

Supplementary Material

Table S1: Minor allele frequencies of the studied SNPs

	MAF in Our Studied Population	Global MAF ^s	Highest Population MAF ^s
MALAT1.rs3200401	T = 0.34	T = 0.14	T = 0.31
PVT1.rs13255292	T = 0.42	T = 0.20	T = 0.43

MAF, minor allele frequency. ^saccording to Ensembl release 102 - November 2020 ©.

Table S2: Hardey-Winberg equilibrium of rs3200401 and rs13255292in CRC group

MALAT.rs3200401.C.T. Exact Test for Hardy-Weinberg Equilibrium (n = 280)						
	CC	CT	TT	C	T	<i>p</i> Value
All subjects	73	110	57	256	224	0.24
CONTROL	42	48	10	132	68	0.66
CRC	31	62	47	124	156	0.23
PVT.rs13255292.C.T. Exact Test for Hardy-Weinberg Equilibrium (n = 280)						
	CC	CT	TT	C	T	<i>p</i> Value
All subjects	95	117	28	307	173	0.4
CONTROL	31	55	14	117	83	0.22
CRC	64	62	14	190	90	1

Hardey-Winberg equilibrium was done by chi-square test. $p < 0.05$ means statistical significance. AIC: Akaike's Information Criteria, BIC: Bayesian Information Criteria.

Table S3: MALAT1 rs3200401 CT association with control and AP groups

MALAT1 rs3200401 CT Association with Control and AP Groups (n = 140, Adjusted by AGE+GENDER)							
Model	Genotype	CONTROL	AP	OR (95% CI)	P-value	AIC	BIC
Codominant	C/C	42 (42%)	17 (42.5%)	1.00	0.26	167	181.7
	C/T	48 (48%)	15 (37.5%)	0.94 (0.41–2.20)			
	T/T	10 (10%)	8 (20%)	2.37 (0.76–7.37)			
Dominant	C/C	42 (42%)	17 (42.5%)	1.00	0.65	167.5	179.2
	C/T-T/T	58 (58%)	23 (57.5%)	1.20 (0.55-2.60)			
Recessive	C/C-C/T	90 (90%)	32 (80%)	1.00	0.1	165	176.7
	T/T	10 (10%)	8 (20%)	2.44 (0.85–6.98)			
Overdominant	C/C-T/T	52 (52%)	25 (62.5%)	1.00	0.48	167.2	178.9
	C/T	48 (48%)	15 (37.5%)	0.76 (0.35–1.64)			
Log-additive	---	---	---	1.38 (0.80–2.41)	0.25	166.3	178.1

SNPs association was done using SNPstat software analysis. $p < 0.05$ means statistical significance. AIC: Akaike's Information Criteria, BIC: Bayesian Information Criteria.

Table S4: *PVT1 rs13255292* CT association with control and AP groups

<i>PVT1 rs13255292</i> CT Association with Control and AP Groups(<i>n</i> = 140, Adjusted by AGE+GENDER)							
Model	Genotype	CONTROL	AP	OR (95% CI)	P-value	AIC	BIC
Codominant	CC	31 (31%)	16 (40%)	1.00	0.7	169	183.7
	CT	55 (55%)	20 (50%)	0.79 (0.35–1.79)			
	TT	14 (14%)	4 (10%)	0.60 (0.16–2.20)			
Dominant	CC	31 (31%)	16 (40%)	1.00	0.47	167.1	178.9
	CT-TT	69 (69%)	24 (60%)	0.75 (0.34–1.65)			
Recessive	CC-CT	86 (86%)	36 (90%)	1.00	0.53	167.3	179
	TT	14 (14%)	4 (10%)	0.69 (0.20–2.31)			
Overdominant	CC-TT	45 (45%)	20 (50%)	1.00	0.78	167.6	179.4
	CT	55 (55%)	20 (50%)	0.90 (0.42–1.92)			
Log-additive	---	---	---	0.78 (0.43–1.40)	0.4	167	178.7

SNPs association was done using SNPstat software analysis. $p < 0.05$ means statistical significance. AIC: Akaike's Information Criteria, BIC: Bayesian Information Criteria.

