**Supplementary Table 2.** Clinical features of HNSCC patients in TCGA database.

|  |  |  |
| --- | --- | --- |
| **Variable** | **Number of samples (%)** | **Total (*N=527*)** |
| Age: |  | 527 |
| <=65 | 345 (65.5%) |  |
| >65 | 182 (34.5%) |  |
| Gender: |  | 527 |
| female | 142 (26.9%) |  |
| male | 385 (73.1%) |  |
| Race: |  | 513 |
| american indian or alaska native | 2 (0.39%) |  |
| asian | 11 (2.14%) |  |
| black or african american | 48 (9.36%) |  |
| white | 452 (88.1%) |  |
| Stage: |  | 513 |
| I | 21 (4.09%) |  |
| II | 98 (19.1%) |  |
| III | 107 (20.9%) |  |
| IV | 287 (55.9%) |  |
| AJCC T: |  | 511 |
| T1 | 37 (7.24%) |  |
| T2 | 151 (29.5%) |  |
| T3 | 139 (27.2%) |  |
| T4 | 184 (36.0%) |  |
| AJCC N: |  | 505 |
| N0 | 245 (48.5%) |  |
| N1 | 85 (16.8%) |  |
| N2 | 166 (32.9%) |  |
| N3 | 9 (1.78%) |  |
| AJCC M: |  | 501 |
| M0 | 495 (98.8%) |  |
| M1 | 6 (1.20%) |  |
| Grade: |  | 505 |
| G1 | 63 (12.5%) |  |
| G2 | 310 (61.4%) |  |
| G3 | 125 (24.8%) |  |
| G4 | 7 (1.39%) |  |
| Alcohol history: |  | 516 |
| No | 165 (32.0%) |  |
| Yes | 351 (68.0%) |  |
| Smoke history: |  | 514 |
| Lifelong Non-smoker | 122 (23.7%) |  |
| Current smoker | 177 (34.4%) |  |
| Current reformed smoker for > 15 years | 73 (14.2%) |  |
| Current reformed smoker for ≤15 years | 140 (27.2%) |  |
| Current reformed smoker, duration not specified | 2 (0.39%) |  |
| Site: |  | 527 |
| larynx | 126 (23.9%) |  |
| oral cavity | 344 (65.3%) |  |
| other | 1 (0.19%) |  |
| pharynx | 56 (10.6%) |  |
| Radiation therapy: |  | 416 |
| NO | 144 (34.6%) |  |
| YES | 272 (65.4%) |  |
| Therapy outcome: |  | 383 |
| Complete Remission/Response | 338 (88.3%) |  |
| Partial Remission/Response | 6 (1.57%) |  |
| Stable Disease | 5 (1.31%) |  |
| Persistent Disease | 4 (1.04%) |  |
| Progressive Disease | 30 (7.83%) |  |
| Lymphovascular invasion present: |  | 355 |
| NO | 231 (65.1%) |  |
| YES | 124 (34.9%) |  |
| HPV: |  | 101 |
| Negative | 57 (56.4%) |  |
| Positive | 44 (43.6%) |  |

**Supplementary Table 2.** The differential expression levels and classification of differential expressed homeobox genes between HNSCC tumor and normal samples.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Gene** | **Class** | **Log2(FC)** | **Average Expression** | **P value** |
| HOXC6 | ANTP | 4.246 | 6.241 | 3.37E-51 |
| HOXD11 | ANTP | 5.754 | 7.120 | 1.02E-50 |
| HOXC9 | ANTP | 4.164 | 5.781 | 2.70E-48 |
| HOXA10 | ANTP | 4.148 | 6.953 | 1.44E-41 |
| LBX2 | ANTP | 2.502 | 5.096 | 3.33E-39 |
