**Table S1. Clinical data of 154 women (GEO microarray submission)**

| **Sample** | **Title** | **CEL file** | **Gestational Age at Sampling** | **Gestational Age at Delivery** | **Del <48hrs** | **Del <7days** | **PTB <37 weeks** |
| --- | --- | --- | --- | --- | --- | --- | --- |
| T-102 | wholeblood\_woman\_T-102 | U133Plus2\_011207W\_SL54\_T102 | 31.14 | 31.14 | 1 | 1 | 1 |
| T-129 | wholeblood\_woman\_T-129 | U133Plus2\_011907W\_SL70\_T129 | 32.43 | 37.71 | 0 | 0 | 0 |
| T-150 | wholeblood\_woman\_T-150 | U133Plus2\_101707W(2)\_SL35\_T150 | 24.86 | 24.86 | 1 | 1 | 1 |
| T-072 | wholeblood\_woman\_T-072 | U133Plus2\_101707W(2)\_SL48\_T072 | 32.29 | 34.29 | 0 | 0 | 1 |
| T-046 | wholeblood\_woman\_T-046 | U133Plus2\_010307W\_SL28\_T046 | 31.29 | 37.43 | 0 | 0 | 0 |
| T-243 | wholeblood\_woman\_T-243 | U133Plus2\_101007W\_SL20\_T243 | 26.00 | 37.43 | 0 | 0 | 0 |
| T-194 | wholeblood\_woman\_T-194 | U133Plus2\_102507W(2)\_SL56\_T194 | 33.86 | 38.00 | 0 | 0 | 0 |
| T-188 | wholeblood\_woman\_T-188 | U133Plus2\_102507W(2)\_SL53\_T188 | 34.29 | 37.57 | 0 | 0 | 0 |
| T-109 | wholeblood\_woman\_T-109 | U133Plus2\_011907W\_SL61\_T109 | 32.00 | 39.00 | 0 | 0 | 0 |
| T-160 | wholeblood\_woman\_T-160 | U133Plus2\_101707W(2)\_SL37\_T160 | 26.57 | 27.14 | 0 | 1 | 1 |
| T-268 | wholeblood\_woman\_T-268 | U133Plus2\_103107W(2)\_SL74\_T268 | 26.14 | 26.14 | 1 | 1 | 1 |
| T-048 | wholeblood\_woman\_T-048 | U133Plus2\_010307W\_SL29\_T048 | 34.43 | 34.71 | 1 | 1 | 1 |
| T-153 | wholeblood\_woman\_T-153 | U133Plus2\_101707W(2)\_SL36\_T153 | 29.14 | 31.86 | 0 | 0 | 1 |
| T-085 | wholeblood\_woman\_T-085 | U133Plus2\_011207W\_SL48\_T085 | 33.43 | 33.57 | 1 | 1 | 1 |
| T-090 | wholeblood\_woman\_T-090 | U133Plus2\_011207W\_SL51\_T090 | 30.43 | 36.86 | 0 | 0 | 1 |
| T-238 | wholeblood\_woman\_T-238 | U133Plus2\_101007W\_SL17\_T238 | 31.14 | 38.00 | 0 | 0 | 0 |
| T-007 | wholeblood\_woman\_T-007 | U133Plus2\_101707W\_SL25\_T007 | 32.29 | 36.43 | 0 | 0 | 1 |
| T-045 | wholeblood\_woman\_T-045 | U133Plus2\_010307W\_SL27\_T045 | 30.14 | 37.57 | 0 | 0 | 0 |
| T-157 | wholeblood\_woman\_T-157 | U133Plus2\_011907W\_SL82\_T157 | 27.57 | 40.71 | 0 | 0 | 0 |
| T-023 | wholeblood\_woman\_T-023 | U133Plus2\_112505\_XW\_SL06B | 31.86 | 31.86 | 1 | 1 | 1 |
| T-053 | wholeblood\_woman\_T-053 | U133Plus2\_011207W\_SL33\_T053 | 28.71 | 39.71 | 0 | 0 | 0 |
| T-004 | wholeblood\_woman\_T-004 | U133Plus2\_120606W\_SL03\_T004 | 32.14 | 37.43 | 0 | 0 | 0 |
| T-273 | wholeblood\_woman\_T-273 | U133Plus2\_103107W(2)\_SL77\_T273 | 25.71 | 39.43 | 0 | 0 | 0 |
| T-204 | wholeblood\_woman\_T-204 | U133Plus2\_102507W(2)\_SL61\_T204 | 32.86 | 33.14 | 1 | 1 | 1 |
| T-141 | wholeblood\_woman\_T-141 | U133Plus2\_101707W(2)\_SL33\_T141 | 26.86 | 40.00 | 0 | 0 | 0 |
| T-166 | wholeblood\_woman\_T-166 | U133Plus2\_101707W(2)\_SL41\_T166 | 32.71 | 38.00 | 0 | 0 | 0 |
| T-028 | wholeblood\_woman\_T-028 | U133Plus2\_120606W\_SL16\_T028 | 29.57 | 29.86 | 1 | 1 | 1 |
| T-006 | wholeblood\_woman\_T-006 | U133Plus2\_120606W\_SL05\_T006 | 34.71 | 34.86 | 1 | 1 | 1 |
| T-154 | wholeblood\_woman\_T-154 | U133Plus2\_011907W\_SL80\_T154 | 28.00 | 28.43 | 0 | 1 | 1 |
| T-255 | wholeblood\_woman\_T-255 | U133Plus2\_103107W(2)\_SL69\_T255 | 29.43 | 39.57 | 0 | 0 | 0 |
| T-158 | wholeblood\_woman\_T-158 | U133Plus2\_103107W(2)\_SL92\_T158 | 32.57 | 32.57 | 1 | 1 | 1 |
| T-168 | wholeblood\_woman\_T-168 | U133Plus2\_103107W(2)\_SL93\_T168 | 33.71 | 33.86 | 1 | 1 | 1 |
| T-016 | wholeblood\_woman\_T-016 | U133Plus2\_112505\_XW\_SL04B | 34.57 | 40.14 | 0 | 0 | 0 |
| T-249 | wholeblood\_woman\_T-249 | U133Plus2\_101007W\_SL22\_T249 | 35.43 | 35.71 | 1 | 1 | 1 |
| T-193 | wholeblood\_woman\_T-193 | U133Plus2\_102507W(2)\_SL55\_T193 | 29.14 | 29.14 | 1 | 1 | 1 |
| T-136 | wholeblood\_woman\_T-136 | U133Plus2\_101707W(2)\_SL32\_T136 | 31.71 | 38.57 | 0 | 0 | 0 |
| T-290 | wholeblood\_woman\_T-290 | U133Plus2\_103107W(2)\_SL87\_T290 | 30.14 | 30.43 | 1 | 1 | 1 |
| T-225 | wholeblood\_woman\_T-225 | U133Plus2\_101007W\_SL08\_T225 | 24.43 | 24.43 | 1 | 1 | 1 |
| T-127 | wholeblood\_woman\_T-127 | U133Plus2\_011907W\_SL69\_T127 | 27.14 | 28.00 | 0 | 1 | 1 |
| T-272 | wholeblood\_woman\_T-272 | U133Plus2\_103107W(2)\_SL76\_T272 | 32.43 | 36.71 | 0 | 0 | 1 |
| T-097 | wholeblood\_woman\_T-097 | U133Plus2\_011207W\_SL53\_T097 | 27.71 | 41.00 | 0 | 0 | 0 |
| T-142 | wholeblood\_woman\_T-142 | U133Plus2\_011907W\_SL76\_T142 | 33.86 | 33.86 | 1 | 1 | 1 |
| T-070 | wholeblood\_woman\_T-070 | U133Plus2\_011207W\_SL43\_T070 | 30.14 | 38.71 | 0 | 0 | 0 |
| T-221 | wholeblood\_woman\_T-221 | U133Plus2\_101007W\_SL06\_T221 | 31.86 | 31.86 | 1 | 1 | 1 |
| T-002 | wholeblood\_woman\_T-002 | U133Plus2\_120606W\_SL02\_T002 | 28.57 | 40.00 | 0 | 0 | 0 |
| T-079 | wholeblood\_woman\_T-079 | U133Plus2\_011207W\_SL46\_T079 | 30.14 | 39.43 | 0 | 0 | 0 |
| T-234 | wholeblood\_woman\_T-234 | U133Plus2\_101007W\_SL14\_T234 | 33.00 | 33.57 | 0 | 1 | 1 |
| T-262 | wholeblood\_woman\_T-262 | U133Plus2\_103107W(2)\_SL72\_T262 | 34.71 | 39.00 | 0 | 0 | 0 |
| T-035 | wholeblood\_woman\_T-035 | U133Plus2\_120606W\_SL20\_T035 | 32.57 | 39.71 | 0 | 0 | 0 |
| T-022 | wholeblood\_woman\_T-022 | U133Plus2\_101707W\_SL26\_T022 | 31.00 | 36.43 | 0 | 0 | 1 |
| T-263 | wholeblood\_woman\_T-263 | U133Plus2\_103107W(2)\_SL73\_T263 | 33.29 | 39.29 | 0 | 0 | 0 |
| T-042 | wholeblood\_woman\_T-042 | U133Plus2\_010307W\_SL25\_T042 | 33.86 | 37.00 | 0 | 0 | 0 |
| T-288 | wholeblood\_woman\_T-288 | U133Plus2\_111307W(2)\_SL95\_T288 | 33.57 | 39.57 | 0 | 0 | 0 |
| T-169 | wholeblood\_woman\_T-169 | U133Plus2\_103107W(2)\_SL94\_T169 | 32.57 | 32.57 | 1 | 1 | 1 |
| T-068 | wholeblood\_woman\_T-068 | U133Plus2\_011207W\_SL41\_T068 | 34.43 | 34.43 | 1 | 1 | 1 |
| T-055 | wholeblood\_woman\_T-055 | U133Plus2\_011207W\_SL35\_T055 | 33.14 | 37.57 | 0 | 0 | 0 |
| T-197 | wholeblood\_woman\_T-197 | U133Plus2\_102507W(2)\_SL58\_T197 | 29.86 | 31.14 | 0 | 0 | 1 |
| T-049 | wholeblood\_woman\_T-049 | U133Plus2\_010307W\_SL30\_T049 | 35.14 | 39.00 | 0 | 0 | 0 |
| T-212 | wholeblood\_woman\_T-212 | U133Plus2\_101007W\_SL01\_T212 | 32.57 | 32.71 | 1 | 1 | 1 |
| T-237 | wholeblood\_woman\_T-237 | U133Plus2\_101007W\_SL16\_T237 | 33.29 | 34.00 | 0 | 1 | 1 |
| T-119 | wholeblood\_woman\_T-119 | U133Plus2\_011907W\_SL65\_T119 | 32.43 | 40.29 | 0 | 0 | 0 |
| T-274 | wholeblood\_woman\_T-274 | U133Plus2\_103107W(2)\_SL78\_T274 | 26.14 | 26.14 | 1 | 1 | 1 |
| T-096 | wholeblood\_woman\_T-096 | U133Plus2\_101707W(2)\_SL31\_T096 | 33.14 | 37.71 | 0 | 0 | 0 |
| T-300 | wholeblood\_woman\_T-300 | U133Plus2\_103107W(2)\_SL90\_T300 | 25.29 | 25.29 | 1 | 1 | 1 |
| T-175 | wholeblood\_woman\_T-175 | U133Plus2\_101707W(2)\_SL45\_T175 | 33.29 | 35.14 | 0 | 0 | 1 |
| T-013 | wholeblood\_woman\_T-013 | U133Plus2\_112505\_XW\_SL03B | 32.57 | 32.57 | 1 | 1 | 1 |
| T-224 | wholeblood\_woman\_T-224 | U133Plus2\_101007W\_SL07\_T224 | 31.00 | 31.14 | 1 | 1 | 1 |
| T-014 | wholeblood\_woman\_T-014 | U133Plus2\_120606W\_SL10\_T014 | 32.00 | 40.29 | 0 | 0 | 0 |
| T-155 | wholeblood\_woman\_T-155 | U133Plus2\_011907W\_SL81\_T155 | 29.00 | 38.57 | 0 | 0 | 0 |
| T-217 | wholeblood\_woman\_T-217 | U133Plus2\_101007W\_SL03\_T217 | 31.86 | 36.14 | 0 | 0 | 1 |
| T-183 | wholeblood\_woman\_T-183 | U133Plus2\_102507W(2)\_SL52\_T183 | 34.57 | 34.57 | 1 | 1 | 1 |
| T-284 | wholeblood\_woman\_T-284 | U133Plus2\_103107W(2)\_SL84\_T284 | 28.43 | 39.00 | 0 | 0 | 0 |
| T-172 | wholeblood\_woman\_T-172 | U133Plus2\_111307W(2)\_SL96\_T172 | 31.29 | 40.00 | 0 | 0 | 0 |
| T-173 | wholeblood\_woman\_T-173 | U133Plus2\_101707W(2)\_SL43\_T173 | 28.71 | 38.43 | 0 | 0 | 0 |
| T-275 | wholeblood\_woman\_T-275 | U133Plus2\_103107W(2)\_SL79\_T275 | 26.43 | 26.86 | 0 | 1 | 1 |
| T-144 | wholeblood\_woman\_T-144 | U133Plus2\_011907W\_SL77\_T144 | 26.29 | 26.71 | 0 | 1 | 1 |
| T-278 | wholeblood\_woman\_T-278 | U133Plus2\_103107W(2)\_SL80\_T278 | 31.43 | 40.00 | 0 | 0 | 0 |
| T-170 | wholeblood\_woman\_T-170 | U133Plus2\_101707W(2)\_SL42\_T170 | 29.00 | 39.86 | 0 | 0 | 0 |
| T-089 | wholeblood\_woman\_T-089 | U133Plus2\_011207W\_SL50\_T089 | 31.43 | 38.00 | 0 | 0 | 0 |
| T-203 | wholeblood\_woman\_T-203 | U133Plus2\_102507W(2)\_SL60\_T203 | 25.86 | 39.00 | 0 | 0 | 0 |
| T-051 | wholeblood\_woman\_T-051 | U133Plus2\_011207W\_SL32\_T051 | 32.00 | 33.00 | 0 | 1 | 1 |
| T-003 | wholeblood\_woman\_T-003 | U133Plus2\_112505\_XW\_SL01B | 28.57 | 38.57 | 0 | 0 | 0 |
| T-012 | wholeblood\_woman\_T-012 | U133Plus2\_120606W\_SL09\_T012 | 32.57 | 37.57 | 0 | 0 | 0 |
| T-252 | wholeblood\_woman\_T-252 | U133Plus2\_101007W\_SL24\_T252 | 28.71 | 29.14 | 0 | 1 | 1 |
| T-106 | wholeblood\_woman\_T-106 | U133Plus2\_011907W\_SL59\_T106 | 32.86 | 33.00 | 1 | 1 | 1 |
