**Supplemental Table 1: List of the 306 RefSeq annotated transcripts significantly modulated in 99mTcO4−-exposed thyroids.**

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| --- | --- | --- | --- | --- | --- |
| **Gene****Name** | **Agilent Probe ID** | **Accession** | **AveExp** | **log2 (Tc/Ct)** | **Description** |
| Aaas | A\_52\_P301374 | NM\_153416 | 11.06 | 1.69 | achalasia. adrenocortical insufficiency. alacrimia (Aaas)  |
| Abhd4 | A\_51\_P406020 | NM\_134076 | 15.50 | 1.15 | abhydrolase domain containing 4 (Abhd4). transcript variant 1  |
| Acer2 | A\_55\_P2367463 | NM\_139306 | 7.64 | 1.03 | alkaline ceramidase 2 (Acer2)  |
| Adm2 | A\_55\_P2181386 | NM\_182928 | 7.00 | -1.06 | adrenomedullin 2 (Adm2)  |
| Aen | A\_55\_P2141860 | NM\_026531 | 14.42 | 2.00 | apoptosis enhancing nuclease (Aen). transcript variant 1  |
| Alox5 | A\_51\_P247249 | NM\_009662 | 9.69 | 1.58 | arachidonate 5-lipoxygenase (Alox5)  |
| Ano1 | A\_55\_P2038747 | NM\_178642 | 12.22 | -1.11 | anoctamin 1. calcium activated chloride channel (Ano1). transcript variant 1  |
| Anxa8 | A\_51\_P207591 | NM\_013473 | 11.21 | 2.10 | annexin A8 (Anxa8)  |
| Aox1 | A\_51\_P333111 | NM\_009676 | 13.19 | 1.39 | aldehyde oxidase 1 (Aox1)  |
| Apaf1 | A\_51\_P417701 | NM\_001042558 | 8.14 | 1.23 | apoptotic peptidase activating factor 1 (Apaf1). transcript variant 1  |
| Aplnr | A\_52\_P97572 | NM\_011784 | 9.85 | -1.29 | apelin receptor (Aplnr)  |
| Aqp6 | A\_55\_P2182955 | NM\_175087 | 11.34 | -1.29 | aquaporin 6 (Aqp6)  |
| Arhgef33 | A\_66\_P107482 | NM\_001145452 | 8.71 | -1.61 | Rho guanine nucleotide exchange factor (GEF) 33 (Arhgef33)  |
| Arl8a | A\_51\_P224593 | NM\_026823 | 12.51 | 1.01 | ADP-ribosylation factor-like 8A (Arl8a)  |
| Armc2 | A\_55\_P2120469 | NM\_001034858 | 10.89 | -1.68 | armadillo repeat containing 2 (Armc2)  |
| Asgr1 | A\_55\_P2003824 | NM\_009714 | 13.97 | -1.39 | asialoglycoprotein receptor 1 (Asgr1)  |
| Ass1 | A\_55\_P2143070 | NM\_007494 | 11.17 | 3.13 | argininosuccinate synthetase 1 (Ass1)  |
| Atp6v0a4 | A\_55\_P1953003 | NM\_080467 | 7.45 | -1.26 | ATPase. H+ transporting. lysosomal V0 subunit A4 (Atp6v0a4)  |
| Atp6v1d | A\_51\_P393598 | NM\_023721 | 14.43 | 1.01 | ATPase. H+ transporting. lysosomal V1 subunit D (Atp6v1d)  |
| Batf | A\_51\_P114616 | NM\_016767 | 9.62 | -1.15 | basic leucine zipper transcription factor. ATF-like (Batf)  |
| Bax | A\_55\_P2137406 | NM\_007527 | 13.21 | 1.95 | BCL2-associated X protein (Bax)  |
| Bbc3 | A\_51\_P248122 | NM\_133234 | 12.37 | 1.77 | BCL2 binding component 3 (Bbc3). nuclear gene encoding mitochondrial protein  |
| Bcl2a1d | A\_55\_P1978424 | NM\_007536 | 8.71 | -1.43 | B-cell leukemia/lymphoma 2 related protein A1d (Bcl2a1d)  |
| Bcl2l1 | A\_52\_P510877 | NM\_009743 | 9.01 | 1.52 | BCL2-like 1 (Bcl2l1). nuclear gene encoding mitochondrial protein  |
| Bdh1 | A\_55\_P2181753 | NM\_001122683 | 8.18 | -1.23 | 3-hydroxybutyrate dehydrogenase. type 1 (Bdh1). transcript variant 2  |
| Bloc1s2 | A\_55\_P1984825 | NM\_028607 | 11.68 | 1.01 | biogenesis of lysosome-related organelles complex-1. subunit 2 (Bloc1s2)  |
| Bmf | A\_55\_P2029106 | NM\_138313 | 11.21 | -1.37 | BCL2 modifying factor (Bmf)  |
| Btg2 | A\_52\_P31543 | NM\_007570 | 11.88 | 1.72 | B-cell translocation gene 2. anti-proliferative (Btg2)  |
| Cabp5 | A\_55\_P2033215 | NM\_013877 | 14.64 | 1.30 | calcium binding protein 5 (Cabp5)  |
| Cacnb3 | A\_51\_P259009 | NM\_007581 | 9.98 | 1.14 | calcium channel. voltage-dependent. beta 3 subunit (Cacnb3). transcript variant 1  |
| Calml3 | A\_55\_P2083317 | NM\_027416 | 10.33 | 2.49 | calmodulin-like 3 (Calml3)  |
| Camkk1 | A\_55\_P2113165 | NM\_018883 | 11.33 | -1.15 | calcium/calmodulin-dependent protein kinase kinase 1. alpha (Camkk1)  |
| Capn6 | A\_52\_P474089 | NM\_007603 | 10.99 | -1.25 | calpain 6 (Capn6)  |
| Cbs | A\_55\_P2078670 | NM\_144855 | 9.94 | 2.26 | cystathionine beta-synthase (Cbs). transcript variant 1  |
| Ccdc144b | A\_55\_P2000798 | NM\_178418 | 11.57 | 1.67 | coiled-coil domain containing 144B (Ccdc144b)  |
| Ccng1 | A\_52\_P612803 | NM\_009831 | 14.03 | 1.78 | cyclin G1 (Ccng1)  |
| Ccr5 | A\_52\_P578732 | NM\_009917 | 7.09 | -1.10 | chemokine (C-C motif) receptor 5 (Ccr5)  |