| HOXC11 | ANTP | 4.913 | 6.111 | 1.95E-38 |
| HOXC8 | ANTP | 4.030 | 5.284 | 4.89E-38 |
| SHOX2 | PRD | 3.280 | 7.493 | 3.03E-35 |
| HOXD10 | ANTP | 4.219 | 8.089 | 1.30E-34 |
| HOXC13 | ANTP | 4.434 | 8.046 | 1.10E-32 |
| HOXC4 | ANTP | 3.027 | 6.318 | 1.02E-30 |
| GBX2 | ANTP | 3.664 | 4.170 | 2.89E-30 |
| HOXA11 | ANTP | 3.971 | 4.681 | 3.96E-30 |
| HOXD9 | ANTP | 2.124 | 7.872 | 4.99E-29 |
| LHX5 | LIM | 4.350 | 5.301 | 1.97E-28 |
| HOXA1 | ANTP | 2.667 | 7.586 | 2.76E-28 |
| EN1 | ANTP | 4.284 | 7.163 | 2.13E-27 |
| HOXD8 | ANTP | 1.779 | 7.615 | 4.96E-24 |
| CDX1 | ANTP | 2.486 | 4.162 | 3.52E-23 |
| HOXD13 | ANTP | 4.859 | 6.007 | 1.86E-22 |
| HOXB7 | ANTP | 3.655 | 7.808 | 3.64E-22 |
| HOXC10 | ANTP | 4.661 | 6.736 | 8.68E-22 |
| HOXB9 | ANTP | 4.244 | 4.892 | 2.70E-21 |
| DLX1 | ANTP | 2.824 | 6.669 | 9.50E-21 |
| LHX2 | LIM | 3.381 | 5.525 | 4.90E-19 |
| LHX1 | LIM | 4.149 | 4.800 | 7.77E-19 |
| HOPX | PRD | -2.673 | 11.289 | 7.01E-18 |
| DLX6 | ANTP | 3.059 | 5.927 | 9.07E-18 |
| ONECUT2 | CUT | 2.786 | 5.473 | 1.15E-17 |
| HOXA13 | ANTP | 3.351 | 4.166 | 3.77E-17 |
| BARX2 | ANTP | -2.828 | 10.042 | 4.16E-17 |
| EN2 | ANTP | 2.794 | 5.709 | 1.08E-14 |
| DLX2 | ANTP | 2.635 | 5.745 | 1.42E-14 |
| PAX5 | PRD | 2.579 | 6.563 | 1.97E-14 |
| HOXC5 | ANTP | 1.695 | 2.044 | 1.97E-14 |
| NKX6-1 | ANTP | 2.282 | 4.050 | 6.50E-13 |
| TLX2 | ANTP | 2.488 | 3.541 | 8.47E-13 |
| HOXD12 | ANTP | 1.663 | 1.656 | 2.34E-12 |
| MEIS3 | TALE | 1.618 | 8.098 | 4.18E-12 |
| ONECUT3 | CUT | 2.264 | 3.260 | 1.00E-11 |
| HOXB6 | ANTP | 1.855 | 5.204 | 6.42E-11 |
| EMX1 | ANTP | 2.167 | 4.779 | 8.64E-11 |
| VAX1 | ANTP | 2.505 | 3.293 | 1.69E-10 |
| PKNOX2 | TALE | -1.957 | 5.657 | 1.88E-10 |
| HOXA6 | ANTP | 1.981 | 3.801 | 4.12E-10 |
| NKX3-2 | ANTP | 2.039 | 4.559 | 5.24E-10 |
| HOXA5 | ANTP | 1.802 | 6.101 | 5.85E-10 |
| HOXD1 | ANTP | 1.653 | 3.631 | 5.85E-10 |
| ONECUT1 | CUT | 1.624 | 1.872 | 1.03E-09 |
| DLX5 | ANTP | 1.583 | 8.737 | 1.21E-09 |
| PBX1 | TALE | -1.807 | 10.275 | 2.14E-09 |
| LMX1A | LIM | -1.532 | 1.379 | 2.24E-09 |
| LHX9 | LIM | 2.365 | 3.628 | 2.88E-09 |
| HOXB8 | ANTP | 1.908 | 2.785 | 1.96E-08 |
| DMBX1 | PRD | 1.907 | 3.187 | 2.19E-08 |
| MIXL1 | PRD | 1.654 | 3.651 | 2.19E-08 |
| HOXA7 | ANTP | 2.281 | 5.027 | 2.94E-08 |
| MNX1 | ANTP | 1.717 | 3.180 | 3.41E-08 |
| HOXA9 | ANTP | 2.073 | 4.850 | 3.75E-08 |
| HOXB5 | ANTP | 1.597 | 4.072 | 4.87E-08 |
| NKX2-3 | ANTP | -2.356 | 3.571 | 3.97E-07 |
| MEOX2 | ANTP | -1.601 | 5.319 | 6.05E-07 |
