Supplemental Table 1. Summary of Association Results in the GoKinD Collection for SNPs in Linkage Disequilibrium (r^2 > 0.80) with the Leading SNPs on Chromosomes 1 (rs6671557) and 13 (rs1411766).

SNP	Position (basepair)	Location	Linkage Disequilibrium with Leading SNP (r^2)	Risk allele (non-risk allele)	Risk allele frequencies, *P*-values, and ORs for the GoKinD collection			
					Controls (*n*=885)	Cases (*n*=820)	*P*-value	OR (95% CI)
Chromosome 1: rs6671557, *NEGR1* region								
rs12030511	71,881,386	Intron 4	0.92	A(C)	0.04	0.06	5.0×10^{-4}	1.77 (1.28-2.45)
rs12031842	71,907,260	Intron 4	0.92	A(G)	0.04	0.06	5.0×10^{-4}	1.77 (1.28-2.45)
rs12031657	71,917,344	Intron 4	0.92	C(G)	0.04	0.06	3.7×10^{-4}	1.77 (1.28-2.45)
rs12041607	71,928,607	Intron 4	0.94	C(T)	0.04	0.06	1.8×10^{-4}	1.79 (1.30-2.48)
rs7531512	71,939,625	Intron 3	0.96	T(C)	0.03	0.06	1.3×10^{-4}	1.86 (1.34-2.58)
rs12037107	71,978,890	Intron 3	0.97	A(T)	0.03	0.06	1.3×10^{-4}	1.88 (1.35-2.60)
rs12030035	71,980,671	Intron 3	0.97	T(G)	0.03	0.06	1.3×10^{-4}	1.88 (1.35-2.60)
rs17091704	71,981,505	Intron 3	0.97	C(T)	0.03	0.06	1.3×10^{-4}	1.88 (1.35-2.60)
rs17091710	71,984,531	Intron 3	0.97	A(G)	0.03	0.06	1.3×10^{-4}	1.88 (1.35-2.60)
rs12043796	71,987,617	Intron 3	0.97	T(A)	0.03	0.06	1.3×10^{-4}	1.88 (1.35-2.60)
rs12023733	71,988,582	Intron 3	0.97	A(C)	0.03	0.06	5.0×10^{-4}	1.88 (1.35-2.60)
rs6671557	**71,992,909**	**Intron 3**	**---**	**A(C)**	**0.03**	**0.07**	**4.9×10^{-5}**	**1.98 (1.43-2.43)**

rs6697370	72,011,279	Intron 3	0.92	A(C)	0.04	0.07	3.4×10^{-4}	1.74 (1.28-2.36)
rs12048869	72,017,041	Intron 2	0.95	C(T)	0.03	0.06	1.6×10^{-4}	1.87 (1.34-2.60)
rs7528030	72,019,865	Intron 2	0.95	G(A)	0.03	0.06	1.6×10^{-4}	1.87 (1.34-2.60)
rs12024388*	72,026,165	Intron 2	0.95	C(T)	0.03	0.06	1.6×10^{-4}	1.87 (1.34-2.60)
rs11584866	72,028,565	Intron 2	0.95	A(C)	0.03	0.06	1.6×10^{-4}	1.87 (1.34-2.60)
rs12040327	72,036,627	Intron 2	0.95	T(C)	0.03	0.06	1.6×10^{-4}	1.87 (1.34-2.60)
rs11578097	72,041,472	Intron 2	0.95	C(G)	0.03	0.06	1.6×10^{-4}	1.87 (1.34-2.60)
rs11588321	72,046,203	Intron 2	0.93	T(C)	0.03	0.06	3.9×10^{-4}	1.81 (1.30-2.52)
rs6701156	72,048,147	Intron 2	0.93	C(T)	0.03	0.06	3.9×10^{-4}	1.81 (1.30-2.52)
rs12078969	72,053,759	Intron 2	0.91	C(T)	0.03	0.06	5.4×10^{-4}	1.79 (1.28-2.50)
Chromosome 13: rs1411766, *MYO16-IRS2* region								
rs1411766*	**109,050,161**	**Intergenic**	**---**	**A(G)**	**0.32**	**0.39**	**1.8×10^{-6}**	**1.41 (1.23-1.63)**
rs17412858*	109,050,609	Intergenic	0.99	G(A)	0.32	0.39	2.1×10^{-6}	1.41 (1.22-1.62)
rs9555618	109,051,201	Intergenic	0.99	A(G)	0.32	0.39	2.1×10^{-6}	1.41 (1.22-1.62
rs9515085*	109,056,783	Intergenic	0.91	G(T)	0.34	0.41	2.2×10^{-5}	1.35 (1.18-1.56)
rs329918	109,058,779	Intergenic	0.86	G(C)	0.33	0.40	5.0×10^{-5}	1.34 (1.16-1.54)
rs1547241	109,071,606	Intergenic	0.82	C(G)	0.30	0.37	2.7×10^{-5}	1.36 (1.18-1.57)

Genotyped and imputed SNPs in linkage disequilibrium with the leading SNPs on chromosomes 1 (rs6671557) and 13 (rs1411766). *P*-values and odds ratios (ORs) for case and control comparisons of the GoKinD collection were calculated using stratified additive tests of association using the Cochran-Mantel-Haenszel method, adjusting for both gender and JDC/GWU strata. SNP positions and locations are in reference to NCBI Build 36.1.

* SNPs genotyped on the Affymetrix 5.0 500K SNP Array.