

**Supplementary Table1. Characteristics of tumor samples.**

| ID      | Age/Sex | Type*      | Lymph node<br>metastasis | RNA**   |       |
|---------|---------|------------|--------------------------|---------|-------|
|         |         |            |                          | control | tumor |
| case 2  | 75/M    | diffuse    | +                        |         | x     |
| case 4  | 72/M    | intestinal | -                        |         | x     |
| case 5  | 76/F    | intestinal | +                        |         | x     |
| case 9  | 52/F    | diffuse    | +                        | x       | x     |
| case 10 | 79/M    | diffuse    | +                        |         | x     |
| case 11 | 79/F    | diffuse    | +                        |         | x     |
| case 12 | 87/M    | diffuse    | +                        | x       | x     |
| case 14 | 77/M    | intestinal | -                        | x       | x     |
| case 15 | 74/F    | intestinal | -                        |         | x     |
| case 17 | 77/F    | intestinal | +                        |         | x     |
| case 18 | 65/M    | intestinal | +                        |         | x     |
| case 19 | 58/M    | intestinal | +                        |         | x     |
| case 20 | 82/M    | diffuse    | -                        |         | x     |
| case 21 | 69/F    | intestinal | +                        |         | x     |
| case 22 | 62/M    | intestinal | -                        |         | x     |
| case 23 | 78/M    | diffuse    | +                        | x       | x     |
| case 24 | 71/M    | diffuse    | +                        | x       | x     |
| case 25 | 78/M    | intestinal | +                        |         | x     |
| case 26 | 73/M    | intestinal | -                        |         | x     |
| case 27 | 78/M    | intestinal | -                        |         | x     |
| case 28 | 73/M    | intestinal | +                        |         | x     |
| case 30 | 81/F    | intestinal | -                        |         | x     |

\* According to Lauren classification.

\*\* Samples for RNA extraction.

**Supplementary Table 2. Sequences of oligonucleotides for siPDK1, si14-3-3 $\zeta$ , WT-3'UTR and MUT-3'UTR**

| siRNA/3'UTR         | Sense Sequence (5'→3')                        | Antiense Sequence (5'→3')                     |
|---------------------|-----------------------------------------------|-----------------------------------------------|
| <b>siRNAs</b>       |                                               |                                               |
| siPDK1              | UACUGCUCUAUGUUGCUGCCUGACC                     | GGUCAGGCAGCAACAUAGAGCAGUA                     |
| si14-3-3 $\zeta$    | UCCAGCUUCGUCUCCUUGGGUAUCC                     | GGAUACCCAAGGAGACGAAGCUGAA                     |
| <b>3'UTR target</b> |                                               |                                               |
| WT-3'UTR            | CGGACTAGTTTTAGGCAACCTAAGAA<br>CAAATGAAGCTTGGG | CCCAAGCTTCATTTGTTCTTAGGTTGC<br>CTAAAAGTAGTCCG |
| MUT-3'UTR           | CGGACTAGTTTTAGGCAACCTAACAT<br>GTAATGAAGCTTGGG | CCCAAGCTTCATTACATGTTAGGTTGC<br>CTAAAAGTAGTCCG |

### Supplementary Table 3. List of miRNAs differentially expressed between tumor and normal tissues.

#### (A) Downregulated miRNAs in tumor.

| ID (miRBase 9.1) | Tumor       |      |        | Normal      |      |        | Corrected |                  |                   |
|------------------|-------------|------|--------|-------------|------|--------|-----------|------------------|-------------------|
|                  | Fold change | SD   | Raw    | Fold change | SD   | Raw    | P-value   | Mature accession | ID (miRBase 13.0) |
| hsa-miR-204      | 0.01        | 0.02 | 0.3    | 0.95        | 0.48 | 122.4  | 0.0102    | MIMAT0000265     | hsa-miR-204       |
| hsa-miR-551b     | 0.06        | 0.37 | 2.2    | 1.16        | 1.13 | 15.6   | 0.0204    | MIMAT0003233     | hsa-miR-551b      |
| hsa-miR-133a     | 0.07        | 0.90 | 20.6   | 1.03        | 0.19 | 17.9   | 0.0303    | MIMAT0000427     | hsa-miR-133a      |
| hsa-miR-139      | 0.10        | 0.49 | 2.8    | 1.01        | 0.32 | 11.4   | 0.0226    | MIMAT0000250     | hsa-miR-139-5p    |
| hsa-miR-133b     | 0.10        | 1.10 | 42.5   | 1.03        | 0.19 | 31.3   | 0.0451    | MIMAT0000770     | hsa-miR-133b      |
| hsa-miR-375      | 0.15        | 0.52 | 809.2  | 1.07        | 0.25 | 1610.5 | 0.0204    | MIMAT0000728     | hsa-miR-375       |
| hsa-miR-30a-3p   | 0.15        | 1.01 | 3.9    | 1.15        | 0.54 | 10.7   | 0.0394    | MIMAT0000088     | hsa-miR-30a*      |
| hsa-miR-29c      | 0.16        | 0.15 | 1667.4 | 1.03        | 0.27 | 8819.3 | 0.0102    | MIMAT0000681     | hsa-miR-29c       |
| hsa-miR-363      | 0.17        | 0.76 | 63.6   | 1.03        | 0.57 | 91.4   | 0.0451    | MIMAT0000707     | hsa-miR-363       |
| hsa-miR-582      | 0.18        | 0.37 | 3.0    | 0.93        | 0.38 | 9.4    | 0.0204    | MIMAT0003247     | hsa-miR-582-5p    |
| hsa-miR-148a     | 0.19        | 0.43 | 1176.0 | 1.13        | 0.31 | 3422.1 | 0.0259    | MIMAT0000243     | hsa-miR-148a      |
| hsa-miR-30a-5p   | 0.30        | 0.37 | 220.0  | 1.11        | 0.36 | 572.8  | 0.0284    | MIMAT0000087     | hsa-miR-30a       |
| hsa-miR-30e-5p   | 0.34        | 0.28 | 363.8  | 1.01        | 0.36 | 915.3  | 0.0147    | MIMAT0000692     | hsa-miR-30e       |
| hsa-miR-497      | 0.42        | 0.42 | 49.3   | 1.12        | 0.49 | 96.9   | 0.0284    | MIMAT0002820     | hsa-miR-497       |
| hsa-miR-572      | 0.42        | 0.37 | 179.8  | 1.25        | 0.69 | 471.8  | 0.0259    | MIMAT0003237     | hsa-miR-572       |
| hsa-miR-638      | 0.46        | 0.34 | 1480.5 | 1.13        | 0.57 | 3327.4 | 0.0303    | MIMAT0003308     | hsa-miR-638       |
| hsa-miR-195      | 0.47        | 0.39 | 251.7  | 1.04        | 0.48 | 461.4  | 0.0451    | MIMAT0000461     | hsa-miR-195       |

#### (B) Upregulated miRNAs in tumor.

| ID (miRBase 9.1) | Tumor       |             |       | Normal      |        |      | Corrected |                  |                   |
|------------------|-------------|-------------|-------|-------------|--------|------|-----------|------------------|-------------------|
|                  | Fold change | SD          | Raw   | Fold change | SD     | Raw  | P-value   | Mature accession | ID (miRBase 13.0) |
| hsa-miR-550      | 1772.69     | 1938.1<br>4 | 24.0  | 5.76        | 211.06 | -0.3 | 0.0102    | MIMAT0003257     | hsa-miR-550*      |
| hsa-miR-18a*     | 1389.48     | 1974.4<br>5 | 19.8  | 2.79        | 176.58 | -1.0 | 0.0102    | MIMAT0002891     | hsa-miR-18a*      |
| hsa-miR-196a     | 113.68      | 289.04      | 180.6 | 1.03        | 2.82   | 1.1  | 0.0102    | MIMAT0000226     | hsa-miR-196a      |
| hsa-miR-615      | 91.59       | 3163.6<br>8 | 5.5   | 1.00        | 164.65 | -2.3 | 0.0226    | MIMAT0003283     | hsa-miR-615-3p    |
| hsa-miR-425-3p   | 90.57       | 2933.2<br>3 | 3.8   | 1.65        | 190.69 | -1.7 | 0.0394    | MIMAT0001343     | hsa-miR-425*      |
| hsa-miR-181a*    | 52.46       | 1524.3<br>7 | 3.2   | 1.00        | 164.59 | -1.5 | 0.0303    | MIMAT0000270     | hsa-miR-181a*     |
| hsa-miR-431      | 41.22       | 971.62      | 2.2   | 1.00        | 232.89 | -1.6 | 0.0303    | MIMAT0001625     | hsa-miR-431       |
| hsa-miR-196b     | 32.83       | 321.19      | 97.7  | 0.63        | 2.12   | 0.9  | 0.0134    | MIMAT0001080     | hsa-miR-196b      |
| hsa-miR-224      | 29.57       | 184.52      | 117.3 | 0.56        | 5.23   | 0.9  | 0.0102    | MIMAT0000281     | hsa-miR-224       |