| LMX1B | LIM | 1.909 | 6.200 | 3.28E-06 |
| ISL1 | LIM | -2.055 | 3.755 | 5.18E-06 |
| LHX3 | LIM | 1.677 | 2.405 | 5.75E-06 |
| HOXB13 | ANTP | 2.334 | 3.831 | 7.27E-06 |
| LBX1 | ANTP | -1.527 | 2.197 | 2.80E-05 |
| TLX1 | ANTP | -2.106 | 3.138 | 3.20E-05 |
| HMX2 | ANTP | 1.547 | 1.835 | 4.38E-05 |
| TLX3 | ANTP | 1.940 | 2.223 | 0.000282 |
| IRX6 | TALE | -1.515 | 4.870 | 0.001306 |
| POU6F2 | POU | 1.559 | 4.073 | 0.006258 |

**Supplementary Table 3.** The KEGG-GSEA results of 8 selected LHXs in HNSCC.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **LHX** | **KEGG Gene Sets ID** | **ES** | **NES** | **p.adj** | **FDR q-val** |
| ISL1 |  |  |  |  |  |
|  | KEGG CYTOSOLIC DNA SENSING PATHWAY | -0.590 | -2.389 | 2.42E-05 | 2.01E-05 |
|  | KEGG PROTEASOME | -0.515 | -2.086 | 7.16E-04 | 5.94E-04 |
|  | KEGG ANTIGEN PROCESSING AND PRESENTATION | -0.402 | -1.962 | 5.40E-03 | 4.49E-03 |
|  | KEGG RNA DEGRADATION | -0.409 | -1.750 | 1.12E-02 | 9.30E-03 |
|  | KEGG RIG I LIKE RECEPTOR SIGNALING PATHWAY | -0.388 | -1.704 | 1.96E-02 | 1.62E-02 |
| LHX1 |  |  |  |  |  |
|  | KEGG ECM RECEPTOR INTERACTION | 0.574 | 2.559 | 1.71E-10 | 1.32E-10 |
|  | KEGG METABOLISM OF XENOBIOTICS BY CYTOCHROME P450 | -0.738 | -2.053 | 2.04E-10 | 1.58E-10 |
|  | KEGG CYTOSOLIC DNA SENSING PATHWAY | 0.645 | 2.642 | 7.70E-08 | 5.94E-08 |
|  | KEGG RIG I LIKE RECEPTOR SIGNALING PATHWAY | 0.470 | 2.156 | 8.39E-05 | 6.47E-05 |
|  | KEGG DRUG METABOLISM OTHER ENZYMES | -0.661 | -1.801 | 8.60E-05 | 6.63E-05 |
| LHX2 |  |  |  |  |  |
|  | KEGG RIBOSOME | -0.604 | -2.525 | 4.88E-09 | 4.24E-09 |
|  | KEGG ECM RECEPTOR INTERACTION | -0.524 | -2.215 | 1.91E-05 | 1.66E-05 |
|  | KEGG OXIDATIVE PHOSPHORYLATION | -0.382 | -1.690 | 8.17E-04 | 7.09E-04 |
|  | KEGG TIGHT JUNCTION | -0.383 | -1.708 | 1.05E-03 | 9.07E-04 |
|  | KEGG CYTOSOLIC DNA SENSING PATHWAY | -0.522 | -1.896 | 6.20E-03 | 5.38E-03 |
| LHX3 |  |  |  |  |  |
|  | KEGG RIBOSOME | 0.546 | 1.919 | 4.66E-03 | 4.45E-03 |
|  | KEGG SPLICEOSOME | 0.452 | 1.681 | 3.70E-02 | 3.54E-02 |
| LHX5 |  |  |  |  |  |
|  | KEGG PRIMARY IMMUNODEFICIENCY | -0.753 | -2.150 | 9.66E-05 | 8.42E-05 |
|  | KEGG RIBOSOME | 0.535 | 1.960 | 1.13E-03 | 9.88E-04 |
|  | KEGG FOCAL ADHESION | 0.394 | 1.626 | 2.77E-03 | 2.41E-03 |
|  | KEGG T CELL RECEPTOR SIGNALING PATHWAY | -0.534 | -1.829 | 2.77E-03 | 2.41E-03 |
|  | KEGG NATURAL KILLER CELL MEDIATED CYTOTOXICITY | -0.506 | -1.761 | 3.00E-03 | 2.62E-03 |
| LHX9 |  |  |  |  |  |
|  | KEGG CYTOKINE CYTOKINE RECEPTOR INTERACTION | -0.485 | -1.784 | 1.23E-05 | 9.47E-06 |
