Supplemental Table 1. VAAST genes with most significant p-values in family 1168 sorted by rank

Most Significant Shared Variant Genes in Family 1168			
Rank	**Gene**	**P-value**	**Score**
1	PDE4DIP	1.67E-06	512.629
2	HEATR1	1.67E-06	337.392
3	HRNR	1.67E-06	310.495
4	OR6N1	1.67E-06	247.075
5	USH2A	1.67E-06	235.228
6	OR2L8	1.67E-06	234.921
7	OR11L1	1.67E-06	231.181
8	OR2M7	1.67E-06	192.864
9	EXO1	1.67E-06	189.517
10	OR2W3	1.67E-06	184.782
11	KIR3DL1	1.67E-06	178.513
12	CR1	1.67E-06	174.309
13	LGALS8	1.67E-06	173.868
14	SPTA1	1.67E-06	170.285
15	NES	1.67E-06	169.467
16	OR14I1	1.67E-06	167.385
17	OR4C3	1.67E-06	158.420
18	KIAA1614	1.67E-06	151.236
19	KIAA1324	1.67E-06	148.598
20	PEAR1	1.67E-06	145.222
21	TCHH	1.67E-06	135.753
22	CENPF	1.67E-06	121.825
23	OR2G2	1.67E-06	119.260
24	FCRL5	1.67E-06	119.033
25	IFI16	1.67E-06	118.950
26	CHIA	1.67E-06	117.826
27	PGLYRP4	1.67E-06	115.088
28	TOR1AIP1	1.67E-06	113.727
29	TLR5	1.67E-06	113.513
30	DTL	1.67E-06	112.777
31	CCDC76	1.67E-06	112.564
32	FAM71A	1.67E-06	112.360
33	OR2T11	1.67E-06	111.329
34	LAMC1	1.67E-06	111.244
35	OR2C3	1.67E-06	109.797
36	CDC27	1.67E-06	105.246
37	OR9G9	1.67E-06	104.258
38	OR2T6	1.67E-06	98.889

39	OR2B11	1.67E-06	97.796
40	THEM5	1.67E-06	95.040
41	IQGAP3	1.67E-06	93.682
42	OR10J1	1.67E-06	93.464
43	ADAR	1.67E-06	92.914
44	MRPL9	1.67E-06	91.190
45	F5	1.67E-06	91.081
46	PTGFRN	1.67E-06	87.937
47	ZNF805	1.67E-06	83.064
48	OR2T12	1.67E-06	82.076
49	IGSF3	1.67E-06	81.485
50	OR14C36	1.67E-06	79.059
51	ADAM15	1.67E-06	77.869
52	AKNAD1	1.67E-06	77.606
53	ASTN1	1.67E-06	76.817
54	KIR2DL4_DUP_01	1.67E-06	75.509
55	CR1L	1.67E-06	75.217
56	ARHGEF11	1.67E-06	74.387
57	MUC6	1.67E-06	74.285
58	ZNF695	1.67E-06	73.252
59	FAM104B_DUP_01	1.67E-06	72.298
60	HYDIN	1.67E-06	68.669
61	EPS8L3	1.67E-06	65.993
62	CTBP2	1.67E-06	60.405
63	GPR37L1	1.67E-06	58.488
64	F13B	1.67E-06	57.598
65	RRNAD1	1.67E-06	57.520
66	MYBPHL	1.67E-06	57.296
67	BCL2L15	1.67E-06	57.296
68	TMEM81	1.67E-06	57.090
69	PRODH	1.67E-06	57.090
70	CR2	1.67E-06	56.757
71	CSF1	1.67E-06	56.540
72	PRG4	1.67E-06	56.537
73	ASPM	1.67E-06	56.324
74	ACP6	1.67E-06	56.072
75	DSTYK	1.67E-06	55.948
76	ITPKB	1.67E-06	55.701
77	XKR3	1.67E-06	55.660
78	PTPN22	1.67E-06	55.650
79	TRIM33	1.67E-06	55.627
80	OR14A16	1.67E-06	55.627
81	MIA3	1.67E-06	55.609

82	C1orf111	1.67E-06	55.430
83	CDC42BPA	1.67E-06	55.430
84	CEP350	1.67E-06	55.377
85	ANKRD35	1.67E-06	55.377
86	PPP1R15B	1.67E-06	55.357
87	AHCTF1	1.67E-06	55.357
88	FAM63A	1.67E-06	55.252
89	C1orf116	1.67E-06	54.916
90	C1orf204	1.67E-06	54.758
91	RGS16	1.67E-06	54.659
92	LYPLAL1	1.67E-06	54.637
93	OR2T27	1.67E-06	54.609
94	CD101	1.67E-06	54.464
95	PRSS38	1.67E-06	54.464
96	SYT11	1.67E-06	54.420
97	S100A7	1.67E-06	54.321
98	RXFP4	1.67E-06	54.095
99	CNST	1.67E-06	54.095
100	EPRS	1.67E-06	53.814
101	FNDC7	1.67E-06	52.918
102	TSHB	1.67E-06	52.518
103	ASH1L	1.67E-06	52.518
104	PRSS3	1.67E-06	52.518
105	DBT	1.67E-06	52.485
106	PPM1J	1.67E-06	52.355
107	PM20D1	1.67E-06	52.296
108	APOBEC4	1.67E-06	50.179
109	SETD8	1.67E-06	50.131
110	HMCN1	1.67E-06	49.473
111	COL11A1	1.67E-06	49.220
112	RNASEL	1.67E-06	48.934
113	BGLAP	1.67E-06	47.003
114	LRRC71	1.67E-06	46.590
115	OR10T2	1.67E-06	45.585
116	ITLN1	1.67E-06	41.033
117	OR6K3	1.67E-06	40.721
118	FMN2	1.67E-06	40.220
119	ITLN2	1.67E-06	40.220
120	SMYD2	1.67E-06	39.954
121	URB2	1.67E-06	39.747
122	ST7L	1.67E-06	39.712
123	EDEM3	1.67E-06	39.623
124	LEFTY1	1.67E-06	38.831

