**Supplementary Table 1.** Clinical characteristics of patients in TCGA (n=222).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Variables | n | % | HR(95%CI) | P value |
| Age |  |  |  |  |
| >60 | 104 | 0.47 | 1.425(0.832−2.439) | 0.197 |
| ≤60 | 118 | 0.53 |  |  |
| Gender |  |  |  |  |
| male | 153 | 0.69 | 0.735(0.423−1.280) | 0.277 |
| female | 69 | 0.31 |  |  |
| BMI |  |  |  |  |
| >25 | 106 | 0.48 | 1.237(0.728−2.101) | 0.431 |
| ≤25 | 116 | 0.52 |  |  |
| AFP  |  |  |  |  |
| >300 | 54 | 0.24 | 1.204(0.667−2.172) | 0.537 |
| ≤300 | 168 | 0.76 |  |  |
| Vascular Invasion |  |  |  |  |
| yes | 76 | 0.34 | 2.238(1.295−3.868) | 0.004 |
| no | 146 | 0.66 |  |  |
| Grade |  |  |  |  |
| G3+G4 | 100 | 0.45 | 1.500(0.880−2.557) | 0.136 |
| G1+G2 | 122 | 0.55 |  |  |
| TNM stage |  |  |  |  |
| Stage III+ IV | 42 | 0.19 | 2.643(1.530−4.566) | <0.001 |
| Stage I+ II | 180 | 0.81 |  |  |
| Risk |  |  |  |  |
| high | 41 | 0.18 | 3.070(1.732−5.441) | <0.001 |
| low | 181 | 0.82 |  |  |

**Supplementary Table 2.** Clinical characteristics of patients in ICGC (n=229).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Variables | n | % | HR(95%CI) | P value |
| Age |  |  |  |  |
| >60 | 180 | 0.79 | 0.828(0.405−1.696) | 0.607 |
| ≤60 | 49 | 0.21 |  |  |
| Gender |  |  |  |  |
| male | 168 | 0.73 | 0.459(0.243−0.869) | 0.017 |
| female | 61 | 0.27 |  |  |
| Prior Malignancy |  |  |  |  |
| yes | 30 | 0.13 | 1.923(0.843−4.384) | 0.120 |
| no | 199 | 0.87 |  |  |
| TNM stage |  |  |  |  |
| Stage III+ IV | 88 | 0.38 | 2.303(1.233−4.301) | 0.009 |
| Stage I+ II | 141 | 0.62 |  |  |
| Risk |  |  |  |  |
| high | 47 | 0.21 | 4.703(2.519−8.783) | <0.001 |
| low | 182 | 0.79 |  |  |

**Supplementary Table 3.** Gene set enrichment analysis for high‐risk group with KEGG pathway gene sets gene symbols using the TCGA and ICGC datasets.

