**Supplementary Table S1.** Fold change expression of positive and negative controls and genes of interest across all 52 glioma samples (high (IDH1-) vs. low (IDH1+) tumor grade).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Probeset ID | Entrez Gene | Gene Symbol | Gene Title | p-value | Fold-Change  (+ vs. -) |
| 221821\_s\_at | 54934 | KANSL2 | KAT8 regulatory NSL complex subunit 2 | 0.316849 | -1.17002 |
| 221820\_s\_at | 84148 | KAT8/MOF | K(lysine) acetyltransferase 8 | 0.0040691 | 1.28226 |
| 214885\_at | 84148 | KAT8/MOF | K(lysine) acetyltransferase 9 | 0.0484258 | 1.20058 |
| 205289\_at | 650 | BMP2 | bone morphogenetic protein 2 | 6.64E-11 | 9.06 |
| 205290\_s\_at | 650 | BMP2 | bone morphogenetic protein 2 | 1.02E-08 | 9.47758 |
| 205165\_at | 1951 | CELSR3 | cadherin, EGF LAG seven-pass G-type receptor 3 | 9.39E-06 | 2.86 |
| 40020\_at | 1951 | CELSR3 | cadherin, EGF LAG seven-pass G-type receptor 3 | 1.64E-05 | 2.68195 |
| 204995\_at | 8851 | CDK5R1 | cyclin-dependent kinase 5, regulatory subunit 1 | 6.43E-06 | 2.86183 |
| 203680\_at | 5577 | PRKAR2B | protein kinase, cAMP-dependent, regulatory, type II, beta | 0.00265647 | 2.21 |
| 208017\_s\_at | 4168 | MCF2 | MCF.2 cell line derived transforming sequence | 3.03E-06 | 3.08 |
| 204850\_s\_at | 1641 | DCX | doublecortin | 7.76E-08 | 9.61 |
| 204851\_s\_at | 1641 | DCX | doublecortin | 4.38E-07 | 10.0656 |
| 214930\_at | 26050 | SLITRK5 | SLIT and NTRK-like family, member 5 | 7.46E-12 | 8.58 |
| 229725\_at | 23305 | ACSL6 | acyl-CoA synthetase long-chain family member 6 | 0.00026587 | 3.08 |
| 213683\_at | 23305 | ACSL6 | acyl-CoA synthetase long-chain family member 6 | 0.0002852 | 2.17 |
| 211207\_s\_at | 23305 | ACSL6 | acyl-CoA synthetase long-chain family member 6 | 0.00124553 | 2.32 |
| 210512\_s\_at | 7422 | VEGF | vascular endothelial growth factor A | 4.59E-09 | -7.94 |
| 212171\_x\_at | 7422 | VEGF | vascular endothelial growth factor A | 2.59E-08 | -7.37 |
| 211527\_x\_at | 7422 | VEGF | vascular endothelial growth factor A | 6.55E-07 | -8.14 |
| 210513\_s\_at | 7422 | VEGF | vascular endothelial growth factor A | 2.95E-06 | -4.91 |
| 210840\_s\_at | 8826 | IQGAP1 | IQ motif containing GTPase activating protein 1 | 1.48E-11 | -3.87 |
| 200791\_s\_at | 8826 | IQGAP1 | IQ motif containing GTPase activating protein 1 | 4.29E-10 | -4.03 |
| 202803\_s\_at | 3689 | ITGB2 | integrin, beta 2 (complement component 3 receptor 3 and 4 subunit) | 0.0001093 | -3.53 |
| 1555349\_a\_at | 3689 | ITGB2 | integrin, beta 2 (complement component 3 receptor 3 and 4 subunit) | 0.00207378 | -2.72 |
| 229273\_at | 6299 | SALL1 | spalt-like transcription factor 1 | 4.30E-05 | -2.12 |
| 230258\_at | 169792 | GLIS3 | GLIS family zinc finger 3 | 1.84E-06 | -3.72 |
| 229435\_at | 169792 | GLIS3 | GLIS family zinc finger 3 | 3.13E-06 | -3.54 |
| 205111\_s\_at | 51196 | PLCE1 | phospholipase C, epsilon 1 | 7.69E-06 | -2.64 |
| 205112\_at | 51196 | PLCE1 | phospholipase C, epsilon 1 | 0.0001741 | -2.43 |
| 201324\_at | 2012 | EMP1 | epithelial membrane protein 1 | 2.92E-10 | -7.163 |
| 201325\_s\_at | 2012 | EMP1 | epithelial membrane protein 1 | 6.23E-08 | -4.903 |
| 213895\_at | 2012 | EMP1 | epithelial membrane protein 1 | 1.71E-07 | -2.87 |
| 204924\_at | 7097 | TLR2 | toll-like receptor 2 | 4.06E-06 | -3.87 |
| 225471\_s\_at | 208 | AKT2 | v-akt murine thymoma viral oncogene homolog 2 | 3.36E-06 | -2.31 |
| 221427\_s\_at | 81669 | CCNL2 | cyclin L2 | 0.00070553 | -2.10 |
| 203665\_at | 3162 | HMOX1 | heme oxygenase 1 | 0.00254974 | -3.09 |
| 212185\_x\_at | 4502 | MT2A | metallothionein 2A | 0.00040346 | -2.26 |
| 218205\_s\_at | 2872 | MKNK2 | MAP kinase interacting serine/threonine kinase 2 | 1.02E-07 | -2.04 |
| 223199\_at | 2872 | MKNK2 | MAP kinase interacting serine/threonine kinase 2 | 2.16E-05 | -2.25 |
| 1555229\_a\_at | 716 | C1S | complement component 1, s subcomponent | 0.00108191 | -2.19 |
| 208747\_s\_at | 716 | C1S | complement component 1, s subcomponent | 2.33E-08 | -6.07 |
| 202953\_at | 713 | C1QB | complement component 1, q subcomponent, B chain | 7.65E-05 | -4.07 |
| 225353\_s\_at | 714 | C1QC | complement component 1, q subcomponent, C chain | 0.00094097 | -2.96 |
| 218232\_at | 712 | C1QA | complement component 1, q subcomponent, A chain | 5.67E-05 | -3.80 |
| 200986\_at | 710 | SERPING1 | serpin peptidase inhibitor, clade G (C1 inhibitor), member 1 | 2.29E-13 | -14.67 |