**Supplementary Material**

**Supplementary Table 1**Clinical characteristics of the six enrolled patients

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| number | Sex | Age at surgery(years) | Tumor size(cm) | TNM | Histological grade |
| C1 | Female | 51 | 3.2 | T3N0M0 | High |
| C2 | Male | 65 | 1.5 | T2N0M0 | High |
| C3 | Male | 45 | 3.5 | T2N0M0 | High |
| C4 | Male | 53 | 2.5 | T4aN2M0 | Middle |
| C5 | Male | 43 | 2.0 | T2N2M0 | High |
| C6 | Male | 48 | 3.0 | T2N0M0 | Middle |

**Supplementary Table 2 The GSEA results of four-lncRNA**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **lncRNA** | **GS follow link to MSIGDB** | **SIZE** | **ES** | **NES** | **NOM p-val** | **FDR q-val** |
| LINC00152 | GO\_CHANNEL\_REGULATOR\_ACTIVITY | 1 | 0.997491 | 1.346958 | 0.008197 | 1 |
|  | GO\_CALCIUM\_CHANNEL\_REGULATOR\_ACTIVITY | 1 | 0.997491 | 1.346958 | 0.008197 | 1 |
|  | GO\_ION\_CHANNEL\_REGULATOR\_ACTIVITY | 1 | 0.997491 | 1.346958 | 0.008197 | 1 |
|  | GO\_SINGLE\_FERTILIZATION | 1 | 0.978635 | 1.302637 | 0.023158 | 1 |
|  | GO\_MEMBRANE\_FUSION | 1 | 0.978635 | 1.302637 | 0.023158 | 1 |
|  | GO\_SEXUAL\_REPRODUCTION | 1 | 0.978635 | 1.302637 | 0.023158 | 1 |
|  | GO\_CELLULAR\_PROCESS\_INVOLVED\_IN\_REPRODUCTION\_IN\_MULTICELLULAR\_ORGANISM | 1 | 0.978635 | 1.302637 | 0.023158 | 1 |
|  | GO\_MULTI\_ORGANISM\_REPRODUCTIVE\_PROCESS | 1 | 0.978635 | 1.302637 | 0.023158 | 1 |
|  | GO\_PLASMA\_MEMBRANE\_FUSION | 1 | 0.978635 | 1.302637 | 0.023158 | 1 |
|  | GO\_MEMBRANE\_ORGANIZATION | 1 | 0.978635 | 1.302637 | 0.023158 | 1 |
|  | GO\_FERTILIZATION | 1 | 0.978635 | 1.302637 | 0.023158 | 1 |
|  | GO\_REPRODUCTION | 1 | 0.978635 | 1.302637 | 0.023158 | 1 |
|  | GO\_MULTICELLULAR\_ORGANISM\_REPRODUCTION | 1 | 0.978635 | 1.302637 | 0.023158 | 1 |
|  | GO\_FUSION\_OF\_SPERM\_TO\_EGG\_PLASMA\_MEMBRANE\_INVOLVED\_IN\_SINGLE\_FERTILIZATION | 1 | 0.978635 | 1.302637 | 0.023158 | 1 |
|  | GO\_CELL\_MOTILITY | 2 | 0.90619 | 1.464428 | 0.037328 | 1 |
|  | GO\_LOCOMOTION | 2 | 0.90619 | 1.464428 | 0.037328 | 0.6605 |
|  | GO\_REGULATION\_OF\_CELLULAR\_COMPONENT\_MOVEMENT | 2 | 0.90619 | 1.464428 | 0.037328 | 0.440334 |
|  | GO\_REGULATION\_OF\_GTPASE\_ACTIVITY | 2 | -0.95186 | -1.51114 | 0.009542 | 0.105536 |
|  | GO\_ENZYME\_ACTIVATOR\_ACTIVITY | 2 | -0.95186 | -1.51114 | 0.009542 | 0.079152 |
|  | GO\_NUCLEOSIDE\_TRIPHOSPHATASE\_REGULATOR\_ACTIVITY | 2 | -0.95186 | -1.51114 | 0.009542 | 0.063321 |
|  | GO\_POSITIVE\_REGULATION\_OF\_GTPASE\_ACTIVITY | 2 | -0.95186 | -1.51114 | 0.009542 | 0.052768 |
|  | GO\_GTPASE\_REGULATOR\_ACTIVITY | 2 | -0.95186 | -1.51114 | 0.009542 | 0.04523 |
|  | GO\_INFLAMMATORY\_RESPONSE | 1 | -0.99234 | -1.32646 | 0.013333 | 0.389442 |
|  | GO\_REGULATION\_OF\_INFLAMMATORY\_RESPONSE | 1 | -0.99234 | -1.32646 | 0.013333 | 0.361625 |
|  | GO\_POSITIVE\_REGULATION\_OF\_INFLAMMATORY\_RESPONSE | 1 | -0.99234 | -1.32646 | 0.013333 | 0.337516 |
|  | GO\_MIRNA\_BINDING | 1 | -0.99234 | -1.32646 | 0.013333 | 0.316422 |
|  | GO\_RIBONUCLEOPROTEIN\_COMPLEX\_BINDING | 1 | -0.99234 | -1.32646 | 0.013333 | 0.297808 |
|  | GO\_REGULATORY\_RNA\_BINDING | 1 | -0.99234 | -1.32646 | 0.013333 | 0.281264 |
|  | GO\_NEGATIVE\_REGULATION\_OF\_GENE\_SILENCING\_BY\_MIRNA | 1 | -0.99234 | -1.32646 | 0.013333 | 0.26646 |
