

**Summary of case-control by quartile analysis of dNA.DZ twins**

Language	Q4 (N = 17)	CHR	SNP	BP	A1	F_A	F_U	A2	CHISQ	OR	UNADJ	BONF	FDR_BH	Band	Alleles	Gene(s)	Role
		8	rs17595454	18377451	T	0.281	0.081	C	16.8	4.429	4.16E-05	3.70E-03	3.70E-03	p22	C/T		
Nonverbal	Q4 (N = 15)	CHR	SNP	BP	A1	F_A	F_U	A2	CHISQ	OR	UNADJ	BONF	FDR_BH	Band	Alleles	Gene(s)	Role
		3	rs17564921	148372345	C	0.233	0.069	A	12.39	4.111	4.32E-04	3.93E-02	1.81E-02	q24	A C	RP11-649A	intrinsic
		5	rs17211823	128158012	C	0.233	0.069	T	12.31	4.096	4.49E-04	4.09E-02	1.81E-02	q23.3	T C	SLC27A6	intrinsic
		7	rs4719155	70745160	A	0.533	0.258	G	11.78	3.29	5.99E-04	5.45E-02	1.81E-02	q11.22	A G	WBSCR17	intrinsic
		22	rs6005657	26565087	T	0.333	0.128	C	11.25	3.42	7.97E-04	7.25E-02	1.81E-02	q12.1			
		9	rs6479471	95084239	T	0.300	0.114	G	10.04	3.316	1.53E-03	1.39E-01	2.75E-02	q22.31	G T	WNK2	intrinsic
		4	rs2342654	156369261	T	0.333	0.141	C	9.086	3.053	2.58E-03	2.34E-01	2.75E-02	q32.1			
		9	rs7022051	95042804	T	0.300	0.120	C	9.073	3.142	2.59E-03	2.36E-01	2.75E-02	q22.31	C T	WNK2	intrinsic
		9	rs7857220	95064873	C	0.300	0.120	T	9.068	3.141	2.60E-03	2.37E-01	2.75E-02	q22.31	T C	WNK2	intrinsic (5upstream)
		18	rs8084568	57190720	T	0.233	0.082	C	8.988	3.409	2.72E-03	2.47E-01	2.75E-02	q21.33	C T	CDH20	intrinsic
		7	rs10224816	9678184	C	0.267	0.106	T	8.147	3.085	4.31E-03	3.93E-01	3.93E-02	p21.3			
		10	rs497204	80306297	A	0.167	0.052	G	7.935	3.668	4.85E-03	4.41E-01	4.01E-02	q22.3			
		10	rs772822	80304750	C	0.133	0.037	T	7.606	3.991	5.82E-03	5.29E-01	4.41E-02	q22.3			
		17	rs4387653	68659971	T	0.367	0.177	C	7.291	2.686	6.93E-03	6.31E-01	4.85E-02	q25.1			
		20	rs17805193	59138980	T	0.167	0.055	C	6.996	3.416	8.17E-03	7.43E-01	5.31E-02	q13.33			
		8	rs11984453	4491939	A	0.200	0.079	G	5.969	2.92	1.46E-02	1.00E+00	8.83E-02	p23.2	G A	CSMD1	intrinsic
Play	Q4 (N = 16)	CHR	SNP	BP	A1	F_A	F_U	A2	CHISQ	OR	UNADJ	BONF	FDR_BH	Band	Alleles	Gene(s)	Role
		20	rs2427386	60794328	T	0.625	0.346	C	10.92	3.151	9.53E-04	1.67E-01	9.03E-02	q13.33			
		16	rs1801255	56247306	C	0.469	0.229	A	10.28	2.968	1.35E-03	2.35E-01	9.03E-02	q21	A C	GPR56	coding
		6	rs853884	36576111	T	0.219	0.073	C	9.949	3.574	1.61E-03	2.82E-01	9.03E-02	p21.31	A G	STK38	intrinsic
		1	rs2255340	230002773	A	0.469	0.243	G	8.738	2.744	3.12E-03	5.45E-01	9.03E-02	q42.2	T C	DISC1	intrinsic
