Supplemental Figure 1. Details parallel those outlined in Figure 5 legend.

## Supplemental TABLE 1 Subject Information

| | | | | Antibody Status (embolded is positive) | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Sample Identifier** | **Gender** | **HbA1c(%)** | **Number of detected AA specificities (0-4)** | **GAD** | **IA2** | **IAA** | **ZnT8** | **Age at Visit** | **Age at Diagnosis** | **Plasma Glucose (mg/dl)** | **BMI** | **Serum Signature [S] AddBack [A] Cytokine ELISA [C]** | **Positive for AA at One or More Later Time Points** |
| **Auto-antibody-negative (AA-) Low HLA Risk Siblings (nonDR3 nonDR4)** | | | | | | | | | | | | | |
| LR135 | Male | Not tested | 0 | -0.006 | -0.0017 | 0 | -0.0118 | 9.4575 | | 82 | 19.1 | SC | No |
| LR293 | Male | Not tested | 0 | 0.002 | 0.0005 | 0.03 | -0.0003 | 8.8466 | | 94 | 15.5 | SC | No |
| LR1846 | Male | Not tested | 0 | 0.0129 | -0.0007 | -0.0084 | -0.013 | 8.2192 | | 96 | 15.5 | SC | No |
| LR1918 | Female | Not tested | 0 | 0.0082 | -0.0011 | -0.0034 | -0.01 | 9.0822 | | 94 | 16.5 | SC | No |
| LR1922 | Male | Not tested | 0 | 0.0229 | -0.0017 | 0.0065 | -0.008 | 7.4521 | | 96 | 17.0 | SC | No |
| LR1940 | Male | Not tested | 0 | 0.0107 | 0.0003 | -0.0017 | -0.011 | 7.0192 | | 94 | 16.4 | SC | No |
| LR1976 | Male | Not tested | 0 | 0.0075 | -0.0009 | 0 | -0.007 | 8.0712 | | 83 | 18.3 | SC | No |
| LR1982 | Female | Not tested | 0 | 0.0146 | -0.0012 | 0.0027 | -0.006 | 6.5589 | | 93 | 19.1 | SC | No |
| LR2110 | Female | Not tested | 0 | 0.005 | -0.0016 | 0 | -0.002 | 8.7068 | | 107 | 19.9 | SC | No |
| LR2138 | Male | Not tested | 0 | -0.0094 | 0.0011 | 0.0115 | -0.01 | 7.3178 | | 95 | 15.9 | SC | No |
| LR2532 | Male | Not tested | 0 | -0.0075 | -0.0018 | -0.0071 | -0.0044 | 8.0027 | | 82 | 15.0 | SC | No |
| LR2560 | Female | Not tested | 0 | 0.0002 | -0.0017 | 0.0108 | -0.0028 | 9.2932 | | 93 | 16.0 | SC | No |
| LR2215 | Female | Not tested | 0 | -0.0014 | -0.0021 | -0.0066 | -0.01 | 7.1123 | | 80 | 15.3 | SC | No |
| LR2707 | Female | Not tested | 0 | -0.0002 | 0 | -0.003 | 0.014 | 6.1945 | | 94 | 15.9 | SC | No |
| LR15 | Female | Not tested | 0 | 0.0059 | -0.0003 | 0.0119 | -0.0099 | 8.8548 | | 128 | 18.2 | S | No |
| LR88 | Male | Not tested | 0 | -0.0177 | 0.001 | 0.009 | -0.0083 | 5.5068 | | 91 | 16.7 | SC | No |
| LR101 | Female | Not tested | 0 | -0.0171 | -0.001 | 0.0112 | -0.0098 | 5.1041 | | 86 | 17.6 | SC | No |
| LR342 | Female | Not tested | 0 | 0.0117 | 0.0009 | 0.0033 | -0.0009 | 8.1836 | | 96 | 14.5 | SA | No |
| LR345 | Male | Not tested | 0 | -0.002 | -0.0002 | 0.0165 | 0.0019 | 9.6959 | | 98 | 15.7 | SC | No |
| LR356 | Male | Not tested | 0 | -0.0049 | -0.0046 | 0.0025 | -0.0058 | 5.3671 | | 98 | 18.9 | S | No |
| LR884 | Female | Not tested | 0 | -0.0071 | 0.0023 | 0.0035 | -0.0058 | 7.3123 | | 102 | 15.4 | SC | No |
| LR890 | Male | Not tested | 0 | -0.0027 | -0.0014 | -0.0017 | -0.0039 | 5.7425 | | 158 | 13.9 | S | No |
| LR992 | Female | Not tested | 0 | -0.0032 | 0.0002 | 0 | -0.0075 | 5.1205 | | 75 | 16.1 | S | No |
| LR1050 | Female | Not tested | 0 | 0.0045 | 0.0018 | 0.0031 | -0.0021 | 8.2877 | | 95 | 21.6 | SC | No |
| LR1226 | Female | Not tested | 0 | 0.0072 | -0.0005 | -0.0154 | 0.018 | 9.6849 | | 78 | 17.3 | S | No |
| LR1477 | Male | Not tested | 0 | 0.0028 | 0.0005 | 0.0039 | -0.01 | 8.8 | | 82 | 25.5 | SC | No |
| LR1700 | Male | Not tested | 0 | 0 | -0.003 | 0 | -0.011 | 5.4384 | | 90 | 15.8 | S | No |
| LR1857 | Female | Not tested | 0 | 0.0104 | -0.003 | -0.0017 | -0.013 | 8.3507 | | 106 | 14.2 | S | No |
| LR140 | Female | Not tested | 0 | -0.0006 | -0.0018 | 0.01 | -0.0016 | 11.5562 | | 79 | 15.2 | SC | No |
| LR158 | Female | Not tested | 0 | -0.0001 | -0.0001 | 0.0035 | -0.0086 | 11.3589 | | 89 | 18.0 | S | No |
| LR1497 | Male | Not tested | 0 | 0.0116 | -0.0019 | 0.0014 | -0.002 | 10.537 | | 83 | 14.5 | SC | No |
| LR185 | Male | Not tested | 0 | 0.0068 | 0.0024 | -0.0066 | -0.0112 | 11.7973 | | 99 | 30.1 | SC | No |
| LR1592 | Male | Not tested | 0 | 0.0584 | -0.0014 | -0.0032 | -0.009 | 11.5233 | | 89 | 17.4 | SC | No |
| LR2091 | Female | Not tested | 0 | 0.0023 | -0.0024 | 0.003 | -0.002 | 11.5342 | | 76 | 19.1 | SA | No |
| LR2489 | Male | Not tested | 0 | -0.0074 | -0.0021 | 0 | -0.002 | 11.2082 | | 84 | 16.8 | S | No |
| LR2683 | Male | Not tested | 0 | 0.0008 | -0.002 | -0.0041 | -0.005 | 10.7041 | | 85 | 15.5 | S | No |
| LR2696 | Female | Not tested | 0 | -0.0002 | -0.0009 | 0.0427 | -0.007 | 10.1836 | | 81 | 22.8 | S | No |
| LR2761 | Male | Not tested | 0 | -0.0017 | 0.0002 | 0.0093 | -0.003 | 10.6959 | | 97 | 23.8 | S | No |
| LR2379 | Female | Not tested | 0 | 0.0016 | -0.0006 | 0.0077 | -0.006 | 5.0986 | | 76 | 14.5 | SC | No |
| LR2477 | Male | Not tested | 0 | -0.0026 | 0.0015 | 0.0057 | -0.005 | 8.7014 | | 130 | 15.3 | SC | No |
| LR2549 | Male | Not tested | 0 | -0.0019 | 0.0003 | 0.0075 | -0.0064 | 7.4137 | | 118 | 15.1 | SC | No |
| LR2731 | Male | Not tested | 0 | -0.0021 | 0.0001 | -0.0052 | -0.009 | 8.5562 | | 76 | 16.2 | SCA | No |
| LR883 | Female | Not tested | 0 | -0.0036 | 0.0001 | 0.0139 | -0.0075 | 9.5644 | | 99 | 16.7 | C | No |
| LR1858 | Female | Not tested | 0 | 0.0148 | -0.0028 | -0.005 | -0.011 | 5.9534 | | 108 | 14.6 | C | No |
| **Recent onset T1DM** | | | | | | | | | | | | | |
| RO1973 | Female | 8.1 | 4 | **0.1504** | **0.4984** | **0.3321** | **0.657** | 12.2 | 11.8 | 82 | 24.1 | S | |
| RO2130 | Male | 5.5 | 2 | 0.0524 | 0.0015 | **2.3055** | **0.131** | 15.6 | 15.4 | 71 | 23.2 | S | |
| RO2312 | Female | 10.4 | 4 | **0.2769** | **1.3095** | **0.0917** | **0.812** | 14.6 | 14.6 | 199 | 16.9 | SC | |
| RO1964 | Female | 9.8 | 4 | **0.6068** | **0.7542** | **0.6435** | **0.447** | 9.8 | 9.8 | 116 | 17.9 | SC | |
| RO2348 | Female | 5.5 | 4 | **0.1312** | **0.1777** | **1.9395** | **0.701** | 9.6 | 9.4 | 84 | 14.6 | SC | |
| RO2366 | Male | 7.7 | 1 | 0.0615 | -0.0003 | **0.1669** | -0.009 | 7.7 | 7.5 | 177 | 15.5 | SC | |
| RO2598 | Male | 7.9 | 4 | **0.1275** | **0.0036** | **4.9503** | **0.089** | 6.7 | 6.2 | 103 | 17.2 | SC | |
| RO1939 | Female | 6.8 | 4 | **0.1129** | **0.8125** | **0.5275** | **0.92** | 11.2 | 11.0 | 230 | 18.4 | SCA | |
| RO2109 | Female | 7 | 4 | **0.1598** | **1.161** | **7.0612** | **0.621** | 10.3 | 9.9 | 267 | 20.5 | SCA | |
| RO253 | Male | 6.4 | 4 | **0.1177** | **1.2554** | **3.0061** | **0.7596** | 10.7 | 10.4 | 89 | 24.3 | SCA | |
| RO2024 | Female | Not tested | 0 | N/A | N/A | N/A | N/A | 10.4 | 10.0 | N/A | 15.0 | SA | |
| RO1037 | Male | 5.4 | 4 | **0.0895** | **0.6347** | **2.4508** | **0.1611** | 10.2 | 9.8 | N/A | 19.3 | SCA | |
| RO1437 | Male | 6.8 | 3 | 0.0455 | **0.1381** | **0.4207** | **0.618** | 10.4 | 10.0 | 195 | 16.8 | SCA | |
| RO2944 | Female | 8.6 | 4 | **0.7483** | **0.3721** | **0.274** | **1.195** | 6.5 | 6.4 | 86 | 15.5 | SA | |
| RO2953 | Female | 7.5 | 3 | **0.1535** | **0.7392** | **0.5347** | -0.001 | 9.1 | 8.9 | N/A | 16.5 | SCA | |
| RO2185 | Male | 7.5 | 4 | **1.3191** | **0.567** | **3.6172** | **0.772** | 7.2 | 6.8 | 182 | 14.6 | SCA | |
| RO1707 | Female | 6.5 | 3 | **0.0736** | **0.449** | 0.0397 | **0.425** | 8.0 | 7.7 | 328 | 14.7 | SCA | |
| RO2676 | Female | 8.8 | 4 | **0.7234** | **0.0073** | **0.2875** | **0.131** | 8.1 | 7.8 | 278 | 13.8 | SCA | |
| RO1012 | Female | 8 | 2 | 0.0373 | **0.3809** | **1.0658** | 0.0103 | 9.3 | 9.0 | 156 | 16.3 | SCA | |
| RO246 | Male | 8.8 | 2 | 0.05 | **0.3562** | **0.0772** | N/A | 9.9 | 9.8 | 82 | 15.3 | SCA | |
| RO946 | Female | 7.8 | 4 | **0.8969** | **1.0161** | **3.6723** | **0.6068** | 10.8 | 10.7 | 78 | 22.4 | SCA | |
| RO1442 | Female | 7.2 | 4 | **0.3078** | **0.0165** | **3.2237** | **0.131** | 6.0 | 5.7 | 237 | 18.7 | SCA | |
| RO201 | Male | 8.3 | 4 | **0.1978** | **0.5656** | **0.767** | **0.5919** | 6.7 | 6.4 | 78 | 16.3 | SCA | |
| RO930 | Female | 7.3 | 2 | 0.012 | **0.9537** | **2.4592** | -0.0051 | 6.7 | 6.2 | 92 | 14.3 | SCA | |
| RO62 | Female | 7.4 | 4 | **0.1396** | **0.4377** | **0.102** | **0.0924** | 7.0 | 6.5 | 291 | 19.8 | SCA | |
| RO189 | Female | 7 | 4 | **0.08** | **1.0646** | **0.7346** | **0.6288** | 7.2 | 6.9 | 161 | 15.2 | SCA | |
| RO1057 | Female | 7.1 | 2 | **0.1644** | 0.0014 | **0.1225** | -0.005 | 8.8 | 8.4 | 252 | 15.9 | SCA | |
| RO2808 | Male | 6.4 | 4 | **0.1063** | **0.4445** | **0.5883** | **0.847** | 9.6 | 9.4 | 169 | 22.8 | SCA | |
| RO2991 | Female | 5.6 | 4 | **0.1246** | **0.8591** | **0.1183** | **0.172** | 9.6 | 9.2 | 166 | 20.2 | SA | |
| RO2503 | Male | 7.3 | 2 | 0.029 | **0.0861** | **3.1306** | 0.0034 | 11.1 | 10.7 | 121 | 17.0 | SA | |
| RO2903 | Male | 7.7 | 2 | **0.4621** | -0.003 | **0.7849** | 0 | 11.4 | 11.2 | 81 | 17.3 | SCA | |
| RO972 | Male | 6.9 | 4 | **1.1544** | **1.1083** | **4.6644** | **0.0885** | 11.8 | 11.5 | 139 | 18.8 | SCA | |
| RO2559 | Male | 6.1 | 4 | **0.2532** | **0.0395** | **1.3852** | **0.2487** | 11.8 | 11.4 | 108 | 18.2 | SA | |
| RO2751 | Male | 7.6 | 2 | **0.0806** | -0.0001 | **0.1855** | 0.004 | 11.8 | 11.6 | 82 | 16.2 | SA | |
| RO2936 | Male | 6.2 | 3 | **0.5871** | **0.5838** | **9.2393** | -0.007 | 11.8 | 11.6 | 100 | 17.3 | SA | |
| RO2359 | Female | 8.6 | 3 | 0.0017 | **0.8849** | **0.103** | **0.284** | 12.0 | 11.9 | 77 | 17.6 | SA | |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| RO1997 | Male | 7.1 | 3 | **0.6085** | **0.2183** | **3.529** | -0.005 | 13.0 | 12.8 | 136 | 20.9 | SA | |
| RO3087 | Male | 8.8 | 4 | **0.2383** | **0.1682** | **0.3882** | **0.6379** | 7.8 | 7.2 | 299 | 15.8 | SCA | |
| RO3052 | Female | 7.1 | 3 | **0.308** | **0.041** | **0.7766** | 0.0015 | 9.0 | 8.4 | 238 | 18.5 | SA | |
| RO3153 | Female | 9.5 | 3 | 0.015 | **0.543** | **1.9255** | **0.5183** | 8.0 | 7.4 | 80 | 15.1 | SCA | |
| RO3040 | Male | 8.3 | 3 | 0.0067 | **0.5235** | **0.436** | **0.5023** | 7.5 | 6.9 | 137 | 19.8 | SA | |
| RO3045 | Male | 6.8 | 2 | 0.0285 | -0.0021 | **1.303** | **0.7737** | 11.6 | 11.0 | 106 | 15.8 | SCA | |
| RO3139 | Female | 6.8 | 4 | **1.3488** | **0.1839** | **1.4278** | **0.3987** | 12.5 | 12.0 | 182 | 17.8 | SA | |
| RO159 | Female | 9.8 | 3 | **0.2988** | 0.0002 | **1.4891** | **0.6071** | 6.1 | 5.7 | 63 | 16.1 | SCA | |
| RO1579 | Female | 7.8 | 3 | 0.0495 | **0.5027** | **5.2452** | **0.7** | 7.0 | 6.8 | 231 | 16.0 | SC | |
| RO1225 | Male | 8.8 | 4 | **0.3836** | **0.614** | **1.1782** | **0.308** | 11.8 | 11.3 | 204 | 20.6 | SA | |
| LO2132A6 | Male | 5.5 | 4 | **0.2441** | **1.1301** | **0.8804** | **0.443** | 21.9 | 21.7 | 185 | 27.2 | S | |
| RO2238 | Male | 7.7 | 3 | 0.0327 | **0.5428** | **5.2753** | **0.965** | 5.8 | 5.4 | 199 | 19.5 | C | |
| RO2034 | Male | 6.8 | 4 | **1.1162** | **1.0741** | **1.7151** | **0.915** | 6.0 | 5.8 | 139 | 15.7 | C | |
| RO355 | Female | 6.8 | 3 | 0.0083 | **0.5944** | **0.2184** | **0.3486** | 4.1 | 3.5 | 101 | 17.9 | C | |
| RO814 | Male | 8.3 | 2 | **0.1062** | 0.0047 | **0.1083** | 0.0063 | 5.0 | 4.3 | 256 | N/A | C | |
| RO363 | Female | 7.4 | 1 | 0.0083 | -0.0024 | **1.4439** | -0.0016 | 8.4 | 7.9 | 104 | 14.8 | C | |
| RO1071 | Female | 8.7 | 3 | **1.1759** | **1.0282** | **2.4215** | -0.003 | 11.5 | 11.4 | 186 | 19.4 | C | |
| RO1139 | Female | 6.9 | 4 | **1.7081** | **1.2789** | **3.2528** | **0.286** | 11.0 | 10.8 | 208 | 16.9 | C | |
| RO1329 | Female | 7 | 2 | 0.066 | **0.2404** | **0.61** | -0.002 | 7.2 | 7.1 | 78 | 14.7 | C | |
| RO1470 | Female | 5.7 | 3 | **0.098** | **0.4971** | **2.7758** | 0.003 | 10.6 | 10.4 | 149 | 16.6 | C | |
| RO1475 | Male | 5.8 | 3 | 0.0097 | **0.5294** | **0.6564** | **0.958** | 11.3 | 11.1 | 126 | 20.5 | C | |
| RO1486 | Male | 5.9 | 2 | -0.0004 | -0.0046 | **7.2202** | **0.08** | 6.3 | 5.8 | 139 | 15.3 | C | |
| RO1541 | Female | 6.8 | 2 | 0.0605 | **0.1403** | **0.4607** | -0.003 | 10.2 | 9.8 | 161 | 99.9 | C | |
| RO1559 | Female | 7.5 | 3 | **0.1076** | -0.0002 | **4.1962** | **0.232** | 9.6 | 9.1 | 240 | 15.4 | C | |
| RO1586 | Female | 7.2 | 3 | 0.0022 | **0.505** | **0.6193** | **0.164** | 5.6 | 5.2 | 202 | 20.1 | C | |
| RO1749 | Female | 8.8 | 4 | **0.6031** | **0.7622** | **4.5672** | **0.499** | 5.8 | 5.4 | 176 | 14.4 | C | |
| RO1916 | Female | 7.5 | 4 | **0.9789** | **0.6402** | **0.8433** | **1.165** | 7.2 | 7.0 | 180 | 16.9 | C | |
| RO2522 | Female | 6.9 | 4 | **0.7122** | **0.8799** | **0.4855** | **0.7886** | 7.9 | 7.6 | 168 | 15.4 | C | |
| **Auto-antibody-negative (AA-) High HLA Risk Siblings (DR3 and/or DR4)** | | | | | | | | | | | | | |
| HR49 | Female | Not tested | 1 | -0.0061 | -0.0012 | 0.0149 | 0.0872 | 8.0 | | 118 | 16.2 | SC | Yes |
| HR69 | Female | Not tested | 0 | -0.0055 | -0.0001 | -0.0037 | -0.0079 | 6.3 | | 85 | 15.2 | SC | No |
| HR130 | Male | Not tested | 1 | -0.0031 | 0.0002 | 0.0049 | 0.0426 | 9.4 | | 84 | 18.4 | SC | Yes |
| HR215 | Female | Not tested | 0 | 0.0227 | 0.0006 | 0.01 | -0.0009 | 9.1 | | 97 | 17.2 | SC | No |
| HR229 | Male | Not tested | 0 | 0.0094 | -0.0023 | 0.009 | 0.0017 | 9.5 | | 102 | 18.1 | SCA | No |
| HR334 | Male | Not tested | 0 | 0.006 | -0.0002 | -0.0052 | -0.0023 | 7.8 | | 88 | 16.0 | SC | No |
| HR338 | Male | Not tested | 0 | 0.0029 | 0.0016 | 0 | -0.0056 | 8.7 | | 83 | 14.5 | SC | No |
| HR371 | Male | Not tested | 0 | 0.0039 | -0.0081 | -0.0048 | -0.006 | 7.6 | | 94 | 21.3 | SC | No |
| HR878 | Female | Not tested | 0 | 0.0021 | -0.0006 | -0.0034 | -0.0028 | 8.1 | | 94 | 16.6 | SC | No |
| HR1498 | Female | Not tested | 0 | 0.0268 | -0.0035 | -0.0086 | -0.001 | 7.3 | | 81 | 13.6 | SC | No |
| HR1593 | Female | Not tested | 0 | 0.0073 | -0.0011 | -0.0048 | -0.001 | 5.5 | | 80 | 15.4 | SC | No |
| HR1771 | Female | Not tested | 0 | 0.0233 | -0.0013 | 0.0268 | 0.017 | 8.3 | | 88 | 18.9 | SC | Yes |
| HR2537 | Female | Not tested | 0 | 0.0119 | 0.0003 | 0.002 | -0.0022 | 6.4 | | 83 | 14.4 | SC | Yes |
| HR2251 | Female | Not tested | 0 | 0.0045 | -0.001 | -0.0022 | -0.01 | 7.3 | | 110 | 22.3 | SC | Yes |
| HR2339 | Female | Not tested | 0 | -0.0035 | -0.0025 | 0.0059 | -0.005 | 5.5 | | 77 | 14.3 | SC | No |
| HR182 | Male | Not tested | 0 | 0.0104 | 0.0019 | 0.0131 | -0.0016 | 9.0 | | 90 | 15.0 | SC | No |
| HR1710 | Male | Not tested | 0 | 0.0061 | -0.0015 | 0.0118 | -0.013 | 5.5 | | 93 | 15.5 | S | No |
| HR6 | Female | Not tested | 0 | -0.0062 | -0.0013 | -0.0051 | -0.0032 | 11.1 | | 99 | 23.3 | SC | Yes |
| HR22 | Male | Not tested | 0 | 0.0107 | 0.0004 | -0.0011 | 0.0063 | 11.0 | | 93 | 20.9 | SCA | No |
| HR26 | Female | Not tested | 0 | -0.0049 | 0.002 | -0.0079 | -0.0054 | 11.7 | | 83 | 15.3 | SC | No |
| HR116 | Male | Not tested | 0 | -0.0109 | 0 | 0.0022 | -0.0082 | 10.4 | | 117 | 18.8 | SC | No |
| HR271 | Female | Not tested | 0 | 0.03 | -0.0006 | -0.0081 | 0.0251 | 11.4 | | 87 | 18.8 | SC | No |
| HR1439 | Female | Not tested | 0 | -0.002 | -0.0054 | 0.0017 | -0.005 | 10.4 | | 119 | 25.8 | S | Yes |
| HR1975 | Female | Not tested | 0 | 0.0074 | -0.0006 | -0.0017 | -0.004 | 10.1 | | 82 | 23.9 | SC | No |
| HR2051 | Male | Not tested | 0 | 0.0023 | -0.0031 | -0.0016 | 0.004 | 10.0 | | 95 | 16.6 | SC | No |
| HR2068 | Male | Not tested | 0 | -0.0033 | -0.0005 | 0.0127 | -0.006 | 10.5 | | 76 | 19.0 | SC | No |
| HR2767 | Female | Not tested | 0 | 0.0049 | -0.0007 | 0.013 | -0.004 | 5.4 | | 99 | 15.7 | SC | No |
| HR2684 | Male | Not tested | 0 | -0.0039 | -0.0015 | 0 | -0.008 | 7.1 | | 103 | 14.5 | SC | No |
| HR2490 | Female | Not tested | 0 | 0.0007 | -0.0007 | -0.002 | -0.007 | 9.5 | | 89 | 18.0 | SC | No |
| HR2654 | Female | Not tested | 0 | -0.0012 | -0.0011 | 0.0031 | -0.009 | 8.5 | | 92 | 26.2 | SC | No |
| HR7 | Female | Not tested | 0 | -0.0004 | -0.0004 | -0.0101 | -0.0043 | 8.1 | | 93 | 17.1 | CA | No |
| HR214 | Female | Not tested | 0 | 0.0068 | 0.0028 | 0 | -0.0023 | 10.4 | | 87 | 19.5 | C | No |
| **Unrelated Healthy Controls** | | | | | | | | | | | | | |
| HC2074 | Male | Not tested | 0 | -0.0098 | -0.0043 | 0 | -0.005 | 23.0 | | 87 | 23.8 | SC | |
| HC2302 | Female | Not tested | 1 | 0.0166 | 0.0004 | 0.1812 | -0.009 | 21.3 | | 81 | 19.0 | S | |
| HC2593 | Female | Not tested | 0 | 0.0088 | -0.001 | 0.0088 | 0 | 23.3 | | 82 | 19.1 | S | |
| HC2146 | Female | Not tested | 0 | N/A | N/A | N/A | N/A | 23.9 | | N/A | N/A | SC | |
| HC223 | Female | Not tested | 0 | 0.0037 | -0.0005 | 0.005 | -0.0015 | 13.6 | | 91 | 19.6 | S | |
| HC285 | Female | Not tested | 1 | -0.0117 | 0.0014 | 0.0917 | -0.0115 | 7.6 | | 86 | 16.5 | S | |
| HC233 | Male | Not tested | 0 | 0.005 | -0.0002 | 0.01 | -0.0032 | 8.9 | | 98 | 16.1 | S | |
| HC294 | Male | Not tested | 0 | -0.0069 | 0.001 | 0 | -0.0054 | 11.9 | | 115 | 16.7 | S | |
| HC224 | Female | Not tested | 0 | 0.0057 | 0.0006 | 0 | -0.0075 | 13.7 | | 93 | 23.2 | S | |
| HC217 | Male | Not tested | 0 | -0.0016 | -0.0019 | 0.01 | -0.007 | 10.1 | | 82 | N/A | SC | |
| HC226 | Female | Not tested | 0 | -0.0038 | 0.0005 | 0.01 | -0.0049 | 11.3 | | 77 | 26.8 | S | |
| HC2790 | Female | Not tested | 0 | -0.002 | 0.0017 | 0.0094 | -0.007 | 11.6 | | 126 | 16.2 | SC | |
| HC385 | Male | Not tested | 0 | -0.0091 | -0.0015 | 0.0167 | -0.0101 | 12.3 | | 92 | 19.6 | S | |
| HC295 | Male | Not tested | 0 | -0.0152 | -0.0004 | 0.0048 | -0.0065 | 12.4 | | 96 | 19.4 | SC | |
| HC272 | Female | Not tested | 0 | -0.0068 | 0.0032 | 0.0052 | -0.0104 | 6.3 | | 97 | 19.5 | S | |
| HC375 | Female | Not tested | 0 | N/A | N/A | N/A | N/A | 9.4 | | N/A | 21.4 | SC | |
| HC2614 | Male | Not tested | 0 | -0.0043 | -0.001 | -0.0031 | -0.009 | 10.3 | | 102 | 18.9 | S | |
| HC2301 | Female | Not tested | 0 | 0.009 | 0.0002 | -0.0083 | -0.005 | 10.6 | | 142 | 19.9 | S | |
| HC1006 | Male | Not tested | 0 | 0.0043 | -0.0004 | 0 | -0.0077 | 12.8 | | 95 | 26.1 | S | |
| HC390 | Male | Not tested | 0 | -0.01 | -0.0009 | 0.016 | -0.0023 | 12.9 | | 90 | 14.9 | S | |
| HC322 | Male | Not tested | 0 | -0.0093 | 0.0014 | -0.0105 | -0.0024 | 12.9 | | 102 | 17.0 | SC | |
| HC381 | Female | Not tested | 0 | 0.0001 | 0.0022 | -0.0126 | -0.0098 | 13.1 | | 110 | 25.8 | S | |
| HC379 | Female | Not tested | 0 | -0.0021 | 0.0006 | -0.0126 | -0.005 | 13.4 | | 101 | 22.5 | S | |
| HC227 | Male | Not tested | 0 | 0.0044 | 0.0014 | 0.011 | 0 | 14.1 | | 91 | 21.0 | S | |
| HC1777 | Female | Not tested | 0 | 0.0142 | -0.0005 | 0.0213 | -0.015 | 14.9 | | 90 | 19.0 | S | |
| HC384 | Female | Not tested | 0 | -0.0024 | 0.0007 | 0.0042 | -0.0062 | 15.0 | | 86 | 21.1 | S | |
| HC394 | Female | Not tested | 0 | -0.0066 | 0.0027 | 0.0016 | -0.0077 | 15.2 | | 85 | 31.7 | S | |
| HC1089 | Female | Not tested | 0 | -0.0055 | -0.0001 | -0.0071 | -0.006 | 15.8 | | 78 | 17.4 | SC | |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| HC1142 | Male | Not tested | 0 | 0.0008 | -0.002 | -0.0056 | -0.009 | 16.3 | | 81 | 22.3 | SC |
| HC1265 | Female | Not tested | 0 | 0.0042 | -0.0004 | -0.005 | -0.008 | 16.5 | | 98 | 20.3 | SC |
| HC388 | Male | Not tested | 0 | 0.0003 | -0.0007 | 0 | -0.0057 | 16.5 | | 89 | 30.1 | SC |
| HC1249 | Female | Not tested | 0 | -0.01 | -0.0007 | -0.0041 | -0.007 | 16.6 | | 86 | 28.7 | SC |
| HC2369 | Male | Not tested | 0 | 0.0025 | 0.0009 | -0.0023 | -0.009 | 16.7 | | 95 | 21.8 | SC |
| HC308 | Male | Not tested | 0 | -0.016 | 0.002 | -0.0059 | -0.0074 | 17.1 | | 88 | 20.5 | S |
| HC305 | Male | Not tested | 0 | 0.0019 | 0.0066 | 0.0006 | -0.0046 | 17.1 | | 76 | 25.5 | SC |
| HC304 | Female | Not tested | 0 | 0.0003 | 0.003 | 0.0133 | -0.001 | 17.2 | | 78 | 20.3 | SC |
| HC1601 | Female | Not tested | 0 | 0.0001 | 0.0008 | 0.0032 | 0.003 | 17.2 | | 94 | 22.6 | SC |
| HC1543 | Female | Not tested | 0 | -0.0043 | 0.0003 | 0.0056 | -0.008 | 17.4 | | N/A | 19.6 | SC |
| HC307 | Male | Not tested | 0 | -0.0069 | 0.003 | 0.01 | -0.0065 | 17.6 | | 83 | 26.3 | SC |
| HC1730 | Female | Not tested | 0 | 0.0133 | -0.0003 | 0.0069 | -0.009 | 17.8 | | 76 | 27.7 | SC |
| HC1369 | Female | Not tested | 0 | 0.0246 | -0.0009 | 0.0086 | -0.011 | 21.1 | | 85 | 22.4 | SC |
| HC1365 | Female | Not tested | 0 | 0.0023 | -0.0101 | 0.0174 | -0.009 | 21.8 | | 92 | N/A | SC |
| HC382 | Female | Not tested | 0 | 0.0069 | 0.0004 | 0 | -0.0047 | 13.0 | | 101 | 19.3 | S |
| HC1678 | Female | Not tested | 0 | 0 | -0.003 | -0.01 | -0.005 | 17.8 | | 85 | 20.5 | SC |
| HC1005 | Female | Not tested | 0 | 0.0103 | 0.0019 | 0 | -0.0053 | 16.1 | | 86 | 25.7 | C |
| HC1759 | Male | Not tested | 0 | 0.0101 | -0.0007 | 0.0115 | -0.008 | 16.8 | | 75 | 23.2 | C |
| HC284 | Male | Not tested | 0 | -0.0097 | 0.001 | 0 | -0.0082 | 9.3 | | 86 | 18.9 | C |
| HC1837 | Female | Not tested | 0 | 0.0026 | -0.0009 | 0.0193 | -0.014 | 9.8 | | 98 | N/A | C |
| HC2789 | Female | Not tested | 0 | 0.0008 | -0.0002 | -0.009 | -0.011 | 14.4 | | 93 | 24.6 | C |
| HC1600 | Female | Not tested | 0 | 0.0312 | 0.0002 | -0.0029 | 0.004 | 17.2 | | 92 | 24.0 | C |
| HC1247 | Male | Not tested | 0 | -0.0098 | -0.0005 | -0.0041 | -0.006 | 24.3 | | 90 | 24.6 | C |
| HC2017 | Female | Not tested | 0 | 0.0025 | -0.0013 | 0 | 0.002 | 22.8 | | 88 | 20.7 | C |
| HC2368 | Male | Not tested | 0 | 0.006 | -0.0005 | -0.0135 | -0.007 | 18.1 | | 95 | 17.4 | C |
| **Longitudinal Progressor sample series** | | | | | | | | | | | | |
| RO T1D A1 | Male | Not tested | 0 | 0.0169 | -0.0035 | -0.0017 | -0.0096 | 16.4 | 21.7 | 99 | 23.4 | S |
| RO T1D A2 | Male | Not tested | 1 | 0.0659 | 0.0013 | 0.0044 | **0.4023** | 18.4 | 21.7 | 85 | N/A | S |
| RO T1D A3 | Male | Not tested | 3 | **0.1576** | **0.4249** | 0.0124 | **0.424** | 19.2 | 21.7 | 90 | N/A | S |
| RO T1D A4 | Male | Not tested | 3 | **0.1602** | **1.0131** | 0.0052 | **0.448** | 20.2 | 21.7 | 91 | 26.2 | S |
| RO T1D A5 | Male | Not tested | 3 | **0.3064** | **0.8593** | 0.007 | **0.467** | 21.3 | 21.7 | 123 | 28.1 | S |
| RO T1D A6 | Male | 5.5 | 4 | **0.2441** | **1.1301** | **0.8804** | **0.443** | 21.9 | 21.7 | 185 | 27.2 | S |
| RO T1D B1 | Female | Not tested | 1 | 0.059 | **0.01** | 0.0175 | 0.0022 | 7.5 | 9.0 | 94 | 16.9 | S |
| RO T1D B2 | Female | Not tested | 2 | **0.1518** | **0.2252** | 0.038 | -0.0013 | 8.7 | 9.0 | 98 | N/A | S |
| RO T1D B3 | Female | 6.6 | 3 | **0.1026** | **1.0284** | **0.1886** | -0.0007 | 9.2 | 9.0 | 142 | 16.4 | S |
| RO T1D B4 | Female | 6.8 | 2 | 0.0326 | **0.1231** | **0.5699** | -0.006 | 10.1 | 9.0 | 191 | 16.3 | S |
| RO T1D E1 | Male | Not tested | 4 | **0.2374** | **0.1123** | **0.181** | **0.0518** | 12.9 | 19.3 | 124 | 16.1 | S |
| RO T1D E2 | Male | Not tested | 3 | **0.1358** | **0.1238** | **0.0865** | 0.0045 | 13.9 | 19.3 | 101 | N/A | S |
| RO T1D E3 | Male | Not tested | 3 | **0.1126** | **0.0899** | **0.1222** | -0.001 | 15.0 | 19.3 | 106 | N/A | S |
| RO T1D E4 | Male | Not tested | 3 | **0.1613** | **0.0838** | **0.0939** | 0.011 | 15.4 | 19.3 | 107 | 19.5 | S |
| RO T1D E5 | Male | Not tested | 3 | **0.0849** | **0.0505** | **0.0817** | 0.004 | 15.9 | 19.3 | 95 | 20.0 | S |
| RO T1D E6 | Male | Not tested | 3 | **0.1231** | **0.0852** | **0.054** | -0.006 | 16.4 | 19.3 | 112 | N/A | S |
| RO T1D E7 | Male | Not tested | 3 | **0.0709** | **0.1258** | **0.0847** | -0.001 | 16.9 | 19.3 | 139 | N/A | S |
| RO T1D E8 | Male | Not tested | 1 | 0.0507 | **0.0299** | 0.04 | -0.004 | 18.0 | 19.3 | 144 | 21.0 | S |
| RO T1D F1 | Male | Not tested | 4 | **1.7759** | **0.0407** | **0.1657** | **1.242** | 4.2 | 6.9 | 72 | N/A | S |
| RO T1D F2 | Male | Not tested | 3 | **0.8103** | 0.0032 | **0.0878** | **0.769** | 4.6 | 6.9 | 94 | 18.5 | S |
| RO T1D F3 | Male | Not tested | 4 | **0.6668** | **0.356** | **0.1233** | **1.254** | 5.4 | 6.9 | 104 | 18.1 | S |
| RO T1D F4 | Male | Not tested | 4 | **0.5901** | **0.9015** | **0.1394** | **1.325** | 5.9 | 6.9 | 116 | N/A | S |
| RO T1D F5 | Male | Not tested | 4 | **0.0934** | **0.229** | **0.1706** | **1.178** | 7.0 | 6.9 | 118 | 16.8 | S |
| RO T1D F6 | Male | 6 | 4 | **0.1349** | **0.2102** | **2.9047** | **0.522** | 7.7 | 6.9 | 131 | 19.5 | S |
| RO T1D D1 | Female | Not tested | 0 | -0.002 | -0.0054 | 0.0017 | -0.005 | 10.4 | 17.4 | 119 | 25.8 | S |
| RO T1D D2 | Female | Not tested | 0 | 0.0312 | -0.0014 | 0 | -0.007 | 12.4 | 17.4 | 90 | N/A | S |
| RO T1D D3 | Female | Not tested | 0 | 0.0026 | 0.0015 | 0.0111 | -0.005 | 13.4 | 17.4 | 88 | N/A | S |
| RO T1D D4 | Female | Not tested | 3 | **0.8954** | **0.431** | 0.0128 | **0.271** | 14.4 | 17.4 | 105 | N/A | S |
| RO T1D D5 | Female | Not tested | 3 | **1.2523** | **0.6469** | 0.0028 | **0.2157** | 14.9 | 17.4 | 90 | N/A | S |
| RO T1D D6 | Female | Not tested | 3 | **1.1303** | **1.0491** | -0.0088 | **0.3655** | 15.5 | 17.4 | 110 | N/A | S |
| RO T1D D7 | Female | Not tested | 3 | **0.7322** | **0.9755** | 0.0081 | **0.4358** | 16.0 | 17.4 | 116 | 30.5 | S |
| RO T1D D8 | Female | 7.9 | 4 | **0.7192** | **1.0327** | **0.0932** | **0.4991** | 17.6 | 17.4 | 89 | N/A | S |
| **Longitudinal Auto-antibody-positive (AA+) High HLA Risk Sibling sample series** | | | | | | | | | | | | |
| AA+ HRS A1 | Male | Not tested | 4 | **0.6342** | **0.3731** | **0.0689** | **0.7214** | 14.0 | | 93 | 18.7 | S |
| AA+ HRS A2 | Male | Not tested | 4 | **0.6337** | **0.17** | **0.0857** | **0.744** | 15.1 | | 88 | N/A | S |
| AA+ HRS A3 | Male | Not tested | 4 | **1.0194** | **0.5787** | **0.0575** | **0.8022** | 16.0 | | 82 | N/A | S |
| AA+ HRS A4 | Male | Not tested | 4 | **0.8829** | **0.4392** | **0.1425** | **0.794** | 17.1 | | 58 | N/A | S |
| AA+ HRS A5 | Male | Not tested | 3 | **0.2034** | **0.1397** | 0.0028 | **0.936** | 19.5 | | 79 | 22.5 | S |
| AA+ HRS B1 | Female | Not tested | 3 | 0.0155 | **0.024** | **0.1733** | **0.3372** | 13.4 | | 66 | 17.0 | S |
| AA+ HRS B2 | Female | Not tested | 2 | **0.4579** | **0.5608** | 0 | N/A | 14.0 | | 87 | N/A | S |
| AA+ HRS B3 | Female | Not tested | 3 | **0.5105** | **0.3812** | 0 | **0.04** | 14.7 | | 93 | N/A | S |
| AA+ HRS B4 | Female | Not tested | 2 | **0.5204** | **0.2861** | 0.0113 | 0.025 | 15.8 | | 81 | N/A | S |
| AA+ HRS B5 | Female | Not tested | 3 | **0.7481** | **0.2629** | 0.0087 | **0.055** | 16.5 | | 79 | 18.1 | S |
| AA+ HRS B6 | Female | Not tested | 2 | **0.972** | **0.1117** | 0.0054 | 0.027 | 17.6 | | 116 | N/A | S |
| AA+ HRS B7 | Female | Not tested | 2 | **0.5992** | **0.1056** | -0.0022 | 0.009 | 18.7 | | 137 | 18.4 | S |
| AA+ HRS B8 | Female | Not tested | 2 | **0.4692** | **0.0451** | 0 | 0.005 | 19.7 | | 147 | N/A | S |
| AA+ HRS C1 | Male | Not tested | 1 | 0.0544 | 0.0047 | **0.1241** | -0.01 | 9.2 | | 62 | 16.1 | S |
| AA+ HRS C2 | Male | Not tested | 1 | **0.1193** | -0.0063 | 0.0067 | -0.0045 | 9.8 | | 88 | N/A | S |
| AA+ HRS C3 | Male | Not tested | 1 | **0.0922** | -0.0001 | 0.0134 | 0.006 | 11.0 | | 78 | N/A | S |
| AA+ HRS C4 | Male | Not tested | 2 | **0.1727** | -0.0012 | -0.0018 | **0.158** | 11.5 | | 82 | 16.0 | S |
| AA+ HRS C5 | Male | Not tested | 2 | **0.1212** | 0 | 0.0031 | **0.338** | 12.0 | | 97 | 16.3 | S |
| AA+ HRS C6 | Male | Not tested | 2 | **0.0973** | 0.0008 | 0.0052 | **0.372** | 12.7 | | 82 | N/A | S |
| AA+ HRS C7 | Male | Not tested | 2 | 0.0305 | **0.5402** | 0.0036 | **0.472** | 14.2 | | 81 | 18.1 | S |
| AA+ HRS E1 | Female | Not tested | 0 | -0.0058 | 0.0017 | 0.024 | -0.007 | 12.6 | | 99 | 31.2 | S |
| AA+ HRS E2 | Female | Not tested | 2 | -0.0041 | **0.0038** | **0.2394** | -0.006 | 13.6 | | 77 | N/A | S |
| AA+ HRS E3 | Female | Not tested | 1 | -0.0055 | 0.0007 | **0.3763** | -0.011 | 14.6 | | 94 | N/A | S |
| AA+ HRS E4 | Female | Not tested | 1 | -0.0035 | -0.0016 | **0.3121** | -0.0081 | 15.7 | | 104 | N/A | S |
| AA+ HRS E5 | Female | Not tested | 1 | -0.0053 | -0.0005 | **0.4751** | -0.006 | 16.6 | | 86 | N/A | S |
| AA+ HRS F1 | Male | Not tested | 1 | 0.0034 | -0.0013 | **0.1564** | -0.002 | 11.3 | | 85 | 18.9 | S |
| AA+ HRS F2 | Male | Not tested | 1 | -0.0031 | -0.0078 | **0.1303** | -0.003 | 12.4 | | 78 | N/A | S |
| AA+ HRS F3 | Male | Not tested | 0 | 0.0024 | -0.0009 | 0.0253 | -0.0019 | 13.3 | | 84 | N/A | S |
| AA+ HRS F4 | Male | Not tested | 0 | 0.0033 | 0.0001 | 0.0259 | 0.0021 | 14.3 | | 105 | N/A | S |
| AA+ HRS G1 | Female | Not tested | 0 | 0.0045 | -0.001 | -0.0022 | -0.01 | 7.3 | | 110 | 22.3 | S |
| AA+ HRS G2 | Female | Not tested | 0 | -0.003 | -0.002 | -0.0052 | -0.005 | 8.3 | | 100 | N/A | S |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| AA+ HRS G3 | Female | Not tested | 0 | -0.0054 | -0.0006 | -0.0041 | -0.007 | 9.4 | 85 | N/A | S |
| AA+ HRS G4 | Female | Not tested | 1 | -0.011 | -0.0038 | **0.0622** | -0.0087 | 10.4 | 147 | N/A | S |
| AA+ HRS G5 | Female | Not tested | 0 | 0.0007 | -0.0015 | 0.0211 | -0.0067 | 11.3 | 93 | N/A | S |
| AA+ HRS G6 | Female | Not tested | 0 | -0.0066 | -0.0007 | 0.0158 | -0.0072 | 12.3 | 80 | 26.3 | S |
| AA+ HRS H1 | Female | Not tested | 2 | 0.0143 | **0.0505** | 0.0166 | **0.7273** | 12.0 | 108 | 18.2 | S |
| AA+ HRS H2 | Female | Not tested | 2 | 0.0039 | **0.0091** | -0.0022 | **0.3048** | 13.8 | 74 | N/A | S |
| AA+ HRS H3 | Female | Not tested | 1 | 0.0127 | 0.0021 | 0.0004 | **0.114** | 15.1 | 70 | N/A | S |
| AA+ HRS H4 | Female | Not tested | 0 | 0.0128 | 0.0011 | 0.0236 | 0.029 | 16.0 | 101 | 23.0 | S |
| AA+ HRS H5 | Female | Not tested | 0 | 0.0108 | -0.0002 | 0 | 0.026 | 16.9 | 94 | 23.8 | S |
| AA+ HRS I1 | Female | Not tested | 1 | 0.012 | 0.0003 | **0.1019** | -0.0065 | 2.1 | 93 | 18.0 | S |
| AA+ HRS I2 | Female | Not tested | 1 | 0.0009 | 0.0034 | **0.1403** | -0.0072 | 2.6 | 87 | N/A | S |
| AA+ HRS I3 | Female | Not tested | 2 | **0.0859** | -0.0011 | **2.045** | -0.0039 | 3.2 | 91 | N/A | S |
| AA+ HRS I4 | Female | Not tested | 0 | -0.0041 | -0.0019 | 0.0058 | -0.006 | 4.4 | 76 | N/A | S |
| AA+ HRS I5 | Female | Not tested | 0 | -0.0084 | 0.0003 | 0.007 | -0.006 | 5.4 | 80 | N/A | S |
| AA+ HRS I6 | Female | Not tested | 0 | -0.002 | -0.0004 | -0.0059 | -0.009 | 7.8 | 85 | N/A | S |
| AA+ HRS I7 | Female | Not tested | 0 | -0.0074 | -0.0028 | -0.0042 | -0.0084 | 9.6 | 85 | N/A | S |
| AA+ HRS I8 | Female | Not tested | 0 | 0.0003 | -0.0001 | 0.0078 | -0.0094 | 12.1 | 93 | 19.5 | S |
| AA+ HRS J1 | Male | Not tested | 1 | 0.02 | **0.0144** | 0 | 0.0091 | 5.4 | 76 | 15.3 | S |
| AA+ HRS J2 | Male | Not tested | 1 | 0.0169 | **0.0088** | -0.0019 | 0.003 | 6.4 | 80 | N/A | S |
| AA+ HRS J3 | Male | Not tested | 1 | 0.023 | **0.0081** | 0.0026 | 0.012 | 7.4 | 106 | N/A | S |
| AA+ HRS J4 | Male | Not tested | 0 | 0.0184 | 0.005 | 0.0134 | 0.012 | 8.4 | 82 | N/A | S |
| AA+ HRS J5 | Male | Not tested | 0 | 0.0016 | -0.0001 | 0.0048 | -0.0036 | 12.4 | 83 | N/A | S |
| AA+ HRS J6 | Male | Not tested | 0 | 0.0016 | -0.0001 | 0.0055 | -0.0085 | 14.4 | N/A | N/A | S |

**Longitudinal Auto-antibody-negative (AA-) High HLA Risk Sibling sample series**

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| AA- HRS A1 | Male | Not tested | 0 | -0.0109 | 0 | 0.0022 | -0.0082 | 10.4 | 117 | 18.8 | S |
| AA- HRS A2 | Male | Not tested | 0 | 0.0083 | -0.0001 | 0.0044 | -0.002 | 15.3 | 87 | 19.9 | S |
| AA- HRS A3 | Male | Not tested | 0 | -0.0014 | -0.001 | 0.0022 | -0.007 | 16.5 | 60 | N/A | S |
| AA- HRS A4 | Male | Not tested | 0 | -0.0043 | -0.0011 | 0.0118 | -0.008 | 17.6 | 88 | N/A | S |
| AA- HRS A5 | Male | Not tested | 0 | -0.0048 | 0 | 0.0043 | -0.0045 | 18.9 | 109 | N/A | S |
| AA- HRS B1 | Female | Not tested | 0 | 0.0028 | -0.0005 | 0.0095 | 0.001 | 2.2 | 82 | 17.2 | S |
| AA- HRS B2 | Female | Not tested | 0 | 0.0154 | -0.0008 | 0 | -0.01 | 3.1 | 123 | N/A | S |
| AA- HRS B3 | Female | Not tested | 0 | 0.0071 | -0.0012 | 0.0037 | -0.002 | 4.1 | 92 | N/A | S |
| AA- HRS B4 | Female | Not tested | 0 | 0.0159 | -0.0023 | 0.0054 | -0.0021 | 6.1 | 79 | 13.4 | S |
| AA- HRS C1 | Female | Not tested | 0 | 0.0118 | -0.0017 | 0.0027 | 0.012 | 14.7 | 99 | 19.2 | S |
| AA- HRS C2 | Female | Not tested | 0 | 0.0085 | 0.0007 | 0.0035 | 0.003 | 15.7 | 94 | N/A | S |
| AA- HRS C3 | Female | Not tested | 0 | 0.0076 | -0.0012 | 0.0112 | -0.002 | 16.6 | 66 | N/A | S |
| AA- HRS C4 | Female | Not tested | 0 | 0.0065 | -0.0019 | -0.0077 | 0.0037 | 17.7 | 96 | N/A | S |
| AA- HRS C5 | Female | Not tested | 0 | 0.0053 | -0.0014 | 0.0054 | -0.0021 | 18.6 | 83 | N/A | S |
| AA- HRS D1 | Female | Not tested | 0 | 0.0141 | 0.0027 | 0.0076 | -0.01 | 14.8 | 92 | 38.3 | S |
| AA- HRS D2 | Female | Not tested | 0 | 0.0053 | -0.0006 | 0.0091 | -0.007 | 16.4 | 83 | N/A | S |
| AA- HRS D3 | Female | Not tested | 0 | 0.0029 | -0.0012 | -0.0026 | -0.0073 | 17.4 | 77 | N/A | S |
| AA- HRS D4 | Female | Not tested | 0 | 0.0124 | 0.0006 | 0 | -0.0041 | 18.4 | 93 | N/A | S |
| AA- HRS E2 | Female | Not tested | 0 | 0.0122 | 0.0043 | 0.0017 | -0.003 | 7.1 | 73 | N/A | S |
| AA- HRS E3 | Female | Not tested | 0 | 0.0046 | -0.0009 | 0.003 | -0.004 | 8.1 | 86 | N/A | S |
| AA- HRS E4 | Female | Not tested | 0 | 0.0051 | -0.0021 | -0.0037 | -0.0026 | 9.1 | 79 | N/A | S |
| AA- HRS E5 | Female | Not tested | 0 | 0.0055 | -0.0001 | 0 | -0.0043 | 10.1 | 97 | N/A | S |
| AA- HRS F1 | Female | Not tested | 0 | 0.0268 | -0.0035 | -0.0086 | -0.001 | 7.3 | 81 | 13.6 | S |
| AA- HRS F2 | Female | Not tested | 0 | 0.0123 | -0.0019 | 0.0035 | -0.008 | 9.3 | 82 | N/A | S |
| AA- HRS F3 | Female | Not tested | 0 | 0.0154 | -0.0001 | -0.0068 | 0.001 | 10.3 | 80 | N/A | S |
| AA- HRS F4 | Female | Not tested | 0 | 0.0066 | -0.0024 | -0.0128 | -0.0033 | 11.3 | 89 | N/A | S |
| AA- HRS F5 | Female | Not tested | 0 | 0.0298 | -0.0001 | 0.016 | -0.0034 | 12.3 | 84 | 17.9 | S |
| AA- HRS F6 | Female | Not tested | 0 | 0.0117 | -0.0001 | 0.0036 | -0.0045 | 13.3 | 102 | N/A | S |
| AA- HRS G1 | Female | Not tested | 0 | 0.0073 | -0.0011 | -0.0048 | -0.001 | 5.5 | 80 | 15.4 | S |
| AA- HRS G2 | Female | Not tested | 0 | 0.0212 | 0.0014 | 0.0044 | -0.005 | 6.7 | 132 | N/A | S |
| AA- HRS G3 | Female | Not tested | 0 | -0.0015 | -0.0005 | 0.0027 | -0.003 | 8.0 | 99 | N/A | S |
| AA- HRS G4 | Female | Not tested | 0 | -0.0021 | -0.0032 | 0.0053 | -0.0041 | 11.1 | 94 | 18.4 | S |
| AA- HRS H1 | Male | Not tested | 0 | 0 | -0.001 | 0.033 | -0.011 | 2.9 | 83 | 16.6 | S |
| AA- HRS H2 | Male | Not tested | 0 | 0.0004 | -0.001 | 0.0062 | -0.008 | 5.0 | 80 | N/A | S |
| AA- HRS H3 | Male | Not tested | 0 | -0.0014 | -0.0042 | 0.0113 | -0.007 | 6.7 | 91 | N/A | S |
| AA- HRS H4 | Male | Not tested | 0 | 0.0011 | -0.0004 | 0.0123 | -0.032 | 9.2 | 97 | N/A | S |
| AA- HRS I1 | Male | Not tested | 0 | 0.0088 | 0.0012 | -0.0032 | -0.0028 | 2.1 | 99 | 14.8 | S |
| AA- HRS I2 | Male | Not tested | 0 | -0.0019 | -0.0011 | 0.0096 | -0.005 | 6.0 | 83 | N/A | S |
| AA- HRS I3 | Male | Not tested | 0 | 0.0018 | -0.0006 | -0.0104 | 0.002 | 7.1 | 90 | 15.1 | S |
| AA- HRS I4 | Male | Not tested | 0 | -0.0073 | -0.001 | -0.0018 | 0.0081 | 8.0 | 78 | 15.2 | S |
| AA- HRS I5 | Male | Not tested | 0 | -0.0021 | -0.0024 | 0.0143 | 0 | 9.1 | 89 | N/A | S |
| AA- HRS I6 | Male | Not tested | 0 | 0.01 | -0.0013 | 0.0286 | -0.0077 | 11.2 | N/A | N/A | S |
| AA- HRS J1 | Male | Not tested | 0 | 0.0145 | -0.0003 | -0.0017 | 0.001 | 3.8 | 94 | 15.1 | S |
| AA- HRS J2 | Male | Not tested | 0 | 0.0107 | 0.0018 | 0.0096 | -0.006 | 5.8 | 118 | N/A | S |
| AA- HRS J3 | Male | Not tested | 0 | -0.0048 | 0.0011 | -0.0029 | -0.006 | 6.7 | 85 | N/A | S |
| AA- HRS J4 | Male | Not tested | 0 | -0.0047 | 0.0022 | 0.0036 | -0.009 | 8.1 | 98 | N/A | S |
| AA- HRS J5 | Male | Not tested | 0 | 0.0008 | -0.0018 | -0.0101 | -0.0022 | 8.9 | 89 | 14.8 | S |
| AA- HRS J6 | Male | Not tested | 0 | -0.0017 | 0 | 0.0023 | -0.0094 | 10.0 | 86 | N/A | S |
| AA- HRS J7 | Male | Not tested | 0 | -0.0016 | -0.0004 | 0.0032 | -0.0201 | 11.4 | N/A | N/A | S |
| AA- HRS K1 | Male | Not tested | 0 | 0.0132 | 0.0002 | -0.0017 | -0.005 | 2.2 | 86 | 17.0 | S |
| AA- HRS K2 | Male | Not tested | 0 | 0.0168 | 0.0003 | -0.0067 | -0.009 | 4.2 | 126 | N/A | S |
| AA- HRS K3 | Male | Not tested | 0 | 0.0001 | -0.0004 | 0 | -0.007 | 5.1 | 94 | N/A | S |
| AA- HRS K4 | Male | Not tested | 0 | -0.0042 | 0.0019 | 0.0072 | -0.01 | 6.5 | 96 | N/A | S |
| AA- HRS K5 | Male | Not tested | 0 | -0.0016 | -0.0031 | -0.0101 | -0.0061 | 7.2 | 86 | 15.1 | S |
| AA- HRS K6 | Male | Not tested | 0 | -0.0055 | -0.0032 | -0.0035 | -0.0072 | 8.4 | 94 | N/A | S |
| AA- HRS K7 | Male | Not tested | 0 | -0.0034 | -0.0013 | 0.0011 | -0.0286 | 9.8 | N/A | N/A | S |
| AA- HRS L1 | Female | Not tested | 0 | 0.0042 | -0.0014 | 0 | -0.0023 | 3.1 | 70 | 18.1 | S |
| AA- HRS L2 | Female | Not tested | 0 | 0.0002 | -0.0104 | -0.0027 | -0.006 | 4.1 | 66 | N/A | S |
| AA- HRS L3 | Female | Not tested | 0 | 0.0216 | 0.0005 | 0.0067 | -0.001 | 6.0 | 75 | N/A | S |
| AA- HRS L4 | Female | Not tested | 0 | 0.0069 | -0.0004 | 0 | 0.022 | 7.2 | 75 | N/A | S |

**Longitudinal Auto-antibody-negative (AA-) Low HLA Risk Sibling sample series**

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| AA- LRS B1 | Female | Not tested | 0 | -0.0066 | -0.0028 | 0 | -0.0066 | 5.5 | 94 | 17.5 | S |
| AA- LRS B2 | Female | Not tested | 0 | 0.0116 | -0.0017 | 0.0022 | -0.01 | 8.8 | 72 | N/A | S |
| AA- LRS B3 | Female | Not tested | 0 | -0.0056 | -0.0092 | 0.0106 | -0.009 | 10.2 | 69 | N/A | S |
| AA- LRS B4 | Female | Not tested | 0 | -0.0024 | -0.0005 | 0.0106 | -0.0035 | 14.3 | 70 | N/A | S |
| AA- LRS C1 | Male | Not tested | 0 | -0.0101 | -0.0004 | -0.002 | 0.001 | 4.5 | 78 | 14.6 | S |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| AA- LRS C2 | Male | Not tested | 0 | -0.0074 | -0.002 | 0.008 | -0.0027 | 9.9 | 96 | 15.8 | S |
| AA- LRS C3 | Male | Not tested | 0 | -0.0029 | -0.0007 | -0.001 | 0.0009 | 10.8 | 98 | N/A | S |
| AA- LRS C4 | Male | Not tested | 0 | -0.0028 | -0.0009 | 0.0063 | -0.0059 | 11.8 | 99 | N/A | S |
| AA- LRS C5 | Male | Not tested | 0 | N/A | N/A | N/A | N/A | 12.8 | N/A | N/A | S |
| AA- LRS D1 | Male | Not tested | 0 | 0.0116 | -0.0019 | 0.0014 | -0.002 | 10.5 | 83 | 14.5 | S |
| AA- LRS D2 | Male | Not tested | 0 | -0.0014 | -0.0019 | 0 | -0.001 | 12.5 | 91 | N/A | S |
| AA- LRS D3 | Male | Not tested | 0 | 0.0018 | -0.0002 | 0.0061 | 0.02 | 13.5 | 87 | N/A | S |
| AA- LRS D4 | Male | Not tested | 0 | -0.0106 | -0.0019 | -0.0059 | 0.0018 | 14.5 | 82 | N/A | S |
| AA- LRS D5 | Male | Not tested | 0 | -0.0043 | -0.0003 | 0.0079 | -0.0019 | 15.5 | 89 | 17.2 | S |
| AA- LRS D6 | Male | Not tested | 0 | 0.0017 | -0.0001 | -0.0054 | 0.0032 | 16.5 | 93 | N/A | S |
| AA- LRS E1 | Female | Not tested | 0 | 0.0059 | -0.0013 | -0.0112 | -0.008 | 6.3 | 118 | 17.5 | S |
| AA- LRS E2 | Female | Not tested | 0 | 0.0098 | 0.0001 | -0.0044 | -0.014 | 7.3 | 92 | N/A | S |
| AA- LRS E3 | Female | Not tested | 0 | -0.0026 | -0.0004 | -0.0126 | -0.006 | 8.3 | 78 | N/A | S |
| AA- LRS E4 | Female | Not tested | 0 | -0.0137 | -0.0024 | -0.0118 | -0.0099 | 9.5 | 85 | N/A | S |
| AA- LRS E5 | Female | Not tested | 0 | -0.0022 | -0.001 | -0.0083 | -0.0059 | 10.2 | 97 | N/A | S |
| AA- LRS E6 | Female | Not tested | 0 | -0.0024 | -0.0006 | -0.0122 | -0.0008 | 11.6 | 101 | 18.8 | S |
| AA- LRS E7 | Female | Not tested | 0 | -0.0004 | -0.0007 | 0.0095 | 0.0066 | 12.3 | 99 | N/A | S |
| AA- LRS F1 | Female | Not tested | 0 | 0.0003 | -0.0022 | -0.0078 | -0.006 | 7.4 | 84 | 16.7 | S |
| AA- LRS F2 | Female | Not tested | 0 | -0.0086 | -0.0017 | -0.0022 | -0.004 | 8.4 | 74 | N/A | S |
| AA- LRS F3 | Female | Not tested | 0 | -0.0027 | -0.0037 | 0.007 | -0.0074 | 9.4 | 76 | N/A | S |
| AA- LRS F4 | Female | Not tested | 0 | -0.0003 | -0.0005 | -0.0061 | -0.0086 | 10.6 | 87 | N/A | S |
| AA- LRS F5 | Female | Not tested | 0 | -0.0023 | -0.0007 | 0.0096 | -0.0029 | 11.7 | 84 | N/A | S |
| AA- LRS G1 | Female | Not tested | 0 | 0.02 | -0.002 | 0 | 0.006 | 2.6 | 85 | 15.1 | S |
| AA- LRS G2 | Female | Not tested | 0 | -0.0048 | -0.0012 | -0.0018 | -0.0019 | 7.1 | 81 | 14.1 | S |
| AA- LRS G3 | Female | Not tested | 0 | 0.002 | -0.0016 | 0.0023 | 0.004 | 7.9 | 78 | N/A | S |
| AA- LRS G4 | Female | Not tested | 0 | N/A | N/A | N/A | N/A | 10.0 | N/A | N/A | S |

**Supplemental Table 2: 2422 Regulated probe sets from Cross Sectional Studies (a sortable Excel Spreadsheet with expression levels and statistics for each comparison is available upon request)**

| Probeset ID | Gene Symbol | Gene Title | Mean LRS n=42 | Mean ROT1D T1D n=47 | Mean HRS n=30 | Mean uHC n=44 | Fig1a/b Cross Sect ROT1D: HRSLRS uHC n=1383 | Fig1d/e 4way Venn 1.125 Fold Filter n_total= 1374 | Fig1e LRS 575 138↑=1 437↓=-1 | Fig1e ROT1D 128 36↑=1 92↓=-1 | Fig1e HRS 156 84↑=1 72↓=-1 | Fig1e uHC 647 532↑=1 115↓=-1 | HRS: LRS 612 1= (Log2R≥ 0.263 && FDR≤0.2) | ROT1D: uHC 762 1= (Log2R≥ 0.263 && FDR≤0.2) | ROT1D: HRS 261 1= (Log2R≥ 0.263 && FDR≤0.2) | ROT1D: LRS 468 1= (Log2R≥ 0.263 && FDR≤0.2) | HRS: uHC 635 1= (Log2R≥ 0.263 && FDR≤0.2) | LRS: uHC 1339 1= (Log2R≥ 0.263 && FDR≤0.2) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 204470_at | CXCL1 | chemokine (C-X-C motif) ligand 1 (melanoma growth stimulati | 1.21 | 0.60 | 0.29 | -0.01 | 1 | 1 | 1 | 0 | 0 | -1 | 1 | 1 | 0 | 1 | 0 | 1 |
| 233011_at | ANXA1 | Annexin A1 | -0.09 | 0.44 | 0.22 | -0.15 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 |
| 1554997_a_at | PTGS2 | prostaglandin-endoperoxide synthase 2 (prostaglandin G/H syr | 0.80 | 0.83 | 0.51 | 0.33 | 1 | 1 | 0 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 210367_s_at | PTGES | prostaglandin E synthase | -0.59 | -0.76 | -0.92 | -1.24 | 1 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 235008_at | ANKRD10 | ankyrin repeat domain 10 | -0.58 | -0.10 | -0.39 | -0.57 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 |
| 204112_s_at | HNMT | histamine N-methyltransferase | -0.12 | -0.56 | -0.69 | -1.01 | 1 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 207850_at | CXCL3 | chemokine (C-X-C motif) ligand 3 | 0.64 | 0.21 | -0.01 | -0.25 | 1 | 1 | 1 | 0 | 0 | -1 | 1 | 1 | 0 | 1 | 0 | 1 |
| 236495_at | NAMPT | nicotinamide phosphoribosyltransferase | -0.64 | -0.28 | -0.60 | -0.72 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 |
| 211924_s_at | PLAUR | plasminogen activator, urokinase receptor | -1.40 | -1.65 | -1.88 | -2.07 | 1 | 1 | 1 | 0 | 0 | -1 | 1 | 1 | 0 | 0 | 0 | 1 |
| 233314_at | PTEN | phosphatase and tensin homolog | 0.34 | 0.68 | 0.37 | 0.29 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 218228_s_at | TNKS2 | tankyrase, TRF1-interacting ankyrin-related ADP-ribose polyme | 1.23 | 1.28 | 1.23 | 0.90 | 1 | 1 | 0 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 228478_at | --- | --- | -0.23 | 0.29 | -0.03 | -0.10 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 |
| 230511_at | CREM | cAMP responsive element modulator | -0.68 | -0.76 | -0.95 | -1.15 | 1 | 1 | 0 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1569203_at | CXCL2 | chemokine (C-X-C motif) ligand 2 | -0.59 | -0.90 | -1.01 | -1.26 | 1 | 1 | 1 | 0 | 0 | -1 | 1 | 1 | 0 | 1 | 0 | 1 |
| 242427_at | WAC | WW domain containing adaptor with coiled-coil | 0.08 | 0.51 | 0.33 | 0.15 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 |
| 207075_at | NLRP3 | NLR family, pyrin domain containing 3 | 0.45 | 0.23 | 0.03 | -0.12 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 221345_at | FFAR2 | free fatty acid receptor 2 | 0.84 | 0.51 | 0.46 | 0.17 | 1 | 1 | 1 | 0 | 0 | -1 | 1 | 1 | 0 | 1 | 1 | 1 |
| 201340_s_at | ENC1 | ectodermal-neural cortex 1 (with BTB-like domain) | -0.50 | -0.36 | -0.44 | -0.69 | 1 | 1 | 0 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 204971_at | CSTA | cystatin A (stefin A) | -0.25 | -0.45 | -0.59 | -0.76 | 1 | 1 | 1 | 0 | 0 | -1 | 1 | 1 | 0 | 0 | 0 | 1 |
| 205495_s_at | GNLY | granulysin | 0.53 | 0.50 | 0.55 | 0.20 | 1 | 1 | 0 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 206026_s_at | TNFAIP6 | tumor necrosis factor, alpha-induced protein 6 | -0.08 | -0.27 | -0.42 | -0.58 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 209774_x_at | CXCL2 | chemokine (C-X-C motif) ligand 2 | 0.97 | 0.74 | 0.54 | 0.45 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 209967_s_at | CREM | cAMP responsive element modulator | -0.40 | -0.44 | -0.55 | -0.74 | 1 | 1 | 0 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1568830_at | IRAK3 | interleukin-1 receptor-associated kinase 3 | -0.61 | -0.29 | -0.51 | -0.59 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 |
| 216016_at | NLRP3 | NLR family, pyrin domain containing 3 | -0.19 | -0.17 | -0.19 | -0.46 | 1 | 1 | 0 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 222909_s_at | BAG4 | BCL2-associated athanogene 4 | -0.30 | 0.17 | 0.06 | -0.12 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | 0 |
| 224231_at | PRO0471 | hypothetical LOC28994 | -0.20 | 0.27 | 0.00 | -0.01 | 1 | 1 | -1 | 1 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 |
| 39402_at | IL1B | interleukin 1, beta | 0.52 | 0.25 | 0.14 | -0.04 | 1 | 1 | 1 | 0 | 0 | -1 | 1 | 1 | 0 | 1 | 0 | 1 |
| 201043_s_at | ANP32A | acidic (leucine-rich) nuclear phosphoprotein 32 family, membe | 0.38 | 0.50 | 0.69 | 0.23 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 1 | 0 |
| 205067_at | IL1B | interleukin 1, beta | 0.44 | 0.16 | 0.06 | -0.12 | 1 | 1 | 1 | 0 | 0 | -1 | 1 | 1 | 0 | 1 | 0 | 1 |
| 207388_s_at | PTGES | prostaglandin E synthase | -0.28 | -0.42 | -0.41 | -0.70 | 1 | 1 | 0 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 218839_at | HEY1 | hairy/enhancer-of-split related with YRPW motif 1 | 0.04 | -0.09 | -0.17 | -0.37 | 1 | 1 | 0 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 242163_at | THRAP3 | thyroid hormone receptor associated protein 3 | -0.89 | -0.38 | -0.38 | -0.66 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 1 | 0 | 1 | 1 | 0 |
