

Table SI. Univariate analysis of the prognostic factors related to colorectal cancer (log-rank test).

Variable	Patients (n)	Death n (%)	Mean OS ^a (month)	P-value
Age				
>65	72	25 (34.7)	77.9	0.114
≤65	109	26 (23.9)	87.0	
Sex				
Male	99	32 (32.3)	80.3	0.191
Female	82	19 (23.2)	87.5	
Tumor size				
>5 cm	79	24 (30.4)	81.4	0.706
≤5 cm	102	27 (26.5)	84.8	
Tumor classification				
Tubular adenocarcinoma	143	34 (23.8)	86.9	0.004
Mucinous adenocarcinoma	28	15 (53.6)	59.5	
Others	10	2 (20.0)	87.0	
Vascular & lymphatic infiltration				
No	106	19 (17.9)	93.1	<0.001
Yes	75	32 (42.7)	66.2	
Perineurium invasion				
No	140	29 (20.7)	90.6	<0.001
Yes	41	22 (53.7)	57.3	
Tumor location				
Rectum	86	26 (30.2)	75.9	0.805
Colon	95	25 (26.3)	84.6	
Tumor differentiation				
Medium & high differentiation	147	39 (26.5)	84.3	0.482
Poorly differentiated	34	12 (35.3)	79.7	
TNM stage				
I-II	96	16 (16.7)	94.2	<0.001
III	85	35 (41.2)	71.1	
Programmed death ligand 1				
Negative	150	36 (24.0)	88.2	0.001
Positive	31	15 (1.2)	51.9	

For most characteristics, less than half patients were dead so mean OS time was presented for most of the median OS that could not be calculated. OS, overall survival time.

Table SII. List of genes co-expressed with PD-L1 in CRC from The Cancer Genome Atlas.