Table S5: Correlation between the studied SNPs and clinicopathological factors

<i>MALAT1 rs3200401</i> CT Association with Response Anatominal Site (<i>n</i> = 140, Adjusted by AGE+Age)								<i>PVT1 rs13255292</i> CT Association with Response Anatominal Site (<i>n</i> = 140, Adjusted by AGE+Age)							
Model	Genotype	Rectum	Colon	OR (95% CI)	<i>p</i> Value	AIC	BIC	Model	Genotype	Rectum	Colon	OR (95% CI)	<i>p</i> Value	AIC	BIC
Codominant	T/T	11 (29.7%)	36 (35%)	1	0.54	168.1	179.8	Codominant	C/C	14 (37.8%)	50 (48.5%)	1	0.27	166.6	178.4
	C/T	19 (51.4%)	43 (41.8%)	0.69 (0.29–1.63)					C/T	17 (46%)	45 (43.7%)	0.72 (0.32–1.64)			
	C/C	7 (18.9%)	24 (23.3%)	1.12 (0.38–3.36)					T/T	6 (16.2%)	8 (7.8%)	0.36 (0.11–1.23)			
Dominant	T/T	11 (29.7%)	36 (35%)	1	0.59	167	175.8	Dominant	C/C	14 (37.8%)	50 (48.5%)	1	0.24	165.9	174.7
	C/T-C/C	26 (70.3%)	67 (65%)	0.80 (0.35–1.81)					C/T-T/T	23 (62.2%)	53 (51.5%)	0.63 (0.29–1.36)			
Recessive	T/T-C/T	30 (81.1%)	79 (76.7%)	1	0.48	166.8	175.6	Recessive	C/C-C/T	31 (83.8%)	95 (92.2%)	1	0.15	165.3	174.1
	C/C	7 (18.9%)	24 (23.3%)	1.40 (0.54–3.66)					T/T	6 (16.2%)	8 (7.8%)	0.43 (0.14–1.34)			
Overdominant	T/T-C/C	18 (48.6%)	60 (58.2%)	1	0.28	166.1	174.9	Overdominant	C/C-T/T	20 (54%)	58 (56.3%)	1	0.78	167.2	176
	C/T	19 (51.4%)	43 (41.8%)	0.66 (0.31–1.40)					C/T	17 (46%)	45 (43.7%)	0.90 (0.42–1.91)			

Log-Additive	---	---	---	1.01 (0.60–1.69)	0.97	167.3	176.1	Log-Additive	---	---	---	0.63 (0.36–1.12)	0.12	164.8	173.7
MALAT1 rs3200401 CT Association with Stage (<i>n</i> = 140, Adjusted by AGE+Age)								PVT1 rs13255292 CT Association with Stage (<i>n</i> = 140, Adjusted by AGE+Age)							
Model	Genotype	Stage I+II	Stage=III+IV	OR (95% CI)	<i>p</i> value	AIC	BIC	Model	Genotype	Stage I+II	Stage=III+IV	OR (95% CI)	<i>p</i> Value	AIC	BIC
Codominant	T/T	32 (36.4%)	15 (28.9%)	1	0.33	189.9	201.7	Codominant	C/C	38 (43.2%)	26 (50%)	1	0.76	191.6	203.4
	C/T	35 (39.8%)	27 (51.9%)	1.66 (0.75–3.68)					C/T	41 (46.6%)	21 (40.4%)	0.76 (0.37–1.58)			
	C/C	21 (23.9%)	10 (19.2%)	0.94 (0.35–2.53)					T/T	9 (10.2%)	5 (9.6%)	0.83 (0.25–2.76)			
Dominant	T/T	32 (36.4%)	15 (28.9%)	1	0.38	189.4	198.2	Dominant	C/C	38 (43.2%)	26 (50%)	1	0.47	189.6	198.5
	C/T-C/C	56 (63.6%)	37 (71.2%)	1.39 (0.66–2.92)					C/T-T/T	50 (56.8%)	26 (50%)	0.77 (0.39–1.54)			
Recessive	T/T-C/T	67 (76.1%)	42 (80.8%)	1	0.42	189.5	198.3	Recessive	C/C-C/T	79 (89.8%)	47 (90.4%)	1	0.92	190.1	199
	C/C	21 (23.9%)	10 (19.2%)	0.70 (0.30–1.67)					T/T	9 (10.2%)	5 (9.6%)	0.94 (0.30–2.99)			
Overdominant	T/T-C/C	53 (60.2%)	25 (48.1%)	1	0.14	187.9	196.8	Overdominant	C/C-T/T	47 (53.4%)	31 (59.6%)	1	0.5	189.7	198.5
	C/T	35 (39.8%)	27 (51.9%)	1.70 (0.84–3.42)					C/T	41 (46.6%)	21 (40.4%)	0.79 (0.39–1.58)			
Log-Additive	---	---	---	1.03 (0.64–1.64)	0.91	190.1	199	Log-Additive	---	---	---	0.85 (0.50–1.45)	0.55	189.8	198.6
MALAT1 rs3200401 CT Association with Response Lymphnode Status (<i>n</i> = 140, Adjusted by AGE+Age)								PVT1 rs13255292 CT Association with Response Lymphnode Status (<i>n</i> = 140, Adjusted by AGE+Age)							
Model	Genotype	Absent	Present	OR (95% CI)	<i>p</i> Value	AIC	BIC	Model	Genotype	Absent	Present	OR (95% CI)	<i>p</i> Value	AIC	BIC
Codominant	T/T	25 (28.4%)	22 (42.3%)	1	0.065	186.9	198.7	Codominant	C/C	38 (43.2%)	26 (50%)	1	0.75	191.8	203.6
	C/T	39 (44.3%)	23 (44.2%)	0.67 (0.31–1.46)					C/T	41 (46.6%)	21 (40.4%)	0.76 (0.37–1.57)			
	C/C	24 (27.3%)	7 (13.5%)	0.30 (0.11–0.86)					T/T	9 (10.2%)	5 (9.6%)	0.82 (0.25–2.74)			
Dominant	T/T	25 (28.4%)	22 (42.3%)	1	0.086	187.5	196.3	Dominant	C/C	38 (43.2%)	26 (50%)	1	0.46	189.9	198.7
	C/T-C/C	63 (71.6%)	30 (57.7%)	0.53 (0.26–1.09)					C/T-T/T	50 (56.8%)	26 (50%)	0.77 (0.39–1.54)			
Recessive	T/T-C/T	64 (72.7%)	45 (86.5%)	1	0.035	185.9	194.8	Recessive	C/C-C/T	79 (89.8%)	47 (90.4%)	1	0.92	190.4	199.2

