

Supplementary Information

Kong *et al.*, Gene Expression Correlates of the Cortical Network Underlying Sentence Processing

Table S1. Left hemisphere AICHA atlas regions included in each functional network. See main text for the meanings of the network abbreviations. Region labels in *italic* indicate regions assigned to the language-related network according to either definition, i.e. SmSA, SSA and OcSA.

ID	Label	SmSA	SSA	OcSA	SNN	MDN	DMN
3	<i>G_Frontal_Sup-2-L</i>	YES					YES
29	<i>S_Inf_Frontal-1-L</i>		YES				
31	<i>S_Inf_Frontal-2-L</i>	YES	YES			YES	
33	<i>G_Frontal_Inf_Tri-1-L</i>	YES	YES	YES			
41	<i>G_Frontal_Inf_Orb-1-L</i>	YES					
57	<i>S_Precentral-4-L</i>	YES	YES	YES			
99	<i>G_SupraMarginal-7-L</i>	YES	YES	YES			
103	<i>G_Angular-2-L</i>	YES					YES
105	<i>G_Angular-3-L</i>			YES			YES
111	<i>S_Intraparietal-2-L</i>		YES			YES	
141	<i>G_Occipital_Inf-1-L</i>	YES					
147	<i>G_Insula-anterior-2-L</i>	YES					
149	<i>G_Insula-anterior-3-L</i>	YES	YES				
151	<i>G_Insula-anterior-4-L</i>		YES				
165	<i>G_Temporal_Sup-3-L</i>		YES				
167	<i>G_Temporal_Sup-4-L</i>	YES	YES	YES			
169	<i>S_Sup_Temporal-1-L</i>	YES	YES	YES			
171	<i>S_Sup_Temporal-2-L</i>	YES	YES	YES			
173	<i>S_Sup_Temporal-3-L</i>	YES	YES	YES			
175	<i>S_Sup_Temporal-4-L</i>	YES	YES	YES			
177	<i>S_Sup_Temporal-5-L</i>		YES	YES			YES
179	<i>G_Temporal_Mid-1-L</i>		YES	YES			YES
183	<i>G_Temporal_Mid-3-L</i>	YES	YES	YES			
185	<i>G_Temporal_Mid-4-L</i>	YES	YES				
193	<i>G_Temporal_Inf-4-L</i>	YES	YES			YES	
223	<i>G_Supp_Motor_Area-2-L</i>	YES					
225	<i>G_Supp_Motor_Area-3-L</i>	YES	YES				
229	<i>S_Cingulate-2-L</i>		YES				
263	<i>G_Paracentral_Lobule-4-L</i>	YES					
275	<i>G_Precuneus-6-L</i>	YES			YES	YES	
337	<i>G_Fusiform-4-L</i>		YES				
13	<i>S_Sup_Frontal-4-L</i>						YES
17	<i>S_Sup_Frontal-6-L</i>				YES	YES	
27	<i>G_Frontal_Mid-5-L</i>					YES	
53	<i>S_Precentral-2-L</i>					YES	
81	<i>G_Parietal_Sup-3-L</i>					YES	
83	<i>G_Parietal_Sup-4-L</i>					YES	

85	G_Parietal_Sup-5-L	YES	YES
109	S_Intraparietal-1-L		YES
113	S_Intraparietal-3-L		YES
127	G_Occipital_Lat-5-L		YES
131	G_Occipital_Sup-2-L		
133	G_Occipital_Mid-1-L	YES	YES
135	G_Occipital_Mid-2-L		YES
139	G_Occipital_Mid-4-L	YES	
207	G_Frontal_Sup_Medial-1-L		YES
209	G_Frontal_Sup_Medial-2-L		YES
213	S_Anterior_Rostral-1-L		YES
217	G_Frontal_Med_Orb-2-L		YES
265	G_Precuneus-1-L	YES	
267	G_Precuneus-2-L		YES
269	G_Precuneus-3-L		YES
273	G_Precuneus-5-L	YES	
279	G_Precuneus-8-L	YES	
283	S_Parietooccipital-1-L	YES	
287	S_Parietooccipital-3-L	YES	
289	S_Parietooccipital-4-L	YES	
293	S_Parietooccipital-6-L	YES	
299	G_Calcarine-1-L	YES	
305	G_Lingual-1-L	YES	
309	G_Lingual-3-L	YES	
323	G_ParaHippocampal-2-L	YES	
329	G_ParaHippocampal-5-L	YES	
341	G_Fusiform-6-L	YES	YES
343	G_Fusiform-7-L	YES	YES

Table S2. Overall correlations between the functional networks and their corresponding transcriptomic networks, based on the two resting state datasets BIL&GIN and GEB, and different sets of genes defined by their differential stability across donors in the Allen brain data (see Methods).

