCAN;PTPRS;ITGB5;NCAN;LRP4;LAMC1	4
R-HSA-416482	G alpha (12/13) signalling events	75	8	5.32	0.00026	0.02555	Reactome	1.593	GNA13;TIAM1;ARHGEF17;GNG7;ARHGEF4;PLXNB1;SOS1;ADRA1A	1
R-HSA-204998	Cell death signalling via NRAGE, NRIF and NADE	61	6	4.85	2.30E-03	0.08968	Reactome	1.047	TIAM1;ARHGEF17;UBC;ARHGEF4;SOS1;SQSTM1	1
GO:0046916	cellular transition metal ion homeostasis	93	9	4.78	2.30E-04	0.0439	GO	1.35754	APP;PRNP;MT2A;MT1M;UBC;MT1G;MT3;MT1E;FTL	4
GO:0080135	regulation of cellular response to stress	104	10	4.76	0.00011	0.0266	GO	1.57512	CAMK2B;DNAJB1;HSP90AA1;HSPH1;HSP90AB1;DNAJB6;HSPB8;PTGES3;CRYAB;NPAS2	6
R-HSA-418346	Platelet homeostasis	87	8	4.51	0.00071	0.04265	Reactome	1.37	PPP2CB;PPP2R1B;GNG7;ATP2B4;GNAS;PDE5A;MRVI1;CALM1	2
R-HSA-3371556	Cellular response to heat stress	96	8	4.05	0.0014	0.06347	Reactome	1.197	CAMK2B;HSPA9;DNAJB1;HSP90AA1;HSP90AB1;HSPH1;DNAJB6;PTGES3	5
GO:0080090	regulation of primary metabolic process	139	11	3.85	2.80E-04	0.0498	GO	1.30277	SLC27A1;SMARCD3;RXRA;ID2;PSAP;IRS2;NR1D2;RGL1;PLPP1;NPAS2;FDFT1	8
GO:0001501	skeletal system development	146	11	3.65	0.00043	0.0531	GO	1.27491	BCAN;ANKH;ZBTB16;NCAN;SH3PXD2B;CDH11;GNAS;ITGB8;AEBP1;PKD1;FGFR1	1
GO:0006936	muscle contraction	137	10	3.52	0.001	0.0765	GO	1.11634	RYR1;GJA1;MYBPC1;ITGB5;VIM;CALM1;ADRA1A;CRYAB;SORBS3;SNTA1	5
GO:0050821	protein stabilization	152	11	3.49	6.10E-04	0.0553	GO	1.25727	HSP90AA1;HSP90AB1;PTGES3;LAMP2;FLNA;ATP1B3;SUGT1;CLU;MT3;CRYAB;GAPDH	2
GO:0051128	regulation of cellular component organization	140	10	3.44	0.0012	0.0825	GO	1.08355	ZRANB1;HSP90AA1;ZFYVE16;GSN;FAM107A;TSC2;PHIP;STON2;SNCAIP;IL17RB	9
GO:0072657	protein localization to membrane	160	11	3.3	0.00093	0.0737	GO	1.13253	DLG2;NPC1;PACS1;SH3PXD2B;TTC7B;TSPAN5;FLNA;ATP1B3;EZR;RAMP1;RAB11A	1
R-HSA-71387	Metabolism of carbohydrates	282	16	2.7	0.00062	0.04265	Reactome	1.37	PFKFB2;NCAN;CSGALNACT2;ENO1;BCAN;PPP2CB;PC;PPP2R1B;GLB1;UBC;ALDH1A1;CALM1;TKT;ST3GAL1;GA PDH;PFKP	6
WP3932	Focal Adhesion-PI3K-Akt-mTOR-signaling pathway	303	17	2.68	0.00048	0.034	Wikipathway	1.4685	PDGFRB;PFKFB2;HSP90AA1;HSP90AB1;ITGB5;CAB39L;TSC2;IRS2;LAMC1;PPP2CB;TBC1D1;PPP2R1B;GNG7;PD GFC;ITGB8;SOS1;FGFR1	1
GO:1903507	negative regulation of nucleic acid-templated transcription	444	24	2.6	6.40E-05	0.0174	GO	1.75945	TSC22D4;CTBP2;PRMT2;SMURF2;ZBTB16;FOXG1;PRDM5;NR1D2;PBXIP1;ENO1;PTPRK;MT3;DKK3;BCLAF1;ZN F91;SFPQ;BTAF1;TFDP2;ZNF706;NACC2;ID2;ID4;PLCB1;ZBTB7A	10

Supplementary Table 9 Enrichment Microglia and PVM DGE
Contents

Sheet name	Description
Microglia_amyloid	Gene ontology and pathway enrichment analysis for Microglial genes significantly differentially expressed with amyloid-beta pathology
Microglia_pTau	Gene ontology and pathway enrichment analysis for Microglial genes significantly differentially expressed with pTau pathology
PVM_amyloid	Gene ontology and pathway enrichment analysis for Perivascular Macrophage genes significantly differentially expressed with amyloid-beta pathology
PVM_pTau	Gene ontology and pathway enrichment analysis for Perivascular Macrophage genes significantly differentially expressed with pTau pathology

Analysis performed using enrichR (v 3.0)

Supplementary Table 9 Enrichment Microglia and PVM DGE
Microglia amyloid

geneset	description	size	overlap	odds ratio	pval	FDR	database	X.Log10.FDR	genes	clusters
GO:0097067	cellular response to thyroid hormone stimulus	10	3	28.13	0.00038	0.052	GO	1.284	LMO2;CTSH;CTSS	3
GO:0030889	negative regulation of B cell proliferation	10	3	28.13	3.80E-04	0.052	GO	1.284	LYN;CD300A;MNDA	5
GO:0070585	protein localization to mitochondrion	10	3	28.13	0.00038	0.052	GO	1.284	DNAJA1;LRRK2;HK2	6
GO:0097066	response to thyroid hormone	11	3	24.61	0.00052	0.056	GO	1.2518	LMO2;CTSH;CTSS	3
GO:0010676	positive regulation of cellular carbohydrate metabolic process	13	3	19.69	0.00088	0.077	GO	1.1135	PRKCE;IRS2;SNCA	4
GO:1903320	regulation of protein modification by small protein conjugation or removal	14	3	17.9	0.0011	0.086	GO	1.0655	HSP90AA1;HSP90AB1;UBQLN1	2
GO:0060330	regulation of response to interferon-gamma	14	3	17.9	1.10E-03	8.60E-02	GO	1.0655	HSP90AB1;PARP9;JAK2	2
GO:0061912	selective autophagy	15	3	16.4	1.40E-03	9.90E-02	GO	1.0044	CALCOCO2;UBQLN1;SQSTM1	7
R-HSA-399954	Sema3A PAK dependent Axon repulsion	16	3	15.14	0.00167	0.099	Reactome	1.00436	HSP90AA1;HSP90AB1;PLXNA1	3
GO:0060334	regulation of interferon-gamma-mediated signaling pathway	22	4	14.63	3.00E-04	0.052	GO	1.284	HSP90AB1;PARP14;PARP9;JAK2	2
GO:0045937	positive regulation of phosphate metabolic process	28	4	10.97	0.00079	0.077	GO	1.1135	SDCBP;AKR1B1;NCKAP1L;SNCA	4
GO:0006986	response to unfolded protein	43	6	10.73	4.40E-05	0.018	GO	1.7447	DNAJA1;HSP90AA1;HSP90AB1;HSPA4;HSPB1;HERPUD1	2
GO:0050672	negative regulation of lymphocyte proliferation	29	4	10.53	0.00091	0.077	GO	1.1135	LYN;GPNMB;CD300A;MNDA	5
WP2509	Nanoparticle triggered autophagic cell death	23	3	9.84	0.00487	0.074	Wikipathway	1.1308	ATG10;ULK2;ATG7	4
GO:0010632	regulation of epithelial cell migration	48	6	9.45	8.30E-05	0.028	GO	1.5528	DOCK5;DUSP10;PRKCE;CTSH;EVL;PTPRG	3
WP3937	Microglia Pathogen Phagocytosis Pathway	40	5	9.43	0.00033	0.026	Wikipathway	1.585	LYN;HCK;ITGAM;PIK3CD;NCKAP1L	6
WP400	p38 MAPK Signaling Pathway	34	4	8.77	0.00167	0.037	Wikipathway	1.4318	MKNK1;HSPB1;PLA2G4A;MAPK14	3
GO:0030888	regulation of B cell proliferation	43	5	8.68	0.00046	0.056	GO	1.2518	LYN;CD300A;IRS2;NCKAP1L;MNDA	5
R-HSA-418597	G alpha (z) signalling events	46	5	8.04	0.00064	0.07	Reactome	1.1549	GNG2;ADCY9;PRKCE;GNAS;PRKCA	1
WP2203	Thymic Stromal LymphoPoietin (TSLP) Signaling Pathway	47	5	7.85	7.00E-04	0.028	Wikipathway	1.5528	LYN;NFKBIA;HCK;JAK2;MAPK14	2
WP2371	Parkinsons Disease Pathway	38	4	7.74	0.00254	0.047	Wikipathway	1.3279	APAF1;LRRK2;MAPK14;SNCA	1
WP422	MAPK Cascade	29	3	7.57	0.0094	0.094	Wikipathway	1.0269	RASA3;MBP;MAPK14	1
GO:0043407	negative regulation of MAP kinase activity	61	6	7.21	0.00032	0.052	GO	1.284	LYN;DNAJA1;DUSP10;CD300A;IRAK3;APOE	5
GO:0031346	positive regulation of cell projection organization	63	6	6.96	3.80E-04	0.052	GO	1.284	SCARB2;SNX3;LYN;NAV3;ZNF804A;APOE	5
GO:0051129	negative regulation of cellular component organization	54	5	6.73	1.30E-03	9.90E-02	GO	1.0044	DDX3X;MCTP1;DNAJB6;AKR1B1;IRAK3	8
WP395	IL-4 Signaling Pathway	54	5	6.73	0.00133	0.037	Wikipathway	1.4318	NFKBIA;PIK3CD;IRS2;JAK2;MAPK14	1
WP2374	Oncostatin M Signaling Pathway	65	6	6.72	0.00045	0.026	Wikipathway	1.585	NFKBIA;JUND;PRKCE;PRKCA;JAK2;MAPK14	3
WP2324	AGE/RAGE pathway	66	6	6.61	0.00049	0.026	Wikipathway	1.585	NFKBIA;PLA2G4A;MSN;PRKCA;JAK2;MAPK14	3
WP410	Exercise-induced Circadian Regulation	48	4	5.98	0.00595	0.082	Wikipathway	1.0862	DNAJA1;BTG1;ERC2;HERPUD1	4
GO:0010976	positive regulation of neuron projection development	97	8	5.97	0.00011	0.033	GO	1.4815	SCARB2;SNX3;LYN;ZNF804A;PLXNA1;PLXNC1;APOE;SYT17	5
WP3945	TYROBP Causal Network	61	5	5.88	0.0023	0.046	Wikipathway	1.3372	ABCC4;ITGAM;FKBP15;DPYD;NCKAP1L	6
WP286	IL-3 Signaling Pathway	49	4	5.84	0.00641	0.082	Wikipathway	1.0862	LYN;HCK;PIK3CD;JAK2	2
WP2637	Structural Pathway of Interleukin 1 (IL-1)	49	4	5.84	0.00641	0.082	Wikipathway	1.0862	NFKBIA;MKNK1;MBP;MAPK14	1
GO:0032270	positive regulation of cellular protein metabolic process	91	7	5.52	0.00047	0.056	GO	1.2518	NFKBIA;HSP90AA1;DDX3X;ATG10;RPS27L;MSN;ATG7	1
WP2355	Corticotropin-releasing hormone signaling pathway	93	7	5.39	0.00053	0.026	Wikipathway	1.585	NFKBIA;HSP90AA1;JUND;GNAS;PRKCA;ARRB2;MAPK14	3
WP2864	Apoptosis-related network due to altered Notch3 in ovarian cancer	53	4	5.36	0.00845	0.094	Wikipathway	1.0269	JUND;HSPB1;APOE;SQSTM1	5
WP195	IL-1 signaling pathway	55	4	5.15	0.00961	0.094	Wikipathway	1.0269	NFKBIA;IRAK3;MAPK14;SQSTM1	1
WP2018	RANKL/RANK (Receptor activator of NFKB (ligand)) Signaling Pathway	55	4	5.15	0.00961	0.094	Wikipathway	1.0269	LYN;NFKBIA;MAPK14;SQSTM1	1
GO:0031396	regulation of protein ubiquitination	101	7	4.93	0.00087	0.077	GO	1.1135	DNAJA1;HSP90AA1;HSP90AB1;LRRK2;UBQLN1;ARRB2;MALT1	2
R-HSA-194840	Rho GTPase cycle	122	8	4.66	0.00055	0.07	Reactome	1.1549	ARHGAP9;ARHGAP20;STARD13;GDI2;ARAP1;ARHGAP25;ARHGAP12;FGD2	2
GO:0051056	regulation of small GTPase mediated signal transduction	140	9	4.57	0.00029	0.052	GO	1.284	ARHGAP9;ARHGAP20;STARD13;GDI2;ARAP1;SQSTM1;ARHGAP25;ARHGAP12;FGD2	7
WP23	B Cell Receptor Signaling Pathway	97	6	4.35	0.00359	0.062	Wikipathway	1.2076	LYN;NFKBIA;PIP5K1A;MAPK14;MALT1;RASGRP3	1
WP3929	Chemokine signaling pathway	164	10	4.33	0.00021	0.026	Wikipathway	1.585	LYN;NFKBIA;HCK;ADCY9;GNG2;PIK3CD;PRKX;ARRB2;JAK2;PIK3R5	2
GO:0050821	protein stabilization	152	9	4.19	0.00053	0.056	GO	1.2518	CCT3;MORC3;HSP90AA1;HSP90AB1;ATP1B3;ANK2;NAA16;SUGT1;STK3	2
GO:0043312	neutrophil degranulation	479	26	3.99	2.20E-08	2.10E-05	GO	4.6778	ARHGAP9;CYFIP1;ASAH1;GRN;HSP90AB1;DDX3X;ITGAM;BRI3;GDI2;SNAP23;LRMP;IQGAP2;CTSS;TRPM2;SDCBP;CTSH;NCKAP1L;LTA4H;ATG7;ATP8B4;HSP90AA1;APAF1;CD300A;RAB27A;MAPK14;MNDA	1
GO:0002283	neutrophil activation involved in immune response	483	26	3.95	2.60E-08	2.10E-05	GO	4.6778	ARHGAP9;CYFIP1;ASAH1;GRN;HSP90AB1;DDX3X;ITGAM;BRI3;GDI2;SNAP23;LRMP;IQGAP2;CTSS;TRPM2;SDCBP;CTSH;NCKAP1L;LTA4H;ATG7;ATP8B4;HSP90AA1;APAF1;CD300A;RAB27A;MAPK14;MNDA	1
GO:0002446	neutrophil mediated immunity	487	26	3.92	3.10E-08	2.10E-05	GO	4.6778	ARHGAP9;CYFIP1;ASAH1;GRN;HSP90AB1;DDX3X;ITGAM;BRI3;GDI2;SNAP23;LRMP;IQGAP2;CTSS;TRPM2;SDCBP;CTSH;NCKAP1L;LTA4H;ATG7;ATP8B4;HSP90AA1;APAF1;CD300A;RAB27A;MAPK14;MNDA	1
WP2380	Brain-Derived Neurotrophic Factor (BDNF) signaling pathway	144	8	3.9	0.00161	0.037	Wikipathway	1.4318	NFKBIA;CYFIP1;DOCK3;DPYSL2;IRS2;JAK2;MAPK14;SQSTM1	1
GO:0046777	protein autophosphorylation	175	9	3.6	0.0014	0.1	GO	1	LYN;HCK;PEAK1;LRRK2;MKNK1;ULK2;PRKX;VRK2;JAK2	6
R-HSA-76002	Platelet activation, signaling and aggregation	253	12	3.33	5.10E-04	0.07	Reactome	1.1549	LYN;ABCC4;GNG2;PRKCE;PROS1;PIK3CD;PLA2G4A;PRKCA;ARRB2;JAK2;MAPK14;PIK3R5	1
GO:0016192	vesicle-mediated transport	410	19	3.3	1.80E-05	0.0089	GO	2.0506	DOC2A;LRRK2;SNAP23;RAB27A;GCC2;LRMP;VRK2;ARAP1;SNX30;TRAK1;MIB1;SYT17;CECR2;MYO1E;AP1G2;HEATR5B;DPYSL2;STX6;CYTH1	6
WP3888	VEGFA-VEGFR2 Signaling Pathway	236	11	3.26	0.00099	0.034	Wikipathway	1.4685	NFKBIA;HSP90AA1;ITGB5;PRKCE;MKNK1;HSPB1;PLA2G4A;PRKCA;ARRB2;MAPK14;HERPUD1	3
WP536	Calcium Regulation in the Cardiac Cell	149	7	3.26	0.00772	0.093	Wikipathway	1.0315	ADCY9;GNG2;PRKCE;GNAS;ATP1B3;PRKCA;ARRB2	7
WP382	MAPK Signaling Pathway	246	11	3.12	0.00138	0.037	Wikipathway	1.4318	JUND;DUSP10;LRRK2;MKNK1;HSPB1;PLA2G4A;PRKCA;ARRB2;MAPK14;RASGRP3;STK3	3
R-HSA-194315	Signaling by Rho GTPases	367	16	3.07	0.00016	0.054	Reactome	1.26761	ARHGAP9;RANBP2;CYFIP1;STARD13;GDI2;ARAP1;IQGAP2;ARHGAP25;FGD2;KTN1;ARHGAP12;ARHGAP20;DIAPH2;FMNL1;NCKAP1L;EVL	2
GO:0043065	positive regulation of apoptotic process	307	13	2.96	0.00087	0.077	GO	1.1135	BTG1;DDX3X;APAF1;GRAMD4;FGD2;STK3;DNAJA1;CTSH;MNDA;ATG7;SQSTM1;PPID;SNCA	1
GO:1902531	regulation of intracellular signal transduction	422	17	2.83	0.00026	0.052	GO	1.284	LYN;ARHGAP9;STARD13;LRRK2;GDI2;PRKAG2;HSPB1;VRK2;ARAP1;MAPK14;ARHGAP25;FGD2;ARHGAP12;ARHGAP20;PIP5K1A;SQSTM1;BANP	7
R-HSA-5654743	Signaling by FGFR4	332	13	2.72	0.00175	0.099	Reactome	1.00436	PRKCE;PIK3CD;PRKCA;IRS2;ARRB2;RASGRP3;ADCY9;DUSP10;RASA3;AGO4;MKNK1;PIP5K1A;JAK2	1
R-HSA-5654741	Signaling by FGFR3	333	13	2.71	0.0018	0.099	Reactome	1.00436	PRKCE;PIK3CD;PRKCA;IRS2;ARRB2;RASGRP3;ADCY9;DUSP10;RASA3;AGO4;MKNK1;PIP5K1A;JAK2	1
R-HSA-5654736	Signaling by FGFR1	336	13	2.69	0.00195	0.099	Reactome	1.00436	PRKCE;PIK3CD;PRKCA;IRS2;ARRB2;RASGRP3;ADCY9;DUSP10;RASA3;AGO4;MKNK1;PIP5K1A;JAK2	1
R-HSA-166520	Signalling by NGF	450	16	2.47	0.00148	0.099	Reactome	1.00436	PRKCE;PIK3CD;PRKCA;IRS2;ARRB2;MAPK14;FGD2;RASGRP3;NFKBIA;ADCY9;DUSP10;RASA3;AGO4;PIP5K1A;JAK2;SQSTM1	1
WP2882	Nuclear Receptors Meta-Pathway	319	11	2.37	0.00972	0.094	Wikipathway	1.0269	SLC2A9;ABCC4;HSP90AA1;JUND;HSP90AB1;NAV3;B3GNT5;MAFG;IRS2;SQSTM1;KTN1	5

Supplementary Table 9 Enrichment Microglia and PVM DGE

Microglia tau

geneset	description	size	overlap	odds_ratio	pval	FDR	database	X.Log10.FDR	genes	clusters
WP4337	ncRNAs involved in STAT3 signaling in hepatocellular carcinoma	13	3	35.6	0.00016	0.024	Wikipathway	1.62	ZEB1;JAK2;JAK3	1
GO:0051056	regulation of small GTPase mediated signal transduction	140	7	6.36	2.00E-04	0.062	GO	1.2076	ARHGAP9;STARD13;ARHGAP31;ARAP1;ARHGAP26;SQSTM1;ARHGAP12	2
GO:0002283	neutrophil activation involved in immune response	483	15	4	1.70E-05	0.021	GO	1.6778	ARHGAP9;GRN;ASAH1;BRI3;GAA;SNAP23;ARPC5;IQGAP2;CTSS;CREG1;C3AR1;LTA4H;DNASE1;ATG7;TLR2	1
GO:0043312	neutrophil degranulation	479	14	3.74	6.30E-05	0.031	GO	1.5086	ARHGAP9;GRN;ASAH1;BRI3;GAA;SNAP23;ARPC5;IQGAP2;CTSS;CREG1;C3AR1;LTA4H;ATG7;TLR2	1
GO:0002446	neutrophil mediated immunity	487	14	3.67	7.50E-05	0.031	GO	1.5086	ARHGAP9;GRN;ASAH1;BRI3;GAA;SNAP23;ARPC5;IQGAP2;CTSS;CREG1;C3AR1;LTA4H;ATG7;TLR2	1
GO:1902531	regulation of intracellular signal transduction	422	12	3.6	0.00027	0.068	GO	1.1675	ARHGAP9;STARD13;ARHGAP31;LRRK2;PIP4K2A;HSPB1;VRK2;ARAP1;ARHGAP26;SQSTM1;ARHGAP12;BANP	2

Supplementary Table 9 Enrichment Microglia and PVM DGE
PVM amyloid

geneset	description	size	overlap	odds_ratio	pval	FDR	database	X.Log10.FDR.	genes	clusters
R-HSA-390450	Folding of actin by CCT/TriC	10	4	53.73	4.60E-06	0.0028	Reactome	2.5528	CCT3;TCP1;CCT5;CCT4	7
GO:0070203	regulation of establishment of protein localization to telomere	10	3	34.4	0.00021	0.0398	GO	1.4	TCP1;CCT5;CCT4	5
GO:1904816	positive regulation of protein localization to chromosome, telomeric region	11	3	30.1	2.90E-04	0.0431	GO	1.366	TCP1;CCT5;CCT4	5
GO:1904874	positive regulation of telomerase RNA localization to Cajal body	15	4	29.3	2.90E-05	0.0155	GO	1.81	CCT3;TCP1;CCT5;CCT4	5
GO:1904951	positive regulation of establishment of protein localization	12	3	26.75	0.00039	0.0431	GO	1.366	TCP1;CCT5;CCT4	5
GO:1904872	regulation of telomerase RNA localization to Cajal body	18	4	23.02	6.30E-05	0.0209	GO	1.68	CCT3;TCP1;CCT5;CCT4	5
GO:0030031	cell projection assembly	20	4	20.14	9.70E-05	0.027	GO	1.569	CYFIP1;PARVG;RHOBTB3;NCKAP1L	2
GO:0061912	selective autophagy	15	3	20.06	0.00078	0.0665	GO	1.177	UBQLN1;WDFY3;SQSTM1	4
GO:0031663	lipopolysaccharide-mediated signaling pathway	16	3	18.52	0.00095	0.0719	GO	1.143	HCK;PRKCE;PTPN22	5
GO:0001919	regulation of receptor recycling	17	3	17.19	0.0011	0.0827	GO	1.082	KIF16B;TBC1D16;SNCA	1
GO:0071870	cellular response to catecholamine stimulus	23	4	16.96	1.70E-04	0.036	GO	1.444	GNG2;LRRK2;GNB1;SNCA	7
R-HSA-5620922	BBSome-mediated cargo-targeting to cilium	23	4	16.96	0.00017	0.0349	Reactome	1.4572	CCT3;TCP1;CCT5;CCT4	7
R-HSA-389960	Formation of tubulin folding intermediates by CCT/TriC	25	4	15.34	0.00024	0.0366	Reactome	1.4365	CCT3;TCP1;CCT5;CCT4	7
R-HSA-416700	Other semaphorin interactions	19	3	15.04	0.0016	0.0719	Reactome	1.1433	ITGB1;PLXNA1;PLXNC1	9
R-HSA-389957	Prefoldin mediated transfer of substrate to CCT/TriC	27	4	14	0.00033	0.0399	Reactome	1.399	CCT3;TCP1;CCT5;CCT4	7
R-HSA-6814122	Cooperation of PDCL (PhLP1) and TRiC/CCT in G-protein beta folding	42	6	13.52	1.30E-05	0.0038	Reactome	2.4202	CCT3;GNG2;TCP1;GNB1;CCT5;CCT4	7
GO:0032212	positive regulation of telomere maintenance via telomerase	32	4	11.5	0.00064	0.0595	GO	1.225	CCT3;TCP1;CCT5;CCT4	5
R-HSA-389958	Cooperation of Prefoldin and TriC/CCT in actin and tubulin folding	32	4	11.5	0.00064	0.0649	Reactome	1.1878	CCT3;TCP1;CCT5;CCT4	7
GO:1904358	positive regulation of telomere maintenance via telomere lengthening	34	4	10.73	8.10E-04	0.0665	GO	1.177	CCT3;TCP1;CCT5;CCT4	5
GO:0010632	regulation of epithelial cell migration	48	5	9.39	3.20E-04	0.0431	GO	1.366	MACF1;DUSP10;PRKCE;EVL;PTPRG	4
R-HSA-390471	Association of TriC/CCT with target proteins during biosynthesis	39	4	9.2	0.0014	0.0719	Reactome	1.1433	CCT3;TCP1;CCT5;CCT4	7
GO:0050764	regulation of phagocytosis	41	4	8.7	0.0017	0.0994	GO	1.003	SNX3;HCK;RAB27A;TLR2	5
GO:0031323	regulation of cellular metabolic process	41	4	8.7	0.0017	0.0994	GO	1.003	KIF16B;CACYBP;ABCG1;TBC1D16	1
R-HSA-456926	Thrombin signalling through proteinase activated receptors (PARs)	32	3	8.29	0.0072	0.0977	Reactome	1.0101	GNG2;GNB1;ARRB2	8
R-HSA-392451	G beta:gamma signalling through PI3Kgamma	48	4	7.31	0.003	0.0778	Reactome	1.109	GNG2;GNB1;JAK2;PIK3R5	8
R-HSA-6811440	Retrograde transport at the Trans-Golgi-Network	49	4	7.15	0.0032	0.0778	Reactome	1.109	RHOBTB3;STX6;GCC2;RAB6A	10
GO:0048732	gland development	75	6	7.04	0.00034	0.0431	GO	1.366	THRB;TG;ZBTB1;AKR1B1;MSN;SOD1	6
R-HSA-5620920	Cargo trafficking to the periciliary membrane	51	4	6.84	0.0037	0.0783	Reactome	1.1062	CCT3;TCP1;CCT5;CCT4	7
R-HSA-397795	G-protein beta:gamma signalling	51	4	6.84	0.0037	0.0783	Reactome	1.1062	GNG2;GNB1;JAK2;PIK3R5	8
GO:0007162	negative regulation of cell adhesion	65	5	6.73	0.0013	0.0899	GO	1.046	CD164;PTPRO;PLXNA1;PLXNC1;TGFBI	3
GO:1903076	regulation of protein localization to plasma membrane	67	5	6.51	0.0015	0.0989	GO	1.005	ITGB1;PRKCE;AKR1B1;STX3;SQSTM1	4
GO:0051100	negative regulation of binding	82	6	6.39	0.00056	0.0547	GO	1.262	NFKBIA;BTAF1;IFI16;LRRK2;MITD1;JAK2	7
R-HSA-390466	Chaperonin-mediated protein folding	95	6	5.45	0.0012	0.0719	Reactome	1.1433	CCT3;GNG2;TCP1;GNB1;CCT5;CCT4	7
R-HSA-391251	Protein folding	101	6	5.11	0.0017	0.0719	Reactome	1.1433	CCT3;GNG2;GNB1;TCP1;CCT5;CCT4	7
WP3929	Chemokine signaling pathway	164	9	4.74	0.00022	0.047	Wikipathway	1.328	NFKBIA;HCK;GNG2;GNB1;PRKX;ARRB2;JAK2;SOS1;PIK3R5	1
R-HSA-373760	L1CAM interactions	96	5	4.43	0.007	0.0969	Reactome	1.0137	ITGB1;HSPA8;KCNQ3;MSN;ITGA9	6
R-HSA-157118	Signaling by NOTCH	122	6	4.18	0.0043	0.0809	Reactome	1.0921	KAT2A;TBL1XR1;AGO4;ARRB2;RAB6A;MIB1	1
R-HSA-6811442	Intra-Golgi and retrograde Golgi-to-ER traffic	179	8	3.8	0.0019	0.075	Reactome	1.1249	CYTH4;KIF16B;DCTN4;RHOBTB3;STX6;MAN1C1;GCC2;RAB6A	4
R-HSA-4839726	Chromatin organization	226	9	3.38	0.0022	0.0774	Reactome	1.1113	KAT2A;AEBP2;KDM1B;TBL1XR1;USP22;JADE2;JAK2;CLOCK;SAP30	5
R-HSA-3247509	Chromatin modifying enzymes	226	9	3.38	0.0022	0.0774	Reactome	1.1113	KAT2A;AEBP2;KDM1B;TBL1XR1;USP22;JADE2;JAK2;CLOCK;SAP30	5
R-HSA-76002	Platelet activation, signaling and aggregation	253	10	3.36	0.0013	0.0719	Reactome	1.1433	ABCC4;GNG2;PRKCE;PROS1;GNB1;ARRB2;JAK2;SOS1;PIK3R5;SOD1	11
GO:0070646	protein modification by small protein removal	261	10	3.25	0.0017	0.0994	GO	1.003	SNX3;NFKBIA;KAT2A;USPL1;KDM1B;USP32;USP22;PSME4;AKR1B1;ARRB2	6
GO:0015031	protein transport	326	12	3.13	0.00084	0.0665	GO	1.177	MACF1;RABGAP1L;SNX27;STX6;ATP6V1B2;RAB27A;TBC1D14;STX3;RAB6A;ABCG1;TMED4;TBC1D16	1
R-HSA-512988	Interleukin-3, 5 and GM-CSF signaling	261	9	2.9	0.0056	0.0941	Reactome	1.0264	HCK;DUSP10;RASA3;PTPRA;PSME4;ARRB2;JAK2;SOS1;RASGRP3	2
GO:0043312	neutrophil degranulation	479	16	2.86	0.00035	0.0431	GO	1.366	ARHGAP9;CYFIP1;HSPA8;ATP8B4;PDXK;ATP8A1;APAF1;BRI3;SNAP23;ATP6AP2;RAB27A;TRPM2;NCKAP1L;LTA4H;RAB6A;TLR2	2
GO:0002283	neutrophil activation involved in immune response	483	16	2.84	0.00039	0.0431	GO	1.366	ARHGAP9;CYFIP1;HSPA8;ATP8B4;PDXK;ATP8A1;APAF1;BRI3;SNAP23;ATP6AP2;RAB27A;TRPM2;NCKAP1L;LTA4H;RAB6A;TLR2	2
R-HSA-5654696	Downstream signaling of activated FGFR2	329	11	2.82	0.0029	0.0778	Reactome	1.109	DUSP10;RASA3;PRKAR1A;AGO4;PTPRA;PRKCE;PSME4;ARRB2;JAK2;SOS1;RASGRP3	2
R-HSA-5654716	Downstream signaling of activated FGFR4	329	11	2.82	0.0029	0.0778	Reactome	1.109	DUSP10;RASA3;PRKAR1A;AGO4;PTPRA;PRKCE;PSME4;ARRB2;JAK2;SOS1;RASGRP3	2
R-HSA-5654708	Downstream signaling of activated FGFR3	329	11	2.82	0.0029	0.0778	Reactome	1.109	DUSP10;RASA3;PRKAR1A;AGO4;PTPRA;PRKCE;PSME4;ARRB2;JAK2;SOS1;RASGRP3	2
GO:0002446	neutrophil mediated immunity	487	16	2.81	0.00042	0.0442	GO	1.355	ARHGAP9;CYFIP1;HSPA8;ATP8B4;PDXK;ATP8A1;APAF1;BRI3;SNAP23;ATP6AP2;RAB27A;TRPM2;NCKAP1L;LTA4H;RAB6A;TLR2	2
R-HSA-5654743	Signaling by FGFR4	332	11	2.8	0.0031	0.0778	Reactome	1.109	DUSP10;RASA3;PRKAR1A;AGO4;PTPRA;PRKCE;PSME4;ARRB2;JAK2;SOS1;RASGRP3	2
R-HSA-5654687	Downstream signaling of activated FGFR1	332	11	2.8	0.0031	0.0778	Reactome	1.109	DUSP10;RASA3;PRKAR1A;AGO4;PTPRA;PRKCE;PSME4;ARRB2;JAK2;SOS1;RASGRP3	2
R-HSA-5654741	Signaling by FGFR3	333	11	2.79	0.0032	0.0778	Reactome	1.109	DUSP10;RASA3;PRKAR1A;AGO4;PTPRA;PRKCE;PSME4;ARRB2;JAK2;SOS1;RASGRP3	2
R-HSA-5654736	Signaling by FGFR1	336	11	2.76	0.0034	0.0783	Reactome	1.1062	DUSP10;RASA3;PRKAR1A;AGO4;PTPRA;PRKCE;PSME4;ARRB2;JAK2;SOS1;RASGRP3	2
R-HSA-186763	Downstream signal transduction	341	11	2.72	0.0038	0.0783	Reactome	1.1062	DUSP10;RASA3;PRKAR1A;AGO4;PTPRA;PRKCE;PSME4;ARRB2;JAK2;SOS1;RASGRP3	2
R-HSA-2424491	DAP12 signaling	344	11	2.7	0.004	0.0792	Reactome	1.1013	DUSP10;RASA3;PRKAR1A;AGO4;PTPRA;PRKCE;PSME4;ARRB2;JAK2;SOS1;RASGRP3	2
R-HSA-166520	Signalling by NGF	450	14	2.64	0.0016	0.0719	Reactome	1.1433	PRKCE;ARRB2;RASGRP3;FGD3;NFKBIA;DUSP10;RASA3;PRKAR1A;AGO4;PTPRA;PSME4;JAK2;SOS1;SQSTM1	2
R-HSA-4420097	VEGFA-VEGFR2 Pathway	320	10	2.62	0.007	0.0969	Reactome	1.0137	CYFIP1;DUSP10;RASA3;PTPRA;PSME4;NCKAP1L;ARRB2;JAK2;SOS1;RASGRP3	2
R-HSA-177929	Signaling by EGFR	355	11	2.61	0.0051	0.0937	Reactome	1.0283	DUSP10;RASA3;PRKAR1A;AGO4;PTPRA;PRKCE;PSME4;ARRB2;JAK2;SOS1;RASGRP3	2
R-HSA-449147	Signaling by Interleukins	392	12	2.58	0.0039	0.0783	Reactome	1.1062	HCK;DUSP10;RASA3;PTPRA;PSME4;IRAK3;STX3;ARRB2;JAK2;SOS1;SQSTM1;RASGRP3	2
R-HSA-2172127	DAP12 interactions	359	11	2.58	0.0055	0.0941	Reactome	1.0264	DUSP10;RASA3;PRKAR1A;AGO4;PTPRA;PRKCE;PSME4;ARRB2;JAK2;SOS1;RASGRP3	2
R-HSA-5654738	Signaling by FGFR2	361	11	2.56	0.0058	0.0947	Reactome	1.0237	DUSP10;RASA3;PRKAR1A;AGO4;PTPRA;PRKCE;PSME4;ARRB2;JAK2;SOS1;RASGRP3	2
R-HSA-186797	Signaling by PDGF	364	11	2.54	0.0061	0.0954	Reactome	1.0205	DUSP10;RASA3;PRKAR1A;AGO4;PTPRA;PRKCE;PSME4;ARRB2;JAK2;SOS1;RASGRP3	2
R-HSA-190236	Signaling by FGFR	366	11	2.53	0.0064	0.0957	Reactome	1.0191	DUSP10;RASA3;PRKAR1A;AGO4;PTPRA;PRKCE;PSME4;ARRB2;JAK2;SOS1;RASGRP3	2
R-HSA-194315	Signaling by Rho GTPases	367	11	2.52	0.0065	0.0957	Reactome	1.0191	ARHGAP9;FGD3;ITGB1;CYFIP1;NUDC;DIAPH2;NCKAP1L;EVL;SOS1;ARHGAP25;KTN1	3
R-HSA-187037	NGF signalling via TRKA from the plasma membrane	374	11	2.47	0.0075	0.0983	Reactome	1.0074	DUSP10;RASA3;PRKAR1A;AGO4;PTPRA;PRKCE;PSME4;ARRB2;JAK2;SOS1;RASGRP3	2
R-HSA-199991	Membrane Trafficking	420	12	2.4	0.0066	0.0957	Reactome	1.0191	HSPA8;CYTH4;AP1G2;KIF16B;DCTN4;SNAP23;STX6;RHOBTB3;MAN1C1;GCC2;PUM1;RAB6A	4