	C/C	24 (27.3%)	7 (13.5%)	0.38 (0.15–0.98)					T/T	9 (10.2%)	5 (9.6%)	0.94 (0.30–2.98)			
Overdominant	T/T-C/C	49 (55.7%)	29 (55.8%)	1	0.96	190.4	199.2	Overdominant	C/C-T/T	47 (53.4%)	31 (59.6%)	1	0.5	189.9	198.8
	C/T	39 (44.3%)	23 (44.2%)	1.02 (0.51–2.04)					C/T	41 (46.6%)	21 (40.4%)	0.79 (0.39–1.58)			
Log-Additive	---	---	---	0.57 (0.35–0.93)	0.023	185.2	194	Log-Additive	---	---	---	0.85 (0.50–1.44)	0.54	190	198.8
MALAT1 rs3200401 CT Association with Response Metastasis (n = 140, adjusted by AGE+Age)								PVT rs13255292 CT Association with Response Metastasis (n = 140, Adjusted by AGE+Age)							
Model	Genotype	Absent	Present	OR (95% CI)	p Value	AIC	BIC	Model	Genotype	Absent	Present	OR (95% CI)	p Value	AIC	BIC
Codominant	T/T	36 (31%)	11 (45.8%)	1	0.35	133.8	145.5	Codominant	C/C	52 (44.8%)	12 (50%)	1	0.91	135.7	147.4
	C/T	53 (45.7%)	9 (37.5%)	0.56 (0.21–1.49)					C/T	52 (44.8%)	10 (41.7%)	0.85 (0.34–2.15)			
	C/C	27 (23.3%)	4 (16.7%)	0.45 (0.13–1.59)					T/T	12 (10.3%)	2 (8.3%)	0.74 (0.15–3.76)			
Dominant	T/T	36 (31%)	11 (45.8%)	1	0.16	131.9	140.7	Dominant	C/C	52 (44.8%)	12 (50%)	1	0.68	133.7	142.5
	C/T-C/C	80 (69%)	13 (54.2%)	0.52 (0.21–1.28)					C/T-T/T	64 (55.2%)	12 (50%)	0.83 (0.34–2.01)			
Recessive	T/T-C/T	89 (76.7%)	20 (83.3%)	1	0.39	133.1	142	Recessive	C/C-C/T	104 (89.7%)	22 (91.7%)	1	0.77	133.8	142.6
	C/C	27 (23.3%)	4 (16.7%)	0.60 (0.19–1.96)					T/T	12 (10.3%)	2 (8.3%)	0.80 (0.17–3.82)			
Overdominant	T/T-C/C	63 (54.3%)	15 (62.5%)	1	0.5	133.4	142.3	Overdominant	C/C-T/T	64 (55.2%)	14 (58.3%)	1	0.81	133.8	142.6
	C/T	53 (45.7%)	9 (37.5%)	0.73 (0.30–1.82)					C/T	52 (44.8%)	10 (41.7%)	0.90 (0.37–2.19)			
Log-Additive	---	---	---	0.64 (0.35–1.20)	0.16	131.9	140.7	Log-additive	---	---	---	0.86 (0.43–1.70)	0.66	133.7	14

Correlation was done using SNPstat software analysis. $p < 0.05$ means statistical significance. AIC: Akaike's Information Criteria, BIC: Bayesian Information Criteria.

