

SUPPLEMENTARY TABLES

Supplementary Table 2. qRT-PCR primer sequences.

CCL2	Forward	GATCTCAGTGCAGAGGCTCG
	Reverse	TCTCCTTGGCCACAATGGTC
CD19	Forward	CTCCCATAACCTCCCTGGTCA
	Reverse	GCCCATGACCCACATCTCTC
CTSG	Forward	GAGTCAGACGGAATCGAAACG
	Reverse	CGGAGTGTATCTGTTCCCCTC
RBP5	Forward	CTGGCGTCCCAAATGAAAGA
	Reverse	GAGAGCGGAGATTGGTTGTTCT
ROBO1	Forward	TCCACACAGCAATAGCGAAG
	Reverse	CCTGTAACATGGGCTGGAGT
STC2	Forward	ATGCTACCTCAAGCACGACC
	Reverse	TCTGCTCACACTGAACC
TNFSFR4	Forward	ATGGAAGGGGAAGGGGTTCAACC
	Reverse	TCACAGTGGTACTTGGTTCACAG
ZAP70	Forward	GTTGACTCATCCTCAGAGACGAAT
	Reverse	AGGTTATCGCGCTTCAGGAA
CD247	Forward	GGCACAGTTGCCGATTACAGA
	Reverse	CTGCTGAACTTCACTCTCAGG

Supplementary Table 4. Clinicopathological features of the training set and the test set.

Total	train set (TCGA-HNSC)	test set (GSE65858)	<i>P</i> -value (Chi-Square Test)
	499	270	
Age			
≤65	324	86	<0.001
>65	175	184	
Gender			
Female	133	47	0.004
Male	366	223	
T stage			
T0-1	46	35	0.728
T2	131	80	
T3	96	58	
T4	171	97	
Unknown	55	0	
N stage			
N0	170	94	0.015
N1	65	32	
N2-3	171	144	
Nx	93	0	
M stage			
M0	185	263	0.201

M1	1	7	
Mx	313	0	
NCCN stage			
I	25	18	
II	69	37	
III	78	37	0.302
IV	259	178	
Unknown	68	0	
Grade			
G1	61	NA	
G2	298	NA	
G3	119	NA	NA
G4	2	NA	
Unknown	19	NA	

Supplementary Table 6. Comparisons of somatic variances between high- and low- risk groups.

Gene	Low-mutation (%)	Low-wild (%)	High-mutation (%)	High-wild (%)	P-value (chi-square test)
TP53	134 (54.7)	111 (45.3)	173 (70)	74 (30)	<0.001
TNN	81 (33.1)	164 (66.9)	91 (36.8)	156 (63.2)	0.379
FAT1	49 (20)	196 (80)	54 (21.9)	193 (78.1)	0.612
CDKN2A	44 (18)	201 (82)	44 (17.8)	203 (82.2)	0.966
MUC16	42 (17.1)	203 (82.9)	40 (16.2)	207 (83.8)	0.778
CSMD3	42 (17.1)	203 (82.9)	40 (16.2)	207 (83.8)	0.778
PIK3CA	39 (15.9)	206 (84.1)	40 (16.2)	207 (83.8)	0.934
NOTCH1	39 (15.9)	206 (84.1)	37 (15)	210 (85)	0.773
SYNE1	39 (15.9)	206 (84.1)	35 (14.2)	212 (85.8)	0.588
LRP1B	32 (13.1)	213 (86.9)	35 (14.2)	212 (85.8)	0.72
KMT2D	20 (8.2)	225 (91.8)	42 (17)	205 (83)	0.003
PCLO	27 (11)	218 (89)	32 (13)	215 (87)	0.509
NSD1	34 (13.9)	211 (86.1)	20 (8.1)	227 (91.9)	0.04
DNAH5	27 (11)	218 (89)	27 (10.9)	220 (89.1)	0.975
USH2A	29 (11.8)	216 (88.2)	22 (8.9)	225 (91.1)	0.286
FLG	22 (9)	223 (91)	27 (10.9)	220 (89.1)	0.47
CASP8	27 (11)	218 (89)	20 (8.1)	227 (91.9)	0.27
RYR2	20 (8.2)	225 (91.8)	22 (8.9)	225 (91.1)	0.768
PKHD1L1	17 (6.9)	228 (93.1)	25 (10.1)	222 (89.9)	0.207
XIRP2	25 (10.2)	220 (89.8)	15 (6.1)	232 (93.9)	0.094

Supplementary Table 7. Molecular docking results of the top 10 compounds.

Rank	ZINC ID	Compound name	Binding energy (kcal/mol)
1	ZINC000011679756	Eltrombopag	-8.3
2	ZINC0000116473771	none	-8
3	ZINC000012503187	Conivaptan	-7.8

4	ZINC000003784182	Differin	-7.6
5	ZINC000052955754	Ergotamine	-7.5
6	ZINC000003945984	Vexol	-7.5
7	ZINC000003795819	Palonosetron	-7.4
8	ZINC000084668739	Lifitegrast	-7.4
9	ZINC000003875484	Androxy	-7.3
10	ZINC000064033452	Lumacaftor	-7.3
