Fifty top up-regulated genes at 4ºC in the tPVAT.

| Sequence ID | Gene symbol | Gene name | p-value | Fold change |
|---|---|---|---|---|
| Carbohydrate metabolism | | | | |
| XM_004773546.1 | *Galnt15* | *Polypeptide N-Acetylgalactosaminyltransferase 15* | 5.38E-03 | 4.86 |
| XM_004741919.1 | *Cav1* | *Caveolin 1* | 1.07E-03 | 3.44 |
| Cell cycle | | | | |
| XM_004741923.1 | *Cav2* | *Caveolin 2* | 1.33E-03 | 3.42 |
| XM_004780198.1 | *Cebpd* | *Ccaat/Enhancer Binding Protein (C/Ebp), Delta* | 2.50E-03 | 2.76 |
| XM_004740346.1 | *Ctgf* | *Connective Tisuue Growth Factor* | 3.87E-03 | 3.08 |
| XM_004768767.1 | *Errfi1* | *Erbb Receptor Feedback Inhibitor 1* | 4.51E-03 | 3.50 |
| XM_004737947.1 | *Ghr* | *Growth Hormone Receptor* | 5.30E-03 | 3.09 |
| XM_004758546.1 | *Ndrg2* | *Ndrg Family Member 2* | 7.65E-03 | 2.91 |
| XM_004765797.1 | *Adirf* | *Adipogenesis Regulatory Factor* | 2.76E-02 | 2.68 |
| Cell differentiation and development | | | | |
| XM_004755807.1 | *Gprc5a* | *G Protein-Coupled Receptor, Class C, Group 5, Member A* | 9.84E-03 | 3.56 |
| XM_004782340.1 | *Loc101676727* | *Cytochrome P450 3a12-Like* | 3.02E-03 | 3.74 |
| Cell protection | | | | |
| XM_004744215.1 | *Loc101680117* | *Metallothionein-1e-Like* | 2.51E-03 | 4.61 |
| XM_004766404.1 | *Loc101687859* | *Selenoprotein M* | 6.16E-03 | 2.76 |
| XM_004757964.1 | *Loc101692625* | *Metallothionein-1e Pseudogene* | 2.17E-03 | 5.33 |
| XM_004762982.1 | *Gadd45a* | *Growth Arrest And Dna Damage Inducible Alpha* | 3.79E-03 | 2.74 |
| Cell stress response | | | | |
| XM_004740244.1 | *Sgk1* | *Serum/Glucocorticoid Regulated Kinase 1* | 1.34E-05 | 4.85 |
| XM_004774974.1 | *Cyth3* | *Cytohesin 3* | 7.87E-05 | 2.93 |
| Cell trafficking | | | | |
| XM_004764475.1 | *Fcho2* | Fch Domain Only 2 | 9.42E-04 | 2.63 |
| XM_004743651.1 | *Mal2* | *Mal, T-Cell Differentiation Protein 2* | 4.57E-02 | 3.71 |
| XM_004766342.1 | *Scarb2* | *Scavenger Receptor Class B, Member 2* | 2.12E-03 | 2.84 |
| XM_004753054.1 | *Il1r2* | *Interleukin 1 Receptor, Type Ii* | 3.45E-05 | 4.29 |
| Immune response | | | | |
| XM_004771986.1 | *Nfkbiz* | *Nuclear Factor Of Kappa Light Polypeptide Gene Enhancer In B Cells Inhibitor, Zeta* | 7.23E-03 | 2.84 |
| XM_004739946.1 | *Trem2* | *Triggering Receptor Expressed On Myeloid Cells 2* | 1.58E-02 | 2.73 |
| XM_004747736.1 | *Abca1* | *Atp-Binding Cassette, Subfamily A (Abc1), Member 1* | 7.23E-03 | 3.33 |
