

Supplementary Table 2. Association Analyses of TNIP1 Region including Imputed SNPs

SNP name	position ^a	Allele A ^b	Allele B ^b	Mean Call ^c	Inf ^d	Cases MAF ^e	Controls MAF ^e	OR ^f
rs2233299	150405660	A	G	1.000	1.000	0.311	0.260	1.30
rs13153275	150408592	G	C	0.992	0.982	0.312	0.265	1.28
rs7713567	150411148	T	C	0.946	0.905	0.378	0.326	1.30
rs6579837	150415087	T	G	0.982	0.921	0.142	0.092	1.86
rs2233290	150416696	C	G	0.992	0.957	0.141	0.088	1.92
rs1422673	150419181	T	C	1.000	1.000	0.264	0.188	1.57
rs2042234	150419324	G	A	0.995	0.976	0.142	0.088	1.90
rs2233287	150420290	A	G	1.000	1.000	0.142	0.087	1.88
rs17111708	150423700	A	G	0.992	0.963	0.146	0.091	1.89
rs7732451	150424405	G	A	0.977	0.912	0.182	0.126	1.65
5-150425036	150425036	C	T	0.992	0.962	0.146	0.091	1.89
rs10057690	150425408	C	T	0.992	0.962	0.146	0.091	1.89
rs1559127	150426946	C	T	0.988	0.952	0.175	0.111	1.86
rs6880110	150427283	G	A	0.977	0.925	0.210	0.145	1.65
rs6861227	150427321	G	T	0.977	0.925	0.210	0.145	1.65
rs59926079	150427936	G	A	0.993	0.967	0.146	0.090	1.91
rs58474444	150428073	G	T	0.994	0.968	0.146	0.090	1.91
rs1862364	150428569	G	A	0.982	0.939	0.210	0.145	1.64
5-150429413	150429413	T	C	0.995	0.974	0.145	0.089	1.91
rs4958881	150430429	C	T	1.000	1.000	0.176	0.111	1.82
5-150431268	150431268	T	A	0.986	0.949	0.150	0.095	1.86
rs3792785	150431843	C	T	1.000	1.000	0.159	0.104	1.75
rs13160369	150432389	G	C	0.990	0.967	0.224	0.159	1.57
rs6869605	150433059	C	A	0.995	0.980	0.192	0.126	1.76
5-150433577	150433577	T	C	0.992	0.966	0.154	0.099	1.81
5-150434081	150434081	A	G	0.991	0.965	0.190	0.125	1.78
rs1107239	150434799	A	T	0.992	0.963	0.159	0.103	1.80
rs4958882	150434980	G	C	0.991	0.965	0.190	0.124	1.78
rs3792784	150435865	G	A	0.993	0.970	0.159	0.103	1.80
rs3792783	150435925	G	A	1.000	1.000	0.223	0.157	1.58
rs7731150	150436585	A	G	0.990	0.957	0.159	0.103	1.82
rs7708392	150437678	C	G	0.976	0.944	0.333	0.254	1.51
rs6889239	150437964	C	T	0.976	0.944	0.333	0.254	1.51
rs10036748	150438339	T	C	0.976	0.950	0.332	0.254	1.49
rs7719549	150440240	T	C	0.979	0.908	0.153	0.098	1.89
rs960709	150441242	G	A	0.973	0.944	0.336	0.258	1.49
rs13168551	150442831	C	T	1.000	1.000	0.492	0.423	1.35
rs10067288	150509855	A	G	0.992	0.951	0.108	0.079	1.47
rs10077099	150510867	C	T	0.992	0.954	0.108	0.079	1.48
rs28386800	150511438	T	A	0.992	0.954	0.108	0.079	1.48
rs13167040	150521856	A	G	0.995	0.970	0.108	0.078	1.49
rs10072803	150522414	T	G	0.995	0.971	0.108	0.078	1.49

rs10040086	150525260	G	A	0.996	0.974	0.108	0.078	1.49
rs10072012	150527331	T	C	0.995	0.968	0.108	0.078	1.49
rs10080029	150527544	C	T	0.994	0.965	0.108	0.078	1.49
rs10476763	150528477	A	G	0.992	0.952	0.107	0.077	1.49

a. Base-pair position based on NCBI build 36, HG18.

b. Minor allele (Allele A) and alternative allele (Allele B).

c. Average maximum posterior call from ImputeV2.0 (see Web site). Those SNPs that were genotyped have p Genome data HapMap3 reference genotyping data and only SNPs with >0.90 maximum posterior calls are included.

d. Information (Inf) is a measure of the observed statistical information for the estimate of SNP allele frequency with 1.00 information were genotyped.

e. MAF are the Case and control minor allele frequencies.

f. Odds ratio (OR) and 95% confidence intervals (CI) and are based on an additive model.

g. Association tests and p values for an additive model were determined using SNPTTEST v2 with the SCORE test that were outputted from Impute V2.0.

h. The p values are shown for analyses using no covariates and covariates for population substructure (first five after conditioning on the rs2233290 SNP are shown).

