

Supplementary Materials

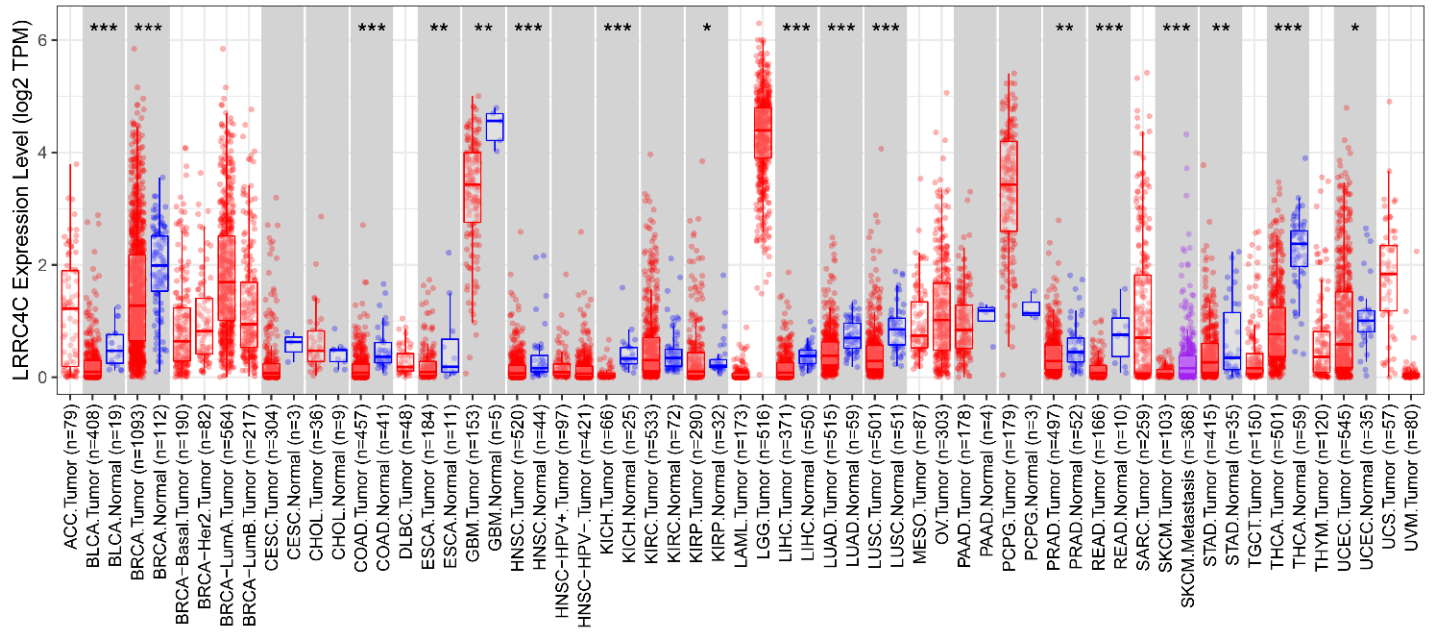


Figure S1. LRR4C expression of different tumor types from the TCGA database was investigated by TIMER 2.0, mainly decreased expression of LRR4C in different tumors compared to normal tissues (*P < 0.05, **P < 0.01, ***P < 0.001).

