

## SUPPLEMENTAL FILES

**Supplemental Table S1: Hardy–Weinberg equilibrium for the five *SPP1* SNPs analyzed**

	Homozygote Reference		Heterozygote		Homozygote variant		<i>p</i> value
	Observed	Expected	Observed	Expected	Observed	Expected	
<b>rs9138</b>	1352	1348.6	1130	1136.8	243	239.6	0.753
<b>rs1126616</b>	1312	1320.2	1168	1151.7	243	251.2	0.459
<b>rs11730582</b>	223	236.3	535	508.3	260	273.3	0.094
<b>rs28357094</b>	133	128.8	798	806.5	1267	1262.8	0.622
<b>rs1126772</b>	908	915.9	570	554.3	76	83.9	0.263

Comparison between groups by means of a Chi-squared test.

**Supplemental Table S2:** Genetic polymorphism of *SPP1* rs1126772 A>G in association with CVE in chronic kidney disease (CKD) patients.

Model	Genotype	No CVE N = 1507 <i>n</i> (%)	CVE N = 106 <i>n</i> (%)	Odds ratio (95% CI)	<i>p</i> value	AIC
Co-dominant	AA	903 (59.9%)	49 (46.2%)	1.00	0.016	779.8
	AG	529 (35.1%)	52 (49.1%)	1.81 (1.21–2.72)*		
	GG	75 (5%)	5 (4.7%)	1.23 (0.48–3.18)		
Dominant	AA	903(59.9)	49(46.2)	1.00	0.006	778.5
	AG-GG	604(40.1)	57(53.8)	1.74 (1.17–2.58)*		
Recessive	AA-AG	1432(95)	101(95.3)	1.00	0.9	786
	GG	75(5)	5(4.7)	0.95 (0.37–2.39)		
Over dominant	AA-GG	978(64.9)	54(50.9)	1.00	0.004	778
	AG	529(35.1)	52(49.1)	1.78 (1.20–2.64)*		
Log-Additive	---	---	---	1.43 (1.05–1.96)*	0.027	781.1
HWE ( <i>p</i> value)	---	0.88	0.098	---	---	---

\*Significant odds ratio. The *p* value is obtained by comparison of Akaike information criterion (AIC) from different models; CVE, cardiovascular events; HWE, Hardy–Weinberg equilibrium.

**Supplemental Table S3:** Genetic polymorphism of *SPP1* rs1126616 C>T in association with CVE in CKD patients.

Model	Genotype	No CVE N = 2609 <i>n</i> (%)	CVE N = 206 <i>n</i> (%)	Odds ratio (95% CI)	<i>p</i> value	AIC
Co-dominant	CC	1276 (48.9%)	87 (42.2%)	1.00	0.062	1474.3
	CT	1097 (42%)	104 (50.5%)	1.39 (1.03–1.87)*		
	TT	236 (9.1%)	15 (7.3%)	0.93 (0.53–1.64)		
Dominant	CC	1276 (48.9%)	87 (42.2%)	1.00	0.064	1474.4
	CT-TT	1333 (51.1%)	119 (57.8%)	1.31 (0.98–1.74)		
Recessive	CC-CT	2373 (91%)	191 (92.7%)	1.00	0.38	1477.1
	TT	236 (9.1%)	15 (7.3%)	0.79 (0.46–1.36)		
Over dominant	CC-TT	1512 (58%)	102 (49.5%)	1.00	0.019	1472.4
	CT	1097 (42%)	104 (50.5%)	1.41 (1.06–1.87)*		
Log-Additive	---	---	---	1.12 (0.90–1.39)	0.3	1476.8
HWE ( <i>p</i> value)	---	1	0.039	---	---	---

\*Significant odds ratio. The *p* value is obtained by comparison of Akaike information criterion (AIC) from different models; CVE, cardiovascular events.