		13	rs2876807	61019136	G	0.188	0.062	A	8.576	3.508	3.41E-03	5.96E-01	9.03E-02	q21.2			
		2	rs10490706	19355330	C	0.406	0.199	T	8.512	2.752	3.53E-03	6.17E-01	9.03E-02	p24.1	T C	AC092594.	intronic
		8	rs11984453	4491939	A	0.219	0.079	G	8.47	3.27	3.61E-03	6.32E-01	9.03E-02	p23.2	G A	CSMD1	intrinsic
		2	rs11690021	239301967	C	0.219	0.080	T	8.191	3.212	4.21E-03	7.37E-01	9.21E-02	q37.3	T C	AC113618.	intronic
Perseverative Behaviors	Q1 (N = 20)	CHR	SNP	BP	A1	F_A	F_U	A2	CHISQ	OR	UNADJ	BONF	FDR_BH	Band	Alleles	Gene(s)	Role
		12	rs2708079	41202340	A	0.125	0.408	G	13.19	0.2072	2.82E-04	7.32E-03	6.48E-03	q12	T C	PRICKLE1	intronic
		9	rs7042145	8394095	T	0.750	0.474	C	12.12	3.33	4.99E-04	1.30E-02	6.48E-03	p24.1	T C	PTPRD	intronic
		5	rs149473	123648735	C	0.000	0.169	T	8.145	0	4.32E-03	1.12E-01	3.74E-02	q23.2			
		4	rs2871491	186937857	A	0.000	0.153	G	7.218	0	7.22E-03	1.88E-01	4.20E-02	q35.1	G A	SORBS2	intronic
		7	rs4337997	22351942	G	0.025	0.189	A	7.016	0.1098	8.08E-03	2.10E-01	4.20E-02	p15.3	A G	RAPGEF5	intronic
		6	rs7756298	40808750	T	0.125	0.315	C	6.638	0.3111	9.98E-03	2.60E-01	4.33E-02	p21.1			
		6	rs12529308	40797708	A	0.125	0.301	C	5.877	0.3312	1.53E-02	3.99E-01	5.68E-02	p21.1			
		9	rs3780457	99962228	T	0.000	0.124	C	5.649	0	1.75E-02	4.54E-01	5.68E-02	q22.33	G A	CORO2A	intronic
		7	rs12333620	22324730	T	0.075	0.218	G	4.772	0.291	2.89E-02	7.52E-01	7.26E-02	p15.3	G T	RAPGEF5	intronic
		7	rs1568571	22341449	G	0.075	0.218	A	4.751	0.2917	2.93E-02	7.61E-01	7.26E-02	p15.3	T C	RAPGEF5	intronic
		2	rs6745182	190533471	C	0.000	0.105	T	4.668	0	3.07E-02	7.99E-01	7.26E-02	q32.2	T C	C2orf88	intronic
		5	rs10059061	95806928	C	0.000	0.097	A	4.313	0	3.78E-02	9.84E-01	8.20E-02	q15	A C	CTD-2337A12.1	
		6	rs6912147	22371817	G	0.000	0.094	A	4.164	0	4.13E-02	1.00E+00	8.26E-02	p22.3	G A	RP3-404K8	intronic
		5	rs1870658	73612235	C	0.000	0.086	T	3.738	0	5.32E-02	1.00E+00	9.22E-02	q13.3			
		5	rs471405	73613440	A	0.000	0.086	G	3.738	0	5.32E-02	1.00E+00	9.22E-02	q13.3			
Q4 (N = 15)	CHR	SNP	BP	A1	F_A	F_U	A2	CHISQ	OR	UNADJ	BONF	FDR_BH	Band	Alleles	Gene(s)	Role	
		6	rs12529308	40797708	A	0.600	0.301	C	12.59	3.477	3.89E-04	1.01E-02	5.26E-03	p21.1			
		7	rs4337997	22351942	G	0.433	0.189	A	11.49	3.275	7.00E-04	1.82E-02	5.26E-03	p15.3			