|                |       |        |         |      |      |        |        |              |                 |
|----------------|-------|--------|---------|------|------|--------|--------|--------------|-----------------|
| hsa-miR-92b    | 25.53 | 130.77 | 19.0    | 0.34 | 6.42 | -1.4   | 0.0134 | MIMAT0003218 | hsa-miR-92b     |
| hsa-miR-135b   | 18.02 | 89.72  | 124.0   | 0.90 | 3.34 | 2.1    | 0.0102 | MIMAT0000758 | hsa-miR-135b    |
| hsa-miR-18a    | 10.66 | 7.99   | 962.8   | 1.02 | 0.47 | 83.5   | 0.0102 | MIMAT0000072 | hsa-miR-18a     |
| hsa-miR-106a   | 9.02  | 5.21   | 2212.5  | 1.04 | 0.58 | 253.9  | 0.0102 | MIMAT0000103 | hsa-miR-106a    |
| hsa-miR-17-5p  | 9.01  | 5.66   | 1830.2  | 1.07 | 0.59 | 212.2  | 0.0102 | MIMAT0000070 | hsa-miR-17      |
| hsa-miR-146a   | 8.86  | 18.74  | 735.5   | 1.00 | 0.60 | 45.4   | 0.0112 | MIMAT0000449 | hsa-miR-146a    |
| hsa-miR-301    | 8.53  | 10.18  | 236.8   | 1.03 | 0.38 | 19.0   | 0.0102 | MIMAT0000688 | hsa-miR-301a    |
| hsa-miR-93     | 8.27  | 5.31   | 1227.2  | 1.05 | 0.49 | 143.5  | 0.0102 | MIMAT0000093 | hsa-miR-93      |
| hsa-miR-19a    | 7.80  | 5.18   | 2188.3  | 1.11 | 0.42 | 278.2  | 0.0102 | MIMAT0000073 | hsa-miR-19a     |
| hsa-miR-20a    | 7.62  | 4.55   | 2857.1  | 1.01 | 0.57 | 372.0  | 0.0102 | MIMAT0000075 | hsa-miR-20a     |
| hsa-miR-18b    | 7.43  | 6.06   | 94.8    | 1.00 | 0.47 | 11.3   | 0.0102 | MIMAT0001412 | hsa-miR-18b     |
| hsa-miR-20b    | 6.84  | 4.22   | 798.7   | 1.07 | 0.55 | 120.2  | 0.0102 | MIMAT0001413 | hsa-miR-20b     |
| hsa-miR-583    | 6.63  | 23.93  | 8.2     | 0.42 | 3.85 | 0.7    | 0.0204 | MIMAT0003248 | hsa-miR-583     |
| hsa-miR-221    | 6.18  | 6.06   | 400.9   | 1.13 | 0.70 | 61.4   | 0.0134 | MIMAT0000278 | hsa-miR-221     |
| hsa-miR-335    | 5.71  | 6.70   | 63.5    | 0.83 | 0.39 | 6.0    | 0.0102 | MIMAT0000765 | hsa-miR-335     |
| hsa-miR-25     | 5.57  | 3.68   | 1255.5  | 1.12 | 0.39 | 221.2  | 0.0102 | MIMAT0000081 | hsa-miR-25      |
| hsa-miR-324-5p | 5.52  | 4.31   | 153.1   | 1.12 | 0.41 | 25.6   | 0.0102 | MIMAT0000761 | hsa-miR-324-5p  |
| hsa-miR-15b    | 5.47  | 2.89   | 1370.8  | 1.11 | 0.51 | 271.9  | 0.0102 | MIMAT0000417 | hsa-miR-15b     |
| hsa-miR-425-5p | 5.27  | 3.47   | 509.6   | 0.98 | 0.38 | 85.1   | 0.0102 | MIMAT0003393 | hsa-miR-425     |
| hsa-miR-92     | 5.24  | 3.15   | 3143.2  | 1.08 | 0.58 | 628.4  | 0.0102 | MIMAT0000092 | hsa-miR-92a     |
| hsa-miR-194    | 5.16  | 3.24   | 4713.8  | 1.27 | 0.69 | 1128.5 | 0.0134 | MIMAT0000460 | hsa-miR-194     |
| hsa-miR-361    | 5.10  | 4.01   | 182.2   | 1.16 | 0.51 | 35.4   | 0.0112 | MIMAT0000703 | hsa-miR-361-5p  |
| hsa-miR-10a    | 4.77  | 8.26   | 607.3   | 1.06 | 0.36 | 79.1   | 0.0303 | MIMAT0000253 | hsa-miR-10a     |
| hsa-miR-222    | 4.70  | 4.20   | 936.6   | 1.22 | 0.59 | 197.2  | 0.0147 | MIMAT0000279 | hsa-miR-222     |
| hsa-miR-7      | 4.68  | 3.87   | 802.8   | 0.88 | 0.32 | 126.5  | 0.0102 | MIMAT0000252 | hsa-miR-7       |
| hsa-miR-455    | 4.59  | 3.44   | 62.7    | 0.85 | 1.55 | 15.4   | 0.0196 | MIMAT0003150 | hsa-miR-455-5p  |
| hsa-miR-362    | 4.42  | 3.31   | 119.3   | 1.01 | 0.26 | 22.8   | 0.0112 | MIMAT0000705 | hsa-miR-362-5p  |
| hsa-miR-454-3p | 4.31  | 3.72   | 48.6    | 0.92 | 0.41 | 8.1    | 0.0102 | MIMAT0003885 | hsa-miR-454     |
| hsa-miR-106b   | 4.30  | 2.86   | 2382.1  | 1.03 | 0.46 | 515.7  | 0.0112 | MIMAT0000680 | hsa-miR-106b    |
| hsa-miR-181c   | 4.26  | 5.24   | 58.2    | 0.89 | 0.63 | 8.7    | 0.0204 | MIMAT0000258 | hsa-miR-181c    |
| hsa-miR-320    | 4.20  | 2.04   | 1416.7  | 1.28 | 0.64 | 435.0  | 0.0134 | MIMAT0000510 | hsa-miR-320a    |
| hsa-miR-21     | 4.05  | 2.17   | 21464.0 | 0.95 | 0.33 | 4687.8 | 0.0102 | MIMAT0000076 | hsa-miR-21      |
| hsa-miR-17-3p  | 4.05  | 2.53   | 300.8   | 1.09 | 0.48 | 74.2   | 0.0102 | MIMAT0000071 | hsa-miR-17*     |
| hsa-miR-155    | 4.03  | 3.28   | 190.1   | 1.15 | 0.63 | 46.5   | 0.0147 | MIMAT0000646 | hsa-miR-155     |
| hsa-miR-34a    | 4.03  | 4.00   | 1422.8  | 1.04 | 0.32 | 276.7  | 0.0134 | MIMAT0000255 | hsa-miR-34a     |
| hsa-miR-19b    | 3.99  | 2.24   | 4842.2  | 1.12 | 0.42 | 1253.7 | 0.0102 | MIMAT0000074 | hsa-miR-19b     |
| hsa-miR-103    | 3.88  | 2.10   | 1857.7  | 1.10 | 0.43 | 499.5  | 0.0102 | MIMAT0000101 | hsa-miR-103     |
| hsa-miR-183    | 3.83  | 6.29   | 88.4    | 0.93 | 0.31 | 13.1   | 0.0284 | MIMAT0000261 | hsa-miR-183     |
| hsa-miR-146b   | 3.81  | 3.18   | 212.2   | 0.84 | 0.51 | 41.4   | 0.0134 | MIMAT0002809 | hsa-miR-146b-5p |
| hsa-miR-181a   | 3.79  | 3.95   | 145.7   | 1.14 | 0.67 | 34.4   | 0.0303 | MIMAT0000256 | hsa-miR-181a    |
| hsa-miR-215    | 3.78  | 2.10   | 2395.3  | 1.15 | 0.58 | 719.9  | 0.0147 | MIMAT0000272 | hsa-miR-215     |
| hsa-miR-192    | 3.74  | 2.04   | 3743.4  | 1.19 | 0.63 | 1191.5 | 0.0170 | MIMAT0000222 | hsa-miR-192     |

|                |      |      |        |      |      |        |        |              |                |
|----------------|------|------|--------|------|------|--------|--------|--------------|----------------|
| hsa-miR-421    | 3.65 | 4.30 | 8.4    | 0.19 | 8.01 | 1.3    | 0.0204 | MIMAT0003339 | hsa-miR-421    |
| hsa-miR-429    | 3.65 | 5.92 | 2019.4 | 1.08 | 0.39 | 358.3  | 0.0170 | MIMAT0001536 | hsa-miR-429    |
| hsa-miR-629    | 3.61 | 3.38 | 32.3   | 0.39 | 4.34 | 6.6    | 0.0204 | MIMAT0003298 | hsa-miR-629*   |
| hsa-miR-503    | 3.53 | 2.94 | 8.6    | 0.99 | 1.49 | 2.5    | 0.0284 | MIMAT0002874 | hsa-miR-503    |
| hsa-miR-181b   | 3.34 | 3.33 | 204.6  | 1.19 | 0.52 | 55.0   | 0.0303 | MIMAT0000257 | hsa-miR-181b   |
| hsa-miR-151    | 3.34 | 2.35 | 177.9  | 1.13 | 0.39 | 53.1   | 0.0204 | MIMAT0000757 | hsa-miR-151-3p |
| hsa-miR-27a    | 3.32 | 2.18 | 1186.0 | 1.02 | 0.56 | 347.3  | 0.0226 | MIMAT0000084 | hsa-miR-27a    |
| hsa-miR-128a   | 3.21 | 2.29 | 34.6   | 0.82 | 0.48 | 8.2    | 0.0134 | MIMAT0000424 | hsa-miR-128    |
| hsa-miR-33     | 3.20 | 2.86 | 310.4  | 1.02 | 0.56 | 86.6   | 0.0284 | MIMAT0000091 | hsa-miR-33a    |
| hsa-miR-34b    | 3.18 | 3.58 | 182.8  | 0.91 | 0.26 | 36.9   | 0.0303 | MIMAT0000685 | hsa-miR-34b*   |
| hsa-miR-493-5p | 3.16 | 3.79 | 10.9   | 0.90 | 1.11 | 1.8    | 0.0147 | MIMAT0002813 | hsa-miR-493*   |
| hsa-miR-223    | 3.13 | 4.33 | 585.6  | 0.90 | 0.70 | 126.2  | 0.0451 | MIMAT0000280 | hsa-miR-223    |
| hsa-miR-532    | 3.11 | 2.34 | 174.0  | 1.01 | 0.27 | 47.2   | 0.0134 | MIMAT0002888 | hsa-miR-532-5p |
| hsa-miR-339    | 3.10 | 2.14 | 264.4  | 0.87 | 0.48 | 69.8   | 0.0196 | MIMAT0000764 | hsa-miR-339-5p |
| hsa-miR-187    | 3.05 | 9.24 | 5.1    | 0.37 | 2.74 | 0.9    | 0.0344 | MIMAT0000262 | hsa-miR-187    |
| hsa-miR-584    | 2.99 | 2.77 | 24.7   | 0.92 | 0.74 | 7.1    | 0.0344 | MIMAT0003249 | hsa-miR-584    |
| hsa-miR-663    | 2.99 | 1.87 | 281.6  | 1.08 | 0.61 | 96.7   | 0.0226 | MIMAT0003326 | hsa-miR-663    |
| hsa-miR-331    | 2.96 | 2.21 | 490.3  | 1.05 | 0.41 | 150.2  | 0.0226 | MIMAT0000760 | hsa-miR-331-3p |
| hsa-miR-23a    | 2.89 | 2.11 | 1821.2 | 0.96 | 0.45 | 543.4  | 0.0226 | MIMAT0000078 | hsa-miR-23a    |
| hsa-miR-107    | 2.89 | 1.72 | 2475.5 | 1.04 | 0.45 | 838.6  | 0.0196 | MIMAT0000104 | hsa-miR-107    |
| hsa-miR-502    | 2.80 | 2.49 | 30.4   | 0.78 | 0.44 | 7.2    | 0.0204 | MIMAT0002873 | hsa-miR-502-5p |
| hsa-miR-374    | 2.67 | 2.18 | 360.1  | 1.08 | 0.34 | 121.5  | 0.0303 | MIMAT0000727 | hsa-miR-374a   |
| hsa-miR-200b   | 2.57 | 3.38 | 5048.1 | 1.05 | 0.38 | 1497.2 | 0.0284 | MIMAT0000318 | hsa-miR-200b   |
| hsa-miR-24     | 2.53 | 2.07 | 4163.1 | 1.09 | 0.39 | 1475.6 | 0.0344 | MIMAT0000080 | hsa-miR-24     |
| hsa-miR-484    | 2.48 | 1.50 | 62.7   | 1.10 | 0.42 | 25.4   | 0.0344 | MIMAT0002174 | hsa-miR-484    |
| hsa-miR-590    | 2.44 | 1.94 | 113.5  | 0.96 | 0.25 | 36.1   | 0.0259 | MIMAT0003258 | hsa-miR-590-5p |
| hsa-miR-345    | 2.39 | 1.71 | 67.9   | 0.92 | 0.49 | 24.5   | 0.0303 | MIMAT0000772 | hsa-miR-345    |
| hsa-miR-15a    | 2.32 | 1.03 | 913.7  | 0.98 | 0.39 | 374.3  | 0.0170 | MIMAT0000068 | hsa-miR-15a    |
| hsa-miR-214    | 2.17 | 1.46 | 215.6  | 1.05 | 0.52 | 92.9   | 0.0394 | MIMAT0000271 | hsa-miR-214    |
| hsa-miR-185    | 2.08 | 1.44 | 387.8  | 1.07 | 0.31 | 176.4  | 0.0394 | MIMAT0000455 | hsa-miR-185    |
| hsa-miR-376b   | 1.86 | 1.67 | 8.6    | 0.76 | 0.73 | 2.9    | 0.0344 | MIMAT0002172 | hsa-miR-376b   |
| hsa-miR-16     | 1.85 | 0.77 | 3698.1 | 1.04 | 0.33 | 2004.5 | 0.0284 | MIMAT0000069 | hsa-miR-16     |
| hsa-miR-423    | 1.81 | 4.31 | 11.9   | 0.24 | 4.04 | 3.5    | 0.0486 | MIMAT0001340 | hsa-miR-423-3p |
| hsa-miR-602    | 1.79 | 4.75 | 16.2   | 0.25 | 1.79 | 3.5    | 0.0259 | MIMAT0003270 | hsa-miR-602    |

MiRNAs are listed in order of the fold changes in tumor.