Lower 95% OR CI ^f	Upper 95% OR CI ^f	p value no covariate	p value all covariate	p value conditioning on rs2233290 ^g
1.13	1.49	2.34E-04	3.04E-04	3.44E-01
1.11	1.47	5.03E-04	7.26E-04	4.05E-01
1.13	1.50	1.62E-04	2.12E-04	1.66E-01
1.50	2.31	1.23E-08	2.13E-08	4.52E-01
1.54	2.38	1.95E-09	3.39E-09	conditioned SNP
1.35	1.83	2.62E-09	5.65E-09	1.67E-02
1.54	2.35	1.98E-09	3.45E-09	9.43E-01
1.52	2.32	2.35E-09	4.54E-09	8.28E-01
1.53	2.33	1.85E-09	2.98E-09	5.23E-01
1.37	1.99	5.44E-08	1.42E-07	5.64E-01
1.53	2.33	1.68E-09	2.71E-09	4.65E-01
1.53	2.33	1.63E-09	2.61E-09	4.44E-01
1.53	2.26	9.00E-11	3.04E-10	1.01E-02
1.39	1.96	3.39E-09	1.78E-08	4.66E-02
1.39	1.96	3.38E-09	1.79E-08	4.64E-02
1.55	2.35	1.13E-09	1.78E-09	2.82E-01
1.55	2.35	1.13E-09	1.77E-09	2.80E-01
1.38	1.95	3.64E-09	1.96E-08	4.47E-02
1.55	2.36	1.01E-09	1.57E-09	2.42E-01
1.51	2.20	1.80E-10	5.56E-10	1.48E-02
1.51	2.29	3.18E-09	4.68E-09	4.73E-01
1.43	2.12	2.29E-08	2.75E-08	5.86E-01
1.33	1.86	1.81E-08	8.02E-08	6.09E-02
1.46	2.11	4.55E-10	1.34E-09	1.65E-02
1.48	2.22	8.55E-09	1.16E-08	5.43E-01
1.48	2.14	3.70E-10	1.03E-09	1.54E-02
1.48	2.20	7.16E-09	8.02E-09	3.63E-01
1.48	2.15	2.90E-10	8.54E-10	1.26E-02
1.47	2.20	8.00E-09	9.04E-09	3.52E-01
1.34	1.86	1.12E-08	6.69E-08	3.85E-02
1.49	2.22	5.45E-09	6.04E-09	3.06E-01
1.31	1.75	3.62E-09	1.16E-08	1.55E-03
1.31	1.75	3.60E-09	1.14E-08	1.53E-03
1.30	1.72	9.76E-09	2.57E-08	2.91E-03
1.53	2.34	2.93E-09	3.34E-09	3.14E-01
1.29	1.71	1.36E-08	3.79E-08	3.54E-03
1.19	1.53	5.70E-06	2.48E-06	1.01E-02
1.17	1.85	5.00E-04	9.06E-04	1.97E-04
1.17	1.86	4.61E-04	8.42E-04	1.82E-04
1.18	1.86	4.41E-04	8.08E-04	1.73E-04
1.19	1.87	3.28E-04	6.09E-04	1.26E-04
1.19	1.87	3.29E-04	6.09E-04	1.26E-04

1.18	1.87	3.35E-04	6.20E-04	1.29E-04
1.19	1.87	3.30E-04	6.26E-04	1.29E-04
1.19	1.87	3.29E-04	6.32E-04	1.30E-04
1.18	1.88	3.27E-04	6.78E-04	1.37E-04

osteior call rates of 1.00. SNPs were imputed using 1000
luded.

determined by the SNPTEST v2 algorithm (see web site). SNPs

st option. Analyses were performed using allele probabilities

re principal components and gender). In addition, the p values