Supplementary Table 9 Enrichment Microglia and PVM DGE
PVM tau

geneset	description	size	overlap	odds_ratio	pval	FDR	database	X.Log10.FDR.	genes	clusters
GO:0016192	vesicle-mediated transport	410	13	5.18	4.60E-06	0.0046	GO	2.337	DOC2A;LRRK2;SNAP23;AGAP1;GCC2;DENND3;VRK2;COMMD1;ARAP1;SNX30;AP1G2;STX3;RAB6A	1

Supplementary Table 10 Astrocyte-microglial Cellchat

Ligand-receptor pairs between astrocytes and microglia

Source	Target	Ligand	Receptor
Amyloid-beta and pTau			
Increased expression			
Astrocytes	Microglia	LAMC1	ITGA1_ITGB1
Astrocytes	Microglia	LAMC1	ITGA2_ITGB1
Astrocytes	Microglia	LAMC1	ITGA6_ITGB1
Astrocytes	Microglia	LAMC1	ITGA7_ITGB1
Astrocytes	Microglia	LAMC1	ITGA9_ITGB1
Astrocytes	Microglia	LAMC1	ITGA6_ITGB4
Astrocytes	Astrocytes	LAMC1	CD44
Astrocytes	Microglia	LAMC1	CD44
Astrocytes	Microglia	APP	CD74
Astrocytes	Microglia	CD99	PILRA
Microglia	Astrocytes	VTN	ITGAV_ITGB8
Microglia	Astrocytes	FN1	ITGAV_ITGB8
Decreased expression			
Astrocytes	Astrocytes	ENTPD1	ADORA2B
Astrocytes	Microglia	ENTPD1	TMIGD3
Astrocytes	Astrocytes	NEGR1	NEGR1
Microglia	Astrocytes	ENTPD1	ADORA2B
Microglia	Microglia	ENTPD1	TMIGD3

Source	Target	Ligand	Receptor
Amyloid-beta only			
Increased expression			
Microglia	Astrocytes	BMP4	BMPR1A_ACVR2A
Microglia	Astrocytes	BMP4	BMPR1A_ACVR2B
Microglia	Astrocytes	BMP4	BMPR1A_BMPR2
Astrocytes	Microglia	CSF1	CSF1R
Microglia	Astrocytes	CXCL12	ACKR3
Astrocytes	Astrocytes	EPO	EPOR
Microglia	Astrocytes	WNT2B	FZD3_LRP5
Microglia	Astrocytes	WNT2B	FZD3_LRP6
Microglia	Astrocytes	WNT5A	FZD3
Decreased expression			
Astrocytes	Microglia	GP1BA	ITGAM_ITGB2
Astrocytes	Microglia	ICAM1	ITGAM_ITGB2

Source	Target	Ligand	Receptor
pTau only			
Increased expression			
Astrocytes	Microglia	C3	C3AR1
Astrocytes	Microglia	C4A	C3AR1

Supplementary Table 11. Co-expression by brain region
Astro MEGENA pTau

	EC+SSC logFC	EC logFC	SSC logFC	EC+SSC adj.P.Val	EC adj.P.Val	SSC adj.P.Val
c1_3	0.209969455	0.086586592	0.104787465	0.494537171	0.829281205	0.853427623
c1_4	-0.10412534	-0.03341178	-0.43906018	0.891013674	0.977895177	0.684705704
c1_5	-0.374587327	-0.182692445	-0.514652051	0.250112001	0.718946433	0.591506073
c1_6	-0.233831533	-0.160468981	-0.314146317	0.353886879	0.687612122	0.620893934
c1_8	-0.006399877	0.046474082	0.829121482	0.976869411	0.912473091	0.356703646
c1_9	1.767123627	1.521437893	3.393577791	1.73E-05	0.002807805	0.000528868
c1_10	-0.450575706	-0.416335484	-0.526121321	0.080747097	0.220209102	0.517030999
c1_11	-0.675226545	-0.771694594	-0.877266879	0.167516441	0.187625331	0.517030999
c1_12	-0.654586064	-0.647352075	-1.26872444	0.051822399	0.155404451	0.148748954
c1_13	1.726224321	1.546332066	3.194656202	0.070538104	0.187625331	0.256574401
c1_16	0.029044349	-0.088261518	-0.231681401	0.905471142	0.829281205	0.728612705
c1_17	0.279000683	0.429602032	0.105145299	0.821398545	0.718946433	0.942923029
c1_18	-0.260231335	-0.275160016	-0.625161757	0.699404505	0.718946433	0.656715189
c1_19	-0.477066394	-0.296903779	-0.546456833	0.204847921	0.687612122	0.60622971
c1_21	-0.488692757	-0.346625158	-0.790713444	0.391330974	0.687612122	0.60622971
c1_22	0.381131129	0.579332504	0.869810269	0.699404505	0.687612122	0.68133077
c1_23	-0.672258624	-0.28951548	-2.230978839	0.65570029	0.854283549	0.517030999
c1_24	0.243893344	0.123831048	0.253608769	0.738485636	0.886474069	0.838766088
c1_25	-0.305731317	-0.203722302	-0.38954185	0.278383298	0.687612122	0.60622971
c1_26	0.173749962	0.128849374	1.146573292	0.691513973	0.797676475	0.203960309
c1_27	-0.621283766	-0.365002282	-0.212423188	0.204847921	0.687612122	0.842961618
c1_28	1.568771222	1.455852329	3.44090193	0.158372208	0.25011119	0.272937336
c1_29	2.054629163	1.70026713	3.901443172	1.10E-05	0.002807805	0.000528868
c1_30	1.284860386	1.4224309	1.910080131	0.182739667	0.207626694	0.517030999
c1_32	-0.893856771	-0.708815547	-1.634464296	0.055847371	0.220209102	0.203960309
c1_33	-0.097328938	-0.12103774	0.301045754	0.821398545	0.814301201	0.684705704
c1_34	-0.778808534	-0.769270668	-1.169076794	0.070538104	0.187625331	0.356703646
c1_36	-0.720942079	-0.808730473	-0.946741085	0.158372208	0.187625331	0.517030999
c1_37	-0.682142356	-0.664222081	-1.362096711	0.046304427	0.155404451	0.122347265
c1_41	1.494312166	1.593539756	2.845252158	0.426124445	0.661179278	0.591506073
c1_46	-0.049693107	-0.16996022	-0.369582916	0.892042551	0.687612122	0.656715189
c1_47	-0.543206289	-0.353603932	-0.622144889	0.184519313	0.687612122	0.591506073
c1_51	0.307168593	0.17807761	0.372971682	0.699404505	0.854283549	0.771829206
c1_53	-0.375104864	-0.244134558	-0.568727844	0.237318411	0.687612122	0.517030999
c1_54	-0.050401422	0.012720654	0.236564912	0.892042551	0.991363452	0.771829206
c1_61	0.04375695	-0.001466045	0.952323306	0.892042551	0.995648442	0.356703646
c1_62	1.175904721	1.392802848	3.233465753	0.355246057	0.462839965	0.356703646
c1_65	1.462043015	1.466579901	2.66817116	0.250112001	0.397662039	0.517030999
c1_66	3.107801305	2.605768628	5.701889208	6.81E-06	0.002180678	0.000528868
c1_78	1.414253003	1.552671262	2.375948197	0.204847921	0.260337685	0.517030999
c1_80	-0.977743629	-0.758464756	-1.942860466	0.046304427	0.206868469	0.122347265
c1_83	-0.153025297	-0.218469684	0.265694295	0.699404505	0.687612122	0.71427619
c1_86	-0.725363854	-0.821625379	-0.921476574	0.158372208	0.187625331	0.517030999
c1_89	1.34206982	1.666133376	2.061422615	0.675523765	0.687612122	0.71427619
c1_92	-0.041206877	-0.167586938	-0.357685837	0.892042551	0.687612122	0.656715189
c1_95	-0.494808375	-0.29052055	-0.413898777	0.745454582	0.865565223	0.853427623
c1_96	0.509790776	0.283008181	0.600588053	0.486139798	0.797676475	0.692048785
c1_99	-0.410030284	-0.26756835	-0.654604206	0.204847921	0.687612122	0.517030999
c1_106	0.053330337	0.009301317	1.011311454	0.892042551	0.991363452	0.343721222
c1_108	3.217133701	2.690251827	5.911239882	5.96E-06	0.002180678	0.000528868
c1_112	-0.064023202	-0.141910924	0.44987701	0.892042551	0.797676475	0.620893934
c1_117	-0.040425998	-0.167888318	-0.360461531	0.892042551	0.687612122	0.656715189
c1_119	-0.437095093	-0.28576295	-0.707227063	0.204559349	0.687612122	0.505944705

Abbreviations:
EC+SSC. enriched data integrated from the entrorhinal and somatosensory cortices
EC, enriched data integrated from the entrorhinal cortex only
SSC, enriched data integrated from the somatosensory cortex only
logFC, log base 2 fold-enrichment
adj P, p-statistic adjusted (corrected) for multiple comparisons

Supplementary Table 11. Co-expression by brain region
Astro MEGENA amyloid beta

	EC+SSC logFC	EC logFC	SSC logFC	EC+SSC adj.P.Val	EC adj.P.Val	SSC adj.P.Val
c1_3	-0.0685978	-0.3353095	0.03727925	0.87592558	0.85130221	0.92594712
c1_4	-0.2938607	-0.0094128	-0.3776985	0.58702809	0.98979302	0.78255525
c1_5	-0.3055878	-0.9175434	-0.1831944	0.54196649	0.56928645	0.78255525
c1_6	-0.0798242	-0.1772709	-0.0739151	0.81806754	0.85130221	0.81337859
c1_8	0.45454087	0.11834588	0.49236906	0.34056063	0.91848015	0.43792409
c1_9	1.55901638	1.6219118	1.56263388	0.00328119	0.47260103	0.02234682
c1_10	-0.3967565	-0.8676133	-0.2853586	0.34017356	0.47260103	0.66464592
c1_11	-0.4001854	-0.3053754	-0.4168698	0.54196649	0.85130221	0.78255525
c1_12	-0.641982	-1.021296	-0.5304819	0.15106985	0.47260103	0.43792409
c1_13	1.18211609	-0.1889966	1.57696668	0.45216946	0.94171736	0.43792409
c1_16	-0.2070248	-0.4372903	-0.1106221	0.5748855	0.84528923	0.8058255
c1_17	-0.4677204	-0.2274868	-0.5556932	0.66930745	0.93565954	0.78255525
c1_18	-0.12794	0.01474733	-0.1578193	0.87592558	0.98979302	0.82202576
c1_19	-0.2909181	-0.8374793	-0.1907987	0.55622458	0.84528923	0.78255525
c1_21	-0.2717455	-0.248987	-0.3118238	0.69807107	0.91531313	0.78255525
c1_22	0.04629163	-1.4443605	0.39915056	0.94583515	0.84528923	0.78255525
c1_23	-1.2347662	-2.9393539	-0.785182	0.53637203	0.56928645	0.78255525
c1_24	0.32810842	0.84969294	0.22455921	0.65985951	0.85130221	0.79846031
c1_25	-0.136221	-0.3282748	-0.1142403	0.70144247	0.85130221	0.79846031
c1_26	0.5448473	0.2076002	0.6024747	0.23903582	0.85130221	0.40069098
c1_27	0.02880558	-0.384192	0.04825671	0.94583515	0.85130221	0.93662154
c1_28	1.86637228	1.64743967	1.89141747	0.22114772	0.84528923	0.43157443
c1_29	1.83633677	2.21566882	1.77098306	0.00257323	0.25626965	0.02234682
c1_30	0.91449117	0.61079509	0.98018826	0.54196649	0.85130221	0.76551102
c1_32	-1.0948526	-2.0171182	-0.867539	0.04952979	0.18286354	0.40069098
c1_33	0.02509367	-0.3581638	0.11060251	0.94583515	0.85130221	0.8058255
c1_34	-0.5958111	-0.8307128	-0.5401993	0.39944538	0.84528923	0.61391286
c1_36	-0.4306353	-0.3397399	-0.4482161	0.54196649	0.85130221	0.78255525
c1_37	-0.6810949	-1.0575858	-0.5700642	0.12659278	0.47260103	0.43157443
c1_41	1.42453998	1.92104982	1.2315618	0.54208445	0.85130221	0.78255525
c1_46	-0.2756828	-0.5243964	-0.1728095	0.54196649	0.84528923	0.78255525
c1_47	-0.333129	-0.9143668	-0.2272183	0.54196649	0.84528923	0.78255525
c1_51	0.38513783	0.9122372	0.28186795	0.61268727	0.85130221	0.78255525
c1_53	-0.2433338	-0.525227	-0.2002507	0.55622458	0.85130221	0.78255525
c1_54	0.30951735	0.48863006	0.22805222	0.54196649	0.85130221	0.78255525
c1_61	0.43549234	0.08897625	0.49587028	0.42199255	0.93565954	0.48014012
c1_62	1.65850416	0.94892294	1.73541336	0.39944538	0.85130221	0.48014012
c1_65	1.45341177	1.00299376	1.55113359	0.53637203	0.85130221	0.66464592
c1_66	2.6690251	3.49747911	2.50187426	0.00257323	0.18286354	0.02409093
c1_78	1.09252491	0.85427586	1.13163768	0.54196649	0.85130221	0.77432122
c1_80	-1.195902	-2.0116939	-0.9957787	0.03148743	0.18286354	0.31222517
c1_83	-0.0218965	-0.4327962	0.07732001	0.94583515	0.85130221	0.84356881
c1_86	-0.4246317	-0.3523738	-0.4367865	0.54196649	0.85130221	0.78255525
c1_89	1.07795942	1.68454228	0.84125558	0.70956245	0.85130221	0.80593049
c1_92	-0.2718478	-0.5236859	-0.1668101	0.54196649	0.84528923	0.78255525
c1_95	0.11038325	0.548457	-0.0540914	0.94583515	0.91531313	0.96305921
c1_96	0.46423896	1.01238633	0.37870692	0.57676712	0.85130221	0.78255525
c1_99	-0.2834049	-0.59116	-0.2342122	0.54196649	0.84528923	0.78255525
c1_106	0.45953251	0.08573897	0.52507626	0.39944538	0.93565954	0.46483555
c1_108	2.77692219	3.64656161	2.60151608	0.00257323	0.18286354	0.02234682
c1_112	0.03699699	-0.408078	0.14600329	0.94583515	0.85130221	0.79846031
c1_117	-0.2740586	-0.5222411	-0.1695483	0.54196649	0.84528923	0.78255525
c1_119	-0.3125646	-0.6400224	-0.2595372	0.54196649	0.84528923	0.78255525

Abbreviations:

EC+SSC. enriched data integrated from the entrorhinal and somatosensory cortices

EC, enriched data integrated from the entrorhinal cortex only

SSC, enriched data integrated from the somatosensory cortex only

logFC, log base 2 fold-enrichment

adj P, p-statistic adjusted (corrected) for multiple comparisons

Supplementary Table 11. Co-expression by brain region
Micro MEGENA pTau

	EC+SSC logFC	EC logFC	SSC logFC	EC+SSC adj.P.Val	EC adj.P.Val	SSC adj.P.Val
c1_2	0.3889342	0.25698269	0.63809355	0.09082358	0.66104138	0.35092058
c1_4	0.05243319	-0.06953	0.28169027	0.86403015	0.94946875	0.75896434
c1_5	0.55451559	0.38766893	0.82657521	0.34118444	0.84034315	0.54051031
c1_6	0.55676076	0.46641014	0.76909696	0.02175517	0.3024769	0.29083393
c1_7	0.0856677	0.06327162	0.14337057	0.70923642	0.93705233	0.81596468
c1_9	-0.6772311	-0.5996857	-1.2682164	0.00568981	0.1386623	0.04396863
c1_10	0.26524604	0.17749242	0.18048013	0.33864461	0.81558817	0.81596468
c1_11	1.26264146	1.13211818	1.8384439	0.00114276	0.05779617	0.07413038
c1_12	0.11666625	0.05901417	0.09036113	0.74114055	0.99192542	0.91065227
c1_13	-0.5553331	-0.433613	-1.0448591	0.4076475	0.8517808	0.50972119
c1_15	-0.4125701	-0.5956293	-0.5340772	0.63600442	0.81558817	0.81596468
c1_16	0.31711974	0.05607661	1.06536247	0.66465647	0.99613423	0.54151794
c1_17	0.4927903	0.31629054	1.12329645	0.34118444	0.8517808	0.39917757
c1_18	0.63238412	0.35812391	0.95706974	0.53244223	0.93051835	0.692999
c1_19	0.68045332	0.57398701	0.95156154	0.09915266	0.46640761	0.41851486
c1_20	-0.7044657	-0.5641027	-1.3968347	0.61966062	0.91594024	0.68804909
c1_21	0.20539898	0.19737837	-0.0469769	0.61966062	0.86346813	0.96381336
c1_22	0.79206528	0.70993091	1.1671645	0.00715181	0.14859344	0.14752295
c1_23	0.73389679	0.46247727	1.44987877	0.09082358	0.66104138	0.23686212
c1_24	-0.9515181	-0.9193275	-1.4512768	0.0708723	0.30765288	0.35092058
c1_25	0.17611588	0.1277958	0.34447257	0.50142631	0.86346813	0.54386407
c1_26	-0.8815427	0.42667963	-2.2688775	0.5930736	0.93705233	0.50972119
c1_27	0.22198898	0.09456777	0.29272984	0.5708343	0.93705233	0.78329096
c1_28	-0.7951167	-0.6995328	-1.4049747	0.00116345	0.05779617	0.02622482
c1_29	-0.1883504	-0.1082889	-0.8243464	0.69739962	0.94946875	0.50598333
c1_30	-0.4233363	-0.46125	-0.8240475	0.4076475	0.66104138	0.50972119
c1_31	0.15483623	0.09491723	-0.0747263	0.60147723	0.93051835	0.91065227
c1_32	0.81050047	0.59410626	1.42749885	0.01578315	0.30765288	0.10633866
c1_33	1.91678471	1.53316247	3.75980479	0.04758611	0.34836187	0.13476059
c1_34	2.37326288	2.23031872	3.21125481	0.0708723	0.30765288	0.41851486
c1_35	0.90437966	0.88060036	0.90930572	0.0708723	0.30394601	0.52546548
c1_36	1.67805728	1.4318068	2.7072539	0.00666631	0.14859344	0.1088137
c1_37	0.92906269	0.82190151	1.52149973	0.2194396	0.58687644	0.44074617
c1_39	0.11238564	0.04790321	0.21661232	0.74312454	0.99192542	0.83081514
c1_41	-0.8579073	-0.6437833	-1.7411784	0.31401775	0.77261876	0.39917757
c1_43	0.2931677	-0.006557	1.08761033	0.69773659	0.99613423	0.54386407
c1_45	0.94652014	0.51744501	1.70701202	0.4076475	0.90122286	0.52776855
c1_49	0.22599382	0.2066097	-0.0032908	0.60147723	0.86346813	0.99583069
c1_55	0.83236923	0.73966447	1.24436709	0.00568981	0.14355945	0.13347364
c1_57	-0.440141	-0.790508	0.56035432	0.63600442	0.66104138	0.81596468
c1_59	-0.1236202	0.00708825	-0.9803402	0.74114055	0.99613423	0.3233766
c1_60	-0.1203953	-0.0910034	-0.1528637	0.66465647	0.93051835	0.83081514
c1_61	1.70182335	1.10475714	4.26978684	5.04E-06	0.05779617	2.49E-07
c1_62	0.61209812	0.48256357	0.90242214	0.26207213	0.66104138	0.50972119
c1_64	0.12271015	-0.0054686	0.12280415	0.74312454	0.99613423	0.90574972
c1_65	-1.224025	-1.0140615	-2.5025081	0.00025809	0.05779617	0.00148331
c1_66	-0.7553239	-0.6426641	-1.3144983	0.01799374	0.25095672	0.13476059
c1_67	-0.6786103	-0.651628	-0.8457462	0.05935084	0.3024769	0.41851486
c1_68	-0.4282399	-0.3988042	-0.983373	0.34118444	0.66104138	0.39917757
c1_71	-0.1307975	-0.0530932	-0.7233793	0.77311157	0.99192542	0.54151794
c1_75	-0.4162099	-0.4472426	-0.8334913	0.41238369	0.66104138	0.50972119
c1_76	0.25410793	0.16409355	0.09246879	0.38632954	0.85313714	0.90574972
c1_78	-0.2113909	-0.1785116	-0.7236163	0.5930736	0.86346813	0.42380353
c1_80	0.04682677	0.08003497	-0.2485582	0.95445959	0.99192542	0.90574972
c1_84	1.0543461	0.99345351	1.29437549	0.0548207	0.3024769	0.41851486
c1_86	0.74635076	0.77451494	0.72423483	0.4076475	0.66104138	0.78329096
c1_92	-0.069685	0.06347007	-0.9900231	0.86403015	0.99192542	0.39917757
c1_93	-0.3531484	-0.1748584	-1.2130777	0.54601788	0.93051835	0.39917757
c1_95	0.004389	-0.1546805	0.80031501	0.99692413	0.94946875	0.6872823
c1_96	-0.798346	-0.4935945	-2.005073	0.04321665	0.57880367	0.03374421
c1_97	-0.30158	-0.2224805	-1.3126415	0.6489216	0.93051835	0.41851486
c1_98	1.22305698	0.80762519	3.27734765	0.01799374	0.37752624	0.006146
c1_99	-0.3981556	-0.2733961	-0.7547349	0.63128941	0.93051835	0.71659356
c1_101	1.84424826	1.20607525	4.39509459	0.00025809	0.14859344	0.00033341
c1_102	1.84132177	1.27616975	4.70995506	0.00117705	0.19333888	0.00048511
c1_104	-1.3203144	-1.1243356	-2.5874652	0.00025434	0.05779617	0.00148331
c1_107	-0.6700038	-0.651698	-0.7815074	0.07069821	0.30394601	0.46706862
c1_109	0.20673802	0.12633776	0.01343379	0.50142631	0.90122286	0.98983235
c1_115	-0.4888015	-0.296463	-1.5393329	0.34866633	0.85313714	0.22393933
c1_117	-0.0671199	-0.1110697	-0.2951285	0.86403015	0.93705233	0.81596468
c1_123	-0.163802	-0.0019391	-1.2917433	0.72948322	0.99613423	0.28513703
c1_127	-0.0027439	-0.0235531	0.44961709	0.99692413	0.99613423	0.88581405
c1_129	-1.3101182	-0.8468487	-3.4361589	0.00723387	0.32088924	0.00217898
c1_130	-0.0613282	-0.0048053	-0.156405	0.88869028	0.99613423	0.90574972
c1_133	1.31131677	0.89777338	3.42760616	0.01578315	0.33496557	0.00610009
c1_137	-1.3503988	-1.1551422	-2.6410179	0.00025434	0.05779617	0.00149985
c1_145	-0.5315062	-0.322906	-1.6772149	0.34866633	0.85313714	0.22393933

Abbreviations:

EC+SSC. enriched data integrated from the entrorhinal and somatosensory cortices

EC, enriched data integrated from the entrorhinal cortex only

SSC, enriched data integrated from the somatosensory cortex only

logFC, log base 2 fold-enrichment

adj P, p-statistic adjusted (corrected) for multiple comparisons

Supplementary Table 11. Co-expression by brain region
Micro MEGENA amyloid beta

	EC+SSC logFC	EC logFC	SSC logFC	EC+SSC adj.P.Val	EC adj.P.Val	SSC adj.P.Val
	0.28621445	0.2517795	0.30998402	0.3505243	0.88012223	0.40433006
c1_4	-0.0089219	-0.4917284	0.12839709	0.97167591	0.88012223	0.8163668
c1_5	0.40246642	0.83233848	0.31481377	0.61573579	0.88012223	0.72097998
c1_6	0.45042163	0.42070902	0.46550336	0.17420161	0.88012223	0.25174748
c1_7	0.0574459	0.02483381	0.05113341	0.85584427	0.95281585	0.91756615
c1_9	-0.5935383	-0.5211907	-0.6443562	0.04994916	0.88012223	0.08642221
c1_10	0.15860408	0.25812517	0.13637002	0.7083544	0.88012223	0.75587443
c1_11	1.23445614	1.74025134	1.10849074	0.00702193	0.72720234	0.05720272
c1_12	0.07633492	0.30860592	0.01620433	0.88612794	0.88012223	0.9713126
c1_13	-0.7658319	-1.5068373	-0.5841297	0.32505855	0.78941021	0.53644556
c1_15	-0.7442633	-2.1214059	-0.346151	0.4932037	0.72720234	0.8163668
c1_16	0.32914242	-0.4777024	0.56398457	0.78911329	0.88012223	0.63104755
c1_17	0.53963754	0.22508539	0.62888976	0.3505243	0.91390058	0.40289734
c1_18	0.31567461	0.90364513	0.2180008	0.84996665	0.88012223	0.91756615
c1_19	0.56016826	0.85102587	0.49602386	0.32175647	0.88012223	0.48907799
c1_20	-0.4173276	0.7660698	-0.7790952	0.85554351	0.88969095	0.71931911
c1_21	-0.023134	-0.3585964	0.07203604	0.95270098	0.88012223	0.91756615
c1_22	0.71174675	0.87978322	0.67175532	0.05083058	0.72720234	0.13805974
c1_23	0.80380827	0.96588862	0.7744411	0.15863307	0.83553707	0.28954353
c1_24	-1.0213823	-0.8597695	-1.1056097	0.13371439	0.88012223	0.1488725
c1_25	0.19464492	0.19699494	0.17822249	0.54595767	0.88012223	0.63734874
c1_26	-0.4033105	0.28073206	-0.8172433	0.85554351	0.95065085	0.72097998
c1_27	0.05211441	-0.2182005	0.13292065	0.93104649	0.88012223	0.82320485
c1_28	-0.7078955	-0.8206685	-0.7123005	0.01802615	0.72720234	0.05811588
c1_29	-0.1806838	0.68027713	-0.4449019	0.82239623	0.88012223	0.53322805
c1_30	-0.2539409	0.17004401	-0.3809773	0.75784903	0.93493456	0.63104755
c1_31	0.03864967	0.22137381	-0.008934	0.93104649	0.88012223	0.9713126
c1_32	0.71201486	0.34838526	0.8279078	0.09880502	0.88012223	0.08731238
c1_33	2.34405012	3.20968799	2.12677747	0.04448631	0.72720234	0.1333457
c1_34	2.32151798	3.754703	1.98179935	0.18698329	0.72720234	0.38267474
c1_35	0.72136248	1.19396525	0.59693885	0.28966349	0.79196722	0.49950978
c1_36	1.5864242	1.91241141	1.52645027	0.04057146	0.72720234	0.10723015
c1_37	1.08925874	1.19621228	1.04382111	0.2333297	0.88012223	0.38267474
c1_39	0.12675927	0.35889192	0.0629181	0.84996665	0.88012223	0.92043894
c1_41	-1.2075868	-2.003908	-1.0256292	0.20141682	0.73750599	0.38267474
c1_43	0.31909275	-0.5395127	0.5735233	0.8063715	0.88012223	0.6334884
c1_45	0.64447456	1.23069865	0.57883832	0.71542382	0.88012223	0.75139539
c1_49	-0.0355969	-0.4464012	0.08370389	0.94825977	0.88012223	0.91756615
c1_55	0.74576561	0.90951044	0.70955353	0.04549691	0.72720234	0.12350564
c1_57	0.43822943	0.40550693	0.43123811	0.76442568	0.91390058	0.75614982
c1_59	-0.4567024	-0.3735673	-0.4956982	0.31801881	0.88012223	0.38267474
c1_60	-0.0835234	-0.2116134	-0.0761718	0.85554351	0.88012223	0.89521536
c1_61	2.22002535	2.56346796	2.14406436	8.05E-08	0.14741304	9.74E-06
c1_62	0.432582	0.13911179	0.51960885	0.54595767	0.95065085	0.53322805
c1_64	-0.0449674	-0.2652646	0.02075246	0.94232908	0.88012223	0.9713126
c1_65	-1.1863077	-1.0181127	-1.270615	0.00293551	0.72720234	0.00651075
c1_66	-0.6879434	-0.9331998	-0.6637068	0.09880502	0.72720234	0.2061413
c1_67	-0.4752627	-0.8403853	-0.4135177	0.32505855	0.79196722	0.5161766
c1_68	-0.4701239	-0.2802081	-0.5357557	0.3505243	0.88012223	0.40433006
c1_71	-0.1417003	0.72877587	-0.4100469	0.85554351	0.88012223	0.60736358
c1_75	-0.2720246	0.1084109	-0.3871203	0.74370686	0.95065085	0.63104755
c1_76	0.11996828	0.29431675	0.08068878	0.8063715	0.88012223	0.89521536
c1_78	-0.2822878	-0.0590671	-0.3588815	0.54595767	0.95065085	0.5161766
c1_80	-0.045938	0.14523151	-0.1212386	0.95270098	0.95065085	0.92043894
c1_84	0.94155992	1.453885	0.80687004	0.19230944	0.73868651	0.38267474
c1_86	0.70170833	0.96408254	0.61143727	0.54595767	0.88012223	0.67092295
c1_92	-0.4899114	-0.5658345	-0.4800648	0.3505243	0.88012223	0.4681655
c1_93	-0.4911137	-0.0660321	-0.6469608	0.47150452	0.95281585	0.40433006
c1_95	0.44593958	0.46995421	0.40762376	0.70259475	0.88012223	0.72097998
c1_96	-1.0803763	-1.4642594	-1.0182553	0.01802615	0.72720234	0.07014024
c1_97	-0.8052462	-0.9065742	-0.7676689	0.28966349	0.88012223	0.40433006
c1_98	1.85299579	2.04058204	1.798252	0.00233741	0.72720234	0.00828658
c1_99	-0.4458738	-0.4313064	-0.5029568	0.71542382	0.89226888	0.67726246
c1_101	2.30975995	3.01379474	2.15311404	9.74E-05	0.25525728	0.00274972
c1_102	2.55917682	2.82792214	2.47103423	9.74E-05	0.61973114	0.00254806
c1_104	-1.2367474	-1.0787915	-1.3157916	0.00293551	0.72720234	0.00651075
c1_107	-0.4539188	-0.8764183	-0.3778604	0.3505243	0.79196722	0.55159814
c1_109	0.07833768	0.26934129	0.03254433	0.85554351	0.88012223	0.95045963
c1_115	-0.7152175	-0.6671317	-0.7556651	0.2333297	0.88012223	0.34148215
c1_117	-0.0454309	0.3466636	-0.1656952	0.94232908	0.88012223	0.82320485
c1_123	-0.6331764	-0.678138	-0.6299211	0.24721439	0.88012223	0.38267474
c1_127	0.25570559	0.35905079	0.19857918	0.85584427	0.93493456	0.91756615
c1_129	-1.794617	-2.0304869	-1.7757673	0.00233741	0.72720234	0.00691303
c1_130	-0.1854679	-0.8568424	-0.023959	0.82239623	0.88012223	0.9713126
c1_133	1.90165309	2.0256814	1.86529559	0.00236777	0.72720234	0.00828658
c1_137	-1.2535807	-1.1074046	-1.3300498	0.00328301	0.72720234	0.00691303
c1_145	-0.7661076	-0.7055193	-0.8101842	0.24308976	0.88012223	0.34567095

Abbreviations:

EC+SSC. enriched data integrated from the entrorhinal and somatosensory cortices

EC, enriched data integrated from the entrorhinal cortex only

SSC, enriched data integrated from the somatosensory cortex only

logFC, log base 2 fold-enrichment

adj P, p-statistic adjusted (corrected) for multiple comparisons

Supplementary Table 11. Co-expression by brain region
Astro SCENIC pTau

	EC+SSC logFC	EC logFC	SSC logFC	EC+SSC adj.P.Val	EC adj.P.Val	SSC adj.P.Val
ATF6(+)	-0.5704126	-0.6370634	-0.796204	0.24051656	0.33728147	0.70583034
BACH1(+)	0.17632055	-0.1113373	2.75656406	0.82661021	0.91743281	0.35565405
BACH2(+)	-0.5116762	-0.5529593	-0.6657926	0.28904535	0.40638161	0.70583034
BHLHE40(+)	0.35145918	0.26342222	1.26764601	0.74760691	0.80609233	0.71835801
CEBPB(+)	1.9902021	1.60713673	4.25054881	0.00350027	0.08169149	0.02111588
CEBPD(+)	0.02555727	-0.0426224	0.46073163	0.96491085	0.9362598	0.77209975
CREB1(+)	-0.2273958	-0.2608146	-0.3446187	0.78791779	0.77241136	0.87467455
CREM(+)	-0.5002123	-0.6998609	0.23859523	0.57080002	0.56508987	0.87715398
CUX1(+)	0.09640714	0.19246167	1.55873757	0.82661021	0.70566486	0.35565405
ELF1(+)	-0.0306712	-0.2574526	0.83521217	0.96491085	0.68375844	0.70583034
ELF2(+)	-0.384321	-0.477186	-0.3219572	0.63175831	0.56508987	0.87467455
EMX2(+)	0.5090767	0.51013464	1.0890619	0.4330182	0.56508987	0.70583034
EPAS1(+)	-0.5336102	-0.4883336	0.61716036	0.4330182	0.56508987	0.76761824
ETV6(+)	-0.8005288	-0.7880842	-0.9238186	0.28904535	0.42593196	0.71835801
FOS(+)	0.86857295	0.48632642	1.5495621	0.24051656	0.56508987	0.5778911
FOXN3(+)	0.16019399	0.20155489	1.09544884	0.7113056	0.68375844	0.4196146
FOXO1(+)	-0.1447325	-0.1291788	0.31757549	0.71999248	0.77241136	0.77209975
FOXO3(+)	-0.4000293	-0.2918592	0.15244769	0.43102402	0.56508987	0.87467455
HSF4(+)	1.19917586	1.05606373	1.55090143	0.24051656	0.37289428	0.70583034
IRF2(+)	-0.4487733	-0.3926318	-0.6309378	0.4330182	0.56508987	0.71835801
JUN(+)	1.05534137	0.63910757	1.82017084	0.23858752	0.56508987	0.44457951
JUNB(+)	0.42376979	0.24169491	0.68009792	0.46820343	0.69769621	0.71835801
JUND(+)	2.17319521	1.67856353	4.1616879	0.00320735	0.08169149	0.03155843
KDM5B(+)	-0.3599056	-0.2835482	-0.6215532	0.63175831	0.69769621	0.77209975
KLF12(+)	-0.2234373	-0.0028467	-0.5860958	0.78791779	0.99626394	0.78344708
LHX2(+)	0.28020649	0.450383	1.08079741	0.69773931	0.56508987	0.70583034
MAF(+)	1.78115629	1.37202653	3.73838024	4.91E-06	0.00391461	0.00012566
MAFG(+)	2.02255627	1.73670951	4.27282634	2.54E-07	0.0002551	5.19E-06
MAX(+)	1.01311788	0.69408897	1.32031825	0.2440587	0.56508987	0.70583034
MXI1(+)	0.30226499	0.27600159	0.91647907	0.4330182	0.56508987	0.44457951
MZF1(+)	0.74897426	0.84103431	1.17104843	0.4330182	0.56508987	0.71835801
NFIC(+)	0.63689611	0.59088923	2.0886891	0.35002321	0.56508987	0.28327956
NR3C1(+)	-0.4738481	-0.4823972	-0.1585677	0.47363716	0.56508987	0.88170392
NRF1(+)	-0.3113683	-0.2756523	-0.1139513	0.4667652	0.56508987	0.87715398
POU3F2(+)	0.25419108	0.34766984	0.98924559	0.72709924	0.68375844	0.71835801
PPARA(+)	0.31431537	0.61760874	1.18784983	0.69773931	0.56508987	0.70583034
RXRA(+)	1.50050287	1.66851128	2.46107829	0.11709091	0.08169149	0.4196146
SMAD1(+)	0.26852461	0.06929968	0.46921767	0.69773931	0.91743281	0.78344708
SREBF1(+)	0.29796894	0.40221932	0.52703677	0.63175831	0.56508987	0.76761824
SREBF2(+)	-0.3300313	-0.1127473	0.2849864	0.4667652	0.79917336	0.78705203
STAT1(+)	-0.6169615	-0.6655176	-0.52388	0.24051656	0.33728147	0.71835801
STAT2(+)	0.53435466	0.4245084	0.65211976	0.57080002	0.68375844	0.78344708
STAT3(+)	0.00349744	-0.2310993	1.1194088	0.99165393	0.68375844	0.48921189
STAT5B(+)	-1.0121072	-0.9096533	-0.8086503	0.23858752	0.35859533	0.71835801
TCF7L1(+)	0.99217559	0.65281727	0.90395231	0.4330182	0.64651678	0.78344708
THRA(+)	1.34008838	1.42608692	2.6375762	0.24051656	0.33728147	0.44457951
ZBTB7A(+)	1.41505859	1.35696128	3.78838528	0.13163587	0.24343402	0.06830307
ZEB1(+)	-0.4276533	-0.4328592	-0.4725881	0.24051656	0.37289428	0.70583034
ZIC2(+)	1.51191896	1.61517222	3.2156493	0.24051656	0.33728147	0.4196146
ZXDC(+)	0.69494504	0.68982086	1.58075907	0.4330182	0.56508987	0.70583034

