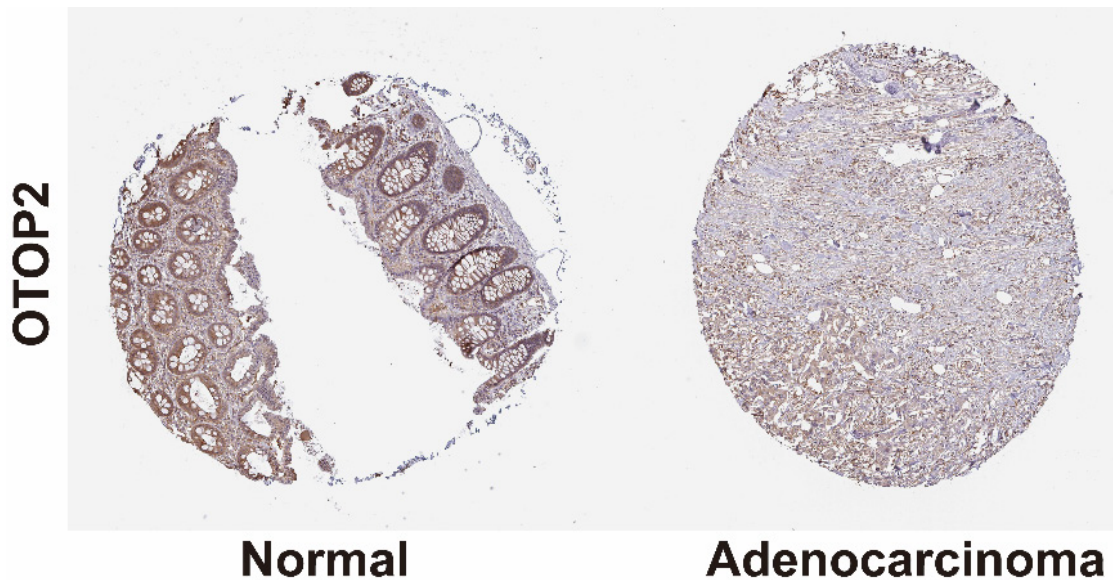


Supplementary Figure 1

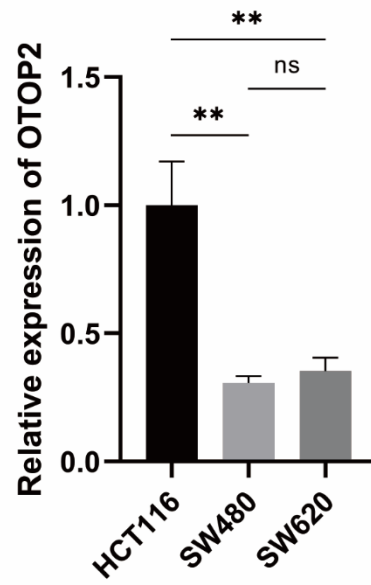
Aberrant mRNA expression of *OTOP2* in TCGA pan-cancer.

(A) Comparison of *OTOP2* mRNA expression between tumor and normal specimens in 33 kinds of cancers. (B) Comparison of *OTOP2* mRNA expression between tumor and paired normal specimens in 23 kinds of cancers ns, $P \geq 0.05$, $*P < 0.05$, $**P < 0.01$, $***P < 0.001$, $****P < 0.0001$.