| Cd163l1 | A\_55\_P1989563 | NM\_172909 | 7.37 | -1.24 | CD163 molecule-like 1 (Cd163l1)  |
| Cd300lf | A\_55\_P2004511 | NM\_001169153 | 10.76 | 1.67 | CD300 antigen like family member F (Cd300lf). transcript variant 1  |
| Cd44 | A\_55\_P2166488 | NM\_009851 | 9.77 | 1.52 | CD44 antigen (Cd44). transcript variant 1  |
| Cd86 | A\_55\_P1971951 | NM\_019388 | 7.70 | -1.12 | CD86 antigen (Cd86)  |
| Cdc42bpg | A\_52\_P105765 | NM\_001033342 | 10.14 | 1.53 | CDC42 binding protein kinase gamma (DMPK-like) (Cdc42bpg)  |
| Cdca7 | A\_55\_P2012498 | NM\_025866 | 10.91 | -1.59 | cell division cycle associated 7 (Cdca7)  |
| Cdh16 | A\_51\_P287100 | NM\_007663 | 14.81 | -1.19 | cadherin 16 (Cdh16). transcript variant 1  |
| Cdkn1a | A\_51\_P363947 | NM\_007669 | 13.02 | 3.87 | cyclin-dependent kinase inhibitor 1A (P21) (Cdkn1a). transcript variant 1  |
| Celf5 | A\_55\_P1972948 | NM\_176954 | 9.91 | 3.31 | CUGBP. Elav-like family member 5 (Celf5)  |
| Ces2c | A\_55\_P2005213 | NM\_145603 | 10.30 | 1.71 | carboxylesterase 2C (Ces2c)  |
| Ces2e | A\_55\_P1959500 | NM\_172759 | 12.82 | 1.68 | carboxylesterase 2E (Ces2e). transcript variant 1  |
| Cgref1 | A\_51\_P372550 | NM\_026770 | 10.94 | 2.81 | cell growth regulator with EF hand domain 1 (Cgref1). transcript variant 1  |
| Chst3 | A\_52\_P390944 | NM\_016803 | 9.13 | -1.70 | carbohydrate (chondroitin 6/keratan) sulfotransferase 3 (Chst3)  |
| Cited4 | A\_52\_P426768 | NM\_019563 | 13.56 | 1.09 | Cbp/p300-interacting transactivator. with Glu/Asp-rich carboxy-terminal domain. 4 (Cited4)  |
| Ckap2 | A\_52\_P162099 | NM\_001004140 | 8.53 | 2.36 | cytoskeleton associated protein 2 (Ckap2)  |
| Cks1b | A\_55\_P2061495 | NM\_016904 | 10.79 | -1.01 | CDC28 protein kinase 1b (Cks1b)  |
| Clec9a | A\_66\_P103027 | NM\_001205363 | 7.04 | -1.15 | C-type lectin domain family 9. member a (Clec9a). transcript variant 1  |
| Cmtm7 | A\_55\_P1973254 | NM\_133978 | 10.84 | -1.25 | CKLF-like MARVEL transmembrane domain containing 7 (Cmtm7). transcript variant 1  |
| Cngb1 | A\_55\_P2100739 | NM\_145601 | 9.46 | -1.14 | cyclic nucleotide gated channel beta 1 (Cngb1). transcript variant 2  |
| Col5a3 | A\_51\_P241995 | NM\_016919 | 11.32 | -1.02 | collagen. type V. alpha 3 (Col5a3)  |
| Cox6b2 | A\_51\_P300506 | NM\_183405 | 12.51 | 4.20 | cytochrome c oxidase subunit VIb polypeptide 2 (Cox6b2). transcript variant 1  |
| Cpt1c | A\_52\_P269942 | NM\_153679 | 10.08 | 2.96 | carnitine palmitoyltransferase 1c (Cpt1c). transcript variant 1  |
| Ctxn1 | A\_52\_P680870 | NM\_183315 | 9.97 | 1.31 | cortexin 1 (Ctxn1)  |
| Cx3cr1 | A\_52\_P99810 | NM\_009987 | 8.13 | -2.25 | chemokine (C-X3-C) receptor 1 (Cx3cr1)  |
| Cxcl12 | A\_55\_P1966204 | NM\_021704 | 10.62 | -1.32 | chemokine (C-X-C motif) ligand 12 (Cxcl12). transcript variant 1  |
| Cxcr6 | A\_55\_P2165199 | NM\_030712 | 8.06 | -1.28 | chemokine (C-X-C motif) receptor 6 (Cxcr6)  |
| Cyp27b1 | A\_55\_P2088237 | NM\_010009 | 7.25 | -1.56 | cytochrome P450. family 27. subfamily b. polypeptide 1 (Cyp27b1). nuclear gene encoding mitochondrial protein  |
| Daf2 | A\_66\_P106385 | NM\_007827 | 9.53 | 1.31 | decay accelerating factor 2 (Daf2)  |
| Dcaf12l2 | A\_55\_P1959973 | NM\_175539 | 12.84 | 1.93 | DDB1 and CUL4 associated factor 12-like 2 (Dcaf12l2)  |
| Dcaf4 | A\_51\_P170641 | NM\_030246 | 11.18 | 1.15 | DDB1 and CUL4 associated factor 4 (Dcaf4). transcript variant 2  |
| Dcbld1 | A\_55\_P1967905 | NM\_025705 | 9.71 | 1.01 | discoidin. CUB and LCCL domain containing 1 (Dcbld1)  |
| Dclk3 | A\_51\_P419637 | NM\_172928 | 9.53 | -1.81 | doublecortin-like kinase 3 (Dclk3)  |
| Dcxr | A\_51\_P181319 | NM\_026428 | 12.26 | 2.91 | dicarbonyl L-xylulose reductase (Dcxr)  |
| Ddit4 | A\_51\_P245796 | NM\_029083 | 14.24 | 2.28 | DNA-damage-inducible transcript 4 (Ddit4)  |
| Ddx25 | A\_51\_P326229 | NM\_013932 | 10.45 | 2.63 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 25 (Ddx25)  |
| Dio1 | A\_51\_P403477 | NM\_007860 | 12.93 | -2.34 | deiodinase. iodothyronine. type I (Dio1)  |
| Dnaja1 | A\_55\_P2087984 | NM\_001164671 | 14.50 | 1.04 | DnaJ (Hsp40) homolog. subfamily A. member 1 (Dnaja1). transcript variant 1  |