|  | KEGG INTESTINAL IMMUNE NETWORK FOR IGA PRODUCTION | -0.682 | -2.017 | 3.10E-04 | 2.39E-04 |
|  | KEGG T CELL RECEPTOR SIGNALING PATHWAY | -0.517 | -1.749 | 1.09E-03 | 8.36E-04 |
|  | KEGG TIGHT JUNCTION | -0.509 | -1.758 | 1.09E-03 | 8.36E-04 |
|  | KEGG CELL ADHESION MOLECULES CAMS | -0.492 | -1.698 | 3.06E-03 | 2.36E-03 |
| LMX1A |  |  |  |  |  |
|  | KEGG RIBOSOME | -0.698 | -3.097 | 1.08E-16 | 7.82E-17 |
|  | KEGG NEUROACTIVE LIGAND RECEPTOR INTERACTION | 0.603 | 1.847 | 2.29E-13 | 1.65E-13 |
|  | KEGG SPLICEOSOME | -0.564 | -2.655 | 4.82E-13 | 3.48E-13 |
|  | KEGG FOCAL ADHESION | 0.586 | 1.785 | 8.07E-09 | 5.83E-09 |
|  | KEGG ECM RECEPTOR INTERACTION | 0.648 | 1.890 | 1.88E-06 | 1.36E-06 |
| LMX1B |  |  |  |  |  |
|  | KEGG DRUG METABOLISM CYTOCHROME P450 | -0.699 | -2.093 | 7.47E-06 | 6.42E-06 |
|  | KEGG METABOLISM OF XENOBIOTICS BY CYTOCHROME P450 | -0.683 | -2.038 | 7.47E-06 | 6.42E-06 |
|  | KEGG NEUROACTIVE LIGAND RECEPTOR INTERACTION | 0.396 | 1.688 | 3.32E-04 | 2.85E-04 |
|  | KEGG PRIMARY IMMUNODEFICIENCY | -0.634 | -1.698 | 4.62E-02 | 3.98E-02 |
|  | KEGG FOCAL ADHESION | 0.348 | 1.457 | 4.62E-02 | 3.98E-02 |

LHX, LIM homeobox gene; ES, enrichment score; NES, normalized enrichment score; p.adj, adjusted p value; FDR q-val, false discovery rate q value.

**Supplementary Table 4.** The Hallmark-GSEA results of 8 selected LHXs in HNSCC.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **LHX** | **Hallmark Gene Set ID** | **ES** | **NES** | **p.adj** | **FDR q-val** |
| ISL1 |  |  |  |  |  |
|  | HALLMARK CHOLESTEROL HOMEOSTASIS | -0.512 | -2.133 | 6.630E-07 | 4.187E-07 |
|  | HALLMARK REACTIVE OXYGEN SPECIES PATHWAY | -0.568 | -2.241 | 8.545E-06 | 5.397E-06 |
|  | HALLMARK MYC TARGETS V2 | -0.456 | -1.833 | 1.783E-04 | 1.126E-04 |
|  | HALLMARK TGF BETA SIGNALING | -0.403 | -1.653 | 3.039E-03 | 1.919E-03 |
|  | HALLMARK PANCREAS BETA CELLS | 0.635 | 1.568 | 8.247E-03 | 5.209E-03 |
|  | HALLMARK KRAS SIGNALING DN | 0.478 | 1.285 | 2.616E-02 | 1.652E-02 |
|  | HALLMARK NOTCH SIGNALING | -0.410 | -1.500 | 3.086E-02 | 1.949E-02 |
| LHX1 |  |  |  |  |  |
|  | HALLMARK IL6 JAK STAT3 SIGNALING | 0.498 | 2.422 | 3.558E-08 | 2.809E-08 |
|  | HALLMARK TGF BETA SIGNALING | 0.520 | 2.319 | 4.173E-05 | 3.294E-05 |
|  | HALLMARK ANGIOGENESIS | 0.589 | 2.424 | 1.545E-04 | 1.219E-04 |
|  | HALLMARK SPERMATOGENESIS | -0.494 | -1.435 | 7.905E-03 | 6.241E-03 |
|  | HALLMARK PANCREAS BETA CELLS | -0.576 | -1.524 | 2.952E-02 | 2.331E-02 |
