

Supplemental Material

Supplemental Table 1. Correlation matrix of quantitative traits

	Word ID	Word Attack	Pass Comp	Speaking	Grammar	SLQ
Word ID	1.00					
Word Attack	0.77	1.00				
Pass Comp	0.76	0.53	1.00			
Speaking	0.57	0.41	0.59	1.00		
Grammar	0.70	0.59	0.67	0.78	1.00	
SLQ	0.67	0.52	0.69	0.87	0.87	1.00

Supplemental Table 2. List of SNP markers for analysis of 13q21

SNP ID	Physical Position	Genetic Position
rs1239684	50062719	53.887
rs1832694	50617813	54.319
rs747781	51451102	54.678
rs726540	52306404	54.973
rs7991623	52515781	55.075
rs1322938	52629757	55.127
rs1382461	54063650	55.741
rs641385	54771025	55.874
rs1409239	56879322	55.952
rs1413119	58237281	56.516
rs1536289	58781782	56.87
rs1414978	58940376	56.982
rs376767	59253329	57.207
rs950400	63696478	59.366
rs1889083	65120691	60.199
rs1831972	65837722	60.575
rs1444387	65842131	60.577
rs980150	66444608	60.863
rs1341518	69874063	63.002
rs768826	70668641	63.918

Supplemental Table 3. Reading impairment LD-PPL analysis of 28 functional SNPs putatively associated with cognition.

SNP	Gene Symbol	Cytogenetic Band	LD-PPL*
rs733722	CHAT	10q11.2	0.017
rs8178981	CHAT	10q11.2	0.0218
rs6265	BDNF	11p13	0.0602
rs12720366	DRD4	11p15.5	0.0121
rs1800496	DRD2	11q23	0.0184
rs6277	DRD2	11q23	0.014
rs6304	HTR2A	13q14.2	0.0138
rs6308	HTR2A	13q14.2	0.0253
rs6314	HTR2A	13q14.2	0.015
rs1799722	BDKRB2	14q32.2	0.0235
rs945032	BDKRB2	14q32.2	0.0207
rs4906902	GABRB3	15q12	0.0193
rs16969968	CHRNA5	15q25.1	0.0151
rs1731017	ABAT	16p13.3	0.0195
rs28936679	AANAT	17q25.1	0.0166
rs1044396	CHRNA4	20q13.33	0.0226
rs4680	COMT	22q11.2	0.0122
rs8192506	DBI	2q14.2	0.0114
rs6280	DRD3	3q13.3	0.0221
rs1229984	ADH1B	4q22	0.0143
rs1799920	HTR1A	5q12.2	0.0215
rs1042711	ADRB2	5q33.1	0.0136
rs1042714	ADRB2	5q33.1	0.0132
rs130060	HTR1B	6q13	0.0124
rs16147	NPY	7p15.1	0.0193
rs324650	CHRM2	7q33	0.0157
rs891398	CHRNA2	8p21	0.0152
rs1611115	DBH	9q34	0.0162
rs2205718	MAOA	Xp11.23	0.021
rs6323	MAOA	Xp11.23	0.0284
rs979605	MAOA	Xp11.23	0.0276
rs979606	MAOA	Xp11.23	0.0199
rs6318	HTR2C	Xq23	0.0147

*LD-PPL analysis, as described in the text, is an analysis of linkage allowing for linkage disequilibrium with the trait that can be useful for mapping traits in large pedigrees. Any values greater than the prior probability of 2% is evidence for linkage/linkage disequilibrium with the trait while values below 2% represent evidence against.

Supplemental Table 4. Alternative 13q21 linkage (cM location) statistics for reading and language traits

	MOD			VC LOD*		
	Univariate	+ LI Threshold	+RI Threshold	Univariate	+ LI Threshold**	+RI Threshold**
LI (Dichotomous)	1.27 (54 cM)			0.44 (63 cM)		
Word Identification	1.58 (60 cM)	1.29 (54 cM)		0.79 (64 cM)	0.84 (64 cM)	
Word Attack	1.48 (64 cM)	1.43 (55 cM)		0.18 (64 cM)	0.38 (63 cM)	
Passage Comprehension	1.63 (59 cM)	1.00 (59 cM)		0.00	0.01 (63 cM)	
RI (Dichotomous)	4.76 (56 cM)			4.38 (56 cM)		
Speaking	1.84 (63 cM)		4.86 (55 cM)	0.21 (63 cM)		2.93 (56 cM)
SLQ	1.38 (60 cM)		4.54 (55 cM)	1.73 (64 cM)		2.75 (56 cM)
Grammar	1.87 (59 cM)		3.89 (56 cM)	0.22 (64 cM)		2.14 (56 cM)

*VC LOD: variance components LOD score from SOLAR v4.2 using ascertainment corrected heritability values and IBD matrices estimated by Loki v2.3.

**Since SOLAR does not have a bivariate threshold model such as the one we use with the PPL and MOD, a simple bivariate model was run where the linkage to the covariation between the traits. As such, this model is not strictly equivalent and offered only for comparison purposes.