Correlated gene	Cytoband	Spearman's r	P-value	Q-value
GBP1	1p22.2	0.8303	2.24x10 ⁻⁶³	4.33x10 ⁻⁵⁹
STAT1	2q32.2	0.7929	5.70x10 ⁻⁵⁴	5.52x10 ⁻⁵⁰
GBP5	1p22.2	0.7904	1.99x10 ⁻⁵³	1.28x10 ⁻⁴⁹
GBP4	1p22.2	0.7775	1.20x10 ⁻⁵⁰	5.81x10 ⁻⁴⁷
SAMD9L	7q21.2	0.7718	1.72x10 ⁻⁴⁹	6.64x10 ⁻⁴⁶
PARP9	3q21.1	0.7683	8.53x10 ⁻⁴⁹	2.75x10 ⁻⁴⁵
CXCL10	4q21.1	0.7508	1.78x10 ⁻⁴⁵	4.92x10 ⁻⁴²
LCP2	5q35.1	0.7470	8.46x10 ⁻⁴⁵	2.05x10 ⁻⁴¹
CXCL9	4q21.1	0.7427	4.92x10 ⁻⁴⁴	1.06x10 ⁻⁴⁰
IFIT3	10q23.31	0.7412	8.88x10 ⁻⁴⁴	1.72x10 ⁻⁴⁰
PDCD1LG2	9p24.1	0.7344	1.28x10 ⁻⁴²	2.26x10 ⁻³⁹
CCL4	17q12	0.7261	3.02x10 ⁻⁴¹	4.87x10 ⁻³⁸
PTPRC	1q31.3-q32.1	0.7224	1.18x10 ⁻⁴⁰	1.76x10 ⁻³⁷
IL2RA	10p15.1	0.7209	2.09x10 ⁻⁴⁰	2.89x10 ⁻³⁷
LCP1	13q14.13	0.7186	4.80x10 ⁻⁴⁰	6.19x10 ⁻³⁷
IDO1	8p11.21	0.7180	5.92x10 ⁻⁴⁰	7.17x10 ⁻³⁷
PLEK	2p14	0.7148	1.84x10 ⁻³⁹	2.10x10 ⁻³⁶
CD80	3q13.33	0.7043	7.05x10 ⁻³⁸	7.58x10 ⁻³⁵
IFNG	12q15	0.7021	1.50x10 ⁻³⁷	1.53x10 ⁻³⁴
MMP12	11q22.2	0.6980	5.87x10 ⁻³⁷	5.68x10 ⁻³⁴
CD86	3q13.33	0.6972	7.74x10 ⁻³⁷	7.14x10 ⁻³⁴
TNFSF13B	13q33.3	0.6942	2.04x10 ⁻³⁶	1.80x10 ⁻³³
CYBB	Xp21.1-p11.4	0.6891	1.05x10 ⁻³⁵	8.82x10 ⁻³³
CCR5	3p21.31	0.6889	1.11x10 ⁻³⁵	8.97x10 ⁻³³
FCER1G	1q23.3	0.6886	1.23x10 ⁻³⁵	9.53x10 ⁻³³
APOL6	22q12.3	0.6881	1.43x10 ⁻³⁵	1.06x10 ⁻³²
FCGR3A	1q23.3	0.6869	2.12x10 ⁻³⁵	1.48x10 ⁻³²
SLC26A3	7q22.3-q31.1	0.6869	2.14x10 ⁻³⁵	1.48x10 ⁻³²
ICOS	2q33.2	0.6849	4.03x10 ⁻³⁵	2.69x10 ⁻³²
RASGRP1	15q14	0.6840	5.24x10 ⁻³⁵	3.38x10 ⁻³²
HAVCR2	5q33.3	0.6839	5.51x10 ⁻³⁵	3.44x10 ⁻³²
IL2RB	22q12.3	0.6837	5.71x10 ⁻³⁵	3.45x10 ⁻³²
BIRC3	11q22.2	0.6801	1.77x10 ⁻³⁴	1.04x10 ⁻³¹
CLEC7A	12p13.2	0.6776	3.81x10 ⁻³⁴	2.17x10 ⁻³¹
FASLG	1q24.3	0.6773	4.10x10 ⁻³⁴	2.27x10 ⁻³¹
IRF1	5q31.1	0.6764	5.53x10 ⁻³⁴	2.97x10 ⁻³¹
TNFRSF9	1p36.23	0.6761	6.07x10 ⁻³⁴	3.18x10 ⁻³¹
OAS2	12q24.13	0.6751	7.99x10 ⁻³⁴	4.07x10 ⁻³¹
PARP14	3q21.1	0.6734	1.36x10 ⁻³³	6.75x10 ⁻³¹
TLR8	Xp22.2	0.6719	2.12x10 ⁻³³	1.03x10 ⁻³⁰
MNDA	1q23.1	0.6697	4.09x10 ⁻³³	1.93x10 ⁻³⁰
FYB1	5p13.1	0.6695	4.36x10 ⁻³³	2.01x10 ⁻³⁰
SAMSN1	21q11.2	0.6686	5.61x10 ⁻³³	2.53x10 ⁻³⁰
XAF1	17p13.1	0.6683	6.06x10 ⁻³³	2.67x10 ⁻³⁰
CCR1	3p21.31	0.6683	6.20x10 ⁻³³	2.67x10 ⁻³⁰
TFEC	7q31.2	0.6679	6.99x10 ⁻³³	2.94x10 ⁻³⁰
CIITA	16p13.13	0.6667	9.94x10 ⁻³³	4.10x10 ⁻³⁰
WARS	14q32.2	0.6655	1.39x10 ⁻³²	5.60x10 ⁻³⁰
1-Mar	4q32.2-q32.3	0.6646	1.80x10 ⁻³²	7.11x10 ⁻³⁰
PLA2G7	6p12.3	0.6634	2.53x10 ⁻³²	9.82x10 ⁻³⁰
IKZF1	7p12.2	0.6619	3.90x10 ⁻³²	1.48x10 ⁻²⁹
CD2	1p13.1	0.6619	3.97x10 ⁻³²	1.48x10 ⁻²⁹
RARRES3	11q12.3	0.6611	4.95x10 ⁻³²	1.81x10 ⁻²⁹
IFIT2	10q23.31	0.6605	5.92x10 ⁻³²	2.12x10 ⁻²⁹
GZMA	5q11.2	0.6595	7.75x10 ⁻³²	2.73x10 ⁻²⁹
SLA	8q24.22	0.6590	8.85x10 ⁻³²	3.06x10 ⁻²⁹

Table SII. Continued.