| Lipid metabolism | | | | |
| XM_004743410.1 | *Dgkb* | *Diacylglycerol Kinase, Beta* | 1.56E-02 | 2.80 |
| XM_004774219.1 | *Fabp4* | *Fatty Acid Binding Protein 4, Adipocyte* | 1.38E-02 | 2.95 |
| XM_004771705.1 | *Retn* | *Resistin* | 2.84E-03 | 2.72 |
| XM_004766965.1 | *Atp6v0d2* | *Atpase, H+ Transporting, Lysosomal V0 Subunit D2* | 1.02E-02 | 2.72 |
| Others | | | | |
| XM_004780129.1 | *Amy2a* | *Amylase, alpha 2A* | 1.24E-03 | 2.92 |
| XM_004776777.1 | *Ctsk* | *Cathepsin K* | 9.26E-03 | 3.92 |
| XM_004755799.1 | *Emp1* | *Epithelial Membrane Protein 1* | 3.47E-02 | 3.52 |
| XM_004766844.1 | *F2rl2* | *Coagulation Factor Ii (Thrombin) Receptor-Like 2* | 2.39E-03 | 4.06 |
| XM_004752563.1 | *F3* | *Coagulation Factor Iii (Thromboplastin, Tissue Factor)* | 6.46E-05 | 4.06 |
| XM_004755885.1 | *Fibin* | *Fin Bud Initiation Factor Homolog (Zebrafish)* | 4.13E-04 | 3.26 |
| XM_004775062.1 | *Klf5* | *Kruppel-Like Factor 5 (Intestinal)* | 2.73E-02 | 3.41 |
| XM_004769265.1 | *Pam* | *Peptidylglycine Alpha-Amidating Monooxygenase* | 8.35E-04 | 2.82 |
| XM_004767845.1 | *Pdk4* | *Pyruvate Dehydrogenase Kinase, Isozyme 4* | 6.41E-03 | 5.73 |
| XM_004759991.1 | *Rbbp8nl* | *Rbbp8 N-Terminal Like* | 1.88E-03 | 3.56 |
| XM_004737647.1 | *Wwc1* | *Ww And C2 Domain Containing 1* | 2.85E-03 | 2.98 |
| XM_004760169.1 | *Dhrs7c* | Dehydrogenase/Reductase (Sdr Family) Member 7c | 4.41E-02 | 2.58 |
| Redox metabolism | | | | |
| XM_004756692.1 | *Fmo2* | *Flavin Containing Monooxygenase 2* | 7.37E-03 | 2.94 |
| XM_004761383.1 | *Upk1b* | Uroplakin 1b | 5.50E-03 | 2.57 |
| Signal transduction | | | | |
| XM_004741918.1 | *Met* | *Met Proto-Oncogen* | 2.17E-03 | 3.05 |
| XM_004772400.1 | *Dst* | *Dystonin* | 7.30E-04 | 3.60 |
| Structure/cytoskeleton | | | | |
| XM_004742842.1 | *Lama3* | *Laminin, Alpha 3* | 5.56E-03 | 3.14 |
| XM_004761362.1 | *Lox* | *Lysyl Oxidase* | 3.94E-03 | 2.75 |
| XM_004766755.1 | *Myom2* | *Myomesin 2* | 2.71E-02 | 2.76 |
| XM_004756105.1 | *Spp1* | *Secreted Phosphoprotein 1* | 7.16E-03 | 3.39 |
| Unknown | | | | |
| XM_004777698.1 | *Loc101672612* | Chromosome Unknown Open Reading Frame, Human C8orf4 | 1.46E-03 | 2.63 |
| XM_004764364.1 | *Loc101686598* | *Chromosome Unknown Open Reading Frame, Human C2orf40* | 1.90E-02 | 3.09 |

Fity top down-regulated genes at 4ºC in the tPVAT.

