

Supplementary Tables

Table 1: Metadata for adult donors.

donor ID	age	sex	ethnicity	# brain regions sampled	# samples
2001	24 yrs	M	Black or African American	327	946
2002	39 yrs	M	Black or African American	348	893
1009	57 yrs	M	White or Caucasian	158	363
1012	31 yrs	M	White or Caucasian	185	529
1015	49 yrs	F	Hispanic	187	470
1016	55 yrs	M	White or Caucasian	200	501

Table 2: Number of brain regions (column 2) for different numbers of donors (column 1) the set of regions were sampled in (Adult Human Brain Atlas).

# donors	# brain regions
1	54
2	158
3	19
4	42
5	36
6	105

Table 3: Table of donors from the Developing Human Brain Atlas.

age	age [weeks]	donor id	donor ID	sex	stage	stage name
8 pcw	8	13058	H376.IIA.51	M	1	prenatal
9 pcw	9	12833	H376.IIA.50	M	1	prenatal
12 pcw	12	12835	H376.IIB.50	F	1	prenatal
12 pcw	12	12960	H376.IIB.51	F	1	prenatal
12 pcw	12	13060	H376.IIB.52	F	1	prenatal
13 pcw	13	12820	H376.IIIA.50	M	1	prenatal
13 pcw	13	12834	H376.IIIA.51	F	1	prenatal
13 pcw	13	12888	H376.IIIA.52	M	1	prenatal
16 pcw	16	12287	H376.IIIB.50	M	1	prenatal
16 pcw	16	12837	H376.IIIB.51	M	1	prenatal
16 pcw	16	12879	H376.IIIB.52	M	1	prenatal
17 pcw	17	12880	H376.IIIB.53	F	1	prenatal
19 pcw	19	12885	H376.IV.53	F	1	prenatal
21 pcw	21	12365	H376.IV.51	F	1	prenatal

21 pcw	21	12886	H376.IV.54	M	1	prenatal
24 pcw	24	12288	H376.IV.50	M	1	prenatal
25 pcw	25	12948	H376.V.51	F	1	prenatal
26 pcw	26	12949	H376.V.52	F	1	prenatal
35 pcw	35	12295	H376.V.50	F	1	prenatal
37 pcw	37	263195015	H376.V.53	M	1	prenatal
4 mos	54	12296	H376.VI.50	M	2	infant
4 mos	54	12889	H376.VI.51	M	2	infant
4 mos	54	12890	H376.VI.52	M	2	infant
10 mos	78	12977	H376.VII.51	M	2	infant
1 yrs	90	12830	H376.VIII.51	F	2	infant
2 yrs	142	12979	H376.VIII.53	F	2	infant
3 yrs	194	12836	H376.VIII.52	F	3	child
3 yrs	194	12980	H376.VIII.54	M	3	child
4 yrs	246	12298	H376.VIII.50	M	3	child
8 yrs	454	12841	H376.IX.51	M	3	child
8 yrs	454	12981	H376.IX.52	M	3	child
11 yrs	610	12289	H376.IX.50	F	3	child
13 yrs	714	12831	H376.X.51	F	4	adolescent
15 yrs	818	12299	H376.X.50	M	4	adolescent
18 yrs	974	12984	H376.X.53	M	4	adolescent
19 yrs	1026	12832	H376.X.52	F	4	adolescent
21 yrs	1130	13057	H376.XI.60	F	5	adult
23 yrs	1234	12300	H376.XI.50	M	5	adult
30 yrs	1598	12290	H376.XI.52	F	5	adult
36 yrs	1910	12302	H376.XI.53	M	5	adult
37 yrs	1962	12303	H376.XI.54	M	5	adult
40 yrs	2118	12304	H376.XI.56	F	5	adult

Table 4: Brain regions (after filtering) in the developing human brain dataset and the number of different ages at which they were sampled.

structure	#ages	# donors
mediodorsal nucleus of thalamus	21	24
primary motor cortex (area M1, area 4)	20	26
primary somatosensory cortex (area S1, areas 3,1,2)	22	26
striatum	21	28
cerebellar cortex	25	29
primary auditory cortex (core)	22	31
orbital frontal cortex	25	31
anterior (rostral) cingulate (medial prefrontal) cortex	25	32
hippocampus (hippocampal formation)	25	32
primary visual cortex (striate cortex, area V1/17)	24	33
amygdaloid complex	24	33

posteroventral (inferior) parietal cortex	25	33
inferolateral temporal cortex (area TEv, area 20)	24	34
ventrolateral prefrontal cortex	26	35
dorsolateral prefrontal cortex	27	35
posterior (caudal) superior temporal cortex (area 22c)	28	36