Correlated gene	Cytoband	Spearman's r	P-value	Q-value
KYNU	2q22.2	0.6579	1.22x10 ⁻³¹	4.15x10 ⁻²⁹
TAGAP	6q25.3	0.6570	1.58x10 ⁻³¹	5.29x10 ⁻²⁹
STX11	6q24.2	0.6568	1.67x10 ⁻³¹	5.47x10 ⁻²⁹
GNLY	2p11.2	0.6564	1.86x10 ⁻³¹	6.00x10 ⁻²⁹
BCL2A1	15q25.1	0.6563	1.90x10 ⁻³¹	6.04x10 ⁻²⁹
TRIM22	11p15.4	0.6561	2.02x10 ⁻³¹	6.31x10 ⁻²⁹
STAT2	12q13.3	0.6530	4.84x10 ⁻³¹	1.49x10 ⁻²⁸
APOBEC3G	22q13.1	0.6528	5.06x10 ⁻³¹	1.53x10 ⁻²⁸
TLR1	4p14	0.6525	5.49x10 ⁻³¹	1.64x10 ⁻²⁸
FCGR2A	1q23.3	0.6522	6.01x10 ⁻³¹	1.76x10 ⁻²⁸
SP140	2q37.1	0.6518	6.71x10 ⁻³¹	1.94x10 ⁻²⁸
JAK2	9p24.1	0.6516	7.08x10 ⁻³¹	2.02x10 ⁻²⁸
ITK	5q33.3	0.6501	1.06x10 ⁻³⁰	2.95x10 ⁻²⁸
APOL4	22q12.3	0.6501	1.06x10 ⁻³⁰	2.95x10 ⁻²⁸
CXCL11	4q21.1	0.6500	1.10x10 ⁻³⁰	3.00x10 ⁻²⁸
FPR3	19q13.41	0.6485	1.64x10 ⁻³⁰	4.42x10 ⁻²⁸
TIGIT	3q13.31	0.6479	1.96x10 ⁻³⁰	5.20x10 ⁻²⁸
APBB1IP	10p12.1	0.6476	2.11x10 ⁻³⁰	5.52x10 ⁻²⁸
RASSF5	1q32.1	0.6475	2.16x10 ⁻³⁰	5.58x10 ⁻²⁸
APOL3	22q12.3	0.6462	3.11x10 ⁻³⁰	7.94x10 ⁻²⁸
NCKAP1L	12q13.13-q13.2	0.6448	4.46x10 ⁻³⁰	1.12x10 ⁻²⁷
STAT4	2q32.2-q32.3	0.6445	4.94x10 ⁻³⁰	1.23x10 ⁻²⁷
SAMHD1	20q11.23	0.6441	5.40x10 ⁻³⁰	1.32x10 ⁻²⁷
IL18RAP	2q12.1	0.6438	5.91x10 ⁻³⁰	1.43x10 ⁻²⁷
HLA-DMA	6p21.32	0.6429	7.47x10 ⁻³⁰	1.79x10 ⁻²⁷
GIMAP4	7q36.1	0.6419	9.73x10 ⁻³⁰	2.30x10 ⁻²⁷
EVI1B	17q11.2	0.6413	1.16x10 ⁻²⁹	2.70x10 ⁻²⁷
LAP3	4p15.32	0.6405	1.40x10 ⁻²⁹	3.24x10 ⁻²⁷
CD53	1p13.3	0.6403	1.49x10 ⁻²⁹	3.39x10 ⁻²⁷
SLAMF8	1q23.2	0.6402	1.52x10 ⁻²⁹	3.42x10 ⁻²⁷
CD226	18q22.2	0.6397	1.76x10 ⁻²⁹	3.91x10 ⁻²⁷
DOCK2	5q35.1	0.6394	1.89x10 ⁻²⁹	4.15x10 ⁻²⁷
IFIH1	2q24.2	0.6377	2.94x10 ⁻²⁹	6.40x10 ⁻²⁷
CD96	3q13.13-q13.2	0.6359	4.78x10 ⁻²⁹	1.03x10 ⁻²⁶
FAM49A	2p24.2	0.6352	5.74x10 ⁻²⁹	1.22x10 ⁻²⁶
CD3G	11q23.3	0.6343	7.23x10 ⁻²⁹	1.52x10 ⁻²⁶
CD84	1q23.3	0.6341	7.47x10 ⁻²⁹	1.56x10 ⁻²⁶
GPR65	14q31.3	0.6341	7.55x10 ⁻²⁹	1.56x10 ⁻²⁶
BTN3A1	6p22.2	0.6333	9.27x10 ⁻²⁹	1.89x10 ⁻²⁶
CMKLR1	12q23.3	0.6331	9.67x10 ⁻²⁹	1.94x10 ⁻²⁶
NCF2	1q25.3	0.6331	9.71x10 ⁻²⁹	1.94x10 ⁻²⁶
HCLS1	3q13.33	0.6331	9.88x10 ⁻²⁹	1.95x10 ⁻²⁶
USP18	22q11.21	0.6330	1.00x10 ⁻²⁸	1.96x10 ⁻²⁶
PRKCB	16p12.2-p12.1	0.6322	1.22x10 ⁻²⁸	2.36x10 ⁻²⁶
GVINP1	11p15.4	0.6321	1.25x10 ⁻²⁸	2.40x10 ⁻²⁶
CCL4L1	17q12	0.6320	1.28x10 ⁻²⁸	2.44x10 ⁻²⁶
DOCK8	9p24.3	0.6315	1.48x10 ⁻²⁸	2.78x10 ⁻²⁶
IFIT5	10q23.31	0.6300	2.14x10 ⁻²⁸	3.98x10 ⁻²⁶
TBX21	17q21.32	0.6287	2.98x10 ⁻²⁸	5.49x10 ⁻²⁶
SLAMF7	1q23.3	0.6286	3.05x10 ⁻²⁸	5.54x10 ⁻²⁶
ICAM1	19p13.2	0.6286	3.08x10 ⁻²⁸	5.54x10 ⁻²⁶
ARHGAP30	1q23.3	0.6286	3.09x10 ⁻²⁸	5.54x10 ⁻²⁶
FCGR3B	1q23.3	0.6277	3.85x10 ⁻²⁸	6.85x10 ⁻²⁶
LRRC8C	1p22.2	0.6266	5.16x10 ⁻²⁸	9.08x10 ⁻²⁶
SRGN	10q22.1	0.6253	7.04x10 ⁻²⁸	1.23x10 ⁻²⁵
ARHGAP25	2p13.3	0.6238	1.02x10 ⁻²⁷	1.76x10 ⁻²⁵

