

Appendix 1 to Wang K-S, Liu X, Zhang, Q-Y, et al. Parent-of-origin effects of *FAS* and *PDLIM1* in attention-deficit/hyperactivity disorder. *J Psychiatry Neurosci* 2011.

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Table S1: Forty-four single nucleotide polymorphisms showing parent-of-origin effect with $p < 0.001$

Chr.	SNP database	Base pair position*	Known gene	A1:A2	T/NT	U	Paternal		Maternal				Parent-of-origin effect	
							χ^2	p	T/NT	U	χ^2	p	Z	p
1	rs17098286	77640412	<i>AK5</i>	G:C	76	42	9.88	0.001671	45	62	2.73	0.0987	3.343	0.0008295
1	rs542494	232490912	<i>SLC35F3</i>	C:T	86	123	6.55	0.01049	120	80	8	0.004678	-3.789	0.0001515
2	rs7603744	2986305	intergenic	G:A	75	51	4.571	0.03251	57	90	7.41	0.006493	3.394	0.0006881
2	rs12617333	213739278	intergenic	C:T	84	121	6.678	0.009761	114	75	7.6	0.005837	-3.755	0.0001734
3	rs7647821	11771917	intergenic	A:G	82	132	11.74	0.0006127	126	103	2.32	0.1277	-3.511	0.0004461
3	rs7627205	113917621	intergenic	A:C	46	94	16.58	0.0000468	78	62	1.84	0.1747	-3.826	0.0001301
3	rs7614907	120559179	<i>CDGAP</i>	T:C	58	25	13.28	0.0002682	26	43	4.7	0.03024	3.998	0.000064
4	rs16869853	20301678	intergenic	A:G	162	215	7.451	0.00634	202	164	3.95	0.047	-3.323	0.0008907
4	rs1452898	72359433	<i>SLC4A4</i>	C:A	107	81	3.596	0.05793	73	119	11	0.0009009	3.665	0.0002471
4	rs7673301	72406891	<i>SLC4A4</i>	T:C	97	73	3.408	0.06487	61	101	9.94	0.001619	3.526	0.0004217
4	rs12503217	111925610	intergenic	C:T	56	75	2.777	0.09563	84	49	9.28	0.002316	-3.31	0.0009318
4	rs17484427	115089316	<i>ARSL</i>	G:C	126	88	6.748	0.009387	90	123	5.11	0.02375	3.42	0.0006274
4	rs6834471	139173534	intergenic	C:T	51	65	1.69	0.1936	77	40	11.7	0.0006247	-3.322	0.0008932
5	rs289008	55717899	intergenic	A:G	32	59	8.1	0.004427	52	34	3.81	0.05089	-3.349	0.0008103
6	rs2582	33082529	<i>HLA-DOA</i>	T:G	117	73	10.19	0.001412	90	117	3.52	0.06057	3.586	0.0003358
6	rs9389004	132901953	<i>TAAR9</i>	A:G	46	20	10.4	0.00126	34	47	2.11	0.1461	3.329	0.0008714
6	rs8192624	132933946	<i>TAAR6</i>	A:G	78	50	6.173	0.01297	51	76	4.96	0.02594	3.307	0.0009444
6	rs9356167	158293358	intergenic	T:C	55	28	8.783	0.00304	41	62	4.28	0.03853	3.543	0.0003955
7	rs6965123	21376762	intergenic	T:C	101	65	7.855	0.005069	70	94	3.53	0.06013	3.292	0.0009939
7	rs7790549	149720965	<i>ZNF775</i>	A:G	77	34	16.81	0.0000413	67	76	0.57	0.4501	3.57	0.0003568
8	rs12114607	63416967	<i>NKAIN3</i>	A:G	71	100	4.918	0.02658	109	73	7.12	0.007619	-3.431	0.0006026
8	rs13255144	119516196	<i>SAMD12</i>	T:C	206	175	2.516	0.1127	167	233	11.2	0.0008081	3.47	0.0005199
8	rs7835137	128744953	intergenic	C:T	61	106	12.13	0.0004973	93	74	2.16	0.1415	-3.49	0.0004833
10	rs12413311	10815999	intergenic	G:A	143	103	6.531	0.0106	109	147	5.66	0.01733	3.476	0.0005083
10	rs9658691	90746143	<i>FAS</i>	C:T	76	67	0.5704	0.4501	53	103	16.1	0.0000592	3.331	0.000864
10	rs11188249	97000369	<i>PDLIM1</i>	G:A	77	75	0.026320.8711		45	99	20.3	0.0000068	3.365	0.0007668
10	rs4465313	113062138	intergenic	A:G	57	95	9.563	0.001985	80	60	2.88	0.08981	-3.349	0.0008122
10	rs4750741	130825576	intergenic	A:G	40	69	7.716	0.005475	56	35	4.85	0.02771	-3.463	0.0005333
13	rs10492402	32606789	<i>STARD13</i>	T:C	64	39	6.068	0.01377	44	72	6.76	0.00933	3.54	0.0004009
13	rs7322586	32610785	<i>STARD13</i>	A:G	66	40	6.377	0.01156	44	70	5.93	0.01489	3.474	0.0005125
14	rs1974173	84493496	intergenic	C:G	149	180	2.921	0.08744	183	130	8.97	0.002738	-3.33	0.0008686
15	rs4777414	69675927	<i>THSD4</i>	C:T	68	88	2.581	0.1082	92	53	10.6	0.001154	-3.437	0.0005874
15	rs12439633	95354542	intergenic	A:G	75	125	12.56	0.0003935	103	86	1.54	0.215	-3.355	0.0007952
16	rs4412964	82113739	<i>CDH13</i>	T:C	163	219	8.505	0.003541	197	157	4.53	0.03326	-3.547	0.0003905
17	rs2644700	729799	<i>NXN</i>	T:C	46	86	12.12	0.0004985	70	54	2.07	0.1508	-3.441	0.0005792
17	rs604229	733578	<i>NXN</i>	T:C	37	75	13.01	0.00031	65	49	2.27	0.1323	-3.6	0.0003183
17	rs12938404	53117603	intergenic	C:G	117	78	7.8	0.005225	81	107	3.6	0.05793	3.296	0.0009825
17	rs6501984	73214462	intergenic†	T:G	80	58	3.507	0.0611	49	84	9.21	0.002406	3.455	0.0005511
18	rs1452643	29741426	<i>NOL4</i>	T:A	145	113	3.969	0.04635	91	131	7.21	0.007261	3.31	0.0009322
18	rs12605124	63226974	intergenic	C:G	87	127	7.477	0.00625	128	98	3.98	0.04598	-3.338	0.000845
19	rs17325700	38923667	<i>CHST8</i>	T:A	90	58	6.966	0.008307	60	88	5.33	0.02092	3.475	0.0005115
20	rs17225746	12264672	intergenic	G:A	72	38	10.61	0.001128	48	68	3.48	0.06218	3.603	0.0003143
21	rs9983727	22427523	intergenic	A:G	40	113	35.06	0.000000032	72	88	1.61	0.2045	-3.459	0.0005413
21	rs2839525	42750006	intergenic	G:T	197	165	2.837	0.09214	167	227	9.16	0.002473	3.304	0.0009524