| T-077 | wholeblood\_woman\_T-077 | U133Plus2\_101707W(2)\_SL49\_T077 | 32.14 | 33.14 | 0 | 1 | 1 |
| T-270 | wholeblood\_woman\_T-270 | U133Plus2\_103107W(2)\_SL75\_T270 | 35.57 | 38.86 | 0 | 0 | 0 |
| T-064 | wholeblood\_woman\_T-064 | U133Plus2\_011207W\_SL38\_T064 | 34.57 | 38.00 | 0 | 0 | 0 |
| T-123 | wholeblood\_woman\_T-123 | U133Plus2\_011907W\_SL67\_T123 | 32.14 | 32.14 | 1 | 1 | 1 |
| T-075 | wholeblood\_woman\_T-075 | U133Plus2\_011207W\_SL44\_T075 | 32.29 | 39.00 | 0 | 0 | 0 |
| T-124 | wholeblood\_woman\_T-124 | U133Plus2\_011907W\_SL68\_T124 | 34.43 | 34.57 | 1 | 1 | 1 |
| T-020 | wholeblood\_woman\_T-020 | U133Plus2\_120606W\_SL14\_T020 | 27.29 | 28.14 | 0 | 1 | 1 |
| T-044 | wholeblood\_woman\_T-044 | U133Plus2\_010307W\_SL26\_T044 | 26.57 | 26.86 | 1 | 1 | 1 |
| T-218 | wholeblood\_woman\_T-218 | U133Plus2\_101007W\_SL04\_T218 | 24.86 | 25.29 | 0 | 1 | 1 |
| T-287 | wholeblood\_woman\_T-287 | U133Plus2\_103107W(2)\_SL86\_T287 | 35.00 | 37.86 | 0 | 0 | 0 |
| T-140 | wholeblood\_woman\_T-140 | U133Plus2\_011907W\_SL75\_T140 | 33.00 | 40.29 | 0 | 0 | 0 |
| T-030 | wholeblood\_woman\_T-030 | U133Plus2\_120606W\_SL18\_T030 | 34.71 | 38.14 | 0 | 0 | 0 |
| T-180 | wholeblood\_woman\_T-180 | U133Plus2\_101707W(2)\_SL47\_T180 | 35.57 | 35.71 | 1 | 1 | 1 |
| T-248 | wholeblood\_woman\_T-248 | U133Plus2\_101007W\_SL21\_T248 | 31.86 | 31.86 | 1 | 1 | 1 |
| T-067 | wholeblood\_woman\_T-067 | U133Plus2\_011207W\_SL40\_T067 | 32.00 | 42.14 | 0 | 0 | 0 |
| T-041 | wholeblood\_woman\_T-041 | U133Plus2\_120606W\_SL24\_T041 | 31.00 | 38.00 | 0 | 0 | 0 |
| T-018 | wholeblood\_woman\_T-018 | U133Plus2\_120606W\_SL13\_T018 | 27.86 | 27.86 | 1 | 1 | 1 |
| T-054 | wholeblood\_woman\_T-054 | U133Plus2\_011207W\_SL34\_T054 | 33.71 | 37.86 | 0 | 0 | 0 |
| T-021 | wholeblood\_woman\_T-021 | U133Plus2\_112505\_XW\_SL05B | 35.00 | 37.00 | 0 | 0 | 0 |
| T-148 | wholeblood\_woman\_T-148 | U133Plus2\_101707W(2)\_SL34\_T148 | 33.29 | 33.29 | 1 | 1 | 1 |
| T-017 | wholeblood\_woman\_T-017 | U133Plus2\_120606W\_SL12\_T017 | 26.29 | 39.86 | 0 | 0 | 0 |
| T-286 | wholeblood\_woman\_T-286 | U133Plus2\_103107W(2)\_SL85\_T286 | 30.29 | 32.71 | 0 | 0 | 1 |
| T-147 | wholeblood\_woman\_T-147 | U133Plus2\_011907W\_SL79\_T147 | 32.14 | 32.43 | 1 | 1 | 1 |
| T-078 | wholeblood\_woman\_T-078 | U133Plus2\_011207W\_SL45\_T078 | 30.71 | 38.71 | 0 | 0 | 0 |
| T-069 | wholeblood\_woman\_T-069 | U133Plus2\_011207W\_SL42\_T069 | 28.00 | 37.57 | 0 | 0 | 0 |
| T-001 | wholeblood\_woman\_T-001 | U133Plus2\_120606W\_SL01\_T001 | 32.00 | 32.00 | 1 | 1 | 1 |
| T-103 | wholeblood\_woman\_T-103 | U133Plus2\_011907W\_SL58\_T103 | 34.43 | 34.43 | 1 | 1 | 1 |
| T-165 | wholeblood\_woman\_T-165 | U133Plus2\_101707W(2)\_SL40\_T165 | 30.00 | 39.86 | 0 | 0 | 0 |
| T-104 | wholeblood\_woman\_T-104 | U133Plus2\_011207W\_SL55\_T104 | 33.57 | 40.14 | 0 | 0 | 0 |
| T-031 | wholeblood\_woman\_T-031 | U133Plus2\_120606W\_SL19\_T031 | 34.14 | 34.29 | 1 | 1 | 1 |
| T-029 | wholeblood\_woman\_T-029 | U133Plus2\_120606W\_SL17\_T029 | 34.43 | 38.14 | 0 | 0 | 0 |
| T-133 | wholeblood\_woman\_T-133 | U133Plus2\_011907W\_SL72\_T133 | 33.00 | 37.00 | 0 | 0 | 0 |
| T-120 | wholeblood\_woman\_T-120 | U133Plus2\_011907W\_SL66\_T120 | 25.29 | 40.71 | 0 | 0 | 0 |
| T-161 | wholeblood\_woman\_T-161 | U133Plus2\_101707W(2)\_SL38\_T161 | 29.86 | 41.00 | 0 | 0 | 0 |
| T-071 | wholeblood\_woman\_T-071 | U133Plus2\_101707W\_SL28\_T071 | 23.71 | 39.14 | 0 | 0 | 0 |
| T-279 | wholeblood\_woman\_T-279 | U133Plus2\_103107W(2)\_SL81\_T279 | 35.00 | 35.29 | 1 | 1 | 1 |
| T-231 | wholeblood\_woman\_T-231 | U133Plus2\_101007W\_SL11\_T231 | 33.71 | 36.86 | 0 | 0 | 1 |
| T-025 | wholeblood\_woman\_T-025 | U133Plus2\_120606W\_SL15\_T025 | 33.29 | 40.00 | 0 | 0 | 0 |
| T-251 | wholeblood\_woman\_T-251 | U133Plus2\_101007W\_SL23\_T251 | 31.14 | 40.43 | 0 | 0 | 0 |
| T-066 | wholeblood\_woman\_T-066 | U133Plus2\_011207W\_SL39\_T066 | 34.00 | 39.14 | 0 | 0 | 0 |
| T-232 | wholeblood\_woman\_T-232 | U133Plus2\_101007W\_SL12\_T232 | 35.71 | 35.71 | 1 | 1 | 1 |
| T-107 | wholeblood\_woman\_T-107 | U133Plus2\_011907W\_SL60\_T107 | 31.71 | 41.00 | 0 | 0 | 0 |
| T-111 | wholeblood\_woman\_T-111 | U133Plus2\_101707W\_SL29\_T111 | 34.00 | 34.14 | 1 | 1 | 1 |
| T-094 | wholeblood\_woman\_T-094 | U133Plus2\_011207W\_SL52\_T094 | 28.71 | 39.29 | 0 | 0 | 0 |
| T-005 | wholeblood\_woman\_T-005 | U133Plus2\_120606W\_SL04\_T005 | 33.14 | 38.43 | 0 | 0 | 0 |
| T-132 | wholeblood\_woman\_T-132 | U133Plus2\_011907W\_SL71\_T132 | 34.71 | 38.57 | 0 | 0 | 0 |
| T-134 | wholeblood\_woman\_T-134 | U133Plus2\_011907W\_SL73\_T134 | 32.71 | 41.57 | 0 | 0 | 0 |
| T-113 | wholeblood\_woman\_T-113 | U133Plus2\_011907W\_SL63\_T113 | 34.00 | 40.43 | 0 | 0 | 0 |
| T-058 | wholeblood\_woman\_T-058 | U133Plus2\_011207W\_SL37\_T058 | 30.29 | 37.86 | 0 | 0 | 0 |
| T-011 | wholeblood\_woman\_T-011 | U133Plus2\_120606W\_SL08\_T011 | 31.57 | 37.00 | 0 | 0 | 0 |
| T-116 | wholeblood\_woman\_T-116 | U133Plus2\_011907W\_SL64\_T116 | 25.43 | 25.43 | 1 | 1 | 1 |
| T-008 | wholeblood\_woman\_T-008 | U133Plus2\_120606W\_SL06\_T008 | 25.71 | 39.29 | 0 | 0 | 0 |
| T-162 | wholeblood\_woman\_T-162 | U133Plus2\_101707W(2)\_SL39\_T162 | 30.71 | 39.00 | 0 | 0 | 0 |
| T-226 | wholeblood\_woman\_T-226 | U133Plus2\_101007W\_SL09\_T226 | 30.14 | 30.29 | 1 | 1 | 1 |
| T-195 | wholeblood\_woman\_T-195 | U133Plus2\_102507W(2)\_SL57\_T195 | 27.14 | 27.14 | 1 | 1 | 1 |
| T-009 | wholeblood\_woman\_T-009 | U133Plus2\_120606W\_SL07\_T009 | 27.00 | 38.00 | 0 | 0 | 0 |
| T-039 | wholeblood\_woman\_T-039 | U133Plus2\_120606W\_SL22\_T039 | 32.57 | 41.57 | 0 | 0 | 0 |
| T-015 | wholeblood\_woman\_T-015 | U133Plus2\_120606W\_SL11\_T015 | 29.86 | 31.57 | 0 | 0 | 1 |
| T-112 | wholeblood\_woman\_T-112 | U133Plus2\_011907W\_SL62\_T112 | 34.00 | 34.00 | 1 | 1 | 1 |
| T-057 | wholeblood\_woman\_T-057 | U133Plus2\_011207W\_SL36\_T057 | 31.86 | 31.86 | 1 | 1 | 1 |
| T-179 | wholeblood\_woman\_T-179 | U133Plus2\_101707W(2)\_SL46\_T179 | 32.14 | 34.14 | 0 | 0 | 1 |
| T-239 | wholeblood\_woman\_T-239 | U133Plus2\_101007W\_SL18\_T239 | 29.71 | 35.57 | 0 | 0 | 1 |
| T-105 | wholeblood\_woman\_T-105 | U133Plus2\_011207W\_SL56\_T105 | 34.86 | 34.86 | 1 | 1 | 1 |
| T-050 | wholeblood\_woman\_T-050 | U133Plus2\_011207W\_SL31\_T050 | 35.00 | 35.29 | 1 | 1 | 1 |
| T-199 | wholeblood\_woman\_T-199 | U133Plus2\_102507W(2)\_SL59\_T199 | 34.00 | 34.00 | 1 | 1 | 1 |
| T-261 | wholeblood\_woman\_T-261 | U133Plus2\_103107W(2)\_SL71\_T261 | 25.43 | 41.29 | 0 | 0 | 0 |
| T-065 | wholeblood\_woman\_T-065 | U133Plus2\_101707W\_SL27\_T065 | 32.00 | 36.00 | 0 | 0 | 1 |
| T-260 | wholeblood\_woman\_T-260 | U133Plus2\_103107W(2)\_SL70\_T260 | 33.14 | 39.57 | 0 | 0 | 0 |
| T-214 | wholeblood\_woman\_T-214 | U133Plus2\_101007W\_SL02\_T214 | 35.29 | 38.14 | 0 | 0 | 0 |

**Table S2. The list of 469 significant differentially expressed genes obtained using *Limma* ranked by magnitude of fold change.**

| **Entrez** | **HGNC Symbol** | **Log2** | **Fold Change** | **% Change** | **Average** | **adj.P.Val** | **Gene Annotation** |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene ID** | **Fold Change** | **Expression** | **(FDR)** |  |  |
| **Up-regulated genes (n=256)** | |  |  |  |  |  |  |  |  |
| 131540 | ZDHHC19 | 1.202 | 2.30 | 129.99 | 4.09 | <0.001 | zinc finger, DHHC-type containing 19 |  |  |
| 3248 | HPGD | 1.049 | 2.07 | 106.87 | 5.80 | 0.047 | hydroxyprostaglandin dehydrogenase 15-(NAD) | |  |
| 53831 | GPR84 | 0.990 | 1.99 | 98.59 | 7.22 | 0.007 | G protein-coupled receptor 84 |  |  |
| 26873 | OPLAH | 0.934 | 1.91 | 91.00 | 6.27 | 0.003 | 5-oxoprolinase (ATP-hydrolysing) |  |  |
| 122402 | TDRD9 | 0.906 | 1.87 | 87.34 | 4.43 | 0.018 | tudor domain containing 9 |  |  |
| 10079 | ATP9A | 0.880 | 1.84 | 84.10 | 7.25 | 0.013 | ATPase, class II, type 9A |  |  |
| 79623 | GALNT14 | 0.879 | 1.84 | 83.89 | 8.47 | <0.001 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14) | | |
| 116369 | SLC26A8 | 0.802 | 1.74 | 74.35 | 6.90 | 0.015 | solute carrier family 26, member 8 |  |  |
| 55755 | CDK5RAP2 | 0.768 | 1.70 | 70.34 | 8.41 | 0.017 | CDK5 regulatory subunit associated protein 2 | |  |
| 399972 | ST3GAL4-AS1 | 0.760 | 1.69 | 69.37 | 8.60 | 0.015 | ST3GAL4 antisense RNA 1 (head to head) |  |  |
| 50486 | G0S2 | 0.758 | 1.69 | 69.08 | 7.11 | 0.006 | G0/G1switch 2 |  |  |
| 9021 | SOCS3 | 0.757 | 1.69 | 68.96 | 7.96 | 0.003 | suppressor of cytokine signaling 3 |  |  |
| 55647 | RAB20 | 0.711 | 1.64 | 63.72 | 8.42 | 0.009 | RAB20, member RAS oncogene family |  |  |
| 6484 | ST3GAL4 | 0.709 | 1.63 | 63.42 | 6.12 | 0.003 | ST3 beta-galactoside alpha-2,3-sialyltransferase 4 | |  |
