

3 analysis.



2 Supplementary Figure 2. Kaplan-Meier survival curves of DSS from the TCGA pan-cancer3 analysis.





2 Supplementary Figure 3. Kaplan-Meier survival curves of PFI from the TCGA pan-cancer3 analysis.

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Supplementary Figure 4



Supplementary Figure 4. A. Heatmap depicting the correlation coefficients between stromal,
immune, and ESTIMATE scores and various cancer types. B. Heatmap illustrates the correlation
of abundance of different immune cell types with the listed cancer types. . ****, P < 0.0001; ***,
P < 0.001; **, P < 0.01; *, P < 0.05; n.s., not significant.



Supplementary Figure 5





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Supplementary Figure 6

GSE74602

GSEI	4002	NES	Pvalue	a value
DNA replication base excision repair	gene ranks	3.01 2.48	2.4^10 ⁻³ 2.5^10 ⁻³	1.2^10 ⁻³ 1.2^10 ⁻³
nomologus recombination	The second	2.22	2.5 ¹⁰⁻³	1.2^10 ⁻³
aminoacyl tRNA biosynthesis	0 8000 16000	2.21	2.6 ^{^10⁻³}	1.2^10 ⁻³
GSE	39393			
steroid biosynthesis	humore en el	1.98	2.3 ¹⁰⁻³	1.6^10-2
DNA replication	There is a second of the secon	1.91	2.3 ⁴ 10 ⁻³	1.6^10 ⁻²
aminoacyl tRNA biosynthesis		1.84	2.3 ¹⁰⁻³	1.6^10 ⁻²
proteasome	1.000.01.01.01.01.01.01.01.01.01.01.01.0	1.91	2.3^10 ⁻³	1.6^10 ⁻²
005	0 7500 15000			
GSE	100243			
steroid biosynthesis	Kanal and a second and a	2.31	3.7 ¹⁰⁻³	4.9^10-2
homologus recombination	10. ··· ··· ··· ··· ·	2.09 1.76	4.7 ¹⁰⁻³	5.1^10-2
RNA polymerase		2.18	5.3 ¹⁰⁻³	5.1^10 ⁻²
base excisión repair	10.11.0000 00 0. 0. 0. 0.	1.84	5.3^10 ⁻³	5.1^10 ⁻²
	0 8000 16000			
GSE	166427			
WNT signaling pathway	harring and the second s	1.54	1.2^10 ⁻³	3.3^10 ⁻²
cell cycle	······································	2.02	1.2^10 ⁻³	3.3^10-2
ribosome		1.80	1.2^10 ⁻³	3.3^10-2
DNA replication	Next in the second seco	1.88	1.2^10 ⁻³ 1 4^10 ⁻³	3.3^10-2
	0 8000 16000			
GSE	43939			
mismatch repair	here a second se	1.99	2.7^10 ⁻³	2.4^10 ⁻²
	here a second seco	2.19	3.0^10 ⁻³	2.4^10 ⁻²
aminoacyl tRNA biosynthesis	· · · · · · · · · · · · · · · · · · ·	2.25	3.3^10 ⁻³	2.4 ¹⁰ 2.4 ¹⁰⁻²
proteasome		1.95	3.3^10-3	2.4^10 ⁻²
	0 10000 20000			
GSE	144259			
ECM receptor interaction		1.64	2.0^10 ⁻³	1.2^10-2
P53 signaling pathway	/ Banking and a second se	2.03	2.1^10 ⁻³	1.2^10-2
pyrimitide metabolism		1.94	2.1^10 ⁻³	1.2^10-2
RNA degradation		2.17	2.1^10 ⁻³	1.2 ^{~10⁻²}
	0 10000 20000			
ТС	CGA			
systemic lupus erythematosus	ha an an ann a sao an	1.41	7.4^10 ⁻³	3.2^10-2
hedgehog signaling bathway	In the second se	1.62 1.40	1.4^10 ⁻² 5.9^10 ⁻²	3.9 ⁴ 10 ⁻²
WNT signaling pathway	home and the second s	1.29	6.1^10-2	1.1^10 ⁻¹
čell cyclé	1.0000000000000000000000000000000000000	1.31	6.2^10 ⁻²	1.1^10 ⁻¹
	0 15000 30000			

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Supplementary Figure 6. Positive enrichment sets of Kyoto Encyclopedia of Genes and Genomes
(KEGG) enrichment analysis of gene expression in colorectal cancer versus normal tissues across
multiple datasets. Gene sets from GSE74602, GSE89393, GSE100243, GSE166427, GSE143939,
GSE144259, and the TCGA are analyzed for pathway enrichment. The pathways are ranked based