125	OR10R2	1.67E-06	38.437
126	CHI3L1	1.67E-06	38.299
127	GPRIN2	1.67E-06	38.299
128	TTF2	1.67E-06	38.230
129	ZNF845	1.67E-06	37.999
130	CHD1L	1.67E-06	37.836
131	SLC6A17	1.67E-06	37.756
132	OR10Z1	1.67E-06	37.738
133	POTEF	1.67E-06	37.557
134	SEMA6C	1.67E-06	37.550
135	HSD3B1	1.67E-06	37.515
136	AGT	1.67E-06	37.484
137	FCGR2A	1.67E-06	37.280
138	SEC16B	1.67E-06	37.280
139	SHISA4_DUP_01	1.67E-06	37.258
140	ARHGAP30	1.67E-06	37.231
141	AXDND1	1.67E-06	37.093
142	SLAMF9	1.67E-06	37.093
143	NSL1	1.67E-06	37.086
144	MTMR11	1.67E-06	37.086
145	ATF6	1.67E-06	37.086
146	ACBD3	1.67E-06	36.942
147	SLC16A1	1.67E-06	36.436
148	SCYL3	1.67E-06	36.003
149	C1orf105	1.67E-06	35.792
150	LBR	1.67E-06	35.792
151	HBXIP	1.67E-06	35.792
152	PLA2G4A	1.67E-06	35.711
153	LGR6	1.67E-06	35.540
154	MOSC1	1.67E-06	35.140
155	GSTM3	1.67E-06	34.977
156	PROK1	1.67E-06	34.977
157	PLEKHA6	1.67E-06	34.977
158	OR13G1	1.67E-06	34.918
159	OR2G3	1.67E-06	34.918
160	VAV3	1.67E-06	34.675
161	MTX1	1.67E-06	34.675
162	EFNA1	1.67E-06	27.648
163	ATP1A4	1.67E-06	26.503
164	DARC	1.67E-06	26.503
165	PBXIP1	1.67E-06	26.503
166	SCCPDH	1.67E-06	26.115
167	SELP	1.67E-06	25.311

168	DENND2C	1.67E-06	25.210
169	LIPK	1.67E-06	24.941
170	IBA57	1.67E-06	24.785
171	FLG2	1.67E-06	24.552
172	CELSR2	1.67E-06	24.339
173	UAP1	1.67E-06	24.339
174	HDGF	1.67E-06	24.289
175	C1orf124	1.67E-06	24.289
176	ADAMTSL4	1.67E-06	24.233
177	CLDN16	1.67E-06	24.233
178	CLCC1	1.67E-06	24.005
179	TCEB3CL_DUP_02	1.67E-06	23.996
180	RPTN	1.67E-06	23.831
181	PLXNA2	1.67E-06	23.831
182	C4BPA	1.67E-06	23.642
183	CAPN2	1.67E-06	23.625
184	EDARADD	1.67E-06	23.607
185	CEP170	1.67E-06	23.540
186	C1orf129	1.67E-06	23.373
187	LHX4	1.67E-06	23.373
188	OR2T4	1.67E-06	23.293
189	PIGC	1.67E-06	23.293
190	BCL9	1.67E-06	23.293
191	PCMTD1	1.67E-06	23.131
192	OR2T1	1.67E-06	22.674
193	METTL13	1.67E-06	22.479
194	LY9	1.67E-06	22.479
195	KCNJ12	1.67E-06	22.435
196	SIPA1L2	1.67E-06	22.328
197	CBWD6	1.67E-06	21.831
198	CD1E	1.67E-06	21.396
199	ADAMTS4	1.67E-06	21.396
200	KDM4DL	1.67E-06	21.396
201	PRSS1	1.67E-06	21.186
202	ADCY10	1.67E-06	20.311

Supplemental Table 2. VAAST genes with most significant p-values in family 1281 sorted by rank

