

**SUPPLEMENTARY TABLES**

**Supplementary Table 3. Univariate Cox regression analyses of clinical information with the overall survival of CRC patients.**

<b>TCGA dataset</b>			
<b>Variable</b>	<b>Univariate regression</b>		
	<b>HR</b>	<b>95% CI</b>	<b>p Value</b>
Risk score	3.8334	2.3288–6.3101	0.0000
Pathologic_stage	2.0305	1.5438–2.6708	0.0000
Pathologic_T	2.5614	1.5665–4.1880	0.0002
Pathologic_N	1.9038	1.4319–2.5313	0.0000
Pathologic_M	3.2602	1.9388–5.4824	0.0000
TP53_mutation	1.8464	1.0562–3.2278	0.0314
KRAS_mutation	0.8982	0.5611–1.4381	0.6549
BRAF_mutation	1.2109	0.6353–2.3080	0.5608

  

<b>GSE39582 dataset</b>			
<b>Variable</b>	<b>Univariate regression</b>		
	<b>HR</b>	<b>95% CI</b>	<b>p Value</b>
Risk score	1.5919	1.1676–2.1702	0.0033
Pathologic_stage	1.9919	1.5290–2.5949	0.0000
Pathologic_T	1.7872	1.2300–2.5968	0.0023
Pathologic_N	1.5973	1.2601–2.0248	0.0001
Pathologic_M	4.6461	2.9194–7.3941	0.0000
TP53_mutation	1.2812	0.8645–1.8987	0.2171
KRAS_mutation	1.2408	0.8407–1.8315	0.2773
BRAF_mutation	1.5943	0.8515–2.9852	0.1449

**Supplementary Table 4. Univariate and multivariate Cox regression analyses of the IRG risk score in GSE39582 datasets with the overall survival of CRC patients.**

<b>GSE39582 dataset</b>						
<b>Variable</b>	<b>Univariate regression</b>			<b>Multivariate regression</b>		
	<b>HR</b>	<b>95% CI</b>	<b>p Value</b>	<b>HR</b>	<b>95% CI</b>	<b>p Value</b>
Risk score	1.5919	1.1676–2.1702	0.0033	1.3746	1.0119–1.8670	0.0418
Pathologic_stage	1.9919	1.5290–2.5949	0	0.9004	0.4943–1.6400	0.7319
Pathologic_T	1.7872	1.2300–2.5968	0.0023	1.2692	0.8539–1.8860	0.2384
Pathologic_N	1.5973	1.2601–2.0248	0.0001	1.3186	0.8702–0.8702	0.1922
Pathologic_M	4.6461	2.9194–7.3941	0	3.8438	1.6796–8.7970	0.0014