| LHX2 |  |  |  |  |  |
|  | HALLMARK MYOGENESIS | -0.760 | -3.458 | 5.204E-50 | 2.848E-50 |
|  | HALLMARK EPITHELIAL MESENCHYMAL TRANSITION | -0.620 | -2.848 | 2.907E-26 | 1.591E-26 |
|  | HALLMARK TNFA SIGNALING VIA NFKB | -0.472 | -2.168 | 6.215E-12 | 3.402E-12 |
|  | HALLMARK INTERFERON ALPHA RESPONSE | -0.512 | -2.142 | 6.951E-07 | 3.805E-07 |
|  | HALLMARK APICAL JUNCTION | -0.391 | -1.783 | 6.951E-07 | 3.805E-07 |
|  | HALLMARK INTERFERON GAMMA RESPONSE | -0.378 | -1.736 | 3.507E-06 | 1.919E-06 |
|  | HALLMARK P53 PATHWAY | -0.365 | -1.679 | 9.521E-06 | 5.211E-06 |
|  | HALLMARK UV RESPONSE DN | -0.408 | -1.877 | 9.521E-06 | 5.211E-06 |
|  | HALLMARK SPERMATOGENESIS | 0.555 | 1.713 | 1.534E-05 | 8.395E-06 |
|  | HALLMARK COAGULATION | -0.409 | -1.867 | 2.729E-05 | 1.494E-05 |
|  | HALLMARK E2F TARGETS | 0.507 | 1.593 | 7.636E-05 | 4.180E-05 |
|  | HALLMARK ANGIOGENESIS | -0.602 | -2.128 | 1.318E-04 | 7.213E-05 |
|  | HALLMARK INFLAMMATORY RESPONSE | -0.337 | -1.532 | 4.043E-04 | 2.213E-04 |
|  | HALLMARK UNFOLDED PROTEIN RESPONSE | -0.369 | -1.607 | 1.439E-03 | 7.875E-04 |
|  | HALLMARK TGF BETA SIGNALING | -0.466 | -1.779 | 1.937E-03 | 1.060E-03 |
|  | HALLMARK KRAS SIGNALING UP | -0.318 | -1.445 | 1.956E-03 | 1.071E-03 |
|  | HALLMARK APOPTOSIS | -0.327 | -1.494 | 3.612E-03 | 1.977E-03 |
|  | HALLMARK HYPOXIA | -0.308 | -1.401 | 3.918E-03 | 2.144E-03 |
|  | HALLMARK PANCREAS BETA CELLS | 0.618 | 1.660 | 4.395E-03 | 2.406E-03 |
|  | HALLMARK PROTEIN SECRETION | -0.346 | -1.438 | 1.679E-02 | 9.190E-03 |
|  | HALLMARK IL2 STAT5 SIGNALING | -0.267 | -1.220 | 3.758E-02 | 2.057E-02 |
| LHX3 |  |  |  |  |  |
|  | HALLMARK E2F TARGETS | 0.529 | 2.092 | 7.916E-08 | 6.333E-08 |
|  | HALLMARK MYC TARGETS V1 | 0.473 | 1.870 | 2.613E-05 | 2.090E-05 |
|  | HALLMARK UV RESPONSE DN | -0.442 | -1.797 | 1.006E-03 | 8.044E-04 |
|  | HALLMARK G2M CHECKPOINT | 0.414 | 1.637 | 2.162E-03 | 1.729E-03 |
|  | HALLMARK MYOGENESIS | 0.408 | 1.612 | 6.587E-03 | 5.270E-03 |
|  | HALLMARK ANDROGEN RESPONSE | -0.432 | -1.695 | 1.028E-02 | 8.224E-03 |
|  | HALLMARK MYC TARGETS V2 | 0.549 | 1.812 | 1.028E-02 | 8.224E-03 |
|  | HALLMARK OXIDATIVE PHOSPHORYLATION | 0.387 | 1.532 | 1.028E-02 | 8.224E-03 |
|  | HALLMARK PANCREAS BETA CELLS | 0.621 | 1.894 | 1.172E-02 | 9.377E-03 |
|  | HALLMARK INFLAMMATORY RESPONSE | -0.348 | -1.477 | 1.516E-02 | 1.213E-02 |
|  | HALLMARK DNA REPAIR | 0.408 | 1.574 | 1.716E-02 | 1.372E-02 |
|  | HALLMARK INTERFERON ALPHA RESPONSE | 0.439 | 1.583 | 3.865E-02 | 3.092E-02 |
