Table S1. Clinical features of 50 patients with OSCC

No.	Age	Sex	Location	TNM	Differentiation
1	81	F	Gingiva	T3N0M0	Well
2	53	M	Floor of mouth	T2N0M0	Poor
3	66	M	Gingiva	T2N2bM0	Moderate
4	67	F	Floor of mouth	T2N0M0	Moderate to poor
5	62	M	Gingiva	T2N0M0	Moderate
6	61	F	Buccal	T2N2bM0	Moderate
7	62	M	Tongue	T1N0M0	Moderate to poor
8	64	M	Floor of mouth	T1N2bM0	Well
9	65	F	Gingiva	T2N0M0	Well
10	46	M	Tongue	T2N2bM0	Moderate to poor
11	70	M	Gingiva	T3N0M0	Moderate
12	62	M	Buccal	T3N2bM0	Moderate to poor
13	50	F	Tongue	T3N2bM0	Moderate
14	34	M	Tongue	T1N2bM0	Moderate to poor
15	51	F	Buccal	T2N1Mo	Poor
16	74	M	Buccal	T2N0M0	Moderate
17	59	M	Tongue	T2N0M0	Moderate to poor
18	57	M	Palate	T3N0M0	Well
19	65	M	Gingiva	T2N0M0	Poor
20	52	M	Palate	T2N1M0	Moderate
21	65	M	Tongue	T2N2bM0	Moderate to poor
22	67	F	Gingiva	T2N2bM0	Moderate
23	77	M	Gingiva	T3N1M0	Poor
24	54	F	Buccal	T1N2bM0	Moderate
25	66	M	Tongue	T2N2cM0	Moderate to poor
26	62	M	Oropharynx	TisN0M0	Well
27	67	F	Buccal	T1N0M0	Well
28	74	F	Gingiva	T3N2bM0	Moderate to poor
29	69	M	Gingiva	T1N2bM0	Moderate
30	63	M	Tongue	T2N2bM0	Moderate
31	43	M	Tongue	T2N2aM0	Poor
32	60	F	Gingiva	T1N0M0	Well
33	62	F	Buccal	T3N0M0	Moderate to poor
34	77	M	Tongue	T3N2bM0	Well
35	56	M	Buccal	T2N1M0	Moderate
36	39	F	Tongue	T3N2bM0	Moderate
37	48	M	Buccal	T1N1M0	Moderate to poor
38	51	M	Floor of mouth	T1N0M0	Well
39	62	F	Oropharynx	T2N0M0	Moderate to poor
40	70	F	Tongue	T2N1M0	Poor
41	52	F	Floor of mouth	T3N2bM0	Poor
42	47	M	Gingiva	T1N1M0	Moderate
43	66	M	Palate	T1N2aM0	Poor
44	61	M	Tongue	T3N1M0	Moderate to poor
45	56	F	Tongue	T2N0M0	Moderate
46	71	M	Tongue	T2N1M0	Moderate
47	42	M	Floor of mouth	T3N2cM0	Moderate to poor

48	33	M	Tongue	T2N2bM0	Moderate
49	45	F	Tongue	T3N2cM0	Well
50	58	F	Buccal	T1N0M0	Moderate

OSCC oral squamous cell carcinoma, F female, M male; TNM classification and tumor stage were determined by the Union for International Cancer Control (UICC).