**Supplementary Table 4. List of genes differentially expressed in pre375-transfected NUGC3 cells and AZ521 cells.**

| Fold change |       | Corrected <i>P</i> * |          | GeneSymbol | Description                                                                                                                  |
|-------------|-------|----------------------|----------|------------|------------------------------------------------------------------------------------------------------------------------------|
| NUGC3       | AZ521 | NUGC3                | AZ521    |            |                                                                                                                              |
| 0.06        | 0.13  | 1.59E-05             | 2.69E-07 | SUB1       | Activated RNA polymerase II transcriptional coactivator p15 (SUB1 homolog) (Positive cofactor 4) (PC4) (p14).                |
| 0.06        | 0.17  | 7.99E-07             | 1.23E-07 | TBC1D5     | TBC1 domain family, member 5 (TBC1D5), mRNA                                                                                  |
| 0.07        | 0.20  | 6.22E-06             | 1.36E-05 | KLK10      | kallikrein-related peptidase 10 (KLK10), transcript variant 1, mRNA                                                          |
| 0.09        | 0.15  | 1.50E-06             | 6.51E-07 | KRT8       | keratin 8 (KRT8), mRNA                                                                                                       |
| 0.10        | 0.16  | 6.48E-06             | 1.84E-07 | PSIP1      | PC4 and SFRS1 interacting protein 1 (PSIP1), transcript variant 2, mRNA                                                      |
| 0.11        | 0.05  | 7.26E-06             | 3.11E-05 | NPPB       | natriuretic peptide precursor B (NPPB), mRNA                                                                                 |
| 0.12        | 0.11  | 1.05E-05             | 3.20E-07 | NUPL1      | KIAA0410 mRNA, partial cds.                                                                                                  |
| 0.13        | 0.23  | 1.61E-05             | 6.18E-07 | YWHAZ      | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ), transcript variant 2, mRNA |
| 0.13        | 0.21  | 2.76E-06             | 1.76E-07 | U69195     | U69195 Soares infant brain 1NIB Homo sapiens cDNA clone 32996, mRNA sequence                                                 |
| 0.14        | 0.21  | 2.11E-06             | 4.02E-07 | RBPJ       | recombination signal binding protein for immunoglobulin kappa J region (RBPJ), transcript variant 4, mRNA                    |
| 0.14        | 0.08  | 3.43E-05             | 1.65E-06 | WDR51B     | WD repeat domain 51B (WDR51B), mRNA                                                                                          |
| 0.14        | 0.21  | 1.16E-05             | 3.60E-06 | SETD7      | SET domain containing (lysine methyltransferase) 7 (SETD7), mRNA                                                             |
| 0.15        | 0.29  | 1.72E-06             | 3.32E-06 | ANKRD1     | ankyrin repeat domain 1 (cardiac muscle) (ANKRD1), mRNA                                                                      |
| 0.16        | 0.28  | 4.23E-05             | 1.70E-06 | EBPL       | emopamil binding protein-like (EBPL), mRNA                                                                                   |
| 0.17        | 0.19  | 2.57E-06             | 9.74E-08 | WWC2       | WW and C2 domain containing 2 (WWC2), mRNA                                                                                   |
| 0.17        | 0.19  | 1.10E-06             | 4.00E-07 | FAM63B     | family with sequence similarity 63, member B (FAM63B), transcript variant 2, mRNA                                            |
| 0.17        | 0.24  | 1.65E-04             | 2.40E-05 | C12orf29   | chromosome 12 open reading frame 29 (C12orf29), mRNA                                                                         |
| 0.17        | 0.19  | 1.57E-05             | 1.16E-06 | MNS1       | meiosis-specific nuclear structural 1 (MNS1), mRNA                                                                           |
| 0.17        | 0.22  | 1.04E-05             | 1.20E-07 | CHSY1      | carbohydrate (chondroitin) synthase 1 (CHSY1), mRNA                                                                          |
| 0.18        | 0.17  | 2.50E-04             | 3.69E-07 | MAT2B      | methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA                                                  |
| 0.19        | 0.10  | 2.00E-06             | 3.79E-07 | ZNF540     | zinc finger protein 540 (ZNF540), mRNA                                                                                       |
| 0.19        | 0.47  | 4.54E-06             | 3.09E-05 | SERTAD2    | SERTA domain containing 2 (SERTAD2), mRNA                                                                                    |
| 0.19        | 0.28  | 2.88E-05             | 2.26E-06 | MTDH       | metadherin (MTDH), mRNA                                                                                                      |
| 0.20        | 0.42  | 3.77E-07             | 2.05E-05 | SLC39A11   | solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), mRNA                                                 |

|      |      |          |          |          |                                                                                                       |
|------|------|----------|----------|----------|-------------------------------------------------------------------------------------------------------|
| 0.20 | 0.44 | 3.46E-05 | 1.67E-05 | FOLR1    | folate receptor 1 (adult) (FOLR1), transcript variant 1, mRNA                                         |
| 0.20 | 0.36 | 7.36E-05 | 2.81E-05 | RASSF8   | clone B4-E11 carcinoma associated protein HOJ-1 mRNA, complete cds, alternatively spliced.            |
| 0.20 | 0.27 | 1.67E-05 | 1.96E-07 | VASN     | vasorin (VASN), mRNA                                                                                  |
| 0.20 | 0.28 | 6.48E-06 | 6.03E-06 | NIN      | ninein (GSK3B interacting protein) (NIN), transcript variant 2, mRNA                                  |
| 0.20 | 0.21 | 9.14E-06 | 5.07E-07 | PHTF2    | putative homeodomain transcription factor 2 (PHTF2), mRNA                                             |
| 0.20 | 0.19 | 3.33E-06 | 7.89E-07 | LDHB     | lactate dehydrogenase B (LDHB), mRNA                                                                  |
| 0.20 | 0.19 | 1.53E-04 | 2.41E-06 | LSM12    | LSM12 homolog (S. cerevisiae) (LSM12), mRNA                                                           |
| 0.21 | 0.23 | 3.77E-07 | 3.62E-05 | ACSL3    | acyl-CoA synthetase long-chain family member 3 (ACSL3), transcript variant 1, mRNA                    |
| 0.21 | 0.32 | 3.04E-05 | 1.96E-07 | SEMA3C   | sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), mRNA |
| 0.21 | 0.12 | 4.68E-07 | 2.09E-06 | CLDN1    | claudin 1 (CLDN1), mRNA                                                                               |
| 0.21 | 0.31 | 6.29E-06 | 1.66E-06 | PAFAH1B1 | platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), mRNA          |
| 0.22 | 0.22 | 3.17E-05 | 7.92E-08 | RG9MTD2  | RNA (guanine-9-) methyltransferase domain containing 2 (RG9MTD2), mRNA                                |
| 0.22 | 0.24 | 2.01E-06 | 5.11E-07 | KPNA4    | karyopherin alpha 4 (importin alpha 3) (KPNA4), mRNA                                                  |
| 0.22 | 0.15 | 6.48E-06 | 1.50E-06 | HDHD1A   | haloacid dehalogenase-like hydrolase domain containing 1A (HDHD1A), mRNA                              |
| 0.23 | 0.26 | 5.63E-05 | 4.74E-06 | GOLGA4   | golgi autoantigen, golgin subfamily a, 4 (GOLGA4), mRNA                                               |
| 0.23 | 0.43 | 1.30E-05 | 4.28E-04 | INSIG2   | insulin induced gene 2 (INSIG2), mRNA                                                                 |
| 0.23 | 0.23 | 1.71E-05 | 1.29E-07 | TTC7B    | tetratricopeptide repeat domain 7B (TTC7B), mRNA                                                      |
| 0.23 | 0.35 | 4.70E-05 | 6.42E-05 | CUGBP2   | CUG triplet repeat, RNA binding protein 2 (CUGBP2), transcript variant 2, mRNA                        |
| 0.23 | 0.29 | 1.35E-05 | 6.43E-05 | SCARNA17 | small Cajal body-specific RNA 17 (SCARNA17) on chromosome 18                                          |
| 0.24 | 0.14 | 4.25E-05 | 5.83E-06 | PHF20L1  | PHD finger protein 20-like 1 (PHF20L1), transcript variant 3, mRNA                                    |
| 0.24 | 0.17 | 5.12E-06 | 1.56E-06 | IL1RAP   | interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, mRNA                         |
| 0.24 | 0.45 | 7.93E-07 | 2.30E-06 | UNC13B   | unc-13 homolog B (C. elegans) (UNC13B), mRNA                                                          |
| 0.24 | 0.13 | 1.73E-04 | 2.38E-07 | FAM36A   | family with sequence similarity 36, member A (FAM36A), mRNA                                           |
| 0.24 | 0.41 | 1.42E-06 | 8.32E-06 | IGFBP3   | insulin-like growth factor binding protein 3 (IGFBP3), transcript variant 1, mRNA                     |
| 0.25 | 0.22 | 3.46E-04 | 2.69E-07 | EEA1     | early endosome antigen 1 (EEA1), mRNA                                                                 |
| 0.25 | 0.42 | 7.88E-05 | 4.34E-06 | ZBTB8    | zinc finger and BTB domain containing 8 (ZBTB8), mRNA                                                 |
| 0.25 | 0.26 | 4.23E-04 | 9.41E-07 | SAMD4A   | mRNA for KIAA1053 protein, partial cds.                                                               |
| 0.25 | 0.26 | 2.89E-06 | 2.07E-07 | TPR      | translocated promoter region (to activated MET oncogene) (TPR), mRNA                                  |
| 0.25 | 0.40 | 2.79E-06 | 5.93E-07 | DDEF2    | development and differentiation enhancing factor 2 (DDEF2), mRNA                                      |

|      |      |          |          |          |                                                                                                              |
|------|------|----------|----------|----------|--------------------------------------------------------------------------------------------------------------|
| 0.25 | 0.31 | 1.39E-04 | 7.43E-07 | TGFB2    | Transforming growth factor beta-2 precursor (TGF-beta-2) (Glioblastoma-derived T-cell suppressor factor)     |
| 0.26 | 0.46 | 5.95E-07 | 9.33E-06 | STX6     | syntaxin 6 (STX6), mRNA                                                                                      |
| 0.26 | 0.38 | 1.42E-06 | 3.10E-07 | ALMS1    | Alstrom syndrome 1 (ALMS1), mRNA                                                                             |
| 0.26 | 0.37 | 1.65E-05 | 3.00E-05 | KIAA0152 | KIAA0152 (KIAA0152), mRNA                                                                                    |
| 0.26 | 0.37 | 2.61E-05 | 1.74E-07 | C11orf54 | chromosome 11 open reading frame 54 (C11orf54), mRNA                                                         |
| 0.26 | 0.48 | 6.14E-05 | 4.45E-05 | TMEM106B | transmembrane protein 106B (TMEM106B), mRNA                                                                  |
| 0.26 | 0.40 | 4.51E-04 | 2.09E-05 | DPY19L1  | DPY-19-like protein 1 (DPY19L1) mRNA, complete cds.                                                          |
| 0.27 | 0.28 | 7.49E-05 | 1.85E-07 | CORO1C   | coronin, actin binding protein, 1C (CORO1C), mRNA                                                            |
| 0.27 | 0.24 | 4.42E-06 | 6.01E-07 | KIAA1191 | KIAA1191 (KIAA1191), transcript variant 1, mRNA                                                              |
| 0.27 | 0.25 | 3.64E-05 | 4.78E-07 | CENPF    | centromere protein F, 350/400ka (mitosin) (CENPF), mRNA                                                      |
| 0.27 | 0.27 | 1.31E-05 | 1.54E-06 | XPR1     | xenotropic and polytropic retrovirus receptor (XPR1), mRNA                                                   |
| 0.27 | 0.24 | 5.95E-07 | 4.73E-06 | RCN2     | reticulocalbin 2, EF-hand calcium binding domain (RCN2), mRNA                                                |
| 0.27 | 0.09 | 5.34E-05 | 1.74E-07 | BIRC3    | baculoviral IAP repeat-containing 3 (BIRC3), transcript variant 1, mRNA                                      |
| 0.28 | 0.30 | 1.57E-05 | 5.84E-07 | NUMB     | numb homolog (Drosophila) (NUMB), transcript variant 1, mRNA                                                 |
| 0.28 | 0.35 | 3.06E-06 | 1.50E-06 | PPP1R2   | protein phosphatase 1, regulatory (inhibitor) subunit 2 (PPP1R2), mRNA                                       |
| 0.28 | 0.25 | 8.28E-06 | 1.71E-06 | SGOL2    | shugoshin-like 2 (S. pombe) (SGOL2), mRNA                                                                    |
| 0.28 | 0.25 | 2.62E-04 | 7.63E-06 | TXNDC10  | thioredoxin domain containing 10 (TXNDC10), mRNA                                                             |
| 0.29 | 0.27 | 0.00122  | 1.43E-05 | CRIM1    | cysteine rich transmembrane BMP regulator 1 (chordin-like) (CRIM1), mRNA                                     |
| 0.29 | 0.48 | 5.95E-07 | 2.28E-05 | CXADR    | coxsackie virus and adenovirus receptor (CXADR), mRNA                                                        |
| 0.29 | 0.27 | 2.07E-06 | 8.55E-08 | VGLL4    | vestigial like 4 (Drosophila) (VGLL4), mRNA                                                                  |
| 0.29 | 0.38 | 2.53E-06 | 1.09E-04 | CDCA7L   | cell division cycle associated 7-like (CDCA7L), mRNA                                                         |
| 0.30 | 0.35 | 2.20E-05 | 6.42E-07 | REEP3    | receptor accessory protein 3 (REEP3), mRNA                                                                   |
| 0.30 | 0.27 | 4.68E-07 | 1.76E-07 | SPAG9    | sperm associated antigen 9 (SPAG9), transcript variant 1, mRNA                                               |
| 0.30 | 0.39 | 1.05E-05 | 2.64E-06 | JAG1     | jagged 1 (Alagille syndrome) (JAG1), mRNA                                                                    |
| 0.30 | 0.33 | 6.96E-05 | 3.66E-07 | AKAP7    | A kinase (PRKA) anchor protein 7 (AKAP7), transcript variant gamma, mRNA                                     |
| 0.30 | 0.35 | 0.00167  | 2.69E-05 | TCF12    | transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12), transcript variant 4, mRNA |
| 0.30 | 0.32 | 2.00E-05 | 1.43E-06 | C3orf34  | chromosome 3 open reading frame 34 (C3orf34), mRNA                                                           |
| 0.30 | 0.40 | 9.89E-06 | 5.98E-05 | PHLDA1   | pleckstrin homology-like domain, family A, member 1 (PHLDA1), mRNA                                           |
| 0.30 | 0.40 | 6.25E-05 | 2.11E-05 | PDGFC    | platelet derived growth factor C (PDGFC), mRNA                                                               |