Table SII. Continued.

Correlated gene	Cytoband	Spearman's r	P-value	Q-value
LILRA6	19q13.42	0.6238	1.03x10 ⁻²⁷	1.77x10 ⁻²⁵
CLEC4A	12p13.31	0.6236	1.07x10 ⁻²⁷	1.82x10 ⁻²⁵
UBE2L6	11q12.1	0.6226	1.37x10 ⁻²⁷	2.31x10 ⁻²⁵
TRAF3IP3	1q32.2	0.6223	1.49x10 ⁻²⁷	2.49x10 ⁻²⁵
DOCK10	2q36.2	0.6216	1.76x10 ⁻²⁷	2.91x10 ⁻²⁵
DDX58	9p21.1	0.6214	1.88x10 ⁻²⁷	3.09x10 ⁻²⁵
IGSF6	16p12.2	0.6207	2.20x10 ⁻²⁷	3.58x10 ⁻²⁵
DDX60	4q32.3	0.6202	2.52x10 ⁻²⁷	4.07x10 ⁻²⁵
PLXNC1	12q22	0.6194	3.04x10 ⁻²⁷	4.87x10 ⁻²⁵
SAMD9	7q21.2	0.6184	3.93x10 ⁻²⁷	6.23x10 ⁻²⁵
FCGR2C	1q23.3	0.6181	4.23x10 ⁻²⁷	6.66x10 ⁻²⁵
BTN3A3	6p22.2	0.6177	4.58x10 ⁻²⁷	7.15x10 ⁻²⁵
CD74	5q33.1	0.6177	4.65x10 ⁻²⁷	7.21x10 ⁻²⁵
MPEG1	11q12.1	0.6173	5.10x10 ⁻²⁷	7.84x10 ⁻²⁵
CCL5	17q12	0.6166	6.07x10 ⁻²⁷	9.25x10 ⁻²⁵
SUCNR1	3q25.1	0.6159	7.08x10 ⁻²⁷	1.07x10 ⁻²⁴
CD300LF	17q25.1	0.6142	1.08x10 ⁻²⁶	1.62x10 ⁻²⁴
CXCL13	4q21.1	0.6140	1.14x10 ⁻²⁶	1.70x10 ⁻²⁴
APOL2	22q12.3	0.6135	1.27x10 ⁻²⁶	1.88x10 ⁻²⁴
APOL1	22q12.3	0.6133	1.32x10 ⁻²⁶	1.94x10 ⁻²⁴
GIMAP5	7q36.1	0.6121	1.78x10 ⁻²⁶	2.58x10 ⁻²⁴
BTK	Xq22.1	0.6115	2.04x10 ⁻²⁶	2.94x10 ⁻²⁴
AQP9	15q21.3	0.6101	2.88x10 ⁻²⁶	4.13x10 ⁻²⁴
FCGR1B	1p11.2	0.6098	3.05x10 ⁻²⁶	4.35x10 ⁻²⁴
ITGAL	16p11.2	0.6091	3.59x10 ⁻²⁶	5.07x10 ⁻²⁴
CLEC2B	12p13.31	0.6084	4.27x10 ⁻²⁶	5.98x10 ⁻²⁴
SELL	1q24.2	0.6083	4.33x10 ⁻²⁶	6.03x10 ⁻²⁴
SH2D1A	Xq25	0.6081	4.53x10 ⁻²⁶	6.27x10 ⁻²⁴
CTLA4	2q33.2	0.6080	4.74x10 ⁻²⁶	6.51x10 ⁻²⁴
SOD2	6q25.3	0.6079	4.79x10 ⁻²⁶	6.53x10 ⁻²⁴
SLFN11	17q12	0.6078	4.90x10 ⁻²⁶	6.64x10 ⁻²⁴
IFI16	1q23.1	0.6067	6.33x10 ⁻²⁶	8.52x10 ⁻²⁴
IHH	2q35	-0.6061	7.25x10 ⁻²⁶	9.68x10 ⁻²⁴