| Dnali1 | A\_55\_P2040723 | NM\_175223 | 8.14 | 1.21 | dynein. axonemal. light intermediate polypeptide 1 (Dnali1)  |
| Dnm3 | A\_52\_P164286 | NM\_001038619 | 8.10 | 1.58 | dynamin 3 (Dnm3). transcript variant 1  |
| Dos | A\_51\_P436817 | NM\_001195268 | 11.87 | 1.27 | downstream of Stk11 (Dos). transcript variant 1  |
| Dtx4 | A\_51\_P144349 | NM\_172442 | 10.95 | -1.21 | deltex 4 homolog (Drosophila) (Dtx4)  |
| Duoxa1 | A\_55\_P2046443 | NM\_145395 | 12.32 | 2.29 | dual oxidase maturation factor 1 (Duoxa1)  |
| Duoxa2 | A\_55\_P2006644 | NM\_025777 | 9.50 | -1.80 | dual oxidase maturation factor 2 (Duoxa2)  |
| Dyrk3 | A\_52\_P232580 | NM\_145508 | 10.47 | 2.10 | dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 (Dyrk3)  |
| Egfl6 | A\_52\_P655687 | NM\_019397 | 7.24 | -1.55 | EGF-like-domain. multiple 6 (Egfl6)  |
| Ei24 | A\_55\_P2175284 | NM\_001199494 | 10.79 | 1.42 | etoposide induced 2.4 mRNA (Ei24). transcript variant 1  |
| Emid1 | A\_55\_P1954277 | NM\_080595 | 10.81 | -1.15 | EMI domain containing 1 (Emid1)  |
| Enc1 | A\_51\_P126437 | NM\_007930 | 11.40 | 1.01 | ectodermal-neural cortex 1 (Enc1)  |
| Epha2 | A\_52\_P518997 | NM\_010139 | 11.32 | 1.84 | Eph receptor A2 (Epha2)  |
| Ephx1 | A\_55\_P2002578 | NM\_010145 | 16.41 | 1.94 | epoxide hydrolase 1. microsomal (Ephx1)  |
| Eppk1 | A\_55\_P2110351 | NM\_144848 | 12.74 | 3.03 | epiplakin 1 (Eppk1)  |
| Ercc5 | A\_66\_P126189 | NM\_011729 | 10.24 | 1.20 | excision repair cross-complementing rodent repair deficiency. complementation group 5 (Ercc5)  |
| Esrrb | A\_55\_P1954302 | NM\_001159500 | 11.77 | -1.81 | estrogen related receptor. beta (Esrrb). transcript variant 2  |
| Evi2a | A\_55\_P2017759 | NM\_001033711 | 8.31 | -1.61 | ecotropic viral integration site 2a (Evi2a). transcript variant 1  |
| Exoc4 | A\_51\_P350403 | NM\_009148 | 10.33 | 1.23 | exocyst complex component 4 (Exoc4)  |
| Fas | A\_55\_P2091676 | NM\_007987 | 11.89 | 1.93 | Fas (TNF receptor superfamily member 6) (Fas). transcript variant 1  |
| Fat1 | A\_55\_P2107502 | NM\_001081286 | 13.54 | 1.32 | FAT tumor suppressor homolog 1 (Drosophila) (Fat1)  |
| Fbxw9 | A\_51\_P357561 | NM\_026791 | 10.47 | 1.12 | F-box and WD-40 domain protein 9 (Fbxw9)  |
| Foxj1 | A\_51\_P456870 | NM\_008240 | 8.56 | 2.10 | forkhead box J1 (Foxj1)  |
| Gadd45g | A\_51\_P315904 | NM\_011817 | 14.44 | 1.55 | growth arrest and DNA-damage-inducible 45 gamma (Gadd45g)  |
| Galnt5 | A\_55\_P2122871 | NM\_172855 | 7.68 | -1.32 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5 (Galnt5)  |
| Gas6 | A\_51\_P172054 | NM\_019521 | 15.86 | 1.32 | growth arrest specific 6 (Gas6)  |
| Gdf15 | A\_55\_P1960735 | NM\_011819 | 14.84 | 4.15 | growth differentiation factor 15 (Gdf15)  |
| Gfer | A\_55\_P2144796 | NM\_023040 | 11.05 | 1.22 | growth factor. erv1 (S. cerevisiae)-like (augmenter of liver regeneration) (Gfer)  |
| Gjb3 | A\_55\_P2014124 | NM\_001160012 | 9.01 | -1.38 | gap junction protein. beta 3 (Gjb3). transcript variant 1  |
| Gmnn | A\_55\_P2128646 | NM\_020567 | 9.56 | -1.34 | geminin (Gmnn)  |
| Gpr34 | A\_55\_P2039684 | NM\_011823 | 7.50 | -1.29 | G protein-coupled receptor 34 (Gpr34)  |
| Gpr65 | A\_51\_P108459 | NM\_008152 | 7.66 | -1.69 | G-protein coupled receptor 65 (Gpr65)  |
| Gramd2 | A\_55\_P1970901 | NM\_001033498 | 9.05 | 1.07 | GRAM domain containing 2 (Gramd2)  |
| Gria3 | A\_52\_P68221 | NM\_016886 | 8.43 | 1.59 | glutamate receptor. ionotropic. AMPA3 (alpha 3) (Gria3)  |
| Grp | A\_51\_P356055 | NM\_175012 | 10.86 | -2.09 | gastrin releasing peptide (Grp)  |
| Gtse1 | A\_51\_P195153 | NM\_013882 | 8.13 | 3.30 | G two S phase expressed protein 1 (Gtse1). transcript variant 2  |
| H2-Aa | A\_52\_P343306 | NM\_010378 | 8.37 | -1.68 | histocompatibility 2. class II antigen A. alpha (H2-Aa)  |
| H2-Ab1 | A\_55\_P1962747 | NM\_207105 | 14.02 | -1.81 | histocompatibility 2. class II antigen A. beta 1 (H2-Ab1)  |
| H2afj | A\_55\_P2099540 | NM\_177688 | 11.06 | 1.55 | H2A histone family. member J (H2afj)  |
| H2-Ea-ps | A\_51\_P222741 | NM\_010381 | 7.76 | -1.35 | histocompatibility 2. class II antigen E alpha. pseudogene (H2-Ea-ps)  |
| H2-Eb1 | A\_55\_P2156731 | NM\_010382 | 13.91 | -1.71 | histocompatibility 2. class II antigen E beta (H2-Eb1)  |
