Supplemental material

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Supplementary Table 1

TCGA Patient information

Variable	Proportion
AJCC stage	
Stage I	16%
Stage II	41%
Stage III	28%
Stage IV	15%
Microsatellite status	
MSS	64%
MSI-L	17%
MSI-H	19%
Age	
<66	50%
>=66	50%
Gender	
Female	45%
Male	55%

Supplementary Table 2

Bioinformatic tools

Bulk transcriptome	
Immune cell abundance	CIBERSORT
ssGSEA	GSVA
GO	clusterProfiler
DEG	Limma
Random forest	ranger
LASSO Cox analysis	glmnet
WGCNA	WGCNA
Single-cell transcriptome	

UMAP	scanpy
cell-cell interactions (CCIs)	SingleCellSignalR
NGS	
Quality control	bcl2fastq
alignment	bwa-mem, Picard, GATK
SNP / Indel calling	VarScan2
CNV identification	FACTERA, ADTEx

Supplementary Table 3

Gene Symbol	ENTREZ ID	Gene Name
ATOH1	474	atonal bHLH transcription factor 1
B3GNT8	374907	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8
SULT1B1	27284	sulfotransferase family 1B member 1
TNFRSF19	55504	TNF receptor superfamily member 19
HOXC4	3221	homeobox C4
HBA1	3039	hemoglobin subunit alpha 1
ENO2	2026	enolase 2
HOXC11	3227	homeobox C11
SYT12	91683	synaptotagmin 12
APOD	347	apolipoprotein D
MTERF	NA	NA
PLAG1	5324	PLAG1 zinc finger
TRIM58	25893	tripartite motif containing 58
TNFAIP2	7127	TNF alpha induced protein 2
TMEM195	NA	NA

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| HOXC8 | 3224 | homeobox C8 |
| LOC100272228 | NA | NA |