Table 5: Classification of ages from the Developing Human Brain Atlas into five developmental stages.

age category	age	stage name
1	prenatal	prenatal
2	0-2 yrs	infant
3	3-11 yrs	child
4	12-19 yrs	adolescent
5	>19 yrs	adult

Table 6: Overview of the numbers of brain regions that were sampled, filtered, statistically analyzed, removed as duplicates or included in the *aba_enrich* output.

	adult	developmental
# measured regions	414	26
# measured regions selected for ABAEnrichment	414	16
# regions in ontology with data annotated (measured+inherited)	677	47
# duplicate regions (inherit from only one subregion)	20	20
# rows per age category in <i>aba_enrich</i> output	657	27

Table 7: Top 20 brain regions from the *aba_enrich* output testing enrichment of oligodendrocyte marker genes compared to the combined sets of neuron and astrocyte marker genes. The top 5 brain regions consist of the entire set of substructures of the white matter with available expression data. Column 1 shows the brain structure id used in the ontology; column 2 the name of the brain structure; column 3 the number of expression cut-offs that led to a FWER below 0.05 (out of 9 cutoffs, which is the default analysis); columns 4 and 5 show the mean and minimum FWER across all expression cut-offs, respectively.

structure_id	structure	times_FWER_under_0.05	mean_FWER	min_FWER
Allen:9241	cingulum bundle, Left	8	0.061	0
Allen:9222	corpus callosum	7	0.027	0
Allen:9242	cingulum bundle, Right	6	0.240	0
Allen:9240	cingulum bundle	6	0.247	0
Allen:9219	Telencephalic White Matter	6	0.255	0

Allen:4506	Reticular Nucleus of Thalamus, Left	5	0.204	0
Allen:9619	lateral medullary reticular group, Right	4	0.252	0.009
Allen:9593	central medullary reticular group, Right	4	0.283	0.003
Allen:4512	Reticular Nucleus of Thalamus, Right	4	0.312	0
Allen:9057	Red Nucleus, Right	4	0.318	0.001
Allen:4787	Dentate Nucleus, Right	4	0.333	0.01
Allen:4790	Globose Nucleus, Right	4	0.336	0.01
Allen:9053	Red Nucleus	4	0.338	0.011
Allen:4780	Cerebellar Nuclei	4	0.356	0.004
Allen:4505	Ventral Thalamus, Left	4	0.358	0.003
Allen:4789	Fastigial Nucleus, Right	4	0.372	0.011
Allen:4788	Emboliform Nucleus, Right	3	0.192	0.005
Allen:12947	Emboliform Nucleus	3	0.221	0.001
Allen:4296	globus pallidus, internal segment, Left	3	0.253	0.002
Allen:4784	Fastigial Nucleus, Left	3	0.261	0.002

Table 8: Numbers of differentially expressed genes in a brain region at a given developmental stage as reported by Kang et al. (Kang *et al.*, 2011). For the analysis of these genes with ABAEnrichment we excluded gene sets containing less than 10 genes. AMY: amygdala, CBC: cerebellar cortex, HIP: hippocampus, MD: mediodorsal nucleus of the thalamus, NCX: neocortex, STR: striatum.

	AMY	CBC	HIP	MD	NCX	STR
prenatal	6	95	42	153	53	84
prenatal & postnatal	4	474	44	371	45	201
postnatal	3	713	20	194	18	125
postnatal & adult	3	1066	40	290	50	284
adult	0	4	4	3	1	3

Table 9: Matching of age categories used in Kang et al. (Kang *et al.*, 2011) and ABAEnrichment.

Kang stage	Kang age	ABAEnrichment stage IDs	ABAEnrichment stages	ABAEnrichment age
prenatal	prenatal	1	Prenatal	prenatal
prenatal & postnatal	prenatal - 11 yrs	1, 2, 3	prenatal, infant, child	prenatal - 11 yrs
postnatal	0 - 19 yrs	2, 3, 4	infant, child, adolescent	0 - 19 yrs
postnatal & adult	> 0.5 yrs	2, 3, 4, 5	infant, child, adolescent, adult	> 0 yrs
adult	> 19 yrs	5	Adult	> 19 yrs

