

Supplemental Table I. Summary of the SNPs from HapMap Caucasian database used for tagSNP selection. SNPs with the same number in the LD cluster column were placed in the same LD cluster ($r^2 \geq 0.95$) by the Tagger program. See Supplemental Figure II for a graphical presentation of the distributions of the LD clusters across the ROCK2 locus.

SNP	Map	Location	LD Cluster	MAF
rs3911110	11,269,075	3'-UTR	1	0.193
rs11694729	11,295,344	Intron 21	1	0.203
rs10454126	11,299,794	Intron 20	1	0.203
rs6721445	11,346,706	Intron 3	1	0.203
rs10194620	11,357,739	Intron 3	1	0.21
rs11695377	11,365,105	Intron 3	1	0.2
rs7593091	11,375,059	Intron 3	1	0.2
rs12692434	11,393,181	Intron 1	1	0.198
rs6733312	11,397,105	Intron 1	1	0.198
rs6713273	11,398,932	Intron 1	1	0.2
rs1562748	11,401,203	Intron 1	1	0.2
rs6749456	11,401,223	Intron 1	1	0.2
rs10203916	11,402,582	Intron 1	1	0.2
rs7355446	11,404,091	Intron 1	1	0.198
rs7563928	11,404,463	Intron 1	1	0.198
rs10210600	11,404,728	Intron 1	1	0.188
rs6432186	11,405,876	Intron 1	1	0.2
rs6755196	11,410,923	Intron 1	1	0.2
rs753770	11,416,120	Intron 1	1	0.2
rs2084577	11,416,687	Intron 1	1	0.2
rs4669710	11,417,111	Intron 1	1	0.2
rs13014721	11,421,331	Intron 1	1	0.188
rs4669713	11,429,137	Intron 1	1	0.2
rs12692437	11,431,159	Intron 1	1	0.2
rs12996399	11,264,437	3'-UTR	2	0.39
rs921322	11,270,258	3'-UTR	2	0.373
rs8996	11,271,475	3'-UTR	2	0.375
rs978906	11,273,874	Exon 34 (UTR)	2	0.361
rs6753921	11,277,353	Intron 33	2	0.375
rs12470004	11,286,630	Intron 28	2	0.375
rs17366657	11,295,112	Intron 21	2	0.373
rs13424069	11,298,059	Intron 21	2	0.373
rs1546597	11,298,854	Intron 20	2	0.375
rs1546598	11,300,688	Intron 19	2	0.375
rs12475086	11,301,202	Intron 19	2	0.373
rs13022598	11,302,936	Intron 18	2	0.362
rs10495582	11,304,906	Intron 18	2	0.375
rs726843	11,306,788	Intron 14	2	0.375
rs10168084	11,317,349	Intron 6	2	0.375
rs1515219	11,319,676	Intron 5	2	0.383
rs17366874	11,322,239	Intron 5	2	0.379
rs7589629	11,323,805	Intron 5	2	0.392
rs11680818	11,324,798	Intron 5	2	0.39
rs6728627	11,332,994	Intron 4	2	0.39
rs10192483	11,334,315	Intron 4	2	0.39