|  |  |  |
| --- | --- | --- |
|  | **TCGA** | **ICGC** |
| **NAME** | **SIZE** | **ES** | **NES** | **NOM p-val** | **FDR q-val** | **SIZE** | **ES** | **NES** | **NOM p-val** | **FDR q-val** |
| KEGG\_PROGESTERONE\_MEDIATED\_OOCYTE\_MATURATION | 85 | 0.68  | 2.06  | 0.00  | 0.00  | 85 | 0.50  | 1.81  | 0.00  | 0.06  |
| KEGG\_CELL\_CYCLE | 124 | 0.76  | 2.01  | 0.00  | 0.00  | 124 | 0.65  | 2.13  | 0.00  | 0.01  |
| KEGG\_RNA\_DEGRADATION | 59 | 0.74  | 2.01  | 0.00  | 0.00  | 52 | 0.71  | 2.22  | 0.00  | 0.00  |
| KEGG\_SPLICEOSOME | 127 | 0.79  | 2.02  | 0.00  | 0.00  | 122 | 0.70  | 2.12  | 0.00  | 0.00  |
| KEGG\_PYRIMIDINE\_METABOLISM | 98 | 0.66  | 2.07  | 0.00  | 0.00  | 96 | 0.57  | 2.01  | 0.00  | 0.01  |
| KEGG\_UBIQUITIN\_MEDIATED\_PROTEOLYSIS | 134 | 0.71  | 2.01  | 0.00  | 0.00  | 130 | 0.56  | 2.03  | 0.00  | 0.01  |
| KEGG\_VASOPRESSIN\_REGULATED\_WATER\_REABSORPTION | 44 | 0.72  | 2.05  | 0.00  | 0.00  | 43 | 0.52  | 1.68  | 0.01  | 0.13  |
| KEGG\_PURINE\_METABOLISM | 158 | 0.61  | 2.15  | 0.00  | 0.00  | 149 | 0.49  | 2.00  | 0.00  | 0.01  |
| KEGG\_BLADDER\_CANCER | 42 | 0.67  | 1.98  | 0.00  | 0.00  | 40 | 0.49  | 1.60  | 0.01  | 0.16  |
| KEGG\_NUCLEOTIDE\_EXCISION\_REPAIR | 44 | 0.76  | 1.97  | 0.00  | 0.00  | 44 | 0.65  | 1.98  | 0.00  | 0.01  |
| KEGG\_BASE\_EXCISION\_REPAIR | 35 | 0.75  | 1.94  | 0.00  | 0.00  | 33 | 0.68  | 2.05  | 0.00  | 0.01  |
| KEGG\_OOCYTE\_MEIOSIS | 112 | 0.70  | 2.15  | 0.00  | 0.00  | 110 | 0.55  | 2.06  | 0.00  | 0.01  |
| KEGG\_AMINOACYL\_TRNA\_BIOSYNTHESIS | 41 | 0.73  | 1.89  | 0.00  | 0.00  | 41 | 0.67  | 1.89  | 0.01  | 0.03  |
| KEGG\_THYROID\_CANCER | 29 | 0.68  | 1.90  | 0.00  | 0.01  | 29 | 0.48  | 1.62  | 0.02  | 0.15  |
| KEGG\_PATHOGENIC\_ESCHERICHIA\_COLI\_INFECTION | 56 | 0.67  | 1.89  | 0.00  | 0.01  | 53 | 0.55  | 1.77  | 0.01  | 0.08  |
| KEGG\_WNT\_SIGNALING\_PATHWAY | 150 | 0.59  | 1.90  | 0.00  | 0.01  | 149 | 0.38  | 1.52  | 0.03  | 0.22  |
| KEGG\_ADHERENS\_JUNCTION | 73 | 0.66  | 1.91  | 0.00  | 0.01  | 68 | 0.47  | 1.63  | 0.01  | 0.17  |
| KEGG\_COLORECTAL\_CANCER | 62 | 0.66  | 1.88  | 0.00  | 0.01  | 62 | 0.49  | 1.73  | 0.01  | 0.10  |
| KEGG\_CHRONIC\_MYELOID\_LEUKEMIA | 73 | 0.67  | 1.90  | 0.00  | 0.01  | 73 | 0.47  | 1.63  | 0.02  | 0.16  |
| KEGG\_HOMOLOGOUS\_RECOMBINATION | 28 | 0.79  | 1.87  | 0.00  | 0.01  | 26 | 0.71  | 1.92  | 0.00  | 0.02  |
| KEGG\_SMALL\_CELL\_LUNG\_CANCER | 84 | 0.62  | 1.85  | 0.00  | 0.01  | 84 | 0.43  | 1.55  | 0.03  | 0.20  |
| KEGG\_ENDOMETRIAL\_CANCER | 52 | 0.64  | 1.86  | 0.00  | 0.01  | 52 | 0.44  | 1.57  | 0.04  | 0.18  |
| KEGG\_NON\_SMALL\_CELL\_LUNG\_CANCER | 54 | 0.64  | 1.86  | 0.00  | 0.01  | 54 | 0.48  | 1.69  | 0.00  | 0.13  |
| KEGG\_DNA\_REPLICATION | 36 | 0.83  | 1.85  | 0.00  | 0.01  | 36 | 0.78  | 1.95  | 0.00  | 0.02  |
| KEGG\_N\_GLYCAN\_BIOSYNTHESIS | 46 | 0.64  | 1.84  | 0.00  | 0.01  | 46 | 0.55  | 1.79  | 0.02  | 0.08  |
| KEGG\_BASAL\_TRANSCRIPTION\_FACTORS | 35 | 0.69  | 1.85  | 0.00  | 0.01  | 35 | 0.56  | 1.78  | 0.00  | 0.08  |
| KEGG\_RENAL\_CELL\_CARCINOMA | 70 | 0.62  | 1.84  | 0.00  | 0.01  | 66 | 0.48  | 1.63  | 0.03  | 0.16  |
| KEGG\_RNA\_POLYMERASE | 29 | 0.69  | 1.82  | 0.00  | 0.01  | 29 | 0.62  | 1.75  | 0.02  | 0.09  |
| KEGG\_PANCREATIC\_CANCER | 70 | 0.66  | 1.82  | 0.00  | 0.01  | 69 | 0.50  | 1.67  | 0.01  | 0.14  |
| KEGG\_MISMATCH\_REPAIR | 23 | 0.79  | 1.79  | 0.00  | 0.01  | 23 | 0.74  | 1.92  | 0.00  | 0.02  |
| KEGG\_PROSTATE\_CANCER | 89 | 0.56  | 1.75  | 0.00  | 0.02  | 89 | 0.40  | 1.51  | 0.03  | 0.22  |

**Supplementary Table 4.** Gene set enrichment analysis for low‐risk group with KEGG pathway gene sets gene symbols using the TCGA and ICGC datasets。

|  |  |  |
| --- | --- | --- |
|  | **TCGA** | **ICGC** |
| **NAME** | **SIZE** | **ES** | **NES** | **NOM p-val** | **FDR q-val** | **SIZE** | **ES** | **NES** | **NOM p-val** | **FDR q-val** |
| KEGG\_COMPLEMENT\_AND\_COAGULATION\_CASCADES | 69 | -0.78  | -2.14  | 0.00  | 0.00  | 69 | -0.84  | -2.29  | 0.00  | 0.00  |
| KEGG\_GLYCINE\_SERINE\_AND\_THREONINE\_METABOLISM | 31 | -0.78  | -2.00  | 0.00  | 0.00  | 31 | -0.67  | -1.69  | 0.03  | 0.14  |
| KEGG\_PRIMARY\_BILE\_ACID\_BIOSYNTHESIS | 16 | -0.92  | -2.01  | 0.00  | 0.00  | 16 | -0.87  | -1.94  | 0.00  | 0.04  |
| KEGG\_RETINOL\_METABOLISM | 64 | -0.71  | -2.02  | 0.00  | 0.00  | 63 | -0.67  | -1.81  | 0.02  | 0.06  |
| KEGG\_DRUG\_METABOLISM\_CYTOCHROME\_P450 | 71 | -0.72  | -2.02  | 0.00  | 0.00  | 72 | -0.71  | -1.91  | 0.01  | 0.03  |
| KEGG\_PPAR\_SIGNALING\_PATHWAY | 69 | -0.57  | -1.77  | 0.01  | 0.02  | 69 | -0.56  | -1.81  | 0.01  | 0.07  |
| KEGG\_LINOLEIC\_ACID\_METABOLISM | 29 | -0.55  | -1.65  | 0.01  | 0.04  | 29 | -0.66  | -1.92  | 0.00  | 0.04  |