		SMSA	SSA	OCSA	SNN	MDN	DMN
TOP 5%	BIL&GIN	0.19	0.26	0.42	0.24	0.39	0.4
	GEB	0.19	0.24	0.35	0.33	0.5	0.6
TOP 10%	BIL&GIN	0.16	0.23	0.36	0.22	0.37	0.3
	GEB	0.15	0.21	0.26	0.31	0.46	0.54
BOTTOM 5%	BIL&GIN	0.05	-0.002	0.14	0.23	0.05	-0.01
	GEB	0.02	-0.005	0.02	0.14	0.05	0.15
BOTTOM 10%	BIL&GIN	0.06	-0.0006	0.16	0.23	0.04	0.0004
	GEB	0.03	-0.003	0.05	0.15	0.03	0.16

Spearman correlations in bold indicate being significant ($p < 0.05$).

Table S3. Overall correlations between the functional networks and their corresponding transcriptomic networks, after controlling for inter-regional spatial distance, based on the top 5% of genes by differential stability across donors in the Allen brain data (see Methods).

	BIL&GIN		GEB	
	rho	<i>p</i>	rho	<i>p</i>
SMSA	0.2	0.0052	0.2	0.0054
SSA	0.33	1.04E-06	0.33	1.48E-06
OCSA	0.56	3.90E-06	0.41	0.0013
SNN	0.3	0.00019	0.32	4.29E-05
MDN	0.34	0.00014	0.35	7.24E-05
DMN	0.49	8.37E-05	0.45	0.00029

Spearman correlations in bold indicate being significant ($p < 0.01$).

Table S4. The consensus gene set for the sentence processing network.

GENE	GENE_NAME	ENTREZ_ID	CHR.
ANK1	ankyrin 1, erythrocytic	286	8
ASGR2	asialoglycoprotein receptor 2	433	17
COX7A1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)	1346	19
GLDC	glycine dehydrogenase (decarboxylating)	2731	9
KCNS2	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 2	3788	8
LAIR2	leukocyte-associated immunoglobulin-like receptor 2	3904	19
LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	3937	5
LY6H	lymphocyte antigen 6 complex, locus H	4062	8
MET	met proto-oncogene (hepatocyte growth factor receptor)	4233	7
MGP	matrix Gla protein	4256	12
SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	5176	17
PRRX1	paired related homeobox 1	5396	1
ROBO1	roundabout, axon guidance receptor, homolog 1 (Drosophila)	6091	3
TGFB1	transforming growth factor, beta-induced, 68kDa	7045	5
TRPC6	transient receptor potential cation channel, subfamily C, member 6	7225	11
ZYX	zyxin	7791	7
DIRAS3	DIRAS family, GTP-binding RAS-like 3	9077	1
FAM65B	family with sequence similarity 65, member B	9750	6
ARHGAP25	Rho GTPase activating protein 25	9938	2
FRAT1	frequently rearranged in advanced T-cell lymphomas	10023	10
SPON2	spondin 2, extracellular matrix protein	10417	4
CNTN6	contactin 6	27255	3
CDR2L	cerebellar degeneration-related protein 2-like	30850	17
VILL	villin-like	50853	3
HR	hairless homolog (mouse)	55806	8
NT5M	5',3'-nucleotidase, mitochondrial	56953	17
SHD	Src homology 2 domain containing transforming protein D	56961	19
ELMO3	engulfment and cell motility 3	79767	16
MAGED4B	melanoma antigen family D, 4B	81557	X
C12ORF23	chromosome 12 open reading frame 23	90488	12
GLCCI1	glucocorticoid induced transcript 1	113263	7
SLC22A9	solute carrier family 22 (organic anion transporter), member 9	114571	11
GPRIN1	G protein regulated inducer of neurite outgrowth 1	114787	5
LOC145837	uncharacterized LOC145837	145837	15
CBLN2	cerebellin 2 precursor	147381	18
FAM162B	family with sequence similarity 162, member B	221303	6
PGM2L1	phosphoglucomutase 2-like 1	283209	11
IGSF22	immunoglobulin superfamily, member 22	283284	11
KIAA1875	KIAA1875	340390	8
CTXN3	cortexin 3	613212	5
IQCJ	IQ motif containing J	654502	3

Table S5. Preferential expression of the consensus set of genes for sentence processing network connectivity, when contrasting sentence processing regions against regions of the comparison networks.

