**Supplementary Table 1. Genes most similar to SKA family members in LIHC (GEPIA)**

|  |  |
| --- | --- |
| **Classification** | **Similar genes** |
| SKA1 | KIF11, NCAPG, NDC80, CDK1, ANLN, CEP55, GTSE1, KPNA2, KIF4A, CENPA |
| SKA2 | PRR11, KIF18B, CTD-2510F5.4, CBX1, PHF19, TPX2, ZWINT, CCNB2, KPNA2, HAUS1 |
| SKA3 | KIFC1, TPX2, NCAPG, HJURP, SGOL1, TTK, MELK, CKAP2L, GINS1, CDK1 |

LIHC, liver hepatocellular carcinoma.

**Supplementary Table 2. GO and KEGG enrichment analysis of SKA family genes and their most similar genes in LIHC**

| **ONTOLOGY** | **ID** | **Description** | **Gene ratio** | **Bg ratio** | ***p*-value** | ***p*-adjust** | ***q*-value** |
| --- | --- | --- | --- | --- | --- | --- | --- |
| BP | GO:0007059 | chromosome segregation | 11/26 | 321/18670 | 2.01e-13 | 9.24e-11 | 5.58e-11 |
| BP | GO:0140014 | mitotic nuclear division | 10/26 | 264/18670 | 1.17e-12 | 2.70e-10 | 1.63e-10 |
| BP | GO:0000280 | nuclear division | 10/26 | 407/18670 | 8.45e-11 | 1.30e-08 | 7.83e-09 |
| BP | GO:0048285 | organelle fission | 10/26 | 449/18670 | 2.20e-10 | 2.54e-08 | 1.53e-08 |
| BP | GO:1902850 | microtubule cytoskeleton organization involved in mitosis | 7/26 | 131/18670 | 4.19e-10 | 3.86e-08 | 2.33e-08 |
| CC | GO:0005819 | spindle | 13/27 | 347/19717 | 2.00e-16 | 1.62e-14 | 7.56e-15 |
| CC | GO:0000775 | chromosome, centromeric region | 10/27 | 193/19717 | 4.66e-14 | 1.89e-12 | 8.84e-13 |
| CC | GO:0098687 | chromosomal region | 11/27 | 349/19717 | 4.62e-13 | 1.25e-11 | 5.84e-12 |
| CC | GO:0005876 | spindle microtubule | 7/27 | 59/19717 | 1.26e-12 | 2.55e-11 | 1.19e-11 |
| CC | GO:0000779 | condensed chromosome, centromeric region | 8/27 | 118/19717 | 2.61e-12 | 4.20e-11 | 1.97e-11 |
| MF | GO:0008017 | microtubule binding | 6/25 | 246/17697 | 9.63e-07 | 5.01e-05 | 3.14e-05 |
| MF | GO:0003777 | microtubule motor activity | 4/25 | 84/17697 | 5.54e-06 | 1.01e-04 | 6.36e-05 |
| MF | GO:0015631 | tubulin binding | 6/25 | 336/17697 | 5.85e-06 | 1.01e-04 | 6.36e-05 |
| MF | GO:0003774 | motor activity | 4/25 | 136/17697 | 3.72e-05 | 4.84e-04 | 3.04e-04 |
| MF | GO:0008574 | ATP-dependent microtubule motor activity, plus-end-directed | 2/25 | 26/17697 | 6.10e-04 | 0.006 | 0.004 |
| KEGG | hsa04115 | p53 signaling pathway | 3/5 | 73/8076 | 7.00e-06 | 7.70e-05 | 3.68e-05 |
| KEGG | hsa04110 | Cell cycle | 3/5 | 124/8076 | 3.45e-05 | 1.90e-04 | 9.09e-05 |
| KEGG | hsa04914 | Progesterone-mediated oocyte maturation | 2/5 | 100/8076 | 0.001 | 0.005 | 0.003 |
| KEGG | hsa04114 | Oocyte meiosis | 2/5 | 129/8076 | 0.002 | 0.007 | 0.003 |
| KEGG | hsa04218 | Cellular senescence | 2/5 | 156/8076 | 0.004 | 0.008 | 0.004 |

LIHC, liver hepatocellular carcinoma; GO, gene ontology; KEGG, and Kyoto Encyclopedia of Genes and Genomes.