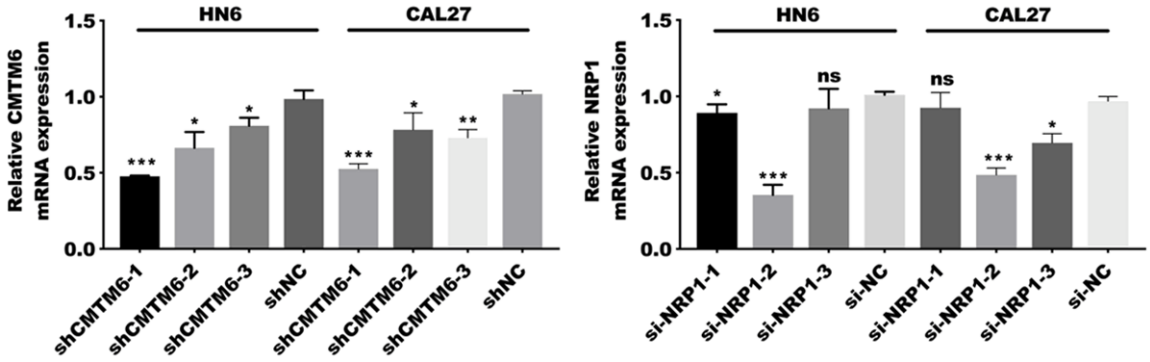
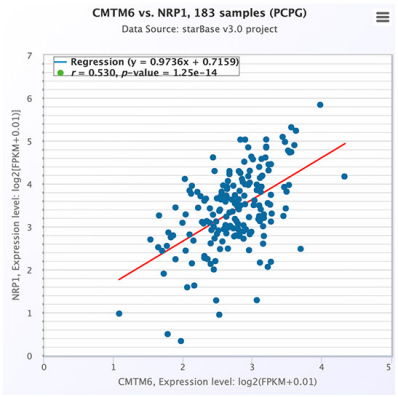
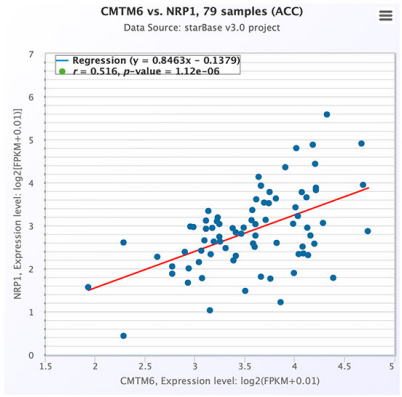
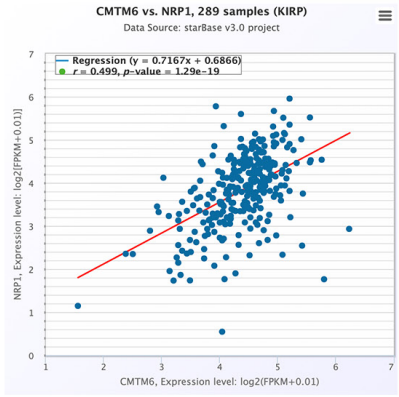
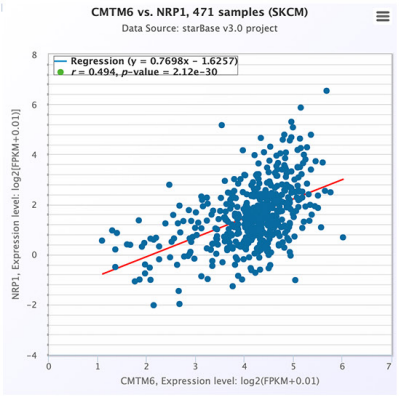


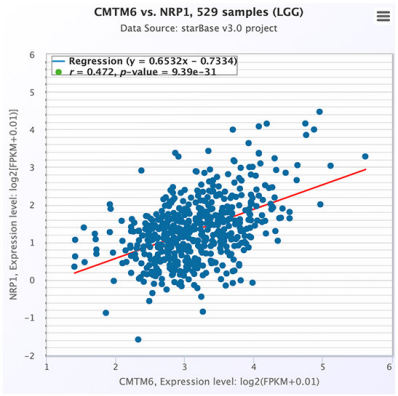
Figure S1. The interference efficiency was determined by qRT-PCR. The sequences of shCMTM6-1 and si-NRP1-2 and the corresponding control were introduced in this study.

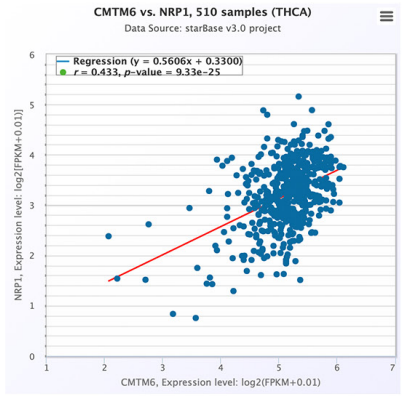

CMTM6 vs. NRP1, 183 samples (PCPG)
Data Source: starBase v3.0 project
Regression (y = 0.9736x + 0.7159)
r = 0.530, p-value = 1.25e-14
NRP1, Expression level: log2[FPKM+0.01)]
CMTM6, Expression level: log2(FPKM+0.01)

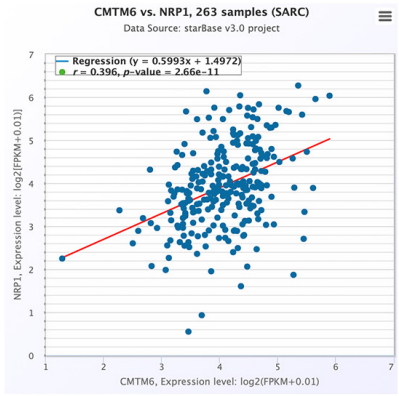

CMTM6 vs. NRP1, 79 samples (ACC)
Data Source: starBase v3.0 project
Regression (y = 0.8463x − 0.1379)
r = 0.516, p-value = 1.12e-06
NRP1, Expression level: log2[FPKM+0.01)]
CMTM6, Expression level: log2(FPKM+0.01)