|      |      |          |          |         |                                                                                                                             |
|------|------|----------|----------|---------|-----------------------------------------------------------------------------------------------------------------------------|
| 0.30 | 0.40 | 2.01E-06 | 1.24E-05 | KCNN4   | potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4 (KCNN4), mRNA                     |
| 0.30 | 0.26 | 7.99E-07 | 1.56E-06 | CSTF2   | cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa (CSTF2), mRNA                                                     |
| 0.31 | 0.28 | 7.19E-05 | 2.69E-07 | FAM3C   | family with sequence similarity 3, member C (FAM3C), transcript variant 1, mRNA                                             |
| 0.31 | 0.32 | 3.81E-05 | 7.30E-06 | DCUN1D4 | DCN1, defective in cullin neddylation 1, domain containing 4 ( <i>S. cerevisiae</i> ) (DCUN1D4), transcript variant 2, mRNA |
| 0.31 | 0.27 | 3.29E-05 | 8.55E-08 | PRDX1   | peroxiredoxin 1 (PRDX1), transcript variant 1, mRNA                                                                         |
| 0.31 | 0.40 | 2.82E-04 | 4.45E-04 | OSBPL8  | oxysterol binding protein-like 8 (OSBPL8), transcript variant 1, mRNA                                                       |
| 0.31 | 0.32 | 4.94E-06 | 1.03E-06 | TGM2    | transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM2), transcript variant 1, mRNA          |
| 0.32 | 0.29 | 6.71E-04 | 7.27E-06 | WTAP    | Wilms tumor 1 associated protein (WTAP), transcript variant 3, mRNA                                                         |
| 0.32 | 0.31 | 3.47E-06 | 3.97E-07 | KCTD10  | potassium channel tetramerisation domain containing 10 (KCTD10), mRNA                                                       |
| 0.32 | 0.27 | 3.84E-06 | 5.57E-07 | MBD2    | methyl-CpG binding domain protein 2 (MBD2), transcript variant 1, mRNA                                                      |
| 0.32 | 0.33 | 3.70E-05 | 1.14E-06 | ENOPH1  | enolase-phosphatase 1 (ENOPH1), mRNA                                                                                        |
| 0.32 | 0.43 | 1.10E-06 | 1.33E-06 | PAPD4   | PAP associated domain containing 4 (PAPD4), mRNA                                                                            |
| 0.32 | 0.39 | 1.85E-04 | 1.02E-04 | DIP2C   | DIP2 disco-interacting protein 2 homolog C ( <i>Drosophila</i> ) (DIP2C), mRNA                                              |
| 0.32 | 0.41 | 8.12E-04 | 1.26E-06 | IFT80   | intraflagellar transport 80 homolog ( <i>Chlamydomonas</i> ) (IFT80), mRNA                                                  |
| 0.32 | 0.27 | 9.23E-06 | 2.53E-07 | CALU    | calumenin (CALU), mRNA                                                                                                      |
| 0.33 | 0.47 | 3.32E-04 | 3.63E-04 | FSTL3   | follicle-stimulating-like 3 (secreted glycoprotein) (FSTL3), mRNA                                                           |
| 0.33 | 0.47 | 6.58E-07 | 1.01E-06 | FVT1    | follicular lymphoma variant translocation 1 (FVT1), mRNA                                                                    |
| 0.33 | 0.27 | 4.04E-06 | 1.62E-07 | EXO1    | exonuclease 1 (EXO1), transcript variant 3, mRNA                                                                            |
| 0.33 | 0.29 | 3.32E-05 | 4.56E-07 | PTPMT1  | protein tyrosine phosphatase, mitochondrial 1, mRNA (cDNA clone MGC:31981 IMAGE:4591438), complete cds.                     |
| 0.33 | 0.17 | 1.70E-04 | 9.72E-06 | EIF2S1  | eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa (EIF2S1), mRNA                                           |
| 0.33 | 0.34 | 3.51E-06 | 4.51E-07 | OPA1    | optic atrophy 1 (autosomal dominant) (OPA1), nuclear gene encoding mitochondrial protein, transcript variant 8, mRNA        |
| 0.33 | 0.40 | 1.90E-05 | 2.17E-05 | STK38L  | serine/threonine kinase 38 like (STK38L), mRNA                                                                              |
| 0.33 | 0.29 | 8.17E-05 | 3.92E-07 | PLEKHA3 | pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 3 (PLEKHA3), mRNA                |
| 0.33 | 0.49 | 8.01E-05 | 2.74E-06 | PRKX    | protein kinase, X-linked (PRKX), mRNA                                                                                       |
| 0.33 | 0.30 | 1.42E-06 | 3.65E-07 | OGFOD1  | 2-oxoglutarate and iron-dependent oxygenase domain containing 1 (OGFOD1), mRNA                                              |
| 0.33 | 0.32 | 4.97E-06 | 1.72E-06 | TH1L    | TH1-like ( <i>Drosophila</i> ) (TH1L), transcript variant 1, mRNA                                                           |
| 0.34 | 0.39 | 5.27E-05 | 9.95E-06 | TMEM111 | Transmembrane protein 111.                                                                                                  |
| 0.34 | 0.23 | 9.16E-05 | 2.60E-07 | SEC23A  | Sec23 homolog A ( <i>S. cerevisiae</i> ) (SEC23A), mRNA                                                                     |
| 0.34 | 0.49 | 0.00116  | 2.49E-05 | TXNDC4  | thioredoxin domain containing 4 (endoplasmic reticulum) (TXNDC4), mRNA                                                      |

|      |      |          |          |           |                                                                                                                   |
|------|------|----------|----------|-----------|-------------------------------------------------------------------------------------------------------------------|
| 0.34 | 0.29 | 1.42E-06 | 2.69E-07 | MAPKAP1   | mitogen-activated protein kinase associated protein 1 (MAPKAP1), transcript variant 1, mRNA                       |
| 0.34 | 0.29 | 2.75E-05 | 1.96E-07 | SENP1     | SUMO1/sentrin specific peptidase 1 (SENP1), mRNA                                                                  |
| 0.34 | 0.49 | 2.05E-04 | 8.05E-07 | NETO2     | neuropilin (NRP) and tolloid (TLL)-like 2 (NETO2), mRNA                                                           |
| 0.34 | 0.36 | 5.42E-06 | 5.72E-07 | USP31     | ubiquitin specific peptidase 31 (USP31), mRNA                                                                     |
| 0.34 | 0.42 | 1.05E-05 | 0.00101  | ACSL4     | acyl-CoA synthetase long-chain family member 4 (ACSL4), transcript variant 1, mRNA                                |
| 0.34 | 0.37 | 1.37E-05 | 2.74E-06 | HOMER2    | homer homolog 2 (Drosophila) (HOMER2), transcript variant 2, mRNA                                                 |
| 0.34 | 0.35 | 1.55E-05 | 7.92E-08 | C14orf159 | chromosome 14 open reading frame 159 (C14orf159), mRNA                                                            |
| 0.34 | 0.25 | 1.01E-04 | 5.26E-05 | SLC35B4   | solute carrier family 35, member B4 (SLC35B4), mRNA                                                               |
| 0.35 | 0.26 | 2.32E-05 | 6.40E-07 | U88048    | Human clone KiSS-16 unknown product mRNA, complete cds.                                                           |
| 0.35 | 0.46 | 2.16E-05 | 1.11E-05 | RAB6A     | RAB6A, member RAS oncogene family (RAB6A), transcript variant 1, mRNA                                             |
| 0.35 | 0.32 | 1.45E-05 | 9.91E-07 | MKRN1     | znf-xp protein mRNA, complete cds.                                                                                |
| 0.35 | 0.40 | 2.21E-06 | 1.78E-06 | SH3D19    | SH3 domain protein D19 (SH3D19), mRNA                                                                             |
| 0.35 | 0.37 | 5.35E-05 | 3.28E-06 | NUS1      | nuclear undecaprenyl pyrophosphate synthase 1 homolog ( <i>S. cerevisiae</i> ) (NUS1), mRNA                       |
| 0.35 | 0.33 | 1.42E-06 | 8.01E-07 | C1QBP     | complement component 1, q subcomponent binding protein (C1QBP), nuclear gene encoding mitochondrial protein, mRNA |
| 0.35 | 0.38 | 1.30E-05 | 4.70E-05 | B3GALNT1  | beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group) (B3GALNT1), transcript variant 1, mRNA       |
| 0.35 | 0.23 | 2.23E-05 | 2.56E-07 | CTGF      | connective tissue growth factor (CTGF), mRNA                                                                      |
| 0.36 | 0.30 | 4.51E-05 | 2.46E-06 | HK2       | hexokinase 2 (HK2), mRNA                                                                                          |
| 0.36 | 0.37 | 0.00176  | 1.88E-05 | PTPN12    | protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA                                                 |
| 0.36 | 0.18 | 4.74E-04 | 6.04E-07 | C14orf145 | chromosome 14 open reading frame 145 (C14orf145), mRNA                                                            |
| 0.36 | 0.44 | 7.90E-05 | 1.12E-04 | ZFP36L2   | zinc finger protein 36, C3H type-like 2 (ZFP36L2), mRNA                                                           |
| 0.36 | 0.40 | 1.57E-05 | 7.27E-05 | ATG7      | mRNA; cDNA DKFZp434N0735 (from clone DKFZp434N0735); partial cds.                                                 |
| 0.36 | 0.31 | 1.23E-04 | 2.28E-07 | RPGRIP1L  | KIAA1005 protein (KIAA1005), mRNA                                                                                 |
| 0.36 | 0.40 | 1.24E-04 | 2.06E-06 | DGKD      | diacylglycerol kinase, delta 130kDa (DGKD), transcript variant 2, mRNA                                            |
| 0.36 | 0.31 | 4.56E-04 | 5.84E-07 | CCDC59    | coiled-coil domain containing 59 (CCDC59), mRNA                                                                   |
| 0.36 | 0.26 | 7.67E-05 | 2.52E-06 | TSC22D2   | TSC22 domain family, member 2 (TSC22D2), mRNA                                                                     |
| 0.36 | 0.36 | 1.01E-06 | 1.23E-07 | RB1CC1    | RB1-inducible coiled-coil 1 (RB1CC1), mRNA                                                                        |
| 0.37 | 0.25 | 1.59E-05 | 2.54E-07 | KIAA0286  | KIAA0286 protein (KIAA0286), mRNA                                                                                 |
| 0.37 | 0.43 | 5.16E-05 | 1.14E-04 | DNAH11    | dynein, axonemal, heavy chain 11 (DNAH11), mRNA                                                                   |
| 0.37 | 0.34 | 2.21E-04 | 6.04E-07 | DAZAP2    | DAZ associated protein 2 (DAZAP2), mRNA                                                                           |

