

ORIGINAL RESEARCH ARTICLE

Expression of MXRA7 and its prognostic significance in human bladder cancer

Supplementary File

Table S1. Statistical summary of variance analysis results with the FC=1.5 and 2.0

Significance threshold	Fold change=1.5		Fold change=2.0	
	Up	Down	Up	Down
$p < 0.05$	849	287	230	63
$p < 0.01$	845	286	230	63
FDR < 0.05	846	286	230	63
FDR < 0.01	809	280	227	62

Table S2. KEGG pathway enrichment analysis with gene involvement and *p* values

Term	Count	%	<i>p</i> -value	Genes
hsa04820: Cytoskeleton in muscle cells	35	15.22	1.94E-26	<i>SYNPO2, COL11A1, ELN, FHL1, LMOD1, NID1, THBS2, THBS1, FBLN2, ACTG2, COMP, PDLIM3, MYH11, FLNC, PDLIM4, TPM2, TPM1, FN1, BGN, DCN, COL1A1, COL3A1, VCAN, ACTC1, DES, COL1A2, COL5A1, COL6A2, COL5A2, COL6A1, COL6A3, VIM, ITGA5, MYL9, FBN1</i>
hsa04510: Focal adhesion	19	8.26	2.06E-10	<i>PDGFRB, ACTN1, CAV1, TNC, FN1, LAMC2, THBS2, THBS1, MYLK, COL1A1, COMP, COL1A2, COL6A2, COL6A1, SPPI, FLNA, COL6A3, ITGA5, MYL9</i>
hsa04974: Protein digestion and absorption	14	6.09	1.34E-09	<i>COL16A1, COL11A1, ELN, COL12A1, COL1A1, COL3A1, COL1A2, COL5A1, COL6A2, COL5A2, COL6A1, COL8A2, COL6A3, COL10A1</i>
hsa04512: ECM-receptor interaction	13	5.65	2.21E-09	<i>TNC, FN1, LAMC2, THBS2, THBS1, COL1A1, COMP, COL1A2, COL6A2, COL6A1, SPPI, COL6A3, ITGA5</i>
hsa05205: Proteoglycans in cancer	14	6.09	3.59E-06	<i>LUM, MMP2, CAV1, FN1, TWIST1, MSN, THBS1, MMP9, DCN, COL1A1, COL1A2, FLNA, ITGA5, FGFR1</i>
hsa04151: PI3K-Akt signaling pathway	18	7.83	7.04E-06	<i>PDGFRB, CSF1R, TNC, FN1, LAMC2, THBS2, OSMR, THBS1, COL1A1, COMP, COL1A2, COL6A2, CREB3L1, COL6A1, SPPI, COL6A3, ITGA5, FGFR1</i>