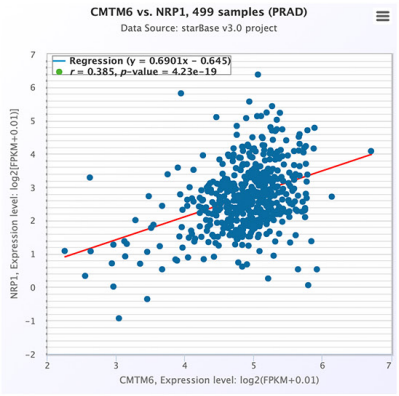

CMTM6 vs. NRP1, 289 samples (KIRP)
Data Source: starBase v3.0 project
Regression (y = 0.7167x + 0.6866)
r = 0.495, p-value = 1.29e-19
NRP1, Expression level: log2[FPKM+0.01)]
CMTM6, Expression level: log2(FPKM+0.01)

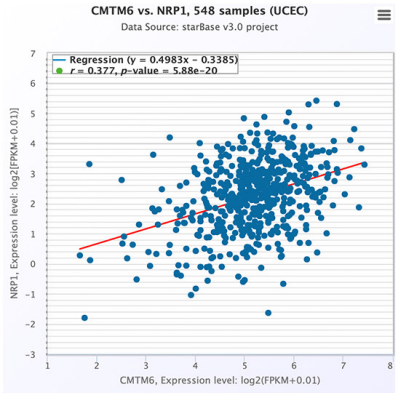

CMTM6 vs. NRP1, 471 samples (SKCM)
Data Source: starBase v3.0 project
Regression (y = 0.7698x − 1.6257)
r = 0.494, p-value = 2.12e-30
NRP1, Expression level: log2[FPKM+0.01)]
CMTM6, Expression level: log2(FPKM+0.01)

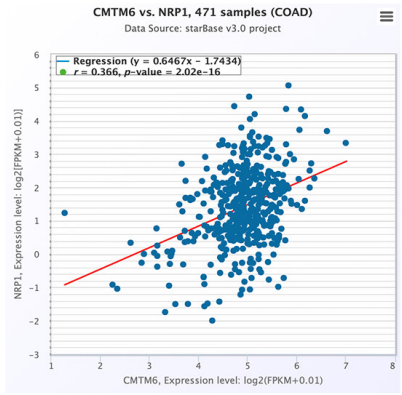

CMTM6 vs. NRP1, 529 samples (LGG)
Data Source: starBase v3.0 project
Regression (y = 0.6532x − 0.7334)
r = 0.472, p-value = 9.39e-31
NRP1, Expression level: log2[FPKM+0.01)]
CMTM6, Expression level: log2(FPKM+0.01)

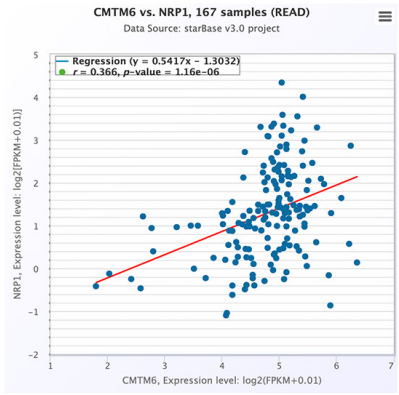

CMTM6 vs. NRP1, 510 samples (THCA)
Data Source: starBase v3.0 project
Regression (y = 0.5606x + 0.3300)
r = 0.433, p-value = 9.33e-25
NRP1, Expression level: log2[FPKM+0.01)]
CMTM6, Expression level: log2(FPKM+0.01)

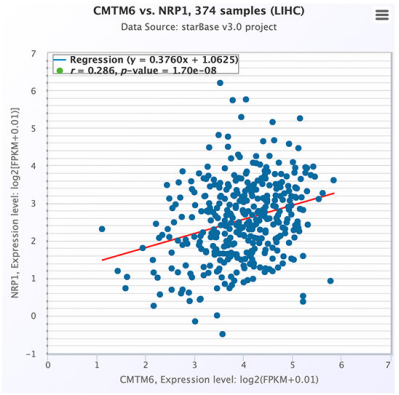

CMTM6 vs. NRP1, 263 samples (SARC)
Data Source: starBase v3.0 project
Regression (y = 0.5993x + 1.4972)
r = 0.396, p-value = 2.66e-11
NRP1, Expression level: log2[FPKM+0.01)]
CMTM6, Expression level: log2(FPKM+0.01)