GENE	T	DF	SIG. (2-TAILED)	MEAN DIFFERENCE	STD. ERROR DIFFERENCE	95% CI OF THE DIFFERENCE		FDR_P
ANK1	-2.275	61.585	0.026378	-0.29684	0.130462	-0.55767	-0.03602	0.098319
ASGR2	1.264	59.608	0.211	0.1527	0.120766	-0.0889	0.394301	0.286985
COX7A1	0.262	59.983	0.793969	0.033411	0.127364	-0.22136	0.288178	0.793969
GLDC	1.716	53.484	0.091937	0.151093	0.088046	-0.02547	0.327654	0.169536
KCNS2	1.373	40.608	0.177323	0.138121	0.100606	-0.06512	0.341358	0.269268
LAIR2	1.982	56.66	0.052383	0.348645	0.17594	-0.00372	0.701005	0.124933
LCP2	1.827	62.881	0.072423	0.226678	0.124061	-0.02125	0.474602	0.156282
LY6H	4.036	52.416	0.000178	0.518619	0.12849	0.260834	0.776404	0.003819
MET	-0.592	60.243	0.556127	-0.15925	0.26905	-0.69739	0.378882	0.584646
MGP	2.874	53.879	0.005797	0.545522	0.189843	0.16489	0.926155	0.039611
SERPINF1	3.851	45.857	0.000363	0.499352	0.129672	0.238313	0.760391	0.003819
PRRX1	-1.701	57.254	0.094331	-0.13388	0.0787	-0.29146	0.023694	0.169536
ROBO1	1.695	61.486	0.095105	0.108899	0.064241	-0.01954	0.237337	0.169536
TGFBI	1.248	59.299	0.216989	0.241808	0.193779	-0.1459	0.629518	0.286985
TRPC6	1.47	61.16	0.146672	0.124961	0.085004	-0.04501	0.294928	0.240542
ZYX	-0.845	63.94	0.401502	-0.0827	0.097918	-0.27831	0.112919	0.448392
DIRAS3	2.646	62.554	0.010294	0.206882	0.078192	0.050607	0.363158	0.052756
FAM65B	3.876	56.99	0.000277	0.475978	0.122814	0.230046	0.721911	0.003819
ARHGAP25	1.956	63.696	0.054849	0.220125	0.112536	-0.00471	0.444961	0.124933
FRAT1	-2.162	61.386	0.034562	-0.20808	0.096265	-0.40055	-0.01561	0.099955
SPON2	3.782	57.48	0.000373	0.619676	0.163847	0.291638	0.947714	0.003819
CNTN6	1.414	58.89	0.162508	0.161233	0.113993	-0.06688	0.389343	0.256262
CDR2L	-2.026	60.661	0.047118	-0.18518	0.091381	-0.36793	-0.00243	0.12074
VILL	-1.143	63.961	0.257482	-0.0705	0.061702	-0.19376	0.052767	0.329898
HR	-1.802	62.44	0.076358	-0.14571	0.080854	-0.30731	0.015895	0.156533
NT5M	-1.289	62.833	0.202002	-0.09297	0.072107	-0.23707	0.05113	0.28559
SHD	-0.938	62.914	0.351778	-0.1257	0.133994	-0.39347	0.142073	0.424203
ELMO3	-1.299	63.999	0.198597	-0.16419	0.126393	-0.41669	0.088311	0.28559
MAGED4B	2.666	62.135	0.009776	0.183261	0.068745	0.045847	0.320674	0.052756
C12ORF23	3.269	64	0.001738	0.197655	0.06046	0.076873	0.318437	0.01425
GLCCI1	-1.063	63.122	0.291919	-0.09197	0.086539	-0.2649	0.080954	0.362688
SLC22A9	1.672	62.007	0.099652	0.221549	0.132541	-0.0434	0.486493	0.170239
GPRIN1	2.194	63.8	0.031874	0.109142	0.049742	0.009764	0.208519	0.099955
LOC145837	0.649	56.511	0.518946	0.03438	0.05297	-0.07171	0.140471	0.559915
CBLN2	2.468	50.079	0.017038	0.395125	0.160086	0.073595	0.716654	0.077616
FAM162B	0.84	56.843	0.404647	0.09039	0.107658	-0.1252	0.305985	0.448392
PGM2L1	2.362	63.853	0.021263	0.126594	0.053608	0.019496	0.233692	0.08718
IGSF22	2.204	63.996	0.031107	0.154815	0.070233	0.014507	0.295122	0.099955
KIAA1875	-2.136	63.417	0.036569	-0.20559	0.096263	-0.39793	-0.01325	0.099955
CTXN3	0.517	63.921	0.607064	0.130138	0.251805	-0.37291	0.633188	0.622241
IQCI	0.886	63.957	0.378901	0.075186	0.084854	-0.09433	0.244703	0.443856