rs12478098	11,335,116	Intron 4	2	0.39
rs6716447	11,336,173	Intron 4	2	0.381
rs3771106	11,340,710	Intron 3	2	0.383
rs6730673	11,344,270	Intron 3	3	0.254
rs7568064	11,345,597	Intron 3	3	0.242
rs6759490	11,351,763	Intron 3	3	0.233
rs10192593	11,352,010	Intron 3	3	0.241
rs7558664	11,355,844	Intron 3	3	0.246
rs4668720	11,356,412	Intron 3	3	0.242
rs12692433	11,359,291	Intron 3	3	0.263
rs7563468	11,381,873	Intron 1	3	0.246
rs7575837	11,395,474	Intron 1	3	0.242
rs12692435	11,395,696	Intron 1	3	0.246
rs6736240	11,401,030	Intron 1	3	0.241
rs2122384	11,401,910	Intron 1	3	0.241
rs12994807	11,402,043	Intron 1	3	0.237
rs7355489	11,403,902	Intron 1	3	0.242
rs12992581	11,406,971	Intron 1	3	0.246
rs6755337	11,410,883	Intron 1	3	0.242
rs10929732	11,434,090	Intron 1	3	0.242
rs13018466	11,267,824	3'-UTR	4	0.423
rs2011812	11,290,796	Intron 24	4	0.417
rs17366643	11,295,102	Intron 21	4	0.409
rs13423864	11,297,847	Intron 21	4	0.424
rs7598032	11,303,798	Intron 18	4	0.415
rs9808232	11,309,718	Exon 10	4	0.417
rs2056103	11,315,354	Intron 6	4	0.425
rs13393192	11,319,264	Intron 5	4	0.414
rs13397757	11,321,366	Intron 5	4	0.414
rs13404430	11,331,711	Intron 4	4	0.433
rs2044758	11,329,046	Intron 4	5	0.195
rs9287728	11,330,275	Intron 4	5	0.195
rs2357996	11,331,127	Intron 4	5	0.184
rs1868584	11,348,481	Intron 3	5	0.195
rs965665	11,349,473	Intron 3	5	0.192
rs6432183	11,350,090	Intron 3	5	0.195
rs6432184	11,350,147	Intron 3	5	0.195
rs1562749	11,355,875	Intron 3	5	0.195
rs2290156	11,283,806	Intron 31	6	0.308
rs11676201	11,322,080	Intron 5	6	0.31
rs10187981	11,329,270	Intron 4	6	0.305
rs1868585	11,333,427	Intron 4	6	0.305
rs10929727	11,334,812	Intron 4	6	0.305
rs4303693	11,358,814	Intron 3	7	0.22
rs10803732	11,359,581	Intron 3	7	0.216
rs10178332	11,359,615	Intron 3	7	0.22
rs6710031	11,359,715	Intron 3	7	0.205
rs7589152	11,371,435	Intron 3	8	0.4
rs2122383	11,387,366	Intron 1	8	0.4
rs1901010	11,422,701	Intron 1	8	0.4
rs16857265	11,281,010	Intron 33	9	0.068
rs11884214	11,320,684	Intron 5	9	0.069
rs7593683	11,405,690	Intron 1	9	0.07
rs6716817	11,336,432	Intron 4	10	0.5

rs4477886	11,338,892	Intron 4	10	0.5
rs4669702	11,354,050	Intron 1	11	0.288
rs12622447	11,426,043	Intron 1	11	0.292
rs10929728	11,362,081	Intron 3	12	0.358
rs7581184	11,440,129	5'-UTR	13	0.408
rs10167277	11,316,598	Intron 6	14	0.379
rs4669708	11,397,149	Intron 1	15	0.417
rs4669700	11,352,136	Intron 3	16	0.195
rs17366517	11,271,266	3'-UTR	17	0.11
rs12479227	11,344,951	Intron 3	18	0.059

Supplemental Table II. ROCK2 SNP physical map locations on chromosome 2, minor allele (M.A.) frequencies (MAF), Hardy-Weinberg equilibrium (HWE) test statistics (p-value) and genotype call rates (%Geno) in the HYPGENE study

SNP	Position	HWE	%Geno	MAF	M.A.
rs17366517	11,271,266	1	100	0.064	G
rs6753921	11,277,353	0.6411	100	0.477	A
rs16857265	11,281,010	0.6137	100	0.056	G
rs9808232	11,309,718	0.3625	100	0.48	C
rs2056103	11,315,354	0.5503	99.8	0.475	T
rs10167277	11,316,598	0.9839	99.7	0.336	A
rs10929727	11,334,812	0.5488	99.8	0.279	G
rs4477886	11,338,892	0.5008	100	0.451	A
rs12479227	11,344,951	0.6866	100	0.053	A
rs965665	11,349,473	0.9515	100	0.128	C
rs4669700	11,352,136	0.5186	99.8	0.216	G
rs4669702	11,354,050	0.5639	100	0.279	A
rs10178332	11,359,615	0.9401	99.8	0.131	C
rs10929728	11,362,081	0.9494	100	0.336	G
rs2122383	11,387,366	0.8746	100	0.48	T
rs6755196	11,410,923	0.9331	100	0.131	A
rs10929732	11,434,090	0.6142	100	0.182	A
rs7581184	11,440,129	0.5242	100	0.381	G

Supplemental Table III. Pairwise linkage disequilibria (D' above and r^2 below diagonal) among the ROCK2 SNPs in the HYPGENE cohort.