1	on Normalized Enrichment Score (NES), P value and false discovery rate (FDR) q-values. Dotted				
2	lines across the enrichment plots indicate the threshold for statistical significance. Pathways with a				
3	P value less than 0.05 are considered significantly enriched and are indicated with asterisks.				
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GSE74602 gene ranks -1.88 natural killer cell mediated cytotoxicity calcium signaling pathway regulation of actin cytoskeleton neuroactive ligand receptor interaction olfactory transduction -1.62 -2.09 0 8000 16000 GSE893933 adipocytokine signaling pathway phosphatidylinositol signaling system vascular smooth muscle contraction calcium signaling pathway MAPK signaling pathway -1.64	P value 1.4^10 ⁻³ 1.4^10 ⁻³ 1.3^10 ⁻³ 1.3^10 ⁻³ 1.7^10 ⁻³ 1.7^10 ⁻³ 1.6^10 ⁻³ 1.6^10 ⁻³ 1.4^10 ⁻³	q value 1.2^10 ⁻³ 1.2^10 ⁻³ 1.2^10 ⁻³ 1.2^10 ⁻³ 1.2^10 ⁻³ 1.5^10 ⁻² 1.5^10 ⁻² 1.5^10 ⁻² 1.5^10 ⁻² 1.5^10 ⁻² 1.5^10 ⁻²
GSE100243 taste transduction metabolism of xenobiotics by cytochrome drug metabolism cytochrome neuroactive ligand receptor interaction olfactory transduction 0 8000 16000	1.2^10 ⁻³ 1.2^10 ⁻³ 1.2^10 ⁻³ 1.0^10 ⁻³ 1.0^10 ⁻³	2.3^10 ⁻² 2.3^10 ⁻² 2.3^10 ⁻² 2.3^10 ⁻² 2.3^10 ⁻²
GSE166427 fatty acid metabolism steroid hormone biosynthesis linoleic acid metabolism butanoate metabolism pentose and glucuronate interconversions 0 8000 16000	3.9^10 ⁻³ 3.8^10 ⁻³ 3.7^10 ⁻³ 3.7^10 ⁻³ 3.4^10 ⁻³	3.3^10 ⁻² 3.3^10 ⁻² 3.3^10 ⁻² 3.3^10 ⁻² 3.3^10 ⁻²
GSE143939 cell adhesion molecules cams calcium signaling pathway neuroactive ligand receptor interaction chemokine signaling pathway cytokine cytokine receptor interaction 0 1000 20000	1.3^10 ⁻³ 1.2^10 ⁻³ 1.2^10 ⁻³ 1.2^10 ⁻³ 1.2^10 ⁻³	1.7^10 ⁻² 1.7^10 ⁻² 1.7^10 ⁻² 1.7^10 ⁻² 1.7^10 ⁻²
GSE144259 steroid hormone biosynthesis intestinal immune network for IGA proximal tubule bicarbonate reclamation pentose and glucuronate interconversion 0 10000 20000	1.9^10 ⁻³ 1.9^10 ⁻³ 1.8^10 ⁻³ 1.8^10 ⁻³ 1.8^10 ⁻³	1.2^10 ⁻² 1.2^10 ⁻² 1.2^10 ⁻² 1.2^10 ⁻² 1.2^10 ⁻²
pentose and glucuronate interconversions asthma ascorbate and aldarate metabolism proximal tubule bicarbonate reclamation -2.38 0 15000	4.0^10 ⁻³ 4.0^10 ⁻² 4.0^10 ⁻² 3.8^10 ⁻² 3.7^10 ⁻²	3.2^10 ⁻² 3.2^10 ⁻² 3.2^10 ⁻² 3.2^10 ⁻² 3.2^10 ⁻²

Supplementary Figure 7. Negative enrichment sets of Kyoto Encyclopedia of Genes and Genomes
(KEGG) enrichment analysis of gene expression in colorectal cancer versus normal tissues across
multiple datasets. Gene sets from GSE74602, GSE89393, GSE100243, GSE166427, GSE143939,
GSE144259, and the TCGA are analyzed for pathway enrichment. The pathways are ranked based
on Normalized Enrichment Score (NES), *P* value and false discovery rate (FDR) q-values. Dotted

7 lines across the enrichment plots indicate the threshold for statistical significance. Pathways with a

1	P value less than 0.05 are considered significantly enriched and are indicated with asterisks.
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Supplementary Figure 8. The roles of STC2 in HIEC6 normal colorectal cells. A. The relative
expression of STC2 in CCLE database. B. Colony formation ability of HIEC6 after STC2 siRNA
transfection. C. Transwell migration ability of HIEC6 after STC2 siRNA transfection. n.s., not
significant.

1 Supplementary Table 1. Differentially expressed genes of 7 independent datasets (GSE74602,

GEO number	Gene ID	Gene name	Adjust P value	P value	Log2FC
GSE74602	ILMN_1691884	STC2	2.08E-11	1.22E-12	2.0051247
GSE89393	8614	STC2	5.97E-04	2.05E-05	3.171764
GSE100243	8614	STC2	4.92E-08	2.45E-11	3.342787
GSE166427	11721436_a_at	STC2	3.72E-41	2.35E-42	1.78
GSE143939	8614	STC2	8.77E-15	8.62E-17	3.751376
GSE144259	8614	STC2	8.11E-08	3.78E-10	3.852166
TCGA	ENSG00000113739.10	STC2	1.19E-54	1.46E-52	3.594413

2 GSE89393, GSE100243, GSE166427, GSE143939, GSE144259, and TCGA-COAD).