Supplementary Figure 2

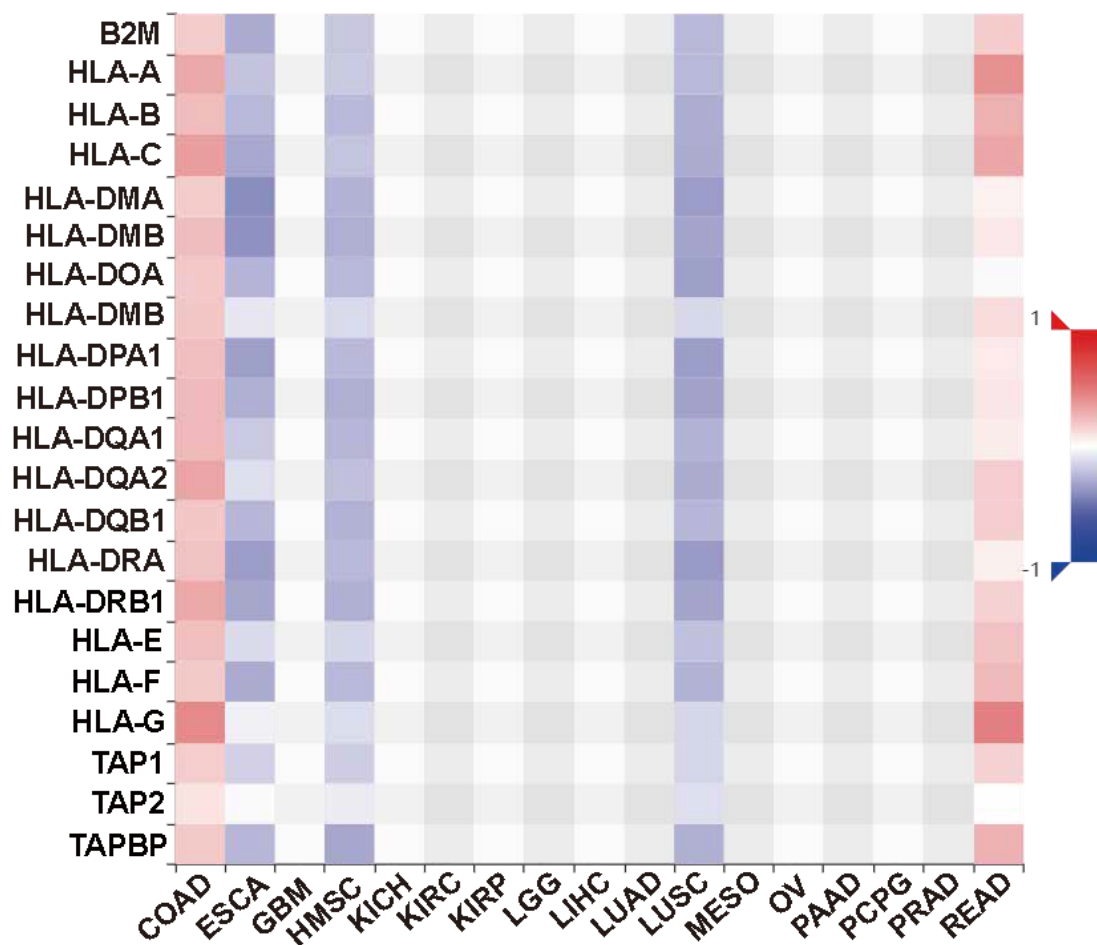
Immunohistochemistry staining images of *OTOP2* in normal colon mucosa and COAD from HPA dataset.



Supplementary Figure 3

***OTOP2* endogenous expression in HCT116, SW480 and SW620 COAD cell lines.**

The relative expression of *OTOP2* in different COAD cell lines was detected using qRT-PCR. ns, $P \geq 0.05$, ** $P < 0.01$.



Supplementary Figure 4

Correlation of *OTOP2* expression with the expression of MHC molecules in pan-cancer from TISIDB.