| LHX5 |  |  |  |  |  |
|  | HALLMARK EPITHELIAL MESENCHYMAL TRANSITION | 0.550 | 2.299 | 4.760E-12 | 4.008E-12 |
|  | HALLMARK ALLOGRAFT REJECTION | -0.563 | -2.043 | 1.785E-09 | 1.504E-09 |
|  | HALLMARK MYOGENESIS | 0.438 | 1.829 | 2.793E-05 | 2.352E-05 |
|  | HALLMARK GLYCOLYSIS | 0.394 | 1.647 | 1.427E-03 | 1.201E-03 |
|  | HALLMARK COAGULATION | 0.437 | 1.732 | 1.470E-03 | 1.238E-03 |
|  | HALLMARK E2F TARGETS | -0.431 | -1.565 | 2.782E-03 | 2.343E-03 |
|  | HALLMARK ANGIOGENESIS | 0.576 | 1.791 | 1.454E-02 | 1.225E-02 |
|  | HALLMARK APICAL JUNCTION | 0.350 | 1.462 | 1.479E-02 | 1.246E-02 |
|  | HALLMARK INTERFERON GAMMA RESPONSE | -0.402 | -1.459 | 1.479E-02 | 1.246E-02 |
|  | HALLMARK HEDGEHOG SIGNALING | 0.532 | 1.654 | 4.112E-02 | 3.463E-02 |
| LHX9 |  |  |  |  |  |
|  | HALLMARK MYOGENESIS | -0.706 | -2.559 | 4.377E-25 | 3.410E-25 |
|  | HALLMARK ALLOGRAFT REJECTION | -0.512 | -1.856 | 4.822E-06 | 3.756E-06 |
|  | HALLMARK KRAS SIGNALING UP | -0.431 | -1.563 | 1.062E-02 | 8.270E-03 |
|  | HALLMARK INFLAMMATORY RESPONSE | -0.430 | -1.558 | 1.062E-02 | 8.270E-03 |
|  | HALLMARK IL2 STAT5 SIGNALING | -0.429 | -1.552 | 1.289E-02 | 1.004E-02 |
|  | HALLMARK INTERFERON ALPHA RESPONSE | 0.423 | 1.607 | 2.780E-02 | 2.165E-02 |
|  | HALLMARK MYC TARGETS V2 | 0.450 | 1.564 | 3.967E-02 | 3.090E-02 |
|  | HALLMARK XENOBIOTIC METABOLISM | -0.396 | -1.433 | 3.967E-02 | 3.090E-02 |
| LMX1A |  |  |  |  |  |
|  | HALLMARK MYOGENESIS | 0.783 | 2.379 | 9.017E-40 | 6.328E-40 |
|  | HALLMARK EPITHELIAL MESENCHYMAL TRANSITION | 0.653 | 1.985 | 1.344E-15 | 9.434E-16 |
|  | HALLMARK MYC TARGETS V2 | -0.627 | -2.550 | 4.247E-08 | 2.980E-08 |
|  | HALLMARK DNA REPAIR | -0.435 | -2.027 | 5.406E-08 | 3.794E-08 |
|  | HALLMARK INTERFERON ALPHA RESPONSE | -0.463 | -1.991 | 6.334E-06 | 4.445E-06 |
|  | HALLMARK UV RESPONSE DN | 0.518 | 1.553 | 2.224E-03 | 1.561E-03 |
|  | HALLMARK KRAS SIGNALING DN | 0.479 | 1.456 | 2.690E-03 | 1.888E-03 |
|  | HALLMARK UNFOLDED PROTEIN RESPONSE | -0.345 | -1.532 | 5.861E-03 | 4.113E-03 |
|  | HALLMARK KRAS SIGNALING UP | 0.459 | 1.395 | 1.763E-02 | 1.237E-02 |
| LMX1B |  |  |  |  |  |
|  | HALLMARK EPITHELIAL MESENCHYMAL TRANSITION | 0.523 | 2.193 | 1.309E-09 | 1.075E-09 |
|  | HALLMARK INTERFERON ALPHA RESPONSE | 0.547 | 2.078 | 1.615E-05 | 1.326E-05 |
|  | HALLMARK ANGIOGENESIS | 0.576 | 1.828 | 2.278E-02 | 1.870E-02 |

LHX, LIM homeobox gene; ES, enrichment score; NES, normalized enrichment score; p.adj, adjusted p value; FDR q-val, false discovery rate q value.