Abbreviations:
EC+SSC. enriched data integrated from the entrorhinal and somatosensory cortices
EC, enriched data integrated from the entrorhinal cortex only
SSC, enriched data integrated from the somatosensory cortex only
logFC, log base 2 fold-enrichment
adj P, p-statistic adjusted (corrected) for multiple comparisons

Supplementary Table 11. Co-expression by brain region
Astro SCENIC amyloid beta

	EC+SSC logFC	EC logFC	SSC logFC	EC+SSC adj.P.Val	EC adj.P.Val	SSC adj.P.Val
MAFG(+)	2.16043704	2.44518777	2.08663319	0.75909415	0.99074719	0.88033409
JUND(+)	1.80125266	1.67105143	1.90987204	0.66192677	0.99074719	0.63393125
MAF(+)	1.78283311	2.05591276	1.74497506	0.76151024	0.99074719	0.88033409
CEBPB(+)	1.758833	1.2462505	1.92723855	0.98073559	0.99074719	0.90424445
ZBTB7A(+)	1.7267681	1.12965662	1.82196234	0.0974182	0.99074719	0.18211344
RXRA(+)	1.58920745	2.1257538	1.39663657	0.94872186	0.99074719	0.90424445
ZIC2(+)	1.34603471	0.30707817	1.56438833	0.95149261	0.99074719	0.90424445
THRA(+)	1.02025633	0.50908216	1.11918569	0.95149261	0.99074719	0.98156944
BACH1(+)	0.99991124	0.06215105	1.19052437	0.30219653	0.99074719	0.63393125
CUX1(+)	0.80510524	0.55416651	0.78039146	0.833453	0.99074719	0.88033409
NFIC(+)	0.74866007	0.011833	0.904649	0.94872186	0.99074719	0.90424445
JUN(+)	0.69983929	0.756612	0.76921112	0.833453	0.99074719	0.88033409
FOS(+)	0.60594817	0.85846178	0.612026	0.95149261	0.99074719	0.88033409
HSF4(+)	0.6015534	0.03141358	0.80447478	0.82368204	0.99074719	0.88033409
FOXN3(+)	0.56199519	0.33659018	0.56729546	0.76151024	0.99074719	0.88033409
LHX2(+)	0.54559942	0.04027333	0.61005892	0.47959146	0.99074719	0.63393125
MXI1(+)	0.5280923	0.58804356	0.49057691	0.94872186	0.99074719	0.88033409
PPARA(+)	0.487788	-0.1583007	0.56368457	0.94872186	0.99074719	0.90424445
SMAD1(+)	0.46997734	1.11045689	0.3327915	0.82368204	0.99074719	0.88033409
ZXDC(+)	0.40912944	-0.4624874	0.62385447	0.833453	0.99074719	0.88033409
EMX2(+)	0.35011247	-0.3635828	0.52971293	0.75909415	0.99074719	0.88033409
TCF7L1(+)	0.34589348	0.96417771	0.28468003	0.95149261	0.99074719	0.88033409
STAT3(+)	0.34495275	-0.0393641	0.44473142	0.09968397	0.99074719	0.19738033
MAX(+)	0.31199521	-0.0216834	0.48501212	0.82368204	0.99074719	0.88033409
ELF1(+)	0.29067097	0.06564283	0.35376424	0.95149261	0.99074719	0.90424445
POU3F2(+)	0.16422578	-0.9549772	0.4223869	0.76151024	0.99074719	0.88033409
FOXO1(+)	0.15990684	-0.0436099	0.17874265	0.00019489	0.24387402	0.00519284
CEBPD(+)	0.14538103	0.25349507	0.1118761	4.18E-06	0.16985049	0.00030354
MZF1(+)	0.14432977	-1.0264395	0.44718924	0.94872186	0.99074719	0.88033409
FOXO3(+)	0.12676411	-0.0744989	0.11422427	0.46313726	0.99074719	0.63393125
JUNB(+)	0.11473851	-0.2060379	0.24268679	0.95149261	0.99074719	0.88033409
EPAS1(+)	0.08711177	-0.8865995	0.2670273	0.64749665	0.99074719	0.63393125
SREBF2(+)	0.00868384	-0.8117957	0.14609843	0.94872186	0.99074719	0.90424445
SREBF1(+)	-0.0108155	-0.9363088	0.21788208	0.94872186	0.99074719	0.90424445
STAT2(+)	-0.0288668	-0.8231499	0.22434537	0.95149261	0.99074719	0.88033409
BHLHE40(+)	-0.0628322	-1.6824341	0.36579972	0.82368204	0.99074719	0.88033409
CREM(+)	-0.1033828	-0.5866838	0.01771331	0.18254764	0.99074719	0.63393125
NRF1(+)	-0.1228689	-0.4666848	-0.0598566	0.82368204	0.99074719	0.88033409
KLF12(+)	-0.1237905	-0.1846646	-0.1478859	0.98073559	0.99074719	0.88033409
CREB1(+)	-0.1739085	-0.179287	-0.1710888	0.98073559	0.99074719	0.90424445
NR3C1(+)	-0.1744231	-0.6133515	-0.0876041	0.76151024	0.99074719	0.88033409
ELF2(+)	-0.2155732	-0.5369298	-0.1271564	0.98073559	0.99074719	0.90424445
ZEB1(+)	-0.2335462	-0.4015488	-0.1997702	0.82368204	0.99074719	0.88033409
IRF2(+)	-0.3039456	-0.481016	-0.2756246	0.833453	0.99074719	0.88033409
STAT1(+)	-0.3849366	-0.6837775	-0.3165193	0.94872186	0.99074719	0.90424445
BACH2(+)	-0.388485	-0.6881902	-0.3066739	0.75909415	0.99074719	0.88033409
STAT5B(+)	-0.3911637	-0.7288005	-0.3569506	0.11455425	0.99074719	0.23485792
KDM5B(+)	-0.4324054	-0.9411273	-0.3102962	0.82368204	0.99074719	0.88033409
ATF6(+)	-0.4516215	-0.6916475	-0.3808242	0.66192677	0.99074719	0.63393125
ETV6(+)	-0.4561183	-0.561693	-0.4451267	0.87107938	0.99074719	0.88033409

Abbreviations:

EC+SSC. enriched data integrated from the entrorhinal and somatosensory cortices

EC, enriched data integrated from the entrorhinal cortex only

SSC, enriched data integrated from the somatosensory cortex only

logFC, log base 2 fold-enrichment

adj P, p-statistic adjusted (corrected) for multiple comparisons

Supplementary Table 11. Co-expression by brain region
Micro SCENIC pTau

	EC+SSC	EC	SSC	EC+SSC	EC	SSC
	logFC	logFC	logFC	adj.P.Val	adj.P.Val	adj.P.Val
CEBPZ(+)	2.02360699	1.30068162	4.011485	0.66252635	0.99320192	0.66641653
JUND(+)	1.93174745	1.34498383	4.07308374	0.332036	0.97799424	0.77758317
MAFG(+)	1.77006547	1.36417611	3.48409983	0.44139883	0.83680157	0.89447348
PPARG(+)	1.4642543	1.26292855	2.53243478	0.18391742	0.83680157	0.21058647
CEBPA(+)	1.30132369	1.1187422	1.96525314	0.66252635	0.99320192	0.56831944
USF2(+)	1.21551265	0.84309925	1.93977527	0.69320395	0.99320192	0.95562574
ATF1(+)	1.20363539	0.85356834	2.60943802	0.18121474	0.74909873	0.14149058
HBP1(+)	1.15227902	0.65667676	2.7012595	1.07E-05	0.0421475	0.00049345
RXRA(+)	1.08209439	0.68786761	2.91785159	0.44139883	0.99320192	0.93192726
MXD4(+)	1.02709352	0.76142748	1.91436392	1.95E-06	0.01664135	0.00596503
PRDM1(+)	1.00882044	0.59963859	2.59179375	0.66252635	0.99320192	0.92808659
SP4(+)	0.99130052	0.74427077	1.29202954	0.00761321	0.74909873	0.01971859
NFATC1(+)	0.95805943	0.78314085	1.58752157	0.10008106	0.83584448	0.2006788
ZNF84(+)	0.95594988	1.02639862	1.01620001	0.11913249	0.83680157	0.19355423
GABPA(+)	0.8938612	0.63488228	1.32107475	0.03414685	0.74909873	0.15487566
MITF(+)	0.78622788	0.55832318	1.39810482	0.65763189	0.99320192	0.26992799
PBX3(+)	0.77020499	0.59814081	1.28234723	0.23656604	0.99320192	0.12477924
MAFB(+)	0.76982436	0.63089399	1.08872691	0.07127508	0.74909873	0.06322458
ELF2(+)	0.74586361	0.48210884	1.78383095	0.86805346	0.99320192	0.95562574
FOXO3(+)	0.73688093	0.53395896	1.25391638	0.6901537	0.99320192	0.49692654
NR2C2(+)	0.73631358	0.49932385	1.44488827	0.98912805	0.99320192	0.95562574
CEBPD(+)	0.7236813	0.44153949	1.51238026	0.94390138	0.99320192	0.93192726
DEAF1(+)	0.70685816	0.39283263	2.35902001	0.10008106	0.83680157	0.38877048
IRF3(+)	0.69745978	0.66114835	0.95642157	0.28103221	0.97564051	0.22814781
RFX3(+)	0.64899469	0.37540782	1.51885085	0.87695571	0.99320192	0.93192726
PKNOX1(+)	0.64231906	0.72946512	0.63877748	0.08954209	0.83680157	0.2006788
CREB1(+)	0.6230812	0.44431101	1.045731	0.50395849	0.99320192	0.33259117
NFE2L2(+)	0.62201002	0.42101012	1.14054224	0.69320395	0.99320192	0.21058647
GTF2IRD1(+)	0.61965944	0.71813652	0.18743291	0.66252635	0.92366805	0.59088824
CLOCK(+)	0.60117454	0.36492292	1.2352647	0.29820514	0.97799424	0.7199222
ELK4(+)	0.54204694	0.30800975	0.99897937	0.6901537	0.99320192	0.2339933
YY1(+)	0.53081238	0.32217698	1.06675153	0.86805346	0.99320192	0.78096886
KLF6(+)	0.52794505	0.39044069	0.80370989	0.97462413	0.99320192	0.92279426
STAT5A(+)	0.50056836	0.26924195	1.56935296	0.88918958	0.99320192	0.83099838
FOXO1(+)	0.48372757	0.37445399	0.63821766	0.09409829	0.74909873	0.38877048
ZNF736(+)	0.47432008	0.35420394	0.35869493	0.00034204	0.19597919	0.01683629
NR3C1(+)	0.47148258	0.33880157	0.64556171	0.74081342	0.99320192	0.9192038
NR2C1(+)	0.46683224	0.40059656	0.6597203	0.332036	0.97102603	0.60990447
ZNF337(+)	0.46096905	0.40002277	0.46943486	0.66252635	0.97972717	0.95562574
TCF7L2(+)	0.42959844	0.3427332	0.85551969	0.49074724	0.99320192	0.46792746
CREM(+)	0.42557396	0.18968295	1.30901869	0.90396828	0.99320192	0.93192726
TFEC(+)	0.42516282	0.28294148	0.65240926	0.39757063	0.99320192	0.30569834
NRF1(+)	0.40455178	0.27109198	0.52567918	0.94527065	0.99320192	0.93192726
SP3(+)	0.39246112	0.13134939	0.84075125	0.16732869	0.74909873	0.38877048
MAX(+)	0.3840162	0.21018519	0.76158829	0.92272817	0.99320192	0.88091789
ARNT(+)	0.35194872	0.23685323	0.33457181	0.69320395	0.99320192	0.27602517
IRF5(+)	0.32481056	0.43197335	-0.5261553	0.62439425	0.99320192	0.51941241
ELF1(+)	0.31852241	0.19334771	0.4514925	0.12951775	0.74909873	0.43856698
SMAD5(+)	0.267397	0.10396435	0.34154457	0.48029042	0.76959719	0.63930085
RUNX2(+)	0.26541553	0.11347696	0.49607916	0.44139883	0.99320192	0.07035581
KDM5B(+)	0.25913018	-0.0084646	1.11330208	0.66252635	0.99320192	0.51941241
FLI1(+)	0.23933032	0.14674815	0.2448134	5.17E-06	0.10830003	3.27E-05
HIF1A(+)	0.23575363	0.03959024	0.6263175	0.88918958	0.99472977	0.83099838
BHLHE41(+)	0.20839522	0.13663933	0.08781787	0.17455472	0.74909873	0.14375323
NFYC(+)	0.19783984	0.16785673	0.07425212	0.44139883	0.97972717	0.63663305
ETS2(+)	0.19462531	0.01442935	0.59492053	0.03412555	0.6193808	0.21058647
JDP2(+)	0.19063932	0.02200045	0.57438544	4.14E-07	0.01791523	2.18E-05
FOS(+)	0.1812037	-0.0734378	0.93405087	0.07127508	0.83680157	0.15487566
CEBPB(+)	0.17237586	0.13098196	0.12703154	0.00062361	0.26421075	0.01783073
IRF2(+)	0.15927551	0.03958574	0.42671847	0.90396828	0.99320192	0.92589421
TAL1(+)	0.13718094	0.07246904	0.18280233	0.00034204	0.19597919	0.00680368
TCF12(+)	0.13178868	0.07065008	0.00916493	0.48681812	0.97972717	0.63663305
ATF6(+)	0.11654684	0.01167085	0.06792494	0.03497498	0.74909873	0.12879695
ZNF121(+)	0.11158159	-0.141179	0.88365522	0.76823188	0.99320192	0.63663305
FOXP2(+)	0.10215251	0.05003918	-0.1374755	0.54657186	0.93623583	0.51941241
E2F3(+)	0.10082374	0.02985932	0.33835856	0.78456656	0.99320192	0.95562574
HIVEP1(+)	0.09657686	-0.0200614	0.44126427	0.66252635	0.99320192	0.83099838
SP1(+)	0.0861323	0.02191064	-0.1346337	0.00154873	0.46456262	0.01272303
FOXN3(+)	0.08334798	0.06900745	-0.3745977	0.0149238	0.6193808	0.2006788
RREB1(+)	0.07686304	0.05211967	0.01691515	0.87695571	0.99320192	0.92808659
ELK3(+)	0.07174795	0.08088661	-0.1171702	0.07127508	0.74909873	0.38877048
ZNF91(+)	0.06221883	0.01325206	-0.0307406	0.0004734	0.19597919	0.0216554
CUX1(+)	0.05153185	-0.0058067	0.03064998	0.69320395	0.99320192	0.92312712
ZNF131(+)	0.03161921	0.04414345	0.33394965	0.98108974	0.99320192	0.62965325
FOXK1(+)	0.01698354	-0.0261437	0.17214381	0.29820514	0.99320192	0.05828641
REL(+)	0.00892894	-0.249104	0.47572346	0.07127508	0.74909873	0.2006788
DNMT1(+)	-0.0075994	-0.165056	0.1578728	0.02388461	0.74909873	0.01272303
POU2F1(+)	-0.0318802	0.09210051	-1.1816004	0.18121474	0.74909873	0.46792746
SPI1(+)	-0.070635	-0.0762795	-0.3349078	0.98912805	0.99320192	0.91803759
ETV5(+)	-0.1015499	-0.0626313	-0.624573	0.44139883	0.99320192	0.40950315
HSF1(+)	-0.102469	-0.1310221	-0.5535107	0.88918958	0.99320192	0.98778772
IKZF1(+)	-0.1062433	-0.0776105	-0.5899552	0.21665757	0.83680157	0.12477924
ETV6(+)	-0.1162079	-0.1600784	-0.3278265	0.65763189	0.99320192	0.70948337
NFIC(+)	-0.12901	-0.0466144	-0.4606104	0.332036	0.97972717	0.21058647
STAT2(+)	-0.1688336	-0.1545279	-0.3876425	0.66252635	0.99320192	0.32284192
CREB3L2(+)	-0.1701432	-0.0957416	-0.7143473	0.69320395	0.99320192	0.90171864
STAT3(+)	-0.1864918	-0.167789	-0.5730973	0.13835457	0.99320192	0.19355423
MLXIP(+)	-0.1951093	-0.1594735	-0.5992198	0.90753078	0.99320192	0.95562574
HDX(+)	-0.1980214	-0.4643388	0.47364174	0.62144402	0.99320192	0.62965325
ZNF143(+)	-0.2086535	-0.1762753	-0.8944345	0.29451668	0.90502533	0.62965325
IRF8(+)	-0.2132648	-0.0962171	-1.0177585	0.84882271	0.99320192	0.63930085
ARID3A(+)	-0.2319134	-0.1423541	-0.5143935	0.13964249	0.81163339	0.12879695
FOXJ3(+)	-0.2650497	-0.2199901	-1.0307005	0.07127508	0.74909873	0.12477924
ZBTB7A(+)	-0.2699807	-0.1531737	-0.9211723	0.0149238	0.4747591	0.03056052
NFKB1(+)	-0.2821358	-0.3034218	-0.6522849	0.69320395	0.99320192	0.70948337
NR6A1(+)	-0.3139641	-0.1924732	-0.62212	0.62439425	0.99320192	0.45131892
POU2F2(+)	-0.3641624	-0.1806407	-1.4474692	0.74081342	0.99320192	0.63930085
ZFP64(+)	-0.3684266	-0.3026862	-0.2109295	0.80664324	0.99320192	0.92808659
RUNX1(+)	-0.37067	-0.2696279	-1.1343185	0.78728502	0.99320192	0.98778772
BACH1(+)	-0.3726531	-0.319021	-0.9846899	0.35748705	0.93623583	0.43856698
XBP1(+)	-0.4067783	-0.3645339	-1.0031071	0.04169109	0.74909873	0.21058647
KLF3(+)	-0.4805302	-0.4247323	-1.2094009	0.71385245	0.99320192	0.81752281
SREBF2(+)	-0.4863871	-0.3418996	-1.0459906	0.04169109	0.74909873	0.2006788
SREBF1(+)	-0.5777748	-0.4341272	-1.3956751	0.21665757	0.77745662	0.19271617
UBP1(+)	-0.6684919	-0.6240224	-1.2934663	0.06766887	0.77745662	0.13902148
HIVEP2(+)	-0.6850372	-0.7008295	-1.0547959	0.69320395	0.99320192	0.51941241
ATF4(+)	-0.6927651	-0.3793959	-1.8232206	0.86805346	0.99320192	0.95562574
SMAD3(+)	-0.7390278	-0.2213599	-2.9077825	0.94527065	0.99320192	0.86690892
STAT1(+)	-0.8053604	-0.6444821	-1.6951734	0.98912805	0.99320192	0.95562574
CTCF(+)	-0.8555201	-0.6272595	-2.0181607	0.84705175	0.99320192	0.66641653
ARNTL(+)	-1.0313822	-1.1348747	-0.7255518	0.84705175	0.99320192	0.94713967
RBPJ(+)	-1.4683626	-1.4129889	-1.996633	0.84882271	0.99320192	0.95562574
BCL6(+)	-1.5358769	-1.2803238	-2.8333424	0.54657186	0.93623583	0.83099838
SOX5(+)	-1.9545966	-0.8168246	-3.8970555	0.87695571	0.99320192	0.96353515

Abbreviations:
EC+SSC. enriched data integrated from the entrorhinal and somatosensory cortices
EC, enriched data integrated from the entrorhinal cortex only
SSC, enriched data integrated from the somatosensory cortex only
logFC, log base 2 fold-enrichment
adj P, p-statistic adjusted (corrected) for multiple comparisons

Supplementary Table 11. Co-expression by brain region
Micro SCENIC amyloid beta

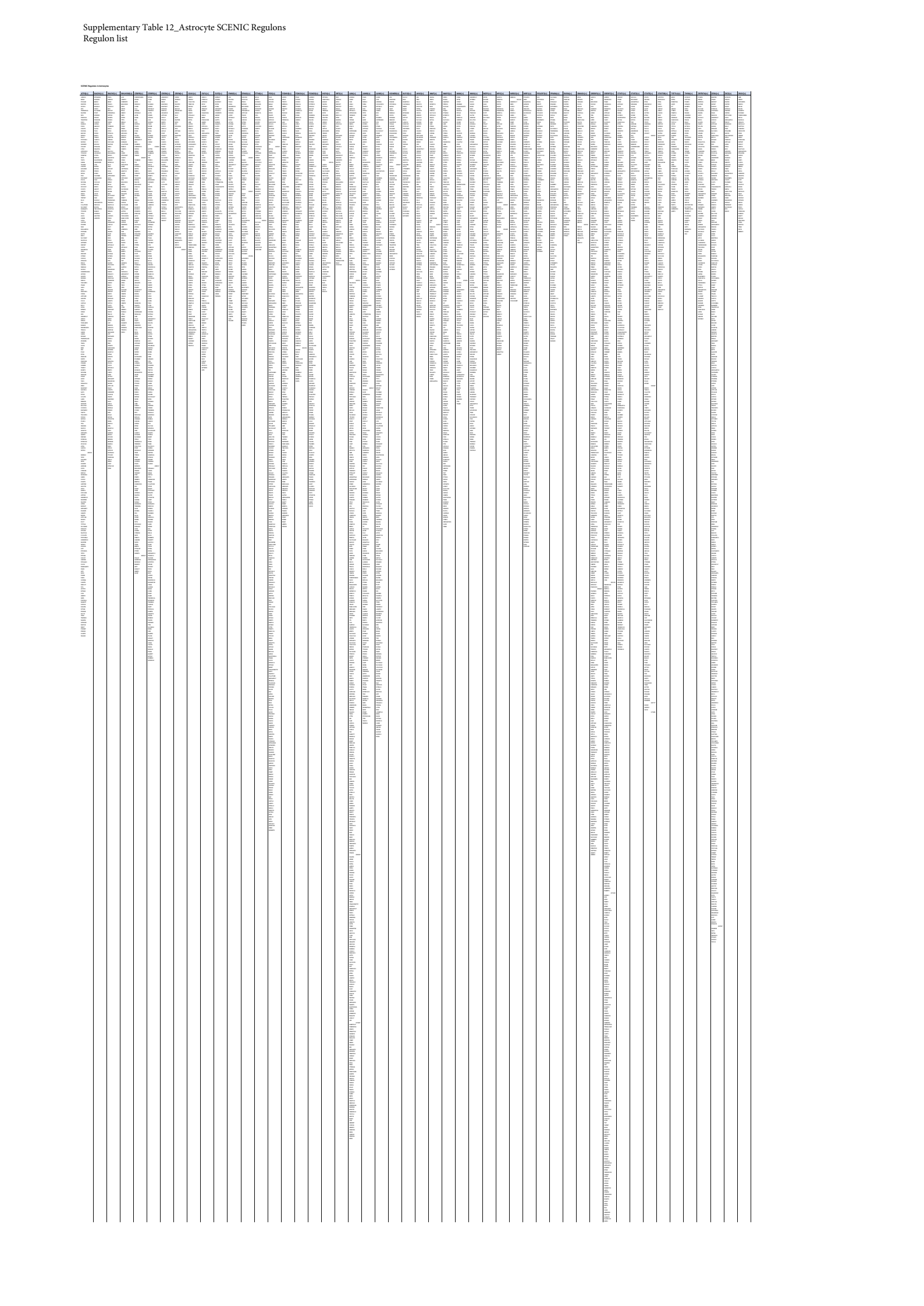
	EC+SSC	EC	SSC	EC+SSC	EC	SSC
	logFC	logFC	logFC	adj.P.Val	adj.P.Val	adj.P.Val
JUND(+)	2.10858666	2.71312689	2.01463436	0.6135928	0.97467485	0.75108676
MAFG(+)	1.96584201	2.58974227	1.82700642	0.6555096	0.97467485	0.73816027
CEBPZ(+)	1.79773651	2.61993099	1.72097275	0.64681448	0.97467485	0.84048852
PPARG(+)	1.78090972	3.07495631	1.44004201	0.14392743	0.97467485	0.2291726
ATF1(+)	1.53969351	1.84102568	1.48558022	0.6135928	0.97467485	0.37470741
RXRA(+)	1.36833465	0.79173056	1.53838384	0.90529119	0.97467485	0.95480033
DEAF1(+)	1.25431846	1.24274714	1.2331529	0.14392743	0.97467485	0.16359441
PRDM1(+)	1.24663405	0.85629004	1.36516354	0.00080446	0.7261037	0.0006764
CEBPA(+)	1.12345784	1.56849774	1.02377225	0.90529119	0.97467485	0.95480033
HBP1(+)	0.97299822	-0.1407426	1.32856708	0.00101798	0.41961605	0.01080401
MXD4(+)	0.94728392	0.69349055	1.04349006	0.84906737	0.97467485	0.95480033
ELF2(+)	0.86689643	0.64466774	0.92879846	0.03842032	0.97467485	0.03221737
USF2(+)	0.83025286	1.08111881	0.83478755	0.25166887	0.97467485	0.37470741
MITF(+)	0.78862447	0.97446876	0.75756449	0.14232381	0.97467485	0.2291726
RFX3(+)	0.78014029	0.64452383	0.82646859	0.08642913	0.95181607	0.21725393
ZNF84(+)	0.7680863	1.56822728	0.56738366	0.59487273	0.97467485	0.37470741
SP4(+)	0.72392122	0.70961192	0.76911984	0.10674311	0.97467485	0.11880578
STAT5A(+)	0.71999043	-0.1193214	0.95313666	0.12310499	0.97467485	0.08633399
NR2C2(+)	0.70579183	0.56202367	0.75955938	0.96124986	0.97467485	0.99593471
GABPA(+)	0.70103221	0.61733548	0.76591543	0.54768579	0.97467485	0.51826733
CEBPD(+)	0.69846501	0.42388332	0.79989371	0.98592153	0.97467485	0.96988529
PBX3(+)	0.6901007	0.82524804	0.66623257	0.81639724	0.97467485	0.96988529
NFE2L2(+)	0.68001175	1.0380276	0.59348668	0.25166887	0.97467485	0.42434744
CLOCK(+)	0.67925451	0.79422903	0.65987271	0.27486827	0.97467485	0.32176868
ZNF121(+)	0.66109252	1.53497849	0.42718808	0.89322805	0.97467485	0.94813667
ELK4(+)	0.64674849	1.01017334	0.5650573	0.08141195	0.7261037	0.2291726
CREM(+)	0.64572778	0.34660005	0.72880449	0.59487273	0.97467485	0.42746698
MAFB(+)	0.63629375	1.23631338	0.49904344	0.24482702	0.97467485	0.28402905
FOXO3(+)	0.62924646	0.45810404	0.6900197	0.55503633	0.97467485	0.51948413
YY1(+)	0.60378483	0.92766513	0.52185767	0.6135928	0.97467485	0.73816027
CREB1(+)	0.6008591	0.81088052	0.55551047	0.69378429	0.97467485	0.48585008
NFATC1(+)	0.55925603	0.13562013	0.70242016	0.85163063	0.97467485	0.8226552
IRF3(+)	0.55504986	0.44314718	0.57501384	0.98996427	0.97467485	0.90285224
KLF6(+)	0.52519855	0.82206495	0.44907698	0.6555096	0.97467485	0.84048852
GTF2IRD1(+)	0.50336099	1.04434061	0.38067734	0.59487273	0.97467485	0.39439599
PKNOX1(+)	0.50118045	1.14717416	0.30913722	0.01541148	0.97467485	0.02060789
ZNF337(+)	0.48319635	1.44085084	0.27648935	0.78250926	0.97467485	0.9037657
SP3(+)	0.47127935	0.66969664	0.4489472	0.59487273	0.97467485	0.56237253
JDP2(+)	0.46414559	1.01852047	0.31239775	0.76511823	0.97467485	0.89683736
NR3C1(+)	0.41920212	0.6834957	0.35577519	0.64681448	0.97467485	0.51948413
TFEC(+)	0.40665499	0.64709544	0.34688514	0.94081254	0.97467485	0.95480033
TCF7L2(+)	0.39422503	0.1987898	0.43159168	0.3385576	0.97467485	0.39978167
E2F3(+)	0.39382218	1.51701681	0.05752705	0.9229002	0.97467485	0.90285224
NRF1(+)	0.37659924	0.68120651	0.30197299	0.23092846	0.95181607	0.41328181
NR2C1(+)	0.36297445	0.27126435	0.38663084	0.84906737	0.97467485	0.90110268
SMAD5(+)	0.34701161	0.93466967	0.19631426	0.3385576	0.97467485	0.3726643
MAX(+)	0.34456808	0.19373344	0.39677356	0.82208656	0.97467485	0.57081476
HIF1A(+)	0.29760225	0.27106608	0.31219862	0.35540546	0.97467485	0.40679859
ZNF736(+)	0.29620765	-0.1200791	0.46564985	0.55503633	0.97467485	0.42434744
ELF1(+)	0.28330267	0.47514292	0.23613752	0.0527374	0.97467485	0.07599759
ZNF131(+)	0.26883695	0.30167532	0.23603966	0.25166887	0.7261037	0.51948413
FOXO1(+)	0.24194356	-0.1857187	0.36824311	3.41E-05	0.30328482	0.00058234
ARNT(+)	0.22249329	0.34205412	0.20502473	0.94081254	0.97467485	0.89683736
RUNX2(+)	0.20382575	-0.042903	0.26217362	0.23092846	0.97467485	0.2291726
FOS(+)	0.1966618	-0.2901481	0.34565904	0.55503633	0.97467485	0.62098903
ETS2(+)	0.19137736	-0.1325685	0.2815936	0.15209178	0.7261037	0.37470741
HIVEP1(+)	0.18366296	-0.3716439	0.34906618	1.49E-06	0.12474136	0.00012574
NFYC(+)	0.18266688	0.64038629	0.04974378	0.20276356	0.97467485	0.2291726
HDX(+)	0.16184017	0.29684954	0.14365575	0.00713782	0.7261037	0.02303505
KDM5B(+)	0.16085555	-0.9460908	0.50015346	0.89322805	0.97467485	0.92367062
FLI1(+)	0.16003315	0.23042015	0.14040163	0.0093804	0.97467485	0.00992806
CEBPB(+)	0.09547688	0.56198274	-0.0337508	0.76511823	0.97467485	0.73816027
TCF12(+)	0.09037965	0.18788806	0.05193631	0.05551338	0.7261037	0.1774802
IRF2(+)	0.09019772	-0.3596811	0.20798512	0.64681448	0.97467485	0.57890008
TAL1(+)	0.08241556	0.04979575	0.07458119	0.59487273	0.99021368	0.48585008
ATF6(+)	0.05543575	0.15456708	0.03114065	0.84906737	0.97467485	0.9590013
BHLHE41(+)	0.05059706	0.14493923	0.02838056	0.78416308	0.97467485	0.84048852
ZNF91(+)	0.04364869	0.2479786	-0.0139426	0.01541148	0.97467485	0.02060789
DNMT1(+)	0.03923338	0.33673665	-0.0406414	0.08141195	0.7261037	0.2291726
CUX1(+)	0.01754756	0.03974091	0.00100168	0.94081254	0.97467485	0.91631633
FOXK1(+)	0.01185011	-0.3916997	0.10255302	0.18190533	0.7377801	0.39439599
REL(+)	0.01125299	-0.5123932	0.17183204	0.01541148	0.7261037	0.04119279
RREB1(+)	0.01002731	0.05071753	-0.0183536	0.81639724	0.97467485	0.92483778
SP1(+)	-0.0052368	0.39546314	-0.1126945	0.66164427	0.97467485	0.69087832
ELK3(+)	-0.0831003	-0.1926175	-0.0695852	0.05551338	0.97467485	0.06728856
FOXP2(+)	-0.1106292	-0.2379244	-0.0759732	0.05888101	0.7261037	0.2291726
NR6A1(+)	-0.163015	0.55129774	-0.4003511	0.01541148	0.97467485	0.02060789
SPI1(+)	-0.1756247	0.07591074	-0.2517883	0.59487273	0.97467485	0.48585008
ETV6(+)	-0.1824806	-0.1597766	-0.1953703	0.9912805	0.97467485	0.94813667
CREB3L2(+)	-0.2167737	0.21951234	-0.3563049	0.43713168	0.97467485	0.42434744
NFIC(+)	-0.2244983	-0.1296657	-0.2759506	0.9912805	0.97467485	0.96988529
IKZF1(+)	-0.2667396	-0.1500661	-0.311221	0.07956015	0.97467485	0.10560316
HSF1(+)	-0.2683616	-0.2271924	-0.2722753	0.76511823	0.97467485	0.73816027
FOXN3(+)	-0.2884353	-0.6136788	-0.2010742	0.27486827	0.97467485	0.28402905
ZFP64(+)	-0.2981261	-0.9438932	-0.1412767	0.54633488	0.97467485	0.42434744
NFKB1(+)	-0.3013876	-0.0086007	-0.3880634	0.66164427	0.97467485	0.89683736
ETV5(+)	-0.3044106	-0.2195474	-0.3363079	0.27450036	0.97467485	0.32176868
ARID3A(+)	-0.307664	-0.6871728	-0.2397952	0.9912805	0.97467485	0.94813667
MLXIP(+)	-0.3099508	-0.3044689	-0.3154865	0.59487273	0.97467485	0.62098903
STAT3(+)	-0.3164198	-0.2746324	-0.3433149	0.59487273	0.97467485	0.57081476
STAT2(+)	-0.3303284	-0.2750332	-0.3669335	0.64681448	0.97467485	0.49912669
FOXJ3(+)	-0.332092	0.4673816	-0.5369262	0.08141195	0.97467485	0.08633399
IRF5(+)	-0.347826	0.05761403	-0.4531933	0.0356462	0.7261037	0.10549339
ZNF143(+)	-0.4146618	-0.3139585	-0.4484589	0.00440811	0.7261037	0.00992806
XBP1(+)	-0.4238661	0.15419508	-0.5929116	0.52975368	0.97467485	0.45732278
ZBTB7A(+)	-0.4248297	0.54752224	-0.7245477	0.39902105	0.97467485	0.41898923
BACH1(+)	-0.4719341	-0.2541694	-0.5469609	0.67759371	0.97467485	0.59667177
POU2F1(+)	-0.5139362	-0.296377	-0.5617591	0.90582018	0.97467485	0.94813667
KLF3(+)	-0.5186406	-0.3177074	-0.5871817	0.89322805	0.97467485	0.95480033
IRF8(+)	-0.5311481	-0.4502079	-0.5697692	0.55317162	0.97467485	0.48585008
RUNX1(+)	-0.5924371	-0.4981864	-0.6436958	0.1091573	0.7261037	0.28778871
UBP1(+)	-0.6423118	-0.6243985	-0.6402247	0.78416308	0.97467485	0.84048852
SREBF2(+)	-0.6639154	-1.0087635	-0.6070903	0.28453093	0.97467485	0.37470741
POU2F2(+)	-0.7072758	-0.4800982	-0.7968847	0.28453093	0.97467485	0.1774802
HIVEP2(+)	-0.7301093	-1.3181973	-0.5774123	0.0784512	0.7261037	0.2291726
SREBF1(+)	-0.7811151	-0.5683558	-0.8663342	0.59487273	0.97467485	0.3726643
ARNTL(+)	-0.7990533	-1.9337246	-0.5234954	0.90582018	0.97467485	0.9590013
ATF4(+)	-0.8791908	1.13293311	-1.4687331	0.72664204	0.97467485	0.89683736
CTCF(+)	-0.8844259	-0.3764021	-1.0658722	0.9229002	0.97467485	0.95480033
RBPJ(+)	-0.9343975	-0.6561521	-1.0593962	0.68889642	0.97467485	0.73816027
STAT1(+)	-1.0944054	-1.0841363	-1.1431256	0.85163063	0.97467485	0.94813667
SMAD3(+)	-1.1561728	-0.4335327	-1.3778226	0.9229002	0.97721345	0.91631633
BCL6(+)	-1.4812539	-1.3954052	-1.5625628	0.67759371	0.97467485	0.84048852
SOX5(+)	-1.8151461	-2.5669701	-1.8133615	0.92540241	0.97467485	0.96988529

