**Supporting information**

**Figure S1.** Correlations between SRGAPs expression and tumor stage in HCC patients (**GEPIA**).

Table S1. DNA methylation sites of SRGAP1 in HCC.

Table S2. Top 20 GO enrichment terms.

Table S3. Top 20 Reactome enrichment terms.

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**Figure S1.** Correlations between SRGAPs expression and tumor stage in HCC patients (GEPIA). The expression of SRGAP1 and SRGAP2 was correlated with the pathological stage of CRC patients (p < 0.05).

**Table S1. DNA methylation sites of SRGAP1 in HCC.**

|  |  |  |
| --- | --- | --- |
| Methylation sites | Pearson-r | p-value |
| cg25022612 | 0.003 | 0.146 |
| cg05970811 | 0.000 | -0.205 |
| cg04581832 | 0.030 | -0.107 |
| cg20746096 | 0.805 | 0.012 |
| cg15326887 | 0.003 | -0.143 |
| cg05850206 | 0.270 | -0.054 |
| cg22610533 | 0.233 | 0.059 |
| cg14479829 | 0.077 | -0.087 |
| cg15628953 | 0.877 | 0.008 |
| cg05205563 | 0.085 | -0.085 |
| cg19191401 | 0.001 | -0.167 |
| cg01826959 | 0.003 | -0.144 |
| cg07973246 | **0.000** | **-0.282** |
| cg26214431 | 0.025 | -0.110 |
| cg10910080 | 0.000 | 0.366 |
| cg23818595 | 0.000 | 0.432 |
| cg23818595 | 0.000 | 0.432 |
| cg16792014 | 0.041 | 0.101 |
| cg03529189 | 0.116 | 0.077 |
| cg11441533 | 0.000 | -0.385 |
| cg11441533 | 0.000 | -0.385 |
| cg17430032 | 0.000 | 0.336 |
| cg11226252 | 0.000 | 0.438 |
| cg15260552 | 0.138 | 0.073 |
| cg14211977 | 0.000 | 0.353 |
| cg14122749 | 0.000 | 0.588 |
| cg26987521 | 0.000 | 0.480 |
| cg26987521 | 0.000 | 0.480 |
| cg05197667 | 0.086 | 0.084 |
| cg04938109 | 0.000 | 0.406 |
| cg11362183 | 0.290 | 0.052 |
| cg00781208 | 0.002 | 0.155 |
| cg06919312 | 0.000 | 0.320 |
| cg09734541 | 0.000 | 0.414 |
| cg01668352 | 0.037 | -0.102 |
| cg20826165 | 0.001 | 0.166 |
| cg15837333 | 0.000 | 0.405 |
| cg17737263 | 0.000 | 0.469 |
| cg22510727 | 0.000 | 0.369 |
| cg24052246 | 0.000 | 0.279 |

**Table S2. Top 20 GO enrichment terms.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Group | Term | Description | LogP | Gene In Term |
| 1 | Cellular Components | extracellular matrix | -14.25736201 | 53/569 |
| 2 | Biological Processes | inorganic ion homeostasis | -14.20232038 | 62/749 |
| 3 | Biological Processes | regulated exocytosis | -13.57316058 | 47/798 |
| 4 | Biological Processes | acute inflammatory response | -12.47938227 | 24/224 |
| 5 | Biological Processes | anion transport | -10.82897616 | 38/656 |
| 6 | Biological Processes | synapse organization | -10.09099627 | 24/433 |
| 7 | Biological Processes | monocarboxylic acid metabolic process | -10.07678338 | 37/664 |
| 8 | Molecular Functions | endopeptidase inhibitor activity | -8.987255191 | 23/183 |
| 9 | Cellular Components | endoplasmic reticulum lumen | -8.777258466 | 30/308 |
| 10 | Biological Processes | response to toxic substance | -8.555624163 | 30/523 |
| 11 | Biological Processes | organic hydroxy compound metabolic process | -8.530047445 | 31/556 |
| 12 | Biological Processes | platelet degranulation | -8.520618602 | 15/129 |
| 13 | Biological Processes | glutamine family amino acid metabolic process | -8.469291713 | 12/76 |
| 14 | Molecular Functions | receptor regulator activity | -8.096805992 | 40/534 |
| 15 | Biological Processes | renal system development | -8.052633527 | 28/293 |
| 16 | Biological Processes | response to bacterium | -8.033224534 | 36/754 |
| 17 | Biological Processes | cofactor metabolic process | -7.711357891 | 31/603 |
| 18 | Molecular Functions | calcium ion binding | -7.674211588 | 47/712 |
| 19 | Biological Processes | antibiotic metabolic process | -7.541397077 | 15/152 |
| 20 | Biological Processes | regulation of cell morphogenesis involved in differentiation | -7.521723846 | 28/310 |

**Table S3. Top 20 Reactome enrichment terms.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Group | Term | Description | LogP | Gene In Term | |
| 1 | R-HSA-6798695 | Neutrophil degranulation | -10.0788 | 31/480 |
| 2 | R-HSA-381426 | Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs) | -9.67561 | 16/125 |
| 3 | R-HSA-166658 | Complement cascade | -8.69277 | 11/58 |
| 4 | R-HSA-76002 | Platelet activation, signaling and aggregation | -8.61767 | 21/263 |
| 5 | R-HSA-382551 | Transport of small molecules | -6.88246 | 33/728 |
| 6 | R-HSA-556833 | Metabolism of lipids | -6.73368 | 33/739 |
| 7 | R-HSA-5686938 | Regulation of TLR by endogenous ligand | -6.40423 | 6/19 |
| 8 | R-HSA-373076 | Class A/1 (Rhodopsin-like receptors) | -6.27964 | 27/335 |
| 9 | R-HSA-1474244 | Extracellular matrix organization | -6.1005 | 25/301 |
| 10 | R-HSA-9033658 | Blood group systems biosynthesis | -5.91371 | 7/22 |
| 11 | R-HSA-71291 | Metabolism of amino acids and derivatives | -5.43512 | 20/374 |
| 12 | R-HSA-6785807 | Interleukin-4 and Interleukin-13 signaling | -5.14585 | 13/108 |
| 13 | R-HSA-211859 | Biological oxidations | -4.76022 | 14/222 |
| 14 | R-HSA-189483 | Heme degradation | -4.22507 | 4/14 |
| 15 | R-HSA-163125 | Post-translational modification: synthesis of GPI-anchored proteins | -4.15824 | 7/93 |
| 16 | R-HSA-8957322 | Metabolism of steroids | -3.73589 | 10/151 |
| 17 | R-HSA-1475029 | Reversible hydration of carbon dioxide | -3.65818 | 4/12 |
| 18 | R-HSA-9683673 | Maturation of protein 3a | -3.483 | 3/9 |
| 19 | R-HSA-76009 | Platelet Aggregation (Plug Formation) | -3.40113 | 5/39 |
| 20 | R-HSA-397014 | Muscle contraction | -3.26854 | 15/207 |