|  | GO\_POSITIVE\_REGULATION\_OF\_CELL\_POPULATION\_PROLIFERATION | 4 | -0.8645 | -1.5792 | 0.017613 | 0.086961 |
|  | GO\_REGULATION\_OF\_CELL\_POPULATION\_PROLIFERATION | 4 | -0.8645 | -1.5792 | 0.017613 | 0.043481 |
| LINC01405 | GO\_NUCLEAR\_OUTER\_MEMBRANE\_ENDOPLASMIC\_RETICULUM\_MEMBRANE\_NETWORK | 2 | -0.9922 | -1.33064 | 0.011321 | 0.577555 |
|  | GO\_OXIDATION\_REDUCTION\_PROCESS | 1 | -0.9922 | -1.33063 | 0.011321 | 0.551302 |
|  | GO\_VESICLE\_MEMBRANE | 1 | -0.9922 | -1.33063 | 0.011321 | 0.527333 |
|  | GO\_OXIDOREDUCTASE\_ACTIVITY\_OXIDIZING\_METAL\_IONS | 1 | -0.9922 | -1.33063 | 0.011321 | 0.50536 |
|  | GO\_COFACTOR\_BINDING | 1 | -0.9922 | -1.33063 | 0.011321 | 0.485146 |
|  | GO\_TETRAPYRROLE\_BINDING | 1 | -0.9922 | -1.33063 | 0.011321 | 0.466486 |
|  | GO\_OXIDOREDUCTASE\_ACTIVITY | 1 | -0.9922 | -1.33063 | 0.011321 | 0.449209 |
|  | GO\_OXIDOREDUCTASE\_ACTIVITY\_OXIDIZING\_METAL\_IONS\_OXYGEN\_AS\_ACCEPTOR | 1 | -0.9922 | -1.33063 | 0.011321 | 0.433166 |
|  | GO\_DEFENSE\_RESPONSE | 4 | -0.80819 | -1.58292 | 0.012097 | 0.230463 |
|  | GO\_G\_PROTEIN\_COUPLED\_RECEPTOR\_SIGNALING\_PATHWAY | 1 | -0.98596 | -1.36186 | 0.01751 | 0.850852 |
|  | GO\_GTPASE\_ACTIVITY | 1 | -0.98596 | -1.36186 | 0.01751 | 0.756313 |
|  | GO\_HYDROLASE\_ACTIVITY\_ACTING\_ON\_ACID\_ANHYDRIDES | 1 | -0.98596 | -1.36186 | 0.01751 | 0.680682 |
|  | GO\_REGULATION\_OF\_G\_PROTEIN\_COUPLED\_RECEPTOR\_SIGNALING\_PATHWAY | 1 | -0.98596 | -1.36186 | 0.01751 | 0.618802 |
|  | GO\_RESPONSE\_TO\_BIOTIC\_STIMULUS | 3 | -0.82203 | -1.4544 | 0.034682 | 0.64275 |
|  | GO\_ENDOPLASMIC\_RETICULUM | 2 | -0.88578 | -1.36078 | 0.03992 | 0.576535 |
|  | GO\_POSITIVE\_REGULATION\_OF\_HYDROLASE\_ACTIVITY | 3 | -0.84188 | -1.44842 | 0.046642 | 0.511583 |
|  | GO\_POSITIVE\_REGULATION\_OF\_CATALYTIC\_ACTIVITY | 3 | -0.84188 | -1.44842 | 0.046642 | 0.409266 |
|  | GO\_POSITIVE\_REGULATION\_OF\_MOLECULAR\_FUNCTION | 3 | -0.84188 | -1.44842 | 0.046642 | 0.341055 |
|  | HALLMARK\_P53\_PATHWAY | 1 | -0.97592 | -1.29671 | 0.062619 | 0.046284 |
| RP11-54H7.4 | GO\_NEGATIVE\_REGULATION\_OF\_PHOSPHORYLATION | 2 | -0.9279 | -1.44626 | 0.02243 | 1 |
|  | GO\_REGULATION\_OF\_PHOSPHORYLATION | 2 | -0.9279 | -1.44626 | 0.02243 | 0.52685 |
|  | GO\_REGULATION\_OF\_INTRACELLULAR\_SIGNAL\_TRANSDUCTION | 2 | -0.9279 | -1.39113 | 0.039526 | 0.321743 |
|  | GO\_CELL\_MOTILITY | 2 | -0.91243 | -1.42158 | 0.044266 | 0.482154 |
|  | GO\_LOCOMOTION | 2 | -0.91243 | -1.42158 | 0.044266 | 0.361616 |
|  | GO\_REGULATION\_OF\_CELLULAR\_COMPONENT\_MOVEMENT | 2 | -0.91243 | -1.42158 | 0.044266 | 0.289293 |
| RP11-760H22.2 | GO\_NEGATIVE\_REGULATION\_OF\_PHOSPHORUS\_METABOLIC\_PROCESS | 3 | 0.878917 | 1.55002 | 0.008333 | 0.360647 |
|  | GO\_REGULATION\_OF\_PHOSPHORUS\_METABOLIC\_PROCESS | 3 | 0.878917 | 1.55002 | 0.008333 | 0.180324 |
|  | GO\_NEGATIVE\_REGULATION\_OF\_PHOSPHORYLATION | 2 | 0.931289 | 1.447353 | 0.022965 | 0.607042 |
|  | GO\_REGULATION\_OF\_PHOSPHORYLATION | 2 | 0.931289 | 1.447353 | 0.022965 | 0.455281 |
|  | GO\_NUCLEIC\_ACID\_PHOSPHODIESTER\_BOND\_HYDROLYSIS | 1 | 0.969547 | 1.341251 | 0.026316 | 0.821226 |
|  | GO\_HYDROLASE\_ACTIVITY\_ACTING\_ON\_ESTER\_BONDS | 1 | 0.969547 | 1.341251 | 0.026316 | 0.746569 |
|  | GO\_NUCLEASE\_ACTIVITY | 1 | 0.969547 | 1.341251 | 0.026316 | 0.684355 |
|  | GO\_EXONUCLEASE\_ACTIVITY | 1 | 0.969547 | 1.341251 | 0.026316 | 0.631713 |