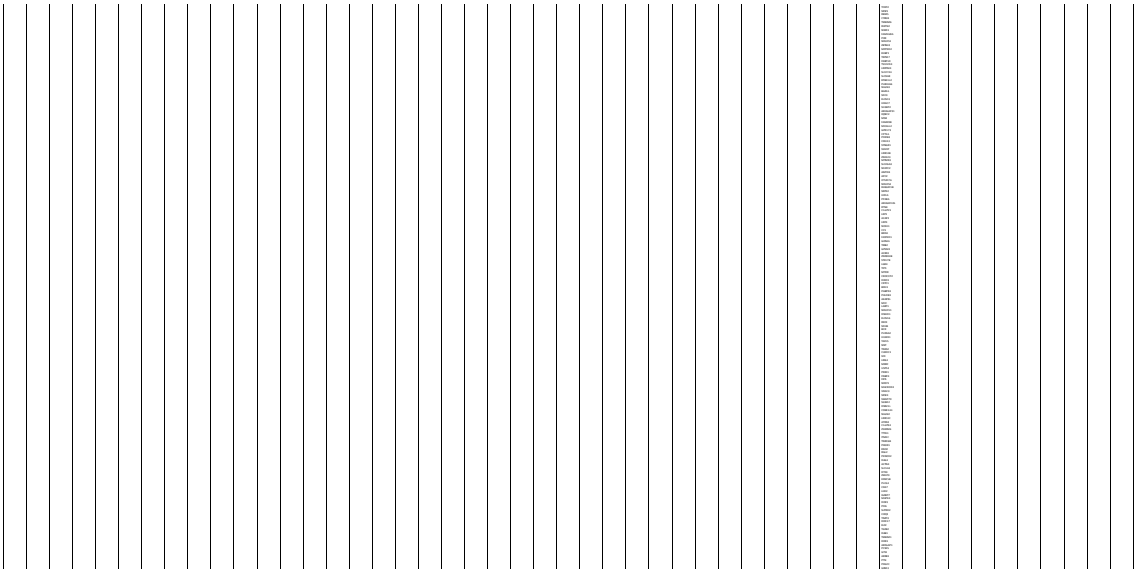
Abbreviations:
EC+SSC. enriched data integrated from the entrorhinal and somatosensory cortices
EC, enriched data integrated from the entrorhinal cortex only
SSC, enriched data integrated from the somatosensory cortex only
logFC, log base 2 fold-enrichment
adj P, p-statistic adjusted (corrected) for multiple comparisons

Supplementary Table 12_Astrocyte SCENIC Regulons
Contents

Sheet name	Description
Regulon_list	SCENIC Regulons in Astrocytes
Pathology_correlation	logFC of the enrichment (AUCell and limma) of regulons with amyloid-beta and pTau pathology
Enrichment_other_datasets	logFC of the enrichment (AUCell and limma) of regulons in AD samples compared to Control samples from previous studies
RSS	Regulon specificity scores (RSS) in astrocytic subclusters

Supplementary Table 12_Astrocyte SCENIC Regulons
Regulon list





Supplementary Table 12_Astrocyte SCENIC Regulons
Pathology correlation

Positive logFC values indicate a higher enrichment with pathology

Amyloid-pathology

	logFC	P.Value	adj.P.Val
ATF6(+)	-0.45162152	0.219807276	0.75909415
BACH1(+)	0.99991124	0.158862425	0.661926769
BACH2(+)	-0.38848501	0.289373889	0.761510236
BHLHE40(+)	-0.06283222	0.943278342	0.980735587
CEBPB(+)	1.758833	0.005845092	0.097418201
CEBPD(+)	0.14538103	0.739029283	0.948721863
CREB1(+)	-0.17390851	0.806523052	0.951492609
CREM(+)	-0.10338278	0.8753732	0.951492609
CUX1(+)	0.80510524	0.042307514	0.30219653
ELF1(+)	0.29067097	0.500071801	0.833453001
ELF2(+)	-0.21557322	0.718945682	0.948721863
EMX2(+)	0.35011247	0.482105905	0.833453001
EPAS1(+)	0.08711177	0.865413844	0.951492609
ETV6(+)	-0.45611834	0.421836048	0.823682038
FOS(+)	0.60594817	0.281516649	0.761510236
FOXN3(+)	0.56199519	0.086326462	0.479591458
FOXO1(+)	0.15990684	0.609672646	0.948721863
FOXO3(+)	0.12676411	0.710487684	0.948721863
HSF4(+)	0.6015534	0.39866643	0.823682038
IRF2(+)	-0.30394561	0.474705582	0.833453001
JUN(+)	0.69983929	0.227728245	0.75909415
JUNB(+)	0.11473851	0.802100389	0.951492609
JUND(+)	1.80125266	0.007974718	0.099683973
KDM5B(+)	-0.43240535	0.42831466	0.823682038
KLF12(+)	-0.12379047	0.854263701	0.951492609
LHX2(+)	0.54559942	0.287951622	0.761510236
MAF(+)	1.78283311	7.79572E-06	0.000194893
MAFG(+)	2.16043704	8.35599E-08	4.178E-06
MAX(+)	0.31199521	0.641374857	0.948721863
MXI1(+)	0.5280923	0.074101962	0.463137264
MZF1(+)	0.14432977	0.834651429	0.951492609
NFIC(+)	0.74866007	0.129499329	0.647496645
NR3C1(+)	-0.17442311	0.740003053	0.948721863
NRF1(+)	-0.12286888	0.705776875	0.948721863
POU3F2(+)	0.16422578	0.777708925	0.951492609
PPARA(+)	0.487788	0.403679752	0.823682038
RXRA(+)	1.58920745	0.021905717	0.18254764
SMAD1(+)	0.46997734	0.362203868	0.823682038
SREBF1(+)	-0.01081548	0.980735587	0.980735587
SREBF2(+)	0.00868384	0.980151455	0.980735587
STAT1(+)	-0.3849366	0.280741626	0.761510236
STAT2(+)	-0.02886683	0.96711018	0.980735587
STAT3(+)	0.34495275	0.375765428	0.823682038
STAT5B(+)	-0.39116367	0.491584816	0.833453001
TCF7L1(+)	0.34589348	0.72117034	0.948721863
THRA(+)	1.02025633	0.21763443	0.75909415
ZBTB7A(+)	1.7267681	0.011455425	0.114554252
ZEB1(+)	-0.2335462	0.385243804	0.823682038
ZIC2(+)	1.34603471	0.151556854	0.661926769
ZXDC(+)	0.40912944	0.540069218	0.871079384

pTau pathology

	logFC	P.Value	adj.P.Val
ATF6(+)	-0.57041255	0.071032684	0.240516557
BACH1(+)	0.176320553	0.772281594	0.826610214
BACH2(+)	-0.511676224	0.104056327	0.289045354
BHLHE40(+)	0.351459185	0.642941942	0.747606909
CEBPB(+)	1.990202098	0.000280022	0.003500274
CEBPD(+)	0.025557271	0.945612631	0.964910848
CREB1(+)	-0.227395766	0.709126012	0.787917792
CREM(+)	-0.500212289	0.376728012	0.570800018
CUX1(+)	0.096407136	0.777013601	0.826610214
ELF1(+)	-0.030671224	0.933939732	0.964910848
ELF2(+)	-0.384320963	0.454865986	0.631758314
EMX2(+)	0.509076703	0.233829826	0.433018196
EPAS1(+)	-0.533610219	0.226527986	0.433018196
ETV6(+)	-0.800528842	0.100558201	0.289045354
FOS(+)	0.868572951	0.072154967	0.240516557
FOXN3(+)	0.160193988	0.56904448	0.7113056
FOXO1(+)	-0.144732495	0.59039383	0.719992475
FOXO3(+)	-0.400029345	0.172409608	0.431024019
HSF4(+)	1.199175857	0.05001219	0.240516557
IRF2(+)	-0.44877328	0.218901785	0.433018196
JUN(+)	1.055341374	0.034104515	0.238587522
JUNB(+)	0.42376979	0.280922056	0.468203426
JUND(+)	2.173195207	0.000192441	0.00320735
KDM5B(+)	-0.359905597	0.442515575	0.631758314
KLF12(+)	-0.223437301	0.69935643	0.787917792
LHX2(+)	0.28020649	0.524974605	0.697739308
MAF(+)	1.78115629	1.9626E-07	4.9065E-06
MAFG(+)	2.022556267	5.08773E-09	2.54386E-07
MAX(+)	1.013117875	0.078098786	0.244058705
MXI1(+)	0.30226499	0.233758063	0.433018196
MZF1(+)	0.74897426	0.207031397	0.433018196
NFIC(+)	0.636896113	0.133008821	0.350023214
NR3C1(+)	-0.473848116	0.293655041	0.473637163
NRF1(+)	-0.311368313	0.265088596	0.466765198
POU3F2(+)	0.254191082	0.610763365	0.727099244
PPARA(+)	0.314315368	0.530801873	0.697739308
RXRA(+)	1.50050287	0.011709091	0.117090913
SMAD1(+)	0.268524609	0.54423666	0.697739308
SREBF1(+)	0.297968938	0.438396853	0.631758314
SREBF2(+)	-0.330031289	0.270723815	0.466765198
STAT1(+)	-0.616961538	0.044029224	0.240516557
STAT2(+)	0.534354658	0.373956868	0.570800018
STAT3(+)	0.003497443	0.991653925	0.991653925
STAT5B(+)	-1.012107233	0.038174004	0.238587522
TCF7L1(+)	0.992175592	0.233066438	0.433018196
THRA(+)	1.340088381	0.0592611	0.240516557
ZBTB7A(+)	1.415058587	0.015796304	0.131635865
ZEB1(+)	-0.4276533	0.064022153	0.240516557
ZIC2(+)	1.511918955	0.060612178	0.240516557
ZXDC(+)	0.694945043	0.225396939	0.433018196

Supplementary Table 12_Astrocyte SCENIC Regulons Enrichment other datasets

Positive logFC values indicate a higher enrichment in AD compared to Control

Grubman et al 2019, doi: 10.1038/s41593-019-0539-4

GRUBMAN	logFC	P.Value	adj.P.Val
ARNT(+)	0.099637423	0.06670431	0.08923956
ATF1(+)	0.403615878	9.0133E-05	0.00016224
ATF6(+)	-0.032999094	0.09231015	0.1218494
ATF6B(+)	0.753332036	3.1243E-44	2.2094E-43
BACH1(+)	0.152486433	0.00051193	0.00085901
BACH2(+)	0.049450116	0.00658435	0.00972911
BBX(+)	0.050759644	0.48896712	0.53195324
BHLHE40(+)	0.250459801	4.97E-09	1.2616E-08
BHLHE41(+)	-0.178596727	0.00045069	0.00078278
CEBPB(+)	0.270356694	1.0841E-25	5.1108E-25
CEBPD(+)	0.457086159	1.5095E-92	2.9889E-91
CLOCK(+)	0.075822984	0.33739066	0.39579554
CREB1(+)	-0.252264013	6.1005E-08	1.438E-07
CREB3L2(+)	-0.151450128	4.8765E-05	8.9403E-05
CREM(+)	0.005267521	0.85377626	0.8713799
CUX1(+)	-0.104720305	2.188E-07	4.8136E-07
DEAF1(+)	-0.076547378	0.40836097	0.45424423
E2F3(+)	-0.084709901	0.49764045	0.53550439
ELF1(+)	0.166675132	6.443E-11	1.7737E-10
ELF2(+)	0.223771354	1.8462E-07	4.1539E-07
EMX2(+)	-0.08611705	4.4581E-05	8.3274E-05
EPAS1(+)	-0.168100668	6.6869E-13	2.0193E-12
ETV6(+)	0.153551284	1.3225E-06	2.7276E-06
FOS(+)	0.445049944	1.4497E-86	2.392E-85
FOXG1(+)	-0.203036242	0.00793911	0.01155841
FOXJ3(+)	0.071442645	0.27881468	0.33661773
FOXK1(+)	0.446910601	0.44998-11	1.7737E-10
FOXN2(+)	0.009403536	0.95286647	0.95286647
FOXN3(+)	-0.18543951	6.3932E-37	3.5163E-36
FOXO1(+)	-0.264935027	8.0329E-70	9.9407E-69
FOXO3(+)	-0.198201466	6.3729E-28	3.1546E-27
GABPA(+)	0.052719853	0.37199355	0.42822514
HMGN3(+)	-0.024483095	0.7682069	0.80055245
HSF4(+)	0.437984447	1.4975E-39	8.7209E-39
IRF2(+)	-0.128854362	2.9555E-07	6.2254E-07
JDP2(+)	0.555903253	9.7447E-40	6.0295E-39
JUN(+)	0.44783139	2.5426E-94	6.293E-93
JUNB(+)	0.378150695	1.0004E-77	1.4148E-76
JUND(+)	0.432033001	3.9342E-69	4.3276E-68
KDM5B(+)	-0.086590118	0.00969577	0.01371259
KLF12(+)	-0.134129894	0.00131579	0.00206766
KLF15(+)	0.371934596	2.3843E-08	5.7573E-08
LHX2(+)	-0.365828214	2.3737E-52	1.9583E-51
MAF(+)	0.255201659	1.9628E-42	1.2954E-41
MAFG(+)	0.321747135	1.0735E-62	1.0628E-61
MAX(+)	0.230298643	2.1668E-17	7.6611E-17
MEF2C(+)	-0.361546742	4.1358E-06	7.8739E-06
MXI1(+)	-0.109767821	7.1324E-16	2.3537E-15
MZF1(+)	0.204920021	3.2461E-16	1.1081E-15
NFE2L2(+)	0.05395254	0.3274823	0.39061142
NFIA(+)	-0.112524851	5.3762E-09	1.3306E-08
NFIB(+)	-0.366955829	5.4751E-23	2.0848E-22
NFIC(+)	0.603585939	2.909E-131	1.44E-129
NFIX(+)	0.357705201	0.00017135	0.00030293
NFKB1(+)	-0.078864974	0.37766786	0.42975998
NR3C1(+)	-0.115071739	0.00050081	0.00085483
NRF1(+)	-0.081664133	3.961E-06	7.84E-06
PBX3(+)	-0.137820485	0.10539579	0.13729189
PKNOX2(+)	-0.025598301	0.73201287	0.77094972
POU2F1(+)	-0.609346025	5.6001E-25	2.4105E-24
POU3F2(+)	-0.266582154	5.404E-20	1.9815E-19
POU6F2(+)	-1.171524738	2.138E-147	2.117E-145
PPARA(+)	0.174756666	4.306E-11	1.2538E-10
PRDM16(+)	-0.20504553	0.0006157	0.00099925
PRRX1(+)	0.717320176	2.8806E-29	6.6725E-29
RFX3(+)	-0.03551014	0.18523593	0.23510714
RFX7(+)	-0.186002618	0.02833216	0.03842307
RREB1(+)	0.1266868	0.02521497	0.03467059
RXRA(+)	0.203622008	1.394E-07	3.2095E-07
SETBP1(+)	-0.253136706	0.00502619	0.00753928
SMAD1(+)	0.296187188	6.6613E-15	2.1273E-14
SMAD3(+)	-0.022737216	0.86461844	0.87344108
SMAD5(+)	-0.097435427	0.16476357	0.21183887
SOX9(+)	-0.014441699	0.83892965	0.8651462
SP3(+)	0.064288192	0.40019245	0.45021651
SP4(+)	0.198864425	0.01586805	0.02212587
SREBF1(+)	-0.011754792	0.44361511	0.48797662
SREBF2(+)	-0.010688691	0.33982445	0.39579554
STAT1(+)	0.103414606	6.7312E-13	2.0193E-12
STAT2(+)	0.2085996	1.1028E-10	2.9508E-10
STAT3(+)	0.411479394	3.47E-123	1.145E-121
STAT5B(+)	0.225061716	2.5514E-10	6.6472E-10
TCF7L1(+)	0.283555117	2.7504E-07	5.9192E-07
TEAD1(+)	-0.112395675	0.00198969	0.0030778
TFCP2(+)	-0.082539542	0.20633408	0.25533842
TFDP2(+)	0.219861425	0.008476	0.01216122
THRA(+)	0.379336245	9.5484E-24	3.9387E-23
THRB(+)	-0.192886515	1.8218E-06	3.6808E-06
USF2(+)	0.472102048	1.3664E-23	5.4108E-23
YY1(+)	0.28901439	0.00083578	0.00133456
ZBTB7A(+)	0.539088469	4.4906E-55	4.0416E-54
ZEB1(+)	-0.125726264	3.9994E-25	1.7997E-24
ZIC2(+)	0.146935276	0.0005497	0.00090701
ZNF148(+)	0.119343492	0.24641617	0.30117532
ZNF33A(+)	0.354956205	0.00420087	0.00639824
ZNF345(+)	0.157952498	4.1151E-06	7.8739E-06
ZNF721(+)	-0.075086975	0.19302271	0.24188922
ZNF770(+)	-0.036472113	0.56913137	0.60584952
ZXDC(+)	0.555858781	8.6193E-46	6.5639E-45

Mathys et al 2019, doi: 10.1038/s41586-019-1195-2

MATHYS	logFC	P.Value	adj.P.Val
ARNT(+)	-0.0513575	0.03274419	0.06233989
ATF1(+)	0.05012142	0.37212823	0.45489012
ATF6(+)	-0.0460846	5.4051E-05	0.00025481
ATF6B(+)	-0.0154542	0.71315468	0.75124361
BACH1(+)	0.04535955	0.02905056	0.05639227
BACH2(+)	-0.0230165	0.0383135	0.07046316
BBX(+)	-0.0224825	0.52319967	0.59536515
BHLHE40(+)	-0.0059154	0.77761446	0.78814403
BHLHE41(+)	0.02875962	0.34290567	0.42971723
CEBPB(+)	0.11311205	1.7831E-12	1.6048E-11
CEBPD(+)	0.07791874	1.2009E-10	9.1452E-10
CLOCK(+)	-0.0688829	0.08608803	0.1311187
CREB1(+)	-0.0908631	0.00013122	0.00059048
CREB3L2(+)	0.01195983	0.56104952	0.63118071
CREM(+)	-0.0169849	0.33283978	0.42245049
CUX1(+)	-0.0225654	0.0436885	0.0786393
DEAF1(+)	0.12416097	0.02611353	0.05289591
E2F3(+)	0.0415936	0.50999615	0.5870886
ELF1(+)	0.0243389	0.07398886	0.12008027
ELF2(+)	-0.0471562	0.01590181	0.03577907
EMX2(+)	0.01962576	0.14015531	0.19542783
EPAS1(+)	-0.0357213	0.00509574	0.01363455
ETV6(+)	-0.0095945	0.61415834	0.66815029
FOS(+)	0.09803913	1.3174E-14	1.3043E-13
FOXG1(+)	-0.1005859	0.02282636	0.04912629
FOXJ3(+)	0.02497975	0.46684271	0.55683649
FOXK1(+)	0.05299688	0.06699784	0.11362454
FOXN2(+)	-0.0694849	0.27890065	0.35858655
FOXN3(+)	-0.0235211	0.01144434	0.0276339
FOXO1(+)	-0.0269052	0.00497472	0.01363455
FOXO3(+)	-0.0427969	2.0949E-05	0.00010915
GABPA(+)	5.4666E-05	0.99868362	0.99868362
HMGN3(+)	0.07480058	0.10368631	0.15552947
HSF4(+)	0.12346621	9.149E-12	7.5483E-11
IRF2(+)	-0.0325936	0.01875105	0.04235231
JDP2(+)	0.10339218	0.00022449	0.00096627
JUN(+)	0.10140345	3.8295E-17	7.1455E-16
JUNB(+)	0.06362295	2.2657E-08	1.4019E-07
JUND(+)	0.14725293	1.5893E-26	1.5734E-24
KDM5B(+)	-0.043344	0.0135902	0.03203405
KLF12(+)	-0.0390356	0.0637498	0.11072333
KLF15(+)	0.08633113	0.01568033	0.03577907
LHX2(+)	-0.0229024	0.08197279	0.12680166
MAF(+)	0.11686089	6.0835E-19	2.0075E-17
MAFG(+)	0.10396709	2.6059E-16	3.6855E-15
MAX(+)	0.01815821	0.24274635	0.31620906
MEF2C(+)	-0.0692448	0.07012819	0.11571151
MXI1(+)	0.01657382	0.07677374	0.12064444
MZF1(+)	0.05257169	0.00042141	0.00166877
NFE2L2(+)	-0.0177794	0.50128138	0.58384537
NFIA(+)	-0.0156774	0.19231585	0.25728743
NFIB(+)	-0.0095895	0.62738114	0.67511666
NFIC(+)	0.12059472	3.6127E-18	8.9415E-17
NFIX(+)	0.06016597	0.14822316	0.20380684
NFKB1(+)	-0.0325809	0.48622488	0.57305075
NR3C1(+)	-0.042584	0.00958817	0.02273071
NRF1(+)	0.01286619	0.01728607	0.03577907
PBX3(+)	0.04352235	0.36953667	0.45489012
PKNOX2(+)	-0.0276221	0.44332393	0.53523255
POU2F1(+)	-0.0975655	0.00044656	0.00170036
POU3F2(+)	0.02310722	0.12211329	0.17778259
POU6F2(+)	-0.0951587	2.2581E-05	0.00011177
PPARA(+)	0.02267829	0.10567338	0.15614425
PRDM16(+)	-0.1498858	6.56E-10	4.6389E-09
PRRX1(+)	0.28419233	4.3306E-17	7.145E-16
RFX3(+)	0.05025817	0.00489446	0.01363455
RFX7(+)	0.05386826	0.21448133	0.28311535
RREB1(+)	-0.0071858	0.76254806	0.78637768
RXRA(+)	0.09781833	1.39E-06	7.645E-06
SETBP1(+)	-0.0951111	0.03843445	0.07046316
SMAD1(+)	0.02751199	0.12610138	0.17834338
SMAD3(+)	0.03961851	0.5806393	0.64589595
SMAD5(+)	-0.0689737	0.06771563	0.11362454
SOX9(+)	0.08440947	0.02618081	0.05289591
SP3(+)	-0.1086029	0.00489485	0.01363455
SP4(+)	-0.0150003	0.71534387	0.75124361
SREBF1(+)	0.03096675	0.00230477	0.00752308
SREBF2(+)	-0.0250162	0.00113714	0.00416953
STAT1(+)	0.00351939	0.72089033	0.75124361
STAT2(+)	0.05647531	0.00335287	0.01037295
STAT3(+)	0.03410735	0.00226824	0.00752308
STAT5B(+)	-0.0658069	0.00024597	0.00101463
TCF7L1(+)	0.07776278	0.00392699	0.01178096
TEAD1(+)	0.03583915	0.06359673	0.11072333
TFCP2(+)	-0.0448445	0.15138684	0.20530543
TFDP2(+)	0.12872399	0.00235571	0.00752308
THRA(+)	0.1668959	5.3795E-15	6.6571E-14
THRB(+)	0.03333472	0.12442268	0.17834338
USF2(+)	0.21006943	8.0977E-15	8.9075E-14
YY1(+)	0.11526984	0.02382517	0.05018494
ZBTB7A(+)	0.17845259	1.0402E-24	5.149E-23
ZEB1(+)	-0.0224368	0.00680966	0.01728607
ZIC2(+)	0.11303271	5.5966E-07	3.2592E-06
ZNF148(+)	-0.0253648	0.61144902	0.66815029
ZNF33A(+)	0.13760966	0.02818454	0.05580539
ZNF345(+)	0.03454877	0.07580805	0.12064444
ZNF721(+)	-0.0068647	0.78018298	0.78814403
ZNF770(+)	0.22323078	2.096E-09	1.3834E-08
ZXDC(+)	0.06033212	0.00229078	0.00752308

Zhou et al 2020, doi: 10.1038/s41591-019-0695-9

ZHOU	logFC	P.Value	adj.P.Val
ARNT(+)	-0.0483756	0.01157685	0.01380853
ATF1(+)	0.16509118	8.1903E-06	1.142E-05
ATF6(+)	-0.1674649	1.641E-95	6.0168E-95
ATF6B(+)	-0.0414888	0.00130865	0.00166098
BACH1(+)	0.0568632	0.00097246	0.00126675
BACH2(+)	-0.3208039	2.714E-264	3.359E-263
BBX(+)	0.01214617	0.64515708	0.65845929
BHLHE40(+)	-0.2931876	3.006E-185	1.984E-184
BHLHE41(+)	0.14083143	2.053E-24	4.065E-24
CEBPB(+)	-0.0088439	0.23625739	0.2514998
CEBPD(+)	-0.3651484	0	0
CLOCK(+)	-0.1628441	2.9681E-07	4.4521E-07
CREB1(+)	-0.0120692	0.3987012	0.41548861
CREB3L2(+)	-0.3096591	8.2363E-74	2.4709E-73
CREM(+)	-0.3534133	3.5107E-91	1.2413E-90
CUX1(+)	0.25121291	1.828E-104	6.962E-104
DEAF1(+)	-0.1446858	2.7243E-07	4.1493E-07
E2F3(+)	-0.101573	0.02447628	0.02817618
ELF1(+)	-0.0888424	9.3865E-16	1.5488E-15
ELF2(+)	-0.1426233	8.0995E-30	1.7061E-29
EMX2(+)	0.05643371	7.1396E-14	1.1587E-13
EPAS1(+)	-0.0267898	0.00843235	0.01018052
ETV6(+)	-0.523923	0	2.254E-307
FOS(+)	-0.2333446	1.742E-184	1.078E-183
FOXG1(+)	0.26180452	2.2093E-22	4.0505E-22
FOXJ3(+)	-0.3300446	2.2257E-24	4.3206E-24
FOXK1(+)	-0.3080829	2.1583E-33	4.7482E-33
FOXN2(+)	0.09757945	0.04426168	0.0492349
FOXN3(+)	0.24615805	6.75E-150	3.713E-149
FOXO1(+)	0.1890049	2.8586E-86	9.129E-86
FOXO3(+)	-0.0048318	0.60922688	0.62826522
GABPA(+)	-0.0589419	0.00098979	0.00127259
HMGN3(+)	0.19413097	1.1949E-22	2.2749E-22
HSF4(+)	0.14383821	1.5608E-49	3.6789E-49
IRF2(+)	-0.0311396	0.00802122	0.00980372
JDP2(+)	0.11615516	5.1704E-20	9.3067E-20
JUN(+)	-0.1761119	1.791E-137	8.443E-137
JUNB(+)	-0.2137826	4.976E-230	4.927E-229
JUND(+)	0.07972626	9.0689E-30	1.8705E-29
KDM5B(+)	-0.000649	0.95544618	0.95544618
KLF12(+)	0.32226108	1.0505E-70	3.0588E-70
KLF15(+)	0.51780642	7.185E-130	3.233E-129
LHX2(+)	0.30382553	3.909E-160	2.277E-159
MAF(+)	0.23870648	1.868E-191	1.321E-190
MAFG(+)	0.21951602	4.551E-211	3.754E-210
MAX(+)	-0.0930961	1.9629E-32	4.2246E-32
MEF2C(+)	0.44726332	3.3706E-48	7.7603E-48
MXI1(+)	0.19964038	4.821E-129	2.075E-128
MZF1(+)	0.13140432	9.1437E-57	2.3211E-56
NFE2L2(+)	-0.1705761	1.4527E-22	2.7135E-22
NFIA(+)	-0.2066143	3.8036E-65	1.0759E-64
NFIB(+)	0.57391109	1.932E-148	1.007E-147
NFIC(+)	0.19150425	4.038E-106	1.599E-105
NFIX(+)	0.15191031	6.3324E-05	8.4717E-05
NFKB1(+)	-0.081234	0.04324681	0.04865266
NR3C1(+)	0.06860624	4.2031E-09	6.5016E-09
NRF1(+)	0.09156722	3.244E-29	6.554BE-29
PBX3(+)	-0.1831816	3.9131E-07	5.782E-07
PKNOX2(+)	-0.6214379	2.8351E-86	9.129E-86
POU2F1(+)	0.10267349	2.3936E-05	3.2911E-05
POU3F2(+)	0.34508937	2.887E-200	2.199E-199
POU6F2(+)	0.36667986	1.5946E-51	3.8503E-51
PPARA(+)	0.42346995	9.954E-217	8.959E-216
PRDM16(+)	0.41155434	1.5156E-75	4.6889E-75
PRRX1(+)	-0.3644761	3.8383E-63	1.0555E-62
RFX3(+)	-0.0285815	0.14997464	0.16138575
RFX7(+)	0.00956211	0.8518988	0.86059165
RREB1(+)	0.05265918	0.02585397	0.02942003
RXRA(+)	0.32607111	1.112E-124	4.586E-124
SETBP1(+)	-0.1973559	6.8711E-06	9.7177E-06
SMAD1(+)	-0.172341	7.056E-38	1.5876E-37
SMAD3(+)	-0.2854402	2.7983E-06	3.6181E-06
SMAD5(+)	-0.0454626	0.14213067	0.15462567
SOX9(+)	0.0721737	5.0791E-05	6.8881E-05
SP3(+)	-0.041772	0.04755104	0.05230614
SP4(+)	-0.0726088	0.00788992	0.00976377
SREBF1(+)	0.11331938	3.6763E-59	9.5777E-59
SREBF2(+)	0.05190171	9.0821E-17	1.5502E-16
STAT1(+)	-0.3647124	0	0
STAT2(+)	-0.033852	6.4181E-05	8.4719E-05
STAT3(+)	-0.3251187	0	0
STAT5B(+)	-0.6497243	0	0
TCF7L1(+)	-0.0234106	0.28737942	0.30266556
TEAD1(+)	0.15850693	2.1905E-16	3.6756E-16
TFCP2(+)	-0.0593879	0.02146243	0.02499742
TFDP2(+)	0.18899464	9.3787E-10	1.4976E-09
THRA(+)	0.41615045	1.302E-275	2.149E-274
THRB(+)	0.24770037	6.2178E-19	1.0992E-18
USF2(+)	0.31409827	3.571E-140	1.767E-139
YY1(+)	0.14724206	2.8989E-09	4.5554E-09
ZBTB7A(+)	0.43140901	3.517E-254	3.869E-253
ZEB1(+)	-0.0572443	6.3665E-18	1.1058E-17
ZIC2(+)	0.48401403	4.463E-273	6.312E-272
ZNF148(+)	0.0990596	0.01943571	0.02290637
ZNF33A(+)	-0.1366392	0.00267753	0.00335538
ZNF345(+)	-0.2324251	4.7588E-63	1.2733E-62
ZNF721(+)	-0.144385	5.3929E-06	7.7377E-06
ZNF770(+)	0.35986503	2.2879E-55	5.6626E-55
ZXDC(+)	0.24440378	4.7042E-89	1.6059E-88

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GERRITS	logFC	P.Value	adj.P.Val
ARNT(+)	0.04693601	8.1177E-39	1.2364E-38
ATF1(+)	0.00336404	0.70520533	0.7124013
ATF6(+)	0.03833862	2.551E-101	4.952E-101
ATF6B(+)	0.1755939	0	0
BACH1(+)	-0.023392	8.4005E-13	1.0396E-12
BACH2(+)	0.05826938	2.139E-220	6.051E-220
BBX(+)	0.18591219	9.482E-226	2.761E-225
BHLHE40(+)	0.21926047	0	0
BHLHE41(+)	0.05410382	5.7723E-11	7.0551E-11
CEBPB(+)	0.263355	0	0
CEBPD(+)	0.16662419	0	0
CLOCK(+)	0.13318645	5.4874E-84	1.006E-83
CREB1(+)	0.03367205	8.6346E-20	1.171E-19
CREB3L2(+)	0.06883034	2.605E-105	5.372E-105
CREM(+)	0.06472286	3.708E-103	7.492E-103
CUX1(+)	-0.0737991	0	0
DEAF1(+)	0.20198425	1.7443E-61	2.9774E-61
E2F3(+)	-0.0297835	0.00822882	0.0090517
ELF1(+)	0.0760994	0	0
ELF2(+)	0.07425305	2.857E-113	6.149E-113
EMX2(+)	-0.0313412	3.6098E-39	5.5839E-39
EPAS1(+)	-0.07252	3.372E-155	8.142E-155
ETV6(+)	0.0881641	1.314E-212	3.613E-212
FOS(+)	0.18715497	0	0
FOXG1(+)	0.02638735	0.00816198	0.0090517
FOXJ3(+)	0.07512645	3.827E-56	6.2122E-56
FOXK1(+)	0.06843595	2.346E-71	4.0748E-71
FOXN2(+)	0.00012198	0.99143649	0.99143649
FOXN3(+)	-0.1250162	0	0
FOXO1(+)	-0.0595664	1.779E-265	5.68E-265
FOXO3(+)	-0.0602744	2.073E-284	6.84E-284
GABPA(+)	0.06800626	9.5604E-22	1.3146E-21
HMGN3(+)	0.18663302	3.2372E-88	6.0469E-88
HSF4(+)	0.00201914	0.53339708	0.55006574
IRF2(+)	-0.0117966	1.1748E-09	1.4184E-09
JDP2(+)	0.07416071	4.626E-110	9.744E-110
JUN(+)	0.21095065	0	0
JUNB(+)	0.18038256	0	0
JUND(+)	0.17874921	0	0
KDM5B(+)	0.01133517	4.9206E-05	5.731E-05
KLF12(+)	-0.154334	0	0
KLF15(+)	-0.267195	1.431E-290	4.887E-290
LHX2(+)	-0.1607619	0	0
MAF(+)	0.02925182	1.0121E-37	1.4735E-37
MAFG(+)	-0.0020431	0.32474561	0.33841911
MAX(+)	0.15975549	0	0
MEF2C(+)	-0.2148801	3.316E-140	7.461E-140
MXI1(+)	-0.0672971	0	0
MZF1(+)	-0.0180369	3.0694E-09	3.6175E-09
NFE2L2(+)	0.11166843	2.134E-143	4.912E-143
NFIA(+)	0.04380959	6.766E-118	1.489E-117
NFIB(+)	-0.0416796	1.498E-38	2.247E-38
NFIC(+)	-0.0173671	5.1315E-15	6.4306E-15
NFIX(+)	0.06236265	7.3728E-18	9.4793E-18
NFKB1(+)	0.11971257	1.3746E-53	2.195E-53
NR3C1(+)	0.04890163	1.1212E-71	1.9821E-71
NRF1(+)	-0.0060071	5.7148E-05	6.6787E-05
PBX3(+)	0.07524011	1.2559E-19	1.6578E-19
PKNOX2(+)	-0.0074434	0.17005593	0.18102728
POU2F1(+)	-0.0537913	1.4103E-27	1.9664E-27
POU3F2(+)	-0.1206947	0	0
POU6F2(+)	-0.2514792	0	0
PPARA(+)	-0.2560576	0	0
PRDM16(+)	-0.1975164	0	0
PRRX1(+)	0.3724188	0	0
RFX3(+)	0.085583	1.166E-243	3.497E-243
RFX7(+)	0.08066767	6.9103E-31	9.9148E-31
RREB1(+)	-0.0530798	1.0733E-60	1.771E-60
RXRA(+)	-0.2191548	0	0
SETBP1(+)	-0.2044357	5.573E-148	1.314E-147
SMAD1(+)	0.12359679	0	0
SMAD3(+)	-0.0139289	0.19755	0.20805798
SMAD5(+)	0.13920751	6.369E-102	1.261E-101
SOX9(+)	-0.0984124	4.4535E-30	6.2985E-30
SP3(+)	0.02171797	0.00140348	0.00157891
SP4(+)	-0.0135649	0.05616291	0.06043618
SREBF1(+)	-0.0634101	7.113E-258	2.201E-257
SREBF2(+)	-0.0745536	0	0
STAT1(+)	0.0874192	0	0
STAT2(+)	0.18519737	0	0
STAT3(+)	0.1108165	0	0
STAT5B(+)	0.0260669	1.0507E-19	1.4057E-19
TCF7L1(+)	0.07907627	6.6509E-74	1.1972E-73
TEAD1(+)	0.0012978	0.6512901	0.66471876
TFCP2(+)	-0.0639488	3.2637E-43	5.1287E-43
TFDP2(+)	0.06214607	7.0139E-19	9.1365E-19
THRA(+)	-0.1456633	3.741E-193	9.747E-193
THRB(+)	-0.0198954	1.7541E-09	2.0923E-09
USF2(+)	0.22629589	1.441E-194	3.856E-194
YY1(+)	0.18714004	8.706E-98	1.6575E-97
ZBTB7A(+)	-0.106719	7.195E-192	1.826E-191
ZEB1(+)	0.03240258	1.757E-186	4.35E-186
ZIC2(+)	-0.2464407	0	0
ZNF148(+)	0.07121422	8.1281E-17	1.0316E-16
ZNF33A(+)	0.12682515	9.4342E-38	1.394E-37
ZNF345(+)	0.13630409	0	0
ZNF721(+)	-0.056603	2.4703E-61	4.145E-61
ZNF770(+)	-0.0323917	0.0002215	0.00025205
ZXDC(+)	-0.0060479	0.04988431	0.05426974