| 199675 | C19orf59 | 0.701 | 1.63 | 62.62 | 12.28 | 0.005 | chromosome 19 open reading frame 59 |  |  |
| 2015 | EMR1 | 0.699 | 1.62 | 62.29 | 8.74 | 0.025 | egf-like module containing, mucin-like, hormone receptor-like 1 | | |
| 5209 | PFKFB3 | 0.685 | 1.61 | 60.74 | 11.06 | 0.012 | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 | | |
| 731424 | LOC731424 | 0.683 | 1.61 | 60.51 | 8.60 | 0.045 | uncharacterized LOC731424 |  |  |
| 57699 | CPNE5 | 0.654 | 1.57 | 57.40 | 7.65 | 0.023 | copine V |  |  |
| 114548 | NLRP3 | 0.654 | 1.57 | 57.36 | 4.55 | 0.015 | NLR family, pyrin domain containing 3 |  |  |
| 51776 | ZAK | 0.654 | 1.57 | 57.35 | 7.57 | 0.002 | sterile alpha motif and leucine zipper containing kinase AZK | | |
| 100288432 | IL10RB-AS1 | 0.649 | 1.57 | 56.86 | 6.75 | 0.017 | IL10RB antisense RNA 1 (head to head) |  |  |
| 57089 | ENTPD7 | 0.644 | 1.56 | 56.24 | 3.06 | 0.006 | ectonucleoside triphosphate diphosphohydrolase 7 | |  |
| 92162 | TMEM88 | 0.638 | 1.56 | 55.65 | 4.96 | 0.012 | transmembrane protein 88 |  |  |
| 5447 | POR | 0.634 | 1.55 | 55.15 | 8.93 | 0.008 | P450 (cytochrome) oxidoreductase |  |  |
| 5990 | RFX2 | 0.620 | 1.54 | 53.67 | 7.40 | 0.037 | regulatory factor X, 2 (influences HLA class II expression) | | |
| 116844 | LRG1 | 0.617 | 1.53 | 53.34 | 11.51 | 0.013 | leucine-rich alpha-2-glycoprotein 1 |  |  |
| 266747 | RGL4 | 0.612 | 1.53 | 52.87 | 9.83 | 0.018 | ral guanine nucleotide dissociation stimulator-like 4 | |  |
| 84034 | EMILIN2 | 0.611 | 1.53 | 52.77 | 6.84 | 0.015 | elastin microfibril interfacer 2 |  |  |
| 11138 | TBC1D8 | 0.605 | 1.52 | 52.08 | 7.96 | 0.030 | TBC1 domain family, member 8 (with GRAM domain) | |  |
| 1230 | CCR1 | 0.605 | 1.52 | 52.07 | 11.07 | 0.022 | chemokine (C-C motif) receptor 1 |  |  |
| 10865 | ARID5A | 0.604 | 1.52 | 52.04 | 8.09 | 0.004 | AT rich interactive domain 5A (MRF1-like) |  |  |
| 151056 | PLB1 | 0.598 | 1.51 | 51.40 | 7.93 | 0.004 | phospholipase B1 |  |  |
| 2355 | FOSL2 | 0.593 | 1.51 | 50.88 | 7.16 | 0.021 | FOS-like antigen 2 |  |  |
| 5055 | SERPINB2 | 0.592 | 1.51 | 50.75 | 3.33 | 0.034 | serpin peptidase inhibitor, clade B (ovalbumin), member 2 | | |
| 7378 | UPP1 | 0.586 | 1.50 | 50.15 | 10.30 | 0.006 | uridine phosphorylase 1 |  |  |
| 5008 | OSM | 0.584 | 1.50 | 49.93 | 6.15 | 0.039 | oncostatin M |  |  |
| 23564 | DDAH2 | 0.579 | 1.49 | 49.41 | 8.20 | 0.003 | dimethylarginine dimethylaminohydrolase 2 | |  |
| 83853 | ROPN1L | 0.577 | 1.49 | 49.22 | 9.18 | 0.038 | rhophilin associated tail protein 1-like |  |  |
| 64651 | CSRNP1 | 0.576 | 1.49 | 49.10 | 9.35 | 0.014 | cysteine-serine-rich nuclear protein 1 |  |  |
| 5768 | QSOX1 | 0.576 | 1.49 | 49.10 | 7.49 | 0.023 | quiescin Q6 sulfhydryl oxidase 1 |  |  |
| 9605 | VPS9D1 | 0.571 | 1.49 | 48.57 | 7.09 | 0.003 | VPS9 domain containing 1 |  |  |
| 100506119 | LOC100506119 | 0.571 | 1.49 | 48.52 | 5.95 | 0.018 | uncharacterized LOC100506119 |  |  |
| 54512 | EXOSC4 | 0.570 | 1.48 | 48.42 | 7.57 | 0.002 | exosome component 4 |  |  |
| 222487 | GPR97 | 0.569 | 1.48 | 48.36 | 11.04 | 0.025 | G protein-coupled receptor 97 |  |  |
| 147015 | DHRS13 | 0.562 | 1.48 | 47.59 | 10.29 | 0.006 | dehydrogenase/reductase (SDR family) member 13 | |  |
| 1263 | PLK3 | 0.550 | 1.46 | 46.44 | 6.65 | 0.012 | polo-like kinase 3 |  |  |
| 100506115 | LOC100506115 | 0.541 | 1.45 | 45.48 | 11.60 | 0.022 | uncharacterized LOC100506115 |  |  |
| 8870 | IER3 | 0.532 | 1.45 | 44.56 | 9.18 | 0.028 | immediate early response 3 |  |  |
| 2153 | F5 | 0.531 | 1.45 | 44.52 | 8.02 | 0.032 | coagulation factor V (proaccelerin, labile factor) | |  |
| 4016 | LOXL1 | 0.528 | 1.44 | 44.16 | 4.08 | 0.018 | lysyl oxidase-like 1 |  |  |
| 79650 | USB1 | 0.521 | 1.43 | 43.50 | 9.19 | 0.003 | U6 snRNA biogenesis 1 |  |  |
| 3101 | HK3 | 0.521 | 1.43 | 43.50 | 10.36 | 0.003 | hexokinase 3 (white cell) |  |  |
| 200931 | SLC51A | 0.517 | 1.43 | 43.12 | 2.63 | 0.036 | solute carrier family 51, alpha subunit |  |  |
| 79865 | TREML2 | 0.514 | 1.43 | 42.77 | 9.54 | 0.037 | triggering receptor expressed on myeloid cells-like 2 | |  |
| 7100 | TLR5 | 0.512 | 1.43 | 42.59 | 10.68 | 0.013 | toll-like receptor 5 |  |  |
| 55129 | ANO10 | 0.504 | 1.42 | 41.84 | 7.46 | 0.019 | anoctamin 10 |  |  |
| 220929 | ZNF438 | 0.495 | 1.41 | 40.96 | 7.62 | 0.045 | zinc finger protein 438 |  |  |
| 79134 | TMEM185B | 0.495 | 1.41 | 40.91 | 7.65 | 0.032 | transmembrane protein 185B |  |  |
| 2992 | GYG1 | 0.494 | 1.41 | 40.82 | 13.16 | 0.012 | glycogenin 1 |  |  |
| 23095 | KIF1B | 0.493 | 1.41 | 40.72 | 8.75 | 0.031 | kinesin family member 1B |  |  |
| 2242 | FES | 0.489 | 1.40 | 40.33 | 9.26 | 0.007 | feline sarcoma oncogene |  |  |
| 83862 | TMEM120A | 0.486 | 1.40 | 40.08 | 9.61 | 0.012 | transmembrane protein 120A |  |  |
| 57655 | GRAMD1A | 0.484 | 1.40 | 39.85 | 9.76 | 0.010 | GRAM domain containing 1A |  |  |
| 147699 | PPM1N | 0.478 | 1.39 | 39.27 | 3.28 | 0.006 | protein phosphatase, Mg2+/Mn2+ dependent, 1N (putative) | | |
| 10211 | FLOT1 | 0.473 | 1.39 | 38.82 | 11.56 | 0.003 | flotillin 1 |  |  |
| 84649 | DGAT2 | 0.466 | 1.38 | 38.17 | 11.49 | 0.015 | diacylglycerol O-acyltransferase 2 |  |  |
| 6253 | RTN2 | 0.466 | 1.38 | 38.14 | 5.55 | 0.017 | reticulon 2 |  |  |
| 2131 | EXT1 | 0.464 | 1.38 | 37.97 | 7.95 | 0.019 | exostosin 1 |  |  |
| 3732 | CD82 | 0.461 | 1.38 | 37.62 | 9.96 | 0.003 | CD82 molecule |  |  |
| 9435 | CHST2 | 0.453 | 1.37 | 36.89 | 8.91 | 0.026 | carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 | | |
| 8291 | DYSF | 0.448 | 1.36 | 36.40 | 12.77 | 0.014 | dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) | | |
| 8530 | CST7 | 0.447 | 1.36 | 36.37 | 13.49 | 0.019 | cystatin F (leukocystatin) |  |  |
| 960 | CD44 | 0.447 | 1.36 | 36.31 | 10.65 | 0.005 | CD44 molecule (Indian blood group) |  |  |
| 10435 | CDC42EP2 | 0.446 | 1.36 | 36.22 | 6.51 | 0.017 | CDC42 effector protein (Rho GTPase binding) 2 | |  |
| 9895 | TECPR2 | 0.439 | 1.36 | 35.61 | 9.25 | 0.021 | tectonin beta-propeller repeat containing 2 |  |  |
| 2319 | FLOT2 | 0.435 | 1.35 | 35.17 | 11.28 | 0.015 | flotillin 2 |  |  |
| 22926 | ATF6 | 0.427 | 1.34 | 34.46 | 10.19 | 0.015 | activating transcription factor 6 |  |  |
| 3985 | LIMK2 | 0.425 | 1.34 | 34.25 | 10.66 | 0.023 | LIM domain kinase 2 |  |  |
| 84418 | CYSTM1 | 0.418 | 1.34 | 33.60 | 13.22 | 0.017 | cysteine-rich transmembrane module containing 1 | |  |
| 27342 | RABGEF1 | 0.413 | 1.33 | 33.18 | 9.37 | 0.037 | RAB guanine nucleotide exchange factor (GEF) 1 | |  |
| 100506550 |  | 0.399 | 1.32 | 31.90 | 7.16 | 0.020 |  |  |  |
| 84925 | DIRC2 | 0.398 | 1.32 | 31.77 | 6.90 | 0.023 | disrupted in renal carcinoma 2 |  |  |
| 7090 | TLE3 | 0.398 | 1.32 | 31.76 | 9.75 | 0.036 | transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) | | |
| 3566 | IL4R | 0.398 | 1.32 | 31.73 | 10.14 | 0.029 | interleukin 4 receptor |  |  |
| 3640 | INSL3 | 0.396 | 1.32 | 31.57 | 4.66 | 0.003 | insulin-like 3 (Leydig cell) |  |  |
| 3687 | ITGAX | 0.394 | 1.31 | 31.39 | 11.49 | 0.018 | integrin, alpha X (complement component 3 receptor 4 subunit) | | |
| 3553 | IL1B | 0.393 | 1.31 | 31.33 | 10.25 | 0.044 | interleukin 1, beta |  |  |
| 51317 | PHF21A | 0.393 | 1.31 | 31.32 | 8.82 | 0.028 | PHD finger protein 21A |  |  |
| 10162 | LPCAT3 | 0.389 | 1.31 | 30.97 | 6.81 | 0.037 | lysophosphatidylcholine acyltransferase 3 |  |  |
| 27180 | SIGLEC9 | 0.388 | 1.31 | 30.84 | 7.89 | 0.046 | sialic acid binding Ig-like lectin 9 |  |  |
| 10226 | PLIN3 | 0.387 | 1.31 | 30.73 | 10.58 | 0.027 | perilipin 3 |  |  |
| 9489 | PGS1 | 0.386 | 1.31 | 30.72 | 11.28 | 0.039 | phosphatidylglycerophosphate synthase 1 | |  |
| 3726 | JUNB | 0.386 | 1.31 | 30.65 | 10.72 | 0.013 | jun B proto-oncogene |  |  |
| 8563 | THOC5 | 0.375 | 1.30 | 29.65 | 9.83 | 0.015 | THO complex 5 |  |  |
| 10538 | BATF | 0.373 | 1.30 | 29.51 | 8.27 | 0.005 | basic leucine zipper transcription factor, ATF-like | |  |
| 4043 | LRPAP1 | 0.373 | 1.29 | 29.47 | 9.89 | 0.015 | low density lipoprotein receptor-related protein associated protein 1 | | |
| 24144 | TFIP11 | 0.372 | 1.29 | 29.38 | 9.07 | 0.032 | tuftelin interacting protein 11 |  |  |
| 26502 | NARF | 0.371 | 1.29 | 29.34 | 11.43 | 0.003 | nuclear prelamin A recognition factor |  |  |
| 10603 | SH2B2 | 0.369 | 1.29 | 29.14 | 9.86 | 0.048 | SH2B adaptor protein 2 |  |  |
| 148479 | PHF13 | 0.366 | 1.29 | 28.85 | 6.66 | 0.048 | PHD finger protein 13 |  |  |
| 90007 | MIDN | 0.364 | 1.29 | 28.70 | 5.76 | 0.025 | midnolin |  |  |
| 377 | ARF3 | 0.364 | 1.29 | 28.69 | 9.32 | 0.015 | ADP-ribosylation factor 3 |  |  |
| 84674 | CARD6 | 0.364 | 1.29 | 28.66 | 10.53 | 0.023 | caspase recruitment domain family, member 6 | |  |