| 206366_x_at | XCL1 | chemokine (C motif) ligand 1 | 0.73 | 0.59 | 0.57 | 0.32 | 1 | 1 | 0 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 240626_at | --- | --- | 0.14 | 0.37 | 0.20 | 0.10 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 37145_at | GNLY | granulysin | 0.55 | 0.51 | 0.57 | 0.24 | 1 | 1 | 0 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1569573_at | AVEN | apoptosis, caspase activation inhibitor | -0.17 | -0.23 | -0.21 | 0.03 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1570409_x_at | --- | --- | -0.85 | -0.85 | -0.80 | -0.59 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1554152_a_at | OGDH | oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) | -0.70 | -0.64 | -0.59 | -0.37 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1557077_a_at | --- | --- | -0.19 | -0.29 | -0.23 | -0.01 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1557238_s_at | Setd5 | SET domain containing 5 | -0.28 | -0.26 | -0.26 | 0.00 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1558078_at | --- | --- | -0.27 | -0.30 | -0.26 | -0.04 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1558792_x_at | AP2A1 | Adaptor-related protein complex 2, alpha 1 subunit | -0.13 | -0.21 | -0.16 | 0.06 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1560014_s_at | PDXDC1 | pyridoxal-dependent decarboxylase domain containing 1 | -0.07 | -0.15 | -0.12 | 0.12 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1560800_at | --- | --- | -0.81 | -1.06 | -0.79 | -0.79 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1561128_at | STK10 | serine/threonine kinase 10 | -0.27 | -0.36 | -0.31 | -0.09 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1562481_at | --- | --- | -0.62 | -0.56 | -0.60 | -0.29 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1563460_at | --- | --- | 0.01 | -0.04 | -0.02 | 0.22 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1569189_at | TTC9C | tetratricopeptide repeat domain 9C | -0.14 | -0.19 | -0.21 | 0.08 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 202940_at | WNK1 | WNK lysine deficient protein kinase 1 | -0.12 | -0.33 | -0.15 | -0.06 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 205822_s_at | HMGCS1 | 3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble) | 0.13 | -0.05 | 0.18 | 0.22 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 206169_x_at | ZC3H7B | zinc finger CCCH-type containing 7B | 0.06 | 0.05 | 0.12 | 0.32 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 210985_s_at | SP100 | SP100 nuclear antigen | -0.93 | -0.89 | -0.86 | -0.62 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 217653_x_at | TRPM6 | transient receptor potential cation channel, subfamily M, mem | -0.08 | -0.14 | -0.04 | 0.13 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 228549_at | TMEM63A | transmembrane protein 63A | 0.12 | 0.11 | 0.18 | 0.38 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 232161_x_at | PTPN4 | protein tyrosine phosphatase, non-receptor type 4 (megakaryc | -0.24 | -0.23 | -0.28 | 0.04 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 232346_at | LOC388692 | hypothetical LOC388692 | -0.05 | -0.10 | -0.08 | 0.17 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 232521_at | PCSK7 | proprotein convertase subtilisin/kexin type 7 | -0.05 | -0.11 | -0.13 | 0.15 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 233405_at | Fip1l1 | FIP1 like 1 (S. cerevisiae) | -0.36 | -0.25 | -0.28 | 0.02 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 235274_at | --- | --- | -0.17 | -0.16 | -0.21 | 0.11 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 236778_at | Atrx | alpha thalassemia/mental retardation syndrome X-linked (RAD | -0.42 | -0.29 | -0.37 | -0.03 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 237878_at | Map2k2 /// LC | mitogen-activated protein kinase kinase 2 pseudogene; mitoge | -0.35 | -0.44 | -0.35 | -0.17 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 238913_at | Cpsf6 | cleavage and polyadenylation specific factor 6, 68kDa | -0.08 | -0.09 | -0.09 | 0.17 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 239751_at | LOC10050686( | hypothetical LOC100506860 | -0.35 | -0.61 | -0.38 | -0.34 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 239893_at | MCTP2 | multiple C2 domains, transmembrane 2 | 0.05 | 0.09 | 0.08 | 0.36 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 242740_at | --- | --- | -0.49 | -0.44 | -0.39 | -0.17 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 242772_x_at | --- | --- | -0.41 | -0.33 | -0.52 | -0.06 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 242859_at | tfcp2 | transcription factor CP2 | -0.34 | -0.41 | -0.36 | -0.14 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 243031_at | rtn4 | reticulon 4 | -0.75 | -0.71 | -0.62 | -0.43 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 243899_at | ARL17A | ADP-ribosylation factor-like 17A | -0.30 | -0.37 | -0.29 | -0.11 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1554670_at | GGA1 | golgi-associated, gamma adaptin ear containing, ARF binding p | -0.84 | -0.86 | -0.86 | -0.58 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1556621_a_at | CHFR | checkpoint with forkhead and ring finger domains | -0.54 | -0.54 | -0.43 | -0.26 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1556931_at | CDC42P2 /// C | cell division cycle 42 (GTP binding protein, 25kDa); cell division | -0.56 | -0.52 | -0.41 | -0.23 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1557828_a_at | C5orf28 | Chromosome 5 open reading frame 28 | -0.03 | -0.11 | -0.05 | 0.18 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1562316_at | PIGU | phosphatidylinositol glycan anchor biosynthesis, class U | -0.17 | -0.36 | -0.18 | -0.07 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1564093_at | NEK1 | NIMA (never in mitosis gene a)-related kinase 1 | -0.45 | -0.50 | -0.44 | -0.23 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1565595_at | Slc6a16 | solute carrier family 6, member 16 | -0.13 | -0.10 | -0.06 | 0.18 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1568943_at | INPP5D | inositol polyphosphate-5-phosphatase, 145kDa | -0.06 | -0.08 | 0.00 | 0.19 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1569142_at | TRIM13 | tripartite motif-containing 13 | -0.58 | -0.68 | -0.61 | -0.40 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1569180_at | --- | --- | 0.05 | -0.01 | 0.03 | 0.27 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 214833_at | TMEM63A | transmembrane protein 63A | -0.06 | -0.08 | -0.06 | 0.20 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 215392_at | usp3 | ubiquitin specific peptidase 3 | -0.10 | -0.18 | -0.19 | 0.10 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 221191_at | STAG3L1 | stromal antigen 3-like 1 | -0.05 | -0.14 | -0.12 | 0.14 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 223314_at | TSPAN14 | tetraspanin 14 | 0.02 | -0.05 | -0.02 | 0.23 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 236060_at | METTL14 | methyltransferase like 14 | -0.07 | -0.14 | -0.09 | 0.14 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 239660_at | RALGAPA2 | Ral GTPase activating protein, alpha subunit 2 (catalytic) | 0.16 | 0.13 | 0.18 | 0.42 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 239771_at | CAND1 | cullin-associated and neddylation-dissociated 1 | 0.43 | 0.43 | 0.45 | 0.71 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 242241_x_at | Tmem50a | transmembrane protein 50A | -0.05 | -0.13 | -0.06 | 0.16 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 243264_s_at | C8orf44 /// SG | chromosome 8 open reading frame 44 /// serum/glucocorticoi | -0.32 | -0.37 | -0.34 | -0.09 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 243910_x_at | CAND1 | cullin-associated and neddylation-dissociated 1 | -0.16 | -0.26 | -0.24 | 0.02 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 243996_at | NPR2 | natriuretic peptide receptor B/guanylate cyclase B (atrionatriu | -0.11 | -0.08 | -0.10 | 0.20 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1553265_at | SLC23A3 | solute carrier family 23 (nucleobase transporters), member 3 | -0.34 | -0.44 | -0.37 | -0.16 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1559161_at | PDCL | phosducin-like | -0.54 | -0.51 | -0.68 | -0.22 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1559362_at | SIK3 | serine/threonine-protein kinase QSK | -0.33 | -0.44 | -0.43 | -0.15 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1562031_at | JAK2 | Janus kinase 2 | -0.03 | -0.11 | -0.11 | 0.17 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1569320_at | GPBP1L1 | GC-rich promoter binding protein 1-like 1 | -0.28 | -0.35 | -0.32 | -0.07 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1570022_at | C3orf1 | chromosome 3 open reading frame 1 | -0.43 | -0.60 | -0.42 | -0.31 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 209865_at | SLC35A3 | solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNA | -0.20 | -0.31 | -0.37 | -0.01 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 214982_at | SNRNP200 | small nuclear ribonucleoprotein 200kDa (U5) | -0.26 | -0.29 | -0.31 | -0.01 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 215162_at | RALGAPA1 | Ral GTPase activating protein, alpha subunit 1 (catalytic) | 0.08 | -0.02 | 0.05 | 0.27 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 217671_at | rfx3 | regulatory factor X, 3 (influences HLA class II expression) | -0.04 | -0.11 | -0.11 | 0.18 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 232000_at | TTC39B | Tetratricopeptide repeat domain 39B | 0.09 | 0.12 | 0.17 | 0.41 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 233824_at | --- | --- | -0.93 | -1.01 | -1.08 | -0.72 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 233931_at | zfr | zinc finger RNA binding protein | -0.66 | -0.72 | -0.73 | -0.43 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 237412_at | BCAS3 | breast carcinoma amplified sequence 3 | -0.16 | -0.24 | -0.14 | 0.04 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 239042_at | TSR1 | TSR1, 20S rRNA accumulation, homolog (S. cerevisiae) | -0.17 | -0.25 | -0.19 | 0.04 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 239809_at | KLF7 | Kruppel-like factor 7 (ubiquitous) | -0.05 | -0.04 | -0.07 | 0.25 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 242176_at | MEF2A | Myocyte enhancer factor 2A | -0.26 | -0.36 | -0.26 | -0.07 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 242440_at | --- | --- | -0.31 | -0.37 | -0.32 | -0.08 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1552788_a_at | HELB | helicase (DNA) B | -0.23 | -0.41 | -0.20 | -0.10 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1556828_at | --- | --- | 0.19 | -0.06 | 0.15 | 0.24 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1557197_a_at | LGALS3 | lectin, galactoside-binding, soluble, 3 | -2.21 | -2.23 | -2.33 | -1.93 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1558569_at | LOC10013154 | Hypothetical LOC100131541 | -0.33 | -0.44 | -0.39 | -0.14 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1560386_at | xpo1 | exportin 1 (CRM1 homolog, yeast) | -0.47 | -0.44 | -0.47 | -0.13 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1560391_at | pigl | phosphatidylinositol glycan anchor biosynthesis, class L | -0.12 | -0.14 | -0.27 | 0.16 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1561600_at | SSH2 | slingshot homolog 2 (Drosophila) | -0.05 | -0.15 | -0.06 | 0.15 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1561660_at | MCART6 | mitochondrial carrier triple repeat 6 | 0.29 | 0.18 | 0.23 | 0.48 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1569128_at | C3orf38 | chromosome 3 open reading frame 38 | -0.39 | -0.44 | -0.41 | -0.13 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1570505_at | ABCB4 | ATP-binding cassette, sub-family B (MDR/TAP), member 4 | -0.09 | -0.06 | 0.00 | 0.24 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 215070_x_at | RABGAP1 | RAB GTPase activating protein 1 | -0.39 | -0.50 | -0.38 | -0.20 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 217701_x_at | Atrx | alpha thalassemia/mental retardation syndrome X-linked (RAD | -0.50 | -0.50 | -0.54 | -0.20 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 223814_at | TRNT1 | tRNA nucleotidyl transferase, CCA-adding, 1 | -0.19 | -0.43 | -0.23 | -0.13 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 231848_x_at | ZNF207 | zinc finger protein 207 | -0.16 | -0.28 | -0.26 | 0.02 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 231886_at | LOC10013482 | similar to hCG1739109 | -0.23 | -0.34 | -0.26 | -0.04 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 232002_at | GPI | glucose phosphate isomerase | -0.04 | -0.17 | -0.14 | 0.13 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 232688_at | BMP2K | BMP2 inducible kinase | -0.23 | -0.41 | -0.22 | -0.12 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 233239_at | ZNF407 | zinc finger protein 407 | -0.07 | -0.15 | -0.07 | 0.15 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 233248_at | C1orf43 | chromosome 1 open reading frame 43 | -0.32 | -0.41 | -0.33 | -0.11 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 239151_at | LOC399753 | hypothetical LOC399753 | -0.08 | -0.25 | 0.00 | 0.05 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 242228_at | BICD1 | bicaudal D homolog 1 (Drosophila) | -0.44 | -0.53 | -0.42 | -0.23 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 242261_at | IREB2 | iron-responsive element binding protein 2 | -0.23 | -0.27 | -0.24 | 0.04 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 244847_at | FAM13B | family with sequence similarity 13, member B | -0.77 | -0.74 | -0.66 | -0.44 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1552627_a_at | ARHGAP5 | Rho GTPase activating protein 5 | -0.65 | -0.54 | -0.56 | -0.23 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1557409_at | SPG7 | spastic paraplegia 7 (pure and complicated autosomal recessiv | -0.27 | -0.29 | -0.25 | 0.02 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1557581_x_at | CABIN1 | calcineurin binding protein 1 | -0.16 | -0.19 | -0.21 | 0.12 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1558922_at | Tia1 | TIA1 cytotoxic granule-associated RNA binding protein | -0.23 | -0.23 | -0.19 | 0.08 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1560013_at | PDXDC1 | pyridoxal-dependent decarboxylase domain containing 1 | -0.19 | -0.25 | -0.22 | 0.06 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1560676_at | SIAH3 | seven in absentia homolog 3 (Drosophila) | 0.53 | 0.69 | 0.75 | 1.00 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1560779_a_at | ZNF568 | Zinc finger protein 568 | -0.03 | -0.17 | -0.11 | 0.15 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1563051_at | OSBP | oxysterol binding protein | -0.07 | -0.09 | -0.05 | 0.22 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1569706_at | MYSM1 | Myb-like, SWIRM and MPN domains 1 | -0.36 | -0.48 | -0.34 | -0.16 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 215398_at | Cdc73 | cell division cycle 73, Paf1/RNA polymerase II complex compor | -0.30 | -0.36 | -0.37 | -0.05 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 215626_at | dock9 | dedicator of cytokinesis 9 | 0.09 | 0.06 | 0.15 | 0.36 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 215991_s_at | KIAA0090 | KIAA0090 | -0.48 | -0.59 | -0.46 | -0.27 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 217529_at | ORAI2 | ORAI calcium release-activated calcium modulator 2 | -0.64 | -0.66 | -0.62 | -0.36 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 221231_s_at | C14orf102 | chromosome 14 open reading frame 102 | -0.23 | -0.31 | -0.25 | -0.01 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 222412_s_at | SSR3 | signal sequence receptor, gamma (translocon-associated prote | -0.85 | -0.97 | -0.85 | -0.66 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 222906_at | FLVCR1 | feline leukemia virus subgroup C cellular receptor 1 | -0.19 | -0.27 | -0.18 | 0.04 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 234643_x_at | ACSM1 | acyl-CoA synthetase medium-chain family member 1 | -0.37 | -0.35 | -0.35 | -0.05 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 234645_at | MAML2 | mastermind-like 2 (Drosophila) | -0.22 | -0.32 | -0.35 | -0.01 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 237377_at | IGF1R | insulin-like growth factor 1 receptor | -0.23 | -0.26 | -0.20 | 0.04 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 237877_at | POLH | polymerase (DNA directed), eta | -0.63 | -0.70 | -0.68 | -0.39 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 239635_at | RBM14 | RNA binding motif protein 14 | -0.31 | -0.45 | -0.34 | -0.14 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 239936_at | DLEU2 | deleted in lymphocytic leukemia 2 (non-protein coding) | -0.49 | -0.74 | -0.55 | -0.43 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 239963_at | --- | --- | 0.27 | 0.07 | 0.40 | 0.38 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 |
| 1557987_at | LOC641298 | SMG1 homolog, phosphatidylinositol 3-kinase-related kinase p | -0.61 | -0.45 | -0.55 | -0.13 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1559045_at | LOC10012828 | hypothetical LOC100128288 | -0.19 | -0.33 | -0.31 | -0.02 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1559201_a_at | ostf1 | osteoclast stimulating factor 1 | -0.32 | -0.33 | -0.22 | -0.02 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1559437_at | --- | --- | -0.12 | -0.22 | -0.10 | 0.09 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1559848_at | NSUN4 | NOP2/Sun domain family, member 4 | -0.28 | -0.35 | -0.29 | -0.03 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1565889_at | tab2 | mitogen-activated protein kinase kinase kinase 7 interacting pr | -0.17 | -0.26 | -0.25 | 0.07 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1569578_at | LOC10012826 | ankyrin repeat domain 11; hypothetical protein LOC100128265 | -0.34 | -0.24 | -0.28 | 0.08 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1569948_at | --- | --- | -0.35 | -0.44 | -0.38 | -0.12 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1570338_at | --- | --- | -0.55 | -0.85 | -0.64 | -0.53 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 |
| 204270_at | SKI | v-ski sarcoma viral oncogene homolog (avian) | -0.87 | -0.56 | -0.55 | -0.24 | 1 | 1 | -1 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 1 | 1 |
| 215137_at | --- | --- | -0.05 | -0.19 | -0.07 | 0.13 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 232665_x_at | SMURF1 | SMAD specific E3 ubiquitin protein ligase 1 | -0.37 | -0.49 | -0.50 | -0.17 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 233055_at | --- | --- | -0.17 | -0.28 | -0.22 | 0.04 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 233957_at | tab2 | mitogen-activated protein kinase kinase kinase 7 interacting pr | -0.88 | -0.68 | -0.59 | -0.37 | 1 | 1 | -1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 234112_at | Cblb | Cas-Br-M (murine) ecotropic retroviral transforming sequence | 0.08 | -0.21 | 0.01 | 0.10 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 |
| 238342_at | --- | --- | -0.24 | -0.33 | -0.27 | -0.01 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 239614_x_at | GLS | glutaminase | -0.33 | -0.21 | -0.31 | 0.11 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 241732_at | cdkal1 | CDK5 regulatory subunit associated protein 1-like 1 | -0.15 | -0.25 | -0.16 | 0.07 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 241860_at | STK17B | serine/threonine kinase 17b | -0.58 | -0.39 | -0.26 | -0.07 | 1 | 1 | -1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 241954_at | FDFT1 | Farnesyl-diphosphate farnesyltransferase 1 | -0.11 | -0.08 | -0.06 | 0.24 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 244872_at | RBBP4 | retinoblastoma binding protein 4 | -0.52 | -0.53 | -0.66 | -0.21 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1552633_at | ZNF101 | zinc finger protein 101 | 0.16 | 0.08 | 0.21 | 0.41 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1554057_at | LOC645676 | hypothetical LOC645676 | -0.13 | -0.35 | -0.14 | -0.02 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1557996_at | LOC10013283 | postmeiotic segregation increased 2-like 5-like | -0.33 | -0.44 | -0.43 | -0.11 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1558220_at | MUC20 | Mucin 20, cell surface associated | -0.33 | -0.44 | -0.36 | -0.11 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1558418_at | PIAS1 | protein inhibitor of activated STAT, 1 | -0.35 | -0.55 | -0.38 | -0.22 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1558802_at | TM2D1 | TM2 domain containing 1 | -0.30 | -0.41 | -0.33 | -0.09 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1559449_a_at | ZNF254 | Zinc finger protein 254 | -0.33 | -0.34 | -0.36 | -0.01 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1561973_at | SMARCC2 | SWI/SNF related, matrix associated, actin dependent regulator | -0.34 | -0.39 | -0.35 | -0.06 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1569041_at | JMJD1C | jumonji domain containing 1C | -0.23 | -0.37 | -0.38 | -0.04 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 207115_x_at | MBTD1 | mbt domain containing 1 | -0.15 | -0.23 | -0.23 | 0.10 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 207786_at | CYP2R1 | cytochrome P450, family 2, subfamily R, polypeptide 1 | 0.01 | -0.24 | -0.03 | 0.09 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 215252_at | DNAJC7 | DnaJ (Hsp40) homolog, subfamily C, member 7 | -0.44 | -0.48 | -0.39 | -0.15 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 215318_at | N4BP2L2-IT | N4BP2L2 intronic transcript (non-protein coding) | -0.47 | -0.48 | -0.56 | -0.15 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 216766_at | Prkce | protein kinase C, epsilon | -0.45 | -0.58 | -0.51 | -0.24 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 219574_at | MARCH1 | membrane-associated ring finger (C3HC4) 1 | 0.02 | -0.01 | 0.08 | 0.31 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 219980_at | C4orf29 | chromosome 4 open reading frame 29 | -0.15 | -0.25 | -0.21 | 0.09 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 232020_at | SMURF2 | SMAD specific E3 ubiquitin protein ligase 2 | -0.29 | -0.27 | -0.37 | 0.06 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 232338_at | ZNF431 | zinc finger protein 431 | -0.10 | -0.23 | -0.25 | 0.10 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 240720_at | --- | --- | -0.20 | -0.32 | -0.18 | 0.00 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1552621_at | POLR2J2 | polymerase (RNA) II (DNA directed) polypeptide J2 | -0.20 | -0.41 | -0.23 | -0.07 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1557293_at | LOC440993 | hypothetical LOC440993 | -0.50 | -0.49 | -0.57 | -0.16 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1557360_at | LRPPRC | leucine-rich PPR-motif containing | -0.03 | -0.16 | -0.06 | 0.18 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1557737_s_at | NKTR | natural killer-tumor recognition sequence | -0.13 | -0.24 | -0.30 | 0.10 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1558698_at | ZNF264 | zinc finger protein 264 | -0.52 | -0.68 | -0.52 | -0.35 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1560172_at | INTS10 | integrator complex subunit 10 | 0.00 | -0.10 | -0.07 | 0.24 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1564438_at | --- | --- | -0.94 | -1.07 | -0.97 | -0.74 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1569864_at | SERAC1 | serine active site containing 1 | -0.42 | -0.51 | -0.45 | -0.17 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 215043_s_at | SMA4 /// SMA | glucuronidase, beta pseudogene /// glucuronidase, beta pseud | -0.12 | -0.28 | -0.26 | 0.06 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 215191_at | KDM2A | lysine (K)-specific demethylase 2A | -0.57 | -0.72 | -0.76 | -0.38 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 215586_at | PPP3CB | protein phosphatase 3 (formerly 2B), catalytic subunit, beta isc | -0.44 | -0.47 | -0.42 | -0.13 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 217704_x_at | SUZ12P | Suppressor of zeste 12 homolog pseudogene | -0.23 | -0.34 | -0.22 | 0.00 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 232896_at | ERBB2IP | Erbb2 interacting protein | -0.26 | -0.39 | -0.32 | -0.05 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 233515_at | KRR1 | KRR1, small subunit (SSU) processome component, homolog (y | -0.10 | -0.19 | -0.12 | 0.15 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 238317_x_at | RBMS1 | RNA binding motif, single stranded interacting protein 1 | -0.32 | -0.27 | -0.10 | 0.07 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 241716_at | HSPD1 | heat shock 60kDa protein 1 (chaperonin) | -0.24 | -0.37 | -0.29 | -0.03 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 242433_at | ZBTB11 | zinc finger and BTB domain containing 11 | -0.11 | -0.32 | -0.12 | 0.02 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 243229_at | --- | --- | 0.17 | -0.16 | 0.14 | 0.18 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 |
| 1559490_at | LRCH3 | leucine-rich repeats and calponin homology (CH) domain conta | -0.22 | -0.33 | -0.25 | 0.02 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1560209_at | --- | --- | -0.25 | -0.37 | -0.25 | -0.02 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1560696_x_at | QTRTD1 | queuine tRNA-ribosyltransferase domain containing 1 | -0.42 | -0.62 | -0.44 | -0.27 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1561893_at | egln1 | egl nine homolog 1 (C. elegans) | -0.33 | -0.45 | -0.42 | -0.10 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1569392_at | TECR | trans-2,3-enoyl-CoA reductase | -0.13 | -0.27 | -0.17 | 0.08 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 210965_x_at | CDK13 | cyclin-dependent kinase 13 | -0.32 | -0.37 | -0.32 | -0.02 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 227891_s_at | TAF15 | TAF15 RNA polymerase II, TATA box binding protein (TBP)-asso | 0.01 | -0.16 | -0.06 | 0.19 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 234459_at | PPHLN1 | periphilin 1 | -0.07 | -0.23 | -0.10 | 0.12 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 236032_at | DNM1L | dynamin 1-like | 0.18 | 0.00 | 0.20 | 0.35 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 238079_at | TPM3 | tropomyosin 3 | -0.53 | -0.63 | -0.58 | -0.28 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 238769_at | MAP4K4 | mitogen-activated protein kinase kinase kinase kinase 4 | -0.23 | -0.23 | -0.08 | 0.12 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 238982_at | DENR | density-regulated protein | -0.20 | -0.26 | -0.16 | 0.10 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 241885_at | taf15 | TAF15 RNA polymerase II, TATA box binding protein (TBP)-asso | -0.20 | -0.29 | -0.22 | 0.06 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 242527_at | C18orf1 | chromosome 18 open reading frame 1 | -0.26 | -0.28 | -0.17 | 0.07 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1560443_at | SMCHD1 | structural maintenance of chromosomes flexible hinge domain | 0.06 | -0.25 | -0.08 | 0.11 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 |
| 1561092_at | klhdc4 | kelch domain containing 4 | 0.05 | -0.17 | 0.08 | 0.19 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1562270_at | ARHGEF7 | Rho guanine nucleotide exchange factor (GEF) 7 | -0.45 | -0.47 | -0.45 | -0.12 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1563724_at | SACS | spastic ataxia of Charlevoix-Saguenay (sacsin) | -0.05 | -0.23 | 0.01 | 0.13 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1564972_x_at | SETDB2 | SET domain, bifurcated 2 | 0.05 | -0.12 | 0.11 | 0.24 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1568858_at | ubfd1 | ubiquitin family domain containing 1 | -0.28 | -0.35 | -0.29 | 0.01 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 215330_at | FLJ43663 | hypothetical LOC378805 | -0.62 | -0.57 | -0.55 | -0.21 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 215986_at | --- | --- | -0.62 | -0.74 | -0.69 | -0.38 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 233724_at | ARNT | aryl hydrocarbon receptor nuclear translocator | -0.47 | -0.61 | -0.52 | -0.25 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 239008_at | NCRNA00182 | Non-protein coding RNA 182 | -1.18 | -0.92 | -0.83 | -0.56 | 1 | 1 | -1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 243067_at | --- | --- | -0.04 | -0.28 | -0.01 | 0.08 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 243673_at | RBM41 | RNA binding motif protein 41 | -0.25 | -0.39 | -0.37 | -0.03 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1556318_s_at | CAND1 | cullin-associated and neddylation-dissociated 1 | -0.10 | -0.24 | -0.19 | 0.13 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1557551_at | Cyth1 | cytohesin 1 | -0.52 | -0.56 | -0.59 | -0.19 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1560814_a_at | C15orf57 | chromosome 15 open reading frame 57 | -0.50 | -0.45 | -0.47 | -0.08 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1566980_at | MAPK1IP1L | mitogen-activated protein kinase 1 interacting protein 1-like | -0.29 | -0.52 | -0.31 | -0.15 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1569527_at | STAU1 | staufen, RNA binding protein, homolog 1 (Drosophila) | -0.37 | -0.51 | -0.49 | -0.14 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 215555_at | C1orf63 | chromosome 1 open reading frame 63 | -0.18 | -0.31 | -0.18 | 0.06 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 232759_at | Invs | inversin | -0.03 | -0.20 | -0.19 | 0.17 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 235442_at | CXorf56 | chromosome X open reading frame 56 | -0.74 | -0.79 | -0.60 | -0.42 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 237586_at | EPS15 | epidermal growth factor receptor pathway substrate 15 | -0.50 | -0.43 | -0.36 | -0.06 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 239651_at | ANAPC5 | anaphase promoting complex subunit 5 | -0.14 | -0.03 | -0.02 | 0.33 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 241723_at | IQGAP2 | IQ motif containing GTPase activating protein 2 | -0.16 | -0.31 | -0.20 | 0.05 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 242879_x_at | Akt3 | v-akt murine thymoma viral oncogene homolog 3 (protein kina | -0.70 | -0.65 | -0.66 | -0.28 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1556849_at | Rnf38 | ring finger protein 38 | -0.14 | -0.20 | -0.19 | 0.18 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1557289_s_at | GTF2IRD2 | GTF2I repeat domain containing 2 | -0.09 | -0.16 | -0.06 | 0.22 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1558719_s_at | RPAIN | RPA interacting protein | 0.05 | -0.26 | -0.03 | 0.12 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 |
| 1559039_at | DHX36 | DEAH (Asp-Glu-Ala-His) box polypeptide 36 | -0.08 | -0.17 | -0.12 | 0.21 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1560349_at | COMMD10 | COMM domain containing 10 | -0.25 | -0.48 | -0.29 | -0.09 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 208154_at | --- | --- | -0.24 | -0.32 | -0.25 | 0.06 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 213650_at | LOC10050974 | Golgin subfamily A member 8B-like | -0.03 | -0.16 | 0.03 | 0.22 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 215866_at | EEF1G | eukaryotic translation elongation factor 1 gamma | -0.36 | -0.60 | -0.42 | -0.21 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 216983_s_at | ZNF224 | zinc finger protein 224 | -0.23 | -0.45 | -0.27 | -0.07 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 220216_at | C8orf44 | chromosome 8 open reading frame 44 | -0.43 | -0.58 | -0.53 | -0.21 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 231979_at | --- | --- | -0.32 | -0.43 | -0.40 | -0.05 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 239937_at | ZNF207 | Zinc finger protein 207 | -0.02 | -0.20 | -0.12 | 0.18 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 241788_x_at | actn4 | actinin, alpha 4 | -0.76 | -0.92 | -0.76 | -0.54 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1555379_at | FAM159A | family with sequence similarity 159, member A | -0.26 | -0.34 | -0.14 | 0.05 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1556462_a_at | Klf12 | Kruppel-like factor 12 | 0.06 | -0.26 | 0.18 | 0.13 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 |
| 1557145_at | STK38 | Serine/threonine kinase 38 | -0.13 | -0.23 | -0.14 | 0.16 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1562161_at | --- | --- | -0.17 | -0.30 | -0.19 | 0.09 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1564639_at | LOC389906 | Similar to Serine/threonine-protein kinase PRKX (Protein kinas | -0.18 | -0.28 | -0.18 | 0.11 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1564640_at | MGA | MAX gene associated | -0.28 | -0.46 | -0.36 | -0.08 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1565810_at | Ppp3r1 | protein phosphatase 3 (formerly 2B), regulatory subunit B, alph | -0.58 | -0.63 | -0.51 | -0.24 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 207474_at | SNRK | SNF related kinase | -0.09 | -0.24 | -0.16 | 0.14 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 210867_at | CNOT4 | CCR4-NOT transcription complex, subunit 4 | -0.36 | -0.52 | -0.44 | -0.12 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 215123_at | NPIPL3 | nuclear pore complex interacting protein-like 3 | -0.46 | -0.59 | -0.49 | -0.19 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 216850_at | SNRPN | small nuclear ribonucleoprotein polypeptide N | -0.07 | -0.30 | -0.02 | 0.09 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 220586_at | CHD9 | chromodomain helicase DNA binding protein 9 | -0.26 | -0.38 | -0.36 | 0.01 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 231829_at | MAVS | mitochondrial antiviral signaling protein | -0.33 | -0.50 | -0.36 | -0.11 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 236887_at | KIN | KIN, antigenic determinant of recA protein homolog (mouse) | -0.54 | -0.67 | -0.63 | -0.27 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 242549_at | PRKD3 | protein kinase D3 | -0.38 | -0.42 | -0.30 | -0.03 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 243360_at | Tmed4 | transmembrane emp24 protein transport domain containing 4 | -0.48 | -0.58 | -0.48 | -0.19 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1554948_at | --- | --- | -0.83 | -0.95 | -0.95 | -0.55 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1558515_at | NCRNA00182 | non-protein coding RNA 182 | -0.79 | -0.78 | -0.86 | -0.38 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1562238_at | USPL1 | ubiquitin specific peptidase like 1 | -0.04 | -0.28 | -0.04 | 0.12 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1564753_at | LASS6 | LAG1 homolog, ceramide synthase 6 | 0.34 | 0.14 | 0.32 | 0.54 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1566040_at | LOC10028865 | Similar to hCG2003116 | 0.00 | -0.14 | -0.04 | 0.27 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 215308_at | XRCC6 | X-ray repair complementing defective repair in Chinese hamst | -0.48 | -0.73 | -0.45 | -0.33 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 216813_at | --- | --- | -0.80 | -0.90 | -0.85 | -0.50 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 219341_at | CLN8 | ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with m | -1.32 | -1.55 | -1.36 | -1.16 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 223036_at | FARSB | phenylalanyl-tRNA synthetase, beta subunit | -0.13 | -0.30 | -0.23 | 0.10 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 232330_at | C7orf44 | chromosome 7 open reading frame 44 | -0.07 | -0.07 | -0.05 | 0.33 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 232879_at | CRTC3 | CREB regulated transcription coactivator 3 | -0.16 | -0.32 | -0.24 | 0.08 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 235028_at | --- | --- | -0.43 | -0.65 | -0.67 | -0.25 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 238393_at | bmpr2 | bone morphogenetic protein receptor, type II (serine/threonin | -1.12 | -1.26 | -1.16 | -0.85 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 243796_at | Hexim2 | hexamthylene bis-acetamide inducible 2 | -0.33 | -0.54 | -0.24 | -0.15 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 243876_at | Fnbp1 | formin binding protein 1 | -0.22 | -0.29 | -0.18 | 0.11 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 244418_at | RTN3 | reticulon 3 | -0.89 | -0.98 | -0.82 | -0.59 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1557527_at | Runx1 | runt-related transcription factor 1 | -1.56 | -1.69 | -1.72 | -1.28 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 205010_at | GNL3L | guanine nucleotide binding protein-like 3 (nucleolar)-like | -0.47 | -0.69 | -0.49 | -0.28 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 211459_at | MAP3K2 | mitogen-activated protein kinase kinase kinase 2 | -0.79 | -0.93 | -0.93 | -0.52 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 215012_at | ZNF451 | zinc finger protein 451 | 0.02 | -0.21 | -0.09 | 0.20 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 215375_x_at | LRRFIP1 | Leucine rich repeat (in FLII) interacting protein 1 | -0.86 | -0.94 | -0.83 | -0.53 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 215558_at | UBR2 | ubiquitin protein ligase E3 component n-recognin 2 | -0.30 | -0.50 | -0.44 | -0.09 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 220338_at | RALGPS2 | Ral GEF with PH domain and SH3 binding motif 2 | -0.06 | -0.28 | -0.14 | 0.13 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 238723_at | ATXN3 | ataxin 3 | -0.55 | -0.71 | -0.68 | -0.30 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1552787_at | HELB | helicase (DNA) B | -0.44 | -0.59 | -0.41 | -0.17 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1553726_s_at | C6orf170 | chromosome 6 open reading frame 170 | -0.25 | -0.46 | -0.38 | -0.03 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1559025_at | SEPT9 | septin 9 | -0.15 | -0.25 | -0.10 | 0.18 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1560112_at | WDFY2 | WD repeat and FYVE domain containing 2 | -0.28 | -0.42 | -0.35 | 0.00 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1563364_at | --- | --- | -0.15 | -0.35 | -0.31 | 0.07 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1566966_at | DPYD | dihydropyrimidine dehydrogenase | -0.74 | -0.95 | -0.82 | -0.53 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 239405_at | RAB7A | RAB7A, member RAS oncogene family | -0.99 | -1.06 | -1.01 | -0.63 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 242126_at | ext1 | exostoses (multiple) 1 | -0.15 | -0.30 | -0.08 | 0.12 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 242182_x_at | ITCH | itchy E3 ubiquitin protein ligase homolog (mouse) | -0.43 | -0.57 | -0.52 | -0.15 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1554478_a_at | HEATR3 | HEAT repeat containing 3 | -0.86 | -0.84 | -0.76 | -0.41 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1556658_a_at | Mbnl1 | muscleblind-like (Drosophila) | -0.07 | -0.31 | -0.23 | 0.12 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1557270_at | --- | --- | -0.24 | -0.45 | -0.35 | -0.02 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1560662_s_at | WHAMML1 //, | WAS protein homolog associated with actin, golgi membranes | 0.15 | -0.04 | 0.19 | 0.39 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1561733_at | INPP5A | inositol polyphosphate-5-phosphatase, 40kDa | -0.25 | -0.48 | -0.28 | -0.05 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1564424_at | Esyt2 | family with sequence similarity 62 (C2 domain containing), me | 0.04 | -0.23 | -0.02 | 0.20 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 205594_at | ZNF652 | zinc finger protein 652 | -0.59 | -0.72 | -0.64 | -0.29 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 215390_at | c9orf5 | chromosome 9 open reading frame 5 | -0.25 | -0.44 | -0.36 | -0.01 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 217534_at | FAM49B | family with sequence similarity 49, member B | -0.49 | -0.66 | -0.55 | -0.23 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 232466_at | CUL4A | Cullin 4A | -0.11 | -0.28 | -0.22 | 0.15 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 235030_at | FAM55C | family with sequence similarity 55, member C | -0.70 | -0.71 | -0.58 | -0.28 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 235058_at | GPN2 | GPN-loop GTPase 2 | -0.36 | -0.54 | -0.37 | -0.11 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 236944_at | --- | --- | -0.11 | -0.38 | -0.18 | 0.05 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 242576_x_at | N4BP2L2 | NEDD4 binding protein 2-like 2 | -0.28 | -0.49 | -0.34 | -0.05 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 242797_x_at | zfr | zinc finger RNA binding protein | -0.39 | -0.57 | -0.58 | -0.14 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1557580_at | CABIN1 | calcineurin binding protein 1 | -0.29 | -0.30 | -0.34 | 0.13 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1562250_at | SEMA4D | sema domain, immunoglobulin domain (Ig), transmembrane d | -0.21 | -0.29 | -0.26 | 0.15 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1562467_at | ppp3ca | protein phosphatase 3 (formerly 2B), catalytic subunit, alpha is | -0.74 | -0.95 | -0.79 | -0.51 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 216765_at | MAP2K5 | Mitogen-activated protein kinase kinase 5 | -0.35 | -0.53 | -0.34 | -0.09 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 232295_at | GFM1 | G elongation factor, mitochondrial 1 | -0.24 | -0.38 | -0.36 | 0.06 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 233554_at | UBAC2 | UBA domain containing 2 | -0.04 | -0.29 | -0.21 | 0.15 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 242423_x_at | --- | --- | -0.30 | -0.47 | -0.30 | -0.03 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1563173_at | --- | --- | -0.16 | -0.35 | -0.04 | 0.11 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1564820_at | LOC10013081 | RAB6C, member RAS oncogene family; RAB6A, member RAS or | -0.75 | -0.83 | -0.80 | -0.37 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1569538_at | --- | --- | -0.70 | -0.76 | -0.72 | -0.31 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 207735_at | RNF125 | ring finger protein 125 | -0.03 | -0.46 | -0.21 | -0.01 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 |
| 212172_at | AK2 | adenylate kinase 2 | -0.17 | -0.34 | -0.25 | 0.12 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 216373_at | TAPT1 | transmembrane anterior posterior transformation 1 | -0.48 | -0.49 | -0.38 | -0.04 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 222319_at | nap1l4 | nucleosome assembly protein 1-like 4 | -0.15 | -0.40 | -0.28 | 0.05 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 224098_at | ABAT | 4-aminobutyrate aminotransferase | -0.84 | -0.91 | -0.83 | -0.46 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 234149_at | THRAP3 | thyroid hormone receptor associated protein 3 | -0.62 | -0.75 | -0.67 | -0.30 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 243023_at | --- | --- | -0.09 | -0.23 | -0.02 | 0.22 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 244010_at | MLL3 | myeloid/lymphoid or mixed-lineage leukemia 3 | -0.41 | -0.60 | -0.53 | -0.15 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1555199_at | GOSR1 | golgi SNAP receptor complex member 1 | -0.63 | -0.78 | -0.74 | -0.31 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1562307_at | RNF24 | ring finger protein 24 | -0.97 | -1.20 | -1.13 | -0.73 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1570571_at | CCDC91 | Coiled-coil domain containing 91 | -0.25 | -0.42 | -0.30 | 0.04 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 214918_at | HNRNPM | heterogeneous nuclear ribonucleoprotein M | -0.54 | -0.56 | -0.50 | -0.11 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 215474_at | NSMCE2 | non-SMC element 2, MMS21 homolog (S. cerevisiae) | -0.74 | -0.92 | -0.69 | -0.45 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 224031_at | STK17A | serine/threonine kinase 17a | -0.27 | -0.38 | -0.13 | 0.08 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1552867_at | zmym2 | zinc finger, MYM-type 2 | -0.73 | -0.88 | -0.92 | -0.40 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1559139_at | NOC2L | nucleolar complex associated 2 homolog (S. cerevisiae) | -0.11 | -0.34 | -0.19 | 0.13 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1559987_at | MSI2 | musashi homolog 2 (Drosophila) | -0.30 | -0.46 | -0.28 | 0.01 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1570415_at | DDX52 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 52 | -0.31 | -0.54 | -0.31 | -0.07 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 205238_at | TRMT2B | TRM2 tRNA methyltransferase 2 homolog B (S. cerevisiae) | -0.45 | -0.70 | -0.53 | -0.23 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 208077_at | C9orf38 | chromosome 9 open reading frame 38 | 0.51 | 0.17 | 0.65 | 0.64 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 |
| 239453_at | Fnbp1 | formin binding protein 1 | -0.15 | -0.36 | -0.13 | 0.11 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1564970_at | SETDB2 | SET domain, bifurcated 2 | -0.08 | -0.25 | -0.04 | 0.23 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1569311_at | --- | --- | -0.21 | -0.46 | -0.35 | 0.02 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 212182_at | NUDT4 /// NU | nudix (nucleoside diphosphate linked moiety X)-type motif 4 // | -0.18 | -0.36 | -0.12 | 0.12 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 215900_at | PPPDE1 | PPPDE peptidase domain containing 1 | -0.42 | -0.64 | -0.45 | -0.16 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 232535_at | --- | --- | -0.66 | -0.86 | -0.63 | -0.37 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1557512_at | CLIP1 | CAP-GLY domain containing linker protein 1 | -0.61 | -0.92 | -0.69 | -0.42 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1557562_at | GRIPAP1 | GRIP1 associated protein 1 | -0.54 | -0.70 | -0.55 | -0.20 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 205727_at | TEP1 | telomerase-associated protein 1 | -0.68 | -0.98 | -0.72 | -0.48 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 215889_at | SKIL | SKI-like oncogene | -1.26 | -1.20 | -0.90 | -0.71 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 235220_at | YIPF4 | Yip1 domain family, member 4 | -0.69 | -0.79 | -0.69 | -0.28 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 215029_at | AKIRIN1 | akirin 1 | -0.60 | -0.90 | -0.77 | -0.39 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1556657_at | Mbnl1 | muscleblind-like (Drosophila) | -0.12 | -0.49 | -0.31 | 0.03 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1562412_at | GPR89A /// GI | G protein-coupled receptor 89C; G protein-coupled receptor 8 | -0.29 | -0.34 | -0.18 | 0.18 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 236237_at | kiaa1370 | KIAA1370 | 0.15 | -0.09 | 0.14 | 0.42 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 236985_at | EIF4BP7 /// EI | similar to eukaryotic translation initiation factor 4H; eukaryotic | -0.42 | -0.58 | -0.30 | -0.06 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 238785_at | --- | --- | -0.67 | -0.83 | -0.53 | -0.31 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1566191_at | SUZ12 | Suppressor of zeste 12 homolog (Drosophila) | -0.45 | -0.64 | -0.53 | -0.11 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1570249_x_at | GNB1 | guanine nucleotide binding protein (G protein), beta polypepti | -0.75 | -0.92 | -0.72 | -0.38 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 210556_at | NFATC3 | nuclear factor of activated T-cells, cytoplasmic, calcineurin-dep | -0.23 | -0.43 | -0.28 | 0.09 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 233866_at | KLHL5 | kelch-like 5 (Drosophila) | -0.46 | -0.57 | -0.39 | -0.04 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 235061_at | PPM1K | protein phosphatase, Mg2+/Mn2+ dependent, 1K | -0.11 | -0.33 | -0.18 | 0.19 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 238931_at | METT10D | methyltransferase 10 domain containing | -0.44 | -0.73 | -0.39 | -0.19 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1569540_at | nlk | nemo-like kinase | -0.50 | -0.79 | -0.66 | -0.26 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1554306_at | ITPKB | inositol 1,4,5-trisphosphate 3-kinase B | -0.55 | -0.66 | -0.52 | -0.11 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1560048_at | --- | --- | -0.46 | -0.74 | -0.56 | -0.19 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 215175_at | PCNX | pecanex homolog (Drosophila) | -0.61 | -0.84 | -0.60 | -0.27 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 232861_at | PDP2 | pyruvate dehyrogenase phosphatase catalytic subunit 2 | -0.79 | -0.71 | -0.79 | -0.15 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 235551_at | WDR4 | WD repeat domain 4 | -0.59 | -0.73 | -0.64 | -0.17 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1555317_at | POLK | polymerase (DNA directed) kappa | -0.43 | -0.74 | -0.46 | -0.17 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 234148_at | LRRC8D | leucine rich repeat containing 8 family, member D | -0.33 | -0.46 | -0.38 | 0.11 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 243134_at | --- | --- | -0.47 | -0.65 | -0.51 | -0.09 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 220900_at | --- | --- | -0.42 | -0.77 | -0.38 | -0.18 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 242974_at | CD47 | CD47 molecule | 0.04 | -0.36 | -0.06 | 0.23 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 0 |
