

Combined model				Variant 1			Variant 2		
log10(BF)	p-value	log10(BF)		Coordinate	Gene	Funcitonal annotation	Coordinate	Gene	Funcitonal annotation
8.21	7.80E-07	6.94		20:48129705_G/T,A	PTGIS	STOP_GAINED	16:81348733_G/T	GAN	NON_SYNONYMOUS_CODING
7.12	2.73E-06	6.47		4:90743415_T/C	SNCA	NON_SYNONYMOUS_CODING	2:179659911_G/A	TTN	NON_SYNONYMOUS_CODING
7.35	2.26E-06	6.43		3:53213690_G/C	PRKCD	NON_SYNONYMOUS_CODING	14:75746689_C/T	FOS	NON_SYNONYMOUS_CODING
6.80	2.82E-06	6.36		2:242795125_G/A	PDCD1	NON_SYNONYMOUS_CODING	8:13356801_G/A	DLC1	NON_SYNONYMOUS_CODING
6.35	3.85E-06	6.22		11:57582923_G/A	CTNND1	AA_modification:Phosphoserine	2:220420784_G/A	OBSL1	NON_SYNONYMOUS_CODING
8.08	6.60E-06	6.07		1:112298763_T/C	DDX20	NON_SYNONYMOUS_CODING	3:125826058_T/C	ALDH1L1	NON_SYNONYMOUS_CODING
7.22	4.77E-06	6.04		2:179457146_G/A	TTN	NON_SYNONYMOUS_CODING	22:35695930_C/A	TOM1	NON_SYNONYMOUS_CODING
7.20	9.62E-06	6.00		1:45797504_C/G	MUTYH	NON_SYNONYMOUS_CODING	8:30982425_T/G	WRN	NON_SYNONYMOUS_CODING
7.45	1.58E-05	5.90		16:4855278_A/G	GLYR1	AA_modification:Phosphoserine	8:13259100_G/A	DLC1	NON_SYNONYMOUS_CODING
6.81	1.55E-05	5.81		11:45975129_C/T	PHF21A	NON_SYNONYMOUS_CODING	19:49458190_C/A	BAX	NON_SYNONYMOUS_CODING
8.67	1.02E-05	5.81		7:128490102_G/A	FLNC	NON_SYNONYMOUS_CODING	8:13357339_G/C	DLC1	NON_SYNONYMOUS_CODING
6.42	9.91E-06	5.79		11:236090_G/A	SIRT3	NON_SYNONYMOUS_CODING	4:110615838_C/T	CASP6	NON_SYNONYMOUS_CODING
7.87	1.08E-05	5.79		8:144993930_C/G	PLEC	NON_SYNONYMOUS_CODING	14:73422258_C/G	DCAF4	NON_SYNONYMOUS_CODING
7.86	2.30E-05	5.70		1:45224997_A/C	KIF2C	NON_SYNONYMOUS_CODING	2:108921032_C/T	SULT1C2	NON_SYNONYMOUS_CODING
6.47	1.56E-05	5.68		11:134252895_C/T	B3GAT1	NON_SYNONYMOUS_CODING	15:75012984_T/C	CYP1A1	NON_SYNONYMOUS_CODING
5.67	1.24E-05	5.63		6:116441645_C/G	COL10A1	NON_SYNONYMOUS_CODING	20:30072135_G/A	REM1	NON_SYNONYMOUS_CODING
7.40	2.89E-05	5.61		1:201016295_G/A	CACNA1S	NON_SYNONYMOUS_CODING	19:17000695_G/A	F2RL3	NON_SYNONYMOUS_CODING
5.87	8.39E-07	5.59		7:43351409_T/G	HECW1	NON_SYNONYMOUS_CODING	2:219294200_A/G	VIL1	NON_SYNONYMOUS_CODING
5.84	2.34E-05	5.58		15:67457334_A/G	SMAD3	NON_SYNONYMOUS_CODING	1:201052381_A/G	CACNA1S	NON_SYNONYMOUS_CODING
7.00	1.46E-05	5.56		10:53822300_A/G	PRKG1	NON_SYNONYMOUS_CODING	9:140007465_G/A	DPP7	NON_SYNONYMOUS_CODING
6.93	2.96E-05	5.56		2:225362477_C/T	CUL3	NON_SYNONYMOUS_CODING	9:120476787_C/G	TLR4	STOP_GAINED