| Sequence ID | Gene symbol | Gene name | p-value | Fold change |
|---|---|---|---|---|
| Cell cycle | | | | |
| XM_004737693.1 | *Ccnjl* | *Cyclin J-Like* | 8.35E-04 | -7.68 |
| XM_004766651.1 | *Cdca3* | *Cell Division Cycle Associated 3* | 1.22E-03 | -4.61 |
| XM_004740751.1 | *Cdca8* | *Cell Division Cycle Associated 8* | 3.79E-04 | -4.44 |
| XM_004774496.1 | *Cdkn2c* | *Cyclin-Dependent Kinase Inhibitor 2c (P18, Inhibits Cdk4)* | 2.05E-04 | -5.05 |
| XM_004741203.1 | *E2f2* | *E2f Transcription Factor 2* | 3.77E-05 | -4.40 |
| XM_004740483.1 | *Kif2c* | *Kinesis Family Member 2 C* | 4.35E-04 | -5.06 |
| XM_004751880.1 | *Mki67* | *Antigen Identified By Monoclonal Antibody Ki-67* | 4.88E-04 | -6.53 |
| XM_004745791.1 | *Rrm2* | *Ribonucleotide Reductase M2* | 9.91E-04 | -4.66 |
| XM_004748404.1 | *Spc24* | *Spc24, Ndc80 Kinetochore Complex Component* | 1.07E-03 | -4.82 |
| XM_004741128.1 | *Stmn1* | *Stathmin1* | 3.14E-03 | -5.62 |
| XM_004742802.1 | *Tyms* | *Thymidylate Synthetase* | 3.77E-04 | -4.62 |
| XM_004771486.1 | *Uhrf1* | *Ubiquitin-Like With Phd And Ring Finger Domain 1* | 5.42E-03 | -6.10 |
| Immune response | | | | |
| XM_004771683.1 | *Ccl25* | *Chemokine (C-C Motif) Ligand 25* | 3.29E-03 | -6.86 |
| XM_004760815.1 | *Ccr9* | *Chemokine (C-C Motif) Receptor 9* | 7.86E-03 | -7.07 |
| XM_004775803.1 | *Cd1d* | *Cd1d Molecule* | 8.33E-03 | -7.81 |
| XM_004775804.1 | *Cd1e* | *Cd1e Molecule* | 5.26E-03 | -5.60 |
| XM_004749949.1 | *Cd3g* | *Cd3g Molecule, Gamma (Cd3-Tcr Complex)* | 2.12E-02 | -4.94 |
| XM_004741105.1 | *Cd52* | *Cd52 Molecule* | 2.69E-03 | -6.13 |
| XM_004742367.1 | *Cd8a* | *Cd8a Molecule* | 1.87E-02 | -5.42 |
| XM_004762280.1 | *Itgb2* | *Integrin, Beta 2 (Complement Component 3 Receptor 3 And 4 Subunit)* | 1.50E-02 | -4.57 |
| XM_004740918.1 | *Lck* | *Lymphocyte-Specific Protein Tyrosine Kinase* | 7.00E-03 | -5.35 |
| XM_004775799.1 | *Loc101690640* | *T-Cell Surface Glycoprotein Cd1a-Like* | 3.52E-03 | -7.85 |
| XM_004778740.1 | *Prss16* | *Protease, Serine 16 (Thymus)* | 9.38E-03 | -9.75 |
| XM_004739882.1 | *Ptcra* | *Pre T-Cell Antigen Receptor Alpha* | 2.72E-03 | -7.42 |
| XM_004756002.1 | *Rag1* | *Recombination Activating Gene 1* | 1.26E-02 | -7.63 |
| XM_004756007.1 | *Rag2* | *Recombination Activating Gene 2* | 8.93E-03 | -5.74 |
| XM_004769506.1 | *Tbata* | *Thymus, Brain And Testes Associated* | 5.53E-04 | -9.81 |
| XM_004740174.1 | *Themis* | *Thymocyte Selection Associated* | 8.36E-03 | -4.93 |
| Lipid metabolism | | | | |
| XM_004773512.1 | *Dgkd* | *Diacylglycerol Kinase, Delta* | 1.82E-03 | -4.48 |
| XM_004748113.1 | *Loc101691931* | *Cytochrome P450 2u1-Like* | 7.29E-03 | -5.76 |
| Others | | | | |
| XM_004741734.1 | *Akr1b1* | *Ldo-Keto Reductase Family 1, Member B1 (Aldose Reductase)* | 3.83E-03 | -6.46 |