|      |      |          |          |          |                                                                                                                                   |
|------|------|----------|----------|----------|-----------------------------------------------------------------------------------------------------------------------------------|
| 0.37 | 0.32 | 6.60E-04 | 8.40E-06 | NUDT21   | nudix (nucleoside diphosphate linked moiety X)-type motif 21 (NUDT21), mRNA                                                       |
| 0.37 | 0.37 | 3.75E-05 | 1.62E-05 | ZNF404   | zinc finger protein 404 (ZNF404), mRNA                                                                                            |
| 0.37 | 0.30 | 4.65E-04 | 4.64E-07 | USP1     | ubiquitin specific peptidase 1 (USP1), transcript variant 1, mRNA                                                                 |
| 0.37 | 0.45 | 1.65E-05 | 3.49E-06 | ARNTL2   | cycle-like factor CLIF mRNA, complete cds.                                                                                        |
| 0.37 | 0.26 | 2.33E-05 | 3.54E-07 | UXS1     | UDP-glucuronate decarboxylase 1 (UXS1), mRNA                                                                                      |
| 0.37 | 0.29 | 1.02E-04 | 1.53E-06 | TMEM170  | mRNA; cDNA DKFZp686O1555 (from clone DKFZp686O1555).                                                                              |
| 0.37 | 0.35 | 8.16E-04 | 2.98E-06 | FKBP1A   | FK506 binding protein 1A, 12kDa (FKBP1A), transcript variant 12A, mRNA                                                            |
| 0.37 | 0.30 | 9.49E-05 | 2.64E-07 | C6orf182 | chromosome 6 open reading frame 182 (C6orf182), mRNA                                                                              |
| 0.38 | 0.46 | 2.67E-05 | 5.49E-05 | BCL10    | B-cell CLL/lymphoma 10 (BCL10), mRNA                                                                                              |
| 0.38 | 0.41 | 1.55E-04 | 4.25E-07 | CBWD2    | COBW domain containing 2 (CBWD2), mRNA                                                                                            |
| 0.38 | 0.30 | 7.99E-07 | 1.83E-06 | UBE3A    | ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript variant 3, mRNA |
| 0.38 | 0.49 | 1.90E-06 | 1.62E-04 | DUSP6    | dual specificity phosphatase 6 (DUSP6), transcript variant 1, mRNA                                                                |
| 0.38 | 0.38 | 3.62E-04 | 2.38E-07 | CBWD3    | COBW domain containing 3 (CBWD3), mRNA                                                                                            |
| 0.38 | 0.44 | 1.06E-04 | 5.70E-05 | ZNF614   | zinc finger protein 614 (ZNF614), mRNA                                                                                            |
| 0.38 | 0.41 | 1.18E-06 | 9.32E-06 | SNRPA1   | small nuclear ribonucleoprotein polypeptide A' (SNRPA1), mRNA                                                                     |
| 0.39 | 0.47 | 3.77E-07 | 2.65E-05 | STRBP    | spermatid perinuclear RNA binding protein (STRBP), mRNA                                                                           |
| 0.39 | 0.24 | 5.09E-05 | 7.82E-06 | SGMS2    | sphingomyelin synthase 2 (SGMS2), mRNA                                                                                            |
| 0.39 | 0.47 | 2.19E-05 | 1.76E-07 | PHF3     | PHD finger protein 3 (PHF3), mRNA                                                                                                 |
| 0.39 | 0.44 | 0.00108  | 2.93E-04 | DUT      | dUTP pyrophosphatase (DUT), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA                               |
| 0.39 | 0.35 | 2.53E-06 | 2.90E-05 | CDKN2B   | cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (CDKN2B), transcript variant 2, mRNA                                    |
| 0.39 | 0.41 | 5.08E-05 | 2.59E-07 | GFM2     | G elongation factor, mitochondrial 2 (GFM2), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA              |
| 0.39 | 0.36 | 0.00627  | 8.42E-04 | SET      | SET translocation (myeloid leukemia-associated) (SET), mRNA                                                                       |
| 0.39 | 0.35 | 6.97E-05 | 6.25E-07 | ENAH     | enabled homolog (Drosophila) (ENAH), transcript variant 1, mRNA                                                                   |
| 0.39 | 0.38 | 2.27E-05 | 2.26E-05 | METTL2B  | methyltransferase like 2B (METTL2B), mRNA                                                                                         |
| 0.40 | 0.40 | 7.17E-06 | 7.78E-05 | FAM44A   | family with sequence similarity 44, member A (FAM44A), mRNA                                                                       |
| 0.40 | 0.45 | 2.46E-05 | 5.89E-07 | CCDC32   | coiled-coil domain containing 32 (CCDC32), transcript variant 2, mRNA                                                             |
| 0.40 | 0.27 | 1.03E-04 | 6.18E-07 | SNX25    | sorting nexin 25 (SNX25), mRNA                                                                                                    |
| 0.40 | 0.31 | 7.28E-06 | 2.45E-07 | C15orf41 | chromosome 15 open reading frame 41 (C15orf41), mRNA                                                                              |
| 0.40 | 0.38 | 5.62E-04 | 2.53E-07 | PAFAH2   | Platelet-activating factor acetylhydrolase 2, cytoplasmic (EC 3.1.1.47) (Serine-dependent phospholipase A2) (HSD-PLA2).           |

|      |      |          |          |          |                                                                                                                                   |
|------|------|----------|----------|----------|-----------------------------------------------------------------------------------------------------------------------------------|
| 0.40 | 0.44 | 8.09E-05 | 1.58E-06 | APPL2    | adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2 (APPL2), mRNA                             |
| 0.40 | 0.40 | 8.00E-07 | 4.28E-07 | EBAG9    | estrogen receptor binding site associated, antigen, 9 (EBAG9), transcript variant 1, mRNA                                         |
| 0.40 | 0.24 | 4.83E-06 | 8.74E-06 | FAM33A   | family with sequence similarity 33, member A (FAM33A), mRNA                                                                       |
| 0.40 | 0.38 | 0.00111  | 2.24E-07 | SNAPC1   | small nuclear RNA activating complex, polypeptide 1, 43kDa (SNAPC1), mRNA                                                         |
| 0.40 | 0.33 | 2.18E-04 | 1.09E-04 | KIAA1212 | KIAA1212 (KIAA1212), mRNA                                                                                                         |
| 0.40 | 0.27 | 2.11E-04 | 2.32E-07 | WDR1     | WD repeat domain 1 (WDR1), transcript variant 1, mRNA                                                                             |
| 0.40 | 0.30 | 1.65E-04 | 5.19E-07 | PPP2R3C  | protein phosphatase 2 (formerly 2A), regulatory subunit B", gamma (PPP2R3C), mRNA                                                 |
| 0.40 | 0.16 | 3.74E-06 | 2.85E-06 | TNS3     | tensin 3 (TNS3), mRNA                                                                                                             |
| 0.40 | 0.47 | 2.81E-04 | 1.02E-05 | EXOC6    | exocyst complex component 6 (EXOC6), transcript variant 2, mRNA                                                                   |
| 0.41 | 0.22 | 3.27E-04 | 2.48E-06 | TMED5    | transmembrane emp24 protein transport domain containing 5 (TMED5), mRNA                                                           |
| 0.41 | 0.39 | 1.67E-04 | 1.93E-05 | LHFPL2   | lipoma HMGIC fusion partner-like 2 (LHFPL2), mRNA                                                                                 |
| 0.41 | 0.40 | 5.04E-05 | 5.02E-06 | RLF      | rearranged L-myc fusion (RLF), mRNA                                                                                               |
| 0.41 | 0.36 | 2.50E-04 | 3.51E-06 | CHPT1    | choline phosphotransferase 1 (CHPT1), mRNA                                                                                        |
| 0.41 | 0.39 | 6.62E-05 | 6.33E-05 | AZI2     | 5-azacytidine induced 2 (AZI2), mRNA                                                                                              |
| 0.41 | 0.33 | 8.01E-04 | 1.79E-04 | MYBL1    | v-myb myeloblastosis viral oncogene homolog (avian)-like 1 (MYBL1), mRNA                                                          |
| 0.41 | 0.37 | 3.29E-05 | 2.91E-05 | MIRH1    | chromosome 13 open reading frame 25, mRNA (cDNA clone IMAGE:4838522).                                                             |
| 0.41 | 0.41 | 0.0019   | 5.44E-06 | NXT2     | nuclear transport factor 2-like export factor 2 (NXT2), mRNA                                                                      |
| 0.41 | 0.40 | 1.00E-04 | 1.17E-06 | ZFP91    | zinc finger protein 91 homolog (mouse) (ZFP91), transcript variant 1, mRNA                                                        |
| 0.41 | 0.34 | 1.77E-05 | 2.81E-07 | CNN3     | calponin 3, acidic (CNN3), mRNA                                                                                                   |
| 0.41 | 0.38 | 1.78E-05 | 1.39E-06 | GRPEL2   | GrpE-like 2, mitochondrial (E. coli) (GRPEL2), nuclear gene encoding mitochondrial protein, mRNA                                  |
| 0.41 | 0.40 | 2.56E-05 | 6.51E-07 | GTPBP4   | Nucleolar GTP-binding protein 1 (Chronic renal failure gene protein) (GTP-binding protein NGB).                                   |
| 0.42 | 0.38 | 7.59E-04 | 1.11E-05 | SIPA1L3  | signal-induced proliferation-associated 1 like 3 (SIPA1L3), mRNA                                                                  |
| 0.42 | 0.47 | 1.09E-04 | 2.09E-05 | WHSC1L1  | Wolf-Hirschhorn syndrome candidate 1-like 1 (WHSC1L1), transcript variant short, mRNA                                             |
| 0.42 | 0.41 | 8.14E-07 | 1.43E-06 | LMAN2    | lectin, mannose-binding 2 (LMAN2), mRNA                                                                                           |
| 0.42 | 0.37 | 1.46E-05 | 2.56E-07 | HSP90AA1 | heat shock protein 90kDa alpha (cytosolic), class A member 1 (HSP90AA1), transcript variant 2, mRNA                               |
| 0.42 | 0.47 | 4.85E-04 | 1.09E-04 | DPYSL3   | dihydropyrimidinase-like 3 (DPYSL3), mRNA                                                                                         |
| 0.42 | 0.41 | 9.29E-06 | 3.54E-07 | PEBP1    | phosphatidylethanolamine binding protein 1 (PEBP1), mRNA                                                                          |
| 0.42 | 0.32 | 1.75E-04 | 1.27E-06 | SLC7A6   | solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 (SLC7A6), transcript variant 1, mRNA               |
| 0.42 | 0.39 | 4.62E-04 | 5.62E-06 | AMMECR1  | Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene 1, transcript variant 1, mRNA |