hsa05133: Pertussis	9	3.91	9.68E-06	<i>C1QB, C3, C1QA, C1S, C1R, SERPING1, CD14, ITGA5, C1QC</i>
hsa04610: Complement and coagulation cascades	9	3.91	2.37E-05	<i>C1QB, C3, C1QA, SERPING1, C1QC, SERPINA1, C1S, C1R, F13A1</i>
hsa04145: Phagosome	11	4.78	5.10E-05	<i>MRC2, C3, COMP, FCGR3A, TUBB6, TUBA1A, C1R, CD14, ITGA5, THBS2, THBS1</i>
hsa05150: <i>Staphylococcus aureus</i> infection	9	3.91	5.99E-05	<i>C1QB, C3, C1QA, FCGR3A, C1S, C1R, KRT14, ICAM1, C1QC</i>
hsa05165: Human papillomavirus infection	15	6.52	1.59E-04	<i>PDGFRB, TNC, FN1, LAMC2, THBS2, THBS1, COL1A1, COMP, COL1A2, COL6A2, CREB3L1, COL6A1, SPPI, COL6A3, ITGA5</i>
hsa04933: AGE-RAGE signaling pathway in diabetic complications	8	3.48	4.27E-04	<i>COL1A1, COL3A1, COL1A2, TGFB3, MMP2, FN1, CCL2, ICAM1</i>
hsa05146: Amoebiasis	8	3.48	4.81E-04	<i>COL1A1, COL3A1, COL1A2, TGFB3, ACTN1, FN1, LAMC2, CD14</i>
hsa05144: Malaria	6	2.61	5.51E-04	<i>COMP, TGFB3, CCL2, THBS2, THBS1, ICAM1</i>
hsa04350: TGF-beta signaling pathway	8	3.48	6.41E-04	<i>GREM1, TGFB3, INHBA, EMP3, FMOD, THBS1, DCN, FBN1</i>
hsa04670: Leukocyte migration, transendothelial	8	3.48	9.80E-04	<i>CXCL12, ACTN1, MMP2, MSN, THY1, MYL9, MMP9, ICAM1</i>
hsa04148: Efferocytosis	9	3.91	1.24E-03	<i>C1QB, C1QA, SLC16A1, AXL, SPHK1, MFGE8, GAS6, THBS1, C1QC</i>
hsa05322: Systemic lupus erythematosus	8	3.48	2.78E-03	<i>C1QB, C3, C1QA, FCGR3A, C1S, C1R, ACTN1, C1QC</i>
hsa05414: Dilated cardiomyopathy	7	3.04	2.98E-03	<i>ACTC1, PLN, DES, TGFB3, TPM2, TPM1, ITGA5</i>
hsa04810: Regulation of actin cytoskeleton	10	4.35	3.99E-03	<i>PDGFRB, CXCL12, ACTN1, FN1, MSN, MYH11, ITGA5, MYL9, FGFR1, MYLK</i>
hsa04814: Motor proteins	9	3.91	5.28E-03	<i>ACTA2, TUBB6, ACTC1, TUBA1A, TPM2, TPM1, MYH11, MYL9, ACTG2</i>