Chr. = chromosome; SNP = single nucleotide polymorphism; T/NT = transmitted/nontransmitted allele.

*Physical position is based on NCBI Genome Build 36.3.

†Between LOC100128672 and LOC100132174.

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Table S2: Eight single nucleotide polymorphisms within *FAS* and *PDLIM1* genes

Chr.	SNP database	Base pair position*	Known gene	GT	AF	All transmissions			Maternal			Paternal			Parent-of-origin effect		
						T/NT	χ^2 †	<i>p</i>	T/NT	χ^2	<i>p</i>	T/NT	χ^2	<i>p</i>	χ^2 ‡	Z§	<i>p</i> ¶
10	rs9658691	90746143	<i>FAS</i>	C/T	0.10	128/169	5.66	0.017	53/103	16.1	0.000059	76/67	0.57	0.45	11.1	3.33	0.00086
10	rs1926194	90750298	<i>FAS</i>	G/A	0.44	411/401	1.03	0.12	218/206	0.34	0.56	193/195	0.01	0.92	0.23	0.50	0.63
10	rs9658786	50766329	<i>FAS</i>	T/C	0.14	189/205	0.64	0.42	83/118	6.10	0.014	106/87	1.87	0.17	7.33	2.70	0.007
10	rs17525629	96996845	<i>PDLIM1</i>	G/T	0.11	175/170	1.92	0.17	87/67	2.83	0.09	87/83	0.09	0.76	0.92	1.01	0.32
10	rs11188249	97000369	<i>PDLIM1</i>	G/A	0.10	122/174	9.14	0.0025	45/99	20.3	0.0000068	77/75	0.03	0.87	11.5	3.37	0.00077
10	rs2296961	97013620	<i>PDLIM1</i>	C/T	0.30	332/386	4.06	0.04	170/191	1.34	0.25	163/194	2.87	0.09	0.15	0.39	0.69
10	rs1745855	97020367	<i>PDLIM1</i>	A/G	0.08	112/118	0.16	0.69	55/63	0.55	0.46	58/56	0.04	0.85	0.42	0.65	0.51
10	rs11188256	97027568	<i>PDLIM1</i>	C/T	0.22	306/238	8.50	0.0036	165/104	13.9	0.00019	142/135	0.18	0.67	5.63	2.37	0.018

AF = minor allele frequency of the SNP in founders; Chr. = chromosome; GT = genotype for the SNP; SNP = single nucleotide polymorphism; T/NT = transmitted/nontransmitted allele.
 *Physical position is based on NCBI Genome Build 36.3.
 † χ^2 transmission disequilibrium test statistic.
 ‡ χ^2 based on a 2 × 2 contingency test to evaluate the difference in transmission frequency between paternal and maternal haplotypes.
 §Z score for difference in paternal versus maternal odds ratios.
 ¶Nominal *p* value, asymptotic for parent-of-origin test.