**Supplemental Table S4:** Genetic polymorphism of *SPP1* rs9138 A>C in association with CVE in CKD patients.

Model	Genotype	No CVE N = 2609 n (%)	CVE N = 206 n (%)	Odds ratio (95% CI)	p value	AIC
Co-dominant	AA	1313 (50.3%)	91 (44.2%)	1.00	0.086	1475.3
	AC	1062 (40.7%)	100 (48.5%)	1.36 (1.01–1.83)*		
	CC	236 (9%)	15 (7.3%)	0.92 (0.52–1.61)		
Dominant	AA	1313 (50.3%)	91 (44.2%)	1.00	0.091	1475.3
	AC-CC	1298 (49.7%)	115 (55.8%)	1.28 (0.96–1.70)		
Recessive	AA-AC	2375 (91%)	191 (92.7%)	1.00	0.38	1477.4
	CC	236 (9%)	15 (7.3%)	0.79 (0.46–1.36)		
Over dominant	AA-CC	1549 (59.3%)	106 (51.5%)	1.00	0.028	1473.3
	AC	1062 (40.7%)	100 (48.5%)	1.38 (1.04–1.83)*		
Log-Additive	---	---	---	1.11 (0.89–1.37)	0.36	1477.3
HWE (p value)	---	0.32	0.11	---	---	---

\*Significant odds ratio. The p value is obtained by comparison of Akaike information criterion (AIC) from different models. CVE, cardiovascular events.

**Supplemental Table S5:** Genetic polymorphism of *SPP1* rs11730582 C>T in association with CVE in CKD patients.

Model	Genotype	No CVE N = 2609 n (%)	CVE N = 206 n (%)	Odds ratio (95% CI)	p value	AIC
Co-dominant	CC	224(22.4%)	12(23.1%)	1.00	0.72	419.3
	CT	514(51.5%)	29(55.8%)	1.05 (0.53–2.10)		
	TT	260(26.1%)	11(21.1%)	0.79 (0.34–1.82)		
Dominant	CC	224(22.4%)	12(23.1%)	1.00	0.92	417.9
	CT-TT	774(77.6%)	40(76.9%)	0.96 (0.50–1.87)		
Recessive	CC-CT	738(74%)	41(78.8%)	1.00	0.42	417.3
	TT	260(26.1%)	11(21.1%)	0.76 (0.39–1.50)		
Over dominant	CC-TT	484(48.5%)	23(44.2%)	1.19 (0.68–2.08)	0.55	417.6
	CT	514(51.5%)	29(55.8%)	1.19 (0.68–2.08)		
Log-Additive	---	---	---	0.89 (0.60–1.33)	0.58	417.6
HWE (p value)	---	0.34	0.58	---	---	---

\*Significant odds ratio. The p value is obtained by comparison of Akaike information criterion (AIC) from different models.

**Supplemental Table S6:** Genetic polymorphism of *SPP1* rs28357094 G/T in association with CVE in CKD patients

Model	Genotype	No CVE N = 2609 n (%)	CVE N = 206 n (%)	Odds ratio (95% CI)	p value	AIC
Co-dominant	GG	126(6%)	8(5.3%)	1.00	0.7	1113.2
	GT	751(35.7%)	59(39.1%)	1.24 (0.58–2.65)		
	TT	1225(58.3%)	84(55.6%)	1.08 (0.51–2.28)		
Dominant	GG	126(6%)	8(5.3%)	1.00	0.72	1111.7
	GT-TT	1976(94%)	143(94.7%)	1.14 (0.55–2.38)		
Recessive	GG-GT	877(41.7%)	67(44.4%)	1.00	0.52	1111.5
	TT	1225(58.3%)	84(55.6%)	0.90 (0.64–1.25)		
Over dominant	GG-TT	1351(64.3%)	92(60.9%)	1.00	0.41	1111.2
	GT	751(35.7%)	59(39.1%)	1.15 (0.82–1.62)		
Log-Additive	---	---	---	0.95 (0.73–1.24)	0.7	1111.7
HWE (p value)	---	0.44	0.67	---	---	---

\*Significant odds ratio. The p value is obtained by comparison of Akaike information criterion (AIC) from different models.