**Supplementary Table 3. Relationships between SKA genes expression and clinicopathological features in LIHC patients in TCGA database**

| **Characteristic** | **Low expression****of SKA1** | **High expression****of SKA1** | ***p*** | **Low expression****of SKA2** | **High expression****of SKA2** | ***p*** | **Low expression****of SKA3** | **High expression****of SKA3** | ***p*** |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| n | 187 | 187 |  | 187 | 187 |  | 187 | 187 |  |
| Age, n (%) |  |  | 0.133 |  |  | **0.011** |  |  | 0.055 |
| <=60 | 81 (21.7%) | 96 (25.7%) |  | 76 (20.4%) | 101 (27.1%) |  | 79 (21.2%) | 98 (26.3%) |  |
| >60 | 106 (28.4%) | 90 (24.1%) |  | 111 (29.8%) | 85 (22.8%) |  | 108 (29%) | 88 (23.6%) |  |
| Gender, n (%) |  |  | 0.122 |  |  | 1.000 |  |  | 0.507 |
| Female | 53 (14.2%) | 68 (18.2%) |  | 61 (16.3%) | 60 (16%) |  | 57 (15.2%) | 64 (17.1%) |  |
| Male | 134 (35.8%) | 119 (31.8%) |  | 126 (33.7%) | 127 (34%) |  | 130 (34.8%) | 123 (32.9%) |  |
| T stage, n (%) |  |  | **< 0.001** |  |  | **0.022** |  |  | **0.031** |
| T1 | 110 (29.6%) | 73 (19.7%) |  | 104 (28%) | 79 (21.3%) |  | 105 (28.3%) | 78 (21%) |  |
| T2 | 36 (9.7%) | 59 (15.9%) |  | 46 (12.4%) | 49 (13.2%) |  | 41 (11.1%) | 54 (14.6%) |  |
| T3 | 34 (9.2%) | 46 (12.4%) |  | 29 (7.8%) | 51 (13.7%) |  | 33 (8.9%) | 47 (12.7%) |  |
| T4 | 4 (1.1%) | 9 (2.4%) |  | 6 (1.6%) | 7 (1.9%) |  | 5 (1.3%) | 8 (2.2%) |  |
| N stage, n (%) |  |  | 1.000 |  |  | 0.625 |  |  | 1.000 |
| N0 | 126 (48.8%) | 128 (49.6%) |  | 120 (46.5%) | 134 (51.9%) |  | 117 (45.3%) | 137 (53.1%) |  |
| N1 | 2 (0.8%) | 2 (0.8%) |  | 1 (0.4%) | 3 (1.2%) |  | 2 (0.8%) | 2 (0.8%) |  |
| M stage, n (%) |  |  | 0.358 |  |  | 0.342 |  |  | 0.348 |
| M0 | 129 (47.4%) | 139 (51.1%) |  | 124 (45.6%) | 144 (52.9%) |  | 126 (46.3%) | 142 (52.2%) |  |
| M1 | 3 (1.1%) | 1 (0.4%) |  | 3 (1.1%) | 1 (0.4%) |  | 3 (1.1%) | 1 (0.4%) |  |
| AFP (ng/ml), n (%) |  |  | **< 0.001** |  |  | **0.003** |  |  | **< 0.001** |
| <=400 | 126 (45%) | 89 (31.8%) |  | 123 (43.9%) | 92 (32.9%) |  | 126 (45%) | 89 (31.8%) |  |
| >400 | 21 (7.5%) | 44 (15.7%) |  | 23 (8.2%) | 42 (15%) |  | 15 (5.4%) | 50 (17.9%) |  |
| Child-Pugh grade, n (%) |  |  | 1.000 |  |  | 0.359 |  |  | 0.363 |
| A | 119 (49.4%) | 100 (41.5%) |  | 122 (50.6%) | 97 (40.2%) |  | 119 (49.4%) | 100 (41.5%) |  |
| B | 11 (4.6%) | 10 (4.1%) |  | 9 (3.7%) | 12 (5%) |  | 9 (3.7%) | 12 (5%) |  |
| C | 1 (0.4%) | 0 (0%) |  | 1 (0.4%) | 0 (0%) |  | 1 (0.4%) | 0 (0%) |  |
| Fibrosis Ishak score, n (%) |  |  | 0.711 |  |  | 0.298 |  |  | 0.436 |
| 0 | 46 (21.4%) | 29 (13.5%) |  | 47 (21.9%) | 28 (13%) |  | 47 (21.9%) | 28 (13%) |  |
| 1/2 | 18 (8.4%) | 13 (6%) |  | 15 (7%) | 16 (7.4%) |  | 15 (7%) | 16 (7.4%) |  |
| 3/4 | 14 (6.5%) | 14 (6.5%) |  | 13 (6%) | 15 (7%) |  | 14 (6.5%) | 14 (6.5%) |  |
| 5/6 | 44 (20.5%) | 37 (17.2%) |  | 41 (19.1%) | 40 (18.6%) |  | 43 (20%) | 38 (17.7%) |  |
| Vascular invasion, n (%) |  |  | 0.181 |  |  | 0.950 |  |  | 0.142 |
| No | 118 (37.1%) | 90 (28.3%) |  | 110 (34.6%) | 98 (30.8%) |  | 114 (35.8%) | 94 (29.6%) |  |
| Yes | 53 (16.7%) | 57 (17.9%) |  | 57 (17.9%) | 53 (16.7%) |  | 50 (15.7%) | 60 (18.9%) |  |
| Albumin(g/dl), n (%) |  |  | 1.000 |  |  | 0.387 |  |  | 1.000 |
| <3.5 | 38 (12.7%) | 31 (10.3%) |  | 32 (10.7%) | 37 (12.3%) |  | 37 (12.3%) | 32 (10.7%) |  |
| ≥3.5 | 126 (42%) | 105 (35%) |  | 123 (41%) | 108 (36%) |  | 122 (40.7%) | 109 (36.3%) |  |
| Prothrombin time, n (%) |  |  | **0.046** |  |  | **0.006** |  |  | 0.062 |
| ≤4 | 103 (34.7%) | 105 (35.4%) |  | 95 (32%) | 113 (38%) |  | 100 (33.7%) | 108 (36.4%) |  |
| >4 | 56 (18.9%) | 33 (11.1%) |  | 57 (19.2%) | 32 (10.8%) |  | 54 (18.2%) | 35 (11.8%) |  |