Most Significant Shared Variant Genes in Family 1281			
Rank	**Gene**	**P-value**	**Score**
1	HRNR	1.67E-06	537.335
2	PDE4DIP	1.67E-06	529.390
3	USH2A	1.67E-06	297.292
4	OR2L8	1.67E-06	234.921
5	SPTA1	1.67E-06	234.171
6	OR11L1	1.67E-06	231.181
7	OR6N1	1.67E-06	228.362
8	OR2W3	1.67E-06	215.566
9	IFI16	1.67E-06	190.834
10	EXO1	1.67E-06	177.373
11	FCRL5	1.67E-06	171.167
12	HEATR1	1.67E-06	171.124
13	KIAA1324	1.67E-06	168.173
14	OVGP1	1.67E-06	157.966
15	KIR3DL1	1.67E-06	146.413
16	IGSF3	1.67E-06	134.528
17	OR10R2	1.67E-06	134.258
18	LGR6	1.67E-06	133.677
19	OR14I1	1.67E-06	131.007
20	ASPM	1.67E-06	130.247
21	OR2C3	1.67E-06	130.028
22	CHIA	1.67E-06	126.557
23	OR13G1	1.67E-06	123.546
24	OR10X1	1.67E-06	120.470
25	PGLYRP4	1.67E-06	115.088
26	ECM1	1.67E-06	114.953
27	TCHH	1.67E-06	114.525
28	DUSP27	1.67E-06	114.130
29	THEM5	1.67E-06	113.804
30	TLR5	1.67E-06	113.513
31	COL11A1	1.67E-06	113.190
32	KIAA1614	1.67E-06	113.125
33	DTL	1.67E-06	112.777
34	FAM71A	1.67E-06	112.360
35	ASTN1	1.67E-06	111.574
36	OR2T11	1.67E-06	111.329
37	TNR	1.67E-06	107.386
38	IQGAP3	1.67E-06	105.922

39	CDC27	1.67E-06	105.246
40	OR2G2	1.67E-06	104.183
41	CENPF	1.67E-06	103.834
42	OR4C3	1.67E-06	102.501
43	OR2M7	1.67E-06	102.453
44	HMCN1	1.67E-06	101.611
45	DNAH14	1.67E-06	100.871
46	MUC6	1.67E-06	100.824
47	VAV3	1.67E-06	98.540
48	CR1L	1.67E-06	97.057
49	CAPN9	1.67E-06	94.835
50	CHD1L	1.67E-06	94.431
51	OR10J1	1.67E-06	93.464
52	ITPKB	1.67E-06	89.898
53	KCNJ12	1.67E-06	87.503
54	CSF1	1.67E-06	80.732
55	TOR1AIP1	1.67E-06	78.971
56	KIR3DL2	1.67E-06	78.295
57	OR9G9	1.67E-06	78.170
58	RNASEL	1.67E-06	78.147
59	LGALS8	1.67E-06	77.914
60	GPRIN2	1.67E-06	77.850
61	CD101	1.67E-06	77.697
62	FAM177B	1.67E-06	77.626
63	ADAR	1.67E-06	76.922
64	CAPN2	1.67E-06	76.667
65	CFH	1.67E-06	76.525
66	LAMC1	1.67E-06	76.488
67	CDC42BPA	1.67E-06	75.028
68	OR10T2	1.67E-06	74.799
69	C1orf68	1.67E-06	74.518
70	NSL1	1.67E-06	74.004
71	MAGEC1	1.67E-06	72.628
72	FAM104B_DUP_01	1.67E-06	72.298
73	PTGFRN	1.67E-06	71.945
74	CR1	1.67E-06	71.815
75	SWT1	1.67E-06	69.177
76	HYDIN	1.67E-06	68.669
77	TNN	1.67E-06	63.405
78	FNDC7	1.67E-06	63.335
79	ATF6	1.67E-06	62.191
80	KIR3DL3	1.67E-06	61.579
81	PM20D1	1.67E-06	60.220

82	EFNA1	1.67E-06	59.633
83	ATP1A4	1.67E-06	58.488
84	GPR37L1	1.67E-06	58.488
85	LCE5A	1.67E-06	57.652
86	F13B	1.67E-06	57.598
87	RRNAD1	1.67E-06	57.520
88	SMYD2	1.67E-06	57.332
89	MYBPHL	1.67E-06	57.296
90	BCL2L15	1.67E-06	57.296
91	PRODH	1.67E-06	57.090
92	EPS8L3	1.67E-06	56.926
93	PRG4	1.67E-06	56.537
94	ADAMTSL4	1.67E-06	56.218
95	FLVCR1	1.67E-06	56.183
96	ACP6	1.67E-06	56.072
97	OR2B11	1.67E-06	56.072
98	OR14C36	1.67E-06	55.663
99	C1orf227	1.67E-06	55.627
100	TRIM33	1.67E-06	55.627
101	OR14A16	1.67E-06	55.627
102	TTF2	1.67E-06	55.609
103	MIA3	1.67E-06	55.609
104	C1orf111	1.67E-06	55.430
105	JMJD4	1.67E-06	55.430
106	SH2D2A	1.67E-06	55.357
107	PPP1R15B	1.67E-06	55.357
108	ADAM15	1.67E-06	55.347
109	FAM63A	1.67E-06	55.252
110	SEMA6C	1.67E-06	54.928
111	PEAR1	1.67E-06	54.916
112	C1orf116	1.67E-06	54.916
113	APOA1BP	1.67E-06	54.769
114	DIEXF	1.67E-06	54.758
115	C1orf204	1.67E-06	54.758
116	SEC16B	1.67E-06	54.659
117	UBQLN4	1.67E-06	54.637
118	LYPLAL1	1.67E-06	54.637
119	OR2T27	1.67E-06	54.609
120	SLAMF9	1.67E-06	54.472
121	PRSS38	1.67E-06	54.464
122	SYT11	1.67E-06	54.420
123	S100A7	1.67E-06	54.321
124	RXFP4	1.67E-06	54.095