Table 10: Enrichment analyses results using sets of differentially expressed genes in a given brain region reported by Kang et al. (Kang *et al.*, 2011). For each combination of developmental stage and region, with more than 10 genes (Supplementary table S8), and for all matching ABAEnrichment developmental stages (Supplementary table S9) the ABAEnrichment results of the corresponding brain regions are displayed. AMY: amygdala, CBC: cerebellar cortex, HIP: hippocampus, MD: mediodorsal nucleus of the thalamus, NCX: neocortex, STR: striatum. The first two columns show the developmental stage and brain regions analyzed by Kang et al. and column 3 the number of genes that Kang et al. found to be differentially expressed in the given gene-age-combination. Column 4 shows the rank that brain regions got in the enrichment analysis with ABAEnrichment at the developmental stage in column 5. Developmental stages as used in Kang et al. may refer to multiple stages in ABAEnrichment. Column 6 shows the number of expression cutoffs that led to a FWER below 0.05 (out of 9 cutoffs) and column 7 and 8 show the mean and minimum FWER across all expression cutoffs, respectively.

Kang stage	Kang region	# genes	ABAEnrichment rank	ABAEnrichment stage	times FWER under 0.05	mean FWER	min FWER
prenatal	CBC	95	1	1	6	0.091	0
prenatal & postnatal	CBC	474	1	1	6	0.124	0
prenatal & postnatal	CBC	474	1	2	9	0.000	0
prenatal & postnatal	CBC	474	1	3	9	0.001	0
postnatal & adult	CBC	1066	1	2	9	0.000	0
postnatal & adult	CBC	1066	1	3	9	0.000	0
postnatal & adult	CBC	1066	1	4	9	0.000	0
postnatal & adult	CBC	1066	1	5	9	0.000	0
postnatal	CBC	713	1	2	9	0.000	0
postnatal	CBC	713	1	3	9	0.000	0
postnatal	CBC	713	1	4	9	0.000	0
prenatal	HIP	42	1	1	0	0.587	0.25
prenatal & postnatal	HIP	44	1	1	0	0.760	0.37
prenatal & postnatal	HIP	44	1	2	0	0.510	0.35
prenatal & postnatal	HIP	44	1	3	0	0.639	0.4
postnatal & adult	HIP	40	1	2	0	0.492	0.28
postnatal & adult	HIP	40	1	3	0	0.458	0.25
postnatal & adult	HIP	40	1	4	0	0.390	0.12
postnatal & adult	HIP	40	1	5	0	0.591	0.2
postnatal	HIP	20	1	2	0	0.487	0.22
postnatal	HIP	20	1	3	0	0.494	0.26
postnatal	HIP	20	1	4	0	0.451	0.1
prenatal	MD	153	1	1	9	0.006	0
prenatal & postnatal	MD	371	1	1	9	0.003	0
prenatal & postnatal	MD	371	1	2	9	0.000	0
prenatal & postnatal	MD	371	1	3	9	0.000	0