IL10RA	11q23.3	0.6060	7.56x10 ⁻²⁶	9.97x10 ⁻²⁴
LAG3	12p13.31	0.6060	7.57x10 ⁻²⁶	9.97x10 ⁻²⁴
TLR6	4p14	0.6059	7.73x10 ⁻²⁶	1.01x10 ⁻²³
UBD	6p22.1	0.6053	8.74x10 ⁻²⁶	1.14x10 ⁻²³
CXCR6	3p21.31	0.6053	8.84x10 ⁻²⁶	1.14x10 ⁻²³
CLEC12A	12p13.31	0.6050	9.47x10 ⁻²⁶	1.21x10 ⁻²³
GBP2	1p22.2	0.6044	1.08x10 ⁻²⁵	1.38x10 ⁻²³
C1ORF162	1p13.2	0.6043	1.11x10 ⁻²⁵	1.40x10 ⁻²³
SP110	2q37.1	0.6041	1.16x10 ⁻²⁵	1.46x10 ⁻²³
IRF9	14q12	0.6039	1.22x10 ⁻²⁵	1.52x10 ⁻²³
FGL2	7q11.23	0.6038	1.26x10 ⁻²⁵	1.56x10 ⁻²³
KLRK1	12p13.2	0.6036	1.32x10 ⁻²⁵	1.63x10 ⁻²³
IFI44L	1p31.1	0.6032	1.43x10 ⁻²⁵	1.75x10 ⁻²³
AIF1	6p21.33	0.6028	1.58x10 ⁻²⁵	1.92x10 ⁻²³
RHOH	4p14	0.6023	1.76x10 ⁻²⁵	2.13x10 ⁻²³
NRP1	10p11.22	0.6021	1.83x10 ⁻²⁵	2.20x10 ⁻²³
LILRB4	19q13.42	0.6016	2.06x10 ⁻²⁵	2.46x10 ⁻²³
CD163	12p13.31	0.6014	2.18x10 ⁻²⁵	2.59x10 ⁻²³

Based on the condition of $r > 0.6$, 164 genes were selected for pathway enrichment analysis.

Table SIII. Top pathways sorted by the number of genes following pathway enrichment analysis using the Kyoto Encyclopedia for Genes and Genomes database.

Rank	Pathway	No. of hits
1	ko04060 Cytokine-cytokine receptor interaction	16
2	ko04062 Chemokine signaling pathway	15
3	ko04514 Cell adhesion molecules	12
4	ko05152 Tuberculosis	12
5	ko05162 Measles	11
6	ko04620 Toll-like receptor signaling pathway	11
7	ko05164 Influenza A	11
8	ko05200 Pathways in cancer	10
9	ko05169 Epstein-Barr virus infection	9
9	ko04630 JAK-STAT signaling pathway	9
9	ko04380 Osteoblast differentiation	9
9	ko05167 Kaposi sarcoma-associated herpesvirus infection	9
9	ko05168 Herpes simplex infection	9