**Supplementary Table 1.** miRNA assays and sequences for validation of miRNA gene expression.

|  |  |
| --- | --- |
| miRNA assay | Sequence |
| hsa-miR-1280 | UCCCACCGCUGCCACCC |
| hsa-miR-4274 | CAGCAGUCCCUCCCCCUG |
| hsa-miR-2116-3p | CCUCCCAUGCCAAGAACUCCC |
| hsa-miR-3675-3p | CAUCUCUAAGGAACUCCCCCAA |
| hsa-let-7b-3p | CUAUACAACCUACUGCCUUCCC |
| hsa-miR-3131 | UCGAGGACUGGUGGAAGGGCCUU |
| hsa-miR-1910 | CCAGUCCUGUGCCUGCCGCCU |
| hsa-miR-4310 | GCAGCAUUCAUGUCCC |
| hsa-miR-92a-3p | UAUUGCACUUGUCCCGGCCUGU |

**Supplementary Table 2.** The −∆∆Ct values for the 9 candidate miRNAs in Cohort 1.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| N | iNPH21 | PS18 | AD16 | *p-value**p1=iNPH:PS**p2=iNPH:AD**p3=PS:AD* |
| has-miR-1280  | -4.87[-4.95~-4.25] | -2.93[-3.22~-2.81] | -3.65[-3.92~-3.03] | *\*p1>0.0001, \*p2>0.0001, \*p3=0.008* |
| has-let-7b  | -2.64[-4.29~-1.85] | -1.29[-2.05~1.10] | -4.24[-6.54~-0.47] | *\*p1=0.012, \*p3=0.011* |
| has-miR-4274  | **-8.90****[-10.07~-7.77]** | **-5.14****[-6.83~-3.11]** | **-9.92****[-10.94~-7.12]** | ***\*p1>0.0001, \*p3>0.0001*** |
| has-miR-2116  | -1.41[-1.97~-0.21] | 1.50[0.08~4.86] | -1.76[-3.90~-0.77] | *\*p1=0.002, \*p3>0.0001* |
| has-miR-3675  | -1.01[-1.47~0.39] | 2.25[1.15~4.14] | -3.53[-4.30~-1.21] | *\*p1>0.0001, \*p2>0.0001, \*p3>0.0001* |
| has-miR-92a  | -3.03[-3.93~-2.05] | -1.07[-2.21~0.96] | -3.34[-5.04~0.73] | *\*p1=0.001, p3=0.180* |
| has-miR-3131  | -0.13[-0.94~0.24] | 2.29[0.26~3.37] | -0.70[-1.81~0.51] | *\*p1=0.033, \*p3=0.014* |
| has-miR-1910  | -1.56[-2.33~-0.42] | 0.68[-0.83~2.76] | -3.09[-3.63~-1.96] | *\*p1=0.003, \*p2=0.004, \*p3>0.0001* |
| has-miR-4310  | -1.70[-2.98~-0.91] | 1.15[-0.58~2.75] | -3.82[-4.11~-2.53] | *\*p1=0.001, \*p2=0.013, \*p3>0.0001* |

Data are shown as median values with interquartile range. p<0.05, statistically significant (ANOVA and Dunnett’s test\*).

**Supplementary Table 3.** ROC analysis of the tested miRNAs comparing the iNPH and PS groups in Cohort 1.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| miRNA name | AUC | Cut-off value ( -∆∆Ct) | Sensitivity | Specificity | *p-value* |
| miR-1280 | \*0.997 | -8.77 | 1.00 | 1.00 | *\*\*\*<0.0001* |
| miR-let-7b | \*\*0.789 | -1.98 | 0.75 | 0.71 | *\*\*\*0.003* |
| miR-4274 | **\*0.908** | **-7.70** | **0.88** | **0.81** | *\*\*\*<0.0001* |
| miR-2116 | \*\*0.875 | 0.03 | 0.88 | 0.81 | *\*\*\*<0.0001* |
| miR-3675 | \*\*0.878 | 0.99 | 0.81 | 0.95 | *\*\*\*<0.0001* |
| miR-92a | \*\*0.845 | -1.96 | 0.75 | 0.14 | *\*\*\*<0.0001* |
| miR-3131 | \*\*0.860 | 0.33 | 0.81 | 0.81 | *\*\*\*<0.0001* |
| miR-1910 | \*\*0.848 | -0.59 | 0.81 | 0.76 | *\*\*\*<0.0001* |
| miR-4310 | \*\*0.866 | -0.71 | 0.88 | 0.81 | *\*\*\*<0.0001* |

AUC, area under the curve; ROC, receiver operator characteristic. \*AUC 0.9–1.0, high accuracy; \*\*AUC 0.7–0.9, moderate accuracy; \*\*\*p<0.05, statistically significant.

**Supplementary Table 4.** Target genes of the miRNAs involved in various pathways.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Target Genes | Amyloid processing | Dopamine signaling | Axon guidance signaling | CREBSignaling |
| hsa-miR-1280 | JAG2, SRC, ROCK1 |  |  |  |  |
| hsa-miR-4274 | **SLC18A2** |  | O |  |  |
| hsa-miR-2116-3p | SOS1 |  |  | O | O |
| hsa-miR-3675-3p |  |  |  |  |  |
| hsa-miR-92a-3p | CACNA1C, GRIA1,3,4, HECW1, NEFH,L,MPIK3R3, CREB1, FRKAR1B, FRKAR2B, CDK5R1, PRKCE, CPLX2, ITPR1, MAP2K4, NSF, REST, SGK1, SP1, CAMK2A, GRM2, KCNN3, RYR3 | O | O | O | O |
| hsa-let-7b-3p | BCL2L1, CACNA1D,E, CAPN3, CASP3, GRIK2, IGF1, NEFM, NOS1, PAK1, TP53, CRIN3A, AKT2, BACE2, MAPK11, GNG5, IGF1R, MAPK9, NCOR1, NGF, POLR2D, TAF9B, GNAL, GNAT1, NRAS, PLA2G3, PPP2R2A | O | O | O | O |
| hsa-mir-3131 | APH1A | O |  |  |  |
| hsa-miR-1910 | PIK3C2A, HTT, TACR1 |  |  |  | O |
| hsa-mir-4310 | PRKACB, KCNJ11 | O | O |  | O |