

Supplementary Table SII Testing Rare vAriants using Public Data (TRAPD) results.

Gene	Rare + novel variants						P_DOM	P_REC
	Cases count			Controls count				
	HET	CH	HOM	HET	CH	HOM		
<i>HRNR</i>	41	21	6	41	18	2	2.59E-09	0.011
<i>PLA2G4F</i>	32	21	0	19	8	2	4.10E-09	0.002
<i>SLC1A5</i>	46	21	6	45	15	7	1.95E-07	0.025
<i>C10orf120</i>	49	1	18	53	5	11	7.73E-07	0.081
<i>DMXL2</i>	41	26	6	41	25	3	7.73E-07	0.024
<i>ZBTB41</i>	50	2	15	49	3	14	1.37E-06	0.211
<i>FAM184A</i>	55	9	13	54	7	9	1.52E-06	0.023
<i>THAP3</i>	50	3	11	48	2	8	1.77E-06	0.070
Common + novel variants								
<i>LRIT2</i>	33	29	3	25	22	3	1.14E-09	0.008
<i>FMO1</i>	44	18	5	40	13	3	1.16E-09	0.014
<i>HRCT1</i>	41	17	10	42	12	7	2.59E-09	0.007
<i>CSTF2T</i>	25	24	1	13	12	0	4.76E-09	0.000
<i>PSKH2</i>	55	0	12	50	0	8	5.15E-09	0.074
<i>SLC2A1</i>	39	25	4	36	23	5	2.33E-08	0.077
<i>MAB21L3</i>	32	24	7	26	23	2	8.17E-08	0.012
<i>ZNF844</i>	32	28	6	30	27	3	2.03E-07	0.020
<i>DEDD2</i>	20	17	3	9	9	0	3.34E-07	0.001
<i>C2orf91</i>	43	15	9	39	18	8	7.04E-07	0.218
<i>GON4L</i>	34	31	3	35	29	5	7.73E-07	0.068
<i>MCM5</i>	36	8	0	21	2	1	9.71E-07	0.037
<i>SFTPA1</i>	33	21	3	24	16	3	1.02E-06	0.030
<i>PRELP</i>	51	0	16	56	0	10	1.37E-06	0.027
<i>CASP1</i>	26	22	4	18	16	2	2.04E-06	0.008
<i>CELSR3</i>	26	21	0	15	13	1	2.19E-06	0.015
<i>DNAJC16</i>	39	23	9	39	27	5	2.98E-06	0.080
<i>RP1</i>	36	25	9	36	31	4	2.98E-06	0.089
<i>TRIM63</i>	41	26	6	40	28	3	2.98E-06	0.061

Only genome-wide significant results are displayed. Threshold for rare variants was $P=3.1 \times 10^{-6}$ based on 15 998 genes scored. For common variants threshold was $P=3.5 \times 10^{-6}$ based on 14 200 genes scored. Columns are from TRAPD output. For detailed explanation, please see: <https://github.com/mhguo1/TRAPD>.