Table S6. Preferential expression in specific cell-types of the consensus set of genes for the sentence processing network.

GENE	CH R.	ASTROCYTES	NEURON	OLIGODENDROCYTE PRECURSOR CELL	NEWLY FORMED OLIGODENDROCYTE	MYELINATING OLIGODENDROCYTES	MICROGLIA	ENDOTHELIAL CELLS	ZHANG_EN RICH	ZHANG_EN RICH2	ZHANG2014	ZEISEL2015
ANK1	8	0.228	4.395	3.691	1.227	0.340	0.214	0.100	1.191	3.583		Interneuron
ASGR2	17	0.100	0.100	0.100	0.298	0.129	1.318	0.100	4.429	10.255	Microglia	
COX7A1	19	1.514	3.257	0.688	0.379	1.215	0.397	0.686	2.151	2.682	Neuron	Ependymal
GLDC	9	25.924	1.701	11.871	2.398	1.008	0.530	0.112	2.184	10.812	Astrocytes	Astrocyte
KCNS2	8	0.100	2.302	0.105	0.100	0.100	0.100	0.100	21.829	23.022	Neuron	
LAIR2	19											
LCP2	5	0.102	0.323	2.880	0.139	0.321	52.317	14.336	3.649	18.164	Microglia	Microglia
LY6H	8	1.736	225.441	72.095	17.532	7.308	8.442	2.675	3.127	12.859	Neuron	
MET	7	0.196	1.235	0.229	0.143	0.100	0.100	0.346	3.568	5.397	Neuron	
MGP	12	0.428	0.777	2.918	0.397	0.882	0.668	30.488	10.449	34.549	Endothelial Cells	
SERPINF1	17	9.423	2.487	10.790	0.539	1.386	97.531	7.738	9.039	10.350	Microglia	
PRRX1	1	17.844	0.918	15.575	2.600	0.111	0.100	0.556	1.146	6.863		
ROBO1	3	2.399	11.005	11.671	2.815	0.293	0.100	0.432	1.061	4.145	Neuron	Oligodendrocyte Precursor Cell
TGFBI	5	0.446	0.492	2.170	1.386	2.077	24.550	0.845	11.312	11.819	Microglia	Microglia
TRPC6	11	0.100	0.677	0.138	0.100	0.100	0.100	0.100	4.890	6.768	Neuron	
ZYX	7	12.443	12.732	17.570	12.735	20.805	74.186	35.417	2.095	3.566	Microglia	
DIRAS3	1											
FAM65B	6	6.286	30.186	1.074	0.105	0.276	0.976	0.869	4.802	28.112	Neuron	
ARHGAP25	2	0.187	0.230	2.900	0.136	0.362	76.103	18.077	4.210	26.240	Microglia	
FRAT1	10	1.646	5.892	1.594	0.663	1.206	1.676	1.014	3.516	3.579	Neuron	
SPON2	4	0.116	0.367	0.134	0.214	0.100	0.104	1.592	4.336	7.442	Neuron	
CNTN6	3	1.022	2.394	13.467	4.841	0.100	0.137	0.100	2.782	5.626	Oligodendrocyte Precursor Cell	
CDR2L	17	2.975	10.019	16.521	17.275	15.453	0.516	3.515	1.046	1.118		Oligodendrocyte
VILL	3	0.100	0.100	0.100	0.100	0.100	0.100	0.100	1.000	1.000		
HR	8	5.561	1.842	7.492	24.163	12.185	1.056	0.100	1.983	3.225	Newly Formed Oligodendrocyte	
NT5M	17	11.875	16.775	16.512	13.975	15.025	11.235	11.594	1.016	1.116		