| 126014 | OSCAR | 0.363 | 1.29 | 28.64 | 9.47 | 0.046 | osteoclast associated, immunoglobulin-like receptor | |  |
| 56996 | SLC12A9 | 0.363 | 1.29 | 28.62 | 7.17 | 0.015 | solute carrier family 12, member 9 |  |  |
| 90459 | ERI1 | 0.360 | 1.28 | 28.37 | 6.91 | 0.045 | exoribonuclease 1 |  |  |
| 60685 | ZFAND3 | 0.358 | 1.28 | 28.13 | 7.87 | 0.039 | zinc finger, AN1-type domain 3 |  |  |
| 10981 | RAB32 | 0.357 | 1.28 | 28.05 | 10.85 | 0.023 | RAB32, member RAS oncogene family |  |  |
| 64778 | FNDC3B | 0.357 | 1.28 | 28.04 | 9.22 | 0.041 | fibronectin type III domain containing 3B |  |  |
| 55784 | MCTP2 | 0.356 | 1.28 | 27.98 | 8.69 | 0.049 | multiple C2 domains, transmembrane 2 |  |  |
| 3718 | JAK3 | 0.355 | 1.28 | 27.93 | 5.84 | <0.001 | Janus kinase 3 |  |  |
| 1889 | ECE1 | 0.354 | 1.28 | 27.79 | 7.49 | 0.022 | endothelin converting enzyme 1 |  |  |
| 5130 | PCYT1A | 0.353 | 1.28 | 27.74 | 5.94 | 0.030 | phosphate cytidylyltransferase 1, choline, alpha | |  |
| 4298 | MLLT1 | 0.353 | 1.28 | 27.71 | 7.38 | 0.003 | myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1 | | |
| 284207 | METRNL | 0.352 | 1.28 | 27.59 | 9.49 | 0.036 | meteorin, glial cell differentiation regulator-like | |  |
| 113878 | DTX2 | 0.350 | 1.27 | 27.47 | 6.25 | 0.032 | deltex homolog 2 (Drosophila) |  |  |
| 3454 | IFNAR1 | 0.347 | 1.27 | 27.23 | 9.01 | 0.029 | interferon (alpha, beta and omega) receptor 1 | |  |
| 54432 | YIPF1 | 0.346 | 1.27 | 27.11 | 9.87 | 0.013 | Yip1 domain family, member 1 |  |  |
| 126208 | ZNF787 | 0.346 | 1.27 | 27.06 | 7.24 | 0.047 | zinc finger protein 787 |  |  |
| 1992 | SERPINB1 | 0.344 | 1.27 | 26.97 | 13.09 | 0.026 | serpin peptidase inhibitor, clade B (ovalbumin), member 1 | | |
| 632 | BGLAP | 0.343 | 1.27 | 26.88 | 3.94 | 0.029 | bone gamma-carboxyglutamate (gla) protein | |  |
| 83667 | SESN2 | 0.342 | 1.27 | 26.78 | 5.48 | 0.048 | sestrin 2 |  |  |
| 56063 | TMEM234 | 0.340 | 1.27 | 26.59 | 6.05 | 0.038 | transmembrane protein 234 |  |  |
| 283537 | SLC46A3 | 0.340 | 1.27 | 26.58 | 9.54 | 0.014 | solute carrier family 46, member 3 |  |  |
| 54187 | NANS | 0.339 | 1.26 | 26.47 | 9.09 | 0.012 | N-acetylneuraminic acid synthase |  |  |
| 23144 | ZC3H3 | 0.338 | 1.26 | 26.38 | 5.73 | 0.023 | zinc finger CCCH-type containing 3 |  |  |
| 706 | TSPO | 0.337 | 1.26 | 26.31 | 13.24 | 0.004 | translocator protein (18kDa) |  |  |
| 9674 | KIAA0040 | 0.337 | 1.26 | 26.27 | 9.66 | 0.045 | KIAA0040 |  |  |
| 2584 | GALK1 | 0.336 | 1.26 | 26.18 | 5.97 | 0.039 | galactokinase 1 |  |  |
| 132160 | PPM1M | 0.335 | 1.26 | 26.12 | 10.11 | 0.005 | protein phosphatase, Mg2+/Mn2+ dependent, 1M | |  |
| 2800 | GOLGA1 | 0.332 | 1.26 | 25.92 | 5.64 | 0.045 | golgin A1 |  |  |
| 4296 | MAP3K11 | 0.332 | 1.26 | 25.85 | 8.84 | 0.041 | mitogen-activated protein kinase kinase kinase 11 | |  |
| 6195 | RPS6KA1 | 0.332 | 1.26 | 25.85 | 11.09 | 0.014 | ribosomal protein S6 kinase, 90kDa, polypeptide 1 | |  |
| 23534 | TNPO3 | 0.331 | 1.26 | 25.78 | 9.07 | 0.048 | transportin 3 |  |  |
| 3684 | ITGAM | 0.329 | 1.26 | 25.61 | 12.31 | 0.013 | integrin, alpha M (complement component 3 receptor 3 subunit) | | |
| 493 | ATP2B4 | 0.328 | 1.26 | 25.54 | 8.61 | 0.007 | ATPase, Ca++ transporting, plasma membrane 4 | |  |
| 7076 | TIMP1 | 0.328 | 1.26 | 25.51 | 12.08 | 0.042 | TIMP metallopeptidase inhibitor 1 |  |  |
| 8694 | DGAT1 | 0.327 | 1.25 | 25.43 | 8.24 | 0.008 | diacylglycerol O-acyltransferase 1 |  |  |
| 51271 | UBAP1 | 0.326 | 1.25 | 25.32 | 9.36 | 0.023 | ubiquitin associated protein 1 |  |  |
| 51296 | SLC15A3 | 0.325 | 1.25 | 25.26 | 9.30 | 0.033 | solute carrier family 15 (oligopeptide transporter), member 3 | | |
| 28988 | DBNL | 0.324 | 1.25 | 25.18 | 9.49 | 0.026 | drebrin-like |  |  |
| 3516 | RBPJ | 0.323 | 1.25 | 25.09 | 12.68 | 0.015 | recombination signal binding protein for immunoglobulin kappa J region | | |
| 64319 | FBRS | 0.320 | 1.25 | 24.83 | 6.97 | 0.049 | fibrosin |  |  |
| 1084 | CEACAM3 | 0.320 | 1.25 | 24.81 | 9.14 | 0.032 | carcinoembryonic antigen-related cell adhesion molecule 3 | | |
| 3577 | CXCR1 | 0.320 | 1.25 | 24.81 | 12.96 | 0.021 | chemokine (C-X-C motif) receptor 1 |  |  |
| 10295 | BCKDK | 0.319 | 1.25 | 24.79 | 8.37 | 0.022 | branched chain ketoacid dehydrogenase kinase | |  |
| 11025 | LILRB3 | 0.319 | 1.25 | 24.78 | 12.03 | 0.016 | leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 | | |
| 254102 | EHBP1L1 | 0.319 | 1.25 | 24.72 | 8.51 | 0.017 | EH domain binding protein 1-like 1 |  |  |
| 9929 | JOSD1 | 0.317 | 1.25 | 24.54 | 8.50 | 0.013 | Josephin domain containing 1 |  |  |
| 80301 | PLEKHO2 | 0.316 | 1.24 | 24.50 | 10.98 | 0.013 | pleckstrin homology domain containing, family O member 2 | | |
| 3280 | HES1 | 0.315 | 1.24 | 24.38 | 3.61 | 0.022 | hes family bHLH transcription factor 1 |  |  |
| 6483 | ST3GAL2 | 0.315 | 1.24 | 24.37 | 7.84 | 0.030 | ST3 beta-galactoside alpha-2,3-sialyltransferase 2 | |  |
| 27128 | CYTH4 | 0.312 | 1.24 | 24.16 | 9.33 | 0.035 | cytohesin 4 |  |  |
| 28232 | SLCO3A1 | 0.311 | 1.24 | 24.06 | 8.47 | 0.041 | solute carrier organic anion transporter family, member 3A1 | | |
| 3383 | ICAM1 | 0.309 | 1.24 | 23.86 | 7.13 | 0.044 | intercellular adhesion molecule 1 |  |  |
| 7132 | TNFRSF1A | 0.308 | 1.24 | 23.83 | 12.62 | 0.023 | tumor necrosis factor receptor superfamily, member 1A | |  |
| 2590 | GALNT2 | 0.306 | 1.24 | 23.67 | 7.09 | 0.012 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2) | | |
| 642475 | MROH6 | 0.306 | 1.24 | 23.60 | 5.34 | 0.003 | maestro heat-like repeat family member 6 |  |  |
| 2787 | GNG5 | 0.305 | 1.24 | 23.50 | 11.44 | 0.037 | guanine nucleotide binding protein (G protein), gamma 5 | | |
| 55902 | ACSS2 | 0.300 | 1.23 | 23.11 | 7.20 | 0.015 | acyl-CoA synthetase short-chain family member 2 | |  |
| 10938 | EHD1 | 0.298 | 1.23 | 22.94 | 9.74 | 0.015 | EH-domain containing 1 |  |  |
| 967 | CD63 | 0.298 | 1.23 | 22.94 | 13.13 | 0.006 | CD63 molecule |  |  |
| 6515 | SLC2A3 | 0.298 | 1.23 | 22.91 | 12.39 | 0.035 | solute carrier family 2 (facilitated glucose transporter), member 3 | | |
| 5770 | PTPN1 | 0.296 | 1.23 | 22.75 | 7.84 | 0.037 | protein tyrosine phosphatase, non-receptor type 1 | |  |
| 83706 | FERMT3 | 0.294 | 1.23 | 22.58 | 10.94 | 0.027 | fermitin family member 3 |  |  |
| 58986 | TMEM8A | 0.294 | 1.23 | 22.58 | 8.24 | 0.041 | transmembrane protein 8A |  |  |
| 83463 | MXD3 | 0.294 | 1.23 | 22.58 | 8.73 | 0.031 | MAX dimerization protein 3 |  |  |
| 200058 | FLJ23867 | 0.293 | 1.23 | 22.53 | 3.34 | 0.045 | uncharacterized protein FLJ23867 |  |  |
| 79415 | C17orf62 | 0.293 | 1.23 | 22.52 | 12.02 | 0.005 | chromosome 17 open reading frame 62 |  |  |
| 58500 | ZNF250 | 0.292 | 1.22 | 22.43 | 2.60 | 0.013 | zinc finger protein 250 |  |  |
| 100131117 | ZBTB20-AS1 | 0.291 | 1.22 | 22.34 | 2.68 | 0.036 | ZBTB20 antisense RNA 1 |  |  |
| 100290566 |  | 0.290 | 1.22 | 22.27 | 8.06 | 0.020 |  |  |  |
| 10049 | DNAJB6 | 0.290 | 1.22 | 22.23 | 9.04 | 0.034 | DnaJ (Hsp40) homolog, subfamily B, member 6 | |  |
| 4790 | NFKB1 | 0.289 | 1.22 | 22.18 | 9.76 | 0.037 | nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 | | |
| 9673 | SLC25A44 | 0.288 | 1.22 | 22.11 | 10.26 | 0.047 | solute carrier family 25, member 44 |  |  |
| 9683 | N4BP1 | 0.286 | 1.22 | 21.89 | 9.07 | 0.029 | NEDD4 binding protein 1 |  |  |
| 124583 | CANT1 | 0.282 | 1.22 | 21.56 | 9.80 | 0.048 | calcium activated nucleotidase 1 |  |  |
| 7409 | VAV1 | 0.278 | 1.21 | 21.23 | 10.62 | 0.021 | vav 1 guanine nucleotide exchange factor |  |  |
| 54434 | SSH1 | 0.278 | 1.21 | 21.22 | 4.81 | 0.030 | slingshot protein phosphatase 1 |  |  |
| 1523 | CUX1 | 0.278 | 1.21 | 21.21 | 8.86 | 0.021 | cut-like homeobox 1 |  |  |
| 2207 | FCER1G | 0.277 | 1.21 | 21.17 | 14.24 | 0.003 | Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide | | |
| 415116 | PIM3 | 0.275 | 1.21 | 20.97 | 10.59 | 0.019 | pim-3 oncogene |  |  |
| 3055 | HCK | 0.275 | 1.21 | 20.97 | 13.95 | 0.026 | hemopoietic cell kinase |  |  |
| 64374 | SIL1 | 0.274 | 1.21 | 20.91 | 5.70 | 0.036 | SIL1 nucleotide exchange factor |  |  |
| 9961 | MVP | 0.271 | 1.21 | 20.66 | 11.17 | 0.030 | major vault protein |  |  |
| 23307 | FKBP15 | 0.271 | 1.21 | 20.63 | 9.19 | 0.032 | FK506 binding protein 15, 133kDa |  |  |
| 10011 | SRA1 | 0.271 | 1.21 | 20.62 | 10.00 | 0.022 | steroid receptor RNA activator 1 |  |  |
| 9654 | TTLL4 | 0.263 | 1.20 | 19.97 | 4.04 | 0.015 | tubulin tyrosine ligase-like family, member 4 | |  |
| 391 | RHOG | 0.261 | 1.20 | 19.81 | 13.64 | 0.020 | ras homolog family member G |  |  |
| 55737 | VPS35 | 0.260 | 1.20 | 19.78 | 10.99 | 0.014 | vacuolar protein sorting 35 homolog (S. cerevisiae) | |  |