125	CNST	1.67E-06	54.095
126	ZNF805	1.67E-06	53.851
127	SLC16A1	1.67E-06	53.814
128	EPRS	1.67E-06	53.814
129	SCYL3	1.67E-06	53.381
130	F5	1.67E-06	53.381
131	LBR	1.67E-06	53.170
132	PLA2G4A	1.67E-06	53.090
133	ERO1LB	1.67E-06	52.578
134	TSHB	1.67E-06	52.518
135	ASH1L	1.67E-06	52.518
136	PRSS3	1.67E-06	52.518
137	DBT	1.67E-06	52.485
138	PPM1J	1.67E-06	52.355
139	AQP10	1.67E-06	52.047
140	BCLAF1	1.67E-06	50.521
141	SELP	1.67E-06	50.255
142	APOBEC4	1.67E-06	50.179
143	SETD8	1.67E-06	50.131
144	POTED	1.67E-06	49.265
145	CEP89	1.67E-06	47.605
146	NES	1.67E-06	46.659
147	SAA2-SAA4	1.67E-06	46.378
148	C1orf85	1.67E-06	45.604
149	SPRR1A	1.67E-06	45.300
150	ARHGEF11	1.67E-06	45.174
151	PDE10A	1.67E-06	44.201
152	ZNF695	1.67E-06	44.038
153	FCRLB	1.67E-06	41.110
154	OR6K3	1.67E-06	40.721
155	KIR2DL1	1.67E-06	40.142
156	DENND2C	1.67E-06	39.817
157	URB2	1.67E-06	39.747
158	TMEM81	1.67E-06	39.712
159	NUF2	1.67E-06	39.686
160	C1orf162	1.67E-06	39.392
161	PIGR	1.67E-06	39.392
162	CR2	1.67E-06	39.379
163	IL19	1.67E-06	39.162
164	KPRP	1.67E-06	39.159
165	CLDN16	1.67E-06	38.839
166	OR2AK2	1.67E-06	38.694
167	DSTYK	1.67E-06	38.569

168	TBX15	1.67E-06	38.282
169	PTPN22	1.67E-06	38.272
170	C4BPA	1.67E-06	38.248
171	DDX20	1.67E-06	38.248
172	CEP350	1.67E-06	37.999
173	ANKRD35	1.67E-06	37.999
174	LHX4	1.67E-06	37.979
175	FAM46C	1.67E-06	37.537
176	TRAF3IP3	1.67E-06	37.380
177	AXDND1	1.67E-06	37.380
178	RGS16	1.67E-06	37.280
179	SHISA4_DUP_01	1.67E-06	37.258
180	METTL13	1.67E-06	37.086
181	LY9	1.67E-06	37.086
182	SDCCAG8	1.67E-06	36.942
183	CD1E	1.67E-06	36.003
184	BGLAP	1.67E-06	36.003
185	HBXIP	1.67E-06	35.792
186	MOSC1	1.67E-06	35.140
187	LCE1E	1.67E-06	35.107
188	PLEKHA6	1.67E-06	34.977
189	TARBP1	1.67E-06	34.968
190	ADCY10	1.67E-06	34.918
191	BBS9	1.67E-06	32.714
192	CHI3L2	1.67E-06	27.068
193	PAPPA2	1.67E-06	27.068
194	CACNA1S	1.67E-06	26.702
195	KMO	1.67E-06	26.702
196	DCST1	1.67E-06	26.702
197	PIP	1.67E-06	26.674
198	FMO3	1.67E-06	26.179
199	BCAN	1.67E-06	26.179
200	OR2T12	1.67E-06	26.135
201	KIAA1671	1.67E-06	26.135
202	VSIG4	1.67E-06	26.115
203	FMN2	1.67E-06	25.613
204	FRG1	1.67E-06	25.348
205	NUDT22	1.67E-06	25.221
206	FCRL4	1.67E-06	25.105
207	SHMT2_DUP_01	1.67E-06	25.105
208	YIF1B	1.67E-06	25.055
209	TPTE	1.67E-06	25.055
210	C1orf88	1.67E-06	24.729

