

Supplemental Digital Content 1. VEGF-pathway gene SNPs genotyped in the initial cohort. SNPs in bold were also genotyped in a validation cohort, and minor allele frequency (MAF) and Hardy-Weinberg equilibrium (HWE) values are presented from initial/validation cohorts, respectively.

SNP	Gene	Location	Alleles	MAF ^a	HWE p value	Rationale for genotyping
rs3829387	<i>FLT1</i>	5' upstream	A>C	0.20 (0.20)	0.07	Cancer survival association ²
rs7321093	<i>FLT1</i>	5' upstream	C>T	0.42 (0.46)	0.31	Cancer survival association ²
rs7996030	<i>FLT1</i>	intron	G>A	0.17/0.21 (0.24)	0.08/0.20	tSNP ³ /putative function ⁴
rs9554330	<i>FLT1</i>	intron	G>A	0.23 (0.30)	0.48	tSNP ³ /putative function ⁴
rs9319434	<i>FLT1</i>	intron	A>T	0.25 (0.25)	0.45	tSNP ³ /putative function ⁴
rs9513114	<i>FLT1</i>	intron	T>C	0.25 (0.25)	0.005	tSNP ³ /putative function ⁴
rs1853581	<i>FTL1</i>	intron	A>C	0.36 (0.38)	0.72	tSNP ³ /putative function ⁴
rs614820	<i>FLT1</i>	intron	T>C	0.33 (0.31)	0.14	tSNP ³ /putative function ⁴
rs7337610	<i>FLT1</i>	intron	C>T	0.36 (0.35)	0.03	tSNP ³ /putative function ⁴
rs9551465	<i>FLT1</i>	intron	T>A	0.45 (0.42)	0.74	tSNP ³ /putative function ⁴
rs9513112	<i>FLT1</i>	intron	G>A	0.40 (0.33)	0.74	tSNP ³ /putative function ⁴
rs9513087	<i>FLT1</i>	intron	A>T	0.16 (0.19)	0.22	tSNP ³ /putative function ⁴
rs9513095	<i>FLT1</i>	intron	T>C	0.31 (0.30)	0.71	tSNP ³ /putative function ⁴
rs9582036	<i>FLT1</i>	intron	A>C	0.28/0.29 (0.29)	0.15/0.02	tSNP ³ /putative function ⁴
rs542403	<i>FRS2</i>	3'UTR	A>G	0.16 (0.17 [#])	0.36	LCL eQTL ¹
rs7219	<i>GRB2</i>	3'UTR	A>G	0.15 (0.21)	0.35	Putative function ⁵
rs2301113	<i>HIF1A</i>	intron	A>C	0.19 (0.17)	0.20	tSNP ³
rs1951795	<i>HIF1A</i>	intron	C>A	0.17 (0.13)	0.14	tSNP ³
rs11549465	<i>HIF1A</i>	exon (missense)	C>T	0.09 (0.08)	0.62	tSNP ³ /putative function ⁴
rs1551643	<i>KDR</i>	5' upstream	T>A	0.33 (0.32)	0.83	Functional evidence ⁶
rs2071559	<i>KDR</i>	5' upstream	C>T	0.47 (0.50)	0.32	Functional evidence ⁶
rs7667298	<i>KDR</i>	5'UTR	C>T	0.45 (0.49)	0.40	Functional evidence ⁶
rs7655964	<i>KDR</i>	intron	A>C	0.34 (0.30)	1.00	Functional evidence ⁶
rs1870377	<i>KDR</i>	exon (missense)	T>A	0.27 (0.28)	0.30	Functional evidence ⁶
rs12813551	<i>KRAS</i>	intron	T>C	0.38/0.40 (0.41)	0.29/0.60	LCL eQTL ¹
rs10505980	<i>KRAS</i>	intron	G>A	0.34/0.37 (0.39)	0.04/0.59	LCL eQTL ¹