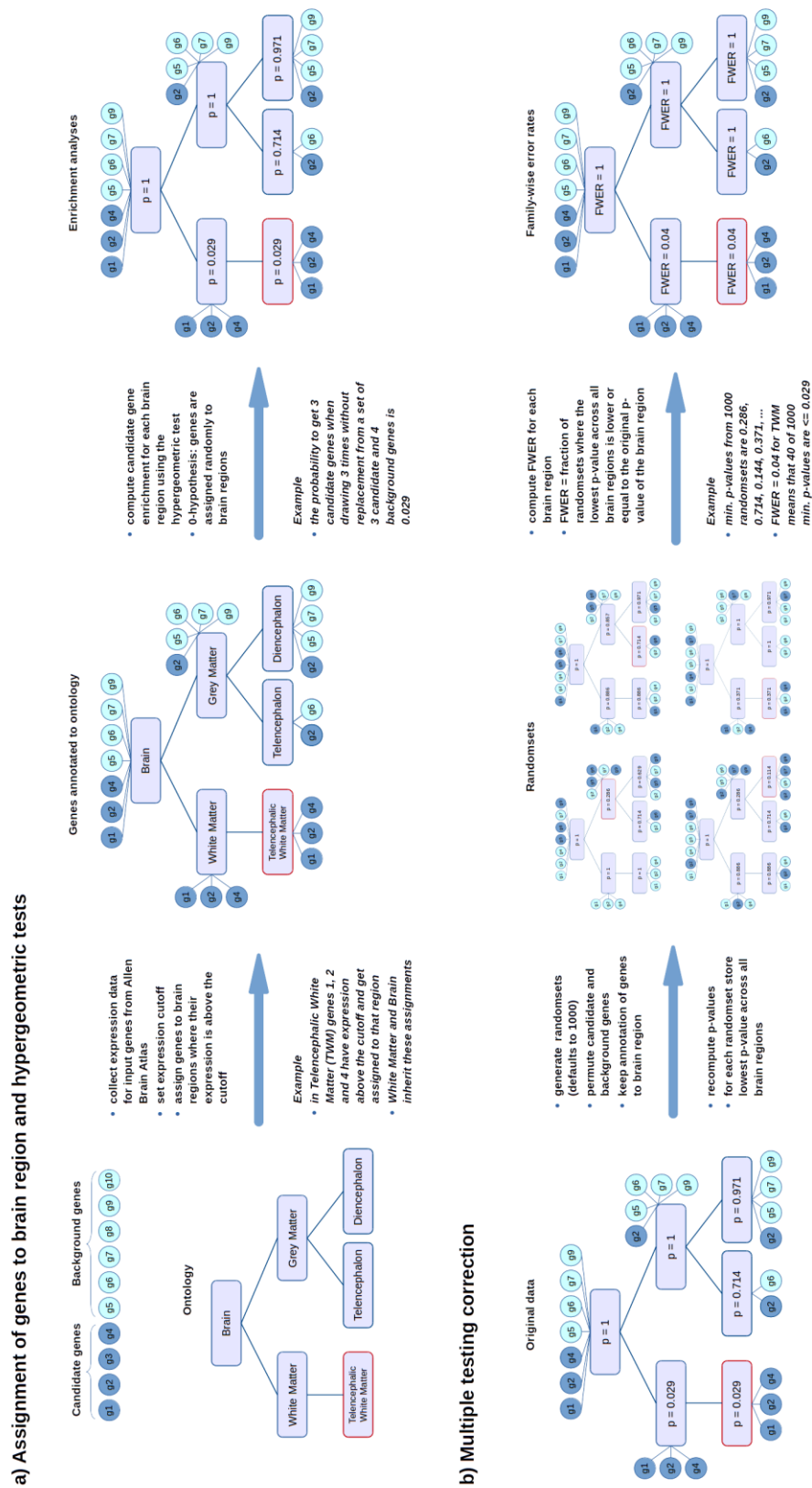
postnatal & adult	MD	290	1	2	9	0.000	0
postnatal & adult	MD	290	1	3	9	0.000	0
postnatal & adult	MD	290	1	4	9	0.003	0
postnatal & adult	MD	290	1	5	9	0.002	0
postnatal	MD	194	1	2	9	0.000	0
postnatal	MD	194	1	3	9	0.000	0
postnatal	MD	194	1	4	9	0.001	0
prenatal	NCX	53	8	1	0	0.333	0.18
prenatal & postnatal	NCX	45	7	1	0	0.605	0.42
prenatal & postnatal	NCX	45	11	2	0	0.708	0.44
prenatal & postnatal	NCX	45	11	3	0	0.756	0.48
postnatal & adult	NCX	50	4	2	0	0.626	0.39
postnatal & adult	NCX	50	4	3	0	0.622	0.35
postnatal & adult	NCX	50	7	4	0	0.571	0.3
postnatal & adult	NCX	50	4	5	0	0.508	0.24
postnatal	NCX	18	8	2	0	0.756	0.5
postnatal	NCX	18	13	3	0	0.773	0.52
postnatal	NCX	18	14	4	0	0.757	0.52
prenatal	STR	84	1	1	7	0.022	0
prenatal & postnatal	STR	201	1	1	7	0.022	0
prenatal & postnatal	STR	201	1	2	8	0.019	0
prenatal & postnatal	STR	201	1	3	8	0.014	0
postnatal & adult	STR	284	1	2	9	0.002	0
postnatal & adult	STR	284	1	3	9	0.002	0
postnatal & adult	STR	284	1	4	9	0.002	0
postnatal & adult	STR	284	1	5	9	0.006	0
postnatal	STR	125	1	2	9	0.002	0
postnatal	STR	125	1	3	9	0.002	0
postnatal	STR	125	1	4	9	0.003	0

References

Kang,H.J. *et al.* (2011) Spatio-temporal transcriptome of the human brain. *Nature*, **478**, 483–489.

Supplementary Figure

Figure 1: Schematic illustration of workflow for enrichment analysis including (a) assignment of genes to brain ontology regions and (b) algorithm for multiple testing correction.



Supplementary data file:

The input gene sets used for the evaluation are stored in the R objects in *gene_sets_evaluation.RData*.