|      |      |          |          |           |                                                                                                     |
|------|------|----------|----------|-----------|-----------------------------------------------------------------------------------------------------|
| 0.42 | 0.31 | 1.90E-05 | 9.66E-06 | RHOQ      | ras homolog gene family, member Q (RHOQ), mRNA                                                      |
| 0.42 | 0.40 | 1.26E-04 | 7.99E-06 | RAB28     | RAB28, member RAS oncogene family (RAB28), transcript variant 2, mRNA                               |
| 0.43 | 0.37 | 0.00235  | 9.07E-06 | RAP2C     | RAP2C, member of RAS oncogene family (RAP2C), mRNA                                                  |
| 0.43 | 0.49 | 6.94E-05 | 2.28E-04 | UBLCP1    | ubiquitin-like domain containing CTD phosphatase 1 (UBLCP1), mRNA                                   |
| 0.43 | 0.49 | 1.24E-05 | 7.02E-06 | CYP20A1   | cytochrome P450, family 20, subfamily A, polypeptide 1 (CYP20A1), mRNA                              |
| 0.43 | 0.44 | 3.72E-06 | 4.45E-05 | EIF4G3    | eukaryotic translation initiation factor 4 gamma, 3 (EIF4G3), mRNA                                  |
| 0.43 | 0.38 | 8.00E-04 | 7.25E-07 | TOR1AIP2  | Torsin-1A-interacting protein 2 (Lumenal domain-like LAP1).                                         |
| 0.43 | 0.36 | 2.23E-05 | 2.21E-06 | OXNAD1    | oxidoreductase NAD-binding domain containing 1 (OXNAD1), mRNA                                       |
| 0.43 | 0.28 | 3.26E-06 | 2.07E-06 | ZNF571    | zinc finger protein 571 (ZNF571), mRNA                                                              |
| 0.43 | 0.26 | 3.05E-05 | 1.46E-06 | SYNCRIP   | synaptotagmin binding, cytoplasmic RNA interacting protein (SYNCRIP), mRNA                          |
| 0.43 | 0.46 | 3.82E-04 | 6.10E-05 | CFL2      | cofilin 2 (muscle) (CFL2), transcript variant 1, mRNA                                               |
| 0.43 | 0.24 | 2.39E-04 | 1.15E-06 | KIAA1524  | mRNA for KIAA1524 protein, partial cds.                                                             |
| 0.43 | 0.40 | 5.83E-05 | 3.37E-04 | HN1       | hematological and neurological expressed 1 (HN1), transcript variant 3, mRNA                        |
| 0.43 | 0.37 | 1.36E-05 | 8.71E-07 | RBBP8     | retinoblastoma binding protein 8 (RBBP8), transcript variant 1, mRNA                                |
| 0.44 | 0.33 | 1.27E-04 | 8.42E-06 | NOLC1     | nucleolar and coiled-body phosphoprotein 1, mRNA (cDNA clone MGC:5049 IMAGE:2900024), complete cds. |
| 0.44 | 0.33 | 2.93E-05 | 2.07E-07 | D15Wsu75e | DNA segment, Chr 15, Wayne State University 75, expressed (D15Wsu75e), mRNA                         |
| 0.44 | 0.46 | 5.82E-05 | 4.29E-05 | RAPGEF1   | Rap guanine nucleotide exchange factor (GEF) 1 (RAPGEF1), transcript variant 2, mRNA                |
| 0.44 | 0.33 | 3.32E-04 | 5.07E-07 | NLE1      | notchless homolog 1 (Drosophila) (NLE1), transcript variant 2, mRNA                                 |
| 0.44 | 0.34 | 2.01E-06 | 4.54E-05 | CREB3     | cAMP responsive element binding protein 3 (CREB3), mRNA                                             |
| 0.44 | 0.24 | 9.89E-05 | 4.68E-06 | ARHGAP11A | Rho GTPase activating protein 11A (ARHGAP11A), transcript variant 1, mRNA                           |
| 0.44 | 0.48 | 3.47E-06 | 1.68E-05 | EXT1      | exostoses (multiple) 1 (EXT1), mRNA                                                                 |
| 0.44 | 0.48 | 5.93E-04 | 2.28E-06 | ARL2BP    | ADP-ribosylation factor-like 2 binding protein (ARL2BP), mRNA                                       |
| 0.44 | 0.27 | 1.20E-04 | 3.84E-06 | TIMM17A   | translocase of inner mitochondrial membrane 17 homolog A (yeast) (TIMM17A), mRNA                    |
| 0.44 | 0.49 | 0.00115  | 2.12E-05 | NCOA7     | nuclear receptor coactivator 7 (NCOA7), mRNA                                                        |
| 0.44 | 0.37 | 9.75E-04 | 1.14E-05 | SLC35A3   | solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member A3, mRNA        |
| 0.44 | 0.47 | 3.07E-05 | 3.10E-05 | TAF3      | Transcription initiation factor TFIID subunit 3 (TBP-associated factor 3)                           |
| 0.45 | 0.40 | 3.91E-06 | 2.24E-07 | METTL2A   | methyltransferase like 2A (METTL2A), mRNA                                                           |
| 0.45 | 0.46 | 2.01E-06 | 1.07E-06 | FYTTD1    | forty-two-three domain containing 1 (FYTTD1), transcript variant 2, mRNA                            |
| 0.45 | 0.43 | 4.69E-06 | 2.28E-06 | PTP4A2    | Protein tyrosine phosphatase type IVA protein 2 (EC 3.1.3.48)                                       |

|      |      |          |          |         |                                                                                                                    |
|------|------|----------|----------|---------|--------------------------------------------------------------------------------------------------------------------|
| 0.45 | 0.48 | 6.07E-04 | 7.60E-06 | MAP2K4  | mitogen-activated protein kinase kinase 4 (MAP2K4), mRNA                                                           |
| 0.45 | 0.35 | 6.00E-06 | 5.40E-06 | ZRF1    | zuotin related factor 1 (ZRF1), mRNA                                                                               |
| 0.45 | 0.42 | 9.10E-06 | 6.05E-07 | TNPO3   | transportin 3 (TNPO3), mRNA                                                                                        |
| 0.45 | 0.26 | 6.95E-05 | 1.24E-06 | GATA6   | GATA binding protein 6 (GATA6), mRNA                                                                               |
| 0.45 | 0.42 | 1.07E-05 | 1.62E-05 | CUL5    | cullin 5 (CUL5), mRNA                                                                                              |
| 0.45 | 0.47 | 0.00349  | 2.87E-06 | AEBP2   | AE binding protein 2 (AEBP2), mRNA                                                                                 |
| 0.45 | 0.46 | 3.04E-06 | 1.94E-06 | GATAD1  | GATA zinc finger domain containing 1 (GATAD1), mRNA                                                                |
| 0.45 | 0.40 | 4.45E-04 | 4.48E-06 | USP46   | ubiquitin specific peptidase 46 (USP46), mRNA                                                                      |
| 0.45 | 0.35 | 6.57E-04 | 7.67E-06 | EMP1    | epithelial membrane protein 1 (EMP1), mRNA                                                                         |
| 0.45 | 0.23 | 3.94E-05 | 4.56E-07 | CTSC    | cathepsin C (CTSC), transcript variant 2, mRNA                                                                     |
| 0.45 | 0.36 | 0.00252  | 1.20E-05 | H19     | H19, imprinted maternally expressed untranslated mRNA (H19) on chromosome 11                                       |
| 0.46 | 0.31 | 1.22E-05 | 6.19E-06 | YAP1    | Yes-associated protein 1, 65kDa (YAP1), mRNA                                                                       |
| 0.46 | 0.34 | 1.52E-04 | 7.78E-07 | AHCYL1  | S-adenosylhomocysteine hydrolase-like 1 (AHCYL1), mRNA                                                             |
| 0.46 | 0.41 | 3.01E-05 | 1.58E-06 | ODF2    | outer dense fiber of sperm tails 2 (ODF2), transcript variant 1, mRNA                                              |
| 0.46 | 0.36 | 4.09E-04 | 9.18E-06 | NDST1   | N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1, mRNA (cDNA clone MGC:9410 IMAGE:3882074), complete cds. |
| 0.46 | 0.40 | 3.55E-04 | 2.76E-04 | MPP5    | membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5) (MPP5), mRNA                                      |
| 0.46 | 0.46 | 0.00729  | 8.06E-05 | SPRED1  | sprouty-related, EVH1 domain containing 1 (SPRED1), mRNA                                                           |
| 0.46 | 0.50 | 1.90E-05 | 4.94E-06 | COG2    | component of oligomeric golgi complex 2 (COG2), mRNA                                                               |
| 0.46 | 0.44 | 1.43E-05 | 9.12E-06 | UGCG    | UDP-glucose ceramide glucosyltransferase (UGCG), mRNA                                                              |
| 0.46 | 0.46 | 1.23E-04 | 1.76E-05 | MRE11A  | MRE11 meiotic recombination 11 homolog A ( <i>S. cerevisiae</i> ) (MRE11A), transcript variant 2, mRNA             |
| 0.46 | 0.42 | 3.83E-06 | 3.62E-06 | PRDX3   | peroxiredoxin 3 (PRDX3), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA                   |
| 0.46 | 0.47 | 6.09E-06 | 8.80E-06 | PPCS    | phosphopantothenoylcysteine synthetase (PPCS), transcript variant 1, mRNA                                          |
| 0.46 | 0.42 | 9.30E-06 | 1.49E-05 | PTPN1   | protein tyrosine phosphatase, non-receptor type 1 (PTPN1), mRNA                                                    |
| 0.46 | 0.45 | 3.35E-06 | 3.29E-05 | F3      | coagulation factor III (thromboplastin, tissue factor) (F3), mRNA                                                  |
| 0.46 | 0.33 | 1.32E-05 | 5.19E-06 | RPN2    | ribophorin II (RPN2), mRNA                                                                                         |
| 0.47 | 0.30 | 2.78E-05 | 2.06E-06 | NT5C2   | 5'-nucleotidase, cytosolic II (NT5C2), mRNA                                                                        |
| 0.47 | 0.44 | 3.62E-05 | 8.54E-07 | C1GALT1 | core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1 (C1GALT1), mRNA                |
| 0.47 | 0.25 | 2.96E-05 | 1.33E-06 | DNMT3B  | DNA (cytosine-5-)-methyltransferase 3 beta (DNMT3B), transcript variant 6, mRNA                                    |
| 0.47 | 0.46 | 1.00E-03 | 2.93E-06 | DR1     | down-regulator of transcription 1, TBP-binding (negative cofactor 2) (DR1), mRNA                                   |