Table S3. GO term enrichment analysis of biological processes, cellular components, and molecular functions, showing the key pathways

Category	Term	Count	%	p-value	Fold enrichment	Genes
GOTERM_BP_D IRECT	GO: 0007155~cell adhesion	41	17.83	3.94E-22	6.96	SRPX, SPON2, SPON1, NRP2, CCL11, COL16A1, TNFAIP6, COL12A1, TNC, DPT, LAMC2, THBS2, THBS1, ICAM1, COMP, ISLR, PDPN, SPP1, CCL2, EMILIN1, CCN2, CCN1, POSTN, FN1, COL1A1, MFAP4, VCAN, CXCL12, COL5A1, FAP, COL6A2, COL6A1, PXDN, ADAM12, CDH11, MXRA8, COL6A3, TGFBI, ITGA5, MFGES, FERMT2
GOTERM_BP_D IRECT	GO: 0030198~extracellular matrix organization	22	9.57	6.24E-16	11.15	POSTN, OLFML2B, COL16A1, COL11A1, MMP2, FBLN2, MMP9, COL1A1, MMP11, SMOC2, COL3A1, ADAMTS2, CCDC80, COL1A2, COL5A1, COL6A2, COL5A2, PXDN, COL8A2, COL10A1, TGFBI, CCN1
GOTERM_BP_D IRECT	GO: 0030335~positive regulation of cell migration	22	9.57	1.50E-11	6.72	PDGFRB, LRRC15, CSF1R, CCL11, TNFAIP6, CCL21, SPHK1, SYNPO2, MMP2, CAV1, TWIST1, LAMC2, THBS1, MYLK, COL1A1, CXCL12, PDPN, MYADM, CCL2, ITGA5, CCN1, FERMT2
GOTERM_BP_D IRECT	GO: 0043066~negative regulation of apoptotic proces	21	9.13	1.48E-06	3.63	CSF1R, ANXA1, HSPB6, SPHK1, IFI6, TWIST1, THBS1, MMP9, FSTL1, GREM1, COMP, SERP1, ACTC1, CHST11, AXL, PDPN, FLNA, CCN1, GAS6, CRYAB, TGM2
GOTERM_BP_D IRECT	GO: 0001525~angiogenesis	20	8.7	1.22E-10	6.83	PDGFRB, ECM1, CLIC4, NRP2, MMP2, CAV1, FN1, THY1, FAP, CALD1, PXDN, COL8A2, CCL2, FLNA, TGFBI, CCN2, ITGA5, MFGES, RAMP1, FGFR1
GOTERM_BP_D IRECT	GO: 0030199~collagen fibril organization	19	8.26	1.49E-20	25.64	FKBP10, LUM, COL11A1, COL12A1, DPT, GREM1, COL1A1, COMP, MMP11, COL3A1, ADAMTS2, SERP2, COL1A2, COL5A1, LOX, COL5A2, COL6A1, PXDN, FMOD
GOTERM_BP_D IRECT	GO: 0006954~inflammatory response	15	6.52	3.49E-04	3.12	CSF1R, ECM1, ANXA1, CCL11, TNFAIP6, CCL21, SPHK1, RARRES2, THBS1, C3, AXL, COL6A1, CCL2, CHI3L1, CD14
GOTERM_BP_D IRECT	GO: 0045766~positive regulation of angiogenesis	14	6.09	4.61E-08	7.53	ECM1, PTGIS, CCL11, HSPB6, SPHK1, TWIST1, THBS1, C3, GREM1, SMOC2, SERP2, ADAM12, CHI3L1, EMILIN1
GOTERM_BP_D IRECT	GO: 0070374~positive regulation of ERK1 and ERK2 cascade	14	6.09	2.19E-06	5.39	PDGFRB, CSF1R, CCL11, CCL21, CAVIN3, MTIX, INHBA, ICAM1, ACTA2, CCL2, CHI3L1, CCN2, GAS6, FERMT2
GOTERM_BP_D IRECT	GO: 0051897~positive regulation of phosphatidyliositol 3-kinase/ protein kinase B signal transduction	13	5.65	2.09E-06	5.94	PDGFRB, CSF1R, IGFBP5, CCL21, FN1, THBS1, DCN, C1QTNF1, AXL, CHI3L1, GAS6, FERMT2, FGFR1

Table S3. (Continued)

