

Table S1. Information of *VEGF* polymorphisms primer set for PCP-RFLP, real-time PCR

Method	Genotype	Reference SNP ID	Primer sequence	Annealing condition	Restriction enzyme	RFLP condition
PCR-RFLP	<i>VEGF</i> +936C>T	rs1570360	Forward: 5'- CGC GTG TCT CTG GAC AGA GTT TCC -3' Reverse: 5'- CGG GGA CAG GCG AGC TTC AG -3'	59°C, with 35 cycles	<i>Mnl</i> I	incubation for 16hr at 37°C
	<i>VEGF</i> +936C>T	rs3025039	Forward: 5'- AAG GAA GAG GAG ACT CTG CGC AGA GC -3' Reverse: 5'- TAA ATG TAT GTA TGT GGG TGG GTG TGT CTA CAG G -3'	68°C, with 35 cycles	<i>Nla</i> III	incubation for 16hr at 37°C
Taqman real-time PCR	<i>VEGF</i> +1451C>T	rs3025040	Forward: 5'- ACG GAC AGA AAG ACA GAT CAC AG -3' Reverse: 5'- CCC AAA GCA CAG CAA TGT C -3' C probe: 5'- [FAM]-TGA GGA CAC C GGC TCT GAC C-[TAMRA] -3' T probe: 5'- [JOE]-TGA GGA CAC T GGC TCT GAC C-[TAMRA] -3'	57°C, with 50 cycles		
	<i>VEGF</i> +1612G>A	rs10434	Forward: 5'- TTC GCT TAC TCT CAC CTG CTT C -3' Reverse: 5'- GCT GTC ATG GGC TGC TTC T -3' G probe: 5'- [FAM]-CCC AGG AG G CCA CTG GCA-[TAMRA] -3' A probe: 5'- [JOE]-CCC AGG AG A CCA CTG GCA-[TAMRA] -3'	65°C, with 50 Cycles		
	<i>VEGF</i> +1725G>A	rs3025053	Forward: 5'- CAT GAC AGC TCC CCT TCC T -3' Reverse: 5'- TGG TTT CAA TGG TGT GAG GAC -3' G probe: 5'- [FAM]-CTT CCT GGG G TGC AGC CTA A-[TAMRA] -3' A probe: 5'- [JOE]-CTT CCT GGG A TGC AGC CTA A-[TAMRA] -3'	68°C, with 35 cycles		

PCR, polymerase chain reaction, RFLP, restriction fragment length polymorphism

Table S2. Comparison of allele frequency in recruited samples and variable population of 1000 genomes.

SNP	Allele	Control	CAD	EAS	CDX	CHB	CHS	JPT	KHV
rs1570360	A	0.838	0.855	0.184	0.167	0.175	0.176	0.168	0.232
	G	0.162	0.145	0.816	0.833	0.825	0.824	0.832	0.768
rs833061	T	0.758	0.766	0.717	0.763	0.728	0.733	0.663	0.702
	C	0.242	0.234	0.283	0.237	0.272	0.267	0.337	0.298
rs3025039	C	0.803	0.820	0.830	0.866	0.816	0.790	0.841	0.843
	T	0.197	0.180	0.827	0.849	0.816	0.790	0.841	0.843
rs3025040	C	0.812	0.824	0.170	0.134	0.184	0.210	0.159	0.157
	T	0.188	0.176	0.173	0.151	0.184	0.210	0.159	0.157
rs10434	G	0.841	0.826	0.780	0.672	0.791	0.800	0.865	0.758
	A	0.159	0.174	0.220	0.328	0.209	0.200	0.135	0.242
rs3025053	G	0.947	0.932	0.864	0.758	0.913	0.862	0.962	0.813
	A	0.053	0.068	0.136	0.242	0.087	0.138	0.038	0.187

EAS, east Asian; CDX, Chinese Dai in Xishuangbanna, China; CHB, Han Chinese in Beijing, China; CHS, Southern Han Chinese; JPT, Japanese in Tokyo, Japan; KHV, Kinh in Ho Chi Minh City, Vietnam

Table S5. Genotype combination of VEGF polymorphisms in CAD patients and control subjects.

Genotype combination	Control subjects (n=422)	CAD patients (n=463)	AOR (95% CI)	P
GG/TT/CC	154 (36.5)	192 (45.5)		
GG/TT/CT	64 (15.2)	70 (16.6)	0.828 (0.545-1.260)	0.378
GG/TT/TT	5 (1.2)	2 (0.5)	0.322 (0.054-1.934)	0.215
GG/TC/CC	36 (8.5)	39 (9.2)	0.827 (0.484-1.413)	0.486
GG/TC/CT	22 (5.2)	28 (6.6)	1.134 (0.594-2.166)	0.704
GG/TC/TT	2 (0.5)	7 (1.7)	3.757 (0.736-19.169)	0.111
GG/CC/CC	5 (1.2)	1 (0.2)	0.161 (0.016-1.591)	0.118
GG/CC/CT	5 (1.2)	0 (0.0)	N/A	N/A
GG/CC/TT	1 (0.2)	0 (0.0)	N/A	N/A
GA/TT/CC	12 (2.8)	3 (0.7)	0.224 (0.059-0.845)	0.027
GA/TT/CT	5 (1.2)	0 (0.0)	N/A	N/A
GA/TC/CC	57 (13.5)	68 (16.1)	0.907 (0.590-1.395)	0.658
GA/TC/CT	25 (5.9)	32 (7.6)	0.843 (0.461-1.541)	0.579
GA/TC/TT	7 (1.7)	4 (0.9)	0.230 (0.054-0.988)	0.048
GA/CC/CC	6 (1.4)	4 (0.9)	0.446 (0.113-1.760)	0.249
GA/CC/CT	5 (1.2)	4 (0.9)	0.533 (0.132-2.158)	0.378
GA/CC/TT	1 (0.2)	0 (0.0)	N/A	N/A
AA/TT/CT	1 (0.2)	0 (0.0)	N/A	N/A
AA/TC/CC	2 (0.5)	0 (0.0)	N/A	N/A
AA/TC/CT	4 (0.9)	0 (0.0)	N/A	N/A
AA/CC/CC	1 (0.2)	4 (0.9)	2.639 (0.261-26.674)	0.411
AA/CC/CT	1 (0.2)	3 (0.7)	2.989 (0.292-30.571)	0.356
AA/CC/TT	1 (0.2)	2 (0.5)	2.075 (0.165-26.177)	0.572

Note: CAD, coronary artery disease; AOR, adjusted odd ratio; CI, confidence interval.

AOR; adjusted by age, gender, hypertension, diabetes mellitus, hyperlipidemia, and smoking