**Supplementary Table 3** All the sequences of lncRNA primers used for qRT-PCR

|  |  |  |
| --- | --- | --- |
| Target ID | Primer | sequence (5’ to 3’) |
| ENST00000562836-CDH1-205 | ForwardReverse | CCTTATGATTCTCTGCTCGTGTTTCAAGTAGTCATAGTCCTGGTCTT |
| ENST00000304425-MIR31HG- | ForwardReverse | CCAGATCCTAGCCTCCAGTTAGGGAAGCACCAGAGAAGTT |
| ENST00000467790-IFI44-204 | ForwardReverse | TGTCTGCCTTGAGAACTTATGAACCACCAAAGCCTGATGCGTTA |
| ENST00000472152-IFI44-206 | ForwardReverse | GGTTCACGTAAATTTCCTCACATCAATAAAACACATCCCTTTGGTCTT |
| ENST00000618966-AL161431 | ForwardReverse | TGGGTTCGTTGTGCATGAGAGGAGGTACGTGTATGACAGCTT |
| ENST00000533110-CTSB-227 | ForwardReverse | AGACCGTACTCCATCCCTCCCTGTTTGTAGGTCGGGCTGT |
| ENST00000568321-HAS3-204 | ForwardReverse | CACAAGTTTCCATGCCGCTGGACGCACGCTTCTCCATCAA |
| ENST00000569117-CDH3-210 | ForwardReverse | GCAACTTATGGCTGTAGTGAATGACCTGGTGGATGTCTCTTGT |
| ENST00000462765-LEPR-206 | ForwardReverse | CTGTGCCAACAGCCAAACTCATGGTACCAATGGTGGGCTG |
| ENST00000462114-AMOT-205 | ForwardReverse | AGAGCGTCTAGAGACTGCCAATTGGTAGAACGGGCAGTGG |
| ENST00000595005-AC020909 | ForwardReverse | GTGCGTGGAATCCTCTATTACCAGGCATTCTGGTCACTGTTC |
| ENST00000331096-LINC01405 | ForwardReverse | TGAAATGTATCTGGCCCAATCGAAAGATGTTCCTCGCCCTCT |
| ENST00000520544-AC091563 | ForwardReverse | CCGTTAGAGCACTGATGACATTACACTACTCTGTGGCAGGAAT |
| ENST00000453722-LINC00511-201  | ForwardReverse | TGATGTCCCAGCACGAGTAGCCACCCAATTCCCCACTTTC |
| ENST00000331944-LINC00152-201 | ForwardReverse | TCCAGCACCTCTACCTGTTGGGACAAGGGATTAAGACACATAGA |
| GAPDH | ForwardReverse | CACCCACTCCTCCACCTTTGATCTCTCTTCCTCTTGTGCTCTTGC |

**Supplementary FIGURE 1** Confirmation of overlapping mRNAs in HNSC by GEPIA. HNSC, head and neck squamous cell carcinoma. (*p*<0.05)

**Supplementary FIGURE 2** (**Continued**)Confirmation of overlapping mRNAs in HNSC by GEPIA. HNSC, head and neck squamous cell carcinoma.

**Supplementary FIGURE 3** Coexpression analysis of TFs and mRNAs in HNSCs analyzed by StarBase. HNSC, head and neck squamous cell carcinoma.

**Supplementary FIGURE 4** (**Continued**) Coexpression analysis of TFs and mRNAs in HNSCs analyzed by StarBase. HNSC, head and neck squamous cell carcinoma.