| 207286_at | CEP135 | centrosomal protein 135kDa | -0.10 | -0.41 | -0.20 | 0.19 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1570248_at | GNB1 | guanine nucleotide binding protein (G protein), beta polypepti | -0.83 | -1.02 | -0.87 | -0.42 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1569312_at | ZNF146 | zinc finger protein 146 | -0.37 | -0.70 | -0.43 | -0.08 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 242691_at | --- | --- | -1.19 | -1.33 | -1.24 | -0.71 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 217594_at | ZCCHC11 | zinc finger, CCHC domain containing 11 | -0.75 | -0.84 | -0.81 | -0.21 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 241879_at | LPP | LIM domain containing preferred translocation partner in lipor | -0.82 | -1.20 | -0.84 | -0.57 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1565743_at | N4BP2L2 | NEDD4 binding protein 2-like 2 | -0.52 | -0.90 | -0.74 | -0.26 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 215659_at | GSDMB | Gasdermin B | -0.22 | -0.44 | -0.28 | 0.20 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1558710_at | ARIH1 | ariadne homolog, ubiquitin-conjugating enzyme E2 binding pro | -0.29 | -0.57 | -0.32 | 0.08 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 216121_at | PUM2 | pumilio homolog 2 (Drosophila) | -0.87 | -1.13 | -0.64 | -0.47 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 206088_at | LRRC37A3 | leucine rich repeat containing 37, member A3 | -0.32 | -0.63 | -0.31 | 0.04 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 210858_x_at | ATM | ataxia telangiectasia mutated | -0.58 | -0.79 | -0.49 | -0.10 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1562283_at | MAPK1 | mitogen-activated protein kinase 1 | -1.20 | -1.53 | -1.43 | -0.83 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 215648_at | NUDCD3 | NudC domain containing 3 | -0.38 | -0.63 | -0.44 | 0.07 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1562028_at | CCND3 | Cyclin D3 | 0.07 | -0.27 | -0.10 | 0.44 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 208442_s_at | ATM | ataxia telangiectasia mutated | -0.62 | -0.96 | -0.54 | -0.19 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 232365_at | SIAH1 | seven in absentia homolog 1 (Drosophila) | -1.02 | -1.36 | -1.08 | -0.56 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1560776_at | Fam18b2 /// f | family with sequence similarity 18, member B2; family with se | -0.44 | -0.82 | -0.51 | 0.04 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 235086_at | THBS1 | thrombospondin 1 | 0.28 | -0.35 | -1.01 | -1.32 | 1 | 1 | 1 | 0 | 0 | -1 | 1 | 1 | 0 | 0 | 0 | 1 |
| 201743_at | CD14 | CD14 molecule | -1.83 | -2.29 | -2.98 | -3.04 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 201109_s_at | THBS1 | thrombospondin 1 | -0.02 | -0.64 | -0.97 | -1.34 | 1 | 1 | 1 | 0 | 0 | -1 | 1 | 1 | 0 | 0 | 0 | 1 |
| 220416_at | ATP8B4 | ATPase, class I, type 8B, member 4 | -1.64 | -1.82 | -2.46 | -2.49 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 201110_s_at | THBS1 | thrombospondin 1 | -0.03 | -0.48 | -0.95 | -1.13 | 1 | 1 | 1 | 0 | 0 | -1 | 1 | 1 | 0 | 0 | 0 | 1 |
| 203887_s_at | THBD | thrombomodulin | -1.91 | -2.39 | -2.97 | -3.03 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 201506_at | TGFBI | transforming growth factor, beta-induced, 68kDa | -3.09 | -3.47 | -3.78 | -4.10 | 1 | 1 | 1 | 0 | 0 | -1 | 1 | 1 | 0 | 0 | 0 | 1 |
| 218469_at | GREM1 | gremlin 1 | -3.08 | -3.22 | -4.15 | -3.83 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 220088_at | C5AR1 | complement component 5a receptor 1 | -1.54 | -1.87 | -2.33 | -2.46 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 202877_s_at | CD93 | CD93 molecule | -0.72 | -1.07 | -1.33 | -1.64 | 1 | 1 | 1 | 0 | 0 | -1 | 1 | 1 | 0 | 0 | 0 | 1 |
| 202878_s_at | CD93 | CD93 molecule | -0.87 | -1.29 | -1.78 | -1.87 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 206569_at | IL24 | interleukin 24 | 0.28 | -0.06 | -0.24 | -0.60 | 1 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 212154_at | SDC2 | syndecan 2 | -2.11 | -2.55 | -2.93 | -3.07 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 201108_s_at | THBS1 | thrombospondin 1 | 0.04 | -0.26 | -0.38 | -0.79 | 1 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 218559_s_at | MAFB | v-maf musculoaponeurotic fibrosarcoma oncogene homolog B | -0.92 | -1.37 | -1.71 | -1.89 | 1 | 1 | 1 | 0 | 0 | -1 | 1 | 1 | 0 | 0 | 0 | 1 |
| 211307_s_at | FCAR | Fc fragment of IgA, receptor for | -0.88 | -1.16 | -1.34 | -1.66 | 1 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 205767_at | EREG | epiregulin | 0.06 | 0.04 | -0.61 | -0.44 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 207674_at | FCAR | Fc fragment of IgA, receptor for | -0.87 | -1.17 | -1.62 | -1.64 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 210146_x_at | LILRB2 | leukocyte immunoglobulin-like receptor, subfamily B (with TM | -1.45 | -1.68 | -1.93 | -2.15 | 1 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 207852_at | CXCL5 | chemokine (C-X-C motif) ligand 5 | -0.34 | -0.79 | -0.97 | -1.25 | 1 | 1 | 1 | 0 | 0 | -1 | 1 | 1 | 0 | 0 | 0 | 1 |
| 230748_at | SLC16A6 | solute carrier family 16, member 6 (monocarboxylic acid trans | -1.42 | -1.65 | -2.09 | -2.09 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 204924_at | TLR2 | toll-like receptor 2 | -0.58 | -0.88 | -1.28 | -1.31 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 202888_s_at | ANPEP | alanyl (membrane) aminopeptidase | -1.46 | -1.77 | -2.15 | -2.20 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 206710_s_at | EPB41L3 | erythrocyte membrane protein band 4.1-like 3 | -1.32 | -1.57 | -1.85 | -1.99 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 212681_at | EPB41L3 | erythrocyte membrane protein band 4.1-like 3 | -1.30 | -1.52 | -1.88 | -1.94 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 213338_at | TMEM158 | transmembrane protein 158 (gene/pseudogene) | -0.44 | -0.61 | -1.10 | -1.03 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 214183_s_at | TKTL1 | transketolase-like 1 | -2.55 | -2.90 | -3.09 | -3.32 | 1 | 1 | 1 | 0 | 0 | -1 | 1 | 1 | 0 | 0 | 0 | 1 |
| 214974_x_at | CXCL5 | chemokine (C-X-C motif) ligand 5 | -0.18 | -0.50 | -0.85 | -0.92 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 202856_s_at | SLC16A3 | solute carrier family 16, member 3 (monocarboxylic acid trans | -1.26 | -1.04 | -1.20 | -1.44 | 1 | 1 | 0 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 219607_s_at | MS4A4A | membrane-spanning 4-domains, subfamily A, member 4 | -3.52 | -3.77 | -3.95 | -4.17 | 1 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 223344_s_at | MS4A7 | membrane-spanning 4-domains, subfamily A, member 7 | -1.07 | -1.29 | -1.43 | -1.69 | 1 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1559910_at | PID1 | phosphotyrosine interaction domain containing 1 | -1.08 | -1.34 | -1.72 | -1.73 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 206214_at | PLA2G7 | phospholipase A2, group VII (platelet-activating factor acetylhy | -2.72 | -3.05 | -3.19 | -3.43 | 1 | 1 | 1 | 0 | 0 | -1 | 1 | 1 | 0 | 0 | 0 | 1 |
| 226066_at | MITF | microphthalmia-associated transcription factor | -1.65 | -1.71 | -2.33 | -2.10 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 219434_at | TREM1 | triggering receptor expressed on myeloid cells 1 | -1.88 | -2.07 | -2.45 | -2.45 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 239336_at | Thbs1 | thrombospondin 1 | -0.04 | -0.02 | -0.05 | -0.41 | 1 | 1 | 0 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 208303_s_at | CRLF2 | cytokine receptor-like factor 2 | -0.64 | -0.56 | -0.71 | -0.92 | 1 | 1 | 0 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 222877_at | NRP2 | neuropilin 2 | -1.34 | -1.06 | -1.43 | -1.42 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 |
| 1562194_at | Zeb2 | zinc finger E-box binding homeobox 2 | -0.89 | -0.88 | -1.01 | -1.23 | 1 | 1 | 0 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 235751_s_at | VMO1 | vitelline membrane outer layer 1 homolog (chicken) | -1.72 | -1.96 | -2.09 | -2.32 | 1 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 204122_at | TYROBP | TYRO protein tyrosine kinase binding protein | -1.53 | -1.75 | -2.06 | -2.09 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 204232_at | FCER1G | Fc fragment of IgE, high affinity I, receptor for; gamma polyper | -1.48 | -1.67 | -1.82 | -2.00 | 1 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 217997_at | PHLDA1 | pleckstrin homology-like domain, family A, member 1 | -1.60 | -1.78 | -2.13 | -2.11 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 223343_at | MS4A7 | membrane-spanning 4-domains, subfamily A, member 7 | -1.16 | -1.34 | -1.53 | -1.67 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1554899_s_at | FCER1G | Fc fragment of IgE, high affinity I, receptor for; gamma polyper | -1.58 | -1.79 | -1.93 | -2.11 | 1 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 204015_s_at | DUSP4 | dual specificity phosphatase 4 | -0.91 | -1.16 | -1.21 | -1.48 | 1 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 234932_s_at | CDCP1 | CUB domain containing protein 1 | -0.04 | -0.07 | -0.12 | -0.39 | 1 | 1 | 0 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 202855_s_at | SLC16A3 | solute carrier family 16, member 3 (monocarboxylic acid trans | -1.35 | -1.22 | -1.34 | -1.52 | 1 | 1 | 0 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 206881_s_at | LILRA3 | leukocyte immunoglobulin-like receptor, subfamily A (without | -0.76 | -0.95 | -0.97 | -1.26 | 1 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 211816_x_at | FCAR | Fc fragment of IgA, receptor for | -0.48 | -0.64 | -0.65 | -0.96 | 1 | 1 | 0 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 224480_s_at | AGPAT9 | 1-acylglycerol-3-phosphate O-acyltransferase 9 | -1.65 | -1.58 | -2.11 | -1.89 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 1 | 1 | 0 | 0 | 0 |
| 200730_s_at | PTP4A1 | protein tyrosine phosphatase type IVA, member 1 | 0.02 | 0.09 | -0.01 | -0.21 | 1 | 1 | 0 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 219558_at | ATP13A3 | ATPase type 13A3 | -1.37 | -1.01 | -1.23 | -1.32 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 |
| 226034_at | DUSP4 | dual specificity phosphatase 4 | -1.02 | -1.17 | -1.27 | -1.47 | 1 | 1 | 0 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1553396_a_at | CCDC13 | coiled-coil domain containing 13 | 0.45 | 0.76 | 0.58 | 0.47 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 |
| 1570364_at | ZNF709 | zinc finger protein 709 | 0.32 | 0.57 | 0.24 | 0.28 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 |
| 222670_s_at | MAFB | v-maf musculoaponeurotic fibrosarcoma oncogene homolog B | -0.77 | -1.10 | -1.25 | -1.39 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | 1 |
| 210773_s_at | FPR2 | formyl peptide receptor 2 | -0.81 | -1.07 | -0.94 | -1.35 | 1 | 1 | 0 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 205126_at | VRK2 | vaccinia related kinase 2 | -1.07 | -1.26 | -1.42 | -1.53 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 224829_at | CPEB4 | cytoplasmic polyadenylation element binding protein 4 | -0.87 | -0.69 | -0.86 | -0.96 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1560225_at | CNR1 | Cannabinoid receptor 1 (brain) | -0.34 | -0.27 | -0.25 | -0.01 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1560762_at | LOC285972 | hypothetical LOC285972 | -0.30 | -0.06 | -0.18 | 0.20 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1560869_a_at | --- | --- | -1.83 | -1.72 | -1.75 | -1.45 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1561654_at | LIMK2 | LIM domain kinase 2 | -0.13 | -0.18 | -0.15 | 0.10 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1566825_at | --- | --- | -0.41 | -0.27 | -0.33 | 0.00 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1570507_at | SFRS2IP | Splicing factor, arginine/serine-rich 2, interacting protein | 0.11 | -0.06 | 0.12 | 0.21 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 227168_at | MIAT | myocardial infarction associated transcript (non-protein coding | 0.41 | 0.39 | 0.40 | 0.67 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 204866_at | PHF16 | PHD finger protein 16 | -0.39 | -0.30 | -0.34 | -0.01 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 205174_s_at | QPCT | glutaminyl-peptide cyclotransferase | -1.83 | -1.78 | -1.85 | -1.50 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 207533_at | CCL1 | chemokine (C-C motif) ligand 1 | 0.41 | 0.66 | 0.54 | 0.94 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 215170_s_at | CEP152 | centrosomal protein 152kDa | -0.16 | -0.25 | -0.32 | 0.03 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 |
| 244219_at | WTAP | Wilms tumor 1 associated protein | -0.13 | -0.41 | -0.18 | -0.13 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 |
| 244546_at | CYCS | cytochrome c, somatic | -0.46 | -0.35 | -0.42 | -0.07 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1559762_at | --- | --- | -0.18 | -0.17 | -0.08 | 0.12 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1566603_s_at | RPUSD3 | RNA pseudouridylate synthase domain containing 3 | -0.33 | -0.27 | -0.28 | 0.02 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 206983_at | CCR6 | chemokine (C-C motif) receptor 6 | -0.34 | -0.36 | -0.28 | -0.08 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 226694_at | AKAP2 /// PAL | A kinase (PRKA) anchor protein 2 /// PALM2-AKAP2 readthroug | -0.80 | -0.58 | -0.58 | -0.29 | 1 | 1 | -1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 207819_s_at | ABCB4 | ATP-binding cassette, sub-family B (MDR/TAP), member 4 | -0.11 | -0.16 | -0.07 | 0.14 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 228304_at | RBM43 | RNA binding motif protein 43 | 0.12 | -0.08 | 0.12 | 0.22 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1556423_at | VASH1 | Vasohibin 1 | -0.87 | -0.82 | -0.82 | -0.52 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1569263_at | --- | --- | -0.02 | 0.03 | 0.14 | 0.34 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 215118_s_at | IGHA1 | Immunoglobulin heavy constant alpha 1 | -0.24 | -0.25 | -0.14 | 0.07 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 202760_s_at | AKAP2 /// PAL | A kinase (PRKA) anchor protein 2 /// PALM2-AKAP2 readthroug | -0.75 | -0.57 | -0.42 | -0.24 | 1 | 1 | -1 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 0 | 1 |
| 231956_at | RNF213 | ring finger protein 213 | -0.06 | -0.19 | -0.06 | 0.14 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 233121_at | ZHX2 | zinc fingers and homeoboxes 2 | -0.26 | -0.32 | -0.24 | 0.01 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 228055_at | NAPSB | napsin B aspartic peptidase pseudogene | -0.35 | -0.31 | -0.20 | 0.03 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 |
| 220704_at | IKZF1 | IKAROS family zinc finger 1 (Ikaros) | 0.30 | 0.28 | 0.32 | 0.63 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 228056_s_at | NAPSB | napsin B aspartic peptidase pseudogene | -0.41 | -0.36 | -0.36 | -0.01 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 232319_at | GGPS1 | geranylgeranyl diphosphate synthase 1 | -0.15 | -0.23 | -0.15 | 0.13 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 1556461_at | Klf12 | Kruppel-like factor 12 | 0.11 | -0.13 | 0.16 | 0.23 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 206157_at | PTX3 | pentraxin 3, long | 0.76 | 1.00 | 0.91 | 1.37 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 242234_at | XAF1 | XIAP associated factor 1 | 0.38 | -0.08 | 0.13 | 0.36 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 |
| 244780_at | SGPP2 | sphingosine-1-phosphate phosphatase 2 | -0.26 | -0.46 | -0.22 | -0.01 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 232584_at | TSHZ2 | teashirt zinc finger homeobox 2 | 0.36 | 0.20 | 0.32 | 0.66 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 213436_at | CNR1 | cannabinoid receptor 1 (brain) | -1.02 | -1.03 | -0.91 | -0.46 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| 210118_s_at | IL1A | interleukin 1, alpha | 1.81 | 1.38 | 1.46 | 1.03 | 0 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1558404_at | LOC644242 | hypothetical LOC644242 | -1.59 | -1.27 | -1.90 | -1.60 | 1 | 1 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 204748_at | PTGS2 | prostaglandin-endoperoxide synthase 2 (prostaglandin G/H syr | 0.87 | 0.66 | 0.50 | 0.34 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1557267_s_at | LOC284952 | hypothetical protein LOC284952 | -0.21 | 0.28 | 0.27 | 0.03 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 202876_s_at | PBX2 | pre-B-cell leukemia homeobox 2 | 0.48 | 0.54 | 0.55 | 0.28 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 208018_s_at | HCK | hemopoietic cell kinase | -1.25 | -1.43 | -1.53 | -1.69 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 205787_x_at | ZC3H11A | zinc finger CCCH-type containing 11A | -0.51 | -0.02 | 0.00 | -0.27 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 207630_s_at | CREM | cAMP responsive element modulator | -0.42 | -0.54 | -0.59 | -0.79 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 216015_s_at | NLRP3 | NLR family, pyrin domain containing 3 | -0.04 | -0.15 | -0.22 | -0.40 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 229389_at | ATG16L2 | ATG16 autophagy related 16-like 2 (S. cerevisiae) | -0.02 | 0.24 | 0.00 | -0.01 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 205114_s_at | CCL3 /// CCL3L | chemokine (C-C motif) ligand 3 /// chemokine (C-C motif) ligan | 0.75 | 0.54 | 0.41 | 0.29 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 208067_x_at | UTY | ubiquitously transcribed tetratricopeptide repeat gene, Y-linke | 0.21 | 0.20 | 0.33 | -0.04 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 213524_s_at | G0S2 | G0/G1switch 2 | 0.35 | 0.20 | 0.20 | -0.04 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 214211_at | FTH1 | ferritin, heavy polypeptide 1 | -1.11 | -1.29 | -1.37 | -1.53 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 216069_at | --- | --- | -0.20 | 0.43 | 0.39 | 0.19 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 238899_at | KIAA1267 | KIAA1267 | -0.72 | -0.20 | -0.45 | -0.44 | 1 | 1 | -1 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 202833_s_at | SERPINA1 | serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, ant | -0.81 | -0.94 | -0.85 | -1.17 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 217813_s_at | SPIN1 | spindlin 1 | -0.53 | -0.11 | -0.17 | -0.34 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 222218_s_at | PILRA | paired immunoglobin-like type 2 receptor alpha | -1.09 | -1.24 | -1.29 | -1.47 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 238954_at | --- | --- | -0.69 | -0.24 | -0.27 | -0.47 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 1558641_at | SPATA24 | spermatogenesis associated 24 | 0.18 | 0.12 | 0.14 | -0.11 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 205476_at | CCL20 | chemokine (C-C motif) ligand 20 | 0.89 | 0.67 | 0.59 | 0.45 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 206025_s_at | TNFAIP6 | tumor necrosis factor, alpha-induced protein 6 | -0.03 | -0.31 | -0.37 | -0.52 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 209057_x_at | CDC5L | CDC5 cell division cycle 5-like (S. pombe) | 0.65 | 0.63 | 0.68 | 0.42 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 210140_at | CST7 | cystatin F (leukocystatin) | 0.61 | 0.47 | 0.59 | 0.24 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 214508_x_at | CREM | cAMP responsive element modulator | -0.36 | -0.49 | -0.49 | -0.71 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 216248_s_at | NR4A2 | nuclear receptor subfamily 4, group A, member 2 | -0.34 | -0.39 | -0.43 | -0.61 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 225954_s_at | MIDN | midnolin | 0.37 | 0.20 | 0.37 | -0.02 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 232204_at | EBF1 | early B-cell factor 1 | 0.38 | 0.31 | 0.32 | 0.09 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 239959_x_at | PDE3B | phosphodiesterase 3B, cGMP-inhibited | 0.76 | 0.70 | 0.79 | 0.48 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1555167_s_at | NAMPT | nicotinamide phosphoribosyltransferase | -0.12 | -0.39 | -0.37 | -0.60 | 0 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1561754_at | FLJ44253 | hypothetical gene supported by AK096952; AK126241; BC0685 | 1.25 | 0.98 | 1.44 | 0.77 | 0 | 1 | 0 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1562836_at | DDX6 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 6 | 0.08 | 0.10 | 0.30 | -0.11 | 0 | 1 | 0 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 209921_at | SLC7A11 | solute carrier family 7, (cationic amino acid transporter, y+ sys | -1.63 | -1.59 | -2.08 | -1.80 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 |
| 211074_at | FOLR1 | folate receptor 1 (adult) | -0.15 | 0.30 | 0.21 | 0.08 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 211429_s_at | SERPINA1 | serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, ant | -0.79 | -0.87 | -0.83 | -1.08 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 212249_at | PIK3R1 | phosphoinositide-3-kinase, regulatory subunit 1 (alpha) | -0.62 | -0.20 | -0.23 | -0.41 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 215352_at | GIMAP5 | GTPase, IMAP family member 5 | -0.06 | 0.53 | 0.40 | 0.33 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 226036_x_at | CASP2 | caspase 2, apoptosis-related cysteine peptidase | 0.50 | 0.42 | 0.56 | 0.21 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 243296_at | NAMPT | Nicotinamide phosphoribosyltransferase | 0.01 | -0.23 | -0.32 | -0.45 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 201631_s_at | IER3 | immediate early response 3 | -0.33 | -0.52 | -0.71 | -0.72 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 210818_s_at | BACH1 | BTB and CNC homology 1, basic leucine zipper transcription fac | -0.50 | -0.20 | -0.43 | -0.40 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 213005_s_at | KANK1 | KN motif and ankyrin repeat domains 1 | -0.81 | -0.78 | -1.16 | -0.98 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 227613_at | ZNF331 | zinc finger protein 331 | -0.21 | -0.32 | -0.21 | -0.51 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 229274_at | GNAS | GNAS complex locus | 0.07 | 0.47 | 0.46 | 0.27 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 200628_s_at | WARS | tryptophanyl-tRNA synthetase | 0.05 | -0.03 | 0.00 | -0.22 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 202388_at | RGS2 | regulator of G-protein signaling 2, 24kDa | 0.31 | 0.11 | 0.18 | -0.08 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 204103_at | CCL4 | chemokine (C-C motif) ligand 4 | 1.23 | 0.93 | 0.97 | 0.74 | 1 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 1 |
| 205731_s_at | NCOA2 | nuclear receptor coactivator 2 | 0.19 | 0.29 | 0.52 | 0.11 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 |
| 219788_at | PILRA | paired immunoglobin-like type 2 receptor alpha | -1.24 | -1.41 | -1.38 | -1.60 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 231697_s_at | TMEM49 | transmembrane protein 49 | -0.47 | -0.10 | -0.16 | -0.29 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 235476_at | TRIM59 | tripartite motif-containing 59 | -0.52 | 0.02 | 0.00 | -0.17 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 236876_at | H1FNT | H1 histone family, member N, testis-specific | 0.12 | 0.10 | 0.18 | -0.08 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 241315_at | FILIP1L | filamin A interacting protein 1-like | 0.52 | 0.50 | 0.62 | 0.30 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 243648_at | ZBED6 | zinc finger, BED-type containing 6 | -0.45 | 0.06 | -0.08 | -0.13 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 201668_x_at | MARCKS | myristoylated alanine-rich protein kinase C substrate | 0.40 | 0.40 | 0.56 | 0.22 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 204794_at | DUSP2 | dual specificity phosphatase 2 | 0.17 | 0.03 | 0.04 | -0.15 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 207219_at | ZNF643 | zinc finger protein 643 | -0.46 | -0.17 | -0.41 | -0.35 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 214567_s_at | XCL1 /// XCL2 | chemokine (C motif) ligand 1 /// chemokine (C motif) ligand 2 | 0.71 | 0.54 | 0.59 | 0.35 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 219653_at | LSM14B | LSM14B, SCD6 homolog B (S. cerevisiae) | 0.44 | 0.34 | 0.48 | 0.16 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 230180_at | DDX17 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 17 | -0.54 | -0.04 | 0.01 | -0.22 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 240773_at | TRIO | triple functional domain (PTPRF interacting) | -1.29 | -0.91 | -1.12 | -1.09 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 206180_x_at | ZNF747 | zinc finger protein 747 | 0.37 | 0.33 | 0.43 | 0.15 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 212762_s_at | TCF7L2 | transcription factor 7-like 2 (T-cell specific, HMG-box) | -0.59 | -0.28 | -0.49 | -0.46 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 217678_at | SLC7A11 | solute carrier family 7, (cationic amino acid transporter, y+ sys | -1.78 | -1.71 | -2.21 | -1.89 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 |
| 223999_at | PPIL2 | peptidylprolyl isomerase (cyclophilin)-like 2 | -0.07 | 0.33 | 0.15 | 0.16 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 237332_at | MON2 | MON2 homolog (S. cerevisiae) | -0.64 | -0.08 | -0.32 | -0.25 | 1 | 1 | -1 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 201266_at | TXNRD1 | thioredoxin reductase 1 | -1.18 | -0.96 | -1.36 | -1.12 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 202912_at | ADM | adrenomedullin | -1.21 | -1.24 | -1.57 | -1.39 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 207528_s_at | SLC7A11 | solute carrier family 7, (cationic amino acid transporter, y+ sys | -1.75 | -1.58 | -2.02 | -1.74 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 212107_s_at | DHX9 | DEAH (Asp-Glu-Ala-His) box polypeptide 9 | -0.44 | -0.05 | -0.04 | -0.21 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 214305_s_at | SF3B1 | splicing factor 3b, subunit 1, 155kDa | -0.22 | 0.23 | 0.19 | 0.07 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 216433_s_at | PRDM2 | PR domain containing 2, with ZNF domain | -0.39 | -0.04 | -0.21 | -0.19 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 222527_s_at | RBM22 | RNA binding motif protein 22 | -0.29 | -0.11 | 0.11 | -0.28 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 |
| 222562_s_at | TNKS2 | tankyrase, TRF1-interacting ankyrin-related ADP-ribose polyme | -0.22 | 0.17 | 0.19 | 0.01 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 224775_at | IWS1 | IWS1 homolog (S. cerevisiae) | -0.12 | 0.00 | 0.23 | -0.15 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 |
| 235645_at | ESCO1 | establishment of cohesion 1 homolog 1 (S. cerevisiae) | -0.13 | 0.20 | 0.40 | 0.05 | 1 | 1 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 | 0 |
| 236005_at | Klf12 | Kruppel-like factor 12 | -0.01 | 0.36 | 0.41 | 0.20 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 238563_at | Abi1 | abl-interactor 1 | -0.16 | 0.21 | 0.02 | 0.04 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 1564002_a_at | AKD1 | adenylate kinase domain containing 1 | -0.17 | 0.16 | 0.20 | 0.01 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 216361_s_at | MYST3 | MYST histone acetyltransferase (monocytic leukemia) 3 | -0.53 | -0.18 | 0.06 | -0.32 | 1 | 1 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 | 0 |
| 222576_s_at | EIF2C1 | eukaryotic translation initiation factor 2C, 1 | -0.12 | 0.06 | 0.25 | -0.09 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 |
| 231897_at | PTGR1 | prostaglandin reductase 1 | -1.76 | -1.63 | -2.00 | -1.78 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 201070_x_at | SF3B1 | splicing factor 3b, subunit 1, 155kDa | -0.25 | 0.16 | 0.14 | 0.02 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 201868_s_at | TBL1X | transducin (beta)-like 1X-linked | -0.52 | -0.10 | -0.16 | -0.24 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 211022_s_at | ATRX | alpha thalassemia/mental retardation syndrome X-linked | -0.43 | -0.07 | 0.04 | -0.21 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 211899_s_at | TRAF4 | TNF receptor-associated factor 4 | -0.02 | 0.02 | 0.22 | -0.12 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 231235_at | NKTR | natural killer-tumor recognition sequence | -0.72 | -0.08 | -0.27 | -0.22 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 235568_at | C19orf59 | chromosome 19 open reading frame 59 | -3.07 | -2.99 | -3.31 | -3.14 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 236946_at | Gpr75 | G protein-coupled receptor 75 | -0.59 | -0.16 | -0.31 | -0.30 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 236962_at | ptbp2 | polypyrimidine tract binding protein 2 | -0.77 | -0.02 | 0.06 | -0.16 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 239014_at | CCAR1 | Cell division cycle and apoptosis regulator 1 | 0.18 | 0.50 | 0.39 | 0.35 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 242306_at | TMEM165 | transmembrane protein 165 | -0.45 | -0.05 | -0.17 | -0.19 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 1558579_at | FLJ37786 | hypothetical LOC642691 | 0.62 | 0.53 | 0.93 | 0.40 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 204864_s_at | IL6ST | interleukin 6 signal transducer (gp130, oncostatin M receptor) | -0.27 | 0.08 | -0.02 | -0.04 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 205411_at | STK4 | serine/threonine kinase 4 | -0.78 | -0.19 | -0.38 | -0.33 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 230681_at | TBRG1 | transforming growth factor beta regulator 1 | -0.14 | 0.21 | 0.17 | 0.08 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 233559_s_at | WDFY1 | WD repeat and FYVE domain containing 1 | -0.57 | -0.17 | -0.16 | -0.29 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 241683_at | HECTD1 | HECT domain containing 1 | -0.10 | 0.15 | 0.35 | 0.02 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 |
| 243293_at | --- | --- | -0.56 | -0.08 | -0.07 | -0.21 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 209803_s_at | PHLDA2 | pleckstrin homology-like domain, family A, member 2 | -0.56 | -0.44 | -0.80 | -0.56 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 217856_at | RBM8A | RNA binding motif protein 8A | 0.01 | 0.36 | 0.34 | 0.24 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 236125_at | DKFZP586I142 | hypothetical protein DKFZp586I1420 | -0.53 | -0.11 | -0.18 | -0.23 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 238281_at | RBMS1 | RNA binding motif, single stranded interacting protein 1 | -0.35 | 0.01 | -0.04 | -0.11 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 238940_at | KLF12 | Kruppel-like factor 12 | -0.52 | 0.01 | -0.07 | -0.11 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 241685_x_at | C5orf53 | chromosome 5 open reading frame 53 | -0.54 | -0.07 | -0.15 | -0.20 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 1555733_s_at | AP1S3 | adaptor-related protein complex 1, sigma 3 subunit | 0.30 | 0.34 | 0.54 | 0.23 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1560142_at | GRIK2 | glutamate receptor, ionotropic, kainate 2 | 0.51 | 0.57 | 0.76 | 0.46 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 201732_s_at | CLCN3 | chloride channel 3 | -0.58 | -0.28 | -0.26 | -0.39 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 202887_s_at | DDIT4 | DNA-damage-inducible transcript 4 | -0.12 | -0.33 | -0.36 | -0.44 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 207334_s_at | TGFBR2 | transforming growth factor, beta receptor II (70/80kDa) | -0.09 | 0.28 | 0.30 | 0.17 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 209675_s_at | HNRNPUL1 | heterogeneous nuclear ribonucleoprotein U-like 1 | 0.10 | 0.12 | 0.30 | 0.01 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 217234_s_at | EZR | ezrin | -0.07 | 0.23 | 0.31 | 0.12 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 228250_at | FNIP1 | folliculin interacting protein 1 | -1.10 | -0.45 | -0.67 | -0.57 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 244568_at | SYNE2 | spectrin repeat containing, nuclear envelope 2 | 0.06 | 0.53 | 0.46 | 0.41 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 1553267_a_at | CNOT6L | CCR4-NOT transcription complex, subunit 6-like | -0.42 | -0.12 | -0.22 | -0.22 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 1557065_at | YLPM1 | YLP motif containing 1 | -0.05 | 0.26 | 0.16 | 0.16 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 205197_s_at | ATP7A | ATPase, Cu++ transporting, alpha polypeptide | -0.46 | -0.11 | -0.25 | -0.21 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 212332_at | RBL2 | retinoblastoma-like 2 (p130) | -0.29 | 0.14 | 0.16 | 0.04 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 212926_at | SMC5 | structural maintenance of chromosomes 5 | -0.34 | -0.07 | -0.12 | -0.17 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 213286_at | ZFR | zinc finger RNA binding protein | -0.73 | -0.30 | -0.34 | -0.40 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 215092_s_at | NFAT5 | nuclear factor of activated T-cells 5, tonicity-responsive | -0.48 | -0.18 | -0.26 | -0.28 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 215589_at | SMURF1 | SMAD specific E3 ubiquitin protein ligase 1 | -0.75 | -0.19 | -0.37 | -0.29 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 217878_s_at | CDC27 | cell division cycle 27 homolog (S. cerevisiae) | -0.08 | 0.07 | 0.34 | -0.03 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 |
| 222387_s_at | VPS35 | vacuolar protein sorting 35 homolog (S. cerevisiae) | -0.41 | -0.10 | -0.01 | -0.20 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 224310_s_at | BCL11B | B-cell CLL/lymphoma 11B (zinc finger protein) | 0.21 | 0.17 | 0.39 | 0.07 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 224580_at | SLC38A1 | solute carrier family 38, member 1 | -0.31 | 0.04 | 0.21 | -0.06 | 1 | 1 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 1 | 0 |
| 227497_at | SOX6 | SRY (sex determining region Y)-box 6 | 0.35 | 0.37 | 0.54 | 0.27 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 238350_at | UBN2 | ubinuclein 2 | -0.70 | -0.22 | -0.30 | -0.33 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 242099_at | --- | --- | 0.05 | 0.33 | 0.26 | 0.23 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 243304_at | LOC286109 | hypothetical protein LOC286109 | -0.58 | -0.18 | -0.19 | -0.28 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 1552417_a_at | NEDD1 | neural precursor cell expressed, developmentally down-regula | -0.16 | 0.18 | 0.24 | 0.09 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 1559822_s_at | MTDH | metadherin | -0.28 | 0.03 | -0.09 | -0.06 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 1562442_a_at | SSBP1 | single-stranded DNA binding protein 1 | -0.18 | 0.16 | 0.07 | 0.07 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 1569238_a_at | --- | --- | -0.37 | -0.07 | -0.19 | -0.16 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 200951_s_at | CCND2 | cyclin D2 | -0.63 | -0.23 | -0.30 | -0.33 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 203958_s_at | ZBTB40 | zinc finger and BTB domain containing 40 | -0.43 | -0.10 | -0.23 | -0.19 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 206341_at | IL2RA | interleukin 2 receptor, alpha | -0.06 | -0.01 | 0.21 | -0.09 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 |
| 208621_s_at | EZR | ezrin | -0.05 | 0.16 | 0.38 | 0.07 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 |
| 219159_s_at | SLAMF7 | SLAM family member 7 | 0.16 | 0.57 | 0.58 | 0.48 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 221092_at | IKZF3 | IKAROS family zinc finger 3 (Aiolos) | -0.84 | -0.29 | -0.24 | -0.37 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 221496_s_at | TOB2 | transducer of ERBB2, 2 | -0.28 | 0.06 | 0.07 | -0.03 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 227062_at | Neat1 | non-protein coding RNA 84 | -1.00 | -0.55 | -0.74 | -0.63 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 228824_s_at | PTGR1 | prostaglandin reductase 1 | -1.83 | -1.72 | -2.02 | -1.81 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 235003_at | UHMK1 | U2AF homology motif (UHM) kinase 1 | -0.64 | -0.23 | -0.06 | -0.32 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 235567_at | RORA | RAR-related orphan receptor A | -0.47 | -0.10 | -0.16 | -0.19 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 236417_at | mfn1 | mitofusin 1 | -0.07 | 0.21 | 0.17 | 0.12 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 242924_at | PITPNB | phosphatidylinositol transfer protein, beta | -0.88 | -0.36 | -0.57 | -0.45 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 244153_at | ZNF207 | zinc finger protein 207 | -0.36 | -0.01 | -0.18 | -0.10 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 244396_at | G3BP1 | GTPase activating protein (SH3 domain) binding protein 1 | -0.19 | 0.14 | 0.10 | 0.05 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 1557910_at | HSP90AB1 | heat shock protein 90kDa alpha (cytosolic), class B member 1 | -0.61 | -0.37 | -0.07 | -0.46 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 |
| 209616_s_at | CES1 | carboxylesterase 1 | -1.50 | -1.61 | -1.91 | -1.69 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 229413_s_at | Pcgf3 | polycomb group ring finger 3 | -0.33 | -0.03 | -0.08 | -0.11 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 230607_at | DENND4A | DENN/MADD domain containing 4A | -0.05 | 0.40 | 0.36 | 0.33 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 232386_at | VPS13C | vacuolar protein sorting 13 homolog C (S. cerevisiae) | -0.24 | 0.01 | 0.04 | -0.07 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 235740_at | MCTP1 | multiple C2 domains, transmembrane 1 | -0.36 | -0.30 | -0.57 | -0.38 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 237741_at | SLC25A36 | Solute carrier family 25, member 36 | 0.06 | 0.39 | 0.45 | 0.30 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 240062_at | FAM3C | family with sequence similarity 3, member C | -0.04 | 0.25 | 0.16 | 0.17 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 242975_s_at | Gnas | GNAS complex locus | -0.26 | 0.14 | 0.18 | 0.06 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 244737_at | KIAA1429 | KIAA1429 | -0.24 | 0.07 | -0.01 | -0.01 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 201879_at | ARIH1 | ariadne homolog, ubiquitin-conjugating enzyme E2 binding pro | -0.53 | -0.18 | -0.27 | -0.25 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 211751_at | LOC653513 // | hypothetical LOC653513 /// phosphodiesterase 4D interacting | -0.33 | -0.32 | -0.08 | -0.39 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 212451_at | SECISBP2L | SECIS binding protein 2-like | -0.31 | 0.01 | 0.09 | -0.06 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 214034_at | ERAP1 | endoplasmic reticulum aminopeptidase 1 | 0.22 | 0.31 | 0.56 | 0.24 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 |
| 220983_s_at | SPRY4 | sprouty homolog 4 (Drosophila) | -0.55 | -0.26 | -0.34 | -0.33 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 223701_s_at | USP47 | ubiquitin specific peptidase 47 | -0.36 | -0.11 | -0.03 | -0.18 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 225800_at | JAZF1 | JAZF zinc finger 1 | -0.08 | 0.21 | 0.24 | 0.13 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 240941_at | ITSN2 | Intersectin 2 | -0.38 | -0.07 | -0.06 | -0.14 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 244733_at | usp33 | ubiquitin specific peptidase 33 | -0.19 | 0.15 | 0.08 | 0.07 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 214843_s_at | USP33 | ubiquitin specific peptidase 33 | -0.15 | 0.20 | 0.13 | 0.14 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 215434_x_at | LOC10028814 | neuroblastoma breakpoint family member /// neuroblastoma | -0.23 | -0.06 | 0.12 | -0.11 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 216595_at | FAM186A | family with sequence similarity 186, member A | 0.52 | 0.47 | 0.70 | 0.41 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 218166_s_at | RSF1 | remodeling and spacing factor 1 | -0.41 | -0.03 | -0.21 | -0.09 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 222313_at | CNOT2 | CCR4-NOT transcription complex, subunit 2 | -0.05 | 0.25 | 0.19 | 0.18 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 223465_at | COL4A3BP | collagen, type IV, alpha 3 (Goodpasture antigen) binding prote | -0.82 | -0.46 | -0.57 | -0.51 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 224012_at | ANKRD20A1 // | ankyrin repeat domain 20 family, member A1 /// ankyrin repea | 0.78 | 0.55 | 0.95 | 0.49 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 1 |
| 227740_at | UHMK1 | U2AF homology motif (UHM) kinase 1 | -0.56 | -0.18 | -0.05 | -0.24 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 229881_at | KLF12 | Kruppel-like factor 12 | 0.02 | 0.32 | 0.36 | 0.26 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 234306_s_at | SLAMF7 | SLAM family member 7 | 0.13 | 0.50 | 0.51 | 0.44 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 235537_at | OCIAD1 | OCIA domain containing 1 | -0.12 | 0.18 | 0.33 | 0.12 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 235574_at | GBP4 | guanylate binding protein 4 | -0.12 | 0.17 | 0.19 | 0.11 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 202118_s_at | CPNE3 | copine III | -0.22 | 0.23 | 0.17 | 0.18 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 212650_at | EHBP1 | EH domain binding protein 1 | -0.15 | 0.19 | 0.17 | 0.14 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 213457_at | MFHAS1 | malignant fibrous histiocytoma amplified sequence 1 | -0.50 | -0.21 | -0.31 | -0.26 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 214615_at | P2RY10 | purinergic receptor P2Y, G-protein coupled, 10 | -0.35 | -0.08 | -0.11 | -0.13 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 223079_s_at | GLS | glutaminase | -0.55 | -0.22 | -0.26 | -0.26 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 226367_at | KDM5A | lysine (K)-specific demethylase 5A | -0.35 | -0.02 | -0.16 | -0.07 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 231597_x_at | --- | --- | 0.67 | 0.37 | 0.91 | 0.32 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 1 |
| 231934_at | TRIM14 | tripartite motif-containing 14 | -0.28 | -0.02 | -0.10 | -0.07 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 233387_s_at | PCNT | pericentrin | -0.26 | -0.08 | 0.14 | -0.13 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 |
| 240951_at | RORA | RAR-related orphan receptor A | -0.36 | -0.13 | -0.09 | -0.18 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 243940_at | TSHZ2 | teashirt zinc finger homeobox 2 | -0.34 | -0.02 | -0.13 | -0.07 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 244171_at | MKLN1 | muskelin 1, intracellular mediator containing kelch motifs | -0.66 | -0.36 | -0.43 | -0.41 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 244669_at | SNHG5 /// SN | small nucleolar RNA host gene 5 (non-protein coding) /// small | -0.02 | 0.40 | 0.48 | 0.35 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 1558678_s_at | MALAT1 | metastasis associated lung adenocarcinoma transcript 1 (non-p | -0.19 | -0.13 | 0.12 | -0.17 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 |
| 1560144_at | --- | --- | 1.07 | 0.74 | 1.42 | 0.70 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 1 |
| 1569830_at | PTPRC | protein tyrosine phosphatase, receptor type, C | -0.48 | -0.20 | -0.12 | -0.24 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 201711_x_at | RANBP2 | RAN binding protein 2 | 0.02 | 0.04 | 0.27 | 0.00 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 202412_s_at | USP1 | ubiquitin specific peptidase 1 | 0.23 | 0.27 | 0.51 | 0.23 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 |
| 208664_s_at | TTC3 | tetratricopeptide repeat domain 3 | -0.36 | 0.00 | 0.09 | -0.04 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 211821_x_at | GYPA | glycophorin A (MNS blood group) | 0.43 | 0.33 | 0.60 | 0.28 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 220946_s_at | SETD2 | SET domain containing 2 | -0.45 | 0.01 | 0.07 | -0.03 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 222600_s_at | UBA6 | ubiquitin-like modifier activating enzyme 6 | -0.45 | -0.14 | -0.20 | -0.18 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 236728_at | LNPEP | leucyl/cystinyl aminopeptidase | -0.16 | 0.10 | 0.21 | 0.06 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 237502_at | CRLS1 | cardiolipin synthase 1 | -0.46 | -0.07 | -0.14 | -0.12 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 239674_at | ARID1B | AT rich interactive domain 1B (SWI1-like) | -0.33 | -0.06 | -0.15 | -0.10 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 241403_at | CLK4 | CDC-like kinase 4 | -0.52 | -0.13 | -0.01 | -0.17 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 241620_at | SMCHD1 | structural maintenance of chromosomes flexible hinge domain | -0.22 | 0.06 | 0.17 | 0.03 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 1558702_at | TEX10 | testis expressed 10 | -0.38 | -0.16 | -0.05 | -0.19 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 1569791_at | STK4 | serine/threonine kinase 4 | -0.36 | -0.05 | -0.06 | -0.08 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 1570371_a_at | EPT1 | Ethanolaminephosphotransferase 1 (CDP-ethanolamine-specifi | -0.15 | -0.04 | 0.17 | -0.06 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 201635_s_at | FXR1 | fragile X mental retardation, autosomal homolog 1 | -0.55 | -0.14 | -0.07 | -0.17 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 209060_x_at | NCOA3 | nuclear receptor coactivator 3 | -0.26 | -0.04 | 0.04 | -0.07 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 210693_at | SPPL2B | signal peptide peptidase-like 2B | -0.04 | 0.22 | 0.24 | 0.18 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 212758_s_at | ZEB1 | zinc finger E-box binding homeobox 1 | -0.14 | 0.00 | 0.17 | -0.03 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 222343_at | BCL2L11 | BCL2-like 11 (apoptosis facilitator) | -0.12 | 0.11 | 0.21 | 0.08 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 226404_at | RBM39 | RNA binding motif protein 39 | -0.14 | 0.19 | 0.13 | 0.16 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 239504_at | LOC731605 // | similar to Bcl-2-associated transcription factor 1 (Btf); BCL2-ass | -0.35 | -0.01 | 0.02 | -0.04 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 240401_at | AATF | apoptosis antagonizing transcription factor | -0.10 | 0.19 | 0.13 | 0.16 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 243473_at | SIK3 | serine/threonine-protein kinase QSK | -0.62 | -0.27 | -0.37 | -0.30 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 244055_at | RYR3 | ryanodine receptor 3 | -0.31 | 0.01 | -0.10 | -0.01 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 208965_s_at | IFI16 | interferon, gamma-inducible protein 16 | 0.01 | 0.23 | 0.37 | 0.21 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 209715_at | CBX5 | chromobox homolog 5 | -0.39 | -0.13 | -0.11 | -0.15 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 209750_at | NR1D2 | nuclear receptor subfamily 1, group D, member 2 | -0.27 | 0.03 | 0.06 | 0.01 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 211993_at | WNK1 | WNK lysine deficient protein kinase 1 | -0.75 | -0.25 | -0.16 | -0.26 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 215220_s_at | TPR | translocated promoter region (to activated MET oncogene) | -0.67 | -0.17 | -0.04 | -0.19 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 215339_at | NKTR | natural killer-tumor recognition sequence | -0.14 | 0.30 | 0.14 | 0.27 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 236645_at | LOC10050631 | hypothetical LOC100506312 | -0.41 | 0.00 | -0.05 | -0.02 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 242422_at | G3BP1 | GTPase activating protein (SH3 domain) binding protein 1 | -0.57 | -0.15 | -0.09 | -0.16 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 242970_at | DIP2B | DIP2 disco-interacting protein 2 homolog B (Drosophila) | -0.44 | -0.18 | -0.15 | -0.20 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 243767_at | --- | --- | -0.38 | -0.04 | -0.10 | -0.06 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 244035_at | BCL2 | B-cell CLL/lymphoma 2 | -0.36 | -0.01 | 0.06 | -0.03 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 1570213_at | --- | --- | 0.32 | 0.31 | 0.60 | 0.30 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 |