Category	Term	Count	%	p-value	Fold enrichment	Genes
GOTERM_CC_DIRECT	GO: 0005615~extracellular space	114	49.57	8.39E-54	5.11	SPON1, SPARC, COL16A1, OLFML2B, COL12A1, TNC, F13A1, ACTG2, ICAM1, COMP, ISLR, IGHG1, LGALS1, EFEMP1, DPYSL3, CCN2, PTGDS, CCN1, KRT6A, POSTN, IGFBP5, SERPINF1, ACTN1, PCOLCE, KRT5, SFRP4, SFRP1, SFRP2, LOX, CD109, COL8A2, SERPING1, HTRA1, DPT, LTBP2, AEBP1, C3, PI3, CD14, IGFBP6, S100A10, CD163, TGFB3, RARRES2, FN1, MSN, INHBA, COL1A1, COL1A2, COL5A1, CILP, COL5A2, TGFBI, FBN1, ECM1, SERPINA1, TNFAIP6, CPXM2, LAMC2, CHRDL2, FCGR3A, C1QTNF1, CTSK, TIMP2, COL10A1, EMILIN1, CPXM1, ANXA1, PTGIS, MMP2, BGN, MMP9, ASPN, DCN, ACTA2, GREM1, MMP11, VCAN, COL6A2, PXDN, COL6A3, CHI3L1, FAM20C, ANGPTL2, GAS6, MFGE8, LRRC15, CCL11, C1S, C1R, COL11A1, PRELP, THBS1, FSTL1, PTHLH, FSTL3, OLFML3, SPP1, CCL2, CTHRC1, CCL21, LUM, SULF1, PODN, SOD3, SULF2, SMOC2, MFAP4, COL3A1, ACTC1, FAP, AXL, FMOD, C1QC
GOTERM_CC_DIRECT	GO: 0005576~extracellular region	110	47.83	1.59E-48	4.78	SPARC, COL16A1, COL12A1, TNC, F13A1, COMP, ISLR, IGHG1, LGALS1, EFEMP1, CCN2, PTGDS, CCN1, TGM2, IGFBP5, SERPINF1, ACTN1, PCOLCE, SFRP4, SFRP1, CCDC80, FNDC1, LOX, CD109, ADAM12, COL8A2, SERPING1 MXRA5, HTRA3, HTRA1, LTBP2, THY1, AEBP1, NID1, FBLN2, C3, ARSI, PI3, CD14, IGFBP6, S100A10, CD163, TGFB3, RARRES2, FN1, INHBA, COL1A1, CXCL12, COL1A2, COL5A1, COL5A2, TGFBI, FBN1, FGFRI, ECM1, NRP2, SERPINA1, HSPB6, TNFAIP6, CPXM2, ELN, LAMC2, ADAMTS2, C1QTNF1, CTSK, TIMP2, COL10A1, EMILIN1, ANXA1, MMP2, BGN, MMP9, DCN, MMP11, VCAN, COL6A2, COL6A1, PXDN, CDH11, FIBIN, COL6A3, CHI3L1, GAS6, MFGE8, C1QB, C1QA, CCL11, C1S, C1R, COL11A1, PRELP, THBS2, THBS1, FSTL1, PTHLH, FSTL3, SPP1, FLNA, CCL2, CTHRC1, CCL21, LUM, SOD3, SULF2, MFAP5, MFAP4, COL3A1, MFAP2, FMOD, C1QC
GOTERM_CC_DIRECT	GO: 0062023~collagen-containing extracellular matrix	85	36.96	2.65E-85	19.00	SRPX, SPON1, ECM1, SERPINA1, SPARC, COL16A1, ELN, COL12A1, TNC, F13A1, LAMC2, ICAM1, COMP, ADAMTS2, EFEMP1, LGALS1, TIMP2, ANXA6, COL10A1, EMILIN1, CCN2, CCN1, TGM2, POSTN, ANXA1, SERPINF1, MMP2, BGN, PCOLCE, MMP9, ASPN, DCN, ADAM19, GREM1, SFRP1, VCAN, SFRP2, LOX, COL6A2, COL6A1, PXDN, COL8A2, COL6A3, ANGPTL2, SERPING1, MXRA7, MFGE8, MXRA5, C1QB, C1QA, LRRC15, COL11A1, HTRA1, DPT, PRELP, LTBP2, AEBP1, THBS2, NID1, THBS1, FBLN2, S100A10, CTHRC1, TGFB3, LUM, RARRES2, FN1, SULF1, PODN, SOD3, MFAP5, COL1A1, MFAP4, COL3A1, CXCL12, COL1A2, COL5A1, CILP, COL5A2, MFAP2, MGP, TGFBI, FMOD, FBN1, C1QC

(Cont'd...)

Table S3. (Continued)