211	ZNF337	1.67E-06	24.688
212	TDRD5	1.67E-06	24.531
213	C1orf110	1.67E-06	24.531
214	IL24	1.67E-06	24.339
215	C1orf129	1.67E-06	24.339
216	TEDDM1	1.67E-06	24.339
217	COL4A5	1.67E-06	24.289
218	INSRR	1.67E-06	24.289
219	C1orf124	1.67E-06	24.289
220	KIR2DL4_DUP_01	1.67E-06	24.289
221	TMEM79_DUP_01	1.67E-06	24.087
222	EFNA3	1.67E-06	24.087
223	HHIPL2	1.67E-06	24.028
224	KIF14	1.67E-06	24.005
225	CLCC1	1.67E-06	24.005
226	TCEB3CL_DUP_02	1.67E-06	23.996
227	DISC1	1.67E-06	23.701
228	NAIF1	1.67E-06	23.701
229	OR2M2	1.67E-06	23.693
230	CGB1	1.67E-06	23.693
231	EDARADD	1.67E-06	23.607
232	SLAMF1	1.67E-06	23.577
233	NOTCH2NL	1.67E-06	23.540
234	AHCTF1	1.67E-06	23.373
235	CREB3L4	1.67E-06	23.293
236	NLRP3	1.67E-06	23.193
237	OR10Z1	1.67E-06	23.131
238	PCMTD1	1.67E-06	23.131
239	METTL11B	1.67E-06	22.931
240	HSD3B1	1.67E-06	22.908
241	AGT	1.67E-06	22.877
242	CD244	1.67E-06	22.798
243	MFSD4	1.67E-06	22.798
244	MR1	1.67E-06	22.674
245	FCGR2A	1.67E-06	22.674
246	FCRL2	1.67E-06	22.628
247	ARHGAP30	1.67E-06	22.624
248	SPRR3	1.67E-06	22.624
249	LAMC2	1.67E-06	22.587
250	RASA2	1.67E-06	22.587
251	CFHR4	1.67E-06	22.491
252	MTMR11	1.67E-06	22.479
253	CRTC2	1.67E-06	22.479

254	RTBDN	1.67E-06	22.362
255	ACBD3	1.67E-06	22.336
256	METTL18	1.67E-06	22.336
257	ATP8B2	1.67E-06	22.016
258	NCF2	1.67E-06	22.016
259	CBWD6	1.67E-06	21.831
260	NAP1L2	1.67E-06	21.829
261	KISS1	1.67E-06	21.396
262	AKNAD1	1.67E-06	21.186
263	AMY2B	1.67E-06	20.934
264	PARP1	1.67E-06	20.934
265	BEND3	1.67E-06	20.934
266	IVL	1.67E-06	20.533
267	CASQ2	1.67E-06	20.533
268	OR6Y1	1.67E-06	20.370
269	GSTM3	1.67E-06	20.370
270	NUP210L	1.67E-06	20.370
271	ILDR2	1.67E-06	20.370
272	XPR1	1.67E-06	20.311
273	ABL2	1.67E-06	20.068
274	NUP98	1.67E-06	19.555
275	NKRF	1.67E-06	18.199

Supplemental Table 3. KEGG pathways with more than three genes from the list of the most significant p-value genes for family 1168

KEGG Pathways Top P-value Genes Family 1168
hsa04740 Olfactory transduction (25)
hsa01100 Metabolic pathways (8)
hsa04610 Complement and coagulation cascades (5)
hsa04640 Hematopoietic cell lineage (4)
hsa04510 Focal adhesion (4)
hsa04972 Pancreatic secretion (4)
hsa05164 Influenza A (4)
hsa04974 Protein digestion and absorption (4)
hsa04080 Neuroactive ligand-receptor interaction (3)
hsa04141 Protein processing in endoplasmic reticulum (3)
hsa05144 Malaria (3)
hsa00520 Amino sugar and nucleotide sugar metabolism (3)
hsa04666 Fc gamma R-mediated phagocytosis (3)
hsa04360 Axon guidance (3)

Supplemental Table 4. KEGG pathways that contained more than three genes from the most significant p-value genes for family 1281

KEGG Pathways Top P-value Genes Family 1281
hsa04740 Olfactory transduction (20)
hsa04510 Focal adhesion (6)
hsa01100 Metabolic pathways (5)
hsa04141 Protein processing in endoplasmic reticulum (4)
hsa04610 Complement and coagulation cascades (4)
hsa04512 ECM-receptor interaction (4)
hsa04972 Pancreatic secretion (3)
hsa04650 Natural killer cell mediated cytotoxicity (3)
hsa05164 Influenza A (3)
hsa04612 Antigen processing and presentation (3)
hsa04974 Protein digestion and absorption (3)

Supplemental Table 5. All novel missense variants in our six other exomes in the six complement and coagulation cascade genes identified by VAAST (for the PolyPhen-2 prediction the HumDiv algorithm was used).

Individual	Gene	Variant	PolyPhen-2
Family 150	*F5*	GLU1390GLN	Benign
Family 150	*F5*	LEU1370PHE	Benign
Family 150	*F5*	PRO1361LEU	Benign
Family 150	*F5*	LEU1357ILE	Benign
Family 1165	*F5*	LEU1370PHE	Benign
Family 1165	*F5*	PRO1361LEU	Benign
Family 1165	*F5*	LEU1357ILE	Benign
Family 1165	*F5*	PHE1334LEU	Benign
Family 1165	*F5*	ARG1220THR	Benign
Family 14w	*CFH*	THR956MET	Probably Damaging

Supplemental Table 6. Complete unadjusted and adjusted additive logistic regression association results for Finnish mothers' Illumina arrays sorted by adjusted p-value. The gene listed is that in which the SNP is located and in parentheses is the VAAST gene the SNP was selected to interrogate within the 10 kb 5' and 3' buffer.

