

Supplementary Table 2. Summary of GWAS and validation results for association with SCD.

Locus	SNP	Chr	Position	Coded /Non-coded allele	AF	GWAS OR (95% CI)	GWAS P	Validation OR (95% CI)	Validation P	Combined P
1	rs11590910	1	91,890,870	C/G	0.360	0.79 (0.72–0.88)	9.66E-06			
2	rs174230	2	159,883,556	T/C	0.013	2.49 (1.78–3.47)	8.58E-08	1.38 (0.99–1.93)	0.03	2.98E-07
	rs4665058	2	159,898,455	A/C	0.014	2.52 (1.80–3.53)	7.07E-08	1.48 (1.05–2.08)	0.01	*1.81E-10
3	rs16880395	4	27,848,761	T/C	0.230	1.30 (1.16–1.46)	5.14E-06	0.97 (0.87–1.07)	0.27	0.01
	rs17619526	4	27,851,492	T/A	0.230	1.31 (1.17–1.47)	4.54E-06			
4	rs2178490	5	30,875,088	G/A	0.207	1.32 (1.17–1.48)	5.63E-06	0.90 (0.81–1.00)	NA	0.11
5	rs1978838	5	106,008,311	A/T	0.234	0.76 (0.67–0.85)	4.19E-06			
	rs12517578	5	106,008,730	G/C	0.234	0.76 (0.67–0.85)	4.41E-06	0.94 (0.85–1.04)	0.12	0.0001
6	rs3193970	10	97,061,998	C/T	0.421	0.78 (0.71–0.86)	1.11E-06	0.96 (0.89–1.05)	0.2	0.0001
	rs10748630	10	97,085,783	T/C	0.482	1.27 (1.15–1.40)	1.47E-06			
7	rs11626637	14	45,792,412	G/A	0.100	0.64 (0.52–0.78)	9.57E-06	1 (0.87–1.16)	NA	0.01
8	rs1318021	16	75,946,589	A/T	0.421	0.75 (0.68–0.83)	3.77E-08			
	rs2650907	16	75,950,708	G/C	0.421	0.75 (0.68–0.83)	4.39E-08	1.03 (0.92–1.13)	NA	0.0005
9	rs9910447	17	31,496,575	T/C	0.117	1.92 (1.46–2.51)	2.43E-06			
	rs1024448	17	31,497,076	T/C	0.116	1.91 (1.47–2.49)	1.29E-06			
10	rs7218928	17	32,338,069	G/A	0.429	0.79 (0.72–0.87)	4.34E-06	1.02 (0.94–1.11)	NA	0.008
11	rs12601622	17	73,560,970	A/G	0.014	6.79 (3.43–13.42)	3.69E-08	0.89 (0.64–1.23)	NA	0.08
12	rs6507566	18	39,939,723	T/G	0.330	1.26 (1.14–1.40)	7.09E-06	0.93 (0.85–1.02)	NA	0.08
13	rs12461046	19	54,924,441	A/T	0.057	2.01 (1.49–2.71)	5.35E-06			

Chr, chromosome; AF, allele frequency of coded allele (study size weighted average). Follow-up genotyping results are reported for 1,730 SCD cases and 10,530 controls, with the exception of rs12601622 (1,460 SCD cases, 10,182 controls), which failed genotyping in the Oregon-SUDS follow-up study. **Bold** indicates nominal significance ($P<0.05$) for validation. P-values for validation are reported as one-sided, and NA indicates opposite direction of effect from GWAS. *Includes ARREST (719 SCD cases, 4,190 controls) and AGNES (670 SCD cases, 654 controls) studies. Follow-up genotyping results are reported for the 11 SNPs which passed genotyping QC.