Supplementary Table 1 Clinical characteristics of the TCGA-COAD patients

characteristics	Low expression of OTOP2	High expression of OTOP2
n	226	228
Pathologic T stage, n (%)		
T1	6 (1.3%)	5 (1.1%)
T2	42 (9.3%)	35 (7.7%)
T3	148 (32.7%)	161 (35.5%)
T4	29 (6.4%)	27 (6%)
Pathologic N stage, n (%)		
N0	129 (28.4%)	138 (30.4%)
N1&N2	97 (21.4%)	90 (19.8%)
Pathologic M stage, n (%)		
M0	158 (39.8%)	175 (44.1%)
M1	29 (7.3%)	35 (8.8%)
Gender, n (%)		
Male	126 (27.8%)	114 (25.1%)
Female	100 (22%)	114 (25.1%)
Race, n (%)		
Asian	9 (3.2%)	2 (0.7%)
Black or African American	34 (12.1%)	25 (8.9%)
White	127 (45%)	85 (30.1%)
Histological type, n (%)		
Mucinous adenocarcinoma	30 (6.7%)	32 (7.1%)
Adenocarcinoma	192 (42.8%)	195 (43.4%)
Age, n (%)		
≤ 65	96 (21.1%)	92 (20.3%)
> 65	130 (28.6%)	136 (30%)

characteristics	Low expression of OTOP2	High expression of OTOP2
n	265	83
Pathologic T stage, n (%)		
T1	3 (0.9%)	0 (0%)
T2	36 (10.3%)	9 (2.6%)
T3	164 (47.1%)	52 (14.9%)
T4	62 (17.8%)	22 (6.3%)
Pathologic N stage, n (%)		
N0	167 (48%)	58 (16.7%)
N1&N2	98 (28.2%)	25 (7.2%)
Pathologic M stage, n (%)		
M0	247 (71%)	75 (21.6%)
M1	18 (5.2%)	8 (2.3%)
Gender, n (%)		
male	127 (36.5%)	48 (13.8%)
female	138 (39.7%)	35 (10.1%)
Race, n (%)		
Asian	265(76.2%)	83(23.9)
Histological type, n (%)		
Mucinous Adenocarcinoma	107 (30.7%)	34 (9.8%)
Adenocarcinoma	158 (45.4%)	49 (14.1%)
Age, n (%)		
≤ 65	189 (54.3%)	68 (19.5%)
> 65	76 (21.8%)	15 (4.3%)

Gene name	Primers (5' - 3')
<i>OTOP2</i>	Forward-ACATCGAGTACAGCCTCTTCG Reverse-CGCTCACTTGAACCTCGTAGAT
<i>TAP1</i>	Forward-AAAGACACTCAACCAGAAGGAG Reverse-CACCAATGTAGAGGATTCCCAC
<i>TAP2</i>	Forward-TGGACGCGGCTTTACTGTG Reverse-GCAGCCCTCTTAGCTTTAGCA
<i>HLA-A</i>	Forward-GACGCCCCCAAACGCATA Reverse-TGGGCAAACCCTCATGCTG
<i>HLA-B</i>	Forward-CAGTTCGTGAGGTTTCGACAG Reverse-CAGCCGTACATGCTCTGGA
<i>HLA-C</i>	Forward-CCATGAGGTATTTGTGGACCG Reverse-TCTCGGACTCTCGTCGTCG
<i>GAPDH</i>	Forward-GGAGCGAGATCCCTCCAAAAT Reverse-GGCTGTTGTCATACTTCTCATGG

Supplementary Table 4 The GSEA enrichment results related to *OTOP2*

ID	Description	Enrichment Score	<i>P</i> .adjust
GO:0000075	cell cycle checkpoint	-0.36974	0.035899
R-HSA-68877	Mitotic Prometaphase	-0.43368	0.000909
R-HSA-68882	Mitotic Anaphase	-0.35777	0.040929
R-HSA-69473	G2/M DNA damage checkpoint	-0.5478	0.019441
R-HSA-69481	G2/M Checkpoints	-0.41192	0.04001
R-HSA-69618	Mitotic Spindle Checkpoint	-0.46972	0.007013
R-HSA-69620	Cell Cycle Checkpoints	-0.38174	0.003471
R-HSA-2555396	Mitotic Metaphase and Anaphase	-0.35893	0.035459