CMTM6 vs. NRP1, 499 samples (PRAD)
Data Source: starBase v3.0 project
Regression (y = 0.6901x − 0.645)
r = 0.385, p-value = 4.23e-19
NRP1, Expression level: log2[FPKM+0.01)]
CMTM6, Expression level: log2(FPKM+0.01)


CMTM6 vs. NRP1, 548 samples (UCEC)
Data Source: starBase v3.0 project
Regression (y = 0.4983x − 0.3385)
r = 0.377, p-value = 5.88e-20
NRP1, Expression level: log2[FPKM+0.01)]
CMTM6, Expression level: log2(FPKM+0.01)


CMTM6 vs. NRP1, 471 samples (COAD)
Data Source: starBase v3.0 project
Regression (y = 0.6467x − 1.7434)
r = 0.366, p-value = 2.02e-16
NRP1, Expression level: log2[FPKM+0.01)]
CMTM6, Expression level: log2(FPKM+0.01)


CMTM6 vs. NRP1, 167 samples (READ)
Data Source: starBase v3.0 project
Regression (y = 0.5417x − 1.3032)
r = 0.366, p-value = 1.16e-06
NRP1, Expression level: log2[FPKM+0.01)]
CMTM6, Expression level: log2(FPKM+0.01)


CMTM6 vs. NRP1, 374 samples (LIHC)
Data Source: starBase v3.0 project
Regression (y = 0.3760x + 1.0625)
r = 0.286, p-value = 1.70e-08
NRP1, Expression level: log2[FPKM+0.01)]
CMTM6, Expression level: log2(FPKM+0.01)

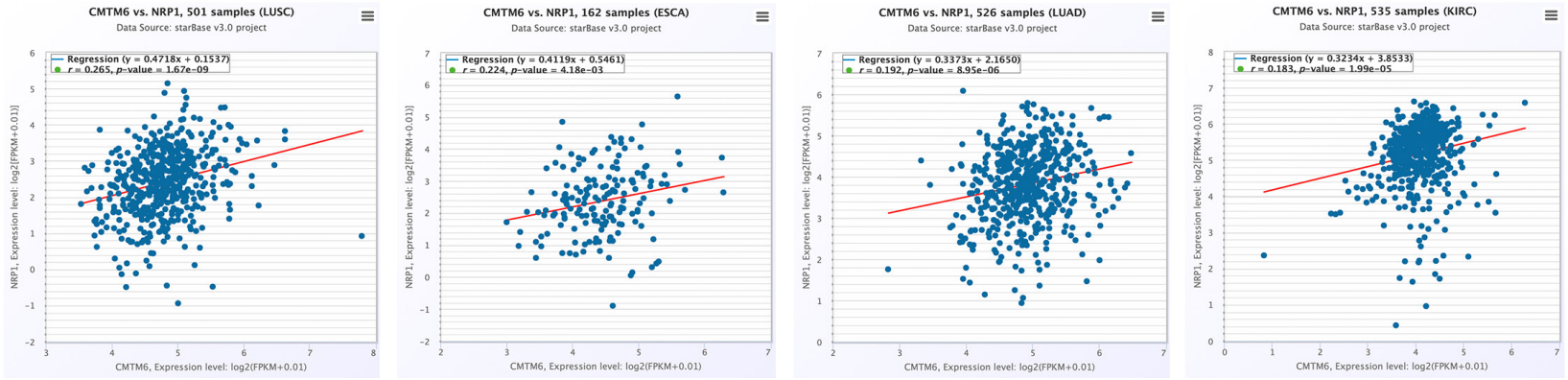


Figure S2. Analysis in The Cancer Genome Atlas (TCGA) of multiple cancer types showed that CMTM6 mRNA expression levels were positively related to NRP1 mRNA levels.