Supplementary Table 12_Astrocyte SCENIC Regulons
Regulon specificity scores

Regulon specificity scores (RSS) in astrocytic subclusters

A high regulon specificity score indicates a relatively specific enrichment of this regulon for a particular subcluster

Regulon	Astro1	Astro2	Astro3	Astro4	Astro5	Astro6
ATF6(+)	0.399	0.378	0.325	0.323	0.287	0.211
BACH1(+)	0.397	0.386	0.316	0.331	0.275	0.209
BACH2(+)	0.400	0.377	0.324	0.326	0.285	0.210
BHLHE40(+)	0.378	0.363	0.316	0.335	0.310	0.215
CEBPB(+)	0.387	0.369	0.320	0.322	0.304	0.216
CEBPD(+)	0.388	0.368	0.322	0.330	0.306	0.213
CREB1(+)	0.399	0.378	0.326	0.317	0.287	0.213
CREM(+)	0.392	0.373	0.319	0.335	0.289	0.210
CUX1(+)	0.403	0.387	0.322	0.316	0.284	0.212
ELF1(+)	0.397	0.376	0.325	0.324	0.290	0.213
ELF2(+)	0.396	0.373	0.325	0.323	0.292	0.212
EMX2(+)	0.402	0.382	0.326	0.315	0.284	0.213
EPAS1(+)	0.404	0.392	0.319	0.329	0.268	0.206
ETV6(+)	0.393	0.373	0.321	0.336	0.287	0.210
FOS(+)	0.381	0.352	0.328	0.321	0.331	0.220
FOXN3(+)	0.407	0.386	0.327	0.309	0.283	0.210
FOXO1(+)	0.408	0.385	0.328	0.312	0.280	0.211
FOXO3(+)	0.407	0.388	0.325	0.318	0.277	0.209
HSF4(+)	0.390	0.365	0.329	0.311	0.309	0.217
IRF2(+)	0.403	0.381	0.327	0.314	0.285	0.211
JUN(+)	0.379	0.352	0.326	0.322	0.334	0.221
JUNB(+)	0.387	0.363	0.325	0.325	0.314	0.216
JUND(+)	0.378	0.354	0.326	0.311	0.335	0.223
KDM5B(+)	0.405	0.387	0.325	0.316	0.276	0.210
KLF12(+)	0.412	0.389	0.328	0.302	0.277	0.207
LHX2(+)	0.411	0.394	0.325	0.310	0.269	0.210
MAF(+)	0.397	0.372	0.328	0.307	0.304	0.217
MAFG(+)	0.396	0.375	0.324	0.311	0.301	0.215
MAX(+)	0.383	0.359	0.329	0.316	0.322	0.217
MXI1(+)	0.407	0.383	0.329	0.310	0.285	0.211
MZF1(+)	0.391	0.376	0.324	0.313	0.295	0.213
NFIC(+)	0.398	0.381	0.322	0.320	0.288	0.212
NR3C1(+)	0.404	0.384	0.325	0.317	0.279	0.210
NRF1(+)	0.404	0.385	0.326	0.316	0.282	0.210
POU3F2(+)	0.405	0.388	0.327	0.306	0.280	0.211
PPARA(+)	0.402	0.390	0.322	0.308	0.282	0.210
RXRA(+)	0.400	0.377	0.327	0.303	0.293	0.215
SMAD1(+)	0.394	0.366	0.330	0.316	0.305	0.215
SREBF1(+)	0.403	0.385	0.324	0.317	0.280	0.212
SREBF2(+)	0.405	0.391	0.322	0.320	0.275	0.209
STAT1(+)	0.397	0.376	0.322	0.331	0.287	0.210
STAT2(+)	0.391	0.370	0.326	0.315	0.305	0.215
STAT3(+)	0.391	0.373	0.320	0.334	0.296	0.211
STAT5B(+)	0.391	0.378	0.316	0.337	0.287	0.207
TCF7L1(+)	0.373	0.339	0.332	0.302	0.359	0.222
THRA(+)	0.395	0.382	0.322	0.307	0.288	0.214
ZBTB7A(+)	0.400	0.387	0.319	0.315	0.279	0.211
ZEB1(+)	0.403	0.380	0.327	0.319	0.285	0.212
ZIC2(+)	0.403	0.392	0.320	0.306	0.270	0.211
ZXDC(+)	0.393	0.377	0.324	0.315	0.297	0.213

Supplementary Table 13_Astrocyte cluster genes
Contents

Sheet name	Description
Astro1	Differentially expressed genes (logFC > 0.25, P-adj <0.05) for Astro1 relative to all other Astro clusters, as defined by the Seurat *FindMarkers* function
Astro2	Differentially expressed genes (logFC > 0.25, P-adj <0.05) for Astro2 relative to all other Astro clusters, as defined by the Seurat *FindMarkers* function
Astro3	Differentially expressed genes (logFC > 0.25, P-adj <0.05) for Astro3 relative to all other Astro clusters, as defined by the Seurat *FindMarkers* function
Astro4	Differentially expressed genes (logFC > 0.25, P-adj <0.05) for Astro4 relative to all other Astro clusters, as defined by the Seurat *FindMarkers* function
Astro5	Differentially expressed genes (logFC > 0.25, P-adj <0.05) for Astro5 relative to all other Astro clusters, as defined by the Seurat *FindMarkers* function
Astro6	Differentially expressed genes (logFC > 0.25, P-adj <0.05) for Astro6 relative to all other Astro clusters, as defined by the Seurat *FindMarkers* function

Supplementary Table 13_Astrocyte cluster genes
Astro1

Gene	avg_logFC	p_val_adj
RERG	0.29684099	1.35E-279
FLRT2	0.28478014	0
DNAH7	0.28422489	1.96E-292
CABLES1	0.28209448	0
SGCD	0.27450058	0
NRXN1	0.27272109	0
ARHGAP24	0.26907198	0
POU6F2	0.26181797	1.18E-180
LINC00499	0.2602252	4.74E-190
CADM2	0.25948372	0
GRM3	0.25762431	0
AL589740.1	0.25595053	3.46E-279
TMEM132C	0.25429668	1.08E-211
PFKFB2	-0.2511389	2.22E-111
ABCC4	-0.253958	2.72E-104
TPST1	-0.259964	4.47E-89
DPP6	-0.2642327	5.37E-26
MATN2	-0.2645049	2.51E-166
GAPDH	-0.2766599	1.07E-84
WWTR1	-0.2769047	1.73E-90
MIR4300HG	-0.2814228	5.48E-39
ID2	-0.2817003	4.45E-76
ELL2	-0.2905541	1.43E-68
FAM189A2	-0.2999035	1.38E-100
PRRX1	-0.3072259	3.73E-183
AEBP1	-0.308911	3.34E-113
EMP1	-0.3107057	3.58E-90
ST6GAL1	-0.3147696	3.68E-136
DPYSL3	-0.3148664	1.00E-168
MAP1B	-0.3179259	5.51E-128
AQP4-AS1	-0.319981	1.41E-95
DGKB	-0.3248432	9.78E-95
HSPB8	-0.3262352	5.74E-105
SERPINI2	-0.3279427	3.78E-224
JUN	-0.3285689	2.37E-212
PLCE1	-0.3289072	9.89E-254
HSPA1A	-0.3314112	5.35E-159
CADPS	-0.3355172	1.38E-53
ARHGEF3	-0.3435124	2.52E-181
NFASC	-0.3440142	4.67E-195
NAV1	-0.3440327	1.01E-245
ANGPT1	-0.344036	6.15E-193
CHI3L1	-0.3514119	2.22E-34
LINC01094	-0.3673278	1.09E-69
Mar-03	-0.3768537	7.48E-135
HSPB1	-0.3836295	7.09E-141
GFAP	-0.3883238	1.96E-284
FOS	-0.3888264	7.19E-218
CERS6	-0.3905995	1.40E-213
HSP90AA1	-0.4187353	6.13E-48
PLEKHA5	-0.4194401	1.17E-124
SMAD9	-0.4218731	0
WDR49	-0.4470404	2.75E-210
ANGPTL4	-0.4529078	1.37E-125
L3MBTL4	-0.4737575	0
UBC	-0.47741	2.92E-193
AQP1	-0.4936864	1.25E-252
MAN1C1	-0.4940081	1.09E-253
CRYAB	-0.5220387	1.68E-125
ADAMTS9-AS	-0.5390772	9.25E-275
GPC6	-0.5963237	0
VCAN	-0.6284829	0
AC073941.1	-0.6338867	0
SNED1	-0.6762329	0
KAZN	-0.7083128	2.37E-300
LINC00609	-0.7646815	2.17E-210
CD44	-0.8307474	0
DPP10	-0.9763978	0

Supplementary Table 13_Astrocyte cluster genes

Astro2

Gene	avg_logFC	p_val_adj
WIF1	0.65492732	0
ZNF98	0.5798912	0
HPSE2	0.54466465	0
SLC1A2	0.4953442	0
GRM3	0.478609	0
RIMS1	0.4720577	0
CALN1	0.45266267	0
ALK	0.44927651	0
SGCD	0.43219285	0
VAV3	0.39827846	0
PTN	0.38721275	0
COL5A3	0.38398238	0
PDE3B	0.38300902	0
PLCB1	0.36936899	0
DGKZ	0.35695577	0
ZNF804B	0.35607417	4.64E-235
KCNIP1	0.35549749	0
SLC4A4	0.35493798	0
HS3ST5	0.34630513	0
CACNB2	0.33255555	0
SPRY4-AS1	0.33030808	0
DLC1	0.329773	0
TBC1D4	0.32144272	0
CABLES1	0.3201073	0
HGF	0.31988012	0
F11-AS1	0.31963704	0
DACH1	0.31338279	0
SLC6A11	0.31335306	0
GLUL	0.31093295	0
ATP1A2	0.30468917	0
CADM1	0.28673064	0
MACROD2	0.28636389	1.48E-300
DGKG	0.28515612	0
ABCD2	0.27931218	0
ARHGAP24	0.27910631	0
MERTK	0.27568961	0
ZNF37BP	0.27528663	0
SLC6A1	0.27460921	0
ARHGAP29	0.26818284	0
LINC01414	0.26723716	4.06E-294
FRMD4A	0.26544646	0
GPC5	0.26408446	0
UNC5C	0.2603363	0
NRXN1	0.25596322	0
ATP1B2	0.25481095	0
RORB	0.25475714	0
AF123462.1	0.25391197	0
SYNE1	0.25207032	0
AC003991.1	0.25124723	1.74E-143
ZFP36L1	-0.2510429	1.14E-94
EMP1	-0.2523361	9.65E-30
S100B	-0.2529402	1.93E-53
FRMPD2	-0.2540806	1.85E-162
ELL2	-0.2543232	2.35E-31
PFKFB2	-0.2549368	1.41E-78
NHS	-0.2549637	2.53E-37
LAMA1	-0.2569462	8.64E-142
MAOB	-0.2603372	1.86E-39
SLC14A1	-0.261082	1.18E-110
FRMD5	-0.2627271	2.20E-45
ID2	-0.2633951	1.03E-18
JUN	-0.2670825	6.01E-74
HSPA1A	-0.2705962	1.13E-38
DPP6	-0.2706461	2.26E-15
PLEC	-0.2833481	5.95E-158
RHPN1	-0.2834412	3.11E-134
MT2A	-0.2837157	2.43E-53
SLC16A9	-0.2861326	1.28E-136
GMPR	-0.2862063	8.46E-141
LAMA4	-0.287502	6.33E-180
PHYHIPL	-0.2881038	5.81E-146
AHNAK	-0.2896777	6.84E-153
ATP9A	-0.2899755	5.70E-130
SYTL4	-0.2907164	7.25E-142
SLC24A4	-0.2948834	1.28E-145
NAV1	-0.2981707	2.36E-113
AL365295.1	-0.3103234	2.14E-92
CACNA2D3	-0.3119067	2.72E-59
CFAP54	-0.3165218	1.67E-149
DCLK2	-0.3228258	3.18E-261
ST6GAL1	-0.3284694	1.20E-114
ARHGEF4	-0.3342926	0
APP	-0.3344475	1.11E-214
SEMA6A	-0.338121	6.62E-241
ARHGEF3	-0.3405883	2.16E-168
HSPB1	-0.3434683	1.06E-46
PCLO	-0.3489165	1.48E-248
HSPB8	-0.3563586	2.01E-91
ABCC4	-0.3584624	6.71E-259
HSP90AA1	-0.3638285	1.93E-16
COL21A1	-0.3663509	7.48E-184
RNF19A	-0.3687813	7.51E-255
PLCE1	-0.3749008	3.26E-242
FAM189A2	-0.375516	1.13E-214
MAP1B	-0.3757787	3.04E-164
ITGB4	-0.3818375	0
NFASC	-0.3902335	6.48E-195
SNTB1	-0.418995	0
MAP2	-0.4208655	0
CFAP47	-0.424722	2.68E-295
PLXDC2	-0.4277555	1.23E-263
MIR4300HG	-0.4295616	4.25E-129
Mar-03	-0.4318213	1.98E-147
UBC	-0.4333512	1.55E-68
AEBP1	-0.4377071	3.39E-239
ADCY8	-0.4453766	0
PRRX1	-0.44648	6.62E-285
AKAP6	-0.4475283	9.45E-251
MAN1C1	-0.4625819	6.20E-175
CNKSR2	-0.4789366	0
LINC01094	-0.4899274	5.64E-179
ST6GALNAC3	-0.4907771	0
DLGAP1	-0.4946348	0
DGKB	-0.4983364	1.04E-242
ANGPT1	-0.5028028	0
CRYAB	-0.5077286	7.02E-78
GFAP	-0.52695	0
SERPINI2	-0.5372419	0
DPYSL3	-0.5686426	0
CERS6	-0.5714971	0
SMAD9	-0.5718598	0
AQP4-AS1	-0.5922584	0
ADAMTS9-AS	-0.5954555	4.54E-293
AQP1	-0.5998363	0
L3MBTL4	-0.6206266	0
GPC6	-0.6396942	0
PLEKHA5	-0.6875978	0
KAZN	-0.7648078	1.30E-258
SNED1	-0.7730962	0
WDR49	-0.7963966	0
AC073941.1	-0.8057698	0
CD44	-0.8422399	0
VCAN	-0.8834694	0
LINC00609	-0.9664157	0
DPP10	-1.9148781	0

Supplementary Table 13_Astrocyte cluster genes
Astro3

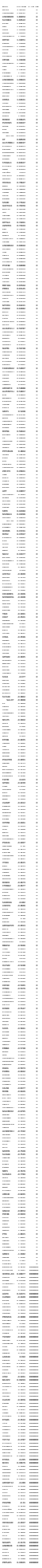
Gene	avg_logFC	p_val_adj
DPP10	0.58248357	0
MAP2	0.33495809	0
CNKSR2	0.3233228	0
MGAT4C	0.30422934	2.81E-300
AC002429.2	0.29220491	5.80E-81
AQP4-AS1	0.28821653	7.21E-161
ST6GALNAC3	0.28686822	4.28E-240
ETNPPL	0.26500617	2.69E-171
RNF219-AS1	0.25550643	1.10E-171
NKAIN3	0.25435679	2.68E-220
DLGAP1	0.2508893	3.88E-157
DPP6	-0.2535668	5.25E-16
SAMD4A	-0.2589852	1.55E-112
UBC	-0.2655249	1.42E-17
DGKZ	-0.2716033	1.17E-142
AC003991.1	-0.2785263	1.47E-44
CADPS	-0.2869106	1.62E-21
GRM3	-0.2913695	3.80E-98
SPRY4-AS1	-0.2936489	1.60E-176
KCNIP1	-0.2938827	8.92E-112
ZNF804B	-0.2952464	2.99E-59
HPSE2	-0.2963166	3.93E-121
SPOCK1	-0.3137926	5.44E-172
HGF	-0.3237446	3.24E-153
ZNF98	-0.3552462	7.64E-110
SGCD	-0.3584275	8.15E-220
KAZN	-0.3799848	1.84E-10
CD44	-0.3822105	2.81E-14
ALK	-0.4244611	8.42E-159
RIMS1	-0.4435366	1.28E-133
CALN1	-0.4721236	2.62E-253
WIF1	-0.4845366	0
CHI3L1	-0.6017334	1.35E-95

Supplementary Table 13_Astrocyte cluster genes

Astro4

Gene	avg_logFC	p_val_adj
CHI3L1	1.099981	0
ANGPTL4	0.6947	0
EMP1	0.68104	1.19E-278
CADPS	0.669407	2.72E-174
AC010655	0.590774	0
TPST1	0.575702	0
SAMD4A	0.559713	0
ARHGEF3	0.548585	0
ADAM12	0.535967	0
BAALC-AS:	0.530254	7.47E-248
ELL2	0.517997	7.18E-287
GNA14	0.489749	0
WWTR1	0.482654	2.67E-153
SLC44A3-A	0.481953	0
CLIC4	0.469592	0
ZFYVE28	0.458296	0
F3	0.457441	0
PKNOX2	0.430184	1.95E-229
CPNE8	0.396825	1.93E-202
IGFBP7	0.395763	0
ETV6	0.392431	1.65E-295
NAMPT	0.387313	9.15E-252
TRIO	0.38277	0
CD44	0.372877	0
BCL6	0.367725	0
ITPKC	0.365588	0
ZFP36	0.364134	0
OSMR	0.354067	0
MAPRE2	0.347255	3.40E-295
OSMR-AS1	0.339252	9.02E-257
FN1	0.337939	3.81E-115
VEGFA	0.337006	1.87E-97
AC099548	0.335416	0
GALNT16	0.334069	0
SLC39A14	0.331067	4.94E-272
PLSCR1	0.330662	4.09E-251
AC003991	0.328879	2.40E-49
MAPK4	0.327836	4.77E-201
NRCAM	0.326492	5.43E-191
NRP1	0.319093	6.42E-93
FAM189A2	0.317757	1.60E-66
DST	0.316717	7.67E-303
GADD45B	0.30733	0
EHBP1	0.306395	7.91E-27
COLEC12	0.304391	7.56E-170
KCND3	0.299463	1.14E-196
CLIP1	0.298869	2.70E-146
BCYRN1	0.298778	3.59E-52
TRIM9	0.298284	3.08E-162
TMTC1	0.296663	1.10E-92
YBX3	0.296054	5.74E-289
TENM4	0.294534	1.89E-215
ACTN1	0.292452	1.28E-261
DTNA	0.292322	0
PLOD2	0.290853	1.56E-122
SCARA3	0.289866	1.17E-229
ANO6	0.289833	5.32E-156
HAP1	0.289733	5.22E-210
MIR100HG	0.287583	1.06E-135
PFKFB3	0.28356	3.28E-255
LPP	0.280524	1.74E-127
ATP1B3	0.277559	1.26E-76
KCNQ3	0.275957	1.47E-81
BAALC	0.274295	8.25E-130
MACF1	0.273006	0
DIP2C	0.271649	3.92E-170
AL354740.	0.271204	3.40E-221
TMTC2	0.269528	2.29E-88
LIMS1	0.268972	2.29E-141
LRRC3B	0.267158	1.93E-127
GLIS3	0.266508	4.03E-75
FAM20C	0.265862	4.90E-241
PAM	0.265539	5.91E-146
EVA1C	0.264128	7.68E-153
NEAT1	0.257951	1.18E-180
NXN	0.257337	1.74E-28
GALNT18	0.25586	3.21E-174
ARHGAP2	0.254693	2.60E-141
AC092691	0.253357	1.55E-80
UNC5C	0.2533	6.75E-106
GALNT2	0.251899	1.44E-112
CRIM1	0.25056	3.92E-132
ATP11A	0.250449	2.03E-118
RFTN2	-0.25044	2.94E-178
CERS6	-0.25116	2.29E-33
PDE4D	-0.25582	9.17E-158
EYA1	-0.25601	7.89E-134
MAML3	-0.26256	3.88E-81
SMAD9	-0.26688	5.80E-60
GPR75-ASI	-0.26768	2.92E-210
DCHS2	-0.27382	6.13E-115
PBX1	-0.27394	9.72E-232
CFAP47	-0.27582	1.16E-75
CAMK2G	-0.27699	4.20E-229
WDR49	-0.27731	1.47E-44
CACNA2D3	-0.27891	2.44E-37
DLGAP1	-0.29815	1.26E-63
LMO3	-0.30161	2.53E-204
ST6GALNA	-0.30185	3.01E-93
NCKAP5	-0.30514	1.26E-213
PHYHIPL	-0.30907	1.63E-166
HSP90AA1	-0.31194	7.46E-21
KAZN	-0.34671	5.89E-05
AC002429	-0.35873	7.98E-107
CNTN1	-0.3603	0
COL21A1	-0.36496	2.28E-164
VCAN	-0.38333	4.62E-57
SLC14A1	-0.39979	3.68E-281
DPP10	-0.41157	1.79E-57
DGKB	-0.45539	4.30E-141
DPP6	-0.57871	3.24E-179
LINC00609	-0.7477	6.17E-186

Supplementary Table 13_Astrocyte cluster genes
Astro5



Supplementary Table 13_Astrocyte cluster genes

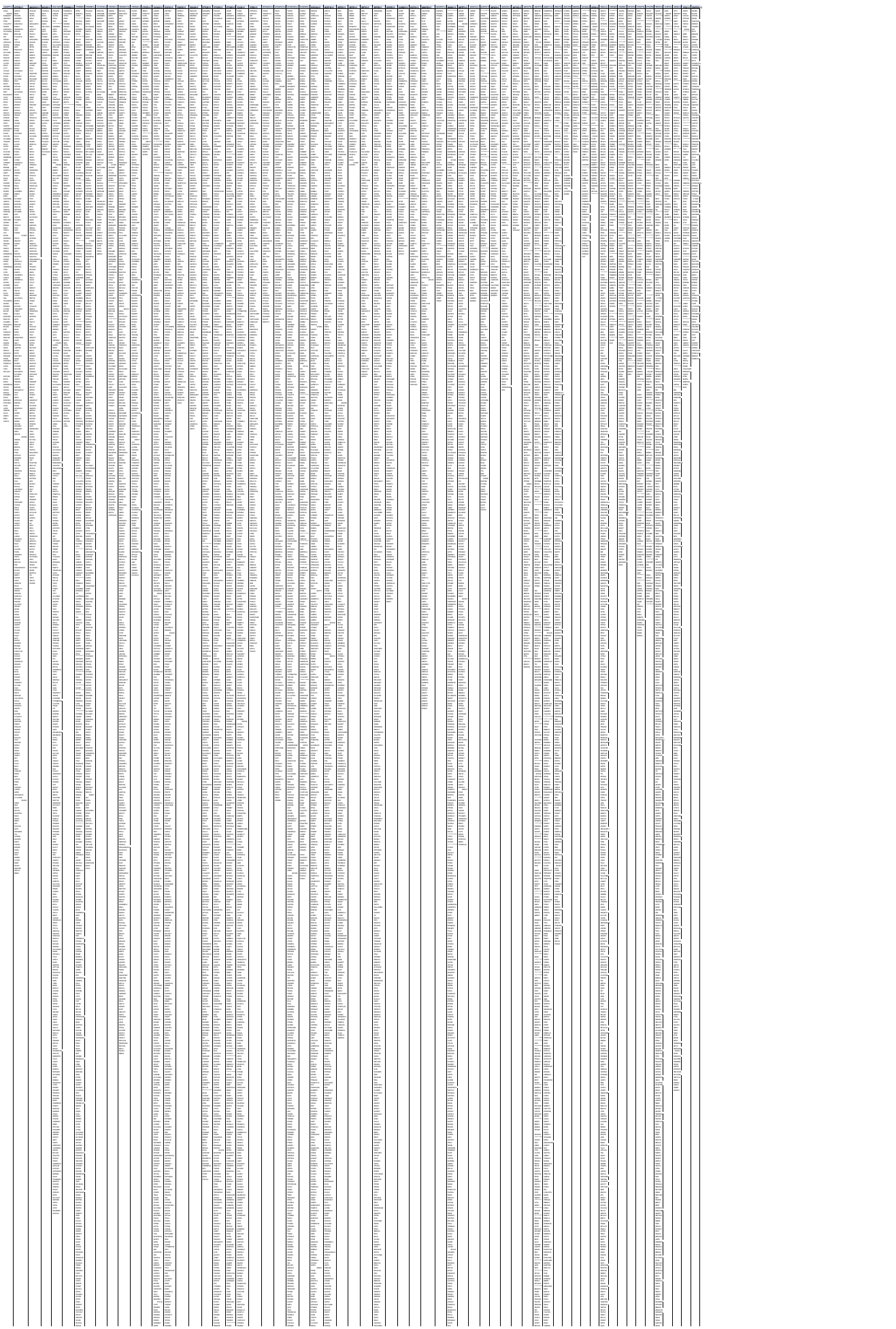
Astro6

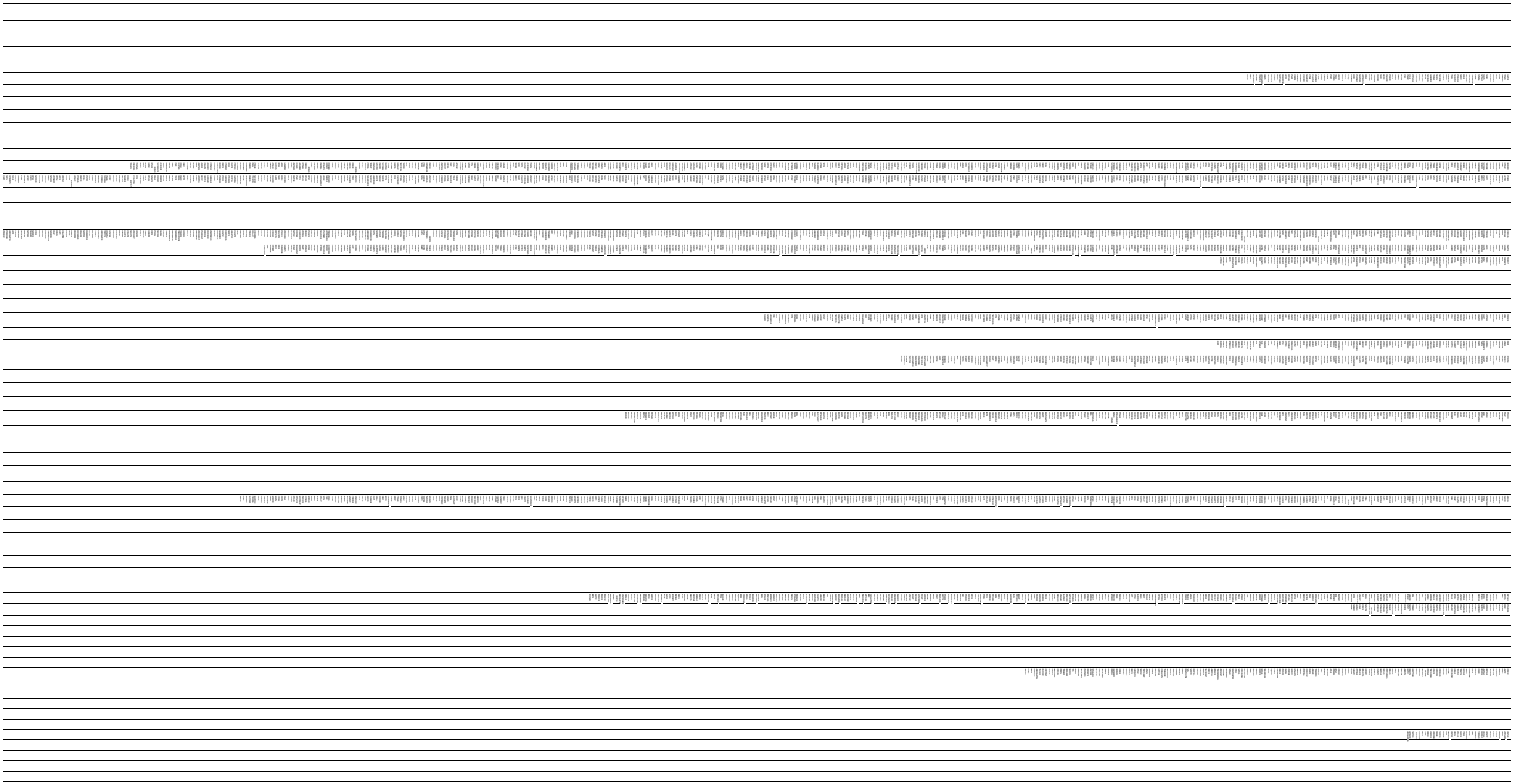
Gene	avg_logFC	p_val_adj
DPP10	1.3077335	0
LINC01411	0.969581	0
SLC38A1	0.9453372	0
ADGRV1	0.8618227	0
SNAI3	0.8518217	0
WDR49	0.8071413	0
AL662796.1	0.8042586	9.99E-212
MAD1L	0.7826516	1.31E-269
LINC01482	0.7577181	0
DUSP1	0.7131801	1.25E-225
VCAN	0.7130575	0
SRARP	0.7056809	2.69E-275
DUSP6	0.7015164	1.36E-256
SRARA	0.6995139	2.17E-278
IER3	0.6828612	6.01E-222
ZNF292	0.6805553	0
ITGB4	0.6650522	7.68E-245
ARRP1	0.6617288	5.65E-251
SHISA6	0.6481817	5.52E-156
NHS	0.6439836	5.55E-170
LINC01622	0.6419857	1.31E-169
CRYAB	0.6213017	5.81E-99
MIR4500HG	0.6131203	5.67E-80
KCNK2	0.6095713	1.65E-260
TNC	0.6070197	1.92E-238
PLCB1	0.6045242	7.62E-183
SPOCK	0.5973827	0
DCLK1	0.5713688	1.13E-197
ARHGEF6	0.5685583	8.56E-258
DPP6	0.5631533	9.65E-121
AQP4-AS1	0.5618627	3.92E-96
MAP2	0.5616021	2.26E-128
SLC1A2	0.5610825	1.08E-205
STXBP6	0.5610625	6.53E-95
AKAP6	0.5598806	2.12E-115
SNTB1	0.5605581	8.82E-115
SHISA2	0.5602327	2.16E-211
ATP1A2	0.5588222	1.04E-208
RYR3	0.5578612	5.06E-168
RASGRF2	0.5568302	3.86E-152
GFAP	0.5533364	3.65E-125
ADCY8	0.5529396	9.03E-120
ATP1B2	0.5519113	1.08E-208
SPON1	0.5516261	1.33E-72
DCLK2	0.5484779	9.53E-157
FAM7?	0.5483979	3.09E-162
GPM6A	0.5460612	1.13E-161
ADAMTS6	0.5455937	5.00E-020
PLCE1	0.5439637	6.79E-108
LINC01844	0.5439607	1.14E-23
ID2	0.5409809	4.13E-23
TMEM132B	0.5407939	1.62E-90
GPC5	0.5406285	1.07E-73
ARHGEF	0.5389767	2.12E-193
ATP1B1	0.5387553	1.13E-178
PLCD	0.5375053	1.58E-56
RNF220	0.535105	8.12E-68
GRIA2	0.5373617	8.63E-96
GPC6	0.5319774	1.79E-81
ADGRV1	0.5314222	1.46E-79
RAPH1	0.5312322	9.80E-79
NPTX	0.5309364	1.23E-95
EVA	0.5295855	2.67E-133
LMO3	0.5278655	3.57E-183
AQP4	0.5273983	2.67E-115
HOPX1	0.5237912	2.85E-20
ADAMTSL1	0.5237552	1.03E-106
GUCY1A3	0.5207553	1.52E-150
INPP4B	0.5208556	6.70E-74
TSBD	0.5208965	9.56E-19
LLPH2	0.5192136	1.16E-78
SLC4A4	0.5190881	1.04E-178
NAV1	0.5187262	9.13E-79
PDS	0.5183703	1.58E-56
SPOCK2	0.5177588	2.86E-87
CHI3L1	0.5169513	2.80E-59
PTPRZ1	0.5167977	1.03E-107
PLEKHA5	0.5167013	9.15E-82
LIMC	0.5158201	6.39E-56
DAAM2	0.5157615	8.43E-68
TANK	0.5156233	1.55E-27
ABCC9	0.5151626	9.25E-115
ADAMTS1	0.5131966	1.03E-107
ANKFY1	0.5123188	9.13E-73
CD44	0.5120644	2.56E-73
AF172928.1	0.5116501	2.71E-63
DUSP3	0.5097519	1.05E-72
SLC7A10	0.5096852	1.03E-107
TSSK4AS1	0.504861	9.63E-50
FAM19A2	0.5023142	5.41E-15
PLEKC2	0.503863	1.71E-90
KCND2	0.5020644	1.21E-56
ITGB8	0.5019222	1.03E-107
SLC7A3	0.5018951	9.70E-43
LINC02296	0.5016681	7.72E-83
SLCO3A1	0.5003776	1.67E-93
CBLN1	0.5017551	6.49E-63
MT1X	0.5010707	2.13E-10
ADGRV1	0.498125	5.72E-171
ATP1A2	0.4978139	1.03E-208
RASL	0.4966855	6.34E-79
ZNRF3	0.4951837	1.92E-82
SRARA1	0.4948868	2.17E-56
PRKG1	0.4938917	6.40E-58
LINC01844	0.4938917	1.14E-23
CTNNA1	0.4919865	1.79E-15
GNAI1	0.4916811	1.03E-69
PXDC1	0.4907766	2.42E-62
AL390876.1	0.4903166	5.75E-64
ID4	0.4902744	1.03E-107
ARHGAP42	0.4900176	6.43E-80
TENM3	0.4899828	1.44E-99
LINC01088	0.4894512	1.38E-63
KMO1	0.4893685	1.08E-54
GAS	0.4892319	1.03E-50
AHNAK	0.4888605	5.72E-45
ANXA5	0.4888605	1.03E-107
JUNB	0.4874837	2.49E-50
ITGB4	0.4874127	2.43E-67
TMEM5	0.4872731	4.49E-49
PPP1R3B	0.4869535	5.08E-125
ARHGAP24	0.4869535	1.03E-107
NPTXR	0.4869502	7.54E-17
HSPJB	0.4867514	1.67E-62
EDNRB	0.4866585	8.84E-58
SPARCL1	0.4862703	8.29E-85
ANXA5	0.4861574	1.03E-107
ANKRD1	0.4861574	9.16E-93
MOXD1	0.4860652	8.01E-60
KRT4/5/6	0.4860317	7.95E-28
DIO	0.4856542	8.41E-58
ZAP70.2	0.486639	2.55E-78
FAT3	0.4855295	1.91E-42
ATP1A1	0.4854138	1.03E-107
IFI16	0.4854076	4.81E-67
RBX2	0.4848051	2.58E-29
LIX1	0.4848122	6.03E-65
SYNDIG1	0.4845947	1.41E-51
ADGRV1	0.4844911	1.03E-107
GAS1	0.4844911	2.69E-34
PBX3	0.4710791	8.51E-28
LINC02099	0.4845675	2.26E-27
STARPS1	0.4844175	3.86E-69
ATP1A2	0.4843917	1.03E-208
DDIT4	0.4843357	1.55E-58
CEP126	0.4839867	1.61E-26
NCAN	0.4843971	5.52E-29
HYDIN	0.4843113	2.76E-55
PRDX1	0.4843395	5.79E-13
PRUNE2	0.4842216	6.18E-26
ITGA7	0.4841837	1.03E-107
SHANK2	0.4839837	1.85E-58
IQCK	0.4839899	5.39E-36
AC008059.1	0.4839211	2.59E-10
GALNT15	0.4839034	1.47E-56
CACNA2D1	0.4838837	1.03E-107
CACNA1C	0.4837897	6.29E-16
TRAPPC	0.4837713	5.29E-21
ZCWCI2	0.4837689	2.07E-43
PCSK5	0.4834977	1.79E-55
ADGRB3	0.4834852	1.03E-107
AC009956.1	0.4834852	2.85E-13
AC009365.1	0.4833832	8.28E-64
SLC6A1	0.4833826	2.94E-43
EIF2B	0.4832776	6.87E-52
ATP1A1	0.4832776	1.03E-107
CTNT3	0.4832625	1.58E-51
NR1	0.4830764	6.77E-47
LRMDA	0.4831655	5.57E-59
IQCA1	0.4830832	9.80E-40
AS0A07527	0.4831826	5.01E-41
PALLD	0.4830699	7.19E-47
ADGRB3	0.4830699	1.03E-107
CDH8-AS1	0.4830699	2.95E-59
JAM2	0.4829518	9.20E-66
MAGI3	0.4829867	2.14E-48
MIR3C-AS1	0.4829393	9.86E-09
ITGB1	0.4829393	1.03E-107
NTN1	0.4728781	8.71E-61
ENOX1	0.4731665	1.12E-57
CHN1	0.4724383	1.46E-54
ADTI	0.4723531	9.90E-39
ANKRD36B	0.4722855	1.03E-107
MIR3208HG	0.4722855	1.57E-54
NR3C2HG	0.4613791	4.65E-59
CRYAA1	0.4613181	1.14E-56
RUBX1	0.4613137	1.52E-60
DPP6AS	0.4613137	1.03E-107
DNAH2	0.4613137	1.57E-54
MIR3208HG	0.4613137	1.57E-54
DNAH1	0.4612491	1.14E-56
RUBX1	0.4611637	1.52E-60
DPP6AS	0.4611637	1.03E-107
ZNF292P	0.4610635	1.89E-61
LINC01622	0.4610635	1.31E-169
RYR1	0.4610627	5.75E-111
LINC02892	0.4608822	2.68E-50
CD47	0.4608388	1.13E-59
MRK1	0.4607124	3.33E-57
ANKRD36B	0.4606855	1.03E-107
GRIA4	0.4606855	3.56E-68
RNF219-AS1	0.4606855	1.22E-50
EIF4	0.4606825	8.48E-52
NKAK1	0.4513681	7.56E-55
ERC2	0.4513681	1.03E-107
GRIA1	0.4507826	1.58E-51
CHST11	0.4506985	6.13E-41
LMO3	0.4504726	2.79E-68
ALK	0.4503206	1.58E-29
ATP7B3	0.4503691	7.85E-57
PACS2B	0.4507524	1.76E-59
ITGA1	0.4501855	1.03E-107
GRIA3	0.4500851	1.57E-71
PTCHD1	0.4500612	1.79E-69
EYA3	0.4500851	7.63E-57
PTN	0.4499723	2.43E-82
SLC4A10	0.4499723	1.03E-107
KLF12	0.4111958	8.09E-60
ASRGL1	0.4109955	4.80E-69
SLC6A1	0.4107796	5.30E-61
C12orf60	0.4104531	4.36E-83
SLC6A12	0.4104531	1.03E-107
GLUL	0.4098268	3.57E-52
TMEM132C	0.4213721	2.29E-55
LIX1	0.4210647	1.46E-54
ADTL	0.4210531	8.92E-39
SLC6A11	0.4210531	1.03E-107
NKAIN2	0.4210531	8.56E-58
PDLIM3	0.4210531	1.03E-107
PTCHD1-AS	0.4210531	1.57E-54
LINC01844	0.4210531	1.57E-54
NKAIN2	0.4210531	1.57E-54
PDLIM3	0.4210531	1.03E-107
SLC6A11	0.4210531	1.03E-107
ASRGL1

