

**Supplementary Table S3.** Association between DFS and genotype subgroups within each treatment group or the combined sunitinib and placebo groups

<b>Gene/SNP</b>	<b>Sunitinib<sup>a</sup></b>		<b>Placebo<sup>b</sup></b>		<b>Combined<sup>c</sup></b>	
<i>VEGFA rs699947</i>	A/C	C/C	A/C	C/C	A/C	C/C
	<i>n</i> = 78	<i>n</i> = 37	<i>n</i> = 69	<i>n</i> = 41	<i>n</i> = 147	<i>n</i> = 78
HR	0.94	1.19	1.19	1.14	1.05	1.17
95% CI	(0.42–2.08)	(0.51–2.82)	(0.63–2.24)	(0.57–2.25)	(0.64–1.71)	(0.68–1.99)
<i>P</i> value	0.789	0.671	0.599	0.734	0.933	0.596
<i>VEGFA rs833061</i>	C/T	T/T	C/T	T/T	C/T	T/T
	<i>n</i> = 80	<i>n</i> = 35	<i>n</i> = 70	<i>n</i> = 40	<i>n</i> = 150	<i>n</i> = 75
HR	0.96	1.16	1.22	1.09	1.07	1.13
95% CI	(0.44–2.11)	(0.49–2.77)	(0.65–2.29)	(0.55–2.18)	(0.66–1.74)	(0.66–1.94)
<i>P</i> value	0.855	0.741	0.507	0.851	0.814	0.719
<i>VEGFR1 rs9554320</i>	A/C	C/C	A/C	C/C	A/C	C/C
	<i>n</i> = 72	<i>n</i> = 50	<i>n</i> = 76	<i>n</i> = 48	<i>n</i> = 148	<i>n</i> = 98
HR	1.44	0.59	2.16	1.74	1.82	1.08

95% CI	(0.56–3.70)	(0.21–1.71)	(0.96–4.86)	(0.74–4.11)	(0.99–3.36)	(0.56–2.10)
<i>P</i> value	0.051	0.068	<b>0.038</b>	0.515	<b>0.006</b>	0.454
<i>VEGFR1 rs9582036</i>	C/A	A/A	C/A	A/A	C/A	A/A
	<i>n</i> = 55	<i>n</i> = 77	<i>n</i> = 70	<i>n</i> = 64	<i>n</i> = 125	<i>n</i> = 141
HR	4.17	1.52	2.83	1.80	3.16	1.55
95% CI	(0.57–30.60)	(0.20–11.36)	(0.87–9.28)	(0.54–5.97)	(1.15–8.69)	(0.56–4.32)
<i>P</i> value	<b>&lt;0.001</b>	<b>0.022</b>	<b>0.027</b>	0.774	<b>&lt;0.001</b>	<b>0.072</b>
<i>VEGFR2 rs2071559</i>	T/C	C/C	T/C	C/C	T/C	C/C
	<i>n</i> = 68	<i>n</i> = 26	<i>n</i> = 68	<i>n</i> = 36	<i>n</i> = 136	<i>n</i> = 62
HR	1.38	1.71	0.60	1.11	0.90	1.39
95% CI	(0.71–2.66)	(0.76–3.85)	(0.34–1.06)	(0.59–2.10)	(0.59–1.39)	(0.84–2.29)
<i>P</i> value	0.352	0.219	0.070	0.956	0.582	0.309
<i>VEGFR2 rs1870377</i>	A/T	T/T	A/T	T/T	A/T	T/T
	<i>n</i> = 46	<i>n</i> = 89	<i>n</i> = 40	<i>n</i> = 89	<i>n</i> = 86	<i>n</i> = 178
HR	–	–	0.83	0.69	0.69	0.53
95% CI	–	–	(0.37–1.88)	(0.32–1.50)	(0.36–1.32)	(0.28–0.98)

<i>P</i> value	–	–	0.807	0.198	0.837	<b>0.018</b>
<i>VEGFR3 rs6877011</i>	C/G	G/G	C/G	G/G	C/G	G/G
	<i>n</i> = 16	<i>n</i> = 5	<i>n</i> = 20	<i>n</i> = 3	<i>n</i> = 36	<i>n</i> = 8
HR	–	–	–	–	–	–
95% CI	–	–	–	–	–	–
<i>P</i> value	–	–	–	–	–	–
<i>LOXL2 rs4872122</i>	A/C	C/C	A/C	C/C	A/C	C/C
	<i>n</i> = 59	<i>n</i> = 59	<i>n</i> = 73	<i>n</i> = 45	<i>n</i> = 132	<i>n</i> = 104
HR	0.73	0.58	0.81	0.65	0.78	0.61
95% CI	(0.36–1.51)	(0.28–1.22)	(0.43–1.50)	(0.33–1.32)	(0.49–1.24)	(0.37–1.01)
<i>P</i> value	0.461	0.221	0.724	0.216	0.514	0.060
<i>eNOS rs2070744</i>	T/C	C/C	T/C	C/C	T/C	C/C
	<i>n</i> = 65	<i>n</i> = 22	<i>n</i> = 70	<i>n</i> = 14	<i>n</i> = 135	<i>n</i> = 36
HR	1.18	0.85	0.67	0.49	0.85	0.61
95% CI	(0.64–2.15)	(0.34–2.12)	(0.40–1.11)	(0.19–1.27)	(0.58–1.25)	(0.32–1.17)
<i>P</i> value	0.596	0.920	0.114	0.065	0.405	0.137