| XM_004741682.1 | *Atp6v0a4* | *Atpare, H+ Transporting, Lysosomal V0 Subunit A4* | 5.70E-04 | -5.41 |
| XM_004768567.1 | *Cdh17* | *Cadherin 17* | 2.00E-03 | -5.79 |
| XM_004738703.1 | *Chchd6* | *Coiled-Coil-Helix-Coiled-Coil-Helix Domain* | 2.22E-03 | -4.87 |
| XM_004749590.1 | *Dntt* | *Dna Nucleotidylexotransferase* | 1.29E-02 | -5.76 |
| XM_004770551.1 | *Drd5* | *Dopamine Receptor D5* | 2.76E-03 | -5.00 |
| XM_004774882.1 | *Loc101676398* | *Phytanoyl-Coa Dioxygenase, Peroxisomal -Like* | 1.28E-03 | -6.53 |
| XM_004778790.1 | *Loc101683777* | *Histone H4 Type Viii-Like* | 8.09E-03 | -5.12 |
| XM_004781521.1 | *Loc101690749* | *Histone H4-Like* | 6.50E-03 | -5.20 |
| XM_004782596.1 | *Loc101690963* | *Phytanoyl-Coa Dioxygenase, Peroxisomal-Like* | 1.54E-03 | -6.01 |
| XM_004774884.1 | *Phyh* | *Phytanoyl-Coa 2-Hydroxylase* | 5.60E-04 | -5.88 |
| XM_004743585.1 | *Sla* | *Src-Like-Adaptor* | 1.82E-02 | -5.29 |
| Protein metabolism/degradation | | | | |
| XM_004754074.1 | *Ctrb1* | *Chymotrypsinogen B1* | 6.23E-03 | -6.11 |
| XM_004750821.1 | *Loc101674311* | *Putative Serine Protease 29-Like* | 1.24E-03 | -7.01 |
| XM_004742552.1 | *Serpind1* | *Serpin Peptidase Inhibitor, Clade D (Heparin Cofactor), Member 1* | 3.86E-04 | -4.63 |
| XM_004746330.1 | *Ube2c* | *Ubiquitin-Conjudatng Enzyme E2c* | 4.78E-04 | -4.87 |
| Signal transduction | | | | |
| XM_004743172.1 | *Rac2* | *Ras-Related C3 Botulinum Substrate 2* | 2.24E-02 | -4.50 |
| XM_004767912.1 | *Rgs16* | *Regulator Of G-Protein Signaling 16* | 3.44E-03 | -4.69 |
| Unknown | | | | |
| XM_004778789.1 | *Loc101683478* | *Uncharacterized* | 9.84E-03 | -9.84 |
| XM_004754742.1 | *Loc101694602* | *Uncharacterized* | 4.52E-04 | -5.57 |

Fifty top up-regulated genes at 4ºC in the IAT.

| Sequence ID | Gene symbol | Gene name | p-value | Fold change |
|---|---|---|---|---|
| Amino acid metabolism | | | | |
| XM_004757114.1 | *Ass1* | *Argininosuccinate Synthase 1* | 6.19E-03 | 4.53 |
| XM_004763011.1 | *Cth* | *Cystathionase (Cystathionine Gamma-Lyase)* | 1.79E-02 | 3.00 |
| XM_004767902.1 | *Glul* | *Glutamate-Ammonia Ligase* | 2.32E-02 | 2.43 |
| Calcium transport | | | | |
| XM_004763794.1 | *Alpk3* | *Alpha-Kinase 3* | 3.91E-02 | 3.20 |
| XM_004773978.1 | *Atp2a1* | *Atpase, Ca++ Transporting, Cardiac Muscle, Fast Twitch 1* | 4.40E-02 | 2.83 |
| XM_004756257.1 | *Cacna1s* | *Calcium Channel, Voltage-Dependent, L Type, Alpha 1S Subunit* | 4.67E-02 | 4.64 |
| XM_004743708.1 | *Ramp1* | *Receptor (G Protein-Coupled) Activity Modifying Protein 1* | 3.99E-02 | 2.49 |
| XM_004740339.1 | *Trdn* | *Triadin* | 2.81E-02 | 3.18 |
| Cell protection | | | | |
| XM_004769485.1 | *Ddit4* | *DNA-Damage-Inducible Transcript 4* | 2.12E-02 | 2.59 |
| XM_004778803.1 | *Gadd45g* | *Growth Arrest And DNA-Damage-Inducible, Gamma* | 2.68E-02 | 3.47 |