Supplementary Table 14_Microglia SCENIC Regulons
Contents

Sheet name	Description
Regulon_list	SCENIC Regulons in Microglia
Pathology_correlation	logFC of the enrichment (AUCell and limma) of regulons with amyloid-beta and pTau
Enrichment_other_datasets	logFC of the enrichment (AUCell and limma) of regulons in AD samples compared to Control samples from previous studies
RSS	Regulon specificity scores (RSS) in microglial subclusters

Supplementary Table 14_Microglia SCENIC Regulons
Regulon list





Supplementary Table 14_Microglia SCENIC Regulons
Pathology correlation

Positive logFC values indicate a higher enrichment with pathology

Amyloid-pathology

Regulon	logFC	P.Value	adj.P.Val
ARID3A(+)	-0.30766399	0.35767844	0.613592801
ARNT(+)	0.222493289	0.414399738	0.655509603
ARNTL(+)	-0.799053268	0.398461863	0.646814477
ATF1(+)	1.539693506	0.036613119	0.143927433
ATF4(+)	-0.879190751	0.355946565	0.613592801
ATF6(+)	0.055435747	0.780041772	0.905291192
BACH1(+)	-0.471934058	0.036129124	0.143927433
BCL6(+)	-1.481253876	2.11699E-05	0.000804456
BHLHE41(+)	0.050597064	0.78617393	0.905291192
CEBPA(+)	1.123457837	3.57186E-05	0.00101798
CEBPB(+)	0.095476879	0.685212265	0.849067372
CEBPD(+)	0.698465011	0.004381265	0.03842032
CEBPZ(+)	1.79773651	0.083174823	0.251668874
CLOCK(+)	0.679254514	0.033708271	0.142323811
CREB1(+)	0.600859102	0.017437457	0.086429133
CREB3L2(+)	-0.216773654	0.321815275	0.594872727
CREM(+)	0.645727784	0.022472234	0.106743113
CTCF(+)	-0.884425855	0.028076577	0.123104992
CUX1(+)	0.017547558	0.919089776	0.961249857
DEAF1(+)	1.254318456	0.245017327	0.547685789
DNMT1(+)	0.03923338	0.951327789	0.985921527
E2F3(+)	0.393822178	0.626865839	0.816397238
ELF1(+)	0.283302671	0.08138693	0.251668874
ELF2(+)	0.866896435	0.098216671	0.274868274
ELK3(+)	-0.083100259	0.757781043	0.893228048
ELK4(+)	0.646748485	0.015711077	0.081411946
ETS2(+)	0.191377356	0.332877643	0.594872727
ETV5(+)	-0.304410621	0.075166189	0.244827017
ETV6(+)	-0.182480649	0.262521055	0.555036335
FLI1(+)	0.160033153	0.36062033	0.613592801
FOS(+)	0.196661805	0.480780341	0.69378429
FOXJ3(+)	-0.332092041	0.702221746	0.851630628
FOXK1(+)	0.011850111	0.963912577	0.989964268
FOXN3(+)	-0.288435331	0.419756149	0.655509603
FOXO1(+)	0.24194356	0.318265928	0.594872727
FOXO3(+)	0.629246462	0.001487072	0.015411476
FOXP2(+)	-0.110629192	0.576585773	0.782509264
GABPA(+)	0.701032211	0.311445972	0.594872727
GTF2IRD1(+)	0.50336099	0.557059766	0.765118233
HBP1(+)	0.972998225	0.3947226	0.646814477
HDX(+)	0.161840172	0.875173993	0.94081254
HIF1A(+)	0.297602249	0.133641158	0.3385576
HIVEP1(+)	0.183662955	0.841944046	0.922900204
HIVEP2(+)	-0.73010935	0.067993626	0.230928456
HSF1(+)	-0.268361554	0.684266832	0.849067372
IKZF1(+)	-0.266739632	0.133317874	0.3385576
IRF2(+)	0.090197722	0.64180442	0.82208656
IRF3(+)	0.55504986	0.143409219	0.355405456
IRF5(+)	-0.347826019	0.266466419	0.555036335
IRF8(+)	-0.531148134	0.006476523	0.052737399
JDP2(+)	0.46414559	0.083889625	0.251668874
JUND(+)	2.108586661	5.98424E-07	3.41102E-05
KDM5B(+)	0.160855547	0.889036053	0.94081254
KLF3(+)	-0.518640632	0.068873399	0.230928456
KLF6(+)	0.525198549	0.267780688	0.555036335
MAFB(+)	0.636293746	0.040024152	0.152091779
MAFG(+)	1.965842011	1.30347E-08	1.48596E-06
MAX(+)	0.344568079	0.056916088	0.202763562
MITF(+)	0.788624468	0.000375675	0.007137823
MLXIP(+)	-0.309950788	0.758013634	0.893228048
MXD4(+)	0.947283925	0.000575989	0.0093804
NFATC1(+)	0.559256028	0.551032728	0.765118233
NFE2L2(+)	0.680011753	0.007623108	0.055513377
NFIC(+)	-0.224498305	0.402840595	0.646814477
NFKB1(+)	-0.301387633	0.324377199	0.594872727
NFYC(+)	0.182666875	0.673351566	0.849067372
NR2C1(+)	0.362974452	0.586271793	0.784163077
NR2C2(+)	0.705791828	0.00139858	0.015411476
NR3C1(+)	0.419202116	0.014567048	0.081411946
NR6A1(+)	-0.16301504	0.89129609	0.94081254
NRF1(+)	0.376599239	0.049465485	0.181905333
PBX3(+)	0.690100696	0.001154073	0.015411476
PKNOX1(+)	0.50118045	0.630201377	0.816397238
POU2F1(+)	-0.513936161	0.432724138	0.661644266
POU2F2(+)	-0.70727584	0.007791351	0.055513377
PPARG(+)	1.780909719	0.008780501	0.058881007
PRDM1(+)	1.246634045	0.001309728	0.015411476
RBPJ(+)	-0.934397493	0.293756717	0.594872727
REL(+)	0.011252987	0.986844139	0.991280498
RFX3(+)	0.780140292	0.184055446	0.437131683
RREB1(+)	0.01002731	0.976605468	0.991280498
RUNX1(+)	-0.592437125	0.013260025	0.07956015
RUNX2(+)	0.203825749	0.55440586	0.765118233
RXRA(+)	1.368334654	0.098856133	0.274868274
SMAD3(+)	-1.156172795	0.239620562	0.546334881
SMAD5(+)	0.347011611	0.43529228	0.661644266
SOX5(+)	-1.815146094	0.093908016	0.274500356
SP1(+)	-0.005236766	0.991280498	0.991280498
SP3(+)	0.471279347	0.312657341	0.594872727
SP4(+)	0.723921223	0.309184536	0.594872727
SPI1(+)	-0.175624691	0.393503101	0.646814477
SREBF1(+)	-0.781115137	0.015563001	0.081411946
SREBF2(+)	-0.663915392	0.003752232	0.035646205
STAT1(+)	-1.094405424	0.000193338	0.004408107
STAT2(+)	-0.330328434	0.227701144	0.529753682
STAT3(+)	-0.316419833	0.164508678	0.399021048
STAT5A(+)	0.719990426	0.457672946	0.677593712
TAL1(+)	0.082415564	0.801583291	0.90582018
TCF12(+)	0.090379649	0.760027374	0.893228048
TCF7L2(+)	0.394225027	0.252323895	0.553171616
TFEC(+)	0.406654991	0.023938005	0.109157302
UBP1(+)	-0.642311756	0.59156162	0.784163077
USF2(+)	0.830252862	0.10732307	0.28453093
XBP1(+)	-0.423866088	0.106299363	0.28453093
YY1(+)	0.603784828	0.012387031	0.078451199
ZBTB7A(+)	-0.424829664	0.333963636	0.594872727
ZFP64(+)	-0.298126062	0.802524897	0.90582018
ZNF121(+)	0.661092519	0.509924237	0.726642037
ZNF131(+)	0.268836951	0.835052499	0.922900204
ZNF143(+)	-0.414661766	0.471350182	0.68889642
ZNF337(+)	0.483196345	0.701558751	0.851630628
ZNF736(+)	0.296207645	0.826339042	0.922900204
ZNF84(+)	0.7680863	0.456126965	0.677593712
ZNF91(+)	0.04364869	0.852344328	0.925402413

pTau pathology

Regulon	logFC	P.Value	adj.P.Val
ARID3A(+)	-0.23191338	0.42424933	0.662526352
ARNT(+)	0.351948719	0.136755694	0.332035996
ARNTL(+)	-1.031382158	0.209083659	0.441398835
ATF1(+)	1.203635392	0.059692497	0.183917424
ATF4(+)	-0.692765103	0.401844395	0.662526352
ATF6(+)	0.116546838	0.498620387	0.693203953
BACH1(+)	-0.372653061	0.056524859	0.181214738
BCL6(+)	-1.535876928	3.74E-07	1.06668E-05
BHLHE41(+)	0.208395223	0.197829772	0.441398835
CEBPA(+)	1.301323688	3.41E-08	1.94604E-06
CEBPB(+)	0.172375865	0.398972614	0.662526352
CEBPD(+)	0.723681302	0.000667826	0.007613211
CEBPZ(+)	2.023606986	0.024581313	0.100081059
CLOCK(+)	0.601174535	0.030305634	0.119132494
CREB1(+)	0.623081203	0.004493006	0.034146845
CREB3L2(+)	-0.170143184	0.370143547	0.657631895
CREM(+)	0.425573962	0.083005629	0.236566043
CTCF(+)	-0.855520054	0.0143472	0.071275079
CUX1(+)	0.051531846	0.730992388	0.86805346
DEAF1(+)	0.706858164	0.450216944	0.690153702
DNMT1(+)	-0.007599392	0.989128047	0.989128047
E2F3(+)	0.100823742	0.885942526	0.943901383
ELF1(+)	0.318522409	0.023933697	0.100081059
ELF2(+)	0.74586361	0.101072989	0.281032213
ELK3(+)	0.071747948	0.758938706	0.876955707
ELK4(+)	0.542046942	0.019636422	0.089542085
ETS2(+)	0.194625308	0.256399934	0.503958492
ETV5(+)	-0.101549859	0.493893147	0.693203953
ETV6(+)	-0.11620793	0.410881785	0.662526352
FLI1(+)	0.23933032	0.115096722	0.298205143
FOS(+)	0.1812037	0.454048488	0.690153702
FOXJ3(+)	-0.265049728	0.725078668	0.86805346
FOXK1(+)	0.016983538	0.940426795	0.974624133
FOXN3(+)	0.083347977	0.788154896	0.889189581
FOXO1(+)	0.483727566	0.021461014	0.094098294
FOXO3(+)	0.736880926	1.80E-05	0.000342037
FOXP2(+)	0.102152513	0.552360884	0.740813421
GABPA(+)	0.8938612	0.136892033	0.332035996
GTF2IRD1(+)	0.619659445	0.404743457	0.662526352
HBP1(+)	1.152279025	0.245373619	0.490747237
HDX(+)	-0.198021429	0.824672817	0.90396828
HIF1A(+)	0.235753634	0.170885621	0.397570629
HIVEP1(+)	0.096576863	0.903811409	0.945270648
HIVEP2(+)	-0.685037194	0.048437252	0.167328688
HSF1(+)	-0.102468989	0.85797532	0.922728175
IKZF1(+)	-0.106243256	0.490768792	0.693203953
IRF2(+)	0.159275507	0.34378417	0.624394253
IRF3(+)	0.69745978	0.034083618	0.129517747
IRF5(+)	0.324810559	0.231719064	0.480290424
IRF8(+)	-0.21326481	0.207733543	0.441398835
JDP2(+)	0.190639319	0.413231943	0.662526352
JUND(+)	1.931747449	1.36E-07	5.16965E-06
KDM5B(+)	0.259130178	0.795590678	0.889189581
KLF3(+)	-0.480530243	0.052060181	0.174554723
KLF6(+)	0.527945052	0.199183538	0.441398835
MAFB(+)	0.769824362	0.004190857	0.034125551
MAFG(+)	1.770065469	3.63E-09	4.14206E-07
MAX(+)	0.384016196	0.014461864	0.071275079
MITF(+)	0.786227879	4.38E-05	0.000623609
MLXIP(+)	-0.195109295	0.823130384	0.90396828
MXD4(+)	1.027093515	1.69E-05	0.000342037
NFATC1(+)	0.958059433	0.239138727	0.486818123
NFE2L2(+)	0.622010015	0.004908769	0.03497498
NFIC(+)	-0.129010018	0.579543345	0.768231875
NFKB1(+)	-0.282135843	0.287669402	0.546571863
NFYC(+)	0.197839844	0.598748164	0.784566559
NR2C1(+)	0.46683224	0.419819756	0.662526352
NR2C2(+)	0.736313584	0.000122268	0.001548726
NR3C1(+)	0.471482584	0.001541436	0.014923801
NR6A1(+)	-0.31396408	0.761566798	0.876955707
NRF1(+)	0.404551777	0.01500528	0.071275079
PBX3(+)	0.770204993	2.91E-05	0.000473399
PKNOX1(+)	0.642319056	0.477004658	0.693203953
POU2F1(+)	-0.031880182	0.955271588	0.981089739
POU2F2(+)	-0.364162361	0.114344049	0.298205143
PPARG(+)	1.464254296	0.013023302	0.071275079
PRDM1(+)	1.00882044	0.002723683	0.023884609
RBPJ(+)	-1.468362649	0.057225707	0.181214738
REL(+)	0.008928944	0.987969083	0.989128047
RFX3(+)	0.64899469	0.202804965	0.441398835
RREB1(+)	0.076863041	0.795581587	0.889189581
RUNX1(+)	-0.370669958	0.074119696	0.216657574
RUNX2(+)	0.265415535	0.374965554	0.657631895
RXRA(+)	1.082094392	0.132522461	0.332035996
SMAD3(+)	-0.739027819	0.386295003	0.662526352
SMAD5(+)	0.267397005	0.488397719	0.693203953
SOX5(+)	-1.954596609	0.037622734	0.138354572
SP1(+)	0.086132304	0.835883614	0.907530781
SP3(+)	0.392461123	0.332527062	0.621444018
SP4(+)	0.99130052	0.108506144	0.294516677
SPI1(+)	-0.070634975	0.692460629	0.848822706
SREBF1(+)	-0.577774762	0.039197893	0.139642495
SREBF2(+)	-0.486387098	0.01440368	0.071275079
STAT1(+)	-0.805360366	0.001570926	0.014923801
STAT2(+)	-0.168833576	0.477352789	0.693203953
STAT3(+)	-0.186491762	0.345059982	0.624394253
STAT5A(+)	0.500568357	0.551778521	0.740813421
TAL1(+)	0.137180939	0.629747794	0.806643241
TCF12(+)	0.131788675	0.607728784	0.787285016
TCF7L2(+)	0.429598441	0.150520864	0.357487051
TFEC(+)	0.425162817	0.006508692	0.041691094
UBP1(+)	-0.668491869	0.519734677	0.713852448
USF2(+)	1.215512645	0.006582804	0.041691094
XBP1(+)	-0.406778321	0.074050802	0.216657574
YY1(+)	0.530812379	0.011278144	0.067668866
ZBTB7A(+)	-0.269980689	0.479173508	0.693203953
ZFP64(+)	-0.368426564	0.721685747	0.86805346
ZNF121(+)	0.111581593	0.89800203	0.945270648
ZNF131(+)	0.03161921	0.977468719	0.989128047
ZNF143(+)	-0.208653521	0.676155341	0.847051745
ZNF337(+)	0.460969049	0.673385548	0.847051745
ZNF736(+)	0.474320081	0.685177813	0.848822706
ZNF84(+)	0.955949878	0.285069868	0.546571863
ZNF91(+)	0.062218833	0.75977231	0.876955707

Supplementary Table 14_Microglia SCENIC Regulons
Enrichment other datasets

Positive logFC values indicate a higher enrichment in AD compared to Control

Grubman et al 2019, doi: 10.1038/s41593-019-0539-4

Regulon	logFC	P.Value	adj.P.Val
ARID3A(+)	0.065790177	0.414411681	0.54414886
ARNT(+)	0.011323944	0.816947588	0.87039276
ARNTL(+)	0.246562868	0.166932903	0.27580219
ATF1(+)	0.298266727	0.023936003	0.05805754
ATF4(+)	0.304139157	0.053837702	0.11159087
ATF6(+)	-0.0407588	0.141052047	0.2399999
BACH1(+)	0.004671262	0.885339319	0.91753348
BCL6(+)	0.712907599	5.31E-20	6.05E-18
BHLHE41(+)	-0.11627466	1.60E-08	2.03E-07
CEBPA(+)	-0.04456437	0.22031134	0.33141938
CEBPB(+)	0.168137596	1.58E-06	1.39E-05
CEBPD(+)	0.020936054	0.506143518	0.62290222
CEBPZ(+)	0.405874434	0.015570874	0.03858869
CLOCK(+)	0.061147778	0.37712979	0.51798549
CREB1(+)	-0.08191564	0.06754245	0.13275585
CREB3L2(+)	0.042473947	0.19479107	0.31276313
CREM(+)	-0.02560956	0.52769335	0.63323202
CTCF(+)	0.48027088	1.89E-07	2.15E-06
CUX1(+)	-0.00522765	0.775737461	0.84833553
DEAF1(+)	-0.32067788	0.100351431	0.18754202
DNMT1(+)	-0.10158929	0.427534479	0.54966852
E2F3(+)	0.140881116	0.339194411	0.48335204
ELF1(+)	-0.05342522	0.000127542	0.00053851
ELF2(+)	-0.07080623	0.556075857	0.66034008
ELK3(+)	-0.16455592	0.000777647	0.00295506
ELK4(+)	0.009387876	0.856408276	0.90398651
ETS2(+)	0.072542731	0.005472693	0.01559717
ETV5(+)	-0.07607583	9.35E-05	0.00042615
ETV6(+)	-0.03436622	0.056862892	0.1157566
FLI1(+)	-0.10626193	1.43E-06	1.35E-05
FOS(+)	0.110278056	0.008374629	0.0216979
FOXJ3(+)	0.217362046	0.137917505	0.23822114
FOXK1(+)	-0.08346639	0.090908245	0.17272567
FOXN3(+)	-0.35464525	1.74E-06	1.42E-05
FOXO1(+)	-0.27888036	4.53E-16	2.58E-14
FOXO3(+)	-0.14045727	6.40E-11	1.46E-09
FOXP2(+)	-0.22448842	9.10E-16	3.46E-14
GABPA(+)	-0.17793075	0.220946255	0.33141938
GTF2IRD1(+)	0.191956572	0.211408196	0.3256829
HBP1(+)	0.133029607	0.429127181	0.54966852
HDX(+)	0.403810971	0.04677092	0.09873861
HIF1A(+)	0.06715334	0.00457403	0.01435105
HIVEP1(+)	-0.31808827	0.042587632	0.09160359
HIVEP2(+)	0.044788169	0.617853148	0.71146726
HSF1(+)	-0.17248669	0.177803236	0.28956527
IKZF1(+)	-0.08939358	5.52E-05	0.00027356
IRF2(+)	-0.12377629	2.26E-05	0.0001431
IRF3(+)	-0.23650095	0.001299551	0.00462965
IRF5(+)	-0.04963109	0.289467905	0.42306848
IRF8(+)	-0.11358217	1.36E-06	1.35E-05
JDP2(+)	0.205116681	2.25E-06	1.71E-05
JUND(+)	0.031213199	0.661064111	0.74615157
KDM5B(+)	-0.12882927	0.48302619	0.60510973
KLF3(+)	-0.04502036	0.365471112	0.51436675
KLF6(+)	-0.02376698	0.781361675	0.84833553
MAFB(+)	0.116931679	0.004756233	0.01435105
MAFG(+)	0.243088504	6.79E-06	4.56E-05
MAX(+)	-0.05910748	0.006000765	0.01668505
MITF(+)	-0.0038824	0.900760556	0.92510544
MLXIP(+)	0.091694215	0.611070922	0.7108376
MXD4(+)	-0.11932225	0.004214686	0.01372783
NFATC1(+)	0.0573854	0.687155112	0.76799689
NFE2L2(+)	0.035615228	0.388404397	0.52712025
NFIC(+)	0.090028738	0.134821071	0.23645542
NFKB1(+)	0.116267628	0.035762341	0.07993935
NFYC(+)	0.054417096	0.515392258	0.62505019
NR2C1(+)	-0.14831974	0.375081245	0.51798549
NR2C2(+)	-0.11613372	0.000475269	0.0018683
NR3C1(+)	-0.08532991	2.80E-06	1.99E-05
NR6A1(+)	0.009724589	0.963788061	0.97231716
NRF1(+)	-0.0069445	0.775287134	0.84833553
PBX3(+)	-0.09735825	0.000869855	0.00319882
PKNOX1(+)	-0.32798042	0.111729542	0.20543819
POU2F1(+)	-0.21192476	0.078052657	0.15081361
POU2F2(+)	-0.19333521	4.25E-05	0.00022003
PPARG(+)	0.350327294	0.004783685	0.01435105
PRDM1(+)	0.237183681	0.007959746	0.02110258
RBPJ(+)	0.390483329	0.027075503	0.06430432
REL(+)	-0.00922516	0.94966914	0.96662752
RFX3(+)	0.31797371	0.031647359	0.07362855
RREB1(+)	-0.17723202	0.010355333	0.02623351
RUNX1(+)	-0.15451579	0.000158234	0.00064424
RUNX2(+)	-0.16851197	0.032523966	0.07415464
RXRA(+)	-0.44488583	0.005259419	0.01537369
SMAD3(+)	0.111644563	0.508157078	0.62290222
SMAD5(+)	0.112301798	0.298870329	0.43128123
SOX5(+)	-0.58611084	3.19E-05	0.00018245
SP1(+)	0.100301103	0.395820006	0.53086448
SP3(+)	0.202736414	0.041488157	0.09093923
SP4(+)	0.282648573	0.067040822	0.13275585
SPI1(+)	0.110370935	3.20E-05	0.00018245
SREBF1(+)	0.141789934	0.007169828	0.01946096
SREBF2(+)	-0.15521876	5.90E-05	0.00028021
STAT1(+)	0.312354514	7.41E-09	1.06E-07
STAT2(+)	0.147140128	0.002383064	0.0082324
STAT3(+)	0.052285269	0.121704142	0.22022654
STAT5A(+)	-0.04332845	0.80434353	0.8650487
TAL1(+)	-0.50397669	1.56E-10	2.97E-09
TCF12(+)	-0.25734932	3.38E-05	0.00018366
TCF7L2(+)	-0.26195246	0.003774436	0.01265546
TFEC(+)	-0.0114614	0.600025359	0.70518444
UBP1(+)	-0.28813975	0.209007649	0.3256829
USF2(+)	-0.01080591	0.88114878	0.91753348
XBP1(+)	0.291744358	5.54E-14	1.58E-12
YY1(+)	0.151000482	9.99E-05	0.00043801
ZBTB7A(+)	0.542982846	3.01E-09	4.91E-08
ZFP64(+)	0.201135467	0.467757004	0.5924922
ZNF121(+)	0.166213815	0.415271499	0.54414886
ZNF131(+)	-0.57032082	0.158453106	0.26564197
ZNF143(+)	0.055838515	0.637561291	0.72681987
ZNF337(+)	0.003339162	0.9915709	0.9915709
ZNF736(+)	1.440424201	0.264285567	0.39127993
ZNF84(+)	-0.23982991	0.12537148	0.22331795
ZNF91(+)	0.056992531	0.206679475	0.3256829

Mathys et al 2019, doi: 10.1038/s41586-019-1195-2

Regulon	logFC	P.Value	adj.P.Val
ARID3A(+)	-0.0865646	0.00491727	0.02548039
ARNT(+)	-0.0409948	0.03609705	0.11757324
ARNTL(+)	-0.051056	0.43070794	0.57232606
ATF1(+)	0.10927631	0.04304913	0.12655403
ATF4(+)	0.10124852	0.12021503	0.27833213
ATF6(+)	-0.0375408	0.00301125	0.01171641
BACH1(+)	-0.0127878	0.41266857	0.5667978
BCL6(+)	-0.0557789	0.120547	0.27833213
BHLHE41(+)	0.0168911	0.14423071	0.30828979
CEBPA(+)	0.09066086	1.25E-06	2.38E-05
CEBPB(+)	0.05603609	4.13E-05	0.00042843
CEBPD(+)	-0.0344038	0.02654307	0.09455968
CEBPZ(+)	-0.06554	0.31341101	0.48464023
CLOCK(+)	0.01401832	0.59464584	0.7289207
CREB1(+)	0.00150418	0.76710432	0.85735189
CREB3L2(+)	-0.0040968	0.75914893	0.85686117
CREM(+)	-0.1849449	3.71E-19	4.23E-17
CTCF(+)	-0.0447483	0.19574812	0.37141915
CUX1(+)	-0.0419594	9.76E-06	0.00013908
DEAF1(+)	-0.0738118	0.37384061	0.53272287
DNMT1(+)	0.04175342	0.43175475	0.57232606
E2F3(+)	-0.0006432	0.99188628	0.99188628
ELF1(+)	-0.0072621	0.33697578	0.50546368
ELF2(+)	-0.0577161	0.20851601	0.37141915
ELK3(+)	0.03682617	0.06496055	0.18062201
ELK4(+)	0.02671352	0.1880481	0.36334718
ETS2(+)	0.01095758	0.36714097	0.53272287
ETV5(+)	0.02939859	0.00465122	0.02524947
ETV6(+)	-0.0219452	0.01480677	0.06028469
FLI1(+)	-0.0096083	0.38398394	0.54042185
FOS(+)	-0.0348309	0.09142528	0.23161072
FOXJ3(+)	-0.0809565	0.20670376	0.37141915
FOXK1(+)	-0.040467	0.03998488	0.12319665
FOXN3(+)	0.03675441	0.32298244	0.49093331
FOXO1(+)	-0.0256418	0.16364445	0.32892763
FOXO3(+)	0.01351197	0.27478314	0.46754146
FOXP2(+)	0.02473346	0.12109995	0.27833213
GABPA(+)	-0.0041366	0.93957014	0.96496392
GTF2IRD1(+)	-0.0168733	0.81220092	0.86533556
HBP1(+)	-0.1523831	0.03607226	0.11757324
HDX(+)	-0.0182339	0.80640478	0.86533556
HIF1A(+)	-0.044277	0.0001401	0.00114082
HIVEP1(+)	-0.246741	0.00037576	0.00285578
HIVEP2(+)	-0.1919884	5.23E-08	1.49E-06
HSF1(+)	0.01227811	0.81128909	0.86533556
IKZF1(+)	0.03541655	0.00871117	0.04137807
IRF2(+)	-0.0479935	0.00011744	0.00102989
IRF3(+)	0.04168949	0.16446381	0.32892763
IRF5(+)	0.09352483	2.25E-05	0.00025638
IRF8(+)	0.04808237	0.00163456	0.01096119
JDP2(+)	-0.0389998	0.02842338	0.09818985
JUND(+)	0.14340658	2.90E-06	4.72E-05
KDM5B(+)	-0.0302602	0.69206187	0.81335106
KLF3(+)	-0.057318	0.00813271	0.04030994
KLF6(+)	0.00038917	0.99160293	0.99188628
MAFB(+)	0.0321633	0.07804426	0.20787212
MAFG(+)	0.06081468	0.01868551	0.07100494
MAX(+)	-0.0082864	0.39904978	0.55477653
MITF(+)	-0.0001532	0.99120474	0.99188628
MLXIP(+)	-0.0510995	0.44919479	0.58860007
MXD4(+)	0.05227225	0.01093867	0.04618548
NFATC1(+)	-0.0837704	0.14951741	0.30990882
NFE2L2(+)	-0.0365476	0.03784044	0.11982806
NFIC(+)	-0.0972918	1.48E-05	0.00018686
NFKB1(+)	-0.010529	0.63704633	0.76445559
NFYC(+)	0.00282035	0.93101575	0.96487086
NR2C1(+)	0.03360148	0.52902257	0.66495228
NR2C2(+)	0.00693321	0.63542118	0.76445559
NR3C1(+)	0.01435672	0.14603201	0.30828979
NR6A1(+)	-0.1008985	0.28845238	0.4765735
NRF1(+)	0.01900801	0.0784079	0.20787212
PBX3(+)	-0.0095226	0.47563357	0.6092385
PKNOX1(+)	-0.1108358	0.11042773	0.27366871
POU2F1(+)	-0.0340216	0.53079524	0.66495228
POU2F2(+)	0.0254127	0.31459103	0.48464023
PPARG(+)	0.01716708	0.73473493	0.83759783
PRDM1(+)	-0.0829477	0.0197741	0.07271764
RBPJ(+)	-0.1079001	0.13767753	0.3018315
REL(+)	-0.1885258	0.00125153	0.00891714
RFX3(+)	0.03058755	0.55564952	0.68852223
RREB1(+)	-0.1061477	0.0017998	0.01139876
RUNX1(+)	-0.0056996	0.79117344	0.86533556
RUNX2(+)	-0.0371196	0.28023355	0.4698033
RXRA(+)	-0.1053198	0.05466744	0.15580219
SMAD3(+)	0.02723361	0.68948129	0.81335106
SMAD5(+)	-0.0366762	0.35584604	0.52683699
SOX5(+)	-0.1720498	0.01025036	0.04618548
SP1(+)	0.01100751	0.79891241	0.86533556
SP3(+)	0.00719795	0.85209388	0.89183077
SP4(+)	-0.0443057	0.46826743	0.60661918
SPI1(+)	0.02989217	0.01071627	0.04618548
SREBF1(+)	-0.0944347	7.68E-05	0.00072997
SREBF2(+)	-0.1298707	2.52E-15	1.44E-13
STAT1(+)	-0.131333	1.01E-09	3.84E-08
STAT2(+)	-0.0361845	0.0432948	0.12655403
STAT3(+)	-0.0352638	0.01835407	0.07100494
STAT5A(+)	-0.0829992	0.17951949	0.35284865
TAL1(+)	0.0485634	0.12451701	0.27833213
TCF12(+)	0.05956772	0.0891348	0.23094018
TCF7L2(+)	0.00635001	0.83790169	0.88445179
TFEC(+)	0.00365253	0.73028457	0.83759783
UBP1(+)	0.03419491	0.73053274	0.83759783
USF2(+)	0.17205802	1.69E-07	3.85E-06
XBP1(+)	0.02162899	0.2008141	0.37141915
YY1(+)	0.01310091	0.43007465	0.57232606
ZBTB7A(+)	0.12544152	0.00285988	0.01715927
ZFP64(+)	0.11107747	0.27289834	0.46754146
ZNF121(+)	-0.0904482	0.22762893	0.39922613
ZNF131(+)	0.09957761	0.37249081	0.53272287
ZNF143(+)	0.0466123	0.30469753	0.48243776
ZNF337(+)	0.11888503	0.30094755	0.48243776
ZNF736(+)	-0.171432	0.29697334	0.48243776
ZNF84(+)	0.0908284	0.20823547	0.37141915
ZNF91(+)	-0.0298208	0.12261348	0.27833213