| 207237_at | KCNA3 | potassium voltage-gated channel, shaker-related subfamily, me | -0.29 | 0.08 | 0.11 | 0.06 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 208601_s_at | TUBB1 | tubulin, beta 1 | 0.38 | 0.54 | 0.80 | 0.53 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 |
| 215698_at | KDM5A | lysine (K)-specific demethylase 5A | -0.78 | -0.32 | -0.43 | -0.33 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 216101_at | --- | --- | -0.19 | 0.03 | 0.20 | 0.02 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 216901_s_at | IKZF1 | IKAROS family zinc finger 1 (Ikaros) | -0.61 | -0.29 | -0.11 | -0.30 | 0 | 1 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 217602_at | PPIA | peptidylprolyl isomerase A (cyclophilin A) | -0.13 | 0.12 | 0.19 | 0.12 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 230014_at | YPEL5 | yippee-like 5 (Drosophila) | -0.34 | 0.02 | 0.14 | 0.01 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 231862_at | CBX5 | chromobox homolog 5 | -0.37 | -0.08 | -0.08 | -0.09 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 234632_x_at | BTNL8 | butyrophilin-like 8 | 0.22 | 0.21 | 0.50 | 0.20 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 237689_at | SARS | Seryl-tRNA synthetase | -0.28 | 0.05 | -0.05 | 0.04 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 239978_at | PITPNB | phosphatidylinositol transfer protein, beta | -0.25 | 0.05 | -0.05 | 0.04 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 240015_at | LOC439949 | hypothetical LOC439949 | 0.08 | 0.36 | 0.36 | 0.35 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 240078_at | SFSWAP | splicing factor, suppressor of white-apricot homolog (Drosophi | -0.30 | 0.00 | -0.01 | -0.01 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 241462_at | --- | --- | 0.18 | 0.63 | 0.55 | 0.62 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 1557519_at | CDC42SE2 | CDC42 small effector 2 | -0.21 | 0.10 | 0.04 | 0.09 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 200806_s_at | HSPD1 | heat shock 60kDa protein 1 (chaperonin) | -0.19 | -0.20 | 0.11 | -0.20 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 206500_s_at | C14orf106 | chromosome 14 open reading frame 106 | -0.24 | 0.05 | 0.16 | 0.05 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 206668_s_at | SCAMP1 | secretory carrier membrane protein 1 | -0.50 | -0.22 | -0.05 | -0.22 | 1 | 1 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 209446_s_at | C7orf44 | chromosome 7 open reading frame 44 | -1.10 | -0.99 | -1.28 | -0.99 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 210800_at | TIMM8A | translocase of inner mitochondrial membrane 8 homolog A (ye | 0.57 | 0.50 | 0.80 | 0.50 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 214251_s_at | NUMA1 | nuclear mitotic apparatus protein 1 | -0.51 | -0.19 | -0.18 | -0.19 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 215342_s_at | RABGAP1L | RAB GTPase activating protein 1-like | -0.13 | 0.07 | 0.25 | 0.07 | 0 | 1 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 221765_at | UGCG | UDP-glucose ceramide glucosyltransferase | -0.76 | -0.33 | -0.31 | -0.33 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 223263_s_at | FGFR1OP2 | FGFR1 oncogene partner 2 | -0.44 | -0.09 | -0.15 | -0.09 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 230106_at | ZXDC | ZXD family zinc finger C | -0.11 | 0.02 | 0.20 | 0.02 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 230434_at | PHOSPHO2 | phosphatase, orphan 2 | -0.21 | 0.05 | 0.09 | 0.05 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 230820_at | SMURF2 | SMAD specific E3 ubiquitin protein ligase 2 | -0.35 | 0.00 | -0.11 | 0.00 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 232257_s_at | C3orf20 | chromosome 3 open reading frame 20 | -1.04 | -0.54 | -0.76 | -0.53 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 233283_at | Fntb | farnesyltransferase, CAAX box, beta | -0.20 | 0.13 | 0.06 | 0.13 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 242496_at | --- | --- | 0.39 | 0.32 | 0.61 | 0.32 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 243182_at | --- | --- | -0.61 | -0.34 | -0.40 | -0.34 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 205809_s_at | WASL | Wiskott-Aldrich syndrome-like | -0.72 | -0.36 | -0.43 | -0.35 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 206548_at | --- | --- | -1.13 | -1.16 | -1.42 | -1.15 | 0 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 207549_x_at | CD46 | CD46 molecule, complement regulatory protein | -0.05 | 0.14 | 0.23 | 0.14 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 213566_at | RNASE6 | ribonuclease, RNase A family, k6 | -1.82 | -2.09 | -1.99 | -2.08 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 224549_x_at | SND1 | staphylococcal nuclease and tudor domain containing 1 | 0.64 | 0.45 | 0.87 | 0.46 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 237184_at | ATXN2 | ataxin 2 | -0.59 | -0.27 | -0.26 | -0.26 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 238706_at | PAPD4 | PAP associated domain containing 4 | -0.31 | 0.04 | -0.08 | 0.05 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 243739_at | RANBP9 | RAN binding protein 9 | -0.59 | -0.17 | -0.18 | -0.16 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 1555812_a_at | ARHGDIB | Rho GDP dissociation inhibitor (GDI) beta | 0.39 | 0.22 | 0.64 | 0.24 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 1557236_at | APOL6 | apolipoprotein L, 6 | -0.25 | 0.03 | -0.04 | 0.05 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 201083_s_at | BCLAF1 | BCL2-associated transcription factor 1 | -0.36 | -0.01 | -0.04 | 0.01 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 213875_x_at | C6orf62 | chromosome 6 open reading frame 62 | -0.87 | -0.64 | -0.51 | -0.62 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 217644_s_at | SOS2 | son of sevenless homolog 2 (Drosophila) | -0.97 | -0.64 | -0.49 | -0.62 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 225046_at | LOC389831 | hypothetical LOC389831 | 0.27 | 0.20 | 0.53 | 0.22 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 230466_s_at | --- | --- | -0.30 | 0.04 | -0.11 | 0.07 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 237784_at | SUB1 | SUB1 homolog (S. cerevisiae) | -1.05 | -0.49 | -0.68 | -0.47 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 239351_at | FKBP3 | FK506 binding protein 3, 25kDa | -0.45 | -0.15 | -0.20 | -0.14 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 241091_at | --- | --- | -0.63 | -0.35 | -0.36 | -0.32 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 201446_s_at | TIA1 | TIA1 cytotoxic granule-associated RNA binding protein | -0.32 | -0.07 | -0.02 | -0.04 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 205596_s_at | SMURF2 | SMAD specific E3 ubiquitin protein ligase 2 | -0.19 | 0.10 | -0.01 | 0.13 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 206928_at | ZNF124 | zinc finger protein 124 | -0.36 | -0.10 | 0.00 | -0.07 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 218748_s_at | EXOC5 | exocyst complex component 5 | -0.94 | -0.67 | -0.63 | -0.64 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 232472_at | FNDC3B | fibronectin type III domain containing 3B | -1.53 | -1.57 | -1.84 | -1.54 | 0 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 238356_at | DOCK11 | dedicator of cytokinesis 11 | -0.48 | -0.14 | -0.19 | -0.11 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 242588_at | --- | --- | -0.33 | -0.02 | -0.04 | 0.02 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 1557227_s_at | TPR | translocated promoter region (to activated MET oncogene) | -0.42 | -0.15 | 0.25 | -0.11 | 0 | 1 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 1 |
| 206667_s_at | SCAMP1 | secretory carrier membrane protein 1 | -0.60 | -0.41 | -0.24 | -0.37 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 212417_at | SCAMP1 | secretory carrier membrane protein 1 | -0.50 | -0.28 | -0.20 | -0.23 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 214786_at | MAP3K1 | mitogen-activated protein kinase kinase kinase 1 | -0.73 | -0.22 | -0.15 | -0.19 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 223890_at | PRO1082 | hypothetical protein PRO1082 | -0.14 | 0.16 | 0.09 | 0.20 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 227510_x_at | MALAT1 | metastasis associated lung adenocarcinoma transcript 1 (non-p | 0.32 | 0.19 | 0.64 | 0.23 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 |
| 1556226_at | PDS5A | PDS5, regulator of cohesion maintenance, homolog A (S. cerev | -0.52 | -0.16 | -0.24 | -0.11 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 201450_s_at | TIA1 | TIA1 cytotoxic granule-associated RNA binding protein | -0.22 | 0.03 | -0.01 | 0.08 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 210807_s_at | SLC16A7 | solute carrier family 16, member 7 (monocarboxylic acid transp | -0.30 | -0.07 | -0.04 | -0.02 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 222714_s_at | LACTB2 | lactamase, beta 2 | -0.59 | -0.35 | -0.40 | -0.30 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 229399_at | C10orf118 | chromosome 10 open reading frame 118 | -0.27 | -0.08 | 0.23 | -0.03 | 0 | 1 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 235653_s_at | THAP6 | THAP domain containing 6 | -0.52 | -0.24 | -0.10 | -0.20 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 239692_at | ILKAP | integrin-linked kinase-associated serine/threonine phosphatase | -0.65 | -0.39 | -0.18 | -0.33 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 240105_at | GCFC1 | chromosome 21 open reading frame 66 | -0.25 | 0.11 | 0.22 | 0.16 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 241532_at | Rmnd5a | required for meiotic nuclear division 5 homolog A (S. cerevisiae | -0.36 | -0.12 | -0.17 | -0.08 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1557436_at | XKR6 | XK, Kell blood group complex subunit-related family, member | -0.45 | -0.17 | -0.09 | -0.11 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 1565913_at | ZC3HAV1 | zinc finger CCCH-type, antiviral 1 | -0.12 | 0.16 | 0.23 | 0.21 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 205885_s_at | ITGA4 | integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 rece | -0.46 | -0.11 | -0.23 | -0.05 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 210717_at | ube2d2 | ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast) | -0.43 | -0.09 | -0.09 | -0.03 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 220771_at | LOC51152 | melanoma antigen | 0.38 | 0.20 | 0.58 | 0.26 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 227345_at | TNFRSF10D | tumor necrosis factor receptor superfamily, member 10d, deco | -0.97 | -0.93 | -1.17 | -0.87 | 0 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 242989_at | --- | --- | -0.33 | -0.09 | -0.15 | -0.03 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 243552_at | MBTD1 | mbt domain containing 1 | -0.40 | -0.16 | -0.08 | -0.09 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 243959_at | MKLN1 | muskelin 1, intracellular mediator containing kelch motifs | -0.69 | -0.36 | -0.30 | -0.31 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 201008_s_at | TXNIP | thioredoxin interacting protein | -0.27 | -0.24 | 0.01 | -0.18 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 223254_s_at | G2E3 | G2/M-phase specific E3 ubiquitin protein ligase | -0.53 | -0.33 | -0.18 | -0.26 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 228986_at | OSBPL8 | oxysterol binding protein-like 8 | -0.73 | -0.43 | -0.25 | -0.36 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 231370_at | PPM1A | Protein phosphatase, Mg2+/Mn2+ dependent, 1A | -0.88 | -0.42 | -0.66 | -0.35 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 |
| 237747_at | fam107b | family with sequence similarity 107, member B | -0.44 | -0.24 | -0.25 | -0.17 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 243631_at | MPHOSPH8 | M-phase phosphoprotein 8 | 0.07 | 0.27 | 0.38 | 0.33 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 244263_at | --- | --- | -0.46 | -0.28 | -0.17 | -0.22 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 210218_s_at | SP100 | SP100 nuclear antigen | -0.76 | -0.44 | -0.39 | -0.35 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 232125_at | --- | --- | -0.44 | -0.13 | 0.01 | -0.05 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 232757_at | mtss1 | metastasis suppressor 1 | -0.15 | -0.15 | -0.43 | -0.07 | 0 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 237376_at | cul3 | cullin 3 | -0.48 | -0.18 | -0.14 | -0.10 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 241889_at | NFKBID | nuclear factor of kappa light polypeptide gene enhancer in B-c | -0.32 | -0.10 | 0.03 | -0.02 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 1556471_at | SCML4 | sex comb on midleg-like 4 (Drosophila) | 0.10 | 0.28 | 0.29 | 0.37 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1558093_s_at | MATR3 | matrin 3 | -0.52 | -0.42 | -0.11 | -0.33 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 210057_at | SMG1 | SMG1 homolog, phosphatidylinositol 3-kinase-related kinase ( | -0.77 | -0.46 | -0.42 | -0.37 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 217656_at | SMARCA4 | SWI/SNF related, matrix associated, actin dependent regulator | -0.14 | 0.04 | 0.07 | 0.13 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 240141_at | papd4 | PAP associated domain containing 4 | -0.60 | -0.30 | -0.24 | -0.21 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 1562230_at | --- | --- | -0.30 | -0.11 | -0.10 | -0.01 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1564053_a_at | YTHDF3 | YTH domain family, member 3 | -0.91 | -0.70 | -0.74 | -0.60 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 206652_at | ZMYM5 | zinc finger, MYM-type 5 | -0.38 | -0.19 | -0.12 | -0.09 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 214881_s_at | UBTF | upstream binding transcription factor, RNA polymerase I | 0.13 | 0.10 | 0.37 | 0.20 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 216527_at | --- | --- | -0.39 | -0.17 | -0.09 | -0.07 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 218967_s_at | PTER | phosphotriesterase related | -0.34 | -0.13 | -0.11 | -0.03 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 227777_at | C10orf18 | chromosome 10 open reading frame 18 | -0.59 | -0.39 | -0.35 | -0.30 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 227884_at | TAF15 | TAF15 RNA polymerase II, TATA box binding protein (TBP)-asso | -0.08 | 0.14 | 0.15 | 0.24 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 207686_s_at | CASP8 | caspase 8, apoptosis-related cysteine peptidase | -0.30 | -0.13 | -0.09 | -0.02 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 211794_at | FYB | FYN binding protein | -0.08 | 0.18 | 0.18 | 0.28 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 219797_at | MGAT4A | mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosam | -0.73 | -0.44 | -0.36 | -0.33 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 232179_at | LOC158863 | Hypothetical protein LOC158863 | -0.91 | -0.47 | -0.56 | -0.36 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 233819_s_at | LTN1 | listerin E3 ubiquitin protein ligase 1 | -0.93 | -0.49 | -0.41 | -0.38 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 212398_at | RDX | radixin | -0.89 | -0.63 | -0.65 | -0.51 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 212392_s_at | PDE4DIP | phosphodiesterase 4D interacting protein | -1.00 | -0.85 | -0.54 | -0.72 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 235430_at | C14orf43 | chromosome 14 open reading frame 43 | -0.45 | -0.15 | -0.01 | -0.02 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 240602_at | HBS1L | HBS1-like (S. cerevisiae) | -0.88 | -0.54 | -0.61 | -0.41 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 244508_at | SEPT7 | Septin 7 | -0.41 | -0.17 | -0.08 | -0.04 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 244846_at | MAP4K4 | mitogen-activated protein kinase kinase kinase kinase 4 | -0.30 | -0.02 | 0.03 | 0.10 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 209203_s_at | BICD2 | bicaudal D homolog 2 (Drosophila) | -0.63 | -0.45 | -0.36 | -0.31 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 236386_at | LOC10050650 | hypothetical LOC100506501 | -0.69 | -0.44 | -0.41 | -0.30 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 244443_at | CHD2 | Chromodomain helicase DNA binding protein 2 | -0.02 | 0.20 | 0.17 | 0.34 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1558111_at | MBNL1 | muscleblind-like (Drosophila) | -0.14 | 0.04 | 0.10 | 0.20 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 204180_s_at | ZBTB43 | zinc finger and BTB domain containing 43 | -0.71 | -0.50 | -0.52 | -0.35 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 224227_s_at | BDP1 | B double prime 1, subunit of RNA polymerase III transcription i | -0.30 | -0.06 | 0.09 | 0.09 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 224989_at | C4orf34 | chromosome 4 open reading frame 34 | -0.48 | -0.24 | -0.24 | -0.10 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 229115_at | DYNC1H1 | dynein, cytoplasmic 1, heavy chain 1 | -0.52 | -0.34 | 0.00 | -0.19 | 1 | 1 | -1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 |
| 243835_at | ZDHHC21 | zinc finger, DHHC-type containing 21 | -0.22 | -0.13 | 0.21 | 0.01 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1553185_at | RASEF | RAS and EF-hand domain containing | 0.45 | 0.28 | 0.62 | 0.44 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 202609_at | EPS8 | epidermal growth factor receptor pathway substrate 8 | -0.40 | -0.01 | -0.22 | 0.15 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 208797_s_at | GOLGA8A | golgin A8 family, member A | -0.11 | 0.10 | 0.42 | 0.26 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 |
| 1554250_s_at | TRIM73 | tripartite motif-containing 73 | -0.10 | 0.01 | -0.08 | 0.18 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1554770_x_at | ZNF785 | zinc finger protein 785 | -0.49 | -0.31 | -0.46 | -0.14 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 204995_at | CDK5R1 | cyclin-dependent kinase 5, regulatory subunit 1 (p35) | 0.17 | 0.28 | 0.25 | 0.45 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 210942_s_at | ST3GAL6 | ST3 beta-galactoside alpha-2,3-sialyltransferase 6 | -1.59 | -1.26 | -1.40 | -1.08 | 0 | 1 | -1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 216683_at | tbca | tubulin folding cofactor A | -0.36 | -0.27 | -0.31 | -0.09 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 217540_at | FAM55C | family with sequence similarity 55, member C | -0.39 | -0.25 | -0.29 | -0.08 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 221986_s_at | KLHL24 | kelch-like 24 (Drosophila) | -0.52 | -0.31 | -0.18 | -0.15 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 223578_x_at | MALAT1 | metastasis associated lung adenocarcinoma transcript 1 (non-p | 0.76 | 0.46 | 0.96 | 0.63 | 1 | 1 | 0 | -1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 226550_at | --- | --- | -0.66 | -0.54 | -0.59 | -0.36 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 232980_at | LMBRD1 | LMBR1 domain containing 1 | -0.15 | -0.06 | -0.09 | 0.11 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1554910_at | PRKD3 | protein kinase D3 | -0.37 | -0.24 | -0.27 | -0.06 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1559289_at | TADA1 | Transcriptional adaptor 1 | -0.44 | -0.31 | -0.39 | -0.13 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1564789_at | --- | --- | -0.76 | -0.72 | -0.93 | -0.54 | 0 | 1 | 0 | 0 | -1 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1565875_at | --- | --- | -0.13 | 0.01 | -0.14 | 0.19 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1569431_at | PAFAH1B2 | platelet-activating factor acetylhydrolase 1b, catalytic subunit | -0.36 | -0.37 | -0.47 | -0.19 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 204956_at | MTAP | methylthioadenosine phosphorylase | -0.06 | 0.07 | 0.04 | 0.25 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 207907_at | TNFSF14 | tumor necrosis factor (ligand) superfamily, member 14 | -2.27 | -2.23 | -2.39 | -2.05 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 215188_at | STK24 | serine/threonine kinase 24 | -1.11 | -0.91 | -0.94 | -0.73 | 0 | 1 | -1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 222473_s_at | ERBB2IP | erbb2 interacting protein | -0.32 | -0.22 | -0.27 | -0.04 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 225237_s_at | MSI2 | musashi homolog 2 (Drosophila) | -0.48 | -0.38 | -0.48 | -0.20 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 227719_at | SMAD9 | SMAD family member 9 | -0.38 | -0.16 | -0.20 | 0.02 | 0 | 1 | -1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 229732_at | ZNF823 | zinc finger protein 823 | 0.03 | 0.13 | 0.07 | 0.31 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 229966_at | EWSR1 | Ewing sarcoma breakpoint region 1 | -0.44 | -0.21 | -0.44 | -0.02 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 231995_at | C9orf82 | chromosome 9 open reading frame 82 | -0.28 | -0.14 | -0.22 | 0.05 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 233664_at | ARL15 | ADP-ribosylation factor-like 15 | -0.63 | -0.64 | -0.75 | -0.46 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 235803_at | CRLF3 | cytokine receptor-like factor 3 | -0.51 | -0.43 | -0.52 | -0.25 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 241275_at | CAPZA1 | Capping protein (actin filament) muscle Z-line, alpha 1 | -0.50 | -0.36 | -0.38 | -0.18 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 244674_at | RBM6 | RNA binding motif protein 6 | -0.73 | -0.51 | -0.67 | -0.33 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1569129_s_at | C3orf38 | chromosome 3 open reading frame 38 | -0.21 | -0.14 | -0.24 | 0.05 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1569472_s_at | TTC3 | tetratricopeptide repeat domain 3 | -0.26 | -0.09 | 0.32 | 0.10 | 1 | 1 | -1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 |
| 203548_s_at | LPL | lipoprotein lipase | -2.69 | -2.72 | -2.92 | -2.53 | 0 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 219730_at | MED18 | mediator complex subunit 18 | -1.10 | -0.90 | -1.04 | -0.71 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 228988_at | ZNF711 | zinc finger protein 711 | -0.15 | -0.07 | -0.08 | 0.11 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 235052_at | ZNF792 | zinc finger protein 792 | 0.08 | 0.18 | 0.13 | 0.37 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 236202_at | --- | --- | -0.24 | -0.10 | -0.09 | 0.09 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 239778_x_at | CAPN7 | calpain 7 | -0.09 | -0.01 | 0.00 | 0.18 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 240265_at | TRAF3IP3 | TRAF3 interacting protein 3 | 0.00 | 0.12 | -0.02 | 0.31 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 241863_x_at | ttc14 | tetratricopeptide repeat domain 14 | -0.23 | -0.01 | -0.17 | 0.18 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 242289_at | --- | --- | -0.02 | 0.05 | -0.02 | 0.25 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 243570_at | SPCS2 | signal peptidase complex subunit 2 homolog (S. cerevisiae) | -0.61 | -0.52 | -0.55 | -0.33 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1555116_s_at | SLC11A1 | solute carrier family 11 (proton-coupled divalent metal ion tra | -2.39 | -2.71 | -2.51 | -2.51 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 1568865_at | FNTB | Farnesyltransferase, CAAX box, beta | -0.14 | -0.15 | -0.23 | 0.05 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 205684_s_at | DENND4C | DENN/MADD domain containing 4C | -0.37 | -0.40 | -0.47 | -0.19 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 220038_at | C8orf44 /// SG | chromosome 8 open reading frame 44 /// serum/glucocorticoi | -1.21 | -1.22 | -1.33 | -1.02 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 228654_at | SPIN4 | spindlin family, member 4 | -0.64 | -0.52 | -0.56 | -0.32 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 228905_at | PCM1 | pericentriolar material 1 | -0.01 | 0.09 | 0.07 | 0.29 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 229075_at | SPATA5 | spermatogenesis associated 5 | -0.27 | -0.21 | -0.33 | -0.01 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 232648_at | PSMA3 | proteasome (prosome, macropain) subunit, alpha type, 3 | -0.51 | -0.23 | -0.25 | -0.03 | 1 | 1 | -1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 |
| 235060_at | LOC10019098 | hypothetical LOC100190986 | -0.50 | -0.36 | -0.33 | -0.16 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 240271_at | mtmr3 | myotubularin related protein 3 | -0.66 | -0.58 | -0.61 | -0.39 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 240789_at | WDR44 | WD repeat domain 44 | -0.21 | -0.20 | -0.29 | 0.00 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 244763_at | MTRF1 | mitochondrial translational release factor 1 | -0.33 | -0.20 | -0.24 | 0.00 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1565692_at | --- | --- | -0.26 | -0.18 | -0.20 | 0.03 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1570115_at | PP12708 | hypothetical LOC100130609 | -0.26 | -0.17 | -0.17 | 0.05 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 214740_at | POLR2J /// PO | polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa /// | -0.74 | -0.46 | -0.50 | -0.25 | 0 | 1 | -1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 219858_s_at | MFSD6 | major facilitator superfamily domain containing 6 | -1.25 | -0.92 | -0.98 | -0.70 | 1 | 1 | -1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 1 | 1 |
| 232614_at | BCL2 | B-cell CLL/lymphoma 2 | -0.12 | -0.09 | -0.19 | 0.12 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 233713_at | SMYD2 | SET and MYND domain containing 2 | 0.06 | 0.17 | 0.14 | 0.38 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 237890_at | Dtnbp1 | dystrobrevin binding protein 1 | -0.14 | 0.11 | 0.09 | 0.32 | 0 | 1 | -1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 238525_at | DDX56 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 56 | -0.23 | -0.25 | -0.31 | -0.05 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 241680_at | MBD3 | methyl-CpG binding domain protein 3 | -0.40 | -0.39 | -0.45 | -0.17 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 241755_at | UQCRC2 | ubiquinol-cytochrome c reductase core protein II | -0.96 | -0.84 | -0.88 | -0.63 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 242563_at | fchsd2 | FCH and double SH3 domains 2 | -0.09 | -0.04 | -0.15 | 0.17 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 244766_at | LOC10027183 | SMG1 homolog, phosphatidylinositol 3-kinase-related kinase p | -0.34 | -0.27 | -0.25 | -0.06 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1557538_at | Med13l | mediator complex subunit 13-like | -0.50 | -0.48 | -0.54 | -0.26 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 209790_s_at | CASP6 | caspase 6, apoptosis-related cysteine peptidase | -0.02 | 0.05 | -0.02 | 0.27 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 211310_at | EZH1 | enhancer of zeste homolog 1 (Drosophila) | -0.42 | -0.20 | -0.19 | 0.02 | 0 | 1 | -1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 223771_at | TMEM87A | Transmembrane protein 87A | 0.02 | 0.02 | -0.04 | 0.25 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 231109_at | CELF2 | CUG triplet repeat, RNA binding protein 2 | -0.26 | -0.06 | -0.04 | 0.16 | 0 | 1 | -1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 232885_at | NCRNA00081 | non-protein coding RNA 81 | -0.33 | -0.34 | -0.39 | -0.12 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 233400_at | CCDC82 | coiled-coil domain containing 82 | -0.09 | -0.04 | -0.06 | 0.18 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 235469_at | FAM133B /// L | family with sequence similarity 133, member B /// family with | -0.13 | -0.05 | -0.05 | 0.17 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 235611_at | SREK1 | splicing regulatory glutamine/lysine-rich protein 1 | -0.23 | -0.07 | -0.19 | 0.16 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 235811_at | Mbnl1 | muscleblind-like (Drosophila) | -0.37 | -0.21 | -0.18 | 0.00 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 236558_at | Mbnl1 | muscleblind-like (Drosophila) | -0.28 | -0.18 | -0.16 | 0.05 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 237333_at | RBBP4 | retinoblastoma binding protein 4 | -0.57 | -0.49 | -0.49 | -0.26 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 243537_at | GIT2 | G protein-coupled receptor kinase interacting ArfGAP 2 | -0.28 | -0.21 | -0.24 | 0.01 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 244473_at | Atf7 | activating transcription factor 7 | -0.51 | -0.45 | -0.42 | -0.23 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1558105_a_at | --- | --- | -0.62 | -0.56 | -0.58 | -0.34 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1559580_at | LRRC39 | leucine rich repeat containing 39 | -0.19 | -0.15 | -0.18 | 0.07 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1559731_x_at | MACROD1 | MACRO domain containing 1 | -0.22 | -0.15 | -0.17 | 0.09 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1559932_at | --- | --- | -0.40 | -0.26 | -0.22 | -0.04 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1562364_at | GVIN1 | GTPase, very large interferon inducible 1 | -0.43 | 0.04 | 0.06 | 0.27 | 1 | 1 | -1 | 0 | 0 | 1 | 1 | 0 | 0 | 1 | 0 | 1 |
| 1562457_at | NCKAP5L | NCK-associated protein 5-like | -0.47 | -0.38 | -0.44 | -0.15 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1565886_at | TRPM7 | transient receptor potential cation channel, subfamily M, mem | -0.23 | -0.21 | -0.25 | 0.02 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 213355_at | ST3GAL6 | ST3 beta-galactoside alpha-2,3-sialyltransferase 6 | -1.65 | -1.28 | -1.48 | -1.05 | 1 | 1 | -1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 1 | 1 |
| 214724_at | DIXDC1 | DIX domain containing 1 | -1.30 | -1.24 | -1.24 | -1.00 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 232412_at | FBXL20 | F-box and leucine-rich repeat protein 20 | -1.23 | -1.06 | -1.15 | -0.83 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 235652_at | SCML1 | sex comb on midleg-like 1 (Drosophila) | 0.00 | 0.11 | 0.07 | 0.35 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 237232_at | Ube2h | ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast) | -0.79 | -0.68 | -0.82 | -0.45 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 239867_at | C19orf2 | chromosome 19 open reading frame 2 | -0.50 | -0.28 | -0.30 | -0.05 | 0 | 1 | -1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 241263_at | --- | --- | -0.86 | -0.76 | -0.81 | -0.52 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1556750_at | LOC153577 | hypothetical protein LOC153577 | -1.28 | -1.14 | -1.22 | -0.90 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1560556_a_at | PLEKHA8 | Pleckstrin homology domain containing, family A (phosphoinos | -0.20 | -0.19 | -0.27 | 0.06 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1563461_at | --- | --- | -0.95 | -0.90 | -1.07 | -0.66 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 216022_at | LOC10013236 | WNK lysine deficient protein kinase 1; hypothetical LOC100132 | -0.40 | -0.31 | -0.34 | -0.07 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 218362_s_at | DIS3 | DIS3 mitotic control homolog (S. cerevisiae) | -0.33 | -0.34 | -0.39 | -0.09 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 225746_at | RAB11FIP4 | RAB11 family interacting protein 4 (class II) | -0.44 | -0.37 | -0.39 | -0.13 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 60794_f_at | ZNF814 | zinc finger protein 814 | -0.51 | -0.42 | -0.37 | -0.18 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1554769_at | ZNF785 | zinc finger protein 785 | -0.56 | -0.43 | -0.55 | -0.18 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1559455_at | --- | --- | -0.46 | -0.38 | -0.50 | -0.13 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1560755_at | Fam149b1 | family with sequence similarity 149, member B1 | -0.24 | -0.21 | -0.23 | 0.04 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1561154_at | GBF1 | golgi-specific brefeldin A resistant guanine nucleotide exchang | -0.41 | -0.36 | -0.36 | -0.11 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1563077_at | LOC10028905 | Hypothetical protein LOC100289058 | -0.46 | -0.43 | -0.41 | -0.18 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1568983_a_at | --- | --- | -0.17 | -0.15 | -0.22 | 0.10 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 211934_x_at | GANAB | glucosidase, alpha; neutral AB | 0.12 | -0.19 | 0.00 | 0.06 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 214815_at | TRIM33 | tripartite motif-containing 33 | -0.24 | -0.26 | -0.28 | -0.01 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 220467_at | --- | --- | -0.06 | -0.05 | -0.09 | 0.20 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 224151_s_at | AK3 | adenylate kinase 3 | -0.03 | -0.01 | 0.03 | 0.24 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 224568_x_at | MALAT1 | metastasis associated lung adenocarcinoma transcript 1 (non-p | 0.08 | 0.02 | 0.85 | 0.26 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 |
| 233231_at | MCCC2 | Methylcrotonoyl-Coenzyme A carboxylase 2 (beta) | -0.21 | -0.17 | -0.28 | 0.08 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 233419_at | --- | --- | -0.12 | -0.17 | -0.23 | 0.08 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 233630_at | CDS2 | CDP-diacylglycerol synthase (phosphatidate cytidylyltransferas | -0.11 | -0.18 | -0.20 | 0.07 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 236153_at | ZNF280D | zinc finger protein 280D | 0.02 | -0.05 | -0.06 | 0.20 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 243751_at | CHD2 | chromodomain helicase DNA binding protein 2 | -0.31 | -0.30 | -0.33 | -0.05 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1560177_at | CCDC66 | coiled-coil domain containing 66 | -0.47 | -0.44 | -0.41 | -0.18 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 203607_at | INPP5F | inositol polyphosphate-5-phosphatase F | -0.43 | -0.32 | -0.36 | -0.07 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 215128_at | --- | --- | -0.04 | -0.13 | -0.15 | 0.14 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 221771_s_at | MPHOSPH8 | M-phase phosphoprotein 8 | -0.37 | -0.37 | -0.41 | -0.11 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 226663_at | ANKRD10 | ankyrin repeat domain 10 | -0.37 | -0.34 | -0.31 | -0.08 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 239131_at | ADNP | activity-dependent neuroprotector homeobox | -0.05 | -0.01 | -0.02 | 0.24 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 242490_at | --- | --- | -0.24 | -0.31 | -0.33 | -0.05 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 239258_at | rhoq /// RHOC | ras homolog gene family, member Q; similar to small GTP bind | -0.99 | -0.98 | -1.08 | -0.70 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 204475_at | MMP1 | matrix metallopeptidase 1 (interstitial collagenase) | -1.43 | -0.84 | -1.29 | -0.54 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 220458_at | --- | --- | -0.43 | -0.46 | -0.52 | -0.16 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 223940_x_at | MALAT1 | metastasis associated lung adenocarcinoma transcript 1 (non-p | 0.45 | 0.15 | 1.09 | 0.51 | 1 | 1 | 0 | -1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 206336_at | CXCL6 | chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic pro | 0.39 | -0.39 | -0.92 | -1.00 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 219890_at | CLEC5A | C-type lectin domain family 5, member A | -2.33 | -2.63 | -3.29 | -3.19 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 216598_s_at | CCL2 | chemokine (C-C motif) ligand 2 | -1.67 | -2.11 | -2.63 | -2.67 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 203980_at | FABP4 | fatty acid binding protein 4, adipocyte | -1.40 | -1.83 | -2.29 | -2.37 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 212158_at | SDC2 | syndecan 2 | -2.31 | -2.81 | -3.25 | -3.32 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 203888_at | THBD | thrombomodulin | -1.61 | -2.05 | -2.29 | -2.51 | 0 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 204620_s_at | VCAN | versican | -2.61 | -3.31 | -3.62 | -3.76 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 208075_s_at | CCL7 | chemokine (C-C motif) ligand 7 | -2.54 | -3.16 | -3.58 | -3.60 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 204619_s_at | VCAN | versican | -2.58 | -3.28 | -3.53 | -3.70 | 0 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 221731_x_at | VCAN | versican | -2.61 | -3.34 | -3.67 | -3.76 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 215101_s_at | CXCL5 | chemokine (C-X-C motif) ligand 5 | -0.44 | -1.10 | -1.17 | -1.47 | 1 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 1 |
| 204059_s_at | ME1 | malic enzyme 1, NADP(+)-dependent, cytosolic | -0.63 | -0.40 | -1.11 | -0.75 | 1 | 1 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 212820_at | DMXL2 | Dmx-like 2 | -1.09 | -1.29 | -1.68 | -1.64 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 211571_s_at | VCAN | versican | -2.64 | -3.13 | -3.29 | -3.46 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 215646_s_at | VCAN | versican | -2.83 | -3.57 | -3.76 | -3.89 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1565162_s_at | MGST1 | microsomal glutathione S-transferase 1 | -2.37 | -2.43 | -3.02 | -2.74 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 |
| 208891_at | DUSP6 | dual specificity phosphatase 6 | -1.39 | -1.54 | -2.03 | -1.85 | 0 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 212298_at | NRP1 | neuropilin 1 | -1.86 | -1.90 | -2.53 | -2.21 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 203535_at | S100A9 | S100 calcium binding protein A9 | -0.71 | -1.02 | -1.24 | -1.32 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 219403_s_at | HPSE | heparanase | -2.23 | -2.45 | -2.85 | -2.75 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 226281_at | DNER | delta/notch-like EGF repeat containing | -1.28 | -1.54 | -1.74 | -1.84 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 202917_s_at | S100A8 | S100 calcium binding protein A8 | -2.08 | -2.51 | -2.68 | -2.80 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 208892_s_at | DUSP6 | dual specificity phosphatase 6 | -1.43 | -1.52 | -2.02 | -1.82 | 0 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 210119_at | KCNJ15 | potassium inwardly-rectifying channel, subfamily J, member 15 | -2.59 | -2.77 | -3.05 | -3.06 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 228937_at | C13orf31 | chromosome 13 open reading frame 31 | -0.91 | -1.12 | -1.49 | -1.41 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 210772_at | FPR2 | formyl peptide receptor 2 | -1.22 | -1.62 | -1.54 | -1.89 | 1 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 1 | 1 |
| 237252_at | THBD | thrombomodulin | -1.15 | -1.32 | -1.46 | -1.59 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 202437_s_at | CYP1B1 | cytochrome P450, family 1, subfamily B, polypeptide 1 | -2.12 | -1.87 | -2.59 | -2.13 | 1 | 1 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 204058_at | ME1 | malic enzyme 1, NADP(+)-dependent, cytosolic | -0.80 | -0.57 | -1.22 | -0.83 | 1 | 1 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 221802_s_at | KIAA1598 | KIAA1598 | -1.45 | -1.63 | -1.94 | -1.89 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 225662_at | ZAK | sterile alpha motif and leucine zipper containing kinase AZK | -0.77 | -0.96 | -1.33 | -1.22 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 |
| 202435_s_at | CYP1B1 | cytochrome P450, family 1, subfamily B, polypeptide 1 | -2.04 | -1.89 | -2.51 | -2.15 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 204151_x_at | AKR1C1 | aldo-keto reductase family 1, member C1 (dihydrodiol dehydro | -0.44 | -0.29 | -0.89 | -0.55 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 205576_at | SERPIND1 | serpin peptidase inhibitor, clade D (heparin cofactor), member | 0.51 | 0.44 | 0.37 | 0.19 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 207316_at | HAS1 | hyaluronan synthase 1 | -0.33 | -0.42 | -0.45 | -0.68 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 209277_at | TFPI2 | tissue factor pathway inhibitor 2 | 0.37 | 0.56 | 0.03 | 0.31 | 1 | 1 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 214681_at | GK | glycerol kinase | -0.98 | -1.15 | -1.43 | -1.40 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 215761_at | DMXL2 | Dmx-like 2 | -0.89 | -1.19 | -1.38 | -1.44 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 223454_at | CXCL16 | chemokine (C-X-C motif) ligand 16 | -1.00 | -1.26 | -1.37 | -1.51 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 224358_s_at | MS4A7 | membrane-spanning 4-domains, subfamily A, member 7 | -1.25 | -1.56 | -1.77 | -1.80 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 225283_at | ARRDC4 | arrestin domain containing 4 | -1.43 | -1.40 | -1.85 | -1.65 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 239519_at | NRP1 | neuropilin 1 | -1.82 | -1.87 | -2.38 | -2.12 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 |
| 242037_at | asph | aspartate beta-hydroxylase | -1.08 | -1.04 | -1.47 | -1.29 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 202381_at | ADAM9 | ADAM metallopeptidase domain 9 | -1.65 | -1.69 | -2.11 | -1.93 | 0 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 205098_at | CCR1 | chemokine (C-C motif) receptor 1 | -2.46 | -2.70 | -2.97 | -2.94 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 205119_s_at | FPR1 | formyl peptide receptor 1 | -1.13 | -1.48 | -1.46 | -1.72 | 1 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 1 | 1 |
| 205237_at | FCN1 | ficolin (collagen/fibrinogen domain containing) 1 | -0.85 | -1.01 | -1.04 | -1.25 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 209135_at | ASPH | aspartate beta-hydroxylase | -1.06 | -1.00 | -1.53 | -1.24 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 |
| 211135_x_at | LILRB3 | leukocyte immunoglobulin-like receptor, subfamily B (with TM | -0.64 | -0.75 | -0.79 | -0.99 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 216370_s_at | TKTL1 | transketolase-like 1 | -1.62 | -1.93 | -1.88 | -2.17 | 1 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 1 | 1 |
| 217996_at | PHLDA1 | pleckstrin homology-like domain, family A, member 1 | -1.27 | -1.45 | -1.74 | -1.69 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 227080_at | ZNF697 | zinc finger protein 697 | -1.45 | -1.45 | -1.89 | -1.69 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 240652_at | --- | --- | -0.93 | -0.91 | -0.85 | -1.15 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1553313_s_at | SLC5A3 | solute carrier family 5 (sodium/myo-inositol cotransporter), me | -0.08 | 0.44 | -0.01 | 0.20 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 201325_s_at | EMP1 | epithelial membrane protein 1 | -1.75 | -1.67 | -2.13 | -1.90 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 202436_s_at | CYP1B1 | cytochrome P450, family 1, subfamily B, polypeptide 1 | -2.04 | -1.96 | -2.55 | -2.19 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 204014_at | DUSP4 | dual specificity phosphatase 4 | -0.77 | -1.09 | -1.05 | -1.32 | 1 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 1 | 1 |
| 207697_x_at | LILRB2 | leukocyte immunoglobulin-like receptor, subfamily B (with TM | -0.90 | -1.14 | -1.18 | -1.37 | 0 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 228188_at | FOSL2 | FOS-like antigen 2 | -0.67 | -0.89 | -0.97 | -1.13 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 1554442_at | BEST1 | bestrophin 1 | -0.31 | -0.37 | -0.40 | -0.59 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1558691_a_at | DOCK4 | dedicator of cytokinesis 4 | -1.34 | -1.41 | -1.34 | -1.63 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 201360_at | CST3 | cystatin C | -0.80 | -0.94 | -0.89 | -1.16 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 207038_at | SLC16A6 | solute carrier family 16, member 6 (monocarboxylic acid transp | -1.63 | -1.86 | -2.03 | -2.08 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 210225_x_at | LILRB3 | leukocyte immunoglobulin-like receptor, subfamily B (with TM | -0.68 | -0.79 | -0.76 | -1.01 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 211653_x_at | AKR1C2 | aldo-keto reductase family 1, member C2 (dihydrodiol dehydro | -0.37 | -0.23 | -0.63 | -0.44 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 222876_s_at | ADAP2 | ArfGAP with dual PH domains 2 | -0.44 | -0.56 | -0.58 | -0.78 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 225955_at | METRNL | meteorin, glial cell differentiation regulator-like | -0.19 | -0.48 | -0.48 | -0.70 | 1 | 1 | 1 | 0 | 0 | -1 | 1 | 0 | 0 | 1 | 0 | 1 |
| 206028_s_at | MERTK | c-mer proto-oncogene tyrosine kinase | -1.58 | -1.71 | -1.73 | -1.92 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 215049_x_at | CD163 | CD163 molecule | -0.57 | -0.76 | -1.04 | -0.97 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 217507_at | SLC11A1 | solute carrier family 11 (proton-coupled divalent metal ion tra | -2.83 | -3.00 | -3.08 | -3.21 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 241866_at | SLC16A7 | solute carrier family 16, member 7 (monocarboxylic acid transp | -0.42 | 0.08 | -0.02 | -0.12 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 241894_at | VMO1 | vitelline membrane outer layer 1 homolog (chicken) | -0.43 | -0.52 | -0.54 | -0.72 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1553142_at | C13orf31 | chromosome 13 open reading frame 31 | -1.02 | -1.20 | -1.41 | -1.40 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 201324_at | EMP1 | epithelial membrane protein 1 | -1.77 | -1.68 | -2.16 | -1.88 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 |