| XM_004757923.1 | *Net1* | *Neuroepithelial Cell Transforming 1* | 5.40E-03 | 3.36 |
| XM_004749869.1 | *Nnmt* | *Nicotinamide N-Methyltransferase* | 4.74E-03 | 2.44 |
| Electron transport chain in mitochondria/oxidative phosphorylation | | | | |
| XM_004762520.1 | *Loc101690488* | *Cytochrome C-Like* | 2.43E-02 | 2.68 |
| XM_004756805.1 | *Loc101686662* | *Cytochrome C Oxidase Protein 20 Homolog* | 3.94E-02 | 2.39 |
| XM_004781049.1 | *Loc101674825* | *Cytochrome C Oxidase Subunit 8B, Mitochondrial-Like* | 4.42E-02 | 3.22 |
| XM_004757734.1 | *Slc25a4* | *Solute Carrier Family 25, Member 4* | 2.29E-02 | 2.44 |
| FA transport | | | | |
| XM_004740951.1 | *Fabp3* | *Fatty Acid Binding Protein 3, Muscle And Heart* | 1.57E-02 | 3.10 |
| XM_004767850.1 | *Pon3* | *Paraoxonase 3* | 1.44E-04 | 6.74 |
| Gene expression regulation | | | | |
| XM_004780198.1 | *Cebpd* | *CCAAT/Enhancer Binding Protein (C/EBP), Delta* | 3.91E-02 | 2.43 |
| XM_004740700.1 | *Heyl* | *Hairy/Enhancer-Of-Split Related With YRPW Motif-Like* | 3.21E-02 | 2.38 |
| XM_004743220.1 | *Maff* | *V-Maf Avian Musculoaponeurotic Fibrosarcoma Oncogene Homolog F* | 4.69E-02 | 2.36 |
| XM_004781266.1 | *Myf6* | *Myogenic Factor 6* | 2.26E-02 | 2.72 |
| Ion transport | | | | |
| XM_004762066.1 | *Atp1b4* | *Atpase, (Na+)/K+ Transporting, Beta 4 Polypeptide* | 3.99E-02 | 3.75 |
| XM_004750299.1 | *Tmc5* | *Transmembrane Channel-Like 5* | 4.22E-04 | 3.59 |
| Others | | | | |
| XM_004751192.1 | *Capn3* | *Calpain 3* | 2.91E-02 | 2.96 |
| XM_004759150.1 | *Ckmt2* | *Creatine Kinase, Mitochondrial 2, Sarcomeric* | 1.97E-02 | 4.07 |
| XM_004770688.1 | *Fkbp5* | *FK506 Binding Protein 5* | 6.83E-03 | 3.10 |
| XM_004752563.1 | *F3* | *Coagulation Factor III (Thromboplastin, Tissue Factor)* | 1.51E-02 | 3.32 |
| XM_004741401.1 | *Hspb7* | *Heat Shock Protein Family, Member 7 (Cardiovascular)* | 2.52E-02 | 7.24 |
| XM_004738170.1 | *Itih4* | *Inter-Alpha-Trypsin Inhibitor Heavy Chain Family Member 4* | 2.15E-02 | 2.34 |
| XM_004743718.1 | *Klhl30* | *Kelch-Like Family Member 30* | 2.98E-02 | 4.66 |
| XM_004770231.1 | *Loc101676773* | *HRAS-Like Suppressor 3* | 2.06E-02 | 2.34 |
| XM_004757964.1 | *Loc101692625* | *Metallothionein-1-Like* | 4.64E-02 | 5.45 |
| XM_004755129.1 | *Loc101674041* | *Putative G Antigen Family E Member 3-Like* | 4.23E-02 | 2.36 |
| XM_004741999.1 | *Loc101681100* | *Transmembrane Protein 229A-Like* | 8.19E-03 | 2.37 |
| XM_004755772.1 | *Pde6h* | *Phosphodiesterase 6H, Cgmp-Specific, Cone, Gamma (Pde6h), Mrna* | 2.90E-02 | 2.82 |
| XM_004777369.1 | *Rasgef1b* | *Rasgef Domain Family, Member 1B* | 1.56E-02 | 2.65 |
| XM_004750746.1 | *Rpl3l* | *Ribosomal Protein L3-Like* | 1.18E-02 | 2.68 |
| XM_004769189.1 | *Smpx* | *Small Muscle Protein, X-Linked* | 4.32E-02 | 6.00 |
| XM_004768064.1 | *Ucp3* | *Uncoupling Protein 3 (Mitochondrial, Proton Carrier)* | 1.03E-02 | 3.06 |
| Signal transduction | | | | |
| XM_004775565.1 | *Asb5* | *Ankyrin Repeat And SOCS Box-Containing 5* | 3.08E-02 | 3.72 |
| XM_004775460.1 | *Mapk12* | *Mitogen-Activated Protein Kinase 12* | 2.03E-02 | 2.43 |
| XM_004756052.1 | *Pdlim5* | *PDZ And LIM Domain 5* | 1.77E-02 | 3.50 |
| XM_004740244.1 | *Sgk1* | *Serum/Glucocorticoid Regulated Kinase 1* | 3.66E-02 | 2.65 |
| XM_004746413.1 | *Sgk2* | *Serum/Glucocorticoid Regulated Kinase 2* | 1.43E-02 | 2.74 |
| Structure/cytoskeleton | | | | |
| XM_004774791.1 | *Actn2* | *Actinin Alpha 2* | 3.69E-02 | 7.62 |
| XM_004741862.1 | *Lmod2* | *Leiomodin 2 (Cardiac)* | 3.68E-02 | 7.05 |
| XM_004747997.1 | *Myoz2* | *Myozenin 2* | 1.07E-02 | 4.93 |
| XM_004776741.1 | *Tmod4* | *Tropomodulin 4* | 4.88E-02 | 3.33 |
| XM_004744005.1 | *Xirp2* | *Xin Actin-Binding Repeat Containing 2* | 1.58E-02 | 5.56 |

Fifty top down-regulated genes at 4ºC in the IAT.

| Sequence ID | Gene symbol | Gene name | p-value | Fold change |
|---|---|---|---|---|
| Cell cycle | | | | |
| XM_004772789.1 | *Fstl1* | *Follistatin-Like 1* | 1.73E-03 | -2.22 |
| XM_004742992.1 | *Igf1* | *Insulin-Like Growth Factor 1* | 4.76E-03 | -2.97 |
| Cell differentiation and development | | | | |
| XM_004772230.1 | *Cpz* | *Carboxypeptidase Z* | 5.52E-04 | -4.32 |
| XM_004739323.1 | *Dact1* | *Dishevelled-Binding Antagonist Of Beta-Catenin 1* | 8.43E-04 | -2.36 |
| XM_004746553.1 | *Gdf5* | *Growth Differentiation Factor 5* | 5.21E-03 | -2.97 |
| XM_004749459.1 | *Kazald1* | *Kazal-Type Serine Peptidase Inhibitor Domain 1* | 8.24E-03 | -2.22 |
| XM_004754862.1 | *Loc101677386* | *Protein Delta Homolog 1-Like* | 9.74E-03 | -2.52 |
| XM_004761315.1 | *Nrep* | *Neuronal Regeneration Related Protein* | 5.91E-04 | -2.25 |
| XM_004772002.1 | *Sfrp2* | *Secreted Frizzled-Related Protein 2* | 1.03E-02 | -3.97 |
| XM_004739496.1 | *Sfrp4* | *Secreted Frizzled-Related Protein 4* | 4.49E-02 | -2.53 |
| XM_004740360.1 | *Trabd2b* | *Trab Domain Containing 2B* | 6.23E-03 | -2.38 |
| XM_004741795.1 | *Kcp* | *Kielin/Chordin-Like Protein* | 7.26E-04 | -2.60 |
| XM_004739586.1 | *Lrrc17* | *Leucine Rich Repeat Containing 17* | 2.80E-03 | -2.80 |
| Food intake control | | | | |
| XM_004754240.1 | *Cck* | *Cholecystokinin* | 6.93E-03 | -4.64 |
| XM_004741831.1 | *Lep* | *Leptin* | 1.84E-02 | -4.28 |
| Others | | | | |
| XM_004757188.1 | *Cercam* | *Cerebral Endothelial Cell Adhesion Molecule* | 1.53E-03 | -2.39 |
| XM_004763149.1 | *Creb3l1* | *Camp Responsive Element Binding Protein 3-Like 1* | 4.27E-03 | -2.88 |
| XM_004741584.1 | *Loc101682426* | *Family with sequence similarity 43, member B* | 1.46E-02 | -2.23 |
| XM_004765489.1 | *Qpct* | *Glutaminyl-Peptide Cyclotransferase* | 1.46E-03 | -2.35 |
| XM_004769061.1 | *Rgag1* | *Retrotransposon Gag Domain Containing 1* | 3.31E-02 | -3.04 |
| XM_004754890.1 | *Srpx* | *Srpxsushi-Repeat-Containing Protein, X-Linked* | 1.31E-03 | -2.27 |
| XM_004779817.1 | *Loc101684445* | *Leukocyte Immunoglobulin-Like Receptor Subfamily A Member 6* | 1.70E-02 | -2.22 |
| Signal transduction | | | | |
| XM_004743168.1 | *C1qtnf6* | *C1q And Tumor Necrosis Factor Related Protein 6* | 3.53E-03 | -2.33 |
| XM_004741223.1 | *Ephb2* | *Eph Receptor B2* | 6.31E-03 | -2.22 |
| XM_004771853.1 | *Klhl31* | *Kelch-Like Family Member 31* | 1.17E-02 | -2.75 |
| XM_004739125.1 | *Tshr* | *Thyroid Stimulating Hormone Receptor* | 2.11E-02 | -3.75 |
| Structure/cytoskeleton | | | | |
| XM_004758676.1 | *Cilp* | *Cartilage Intermediate Layer Protein, Nucleotide Pyrophosphohydrolase* | 1.89E-03 | -3.13 |
| XM_004743495.1 | *Col14a1* | *Collagen, Type XIV, Alpha 1* | 4.70E-04 | -2.99 |
| XM_004740947.1 | *Col16a1* | *Collagen, Type XVI, Alpha 1* | 4.48E-03 | -2.46 |
| XM_004763363.1 | *Col3a1* | *Collagen, Type III, Alpha 1* | 1.93E-04 | -8.58 |
| XM_004743676.1 | *Col6a3* | *Collagen, Type VI, Alpha 3* | 6.77E-03 | -2.31 |
| XM_004759996.1 | *Col9a3* | *Collagen, Type IX, Alpha 3* | 1.99E-03 | -2.26 |
| XM_004768864.1 | *Cthrc1* | *Collagen Triple Helix Repeat Containing 1* | 3.34E-03 | -3.55 |
| XM_004748554.1 | *Dcn* | *Decorin* | 4.49E-03 | -2.53 |
| XM_004772734.1 | *Fkbp10* | *FK506 Binding Protein 10* | 2.71E-03 | -2.40 |
| XM_004756352.1 | *Fmod* | *Fibromodulin* | 6.11E-03 | -2.76 |
| XM_004766993.1 | *Fn1* | *Fibronectin 1* | 1.78E-03 | -3.62 |
| XM_004764820.1 | *Loc101686788* | *Collagen Alpha-1(I) Chain-Like* | 6.74E-03 | -4.41 |
| XM_004767862.1 | *Loc101690329* | *Collagen Alpha-2(I) Chain-Like* | 7.40E-04 | -6.23 |
| XM_004763267.1 | *Loxl2* | *Lysyl Oxidase-Like 2* | 1.03E-03 | -2.52 |
| XM_004748555.1 | *Lum* | *Lumican* | 1.27E-04 | -6.00 |
| XM_004752504.1 | *Mfap5* | *Microfibrillar Associated Protein 5* | 2.84E-02 | -2.26 |
| XM_004781342.1 | *Mmp23b* | *Matrix Metallopeptidase 23B* | 1.60E-03 | -2.36 |
| XM_004775945.1 | *Mpz* | *Myelin Protein Zero* | 9.73E-04 | -4.06 |
| XM_004749294.1 | *Mrc2* | *Mannose Receptor, C Type 2* | 1.57E-03 | -2.68 |
| XM_004761526.1 | *Pcolce* | *Procollagen C-Endopeptidase Enhancer* | 1.74E-03 | -3.24 |
| XM_004779534.1 | *Postn* | *Periostin, Osteoblast Specific Factor* | 6.20E-04 | -4.88 |
| XM_004768014.1 | *Serpinh1* | *Serpin Peptidase Inhibitor, Clade H (Heat Shock Protein 47), Member 1, (Collagen Binding Protein 1)* | 2.64E-03 | -2.68 |
| XM_004778593.1 | *Thbs3* | *Thrombospondin 3* | 4.35E-04 | -2.64 |
| Unknown | | | | |
| XM_004753470.1 | *Loc101686176* | *Uncharacterized LOC101686176* | 1.18E-02 | -2.35 |