rs11047912	<i>KRAS</i>	intron	T>C	0.21 (0.31)	0.03	LCL eQTL ¹
rs10842513	<i>KRAS</i>	intron	C>T	0.11/0.07 (0.11)	0.002/0.11	LCL eQTL ¹
rs4246229	<i>KRAS</i>	intron	A>G	0.43 (0.48)	0.008	LCL eQTL ¹
rs1137282	<i>KRAS</i>	3'-UTR	T>C	0.17 (0.25)	0.14	Putative function ⁵
rs34176876	<i>KRAS</i>	3'-UTR	A>-	0.41 (0.40 ⁵)	0.01	NSCLC association ⁷
rs1133228	<i>MAP2K6</i>	exon (synonymous)	C>A	0.47 (0.41)	0.005 [^]	Putative function ^{4,5}
rs2716197	<i>MAP2K6</i>	intron	T>G	0.33 (0.35)	0.03	Cancer survival association ²
rs2076139	<i>MAPK11</i>	exon (synonymous)	C>T	0.22 (0.30)	0.47	LCL eQTL ¹
rs2228638	<i>NRP1</i>	exon (missense)	G>A	0.07 (0.14)	0.54	Putative function ⁴
rs2359192	<i>PGF</i>	intron	C>A	0.15 (0.19)	0.35	LCL eQTL ¹
rs4356203	<i>PIK3C2A</i>	intron	A>G	0.40 (0.42)	0.18	LCL eQTL ¹
rs17561348	<i>PIK3C2A</i>	intron	T>C	0.29 (0.33)	0.69	LCL eQTL ¹
rs214936	<i>PIK3C2A</i>	exon (synonymous)	A>G	0.44(0.46)	0.62	LCL eQTL ¹
rs11604561	<i>PIK3C2A</i>	exon (missense)	T>C	0.13 (0.11)	0.45	Putative function ⁴
rs935661	<i>PRKCE</i>	intron	A>C	0.46 (0.47)	0.87	LCL eQTL ¹
rs11125055	<i>PRKCE</i>	intron	G>T	0.15 (0.19)	0.09	LCL eQTL ¹
rs3754562	<i>PRKCE</i>	intron	G>C	0.31 (0.32)	0.85	Putative function ⁴
rs7576304	<i>PRKCE</i>	intron	C>T	0.41 (0.44)	0.73	LCL eQTL ¹
rs2345625	<i>PRKCE</i>	intron	C>T	0.45 (0.41)	0.25	LCL eQTL ¹
rs2345626	<i>PRKCE</i>	intron	C>T	0.24 (0.30)	0.07	LCL eQTL tSNP ¹
rs14138	<i>PRKCE</i>	3'-UTR	G>A	0.14 (0.17)	0.19	LCL eQTL ¹
rs699947	<i>VEGFA</i>	5' upstream	C>A	0.44 (0.48)	0.51	NSCLC survival association ⁸
rs1570360	<i>VEGFA</i>	5' upstream	G>A	0.39 (0.28 [#])	1.00	NSCLC survival association ⁸
rs2010963	<i>VEGFA</i>	5'UTR	G>C	0.26 (0.27 [#])	0.13	NSCLC survival association ⁹
rs3024997	<i>VEGFA</i>	intron	G>A	0.26 (0.33)	0.13	LCL eQTL ¹
rs3025006	<i>VEGFA</i>	intron	C>T	0.32 (0.44 [#])	0.02	LCL eQTL ¹
rs3025039	<i>VEGFA</i>	3'UTR	C>T	0.16 (0.17 [#])	0.54	Putative function ⁵

*MAFs from the present study shown with corresponding reference European MAF (CEU HapMap population unless otherwise specified) in brackets.

#reference European MAF from 1,000 Genomes CEU population.

^rs1133228 has shown a $p=0.01$ for HWE in the HapMap CEU population (http://www.ncbi.nlm.nih.gov/projects/SNP/snp_ref.cgi?rs=1133228).

¶reference European MAF from Coriell Cell Repository CEPH panel.

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