

Table S13. Influence of gene polymorphisms on progression-free survival of 127 CRC patients.

Gen	SNPs	Genotype	PFS								
			N	Events	MST (mo)	CI _{95%}	Log-rank p-value	Ref. cat.	Univariate Cox Model		
									HR	CI _{95%}	p-value
VDR	rs1544410 (BsmI)	TT	33	16	73.3	37.0-NR	0.900	-	-	-	-
		CT	47	21	60.6	30.6-NR			-	-	-
		CC	47	19	75.0	35.0-NR			-	-	-
		T	80	37	73.3	38.6-NR	0.900	-	-	-	-
		C	94	40	63.3	38.1-NR	0.700	-	-	-	-
	rs11568820 (Cdx2)	TT	6	1	NR	16.7-NR	0.700	-	-	-	-
		CT	45	23	63.3	41.0-NR			-	-	-
		CC	76	32	105.2	35.0-NR			-	-	-
		T	51	24	63.3	41.0-NR	0.800	-	-	-	-
		C	121	55	63.3	41.0-NR	0.500	-	-	-	-
	rs2228570 (FokI)	GG	52	26	55.1	23.7-NR	0.050	AG	1.650	0.934-2.916	0.085
		AG	63	22	125.4	47.4-NR			1	-	-
		AA	12	8	19.8	6.23-NR			2.542	1.126-5.742	0.025
		G	115	48	75.0	43.8-NR	0.070	G	1.994	0.939-4.232	0.072
		A	75	30	105.2	41.0-NR	0.200	-	-	-	-
	rs7975232 (ApaI)	AA	48	27	43.8	34.5-NR	0.100	-	-	-	-
		AC	51	19	125.9	30.2-NR			-	-	-
		CC	28	10	NR	51.1-NR			-	-	-
		A	99	46	60.6	38.1-NR	0.200	-	-	-	-
	rs731236 (TaqI)	C	79	29	125.9	55.1-NR	0.040	C	1.732	1.019-2.945	0.042
		GG	27	15	41.0	18.6-NR	0.200	-	-	-	-
		AG	48	19	125.4	59.2-NR			-	-	-
		AA	52	22	63.3	30.2-NR			-	-	-
		G	75	34	73.3	43.8-NR	0.900	-	-	-	-
CYP27B1	rs4646536	A	100	41	105.0	51.1-NR	0.090	A	1.670	0.916-3.046	0.094
		AA	71	35	63.3	35.0-NR	0.800	-	-	-	-
		AG	42	15	105.2	37.0-NR			-	-	-
		GG	14	6	NR	17.7-NR			-	-	-
		A	113	50	73.3	41.0-NR	0.800	-	-	-	-
	rs3782130	G	56	21	105.2	38.6-NR	0.500	-	-	-	-
		CC	13	6	59.2	8.5-NR	0.700	-	-	-	-
		CG	43	15	105.2	38.6-NR			-	-	-
		GG	71	35	63.3	35.0-NR			-	-	-
		C	56	21	105.2	38.6-NR	0.400	-	-	-	-
	rs10877012	G	114	50	73.3	41.0-NR	0.900	-	-	-	-
		TT	12	6	59.2	8.5-NR	0.400	-	-	-	-
		GT	45	15	105.2	38.6-NR			-	-	-
		GG	70	35	55.1	35.0-NR			-	-	-
		T	57	21	105.2	38.6-NR	0.300	-	-	-	-
	rs703842	G	115	50	73.3	41.0-NR	0.600	-	-	-	-
		GG	14	6	NR	17.7-NR	0.800	-	-	-	-
		AG	42	15	105.2	37.0-NR			-	-	-
		AA	71	35	63.3	35.0-NR			-	-	-
		G	56	21	105.2	38.6-NR	0.500	-	-	-	-

CYP24A1	rs6068816	CC	89	39	63.3	43.8-NR	0.010	CT	1.241	0.619-2.489	0.543
		CT	28	10	NR	38.6-NR			1	-	-
		TT	10	7	14.2	3.1-NR			3.585	1.355-9.483	0.010
		C	117	49	75.0	47.4-NR	0.004	C	3.030	1.361-6.743	0.006
		T	38	17	75.0	19.8-NR	0.600	-	-	-	-
	rs4809957	GG	8	2	NR	34.5-NR	0.800	-	-	-	-
		GA	37	19	38.6	19.8-NR					
		AA	82	35	75.0	47.4-NR					
		G	45	21	51.1	23.7-NR	0.600	-	-	-	-
		A	119	54	63.3	41.0-NR	0.800	-	-	-	-
CYP2R1	rs10741657	GG	57	25	63.3	43.8-NR	1	-	-	-	-
		AG	56	23	125.4	35.0-NR					
		AA	14	8	60.6	18.6-NR					
		G	113	48	73.3	41.0-NR	0.900	-	-	-	-
		A	70	31	75.0	35.0-NR	1	-	-	-	-
GC	rs7041	AA	27	8	NR	60.6-NR	0.004	CC	1.149	0.440-2.997	0.777
		AC	71	39	38.1	18.5-73.3			2.742	1.321-5.691	0.007
		CC	29	9	125.9	105.8-NR			1	-	-
		A	98	47	55.1	37.0-NR	0.030	CC	2.226	1.083-4.574	0.029
		C	100	48	55.1	37.0-NR	0.100	-	-	-	-
HR, hazard ratio. IC _{95%} , 95% confidence interval. MST, median survival time (months). NR, not reached.											