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Regulon	logFC	P.Value	adj.P.Val
ARID3A(+)	0.00591601	0.81893606	0.83355992
ARNT(+)	0.07180689	6.76E-06	1.33E-05
ARNTL(+)	-0.5494886	5.79E-25	2.75E-24
ATF1(+)	-0.0175924	0.70377484	0.75688992
ATF4(+)	-0.4034802	7.49E-15	2.14E-14
ATF6(+)	0.02352352	0.0349015	0.04852159
BACH1(+)	-0.155263	4.48E-33	2.69E-32
BCL6(+)	-0.6106981	1.84E-113	1.05E-111
BHLHE41(+)	0.05330573	3.65E-08	8.16E-08
CEBPA(+)	0.26514159	9.04E-71	1.29E-69
CEBPB(+)	-0.1057725	2.42E-20	8.35E-20
CEBPD(+)	-0.0395583	0.00034083	0.00061673
CEBPZ(+)	-0.2056508	1.01E-06	2.13E-06
CLOCK(+)	0.05562613	0.00254119	0.0041385
CREB1(+)	0.12779381	8.74E-22	3.21E-21
CREB3L2(+)	-0.023361	0.05587492	0.07515717
CREM(+)	-0.1837623	6.85E-44	4.88E-43
CTCF(+)	-0.0888121	0.00043005	0.00075425
CUX1(+)	-0.0337235	3.23E-05	6.03E-05
DEAF1(+)	0.22601963	2.70E-05	5.13E-05
DNMT1(+)	-0.2260032	1.17E-09	2.78E-09
E2F3(+)	-0.1461465	0.00258599	0.00415215
ELF1(+)	0.03356738	2.55E-06	5.11E-06
ELF2(+)	0.09134014	0.00320113	0.00499902
ELK3(+)	0.29888944	6.05E-63	6.90E-62
ELK4(+)	0.07304802	1.86E-06	3.79E-06
ETS2(+)	-0.0674314	8.24E-08	1.81E-07
ETV5(+)	0.06538082	6.44E-11	1.56E-10
ETV6(+)	-0.0759559	1.91E-16	5.73E-16
FLI1(+)	0.1208166	1.41E-33	8.90E-33
FOS(+)	-0.2799944	9.98E-86	2.28E-84
FOXJ3(+)	-0.0956492	0.0944701	0.12238172
FOXK1(+)	-0.0408257	0.02319539	0.03264536
FOXN3(+)	0.39102445	3.90E-23	1.64E-22
FOXO1(+)	0.32158209	3.91E-91	1.11E-89
FOXO3(+)	0.2493956	4.57E-116	5.21E-114
FOXP2(+)	0.21352037	4.14E-67	5.24E-66
GABPA(+)	0.13266882	0.00412514	0.00627022
GTF2IRD1(+)	-0.2005572	0.00226775	0.00374672
HBP1(+)	0.33144286	2.26E-08	5.26E-08
HDX(+)	-0.1187177	0.20258324	0.25660544
HIF1A(+)	-0.1024423	2.50E-26	1.36E-25
HIVEP1(+)	-0.245241	2.34E-05	4.52E-05
HIVEP2(+)	-0.5796496	7.88E-74	1.28E-72
HSF1(+)	0.02288877	0.62569366	0.68585651
IKZF1(+)	0.10556863	2.91E-19	9.48E-19
IRF2(+)	0.09490015	1.64E-15	4.80E-15
IRF3(+)	0.39999174	2.97E-52	2.42E-51
IRF5(+)	0.1837992	1.19E-23	5.44E-23
IRF8(+)	0.11670303	1.01E-21	3.58E-21
JDP2(+)	-0.1973756	2.04E-43	1.37E-42
JUND(+)	0.01871492	0.2975421	0.36472891
KDM5B(+)	0.09346894	0.06627224	0.08784924
KLF3(+)	-0.1157036	3.72E-12	9.85E-12
KLF6(+)	-0.0985407	0.00013604	0.00025014
MAFB(+)	-0.1218576	1.79E-23	7.83E-23
MAFG(+)	0.07710115	1.05E-06	2.19E-06
MAX(+)	-0.0031125	0.72073788	0.76077887
MITF(+)	0.03316335	0.00328596	0.00506216
MLXIP(+)	0.01775222	0.71386677	0.76056834
MXD4(+)	0.2622179	4.33E-59	4.12E-58
NFATC1(+)	-0.1470567	0.00104113	0.00177147
NFE2L2(+)	0.00647146	0.61448829	0.68011325
NFIC(+)	-0.0585116	0.0012534	0.00210129
NFKB1(+)	-0.1836351	1.84E-22	7.22E-22
NFYC(+)	0.06758689	0.00580225	0.00859035
NR2C1(+)	0.23236926	1.51E-07	3.25E-07
NR2C2(+)	0.20327729	6.09E-52	4.63E-51
NR3C1(+)	0.13706478	1.19E-55	1.04E-54
NR6A1(+)	-0.0752955	0.40323411	0.45757362
NRF1(+)	0.08074232	4.48E-17	1.38E-16
PBX3(+)	0.09762839	2.11E-22	8.01E-22
PKNOX1(+)	-0.0495826	0.40539417	0.45757362
POU2F1(+)	0.0163895	0.73347371	0.76711929
POU2F2(+)	0.15841726	1.59E-11	4.03E-11
PPARG(+)	0.00526504	0.92564966	0.93384125
PRDM1(+)	0.0835767	0.00048408	0.00083615
RBPJ(+)	-0.5766791	1.80E-22	7.22E-22
REL(+)	-0.3036521	2.11E-11	7.20E-11
RFX3(+)	0.04737822	0.35081213	0.42097456
RREB1(+)	-0.0235463	0.36918035	0.43840167
RUNX1(+)	0.06114071	0.00456572	0.00684858
RUNX2(+)	0.33412884	6.70E-26	3.47E-25
RXRA(+)	-0.0153197	0.7828912	0.80405043
SMAD3(+)	0.07160642	0.18164317	0.23266653
SMAD5(+)	0.01463657	0.58492166	0.65373598
SOX5(+)	-0.1736983	0.00750613	0.0109705
SP1(+)	-0.0402841	0.22947779	0.28435291
SP3(+)	-0.0255423	0.33113702	0.40154171
SP4(+)	0.51046958	1.26E-25	6.24E-25
SPI1(+)	-0.1143711	4.07E-20	1.36E-19
SREBF1(+)	-0.379252	3.75E-109	1.43E-107
SREBF2(+)	-0.0982548	6.81E-12	1.76E-11
STAT1(+)	-0.349022	9.37E-76	1.78E-74
STAT2(+)	-0.1738439	3.71E-30	2.12E-29
STAT3(+)	-0.0781153	3.18E-08	7.24E-08
STAT5A(+)	0.08338293	0.07916817	0.1037376
TAL1(+)	0.24298741	5.51E-18	1.74E-17
TCF12(+)	0.08400699	0.01710959	0.02438116
TCF7L2(+)	0.23777223	5.98E-14	1.66E-13
TFEC(+)	0.06588691	2.79E-13	7.58E-13
UBP1(+)	0.11709413	0.22690786	0.2842582
USF2(+)	0.00040153	0.98502058	0.98502058
XBP1(+)	-0.2429234	2.92E-60	3.02E-59
YY1(+)	-0.0039724	0.77587885	0.80405043
ZBTB7A(+)	-0.0388694	0.40137489	0.45757362
ZFP64(+)	0.03185792	0.63761434	0.692267
ZNF121(+)	-0.1976529	0.00041501	0.00073924
ZNF131(+)	0.0665015	0.37744566	0.44359593
ZNF143(+)	-0.0956555	0.00299937	0.00474901
ZNF337(+)	0.13508863	0.03658749	0.0502527
ZNF736(+)	0.10095162	0.39171388	0.45566716
ZNF84(+)	0.16186253	0.01005165	0.01450491
ZNF91(+)	0.02867948	0.05603824	0.07515717

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Regulon	logFC	P.Value	adj.P.Val
ARID3A(+)	-0.0650321	8.49E-123	2.85E-122
ARNT(+)	0.0193968	1.57E-24	2.98E-24
ARNTL(+)	0.03011369	2.59E-05	3.48E-05
ATF1(+)	0.02779037	7.01E-06	9.87E-06
ATF4(+)	0.02665058	0.00179595	0.0021327
ATF6(+)	0.01242027	2.56E-23	4.70E-23
BACH1(+)	0.00570864	0.00017986	0.00023038
BCL6(+)	0.03008598	2.40E-18	4.14E-18
BHLHE41(+)	0.02703326	3.80E-118	1.20E-117
CEBPA(+)	0.13503764	0	0
CEBPB(+)	0.02719357	4.17E-93	1.13E-92
CEBPD(+)	0.05043143	8.07E-223	4.00E-222
CEBPZ(+)	0.03294128	0.00186903	0.00219457
CLOCK(+)	0.05315835	1.21E-97	3.37E-97
CREB1(+)	0.03462694	3.99E-85	9.68E-85
CREB3L2(+)	0.02855114	7.01E-109	2.05E-108
CREM(+)	0.02002385	7.61E-24	1.42E-23
CTCF(+)	-0.1299844	0	0
CUX1(+)	0.01804055	6.36E-83	1.51E-82
DEAF1(+)	0.02335561	0.0044951	0.00507368
DNMT1(+)	0.05789578	1.07E-25	2.07E-25
E2F3(+)	-0.0080443	0.20158607	0.20891647
ELF1(+)	0.04094337	0	0
ELF2(+)	-0.0168393	0.00018813	0.0002383
ELK3(+)	0.00758656	9.15E-05	0.00011987
ELK4(+)	0.05398991	1.59E-163	6.05E-163
ETS2(+)	0.01828868	1.49E-37	3.14E-37
ETV5(+)	0.0371553	4.20E-277	2.39E-276
ETV6(+)	0.02506115	1.40E-139	5.00E-139
FLI1(+)	0.0347343	1.08E-238	5.60E-238
FOS(+)	0.04415796	1.95E-104	5.57E-104
FOXJ3(+)	0.02211524	0.00106497	0.00127796
FOXK1(+)	-0.0037971	0.03576281	0.0388282
FOXN3(+)	0.02458579	1.69E-20	2.96E-20
FOXO1(+)	-0.0540457	1.41E-291	8.91E-291
FOXO3(+)	0.04459014	0	0
FOXP2(+)	-0.0103925	5.20E-14	8.72E-14
GABPA(+)	0.06037339	1.25E-29	2.54E-29
GTF2IRD1(+)	0.03267311	5.56E-08	8.33E-08
HBP1(+)	-0.0224842	0.00427387	0.00487221
HDX(+)	0.03167346	0.00019983	0.00025034
HIF1A(+)	0.03426526	3.45E-172	1.41E-171
HIVEP1(+)	0.02775991	2.13E-05	2.90E-05
HIVEP2(+)	0.01261939	0.00015651	0.00020275
HSF1(+)	-0.0297576	1.25E-08	1.95E-08
IKZF1(+)	0.0296664	7.33E-126	2.53E-125
IRF2(+)	0.02725947	7.34E-116	2.26E-115
IRF3(+)	0.00523415	0.05684717	0.06113752
IRF5(+)	0.13709299	0	0
IRF8(+)	0.01453869	2.11E-26	4.15E-26
JDP2(+)	0.03017731	4.04E-57	9.41E-57
JUND(+)	0.19693189	0	0
KDM5B(+)	0.05457116	1.80E-10	2.90E-10
KLF3(+)	0.00251293	0.23311063	0.23941092
KLF6(+)	0.12076571	2.22E-196	9.71E-196
MAFB(+)	0.13556448	0	0
MAFG(+)	0.14794229	0	0
MAX(+)	0.03100729	9.85E-221	4.68E-220
MITF(+)	0.08190969	0	0
MLXIP(+)	0.00399147	0.56191174	0.56688441
MXD4(+)	0.01353593	1.84E-12	3.04E-12
NFATC1(+)	0.16352404	4.97E-152	1.83E-151
NFE2L2(+)	0.06039838	5.08E-262	2.76E-261
NFIC(+)	-0.0176651	1.13E-21	2.05E-21
NFKB1(+)	0.0728417	1.48E-219	6.75E-219
NFYC(+)	0.04773363	8.06E-48	1.80E-47
NR2C1(+)	0.00823027	0.10478119	0.11163604
NR2C2(+)	0.03104152	1.55E-110	4.65E-110
NR3C1(+)	0.04755058	0	0
NR6A1(+)	-0.0324897	0.00465826	0.00520629
NRF1(+)	0.0390588	3.34E-284	2.00E-283
PBX3(+)	0.06446258	0	0
PKNOX1(+)	0.00344799	0.61926877	0.61926877
POU2F1(+)	-0.0680113	2.54E-48	5.80E-48
POU2F2(+)	0.06140594	7.35E-170	2.89E-169
PPARG(+)	0.27423637	0	0
PRDM1(+)	0.0155501	7.49E-08	1.11E-07
RBPJ(+)	0.04953558	5.48E-11	8.92E-11
REL(+)	0.07910553	2.60E-42	5.60E-42
RFX3(+)	-0.0234896	8.32E-06	1.16E-05
RREB1(+)	0.00770848	0.00188656	0.00219457
RUNX1(+)	0.05263389	1.28E-120	4.18E-120
RUNX2(+)	-0.0113447	7.64E-05	0.00010127
RXRA(+)	0.02756885	2.71E-06	3.92E-06
SMAD3(+)	0.06244106	1.54E-20	2.75E-20
SMAD5(+)	0.05275364	4.83E-45	1.06E-44
SOX5(+)	-0.168867	2.39E-186	1.01E-185
SP1(+)	0.02900759	2.30E-14	3.91E-14
SP3(+)	0.04735179	6.48E-36	1.34E-35
SP4(+)	-0.0190743	0.00095704	0.00116067
SPI1(+)	0.0534056	0	0
SREBF1(+)	-0.0016555	0.49878473	0.5076916
SREBF2(+)	-0.0285733	1.35E-86	3.35E-86
STAT1(+)	0.17025754	0	0
STAT2(+)	0.08431104	0	0
STAT3(+)	0.00672708	1.54E-05	2.12E-05
STAT5A(+)	0.03125692	4.23E-06	6.02E-06
TAL1(+)	-0.0157309	2.74E-08	4.21E-08
TCF12(+)	0.04721587	3.77E-87	9.55E-87
TCF7L2(+)	-0.0126863	1.98E-06	2.89E-06
TFEC(+)	0.04204573	0	0
UBP1(+)	-0.0128076	0.18757191	0.19799257
USF2(+)	0.18463043	0	0
XBP1(+)	0.03490992	3.70E-91	9.59E-91
YY1(+)	0.03367925	7.67E-92	2.03E-91
ZBTB7A(+)	-0.0417609	5.98E-29	1.20E-28
ZFP64(+)	-0.062572	3.47E-10	5.50E-10
ZNF121(+)	-0.0255213	0.0026133

Regulon specificity scores (RSS) in microglial subclusters

A high regulon specificity score indicates a relatively specific enrichment of this regulon for a particular subcluster

Regulon	Micro1	Micro2	Micro3	PVM
ARNT(+)	0.554	0.367	0.297	0.281
ATF6(+)	0.558	0.366	0.296	0.280
BACH1(+)	0.556	0.365	0.299	0.278
BCL6(+)	0.551	0.357	0.302	0.276
BHLHE41(+)	0.559	0.367	0.297	0.277
CEBPA(+)	0.541	0.382	0.292	0.283
CEBPB(+)	0.549	0.370	0.300	0.281
CEBPD(+)	0.543	0.376	0.291	0.290
CLOCK(+)	0.550	0.366	0.296	0.284
CREB1(+)	0.552	0.366	0.300	0.281
CREB3L2(+)	0.554	0.366	0.301	0.278
CREM(+)	0.533	0.380	0.293	0.295
CTCF(+)	0.555	0.356	0.304	0.274
CUX1(+)	0.556	0.368	0.295	0.281
ELF1(+)	0.555	0.368	0.297	0.282
ELK3(+)	0.565	0.360	0.300	0.269
ELK4(+)	0.556	0.363	0.299	0.279
ETS2(+)	0.556	0.370	0.292	0.282
ETV5(+)	0.562	0.363	0.300	0.274
ETV6(+)	0.558	0.365	0.298	0.279
FLI1(+)	0.560	0.363	0.297	0.279
FOS(+)	0.535	0.379	0.294	0.289
FOXK1(+)	0.554	0.366	0.301	0.277
FOXO1(+)	0.562	0.359	0.300	0.274
FOXO3(+)	0.555	0.367	0.294	0.283
FOXP2(+)	0.568	0.359	0.299	0.271
HIF1A(+)	0.549	0.372	0.294	0.286
IKZF1(+)	0.565	0.362	0.299	0.273
IRF2(+)	0.560	0.361	0.299	0.280
IRF3(+)	0.556	0.355	0.305	0.276
IRF5(+)	0.555	0.366	0.294	0.273
IRF8(+)	0.566	0.361	0.302	0.268
JDP2(+)	0.542	0.374	0.295	0.289
JUND(+)	0.524	0.386	0.288	0.291
KLF3(+)	0.554	0.362	0.304	0.277
MAFB(+)	0.527	0.389	0.295	0.290
MAFG(+)	0.526	0.386	0.289	0.293
MAX(+)	0.552	0.368	0.299	0.283
MITF(+)	0.545	0.376	0.293	0.288
MXD4(+)	0.551	0.368	0.298	0.279
NFE2L2(+)	0.545	0.375	0.294	0.287
NFIC(+)	0.553	0.367	0.298	0.278
NFKB1(+)	0.548	0.371	0.297	0.280
NFYC(+)	0.549	0.361	0.301	0.280
NR2C2(+)	0.555	0.365	0.295	0.284
NR3C1(+)	0.556	0.367	0.297	0.281
NRF1(+)	0.556	0.367	0.296	0.281
PBX3(+)	0.549	0.370	0.297	0.285
POU2F2(+)	0.565	0.362	0.300	0.266
RREB1(+)	0.553	0.367	0.293	0.281
RUNX1(+)	0.567	0.357	0.302	0.269
SP3(+)	0.541	0.364	0.304	0.281
SPI1(+)	0.552	0.372	0.297	0.279
SREBF1(+)	0.539	0.376	0.298	0.280
SREBF2(+)	0.561	0.361	0.304	0.271
STAT1(+)	0.549	0.360	0.302	0.284
STAT2(+)	0.547	0.363	0.301	0.289
STAT3(+)	0.557	0.369	0.293	0.278
TFEC(+)	0.556	0.367	0.296	0.282
USF2(+)	0.533	0.379	0.286	0.282
XBP1(+)	0.549	0.366	0.300	0.282
YY1(+)	0.551	0.369	0.297	0.284
ZNF91(+)	0.554	0.365	0.300	0.279

Supplementary Table 15_Microglial cluster genes
Contents

Sheet name	Description
Micro1	Differentially expressed genes (logFC > 0.25, P-adj <0.05) for Micro1 relative to Micro2, Micro3 and PVM clusters, as defined by the Seurat *FindMarkers* function
Micro2	Differentially expressed genes (logFC > 0.25, P-adj <0.05) for Micro2 relative to Micro1, Micro3 and PVM clusters, as defined by the Seurat *FindMarkers* function
Micro3	Differentially expressed genes (logFC > 0.25, P-adj <0.05) for Micro3 relative to Micro1, Micro2 and PVM clusters, as defined by the Seurat *FindMarkers* function
PVM	Differentially expressed genes (logFC > 0.25, P-adj <0.05) for perivascular macrophages (PVMs) relative to all Micro clusters, as defined by the Seurat *FindMarkers* function

Supplementary Table 15_Microglial cluster genes
Micro 1

Gene	avg_logFC	p_val_adj
GRID2	0.426296	4.92E-116
FOXP2	0.405731	0
KHDRBS3	0.393592	0
AC008691.1	0.383815	6.36E-208
AP003481.1	0.371718	0
LINC02232	0.363242	0
ERC2	0.352591	6.40E-244
BLNK	0.34387	0
CPED1	0.341726	0
TLN2	0.336465	0
P2RY12	0.334303	0
IL6ST	0.334208	0
SRGAP2B	0.319873	0
CCDC26	0.319508	1.31E-78
ST6GALNAC3	0.319296	3.45E-281
NAV3	0.316925	0
ABCC4	0.315745	0
CX3CR1	0.313415	0
SRGAP2	0.294314	0
LINC01684	0.293163	1.87E-204
TIAM1	0.290296	2.25E-302
SRGAP2C	0.286308	0
IGSF21	0.283065	0
TMEM156	0.280064	1.15E-278
TMEM163	0.2751	7.13E-140
RASGEF1C	0.274634	0
ADAM28	0.271739	0
OXR1	0.270826	1.87E-196
PRDM11	0.270185	5.03E-150
RUNX2	0.269405	9.18E-283
SERPINB9	0.268154	1.21E-258
DENND3	0.265293	1.20E-284
DOCK8	0.26466	0
P3H2	0.261351	1.50E-180
CSF1R	0.258822	0
AC079015.1	0.256017	2.66E-203
AL034397.3	0.253471	1.35E-208
FARP1	-0.25337	2.80E-36
THRB	-0.25355	3.15E-67
LINGO1	-0.25429	1
SLC26A3	-0.25646	1
PRKCE	-0.26252	1.55E-23
RGL1	-0.26314	0.000764964
OPHN1	-0.27705	5.26E-10
PEAK1	-0.28224	4.54E-08
ATG7	-0.28864	4.26E-53
PPARG	-0.29255	8.74E-30
DST	-0.29944	1.95E-10
AHCYL1	-0.30362	0.031105351
SYNE1	-0.30491	5.57E-21
MITF	-0.30775	1.70E-37
PADI2	-0.31498	1
RASGEF1B	-0.31984	5.20E-13
ARID5B	-0.31991	5.79E-47
ADGRB3	-0.32642	1
NHSL1	-0.32854	2.82E-23
ITSN1	-0.34057	6.47E-32
SAMD4A	-0.34562	9.01E-43
GLIS3	-0.36694	7.31E-19
DTNA	-0.36697	4.68E-30
GAS7	-0.38199	3.35E-68
ACSL1	-0.39436	1.08E-27
HSP90AA1	-0.40643	0.027211268
CPM	-0.41644	5.50E-22
FP236383.1	-0.42706	1.11E-31
MYO1E	-0.53435	3.43E-62
SOX5	-0.53682	7.84E-18
CLU	-0.56208	1.43E-72
DPYD	-0.56575	1.28E-164
SPARCL1	-0.57305	4.85E-71
PITPNC1	-0.58367	3.74E-13
CD163	-0.59056	5.03E-76
STARD13	-0.59437	1.48E-174
NPAS3	-0.66127	8.78E-34
CADM1	-0.83318	5.12E-196
CADM2	-0.86155	1.64E-68
NRXN1	-0.99805	1.26E-63
LRP1B	-1.05399	1.58E-69
GPM6A	-1.12059	5.37E-80
SLC1A2	-1.12851	2.18E-85
CTNNA2	-1.15555	7.65E-73
PCDH9	-1.27376	3.24E-74
LSAMP	-1.31076	7.76E-82

Supplementary Table 15_Microglial cluster genes
Micro 2

Gene	avg_logFC	p_val_adj
MYO1E	1.034973629	0
CD83	0.939272529	0
PTPRG	0.792791756	5.19E-53
GLDN	0.69540176	2.47E-171
PADI2	0.682871159	2.93E-294
OLR1	0.670161405	0
GPNMB	0.663050582	0
TPRG1	0.597623239	1.72E-136
FTL	0.588308809	3.97E-247
PPARG	0.586644016	0
SPP1	0.574038865	2.11E-213
CPM	0.566288465	1.22E-171
FTH1	0.559211388	6.99E-145
GAS7	0.555254181	0
MITF	0.551317616	0
PLA2G7	0.542262432	0
FNIP2	0.507102489	1.30E-227
ARID5B	0.500470407	5.66E-159
ELL2	0.473864184	3.48E-173
AC066613.2	0.464434381	1.99E-102
SOCS6	0.450021194	2.84E-189
DSCAM	0.442546744	4.32E-196
EEPD1	0.438056684	5.89E-93
MAFB	0.432515905	7.86E-298
ADAMTS17	0.428586502	1.03E-87
XYLT1	0.426092521	1.18E-180
ZNF804A	0.417148866	8.02E-138
ITGAX	0.416535559	6.72E-288
RGS1	0.415625085	1.22E-124
WIPF3	0.411128088	1.88E-225
NPL	0.401506766	1.20E-239
ACSL1	0.401051965	3.69E-143
TMSB4X	0.40074146	1.81E-145
ATG7	0.399117621	9.59E-242
RTTN	0.397172784	7.58E-132
SGK1	0.395944014	7.24E-169
RAPGEF1	0.393959883	2.18E-180
SLC2A3	0.385838049	1.59E-38
ASAH1	0.38090979	1.28E-214
APOE	0.368704604	5.10E-157
STARD13	0.367140594	1.17E-138
HSP90AA1	0.365970622	3.48E-05
UGCG	0.360949947	6.12E-168
NHSL1	0.358048468	5.26E-47
APOC1	0.35467153	8.45E-167
MTSS1	0.344554639	9.25E-124
SAT1	0.344197617	3.19E-131
LIMS1	0.3420839	2.99E-127
GNA13	0.340692184	3.31E-103
SUSD1	0.340592938	1.29E-189
FMNL2	0.340047356	2.71E-99
PLEK	0.333732997	2.23E-113
CTSB	0.327938339	7.69E-160
NAMPT	0.326844983	4.22E-38
TPT1	0.324881826	1.02E-71
RPL19	0.324844861	1.49E-82
EEF1A1	0.323259847	2.54E-107
SAMSN1	0.317668409	9.22E-128
MERTK	0.317038415	4.26E-64
PDE8A	0.316887608	3.61E-125
RASSF3	0.316684553	4.97E-153
MGAT1	0.315514157	1.45E-164
KCNMA1	0.314392583	9.33E-81
SRGN	0.314389307	1.85E-62
HIF1A-AS2	0.313179645	2.50E-65
SCIN	0.304768256	2.95E-114
PRKCE	0.301495967	4.75E-94
SLC11A1	0.300605513	6.14E-133
TANC2	0.300254706	7.64E-102
LIPA	0.299363011	7.47E-127
FRMD4B	0.298757924	1.13E-133
CHSY3	0.29719433	2.64E-113
SYTL3	0.296253035	7.86E-93
PDE3B	0.294716976	1.02E-79
HIF1A	0.293495461	1.39E-55
MB21D2	0.290478747	4.11E-80
MALT1	0.290068175	3.38E-118
DENND4C	0.288730518	4.45E-134
HSPH1	0.288608568	4.54E-12
DPYD	0.288111677	3.74E-70
PEAK1	0.287602514	8.07E-82
UBC	0.283037509	9.27E-87
B2M	0.282442111	1.22E-135
RASGRP3	0.276251937	2.90E-106
RPL10	0.272942777	2.36E-96
RPL3P4	0.271205112	2.94E-104
GPX1	0.270111223	5.94E-136
TMSB10	0.269368263	2.92E-69
GBE1	0.268010754	1.78E-63
SLC1A3	0.266953942	2.10E-163
TMEM51	0.266758609	1.62E-103
RPS27A	0.266000885	1.96E-74
PDGFB	0.262844985	4.03E-127
AC008957.2	0.26233044	1.37E-124
PSAP	0.26107703	2.28E-116
ZNF331	0.260827684	4.13E-52
LINC00278	0.26048499	8.01E-20
RPS19	0.258295787	6.64E-107
RPL41	0.257607674	2.48E-78
AC073861.1	0.25702321	4.36E-65
STEAP1B	0.253591391	1.35E-102
SDK1	0.251306791	1.23E-63
CYTH1	0.250315078	3.44E-133
HIVEP1	0.250129219	3.10E-94
PARD3B	-0.250818481	1.83E-12
PSD3	-0.250932091	3.73E-08
TIAM1	-0.251082759	2.79E-29
DST	-0.253984235	8.45E-16
NAV3	-0.257894865	4.52E-91
PDE4D	-0.266891959	2.20E-13
TRPS1	-0.267065734	1.13E-35
C3	-0.268272591	1.53E-39
PLB1	-0.268348624	1.49E-36
MVB12B	-0.281848528	1.14E-51
AL163541.1	-0.282984994	1.80E-18
ST6GALNAC3	-0.2888384	6.01E-55
MS4A6A	-0.290406834	3.48E-45
ARHGAP22	-0.291239115	6.55E-96
NFIA	-0.300833449	3.97E-35
MIR646HG	-0.316547646	9.59E-50
AOAH	-0.325140003	2.27E-131
KHDRBS3	-0.329005452	1.04E-39
FOXP2	-0.333980666	2.07E-97
PRPF38B	-0.334524083	5.50E-18
MIR99AHG	-0.336140898	6.78E-74
LINC01684	-0.339783862	1.59E-46
LINC02232	-0.342419277	2.77E-81
CPED1	-0.343689774	1.21E-111
ORS2K3P	-0.358249809	6.21E-38
PITPNC1	-0.391872636	0.010113825
RASGEF1C	-0.393176105	2.91E-53
AC008691.1	-0.411270902	2.46E-30
ERC2	-0.421075515	2.26E-67
GRID2	-0.443984035	3.78E-38
PRKCA	-0.45561849	1.62E-186
NPAS3	-0.456153323	1.34E-06
MRC1	-0.472046227	1.32E-72
AC244021.1	-0.508333147	3.20E-144
CCDC26	-0.552471709	1.88E-51
CMAHP	-0.575917565	1.04E-163
AP003481.1	-0.593806371	8.80E-131
TMEM163	-0.699433657	1.23E-147
ADGRB3	-0.707419585	2.45E-93
SLC1A2	-0.797840012	3.01E-13
LSAMP	-0.860355715	1.54E-09
PCDH9	-0.883314465	1.17E-15

Supplementary Table 15_Microglial cluster genes
Micro 3

Gene	avg_logFC	p_val_adj
FP236383.1	0.903468016	2.16E-68
AC244021.1	0.85399617	3.19E-240
PRPF38B	0.681818318	1
SON	0.613259139	2.66E-14
BOD1L1	0.600704143	1
NKTR	0.582563757	1
SRRM2	0.546657978	1
PRPF4B	0.520217026	2.17E-09
SLC26A3	0.50213036	8.22E-10
ZNF780B	0.493742786	1.41E-10
RASGEF1C	0.486362304	3.18E-16
GOLGB1	0.481952326	1.06E-21
RASGEF1B	0.472397204	1.23E-20
ZMAT1	0.462644085	6.40E-22
PRRC2C	0.461588156	1
ANKRD12	0.459076811	3.96E-20
AKAP9	0.453506501	5.87E-09
CCDC88A	0.453059473	1
LINGO1	0.449564675	6.48E-10
GOLGA4	0.442204034	1
COL19A1	0.431967398	4.49E-32
C3	0.428529213	7.97E-13
AP003481.1	0.409602196	1
PNISR	0.40960057	1
HIVEP3	0.409222805	0.009464315
XAF1	0.404876905	1.08E-31
SYNDIG1	0.404336292	1.21E-70
BDP1	0.403933909	1.09E-37
KCNIP1	0.393828507	1
TRIP11	0.387737696	7.26E-40
ATRX	0.383873245	1
PCF11	0.381674935	4.01E-46
KBTBD12	0.380321468	4.33E-16
PRR14L	0.374094309	4.97E-37
ZFP36L2	0.366781671	5.11E-18
GCC2	0.366611847	6.81E-41
BPTF	0.352569773	9.35E-10
PARP14	0.35053885	8.27E-25
ORS2K3P	0.349950966	1.96E-05
AC027097.2	0.349168878	1.79E-32
RBM25	0.348194844	9.63E-41
LPAR6	0.345562294	1
ZNF117	0.342860156	1.66E-33
SH3BGRL	0.339500023	1
RESF1	0.336684082	7.22E-40
BAZ1B	0.336621841	9.12E-62
GAK	0.333298215	7.95E-60
MYO1F	0.332338902	1
POU2F2	0.330010803	4.49E-06
FAM228B	0.324377281	3.82E-38
PNN	0.320684365	8.72E-81
ANKRD11	0.320564304	1
SP140	0.316403435	7.35E-41
TTC14	0.315401216	5.00E-45
SAMD9L	0.314696447	9.66E-43
SETX	0.313006053	0.000864941
LILRB1	0.312315476	5.09E-60
CASP8AP2	0.312298071	5.53E-38
AL390728.4	0.312114438	1.20E-58
TAF1D	0.310027601	2.78E-60
AC008691.1	0.305606711	1
HNRNPL	0.294450552	3.56E-46
ANKRD36C	0.292782265	1.01E-48
BIN1	0.290067207	3.72E-28
AOAH	0.288259617	2.30E-10
UPF2	0.287979268	5.59E-75
IFI16	0.287964823	1
DST	0.287857368	1
RBBP6	0.282036122	3.80E-73
GMDS-DT	0.281125699	2.09E-13
MIS18BP1	0.274780277	1.06E-37
NOL8	0.271001816	4.57E-47
CNTRL	0.268866225	1.62E-54
DDX21	0.26628681	6.79E-65
LINC02232	0.265703557	1
INO80D	0.263478056	9.49E-82
EIF5B	0.261373015	3.78E-63
TMEM163	0.259669932	0.001228831
ERCC6L2	0.257080027	1.08E-68
ERICH1	0.256389524	4.37E-74
ZFC3H1	0.256371997	6.85E-67
WNT2B	0.25581022	4.40E-48
AC139887.2	0.255572861	1.09E-72
CHD9	0.255034516	3.43E-11
RIF1	0.254985997	1.02E-71
ZNF37BP	0.254430966	1.11E-57
CALM1	0.250787602	3.62E-81
NPL	-0.252962151	8.98E-279
SRGAP2C	-0.253547791	1.56E-232
MS4A4A	-0.257458014	4.83E-188
ARID5B	-0.259793107	1.12E-158
RPL8	-0.262599179	1.05E-207
SRGAP2B	-0.262956617	3.10E-197
CD81	-0.263352542	0
HLA-A	-0.263403525	2.02E-276
GNA13	-0.263956271	3.19E-298
ENTPD1-AS1	-0.265526176	0
HERPUD1	-0.265898612	5.30E-266
RPL13	-0.271466754	1.61E-273
FCER1G	-0.271828447	5.15E-246
RPS2	-0.273371069	1.61E-257
RPS11	-0.273454595	6.05E-227
LRP4	-0.275752373	2.05E-272
RPL13P12	-0.279041567	8.20E-233
KCTD12	-0.279228312	0
CTSB	-0.281190124	0
TUBA1B	-0.283138631	2.78E-284
GPX1	-0.286709256	4.02E-263
PSAP	-0.288205044	0
MERTK	-0.289653192	2.27E-230
RPLP2	-0.290070436	3.83E-218
OLR1	-0.290589328	1.25E-241
RPS3	-0.291310715	1.23E-271
DPYD	-0.291883606	1.22E-124
ABCA1	-0.292426543	1.64E-225
RGL1	-0.292431222	3.80E-228
HIF1A-AS2	-0.292450953	6.07E-173
RPL3P4	-0.293350496	2.28E-240
RNF144B	-0.298702237	1.38E-243
AIF1	-0.305696305	5.34E-211
AL034397.3	-0.30736848	3.22E-300
RPL11	-0.311877355	7.00E-267
C1QB	-0.311976046	0
SLC2A3	-0.314470945	4.99E-142
RPLP1	-0.315194748	9.27E-242
FCGR3A	-0.316751832	0
MAN1A1	-0.319973522	3.50E-291
ASAH1	-0.322980145	0
HLA-B	-0.323387787	0
ACSL1	-0.326109926	3.50E-265
RPL37A	-0.326830615	4.54E-276
AC079793.1	-0.331658839	4.12E-258
MTSS1	-0.335106585	1.27E-247
RPL10	-0.338711736	1.26E-271
ELL2	-0.340565005	6.27E-245
C1QA	-0.341483577	0
HIF1A	-0.34478454	7.02E-285
RPL19	-0.346172159	6.03E-228
CD14	-0.353639132	3.11E-274
RAB11A	-0.353901608	0
ACTB	-0.354093885	0
STARD13	-0.357761724	2.03E-203
MITF	-0.360754455	6.03E-278
AC011933.4	-0.361069299	8.47E-287
MCF2L2	-0.362924226	1.68E-265
HSPA1A	-0.364203327	4.62E-220
AC016739.1	-0.366612199	4.89E-242
RPL41	-0.368510473	3.12E-263
MYO1E	-0.380117117	2.58E-236
CPM	-0.380971321	1.94E-244
ABHD15-AS1	-0.383697436	0
DLEU7	-0.385432395	2.26E-295
RPS19	-0.387156952	0
HLA-DRB1	-0.394125759	0
SHOC1	-0.396288016	4.54E-270
APOE	-0.398818385	0
TMSB10	-0.404423055	8.55E-255
FAM177B	-0.406356744	1.95E-276
B2M	-0.407035434	0
EEF1A1	-0.409499963	0
AP003086.2	-0.419167962	0
AC044781.1	-0.436834618	0
TPT1	-0.451136388	0
CD163	-0.45392345	5.27E-193
HLA-DRA	-0.476035914	0
SRGN	-0.490217461	4.63E-295
CD74	-0.506698542	0
AC120193.1	-0.53679618	0
TMSB4X	-0.546203537	0
C1QC	-0.574031776	0
FTH1	-0.721541827	2.93E-297
FTL	-0.866049207	0