| Hbegf | A\_51\_P181565 | NM\_010415 | 11.23 | 1.32 | heparin-binding EGF-like growth factor (Hbegf)  |
| Herc2 | A\_55\_P2106429 | NM\_010418 | 12.37 | 1.04 | hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 2 (Herc2)  |
| Heyl | A\_52\_P337259 | NM\_013905 | 9.63 | -1.45 | hairy/enhancer-of-split related with YRPW motif-like (Heyl)  |
| Hist1h2be | A\_55\_P2109128 | NM\_178194 | 9.68 | 1.07 | histone cluster 1. H2be (Hist1h2be). transcript variant 2  |
| Hist2h4 | A\_55\_P1974967 | NM\_033596 | 7.44 | 1.10 | histone cluster 2. H4 (Hist2h4)  |
| Hp | A\_55\_P2048607 | NM\_017370 | 14.56 | 1.16 | haptoglobin (Hp)  |
| Hpgd | A\_51\_P458778 | NM\_008278 | 7.82 | -1.27 | hydroxyprostaglandin dehydrogenase 15 (NAD) (Hpgd)  |
| Hspa1a | A\_55\_P2068459 | NM\_010479 | 11.71 | 1.60 | heat shock protein 1A (Hspa1a)  |
| Hunk | A\_55\_P1967538 | NM\_015755 | 8.71 | -1.74 | hormonally upregulated Neu-associated kinase (Hunk)  |
| Hyal1 | A\_51\_P479408 | NM\_008317 | 10.51 | 1.09 | hyaluronoglucosaminidase 1 (Hyal1)  |
| Il20ra | A\_51\_P340170 | NM\_172786 | 8.61 | 1.48 | interleukin 20 receptor. alpha (Il20ra)  |
| Inf2 | A\_55\_P2085295 | NM\_198411 | 13.96 | 1.67 | inverted formin. FH2 and WH2 domain containing (Inf2)  |
| Inmt | A\_51\_P162162 | NM\_009349 | 11.32 | -1.44 | indolethylamine N-methyltransferase (Inmt)  |
| Inpp5j | A\_55\_P2115871 | NM\_172439 | 10.72 | -1.10 | inositol polyphosphate 5-phosphatase J (Inpp5j)  |
| Ipcef1 | A\_51\_P438657 | NM\_001170800 | 7.07 | -1.29 | interaction protein for cytohesin exchange factors 1 (Ipcef1). transcript variant 1  |
| Irf8 | A\_52\_P354823 | NM\_008320 | 11.00 | -1.24 | interferon regulatory factor 8 (Irf8)  |
| Itga10 | A\_55\_P2111533 | NM\_001081053 | 9.06 | 1.21 | integrin. alpha 10 (Itga10)  |
| Itgax | A\_51\_P303424 | NM\_021334 | 8.19 | -1.69 | integrin alpha X (Itgax)  |
| Itih4 | A\_55\_P2077055 | NM\_018746 | 8.88 | 1.14 | inter alpha-trypsin inhibitor. heavy chain 4 (Itih4). transcript variant 1  |
| Jak3 | A\_55\_P2010912 | NM\_001190830 | 9.39 | 1.02 | Janus kinase 3 (Jak3). transcript variant 2  |
| Kcnj4 | A\_51\_P166740 | NM\_008427 | 7.24 | 1.60 | potassium inwardly-rectifying channel. subfamily J. member 4 (Kcnj4)  |
| Kcnn2 | A\_51\_P309854 | NM\_080465 | 8.69 | -2.01 | potassium intermediate/small conductance calcium-activated channel. subfamily N. member 2 (Kcnn2)  |
| Kit | A\_66\_P128434 | NM\_001122733 | 10.59 | -1.10 | kit oncogene (Kit). transcript variant 1  |
| Klhl14 | A\_55\_P2048085 | NM\_001081403 | 9.93 | -1.58 | kelch-like 14 (Drosophila) (Klhl14)  |
| Klhl26 | A\_51\_P143468 | NM\_178771 | 11.61 | 1.11 | kelch-like 26 (Drosophila) (Klhl26). transcript variant 2  |
| Klra1 | A\_55\_P2004551 | NM\_016659 | 9.47 | 1.51 | killer cell lectin-like receptor. subfamily A. member 1 (Klra1)  |
| Krt73 | A\_55\_P1973970 | NM\_212485 | 9.91 | 1.30 | keratin 73 (Krt73)  |
| Lace1 | A\_51\_P432511 | NM\_145743 | 10.27 | 1.03 | lactation elevated 1 (Lace1)  |
| Lama5 | A\_55\_P2064321 | NM\_001081171 | 13.62 | 1.23 | laminin. alpha 5 (Lama5)  |
| Lass6 | A\_52\_P667287 | NM\_172856 | 7.82 | -1.29 | LAG1 homolog. ceramide synthase 6 (Lass6)  |
| Lcn5 | A\_55\_P1963727 | NM\_007947 | 7.36 | 1.54 | lipocalin 5 (Lcn5). transcript variant 1  |
| Lcn8 | A\_55\_P2051738 | NM\_033145 | 9.17 | 3.35 | lipocalin 8 (Lcn8)  |
| Lgi3 | A\_51\_P356967 | NM\_145219 | 9.09 | -1.41 | leucine-rich repeat LGI family. member 3 (Lgi3)  |
| Lifr | A\_55\_P2159264 | NM\_001113386 | 10.19 | -1.17 | leukemia inhibitory factor receptor (Lifr). transcript variant 2  |
| Lrfn4 | A\_55\_P2138878 | NM\_153388 | 10.32 | -1.22 | leucine rich repeat and fibronectin type III domain containing 4 (Lrfn4)  |
| Ltbp2 | A\_55\_P1970105 | NM\_013589 | 13.24 | 1.05 | latent transforming growth factor beta binding protein 2 (Ltbp2)  |
| Ly86 | A\_51\_P465350 | NM\_010745 | 9.34 | -1.30 | lymphocyte antigen 86 (Ly86)  |
| Lypd6b | A\_51\_P105068 | NM\_027990 | 11.42 | -1.20 | LY6/PLAUR domain containing 6B (Lypd6b)  |
| Mab21l3 | A\_55\_P2090060 | NM\_172295 | 8.89 | 2.26 | mab-21-like 3 (C. elegans) (Mab21l3)  |