LIHC, liver hepatocellular carcinoma; TCGA, The Cancer Genome Atlas.

**Supplementary Table 4. AUCs, optimal cutoff values, sensitivity, specificity and Youden index of SKA1/2/3 mRNA levels for predicting LIHC**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Variable** | **AUC (95% CI)** | **Cutoff value** | **Sensitivity (%)** | **Specificity (%)** | **Youden index (%)** |
| SKA1 | 0.982 (0.970-0.994) | 0.433 | 95.2 | 96.0 | 91.2 |
| SKA2 | 0.887 (0.852-0.922) | 3.279 | 85.0 | 82.0 | 67.0 |
| SKA3 | 0.973 (0.957-0.989) | 0.511 | 92.8 | 92.0 | 84.8 |

AUC, area under the curve; LIHC, liver hepatocellular carcinoma.

**Supplementary Table 5. Primer sequences for qRT-PCR**

|  |  |  |
| --- | --- | --- |
| Genes | Forward | Reverse |
| GAPDH | 5′-GGTTGTCTCCTGCGACTTCA-3′ | 5′-TGGTCCAGGGTTTCTTACTCC-3′ |
| SKA1 | 5′-CCTGAACCCGTAAAGCCT-3′ | 5′-TCATGTACGAAGGAACACCATTG-3′ |
| SKA2 | 5′-ATGGAGGCGGAGGTCGATAA-3′ | 5′-AAGCGGGCATACAAAGTTTGA-3′ |
| SKA3 | 5′-TACACGAGCAAGAAGCCATTAAC-3′ | 5′-GGATACGATGTACCGCTCAAGT-3′ |