CHR	SNP	BP	GENE	MINOR ALLELE	MAJOR ALLELE	ADJ P-VALUE	ADJ OR	UNADJ P-VALUE	UNADJ OR
1	rs6691117	207782931	*CR1*	G	A	1.07E-04	1.732	6.93E-05	1.741
1	EXM133911	197031021	*F13B*	C	T	0.0213	0.5327	0.04428	0.5864
1	EXM-RS12034383	207803595	*CR1*	G	A	0.0307	1.31	0.02107	1.326
1	EXM-RS6656401	207692049	*CR1*	A	G	0.0504	0.7326	0.05833	0.7454
1	EXM144910	207782769	*CR1*	A	G	0.0793	1.477	0.1053	1.423
1	EXM-RS3818361	207784968	*CR1*	T	C	0.0927	0.7726	0.09383	0.7776
1	EXM-RS6701713	207786289	*CR1*	A	G	0.0927	0.7726	0.09383	0.7776
1	EXM144976	207795320	*CR1*	A	G	0.1011	0.7782	0.104	0.784
1	EXM-RS3813948	207269858	*C4BPA*	G	A	0.1553	0.673	0.165	0.6842
1	EXM-RS6677604	196686918	*CFH*	A	G	0.1601	0.752	0.1991	0.7769
1	EXM144922	207782916	*CR1*	A	T	0.1796	0.493	0.127	0.4497
1	EXM144743	207653395	*CR2*	C	A	0.1905	0.7905	0.1542	0.7775
1	EXM-RS1061170	196659237	*CFH*	C	T	0.1964	0.8492	0.1775	0.8459
1	EXM144486	207304980	*C4BPA*	C	G	0.2161	2.305	0.3081	1.987
1	EXM121798	169510139	*F5*	A	G	0.2205	0.7313	0.1913	0.7219
1	EXM121818	169510475	*F5*	T	G	0.2523	0.8353	0.3945	0.878
1	EXM121977	169521853	*F5*	G	A	0.2732	0.7969	0.5509	0.8878
1	EXM121943	169513583	*F5*	T	G	0.3048	0.8082	0.6067	0.9022
1	EXM2250216	169513583	*F5*	T	G	0.3048	0.8082	0.6067	0.9022
1	EXM-RS1329424	196646176	*CFH*	A	C	0.3288	0.8869	0.2994	0.8824
1	EXM133342	196642233	*CFH*	A	G	0.3511	1.135	0.2702	1.158
1	EXM133469	196709816	*CFH*	T	G	0.3593	3.091	0.4045	2.783
1	EXM144433	207286381	*C4BPA*	A	C	0.4025	1.58	0.5381	1.396
1	EXM133467	196709774	*CFH*	T	G	0.4383	1.142	0.6694	1.074
1	EXM122025	169541513	*F5*	G	C	0.4563	1.328	0.5909	1.224
1	EXM121797	169510118	*F5*	A	G	0.4583	0.7704	0.4232	0.7584
1	EXM122022	169529974	*F5*	A	G	0.4843	0.5536	0.4769	0.5498
1	EXM-RS380390	196701051	*CFH*	C	G	0.4857	0.9182	0.4585	0.9149
1	EXM144908	207782707	*CR1*	G	A	0.5277	1.139	0.4767	1.155
1	EXM144887	207760772	*CR1*	G	A	0.5394	1.304	0.5605	1.282
1	EXM121681	169483561	*F5*	C	T	0.5635	0.877	0.9626	1.01
1	EXM122058	169563951	*F5*	G	T	0.5974	0.9059	0.5445	0.8951
1	EXM121903	169511878	*F5*	G	T	0.5975	0.8857	0.9166	1.023
1	EXM-RS17045328	207652176	*CR2*	G	A	0.6030	1.183	0.5552	1.206
1	EXM144740	207653364	*CR2*	G	A	0.6062	0.8743	0.4428	0.8213
1	EXM144473	207300070	*C4BPA*	A	G	0.6458	0.8845	0.5855	0.8667
1	EXM144961	207791434	*CR1*	G	A	0.7044	1.218	0.887	1.075
1	EXM121964	169519112	*F5*	T	C	0.7311	1.115	0.9299	1.027