| Mapk4 | A\_51\_P245895 | NM\_172632 | 7.34 | -1.01 | mitogen-activated protein kinase 4 (Mapk4)  |
| Mapre3 | A\_55\_P2087404 | NM\_133350 | 13.53 | 1.12 | microtubule-associated protein. RP/EB family. member 3 (Mapre3)  |
| Matn4 | A\_55\_P2171206 | NM\_013592 | 10.77 | -1.16 | matrilin 4 (Matn4). transcript variant 1  |
| Mbnl3 | A\_55\_P2106255 | NM\_134163 | 7.88 | -1.17 | muscleblind-like 3 (Drosophila) (Mbnl3)  |
| Mc4r | A\_55\_P2183884 | NM\_016977 | 8.22 | -1.20 | melanocortin 4 receptor (Mc4r)  |
| Mdm2 | A\_55\_P1975475 | NM\_010786 | 14.07 | 2.35 | transformed mouse 3T3 cell double minute 2 (Mdm2)  |
| Mdm4 | A\_52\_P485905 | NM\_008575 | 8.65 | 1.65 | transformed mouse 3T3 cell double minute 4 (Mdm4)  |
| Mfi2 | A\_51\_P324351 | NM\_013900 | 9.19 | -2.08 | antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5 (Mfi2)  |
| Mfsd2a | A\_51\_P279437 | NM\_029662 | 9.02 | 2.23 | major facilitator superfamily domain containing 2A (Mfsd2a)  |
| Mgmt | A\_55\_P2071858 | NM\_008598 | 11.93 | 2.27 | O-6-methylguanine-DNA methyltransferase (Mgmt)  |
| Micall1 | A\_51\_P242414 | NM\_177461 | 12.50 | 1.12 | microtubule associated monoxygenase. calponin and LIM domain containing -like 1 (Micall1)  |
| Mpeg1 | A\_51\_P390538 | NM\_010821 | 10.99 | -1.23 | macrophage expressed gene 1 (Mpeg1)  |
| Mrps6 | A\_52\_P58257 | NM\_080456 | 14.77 | 1.01 | mitochondrial ribosomal protein S6 (Mrps6). nuclear gene encoding mitochondrial protein  |
| Ms4a10 | A\_55\_P2094445 | NM\_023529 | 8.15 | 2.30 | membrane-spanning 4-domains. subfamily A. member 10 (Ms4a10)  |
| Mybl1 | A\_55\_P1966369 | NM\_008651 | 7.29 | 1.39 | myeloblastosis oncogene-like 1 (Mybl1)  |
| Ncs1 | A\_51\_P114062 | NM\_019681 | 9.62 | -1.02 | neuronal calcium sensor 1 (Ncs1)  |
| Net1 | A\_66\_P105736 | NM\_019671 | 12.01 | 1.73 | neuroepithelial cell transforming gene 1 (Net1). transcript variant 1  |
| Neu3 | A\_52\_P357611 | NM\_016720 | 9.61 | 1.93 | neuraminidase 3 (Neu3)  |
| Nkx2-9 | A\_55\_P2042844 | NM\_008701 | 8.52 | 3.56 | NK2 transcription factor related. locus 9 (Drosophila) (Nkx2-9)  |
| Nme5 | A\_55\_P1966102 | NM\_080637 | 11.42 | 1.12 | non-metastatic cells 5. protein expressed in (nucleoside-diphosphate kinase) (Nme5)  |
| Nmur2 | A\_55\_P2179582 | NM\_153079 | 10.55 | 1.48 | neuromedin U receptor 2 (Nmur2)  |
| Notch3 | A\_51\_P220162 | NM\_008716 | 13.03 | 1.06 | Notch gene homolog 3 (Drosophila) (Notch3)  |
| Nrg1 | A\_55\_P1985433 | NM\_178591 | 11.11 | 1.83 | neuregulin 1 (Nrg1)  |
| Nudt10 | A\_55\_P1993807 | NM\_001031664 | 9.51 | -1.00 | nudix (nucleoside diphosphate linked moiety X)-type motif 10 (Nudt10)  |
| Odz4 | A\_55\_P2141084 | NM\_011858 | 14.10 | -1.30 | odd Oz/ten-m homolog 4 (Drosophila) (Odz4)  |
| Olfr1229 | A\_55\_P2142172 | NM\_001011761 | 10.48 | 1.46 | olfactory receptor 1229 (Olfr1229)  |
| Papss2 | A\_55\_P2080021 | NM\_011864 | 14.29 | -1.25 | 3'-phosphoadenosine 5'-phosphosulfate synthase 2 (Papss2). transcript variant 1  |
| Pdgfra | A\_51\_P345649 | NM\_011058 | 9.81 | -1.07 | platelet derived growth factor receptor. alpha polypeptide (Pdgfra). transcript variant 1  |
| Pdzk1ip1 | A\_55\_P2011678 | NM\_001164557 | 11.67 | -1.15 | PDZK1 interacting protein 1 (Pdzk1ip1). transcript variant 1  |
| Per1 | A\_55\_P1970033 | NM\_011065 | 12.68 | 2.20 | period homolog 1 (Drosophila) (Per1). transcript variant 1  |
| Per2 | A\_51\_P282760 | NM\_011066 | 9.62 | 2.04 | period homolog 2 (Drosophila) (Per2)  |
| Perp | A\_51\_P317941 | NM\_022032 | 14.12 | 2.01 | PERP. TP53 apoptosis effector (Perp)  |
| Phlda3 | A\_51\_P329928 | NM\_013750 | 15.82 | 1.41 | pleckstrin homology-like domain. family A. member 3 (Phlda3)  |
| Pigf | A\_51\_P264053 | NM\_008838 | 10.93 | 1.12 | phosphatidylinositol glycan anchor biosynthesis. class F (Pigf)  |
| Pim3 | A\_51\_P189746 | NM\_145478 | 11.85 | 1.05 | proviral integration site 3 (Pim3)  |
| Plcd4 | A\_52\_P327588 | NM\_148937 | 11.75 | 1.97 | phospholipase C. delta 4 (Plcd4). transcript variant 2  |
| Plk2 | A\_51\_P290576 | NM\_152804 | 10.14 | 1.20 | polo-like kinase 2 (Drosophila) (Plk2)  |
| Plk3 | A\_51\_P375201 | NM\_013807 | 9.68 | 1.11 | polo-like kinase 3 (Drosophila) (Plk3)  |