| 3588 | IL10RB | 0.259 | 1.20 | 19.68 | 12.02 | 0.045 | interleukin 10 receptor, beta |  |  |
| 23210 | JMJD6 | 0.258 | 1.20 | 19.61 | 6.78 | 0.031 | jumonji domain containing 6 |  |  |
| 7920 | ABHD16A | 0.258 | 1.20 | 19.59 | 9.27 | 0.020 | abhydrolase domain containing 16A |  |  |
| 51292 | GMPR2 | 0.257 | 1.19 | 19.46 | 10.00 | 0.037 | guanosine monophosphate reductase 2 |  |  |
| 4055 | LTBR | 0.252 | 1.19 | 19.12 | 7.80 | 0.015 | lymphotoxin beta receptor (TNFR superfamily, member 3) | | |
| 7227 | TRPS1 | 0.252 | 1.19 | 19.06 | 4.84 | 0.047 | trichorhinophalangeal syndrome I |  |  |
| 55741 | EDEM2 | 0.250 | 1.19 | 18.92 | 9.34 | 0.023 | ER degradation enhancer, mannosidase alpha-like 2 | |  |
| 64342 | HS1BP3 | 0.249 | 1.19 | 18.80 | 8.67 | 0.046 | HCLS1 binding protein 3 |  |  |
| 8793 | TNFRSF10D | 0.248 | 1.19 | 18.76 | 3.79 | 0.026 | tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain | | |
| 29950 | SERTAD1 | 0.248 | 1.19 | 18.72 | 8.21 | 0.042 | SERTA domain containing 1 |  |  |
| 57053 | CHRNA10 | 0.247 | 1.19 | 18.71 | 2.56 | 0.015 | cholinergic receptor, nicotinic, alpha 10 (neuronal) | |  |
| 11270 | NRM | 0.247 | 1.19 | 18.68 | 8.03 | 0.035 | nurim (nuclear envelope membrane protein) | |  |
| 81894 | SLC25A28 | 0.245 | 1.18 | 18.48 | 8.26 | 0.037 | solute carrier family 25 (mitochondrial iron transporter), member 28 | | |
| 2870 | GRK6 | 0.243 | 1.18 | 18.34 | 9.76 | 0.018 | G protein-coupled receptor kinase 6 |  |  |
| 79180 | EFHD2 | 0.243 | 1.18 | 18.33 | 11.51 | 0.041 | EF-hand domain family, member D2 |  |  |
| 83692 | CD99L2 | 0.243 | 1.18 | 18.32 | 4.64 | 0.029 | CD99 molecule-like 2 |  |  |
| 9922 | IQSEC1 | 0.241 | 1.18 | 18.16 | 10.69 | 0.023 | IQ motif and Sec7 domain 1 |  |  |
| 54926 | UBE2R2 | 0.240 | 1.18 | 18.10 | 11.02 | 0.045 | ubiquitin-conjugating enzyme E2R 2 |  |  |
| 51304 | ZDHHC3 | 0.239 | 1.18 | 18.05 | 7.66 | 0.022 | zinc finger, DHHC-type containing 3 |  |  |
| 6648 | SOD2 | 0.235 | 1.18 | 17.73 | 13.41 | 0.047 | superoxide dismutase 2, mitochondrial |  |  |
| 5265 | SERPINA1 | 0.234 | 1.18 | 17.61 | 14.55 | 0.014 | serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 | | |
| 11035 | RIPK3 | 0.232 | 1.17 | 17.41 | 7.86 | 0.027 | receptor-interacting serine-threonine kinase 3 | |  |
| 4689 | NCF4 | 0.231 | 1.17 | 17.35 | 13.11 | 0.037 | neutrophil cytosolic factor 4, 40kDa |  |  |
| 7177 | TPSAB1 | 0.227 | 1.17 | 17.00 | 6.63 | 0.035 | tryptase alpha/beta 1 |  |  |
| 404201 | WDFY3-AS2 | 0.223 | 1.17 | 16.75 | 2.29 | 0.001 | WDFY3 antisense RNA 2 |  |  |
| 10409 | BASP1 | 0.221 | 1.17 | 16.57 | 14.68 | 0.023 | brain abundant, membrane attached signal protein 1 | |  |
| 22877 | MLXIP | 0.221 | 1.17 | 16.56 | 5.32 | 0.049 | MLX interacting protein |  |  |
| 553115 | PEF1 | 0.218 | 1.16 | 16.28 | 9.84 | 0.012 | penta-EF-hand domain containing 1 |  |  |
| 5937 | RBMS1 | 0.217 | 1.16 | 16.21 | 11.35 | 0.020 | RNA binding motif, single stranded interacting protein 1 | | |
| 55654 | TMEM127 | 0.215 | 1.16 | 16.06 | 9.56 | 0.047 | transmembrane protein 127 |  |  |
| 54838 | WBP1L | 0.213 | 1.16 | 15.88 | 9.91 | 0.046 | WW domain binding protein 1-like |  |  |
| 25923 | ATL3 | 0.208 | 1.16 | 15.53 | 2.54 | 0.016 | atlastin GTPase 3 |  |  |
| 7846 | TUBA1A | 0.207 | 1.15 | 15.42 | 14.34 | 0.022 | tubulin, alpha 1a |  |  |
| 58190 | CTDSP1 | 0.205 | 1.15 | 15.28 | 10.38 | 0.042 | CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1 | | |
| 79709 | COLGALT1 | 0.196 | 1.15 | 14.52 | 6.06 | 0.034 | collagen beta(1-O)galactosyltransferase 1 |  |  |
| 79594 | MUL1 | 0.195 | 1.14 | 14.45 | 6.13 | 0.047 | mitochondrial E3 ubiquitin protein ligase 1 |  |  |
| 7994 | KAT6A | 0.191 | 1.14 | 14.19 | 10.43 | 0.046 | K(lysine) acetyltransferase 6A |  |  |
| 80347 | COASY | 0.189 | 1.14 | 14.00 | 8.17 | 0.032 | CoA synthase |  |  |
| 6821 | SUOX | 0.186 | 1.14 | 13.80 | 3.36 | 0.030 | sulfite oxidase |  |  |
| 226 | ALDOA | 0.186 | 1.14 | 13.79 | 12.58 | 0.041 | aldolase A, fructose-bisphosphate |  |  |
| 26277 | TINF2 | 0.180 | 1.13 | 13.33 | 10.51 | 0.010 | TERF1 (TRF1)-interacting nuclear factor 2 |  |  |
| 7038 | TG | 0.174 | 1.13 | 12.79 | 2.34 | 0.044 | thyroglobulin |  |  |
| 4898 | NRD1 | 0.173 | 1.13 | 12.71 | 11.97 | 0.050 | nardilysin (N-arginine dibasic convertase) |  |  |
| 10221 | TRIB1 | 0.173 | 1.13 | 12.71 | 2.45 | 0.041 | tribbles pseudokinase 1 |  |  |
| 79155 | TNIP2 | 0.171 | 1.13 | 12.56 | 8.87 | 0.026 | TNFAIP3 interacting protein 2 |  |  |
| 7084 | TK2 | 0.166 | 1.12 | 12.22 | 4.85 | 0.022 | thymidine kinase 2, mitochondrial |  |  |
| 8239 | USP9X | 0.161 | 1.12 | 11.84 | 9.32 | 0.037 | ubiquitin specific peptidase 9, X-linked |  |  |
| 2582 | GALE | 0.144 | 1.10 | 10.48 | 2.50 | 0.028 | UDP-galactose-4-epimerase |  |  |
| 23288 | IQCE | 0.140 | 1.10 | 10.23 | 3.59 | 0.044 | IQ motif containing E |  |  |
| 351 | APP | 0.130 | 1.09 | 9.39 | 6.14 | 0.030 | amyloid beta (A4) precursor protein |  |  |
| 10540 | DCTN2 | 0.127 | 1.09 | 9.22 | 10.18 | 0.047 | dynactin 2 (p50) |  |  |
| 6282 | S100A11 | 0.126 | 1.09 | 9.12 | 15.13 | 0.029 | S100 calcium binding protein A11 |  |  |
| 63924 | CIDEC | 0.125 | 1.09 | 9.03 | 2.27 | 0.016 | cell death-inducing DFFA-like effector c |  |  |
| 10018 | BCL2L11 | 0.123 | 1.09 | 8.90 | 5.36 | 0.047 | BCL2-like 11 (apoptosis facilitator) |  |  |
| 2810 | SFN | 0.115 | 1.08 | 8.30 | 3.08 | 0.037 | stratifin |  |  |
| 116986 | AGAP2 | 0.113 | 1.08 | 8.18 | 2.36 | 0.014 | ArfGAP with GTPase domain, ankyrin repeat and PH domain 2 | | |
| 55252 | ASXL2 | 0.106 | 1.08 | 7.64 | 3.28 | 0.038 | additional sex combs like 2 (Drosophila) |  |  |
| 711 | ERC2-IT1 | 0.093 | 1.07 | 6.69 | 2.30 | 0.037 | ERC2 intronic transcript 1 (non-protein coding) | |  |
| 5830 | PEX5 | 0.082 | 1.06 | 5.87 | 2.96 | 0.029 | peroxisomal biogenesis factor 5 |  |  |
| 389792 | IER5L | 0.078 | 1.06 | 5.58 | 3.64 | 0.026 | immediate early response 5-like |  |  |
| 7170 | TPM3 | 0.076 | 1.05 | 5.39 | 2.87 | 0.017 | tropomyosin 3 |  |  |
| 283875 | LINC00514 | 0.067 | 1.05 | 4.78 | 2.23 | 0.026 | long intergenic non-protein coding RNA 514 | |  |
| 100505547 | LOC100505547 | 0.061 | 1.04 | 4.35 | 2.24 | 0.039 | uncharacterized LOC100505547 |  |  |
| 153562 | MARVELD2 | 0.052 | 1.04 | 3.66 | 2.24 | 0.047 | MARVEL domain containing 2 |  |  |
| 6462 | SHBG | 0.027 | 1.02 | 1.86 | 2.22 | 0.023 | sex hormone-binding globulin |  |  |
| **Down-regulated genes (n=213)** | | | | | | | | | |
| 92342 | METTL18 | -0.909 | 0.53 | -46.76 | 3.96 | 0.002 | methyltransferase like 18 |  |  |
| 23015 | GOLGA8A | -0.874 | 0.55 | -45.44 | 8.94 | 0.037 | golgin A8 family, member A |  |  |
| 55900 | ZNF302 | -0.802 | 0.57 | -42.65 | 3.70 | 0.007 | zinc finger protein 302 |  |  |
| 54482 | TRMT13 | -0.797 | 0.58 | -42.46 | 4.87 | 0.047 | tRNA methyltransferase 13 homolog (S. cerevisiae) | |  |
| 1070 | CETN3 | -0.773 | 0.59 | -41.49 | 4.45 | 0.032 | centrin, EF-hand protein, 3 |  |  |
| 79752 | ZFAND1 | -0.771 | 0.59 | -41.41 | 5.87 | 0.040 | zinc finger, AN1-type domain 1 |  |  |
| 26228 | STAP1 | -0.764 | 0.59 | -41.11 | 4.61 | 0.007 | signal transducing adaptor family member 1 | |  |
| 931 | MS4A1 | -0.758 | 0.59 | -40.86 | 7.52 | 0.028 | membrane-spanning 4-domains, subfamily A, member 1 | | |
| 57560 | IFT80 | -0.737 | 0.60 | -40.01 | 4.62 | 0.040 | intraflagellar transport 80 homolog (Chlamydomonas) | |  |
| 10393 | ANAPC10 | -0.729 | 0.60 | -39.65 | 4.42 | 0.047 | anaphase promoting complex subunit 10 |  |  |
| 60592 | SCOC | -0.705 | 0.61 | -38.64 | 4.88 | 0.047 | short coiled-coil protein |  |  |
| 100499177 | THAP9-AS1 | -0.703 | 0.61 | -38.56 | 7.05 | 0.024 | THAP9 antisense RNA 1 |  |  |
| 6741 | SSB | -0.686 | 0.62 | -37.86 | 6.57 | 0.026 | Sjogren syndrome antigen B (autoantigen La) | |  |
| 157567 | ANKRD46 | -0.671 | 0.63 | -37.20 | 4.70 | 0.037 | ankyrin repeat domain 46 |  |  |
| 112942 | CCDC104 | -0.668 | 0.63 | -37.07 | 5.00 | 0.031 | coiled-coil domain containing 104 |  |  |
| 91298 | C12ORF29 | -0.648 | 0.64 | -36.17 | 4.78 | 0.031 | chromosome 12 open reading frame 29 |  |  |
| 5378 | PMS1 | -0.647 | 0.64 | -36.13 | 5.33 | 0.044 | PMS1 postmeiotic segregation increased 1 (S. cerevisiae) | | |
| 8821 | INPP4B | -0.636 | 0.64 | -35.67 | 4.85 | 0.012 | inositol polyphosphate-4-phosphatase, type II, 105kDa | | |
| 84128 | WDR75 | -0.636 | 0.64 | -35.67 | 6.72 | 0.019 | WD repeat domain 75 |  |  |
| 65109 | UPF3B | -0.626 | 0.65 | -35.18 | 4.23 | 0.031 | UPF3 regulator of nonsense transcripts homolog B (yeast) | | |
| 123036 | TC2N | -0.624 | 0.65 | -35.10 | 6.22 | 0.021 | tandem C2 domains, nuclear |  |  |
| 8504 | PEX3 | -0.620 | 0.65 | -34.93 | 4.77 | 0.021 | peroxisomal biogenesis factor 3 |  |  |
