

Table S2. Calculation of multiple testing thresholds. The Ras/MAPK SNP set is shown, including gene, chromosome positions, total SNPs, LD-independent SNPs, and proportion of the genome screened for epistasis (subtracting the X chromosome and gene chromosome proportion from approximate 3 billion bp genome). The last row indicates the threshold calculated by multiplying 5×10^{-8} by the gene or screening proportion x LD-independent SNPs proportion total for gene-based and genome-wide independent thresholds, respectively.

gene	CHR	START	END	N total SNPs	N SNPs ($R^2 < 0.2$)	screening proportion (%)
<i>BRAF</i>	7	140428813	140629564	267	4	89.5
<i>CBL</i>	11	119071986	119183859	74	2	90.3
<i>KRAS</i>	12	25353180	25408854	139	8	90.4
<i>LZTR1</i>	22	21331558	21358326	1	1	93.1
<i>MAP2K1</i>	15	66674211	66788882	276	8	91.4
<i>MAPK1</i>	22	22108947	22226970	218	5	93.1
<i>NF1</i>	17	29416945	29709695	249	4	92
<i>NRAS</i>	1	115242085	115264515	22	4	86.5
<i>PTPN11</i>	12	112851536	112952717	21	4	90.4
<i>RAF1</i>	3	12620100	12710700	187	4	88.2
<i>RASA1</i>	5	86559070	86692743	65	6	88.8
<i>RASA2</i>	3	141200926	141336197	86	4	88.2
<i>RIT1</i>	1	155862599	155885706	28	2	86.5
<i>SHOC2</i>	10	112674301	112778425	164	5	90.3
<i>SOS1</i>	2	39203690	39352604	176	3	86.7
<i>SOS2</i>	14	50578846	50703099	240	4	91.2
<i>SPRED1</i>	15	38540052	38654450	307	5	91.4
17 genes				2520 SNPs	73 ind.	65.72 ind x prop
						2.9×10^{-9}
						7.6×10^{-10}

Abbreviations: CHR chromosome; START start position (bp); END end position (bp)