| Plk5 | A\_55\_P1972297 | NM\_183152 | 8.92 | 2.36 | polo-like kinase 5 (Drosophila) (Plk5)  |
| Pm20d1 | A\_55\_P2159585 | NM\_178079 | 10.14 | 1.57 | peptidase M20 domain containing 1 (Pm20d1)  |
| Pmaip1 | A\_51\_P477121 | NM\_021451 | 8.67 | 2.73 | phorbol-12-myristate-13-acetate-induced protein 1 (Pmaip1)  |
| Polk | A\_55\_P2000533 | NM\_012048 | 10.09 | 2.01 | polymerase (DNA directed). kappa (Polk)  |
| Ppp1r13l | A\_55\_P2074924 | NM\_001010836 | 11.63 | 1.93 | protein phosphatase 1. regulatory (inhibitor) subunit 13 like (Ppp1r13l)  |
| Ppp1r1b | A\_55\_P2026275 | NM\_144828 | 13.89 | -1.85 | protein phosphatase 1. regulatory (inhibitor) subunit 1B (Ppp1r1b)  |
| Pqlc3 | A\_51\_P332652 | NM\_172574 | 11.89 | 1.24 | PQ loop repeat containing (Pqlc3). transcript variant 1  |
| Prdx6 | A\_55\_P2176731 | NM\_007453 | 14.87 | 1.24 | peroxiredoxin 6 (Prdx6)  |
| Pros1 | A\_51\_P393426 | NM\_011173 | 11.35 | 1.38 | protein S (alpha) (Pros1)  |
| Prosapip1 | A\_55\_P2020361 | NM\_197945 | 14.39 | 1.33 | ProSAPiP1 protein (Prosapip1)  |
| Prr15l | A\_52\_P435561 | NM\_146026 | 10.93 | 1.25 | proline rich 15-like (Prr15l)  |
| Psapl1 | A\_52\_P523368 | NM\_175249 | 11.37 | 4.16 | prosaposin-like 1 (Psapl1)  |
| Psrc1 | A\_55\_P2429225 | NM\_001190161 | 9.34 | 3.49 | proline/serine-rich coiled-coil 1 (Psrc1). transcript variant 1  |
| Ptgir | A\_55\_P1994309 | NM\_008967 | 9.04 | -1.37 | prostaglandin I receptor (IP) (Ptgir)  |
| Ptk2b | A\_51\_P311904 | NM\_172498 | 11.70 | 1.98 | PTK2 protein tyrosine kinase 2 beta (Ptk2b). transcript variant 3  |
| Ptpdc1 | A\_55\_P2007871 | NM\_207232 | 12.03 | 1.40 | protein tyrosine phosphatase domain containing 1 (Ptpdc1)  |
| Ptpn22 | A\_51\_P483324 | NM\_008979 | 8.17 | -1.71 | protein tyrosine phosphatase. non-receptor type 22 (lymphoid) (Ptpn22)  |
| Pvt1 | A\_55\_P2051254 | NR\_003368 | 9.11 | 2.33 | plasmacytoma variant translocation 1 (Pvt1). non-coding RNA  |
| Rab3il1 | A\_55\_P1994927 | NM\_144538 | 10.75 | -1.01 | RAB3A interacting protein (rabin3)-like 1 (Rab3il1)  |
| Rabgap1 | A\_55\_P2161923 | NM\_001033960 | 10.02 | 1.54 | RAB GTPase activating protein 1 (Rabgap1). transcript variant 2  |
| Rabgap1l | A\_55\_P2002819 | NM\_013862 | 12.52 | 1.11 | RAB GTPase activating protein 1-like (Rabgap1l). transcript variant 1  |
| Rad51ap1 | A\_55\_P1991688 | NM\_009013 | 8.69 | -1.09 | RAD51 associated protein 1 (Rad51ap1)  |
| Rasgef1b | A\_55\_P2035315 | NM\_145839 | 10.97 | -1.07 | RasGEF domain family. member 1B (Rasgef1b). transcript variant 1  |
| Rbp1 | A\_55\_P2059010 | NM\_011254 | 13.35 | -1.37 | retinol binding protein 1. cellular (Rbp1)  |
| Reep2 | A\_52\_P125467 | NM\_144865 | 8.46 | 1.16 | receptor accessory protein 2 (Reep2). transcript variant 1  |
| Rem2 | A\_51\_P191909 | NM\_080726 | 8.03 | -1.13 | rad and gem related GTP binding protein 2 (Rem2)  |
| Rev1 | A\_51\_P249594 | NM\_019570 | 9.65 | 1.11 | REV1 homolog (S. cerevisiae) (Rev1)  |
| Rhbdf2 | A\_55\_P2028259 | NM\_172572 | 10.93 | 1.25 | rhomboid 5 homolog 2 (Drosophila) (Rhbdf2). transcript variant 1  |
| Rhpn1 | A\_55\_P2077027 | NM\_001163465 | 10.09 | -1.32 | rhophilin. Rho GTPase binding protein 1 (Rhpn1). transcript variant 1  |
| Rimkla | A\_52\_P69194 | NM\_177572 | 8.65 | -1.53 | ribosomal modification protein rimK-like family member A (Rimkla)  |
| Ripk4 | A\_55\_P2035400 | NM\_023663 | 12.69 | 1.47 | receptor-interacting serine-threonine kinase 4 (Ripk4)  |
| Rln1 | A\_52\_P182298 | NM\_011272 | 9.21 | 2.30 | relaxin 1 (Rln1)  |
| Rnf169 | A\_52\_P577729 | NM\_175388 | 12.11 | 1.61 | ring finger protein 169 (Rnf169)  |
| Rnf183 | A\_55\_P1988310 | NM\_153504 | 8.89 | -1.45 | ring finger protein 183 (Rnf183)  |
| Robo3 | A\_55\_P2144886 | NM\_001164767 | 7.81 | 1.00 | roundabout homolog 3 (Drosophila) (Robo3)  |
| Rprm | A\_51\_P278653 | NM\_023396 | 9.44 | 3.29 | reprimo. TP53 dependent G2 arrest mediator candidate (Rprm)  |
| Rps27l | A\_51\_P246903 | NM\_026467 | 15.68 | 1.22 | ribosomal protein S27-like (Rps27l)  |
| Rufy4 | A\_55\_P2031471 | NM\_001034060 | 10.33 | 1.00 | RUN and FYVE domain containing 4 (Rufy4). transcript variant 2  |
| S100a3 | A\_51\_P468456 | NM\_011310 | 8.53 | 1.17 | S100 calcium binding protein A3 (S100a3)  |