| 201490_s_at | PPIF | peptidylprolyl isomerase F | -1.12 | -1.42 | -1.54 | -1.61 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 201785_at | RNASE1 | ribonuclease, RNase A family, 1 (pancreatic) | -1.73 | -1.84 | -1.85 | -2.04 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 204858_s_at | TYMP | thymidine phosphorylase | -0.83 | -1.06 | -1.09 | -1.27 | 0 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 209699_x_at | AKR1C2 | aldo-keto reductase family 1, member C2 (dihydrodiol dehydro | -0.36 | -0.18 | -0.65 | -0.38 | 1 | 1 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 209933_s_at | CD300A | CD300a molecule | -0.07 | -0.15 | -0.16 | -0.35 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 210422_x_at | SLC11A1 | solute carrier family 11 (proton-coupled divalent metal ion tra | -1.20 | -1.30 | -1.29 | -1.50 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 210784_x_at | LILRA6 /// LILF | leukocyte immunoglobulin-like receptor, subfamily A (with TM | -0.64 | -0.75 | -0.75 | -0.95 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 217853_at | TNS3 | tensin 3 | -2.62 | -2.58 | -3.07 | -2.79 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 218856_at | TNFRSF21 | tumor necrosis factor receptor superfamily, member 21 | -3.03 | -3.26 | -3.30 | -3.46 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 222692_s_at | FNDC3B | fibronectin type III domain containing 3B | -1.69 | -1.43 | -1.75 | -1.62 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 |
| 235518_at | SLC8A1 | solute carrier family 8 (sodium/calcium exchanger), member 1 | -1.99 | -2.23 | -2.32 | -2.44 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 238831_at | TMEM33 | transmembrane protein 33 | -0.67 | -0.27 | -0.55 | -0.48 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 1556202_at | SRGAP2 | SLIT-ROBO Rho GTPase activating protein 2 | -0.74 | -0.37 | -0.52 | -0.56 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 210896_s_at | ASPH | aspartate beta-hydroxylase | -1.23 | -1.25 | -1.71 | -1.44 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 211067_s_at | GAS7 | growth arrest-specific 7 | -0.26 | -0.46 | -0.62 | -0.65 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 211336_x_at | LILRB1 | leukocyte immunoglobulin-like receptor, subfamily B (with TM | -0.99 | -1.15 | -1.14 | -1.34 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 212944_at | SLC5A3 | solute carrier family 5 (sodium/myo-inositol cotransporter), m | 0.12 | 0.54 | -0.07 | 0.35 | 1 | 1 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 1 | 1 | 0 |
| 213472_at | HNRNPH1 | heterogeneous nuclear ribonucleoprotein H1 (H) | -0.32 | 0.10 | 0.13 | -0.09 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 214560_at | FPR3 | formyl peptide receptor 3 | -2.75 | -2.77 | -2.68 | -2.96 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 216594_x_at | AKR1C1 | aldo-keto reductase family 1, member C1 (dihydrodiol dehydro | -0.30 | -0.19 | -0.62 | -0.38 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 224996_at | ASPH | aspartate beta-hydroxylase | -0.92 | -0.84 | -1.38 | -1.03 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 |
| 228573_at | ANTXR2 | anthrax toxin receptor 2 | -0.33 | -0.16 | -0.48 | -0.35 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 229900_at | CD109 | CD109 molecule | -1.34 | -1.16 | -1.50 | -1.36 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 204011_at | SPRY2 | sprouty homolog 2 (Drosophila) | -2.56 | -2.32 | -2.87 | -2.50 | 1 | 1 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 208198_x_at | KIR2DS1 | killer cell immunoglobulin-like receptor, two domains, short cy | 0.30 | 0.22 | 0.24 | 0.04 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 211242_x_at | KIR2DL4 | killer cell immunoglobulin-like receptor, two domains, long cyt | 0.19 | 0.08 | 0.15 | -0.10 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 211688_x_at | KIR3DL1 /// KI | killer cell immunoglobulin-like receptor, three domains, long c | 0.55 | 0.44 | 0.44 | 0.26 | 0 | 1 | 0 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 222693_at | FNDC3B | fibronectin type III domain containing 3B | -1.86 | -1.57 | -1.84 | -1.75 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 226364_at | HIP1 | huntingtin interacting protein 1 | -1.44 | -1.48 | -1.87 | -1.66 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 226545_at | CD109 | CD109 molecule | -2.08 | -1.94 | -2.32 | -2.12 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 242871_at | PAQR5 | progestin and adipoQ receptor family member V | -1.77 | -1.67 | -2.06 | -1.85 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 1569773_at | ATP8A1 | ATPase, aminophospholipid transporter (APLT), class I, type 8A | -0.36 | 0.13 | 0.28 | -0.05 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 1 | 1 |
| 224414_s_at | CARD6 | caspase recruitment domain family, member 6 | -0.97 | -0.80 | -1.23 | -0.97 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 237588_at | SMCHD1 | structural maintenance of chromosomes flexible hinge domain | -0.16 | 0.27 | 0.24 | 0.10 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 242732_at | NDUFB9 | NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kD | -0.33 | 0.10 | -0.10 | -0.07 | 1 | 1 | -1 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 210152_at | LILRB4 | leukocyte immunoglobulin-like receptor, subfamily B (with TM | -2.20 | -2.38 | -2.38 | -2.54 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 211192_s_at | CD84 | CD84 molecule | -0.98 | -0.62 | -0.68 | -0.78 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 221060_s_at | TLR4 | toll-like receptor 4 | -0.59 | -0.78 | -0.87 | -0.94 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 205966_at | TAF13 | TAF13 RNA polymerase II, TATA box binding protein (TBP)-asso | -1.41 | -0.96 | -0.99 | -1.11 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 212157_at | SDC2 | syndecan 2 | -1.73 | -2.08 | -2.16 | -2.24 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 230323_s_at | TMEM45B | transmembrane protein 45B | -0.89 | -1.09 | -1.26 | -1.24 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 230422_at | FPR3 | formyl peptide receptor 3 | -3.29 | -3.61 | -3.61 | -3.76 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 232653_at | TRPS1 | trichorhinophalangeal syndrome I | -0.97 | -1.14 | -1.32 | -1.29 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 235180_at | STYX | serine/threonine/tyrosine interacting protein | -0.56 | -0.24 | -0.21 | -0.39 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 242408_at | STYX | serine/threonine/tyrosine interacting protein | -0.64 | -0.23 | -0.22 | -0.37 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 243299_at | VRK2 | Vaccinia related kinase 2 | -1.14 | -1.34 | -1.40 | -1.48 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1554503_a_at | OSCAR | osteoclast associated, immunoglobulin-like receptor | -0.80 | -1.00 | -1.03 | -1.14 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 203889_at | SCG5 | secretogranin V (7B2 protein) | -2.99 | -3.12 | -3.61 | -3.26 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 204088_at | P2RX4 | purinergic receptor P2X, ligand-gated ion channel, 4 | -0.55 | -0.74 | -0.81 | -0.87 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1552703_s_at | CARD16 /// CA | caspase recruitment domain family, member 16 /// caspase 1, | 0.70 | 0.52 | 0.44 | 0.39 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 214041_x_at | RPL37A | Ribosomal protein L37a | -0.18 | 0.19 | 0.20 | 0.06 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 230127_at | --- | --- | -1.02 | -0.89 | -1.35 | -1.02 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 227314_at | ITGA2 | integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) | -0.87 | -0.69 | -1.06 | -0.82 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 229706_at | tcerg1 | transcription elongation regulator 1 | -0.18 | 0.40 | 0.44 | 0.28 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 239819_at | --- | --- | -0.28 | 0.12 | 0.12 | 0.01 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 207545_s_at | NUMB | numb homolog (Drosophila) | -1.20 | -1.07 | -1.44 | -1.19 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 214149_s_at | ATP6V0E1 | ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1 | -0.79 | -0.45 | -0.48 | -0.56 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 227195_at | ZNF503 | zinc finger protein 503 | -1.18 | -1.41 | -1.37 | -1.52 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 237318_at | Slc43a2 | solute carrier family 43, member 2 | -1.45 | -1.63 | -1.73 | -1.74 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 240498_at | ETV6 | ets variant 6 | -1.00 | -0.69 | -0.79 | -0.80 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 240544_at | ZFAND3 | zinc finger, AN1-type domain 3 | -0.61 | -0.29 | -0.43 | -0.40 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 1553252_a_at | BRWD3 | bromodomain and WD repeat domain containing 3 | -0.50 | -0.22 | -0.18 | -0.32 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 1565598_at | RBM47 | RNA binding motif protein 47 | -1.72 | -1.73 | -2.07 | -1.82 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 220253_s_at | LRP12 | low density lipoprotein receptor-related protein 12 | -2.26 | -1.94 | -2.07 | -2.04 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 224311_s_at | CAB39 | calcium binding protein 39 | -0.43 | -0.12 | 0.00 | -0.22 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 244840_x_at | DOCK4 | dedicator of cytokinesis 4 | -1.16 | -1.51 | -1.61 | -1.61 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 202195_s_at | TMED5 | transmembrane emp24 protein transport domain containing 5 | -1.07 | -1.01 | -1.27 | -1.10 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 225188_at | RAPH1 | Ras association (RalGDS/AF-6) and pleckstrin homology domai | -1.64 | -1.70 | -2.01 | -1.79 | 0 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 231644_at | --- | --- | -1.36 | -1.60 | -1.56 | -1.69 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1555977_at | LOC727918 | hypothetical LOC727918 | 0.18 | 0.08 | 0.43 | 0.00 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 1570021_at | LOC360030 | homeobox C14 | -1.05 | -0.64 | -0.87 | -0.72 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 202600_s_at | NRIP1 | nuclear receptor interacting protein 1 | -0.99 | -0.70 | -0.71 | -0.78 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 218273_s_at | PDP1 | pyruvate dehyrogenase phosphatase catalytic subunit 1 | -0.41 | -0.09 | -0.04 | -0.17 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 222679_s_at | DCUN1D1 | DCN1, defective in cullin neddylation 1, domain containing 1 (S | -0.67 | -0.31 | -0.38 | -0.38 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 222880_at | AKT3 | v-akt murine thymoma viral oncogene homolog 3 (protein kina | -0.67 | -0.33 | -0.33 | -0.41 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 235451_at | SMAD5 | SMAD family member 5 | -0.67 | -0.33 | -0.42 | -0.41 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 236327_at | CEPT1 | choline/ethanolamine phosphotransferase 1 | -0.47 | -0.16 | -0.29 | -0.24 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 241345_at | MIR186 /// ZR | microRNA 186 /// zinc finger, RAN-binding domain containing | -0.49 | -0.10 | -0.12 | -0.18 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 202601_s_at | HTATSF1 | HIV-1 Tat specific factor 1 | -0.18 | -0.10 | 0.10 | -0.17 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 |
| 217513_at | C17orf60 | chromosome 17 open reading frame 60 | -1.03 | -1.25 | -1.28 | -1.32 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 217576_x_at | SOS2 | son of sevenless homolog 2 (Drosophila) | -0.22 | 0.03 | 0.11 | -0.04 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 227948_at | FGD4 | FYVE, RhoGEF and PH domain containing 4 | -1.17 | -1.37 | -1.45 | -1.45 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 228181_at | SLC30A1 | solute carrier family 30 (zinc transporter), member 1 | 0.03 | 0.15 | -0.15 | 0.08 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 238644_at | MYSM1 | Myb-like, SWIRM and MPN domains 1 | -0.43 | -0.28 | -0.08 | -0.35 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 |
| 238848_at | OTUD4 | OTU domain containing 4 | -0.60 | -0.28 | -0.22 | -0.35 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 1552553_a_at | NLRC4 | NLR family, CARD domain containing 4 | -1.27 | -1.58 | -1.56 | -1.64 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 1553575_at | ND6 | NADH dehydrogenase, subunit 6 (complex I) | 1.28 | 1.01 | 1.09 | 0.94 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1563445_x_at | CTSL1P8 | cathepsin L1 pseudogene 8 | -1.69 | -1.88 | -1.92 | -1.95 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 201299_s_at | MOBKL1B | MOB1, Mps One Binder kinase activator-like 1B (yeast) | -0.56 | -0.21 | -0.20 | -0.27 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 202869_at | OAS1 | 2',5'-oligoadenylate synthetase 1, 40/46kDa | -0.12 | -0.33 | -0.30 | -0.39 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 210282_at | ZMYM2 | zinc finger, MYM-type 2 | -0.41 | -0.01 | -0.19 | -0.07 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 210873_x_at | APOBEC3A | apolipoprotein B mRNA editing enzyme, catalytic polypeptide- | -0.41 | -0.65 | -0.60 | -0.71 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 213956_at | CEP350 | centrosomal protein 350kDa | -0.26 | 0.10 | 0.07 | 0.04 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 214483_s_at | ARFIP1 | ADP-ribosylation factor interacting protein 1 | -0.85 | -0.57 | -0.52 | -0.63 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 218854_at | DSE | dermatan sulfate epimerase | -1.54 | -1.51 | -1.78 | -1.57 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 219844_at | C10orf118 | chromosome 10 open reading frame 118 | -0.40 | -0.07 | -0.09 | -0.13 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 230742_at | RBM6 | RNA binding motif protein 6 | -0.11 | 0.16 | 0.20 | 0.10 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 244579_at | TRPS1 | trichorhinophalangeal syndrome I | -0.98 | -1.19 | -1.33 | -1.25 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 1555730_a_at | CFL1 | cofilin 1 (non-muscle) | -0.37 | -0.51 | -0.15 | -0.56 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 1563431_x_at | CALM3 | Calmodulin 3 (phosphorylase kinase, delta) | -0.21 | 0.13 | -0.02 | 0.08 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 204628_s_at | ITGB3 | integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) | -0.23 | 0.04 | -0.04 | -0.01 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 220220_at | LRRC37A4 | leucine rich repeat containing 37, member A4 (pseudogene) | -0.23 | 0.16 | 0.12 | 0.11 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 224618_at | ROD1 | ROD1 regulator of differentiation 1 (S. pombe) | -0.44 | -0.14 | -0.22 | -0.18 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 1556812_a_at | ANKRD44 | ankyrin repeat domain 44 | -0.20 | -0.05 | 0.20 | -0.09 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 |
| 1559954_s_at | DDX42 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 42 | -0.60 | -0.26 | -0.15 | -0.30 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 202430_s_at | PLSCR1 | phospholipid scramblase 1 | -1.12 | -1.36 | -1.31 | -1.40 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 212720_at | PAPOLA | poly(A) polymerase alpha | -0.89 | -0.61 | -0.56 | -0.65 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 226184_at | FMNL2 | formin-like 2 | -0.86 | -0.88 | -1.21 | -0.92 | 0 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 227259_at | CD47 | CD47 molecule | -0.20 | 0.15 | 0.08 | 0.11 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 241207_at | mkl1 | megakaryoblastic leukemia (translocation) 1 | -0.71 | -0.33 | -0.32 | -0.37 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 242248_at | PHKB | phosphorylase kinase, beta | -0.21 | 0.05 | 0.10 | 0.02 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 244774_at | PHACTR2 | phosphatase and actin regulator 2 | -0.94 | -0.54 | -0.58 | -0.58 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 33148_at | ZFR | zinc finger RNA binding protein | -0.82 | -0.40 | -0.41 | -0.44 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 1552978_a_at | SCAMP1 | secretory carrier membrane protein 1 | -0.52 | -0.29 | -0.10 | -0.32 | 0 | 1 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 1557626_at | --- | --- | -0.83 | -0.86 | -1.12 | -0.89 | 0 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 202241_at | TRIB1 | tribbles homolog 1 (Drosophila) | -1.17 | -1.15 | -1.43 | -1.18 | 1 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 209013_x_at | TRIO | triple functional domain (PTPRF interacting) | -1.38 | -1.06 | -1.17 | -1.08 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 211973_at | LOC10050762 | hypothetical LOC100507620 | -0.80 | -0.32 | -0.57 | -0.35 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 215767_at | ZNF804A | zinc finger protein 804A | -1.37 | -1.31 | -1.59 | -1.33 | 1 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 229841_at | EIF2C2 | eukaryotic translation initiation factor 2C, 2 | -0.32 | -0.04 | -0.14 | -0.07 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 230265_at | SEL1L | Sel-1 suppressor of lin-12-like (C. elegans) | -0.86 | -0.55 | -0.69 | -0.58 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 238220_at | KDM6A | lysine (K)-specific demethylase 6A | -0.57 | -0.24 | -0.34 | -0.26 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 1555594_a_at | MBNL1 | muscleblind-like (Drosophila) | -0.36 | -0.03 | 0.04 | -0.05 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 1569583_at | EREG | epiregulin | -0.66 | -1.11 | -1.32 | -1.14 | 1 | 1 | 1 | 0 | -1 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 200671_s_at | SPTBN1 | spectrin, beta, non-erythrocytic 1 | -0.29 | -0.05 | 0.04 | -0.08 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 203231_s_at | ATXN1 | ataxin 1 | -0.84 | -0.53 | -0.57 | -0.55 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 208178_x_at | TRIO | triple functional domain (PTPRF interacting) | -1.33 | -0.98 | -1.08 | -1.00 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 209599_s_at | PRUNE | prune homolog (Drosophila) | -0.15 | 0.07 | 0.11 | 0.05 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 212105_s_at | DHX9 | DEAH (Asp-Glu-Ala-His) box polypeptide 9 | -0.92 | -0.56 | -0.49 | -0.57 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 214834_at | PAR5 | Prader-Willi/Angelman syndrome-5 | -0.29 | -0.01 | 0.06 | -0.03 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 236023_at | CDK9 | cyclin-dependent kinase 9 | -0.83 | -0.49 | -0.62 | -0.51 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 236723_at | Hnrnpu | heterogeneous nuclear ribonucleoprotein U (scaffold attachme | -0.58 | -0.24 | -0.20 | -0.26 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 240636_at | C11orf61 | chromosome 11 open reading frame 61 | -0.31 | -0.07 | 0.02 | -0.09 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 240957_at | Vps26a | vacuolar protein sorting 26 homolog A (S. pombe) | -0.80 | -0.51 | -0.51 | -0.53 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 200928_s_at | RAB14 | RAB14, member RAS oncogene family | -0.40 | -0.04 | -0.14 | -0.05 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 224595_at | SLC44A1 | solute carrier family 44, member 1 | -1.13 | -1.28 | -1.51 | -1.29 | 0 | 1 | 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 227152_at | C12orf35 | chromosome 12 open reading frame 35 | -0.14 | 0.18 | 0.27 | 0.16 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 235011_at | MAP3K2 | mitogen-activated protein kinase kinase kinase 2 | -0.94 | -0.64 | -0.72 | -0.66 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 237118_at | ANP32A /// LC | hepatopoietin PCn127; acidic (leucine-rich) nuclear phosphopr | -0.52 | -0.17 | -0.18 | -0.18 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 237554_at | --- | --- | -0.86 | -0.46 | -0.61 | -0.47 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 239871_at | CLTC | Clathrin, heavy chain (Hc) | -0.54 | -0.32 | -0.22 | -0.33 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 224875_at | C5orf24 | chromosome 5 open reading frame 24 | -0.35 | -0.01 | -0.04 | -0.02 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 238884_at | CTNND1 | catenin (cadherin-associated protein), delta 1 | -0.89 | -0.59 | -0.59 | -0.59 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 239742_at | TULP4 | Tubby like protein 4 | -0.39 | -0.11 | -0.10 | -0.11 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 241155_at | PIP4K2A | phosphatidylinositol-5-phosphate 4-kinase, type II, alpha | -0.29 | -0.03 | -0.09 | -0.03 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 60815_at | POLR2J4 | polymerase (RNA) II (DNA directed) polypeptide J4, pseudogen | -0.48 | -0.25 | -0.19 | -0.26 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 1556336_at | RBMX | RNA binding motif protein, X-linked | -0.37 | -0.10 | 0.03 | -0.09 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 1558747_at | SMCHD1 | structural maintenance of chromosomes flexible hinge domain | -0.19 | -0.22 | 0.38 | -0.21 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 |
| 1562527_at | LOC283027 | hypothetical protein LOC283027 | 0.81 | 0.62 | 1.05 | 0.63 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 201073_s_at | SMARCC1 | SWI/SNF related, matrix associated, actin dependent regulator | -0.27 | -0.02 | -0.01 | 0.00 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 208575_at | HIST1H3A | histone cluster 1, H3a | -0.25 | 0.00 | 0.00 | 0.02 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 210436_at | CCT8 | chaperonin containing TCP1, subunit 8 (theta) | -0.34 | -0.12 | -0.02 | -0.11 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 212079_s_at | MLL | myeloid/lymphoid or mixed-lineage leukemia (trithorax homol | -0.37 | -0.09 | -0.01 | -0.09 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 221695_s_at | MAP3K2 | mitogen-activated protein kinase kinase kinase 2 | -0.67 | -0.44 | -0.34 | -0.43 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 222508_s_at | ARGLU1 | arginine and glutamate rich 1 | -0.10 | -0.01 | 0.18 | 0.00 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 223984_s_at | NUPL1 | nucleoporin like 1 | -0.82 | -0.49 | -0.52 | -0.48 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 224152_s_at | PBRM1 | polybromo 1 | -0.76 | -0.54 | -0.45 | -0.53 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 224940_s_at | PAPPA | pregnancy-associated plasma protein A, pappalysin 1 | 0.36 | 0.27 | 0.54 | 0.28 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 235577_at | ZNF652 | zinc finger protein 652 | -0.50 | -0.22 | -0.25 | -0.21 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 237625_s_at | --- | --- | -0.06 | 0.15 | 0.22 | 0.16 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 240613_at | JAK1 | Janus kinase 1 | -0.68 | -0.29 | -0.42 | -0.28 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 242429_at | ZNF567 | zinc finger protein 567 | -0.45 | -0.20 | -0.08 | -0.19 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 243064_at | mtif3 | mitochondrial translational initiation factor 3 | -0.21 | 0.03 | 0.07 | 0.04 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 213638_at | PHACTR1 | phosphatase and actin regulator 1 | -1.46 | -1.07 | -1.13 | -1.06 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 214352_s_at | KRAS | v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog | -0.33 | -0.08 | 0.00 | -0.06 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 215284_at | SNX9 | sorting nexin 9 | -0.47 | -0.20 | -0.28 | -0.18 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 218430_s_at | RFX7 | regulatory factor X, 7 | -0.33 | 0.04 | 0.13 | 0.05 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 235743_at | SNED1 | sushi, nidogen and EGF-like domains 1 | -0.35 | -0.06 | 0.11 | -0.05 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 237813_at | PCBP2 | poly(rC) binding protein 2 | -0.40 | -0.16 | -0.01 | -0.14 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 240246_at | LOC642236 | Similar to FRG1 protein (FSHD region gene 1 protein) | -0.57 | -0.21 | -0.24 | -0.19 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 241347_at | RNF213 | ring finger protein 213 | 0.04 | 0.31 | 0.45 | 0.33 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 241955_at | HECTD1 | HECT domain containing 1 | -0.59 | -0.33 | -0.19 | -0.31 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 1557278_s_at | TNPO1 | Transportin 1 | -0.45 | -0.01 | -0.09 | 0.02 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 204863_s_at | IL6ST | interleukin 6 signal transducer (gp130, oncostatin M receptor) | -0.30 | 0.03 | 0.00 | 0.06 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 211947_s_at | BAT2L2 | HLA-B associated transcript 2-like 2 | -0.30 | -0.03 | 0.11 | 0.01 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 213971_s_at | LOC10051052 | polycomb protein SUZ12-like /// suppressor of zeste 12 homol | -0.47 | -0.20 | -0.18 | -0.17 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 214806_at | BICD1 | bicaudal D homolog 1 (Drosophila) | -0.19 | -0.02 | 0.10 | 0.01 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 240165_at | --- | --- | 0.26 | 0.00 | -0.11 | 0.03 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 244804_at | SQSTM1 | sequestosome 1 | -0.16 | 0.07 | 0.15 | 0.10 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 208930_s_at | ILF3 | interleukin enhancer binding factor 3, 90kDa | -0.26 | -0.03 | 0.00 | 0.01 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 211965_at | ZFP36L1 | zinc finger protein 36, C3H type-like 1 | -0.28 | -0.11 | -0.02 | -0.07 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 212286_at | ANKRD12 | ankyrin repeat domain 12 | -0.32 | -0.01 | -0.14 | 0.03 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 214250_at | NUMA1 | nuclear mitotic apparatus protein 1 | -0.68 | -0.26 | -0.15 | -0.21 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 221705_s_at | SIKE1 | suppressor of IKBKE 1 | -0.40 | -0.18 | -0.07 | -0.14 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 222406_s_at | PNRC2 | proline-rich nuclear receptor coactivator 2 | -0.37 | -0.16 | -0.04 | -0.12 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 226975_at | RNPC3 | RNA-binding region (RNP1, RRM) containing 3 | -0.01 | 0.18 | 0.30 | 0.22 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 233309_at | Tmem2 | transmembrane protein 2 | -0.07 | 0.17 | 0.16 | 0.21 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 233543_s_at | FAM175A | family with sequence similarity 175, member A | -0.09 | 0.19 | 0.22 | 0.22 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 235765_at | TLE4 | transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila | -0.10 | 0.15 | 0.26 | 0.19 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 237577_at | PCNP | PEST proteolytic signal containing nuclear protein | -0.45 | 0.00 | 0.08 | 0.04 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 238159_at | --- | --- | -0.54 | -0.27 | -0.35 | -0.23 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 214499_s_at | BCLAF1 | BCL2-associated transcription factor 1 | -0.17 | 0.07 | 0.08 | 0.12 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 230064_at | --- | --- | -0.28 | 0.01 | 0.13 | 0.06 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 241947_at | LOC10023320 | hypothetical LOC100233209 | -0.06 | 0.17 | 0.18 | 0.22 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 243107_at | CCR7 | chemokine (C-C motif) receptor 7 | -0.27 | 0.01 | 0.28 | 0.07 | 1 | 1 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 243319_at | med31 | mediator complex subunit 31 | -0.48 | -0.17 | -0.24 | -0.12 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 206241_at | KPNA5 | karyopherin alpha 5 (importin alpha 6) | -0.69 | -0.44 | -0.49 | -0.37 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 211000_s_at | IL6ST | interleukin 6 signal transducer (gp130, oncostatin M receptor) | -0.42 | -0.15 | -0.15 | -0.09 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 211081_s_at | MAP4K5 | mitogen-activated protein kinase kinase kinase kinase 5 | -0.77 | -0.32 | -0.26 | -0.27 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 222634_s_at | TBL1XR1 | transducin (beta)-like 1 X-linked receptor 1 | -0.45 | -0.27 | -0.16 | -0.21 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 230028_at | kiaa0907 | KIAA0907 | -0.08 | 0.15 | 0.17 | 0.21 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 235009_at | BOD1L | biorientation of chromosomes in cell division 1-like | -0.35 | -0.08 | 0.27 | -0.02 | 1 | 1 | -1 | 0 | 1 | 0 | 1 | 0 | 1 | 1 | 1 | 1 |
| 236000_s_at | HNRNPD | heterogeneous nuclear ribonucleoprotein D (AU-rich element | -0.27 | -0.05 | 0.06 | 0.01 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 239798_at | --- | --- | 0.04 | 0.28 | 0.23 | 0.34 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 243332_at | GUSBP3 | glucuronidase, beta pseudogene; glucuronidase, beta pseudog | 0.63 | 0.54 | 0.94 | 0.59 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 1565436_s_at | MLL | myeloid/lymphoid or mixed-lineage leukemia (trithorax homol | -0.16 | 0.14 | 0.25 | 0.21 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 201085_s_at | SON | SON DNA binding protein | -0.32 | -0.11 | -0.07 | -0.04 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 210251_s_at | RUFY3 | RUN and FYVE domain containing 3 | -0.42 | -0.21 | -0.21 | -0.14 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 213430_at | RUFY3 | RUN and FYVE domain containing 3 | -0.49 | -0.14 | -0.25 | -0.07 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 223038_s_at | FAM60A | family with sequence similarity 60, member A | -0.02 | 0.20 | 0.35 | 0.27 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 227632_at | TBC1D24 | TBC1 domain family, member 24 | -0.53 | -0.22 | -0.29 | -0.16 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 236356_at | NDUFS1 | NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NAD | -0.64 | -0.28 | -0.40 | -0.21 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 1405_i_at | CCL5 | chemokine (C-C motif) ligand 5 | 0.46 | 0.67 | 0.65 | 0.75 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1557529_at | C12orf51 | chromosome 12 open reading frame 51 | -0.08 | 0.16 | 0.24 | 0.23 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 227101_at | ZNF800 | zinc finger protein 800 | -0.30 | -0.13 | 0.13 | -0.04 | 0 | 1 | -1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 236650_at | --- | --- | -0.14 | 0.06 | 0.16 | 0.14 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 242432_at | --- | --- | -0.67 | -0.30 | -0.25 | -0.22 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 244125_at | MGC70870 | C-terminal binding protein 2 pseudogene | 0.33 | 0.34 | 0.60 | 0.42 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 200607_s_at | RAD21 | RAD21 homolog (S. pombe) | -0.07 | -0.07 | 0.21 | 0.03 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 201065_s_at | GTF2I /// GTF2 | general transcription factor IIi /// general transcription factor I | -0.18 | 0.04 | 0.00 | 0.13 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 204192_at | CD37 | CD37 molecule | 0.00 | -0.05 | 0.24 | 0.03 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 205285_s_at | FYB | FYN binding protein | 0.47 | 0.37 | 0.72 | 0.46 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 214184_at | NPFF | neuropeptide FF-amide peptide precursor | -0.25 | -0.24 | -0.44 | -0.16 | 0 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 219864_s_at | RCAN3 | RCAN family member 3 | -0.54 | -0.35 | -0.22 | -0.26 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 229437_at | MIR155HG | MIR155 host gene (non-protein coding) | 0.85 | 1.10 | 1.02 | 1.20 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 219969_at | TXLNG | taxilin gamma | -0.45 | -0.26 | -0.16 | -0.15 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 230000_at | RNF213 | ring finger protein 213 | -0.16 | 0.09 | 0.11 | 0.19 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 236971_at | clu | clusterin | -0.36 | -0.11 | -0.09 | -0.02 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 242774_at | SYNE2 | spectrin repeat containing, nuclear envelope 2 | -0.20 | -0.12 | 0.29 | -0.01 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 |
| 212979_s_at | FAM115A | family with sequence similarity 115, member A | -0.09 | 0.14 | 0.08 | 0.25 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 217546_at | MT1M | metallothionein 1M | 2.03 | 2.17 | 1.81 | 2.29 | 0 | 1 | 0 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 235643_at | SAMD9L | sterile alpha motif domain containing 9-like | 0.30 | 0.16 | 0.58 | 0.27 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 239487_at | FAM98A | Family with sequence similarity 98, member A | -0.18 | -0.01 | 0.07 | 0.10 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 240990_at | rab5a | RAB5A, member RAS oncogene family | -0.68 | -0.39 | -0.39 | -0.28 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 244794_at | --- | --- | -0.46 | -0.27 | -0.26 | -0.16 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1564430_at | Bat2l2 | BAT2 domain containing 1 | -0.66 | -0.36 | -0.48 | -0.23 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 211538_s_at | HSPA2 | heat shock 70kDa protein 2 | -0.53 | -0.27 | -0.35 | -0.15 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 222538_s_at | APPL1 | adaptor protein, phosphotyrosine interaction, PH domain and | -0.23 | -0.04 | 0.04 | 0.08 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 241508_at | ANKRD12 | ankyrin repeat domain 12 | -0.26 | 0.04 | 0.00 | 0.16 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 204560_at | FKBP5 | FK506 binding protein 5 | -0.09 | 0.11 | 0.15 | 0.25 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 218404_at | SNX10 | sorting nexin 10 | -1.10 | -0.81 | -0.88 | -0.68 | 1 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 242672_at | Rftn1 | raftlin, lipid raft linker 1 | -0.11 | 0.08 | 0.34 | 0.20 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 236505_at | NUP62 | Nucleoporin 62kDa | -0.42 | -0.73 | -0.68 | -0.59 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 203394_s_at | HES1 | hairy and enhancer of split 1, (Drosophila) | 0.87 | 1.13 | 1.14 | 1.28 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 241859_at | PLCL1 | phospholipase C-like 1 | -0.29 | -0.05 | -0.11 | 0.10 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 244791_at | UBAC2 | UBA domain containing 2 | -0.43 | -0.22 | -0.12 | -0.07 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 230352_at | PRPS2 | Phosphoribosyl pyrophosphate synthetase 2 | -0.32 | -0.09 | -0.02 | 0.07 | 0 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 1558971_at | THEMIS | thymocyte selection associated | 0.01 | 0.10 | 0.09 | 0.28 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1559776_at | gm2a | GM2 ganglioside activator | -0.28 | -0.15 | -0.21 | 0.02 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 204165_at | WASF1 | WAS protein family, member 1 | -0.27 | 0.02 | -0.16 | 0.20 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 1 | 1 |
| 240248_at | C10orf46 | chromosome 10 open reading frame 46 | -0.45 | -0.19 | -0.29 | -0.01 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 1 | 1 |
| 243375_at | GRIK1 | glutamate receptor, ionotropic, kainate 1 | -0.15 | -0.04 | -0.14 | 0.13 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 204686_at | IRS1 | insulin receptor substrate 1 | -0.04 | 0.07 | -0.05 | 0.25 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 216117_at | EXOSC2 | exosome component 2 | -0.28 | -0.20 | -0.31 | -0.02 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 223681_s_at | INADL | InaD-like (Drosophila) | -0.13 | 0.01 | -0.10 | 0.19 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 228155_at | C10orf58 | chromosome 10 open reading frame 58 | -0.17 | 0.03 | 0.00 | 0.21 | 0 | 1 | -1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 231873_at | BMPR2 | bone morphogenetic protein receptor, type II (serine/threonin | -0.61 | -0.45 | -0.60 | -0.27 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 232740_at | MCM3AP-AS | MCM3AP antisense RNA (non-protein coding) | -0.08 | -0.03 | -0.11 | 0.16 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 235172_at | --- | --- | -0.40 | -0.18 | -0.16 | 0.00 | 0 | 1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1562255_at | SYTL3 | synaptotagmin-like 3 | 0.00 | -0.30 | 0.09 | -0.11 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 |
| 1570255_s_at | ANKRD20A1 // | ankyrin repeat domain 20 family, member A1 /// ankyrin repea | 1.04 | 0.65 | 1.13 | 0.84 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 |
| 201689_s_at | TPD52 | tumor protein D52 | -0.18 | -0.09 | -0.09 | 0.10 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 201694_s_at | EGR1 | early growth response 1 | -1.07 | -0.84 | -0.82 | -0.65 | 0 | 1 | -1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 206398_s_at | CD19 | CD19 molecule | -0.08 | 0.02 | 0.01 | 0.21 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 220643_s_at | FAIM | Fas apoptotic inhibitory molecule | -0.71 | -0.58 | -0.62 | -0.39 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 229553_at | PGM2L1 | phosphoglucomutase 2-like 1 | 0.03 | 0.17 | 0.19 | 0.36 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 229850_at | KDSR | 3-ketodihydrosphingosine reductase | 0.06 | 0.28 | 0.16 | 0.47 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 229869_at | --- | --- | 0.12 | 0.22 | 0.16 | 0.41 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 231108_at | FUS | fused in sarcoma | -0.22 | -0.04 | -0.11 | 0.15 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 232181_at | PPARGC1B | peroxisome proliferator-activated receptor gamma, coactivato | -0.34 | -0.22 | -0.34 | -0.04 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 242540_at | DNHD1 | dynein heavy chain domain 1 | -0.30 | -0.17 | -0.27 | 0.02 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 243655_x_at | SMARCA4 | SWI/SNF related, matrix associated, actin dependent regulator | -0.29 | -0.21 | -0.21 | -0.02 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1559006_at | --- | --- | -0.31 | -0.24 | -0.33 | -0.04 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1569352_at | FNIP2 | folliculin interacting protein 2 | -2.19 | -1.96 | -2.06 | -1.77 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 242929_at | Rhoh | ras homolog gene family, member H | -0.69 | -0.39 | -0.30 | -0.19 | 1 | 1 | -1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 |
| 203940_s_at | VASH1 | vasohibin 1 | -0.89 | -0.85 | -0.96 | -0.64 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 218930_s_at | TMEM106B | transmembrane protein 106B | -0.06 | 0.00 | 0.00 | 0.21 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 224435_at | C10orf58 | chromosome 10 open reading frame 58 | -0.19 | -0.08 | -0.15 | 0.13 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 238470_at | SYS1 | SYS1 Golgi-localized integral membrane protein homolog (S. ce | -0.36 | -0.25 | -0.38 | -0.04 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 239661_at | AFF1 | AF4/FMR2 family, member 1 | -0.38 | -0.23 | -0.28 | -0.02 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1557113_at | LOC283588 | hypothetical LOC283588 | -0.22 | -0.11 | -0.18 | 0.11 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1565887_at | TRPM7 | Transient receptor potential cation channel, subfamily M, mem | -0.22 | -0.15 | -0.21 | 0.07 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 202814_s_at | HEXIM1 | hexamethylene bis-acetamide inducible 1 | -0.28 | -0.17 | -0.19 | 0.05 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 206279_at | PRKY | protein kinase, Y-linked | -0.08 | -0.02 | -0.07 | 0.20 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 212592_at | IGJ | immunoglobulin J polypeptide, linker protein for immunoglobu | 0.19 | 0.30 | 0.32 | 0.52 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 214705_at | INADL | InaD-like (Drosophila) | 0.17 | 0.28 | 0.14 | 0.51 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 219922_s_at | LTBP3 | latent transforming growth factor beta binding protein 3 | 0.10 | 0.16 | 0.10 | 0.38 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 220068_at | VPREB3 | pre-B lymphocyte 3 | 0.02 | 0.19 | 0.21 | 0.41 | 0 | 1 | -1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 228170_at | OLIG1 | oligodendrocyte transcription factor 1 | -1.91 | -2.18 | -2.00 | -1.96 | 1 | 1 | 0 | -1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 200832_s_at | SCD | stearoyl-CoA desaturase (delta-9-desaturase) | -0.60 | -0.35 | -0.44 | -0.12 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 202581_at | HSPA1A /// HS | heat shock 70kDa protein 1A /// heat shock 70kDa protein 1B | -0.14 | 0.11 | 0.09 | 0.34 | 0 | 1 | -1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 215462_at | PLK3 | polo-like kinase 3 | -0.41 | -0.37 | -0.36 | -0.15 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 217951_s_at | PHF3 | PHD finger protein 3 | -0.15 | -0.09 | -0.04 | 0.14 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 229513_at | STRBP | spermatid perinuclear RNA binding protein | -0.16 | 0.02 | -0.05 | 0.25 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 234150_at | --- | --- | 0.20 | 0.25 | 0.23 | 0.48 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 240019_at | --- | --- | -0.24 | -0.09 | -0.05 | 0.14 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 205267_at | POU2AF1 | POU class 2 associating factor 1 | -0.35 | -0.21 | -0.20 | 0.03 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 230896_at | BEND4 | BEN domain containing 4 | -0.47 | -0.33 | -0.41 | -0.09 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 239278_at | --- | --- | 0.01 | 0.10 | 0.12 | 0.34 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 205934_at | PLCL1 | phospholipase C-like 1 | -0.43 | -0.34 | -0.35 | -0.09 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 209321_s_at | ADCY3 | adenylate cyclase 3 | 0.30 | 0.38 | 0.40 | 0.63 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 233251_at | STRBP | Spermatid perinuclear RNA binding protein | -0.44 | -0.18 | -0.16 | 0.07 | 0 | 1 | -1 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 1 |
| 239649_at | gtf2i /// LOC1 | general transcription factor II, i; general transcription factor II, | -0.46 | -0.27 | -0.34 | -0.03 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1558279_a_at | KDSR | 3-ketodihydrosphingosine reductase | -0.28 | 0.00 | -0.12 | 0.26 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 1 | 1 |
| 202759_s_at | AKAP2 /// PAL | A kinase (PRKA) anchor protein 2 /// PALM2-AKAP2 readthrou | -0.71 | -0.60 | -0.51 | -0.34 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 211721_s_at | ZNF551 | zinc finger protein 551 | -0.10 | -0.10 | -0.05 | 0.17 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 219518_s_at | ELL3 /// SERIN | elongation factor RNA polymerase II-like 3 /// serine incorpora | -0.34 | -0.18 | -0.16 | 0.08 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| 242509_at | C16orf74 | chromosome 16 open reading frame 74 | -0.35 | -0.35 | -0.38 | -0.09 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 210845_s_at | PLAUR | plasminogen activator, urokinase receptor | -1.40 | -1.56 | -1.93 | -1.99 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 219869_s_at | SLC39A8 | solute carrier family 39 (zinc transporter), member 8 | -0.33 | -0.31 | -0.58 | -0.71 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1553626_a_at | C17orf57 | chromosome 17 open reading frame 57 | -0.16 | 0.25 | 0.27 | -0.13 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 1 | 1 | 0 |
| 209267_s_at | SLC39A8 | solute carrier family 39 (zinc transporter), member 8 | -0.17 | -0.24 | -0.57 | -0.62 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 200612_s_at | AP2B1 | adaptor-related protein complex 2, beta 1 subunit | 0.35 | 0.63 | 0.70 | 0.26 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 1 | 1 | 0 |
| 238727_at | LOC440934 | hypothetical LOC440934 | 0.68 | 0.59 | 0.18 | 0.22 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 223168_at | RHOU | ras homolog gene family, member U | -0.73 | -0.84 | -1.18 | -1.21 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 210042_s_at | CTSZ | cathepsin Z | -0.32 | -0.44 | -0.74 | -0.79 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 44783_s_at | HEY1 | hairy/enhancer-of-split related with YRPW motif 1 | 0.06 | -0.09 | -0.27 | -0.42 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 216504_s_at | SLC39A8 | solute carrier family 39 (zinc transporter), member 8 | -0.43 | -0.42 | -0.71 | -0.75 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 230703_at | MAPK1IP1L | mitogen-activated protein kinase 1 interacting protein 1-like | -0.21 | 0.04 | 0.00 | -0.26 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 236228_at | LOC10013074 | hypothetical LOC100130744 | 0.50 | 0.69 | 0.58 | 0.38 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 216392_s_at | SEC23IP | SEC23 interacting protein | -0.44 | -0.22 | -0.22 | -0.51 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 |
| 230085_at | PDK3 | pyruvate dehydrogenase kinase, isozyme 3 | -0.02 | 0.22 | 0.21 | -0.07 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 |
| 201200_at | CREG1 | cellular repressor of E1A-stimulated genes 1 | -1.96 | -1.81 | -2.17 | -2.09 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 |
| 213469_at | PGAP1 | post-GPI attachment to proteins 1 | -0.60 | -0.60 | -0.81 | -0.89 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 215169_at | SLC35E2 | solute carrier family 35, member E2 | 0.12 | 0.49 | 0.41 | 0.21 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 |
| 1563321_s_at | MLLT10 | myeloid/lymphoid or mixed-lineage leukemia (trithorax homol | 0.25 | 0.44 | 0.32 | 0.17 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 204926_at | INHBA | inhibin, beta A | -0.70 | -0.49 | -0.63 | -0.76 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 205088_at | MAMLD1 | mastermind-like domain containing 1 | -0.66 | -0.65 | -0.91 | -0.91 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 |
| 211732_x_at | HNMT | histamine N-methyltransferase | 0.01 | -0.08 | -0.25 | -0.36 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 204735_at | PDE4A | phosphodiesterase 4A, cAMP-specific | -0.94 | -1.08 | -1.26 | -1.35 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 208721_s_at | ANAPC5 | anaphase promoting complex subunit 5 | 0.10 | 0.25 | 0.28 | -0.02 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 |
| 210519_s_at | NQO1 | NAD(P)H dehydrogenase, quinone 1 | -0.86 | -0.71 | -1.13 | -0.97 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 0 |