<i>SH3GL2 rs10963287</i>	C/T	T/T	C/T	T/T	C/T	T/T
	<i>n</i> = 46	<i>n</i> = 11	<i>n</i> = 53	<i>n</i> = 11	<i>n</i> = 99	<i>n</i> = 22
HR	0.70	1.53	1.08	1.22	0.92	1.40
95% CI	(0.36–1.35)	(0.59–3.98)	(0.65–1.79)	(0.51–2.91)	(0.62–1.38)	(0.74–2.66)
<i>P</i> value	0.339	0.996	0.768	0.631	0.742	0.618
<i>CCDC26 rs60315789</i>	–/TAT	TAT/TAT	–/TAT	TAT/TAT	–/TAT	TAT/TAT
	<i>n</i> = 71	<i>n</i> = 42	<i>n</i> = 70	<i>n</i> = 40	<i>n</i> = 141	<i>n</i> = 82
HR	1.52	1.84	1.20	0.95	1.35	1.26
95% CI	(0.70–3.29)	(0.82–4.13)	(0.66–2.20)	(0.47–1.92)	(0.83–2.17)	(0.74–2.13)
<i>P</i> value	0.432	0.123	0.481	0.869	0.264	0.380

HRs calculated using the unstratified Cox proportional hazards model for heterozygous vs. homozygous genotypes. Two-sided *P* value from the unstratified log rank test.

<sup>a</sup> Sunitinib group (homozygous genotypes): *n* = 27 (*VEGF A rs699947 A/A*); *n* = 27 (*VEGF A rs833061 C/C*); *n* = 20 (*VEGFR1 rs9554320 A/A*); *n* = 10 (*VEGFR1 rs9582036 C/C*); *n* = 48 (*VEGFR2 rs2071559 T/T*); *n* = 7 (*VEGFR2 rs1870377 A/A*); *n* = 121 (*VEGFR3 rs6877011 C/C*); *n* = 24 (*LOXL2 rs4872122 A/A*); *n* = 55 (*eNOS rs2070744 T/T*); *n* = 85 (*SH3GL2 rs10963287 C/C*); *n* = 29 (*CCDC26 rs60315789 –/–*).

<sup>b</sup> Placebo group (homozygous genotypes):  $n = 34$  (*VEGF A rs699947 A/A*);  $n = 34$  (*VEGF A rs833061 C/C*);  $n = 20$  (*VEGFR1 rs9554320 A/A*);  $n = 10$  (*VEGFR1 rs9582036 C/C*);  $n = 40$  (*VEGFR2 rs2071559 T/T*);  $n = 15$  (*VEGFR2 rs1870377 A/A*);  $n = 121$  (*VEGFR3 rs6877011 C/C*);  $n = 26$  (*LOXL2 rs4872122 A/A*);  $n = 60$  (*eNOS rs2070744 T/T*);  $n = 80$  (*SH3GL2 rs10963287 C/C*);  $n = 34$  (*CCDC26 rs60315789 -/-*).

<sup>c</sup> Combined group (homozygous genotypes):  $n = 61$  (*VEGF A rs699947 A/A*);  $n = 61$  (*VEGF A rs833061 C/C*);  $n = 40$  (*VEGFR1 rs9554320 A/A*);  $n = 20$  (*VEGFR1 rs9582036 C/C*);  $n = 88$  (*VEGFR2 rs2071559 T/T*);  $n = 22$  (*VEGFR2 rs1870377 A/A*);  $n = 242$  (*VEGFR3 rs6877011 C/C*);  $n = 50$  (*LOXL2 rs4872122 A/A*);  $n = 115$  (*eNOS rs2070744 T/T*);  $n = 165$  (*SH3GL2 rs10963287 C/C*);  $n = 63$  (*CCDC26 rs60315789 -/-*).

Abbreviations: CI=confidence interval; DFS=disease-free survival; SNP=single nucleotide polymorphism; VEGFR=VEGF receptor.