1	EXM144679	207646898	*CR2*	C	T	0.7341	0.95	0.5762	0.9208
1	EXM144874	207755285	*CR1*	A	G	0.7434	0.7922	0.8784	1.109
1	EXM144675	207646462	*CR2*	A	G	0.7572	0.9545	0.5927	0.9241
1	EXM144681	207646923	*CR2*	A	G	0.7579	0.9545	0.5992	0.9254
1	EXM133877	197026289	*F13B*	G	A	0.8023	0.7329	0.7631	0.6907
1	EXM-RS10737680	196679455	*CFH*	C	A	0.8453	1.025	0.6321	1.062
1	EXM-RS1329428	196702810	*CFH*	A	G	0.8453	1.025	0.6321	1.062
1	EXM-RS1410996	196696933	*CFH*	T	C	0.8453	1.025	0.6321	1.062
1	EXM122075	169565346	*F5*	A	C	0.8731	0.9642	0.9244	0.9793
1	EXM121879	169511555	*F5*	C	T	0.8767	1.023	0.7438	0.9545
1	EXM121894	169511734	*F5*	C	T	0.8792	1.022	0.7491	0.9556
1	EXM121896	169511755	*F5*	C	T	0.9022	1.018	0.7251	0.9513
1	EXM144655	207644786	*CR2*	A	T	0.9062	0.8651	0.7631	0.6907
1	EXM121743	169498975	*F5*	C	T	0.9359	0.9892	0.8742	0.9793
1	EXM133490	196712596	*CFH*	T	A	0.9514	0.9559	0.7977	0.8282
1	EXM121985	169524517	*F5*	A	G	0.9666	0.9682	0.6435	1.391
1	EXM144888	207760773	*CR1*	T	C	0.9814	1.003	0.996	0.9993
1	EXM2259849	169527856	*F5*	C	T	0.9866	1.002	0.8072	1.033
1	EXM144899	207762095	*CR1*	T	C	0.9879	0.9815	0.7631	0.6907
1	EXM121732	169497306	*F5*	A	G	0.9993	9E-10	0.9993	8.541E-10
1	EXM121746	169499020	*F5*	C	G	0.9993	1E-09	0.9993	8.541E-10
1	EXM121969	169519883	*F5*	A	G	0.9993	3E+09	0.9993	2.245E+09
1	EXM122036	169555582	*F5*	T	C	0.9993	8E-10	0.9993	8.515E-10
1	EXM133460	196706677	*CFH*	T	G	0.9993	2E+09	0.9993	2.245E+09
1	EXM133479	196711067	*CFH*	T	G	0.9993	2E+09	0.9993	2.245E+09
1	EXM133865	197024914	*F13B*	G	A	0.9993	2E+09	0.9993	2.245E+09
1	EXM144467	207297622	*C4BPA*	A	G	0.9993	2E+09	0.9993	2.245E+09
1	EXM144499	207307932	*C4BPA*	A	G	0.9993	2E+09	0.9993	2.245E+09
1	EXM144639	207643432	*CR2*	G	C	0.9993	1E-09	0.9993	8.541E-10

Supplemental Table 7 Complete unadjusted additive logistic association results for Finnish mothers' Affymetrix 6.0 SNP arrays sorted by p-value.
The gene listed is that in which the SNP is located and in parentheses is the VAAST gene the SNP was selected to interrogate within the 10kb 5' and 3' buffer.

CHR	SNP	BP	GENE	MINOR ALLELE	MAJOR ALLELE	UNADJ P-VALUE	UNADJ OR
1	rs10429953	205855201	*CR1*	G	A	1.31E-04	1.931
1	rs10429943	205856094	*CR1*	T	C	3.74E-04	1.841
1	rs11118166	205848618	*CR1*	G	A	5.78E-04	1.776
1	rs12567990	205748308	*CR1*	T	C	5.82E-04	1.791
1	rs12141045	205838777	*CR1*	G	A	6.22E-04	1.776
1	rs599948	205818862	*CR1*	C	T	7.04E-04	1.664
1	rs677066	205840614	*CR1*	C	T	1.70E-03	1.591
1	rs3753305	167820682	*F5*	G	C	5.52E-03	1.422
1	rs9943077	205361921	*C4BPA*	T	C	0.02323	0.7266
1	rs2491393	205366882	*C4BPA*	G	A	0.03275	1.335
1	rs10489185	167815516	*F5*	A	C	0.03766	0.757
1	rs12080578	205887235	*CR1L (CR1)*	G	A	0.04018	1.525
1	rs17522707	167829686	*SELP (F5)*	A	G	0.04466	0.5847
1	rs4844573	205371523	*C4BPA*	C	T	0.05165	1.28
1	rs2213873	167810401	*F5*	A	G	0.05722	0.7711
1	rs10733086	194943558	*CFH*	A	T	0.06023	0.7854
1	rs2227245	167806704	*F5*	T	C	0.06292	0.7785
1	rs572515	194912884	*CFH*	A	G	0.06589	0.7914
1	rs6691048	167808759	*F5*	T	C	0.0678	0.7857
1	rs4403634	205334714	*C4BPB*	A	C	0.06793	0.797
1	rs6427195	167747800	*F5*	T	A	0.07488	1.609
1	rs12406092	167809755	*F5*	T	C	0.07674	0.7934
1	rs7551623	167740978	*F5*	A	G	0.08331	0.6452
1	rs2491395	205368346	*C4BPA*	T	A	0.08607	1.264
1	rs12032512	205719801	*CR2*	C	G	0.09646	0.8065
1	rs6695321	194942484	*CFH*	G	A	0.1016	1.239
1	rs9332647	167758724	*F5*	G	A	0.1105	0.6706
1	rs11118242	205886936	*CR1L (CR1)*	T	C	0.1129	0.8181
1	rs2274566	205819968	*CR1*	G	A	0.1181	1.227
1	rs1018827	167780630	*F5*	T	C	0.1195	1.501
1	rs4618971	205732684	*CR1*	C	T	0.1263	0.8011
1	rs6662176	167810667	*F5*	T	A	0.1271	0.8195
1	rs6427197	167767214	*F5*	G	T	0.1272	1.484
1	rs9429781	205733845	*CR1*	G	T	0.1343	0.7974
1	rs7542088	167802864	*F5*	A	C	0.1538	0.8256
1	rs1329423	194913010	*CFH*	G	A	0.1547	1.258
1	rs17044576	205701293	*CR2*	G	A	0.1567	1.422
1	rs10801555	194926884	*CFH*	A	G	0.1568	0.8273
1	rs514943	194930536	*CFH*	G	A	0.1569	0.836
1	rs6428357	194942194	*CFH*	T	C	0.1654	0.8365