Table S6: Correlation between the studied parameters and clinicopathological factors

Spearman Correlation	MALAT1	miRNA-101	PVT1	miRNA-186	E-Cadherin	Age	Gender	Anatominal Site	Stage	Lymphnode Status	Metastasis
MALAT1	1.0000	−0.4025	0.3608	−0.3208	−0.3236	0.0953	0.1020	0.1925	0.3340	0.3600	0.3062
miRNA-101	−0.4025	1.0000	0.0132	0.0238	0.3559	−0.0532	0.0071	0.0185	−0.4132	−0.3390	−0.3377
PVT1	0.3608	0.0132	1.0000	−0.4688	−0.3078	0.1436	0.1685	−0.1660	0.4412	0.3181	0.3018
miRNA-186	−0.3208	0.0238	−0.4688	1.0000	0.5002	−0.0440	−0.1413	−0.0266	−0.2976	−0.1790	−0.4011

E-cadherin	-0.1947	0.2302	-0.1831	0.1299	1.0000	0.0247	0.2519	-0.1096	-0.1618	-0.2078	-0.3953
Age	0.0953	-0.0532	0.1436	-0.0440	-0.1060	1.0000	-0.2072	-0.0601	0.0760	0.0545	0.0760
Gender	0.1020	0.0071	0.1685	-0.1413	0.0751	-0.2072	1.0000	-0.1280	0.0132	0.0132	0.0170
Anatominal site	0.1925	0.0185	-0.1660	-0.0266	0.0388	-0.0601	-0.1280	1.0000	-0.2098	-0.1427	0.0577
Stage	0.3348	-0.4132	0.4412	-0.3976	-0.2878	0.0760	0.0132	-0.2098	1.0000	0.6635	0.3172
Lymphnode status	0.3348	-0.3390	0.3181	-0.2790	-0.2288	0.0545	0.0132	-0.1427	0.6635	1.0000	0.4740
Metastasis	0.3062	-0.3377	0.3018	-0.4611	-0.4483	0.0760	0.0170	0.0577	0.3172	0.4740	1.0000
Correlations p Value	MALAT1	miRNA-101	PVT1	miRNA-186	E-Cadherin	Age	Gender	Anatominal Site	Stage	Lymphnode Status	Metastasis
MALAT1		0.0061	0.0149	0.0435	0.0343	0.5285	0.5002	0.2000	0.0231	0.0191	0.0385
miRNA-101	0.0061		0.9323	0.8856	0.0207	0.7287	0.9633	0.9040	0.0048	0.0227	0.0233
PVT1	0.0149	0.9323		0.0019	0.0447	0.3411	0.2629	0.2703	0.0021	0.0312	0.0415
miRNA-186	0.0435	0.8856	0.00199		0.0012	0.7849	0.3780	0.8689	0.0588	0.2627	0.0094
E-cadherin	0.2108	0.1424	0.23418	0.42422		0.8737	0.0991	0.4789	0.2939	0.1759	0.0079
Age	0.5285	0.7287	0.34114	0.78489	0.4882		0.0140	0.4805	0.3724	0.5226	0.3723
Gender	0.5002	0.9633	0.26291	0.37805	0.6238	0.0140		0.1318	0.8768	0.8768	0.8424
Anatominal site	0.2000	0.9040	0.27029	0.86892	0.8000	0.4805	0.1318		0.0129	0.0925	0.4982
Stage	0.0230	0.0048	0.00215	0.05882	0.0552	0.3724	0.8768	0.0129		< 0.0001	< 0.0001
Lymphnode status	0.0230	0.0227	0.03119	0.26269	0.1305	0.5226	0.8768	0.0925	< 0.0001		< 0.0001
Metastasis	0.0385	0.0233	0.04150	0.00935	0.0020	0.3723	0.8424	0.4982	< 0.0001	< 0.0001	

Correlation was done by spearman correlation. $p < 0.05$ means statistical significance.