| Scnn1a | A\_51\_P213691 | NM\_011324 | 13.66 | 1.47 | sodium channel. nonvoltage-gated 1 alpha (Scnn1a)  |
| Scube2 | A\_55\_P2232988 | NM\_020052 | 10.81 | -1.58 | signal peptide. CUB domain. EGF-like 2 (Scube2)  |
| Scx | A\_51\_P380432 | NM\_198885 | 11.60 | -1.69 | scleraxis (Scx)  |
| Sdc1 | A\_52\_P479269 | NM\_011519 | 10.00 | 1.37 | syndecan 1 (Sdc1)  |
| Sec11c | A\_51\_P359262 | NM\_025468 | 11.94 | -1.01 | SEC11 homolog C (S. cerevisiae) (Sec11c)  |
| Serpina3n | A\_51\_P159453 | NM\_009252 | 8.32 | 2.13 | serine (or cysteine) peptidase inhibitor. clade A. member 3N (Serpina3n)  |
| Serpinb6b | A\_55\_P2013043 | NM\_011454 | 10.80 | 1.41 | serine (or cysteine) peptidase inhibitor. clade B. member 6b (Serpinb6b)  |
| Sesn2 | A\_51\_P161354 | NM\_144907 | 12.20 | 1.84 | sestrin 2 (Sesn2)  |
| Sgk2 | A\_55\_P2042923 | NM\_013731 | 7.82 | 1.72 | serum/glucocorticoid regulated kinase 2 (Sgk2)  |
| Sh3bgrl2 | A\_52\_P316933 | NM\_172507 | 10.79 | 1.25 | SH3 domain binding glutamic acid-rich protein like 2 (Sh3bgrl2)  |
| Shc4 | A\_55\_P1968763 | NM\_199022 | 13.90 | 1.56 | SHC (Src homology 2 domain containing) family. member 4 (Shc4)  |
| Siglech | A\_55\_P2165790 | NM\_178706 | 8.15 | -1.45 | sialic acid binding Ig-like lectin H (Siglech)  |
| Slain1 | A\_51\_P147284 | NM\_198014 | 9.16 | -1.04 | SLAIN motif family. member 1 (Slain1)  |
| Slamf8 | A\_51\_P444290 | NM\_029084 | 7.34 | -1.17 | SLAM family member 8 (Slamf8)  |
| Slc10a6 | A\_51\_P173678 | NM\_029415 | 8.04 | 1.25 | solute carrier family 10 (sodium/bile acid cotransporter family). member 6 (Slc10a6)  |
| Slc17a9 | A\_55\_P1998601 | NM\_183161 | 8.65 | -1.12 | solute carrier family 17. member 9 (Slc17a9)  |
| Slc19a2 | A\_51\_P329332 | NM\_054087 | 10.48 | 2.20 | solute carrier family 19 (thiamine transporter). member 2 (Slc19a2)  |
| Slc23a1 | A\_52\_P141628 | NM\_011397 | 11.28 | 3.10 | solute carrier family 23 (nucleobase transporters). member 1 (Slc23a1)  |
| Slc26a10 | A\_52\_P140881 | NM\_177615 | 12.53 | -2.58 | solute carrier family 26. member 10 (Slc26a10)  |
| Slc27a3 | A\_55\_P1958597 | NM\_011988 | 11.41 | 1.03 | solute carrier family 27 (fatty acid transporter). member 3 (Slc27a3)  |
| Slc2a9 | A\_55\_P2008936 | NM\_001102414 | 7.90 | 1.40 | solute carrier family 2 (facilitated glucose transporter). member 9 (Slc2a9). transcript variant 1 |
| Slc44a4 | A\_52\_P517762 | NM\_023557 | 8.20 | -1.25 | solute carrier family 44. member 4 (Slc44a4)  |
| Slc5a3 | A\_52\_P283055 | NM\_017391 | 11.57 | 2.06 | solute carrier family 5 (inositol transporters). member 3 (Slc5a3)  |
| Slc5a5 | A\_51\_P115738 | NM\_053248 | 10.09 | -3.27 | solute carrier family 5 (sodium iodide symporter). member 5 (Slc5a5)  |
| Slco2a1 | A\_55\_P1989673 | NM\_033314 | 12.20 | -1.14 | solute carrier organic anion transporter family. member 2a1 (Slco2a1)  |
| Smoc2 | A\_55\_P2002903 | NM\_022315 | 14.43 | -1.24 | SPARC related modular calcium binding 2 (Smoc2)  |
| Snhg12 | A\_66\_P100249 | NR\_029468 | 11.71 | 1.02 | small nucleolar RNA host gene 12 (Snhg12). non-coding RNA  |
| Socs1 | A\_51\_P279606 | NM\_009896 | 9.72 | -2.12 | suppressor of cytokine signaling 1 (Socs1)  |
| Spdef | A\_55\_P2007249 | NM\_013891 | 9.80 | -1.21 | SAM pointed domain containing ets transcription factor (Spdef)  |
| Spon2 | A\_52\_P381484 | NM\_133903 | 9.29 | -1.56 | spondin 2. extracellular matrix protein (Spon2)  |
| Sstr3 | A\_55\_P2106335 | NM\_009218 | 7.82 | -1.18 | somatostatin receptor 3 (Sstr3)  |
| St3gal1 | A\_51\_P301804 | NM\_009177 | 11.43 | 1.01 | ST3 beta-galactoside alpha-2.3-sialyltransferase 1 (St3gal1)  |
| St6galnac1 | A\_55\_P2118609 | NM\_011371 | 12.53 | 1.39 | ST6 (alpha-N-acetyl-neuraminyl-2.3-beta-galactosyl-1.3)-N-acetylgalactosaminide alpha-2.6-sialyltransferase 1 (St6galnac1)  |
| Sulf2 | A\_52\_P193925 | NM\_028072 | 12.42 | 1.19 | sulfatase 2 (Sulf2). transcript variant 2  |
| Susd4 | A\_55\_P1954393 | NM\_144796 | 11.41 | 2.69 | sushi domain containing 4 (Susd4)  |
| Svop | A\_51\_P282594 | NM\_026805 | 7.88 | 1.62 | SV2 related protein (Svop)  |
| Sytl1 | A\_55\_P2143693 | NM\_031393 | 11.81 | 1.46 | synaptotagmin-like 1 (Sytl1)  |
| Tacr1 | A\_52\_P149545 | NM\_009313 | 7.39 | -1.21 | tachykinin receptor 1 (Tacr1)  |
| Tbx22 | A\_55\_P2089565 | NM\_181319 | 10.46 | 1.81 | T-box 22 (Tbx22). transcript variant 2  |
| Tdgf1 | A\_55\_P1968028 | NM\_011562 | 11.07 | 1.51 | teratocarcinoma-derived growth factor 1 (Tdgf1)  |
| Tdrd3 | A\_55\_P1983036 | NM\_172605 | 11.31 | 1.16 | tudor domain containing 3 (Tdrd3). transcript variant 1  |
| Tekt1 | A\_55\_P2132024 | NM\_011569 | 11.61 | -1.71 | tektin 1 (Tekt1)  |
| Tepp | A\_51\_P450682 | NM\_199455 | 9.04 | -1.24 | testis. prostate and placenta expressed (Tepp). transcript variant 1  |
| Tgm1 | A\_52\_P627816 | NM\_019984 | 9.37 | 1.73 | transglutaminase 1. K polypeptide (Tgm1). transcript variant 2  |
| Them5 | A\_51\_P267441 | NM\_025416 | 7.41 | 1.52 | thioesterase superfamily member 5 (Them5)  |
| Thyn1 | A\_51\_P323620 | NM\_144543 | 13.94 | 1.73 | thymocyte nuclear protein 1 (Thyn1)  |
| Tinagl1 | A\_52\_P418489 | NM\_023476 | 12.28 | 1.16 | tubulointerstitial nephritis antigen-like 1 (Tinagl1). transcript variant 1  |
| Tk1 | A\_55\_P2056496 | NM\_009387 | 9.36 | -1.30 | thymidine kinase 1 (Tk1)  |
| Tlr2 | A\_51\_P452629 | NM\_011905 | 12.15 | -1.24 | toll-like receptor 2 (Tlr2)  |
| Tmem132a | A\_55\_P2113081 | NM\_133804 | 13.61 | 1.36 | transmembrane protein 132A (Tmem132a)  |
| Tmem171 | A\_52\_P799815 | NM\_001025606 | 10.22 | -1.66 | transmembrane protein 171 (Tmem171)  |
| Tmem213 | A\_51\_P401501 | NM\_029921 | 9.16 | -1.08 | transmembrane protein 213 (Tmem213)  |
| Tmprss13 | A\_55\_P2177998 | NM\_001013373 | 10.46 | 1.27 | transmembrane protease. serine 13 (Tmprss13)  |
| Tnfrsf10b | A\_55\_P2027836 | NM\_020275 | 10.96 | 1.96 | tumor necrosis factor receptor superfamily. member 10b (Tnfrsf10b)  |
| Tnfrsf12a | A\_51\_P131408 | NM\_013749 | 13.08 | 1.17 | tumor necrosis factor receptor superfamily. member 12a (Tnfrsf12a). transcript variant 1  |
| Tnn | A\_55\_P2005549 | NM\_177839 | 8.59 | 1.58 | tenascin N (Tnn)  |
| Tob2 | A\_52\_P70854 | NM\_020507 | 12.04 | 1.01 | transducer of ERBB2. 2 (Tob2)  |
| Tomm20l | A\_51\_P518156 | NM\_029227 | 7.34 | 2.26 | translocase of outer mitochondrial membrane 20 homolog (yeast)-like (Tomm20l). nuclear gene encoding mitochondrial protein  |
| Trib1 | A\_52\_P573552 | NM\_144549 | 12.81 | 1.20 | tribbles homolog 1 (Drosophila) (Trib1)  |
| Trim11 | A\_55\_P1962359 | NM\_053168 | 13.14 | 1.38 | tripartite motif-containing 11 (Trim11)  |
| Trp53inp1 | A\_55\_P1973906 | NM\_021897 | 9.42 | 2.24 | transformation related protein 53 inducible nuclear protein 1 (Trp53inp1). transcript variant 1  |
| Tsc22d3 | A\_55\_P1989061 | NM\_001077364 | 14.10 | 1.29 | TSC22 domain family. member 3 (Tsc22d3). transcript variant 1  |
| Tspan1 | A\_51\_P333923 | NM\_133681 | 14.65 | -1.65 | tetraspanin 1 (Tspan1)  |
| Tspan33 | A\_55\_P2086664 | NM\_146173 | 12.08 | -1.52 | tetraspanin 33 (Tspan33)  |
| Tspan4 | A\_55\_P2007713 | NM\_053082 | 11.28 | 1.02 | tetraspanin 4 (Tspan4). transcript variant 1  |
| Vopp1 | A\_55\_P1970120 | NM\_146168 | 12.70 | 1.11 | vesicular. overexpressed in cancer. prosurvival protein 1 (Vopp1)  |
| Vsig8 | A\_55\_P2124233 | NM\_177723 | 9.76 | 1.11 | V-set and immunoglobulin domain containing 8 (Vsig8). transcript variant 1  |
| Wdfy4 | A\_52\_P199614 | NM\_001146022 | 9.34 | -2.00 | WD repeat and FYVE domain containing 4 (Wdfy4)  |
| Wee1 | A\_66\_P136186 | NM\_009516 | 9.38 | 1.17 | WEE 1 homolog 1 (S. pombe) (Wee1)  |
| Wfikkn2 | A\_52\_P625215 | NM\_181819 | 8.54 | -1.55 | WAP. follistatin/kazal. immunoglobulin. kunitz and netrin domain containing 2 (Wfikkn2)  |
| Wisp1 | A\_51\_P220343 | NM\_018865 | 11.35 | -2.08 | WNT1 inducible signaling pathway protein 1 (Wisp1)  |
| Wnt7b | A\_55\_P2274592 | NM\_001163634 | 7.61 | 1.00 | wingless-related MMTV integration site 7B (Wnt7b). transcript variant 2  |
| Zbtb16 | A\_55\_P2024155 | NM\_001033324 | 13.03 | 1.73 | zinc finger and BTB domain containing 16 (Zbtb16)  |
| Zfp365 | A\_55\_P2039320 | NM\_178679 | 10.50 | 3.07 | zinc finger protein 365 (Zfp365)  |
| Zfp688 | A\_55\_P1971759 | NM\_026999 | 11.76 | 1.01 | zinc finger protein 688 (Zfp688)  |
| Zmat3 | A\_51\_P415220 | NM\_009517 | 11.48 | 1.82 | zinc finger matrin type 3 (Zmat3)  |