Supplementary Table 15_Microglial cluster genes
PVMs

Gene	avg_log2FC	p_val_adj
P18K1	2.3561727577	0
CD163	1.5882252	0
SPI0	1.0977172091	0
NAAMP	1.0482539516	7.35E-165
NECP1	1.0299502003	0
SQSAP2	0.9764666572	0
STARD13	0.9492615296	2.14E-275
SLC39A8A	0.9366660819	0
TSPN2	0.9156466003	0
GNC3	0.9078192868	1.49E-256
SMC1	0.8921329011	5.97E-93
TPRE1	0.7923172216	9.68E-216
THMB	0.7585735556	0
LYVE1	0.7295767577	6.82E-181
APBB1IB.3	0.7302883712	0
ACSL1	0.7262992214	1.57E-272
RGS1	0.7159699911	1.31E-107
MS4A6A	0.7027555053	0
CD163L1	0.7008849865	0
FMN1	0.6953176016	0
ITGN1	0.6842375869	9.43E-107
FAM132B	0.6811175316	2.59E-211
SRGN	0.6809403252	1.31E-128
ASPG1	0.6439335176	5.26E-118
PLSRC1	0.6351259618	0
SQSAP2	0.6281138717	7.20E-286
ARHGAP18	0.6308675717	2.07E-199
RYK2	0.6305832771	6.05E-196
IL1S	0.6231162619	0
MS4A6B	0.6021169857	3.79E-295
FNDC3A	0.5991959761	5.33E-139
TRPS1	0.5861919754	9.13E-197
SYNE1	0.5852678241	1.03E-116
EPB41L2	0.5852678241	5.33E-116
CSMP2	0.5851653107	5.13E-117
ALDH6A1.2	0.5741586727	5.38E-169
KHDRBS2	0.5667419516	2.61E-171
PDE8B	0.5622189582	1.96E-81
CPM	0.5564598869	4.86E-107
EDIL	0.5458596822	2.36E-86
CPNE8	0.5395028839	9.13E-176
MAN1A1	0.5375995436	7.32E-188
LRRC2	0.5324518358	6.63E-111
PGAS1	0.5237279532	7.68E-117
C1ET1A	0.5209978496	7.79E-258
MYO5A	0.5086688438	3.58E-121
NPTB1	0.4982507158	7.26E-88
RASA2	0.4962179452	8.13E-106
RBP1	0.4897676234	1.22E-105
NAP1	0.4882.5897	1.93E-83
MS4A6A	0.4869789656	8.77E-255
SPA311	0.4811139917	5.32E-89
FCHO2	0.4806775422	2.92E-77
EVE1	0.4767788556	6.79E-176
DRAM1	0.4766479738	2.27E-168
RAP1GB	0.4755218881	1.53E-117
CNNM4	0.4757213216	1.31E-111
ARHGAP	0.4753.5.2.2	6.68E-106
ABCA1	0.4623078772	1.98E-178
YAP65A	0.4589576332	1.36E-56
RAP1A1B	0.4566228.3	1.37E-83
HNRDB	0.4479881211	2.83E-136
AP1M2	0.4467788.5	9.87E-160
SIDBP	0.4465127573	8.49E-108
TOMP	0.4455168963	8.59E-101
SLC2A9	0.4395459568	5.95E-126
RAN4A7	0.4395647143	8.59E-128
RYR2	0.4376727569	9.42E-83
TNFAIP8	0.4327558265	2.13E-109
RBM43	0.4297668556	9.51E-62
AP1B	0.4261268027	5.16E-80
ATP1B3	0.4263011569	1.46E-82
ATG7	0.4260.8885	7.31E-109
SPATS2L	0.4.57.57858	7.22E-89
DOCK1	0.4153.2766	4.28E-97
NAGK71	0.4066229275	4.38E-87
NP1R	0.4058538.53	1.38E-63
DNM1.2	0.3956667.99	1.82E-80
RAB27A	0.3945398937	8.95E-80
AHNP2	0.3905735866	5.09E-70
GPR153	0.3942.29826	9.68E-72
DOCK3	0.3924.39821	7.23E-101
SLC16A3A	0.3.2.5.5.5.5.5	1.68E-108
LTPR1	0.3909.58211	6.83E-108
ZBTB16	0.3894.55366	2.83E-57
C20orf194	0.3.8.5.27.59	1.46E-79
CSRP2	0.3.8.3.9.3.5.6	4.28E-65
SLC11A1	0.3.8.7.7.5.5.1	1.46E-58
PI16L	0.3.8.2.5.9.5.6	1.28E-89
YIMP1	0.3.8.2.5.8.8.6	2.77E-73
SIN32	0.3.8.3.5.2.9.5.1	1.55E-73
ANAH1	0.3.8.3.2.3.7.2	2.46E-69
SAT1	0.3.6.8.8.5.2.8	1.41E-57
FKBP2.B9	0.3.6.8.3.7.7.6.5	1.56E-73
HNRPU2I1	0.3.6.2.7.2.5.1.2	4.78E-73
SN3A	0.3.6.2.1.2.6.8.9	4.26E-73
RAN9L1	0.3.6.2.5.6.2.1.6	1.77E-63
PREA1A2	0.3.6.2.7.6.7.9.7	1.76E-56
NAN1	0.3.6.2.5.2.9.2.1	5.57E-136
PGBP1	0.3.6.1.6.4.3.8.5	7.08E-84
WWP1	0.3.6.0.7.3.5.8.3	1.46E-54
PLSRC1	0.3.7.7.5.5.1.6.9	1.46E-87
CREM	0.3.2.2.5.7.7.7.7	1.28E-99
PR12	0.3.5.9.5.6.2.1.1	1.28E-99
RAB20	0.3.5.1.1.6.1.2.9	8.26E-64
NFTP	0.3.5.0.9.9.5.6.2	1.56E-72
SHSPX22B	0.3.5.1.6.2.3.7.7	5.45E-58
ATP1A1	0.3.5.0.8.5.2.6.1	1.46E-58
ECSIT.1	0.3.5.7.9.7.5.1.1	6.26E-63
PYSL	0.3.4.6.0.3.8.3.8	8.34E-66
TMEM14	0.3.4.5.6.2.0.2.1	1.78E-67
PDSPC	0.3.4.3.1.5.7.6.2	3.82E-11
CYTH1	0.3.4.0.5.1.8.8.6	1.97E-59
FAM89A	0.3.3.7.6.8.9.5.4	4.76E-61
EGFEP	0.3.3.7.7.8.8.6.5	5.26E-60
MAFB	0.3.5.2.3.7.8.5	4.52E-75
TNFRSF1B	0.3.3.5.1.8.1.2.3	1.76E-56
SPA33	0.3.3.7.6.7.2.5.6	8.45E-63
SERINC5	0.2.9.8.2.7.8.5.9	8.76E-53
CD18	0.2.9.2.6.3.8.7.3	7.50E-59
IFI16	0.2.9.8.5.3.4.6.4	1.38E-75
NMRSB1.EIAH1	0.2.9.8.1.1.6.2.3.6	9.15E-66
C20orf196	0.2.9.8.1.1.5.7.4.2	9.15E-66
LITAF	0.2.9.7.6.6.7.4.2	1.26E-53
PVT1	0.2.9.5.3.8.8.5	6.45E-52
PTH1	0.2.8.7.5.7.6.4.2	3.32E-59
HLA-DRB1	0.2.7.9.5.5.7.4.8	5.67E-56
IL18Rx	0.2.7.7.9.5.9.6.5	9.03E-75
LINC02078	0.2.7.7.5.5.7.5.6	1.79E-14
IAH1E2	0.2.7.7.2.7.5.6.1	4.45E-60
CXXT1S	0.2.7.5.3.4.9.8.6	4.05E-69
SPI3K	0.2.7.4.9.5.7.5.8	3.73E-57
SLC7A11	0.2.7.3.7.5.8.2.7	1.46E-58
NOTCH2	0.2.7.3.7.5.8.2.7	4.95E-63
LIBRN28	0.2.6.8.5.3.9.1.7	4.58E-57
HLA-DRA	0.2.6.7.9.8.9.8.1	2.56E-54
FCHO2	0.2.6.7.2.9.8.1	4.51E-25
SNRNP25B	0.2.6.6.9.8.2.1	9.36E-53
MS4A14	0.2.6.5.8.5.2.5.6	8.96E-65
CTSB	0.2.6.5.1.8.8.5.7	4.32E-54
NAP2	0.2.5.9.5.6.8.3.8	7.34E-60
ZNF438	0.2.6.6.1.2.8.8.5	9.32E-25
ACSBT2.2	0.2.5.8.9.6.0.8.8	1.80E-27
ASAP1.1	0.2.5.8.6.6.0.9.8	6.77E-59
RHOBTB3	0.2.5.8.5.1.0.3.8	1.58E-59
CLEC7A	0.2.5.6.8.8.5.5.2	3.91E-59
NIPSD1	0.2.5.6.5.6.9.5.7	3.71E-62
GAS7	0.2.5.6.5.5.4.2.8	4.96E-58
ACSBT2.1	0.2.5.6.4.6.2.2.6	5.27E-28
LNPK1	0.2.5.6.2.6.0.9.9	2.21E-25
PIK3CB	0.2.5.5.7.7.6.2.9	1.37E-42
ATP1A1	0.2.5.5.7.6.2.2.9	1.37E-42
CD300A	0.2.5.5.6.6.2.2.9	1.37E-42
CHD9	0.2.5.5.6.7.4.3	1.43E-53
RCNK13	0.2.5.2.5.2.1.4.2	1.53E-22
ST6GT1	0.2.5.0.8.7.5.6.8	1.26E-20
SYT17	0.2.5.0.1.1.2.6.1	1.15E-18
DENND3	0.2.4.9.8.6.7.7.3	5.45E-66
C19DC1	0.2.4.9.1.2.6.7.6	9.40E-19
ZNF827	0.2.4.9.0.5.2.6.4	1.58E-23
ZNRF2	0.2.4.9.0.5.2.6.4	1.58E-23
SMN2/2H1	0.2.3.9.9.7.5.6.2	9.48E-24
MAP4K4	0.2.3.9.7.7.8.5.1.4	1.26E-20
CA1764.1D	0.2.3.9.5.5.2.3.6	7.23E-19
PTK2B.1	0.2.3.7.7.5.5.2.2	2.60E-26
EVI1	0.2.3.6.7.5.5.5.6	1.93E-53
NCF4	0.2.3.6.2.1.5.6.8	6.36E-22
LRPB1L	0.2.3.6.0.5.9.5.7	6.25E-53
PCSK2	0.2.2.9.5.5.8.6.1	1.75E-60
NPC1L1	0.2.2.7.5.7.8.7.5	0.07738E355
JAZF1	0.2.2.7.5.0.9.8.7	1.50E-52
GUARX1	0.2.2.7.5.0.8.7.4.3	2.16E-28
PAPPA2	0.2.2.7.5.0.1.6.1.7	8.20E-68
AZIP1.2	0.2.2.7.2.7.5.6.6	2.30E-29
NIPS1.1	0.2.2.7.0.5.8.7.5	6.31E-27
ANKRD40	0.2.2.6.5.6.5.8.2	1.17E-70
P3K2	0.2.2.6.5.0.7.2.8	5.36E-26
P1TPNC1	0.2.2.6.5.0.7.8.6	1
NBEA2	0.2.2.6.3.7.6.5.5	1.35E-55
GRN37	0.2.2.6.2.7.3.9.9.3	6.75E-32
KCP1	0.2.2.5.9.2.5.9.8	1.42E-56
CPSD1	0.2.2.5.1.2.0.5.8	5.19E-38
SRGAP3C	0.2.2.5.0.9.5.5.6	1.25E-53
RASAL2	0.2.2.4.2.3.2.3.9.9	6.03E-58
NUDR1P	0.2.2.3.9.2.5.9.1.7	6.55E-54
SSPP1668	0.2.2.3.2.8.8.8.3	6.28E-29
ITGB2	0.2.2.3.2.8.8.8.3	6.28E-29
RASA3	0.2.2.2.9.2.5.9.8	1.25E-53
2081	0.2.2.1.9.1.2.7.5	2.88E-21
CD22A	0.2.2.1.9.0.7.8.9	1.32E-55
ITGAX	0.2.2.0.7.5.5.5.6.6	9.08E-50
ACCSBT54.1	0.2.1.9.8.5.6.8.8.8	7.56E-56
NBJBP1	0.2.1.9.7.5.5.6.6	1.76E-56
PCCSP2	0.2.1.9.5.8.9.9.6	2.37E-63
KLF12	0.2.1.9.5.7.7.5.8.7	1.01E-56
PPP4C1B	0.2.1.9.5.2.8.6.8.8	2.26E-37
AHNAP2P1	0.2.1.9.5.0.8.5.9.9	5.18E-56
ACCPRD3.1	0.2.1.9.3.3.8.8.5	1.32E-53
SRGAP2	0.2.1.9.3.3.8.8.9	1.53E-123
SEC22.1	0.2.1.9.1.8.8.6.5	1.67E-56
LPCAT2	0.2.1.9.0.2.9.9.1.7	3.32E-73
Mar-05	0.2.1.9.0.2.6.6.9.9	1.31E-60
NPC6k	0.2.1.9.0.2.3.2.2.9	9.96E-56
TUSD2	0.2.1.9.0.2.3.0.9.6	7.88E-51
FAM129A	0.2.1.9.0.2.3.0.2.5	1.76E-29
PLCL1	0.2.1.9.0.0.5.9.2.6	9.39E-21
TJP1	0.2.1.9.0.1.7.6.3.3	1.56E-65
PLEK	0.2.1.9.0.1.7.6.3.3	1.56E-65
SRGAP3B	0.2.1.9.0.1.7.6.3.3	1.56E-65
LAPP1.2	0.2.1.9.0.1.7.6.3.3	1.56E-65
TUNA5	0.2.1.9.0.1.7.6.3.3	1.56E-65
TUNA5	0.2.1.9.0.1.7.6.3.3	1.56E-65
ATP6AP1L	0.2.1.9.0.1.7.6.3.3	1.56E-65
SLAY.2	0.2.1.9.0.1.7.6.3.3	1.56E-65
EMA2	0.2.1.9.0.1.7.6.3.3	1.56E-65
LINC01268	0.2.1.9.0.1.7.6.3.3	1.56E-65
BLNK	0.2.1.9.0.1.7.6.3.3	1.56E-65
LIST	0.2.1.9.0.1.7.6.3.3	1.56E-65
DSBP1A	0.2.1.9.0.1.7.6.3.3	1.56E-65
HTR6.1	0.2.1.9.0.1.7.6.3.3	1.56E-65
GRSDB3P	0.2.1.9.0.1.7.6.3.3	1.56E-65
SYLT1	0.2.1.9.0.1.7.6.3.3	1.56E-65
GJA5	0.2.1.9.0.1.7.6.3.3	1.56E-65
SORL1	0.2.1.9.0.1.7.6.3.3	1.56E-65
PI16.1	0.2.1.9.0.1.7.6.3.3	1.56E-65
NSAT1	0.2.1.9.0.1.7.6.3.3	1.56E-65
CLA5	0.2.1.9.0.1.7.6.3.3	1.56E-65
RFP	0.2.1.9.0.1.7.6.3.3	1.56E-65
SPA31.2	0.2.1.9.0.1.7.6.3.3	1.56E-65
ACSBD3B.1	0.2.1.9.0.1.7.6.3.3	1.56E-65
DOCK8	0.2.1.9.0.1.7.6.3.3	1.56E-65
ITPA2	0.2.1.9.0.1.7.6.3.3	1.56E-65
TENM4	0.2.1.9.0.1.7.6.3.3	1.56E-65
APBB1IP	0.2.1.9.0.1.7.6.3.3	1.56E-65
ZNNT1	0.2.1.9.0.1.7.6.3.3	1.56E-65
SPTBP1	0.2.1.9.0.1.7.6.3.3	1.56E-65
TMEM176A	0.2.1.9.0.1.7.6.3.3	1.56E-65
TMEM176B	0.2.1.9.0.1.7.6.3.3	1.56E-65
SLC1A3	0.2.1.9.0.1.7.6.3.3	1.56E-65
ARHGAP24	0.2.1.9.0.1.7.6.3.3	1.56E-65
FAM49A	0.2.1.9.0.1.7.6.3.3	1.56E-65
CSMD1	0.2.1.9.0.1.7.6.3.3	1.56E-65
DPP6	0.2.1.9.0.1.7.6.3.3	1.56E-65
ZFHX3	0.2.1.9.0.1.7.6.3.3	1.56E-65
ZEB2	0.2.1.9.0.1.7.6.3.3	1.56E-65
ANK3	0.2.1.9.0.1.7.6.3.3	1.56E-65
ADGRL3	0.2.1.9.0.1.7.6.3.3	1.56E-65
ZFPM2	0.2.1.9.0.1.7.6.3.3	1.56E-65
SYNE1	0.2.1.9.0.1.7.6.3.3	1.56E-65
FOXP2	0.2.1.9.0.1.7.6.3.3	1.56E-65
CNTNAP5	0.2.1.9.0.1.7.6.3.3	1.56E-65
ANK1	0.2.1.9.0.1.7.6.3.3	1.56E-65
EGFEM1P	0.2.1.9.0.1.7.6.3.3	1.56E-65
LINC01412	0.2.1.9.0.1.7.6.3.3	1.56E-65
RYR3	0.2.1.9.0.1.7.6.3.3	1.56E-65
KCNIP4	0.2.1.9.0.1.7.6.3.3	1.56E-65
RORA	0.2.1.9.0.1.7.6.3.3	1.56E-65
ADAMTS17	0.2.1.9.0.1.7.6.3.3	1.56E-65
LRRC4C	0.2.1.9.0.1.7.6.3.3	1.56E-65
CADPS2	0.2.1.9.0.1.7.6.3.3	1.56E-65
RBFOX1	0.2.1.9.0.1.7.6.3.3	1.56E-65
GRIA1	0.2.1.9.0.1.7.6.3.3	1.56E-65
KCNMA1	0.2.1.9.0.1.7.6.3.3	1.56E-65
GRM3	0.2.1.9.0.1.7.6.3.3	1.56E-65
GRM5	0.2.1.9.0.1.7.6.3.3	1.56E-65
ERBB4	0.2.1.9.0.1.7.6.3.3	1.56E-65
CSMD3	0.2.1.9.0.1.7.6.3.3	1.56E-65
SHANK2	0.2.1.9.0.1.7.6.3.3	1.56E-65
KALRN	0.2.1.9.0.1.7.6.3.3	1.56E-65
NRG3	0.2.1.9.0.1.7.6.3.3	1.56E-65
NRXN1	0.2.1.9.0.1.7.6.3.3	1.56E-65
CNTN4	0.2.1.9.0.1.7.6.3.3	1.56E-65
CNTN5	0.2.1.9.0.1.7.6.3.3	1.56E-65
CNTN6	0.2.1.9.0.1.7.6.3.3	1.56E-65
CNTNAP2	0.2.1.9.0.1.7.6.3.3	1.56E-65
CNTNAP4	0.2.1.9.0.1.7.6.3.3	1.56E-65
CNTNAP5	0.2.1.9.0.1.7.6.3.3	1.56E-65
NLGN1	0.2.1.9.0.1.7.6.3.3	1.56E-65
NLGN3	0.2.1.9.0.1.7.6.3.3	1.56E-65
NLGN4X	0.2.1.9.0.1.7.6.3.3	1.56E-65
NLGN4Y	0.2.1.9.0.1.7.6.3.3	1.56E-65
NRXN3	0.2.1.9.0.1.7.6.3.3	1.56E-65
PTPRD	0.2.1.9.0.1.7.6.3.3	1.56E-65
PTPRT	0.2.1.9.0.1.7.6.3.3	1.56E-65
SDK1	0.2.1.9.0.1.7.6.3.3	1.56E-65
SDK2	0.2.1.9.0.1.7.6.3.3	1.56E-65
SLC1A2	0.2.1.9.0.1.7.6.3.3	1.56E-65
SLC6A1	0.2.1.9.0.1.7.6.3.3	1.56E-65
SLC6A11	0.2.1.9.0.1.7.6.3.3	1.56E-65
SLC6A17	0.2.1.9.0.1.7.6.3.3	1.56E-65
SLC7A14	0.2.1.9.0.1.7.6.3.3	1.56E-65
SLC35F1	0.2.1.9.0.1.7.6.3.3	1.56E-65
SLC35F3	0.2.1.9.0.1.7.6.3.3	1.56E-65
SLC39A11	0.2.1.9.0.1.7.6.3.3	1.56E-65
SLC39A12	0.2.1.9.0.1.7.6.3.3	1.56E-65
SLC39A14	0.2.1.9.0.1.7.6.3.3	1.56E-65
SLC39A8	0.2.1.9.0.1.7.6.3.3	1.56E-65
SLC4A4	0.2.1.9.0.1.7.6.3.3	1.56E-65
SLC5A3	0.2.1.9.0.1.7.6.3.3	1.56E-65
SLC5A7

Supplementary Table 16_Gene set overrepresentation
Contents

Sheet name	Description
Microglial_cluster_markers	function (those genes whose expression is differentially expressed [logFC > 0.25, P-adj <0.05] relative to other clusters)
Microglial_pTau_DGE	Representation of literature gene lists among the significantly pTau regressed genes, as defined by MAST (logFC >
Microglia_Amyloid_beta_DGE	Representation of literature gene lists among the significantly Amyloid beta regressed genes, as defined by MAST (logFC > 0.25 & P-adj <0.05)
Astrocyte_cluster_markers	function (those genes whose expression is differentially expressed [logFC > 0.25, P-adj <0.05] relative to other clusters)
Astrocyte_pTau_DGE	Representation of literature gene lists among the significantly pTau regressed genes, as defined by MAST (logFC >
Astrocyte_Amyloid_beta_DGE	Representation of literature gene lists among the significantly Amyloid beta regressed genes, as defined by MAST (logFC > 0.25 & P-adj <0.05)
Gene_sets	Gene sets used in the analyses

Analyses (Fisher's exact test) were performed using the "enrichment" function of the R package "bc3net" (https://github.com/cran/bc3net)

The p values associated with the Fisher's exact test correspond to the probability that the overlap between the literature gene sets and the subcluster markers/differentially regressed genes from our dataset has occured by chance.

Supplementary Table 16_Gene set overrepresentation
Microglia cluster markers

Representation of literature gene lists among the cluster marker genes, as defined by the Seurat FindMarkers function (those genes whose expression is differentially expressed [logFC > 0.25, P-adj <0.05] relative to other clusters)

Markers for Micro1

Literature gene list	Overlapping genes (N)	% gene set overlap with sub-clu	Global overlap (N) between the literature gene list and the genes in sub-cluster	pval (Fisher's exact test)	padj (bonferroni)
Core_microglia	7	18.918919	238	1.12E-08	7.87E-08
PIG	2	5.405405	48	1.48E-03	1.03E-02
DAM	2	5.405405	1709	6.06E-01	1.00E+00
ARM	0	0	240	1.00E+00	1.00E+00
IRM	0	0	131	1.00E+00	1.00E+00
IFN_response	0	0	209	1.00E+00	1.00E+00

Total number of markers: 37 genes
"Background" for Micro1 cells (total number of genes expressed): 31364 genes

Markers for Micro2

Literature gene list	Overlapping genes (N)	% gene set overlap with sub-clu	Global overlap (N) between the literature gene list and the genes in sub-cluster	pval (Fisher's exact test)	padj (bonferroni)
Core_microglia	10	9.615385	238	1.09E-08	7.61E-08
PIG	4	3.846154	48	2.34E-05	1.64E-04
DAM	34	32.692308	1703	1.76E-17	1.23E-16
ARM	20	19.230769	238	2.93E-22	2.05E-21
IRM	6	5.769231	130	6.23E-06	4.36E-05
IFN_response	2	1.923077	206	1.60E-01	1.00E+00

Total number of markers: 104 genes
"Background" for Micro2 cells (total number of genes expressed): 30073 genes

Markers for Micro3

Literature gene list	Overlapping genes (N)	% gene set overlap with sub-clu	Global overlap (N) between the literature gene list and the genes in sub-cluster	pval (Fisher's exact test)	padj (bonferroni)
Core_microglia	7	8.045977	237	1.58E-05	1.11E-04
PIG	0	0	46	1.00E+00	1.00E+00
DAM	12	13.793103	1685	1.08E-02	7.59E-02
ARM	3	3.448276	233	4.43E-02	3.10E-01
IRM	5	5.747126	126	6.89E-05	4.82E-04
IFN_response	7	8.045977	204	5.97E-06	4.18E-05

Total number of markers: 87 genes
"Background" for Micro3 cells (total number of genes expressed): 25796 genes

Markers for PVM

Literature gene list	Overlapping genes (N)	% gene set overlap with sub-clu	Global overlap (N) between the literature gene list and the genes in sub-cluster	pval (Fisher's exact test)	padj (bonferroni)
Core_microglia	14	9.271523	236	3.92E-11	2.75E-10
PIG	2	1.324503	47	2.62E-02	1.84E-01
DAM	32	21.192053	1695	3.26E-10	2.28E-09
ARM	12	7.94702	237	6.16E-09	4.31E-08
IRM	6	3.97351	130	7.29E-05	5.11E-04
IFN_response	4	2.649007	206	2.49E-02	1.74E-01

Total number of markers: 151 genes
"Background" for PVM cells (total number of genes expressed): 28254 genes

Sources of gene lists: Core_microglia: Patir et al, 2018, doi.org/10.1002/glia.23572; PIG: Chen et al, 2020, doi.org/10.1016/j.cell.2020.06.038; DAM: Keren-Shaul et al, 2017, doi.org/10.1016/j.cell.2017.05.018; ARM and IRM: Sala-Frigerio et al, 2019, doi.org/10.1016/j.celrep.2019.03.099; IFN_response: Roy et al, 2020, doi.org/10.1172/JCI133737

Supplementary Table 16_Gene set overrepresentation
Microglia pTau DGE

Representation of literature gene lists among the significantly pTau regressed genes, as defined by MAST (logFC > 0.25 & P-adj <0.05)

pTau significantly regressed genes in Total Microglia

Literature gene list	Overlapping genes (N)	% gene set overlap with significan	Global overlap (N) between the literature gene list and the genes in sub-cluster	pval (Fisher's exact test)	padj (bonferroni)
Core_microglia	4	3.669724771	238	0.008851546	0.079663915
PIG	3	2.752293578	48	0.000584626	0.00526163
DAM	24	22.01834862	1712	2.32E-09	2.09E-08
ARM	11	10.09174312	241	6.64E-10	5.97E-09
IRM	4	3.669724771	131	0.001047587	0.009428286
Amyloid_beta-associated genes	12	11.00917431	564	4.99E-07	4.49E-06
pTau-associated genes	1	0.917431193	20	0.065606737	0.590460635
IFN_response	1	0.917431193	224	0.533469567	1

Total number of significantly positively regressed genes: 109 genes
"Background" for Total microglial cells (total number of genes expressed): 32190 genes

pTau significantly regressed genes in PVM

Literature gene list	Overlapping genes (N)	% gene set overlap with significan	Global overlap (N) between the literature gene list and the genes in sub-cluster	pval (Fisher's exact test)	padj (bonferroni)
Core_microglia	1	1.063829787	238	0.502715936	1
PIG	1	1.063829787	48	0.13105508	1
DAM	15	15.95744681	1712	0.000127153	0.001144381
ARM	5	5.319148936	241	0.00072062	0.006485582
IRM	2	2.127659574	131	0.056366414	0.507297726
Amyloid_beta-associated genes	3	3.191489362	564	0.227878431	1
pTau-associated genes	0	0	20	1	1
IFN_response	1	1.063829787	224	0.481780338	1

Total number of significantly positively regressed genes: 94 genes
"Background" for PVM cells (total number of genes expressed): 28254 genes

Sources of gene lists: Core_microglia: Patir et al, 2018, doi.org/10.1002/glia.23572; PIG: Chen et al, 2020, doi.org/10.1016/j.cell.2020.06.038; DAM: Keren-Shaul et al, 2017, doi.org/10.1016/j.cell.2017.05.018; Amyloid_beta-associated genes and pTau-associated genes: Sierksma et al, 2020, doi.org/10.15252/emmm.201910606; ARM and IRM: Sala-Frigerio et al, 2019, doi.org/10.1016/j.celrep.2019.03.099; IFN_response: Roy et al, 2020, doi.org/10.1172/JCI133737

Supplementary Table 16_Gene set overrepresentation
Microglia Amyloid beta DGE

Representation of literature gene lists among the significantly Amyloid beta regressed genes, as defined by MAST (logFC > 0.25 & P-adj <0.05)

Amyloid beta significantly regressed genes in Total Microglia

Literature gene list	Overlapping genes (N)	% gene set overlap with sig	Global overlap (N) between the literature gene list and the genes in sub-cluster	pval (Fisher's exact test)	padj (bonferroni)
Core_microglia	5	2.617801047	238	0.014049382	0.126444442
PIG	4	2.094240838	48	0.000190549	0.001714939
DAM	33	17.27748691	1712	2.10E-09	1.89E-08
ARM	9	4.712041885	241	1.50E-05	0.000135407
IRM	4	2.094240838	131	0.007840369	0.070563323
Amyloid_beta-associated genes	15	7.853403141	564	1.58E-06	1.42E-05
pTau-associated genes	1	0.523560209	20	0.112244672	1
IFN_response	2	1.047120419	224	0.384196414	1

Total number of significantly positively regressed genes: 191 genes
"Background" for Total microglial cells (total number of genes expressed): 32190 genes

pTau significantly regressed genes in PVM

Literature gene list	Overlapping genes (N)	% gene set overlap with sig	Global overlap (N) between the literature gene list and the genes in sub-cluster	pval (Fisher's exact test)	padj (bonferroni)
Core_microglia	4	2.234636872	238	0.044353192	0.399178731
PIG	0	0	48	1	1
DAM	27	15.08379888	1712	9.92E-07	8.92E-06
ARM	4	2.234636872	241	0.046066363	0.414597265
IRM	1	0.558659218	131	0.519040468	1
Amyloid_beta-associated genes	6	3.351955307	564	0.095885673	0.862971054
pTau-associated genes	0	0	20	1	1
IFN_response	2	1.117318436	224	0.354334952	1

Total number of significantly positively regressed genes: 179 genes
"Background" for PVM cells (total number of genes expressed): 28254 genes

Sources of gene lists: Core_microglia: Patir et al, 2018, doi.org/10.1002/glia.23572; PIG: Chen et al, 2020, doi.org/10.1016/j.cell.2020.06.038; DAM: Keren-Shaul et al, 2017, doi.org/10.1016/j.cell.2017.05.018; Amyloid_beta-associated genes and pTau-associated genes: Sierksma et al, 2020, doi.org/10.15252/emmm.201910606; ARM and IRM: Sala-Frigerio et al, 2019, doi.org/10.1016/j.celrep.2019.03.099; IFN_response: Roy et al, 2020, doi.org/10.1172/JCI133737

Supplementary Table 16_Gene set overrepresentation
Astrocyte cluster markers

Representation of literature gene lists among the cluster marker genes, as defined by the Seurat FindMarkers function (those genes whose expression is differentially expressed [logFC > 0.25, P-adj <0.05] relative to other clusters)

Markers for Astro1

Literature gene list	Overlapping genes (N)	% gene set overlap with sub-clu	Global overlap (N) between the literature gene list and the genes in sub-cluster	pval (Fisher's exact test)	padj (bonferroni)
DAA	1	7.692308	215	0.08300404	0.249012
IFN_response	0	0	207	1	1

Total number of markers: 13 genes
"Background" for Astro1 cells (total number of genes expressed): 32369 genes

Markers for Astro2

Literature gene list	Overlapping genes (N)	% gene set overlap with sub-clu	Global overlap (N) between the literature gene list and the genes in sub-cluster	pval (Fisher's exact test)	padj (bonferroni)
DAA	3	6.122449	215	0.00424089	0.012723
IFN_response	1	2.040816	208	0.27081405	0.812442

Total number of markers: 49 genes
"Background" for Astro2 cells (total number of genes expressed): 32399 genes

Markers for Astro3

Literature gene list	Overlapping genes (N)	% gene set overlap with sub-clu	Global overlap (N) between the literature gene list and the genes in sub-cluster	pval (Fisher's exact test)	padj (bonferroni)
DAA	0	0	215	1	1
IFN_response	0	0	206	1	1

Total number of markers: 11 genes
"Background" for Astro3 cells (total number of genes expressed): 31824 genes

Markers for Astro4

Literature gene list	Overlapping genes (N)	% gene set overlap with sub-clu	Global overlap (N) between the literature gene list and the genes in sub-cluster	pval (Fisher's exact test)	padj (bonferroni)
DAA	8	9.638554	215	1.01E-07	3.02E-07
IFN_response	3	3.614458	206	1.70E-02	5.11E-02

Total number of markers: 83 genes
"Background" for Astro4 cells (total number of genes expressed): 31676 genes

Markers for Astro5

Literature gene list	Overlapping genes (N)	% gene set overlap with sub-clu	Global overlap (N) between the literature gene list and the genes in sub-cluster	pval (Fisher's exact test)	padj (bonferroni)
DAA	8	4.761905	215	2.17E-05	6.51E-05
IFN_response	3	1.785714	208	1.01E-01	3.02E-01

Total number of markers: 168 genes
"Background" for Astro5 cells (total number of genes expressed): 31391 genes

Markers for Astro6

Literature gene list	Overlapping genes (N)	% gene set overlap with sub-clu	Global overlap (N) between the literature gene list and the genes in sub-cluster	pval (Fisher's exact test)	padj (bonferroni)
DAA	8	5.031447	215	3.17854E-05	9.54E-05
IFN_response	3	1.886792	200	0.104152983	0.312459

Total number of markers: 159 genes
"Background" for Astro6 cells (total number of genes expressed): 28113 genes
Sources of gene lists: DAA: Habib et al, 2020, doi.org/10.1038/s41593-020-0624-8, IFN_response: Roy et al, 2020, doi.org/10.1172/JCI133737

Supplementary Table 16_Gene set overrepresentation
Astrocyte pTau DGE

Representation of literature gene lists among the significantly pTau regressed genes, as defined by MAST (logFC > 0.25 & P-adj <0.05)

pTau significantly regressed genes in Total Astrocytes

Literature gene list	Overlapping genes (N)	% gene set overlap with significantly regressed	Global overlap (N) between the literature gene list and the genes in sub-cluster	pval (Fisher's exact test)	padj (bonferroni)
DAA	29	9.23566879	215	4.67E-25	1.40E-24
IFN_response	3	0.955414013	225	0.347849121	1

Total number of significantly positively regressed genes: 314 genes
"Background" for Total astrocytes (total number of genes expressed): 33804 genes
Sources of gene lists: DAA: Habib et al, 2020, doi.org/10.1038/s41593-020-0624-8, IFN_response: Roy et al, 2020, doi.org/10.1172/JCI133737

Supplementary Table 16_Gene set overrepresentation
Astrocyte amyloid beta DGE

Representation of literature gene lists among the significantly Amyloid beta regressed genes, as defined by MAST (logFC > 0.25 & P-adj <0.05)

Amyloid beta significantly regressed genes in Total Astrocytes

Literature gene list	Overlapping genes (N)	% gene set overlap with significantly regressed	Global overlap (N) between the literature gene list and the genes in sub-cluster	pval (Fisher's exact test)	padj (bonferroni)
DAA	24	4.606525912	215	5.07E-14	1.52E-13
IFN_response	2	0.383877159	225	0.863615175	1

Total number of significantly positively regressed genes: 521 genes
"Background" for Total astrocytes (total number of genes expressed): 33804 genes
Sources of gene lists: DAA: Habib et al, 2020, doi.org/10.1038/s41593-020-0624-8, IFN_response: Roy et al, 2020, doi.org/10.1172/JCI133737

Supplementary Table 16_Gene set overrepresentation
Gene sets

PAC	ABM	DMB	SMB	Cross_Hemisphere	VPN_Inspiratory	SNA	Amygdala_Retina-associated ganglion cells
Chemical at 20200505 <0.00001 and Log2(2020-05-18/0) >0.5 and Log2(2020-05-18/0) >0.5	Trigonia oval 20200509 <0.00001 and Log2(2020-05-18/0) >0.5 and Log2(2020-05-18/0) >0.5	Trigonia oval at 20200509 <0.00001 and Log2(2020-05-18/0) >0.5 and Log2(2020-05-18/0) >0.5	Tetanic Mucosal at 20171020 <0.00001 and Log2(2020-05-18/0) >0.5 and Log2(2020-05-18/0) >0.5	Front cut at 20200505 <0.00001 and Log2(2020-05-18/0) >0.5	Mucosal 20200505 <0.00001 and Log2(2020-05-18/0) >0.5	Membrane at 20200505 <0.00001 and Log2(2020-05-18/0) >0.5	Sub Nucleus cut_20200505 <0.00001 and Log2(2020-05-18/0) >0.5 and Log2(Genomic 20190505
50 Genes in List	Log10 -10.25 and Z<0.005 154 Genes in List	3855 Genes in List	2490 Genes in list	2400 Genes in list	225 Genes in list	556 Genes in list	20 Genes in list

Hck	ANK2	Lst11	ANK2	ABCC9	AANG	DTAP	Hck1
Kcbt	CST7	CSK1	ANK2	ANK	ACSS2	Vhh	Hck1
Cd8	CPP1	ATAT1	ANK2	ATP	ANAMTR	Cu	CELSSBBa
Cnn	CPL	SLAMF9	ANK2	ANK2	ECM1	ECMP1	Cnn
Cnn	CPL	CSK1	ANK2	ANK2	ECM1	Cnn	Cnn
SERPINA3	CAETA	CAP	ANK2	ANK7	ANN	ANN	PECAM
ANXF	HLA-DQB1	DFF7	ANK2	ANK2	ACSS	CNTN1	CDH1
Cnn	CPL	SLAMF9	ANK2	ANK2	ECM1	Cnn	Cnn
CSK1	HLA-DQB1	ADRB2	ANK2	ATP	ANAMTR	Cu	CELSSBBa