Category	Term	Count	%	p-value	Fold enrichment	Genes
GOTERM_CC_DIRECT	GO: 0070062~extracellular exosome	78	33.91	7.59E-21	3.15	SPON2, CLIC4, ECM1, SERPINA1, COL12A1, ACTG2, ICAM1, COMP, TUBB6, FCGR3A, IGHG1, ISLR, EFEMP1, TUBA1A, LGALS1, ANXA6, EMILIN1, PTGDS, TGM2, KRT6A, ANXA1, SERPINF1, ACTN1, BGN, PCOLCE, KRT5, MMP9, ACTA2, SFRP1, COL6A2, COL6A1, PXDN, CDH11, MXRA8, COL6A3, FAM20C, ANGPTL2, SERPING1, CHI3L1, MFGE8, GAS6,
GOTERM_CC_DIRECT	GO: 0005604~basement membrane	15	6.52	2.87E-12	14.1	SPARC, SERPINF1, TNC, FN1, NID1, THBS2, ACTA2, SMOC2, CCDC80, COL5A1, COL6A1, PXDN, COL8A2, CRYAB, MXRA5, LRRC15, CIR, HTRA1, PRELP, LTBP2, THY1, AEBP1, NID1, THBS1, FSTL1, PTGS1, C3, NT5E, SPP1, FLNA, MYH11, CD14, S100A10, SLC16A1, LUM, FN1, CYBRD1, MSN, SOD3, DES, ACTC1, CXCL12, COL1A2, CILP, AXL, KRT14, MGP, CD248, TGFBI, VIM
GOTERM_CC_DIRECT	GO: 0031012~extracellular matrix	40	17.39	2.01E-34	15.2	SPON2, LRRC15, ECM1, SPON1, OLFML2B, ELN, LTBP2, PRELP, THBS1, FBLN2, COMP, ISLR, ADAMTS2, EFEMP1, TIMP2, PI3, CCN2, CCN1, TGM2, POSTN, LUM, MMP2, RARRES2, FN1, BGN, MMP9, ASPN, COL1A1, MMP11, VCAN, COL5A2, PXDN, MGP, COL8A2, COL6A3, CHI3L1, CD248, TGFBI, FMOD, FBN1
GOTERM_CC_DIRECT	GO: 0005788~endoplasmic reticulum lumen	38	16.52	1.26E-27	11.14	FKBP10, SPON1, SERPINA1, COL16A1, COL11A1, COL12A1, TNC, THBS1, FSTL1, FSTL3, C3, LGALS1, SPP1, COL10A1, ARSI, CCN1, IGFBP5, FN1, GPX8, RCN3, COL1A1, COL3A1, VCAN, SELENOM, COL1A2, COL5A1, COL6A2, COL5A2, COL6A1, COL8A2, MXRA8, SERPING1, COL6A3, FAM20C, MFGE8, GAS6, FBN1, CES1
GOTERM_CC_DIRECT	GO: 0009986~cell surface	30	13.04	1.74E-10	4.16	SRPX, CSF1R, CLIC4, SPARC, THY1, ANTXR1, THBS1, ICAM1, C3, NT5E, S100A10, TNS1, ANXA1, TGFB3, BGN, MSN, SULF1, SULF2, GREM1, SFRP4, SFRP1, FAP, AXL, CD109, PXDN, MXRA8, ITGA5, CRYAB, RAMP1, FERMT2
GOTERM_CC_DIRECT	GO: 0005925~focal adhesion	23	10	2.74E-09	4.82	PDGFRB, ANXA1, SYNPO2, ACTN1, CAV1, FHL1, TNC, MSN, THY1, ICAM1, MRC2, CNN1, ACTC1, FAP, PALLD, ANXA6, FLNA, VIM, FLNC, ITGA5, FERMT2, TNS1, TGM2
GOTERM_CC_DIRECT	GO: 0005581~collagen trimer	21	9.13	5.93E-20	19.15	C1QB, C1QA, COL16A1, COL11A1, COL12A1, PCOLCE, COL1A1, COL3A1, C1QTNF1, COL1A2, COL5A1, LOX, COL6A2, COL5A2, COL6A1, COL8A2, COL6A3, COL10A1, EMILIN1, CTHRC1, C1QC TGFBI, FBN1
GOTERM_CC_DIRECT	GO: 0015629~actin cytoskeleton	15	6.52	2.76E-06	4.87	CLIC4, TAGLN, TPM2, SYNPO2, TPM1, HSPB7, ACTG2, MYLK, ACTA2, CNN1, ACTC1, CALD1, AXL, PALLD, FLNA

(Cont'd...)