|      |      |          |          |          |                                                                                                                                      |
|------|------|----------|----------|----------|--------------------------------------------------------------------------------------------------------------------------------------|
| 0.47 | 0.28 | 7.85E-04 | 2.56E-07 | KLHL7    | kelch-like 7 ( <i>Drosophila</i> ), mRNA (cDNA clone IMAGE:3899090), complete cds.                                                   |
| 0.47 | 0.28 | 9.31E-06 | 8.55E-08 | WWC1     | WW and C2 domain containing 1 (WWC1), mRNA                                                                                           |
| 0.47 | 0.21 | 3.17E-05 | 7.21E-05 | DOK7     | docking protein 7 (DOK7), mRNA                                                                                                       |
| 0.47 | 0.09 | 2.38E-05 | 0.0012   | COL12A1  | collagen, type XII, alpha 1 (COL12A1), transcript variant long, mRNA                                                                 |
| 0.47 | 0.46 | 1.38E-04 | 8.46E-06 | PGM2     | phosphoglucomutase 2 (PGM2), mRNA                                                                                                    |
| 0.48 | 0.48 | 4.61E-05 | 8.45E-07 | GAS8     | growth arrest-specific 8 (GAS8), mRNA                                                                                                |
| 0.48 | 0.39 | 5.62E-04 | 1.00E-05 | CRLF3    | cytokine receptor-like factor 3 (CRLF3), mRNA                                                                                        |
| 0.48 | 0.44 | 3.20E-04 | 4.86E-06 | SUZ12    | suppressor of zeste 12 homolog ( <i>Drosophila</i> ) (SUZ12), mRNA                                                                   |
| 0.48 | 0.40 | 1.39E-04 | 2.02E-05 | AGPAT5   | 1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon) (AGPAT5), mRNA                       |
| 0.48 | 0.37 | 1.94E-04 | 7.26E-06 | HERPUD1  | homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1 (HERPUD1), transcript variant 1, mRNA |
| 0.48 | 0.33 | 1.60E-04 | 3.58E-06 | EIF4EBP2 | eukaryotic translation initiation factor 4E binding protein 2 (EIF4EBP2), mRNA                                                       |
| 0.48 | 0.39 | 2.85E-04 | 2.62E-06 | PSME4    | proteasome (prosome, macropain) activator subunit 4 (PSME4), mRNA                                                                    |
| 0.48 | 0.17 | 1.20E-04 | 2.15E-06 | LYPD5    | LY6/PLAUR domain containing 5 (LYPD5), mRNA                                                                                          |
| 0.48 | 0.44 | 7.28E-05 | 2.42E-05 | RPGR     | retinitis pigmentosa GTPase regulator (RPGR), transcript variant A, mRNA                                                             |
| 0.48 | 0.46 | 1.66E-04 | 2.68E-04 | SH3BP4   | SH3-domain binding protein 4 (SH3BP4), mRNA                                                                                          |
| 0.48 | 0.28 | 1.91E-04 | 1.01E-06 | FAM82C   | family with sequence similarity 82, member C (FAM82C), mRNA                                                                          |
| 0.48 | 0.46 | 1.92E-04 | 1.13E-05 | PRKCA    | protein kinase C, alpha (PRKCA), mRNA                                                                                                |
| 0.48 | 0.35 | 3.34E-04 | 8.54E-06 | TMEM55A  | transmembrane protein 55A (TMEM55A), mRNA                                                                                            |
| 0.49 | 0.44 | 3.47E-06 | 1.13E-05 | HRSP12   | heat-responsive protein 12 (HRSP12), mRNA                                                                                            |
| 0.49 | 0.43 | 0.00173  | 1.29E-06 | EFNB2    | ephrin-B2 (EFNB2), mRNA                                                                                                              |
| 0.49 | 0.50 | 0.00294  | 1.08E-04 | AGTPBP1  | ATP/GTP binding protein 1 (AGTPBP1), mRNA                                                                                            |
| 0.49 | 0.44 | 7.01E-04 | 5.59E-07 | SERP1    | stress-associated endoplasmic reticulum protein 1 (SERP1), mRNA                                                                      |
| 0.49 | 0.44 | 1.82E-05 | 3.51E-05 | USP10    | ubiquitin specific peptidase 10 (USP10), mRNA                                                                                        |
| 0.49 | 0.39 | 1.21E-05 | 4.51E-07 | CDR2     | cerebellar degeneration-related protein 2, 62kDa (CDR2), mRNA                                                                        |
| 0.49 | 0.40 | 0.00167  | 5.96E-05 | ABI2     | abl interactor 2 (ABI2), mRNA                                                                                                        |
| 0.49 | 0.40 | 1.08E-04 | 4.27E-05 | MED8     | mediator of RNA polymerase II transcription, subunit 8 homolog ( <i>S. cerevisiae</i> ) (MED8), transcript variant 1, mRNA           |
| 0.49 | 0.31 | 4.23E-05 | 1.74E-07 | NAT10    | N-acetyltransferase 10 (NAT10), mRNA                                                                                                 |
| 0.49 | 0.36 | 1.61E-04 | 8.71E-07 | UCHL3    | ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) (UCHL3), mRNA                                                      |
| 0.49 | 0.47 | 3.87E-04 | 6.65E-06 | NSFL1C   | NSFL1 (p97) cofactor (p47) (NSFL1C), transcript variant 1, mRNA                                                                      |

|      |       |          |          |          |                                                                                                                                      |
|------|-------|----------|----------|----------|--------------------------------------------------------------------------------------------------------------------------------------|
| 0.49 | 0.49  | 3.32E-04 | 4.13E-05 | CRABP2   | cellular retinoic acid binding protein 2 (CRABP2), mRNA                                                                              |
| 0.50 | 0.41  | 9.92E-04 | 5.72E-07 | DNAJC8   | DnaJ (Hsp40) homolog, subfamily C, member 8 (DNAJC8), mRNA                                                                           |
| 0.50 | 0.43  | 0.0013   | 2.99E-06 | CKAP2    | cytoskeleton associated protein 2 (CKAP2), mRNA                                                                                      |
| 0.50 | 0.50  | 2.22E-05 | 2.32E-04 | CEP70    | centrosomal protein 70kDa (CEP70), mRNA                                                                                              |
| 0.50 | 0.49  | 3.76E-04 | 5.05E-05 | VEZT     | vezatin, adherens junctions transmembrane protein (VEZT), mRNA                                                                       |
| 0.50 | 0.37  | 1.12E-04 | 9.29E-07 | EFTUD2   | elongation factor Tu GTP binding domain containing 2 (EFTUD2), mRNA                                                                  |
| 0.50 | 0.44  | 5.26E-04 | 7.43E-07 | BAZ1A    | bromodomain adjacent to zinc finger domain, 1A (BAZ1A), transcript variant 1, mRNA                                                   |
| 0.50 | 0.42  | 8.30E-04 | 8.09E-06 | RPN1     | ribophorin I (RPN1), mRNA                                                                                                            |
| 0.50 | 0.33  | 2.41E-04 | 1.74E-07 | RPUSD4   | RNA pseudouridylylase domain containing 4 (RPUSD4), mRNA                                                                             |
| 2.01 | 3.98  | 1.98E-04 | 4.00E-07 | C9orf103 | chromosome 9 open reading frame 103 (C9orf103), mRNA                                                                                 |
| 2.02 | 2.10  | 0.0015   | 1.50E-05 | PIGB     | phosphatidylinositol glycan anchor biosynthesis, class B (PIGB), mRNA                                                                |
| 2.03 | 2.26  | 6.81E-04 | 3.94E-04 | KIAA0232 | KIAA0232 gene product (KIAA0232), mRNA                                                                                               |
| 2.04 | 2.22  | 0.0013   | 6.20E-05 | PCGF5    | polycomb group ring finger 5 (PCGF5), mRNA                                                                                           |
| 2.04 | 2.48  | 1.50E-05 | 1.02E-04 | CRLF1    | cytokine receptor-like factor 1 (CRLF1), mRNA                                                                                        |
| 2.06 | 2.07  | 8.08E-04 | 2.78E-05 | NAGPA    | N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase (NAGPA), mRNA                                                     |
| 2.07 | 2.61  | 4.66E-04 | 9.06E-05 | OTX1     | orthodenticle homeobox 1 (OTX1), mRNA                                                                                                |
| 2.09 | 4.20  | 9.27E-04 | 9.83E-07 | SYT15    | synaptotagmin XV (SYT15), transcript variant b, mRNA                                                                                 |
| 2.09 | 3.25  | 2.58E-04 | 4.17E-06 | IFI6     | interferon, alpha-inducible protein 6 (IFI6), transcript variant 3, mRNA                                                             |
| 2.09 | 2.55  | 2.97E-05 | 3.44E-06 | CARD8    | caspase recruitment domain family, member 8 (CARD8), mRNA                                                                            |
| 2.11 | 2.52  | 4.84E-04 | 5.01E-06 | IQCE     | mRNA for KIAA1023 protein, partial cds.                                                                                              |
| 2.12 | 5.09  | 2.28E-04 | 2.12E-05 | ITIH4    | inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), mRNA                                         |
| 2.12 | 2.68  | 4.59E-05 | 3.34E-05 | FAH      | fumarylacetoacetate hydrolase (fumarylacetoacetase) (FAH), mRNA                                                                      |
| 2.13 | 2.85  | 3.09E-04 | 1.76E-07 | TMTC4    | transmembrane and tetratricopeptide repeat containing 4 (TMTC4), transcript variant 1, mRNA                                          |
| 2.13 | 3.37  | 0.04816  | 4.23E-05 | THRA     | thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian) (THRA), transcript variant 1, mRNA |
| 2.14 | 19.06 | 2.13E-04 | 8.96E-07 | DISP2    | dispatched homolog 2 (Drosophila) (DISP2), mRNA                                                                                      |
| 2.14 | 2.73  | 1.17E-04 | 2.49E-06 | RRAGB    | Ras-related GTP binding B (RRAGB), transcript variant RAGBI, mRNA                                                                    |
| 2.15 | 2.38  | 7.37E-06 | 1.30E-06 | IL17RA   | interleukin 17 receptor A (IL17RA), mRNA                                                                                             |
| 2.16 | 4.08  | 0.0022   | 2.83E-05 | RAB3B    | Ras-related protein Rab-3B.                                                                                                          |
| 2.17 | 2.04  | 5.16E-06 | 9.39E-06 | SDC1     | syndecan 1 (SDC1), transcript variant 1, mRNA                                                                                        |



|      |      |          |          |          |                                                                                                 |
|------|------|----------|----------|----------|-------------------------------------------------------------------------------------------------|
| 2.17 | 3.81 | 6.59E-04 | 6.22E-06 | ABHD4    | abhydrolase domain containing 4 (ABHD4), mRNA                                                   |
| 2.18 | 2.14 | 0.00226  | 2.02E-06 | ZFHX2    | mRNA for KIAA1762 protein, partial cds.                                                         |
| 2.20 | 2.32 | 2.71E-04 | 6.84E-04 | TBX19    | T-box 19 (TBX19), mRNA                                                                          |
| 2.20 | 2.67 | 8.40E-05 | 2.36E-06 | BCL2L11  | BCL2-like 11 (apoptosis facilitator) (BCL2L11), transcript variant 1, mRNA                      |
| 2.21 | 8.37 | 9.90E-05 | 5.62E-06 | FZD4     | frizzled homolog 4 (Drosophila) (FZD4), mRNA                                                    |
| 2.21 | 4.60 | 0.0012   | 1.55E-05 | IFIT1    | interferon-induced protein with tetratricopeptide repeats 1 (IFIT1), transcript variant 2, mRNA |
| 2.22 | 2.20 | 0.00126  | 1.06E-05 | FKBP1B   | FK506 binding protein 1B, 12.6 kDa (FKBP1B), transcript variant 2, mRNA                         |
| 2.23 | 3.07 | 3.12E-05 | 3.53E-06 | SP110    | SP110 nuclear body protein (SP110), transcript variant b, mRNA                                  |
| 2.23 | 2.12 | 5.94E-05 | 6.27E-06 | GALM     | galactose mutarotase (aldose 1-epimerase) (GALM), mRNA                                          |
| 2.25 | 2.05 | 2.64E-05 | 1.25E-04 | BAK1     | BCL2-antagonist/killer 1 (BAK1), mRNA                                                           |
| 2.26 | 2.69 | 1.07E-04 | 7.87E-07 | C1orf201 | chromosome 1 open reading frame 201 (C1orf201), mRNA                                            |
| 2.27 | 9.49 | 1.09E-04 | 2.71E-07 | PIK3IP1  | HGFL gene (MGC17330), mRNA                                                                      |
| 2.28 | 2.01 | 3.10E-05 | 3.91E-04 | SLC6A6   | solute carrier family 6 (neurotransmitter transporter, taurine), member 6 (SLC6A6), mRNA        |
| 2.28 | 2.26 | 4.87E-06 | 1.12E-05 | FAM89A   | family with sequence similarity 89, member A (FAM89A), mRNA                                     |
| 2.29 | 3.19 | 2.79E-06 | 9.32E-06 | TNFSF12  | tumor necrosis factor (ligand) superfamily, member 12 (TNFSF12), mRNA                           |
| 2.29 | 3.66 | 0.0018   | 7.91E-06 | PAQR8    | progesterone and adipoQ receptor family member VIII (PAQR8), mRNA                               |
| 2.33 | 2.60 | 2.05E-04 | 1.24E-05 | ZNF688   | zinc finger protein 688 (ZNF688), transcript variant 1, mRNA                                    |
| 2.33 | 2.71 | 1.05E-05 | 1.23E-04 | AQP11    | aquaporin 11 (AQP11), mRNA                                                                      |
| 2.35 | 3.39 | 0.00308  | 4.20E-05 | MOSPD3   | motile sperm domain containing 3 (MOSPD3), transcript variant 1, mRNA                           |
| 2.36 | 6.33 | 1.68E-04 | 7.50E-06 | BATF2    | basic leucine zipper transcription factor, ATF-like 2 (BATF2), mRNA                             |
| 2.36 | 2.62 | 1.01E-05 | 1.46E-06 | RAB3D    | RAB3D, member RAS oncogene family, mRNA (cDNA clone IMAGE:4301650), partial cds.                |
| 2.38 | 2.40 | 2.67E-06 | 1.58E-04 | ZBED1    | zinc finger, BED-type containing 1 (ZBED1), mRNA                                                |
| 2.39 | 7.19 | 2.78E-04 | 4.78E-07 | BDH2     | 3-hydroxybutyrate dehydrogenase, type 2 (BDH2), mRNA                                            |
| 2.40 | 2.09 | 8.65E-06 | 4.59E-06 | SLC25A15 | Mitochondrial ornithine transporter 1 (Solute carrier family 25 member 15).                     |
| 2.42 | 2.64 | 5.22E-05 | 3.56E-06 | CCDC88   | coiled-coil domain containing 88 (CCDC88), mRNA                                                 |
| 2.44 | 6.93 | 0.00126  | 3.17E-07 | PBXIP1   | pre-B-cell leukemia homeobox interacting protein 1 (PBXIP1), mRNA                               |
| 2.48 | 2.47 | 2.20E-05 | 1.01E-06 | GKAP1    | G kinase anchoring protein 1 (GKAP1), mRNA                                                      |
| 2.49 | 2.77 | 2.95E-04 | 1.43E-06 | PROCR    | protein C receptor, endothelial (EPCR) (PROCR), mRNA                                            |
| 2.54 | 4.46 | 1.28E-04 | 1.22E-06 | STAP2    | signal-transducing adaptor protein-2 (STAP2), transcript variant 2, mRNA                        |

|      |      |          |          |          |                                                                                        |
|------|------|----------|----------|----------|----------------------------------------------------------------------------------------|
| 2.55 | 3.14 | 6.48E-05 | 1.76E-07 | SESN1    | sestrin 1 (SESN1), mRNA                                                                |
| 2.57 | 2.70 | 1.04E-04 | 2.41E-06 | FBXO8    | F-box protein 8 (FBXO8), mRNA                                                          |
| 2.62 | 2.46 | 5.93E-04 | 6.67E-06 | GSC      | goosecoid (GSC), mRNA                                                                  |
| 2.63 | 2.55 | 2.50E-05 | 2.83E-05 | SNPH     | syntaphilin (SNPH), mRNA                                                               |
| 2.65 | 3.33 | 2.95E-04 | 9.16E-06 | RTN2     | reticulon 2 (RTN2), transcript variant 1, mRNA                                         |
| 2.65 | 2.83 | 1.16E-05 | 1.93E-05 | TMEM25   | transmembrane protein 25 (TMEM25), mRNA                                                |
| 2.67 | 4.93 | 1.29E-04 | 4.29E-06 | ELL2     | elongation factor, RNA polymerase II, 2 (ELL2), mRNA                                   |
| 2.68 | 2.06 | 3.57E-04 | 4.88E-05 | NRBP1    | nuclear receptor binding protein 1 (NRBP1), mRNA                                       |
| 2.68 | 6.06 | 3.69E-04 | 2.67E-07 | BSN      | bassoon (presynaptic cytomatrix protein) (BSN), mRNA                                   |
| 2.69 | 2.99 | 3.31E-05 | 6.38E-07 | KIAA0513 | KIAA0513 (KIAA0513), mRNA                                                              |
| 2.70 | 2.60 | 1.12E-06 | 1.67E-04 | RRAGC    | Ras-related GTP binding C (RRAGC), mRNA                                                |
| 2.71 | 2.34 | 0.00152  | 2.03E-06 | TMED8    | Protein TMED8.                                                                         |
| 2.71 | 3.70 | 4.21E-05 | 1.27E-04 | LIMD2    | LIM domain containing 2 (LIMD2), mRNA                                                  |
| 2.73 | 2.83 | 4.31E-05 | 1.02E-04 | KIAA1712 | KIAA1712, mRNA (cDNA clone MGC:33587 IMAGE:4823994), complete cds.                     |
| 2.74 | 4.51 | 4.40E-05 | 5.40E-05 | C11orf60 | chromosome 11 open reading frame 60 (C11orf60), mRNA                                   |
| 2.76 | 2.93 | 3.28E-05 | 1.98E-06 | FAM96A   | family with sequence similarity 96, member A (FAM96A), transcript variant 1, mRNA      |
| 2.76 | 2.69 | 1.45E-04 | 5.33E-06 | CMTM4    | CKLF-like MARVEL transmembrane domain containing 4 (CMTM4), transcript variant 1, mRNA |
| 2.79 | 2.44 | 1.12E-04 | 3.56E-05 | APH1B    | anterior pharynx defective 1 homolog B (C. elegans) (APH1B), mRNA                      |
| 2.79 | 4.11 | 3.14E-05 | 3.06E-07 | SLC25A42 | solute carrier family 25, member 42 (SLC25A42), mRNA                                   |
| 2.81 | 7.78 | 1.05E-05 | 1.01E-06 | MR1      | MHC class I related protein 1 isoform D (MR1D) mRNA, complete cds.                     |
| 2.82 | 2.06 | 8.72E-06 | 1.13E-05 | LITAF    | lipopolysaccharide-induced TNF factor (LITAF), mRNA                                    |
| 2.83 | 2.32 | 3.28E-04 | 3.17E-05 | TNNI3    | troponin I type 3 (cardiac) (TNNI3), mRNA                                              |
| 2.84 | 2.06 | 2.62E-05 | 1.84E-05 | SLC4A1AP | solute carrier family 4 (anion exchanger), member 1, adaptor protein (SLC4A1AP), mRNA  |
| 2.84 | 2.38 | 8.73E-05 | 1.28E-05 | SCLY     | selenocysteine lyase (SCLY), mRNA                                                      |
| 2.85 | 2.02 | 0.00152  | 2.02E-05 | ANKRD46  | ankyrin repeat domain 46 (ANKRD46), mRNA                                               |
| 2.86 | 2.71 | 2.79E-04 | 1.35E-04 | VPS37D   | vacuolar protein sorting 37 homolog D (S. cerevisiae) (VPS37D), mRNA                   |
| 2.88 | 2.22 | 1.93E-04 | 5.15E-05 | ZDHHC11  | zinc finger, DHHC-type containing 11 (ZDHHC11), mRNA                                   |
| 2.89 | 4.69 | 3.54E-05 | 1.14E-05 | SAMD11   | sterile alpha motif domain containing 11 (SAMD11), mRNA                                |
| 2.92 | 6.89 | 5.62E-04 | 5.97E-06 | FAM79A   | family with sequence similarity 79, member A (FAM79A), mRNA                            |

|      |      |          |          |          |                                                                                                    |
|------|------|----------|----------|----------|----------------------------------------------------------------------------------------------------|
| 3.01 | 2.51 | 6.90E-05 | 1.81E-05 | KHK      | ketohexokinase (fructokinase) (KHK), transcript variant a, mRNA                                    |
| 3.03 | 4.86 | 3.75E-06 | 2.11E-06 | GDAP1    | ganglioside-induced differentiation-associated protein 1 (GDAP1), transcript variant 1, mRNA       |
| 3.04 | 3.80 | 2.01E-06 | 1.11E-05 | TMEM145  | transmembrane protein 145 (TMEM145), mRNA                                                          |
| 3.16 | 2.33 | 1.10E-05 | 4.79E-07 | AYTL2    | acyltransferase like 2 (AYTL2), mRNA                                                               |
| 3.18 | 2.25 | 2.30E-04 | 7.73E-06 | DCTN5    | dynactin 5 (p25) (DCTN5), mRNA                                                                     |
| 3.19 | 5.22 | 2.32E-04 | 6.78E-06 | CHPF     | chondroitin polymerizing factor (CHPF), mRNA                                                       |
| 3.20 | 2.09 | 2.47E-05 | 3.22E-04 | C20orf46 | chromosome 20 open reading frame 46 (C20orf46), mRNA                                               |
| 3.25 | 2.16 | 3.14E-05 | 1.05E-06 | CTDSP2   | CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2 (CTDSP2), mRNA |
| 3.25 | 2.33 | 7.47E-06 | 1.39E-05 | PRRT3    | proline-rich transmembrane protein 3 (PRRT3), mRNA                                                 |
| 3.31 | 2.83 | 6.53E-07 | 7.46E-06 | MREG     | melanoregulin (MREG), mRNA                                                                         |
| 3.31 | 2.55 | 2.52E-05 | 1.07E-04 | STX3     | syntaxin 3 (STX3), mRNA                                                                            |
| 3.33 | 2.82 | 8.32E-04 | 5.91E-06 | RDH11    | retinol dehydrogenase 11 (all-trans/9-cis/11-cis) (RDH11), mRNA                                    |
| 3.42 | 3.51 | 1.71E-04 | 5.80E-06 | GPR157   | Probable G-protein coupled receptor 157.                                                           |
| 3.44 | 3.45 | 1.10E-05 | 2.77E-06 | CYP2U1   | cytochrome P450, family 2, subfamily U, polypeptide 1 (CYP2U1), mRNA                               |
| 3.45 | 2.44 | 2.19E-06 | 1.59E-06 | SEC24C   | SEC24 related gene family, member C ( <i>S. cerevisiae</i> ) (SEC24C), transcript variant 1, mRNA  |
| 3.50 | 2.65 | 1.72E-04 | 6.13E-05 | ESPNL    | espin-like (ESPNL), mRNA                                                                           |
| 3.53 | 5.39 | 1.78E-05 | 2.52E-06 | CHGB     | chromogranin B (secretogranin 1) (CHGB), mRNA                                                      |
| 3.56 | 3.20 | 1.56E-04 | 6.19E-05 | HOXB13   | homeobox B13 (HOXB13), mRNA                                                                        |
| 3.57 | 3.50 | 1.43E-05 | 8.71E-07 | CMAS     | cytidine monophosphate N-acetylneuraminic acid synthetase (CMAS), mRNA                             |
| 3.62 | 2.10 | 1.04E-05 | 1.13E-05 | SFT2D2   | SFT2 domain containing 2 (SFT2D2), mRNA                                                            |
| 3.72 | 2.73 | 3.41E-06 | 2.51E-05 | FAM126B  | family with sequence similarity 126, member B (FAM126B), mRNA                                      |
| 3.88 | 2.87 | 1.80E-05 | 8.46E-07 | HEY1     | hairy/enhancer-of-split related with YRPW motif 1 (HEY1), transcript variant 1, mRNA               |
| 4.03 | 2.60 | 2.51E-06 | 8.46E-06 | CPOX     | coproporphyrinogen oxidase (CPOX), mRNA                                                            |
| 4.11 | 3.54 | 7.26E-06 | 2.02E-06 | KLHDC8B  | kelch domain containing 8B (KLHDC8B), mRNA                                                         |
| 4.62 | 4.73 | 1.33E-05 | 2.53E-07 | PEX11B   | peroxisomal biogenesis factor 11B (PEX11B), mRNA                                                   |
| 5.89 | 5.73 | 5.70E-06 | 2.81E-04 | ZC3HAV1  | zinc finger CCCH-type, antiviral 1 (ZC3HAV1), transcript variant 2, mRNA                           |
| 6.38 | 3.24 | 3.84E-06 | 7.43E-07 | RIMS3    | regulating synaptic membrane exocytosis 3 (RIMS3), mRNA                                            |
| 7.64 | 7.24 | 1.46E-05 | 7.91E-06 | AXL      | AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA                                     |

\*P-values were calculated by using Student's t test with the Benjamini and Hochberg multiple testing correction.