#	SNP	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	rs17366517		1.00	1.00	1.00	1.00	1.00	0.99	1.00	1.00	1.00	1.00	0.99	1.00	1.00	1.00	1.00	1.00	0.98
2	rs6753921	0.06		1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.99	1.00	1.00	1.00	0.99	1.00	1.00	0.98
3	rs16857265	0.00	0.05		1.00	1.00	1.00	1.00	1.00	0.16	0.99	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.97
4	rs9808232	0.07	0.84	0.06		1.00	1.00	1.00	0.82	1.00	1.00	1.00	1.00	1.00	1.00	0.98	1.00	0.58	0.77
5	rs2056103	0.08	0.82	0.07	0.98		1.00	1.00	0.82	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.57	0.77
6	rs10167277	0.14	0.46	0.12	0.55	0.56		1.00	0.65	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.99	0.98
7	rs10929727	0.17	0.35	0.02	0.42	0.43	0.77		0.55	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.98	0.98
8	rs4477886	0.06	0.75	0.07	0.60	0.61	0.26	0.15		1.00	1.00	1.00	0.55	0.97	0.64	1.00	0.97	0.98	0.67
9	rs12479227	0.00	0.05	0.00	0.06	0.06	0.11	0.14	0.07		1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.96
10	rs965665	0.01	0.13	0.01	0.16	0.16	0.07	0.06	0.18	0.01		1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.92
11	rs4669700	0.02	0.25	0.02	0.30	0.30	0.54	0.71	0.33	0.20	0.04		1.00	1.00	0.99	0.99	1.00	0.97	0.98
12	rs4669702	0.17	0.35	0.02	0.42	0.42	0.76	1.00	0.14	0.14	0.06	0.71		1.00	1.00	1.00	1.00	0.98	0.98
13	rs10178332	0.01	0.14	0.01	0.16	0.17	0.08	0.06	0.17	0.01	0.97	0.04	0.06		1.00	1.00	1.00	1.00	0.92
14	rs10929728	0.14	0.46	0.12	0.55	0.56	1.00	0.77	0.26	0.11	0.07	0.54	0.76	0.08		1.00	1.00	0.99	0.98
15	rs2122383	0.06	0.96	0.06	0.81	0.83	0.46	0.36	0.75	0.05	0.14	0.25	0.35	0.14	0.47		1.00	1.00	0.98
16	rs6755196	0.01	0.14	0.01	0.16	0.17	0.08	0.06	0.17	0.01	0.97	0.04	0.06	1.00	0.08	0.14		1.00	0.92
17	rs10929732	0.02	0.20	0.01	0.08	0.08	0.11	0.08	0.26	0.01	0.66	0.06	0.08	0.68	0.11	0.21	0.68		0.32
18	rs7581184	0.11	0.54	0.09	0.40	0.40	0.79	0.61	0.33	0.08	0.08	0.43	0.61	0.08	0.79	0.55	0.08	0.01	

Supplemental Table IV. Odds ratios (95% confidence limits) for the risk of hypertension for the SNPs in LD block 2 that were associated with hypertension. 'A/A' refers to common allele homozygotes, 'A/a' to heterozygotes, and 'a/a' to minor allele homozygotes. Odds ratios for the minor allele homozygotes under recessive model were identical to those shown in the table ('A/A'+ 'A/a' as a reference group). All p-values are adjusted for baseline age, cardiorespiratory fitness, body mass index, and follow-up time.

SNP	A/A	Odds Ratio (95% CL)			p-value	
		A/a	a/a	Additive	Recessive	
rs965665	1	1.04 (0.78; 1.38)	0.15 (0.04; 0.54)	0.012	0.003	
rs10178332	1	1.06 (0.80; 1.40)	0.20 (0.07; 0.62)	0.017	0.0047	
rs6755196	1	1.05 (0.79; 1.39)	0.20 (0.07; 0.62)	0.017	0.0046	
rs10929732	1	0.99 (0.77; 1.28)	0.40 (0.19; 0.83)	0.048	0.014	

Supplemental Figure I. Linkage disequilibrium (LD) block structure of the ROCK2 SNPs in the Caucasian HapMap data.

Supplemental Figure II. Size and distribution of the 18 LD clusters at the ROCK2 locus from the Caucasian HapMap data. Number of SNPs in each cluster is indicated and the list of individual SNPs is given in Supplemental Table I. Clusters 12 – 18 consist of a single SNP.





NM_004850

ROCK2: Rho-associated