| 1557224_at | FAR2 | fatty acyl CoA reductase 2 | -0.07 | -0.17 | -0.22 | 0.10 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1559691_at | NDUFS1 | NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NAD | -0.10 | -0.28 | -0.18 | -0.02 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1563147_at | --- | --- | 0.03 | -0.07 | 0.05 | 0.20 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1570566_at | LOC10028752 | Hypothetical protein LOC100287529 | -0.10 | -0.27 | -0.08 | 0.00 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 214778_at | MEGF8 | multiple EGF-like-domains 8 | -0.23 | -0.37 | -0.29 | -0.10 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 215086_at | IBTK | inhibitor of Bruton agammaglobulinemia tyrosine kinase | -0.29 | -0.44 | -0.31 | -0.17 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 234041_at | --- | --- | -1.07 | -1.18 | -1.18 | -0.92 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 236582_at | Cpsf6 | cleavage and polyadenylation specific factor 6, 68kDa | -0.27 | -0.31 | -0.17 | -0.05 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1555225_at | C1orf43 | chromosome 1 open reading frame 43 | -0.49 | -0.68 | -0.56 | -0.41 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1556204_a_at | LOC10050781 | hypothetical LOC100507816 /// zinc finger protein 814 | -0.49 | -0.42 | -0.17 | -0.15 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1558670_at | Plekhm2 | pleckstrin homology domain containing, family M (with RUN d | -0.46 | -0.66 | -0.54 | -0.39 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1562033_at | --- | --- | -0.16 | -0.30 | -0.31 | -0.03 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1565888_at | tab2 | mitogen-activated protein kinase kinase kinase 7 interacting pr | 0.06 | -0.10 | -0.06 | 0.17 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1567032_s_at | ZNF160 | zinc finger protein 160 | -0.06 | -0.20 | 0.03 | 0.07 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1570165_at | CHST11 | carbohydrate (chondroitin 4) sulfotransferase 11 | -0.87 | -1.03 | -0.96 | -0.76 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 208268_at | ADAM28 | ADAM metallopeptidase domain 28 | -0.36 | -0.23 | -0.12 | 0.04 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 209508_x_at | CFLAR | CASP8 and FADD-like apoptosis regulator | -0.37 | -0.54 | -0.48 | -0.27 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 214808_at | --- | --- | -0.08 | -0.21 | -0.12 | 0.06 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 215645_at | FLCN | folliculin | -0.35 | -0.56 | -0.50 | -0.29 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 215892_at | ZNF440 | Zinc finger protein 440 | -0.07 | -0.12 | -0.01 | 0.15 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 217536_x_at | --- | --- | -0.04 | -0.20 | -0.08 | 0.08 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 227918_s_at | ZYG11B | zyg-11 homolog B (C. elegans) | -0.72 | -0.56 | -0.36 | -0.29 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 232425_at | SNX25 | sorting nexin 25 | 0.07 | -0.06 | 0.18 | 0.20 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 232927_at | TMTC2 | transmembrane and tetratricopeptide repeat containing 2 | 0.02 | -0.08 | 0.03 | 0.19 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 234210_x_at | ACTR2 | ARP2 actin-related protein 2 homolog (yeast) | -0.42 | -0.53 | -0.45 | -0.26 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 237346_at | TGDS | TDP-glucose 4,6-dehydratase | 0.17 | -0.02 | 0.13 | 0.25 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 239900_x_at | --- | --- | -0.10 | -0.24 | -0.18 | 0.04 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 242851_at | KIAA1919 | KIAA1919 | -0.17 | -0.29 | -0.26 | -0.03 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1552729_at | SNHG7 | small nucleolar RNA host gene 7 (non-protein coding) | 0.26 | 0.16 | 0.32 | 0.43 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1554602_at | RBM8A | RNA binding motif protein 8A | 0.44 | 0.30 | 0.53 | 0.57 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1555425_x_at | SSH2 | slingshot homolog 2 (Drosophila) | -0.11 | -0.26 | -0.14 | 0.02 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1560095_s_at | GNB5 | guanine nucleotide binding protein (G protein), beta 5 | 0.00 | -0.16 | -0.04 | 0.11 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1570048_at | DNAJC24 | DnaJ (Hsp40) homolog, subfamily C, member 24 | -0.02 | -0.16 | -0.04 | 0.13 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 211317_s_at | CFLAR | CASP8 and FADD-like apoptosis regulator | -0.46 | -0.67 | -0.58 | -0.39 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 215083_at | PSPC1 /// LOC | paraspeckle component 1; paraspeckle protein 1 pseudogene | -0.22 | -0.41 | -0.37 | -0.13 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 215933_s_at | HHEX | hematopoietically expressed homeobox | -0.77 | -0.80 | -0.61 | -0.51 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 216029_at | --- | --- | 0.00 | -0.15 | -0.02 | 0.13 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 226825_s_at | TMEM165 | transmembrane protein 165 | -0.50 | -0.79 | -0.65 | -0.51 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 |
| 229514_at | C14orf118 | chromosome 14 open reading frame 118 | -0.31 | -0.46 | -0.42 | -0.18 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 232049_at | --- | --- | -0.09 | -0.22 | -0.10 | 0.06 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 232905_at | GTF2H5 | general transcription factor IIH, polypeptide 5 | 0.00 | -0.13 | -0.05 | 0.16 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 234596_at | --- | --- | -0.20 | -0.36 | -0.24 | -0.07 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 237958_at | MCPH1 | microcephalin 1 | -0.36 | -0.32 | -0.14 | -0.04 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 238011_at | C16orf72 | chromosome 16 open reading frame 72 | -1.03 | -0.89 | -0.76 | -0.61 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 238635_at | C5orf28 | chromosome 5 open reading frame 28 | -0.44 | -0.32 | -0.12 | -0.04 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 241658_at | --- | --- | -0.45 | -0.59 | -0.47 | -0.31 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 241774_at | --- | --- | -0.15 | -0.26 | -0.09 | 0.02 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 243042_at | FAM73A | family with sequence similarity 73, member A | -0.07 | -0.19 | -0.08 | 0.08 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 243055_at | NKTR | natural killer-tumor recognition sequence | 0.04 | -0.10 | 0.05 | 0.17 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1556035_s_at | ZNF207 | zinc finger protein 207 | -0.15 | -0.24 | -0.11 | 0.04 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1560332_at | CHST11 | carbohydrate (chondroitin 4) sulfotransferase 11 | -0.88 | -1.01 | -0.97 | -0.72 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 205917_at | ZNF264 | zinc finger protein 264 | -0.48 | -0.62 | -0.54 | -0.33 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 215336_at | AKAP11 | A kinase (PRKA) anchor protein 11 | 0.10 | -0.13 | -0.06 | 0.17 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 217666_at | SIDT1 | SID1 transmembrane family, member 1 | -0.23 | -0.41 | -0.25 | -0.11 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 220494_s_at | --- | --- | 0.17 | -0.03 | 0.09 | 0.26 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 220735_s_at | SENP7 | SUMO1/sentrin specific peptidase 7 | -0.19 | -0.16 | 0.09 | 0.13 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 221276_s_at | SYNC | syncoilin, intermediate filament protein | -0.30 | -0.31 | -0.18 | -0.02 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 229060_at | YPEL2 | yippee-like 2 (Drosophila) | -0.13 | -0.10 | 0.11 | 0.19 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 232418_at | LZTFL1 | leucine zipper transcription factor-like 1 | -0.12 | -0.29 | -0.15 | 0.01 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 232991_at | ARL17A /// AR | ADP-ribosylation factor-like 17 pseudogene 1; ADP-ribosylatior | 0.15 | -0.09 | 0.03 | 0.19 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 233224_at | kpna3 | karyopherin alpha 3 (importin alpha 4) | -0.11 | -0.24 | -0.18 | 0.06 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 233440_at | --- | --- | -0.03 | -0.21 | -0.11 | 0.07 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 233596_at | uimc1 | ubiquitin interaction motif containing 1 | -0.20 | -0.35 | -0.26 | -0.06 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 234260_at | CDC42SE2 | CDC42 small effector 2 | 0.12 | -0.04 | -0.01 | 0.26 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 |
| 238932_at | --- | --- | -0.16 | -0.30 | -0.17 | -0.01 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 239827_at | C13orf15 | Chromosome 13 open reading frame 15 | -0.55 | -0.51 | -0.32 | -0.21 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 243026_x_at | XIAP | X-linked inhibitor of apoptosis | -0.55 | -0.70 | -0.63 | -0.42 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1555938_x_at | VIM | vimentin | -0.21 | -0.14 | -0.01 | 0.16 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1559044_at | EXOSC1 | exosome component 1 | -0.21 | -0.27 | -0.06 | 0.04 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1561924_at | TOPBP1 | topoisomerase (DNA) II binding protein 1 | -0.15 | -0.31 | -0.23 | -0.01 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1566142_at | GBF1 | golgi-specific brefeldin A resistant guanine nucleotide exchang | -0.26 | -0.43 | -0.38 | -0.13 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1569387_at | CSGALNACT1 | Chondroitin sulfate N-acetylgalactosaminyltransferase 1 | 0.28 | 0.07 | 0.24 | 0.38 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 208485_x_at | CFLAR | CASP8 and FADD-like apoptosis regulator | -0.48 | -0.68 | -0.59 | -0.38 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 215203_at | GOLGA4 | golgin A4 | 0.01 | -0.13 | -0.01 | 0.17 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 216614_at | ITPR2 | inositol 1,4,5-triphosphate receptor, type 2 | -0.18 | -0.34 | -0.35 | -0.04 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 |
| 231875_at | KIF21A | kinesin family member 21A | -0.05 | -0.18 | 0.05 | 0.12 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 232705_at | LRRFIP2 | Leucine rich repeat (in FLII) interacting protein 2 | -0.12 | -0.30 | -0.20 | 0.00 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 233377_at | ARID5B | AT rich interactive domain 5B (MRF1-like) | -0.20 | -0.28 | -0.14 | 0.01 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 233832_at | --- | --- | -0.19 | -0.43 | -0.34 | -0.13 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 242337_at | IGBP1 /// C14 | chromosome 14 open reading frame 19; immunoglobulin (CD7 | -0.08 | -0.24 | -0.09 | 0.06 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1553145_at | FLJ39653 | hypothetical FLJ39653 | -0.10 | -0.25 | -0.13 | 0.06 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1553165_at | SYNRG | synergin, gamma | -0.02 | -0.17 | -0.11 | 0.15 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1556654_at | --- | --- | -0.22 | -0.43 | -0.35 | -0.13 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1557736_at | NKTR | natural killer-tumor recognition sequence | -0.30 | -0.45 | -0.41 | -0.15 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1559121_s_at | ARIH2 | Ariadne homolog 2 (Drosophila) | -0.30 | -0.46 | -0.39 | -0.15 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1559232_a_at | slc33a1 | solute carrier family 33 (acetyl-CoA transporter), member 1 | -0.06 | -0.31 | -0.15 | 0.00 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1562938_at | GPAT2 /// LOC | hypothetical protein LOC150763; similar to hCG1732629; simil | 0.05 | -0.14 | -0.07 | 0.17 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1565703_at | SMAD4 | SMAD family member 4 | 0.00 | -0.23 | -0.17 | 0.08 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1565811_at | Ppp3r1 | protein phosphatase 3 (formerly 2B), regulatory subunit B, alp | -0.02 | -0.12 | 0.03 | 0.19 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1568997_at | POLR1E | polymerase (RNA) I polypeptide E, 53kDa | -0.16 | -0.32 | -0.17 | -0.01 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1570339_x_at | --- | --- | -0.62 | -0.86 | -0.73 | -0.55 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 232556_at | --- | --- | 0.24 | 0.10 | 0.36 | 0.41 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 232704_s_at | LRRFIP2 | leucine rich repeat (in FLII) interacting protein 2 | -0.28 | -0.49 | -0.38 | -0.19 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 239954_at | ZNF160 | zinc finger protein 160 | -0.13 | -0.46 | -0.31 | -0.15 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 |
| 242403_at | ube2d3 /// UB | ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast); | -0.05 | -0.26 | -0.16 | 0.05 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 243108_at | RANBP9 | RAN binding protein 9 | -0.56 | -0.52 | -0.32 | -0.21 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1557064_s_at | HGSNAT | heparan-alpha-glucosaminide N-acetyltransferase | -0.31 | -0.45 | -0.30 | -0.13 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1559528_at | LOC10012991 | hypothetical LOC100129917 | -0.39 | -0.48 | -0.29 | -0.16 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1559739_at | CHPT1 | Choline phosphotransferase 1 | 0.25 | 0.06 | 0.18 | 0.38 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1565804_at | ATXN1 | ataxin 1 | -0.61 | -0.79 | -0.80 | -0.47 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1566448_at | CD6 | CD6 molecule | 0.44 | 0.29 | 0.46 | 0.61 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1569927_at | Msh2 | mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli) | -0.09 | -0.29 | -0.12 | 0.03 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1570441_at | NAPB | N-ethylmaleimide-sensitive factor attachment protein, beta | -0.13 | -0.30 | -0.11 | 0.02 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 210701_at | CFDP1 | craniofacial development protein 1 | -0.24 | -0.46 | -0.46 | -0.14 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 |
| 215281_x_at | POGZ | pogo transposable element with ZNF domain | -0.13 | -0.32 | -0.21 | 0.00 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 224402_s_at | FCRL4 | Fc receptor-like 4 | -0.66 | -0.67 | -0.36 | -0.35 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 1 |
| 233374_at | Hic2 | hypermethylated in cancer 2 | -0.57 | -0.69 | -0.54 | -0.38 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 235680_at | Stat3 | signal transducer and activator of transcription 3 (acute-phase | -0.04 | -0.33 | -0.17 | -0.01 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 |
| 240513_at | EIF3M | Eukaryotic translation initiation factor 3, subunit M | -0.05 | -0.18 | -0.01 | 0.14 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 243037_at | FUBP1 | far upstream element (FUSE) binding protein 1 | -0.10 | -0.26 | -0.26 | 0.05 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1555476_at | IREB2 | iron-responsive element binding protein 2 | -0.05 | -0.19 | 0.05 | 0.14 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1569098_s_at | TP53BP1 | tumor protein p53 binding protein 1 | -0.29 | -0.43 | -0.23 | -0.10 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 215213_at | NUP54 | nucleoporin 54kDa | 0.00 | -0.25 | -0.11 | 0.08 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 215599_at | GUSBP3 | glucuronidase, beta pseudogene 3 | 0.20 | 0.07 | 0.28 | 0.40 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 232622_at | Prkce | protein kinase C, epsilon | -0.05 | -0.21 | -0.08 | 0.12 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 243771_at | PPP1R16B | protein phosphatase 1, regulatory (inhibitor) subunit 16B | -0.27 | -0.30 | -0.13 | 0.04 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1554543_at | SPAG9 | sperm associated antigen 9 | -0.85 | -1.05 | -1.01 | -0.71 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1559964_at | FLJ38717 | FLJ38717 protein | -0.22 | -0.51 | -0.40 | -0.17 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 |
| 1568964_x_at | SPN | sialophorin | 0.00 | -0.18 | -0.08 | 0.16 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 215013_s_at | USP34 | ubiquitin specific peptidase 34 | -0.15 | -0.37 | -0.25 | -0.03 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 216783_at | C15orf60 | chromosome 15 open reading frame 60 | -0.63 | -0.80 | -0.68 | -0.46 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 220710_at | C15orf28 | chromosome 15 open reading frame 28 | -0.24 | -0.42 | -0.35 | -0.08 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 |
| 233458_at | POLR3E | polymerase (RNA) III (DNA directed) polypeptide E (80kD) | 0.01 | -0.25 | -0.09 | 0.09 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 |
| 241869_at | APOL6 | apolipoprotein L, 6 | -0.06 | -0.27 | -0.14 | 0.08 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 243878_at | FOXP1 | forkhead box P1 | -0.06 | -0.04 | 0.14 | 0.30 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 39313_at | WNK1 | WNK lysine deficient protein kinase 1 | -0.33 | -0.52 | -0.41 | -0.18 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1552622_s_at | LOC441259 //, | PMS2 postmeiotic segregation increased 2 (S. cerevisiae)-like / | -0.19 | -0.34 | -0.16 | 0.01 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1563226_at | SLC38A10 | solute carrier family 38, member 10 | -0.35 | -0.55 | -0.40 | -0.19 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1566485_at | FHIT | fragile histidine triad gene | -0.24 | -0.35 | -0.16 | 0.00 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 215521_at | PHC3 | polyhomeotic homolog 3 (Drosophila) | -0.12 | -0.36 | -0.25 | -0.01 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 217591_at | Skil | SKI-like oncogene | -0.68 | -0.86 | -0.76 | -0.51 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1570439_at | MAP3K4 | mitogen-activated protein kinase kinase kinase 4 | -0.24 | -0.44 | -0.41 | -0.08 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 |
| 242029_at | FNDC3B | Fibronectin type III domain containing 3B | -1.21 | -1.45 | -1.32 | -1.09 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1559154_at | SNX1 | sorting nexin 1 | -0.27 | -0.49 | -0.43 | -0.11 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 |
| 224321_at | TMEFF2 | transmembrane protein with EGF-like and two follistatin-like d | -0.89 | -0.87 | -0.64 | -0.50 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 228643_at | --- | --- | -1.14 | -1.03 | -0.69 | -0.66 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 238013_at | PLEKHA2 | pleckstrin homology domain containing, family A (phosphoinos | -0.88 | -0.89 | -0.62 | -0.52 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 241702_at | HNRNPD | heterogeneous nuclear ribonucleoprotein D (AU-rich element | -0.33 | -0.42 | -0.20 | -0.04 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1557571_at | VPS13D | Vacuolar protein sorting 13 homolog D (S. cerevisiae) | -0.65 | -0.76 | -0.49 | -0.34 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1559500_at | VPS8 | vacuolar protein sorting 8 homolog (S. cerevisiae) | -0.77 | -0.85 | -0.58 | -0.44 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1560741_at | SNRPN | small nuclear ribonucleoprotein polypeptide N | 0.15 | -0.11 | 0.05 | 0.30 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1569091_at | zmym2 | zinc finger, MYM-type 2 | -0.45 | -0.71 | -0.61 | -0.30 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 |
| 1569503_at | HEATR5B | HEAT repeat containing 5B | -0.27 | -0.52 | -0.42 | -0.11 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 |
| 215262_at | --- | --- | -0.07 | -0.18 | 0.10 | 0.24 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 240482_at | HDAC3 | histone deacetylase 3 | -0.38 | -0.49 | -0.24 | -0.08 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1560422_at | paaF1 | proteasomal ATPase-associated factor 1 | 0.16 | -0.13 | 0.03 | 0.30 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 1 | 0 |
| 1561181_at | ARID5B | AT rich interactive domain 5B (MRF1-like) | -0.34 | -0.64 | -0.48 | -0.20 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1559347_at | CNOT4 | CCR4-NOT transcription complex, subunit 4 | -0.14 | -0.47 | -0.32 | 0.02 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 1 | 0 |
| 221085_at | TNFSF15 | tumor necrosis factor (ligand) superfamily, member 15 | -0.46 | -0.91 | -0.76 | -0.34 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 212942_s_at | KIAA1199 | KIAA1199 | -1.39 | -1.42 | -2.22 | -2.30 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 203939_at | NT5E | 5'-nucleotidase, ecto (CD73) | -0.70 | -0.87 | -1.47 | -1.54 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 222939_s_at | SLC16A10 | solute carrier family 16, member 10 (aromatic amino acid tran | -1.75 | -1.90 | -2.38 | -2.49 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 218468_s_at | GREM1 | gremlin 1 | -3.00 | -3.15 | -3.90 | -3.74 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 202948_at | IL1R1 | interleukin 1 receptor, type I | -0.37 | -0.54 | -1.16 | -1.04 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 1558871_at | --- | --- | -0.55 | -0.62 | -1.13 | -1.12 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 205403_at | IL1R2 | interleukin 1 receptor, type II | -0.87 | -0.80 | -1.30 | -1.30 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 1553995_a_at | NT5E | 5'-nucleotidase, ecto (CD73) | -0.47 | -0.52 | -0.97 | -0.99 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 207016_s_at | ALDH1A2 | aldehyde dehydrogenase 1 family, member A2 | -1.44 | -1.48 | -2.03 | -1.94 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 225436_at | FAM108C1 | family with sequence similarity 108, member C1 | -1.06 | -1.07 | -1.57 | -1.54 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 1553994_at | NT5E | 5'-nucleotidase, ecto (CD73) | -0.40 | -0.39 | -0.77 | -0.83 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 211372_s_at | IL1R2 | interleukin 1 receptor, type II | -0.72 | -0.63 | -1.00 | -1.05 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 224918_x_at | MGST1 | microsomal glutathione S-transferase 1 | -2.16 | -2.20 | -2.78 | -2.62 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 236220_at | --- | --- | -2.42 | -2.39 | -2.78 | -2.81 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 211776_s_at | EPB41L3 | erythrocyte membrane protein band 4.1-like 3 | -1.33 | -1.49 | -1.78 | -1.88 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 214866_at | PLAUR | plasminogen activator, urokinase receptor | -1.69 | -1.72 | -2.11 | -2.12 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 219093_at | PID1 | phosphotyrosine interaction domain containing 1 | -1.03 | -1.11 | -1.55 | -1.51 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 223952_x_at | DHRS9 | dehydrogenase/reductase (SDR family) member 9 | -2.07 | -2.15 | -2.48 | -2.53 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 231736_x_at | MGST1 | microsomal glutathione S-transferase 1 | -2.15 | -2.23 | -2.76 | -2.61 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 203821_at | HBEGF | heparin-binding EGF-like growth factor | -2.26 | -2.43 | -2.79 | -2.81 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 210664_s_at | TFPI | tissue factor pathway inhibitor (lipoprotein-associated coagula | -0.62 | -0.58 | -1.01 | -0.96 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 203058_s_at | PAPSS2 | 3'-phosphoadenosine 5'-phosphosulfate synthase 2 | -0.88 | -0.91 | -1.18 | -1.28 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 218451_at | CDCP1 | CUB domain containing protein 1 | -0.13 | -0.28 | -0.61 | -0.65 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 222757_s_at | ZAK | sterile alpha motif and leucine zipper containing kinase AZK | -0.65 | -0.77 | -1.09 | -1.14 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 225665_at | ZAK | sterile alpha motif and leucine zipper containing kinase AZK | -0.74 | -0.82 | -1.33 | -1.19 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 229510_at | MS4A14 | membrane-spanning 4-domains, subfamily A, member 14 | -1.37 | -1.52 | -1.87 | -1.89 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 203510_at | MET | met proto-oncogene (hepatocyte growth factor receptor) | -0.65 | -0.71 | -1.16 | -1.06 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 205863_at | S100A12 | S100 calcium binding protein A12 | -1.04 | -1.15 | -1.57 | -1.50 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 209906_at | C3AR1 | complement component 3a receptor 1 | -0.39 | -0.54 | -0.77 | -0.89 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 227034_at | ANKRD57 | ankyrin repeat domain 57 | -1.45 | -1.61 | -2.06 | -1.96 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 209833_at | CRADD | CASP2 and RIPK1 domain containing adaptor with death doma | -0.61 | -0.63 | -0.92 | -0.97 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 215977_x_at | GK | glycerol kinase | -1.22 | -1.32 | -1.51 | -1.66 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 223519_at | ZAK | sterile alpha motif and leucine zipper containing kinase AZK | -0.89 | -0.90 | -1.33 | -1.23 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 224009_x_at | DHRS9 | dehydrogenase/reductase (SDR family) member 9 | -2.17 | -2.27 | -2.64 | -2.61 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 213763_at | HIPK2 | homeodomain interacting protein kinase 2 | -0.76 | -0.59 | -0.77 | -0.93 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 217167_x_at | GK | glycerol kinase | -1.01 | -1.11 | -1.33 | -1.44 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 38037_at | HBEGF | heparin-binding EGF-like growth factor | -2.13 | -2.26 | -2.58 | -2.59 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 204575_s_at | MMP19 | matrix metallopeptidase 19 | -2.02 | -2.10 | -2.42 | -2.42 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 207387_s_at | GK | glycerol kinase | -1.13 | -1.25 | -1.52 | -1.57 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 212657_s_at | IL1RN | interleukin 1 receptor antagonist | -2.48 | -2.39 | -2.87 | -2.71 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 |
| 213258_at | TFPI | tissue factor pathway inhibitor (lipoprotein-associated coagula | -0.76 | -0.82 | -1.24 | -1.14 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 215966_x_at | GK3P | glycerol kinase 3 pseudogene | -1.21 | -1.33 | -1.54 | -1.65 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 217999_s_at | PHLDA1 | pleckstrin homology-like domain, family A, member 1 | -1.67 | -1.77 | -2.03 | -2.08 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 219915_s_at | SLC16A10 | solute carrier family 16, member 10 (aromatic amino acid tran | -1.89 | -1.97 | -2.15 | -2.29 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 202897_at | SIRPA | signal-regulatory protein alpha | -1.22 | -1.30 | -1.56 | -1.61 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 212659_s_at | IL1RN | interleukin 1 receptor antagonist | -2.65 | -2.59 | -2.76 | -2.90 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 237867_s_at | PID1 | phosphotyrosine interaction domain containing 1 | -1.37 | -1.41 | -1.72 | -1.73 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 201666_at | TIMP1 | TIMP metallopeptidase inhibitor 1 | -1.09 | -1.09 | -1.34 | -1.39 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 204614_at | SERPINB2 | serpin peptidase inhibitor, clade B (ovalbumin), member 2 | 0.34 | 0.29 | -0.06 | -0.01 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 215447_at | TFPI | tissue factor pathway inhibitor (lipoprotein-associated coagula | -0.40 | -0.34 | -0.48 | -0.64 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 219496_at | ANKRD57 | ankyrin repeat domain 57 | -1.38 | -1.54 | -1.91 | -1.84 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 228918_at | LOC10028861 | Hypothetical protein LOC100288617 | -2.20 | -2.35 | -2.74 | -2.65 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 203060_s_at | PAPSS2 | 3'-phosphoadenosine 5'-phosphosulfate synthase 2 | -0.76 | -0.86 | -1.01 | -1.15 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 217998_at | PHLDA1 | pleckstrin homology-like domain, family A, member 1 | -0.88 | -0.90 | -1.06 | -1.19 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 222881_at | HPSE | heparanase | -1.88 | -2.01 | -2.23 | -2.30 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 223918_at | ACSL6 | acyl-CoA synthetase long-chain family member 6 | -0.86 | -0.85 | -1.00 | -1.14 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 229521_at | FLJ36031 | hypothetical protein FLJ36031 | -0.69 | -0.69 | -0.95 | -0.98 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 201422_at | IFI30 | interferon, gamma-inducible protein 30 | -2.00 | -2.15 | -2.31 | -2.44 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 201489_at | PPIF | peptidylprolyl isomerase F | -1.08 | -1.21 | -1.51 | -1.49 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 210510_s_at | NRP1 | neuropilin 1 | -0.74 | -0.87 | -1.18 | -1.15 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 212698_s_at | SEPT10 | septin 10 | -1.33 | -1.34 | -1.77 | -1.62 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 205382_s_at | CFD | complement factor D (adipsin) | -0.86 | -0.91 | -1.10 | -1.17 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 205568_at | AQP9 | aquaporin 9 | -0.73 | -0.67 | -0.98 | -0.94 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 |
| 207610_s_at | EMR2 | egf-like module containing, mucin-like, hormone receptor-like | -0.98 | -1.04 | -1.34 | -1.31 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 203936_s_at | MMP9 | matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92k | -1.11 | -1.21 | -1.49 | -1.48 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 236345_at | TBXAS1 | thromboxane A synthase 1 (platelet) | -1.04 | -0.98 | -1.28 | -1.24 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1553224_at | LUZP1 | leucine zipper protein 1 | -0.14 | -0.22 | -0.09 | 0.05 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 204004_at | PAWR | PRKC, apoptosis, WT1, regulator | -0.08 | -0.16 | -0.01 | 0.11 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 206828_at | TXK | TXK tyrosine kinase | 0.43 | 0.32 | 0.48 | 0.58 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 208206_s_at | RASGRP2 | RAS guanyl releasing protein 2 (calcium and DAG-regulated) | 0.63 | 0.46 | 0.60 | 0.73 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 215874_at | ST3GAL1 | ST3 beta-galactoside alpha-2,3-sialyltransferase 1 | -0.81 | -1.08 | -0.92 | -0.82 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 |
| 232279_at | PHF15 | PHD finger protein 15 | 0.15 | 0.04 | 0.09 | 0.32 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1556655_s_at | --- | --- | -0.08 | -0.22 | -0.15 | 0.06 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 211862_x_at | CFLAR | CASP8 and FADD-like apoptosis regulator | -0.48 | -0.68 | -0.60 | -0.40 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 210948_s_at | LEF1 | lymphoid enhancer-binding factor 1 | -0.06 | -0.06 | 0.32 | 0.23 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 |
| 232392_at | SFRS3 | Splicing factor, arginine/serine-rich 3 | 0.61 | 0.48 | 0.73 | 0.77 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 1558748_at | NAPEPLD | N-acyl phosphatidylethanolamine phospholipase D | 0.15 | -0.05 | 0.06 | 0.26 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 244665_at | itga6 | integrin, alpha 6 | 0.55 | 0.37 | 0.49 | 0.68 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 207492_at | NGLY1 | N-glycanase 1 | -0.04 | -0.22 | -0.08 | 0.09 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 216379_x_at | CD24 | CD24 molecule | 0.21 | 0.10 | 0.33 | 0.42 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 242201_at | LOC730323 // | postmeiotic segregation increased 2-like 5; postmeiotic segreg | 0.22 | 0.02 | 0.12 | 0.33 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 243932_at | col19a1 | collagen, type XIX, alpha 1 | -0.13 | -0.18 | -0.01 | 0.14 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 224403_at | FCRL4 | Fc receptor-like 4 | -0.56 | -0.61 | -0.40 | -0.29 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| 235385_at | MARCH1 | membrane-associated ring finger (C3HC4) 1 | -0.06 | 0.10 | 0.29 | 0.43 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| 210511_s_at | INHBA | inhibin, beta A | -0.97 | -1.06 | -1.29 | -1.32 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 209959_at | NR4A3 | nuclear receptor subfamily 4, group A, member 3 | -0.76 | -0.89 | -0.98 | -1.15 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 225342_at | AK4 | adenylate kinase 4 | 0.12 | 0.12 | -0.19 | -0.14 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 217738_at | NAMPT | nicotinamide phosphoribosyltransferase | -0.05 | -0.19 | -0.34 | -0.44 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 207072_at | IL18RAP | interleukin 18 receptor accessory protein | 0.26 | 0.16 | 0.07 | -0.08 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 235179_at | ZNF641 | zinc finger protein 641 | -0.19 | 0.12 | 0.11 | -0.12 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 202007_at | NID1 | nidogen 1 | -1.62 | -1.57 | -1.84 | -1.80 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 224523_s_at | C3orf26 | chromosome 3 open reading frame 26 | -0.16 | -0.23 | -0.43 | -0.46 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1564160_at | DTHD1 | death domain containing 1 | -0.08 | 0.15 | 0.18 | -0.08 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 204493_at | BID | BH3 interacting domain death agonist | -0.80 | -0.68 | -0.98 | -0.91 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 217388_s_at | KYNU | kynureninase (L-kynurenine hydrolase) | -0.92 | -0.94 | -1.21 | -1.16 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 217739_s_at | NAMPT | nicotinamide phosphoribosyltransferase | -0.03 | -0.15 | -0.35 | -0.37 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 202827_s_at | MMP14 | matrix metallopeptidase 14 (membrane-inserted) | 0.01 | -0.14 | -0.22 | -0.34 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 204385_at | KYNU | kynureninase (L-kynurenine hydrolase) | -1.10 | -1.13 | -1.40 | -1.34 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 228570_at | BTBD11 | BTB (POZ) domain containing 11 | 0.05 | -0.10 | -0.20 | -0.31 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 239385_at | TFG | TRK-fused gene | -0.15 | 0.13 | 0.03 | -0.08 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 206380_s_at | CFP | complement factor properdin | -0.17 | -0.29 | -0.37 | -0.49 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 210866_s_at | CNOT4 | CCR4-NOT transcription complex, subunit 4 | -0.09 | 0.14 | 0.26 | -0.06 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 |
| 226189_at | ITGB8 | integrin, beta 8 | -0.59 | -0.66 | -0.70 | -0.87 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 228080_at | LAYN | layilin | 0.24 | 0.16 | 0.08 | -0.04 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 201468_s_at | NQO1 | NAD(P)H dehydrogenase, quinone 1 | -0.57 | -0.45 | -0.78 | -0.64 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 211725_s_at | BID | BH3 interacting domain death agonist | -0.61 | -0.58 | -0.84 | -0.77 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 224588_at | XIST | X (inactive)-specific transcript (non-protein coding) | 0.44 | 0.29 | 0.20 | 0.10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 229272_at | FNBP4 | formin binding protein 4 | -0.09 | 0.18 | 0.27 | -0.01 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 1 | 0 |
| 233261_at | EBF1 | Early B-cell factor 1 | 0.18 | 0.25 | 0.34 | 0.06 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 242781_at | FAM199X | family with sequence similarity 199, X-linked | -0.33 | -0.06 | -0.05 | -0.25 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 244490_at | --- | --- | -0.23 | -0.02 | 0.06 | -0.20 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1558299_at | Sirpa | signal-regulatory protein alpha | -0.86 | -0.98 | -1.13 | -1.15 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 200917_s_at | SRPR | signal recognition particle receptor (docking protein) | -0.22 | 0.01 | 0.11 | -0.17 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 204348_s_at | AK4 | adenylate kinase 4 | 0.32 | 0.44 | 0.17 | 0.26 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 205220_at | GPR109B | G protein-coupled receptor 109B | 0.32 | 0.35 | 0.01 | 0.17 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 210663_s_at | KYNU | kynureninase (L-kynurenine hydrolase) | -0.97 | -1.04 | -1.24 | -1.22 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 213998_s_at | DDX17 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 17 | 0.29 | 0.37 | 0.53 | 0.19 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 220122_at | MCTP1 | multiple C2 domains, transmembrane 1 | -0.25 | -0.09 | -0.43 | -0.27 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 224917_at | MIR21 | microRNA 21 | -0.67 | -0.40 | -0.48 | -0.58 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 227143_s_at | BID | BH3 interacting domain death agonist | -0.69 | -0.62 | -0.90 | -0.80 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 235526_at | SOX6 | SRY (sex determining region Y)-box 6 | 0.47 | 0.51 | 0.63 | 0.33 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 241661_at | JMJD1C | jumonji domain containing 1C | -0.25 | -0.01 | 0.03 | -0.20 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 1554958_at | ZNF641 | zinc finger protein 641 | -0.43 | -0.25 | -0.15 | -0.42 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 |
| 1555125_at | GCFC1 | GC-rich sequence DNA-binding factor 1 | -0.12 | 0.22 | 0.29 | 0.05 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 207391_s_at | PIP5K1A | phosphatidylinositol-4-phosphate 5-kinase, type I, alpha | 0.62 | 0.39 | 0.45 | 0.23 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 212240_s_at | PIK3R1 | phosphoinositide-3-kinase, regulatory subunit 1 (alpha) | -0.02 | 0.09 | 0.18 | -0.08 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 217078_s_at | CD300A | CD300a molecule | -0.16 | -0.33 | -0.32 | -0.50 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 243821_at | MRPS31 | mitochondrial ribosomal protein S31 | -0.19 | 0.05 | 0.08 | -0.12 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 244267_at | Satb1 | SATB homeobox 1 | -0.31 | 0.02 | 0.00 | -0.15 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 201235_s_at | BTG2 | BTG family, member 2 | -0.47 | -0.15 | -0.16 | -0.31 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 201683_x_at | TOX4 | TOX high mobility group box family member 4 | -0.27 | 0.02 | 0.00 | -0.14 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 203990_s_at | KDM6A | lysine (K)-specific demethylase 6A | -0.18 | 0.12 | 0.19 | -0.04 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 211506_s_at | IL8 | interleukin 8 | -0.16 | -0.31 | -0.41 | -0.48 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 211697_x_at | PNO1 | partner of NOB1 homolog (S. cerevisiae) | 0.61 | 0.48 | 0.65 | 0.32 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 213817_at | IRAK3 | interleukin-1 receptor-associated kinase 3 | -1.57 | -1.71 | -1.95 | -1.86 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 243824_at | LOC10050595 | hypothetical LOC100505956 | 0.91 | 0.65 | 1.07 | 0.49 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 36711_at | MAFF | v-maf musculoaponeurotic fibrosarcoma oncogene homolog F | -0.64 | -0.57 | -0.88 | -0.73 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 1555058_a_at | LPGAT1 | lysophosphatidylglycerol acyltransferase 1 | -0.50 | -0.15 | -0.35 | -0.29 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 1555368_x_at | ZNF479 | zinc finger protein 479 | 0.65 | 0.63 | 0.77 | 0.48 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1558080_s_at | DNAJC3 | DnaJ (Hsp40) homolog, subfamily C, member 3 | -1.30 | -1.03 | -1.15 | -1.19 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 201835_s_at | PRKAB1 | protein kinase, AMP-activated, beta 1 non-catalytic subunit | -0.19 | -0.23 | -0.07 | -0.38 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 202631_s_at | APPBP2 | amyloid beta precursor protein (cytoplasmic tail) binding prote | -0.57 | -0.26 | -0.38 | -0.40 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 231779_at | IRAK2 | interleukin-1 receptor-associated kinase 2 | -0.11 | -0.02 | -0.32 | -0.16 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 231899_at | ZC3H12C | zinc finger CCCH-type containing 12C | -0.22 | 0.00 | -0.38 | -0.15 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 238692_at | BTBD11 | BTB (POZ) domain containing 11 | -0.16 | -0.29 | -0.31 | -0.44 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 38158_at | ESPL1 | extra spindle pole bodies homolog 1 (S. cerevisiae) | -0.23 | -0.18 | -0.45 | -0.33 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 1561171_a_at | GOLGA6L1 /// | golgin A6 family-like 1 /// golgin A6 family-like 6 /// transmem | 0.49 | 0.42 | 0.60 | 0.27 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 201328_at | ETS2 | v-ets erythroblastosis virus E26 oncogene homolog 2 (avian) | -0.47 | -0.38 | -0.67 | -0.52 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 201831_s_at | USO1 | USO1 vesicle docking protein homolog (yeast) | -0.25 | 0.02 | 0.11 | -0.13 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 202871_at | TRAF4 | TNF receptor-associated factor 4 | 0.46 | 0.54 | 0.68 | 0.41 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 203141_s_at | AP3B1 | adaptor-related protein complex 3, beta 1 subunit | -0.31 | -0.17 | -0.04 | -0.31 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 |
| 208003_s_at | NFAT5 | nuclear factor of activated T-cells 5, tonicity-responsive | -0.31 | -0.02 | -0.28 | -0.16 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 227952_at | ZNF595 | zinc finger protein 595 | 1.27 | 1.03 | 1.35 | 0.88 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 235815_at | TSHZ2 | teashirt zinc finger homeobox 2 | 0.02 | 0.37 | 0.17 | 0.23 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 238423_at | SYTL3 | synaptotagmin-like 3 | 0.06 | -0.10 | -0.10 | -0.24 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 242352_at | NIPBL | Nipped-B homolog (Drosophila) | -0.19 | 0.11 | 0.18 | -0.02 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 244132_x_at | ZNF518A | Zinc finger protein 518A | 0.15 | 0.44 | 0.16 | 0.30 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 |
| 203479_s_at | OTUD4 | OTU domain containing 4 | -0.33 | -0.04 | 0.00 | -0.17 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 206323_x_at | OPHN1 | oligophrenin 1 | 0.83 | 0.76 | 0.91 | 0.63 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 210384_at | PRMT2 | protein arginine methyltransferase 2 | -0.09 | 0.18 | 0.16 | 0.06 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 214430_at | GLA | galactosidase, alpha | -1.12 | -0.86 | -1.21 | -0.99 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 230464_at | S1PR5 | sphingosine-1-phosphate receptor 5 | 0.41 | 0.28 | 0.30 | 0.14 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 230821_at | ZNF148 | zinc finger protein 148 | -0.03 | 0.26 | 0.12 | 0.12 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 241219_at | --- | --- | 0.05 | 0.27 | 0.32 | 0.14 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 1555367_at | ZNF479 | zinc finger protein 479 | 0.53 | 0.47 | 0.61 | 0.34 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1555913_at | GON4L | gon-4-like (C. elegans) | 0.10 | 0.27 | 0.38 | 0.15 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 1562925_at | --- | --- | 0.48 | 0.29 | 0.48 | 0.17 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 201977_s_at | KIAA0141 | KIAA0141 | -0.24 | -0.02 | 0.03 | -0.15 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 204817_at | ESPL1 | extra spindle pole bodies homolog 1 (S. cerevisiae) | -0.25 | -0.18 | -0.46 | -0.30 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 210943_s_at | LYST | lysosomal trafficking regulator | -0.44 | -0.25 | -0.16 | -0.37 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 213957_s_at | CEP350 | centrosomal protein 350kDa | -0.08 | 0.17 | 0.29 | 0.05 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 230067_at | FAM124A | Family with sequence similarity 124A | 0.06 | -0.11 | -0.08 | -0.23 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 242982_x_at | ITGB8 | integrin, beta 8 | 0.21 | 0.15 | 0.34 | 0.04 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1552736_a_at | NETO1 | neuropilin (NRP) and tolloid (TLL)-like 1 | 0.44 | 0.37 | 0.53 | 0.26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1557166_at | PDCD4 | programmed cell death 4 (neoplastic transformation inhibitor) | 0.42 | 0.62 | 0.70 | 0.51 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 1560495_at | --- | --- | 0.34 | 0.17 | 0.36 | 0.06 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 201708_s_at | NIPSNAP1 | nipsnap homolog 1 (C. elegans) | 0.45 | 0.41 | 0.57 | 0.30 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 206359_at | SOCS3 | suppressor of cytokine signaling 3 | 0.00 | -0.18 | -0.11 | -0.29 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 212570_at | ENDOD1 | endonuclease domain containing 1 | -0.08 | 0.16 | 0.32 | 0.05 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 224424_x_at | ACTR3BP2 | ARP3 actin-related protein 3 homolog B (yeast) pseudogene 2 | 0.57 | 0.41 | 0.61 | 0.31 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 231747_at | CYSLTR1 | cysteinyl leukotriene receptor 1 | 0.12 | 0.39 | 0.36 | 0.29 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 235299_at | SLC41A2 | solute carrier family 41, member 2 | -1.55 | -1.36 | -1.63 | -1.48 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 236696_at | SR140 | U2-associated SR140 protein | 0.02 | 0.26 | 0.37 | 0.15 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 238546_at | SLC8A1 | solute carrier family 8 (sodium/calcium exchanger), member 1 | -0.76 | -0.92 | -0.86 | -1.04 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 238551_at | FUT11 | fucosyltransferase 11 (alpha (1,3) fucosyltransferase) | -0.62 | -0.34 | -0.47 | -0.45 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 240237_at | Clcn3 | chloride channel 3 | -0.45 | -0.20 | -0.19 | -0.31 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 1567913_at | --- | --- | 0.71 | 0.64 | 0.83 | 0.53 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 207509_s_at | LAIR2 | leukocyte-associated immunoglobulin-like receptor 2 | 0.50 | 0.26 | 0.36 | 0.16 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 208042_at | AGGF1 | angiogenic factor with G patch and FHA domains 1 | -0.15 | 0.10 | 0.18 | 0.00 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 209629_s_at | NXT2 | nuclear transport factor 2-like export factor 2 | -0.30 | -0.11 | 0.02 | -0.21 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 211565_at | SH3GL3 | SH3-domain GRB2-like 3 | 0.65 | 0.43 | 0.69 | 0.33 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 224425_x_at | ACTR3BP2 | ARP3 actin-related protein 3 homolog B (yeast) pseudogene 2 | 0.65 | 0.50 | 0.69 | 0.40 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 227277_at | MTDH | metadherin | -0.20 | 0.07 | -0.07 | -0.03 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 241966_at | MYO5A | myosin VA (heavy chain 12, myoxin) | -0.73 | -0.50 | -0.43 | -0.61 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 244154_at | DDHD1 | DDHD domain containing 1 | -0.14 | 0.13 | -0.09 | 0.03 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 204159_at | CDKN2C | cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4) | -0.06 | 0.05 | -0.22 | -0.04 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 207731_at | TMEM161B | transmembrane protein 161B | 0.39 | 0.36 | 0.53 | 0.27 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 208360_s_at | --- | --- | 0.51 | 0.36 | 0.57 | 0.27 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 220882_at | --- | --- | -0.42 | -0.22 | -0.54 | -0.32 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 222246_at | STXBP3 | syntaxin binding protein 3 | -0.20 | 0.07 | -0.03 | -0.02 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 224546_at | --- | --- | 0.48 | 0.33 | 0.64 | 0.24 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 242601_at | HEPACAM2 | HEPACAM family member 2 | 0.53 | 0.48 | 0.67 | 0.39 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 243489_at | --- | --- | 1.13 | 0.83 | 1.11 | 0.75 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1560025_at | --- | --- | 0.60 | 0.47 | 0.66 | 0.39 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 216917_s_at | SYCP1 | synaptonemal complex protein 1 | 0.42 | 0.30 | 0.59 | 0.22 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 219662_at | C2orf49 | chromosome 2 open reading frame 49 | -0.43 | -0.19 | -0.17 | -0.27 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 222439_s_at | THRAP3 | thyroid hormone receptor associated protein 3 | 0.03 | 0.25 | 0.32 | 0.17 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 227093_at | USP36 | Ubiquitin specific peptidase 36 | 0.39 | 0.18 | 0.26 | 0.10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 233536_at | ASXL3 | additional sex combs like 3 (Drosophila) | 0.29 | 0.25 | 0.44 | 0.17 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 233579_at | --- | --- | 0.60 | 0.41 | 0.63 | 0.34 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 234655_at | --- | --- | 0.38 | 0.26 | 0.48 | 0.19 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 244612_at | --- | --- | 0.58 | 0.48 | 0.74 | 0.40 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 201793_x_at | SMG7 | Smg-7 homolog, nonsense mediated mRNA decay factor (C. ele | -0.14 | 0.06 | 0.15 | -0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 216609_at | TXN | Thioredoxin | -0.80 | -0.45 | -0.84 | -0.51 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 |