SHD	19	9.325	14.378	19.730	9.362	3.409	0.886	0.910	1.372	2.107	Interneuron
ELMO3	16	0.623	0.173	0.183	0.100	0.100	0.164	0.330	1.886	3.409	Astrocytes
MAGED4B	X										
C12ORF23	12										
GLCCI1	7	4.252	4.604	7.851	5.422	1.839	0.340	7.182	1.093	1.448	
SLC22A9	11										
GPRIN1	5	0.588	28.585	4.909	1.203	1.539	1.280	0.280	5.823	18.574	Neuron
LOC145837	15										
CBLN2	18	0.101	11.801	0.354	4.057	0.508	0.185	2.503	2.909	4.716	Neuron
FAM162B	6	0.146	0.103	0.100	0.100	0.100	0.100	0.351	2.400	3.402	Endothelial Cells
PGM2L1	11	1.130	14.572	2.629	0.567	1.142	0.742	1.982	5.542	7.351	Neuron
IGSF22	11										
KIAA1875	8										
CTXN3	5	0.100	0.307	0.137	0.102	0.199	0.100	0.100	1.544	2.240	Neuron
IQCJ	3	0.100	0.101	0.346	0.100	0.100	0.100	0.100	3.415	3.462	Oligodendrocyte Precursor Cell

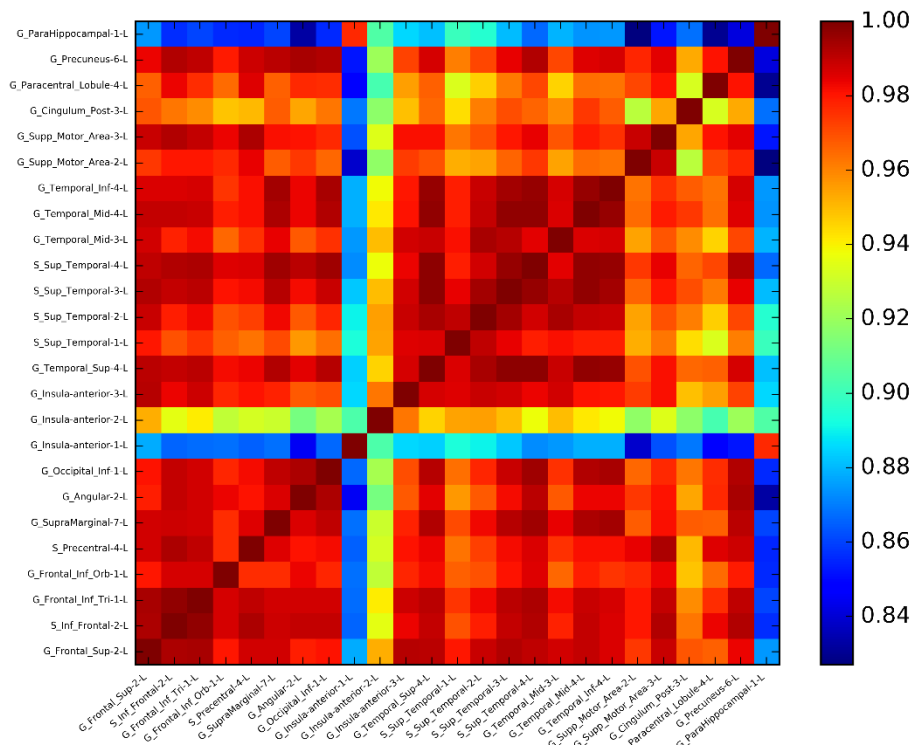


Fig. S1. Two deep cortical areas (G_ParaHippocampal-1 and G_Insula-anterior-1) showing relatively distinct gene expression profiles compared with most of the cortical areas. The gene expression similarity was calculated based on the top 5% genes according to their differential stability across donors.