| 27075 | TSPAN13 | -0.610 | 0.66 | -34.50 | 6.75 | 0.022 | tetraspanin 13 |  |  |
| 34 | ACADM | -0.596 | 0.66 | -33.84 | 7.11 | 0.049 | acyl-CoA dehydrogenase, C-4 to C-12 straight chain | |  |
| 55300 | PI4K2B | -0.594 | 0.66 | -33.75 | 5.32 | 0.047 | phosphatidylinositol 4-kinase type 2 beta |  |  |
| 10892 | MALT1 | -0.594 | 0.66 | -33.73 | 5.88 | 0.018 | mucosa associated lymphoid tissue lymphoma translocation gene 1 | | |
| 117143 | TADA1 | -0.593 | 0.66 | -33.68 | 3.95 | 0.016 | transcriptional adaptor 1 |  |  |
| 57665 | RDH14 | -0.578 | 0.67 | -33.00 | 5.91 | 0.015 | retinol dehydrogenase 14 (all-trans/9-cis/11-cis) | |  |
| 10282 | BET1 | -0.577 | 0.67 | -32.95 | 5.95 | 0.044 | Bet1 golgi vesicular membrane trafficking protein | |  |
| 55006 | TRMT61B | -0.565 | 0.68 | -32.42 | 5.91 | 0.023 | tRNA methyltransferase 61 homolog B (S. cerevisiae) | |  |
| 84365 | NIFK | -0.562 | 0.68 | -32.25 | 6.01 | 0.030 | nucleolar protein interacting with the FHA domain of MKI67 | | |
| 25842 | ASF1A | -0.560 | 0.68 | -32.18 | 7.15 | 0.038 | anti-silencing function 1A histone chaperone | |  |
| 5567 | PRKACB | -0.559 | 0.68 | -32.11 | 6.72 | 0.032 | protein kinase, cAMP-dependent, catalytic, beta | |  |
| 9255 | AIMP1 | -0.558 | 0.68 | -32.10 | 6.61 | 0.041 | aminoacyl tRNA synthetase complex-interacting multifunctional protein 1 | | |
| 138241 | C9ORF85 | -0.554 | 0.68 | -31.89 | 3.96 | 0.031 | chromosome 9 open reading frame 85 |  |  |
| 5311 | PKD2 | -0.552 | 0.68 | -31.82 | 6.39 | 0.028 | polycystic kidney disease 2 (autosomal dominant) | |  |
| 10402 | ST3GAL6 | -0.548 | 0.68 | -31.59 | 7.37 | 0.017 | ST3 beta-galactoside alpha-2,3-sialyltransferase 6 | |  |
| 58478 | ENOPH1 | -0.546 | 0.68 | -31.51 | 7.71 | 0.020 | enolase-phosphatase 1 |  |  |
| 8725 | URI1 | -0.544 | 0.69 | -31.44 | 7.30 | 0.015 | URI1, prefoldin-like chaperone |  |  |
| 29121 | CLEC2D | -0.538 | 0.69 | -31.15 | 6.13 | 0.032 | C-type lectin domain family 2, member D |  |  |
| 81537 | SGPP1 | -0.537 | 0.69 | -31.10 | 5.52 | 0.037 | sphingosine-1-phosphate phosphatase 1 |  |  |
| 9702 | CEP57 | -0.537 | 0.69 | -31.06 | 5.97 | 0.023 | centrosomal protein 57kDa |  |  |
| 1633 | DCK | -0.536 | 0.69 | -31.03 | 8.82 | 0.039 | deoxycytidine kinase |  |  |
| 9166 | EBAG9 | -0.535 | 0.69 | -31.00 | 6.96 | 0.016 | estrogen receptor binding site associated, antigen, 9 | |  |
| 51015 | ISOC1 | -0.532 | 0.69 | -30.86 | 7.09 | 0.044 | isochorismatase domain containing 1 |  |  |
| 92912 | UBE2Q2 | -0.525 | 0.69 | -30.51 | 8.68 | 0.045 | ubiquitin-conjugating enzyme E2Q family member 2 | |  |
| 114908 | TMEM123 | -0.523 | 0.70 | -30.43 | 11.37 | 0.042 | transmembrane protein 123 |  |  |
| 23473 | CAPN7 | -0.522 | 0.70 | -30.36 | 6.08 | 0.015 | calpain 7 |  |  |
| 27334 | P2RY10 | -0.520 | 0.70 | -30.26 | 4.57 | 0.032 | purinergic receptor P2Y, G-protein coupled, 10 | |  |
| 5366 | PMAIP1 | -0.519 | 0.70 | -30.21 | 6.02 | 0.020 | phorbol-12-myristate-13-acetate-induced protein 1 | |  |
| 3646 | EIF3E | -0.517 | 0.70 | -30.12 | 11.84 | 0.045 | eukaryotic translation initiation factor 3, subunit E | |  |
| 57037 | ANKMY2 | -0.516 | 0.70 | -30.07 | 6.27 | 0.035 | ankyrin repeat and MYND domain containing 2 | |  |
| 79738 | BBS10 | -0.513 | 0.70 | -29.91 | 6.47 | 0.045 | Bardet-Biedl syndrome 10 |  |  |
| 56204 | FAM214A | -0.511 | 0.70 | -29.83 | 8.82 | 0.012 | family with sequence similarity 214, member A | |  |
| 83939 | EIF2A | -0.510 | 0.70 | -29.78 | 9.40 | 0.042 | eukaryotic translation initiation factor 2A, 65kDa | |  |
| 202781 | PAXIP1-AS1 | -0.509 | 0.70 | -29.71 | 4.29 | 0.015 | PAXIP1 antisense RNA 1 (head to head) |  |  |
| 159090 | FAM122B | -0.506 | 0.70 | -29.58 | 6.87 | 0.018 | family with sequence similarity 122B |  |  |
| 10800 | CYSLTR1 | -0.505 | 0.70 | -29.54 | 8.63 | 0.020 | cysteinyl leukotriene receptor 1 |  |  |
| 25950 | RWDD3 | -0.503 | 0.71 | -29.42 | 4.34 | 0.018 | RWD domain containing 3 |  |  |
| 9406 | ZRANB2 | -0.501 | 0.71 | -29.33 | 9.59 | 0.045 | zinc finger, RAN-binding domain containing 2 | |  |
| 60487 | TRMT11 | -0.500 | 0.71 | -29.30 | 3.47 | 0.049 | tRNA methyltransferase 11 homolog (S. cerevisiae) | |  |
| 23443 | SLC35A3 | -0.499 | 0.71 | -29.26 | 6.02 | 0.044 | solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member A3 | | |
| 5876 | RABGGTB | -0.498 | 0.71 | -29.19 | 5.07 | 0.020 | Rab geranylgeranyltransferase, beta subunit | |  |
| 55251 | PCMTD2 | -0.494 | 0.71 | -29.00 | 9.80 | 0.018 | protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2 | | |
| 51727 | CMPK1 | -0.492 | 0.71 | -28.88 | 9.80 | 0.023 | cytidine monophosphate (UMP-CMP) kinase 1, cytosolic | | |
| 2287 | FKBP3 | -0.487 | 0.71 | -28.63 | 8.63 | 0.046 | FK506 binding protein 3, 25kDa |  |  |
| 25816 | TNFAIP8 | -0.485 | 0.71 | -28.57 | 10.58 | 0.006 | tumor necrosis factor, alpha-induced protein 8 | |  |
| 7699 | ZNF140 | -0.482 | 0.72 | -28.40 | 5.80 | 0.047 | zinc finger protein 140 |  |  |
| 53371 | NUP54 | -0.481 | 0.72 | -28.37 | 8.16 | 0.046 | nucleoporin 54kDa |  |  |
| 256380 | SCML4 | -0.481 | 0.72 | -28.33 | 8.18 | 0.003 | sex comb on midleg-like 4 (Drosophila) |  |  |
| 7748 | ZNF195 | -0.477 | 0.72 | -28.18 | 3.80 | 0.019 | zinc finger protein 195 |  |  |
| 7443 | VRK1 | -0.477 | 0.72 | -28.14 | 7.52 | 0.023 | vaccinia related kinase 1 |  |  |
| 3945 | LDHB | -0.469 | 0.72 | -27.76 | 12.99 | 0.044 | lactate dehydrogenase B |  |  |
| 9338 | TCEAL1 | -0.468 | 0.72 | -27.73 | 3.40 | 0.045 | transcription elongation factor A (SII)-like 1 | |  |
| 1974 | EIF4A2 | -0.468 | 0.72 | -27.72 | 11.44 | 0.016 | eukaryotic translation initiation factor 4A2 |  |  |
| 11168 | PSIP1 | -0.467 | 0.72 | -27.65 | 8.43 | 0.015 | PC4 and SFRS1 interacting protein 1 |  |  |
| 51747 | LUC7L3 | -0.466 | 0.72 | -27.62 | 9.53 | 0.027 | LUC7-like 3 (S. cerevisiae) |  |  |
| 10772 | SRSF10 | -0.464 | 0.73 | -27.49 | 8.27 | 0.020 | serine/arginine-rich splicing factor 10 |  |  |
| 114932 | MRFAP1L1 | -0.462 | 0.73 | -27.42 | 9.05 | 0.005 | Morf4 family associated protein 1-like 1 |  |  |
| 6726 | SRP9 | -0.462 | 0.73 | -27.38 | 12.21 | 0.029 | signal recognition particle 9kDa |  |  |
| 92106 | OXNAD1 | -0.461 | 0.73 | -27.36 | 7.32 | 0.048 | oxidoreductase NAD-binding domain containing 1 | |  |
| 100506112 | RIMKLB | -0.458 | 0.73 | -27.22 | 5.00 | 0.006 | ribosomal modification protein rimK-like family member B | | |
| 91272 | BOD1 | -0.457 | 0.73 | -27.16 | 6.73 | 0.030 | biorientation of chromosomes in cell division 1 | |  |
| 7503 | XIST | -0.457 | 0.73 | -27.15 | 10.08 | 0.022 | X inactive specific transcript (non-protein coding) | |  |
| 10196 | PRMT3 | -0.456 | 0.73 | -27.10 | 4.70 | 0.047 | protein arginine methyltransferase 3 |  |  |
| 10600 | USP16 | -0.455 | 0.73 | -27.05 | 7.30 | 0.029 | ubiquitin specific peptidase 16 |  |  |
| 9847 | C2CD5 | -0.451 | 0.73 | -26.87 | 8.71 | 0.030 | C2 calcium-dependent domain containing 5 | |  |
| 50854 | C6ORF48 | -0.450 | 0.73 | -26.79 | 10.20 | 0.044 | chromosome 6 open reading frame 48 |  |  |
| 9804 | TOMM20 | -0.432 | 0.74 | -25.89 | 9.78 | 0.030 | translocase of outer mitochondrial membrane 20 homolog (yeast) | | |
| 80746 | TSEN2 | -0.432 | 0.74 | -25.86 | 3.53 | 0.048 | TSEN2 tRNA splicing endonuclease subunit | |  |
| 154 | ADRB2 | -0.429 | 0.74 | -25.71 | 8.23 | 0.038 | adrenoceptor beta 2, surface |  |  |
| 26586 | CKAP2 | -0.429 | 0.74 | -25.71 | 4.90 | 0.040 | cytoskeleton associated protein 2 |  |  |
| 89894 | TMEM116 | -0.428 | 0.74 | -25.66 | 4.06 | 0.024 | transmembrane protein 116 |  |  |
| 136895 | C7ORF31 | -0.427 | 0.74 | -25.61 | 4.71 | 0.003 | chromosome 7 open reading frame 31 |  |  |
| 8434 | RECK | -0.424 | 0.75 | -25.45 | 3.93 | 0.048 | reversion-inducing-cysteine-rich protein with kazal motifs | | |
| 6135 | RPL11 | -0.424 | 0.75 | -25.45 | 13.25 | 0.049 | ribosomal protein L11 |  |  |
| 900 | CCNG1 | -0.423 | 0.75 | -25.40 | 10.34 | 0.022 | cyclin G1 |  |  |
| 55024 | BANK1 | -0.423 | 0.75 | -25.39 | 7.20 | 0.047 | B-cell scaffold protein with ankyrin repeats 1 | |  |
| 55602 | CDKN2AIP | -0.419 | 0.75 | -25.22 | 6.75 | 0.020 | CDKN2A interacting protein |  |  |
| 94101 | ORMDL1 | -0.418 | 0.75 | -25.16 | 6.35 | 0.045 | ORM1-like 1 (S. cerevisiae) |  |  |
| 10208 | USPL1 | -0.416 | 0.75 | -25.03 | 7.27 | 0.028 | ubiquitin specific peptidase like 1 |  |  |
| 5128 | CDK17 | -0.413 | 0.75 | -24.90 | 5.19 | 0.047 | cyclin-dependent kinase 17 |  |  |
| 79657 | RPAP3 | -0.410 | 0.75 | -24.74 | 6.43 | 0.016 | RNA polymerase II associated protein 3 |  |  |
| 4154 | MBNL1 | -0.409 | 0.75 | -24.70 | 10.59 | 0.015 | muscleblind-like splicing regulator 1 |  |  |
| 256586 | LYSMD2 | -0.403 | 0.76 | -24.37 | 11.11 | 0.039 | LysM, putative peptidoglycan-binding, domain containing 2 | | |