Table S3. (Continued)

Category	Term	Count	%	p-value	Fold enrichment	Genes
GOTERM_CC_DIRECT	GO: 0009897~external side of plasma membrane	14	6.09	9.17E-04	2.98	CD163, THY1, OSMR, ANTXR1, THBS1, ICAM1, FCGR3A, NT5E, CXCL12, CTSK, CD248, CD14, ITGA5, MFGE8
GOTERM_CC_DIRECT	GO: 0005856~cytoskeleton	14	6.09	4.70E-03	2.47	TPM1, LMOD1, MSN, ACTG2, ACTA2, CNN1, CALD1, KRT14, VIM, FLNC, IGF2BP2, PDLIM4, FERMT2, TNS1
GOTERM_MF_DIRECT	GO: 0005515~protein binding	177	76.95	9.78E-06	1.2	IFITM3, SPON2, SPON1, SPARC, COL16A1, TNC, F13A1, MT1X, ANTXR1, MYLK, ICAM1, COMP, RGS2, TUBB6, MT2A, IGHG1, LGALS1, EFEMP1, CREB3L1, DPYSL3, CCN2, PTGDS, CCN1, KRT6A, TGM2, TNS1, PDGFRB, POSTN, IGFBP5, SERPINF1, ACTN1, TPM1, PCOLCE, KRT5, GEM, ADAM19, SFRP4, PCP4, SFRP1, SELENOM, RAB31, LOX, RBP1, ADAM12, MYADM, MXRA8, SERPING1, MT1E, CSF1R, RRAD, HTRA3, HTRA1, DPT, TWIST1, LTBP2, THY1, FBLN2, C3, CNN1, CALD1, ARSI, MYH11, CD14, IGFBP6, MSC, S100A10, CD163, TGFB3, RARRES2, CAV1, GFPT2, FN1, CYBRD1, MSN, INHBA, COL1A1, CXCL12, COL1A2, COL5A1, FXYD6, TGFB1, FERMT2, FBN1, FGFR1, FKBP10, SRPX, SYNM, CLIC4, ECM1, NRP2, SERPINA1, TNFAIP6, ELN, FHL1, HSPB7, MRC2, FCGR3A, UCHL1, TUBA1A, C1QTNF1, CTSK, ANXA6, TIMP2, COL10A1, PMEPA1, EMILIN1, ANXA1, PTGIS, SPHK1, MMP2, GPX8, BGN, EMP3, OSMR, MMP9, DCN, ARL4C, GREM1, RCN3, VCAN, PALLD, COL6A2, GAS1, CHI3L1, FAM20C, ANGPTL2, ITGA5, GAS6, CRYAB, CIQB, CIQA, LRRC15, TAGLN, OAT, CCL11, C1S, C1R, SYNPO2, IFI6, THBS2, THBS1, FSTL1, PTHLH, FSTL3, PTGS1, NT5E, PDLIM3,
GOTERM_MF_DIRECT	GO: 0005518~collagen binding	18	7.83	1.98E-18	22.58	LRRC15, SPARC, LUM, FN1, PCOLCE, AEBP1, PODN, NID1, ANTXR1, MMP9, MRC2, COMP, C1QTNF1, LOX, CTSK, COL6A2, COL6A1, TGFB1 PLN, PDPN, SPP1, FLNA, CCL2, FLNC, IGF2BP2, PDLIM4, SLC16A1, PRRX1, CAVIN1, CCL21, LUM, CAVIN3, AHNAK2, SOD3, SMOC2, MFAP4, COL3A1, DES, FAP, AXL, KRT14, MFAP2, MGP, MSRB3, CD248, VIM, RAMP1, C1QC
GOTERM_MF_DIRECT	GO: 0005201~extracellular matrix structural constituent	41	17.83	1.07E-48	30.33	SRPX, ECM1, SPON1, SPARC, COL11A1, ELN, TNC, DPT, LAMC2, LTBP2, PRELP, AEBP1, NID1, THBS2, THBS1, FBLN2, COMP, EFEMP1, EMILIN1, CCN1, CTHRC1, POSTN, LUM, FN1, BGN, PCOLCE, MFAP5, COL1A1, MFAP4, COL3A1, COL1A2, CILP, MFAP2, PXDN, MGP, COL8A2, CHI3L1, TGFB1, MFGE8, MXRA5, FBN1
GOTERM_MF_DIRECT	GO: 0042802~identical protein binding	38	16.52	1.81E-04	1.89	CIQB, NRP2, OAT, SERPINA1, OLFML2B, C1S, C1R, HTRA3, HTRA1, NT5E, C1QTNF1, TUBA1A, PLN, DPYSL3, ANXA6, EMILIN1, FLNC, IGFBP6, SLC16A1, CAVIN1, TGFB3, TPM2, CAV1, TPM1, FN1, CYBRD1, INHBA, MMP9, COL1A1, SFRP1, DES, COL1A2, FAP, TGFB1, VIM, CRYAB, FGFR1, FBN1

(Cont'd...)