| 232792_at | TRIM69 | tripartite motif-containing 69 | -0.77 | -0.47 | -0.70 | -0.54 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 204700_x_at | C1orf107 | chromosome 1 open reading frame 107 | 0.03 | 0.30 | 0.20 | 0.24 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 211637_x_at | IGHA1 /// IGH | immunoglobulin heavy constant alpha 1 /// immunoglobulin h | -0.33 | -0.16 | -0.05 | -0.22 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 214193_s_at | C1orf107 | chromosome 1 open reading frame 107 | 0.00 | 0.29 | 0.15 | 0.24 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 217767_at | C3 | complement component 3 | -1.99 | -1.82 | -2.15 | -1.87 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 232523_at | MEGF10 | multiple EGF-like-domains 10 | 0.45 | 0.33 | 0.61 | 0.27 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 236029_at | FAT3 | FAT tumor suppressor homolog 3 (Drosophila) | 0.50 | 0.43 | 0.64 | 0.37 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1562755_at | --- | --- | 0.87 | 0.64 | 0.99 | 0.59 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 202124_s_at | TRAK2 | trafficking protein, kinesin binding 2 | -0.54 | -0.35 | -0.27 | -0.40 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 203751_x_at | JUND | jun D proto-oncogene | -0.28 | -0.17 | -0.01 | -0.22 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 206715_at | TFEC | transcription factor EC | -1.04 | -0.78 | -1.12 | -0.83 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 |
| 207815_at | PF4V1 | platelet factor 4 variant 1 | 0.55 | 0.86 | 0.72 | 0.80 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 207978_s_at | NR4A3 | nuclear receptor subfamily 4, group A, member 3 | -1.20 | -1.33 | -1.10 | -1.38 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 240013_at | --- | --- | -0.77 | -0.51 | -0.86 | -0.56 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 244539_at | --- | --- | -0.24 | -0.05 | 0.12 | -0.10 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 205782_at | FGF7 | fibroblast growth factor 7 | 0.75 | 0.56 | 0.85 | 0.52 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 206269_at | GCM1 | glial cells missing homolog 1 (Drosophila) | -1.11 | -0.87 | -1.17 | -0.91 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 209716_at | CSF1 | colony stimulating factor 1 (macrophage) | -1.97 | -1.67 | -1.89 | -1.71 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 215801_at | --- | --- | 0.43 | 0.23 | 0.53 | 0.19 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 222626_at | RBM26 | RNA binding motif protein 26 | -0.17 | 0.02 | 0.15 | -0.02 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 231598_x_at | TMEM192 | transmembrane protein 192 | 1.03 | 0.70 | 1.01 | 0.66 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 |
| 239197_s_at | EZH1 | enhancer of zeste homolog 1 (Drosophila) | -0.09 | 0.07 | 0.18 | 0.03 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 244492_at | SLA | Src-like-adaptor | -0.24 | -0.14 | -0.40 | -0.18 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 1569664_at | LOC375010 | ankyrin repeat domain 20 family, member A pseudogene | 0.79 | 0.59 | 0.91 | 0.56 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 201367_s_at | ZFP36L2 | zinc finger protein 36, C3H type-like 2 | 0.02 | -0.15 | 0.16 | -0.18 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 203925_at | GCLM | glutamate-cysteine ligase, modifier subunit | -0.78 | -0.50 | -0.86 | -0.53 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 |
| 209210_s_at | FERMT2 | fermitin family member 2 | -1.82 | -1.42 | -1.90 | -1.45 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 |
| 214409_at | RFPL3S | RFPL3 antisense RNA (non-protein coding) | -1.36 | -0.98 | -1.52 | -1.01 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 |
| 229715_at | DKFZp686O24 | hypothetical protein DKFZp686O24166 | -1.11 | -0.92 | -1.19 | -0.95 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 230302_at | --- | --- | -0.92 | -0.65 | -1.06 | -0.68 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 |
| 240089_at | NFE2L3 | nuclear factor (erythroid-derived 2)-like 3 | -0.90 | -0.59 | -0.77 | -0.62 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 1553856_s_at | P2RY10 | purinergic receptor P2Y, G-protein coupled, 10 | -0.22 | -0.06 | 0.08 | -0.08 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 1559688_at | GRAPL | GRB2-related adaptor protein-like | 0.55 | 0.25 | 0.53 | 0.23 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 |
| 1561489_at | --- | --- | 0.66 | 0.52 | 0.82 | 0.51 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 203828_s_at | IL32 | interleukin 32 | 0.39 | 0.51 | 0.66 | 0.50 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 219507_at | RSRC1 | arginine/serine-rich coiled-coil 1 | -0.33 | -0.16 | -0.04 | -0.18 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 221144_at | TMEM131 | transmembrane protein 131 | 0.54 | 0.39 | 0.67 | 0.36 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 1558982_at | LOC375010 | ankyrin repeat domain 20 family, member A pseudogene | 0.46 | 0.27 | 0.57 | 0.26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 202975_s_at | RHOBTB3 | Rho-related BTB domain containing 3 | -0.69 | -0.35 | -0.54 | -0.36 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 212065_s_at | USP34 | ubiquitin specific peptidase 34 | -0.48 | -0.31 | -0.15 | -0.32 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 233092_s_at | LOC10027184 | hypothetical LOC100271840 | 0.56 | 0.34 | 0.60 | 0.33 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 243386_at | CASZ1 | castor zinc finger 1 | -0.49 | -0.26 | -0.56 | -0.27 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 202976_s_at | RHOBTB3 | Rho-related BTB domain containing 3 | -0.73 | -0.48 | -0.78 | -0.49 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 238756_at | GAS2L3 | Growth arrest-specific 2 like 3 | -1.78 | -1.57 | -1.90 | -1.57 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 202446_s_at | PLSCR1 | phospholipid scramblase 1 | -0.98 | -1.27 | -1.11 | -1.27 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 209286_at | CDC42EP3 | CDC42 effector protein (Rho GTPase binding) 3 | -0.45 | -0.18 | -0.45 | -0.17 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 |
| 217544_at | LOC729806 | similar to hCG1725380 | -0.64 | -0.26 | -0.49 | -0.26 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 222249_at | --- | --- | 0.34 | 0.12 | 0.39 | 0.13 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 228477_at | ARGLU1 | arginine and glutamate rich 1 | -0.27 | 0.10 | -0.10 | 0.11 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 1562745_at | --- | --- | -0.31 | -0.19 | -0.46 | -0.16 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 225054_x_at | LOC10049946 | hypothetical LOC100499466 | -0.40 | -0.24 | -0.10 | -0.22 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 225685_at | CDC42EP3 | CDC42 effector protein (Rho GTPase binding) 3 | -0.45 | -0.23 | -0.47 | -0.21 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 228983_at | --- | --- | -1.02 | -0.78 | -1.03 | -0.76 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 205249_at | EGR2 | early growth response 2 | -2.44 | -2.15 | -2.61 | -2.12 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 1 |
| 221200_at | --- | --- | -1.57 | -1.35 | -1.63 | -1.33 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 232538_at | --- | --- | 0.73 | 0.40 | 0.89 | 0.43 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 1 |
| 1561763_at | --- | --- | -0.31 | -0.05 | -0.15 | -0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 206038_s_at | NR2C2 | nuclear receptor subfamily 2, group C, member 2 | -0.69 | -0.43 | -0.52 | -0.39 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 216176_at | HCRP1 | hepatocellular carcinoma-related HCRP1 | -0.17 | -0.03 | -0.26 | 0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 228487_s_at | Rreb1 | ras responsive element binding protein 1 | -0.93 | -0.66 | -0.81 | -0.62 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 230241_at | --- | --- | -0.53 | -0.38 | -0.65 | -0.34 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 230618_s_at | BAT2L2 | HLA-B associated transcript 2-like 2 | -0.59 | -0.14 | -0.43 | -0.11 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 |
| 237459_at | Cdk17 | PCTAIRE protein kinase 2 | -0.24 | 0.13 | -0.19 | 0.17 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 |
| 1563348_at | RPL15P22 /// | ribosomal protein L15 pseudogene 22; ribosomal protein L15 | -0.30 | -0.06 | -0.34 | -0.01 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 1 |
| 204894_s_at | AOC3 | amine oxidase, copper containing 3 (vascular adhesion protein | -0.58 | -0.43 | -0.66 | -0.38 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 212634_at | KIAA0776 | KIAA0776 | -0.07 | 0.06 | 0.20 | 0.11 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 216452_at | TRPM3 | transient receptor potential cation channel, subfamily M, mem | 0.50 | 0.30 | 0.60 | 0.35 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 221935_s_at | C3orf64 | chromosome 3 open reading frame 64 | -0.53 | -0.34 | -0.56 | -0.29 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 228372_at | C10orf128 | chromosome 10 open reading frame 128 | -1.47 | -1.29 | -1.51 | -1.24 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1556306_at | MLL5 | myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax hom | -0.23 | 0.01 | -0.19 | 0.08 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 204072_s_at | FRY | furry homolog (Drosophila) | -0.23 | -0.01 | -0.34 | 0.05 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 209840_s_at | LRRN3 | leucine rich repeat neuronal 3 | 0.14 | 0.43 | 0.28 | 0.49 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 224898_at | WDR26 | WD repeat domain 26 | -0.62 | -0.41 | -0.50 | -0.36 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 229061_s_at | SLC25A13 | solute carrier family 25, member 13 (citrin) | -0.68 | -0.46 | -0.57 | -0.40 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 239401_at | S1PR1 | sphingosine-1-phosphate receptor 1 | -0.15 | 0.05 | -0.05 | 0.11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 242836_at | Atp1b3 | ATPase, Na+/K+ transporting, beta 3 polypeptide | -0.89 | -0.72 | -1.00 | -0.66 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 202211_at | ARFGAP3 | ADP-ribosylation factor GTPase activating protein 3 | -0.65 | -0.44 | -0.61 | -0.37 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 205092_x_at | ZBTB1 | zinc finger and BTB domain containing 1 | -0.79 | -0.47 | -0.80 | -0.41 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 |
| 208900_s_at | TOP1 | topoisomerase (DNA) I | -0.06 | 0.05 | 0.24 | 0.12 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 209841_s_at | LRRN3 | leucine rich repeat neuronal 3 | 0.11 | 0.41 | 0.16 | 0.48 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 |
| 214684_at | MEF2A | myocyte enhancer factor 2A | -0.75 | -0.59 | -0.80 | -0.52 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 221740_x_at | LOC10050616 | hypothetical LOC100506162 | -0.28 | -0.11 | 0.01 | -0.03 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 229787_s_at | Ogt | O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-ac | -0.27 | 0.09 | -0.16 | 0.17 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 236999_at | PPWD1 | peptidylprolyl isomerase domain and WD repeat containing 1 | -0.33 | -0.10 | -0.18 | -0.04 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 243748_at | eif4e3 | eukaryotic translation initiation factor 4E family member 3 | -0.24 | 0.01 | -0.15 | 0.08 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1557749_at | EHBP1L1 | EH domain binding protein 1-like 1 | -0.54 | -0.32 | -0.37 | -0.25 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1558449_at | --- | --- | -0.21 | -0.07 | 0.07 | 0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 1559401_a_at | znf609 | zinc finger protein 609 | -0.48 | -0.26 | -0.40 | -0.18 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 222101_s_at | DCHS1 | dachsous 1 (Drosophila) | -0.04 | 0.19 | -0.13 | 0.27 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 1 |
| 228496_s_at | CRIM1 | Cysteine rich transmembrane BMP regulator 1 (chordin-like) | -0.50 | -0.34 | -0.53 | -0.26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 228771_at | ADRBK2 | adrenergic, beta, receptor kinase 2 | -0.66 | -0.47 | -0.63 | -0.40 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 236106_at | C17orf67 | chromosome 17 open reading frame 67 | -0.27 | -0.21 | -0.42 | -0.14 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 243036_at | CCDC30 | coiled-coil domain containing 30 | -0.73 | -0.51 | -0.60 | -0.42 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 205884_at | ITGA4 | integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 rece | -0.29 | -0.10 | -0.18 | -0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 206695_x_at | ZNF43 | zinc finger protein 43 | -0.26 | -0.07 | -0.14 | 0.02 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 222587_s_at | GALNT7 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgala | -0.39 | -0.19 | -0.29 | -0.11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 223898_at | ZNF670 | zinc finger protein 670 | -0.57 | -0.39 | -0.64 | -0.30 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 227386_s_at | TMEM200B | transmembrane protein 200B | -0.09 | 0.03 | -0.20 | 0.12 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 230629_s_at | EP400 | E1A binding protein p400 | -0.15 | -0.01 | 0.12 | 0.08 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 230930_at | LOC338620 | hypothetical protein LOC338620 | -0.81 | -0.62 | -0.85 | -0.53 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 231403_at | TRIO | triple functional domain (PTPRF interacting) | -1.41 | -1.18 | -1.27 | -1.09 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 234997_x_at | --- | --- | -0.13 | 0.05 | -0.08 | 0.14 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 235975_at | MTO1 | mitochondrial translation optimization 1 homolog (S. cerevisia | -0.33 | -0.26 | -0.45 | -0.17 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 244359_s_at | LOC401131 | hypothetical LOC401131 | 0.49 | 0.26 | 0.59 | 0.35 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 1559072_a_at | ELFN2 | extracellular leucine-rich repeat and fibronectin type III domai | -0.14 | 0.03 | -0.16 | 0.14 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1569482_at | --- | --- | -0.05 | 0.20 | 0.10 | 0.30 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 202213_s_at | CUL4B | cullin 4B | -0.38 | -0.21 | -0.24 | -0.10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 202438_x_at | IDS | iduronate 2-sulfatase | -0.81 | -0.65 | -0.65 | -0.55 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 224516_s_at | CXXC5 | CXXC finger protein 5 | -1.41 | -1.19 | -1.34 | -1.09 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 229765_at | ZNF207 | zinc finger protein 207 | -0.37 | -0.16 | -0.26 | -0.06 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 231329_at | ITPR1 | inositol 1,4,5-triphosphate receptor, type 1 | -0.23 | -0.05 | -0.19 | 0.05 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 232709_at | --- | --- | -0.43 | -0.21 | -0.39 | -0.11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 236254_at | VPS13B | vacuolar protein sorting 13 homolog B (yeast) | -0.34 | -0.30 | -0.05 | -0.20 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 237841_at | c9orf5 | chromosome 9 open reading frame 5 | -0.36 | 0.08 | -0.21 | 0.18 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 |
| 239346_at | gtf2h3 | general transcription factor IIH, polypeptide 3, 34kDa | -0.20 | -0.07 | -0.23 | 0.04 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 239948_at | NUP153 | nucleoporin 153kDa | -0.06 | 0.13 | 0.01 | 0.23 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 240867_at | rfx3 | regulatory factor X, 3 (influences HLA class II expression) | -0.04 | 0.01 | -0.16 | 0.10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 243640_x_at | ZNF135 | zinc finger protein 135 | 0.06 | 0.24 | 0.18 | 0.34 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1555392_at | LOC10012886 | Testin-related protein TRG | 0.09 | 0.11 | -0.03 | 0.23 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1558924_s_at | CLIP1 | CAP-GLY domain containing linker protein 1 | -0.76 | -0.62 | -0.34 | -0.51 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 1562957_at | --- | --- | -0.30 | -0.15 | -0.04 | -0.04 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 200841_s_at | EPRS | glutamyl-prolyl-tRNA synthetase | -0.41 | -0.25 | -0.16 | -0.14 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 204671_s_at | ANKRD6 | ankyrin repeat domain 6 | -0.55 | -0.47 | -0.65 | -0.36 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 223400_s_at | PBRM1 | polybromo 1 | -0.95 | -0.71 | -0.79 | -0.59 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 224737_x_at | CCAR1 | cell division cycle and apoptosis regulator 1 | -0.25 | -0.14 | -0.30 | -0.04 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 228295_at | WDR59 | WD repeat domain 59 | -0.46 | -0.30 | -0.10 | -0.20 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 238257_at | MLLT10 | Myeloid/lymphoid or mixed-lineage leukemia (trithorax homol | -0.75 | -0.60 | -0.82 | -0.49 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 240432_x_at | KLF7 | Kruppel-like factor 7 (ubiquitous) | -0.13 | 0.02 | -0.01 | 0.14 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 244703_x_at | IPO9 | importin 9 | -0.52 | -0.34 | -0.36 | -0.23 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 209829_at | FAM65B | family with sequence similarity 65, member B | 0.01 | 0.16 | 0.11 | 0.28 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 224484_s_at | BRMS1L | breast cancer metastasis-suppressor 1-like | -0.23 | -0.03 | -0.10 | 0.09 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 229956_at | NR2C1 | nuclear receptor subfamily 2, group C, member 1 | -0.03 | 0.13 | -0.03 | 0.25 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 230752_at | CBX5 | chromobox homolog 5 (HP1 alpha homolog, Drosophila) | -0.33 | -0.15 | -0.18 | -0.03 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 234488_s_at | GMCL1 /// GN | germ cell-less homolog 1 (Drosophila) /// germ cell-less homol | -0.02 | 0.13 | 0.07 | 0.25 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 237999_at | ZDHHC13 | zinc finger, DHHC-type containing 13 | -0.35 | -0.19 | -0.20 | -0.07 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 240703_s_at | HERC1 | hect (homologous to the E6-AP (UBE3A) carboxyl terminus) do | -0.10 | 0.03 | 0.19 | 0.15 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 240762_at | Hnrnpk /// LO | heterogeneous nuclear ribonucleoprotein K; similar to heterog | -0.47 | -0.27 | -0.41 | -0.15 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 242051_at | --- | --- | -0.22 | -0.07 | -0.31 | 0.05 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 242514_at | Gna12 | guanine nucleotide binding protein (G protein) alpha 12 | -1.17 | -1.21 | -1.38 | -1.10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1557895_at | FLJ35934 | FLJ35934 | -0.25 | -0.01 | -0.08 | 0.12 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1565876_x_at | --- | --- | -0.07 | -0.03 | -0.19 | 0.11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 206980_s_at | FLT3LG | fms-related tyrosine kinase 3 ligand | 0.16 | 0.09 | 0.36 | 0.22 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 220148_at | ALDH8A1 | aldehyde dehydrogenase 8 family, member A1 | -0.42 | -0.25 | -0.47 | -0.13 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 221773_at | ELK3 | ELK3, ETS-domain protein (SRF accessory protein 2) | -0.25 | -0.10 | -0.18 | 0.03 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 226675_s_at | MALAT1 | metastasis associated lung adenocarcinoma transcript 1 (non-p | 0.00 | 0.11 | 0.36 | 0.24 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 226794_at | STXBP5 | syntaxin binding protein 5 (tomosyn) | -0.47 | -0.24 | -0.36 | -0.11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 230056_at | BPTF | bromodomain PHD finger transcription factor | -0.30 | -0.19 | -0.34 | -0.06 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 230416_at | SLC18A2 | solute carrier family 18 (vesicular monoamine), member 2 | -0.63 | -0.50 | -0.72 | -0.38 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 230961_at | --- | --- | -0.39 | -0.14 | -0.35 | -0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 235848_x_at | atl2 | atlastin GTPase 2 | -0.32 | -0.17 | -0.31 | -0.05 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 239793_at | KLC1 | kinesin light chain 1 | -0.95 | -0.75 | -0.79 | -0.62 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 240759_at | ACAP2 | ArfGAP with coiled-coil, ankyrin repeat and PH domains 2 | -0.45 | -0.39 | -0.55 | -0.26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 241093_at | SEPT6 | septin 6 | -0.25 | -0.18 | 0.06 | -0.05 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 1560071_a_at | ACOT13 | acyl-CoA thioesterase 13 | -0.59 | -0.50 | -0.67 | -0.37 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1570192_at | --- | --- | -0.56 | -0.36 | -0.47 | -0.22 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 207001_x_at | TSC22D3 | TSC22 domain family, member 3 | 0.26 | 0.00 | 0.27 | 0.13 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 208127_s_at | SOCS5 | suppressor of cytokine signaling 5 | -0.39 | -0.24 | -0.35 | -0.10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 216100_s_at | TOR1AIP1 | torsin A interacting protein 1 | -0.79 | -0.65 | -0.64 | -0.51 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 221904_at | FAM131A | family with sequence similarity 131, member A | -0.20 | -0.51 | -0.37 | -0.37 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 227227_at | LRRC37A | leucine rich repeat containing 37A | -0.24 | -0.11 | -0.10 | 0.02 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 229687_s_at | LOC10028701 | Hypothetical protein LOC100287017 | -0.24 | -0.05 | -0.20 | 0.09 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 230175_s_at | DCBLD2 | Discoidin, CUB and LCCL domain containing 2 | -1.37 | -1.25 | -1.41 | -1.11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 233955_x_at | CXXC5 | CXXC finger protein 5 | -1.26 | -1.11 | -1.14 | -0.97 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 235890_at | TBL1XR1 | transducin (beta)-like 1 X-linked receptor 1 | -0.37 | -0.10 | -0.24 | 0.04 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 |
| 236072_at | ATAD1 | ATPase family, AAA domain containing 1 | 0.08 | 0.15 | 0.00 | 0.29 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 243329_at | Pcgf3 | polycomb group ring finger 3 | -0.72 | -0.53 | -0.55 | -0.39 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 243857_at | MORF4L2 | Mortality factor 4 like 2 | -0.08 | 0.03 | 0.27 | 0.17 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 244187_at | APOOL | Apolipoprotein O-like | 0.06 | -0.21 | -0.13 | -0.07 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 1553186_x_at | RASEF | RAS and EF-hand domain containing | 0.43 | 0.27 | 0.57 | 0.41 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 1555068_at | WNK1 | WNK lysine deficient protein kinase 1 | -0.36 | -0.23 | -0.23 | -0.08 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1557352_at | SQLE | squalene epoxidase | 0.06 | 0.23 | 0.26 | 0.38 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1565566_a_at | STX7 | syntaxin 7 | -0.39 | -0.33 | -0.45 | -0.18 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1566491_at | --- | --- | 0.14 | 0.27 | 0.16 | 0.42 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1570194_x_at | --- | --- | -0.84 | -0.48 | -0.69 | -0.33 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 |
| 204075_s_at | KIAA0562 | KIAA0562 | -0.28 | -0.12 | -0.18 | 0.03 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 206188_at | ZNF623 | zinc finger protein 623 | -0.17 | -0.04 | -0.13 | 0.11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 206239_s_at | SPINK1 | serine peptidase inhibitor, Kazal type 1 | -1.26 | -0.72 | -1.12 | -0.57 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 |
| 228242_at | N4BP2 | NEDD4 binding protein 2 | -0.46 | -0.32 | -0.37 | -0.17 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 229038_at | CWF19L1 | CWF19-like 1, cell cycle control (S. pombe) | -0.68 | -0.58 | -0.71 | -0.43 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 230479_at | --- | --- | -0.35 | -0.13 | -0.22 | 0.03 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 238595_at | --- | --- | -0.47 | -0.35 | -0.42 | -0.20 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 240046_at | ubn2 | ubinuclein 2 | -0.10 | -0.15 | 0.16 | 0.00 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 240824_at | OBFC1 | oligonucleotide/oligosaccharide-binding fold containing 1 | 0.00 | 0.12 | 0.08 | 0.27 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 241988_x_at | SSH2 | slingshot homolog 2 (Drosophila) | -0.06 | 0.05 | -0.07 | 0.20 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 203869_at | USP46 | ubiquitin specific peptidase 46 | -0.44 | -0.29 | -0.34 | -0.14 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 204449_at | PDCL | phosducin-like | -0.18 | -0.08 | -0.14 | 0.08 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 214012_at | ERAP1 | endoplasmic reticulum aminopeptidase 1 | -0.10 | 0.09 | -0.03 | 0.24 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 235167_at | LOC10019098 | hypothetical LOC100190986 | -0.73 | -0.57 | -0.32 | -0.41 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 240892_at | --- | --- | -0.34 | -0.22 | -0.30 | -0.06 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 242055_at | PSMG4 | Proteasome (prosome, macropain) assembly chaperone 4 | 0.09 | 0.19 | 0.19 | 0.36 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 243233_at | RNU6-1 /// RN | RNA, U6 small nuclear 2; RNA, U6 small nuclear 1 | -0.27 | -0.16 | -0.17 | 0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1554339_a_at | COG3 | component of oligomeric golgi complex 3 | -0.54 | -0.39 | -0.22 | -0.21 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1557513_a_at | KLC2 | kinesin light chain 2 | -0.31 | -0.20 | -0.19 | -0.04 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 200762_at | DPYSL2 | dihydropyrimidinase-like 2 | -0.17 | -0.04 | -0.14 | 0.12 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 204969_s_at | RDX | radixin | -0.78 | -0.62 | -0.57 | -0.44 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 220076_at | ANKH | ankylosis, progressive homolog (mouse) | -0.10 | -0.02 | -0.14 | 0.14 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 221079_s_at | METTL2A /// | methyltransferase like 2A /// methyltransferase like 2B | -0.40 | -0.28 | -0.28 | -0.11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 239557_at | lrrfip2 | leucine rich repeat (in FLII) interacting protein 2 | -0.21 | -0.21 | -0.38 | -0.04 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 239655_at | PRDM2 | similar to zinc finger protein RIZ | -0.11 | -0.01 | 0.04 | 0.16 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 243511_at | --- | --- | -0.24 | -0.19 | -0.30 | -0.03 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 207826_s_at | ID3 | inhibitor of DNA binding 3, dominant negative helix-loop-helix | -0.69 | -0.59 | -0.53 | -0.41 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 228156_at | --- | --- | -0.19 | -0.10 | -0.06 | 0.09 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 231913_s_at | BRCC3 | BRCA1/BRCA2-containing complex, subunit 3 | -0.40 | -0.25 | -0.22 | -0.07 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 233406_at | secisbp2l | SECIS binding protein 2-like | 0.35 | 0.18 | 0.51 | 0.36 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 235575_at | LOC440993 | hypothetical LOC440993 | -0.51 | -0.35 | -0.28 | -0.18 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 236268_at | SEC22C | SEC22 vesicle trafficking protein homolog C (S. cerevisiae) | -0.33 | -0.21 | -0.17 | -0.03 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 243495_s_at | ZNF652 | zinc finger protein 652 | -0.50 | -0.38 | -0.19 | -0.19 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1565915_at | ZC3HAV1 | zinc finger CCCH-type, antiviral 1 | -0.21 | -0.06 | 0.08 | 0.13 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 1570629_at | ATF1 | activating transcription factor 1 | 0.00 | -0.12 | 0.18 | 0.07 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 215936_s_at | KIAA1033 | KIAA1033 | -0.48 | -0.40 | -0.19 | -0.21 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 220943_s_at | C2orf56 | chromosome 2 open reading frame 56 | -0.20 | -0.11 | -0.08 | 0.08 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 229318_at | --- | --- | -0.37 | -0.40 | -0.48 | -0.21 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 232013_at | C9orf102 | chromosome 9 open reading frame 102 | -0.39 | -0.24 | -0.18 | -0.05 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1562067_at | CERKL | ceramide kinase-like | -0.32 | -0.35 | -0.49 | -0.15 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 215212_at | --- | --- | -0.16 | -0.09 | -0.05 | 0.11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 242384_at | CPEB4 | cytoplasmic polyadenylation element binding protein 4 | -1.55 | -1.61 | -1.69 | -1.41 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1557419_a_at | ACSL4 | Acyl-CoA synthetase long-chain family member 4 | -0.78 | -0.98 | -1.08 | -0.77 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1559035_a_at | ahr | aryl hydrocarbon receptor | -1.41 | -1.26 | -1.07 | -1.05 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1562505_at | Stk35 | serine/threonine kinase 35 | -0.33 | -0.22 | -0.14 | -0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1570264_at | HMGN1 | high-mobility group nucleosome binding domain 1 | -0.11 | -0.06 | 0.01 | 0.16 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 204638_at | ACP5 | acid phosphatase 5, tartrate resistant | -0.73 | -0.64 | -0.53 | -0.43 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 223815_at | CCDC45 | Coiled-coil domain containing 45 | -0.31 | -0.25 | -0.14 | -0.04 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 231152_at | INO80D | INO80 complex subunit D | -0.28 | -0.12 | -0.06 | 0.09 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 243619_at | FGFR1OP2 | FGFR1 oncogene partner 2 | -0.59 | -0.52 | -0.40 | -0.32 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1556472_s_at | SCML4 | sex comb on midleg-like 4 (Drosophila) | 0.21 | 0.30 | 0.38 | 0.52 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 201295_s_at | WSB1 | WD repeat and SOCS box-containing 1 | -0.51 | -0.38 | -0.15 | -0.15 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 228315_at | ZMAT3 | zinc finger, matrin-type 3 | -0.12 | -0.07 | 0.04 | 0.16 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 236808_at | FGFR1OP2 | FGFR1 oncogene partner 2 | -0.48 | -0.36 | -0.27 | -0.13 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1562817_at | PPP2R5E | protein phosphatase 2, regulatory subunit B', epsilon isoform | -0.01 | -0.11 | 0.17 | 0.12 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 1567044_s_at | lsm14a | LSM14A, SCD6 homolog A (S. cerevisiae) | -0.17 | -0.12 | -0.01 | 0.11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 215201_at | REPS1 | RALBP1 associated Eps domain containing 1 | -0.06 | -0.17 | -0.20 | 0.06 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 229128_s_at | ANP32E | Acidic (leucine-rich) nuclear phosphoprotein 32 family, membe | 0.08 | 0.23 | 0.29 | 0.46 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 233637_at | DCAF8 | DDB1 and CUL4 associated factor 8 | -0.21 | -0.30 | -0.35 | -0.06 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 235722_at | SYNJ2BP | synaptojanin 2 binding protein | -0.38 | -0.24 | -0.02 | -0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 1569225_a_at | SCML4 | sex comb on midleg-like 4 (Drosophila) | 0.22 | 0.26 | 0.36 | 0.50 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 216094_at | WASL | Wiskott-Aldrich syndrome-like | -0.31 | -0.58 | -0.46 | -0.34 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 221015_s_at | CDADC1 | cytidine and dCMP deaminase domain containing 1 | 0.14 | 0.00 | -0.03 | 0.24 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 228697_at | HINT3 | histidine triad nucleotide binding protein 3 | -0.34 | -0.23 | -0.14 | 0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 242472_x_at | FNBP4 | Formin binding protein 4 | 0.06 | -0.01 | -0.08 | 0.22 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1558937_s_at | GUSBP3 | glucuronidase, beta pseudogene; glucuronidase, beta pseudog | -0.28 | -0.24 | -0.12 | 0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1564248_at | NSUN3 | NOL1/NOP2/Sun domain family, member 3 | 0.10 | -0.17 | -0.01 | 0.07 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 217208_s_at | DLG1 | discs, large homolog 1 (Drosophila) | -0.42 | -0.41 | -0.17 | -0.16 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 232569_at | --- | --- | 0.03 | -0.10 | 0.24 | 0.15 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 233034_at | RBMS1 | RNA binding motif, single stranded interacting protein 1 | -0.60 | -0.48 | -0.33 | -0.23 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 237803_x_at | --- | --- | -0.16 | -0.12 | 0.03 | 0.13 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 229116_at | CNKSR2 | connector enhancer of kinase suppressor of Ras 2 | 0.10 | 0.14 | 0.24 | 0.40 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 239164_at | rab12 | RAB12, member RAS oncogene family | -0.47 | -0.45 | -0.34 | -0.19 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 239243_at | ZNF638 | zinc finger protein 638 | -0.30 | -0.41 | -0.43 | -0.15 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 242693_at | CDK13 | cell division cycle 2-like 5 (cholinesterase-related cell division c | -0.41 | -0.32 | -0.22 | -0.06 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 203645_s_at | CD163 | CD163 molecule | -0.66 | -0.74 | -1.18 | -1.08 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 201809_s_at | ENG | endoglin | -1.60 | -1.75 | -2.09 | -2.07 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 210004_at | OLR1 | oxidized low density lipoprotein (lectin-like) receptor 1 | -2.79 | -2.94 | -3.36 | -3.26 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 224341_x_at | TLR4 | toll-like receptor 4 | -1.19 | -1.34 | -1.70 | -1.66 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 208893_s_at | DUSP6 | dual specificity phosphatase 6 | -1.43 | -1.56 | -1.93 | -1.87 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 204271_s_at | EDNRB | endothelin receptor type B | 0.15 | 0.04 | -0.11 | -0.22 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 210512_s_at | VEGFA | vascular endothelial growth factor A | -3.60 | -3.63 | -4.03 | -3.89 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 213446_s_at | IQGAP1 | IQ motif containing GTPase activating protein 1 | -0.94 | -0.53 | -0.47 | -0.79 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 1 | 0 |
| 200998_s_at | CKAP4 | cytoskeleton-associated protein 4 | -0.92 | -0.94 | -1.07 | -1.19 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 206701_x_at | EDNRB | endothelin receptor type B | 0.07 | 0.01 | -0.14 | -0.24 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 207233_s_at | MITF | microphthalmia-associated transcription factor | -1.46 | -1.48 | -1.87 | -1.73 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 208702_x_at | APLP2 | amyloid beta (A4) precursor-like protein 2 | -1.20 | -1.26 | -1.47 | -1.51 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 210665_at | TFPI | tissue factor pathway inhibitor (lipoprotein-associated coagula | -0.45 | -0.42 | -0.74 | -0.68 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 225262_at | FOSL2 | FOS-like antigen 2 | -0.77 | -0.92 | -1.02 | -1.17 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 238435_at | LOC10050666 | hypothetical LOC100506661 | -0.61 | -0.32 | -0.33 | -0.56 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 1552701_a_at | CARD16 | caspase recruitment domain family, member 16 | 0.29 | 0.14 | -0.01 | -0.10 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 203504_s_at | ABCA1 | ATP-binding cassette, sub-family A (ABC1), member 1 | -2.25 | -2.16 | -2.57 | -2.40 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 205003_at | DOCK4 | dedicator of cytokinesis 4 | -1.53 | -1.62 | -1.89 | -1.86 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 209278_s_at | TFPI2 | tissue factor pathway inhibitor 2 | 0.49 | 0.58 | 0.17 | 0.34 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 212473_s_at | MICAL2 | microtubule associated monoxygenase, calponin and LIM dom | -0.19 | -0.15 | -0.48 | -0.39 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 225842_at | PHLDA1 | pleckstrin homology-like domain, family A, member 1 | -1.30 | -1.40 | -1.73 | -1.64 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 |
| 227484_at | SRGAP1 | SLIT-ROBO Rho GTPase activating protein 1 | -1.59 | -1.63 | -1.76 | -1.87 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 227889_at | LPCAT2 | lysophosphatidylcholine acyltransferase 2 | -1.16 | -1.26 | -1.42 | -1.50 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 202071_at | SDC4 | syndecan 4 | -0.82 | -0.84 | -1.15 | -1.06 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 203603_s_at | ZEB2 | zinc finger E-box binding homeobox 2 | -1.08 | -1.00 | -1.30 | -1.23 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 204526_s_at | TBC1D8 | TBC1 domain family, member 8 (with GRAM domain) | -0.99 | -1.09 | -1.33 | -1.32 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 205349_at | GNA15 | guanine nucleotide binding protein (G protein), alpha 15 (Gq c | -0.97 | -1.06 | -1.29 | -1.29 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 213816_s_at | MET | met proto-oncogene (hepatocyte growth factor receptor) | -0.45 | -0.16 | -0.27 | -0.39 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 228846_at | MXD1 | MAX dimerization protein 1 | -1.72 | -1.77 | -2.08 | -2.00 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 241617_x_at | uimc1 | ubiquitin interaction motif containing 1 | 0.23 | 0.34 | 0.40 | 0.11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1560060_s_at | VPS37C | vacuolar protein sorting 37 homolog C (S. cerevisiae) | -1.01 | -1.06 | -1.34 | -1.29 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 |
| 200727_s_at | ACTR2 | ARP2 actin-related protein 2 homolog (yeast) | -0.74 | -0.42 | -0.47 | -0.64 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 203104_at | CSF1R | colony stimulating factor 1 receptor | -1.32 | -1.46 | -1.76 | -1.68 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 206176_at | BMP6 | bone morphogenetic protein 6 | -0.99 | -1.06 | -1.25 | -1.28 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 207085_x_at | CSF2RA | colony stimulating factor 2 receptor, alpha, low-affinity (granul | -1.55 | -1.65 | -1.84 | -1.86 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 216316_x_at | GK /// GK3P | glycerol kinase /// glycerol kinase 3 pseudogene | -0.92 | -1.06 | -1.18 | -1.28 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 221210_s_at | NPL | N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synth | -2.26 | -2.37 | -2.55 | -2.59 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 230266_at | RAB7B | RAB7B, member RAS oncogene family | -2.12 | -2.17 | -2.52 | -2.38 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 200878_at | EPAS1 | endothelial PAS domain protein 1 | -0.84 | -0.89 | -1.00 | -1.10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 202252_at | RAB13 | RAB13, member RAS oncogene family | -1.37 | -1.47 | -1.74 | -1.69 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 202345_s_at | FABP5 | fatty acid binding protein 5 (psoriasis-associated) | -2.12 | -2.27 | -2.54 | -2.49 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 202375_at | SEC24D | SEC24 family, member D (S. cerevisiae) | -0.66 | -0.60 | -0.91 | -0.81 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 203833_s_at | TGOLN2 | trans-golgi network protein 2 | -0.84 | -0.56 | -0.68 | -0.77 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 204324_s_at | GOLIM4 | golgi integral membrane protein 4 | -1.03 | -0.70 | -0.74 | -0.91 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 204834_at | FGL2 | fibrinogen-like 2 | -0.71 | -0.79 | -0.86 | -0.99 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 205099_s_at | CCR1 | chemokine (C-C motif) receptor 1 | -2.52 | -2.67 | -2.95 | -2.88 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 206034_at | SERPINB8 | serpin peptidase inhibitor, clade B (ovalbumin), member 8 | -0.39 | -0.41 | -0.70 | -0.62 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 209191_at | TUBB6 | tubulin, beta 6 | -1.58 | -1.56 | -1.88 | -1.77 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 209568_s_at | RGL1 | ral guanine nucleotide dissociation stimulator-like 1 | 0.17 | 0.05 | -0.04 | -0.16 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 214696_at | C17orf91 | chromosome 17 open reading frame 91 | -0.78 | -0.73 | -1.08 | -0.94 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 224374_s_at | EMILIN2 | elastin microfibril interfacer 2 | -0.80 | -0.89 | -1.06 | -1.09 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 228152_s_at | DDX60L | DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like | -0.88 | -0.97 | -1.18 | -1.18 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 229435_at | GLIS3 | GLIS family zinc finger 3 | -1.64 | -1.62 | -1.92 | -1.82 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 201952_at | ALCAM | activated leukocyte cell adhesion molecule | -1.67 | -1.70 | -2.00 | -1.90 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 203921_at | CHST2 | carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 | 0.15 | 0.01 | -0.05 | -0.18 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 204204_at | SLC31A2 | solute carrier family 31 (copper transporters), member 2 | -1.49 | -1.43 | -1.73 | -1.63 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 204351_at | S100P | S100 calcium binding protein P | -0.71 | -0.80 | -0.95 | -0.99 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 206011_at | CASP1 | caspase 1, apoptosis-related cysteine peptidase (interleukin 1, | 0.90 | 0.83 | 0.67 | 0.63 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 206522_at | MGAM | maltase-glucoamylase (alpha-glucosidase) | -1.46 | -1.57 | -1.84 | -1.77 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 218833_at | ZAK | sterile alpha motif and leucine zipper containing kinase AZK | -0.90 | -0.99 | -1.17 | -1.18 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 219053_s_at | VPS37C | vacuolar protein sorting 37 homolog C (S. cerevisiae) | -1.05 | -1.08 | -1.34 | -1.27 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 223019_at | FAM129B | family with sequence similarity 129, member B | -1.51 | -1.60 | -1.92 | -1.80 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 |