| 5471 | PPAT | -0.402 | 0.76 | -24.31 | 2.88 | 0.044 | phosphoribosyl pyrophosphate amidotransferase | |  |
| 7336 | UBE2V2 | -0.401 | 0.76 | -24.26 | 7.82 | 0.023 | ubiquitin-conjugating enzyme E2 variant 2 |  |  |
| 84248 | FYTTD1 | -0.401 | 0.76 | -24.25 | 7.92 | 0.044 | forty-two-three domain containing 1 |  |  |
| 29945 | ANAPC4 | -0.399 | 0.76 | -24.18 | 7.67 | 0.031 | anaphase promoting complex subunit 4 |  |  |
| 387751 | GVINP1 | -0.397 | 0.76 | -24.04 | 7.85 | 0.047 | GTPase, very large interferon inducible pseudogene 1 | |  |
| 115426 | UHRF2 | -0.395 | 0.76 | -23.97 | 8.98 | 0.020 | ubiquitin-like with PHD and ring finger domains 2, E3 ubiquitin protein ligase | | |
| 51574 | LARP7 | -0.395 | 0.76 | -23.96 | 7.58 | 0.021 | La ribonucleoprotein domain family, member 7 | |  |
| 403313 | PPAPDC2 | -0.392 | 0.76 | -23.80 | 6.04 | 0.049 | phosphatidic acid phosphatase type 2 domain containing 2 | | |
| 8575 | PRKRA | -0.388 | 0.76 | -23.56 | 7.09 | 0.039 | protein kinase, interferon-inducible double stranded RNA dependent activator | | |
| 22890 | ZBTB1 | -0.387 | 0.76 | -23.51 | 6.13 | 0.028 | zinc finger and BTB domain containing 1 |  |  |
| 60526 | C2ORF43 | -0.384 | 0.77 | -23.37 | 3.99 | 0.041 | chromosome 2 open reading frame 43 |  |  |
| 113791 | PIK3IP1 | -0.370 | 0.77 | -22.62 | 9.10 | 0.047 | phosphoinositide-3-kinase interacting protein 1 | |  |
| 7163 | TPD52 | -0.370 | 0.77 | -22.61 | 5.44 | 0.022 | tumor protein D52 |  |  |
| 100505971 |  | -0.368 | 0.77 | -22.54 | 4.63 | 0.017 |  |  |  |
| 285331 | CCDC66 | -0.367 | 0.78 | -22.46 | 3.53 | 0.033 | coiled-coil domain containing 66 |  |  |
| 127018 | LYPLAL1 | -0.366 | 0.78 | -22.40 | 7.45 | 0.018 | lysophospholipase-like 1 |  |  |
| 29078 | NDUFAF4 | -0.364 | 0.78 | -22.33 | 3.99 | 0.045 | NADH dehydrogenase (ubiquinone) complex I, assembly factor 4 | | |
| 171586 | ABHD3 | -0.362 | 0.78 | -22.22 | 10.13 | 0.045 | abhydrolase domain containing 3 |  |  |
| 79017 | GGCT | -0.362 | 0.78 | -22.21 | 7.40 | 0.026 | gamma-glutamylcyclotransferase |  |  |
| 100506710 | LOC100506710 | -0.361 | 0.78 | -22.14 | 8.73 | 0.044 | endogenous Bornavirus-like nucleoprotein 2 pseudogene | | |
| 6342 | SCP2 | -0.361 | 0.78 | -22.12 | 10.10 | 0.047 | sterol carrier protein 2 |  |  |
| 132 | ADK | -0.358 | 0.78 | -21.96 | 4.09 | 0.031 | adenosine kinase |  |  |
| 285989 | ZNF789 | -0.355 | 0.78 | -21.80 | 4.21 | 0.045 | zinc finger protein 789 |  |  |
| 221294 | NT5DC1 | -0.354 | 0.78 | -21.75 | 5.44 | 0.048 | 5'-nucleotidase domain containing 1 |  |  |
| 2188 | FANCF | -0.350 | 0.78 | -21.57 | 5.45 | 0.027 | Fanconi anemia, complementation group F |  |  |
| 55299 | BRIX1 | -0.350 | 0.78 | -21.53 | 3.68 | 0.032 | BRX1, biogenesis of ribosomes, homolog (S. cerevisiae) | | |
| 100506969 |  | -0.350 | 0.78 | -21.52 | 6.10 | 0.031 |  |  |  |
| 203522 | DDX26B | -0.347 | 0.79 | -21.36 | 6.16 | 0.038 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B | |  |
| 4673 | NAP1L1 | -0.346 | 0.79 | -21.34 | 8.54 | 0.048 | nucleosome assembly protein 1-like 1 |  |  |
| 7705 | ZNF146 | -0.346 | 0.79 | -21.30 | 4.48 | 0.020 | zinc finger protein 146 |  |  |
| 9666 | DZIP3 | -0.344 | 0.79 | -21.22 | 3.39 | 0.039 | DAZ interacting zinc finger protein 3 |  |  |
| 79886 | CAAP1 | -0.342 | 0.79 | -21.13 | 5.06 | 0.033 | caspase activity and apoptosis inhibitor 1 |  |  |
| 23347 | SMCHD1 | -0.340 | 0.79 | -21.00 | 10.86 | 0.041 | structural maintenance of chromosomes flexible hinge domain containing 1 | | |
| 11335 | CBX3 | -0.338 | 0.79 | -20.88 | 9.94 | 0.049 | chromobox homolog 3 |  |  |
| 29902 | FAM216A | -0.338 | 0.79 | -20.87 | 3.92 | 0.036 | family with sequence similarity 216, member A | |  |
| 5884 | RAD17 | -0.338 | 0.79 | -20.86 | 6.54 | 0.013 | RAD17 homolog (S. pombe) |  |  |
| 10473 | HMGN4 | -0.337 | 0.79 | -20.82 | 10.77 | 0.018 | high mobility group nucleosomal binding domain 4 | |  |
| 64924 | SLC30A5 | -0.336 | 0.79 | -20.78 | 6.38 | 0.046 | solute carrier family 30 (zinc transporter), member 5 | |  |
| 80218 | NAA50 | -0.333 | 0.79 | -20.62 | 7.80 | 0.032 | N(alpha)-acetyltransferase 50, NatE catalytic subunit | |  |
| 84992 | PIGY | -0.333 | 0.79 | -20.60 | 9.26 | 0.047 |  |  |  |
| 29883 | CNOT7 | -0.331 | 0.79 | -20.53 | 6.91 | 0.044 | CCR4-NOT transcription complex, subunit 7 | |  |
| 51012 | SLMO2 | -0.328 | 0.80 | -20.31 | 6.75 | 0.016 | slowmo homolog 2 (Drosophila) |  |  |
| 7763 | ZFAND5 | -0.327 | 0.80 | -20.28 | 11.48 | 0.013 | zinc finger, AN1-type domain 5 |  |  |
| 84329 | HVCN1 | -0.326 | 0.80 | -20.24 | 9.79 | 0.023 | hydrogen voltage-gated channel 1 |  |  |
| 5716 | PSMD10 | -0.326 | 0.80 | -20.23 | 7.76 | 0.045 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 10 | | |
| 2971 | GTF3A | -0.325 | 0.80 | -20.16 | 11.76 | 0.040 | general transcription factor IIIA |  |  |
| 51562 | MBIP | -0.323 | 0.80 | -20.05 | 4.38 | 0.029 | MAP3K12 binding inhibitory protein 1 |  |  |
| 81853 | TMEM14B | -0.321 | 0.80 | -19.97 | 10.38 | 0.047 | transmembrane protein 14B |  |  |
| 139341 | FUNDC1 | -0.320 | 0.80 | -19.91 | 7.60 | 0.015 | FUN14 domain containing 1 |  |  |
| 100507399 | HCG8 | -0.320 | 0.80 | -19.89 | 2.50 | 0.047 | HLA complex group 8 |  |  |
| 7381 | UQCRB | -0.319 | 0.80 | -19.85 | 5.23 | 0.029 | ubiquinol-cytochrome c reductase binding protein | |  |
| 29767 | TMOD2 | -0.318 | 0.80 | -19.78 | 3.70 | 0.029 | tropomodulin 2 (neuronal) |  |  |
| 2339 | FNTA | -0.317 | 0.80 | -19.72 | 10.76 | 0.022 | farnesyltransferase, CAAX box, alpha |  |  |
| 23484 | LEPROTL1 | -0.312 | 0.81 | -19.47 | 10.20 | 0.013 | leptin receptor overlapping transcript-like 1 | |  |
| 23568 | ARL2BP | -0.312 | 0.81 | -19.45 | 6.70 | 0.033 | ADP-ribosylation factor-like 2 binding protein | |  |
| 8562 | DENR | -0.310 | 0.81 | -19.32 | 9.27 | 0.031 | density-regulated protein |  |  |
| 3796 | KIF2A | -0.309 | 0.81 | -19.28 | 8.44 | 0.028 | kinesin heavy chain member 2A |  |  |
| 51193 | ZNF639 | -0.304 | 0.81 | -19.01 | 4.72 | 0.037 | zinc finger protein 639 |  |  |
| 81688 | C6ORF62 | -0.302 | 0.81 | -18.87 | 10.66 | 0.018 | chromosome 6 open reading frame 62 |  |  |
| 84265 | POLR3GL | -0.296 | 0.81 | -18.55 | 9.05 | 0.015 | polymerase (RNA) III (DNA directed) polypeptide G (32kD)-like | | |
| 100506087 |  | -0.295 | 0.82 | -18.48 | 8.09 | 0.035 |  |  |  |
| 23635 | SSBP2 | -0.293 | 0.82 | -18.40 | 8.28 | 0.014 | single-stranded DNA binding protein 2 |  |  |
| 55330 | BLOC1S4 | -0.292 | 0.82 | -18.33 | 7.78 | 0.023 | biogenesis of lysosomal organelles complex-1, subunit 4, cappuccino | | |
| 7884 | SLBP | -0.292 | 0.82 | -18.32 | 9.73 | 0.015 | stem-loop binding protein |  |  |
| 25875 | LETMD1 | -0.291 | 0.82 | -18.29 | 8.69 | 0.047 | LETM1 domain containing 1 |  |  |
| 10541 | ANP32B | -0.291 | 0.82 | -18.26 | 12.38 | 0.030 | acidic (leucine-rich) nuclear phosphoprotein 32 family, member B | | |
| 55591 | VEZT | -0.286 | 0.82 | -17.99 | 3.11 | 0.026 | vezatin, adherens junctions transmembrane protein | |  |
| 5283 | PIGH | -0.285 | 0.82 | -17.91 | 7.66 | 0.039 | phosphatidylinositol glycan anchor biosynthesis, class H | | |
| 55082 | ARGLU1 | -0.276 | 0.83 | -17.39 | 8.10 | 0.047 | arginine and glutamate rich 1 |  |  |
| 689 | BTF3 | -0.273 | 0.83 | -17.25 | 13.45 | 0.023 | basic transcription factor 3 |  |  |
| 5734 | PTGER4 | -0.273 | 0.83 | -17.24 | 6.05 | 0.045 | prostaglandin E receptor 4 (subtype EP4) |  |  |
| 7852 | CXCR4 | -0.273 | 0.83 | -17.22 | 12.60 | 0.047 |  |  |  |
| 55278 | QRSL1 | -0.272 | 0.83 | -17.19 | 3.02 | 0.029 | glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1 | | |
| 51669 | TMEM66 | -0.269 | 0.83 | -17.03 | 12.78 | 0.026 | transmembrane protein 66 |  |  |
| 55787 | TXLNG | -0.264 | 0.83 | -16.70 | 3.43 | 0.022 | taxilin gamma |  |  |
| 22889 | KIAA0907 | -0.263 | 0.83 | -16.64 | 9.40 | 0.030 | KIAA0907 |  |  |
| 64864 | RFX7 | -0.262 | 0.83 | -16.62 | 4.81 | 0.031 | regulatory factor X, 7 |  |  |
| 23029 | RBM34 | -0.260 | 0.83 | -16.50 | 4.78 | 0.010 | RNA binding motif protein 34 |  |  |
| 90411 | MCFD2 | -0.255 | 0.84 | -16.22 | 7.42 | 0.013 | multiple coagulation factor deficiency 2 |  |  |
| 90634 | N4BP2L1 | -0.254 | 0.84 | -16.17 | 4.88 | 0.048 | NEDD4 binding protein 2-like 1 |  |  |
| 11146 | GLMN | -0.254 | 0.84 | -16.12 | 3.05 | 0.047 | glomulin, FKBP associated protein |  |  |
| 79612 | NAA16 | -0.250 | 0.84 | -15.91 | 3.83 | 0.031 | N(alpha)-acetyltransferase 16, NatA auxiliary subunit | |  |
| 54680 | ZNHIT6 | -0.246 | 0.84 | -15.69 | 3.03 | 0.030 | zinc finger, HIT-type containing 6 |  |  |
| 9465 | AKAP7 | -0.246 | 0.84 | -15.68 | 5.76 | 0.044 | A kinase (PRKA) anchor protein 7 |  |  |