1	rs11803956	205869644	*CR1*	T	C	0.1693	1.187
1	rs10779340	205883648	*CR1*	C	T	0.1704	1.187
1	rs1831282	194940616	*CFH*	A	C	0.1724	0.8445
1	rs395544	194964895	*CFH*	A	G	0.1894	0.8456
1	rs2182911	205726694	*CR2*	G	A	0.203	0.8308
1	rs1759007	195294229	*F13B*	T	C	0.2242	0.7253
1	rs10801556	194927087	*CFH*	T	C	0.2281	0.8539
1	rs17258982	205719987	*CR2*	C	T	0.2337	0.7363
1	rs6690215	205722673	*CR2*	C	T	0.2468	0.86
1	rs4844597	205737892	*CR1*	C	T	0.2732	0.8503
1	rs742855	194972143	*CFH*	G	A	0.2843	1.212
1	rs7518773	195278259	*F13B*	A	G	0.2971	1.137
1	rs10737680	194946078	*CFH*	G	T	0.2977	1.146
1	rs974793	167745278	*F5*	T	C	0.2998	1.172
1	rs203687	194940893	*CFH*	C	T	0.3151	0.8774
1	rs1759008	195293518	*F13B*	T	G	0.3161	0.7802
1	rs3917843	167826881	*SELP (F5)*	T	C	0.3344	0.8381
1	rs9332627	167764444	*F5*	T	C	0.3483	1.153
1	rs3820060	167751176	*F5*	G	T	0.3557	1.134
1	rs403846	194963360	*CFH*	A	G	0.3581	0.8845
1	rs1627765	195299666	*F13B*	C	T	0.371	0.8008
1	rs424535	194975846	*CFH*	T	A	0.3888	1.124
1	rs10754209	195278200	*F13B*	A	T	0.3949	1.111
1	rs4915148	195302161	*F13B*	T	C	0.437	0.8258
1	rs857021	195274102	*F13B*	A	G	0.437	0.8258
1	rs2182913	205727001	*CR2*	T	C	0.4498	0.9044
1	rs3849266	205819613	*CR1*	T	C	0.4527	1.112
1	rs1571344	205737551	*CR1*	G	A	0.4535	1.185
1	rs3917820	167831369	*SELP (F5)*	T	C	0.4566	1.172
1	rs4656685	167750468	*F5*	A	G	0.4634	1.123
1	rs1759009	195293295	*F13B*	T	C	0.5075	0.847
1	rs3766104	167755647	*F5*	T	A	0.5089	0.8546
1	rs17020993	205355015	*C4BPA*	G	A	0.5116	1.145
1	rs7519408	205727912	*CR2*	C	G	0.5476	0.9042
1	rs3917824	167831206	*SELP (F5)*	G	C	0.5669	1.13
1	rs3917819	167831513	*SELP (F5)*	G	A	0.598	1.13
1	rs9332600	167779537	*F5*	T	C	0.6052	1.077
1	rs8942	205336542	*C4BPB*	A	G	0.6097	1.113
1	rs6128	167829528	*SELP (F5)*	A	G	0.6377	0.9326
1	rs9332619	167766972	*F5*	T	C	0.6544	1.069
1	rs9332661	167755827	*F5*	C	T	0.666	1.101
1	rs6661764	205875008	*CR1*	C	G	0.7046	1.05
1	rs4524	167778379	*F5*	G	A	0.7397	1.049
1	rs7527218	205690452	*CR2*	C	T	0.7508	1.041
1	rs6662593	167779218	*F5*	T	C	0.7594	1.045
1	rs3766110	167781807	*F5*	C	A	0.7746	0.9597

1	rs1986158	205737367	*CR1*	G	A	0.7833	1.065
1	rs6029	167796597	*F5*	A	G	0.7891	0.9636
1	rs12025910	167745405	*F5*	C	T	0.797	1.059
1	rs17615	205713085	*CR2*	A	G	0.8337	0.9697
1	rs9332618	167767105	*F5*	T	C	0.8377	0.9661
1	rs11120211	205343002	*C4BPA*	A	G	0.8424	1.054
1	rs2019727	194941337	*CFH*	T	A	0.8471	1.037
1	rs2940253	205712366	*CR2*	C	G	0.8611	0.9746
1	rs9332595	167780979	*F5*	C	G	0.8669	0.9767
1	rs11120218	205345074	*C4BPA*	T	C	0.8718	1.032
1	rs9332640	167760350	*F5*	G	C	0.8719	0.9804
1	rs511678	205711905	*CR2*	C	G	0.8976	0.981
1	rs1410408	205732931	*CR1*	T	C	0.9113	0.9738
1	rs311311	205706318	*CR2*	C	G	0.9124	0.984
1	rs6015	167786518	*F5*	T	C	0.9447	1.014
1	rs9429774	205712518	*CR2*	T	C	0.9519	0.9912
1	rs916438	167766283	*F5*	A	T	0.9561	0.993