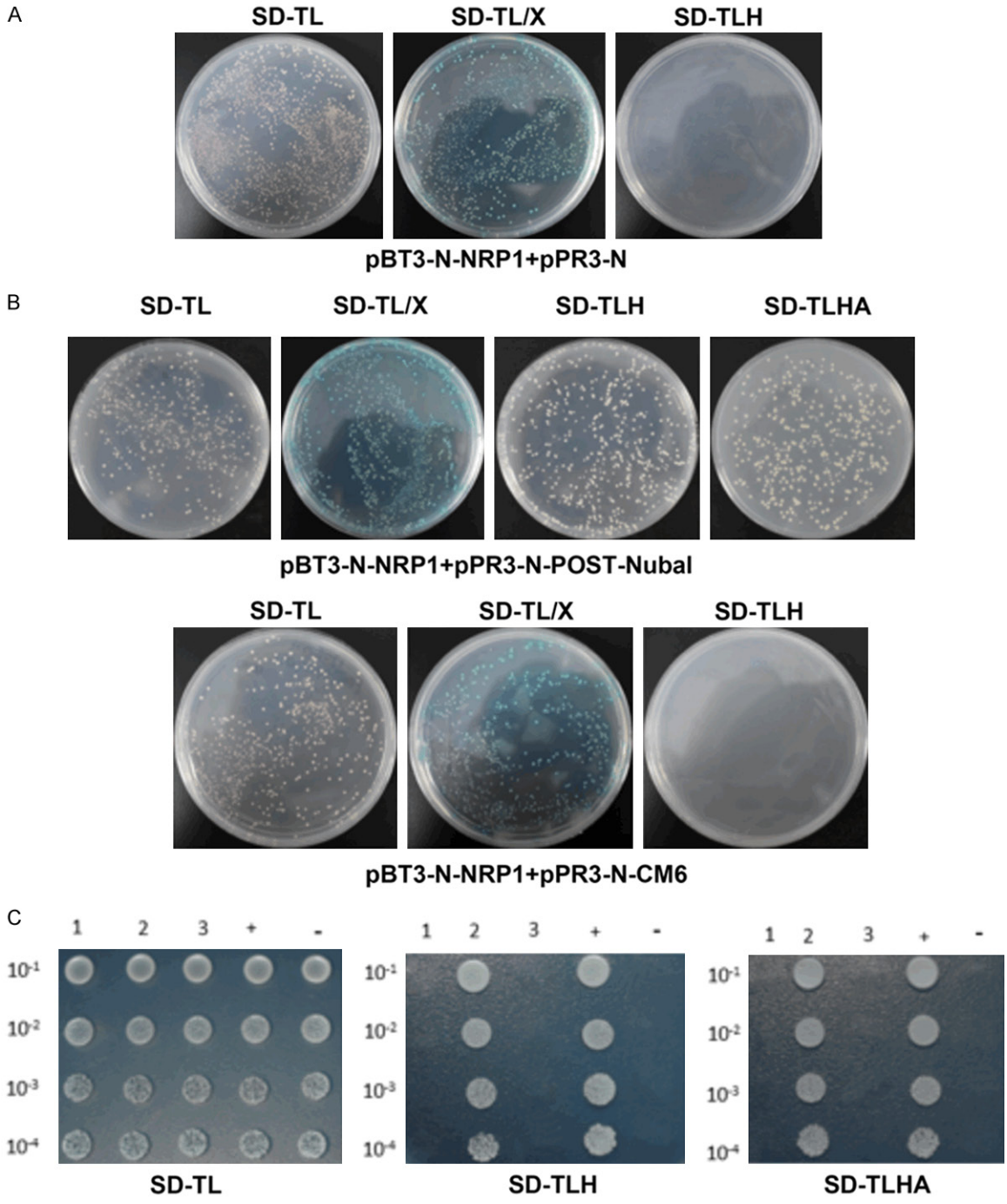


Figure S3. The Yeast two-hybrid assay was performed to verify the physical interaction between NRP1 and CMTM6. The DNA sequences encoding NRP1 and CMTM6 gene were cloned into the PBT3-N and PPR3-N vector, respectively. NRP1 worked as the Bait (pBT3-N-NRP1). CMTM6 was the Prey (pPR3-N-CM6). A. Bait plasmid toxicity detection and self-activation detection. The three plates from left to right were SD/-Leu/-Trp, SD/-Leu/-Trp/X, SD/-Leu/-Trp/-His. B. Both recombinant plasmids were co-transformed into the yeast strain NMY51. Protein interaction enables the yeast to make the His3 enzyme, thereby permitting histidine biosynthesis and growth on His minimal medium. Colony formation was not detected in the SD/-Leu/-Trp/-His plate, therefore, protein interaction was not existed. C. Point board verified the result. 1: co-transformation of pBT3-N-NRP1 and pPR3-N. 2: co-transformation of pBT3-N-CM6 and pPR3-N-POST-Nubal. 3: co-transformation of pBT3-N-NRP1 and pPR3-N-CM6. +: co-transformation of pTSU2-APP and pNubG-Fe65 (positive control). -: co-transformation of pBT3-SUC and PPR3-N (negative control).