Table S3. (Continued)

Category	Term	Count	%	p-value	Fold enrichment	Genes
GOTERM_MF_DIRECT	GO: 0005509~calcium ion binding	33	14.35	1.34E-10	3.83	<i>FKBP10, SPARC, C1S, TNFAIP6, C1R, LTBP2, NID1, THBS2, THBS1, FBLN2, FSTL1, COMP, EFEMP1, ANXA6, S100A10, TGM2, ANXA1, ACTN1, SULF1, ASPN, SULF2, RCN3, SMOC2, PCP4, VCAN, MGP, CDH11, FAM20C, CD248, ITGA5, GAS6, MYL9, FBNI</i>
GOTERM_MF_DIRECT	GO: 0008201~heparin binding	23	10	3.50E-16	10.59	<i>POSTN, NRP2, COL11A1, FN1, PRELP, LAMC2, LTBP2, PCOLCE, THBS2, THBS1, SOD3, FSTL1, COL1A1, COMP, SMOC2, SFRP1, CCDC80, COL5A1, ANXA6, CCN2, CCN1, FGFR1, FBNI</i>
GOTERM_MF_DIRECT	GO: 0005178~integrin binding	22	9.57	2.06E-16	11.76	<i>COL16A1, ACTN1, TNC, FN1, LAMC2, THY1, THBS1, ICAM1, COMP, COL3A1, CXCL12, SFRP2, COL5A1, FAP, SPPI, TGFBI, CCN2, ITGA5, CCN1, MFGES, FERMT2, FBNI</i>

Table S4. Multivariate analysis results of preliminary Cox regression model ($n=325$, all muscle-invasive tumors)

Term	Regression coefficient	<i>p</i> -value	HR	HR 95% CI
Age	0.03	0.01	1.03	1.01~1.05
BMI	-0.01	0.77	1.00	0.96~1.03
MXRA7	0.32	0.04	1.38	1.01~1.87
Risk score	0.87	0.00	2.38	1.73~3.26
Sex				
Female	-	-	-	-
Male	0.03	0.89	1.02	0.69~1.53
Expression level (MXRA7)				
High	-	-	-	-
Low	0.83	0.01	2.28	1.25~4.18
Cancer status				
Tumor-free	-	-	-	-
With tumor	0.86	0.00	2.36	1.63~3.40
Stage				
Stage I	-	-	-	-
Stage II	-1.07	0.30	0.34	0.04~2.65
Stage III	-1.17	0.26	0.31	0.04~2.41
Stage IV	-1.15	0.27	0.32	0.04~2.44
Tumor grade				
High grade	-	-	-	-
Low grade	0.80	0.03	2.22	1.08~4.56
Clinical_T				
T1	-	-	-	-
T2	1.07	0.75	2.93	0.68~12.65
T3	1.14	0.75	3.14	0.73~13.54
T4	1.27	0.78	3.56	0.78~16.32
Clinical_N				
N0	-	-	-	-
N1	0.11	0.69	1.11	0.66~1.88
N2	0.46	0.05	1.59	1.01~2.51
N3	1.29	0.03	3.62	1.17~11.19
NX	0.81	0.02	2.25	1.16~4.35
Clinical_M				
M0	-	-	-	-
M1	-0.79	0.11	0.46	0.17~1.21
MX	-0.03	0.89	0.97	0.66~1.43

Notes: C-index=0.60, 95% CI=0.60-0.60.

Abbreviations: BMI: Body mass index; CI: Confidence interval.