| 10286 | BCAS2 | -0.245 | 0.84 | -15.62 | 8.29 | 0.030 | breast carcinoma amplified sequence 2 |  |  |
| 100505641 | FGD5-AS1 | -0.243 | 0.85 | -15.50 | 9.99 | 0.045 | FGD5 antisense RNA 1 |  |  |
| 51696 | HECA | -0.240 | 0.85 | -15.34 | 11.28 | 0.030 | headcase homolog (Drosophila) |  |  |
| 84240 | ZCCHC9 | -0.237 | 0.85 | -15.16 | 7.96 | 0.046 | zinc finger, CCHC domain containing 9 |  |  |
| 4907 | NT5E | -0.233 | 0.85 | -14.93 | 2.80 | 0.030 | 5'-nucleotidase, ecto (CD73) |  |  |
| 80008 | TMEM156 | -0.227 | 0.85 | -14.58 | 4.57 | 0.020 | transmembrane protein 156 |  |  |
| 7109 | TRAPPC10 | -0.219 | 0.86 | -14.08 | 7.12 | 0.047 | trafficking protein particle complex 10 |  |  |
| 54842 | MFSD6 | -0.216 | 0.86 | -13.90 | 3.33 | 0.041 | major facilitator superfamily domain containing 6 | |  |
| 3189 | HNRNPH3 | -0.205 | 0.87 | -13.24 | 8.96 | 0.048 | heterogeneous nuclear ribonucleoprotein H3 (2H9) | |  |
| 100507463 | TAPSAR1 | -0.204 | 0.87 | -13.21 | 11.34 | 0.040 | TAP1 and PSMB8 antisense RNA 1 |  |  |
| 8634 | RTCA | -0.204 | 0.87 | -13.19 | 8.55 | 0.039 | RNA 3'-terminal phosphate cyclase |  |  |
| 54940 | OCIAD1 | -0.201 | 0.87 | -12.99 | 9.58 | 0.042 | OCIA domain containing 1 |  |  |
| 55573 | CDV3 | -0.198 | 0.87 | -12.85 | 8.50 | 0.028 | CDV3 homolog (mouse) |  |  |
| 84864 | MINA | -0.188 | 0.88 | -12.24 | 3.37 | 0.048 | MYC induced nuclear antigen |  |  |
| 10904 | BLCAP | -0.184 | 0.88 | -12.00 | 9.18 | 0.048 | bladder cancer associated protein |  |  |
| 55617 | TASP1 | -0.183 | 0.88 | -11.90 | 2.44 | 0.049 | taspase, threonine aspartase, 1 |  |  |
| 93621 | MRFAP1 | -0.178 | 0.88 | -11.59 | 13.17 | 0.018 | Morf4 family associated protein 1 |  |  |
| 9221 | NOLC1 | -0.177 | 0.88 | -11.53 | 4.45 | 0.031 | nucleolar and coiled-body phosphoprotein 1 | |  |
| 201229 | LYRM9 | -0.163 | 0.89 | -10.69 | 3.54 | 0.028 | LYR motif containing 9 |  |  |
| 54014 | BRWD1 | -0.161 | 0.89 | -10.53 | 3.25 | 0.047 | bromodomain and WD repeat domain containing 1 | |  |
| 5108 | PCM1 | -0.159 | 0.90 | -10.43 | 6.34 | 0.037 | pericentriolar material 1 |  |  |
| 10495 | ENOX2 | -0.083 | 0.94 | -5.62 | 2.92 | 0.050 | ecto-NOX disulfide-thiol exchanger 2 |  |  |
| 5191 | PEX7 | -0.068 | 0.95 | -4.63 | 2.48 | 0.042 | peroxisomal biogenesis factor 7 |  |  |
| 567 | B2M | -0.053 | 0.96 | -3.58 | 15.39 | 0.047 | beta-2-microglobulin |  |  |

**Table S3. Microarray and quantitative real time-PCR of the selected 28 genes.**

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Forward Primer (5’ to 3’)** | **Reverse Primer (5’ to 3’)** | **RT-PCR** | | | | | **Microarray** | | | | |
| **Gene** |  |  | **Fold Change**  **(Log2)** | **Fold**  **Change** | ***sPTB within 48 hours***  ***(median (25th, 75th percentile))*** | ***No sPTB within 48 hours (median (25th, 75th percentile)*** | ***LogXact***  ***p* Value** | **Fold**  **Change**  **(Log2)** | **Fold**  **Change** | ***sPTB within 48 hours***  ***(median (25th, 75th percentile))*** | ***No sPTB within 48 hours (median (25th, 75th percentile))*** | ***Limma* FDR** |
| *ANAPC10* | AGTTTCGGCAAGCAGCCAGAATA | TCCAACTGCTTGGGGTCAGCAC | -0.17 | 0.89 | 0.91 (0.70, 1.13) | 1.03 (0.82, 1.38) | 0.127 | -0.73 | 0.60 | 3.68 (3.31, 4.43) | 4.54 (3.66, 5.76) | 0.047 |
| *ANKRD46* | TGCTCGTTCGAGTCGCAGATCC | TTCGTTCAGTGGTCACTCAGCAGTT | -0.13 | 0.92 | 0.95 (0.78, 1.11) | 1.04 (0.74, 1.31) | 0.179 | -0.67 | 0.63 | 4.30 (3.89, 4.70) | 4.81 (4.17, 5.64) | 0.037 |
| *ATP9A* | GGCTCACAGCACGAGGCACAG | CATGTCGGCAGGGACCCGC | 0.85 | 1.80 | 1.22 (0.75, 3.05) | 0.68 (0.43, 1.36) | 0.010 | 0.88 | 1.84 | 7.86 (6.73, 8.92) | 6.71 (6.15, 7.78) | 0.013 |
| *C19orf59* | CAGCCAAGAATCAAGGTGCCCA | GGGACTTGGCTCGTGGGTCG | 0.67 | 1.59 | 1.35 (0.84, 2.31) | 0.84 (0.38, 1.25) | <0.001 | 0.70 | 1.63 | 12.85 (12.07, 13.38) | 12.18 (11.59, 12.64) | 0.005 |
| *CCDC104* | GAGCCCACAGTGCATTCCAGTGA | TTTTAACTTCTGAGGGTGGGTGTGC | -0.08 | 0.94 | 0.93 (0.77, 1.25) | 0.98 (0.75, 1.29) | 0.891 | -0.67 | 0.63 | 4.73 (3.95, 5.18) | 5.13 (4.39, 6.09) | 0.031 |
| *CCR1* | GTCCCTTGGAACCAGAGAGAAGCC | GGCACGGAGTTGCATCCCCATA | 0.67 | 1.59 | 1.34 (0.81, 1.85) | 0.85 (0.57, 1.13) | 0.003 | 0.60 | 1.52 | 11.57 (10.92, 12.12) | 10.97 (10.37, 11.35) | 0.022 |
| *CDK5RAP2* | ATTGCAGTCTCTCCGAGTGGAGCTG | TCTCCCGACGCCTCTCTCAGTCT | 0.44 | 1.35 | 1.19 (0.99, 1.40) | 0.88 (0.75, 1.05) | <0.001 | 0.77 | 1.70 | 8.73 (7.73, 10.10) | 8.12 (7.44, 8.80) | 0.017 |
| *CETN3* | TGGGCGTCTTGCTGCCTTGG | CCACTACAAGCTCACTTCTCAGAGC | -0.49 | 0.71 | 0.77 (0.59, 1.17) | 1.08 (0.70, 1.72) | 0.052 | -0.77 | 0.59 | 4.20 (3.01, 4.36) | 4.41 (3.98, 5.70) | 0.032 |
| *EMILIN2* | AACCCCAGCACCGGGGTCTT | GGCGTCTCTCTCGGGGGTGA | 0.60 | 1.52 | 1.36 (1.06, 1.72) | 0.89 (0.65, 1.16) | <0.001 | 0.61 | 1.53 | 7.29 (6.79, 7.84) | 6.83 (6.17, 7.20) | 0.015 |
| *EMR1* | TGCTCAACGGCCAGGTACGAGA | CCCGTCTTGGAAGCGGATGGC | 0.78 | 1.72 | 1.32 (0.75, 2.25) | 0.77 (0.65, 1.11) | 0.001 | 0.70 | 1.62 | 9.14 (8.64, 10.01) | 8.58 (7.89, 9.15) | 0.025 |
| *G0S2* | TGCCACTAAGGTCATTCCCGCCT | CCTTGCGCTTCTGGGCCATCA | 0.73 | 1.65 | 1.33 (0.96, 2.03) | 0.81 (0.60, 1.25) | <0.001 | 0.76 | 1.69 | 7.56 (7.10, 8.05) | 6.83 (6.26, 7.53) | 0.006 |
| *GALNT14* | AAGTGCAGACCCCTAAGCCTTCG | TCGTCACCAACGCGCCACTT | 0.80 | 1.74 | 1.30 (1.00, 2.15) | 0.75 (0.48, 1.16) | 0.001 | 0.88 | 1.84 | 9.04 (8.46, 9.58) | 8.27 (7.86, 8.66) | <0.001 |
| *GPR84* | CCACCAGAAAGGACTGCTCTTTGGG | GCTGTTCCACATGATAGAGGCTGAG | 0.96 | 1.94 | 1.36 (0.82, 2.38) | 0.70 (0.50, 1.28) | 0.001 | 0.99 | 1.99 | 8.00 (6.77, 8.78) | 6.78 (6.40, 7.64) | 0.007 |
| *IFT80* | TGGCTCCCTGGTTCACATCAGCA | TGGTTTGCTCCTTAACAAAGCGACA | -0.11 | 0.93 | 0.93 (0.73, 1.15) | 1.00 (0.78, 1.43) | 0.132 | -0.74 | 0.60 | 4.28 (3.39, 4.84) | 4.84 (4.01, 5.84) | 0.040 |
| *METTL18* | GTCCGGAGGAGGCGTTGTGAGG | TCCTCTTTCCAAGCAGCTCTGGGG | -0.41 | 0.75 | 0.79 (0.67, 1.11) | 1.05 (0.80, 1.48) | 0.018 | -0.91 | 0.53 | 3.46 (2.73, 3.79) | 4.20 (3.52, 5.00) | 0.002 |
| *MS4A1* | AGGCCTTGGAGACTCAGATCCTGA | TGTCAGTCTCTTCCCCACAGAATGG | -0.71 | 0.61 | 0.81 (0.56, 1.27) | 1.33 (0.75, 1.63) | 0.003 | -0.76 | 0.59 | 6.93 (6.09, 7.55) | 7.76 (6.97, 8.69) | 0.028 |
| *NLRP3* | CGCCCTCGGTGACTTCGGAA | CAGCAGCTGACCAACCAGAGCT | 0.52 | 1.43 | 1.19 (0.98, 1.89) | 0.83 (0.68, 1.09) | 0.001 | 0.65 | 1.57 | 4.83 (4.37, 5.39) | 4.42 (4.11, 4.75) | 0.015 |
| *OPLAH* | ATCAACACCGTGGCAGCGGG | ACAGGGCCCCCTTTGCGGTA | 0.57 | 1.48 | 1.20 (0.81, 2.01) | 0.81 (0.62, 1.27) | 0.003 | 0.93 | 1.91 | 6.62 (5.89, 7.90) | 5.82 (5.26, 6.69) | 0.003 |
| *PFKFB3* | CGCGAAGATGCCGTTGGAACTGA | GGCCCACAGGATCTGGGCAACGA | 0.80 | 1.74 | 1.44 (0.91, 1.89) | 0.82 (0.52, 1.19) | 0.001 | 0.68 | 1.61 | 11.52 (10.91, 12.32) | 10.95 (10.40, 11.40) | 0.012 |
| *PMS1* | GCGCTAGCAGGAAGCTGCTCTG | GCTCTTTTACAACACTGACCACCGA | -0.29 | 0.82 | 0.92 (0.79, 1.13) | 1.12 (0.82, 1.33) | 0.025 | -0.65 | 0.64 | 4.93 (4.40, 5.36) | 5.40 (4.62, 6.35) | 0.044 |
| *RAB20* | GGGGGCGCTGGGGGTTCTTA | GCGCCGCTCCATATACCGCT | 0.56 | 1.47 | 1.15 (0.81, 2.05) | 0.78 (0.62, 1.09) | 0.001 | 0.71 | 1.64 | 8.78 (8.35, 9.47) | 8.15 (7.65, 8.71) | 0.009 |
| *SCOC* | GCGCCTCAAGCGGAAGACCATT | ACTGCATCCATGTCAGCATTCATCA | -0.07 | 0.95 | 0.94 (0.73, 1.16) | 0.98 (0.76, 1.41) | 0.153 | -0.70 | 0.61 | 4.37 (3.80, 4.81) | 4.81 (4.31, 6.01) | 0.047 |
| *SOCS3* | CTGCGGGCTGGCGAAGGAAA | CCCAAGCCCTTCTCCCCGGA | 0.78 | 1.71 | 1.38 (0.81, 2.17) | 0.81 (0.53, 1.22) | 0.003 | 0.76 | 1.69 | 8.45 (7.51, 9.13) | 7.77 (7.14, 8.22) | 0.003 |
| *ST3GAL4* | TGCACATTGCCGGCTTTGGC | CCTGACCCCGCCATGGACTTG | 0.76 | 1.69 | 1.39 (0.91, 1.71) | 0.82 (0.63, 1.01) | <0.001 | 0.71 | 1.63 | 9.15 (8.41, 9.81) | 8.41 (7.71, 9.03) | 0.003 |
| *STAP1* | GCGAAATTCACCCTTGTTTTGCCG | GGGGAACTGACAGCTCTGTTACTGT | -0.60 | 0.66 | 0.81 (0.66, 1.19) | 1.23 (0.72, 1.61) | 0.007 | -0.76 | 0.59 | 4.10 (3.52, 4.52) | 4.78 (4.09, 5.50) | 0.007 |
| *TSPAN13* | ACCACTCGTGCTCGCCATGTG | GTCAGCCAAACACCCAGGATCTCTG | -0.03 | 0.98 | 0.97 (0.72, 1.35) | 1.00 (0.75, 1.18) | 0.766 | -0.61 | 0.66 | 6.32 (5.92, 6.80) | 7.09 (6.37, 7.55) | 0.022 |
| *ZDHHC19* | TCGGCCGACCGCACCTACAA | GCTTCAGCCATGTACTTGGGTCCC | 0.98 | 1.97 | 1.55 (0.84, 2.76) | 0.79 (0.26, 1.40) | 0.021 | 1.20 | 2.30 | 4.66 (3.95, 5.51) | 3.47 (3.19, 4.21) | <0.001 |
| *ZFAND1* | AGCATTGCCGGCAGCGAGATTTT | CAGGACAACCATGAGACTCCCTGCT | -0.29 | 0.82 | 0.87 (0.68, 1.17) | 1.06 (0.80, 1.35) | 0.058 | -0.77 | 0.59 | 5.35 (4.68, 6.31) | 6.18 (5.12, 6.99) | 0.040 |
| *SDHA* | TGGGAACAAGAGGGCATCTG | CCACCACTGCATCAAATTCATG | *(Housekeeping)* | | | | | *(Housekeeping)* | | | | |
| *TBP* | TGCACAGGAGCCAAGAGTGAA | CACATCACAGCTCCCCACCA | *(Housekeeping)* | | | | | *(Housekeeping)* | | | | |
| *YWHAZ* | ACTTTTGGTACATTGTGGCTTCAA | CCGCCAGGACAAACCAGTAT | *(Housekeeping)* | | | | | *(Housekeeping)* | | | | |