**Supplementary Table 6. The RT-qPCR primer sequences and antibodies were used in this article.**

<b>The RT-qPCR primer sequences</b>		
<b>Gene</b>	<b>Forward primer</b>	<b>Reverse primer</b>
<i>ITGAX (CD11c)</i>	AGAGCTGTGATAAGCCAGTTCC	AATTCCTCGAAAGTGAAGTGTGT
<i>CD80</i>	GGCCCGAGTACAAGAACCG	TCGTATGTGCCCTCGTCAGAT
<i>ARG1</i>	GTGGAAACTTGCATGGACAAC	AATCCTGGCACATCGGGAATC
<i>CD163</i>	TTTGTCAACTTGAGTCCCTTAC	TCCCGCTACACTTGTTTTAC
<i>TIMP1</i>	ACCACCTTATACCAGCGTTATGA	GGTGTAGACGAACCGGATGTC
<i>18S</i>	GCAGAATCCACGCCAGTACAAGAT	TCTTCTTCAGTCGCTCCAGGTCTT
<i>ARPC1B</i>	CAAGGACCGCACCCAGATT	TGCCGCAGGTCACAATACG
<i>C5</i>	ACAGTCATAGAGTCTACAGGTGG	CCAACTGGTCAAGCGAATCTT
<i>CCL1</i>	CTCATTTGCGGAGCAAGAGAT	GCCTCTGAACCCATCCAACCTG
<i>CCL2</i>	AGAATCACCAGCAGCAAGTGTCC	TCCTGAACCCACTTCTGCTTGG
<i>CCL3</i>	AGTTCTCTGCATCACTTGCTG	CGGCTTCGCTTGGTTAGGAA
<i>CCL4</i>	CTGTGCTGATCCCAGTGAATC	TCAGTTCAGTTCAGGTCATACA
<i>CCL5</i>	CCTGCTGCTTTGCCTACATTGC	ACACACTTGGCGGTTCTTTCCGG
<i>CD40LG</i>	ACATACAACCAAACCTTCTCCCG	GCAAAAAGTGCTGACCCAATCA
<i>CXCL1</i>	AGCTTGCCCTCAATCCTGCATCC	TCCTTCAGGAACAGCCACCAGT
<i>CXCL10</i>	GGTGAGAAGAGATGTCTGAATCC	GTCCATCCTTGAAGCACTGCA
<i>CXCL11</i>	GACGCTGTCTTTGCATAGGC	GGATTTAGGCATCGTTGTCCTTT
<i>CXCL12</i>	ATTCTCAACACTCCAAACTGTGC	ACTTTAGCTTCGGGTCAATGC
<i>G-CSF</i>	GCTGCTTGAGCCAACCTCCATA	GAACGCGGTACGACACCTC
<i>GM-CSF</i>	TCCTGAACCTGAGTAGAGACAC	TGCTGCTTGTAGTGGCTGG
<i>ICAM1</i>	ATGCCCAGACATCTGTGTCC	GGGGTCTCTATGCCCAACAA
<i>IFNG</i>	GAGTGTGGAGACCATCAAGGAAG	TGCTTTGCGTTGGACATTCAAGTC
<i>IL10</i>	TCTCCGAGATGCCTTCAGCAGA	TCAGACAAGGCTTGGCAACCCA
<i>IL12</i>	CCTTGCACCTTCTGAAGAGATTGA	ACAGGGCCATCATAAAAGAGGT
<i>IL13</i>	CCTCATGGCGCTTTTGTTGAC	TCTGGTTCTGGGTGATGTTGA
<i>IL16</i>	GCCGAAGACCCTTGGGTTAG	GCTGGCATTGGGCTGTAGA
<i>IL17a</i>	TCCCACGAAATCCAGGATGC	GGATGTTCAAGGTTGACCATCAC
<i>IL18</i>	TCTTCATTGACCAAGGAAATCGG	TCCGGGGTGCATTATCTCTAC
<i>IL1a</i>	TGGTAGTAGCAACCAACGGGA	ACTTTGATTGAGGGCGTCATTC
<i>IL1b</i>	CCACAGACCTTCCAGGAGAATG	GTGCAGTTCAGTGATCGTACAGG
<i>IL1ra</i>	CATTGAGCCTCATGCTCTGTT	CGCTGTCTGAGCGGATGAA
<i>IL2</i>	AACTCCTGTCTTGCATTGCAC	GCTCCAGTTGTAGCTGTGTTT
<i>IL21</i>	TAGAGACAAACTGTGAGTGGTCA	GGGCATGTTAGTCTGTGTTTCTG
<i>IL25</i>	CAGGTGGTTGCATTCTTGGC	GAGCCGGTTCAAGTCTCTGT
<i>IL27/</i>	ACCGCTTTGCGGAATCTCA	AGGTCAGGGAAACATCAGGGA
<i>IL32a</i>	TGGCGGCTTATTATGAGGAGC	CTCGGCACCGTAATCCATCTC
<i>IL4</i>	CCAACCTGCTTCCCCCTCTG	TCTGTTACGGTCAACTCGGTG
<i>IL5</i>	TGGAGCTGCCTACGTGTATG	TTCGATGAGTAGAAAGCAGTGC
<i>IL6</i>	AGACAGCCACTCACCTCTTCAG	TTCTGCCAGTGCCTCTTTGCTG
<i>IL8</i>	ACTGAGAGTGATTGAGAGTGGAC	AACCCTCTGCACCCAGTTTTT
<i>SerpineE1</i>	ACCGCAACGTGGTTTTCTCA	TTGAATCCCATAGCTGCTTGAAT
<i>TNFa</i>	CCTCTCTCTAATCAGCCCTCTG	GAGGACCTGGGAGTAGATGAG
<i>TREM1</i>	GAACCTCCGAGCTGCAACTAAA	TCTAGCGTGTAGTCACATTTTAC
<i>ATF3</i>	CGCTGGAATCAGTCACTGTCAG	CTTGTTTCGGCACTTTGCAGCTG
<i>IRF2</i>	CATGCGGCTAGACATGGGTG	GCTTTCCTGTATGGATTGCC

<i>CEBPA</i>	AGGAGGATGAAGCCAAGCAGCT	AGTGCGCGATCTGGAACTGCAG
<i>CEBPB</i>	CTTCAGCCCGTACCTGGAG	GGAGAGGAAGTCGTGGTGC

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**The antibodies**

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<b>Antibody</b>	<b>Identifier</b>
Anti-p Erk1/2	4370
Anti-Erk1/2	4695
Anti-CCL2	ab214819
Anti-ICAM1	ab282575
Anti-TIMP1	16644-1-AP
Anti-GAPDH	ab8245
ERK1/2 inhibitor 1	HY-112287

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