| 224828_at | CPEB4 | cytoplasmic polyadenylation element binding protein 4 | -1.52 | -1.17 | -1.20 | -1.36 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 226517_at | BCAT1 | branched chain amino-acid transaminase 1, cytosolic | -1.62 | -1.63 | -1.91 | -1.84 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 1563745_a_at | LOC283050 | hypothetical LOC283050 | -2.29 | -2.29 | -2.56 | -2.48 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 201976_s_at | MYO10 | myosin X | -1.08 | -1.14 | -1.36 | -1.33 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 205685_at | CD86 | CD86 molecule | -1.58 | -1.67 | -1.70 | -1.86 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 210427_x_at | ANXA2 | annexin A2 | -1.06 | -1.14 | -1.33 | -1.33 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 213095_x_at | AIF1 | allograft inflammatory factor 1 | -0.61 | -0.75 | -0.78 | -0.94 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 218035_s_at | RBM47 | RNA binding motif protein 47 | -1.72 | -1.60 | -1.96 | -1.79 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 223405_at | NPL | N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synth | -2.01 | -2.12 | -2.28 | -2.31 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1559485_at | ATG2B | ATG2 autophagy related 2 homolog B (S. cerevisiae) | -0.10 | 0.17 | 0.06 | -0.01 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 1560492_at | CRADD | CASP2 and RIPK1 domain containing adaptor with death doma | -0.59 | -0.71 | -0.82 | -0.89 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 203505_at | ABCA1 | ATP-binding cassette, sub-family A (ABC1), member 1 | -2.02 | -1.94 | -2.22 | -2.12 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 204359_at | FLRT2 | fibronectin leucine rich transmembrane protein 2 | -2.18 | -2.28 | -2.39 | -2.46 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 207376_at | VENTX | VENT homeobox homolog (Xenopus laevis) | -0.04 | -0.13 | -0.28 | -0.31 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 218676_s_at | PCTP | phosphatidylcholine transfer protein | -0.54 | -0.64 | -0.80 | -0.82 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 219799_s_at | DHRS9 | dehydrogenase/reductase (SDR family) member 9 | -1.38 | -1.48 | -1.68 | -1.66 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 225116_at | HIPK2 | homeodomain interacting protein kinase 2 | -0.58 | -0.69 | -0.89 | -0.86 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 227647_at | KCNE3 | potassium voltage-gated channel, Isk-related family, member 3 | -1.53 | -1.69 | -1.83 | -1.87 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 233888_s_at | SRGAP1 | SLIT-ROBO Rho GTPase activating protein 1 | -0.54 | -0.64 | -0.69 | -0.82 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 236787_at | LOC100507286 | hypothetical LOC100507286 | -1.66 | -1.55 | -1.83 | -1.73 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 208438_s_at | FGR | Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolo | -1.17 | -1.06 | -1.34 | -1.23 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 212501_at | CEBPB | CCAAT/enhancer binding protein (C/EBP), beta | -1.90 | -1.99 | -2.24 | -2.16 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 212606_at | WDFY3 | WD repeat and FYVE domain containing 3 | -1.74 | -1.86 | -1.97 | -2.03 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 214875_x_at | APLP2 | amyloid beta (A4) precursor-like protein 2 | -1.14 | -1.23 | -1.36 | -1.40 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 218880_at | FOSL2 | FOS-like antigen 2 | -0.83 | -0.96 | -0.99 | -1.13 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 233506_at | --- | --- | -0.87 | -0.66 | -0.97 | -0.83 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 1555728_a_at | MS4A4A | membrane-spanning 4-domains, subfamily A, member 4 | -3.21 | -3.41 | -3.37 | -3.57 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 200782_at | ANXA5 | annexin A5 | -0.96 | -0.91 | -1.19 | -1.07 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 200999_s_at | CKAP4 | cytoskeleton-associated protein 4 | -0.99 | -1.06 | -1.28 | -1.21 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 201858_s_at | SRGN | serglycin | -0.64 | -0.78 | -0.89 | -0.94 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 208426_x_at | KIR2DL4 /// KI | killer cell immunoglobulin-like receptor, two domains, long cyt | 0.31 | 0.18 | 0.18 | 0.02 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 209901_x_at | AIF1 | allograft inflammatory factor 1 | -0.69 | -0.92 | -0.86 | -1.07 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 210423_s_at | SLC11A1 | solute carrier family 11 (proton-coupled divalent metal ion tra | -1.97 | -2.12 | -2.16 | -2.28 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 210872_x_at | GAS7 | growth arrest-specific 7 | -0.18 | -0.30 | -0.36 | -0.46 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 211532_x_at | KIR2DS2 | killer cell immunoglobulin-like receptor, two domains, short cy | 0.57 | 0.38 | 0.48 | 0.22 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 216676_x_at | KIR3DL3 | killer cell immunoglobulin-like receptor, three domains, long c | 0.48 | 0.37 | 0.34 | 0.21 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 225612_s_at | B3GNT5 | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase | -1.24 | -1.29 | -1.52 | -1.45 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 226905_at | FAM101B | family with sequence similarity 101, member B | -0.55 | -0.35 | -0.65 | -0.52 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 238762_at | MTHFD2L | methylenetetrahydrofolate dehydrogenase (NADP+ dependent | -0.76 | -0.68 | -0.94 | -0.83 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 1554390_s_at | ACTR2 | ARP2 actin-related protein 2 homolog (yeast) | -0.84 | -0.55 | -0.66 | -0.70 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 1554600_s_at | LMNA | lamin A/C | -0.35 | -0.50 | -0.51 | -0.65 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 204143_s_at | ENOSF1 | enolase superfamily member 1 | -0.85 | -0.98 | -0.92 | -1.13 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 205896_at | SLC22A4 | solute carrier family 22 (organic cation/ergothioneine transpor | -1.73 | -1.86 | -2.03 | -2.01 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 207314_x_at | KIR3DL1 /// KI | killer cell immunoglobulin-like receptor, three domains, long c | 0.55 | 0.44 | 0.47 | 0.29 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 209393_s_at | EIF4E2 | eukaryotic translation initiation factor 4E family member 2 | -0.25 | -0.37 | -0.45 | -0.53 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 221840_at | PTPRE | protein tyrosine phosphatase, receptor type, E | -1.23 | -1.23 | -1.53 | -1.38 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 223551_at | PKIB | protein kinase (cAMP-dependent, catalytic) inhibitor beta | 0.54 | 0.30 | 0.38 | 0.14 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 227013_at | LATS2 | LATS, large tumor suppressor, homolog 2 (Drosophila) | -0.91 | -0.91 | -1.18 | -1.06 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 229865_at | FNDC3B | fibronectin type III domain containing 3B | -2.20 | -2.09 | -2.38 | -2.24 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 235146_at | TMCC3 | transmembrane and coiled-coil domain family 3 | -1.17 | -1.33 | -1.42 | -1.48 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 203297_s_at | JARID2 | jumonji, AT rich interactive domain 2 | -0.70 | -0.80 | -0.97 | -0.94 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 203298_s_at | JARID2 | jumonji, AT rich interactive domain 2 | -0.84 | -0.93 | -1.13 | -1.08 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 208262_x_at | MEFV | Mediterranean fever | 0.60 | 0.39 | 0.61 | 0.25 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 210904_s_at | IL13RA1 | interleukin 13 receptor, alpha 1 | -0.84 | -0.97 | -0.92 | -1.11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 213926_s_at | AGFG1 | ArfGAP with FG repeats 1 | -0.59 | -0.32 | -0.24 | -0.46 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 224615_x_at | HM13 | histocompatibility (minor) 13 | -0.39 | -0.52 | -0.52 | -0.66 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 229940_at | SETD3 | SET domain containing 3 | -0.79 | -0.87 | -1.08 | -1.00 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 235407_at | --- | --- | -1.07 | -1.01 | -1.30 | -1.15 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 242397_at | Olr1 | oxidized low density lipoprotein (lectin-like) receptor 1 | -2.55 | -2.68 | -2.75 | -2.82 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 204184_s_at | ADRBK2 | adrenergic, beta, receptor kinase 2 | -0.67 | -0.40 | -0.54 | -0.53 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 207704_s_at | GAS7 | growth arrest-specific 7 | 0.09 | -0.07 | -0.12 | -0.20 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 210184_at | ITGAX | integrin, alpha X (complement component 3 receptor 4 subuni | -1.12 | -1.13 | -1.42 | -1.26 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 213895_at | EMP1 | epithelial membrane protein 1 | -1.75 | -1.68 | -1.98 | -1.81 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 222651_s_at | TRPS1 | trichorhinophalangeal syndrome I | -0.85 | -0.98 | -1.08 | -1.11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 227854_at | fancl | Fanconi anemia, complementation group L | -1.00 | -1.17 | -1.29 | -1.30 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 242853_at | FLJ34208 | hypothetical protein LOC401106 | -0.69 | -0.76 | -0.95 | -0.90 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 1555833_a_at | IRGQ | immunity-related GTPase family, Q | -0.45 | -0.55 | -0.73 | -0.67 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 204542_at | ST6GALNAC2 | ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acet | -0.69 | -0.84 | -0.72 | -0.96 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 208836_at | ATP1B3 | ATPase, Na+/K+ transporting, beta 3 polypeptide | -0.83 | -0.72 | -1.01 | -0.85 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 213164_at | SLC5A3 | solute carrier family 5 (sodium/myo-inositol cotransporter), m | 0.16 | 0.45 | 0.01 | 0.33 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 |
| 214007_s_at | TWF1 | twinfilin, actin-binding protein, homolog 1 (Drosophila) | -0.65 | -0.38 | -0.26 | -0.51 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 224576_at | ERGIC1 | endoplasmic reticulum-golgi intermediate compartment (ERGI | -0.21 | -0.37 | -0.22 | -0.49 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 224919_at | MRPS6 | mitochondrial ribosomal protein S6 | -0.04 | 0.27 | -0.08 | 0.15 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 |
| 226489_at | TMCC3 | transmembrane and coiled-coil domain family 3 | -0.82 | -0.97 | -1.01 | -1.09 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1554508_at | PIK3AP1 | phosphoinositide-3-kinase adaptor protein 1 | -1.15 | -0.90 | -0.86 | -1.02 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 207104_x_at | LILRB1 | leukocyte immunoglobulin-like receptor, subfamily B (with TM | -0.67 | -0.85 | -0.78 | -0.97 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 215051_x_at | AIF1 | allograft inflammatory factor 1 | -0.60 | -0.76 | -0.72 | -0.88 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 216907_x_at | KIR3DL1 /// KI | killer cell immunoglobulin-like receptor, three domains, long c | 0.46 | 0.27 | 0.34 | 0.15 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 219631_at | LRP12 | low density lipoprotein receptor-related protein 12 | -2.01 | -1.84 | -2.11 | -1.95 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 235458_at | HAVCR2 | hepatitis A virus cellular receptor 2 | -1.31 | -1.30 | -1.58 | -1.42 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| 1557885_at | C9orf41 | chromosome 9 open reading frame 41 | 0.20 | 0.19 | 0.37 | 0.09 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 210340_s_at | CSF2RA | colony stimulating factor 2 receptor, alpha, low-affinity (granul | -1.66 | -1.79 | -1.99 | -1.89 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 211397_x_at | KIR2DL2 | killer cell immunoglobulin-like receptor, two domains, long cyt | 0.57 | 0.40 | 0.44 | 0.30 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 212297_at | ATP13A3 | ATPase type 13A3 | -1.08 | -1.16 | -1.42 | -1.26 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 218368_s_at | TNFRSF12A | tumor necrosis factor receptor superfamily, member 12A | -0.82 | -0.68 | -0.95 | -0.79 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 223143_s_at | AKIRIN2 | akirin 2 | -0.71 | -0.83 | -0.63 | -0.94 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 230413_s_at | AP1S2 | Adaptor-related protein complex 1, sigma 2 subunit | -0.88 | -0.60 | -0.83 | -0.70 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 234196_at | tmcc3 | transmembrane and coiled-coil domain family 3 | -0.93 | -1.13 | -1.08 | -1.23 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1559249_at | ATXN1 | ataxin 1 | -0.79 | -0.52 | -0.66 | -0.62 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 203935_at | ACVR1 | activin A receptor, type I | -0.93 | -0.76 | -1.09 | -0.85 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 226490_at | NHSL1 | NHS-like 1 | 0.09 | -0.02 | 0.20 | -0.10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 226534_at | KITLG | KIT ligand | 0.58 | 0.35 | 0.44 | 0.27 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 202794_at | INPP1 | inositol polyphosphate-1-phosphatase | -0.58 | -0.66 | -0.84 | -0.74 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 205191_at | RP2 | retinitis pigmentosa 2 (X-linked recessive) | -1.09 | -0.92 | -1.23 | -1.00 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 208997_s_at | UCP2 | uncoupling protein 2 (mitochondrial, proton carrier) | -0.16 | -0.19 | 0.00 | -0.26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 213979_s_at | Ctbp1 | C-terminal binding protein 1 | -0.22 | 0.04 | -0.13 | -0.04 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 217975_at | WBP5 | WW domain binding protein 5 | -1.46 | -1.26 | -1.59 | -1.34 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 240137_at | tdrd6 | tudor domain containing 6 | -3.06 | -3.32 | -3.20 | -3.39 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 208750_s_at | ARF1 | ADP-ribosylation factor 1 | -0.45 | -0.58 | -0.37 | -0.65 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 228603_at | ACTR3 | ARP3 actin-related protein 3 homolog (yeast) | -0.46 | -0.16 | -0.30 | -0.23 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 201040_at | GNAI2 | guanine nucleotide binding protein (G protein), alpha inhibitin | -0.11 | -0.22 | 0.03 | -0.28 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 212595_s_at | DAZAP2 | DAZ associated protein 2 | -0.26 | -0.38 | -0.10 | -0.44 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 217137_x_at | --- | --- | 0.70 | 0.58 | 0.79 | 0.52 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 218506_x_at | GLYR1 | glyoxylate reductase 1 homolog (Arabidopsis) | -0.03 | -0.14 | -0.29 | -0.21 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 228754_at | SLC6A6 | solute carrier family 6 (neurotransmitter transporter, taurine), | -0.84 | -0.64 | -0.91 | -0.70 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 238420_at | Taok1 | TAO kinase 1 | -0.54 | -0.31 | -0.18 | -0.37 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 1553944_at | MIA2 | melanoma inhibitory activity 2 | 0.27 | 0.16 | 0.39 | 0.11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 212075_s_at | CSNK2A1 | casein kinase 2, alpha 1 polypeptide | -0.35 | -0.17 | -0.05 | -0.22 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 229010_at | CBL | Cas-Br-M (murine) ecotropic retroviral transforming sequence | -1.14 | -0.84 | -1.01 | -0.89 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 231038_s_at | srebf2 | sterol regulatory element binding transcription factor 2 | -0.50 | -0.14 | -0.39 | -0.18 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 201950_x_at | CAPZB | capping protein (actin filament) muscle Z-line, beta | 0.00 | -0.07 | 0.17 | -0.11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 205552_s_at | OAS1 | 2',5'-oligoadenylate synthetase 1, 40/46kDa | -0.46 | -0.75 | -0.57 | -0.79 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 213382_at | MST1 /// MST | macrophage stimulating 1 (hepatocyte growth factor-like) /// r | 0.37 | 0.18 | 0.45 | 0.14 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 213734_at | WSB2 | WD repeat and SOCS box-containing 2 | -0.96 | -0.69 | -0.92 | -0.73 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 225937_at | CUX1 | cut-like homeobox 1 | -0.98 | -0.71 | -0.89 | -0.76 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 1557348_at | --- | --- | 0.39 | 0.24 | 0.49 | 0.21 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 208624_s_at | EIF4G1 | eukaryotic translation initiation factor 4 gamma, 1 | -0.35 | -0.20 | -0.08 | -0.23 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 214155_s_at | LARP4 | La ribonucleoprotein domain family, member 4 | -0.75 | -0.53 | -0.81 | -0.57 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 225412_at | TMEM87B | transmembrane protein 87B | -0.17 | 0.03 | 0.12 | 0.00 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 228365_at | CPNE8 | copine VIII | -0.44 | -0.28 | -0.57 | -0.31 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 242787_at | INCENP | inner centromere protein antigens 135/155kDa | -0.64 | -0.36 | -0.51 | -0.39 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 235777_at | ANKRD44 | ankyrin repeat domain 44 | 0.90 | 0.63 | 0.76 | 0.61 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 221561_at | SOAT1 | sterol O-acyltransferase 1 | -2.35 | -2.02 | -2.25 | -2.03 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 229926_at | --- | --- | -0.77 | -0.53 | -0.79 | -0.53 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 242701_at | TBRG1 | transforming growth factor beta regulator 1 | -0.22 | -0.05 | 0.06 | -0.07 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 216388_s_at | LTB4R | leukotriene B4 receptor | 0.15 | 0.05 | -0.12 | 0.05 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 202923_s_at | GCLC | glutamate-cysteine ligase, catalytic subunit | -0.58 | -0.27 | -0.50 | -0.26 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 207201_s_at | SLC22A1 | solute carrier family 22 (organic cation transporter), member 1 | 0.56 | 0.93 | 0.71 | 0.94 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 219679_s_at | WAC | WW domain containing adaptor with coiled-coil | -0.46 | -0.32 | -0.19 | -0.32 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 222330_at | PDE3B | phosphodiesterase 3B, cGMP-inhibited | -0.26 | 0.03 | -0.13 | 0.04 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 244532_x_at | LOC401131 | hypothetical LOC401131 | 0.56 | 0.33 | 0.61 | 0.34 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1565358_at | RARA | retinoic acid receptor, alpha | 0.84 | 0.46 | 0.70 | 0.49 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 207419_s_at | RAC2 | ras-related C3 botulinum toxin substrate 2 (rho family, small G | 0.07 | -0.13 | 0.14 | -0.12 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 213741_s_at | KPNA1 | karyopherin alpha 1 (importin alpha 5) | -0.72 | -0.43 | -0.58 | -0.42 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 222424_s_at | NUCKS1 | nuclear casein kinase and cyclin-dependent kinase substrate 1 | -0.18 | 0.13 | -0.01 | 0.15 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 236761_at | LHFPL3 | lipoma HMGIC fusion partner-like 3 | 0.46 | 0.29 | 0.58 | 0.31 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 238716_at | FAM85A | family with sequence similarity 85, member A | -0.12 | 0.05 | 0.15 | 0.07 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 1554873_at | CSPP1 | centrosome and spindle pole associated protein 1 | -0.03 | 0.06 | 0.24 | 0.08 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 209326_at | SLC35A2 | solute carrier family 35 (UDP-galactose transporter), member | -1.09 | -0.86 | -1.13 | -0.83 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 214551_s_at | CD7 | CD7 molecule | 0.31 | 0.16 | 0.45 | 0.18 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 218911_at | YEATS4 | YEATS domain containing 4 | -0.34 | -0.06 | -0.27 | -0.02 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 223515_s_at | COQ3 | coenzyme Q3 homolog, methyltransferase (S. cerevisiae) | -0.51 | -0.32 | -0.60 | -0.29 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 225202_at | RHOBTB3 | Rho-related BTB domain containing 3 | -0.71 | -0.44 | -0.66 | -0.41 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 235360_at | PLEKHM3 | pleckstrin homology domain containing, family M, member 3 | -0.82 | -0.62 | -0.87 | -0.59 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 242117_at | MAP3K3 | mitogen-activated protein kinase kinase kinase 3 | -0.88 | -0.60 | -0.79 | -0.57 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 243476_at | NF1 | neurofibromin 1 | -0.73 | -0.52 | -0.77 | -0.49 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 203491_s_at | CEP57 | centrosomal protein 57kDa | -0.17 | -0.02 | 0.12 | 0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 204312_x_at | CREB1 | cAMP responsive element binding protein 1 | -0.38 | -0.26 | -0.10 | -0.22 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 212794_s_at | KIAA1033 | KIAA1033 | -0.42 | -0.26 | -0.12 | -0.23 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 214723_x_at | ANKRD36 | ankyrin repeat domain 36 | 0.08 | 0.23 | 0.40 | 0.27 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 229359_at | ASXL2 | additional sex combs like 2 (Drosophila) | -0.60 | -0.37 | -0.49 | -0.33 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 230628_at | EP400 | E1A binding protein p400 | -0.09 | 0.06 | 0.21 | 0.11 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 233063_s_at | --- | --- | -0.02 | 0.10 | 0.29 | 0.14 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 237009_at | CD69 | CD69 molecule | -0.10 | 0.04 | 0.17 | 0.08 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 237322_at | MIAT | myocardial infarction associated transcript (non-protein coding | 0.16 | 0.39 | 0.31 | 0.43 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 241814_at | RANBP9 | RAN binding protein 9 | 0.07 | 0.14 | 0.34 | 0.18 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 244423_at | fam107b | family with sequence similarity 107, member B | -1.17 | -0.92 | -1.04 | -0.88 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1555991_s_at | C22orf42 | chromosome 22 open reading frame 42 | 0.25 | 0.36 | 0.12 | 0.41 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1557049_at | BTBD19 | BTB (POZ) domain containing 19 | -0.83 | -0.71 | -0.98 | -0.65 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 1569107_s_at | ZNF642 | zinc finger protein 642 | -0.57 | -0.33 | -0.53 | -0.28 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 200799_at | HSPA1A | heat shock 70kDa protein 1A | -0.58 | -0.33 | -0.48 | -0.28 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 204170_s_at | CKS2 | CDC28 protein kinase regulatory subunit 2 | 0.09 | 0.32 | 0.17 | 0.36 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 207957_s_at | PRKCB | protein kinase C, beta | -0.47 | -0.25 | -0.39 | -0.20 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 208536_s_at | BCL2L11 | BCL2-like 11 (apoptosis facilitator) | -0.19 | -0.06 | 0.14 | -0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 225939_at | EIF4E3 | eukaryotic translation initiation factor 4E family member 3 | -0.21 | 0.05 | -0.19 | 0.10 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 |
| 232065_x_at | CENPL | centromere protein L | -0.24 | 0.00 | -0.20 | 0.05 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 202922_at | GCLC | glutamate-cysteine ligase, catalytic subunit | -0.37 | -0.16 | -0.34 | -0.10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 208103_s_at | ANP32E | acidic (leucine-rich) nuclear phosphoprotein 32 family, membe | -0.27 | -0.06 | -0.16 | 0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 210995_s_at | TRIM23 | tripartite motif-containing 23 | -0.37 | -0.22 | -0.04 | -0.15 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 213092_x_at | DNAJC9 | DnaJ (Hsp40) homolog, subfamily C, member 9 | -0.30 | -0.09 | -0.18 | -0.04 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 219073_s_at | OSBPL10 | oxysterol binding protein-like 10 | -0.54 | -0.21 | -0.43 | -0.14 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 |
| 222838_at | SLAMF7 | SLAM family member 7 | 0.29 | 0.52 | 0.40 | 0.58 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 225633_at | DPY19L3 | dpy-19-like 3 (C. elegans) | 0.06 | 0.29 | 0.16 | 0.34 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 230913_at | --- | --- | 0.46 | 0.63 | 0.38 | 0.69 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 238890_at | BRWD1 | bromodomain and WD repeat domain containing 1 | -0.36 | -0.09 | -0.35 | -0.03 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 |
| 243740_at | --- | --- | -0.33 | -0.12 | -0.31 | -0.06 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 244822_at | GART | phosphoribosylglycinamide formyltransferase, phosphoribosyl | -0.17 | 0.08 | -0.01 | 0.14 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 37433_at | PIAS2 | protein inhibitor of activated STAT, 2 | -0.42 | -0.14 | -0.33 | -0.08 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| 1568680_s_at | YTHDC2 | YTH domain containing 2 | -0.13 | 0.00 | 0.15 | 0.07 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 201101_s_at | BCLAF1 | BCL2-associated transcription factor 1 | -0.06 | 0.02 | 0.21 | 0.09 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 204446_s_at | ALOX5 | arachidonate 5-lipoxygenase | -0.95 | -0.74 | -0.83 | -0.67 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 208859_s_at | ATRX | alpha thalassemia/mental retardation syndrome X-linked | -0.14 | 0.03 | 0.16 | 0.10 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 209648_x_at | SOCS5 | suppressor of cytokine signaling 5 | -0.33 | -0.11 | -0.25 | -0.04 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 211968_s_at | HSP90AA1 | heat shock protein 90kDa alpha (cytosolic), class A member 1 | -0.24 | -0.08 | 0.04 | -0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 224834_at | UBTD2 | ubiquitin domain containing 2 | -0.43 | -0.21 | -0.32 | -0.13 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 226913_s_at | SOX8 | SRY (sex determining region Y)-box 8 | -0.19 | 0.10 | -0.10 | 0.17 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 |
| 234986_at | GCLM | glutamate-cysteine ligase, modifier subunit | -0.63 | -0.46 | -0.73 | -0.38 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| 1555920_at | CBX3 | Chromobox homolog 3 (HP1 gamma homolog, Drosophila) | -0.31 | -0.06 | -0.21 | 0.02 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 203213_at | CDK1 | cyclin-dependent kinase 1 | -0.99 | -0.84 | -1.08 | -0.76 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 212113_at | ATXN7L3B | ataxin 7-like 3B | -0.28 | -0.06 | -0.14 | 0.02 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 218783_at | INTS7 | integrator complex subunit 7 | -0.20 | 0.02 | -0.22 | 0.10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 220459_at | MCM3AP-AS | MCM3AP antisense RNA (non-protein coding) | 0.20 | 0.44 | 0.34 | 0.52 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 224827_at | UBTD2 | ubiquitin domain containing 2 | -0.29 | -0.06 | -0.21 | 0.02 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 225520_at | MTHFD1L | methylenetetrahydrofolate dehydrogenase (NADP+ dependen | -0.39 | -0.18 | -0.32 | -0.09 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 225922_at | FNIP2 | folliculin interacting protein 2 | -1.61 | -1.36 | -1.47 | -1.28 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 225962_at | ZNRF1 | zinc and ring finger 1 | 0.18 | 0.30 | 0.11 | 0.39 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 227156_at | CASK | calcium/calmodulin-dependent serine protein kinase (MAGUK | -0.06 | 0.12 | -0.01 | 0.20 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 236140_at | GCLM | glutamate-cysteine ligase, modifier subunit | -0.62 | -0.43 | -0.70 | -0.35 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1558972_s_at | THEMIS | thymocyte selection associated | 0.17 | 0.35 | 0.25 | 0.44 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 205659_at | HDAC9 | histone deacetylase 9 | 0.39 | 0.61 | 0.48 | 0.70 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 212637_s_at | WWP1 | WW domain containing E3 ubiquitin protein ligase 1 | -0.15 | 0.05 | -0.06 | 0.14 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 222564_at | POGK | pogo transposable element with KRAB domain | -0.20 | -0.05 | -0.25 | 0.03 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 223588_at | THAP2 | THAP domain containing, apoptosis associated protein 2 | -0.73 | -0.48 | -0.76 | -0.40 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 1 |
| 224802_at | NDFIP2 | Nedd4 family interacting protein 2 | -0.16 | 0.01 | -0.10 | 0.10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 225619_at | SLAIN1 | SLAIN motif family, member 1 | -0.07 | 0.12 | 0.01 | 0.21 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 228069_at | FAM54A | family with sequence similarity 54, member A | -0.86 | -0.59 | -0.79 | -0.50 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 |
| 228556_at | YTHDC1 | YTH domain containing 1 | -0.13 | 0.00 | 0.24 | 0.09 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 229226_at | MMS19 | MMS19 nucleotide excision repair homolog (S. cerevisiae) | -0.19 | 0.01 | -0.17 | 0.10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 239146_at | CLDND1 | claudin domain containing 1 | -0.24 | -0.04 | -0.26 | 0.05 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 91816_f_at | MEX3D | mex-3 homolog D (C. elegans) | -0.88 | -0.84 | -1.02 | -0.74 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1560570_a_at | --- | --- | -0.27 | -0.11 | -0.24 | -0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 202419_at | KDSR | 3-ketodihydrosphingosine reductase | 0.03 | 0.20 | 0.15 | 0.30 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 204240_s_at | SMC2 | structural maintenance of chromosomes 2 | -0.09 | 0.07 | 0.02 | 0.18 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 213373_s_at | CASP8 | caspase 8, apoptosis-related cysteine peptidase | 0.22 | 0.41 | 0.26 | 0.51 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 213922_at | TTBK2 | tau tubulin kinase 2 | -0.09 | 0.09 | -0.01 | 0.19 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 214313_s_at | EIF5B | Eukaryotic translation initiation factor 5B | -0.12 | 0.08 | -0.18 | 0.18 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 221290_s_at | MUM1 | melanoma associated antigen (mutated) 1 | -0.29 | -0.07 | -0.27 | 0.03 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 222108_at | AMIGO2 | adhesion molecule with Ig-like domain 2 | 0.15 | 0.39 | 0.25 | 0.49 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 223062_s_at | PSAT1 | phosphoserine aminotransferase 1 | -0.23 | -0.10 | -0.36 | 0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 227295_at | IKBIP | IKBKB interacting protein | -0.03 | 0.17 | 0.07 | 0.27 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 228084_at | PLA2G12A | phospholipase A2, group XIIA | 0.18 | 0.37 | 0.31 | 0.47 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 229588_at | DNAJC10 | DnaJ (Hsp40) homolog, subfamily C, member 10 | -0.13 | 0.02 | -0.17 | 0.11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 229809_at | POU6F1 | POU class 6 homeobox 1 | -0.39 | -0.30 | -0.47 | -0.19 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 230120_s_at | PLGLB2 | plasminogen-like B2 | -0.21 | -0.04 | -0.15 | 0.06 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 230893_at | DNAJC21 | DnaJ (Hsp40) homolog, subfamily C, member 21 | -0.14 | 0.05 | -0.03 | 0.15 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 235286_at | Cklf | chemokine-like factor | -0.59 | -0.42 | -0.58 | -0.32 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 238004_at | PGBD2 | piggyBac transposable element derived 2 | -0.28 | -0.08 | -0.22 | 0.02 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 238315_s_at | ZNF567 | zinc finger protein 567 | -0.29 | -0.17 | 0.01 | -0.08 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 238378_at | --- | --- | -0.34 | -0.18 | -0.28 | -0.07 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 47560_at | LPHN1 | latrophilin 1 | -0.15 | 0.03 | -0.15 | 0.13 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1558517_s_at | LRRC8C | leucine rich repeat containing 8 family, member C | -0.22 | -0.03 | -0.08 | 0.08 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1569566_at | TBC1D1 | TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 | -0.25 | 0.00 | -0.10 | 0.11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 202660_at | ITPR2 | inositol 1,4,5-triphosphate receptor, type 2 | -0.26 | -0.09 | -0.25 | 0.02 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 210461_s_at | ABLIM1 | actin binding LIM protein 1 | -0.40 | -0.25 | -0.21 | -0.14 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 214848_at | YWHAZ | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase acti | -0.49 | -0.30 | -0.42 | -0.19 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 217599_s_at | MDFIC | MyoD family inhibitor domain containing | -0.77 | -0.52 | -0.62 | -0.42 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 222074_at | UROD | uroporphyrinogen decarboxylase | -0.05 | 0.03 | -0.13 | 0.14 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 225066_at | PPP2R2D | protein phosphatase 2, regulatory subunit B, delta | -0.50 | -0.25 | -0.39 | -0.14 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 226460_at | FNIP2 | folliculin interacting protein 2 | -1.46 | -1.24 | -1.34 | -1.13 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 228297_at | cnn3 | calponin 3, acidic | 0.11 | 0.28 | 0.22 | 0.39 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 235122_at | HIVEP3 | human immunodeficiency virus type I enhancer binding protei | -2.18 | -1.92 | -2.14 | -1.81 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 235363_at | --- | --- | -0.15 | -0.01 | -0.19 | 0.10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 238341_at | LOC10050639 | hypothetical LOC100506395 | -0.46 | -0.22 | -0.33 | -0.11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 241370_at | LOC286052 | hypothetical protein LOC286052 | -0.23 | -0.02 | -0.20 | 0.09 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 208661_s_at | TTC3 | tetratricopeptide repeat domain 3 | -0.03 | 0.10 | 0.27 | 0.21 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 209146_at | SC4MOL | sterol-C4-methyl oxidase-like | -0.02 | 0.14 | 0.09 | 0.26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 212386_at | TCF4 | transcription factor 4 | -0.07 | 0.09 | 0.07 | 0.21 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 218073_s_at | TMEM48 | transmembrane protein 48 | -0.44 | -0.28 | -0.35 | -0.16 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 218236_s_at | PRKD3 | protein kinase D3 | -0.28 | -0.11 | -0.19 | 0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 218538_s_at | MRS2 | MRS2 magnesium homeostasis factor homolog (S. cerevisiae) | -0.26 | -0.07 | -0.11 | 0.05 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 226287_at | CCDC34 | coiled-coil domain containing 34 | 0.15 | 0.31 | 0.20 | 0.43 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 227177_at | CORO2A | coronin, actin binding protein, 2A | -0.08 | 0.07 | -0.05 | 0.19 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 230091_at | SRPK2 | SFRS protein kinase 2 | -0.30 | -0.11 | -0.28 | 0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 234297_at | RGS8 /// SDHA | Regulator of G-protein signaling 8 /// Succinate dehydrogenase | -0.15 | 0.01 | -0.19 | 0.13 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 236704_at | LOC10050597 | hypothetical LOC100505971 | -0.25 | -0.09 | -0.21 | 0.03 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 238695_s_at | RAB39B | RAB39B, member RAS oncogene family | -0.23 | -0.04 | -0.10 | 0.07 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 243675_at | --- | --- | -1.82 | -1.59 | -1.76 | -1.47 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1555526_a_at | SEPT6 | septin 6 | 0.23 | 0.21 | 0.47 | 0.34 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 1556332_at | --- | --- | -0.43 | -0.32 | -0.47 | -0.20 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 1557222_at | --- | --- | 0.17 | 0.32 | 0.22 | 0.45 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1570621_at | AFF1 | AF4/FMR2 family, member 1 | -0.64 | -0.50 | -0.33 | -0.37 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 201151_s_at | MBNL1 | muscleblind-like (Drosophila) | -0.19 | -0.03 | 0.14 | 0.09 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 201693_s_at | EGR1 | early growth response 1 | -0.35 | -0.13 | -0.18 | 0.00 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 203401_at | PRPS2 | phosphoribosyl pyrophosphate synthetase 2 | -0.09 | 0.08 | -0.02 | 0.21 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 203803_at | PCYOX1 | prenylcysteine oxidase 1 | -0.09 | 0.08 | 0.03 | 0.21 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 204432_at | SOX12 | SRY (sex determining region Y)-box 12 | 0.01 | 0.20 | 0.11 | 0.33 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 205229_s_at | COCH | coagulation factor C homolog, cochlin (Limulus polyphemus) | -0.23 | -0.04 | -0.07 | 0.09 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 213954_at | FAM169A | family with sequence similarity 169, member A | -0.05 | 0.11 | 0.14 | 0.24 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 217104_at | ST20 | suppressor of tumorigenicity 20 | -0.71 | -0.63 | -0.85 | -0.50 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 228658_at | MIAT | myocardial infarction associated transcript (non-protein codin | 0.37 | 0.53 | 0.40 | 0.66 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 228955_at | LRP8 | low density lipoprotein receptor-related protein 8, apolipoprot | -0.15 | -0.01 | -0.13 | 0.12 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 228990_at | SNHG12 | small nucleolar RNA host gene 12 (non-protein coding) | -0.14 | 0.04 | -0.03 | 0.17 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 230252_at | LPAR5 | lysophosphatidic acid receptor 5 | -0.19 | -0.05 | -0.14 | 0.08 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 235102_x_at | SNORD3B-2 // | small nucleolar RNA, C/D box 3B-1; small nucleolar RNA, C/D b | -0.16 | 0.01 | 0.00 | 0.13 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 237035_at | WWOX | WW domain containing oxidoreductase | 0.23 | 0.43 | 0.39 | 0.57 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 242887_at | KCMF1 | potassium channel modulatory factor 1 | -0.43 | -0.27 | -0.25 | -0.14 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 242915_at | ZNF682 | zinc finger protein 682 | 0.11 | 0.25 | 0.13 | 0.39 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1559125_at | C16orf53 | Chromosome 16 open reading frame 53 | -0.16 | -0.01 | -0.11 | 0.14 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1562249_at | LOC285965 | hypothetical LOC285965 | 0.13 | 0.30 | 0.23 | 0.44 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1565544_at | RNF141 | ring finger protein 141 | -0.55 | -0.33 | -0.54 | -0.20 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 203158_s_at | GLS | glutaminase | -0.68 | -0.45 | -0.53 | -0.31 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 204040_at | RNF144A | ring finger protein 144A | 0.19 | 0.32 | 0.21 | 0.46 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 209153_s_at | TCF3 | transcription factor 3 (E2A immunoglobulin enhancer binding f | -0.19 | -0.01 | -0.14 | 0.13 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 209257_s_at | SMC3 | structural maintenance of chromosomes 3 | 0.10 | -0.01 | 0.30 | 0.13 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 212538_at | DOCK9 | dedicator of cytokinesis 9 | -0.02 | 0.11 | 0.09 | 0.26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 225767_at | LOC284801 | hypothetical protein LOC284801 | 0.66 | 0.81 | 0.82 | 0.96 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 228859_at | C4orf21 | chromosome 4 open reading frame 21 | -0.03 | 0.14 | 0.07 | 0.28 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 229072_at | RAB30 | RAB30, member RAS oncogene family | -0.22 | -0.07 | -0.08 | 0.07 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 230808_at | FNTA | farnesyltransferase, CAAX box, alpha | -0.39 | -0.26 | -0.20 | -0.12 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 231941_s_at | MUC20 | mucin 20, cell surface associated | -0.40 | -0.27 | -0.44 | -0.13 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 235046_at | INPP4B | inositol polyphosphate-4-phosphatase, type II, 105kDa | -0.16 | 0.01 | -0.11 | 0.15 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 236208_at | MOCS2 | molybdenum cofactor synthesis 2 | -0.09 | 0.05 | -0.04 | 0.19 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 236215_at | FAM164A | family with sequence similarity 164, member A | -0.20 | -0.07 | -0.11 | 0.07 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 236612_at | Sgpp1 | sphingosine-1-phosphate phosphatase 1 | -0.13 | 0.03 | 0.11 | 0.17 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 236665_at | CCDC18 | coiled-coil domain containing 18 | -0.63 | -0.51 | -0.50 | -0.37 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 242292_at | NCRNA00246B | non-protein coding RNA 246B | -0.09 | 0.04 | -0.02 | 0.19 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 244177_at | ing1 | inhibitor of growth family, member 1 | -0.34 | -0.17 | -0.27 | -0.02 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 201675_at | AKAP1 | A kinase (PRKA) anchor protein 1 | 0.19 | 0.31 | 0.29 | 0.45 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 205316_at | SLC15A2 | solute carrier family 15 (H+/peptide transporter), member 2 | -0.21 | -0.19 | -0.32 | -0.04 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 215177_s_at | ITGA6 | integrin, alpha 6 | 0.21 | 0.31 | 0.55 | 0.47 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 225144_at | BMPR2 | bone morphogenetic protein receptor, type II (serine/threonin | -0.72 | -0.53 | -0.68 | -0.38 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 238176_at | RAPGEF2 | Rap guanine nucleotide exchange factor (GEF) 2 | -0.46 | -0.39 | -0.51 | -0.24 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 238604_at | --- | --- | -0.02 | 0.10 | 0.06 | 0.25 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 241763_s_at | FBXO32 | F-box protein 32 | 0.15 | 0.29 | 0.31 | 0.44 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 242245_at | SYDE2 | synapse defective 1, Rho GTPase, homolog 2 (C. elegans) | 0.19 | 0.40 | 0.20 | 0.55 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 55872_at | ZNF512B | zinc finger protein 512B | -0.15 | 0.09 | -0.12 | 0.24 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1552398_a_at | CLEC12A | C-type lectin domain family 12, member A | -1.03 | -0.88 | -1.00 | -0.73 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 1555261_at | maeA | macrophage erythroblast attacher | -0.33 | -0.21 | -0.15 | -0.05 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1560798_at | NCOA1 | nuclear receptor coactivator 1 | -0.34 | -0.21 | -0.46 | -0.05 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 204430_s_at | SLC2A5 | solute carrier family 2 (facilitated glucose/fructose transporter | -0.36 | -0.18 | -0.29 | -0.03 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 205739_x_at | ZNF107 | zinc finger protein 107 | 0.00 | 0.16 | 0.09 | 0.32 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 207996_s_at | C18orf1 | chromosome 18 open reading frame 1 | 0.06 | 0.19 | 0.16 | 0.35 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 217418_x_at | MS4A1 | membrane-spanning 4-domains, subfamily A, member 1 | -0.26 | -0.15 | 0.04 | 0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 229571_at | --- | --- | -0.23 | -0.11 | -0.06 | 0.05 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 242918_at | NASP | Nuclear autoantigenic sperm protein (histone-binding) | 0.13 | 0.24 | 0.47 | 0.41 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 1565830_at | KIAA1731 | KIAA1731 | -0.43 | -0.35 | -0.49 | -0.18 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 200800_s_at | HSPA1A /// HS | heat shock 70kDa protein 1A /// heat shock 70kDa protein 1B | -0.43 | -0.26 | -0.28 | -0.10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 228167_at | KLHL6 | kelch-like 6 (Drosophila) | -0.24 | -0.12 | -0.13 | 0.04 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 228599_at | MS4A1 | membrane-spanning 4-domains, subfamily A, member 1 | -0.30 | -0.12 | -0.17 | 0.05 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 229256_at | PGM2L1 | phosphoglucomutase 2-like 1 | -0.09 | 0.12 | 0.03 | 0.29 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 235051_at | CCDC50 | coiled-coil domain containing 50 | -0.15 | -0.02 | 0.13 | 0.15 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 237560_at | MRPS5 | Mitochondrial ribosomal protein S5 | -0.47 | -0.35 | -0.36 | -0.19 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 239644_at | ZC3H8 | zinc finger CCCH-type containing 8 | 0.21 | 0.31 | 0.27 | 0.48 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 243841_at | SYNE2 | spectrin repeat containing, nuclear envelope 2 | -0.24 | -0.14 | -0.03 | 0.03 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 244663_at | --- | --- | -0.18 | -0.06 | -0.21 | 0.11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| 203881_s_at | DMD | dystrophin | 0.28 | 0.37 | 0.49 | 0.55 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 222292_at | CD40 | CD40 molecule, TNF receptor superfamily member 5 | -0.08 | 0.01 | 0.07 | 0.19 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 207655_s_at | BLNK | B-cell linker | -0.31 | -0.15 | -0.12 | 0.04 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 209761_s_at | SP110 | SP110 nuclear body protein | 0.35 | 0.19 | 0.55 | 0.38 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 210356_x_at | MS4A1 | membrane-spanning 4-domains, subfamily A, member 1 | -0.24 | -0.14 | 0.05 | 0.05 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 210786_s_at | FLI1 | Friend leukemia virus integration 1 | -0.38 | -0.30 | -0.15 | -0.12 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 207901_at | IL12B | interleukin 12B (natural killer cell stimulatory factor 2, cytotoxi | 0.36 | 0.43 | 0.67 | 0.63 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 212382_at | TCF4 | transcription factor 4 | -0.33 | -0.20 | -0.04 | -0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 219517_at | ELL3 /// SERIN | elongation factor RNA polymerase II-like 3 /// serine incorpora | -0.07 | -0.01 | 0.05 | 0.19 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 228818_at | TPD52 | tumor protein D52 | -0.16 | -0.04 | 0.03 | 0.17 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 233252_s_at | STRBP | spermatid perinuclear RNA binding protein | -0.08 | 0.01 | 0.07 | 0.20 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 240286_at | GPM6B | glycoprotein M6B | -0.34 | -0.28 | -0.22 | -0.08 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 219497_s_at | BCL11A | B-cell CLL/lymphoma 11A (zinc finger protein) | -0.10 | -0.01 | 0.07 | 0.20 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 241762_at | FBXO32 | F-box protein 32 | 0.11 | 0.24 | 0.34 | 0.46 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 202971_s_at | DYRK2 | dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 | 0.01 | 0.07 | 0.18 | 0.28 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 206693_at | IL7 | interleukin 7 | -0.41 | -0.29 | -0.20 | -0.07 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 213506_at | F2RL1 | coagulation factor II (thrombin) receptor-like 1 | 0.34 | 0.40 | 0.50 | 0.63 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 239292_at | --- | --- | -0.17 | -0.09 | -0.01 | 0.12 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 242968_at | --- | --- | -0.04 | -0.12 | -0.20 | 0.09 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 212827_at | IGHM | immunoglobulin heavy constant mu | -0.08 | -0.03 | 0.12 | 0.20 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 228956_at | UGT8 | UDP glycosyltransferase 8 | 0.17 | 0.04 | 0.31 | 0.27 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 235401_s_at | FCRLA | Fc receptor-like A | -0.19 | -0.14 | -0.02 | 0.09 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 1569599_at | SAMSN1 | SAM domain, SH3 domain and nuclear localization signals 1 | -0.59 | -0.68 | -0.31 | -0.43 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 201465_s_at | JUN | jun proto-oncogene | -0.36 | -0.23 | -0.07 | 0.02 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 206255_at | BLK | B lymphoid tyrosine kinase | -0.16 | -0.14 | -0.04 | 0.11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |