**Supplementary Materials**

**Supplementary Table I. Sequence of primers used for RTPCR and MSPCR**

**Primers for RTPCR**

**Primer Name Sequence (5' to 3')**

mTGFB2-F1 CAC CAA AGT CCT CAG CCT GT

mTGFB2-R1 GCT GTT CGA TCT TGG GCG TA

mIL6RA-F1 GAT GCC TTG CGA GGA GTG AA

mIL6RA-R1 CTG GGC TCT GCT ATC CAA GG

mTRPM2-F1 ACA AAG GGT ACG TGG ATG ACC

mTRPM2-R1 GAG TGT GCA GGT TCT CTT CCA

mSlc25a12-F1 AAG ACC CGG ATG CAA AAC CA

mSlc25a12-R1 TGG GAT CAG ACC TCG GTA CA

mSKI-F1 CCT GCA CCA GGA GCT AGA AT

mSKI-R1 GGA CTC GTT GGC CTC TTT CA

mCARTPT-F1 GCG CTA TGT TGC AGA TCG AAG

mCARTPT-R1 AGC GTC ACA CAT GGG GAC TTG

mSMAD3-F2 GAG ACG CCA GTT CTA CCT C

mSMAD3-R2 TCA ATG CCA GCA GGG AAG TT

mSMAD2-F1 GAG AGT TGA GAC CCC AGT CTT G

mSMAD2-R1 CTG GAA TGG AGT GGG TGT AGT C

mPDE10A-F1 CAT CCG CAA AGC CAT CAT CG

mPDE10A-R1 GAT GAC ACG GTC TCG ATG GG

mGAL3ST1-F1 AGA ACA GGG CAA AGT GCC TC

mGAL3ST1-R1 AGT CCC CCA TTG CCA TTG TC

mP4HA2-F1 CAG AGC TAT TGC AGG TCG CA

mP4HA2-R1 CCC AGT CCC TAA ACG CTT GA

mCREBZF-F1 AAA GGT GGT GGG AGG GGA AT

mCREBZF-R1 CGC AAC TCT GAA CAA GGG GA

mPRKG2-F1 ACG TGG ACA TTC TGT GGG AC

mPRKG2-R1 CAG AAA AGG GAG GGT TGC CC

mFAM198b-F1 AGT GAA GTG TTC GCC TTC CA

mFAM198b-R1 AGG TCG GCC ATC TTG GAT GA

mIL36b-F1 CAT GGA TCC TCA CAA TCT CCC A

mIL36b-R1 GAC AGG CTT GAC ATT GTT GCT

mMSR1-F1 AGT GTA GGC GGA TCA ACC CC

mMSR1-R1 TGT CCA GCC CGT ATA TCC CA

mPLCL2-F1 GGG CTG AAG GAA CGG AAA CT

mPLCL2-R1 AAG ATC CGC TTG CCC CTT TA

mUNC-F1 AAA CAC GTG CGT GAC TTT CG

mUNC-R1 CCG TAG CCC AGG GCA AAA

mBMP3-F1 CAG CCG CAG GAA CTC CTC AAA

mBMP3-R1 CAA CGT AGA AAT ACA GTG TGG CTG

mMECP2-F1 CAC CTT GCC TGA AGG TTG GA

mMECP2-R1 AAG CTT TTC CCT GGG GAT TGA T

mMBD4-F1 TCA ATC GGA CCT CAG GCA AG

mMBD4-R1 GCA CGG AGA TCG TAG AGA CC

mMBD3-F1 TTA CTA TAG CCC CAG CGG GA

mMBD3-R1 GAA GTC GAA GGT GCT GAG GT

mMBD2-F1 GGT CTT CAA GGA GTC GGT CC

mMBD2-R1 GTT CTT TTC CAC GGC AGC AG

mMBD1-F1 TGT TTA AGC GAG TCG GCT GT

mMBD1-R1 TAA TCC GCA GGC ATC GTC TC

mDNMT3B-F1 CCT CCG ACG CAG GAA AGA TT

mDNMT3B-R1 ACT TGG GTG GCT CCT GAA AT

mDNMT3A-F1 GGG CCA CAC GGC AGA G

mDNMT3A-R1 TGC CGT GGT CTT TGT AAG CA

mDNMT1-F1 GTC GGA CAG TGA CAC CCT TT

mDNMT1-R1 TTT AGT GGG GCC CTT CGT G

mTET1-F GCT GGA TTG AAG GAA CAG GA

mTET1-R GTC TCC ATG AGC TCC CTG AC

mTET2-F GTC AAC AGG ACA TGA TCC AGG AG

mTET2-R CCT GTT CCA TCA GGC TTG CT

mTET3-F CCG TGA CTG TGC TCT CAA CT

mTET3-R TTC TAT CCG GGA ACT CAT GG

mAID-F1 ACC GAT ATG GAC AGC CTT CTG

mAID-R1 ACC ACG TAG CAG AGG TAG GT

mSMUG1-F1 GAT TCA GGG GTT CCA GTC CC

mSMUG1-R1 CTG TCA CCT GCA AAG GCA AAT

mTDG-F1 GAT CCT GTG GTG AGT CCG C

mTDG-R1 TTG CTC CAG AGA ATA GCT GCG

**Primers for MSPCR**

**Primer Name Sequence (5' to 3')**

mMS-TGFB2-MF1 ATT TAT TTG CGG AGA GAA GGA TC

mMS-TGFB2-MR1 CAA AAA CGA CAA CGA TCG AC

mMS-TGFB2-UF1 AAT TTA TTT GTG GAG AGA AGG ATT G

mMS-TGFB2-UR1 ACC AAA AAC AAC AAC AAT CAA C

mMS-SMAD2-F1 TAA TCG TAC GGA TAA GAA TAG TTC G

mMS-SMAD2-R1 TCG TAA AAC CGA AAT AAA CAC GTA

mUS-SMAD2-F1 AAT ATT AAT TGT ATG GAT AAG AAT AGT TTG

mUS-SMAD2-R1 TCA TAA AAC CAA AAT AAA CAC ATA

mMS-smad3-F1 GTT TTG GTT GGT TTT GTA AGG C

mMS-smad3-R1 GAA AAT CGA AAA CAC GAC GA

mUS-smad3-F1 TTT TGG TTG GTT TTG TAA GGT G

mUS-smad3-R1 CTA CAA AAA TCA AAA ACA CAA CAA C

mMS-IL6RA-F1 TGT TTT ATT GTT GTT AGG ACG GTC

mMS-IL6RA-R1 AAC ATA CTT CCT TCT ACG CGA A

mUS-IL6RA-F1 TTT TAT TGT TGT TAG GAT GGT TGG

mUS-IL6RA-R1 ATC AAC ATA CTT CCT TCT ACA CAA A

mMS-TRPM2-F1 GGT GTT TCG AAG AGG TTG ATT C

mMS-TRPM2-R1 AAT ACC TAC TCA AAA ACC GCG

mUS-TRPM2-F1 GTG TTT TGA AGA GGT TGA TTT GT

mUS-TRPM2-R1 AAT ACC TAC TCA AAA ACC ACA CA

mMS-SLC25A12-F1 TTA TAT TGC GCG TTG GAA TTC

mMS-SLC25A12-R1 ACC TTA ACC GCC ATA CTA TAC TCG

mUS-SLC25A12-F1 TTT GTT TAT ATT GTG TGT TGG AAT TT

mUS-SLC25A12-R1 ATC ACC TTA ACC ACC ATA CTA TAC TCA

mMS-CARTPT-F1 GCG TAG AGT TTC GTT TTC GG

mMS-CARTPT-R1 GAC TTC TTA TAA CCG ATT AAA ATC GAA

mUS-CARTPT-F1 ATT TGT GTG TAG AGT TTT GTT TTT GG

mUS-CARTPT-R1 TCC AAC TTC TTA TAA CCA ATT AAA ATC A

mMS-SKI-F1 TAA AGT CGA GTT TGG TCG AGT TC

mMS-SKI-R1 CGC GTT ATT TAT TAC CGT ACG TC

mUS-SKI-F1 ATA AAG TTG AGT TTG GTT GAG TTT G

mUS-SKI-R1 TCC CAC ATT ATT TAT TAC CAT ACA TC

mMS-PDE10A-F1 TTT TTT TGG AAT TTC GGT GC

mMS-PDE10A-R1 CTA AAA CCC CCA ATA AAA CTA ACG T

mUS-PDE10A-F1 GTT TTT TTG GAA TTT TGG TGT G

mUS-PDE10A-R1 TAA AAC CCC CAA TAA AAC TAA CAT A

mMS-BMP3-MF1 TAA ATA AAT TTA TTG TTT GTG ACG A

mMS-BMP3-MR1 ACT AAA TAA AAA CAT CTT TTC CGA C

mMS-BMP3-UF1 TTA AAT AAA TTT ATT GTT TGT GAT GA

mMS-BMP3-UR1 ACT AAA TAA AAA CAT CTT TTC CAA C

mMS-PRKG2-MF1 GTT TCG GGT TTT TTT ACG TTA C

mMS-PRKG2-MR1 TAC TAC CGC CTA ACT ACT CTA CGA A

mMS-PRKG2-UF1 GGG TTT TGG GTT TTT TTA TGT TAT

mMS-PRKG2-UR1 TAC TAC CAC CTA ACT ACT CTA CAA A

mMS-GAL3ST1-MF1 TTT TGT GTT TTT TGG GTA GGC

mMS-GAL3ST1-R1 AAA CCT AAT CCA TAC CCC CG

mMS-GAL3ST1-UF1 TAG TTT TTG TGT TTT TTG GGT AGG T

mMS-GAL3ST1-UR1 AAA CCT AAT CCA TAC CCC CAC

**Supplementary Table II. Differentially methylated candidate revealed in MeDIP-seq (Known genes only)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Symbol** | **Name** | **RefSeq** | **Chromosome** | **Cytoband** | **Functions** |
| *Acox2* | acyl-Coenzyme A oxidase 2, branched chain | NM\_001161667 | 14 | 14 A1 | oxidizes the coa esters of the bile acid intermediates di- and tri-hydroxycholestanoic acids. |
| *Ak4* | adenylate kinase 4 | NM\_001177602 | 4 | 4 C6 | catalyzes the reversible transfer of the terminal phosphate group between atp and amp. may also be active with gtp (by similarity). |
| *Aldh18a1* | aldehyde dehydrogenase 18 family, member A1 | NM\_019698 | 19 | 19 C3 | 3-chloroallyl aldehyde dehydrogenase activity |
| *Aldh3b1* | aldehyde dehydrogenase 3 family, member B1 | NM\_026316 | 19 | 19 A | oxidizes medium and long chain saturated and unsaturated aldehydes. |
| *Atg14* | autophagy related 14 | NM\_172599.4 | 14 | C1 | required for both basal and inducible autophagy |
| *Bmp3* | bone morphogenetic protein 3 | NM\_173404.3 | 5 | E3 | negatively regulates bone density. antagonizes the ability of certain osteogenic bmps to induce osteoprogenitor differentitation and ossification. |
| *Cdh4* | cadherin 4 | NM\_009867 | 2 | 2 H4 | cadherins are calcium dependent cell adhesion proteins. |
| *Cdh8* | cadherin 8 | NM\_001039154 | 8 | 8 D1 | cadherins are calcium dependent cell adhesion proteins |
| *Cpped1* | calcineurin-like phosphoesterase domain containing 1 | NM\_146067 | 16 | 16 A1 | hydrolase activity |
| *Cacna1d* | calcium channel, voltage-dependent, L type, alpha 1D subunit | NM\_001083616 | 14 | 14 B | voltage-sensitive calcium channels (vscc) mediate the entry of calcium ions into excitable cells and are also involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release |
| *Camk1d* | calcium/calmodulin-dependent protein kinase ID | NM\_177343 | 2 | 2 A1 | calcium/calmodulin-dependent protein kinase that operates in the calcium-triggered camkk-camk1 signaling cascade and, upon calcium influx, activates creb-dependent gene transcription |
| *Cartpt* | CART prepropeptide | NM\_001081493 | 13 | 13 | satiety factor closely associated with the actions of leptin and neuropeptide |
| *Cdk5rap2* | CDK5 regulatory subunit associated protein 2 | NM\_145990 | 4 | 4 C2 | potential regulator of cdk5 activity via its interaction with cdk5r1 |
| *Cdc42* | cell division cycle 42 homolog (S. cerevisiae) | NM\_001243769 | 4 | 4 D3 | plasma membrane-associated small gtpase which cycles between an active gtp-bound and an inactive gdp-bound state |
| *Chrdl1* | chordin-like 1 | NM\_001114385 | X | X F3 | antagonizes the function of bmp4 by binding to it and preventing its interaction with receptors |
| *Ccdc89* | coiled-coil domain containing 89 | NM\_027298 | 7 | 7 | chromosome segregation protein binding |
| *Ccbe1* | collagen and calcium binding EGF domains 1 | NM\_178793 | 18 | 18 E1 | required for lymphangioblast budding and angiogenic sprouting from venous endothelium during embryogenesis. |
| *Crebzf* | CREB/ATF bZIP transcription factor | NM\_145151 | 7 | 7 E1 | strongly activates transcription when bound to hcfc1 |
| *Cyp7b1* | cytochrome P450, family 7, subfamily b, polypeptide 1 | NM\_007825 | 3 | 3 A1 | 25-hydroxycholesterol 7alpha-hydroxylase activity |
| *Dock2* | dedicator of cyto-kinesis 2 | NM\_033374 | 11 | 11 | involved in cytoskeletal rearrangements required for lymphocyte migration in response of chemokines. activates rac1 and rac2, but not cdc42, by functioning as a guanine nucleotide exchange factor (gef), which exchanges bound gdp for free gtp. |
| *Dera* | 2-deoxyribose-5-phosphate aldolase homolog (C. elegans) | NM\_172733 | 6 | 6 G1 | catalyzes a reversible aldol reaction between acetaldehyde and d-glyceraldehyde 3-phosphate to generate 2-deoxy- d-ribose 5-phosphate (by similarity). |
| *Dnajc6* | DnaJ (Hsp40) homolog, subfamily C, member 6 | NM\_001164583 | 4 | 4 C6 | recruits hspa8/hsc70 to clathrin-coated vesicles and promotes uncoating of clathrin-coated vesicles (by similarity). |
| *Dync1i2* | dynein cytoplasmic 1 intermediate chain 2 | NM\_001198872 | 2 | 2 C2 | acts as one of several non-catalytic accessory components of the cytoplasmic dynein 1 complex that are thought to be involved in linking dynein to cargos and to adapter proteins that regulate dynein function. |
| *Fam107a* | family with sequence similarity 107, member A | NM\_183187 | 14 | 14 A1 | suppresses cell growth. may play a role in tumor development. |
| *Fam174a* | family with sequence similarity 174, member A | NM\_026321 | 1 | 1 D | unknown molecular function |
| *Fam198b* | family with sequence similarity 198, member B | NM\_133187 | 3 | 3 E3 | unknown molecular function |
| *Fam83b* | family with sequence similarity 83, member B | NM\_001045518 | 9 | 9 D | unknown molecular function |
| *Fbxw4* | F-box and WD-40 domain protein 4 | NM\_013907 | 19 | 19 C3 | probably recognizes and binds to some phosphorylated proteins and promotes their ubiquitination and degradation. may participate in wnt signaling. |
| *Fbxo34* | F-box protein 34 | NM\_001146085 | 14 | 14 C1 | substrate-recognition component of the scf (skp1-cul1-f- box protein)-type e3 ubiquitin ligase complex (by similarity). |
| *Fign* | fidgetin | NM\_021716 | 2 | 2 C1.3 | nucleoside-triphosphatase activity |
| *Foxi1* | forkhead box I1 | NM\_023907 | 11 | 11 17.0 cM | transcriptional activator required for the development of normal hearing, sense of balance and kidney function |
| *Foxk1* | forkhead box K1 | NM\_199068 | 5 | 5 G2 | transcriptional regulator that binds to the upstream enhancer region (ccac box) of myoglobin gene. has a role in myogenic differentiation and in remodeling processes of adult muscles that occur in response to physiological stimuli (by similarity). |
| *Gal3st1* | galactose-3-O-sulfotransferase 1 | NM\_001177691 | 11 | 11 A1 | catalyzes the sulfation of membrane glycolipids. |
| *Golga7b* | golgi autoantigen, golgin subfamily a, 7B | NM\_001141983 | 19 | 19 | may be involved in protein transport from golgi to cell surface (by similarity). |
| *Iyd* | iodotyrosine deiodinase | NM\_027391 | 10 | 10 A1 | catalyzes the oxidative nadph-dependent deiodination of monoiodotyrosine (l-mit) or diiodotyrosine (l-dit). |
| *Lbx1* | ladybird homeobox homolog 1 (Drosophila) | NM\_010691 | 19 | 19 | transcription factor required for the development of gabaergic interneurons in the dorsal horn of the spinal cord and migration and further development of hypaxial muscle precursor cells for limb muscles, diaphragm and hypoglossal cord (by similarity). |
| *Lman1* | lectin, mannose-binding, 1 | NM\_001172062 | 18 | 18 E1 | may recognize sugar residues of glycoproteins, glycolipids, or glycosylphosphatidyl inositol anchors and may be involved in the sorting or recycling of proteins, lipids, or both. |
| *Lrr1* | leucine rich repeat protein 1 | NM\_001081406 | 12 | 12 | may negatively regulate the 4-1bb-mediated signaling cascades which result in the activation of nk-kappab and jnk1. |
| *Lypd6* | LY6/PLAUR domain containing 6 | NM\_177139 | 2 | 2 C1.1 | modulation of calcium influx |
| *Lypd6b* | LY6/PLAUR domain containing 6B | NM\_027990 | 2 | 2 C1.1 | modulation of calcium influx |
| *Lyplal1* | lysophospholipase-like 1 | NM\_146106 | 1 | 1 H5 | does not exhibit phospholipase nor triacylglycerol lipase activity, able to hydrolyze only short chain substrates due to its shallow active site. |
| *Msr1* | macrophage scavenger receptor 1 | NM\_001113326 | 8 | 8 A4 | membrane glycoproteins implicated in the pathologic deposition of cholesterol in arterial walls during atherogenesis |
| *Mir218-2* | microRNA 218-2 | NR\_029799.1 | 11 | 11 | unknown molecular function |
| *Mir551b* | microRNA 551b | NR\_030422.1 | 3 | 3 | unknown molecular function |
| *Mid1* | midline 1 | NM\_010797 | X | X F5 and Y | may have e3 ubiquitin ligase activity which targets the catalytic subunit of protein phosphatase 2 for degradation. |
| *Morn1* | MORN repeat containing 1 | NM\_001081100 | 4 | 4 E2 | unknown molecular function |
| *Mkln1* | muskelin 1, intracellular mediator containing kelch motifs | NM\_013791 | 6 | 6 | acts as a mediator of cell spreading and cytoskeletal responses to the extracellular matrix component thrombospondin 1 (by similarity). |
| *Mdfic* | MyoD family inhibitor domain containing | NM\_175088 | 6 | 6 A1 | acts as a transcriptional activator or repressor. inhibits the transcriptional activation of zic family proteins zic1, zic2 and zic3. |
| *Ndst4* | N-deacetylase/N-sulfotransferase (heparin glucosaminyl) 4 | NM\_022565 | 3 | 3 H1 | essential bifunctional enzyme that catalyzes both the n- deacetylation and the n-sulfation of glucosamine (glcnac) of the glycosaminoglycan in heparan sulfate. |
| *Nemf* | nuclear export mediator factor | NM\_025441 | 12 | 12 | plays a role in nuclear export. |
| *Pak3* | p21 protein (Cdc42/Rac)-activated kinase 3 | NM\_001195046 | X | X F2 | serine/threonine protein kinase that plays a role in a variety of different signaling pathways including cytoskeleton regulation, cell migration, or cell cycle regulation |
| *Pde10a* | phosphodiesterase 10A | NM\_011866 | 17 | 17 A1 | plays a role in signal transduction by regulating the intracellular concentration of cyclic nucleotides. |
| *Plcl2* | phospholipase C-like 2 | NM\_013880.3 | 17 | C | may play an role in the regulation of ins(1,4,5)p3 around the endoplasmic reticulum (by similarity). |
| *Plekhg1* | pleckstrin homology domain containing, family G (with RhoGef domain) member 1 | NM\_001033253 | 10 | 10 A1 | unknown molecular function |
| *Phldb2* | pleckstrin homology-like domain, family B, member 2 | NM\_001252442 | 16 | 16 B5 | may play a role in acetyl-choline receptor (achr) aggregation in the postsynaptic membrane (by similarity). |
| *Podxl* | podocalyxin-like | NM\_013723 | 6 | 6 A3.3 | involved in the regulation of both adhesion and cell morphology and cancer progression. |
| *Kcnh7* | potassium voltage-gated channel, subfamily H (eag-related), member 7 | NM\_133207 | 2 | 2 C1.3 | pore-forming (alpha) subunit of voltage-gated potassium channel. |
| *Prrg1* | proline rich Gla (G-carboxyglutamic acid) 1 | NM\_001164275 | X | X B | proline rich Gla (G-carboxyglutamic acid) 1 |
| *P4ha2* | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide | NM\_001136076 | 11 | 11 A5-B1 | catalyzes the post-translational formation of 4- hydroxyproline in -xaa-pro-gly- sequences in collagens and other proteins. |
| *Prkg2* | protein kinase, cGMP-dependent, type II | NM\_008926 | 5 | 5 E3 | cGMP-dependent protein kinase activity |
| *Rnf32* | ring finger protein 32 | NM\_021470 | 5 | 5 B1 | may play a role in sperm formation. |
| *Sec14l4* | SEC14-like 4 (S. cerevisiae) | NM\_146013 | 11 | 11 A1 | probable hydrophobic ligand-binding protein; may play a role in the transport of hydrophobic ligands like tocopherol, squalene and phospholipids. |
| *Setd4* | SET domain containing 4 | NM\_145482 | 16 | 16 C4 | methyltransferase activity |
| *Sfi1* | Sfi1 homolog, spindle assembly associated (yeast) | NM\_030207 | 11 | 11 A1 | plays a role in the dynamic structure of centrosome- associated contractile fibers via its interaction with cetn2. |
| *Sdk1* | sidekick homolog 1 (chicken) | NM\_177879 | 5 | 5 G2 | cell adhesion protein that guides axonal terminals to specific synapses in developing neurons. |
| *Slit3* | slit homolog 3 (Drosophila) | NM\_011412 | 11 | 11 A5 | may act as molecular guidance cue in cellular migration |
| *Smad3* | MAD homolog 3 (Drosophila) | NM\_016769 | 9 | 9 D | receptor-regulated smad (r-smad) that is an intracellular signal transducer and transcriptional modulator activated by tgf-beta (transforming growth factor) and activin type 1 receptor kinases |
| *Smad2* | SMAD homolog2 | NM\_001252481 | 18 | E3 | receptor-regulated smad (r-smad) that is an intracellular signal transducer and transcriptional modulator activated by tgf-beta (transforming growth factor) and activin type 1 receptor kinases |
| *Slc15a5* | solute carrier family 15, member 5 | NM\_177787 | 6 | 6 G1 | proton oligopeptide cotransporter  (potential). |
| *Slc25a12* | solute carrier family 25 (mitochondrial carrier, Aralar), member 12 | NM\_172436 | 2 | 2 C2 | catalyzes the calcium-dependent exchange of cytoplasmic glutamate with mitochondrial aspartate across the mitochondrial inner membrane. |
| *Sp110* | Sp110 nuclear body protein | NM\_030194 | 1 | 1 C5 | transcription factor |
| *She* | src homology 2 domain-containing transforming protein E | NM\_172530.3 | 3 | F1 | unknown molecular function |
| *Sox5* | SRY-box containing gene 5 | NM\_001113559 | 6 | 6 G3 | binds specifically to the dna sequence 5'-aacaat-3'. |
| *Stxbp5* | syntaxin binding protein 5 (tomosyn) | NM\_001081344 | 10 | 10 | plays a regulatory role in calcium-dependent exocytosis and neurotransmitter release. |
| *Tlx1* | T cell leukemia, homeobox 1 | NM\_021901 | 19 | 19 C3 | controls the genesis of the spleen. binds to the dna sequence 5'-ggcggtaagtgg-3'. |
| *Tfap2a* | transcription factor AP-2, alpha | NM\_001122948 | 13 | 13 A5-B1 | sequence-specific dna-binding protein that interacts with inducible viral and cellular enhancer elements to regulate transcription of selected genes |
| *Tgfb2* | transforming growth factor, beta 2 | NM\_009367 | 1 | 1 H5 | tgf-beta 2 has suppressive effects on interleukin-2 dependent t-cell growth. |
| *Trpm2* | transient receptor potential cation channel, subfamily M, member 2 | NM\_138301 | 10 | 10 C1 | nonselective, voltage-independent cation channel mediating sodium and calcium ion influx. |
| *Usp24* | ubiquitin specific peptidase 24 | NM\_183225.2 | 4 | C7 | involved in the ubiquitin-dependent proteolytic pathway in conjunction with the 26s proteasome (by similarity). |
| *Unc93b1* | unc-93 homolog B1 (C. elegans) | NM\_001161428 | 19 | 19 A | plays an important role in innate and adaptive immunity by regulating nucleotide-sensing toll-like receptor (tlr) signaling. |
| *Vps13a* | vacuolar protein sorting 13A (yeast) | NM\_173028 | 19 | 19 B | may play a role in the control of protein cycling through the trans-golgi network to early and late endosomes, lysosomes and plasma membrane. |
| *Ski* | ski sarcoma viral oncogene homolog | NM\_011385.2 | 4 | E2 | may play a role in terminal differentiation of skeletal muscle cells but not in the determination of cells to the myogenic lineage. functions as a repressor of tgf-beta signaling. |
| *Ypel5* | yippee-like 5 (Drosophila) | NM\_027166 | 17 | 17 | involved in cell cycle progression |
| *Zc3h15* | zinc finger CCCH-type containing 15 | NM\_026934 | 2 | 2 | protects drg1 from proteolytic degradation (by similarity). |