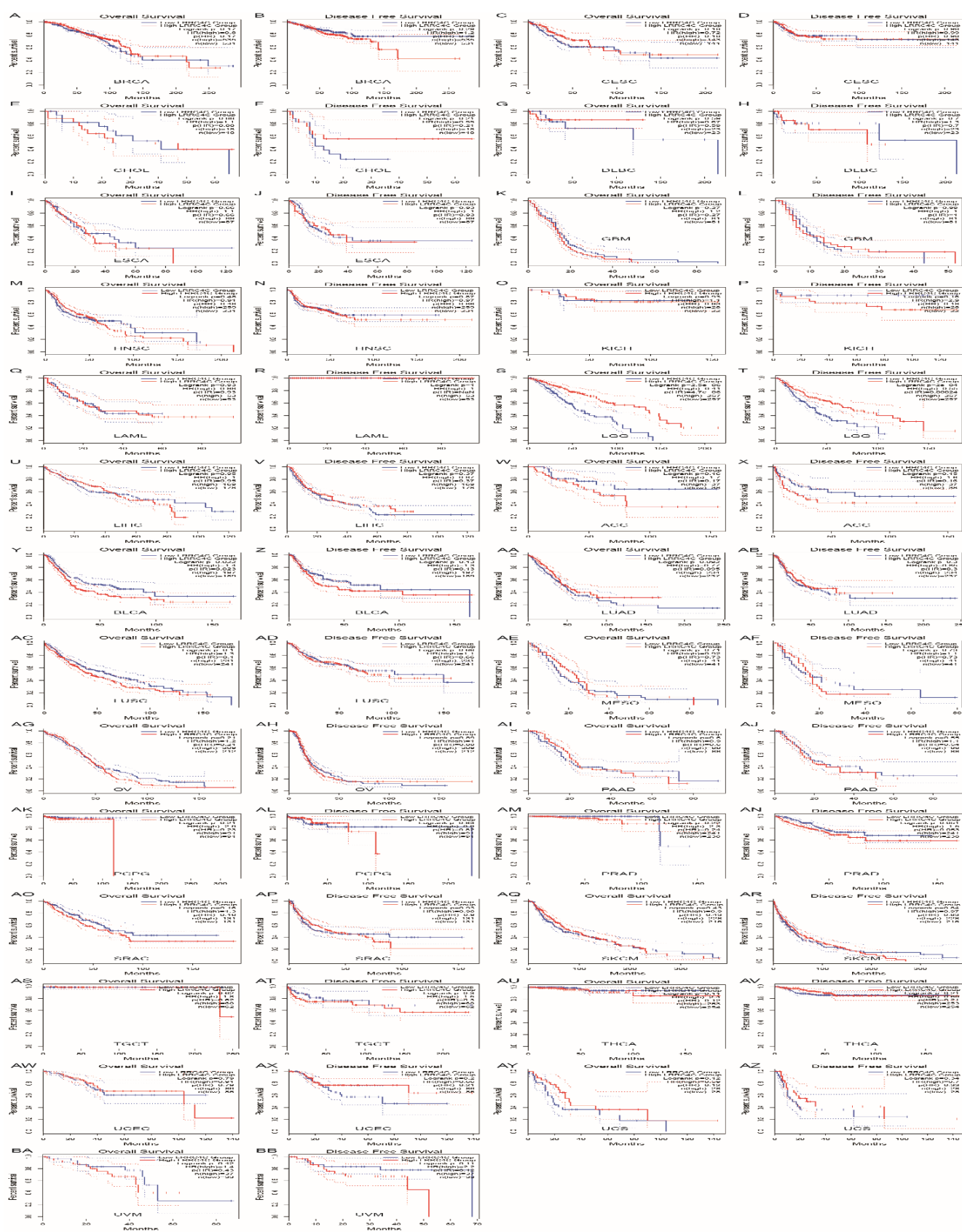


Figure S2. Correlation of LRRC4C expression with prognosis in diverse types of cancer in TCGA.

Supplementary Table 1. Univariate COX regression analysis with 58 DEGs among colon cancer patients from TCGA and GSE39582, listing the significant factors with $p < 0.05$.

DEGs	HR	95%CI lower	95%CI upper	P-value
COAD-OS				
<i>LRRC4C</i>	1.09	1.01	1.18	0.006
HAMP	1.04	1.00	1.09	0.023
GSE39582-OS				
<i>LRRC4C</i>	3.71	2.45	4.96	2.14e-04
MCEMP1	1.38	1.07	1.69	3.78e-04
CR1	1.91	1.29	2.53	0.001
SEMA3D	4.18	2.81	5.55	0.002
CYP1B1	1.20	1.02	1.37	0.002
LINC01094	1.31	1.05	1.56	0.005
KCNJ15	1.40	1.08	1.73	0.006
STAC	1.69	1.19	2.20	0.006
MARCO	1.35	1.06	1.64	0.008
FCN1	1.27	1.04	1.50	0.010
SV2B	2.20	1.44	2.95	0.015
DCLK1	1.39	1.07	1.70	0.016
LILRA2	1.70	1.19	2.21	0.018
FMO2	1.45	1.09	1.81	0.022
HS3ST2	1.35	1.06	1.63	0.034
GAS1	1.15	1.02	1.29	0.034
PPP2R2B	2.08	1.38	2.79	0.035
TREM1	1.13	1.01	1.25	0.038
CNTN1	1.76	1.22	2.30	0.044
GSE39582-DFS				
SEMA3D	6.12	4.38	7.85	2.26e-05
MARCO	1.58	1.14	2.02	4.37e-04
MCEMP1	1.39	1.07	1.70	0.002
KCND2	2.21	1.45	2.98	0.003
STAC	1.83	1.25	2.41	0.008
<i>LRRC4C</i>	2.70	1.75	3.66	0.016
APCDD1L	1.91	1.29	2.53	0.027
LILRA2	1.72	1.20	2.23	0.038
ABCA6	1.34	1.06	1.63	0.043
FCN1	1.25	1.04	1.47	0.044

HR: hazard ratio; CI: confidence interval; DEGs: differentially expressed genes; OS: overall survival; DFS: disease free survival. COAD: colon adenocarcinoma, STAD: stomach adenocarcinoma.

Supplementary Table 2. GSEA results for COAD and STAD samples with high LRRC4C expression and low expression, only gene sets with NOM $p < 0.05$ and FDR $q < 0.08$ were considered significant, listing the top 15 significant gene sets.

Name	NOM p-value	FDR q-value
LRRC4C high expression-COAD-HALLMARK		
HALLMARK_MYOGENESIS	<0.0001	0.0042
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	0.0020	0.0024
HALLMARK_KRAS_SIGNALING_UP	<0.0001	0.0016
HALLMARK_ANGIOGENESIS	<0.0001	0.0028
HALLMARK_UCV_RESPONSE_DN	0.0020	0.0026
HALLMARK_APICAL_JUNCTION	0.0040	0.0056
HALLMARK_INFLAMMATORY_RESPONSE	0.0078	0.0063
HALLMARK_COAGULATION	0.0020	0.0061
HALLMARK_HEDGEHOG_SIGNALING	0.0120	0.0142
HALLMARK_COMPLEMENT	0.0172	0.0139
HALLMARK_IL2_STAT5_SIGNALING	0.0174	0.0190
HALLMARK_APICAL_SURFACE	0.0136	0.0423
HALLMARK_IL6_JAK_STAT3_SIGNALING	0.0470	0.0400
HALLMACRK_ALLOGRAFT_REJECTION	0.0434	0.0407
HALLMARK_KRAS_SIGNALING_DN	0.0108	0.0467
LRRC4C low expression-COAD-HALLMARK		
HALLMARK_OXIDATIVE_PHOSPHORYLATION	<0.0001	0.0338
HALLMARK_E2F_TARGETS	0.0062	0.0233
HALLMARK_MYC_TARGETS_V1	<0.0001	0.0496
HALLMARK_MYC_TARGETS_V2	<0.0001	0.0485
HALLMARK_PEROXISOME	0.0144	0.0405
HALLMARK_DNA_REPAIR	0.0230	0.0402
LRRC4C high expression-COAD-C7		
GSE21063_WT_VS_NFATC1_KO_16H_ANTI_IGM_STIM_BCELL_DN	<0.0001	0.0010
GSE28737_BCL6_HET_VS_BCL6_KO_MARGINAL_ZONE_BCELL_UP	<0.0001	0.0011
GSE3982_BCELL_VS_EFF_MEMORY_CD4_TCELL_DN	<0.0001	0.0021
GSE21380_NON_TFH_VS_TFH_CD4_TCELL_UP	<0.0001	0.0053
GSE23114_WT_VS_SLE2C1_MOUSE_PERITONEAL_CAVITY_B1A_BCELL_DN	<0.0001	0.0084
GSE13522_CTRL_VS_T_CRUZI_BRAZIL_STRAIN_INF_SKIN_UP	<0.0001	0.0093
GSE3982_EFF_MEMORY_CD4_TCELL_VS_TH1_UP	<0.0001	0.0094
GSE37301_HEMATOPOIETIC_STEM_CELL_VS_CD4_TCELL_DN	<0.0001	0.0107
GSE27786_NKTCELL_VS_ERYTHROBLAST_DN	<0.0001	0.0133
GSE19825_NAIVE_VS_IL2RAHIGH_DAY3_EFF_CD8_TCELL_UP	<0.0001	<0.0001
GSE1791_CTRL_VS_NEUROMEDINU_IN_T_CELL_LINE_0.8H_DN	<0.0001	<0.0001
GSE19825_NAIVE_VS_IL2RALOW_DAY3_EFF_CD8_TCELL_UP	<0.0001	<0.0001
GSE23502_BM_VS_COLON_TUMOR_HDC_KO_MYELOID_DERIVED_SUPPRESSOR_CELL_UP	<0.0001	<0.0001
GSE13411_NAIVE_VS_MEMORY_BCELL_UP	<0.0001	<0.0001

Name	NOM p-value	FDR q-value
LRRC4C low expression-COAD-C7		
GSE22886_NAIVE_CD4_TCELL_VS_48H_ACT_TH1_DN	0.0490	0.0250
LRRC4C high expression-STAD-HALLMARK		
HALLMARK_MYOGENESIS	<0.0001	0.0188
HALLMARK_APICAL_JUNCTION	0.0039	0.0537
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	0.0131	0.0506
HALLMARK_UV_RESPONSE_DN	0.0083	0.0545
HALLMARK_KRAS_SIGNALING_UP	0.0179	0.0652
HALLMARK_ANGIOGENESIS	0.0094	0.0575
HALLMARK_COAGULATION	0.0191	0.0780
HALLMARK_KRAS_SIGNALING_DN	0.0020	0.0772
HALLMARK_HEDGEHOG_SIGNALING	0.0242	0.0768
HALLMARK_IL2_STAT5_SIGNALING	0.0433	0.0718
LRRC4C low expression-STAD-HALLMARK		
HALLMARK_OXIDATIVE_PHOSPHORYLATION	0.0020	0.0014
HALLMARK_MYC_TARGETS_V1	<0.0001	0.00333
HALLMARK_MYC_TARGETS_V2	<0.0001	0.0129
HALLMARK_DNA_REPAIR	0.01	0.0135
HALLMARK_E2F_TARGETS	<0.0001	0.0123
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	0.0175	0.0120
HALLMARK_MTORC1_SIGNALING	0.0101	0.0104
HALLMARK_G2M_CHECKPOINT	0.0020	0.0119
HALLMARK_FATTY_ACID_METABOLISM	0.0238	0.0473
HALLMARK_GLYCOLYSIS	0.0178	0.0436
HALLMARK_PEROXISOME	0.0215	0.0678
HALLMARK_CHOLESTEROL_HOMEOSTASIS	0.0478	0.0793
LRRC4C high expression-STAD-C7		
GSE23114_WT_VS_SLE2C1_MOUSE_PERITONEAL_CAVITY_B1A_BCELL_DN	<0.0001	0.0500
GSE12484_HEALTHY_VS_PERIDONTITIS_NEUTROPHILS_UP	<0.0001	0.0499
GSE28737_BCL6_HET_VS_BCL6_KO_MARGINAL_ZONE_BCELL_UP	<0.0001	0.0498
GSE37301_HEMATOPOIETIC_STEM_CELL_VS_CD4_TCELL_DN	<0.0001	0.0497
GSE3982_BCELL_VS_EFF_MEMORY_CD4_TCELL_DN	<0.0001	0.0497
GSE21063_WT_VS_NFATC1_KO_16H_ANTI_IGM_STIM_BCELL_DN	<0.0001	0.04945928
GSE13522_CTRL_VS_T_CRUZI_BRAZIL_STRAIN_INF_SKIN_UP	<0.0001	0.0494
GSE21380_NON_TFH_VS_TFH_CD4_TCELL_UP	<0.0001	0.0485
GSE27786_NKTCELL_VS_ERYTHROBLAST_DN	<0.0001	0.0490
GSE28783_CTRL_ANTI_MIR_VS_UNTREATED_ATHEROSCLEROSIS_MACROPHAGE_UP	<0.0001	0.0423
GSE37301_CD4_TCELL_VS_RAG2_KO_NK_CELL_UP	<0.0001	0.0423
GSE21546_UNSTIM_VS_ANTI_CD3_STIM_DP_THYMOCYTES_UP	<0.0001	0.0423
GSE43863_NAIVE_VS_LY6C_INT_CXCR5POS_CD4_EFF_TCELL_D6_LCMV_DN	<0.0001	0.0423
GSE29949_MICROGLIA_BRAIN_VS_MONOCYTE_BONE_MARROW_UP	0.0021	0.0423

Name	NOM p-value	FDR q-value
GSE13485_DAY3_VS_DAY21_YF17D_VACCINE_PBMC_DN	<0.0001	0.0423
GSE10325_LUPUS_CD4_TCELL_VS_LUPUS_BCELL_UP	0.0199	0.0423
LRRC4C low expression-STAD-C7		
GSE15930_NAIVE_VS_48H_IN_VITRO_STIM_CD8_TCELL_DN	0.0199	0.007
GSE21360_SECONDARY_VS_TERTIARY_MEMORY_CD8_TCELL_UP	0.0197	0.017
GSE15930_NAIVE_VS_48H_IN_VITRO_STIM_IFNAB_CD8_TCELL_DN	0.0110	0.019
GSE41867_DAY6_VS_DAY8_LCMV_ARMSTRONG_EFFECTOR_CD8_TCELL_DN	0.0140	0.019
GSE22886_NAIVE_CD4_TCELL_VS_48H_ACT_TH1_DN	0.0086	0.044

GSEA: Gene Set Enrichment Analysis, COAD: colon adenocarcinoma, STAD: stomach adenocarcinoma.