Table S3: Fourteen single nucleotide polymorphisms within 7 genes showing paternal or maternal transmissions or parent-of-origin effect

Chr.	SNP database	Base pair position*	Known gene	GT	AF	HW†	All transmissions			Maternal			Paternal			Parent-of-origin effect		
							T/NT	χ^2 ‡	<i>p</i>	T/NT	χ^2	<i>p</i>	T/NT	χ^2	<i>p</i>	χ^2 §	Z¶	<i>p</i> **
5	rs3863145	1445711	<i>DAT1</i>	A/G	0.28	0.73	309/362	4.19	0.04	161/172	0.36	0.55	148/190	5.22	0.022	1.40	1.19	0.23
5	rs11564772	1451007	<i>DAT1</i>	T/C	0.08	0.20	107/114	0.22	0.64	45/61	2.42	0.12	62/53	0.70	0.40	2.90	1.70	0.089
7	rs880028	50537630	<i>DDC</i>	G/A	0.22	0.57	229/297	8.79	0.003	108/152	7.79	0.0053	122/144	1.98	0.16	1.01	1.0	0.32
11	rs12288512	2770424	<i>BDNF</i>	A/G	0.22	0.98	256/352	15.2	0.000099	132/174	3.20	0.016	124/178	9.66	0.0019	0.27	0.52	0.60
12	rs17110477	7063013	<i>TPH2</i>	A/T	0.25	0.16	300/349	3.70	0.054	162/168	0.15	0.70	139/180	5.53	0.019	1.99	1.41	0.16
12	rs7978482	7065224	<i>TPH2</i>	T/C	0.18	0.38	268/214	6.05	0.014	126/107	1.39	0.24	143/106	5.21	0.023	0.55	0.74	0.46
18	rs1477941	11682440	<i>GNAL</i>	G/C	0.10	0.62	122/169	7.59	0.0059	57/89	7.01	0.0081	65/80	1.55	0.21	1.01	1.0	0.32
18	rs10468679	11685676	<i>GNAL</i>	T/C	0.06	0.02	62/107	11.9	0.00054	30/59	9.56	0.002	33/49	3.16	0.075	0.78	0.88	0.37
18	rs8087897	11687824	<i>GNAL</i>	A/G	0.10	0.53	47/102	20.3	0.0000066	24/58	14.1	0.0002	23/44	6.58	0.01	0.44	0.66	0.51
20	rs3787303	10156748	<i>SNAP25</i>	G/A	0.18	0.10	219/239	0.35	0.35	118/110	0.28	0.60	101/129	3.41	0.065	2.82	1.68	0.093
20	rs3787283	10232418	<i>SNAP25</i>	G/A	0.34	0.85	375/364	0.16	0.68	174/195	1.95	0.27	201/169	2.77	0.096	3.80	1.95	0.051
22	rs12160908	24258620	<i>ADRBK2</i>	T/C	0.22	0.06	152/224	13.8	0.00021	75/114	6.79	0.0092	75/111	7.1	0.0081	0.02	0.06	0.95
22	rs496796	24262542	<i>ADRBK2</i>	C/G	0.50	0.13	389/396	0.06	0.61	203/179	1.51	0.22	186/217	2.38	0.12	3.83	1.96	0.05
22	rs652099	24264878	<i>ADRBK2</i>	A/C	0.18	0.98	243/247	0.04	0.86	110/135	2.55	0.11	133/112	1.8	0.18	4.32	2.08	0.038

AF = minor allele frequency of the SNP in founders; Chr. = chromosome; GT = genotype for the SNP; SNP = single nucleotide polymorphism; T/NT = transmitted/nontransmitted allele.
 *Physical position is based on NCBI Genome Build 36.3.
 †*p* value for Hardy-Weinberg equilibrium test.
 ‡ χ^2 transmission disequilibrium test statistic.
 § χ^2 based on a 2 × 2 contingency test to evaluate the difference in transmission frequency between paternal and maternal haplotypes.
 ¶Z score for difference in paternal versus maternal odds ratios.
 **Nominal *p* value, asymptotic for parent-of-origin test.

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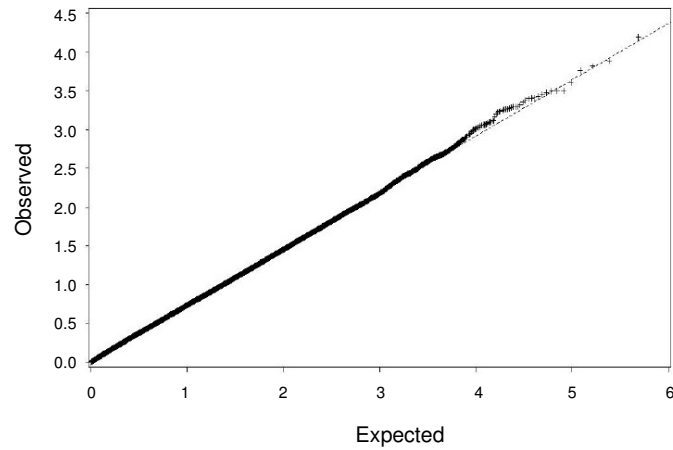


Fig. S1: Q-Q plot of observed versus expected $-\log_{10}(p)$ values for parent-of-origin effects.