**Table S3:** Links to enriched GO terms for clusters and lists of genes in these clusters.

# Cluster 1

## Enriched Terms:

| Gene to GO BP Conditional test for over-representation GOBPID | Pvalue | OddsRatio | ExpCount | Count | Size | Term |
|---|---|---|---|---|---|---|
| **GO:0043436** | 0 | 2,017 | 26 | 43 | 181 | oxoacid metabolic process |
| **GO:0044248** | 0 | 1,844 | 35 | 53 | 241 | cellular catabolic process |
| **GO:0006399** | 0,001 | 3,693 | 5 | 12 | 32 | tRNA metabolic process |
| **GO:0006520** | 0,001 | 2,591 | 9 | 19 | 66 | cellular amino acid metabolic process |
| **GO:0006418** | 0,002 | 3,827 | 4 | 10 | 26 | tRNA aminoacylation for protein translation |
| **GO:0043038** | 0,002 | 3,827 | 4 | 10 | 26 | amino acid activation |
| **GO:0006166** | 0,003 | Inf | 0 | 3 | 3 | purine ribonucleoside salvage |
| **GO:0043086** | 0,003 | 2,445 | 9 | 17 | 60 | negative regulation of catalytic activity |
| **GO:0010033** | 0,003 | 1,695 | 31 | 45 | 220 | response to organic substance |
| **GO:0046686** | 0,003 | 3,209 | 5 | 11 | 32 | response to cadmium ion |
| **GO:0070647** | 0,004 | 2,176 | 12 | 21 | 81 | protein modification by small protein conjugation or removal |
| **GO:0044282** | 0,004 | 1,958 | 16 | 26 | 109 | small molecule catabolic process |
| **GO:0006584** | 0,005 | 12,075 | 1 | 4 | 6 | catecholamine metabolic process |
| **GO:0018958** | 0,005 | 12,075 | 1 | 4 | 6 | phenol-containing compound metabolic process |
| **GO:0034311** | 0,005 | 12,075 | 1 | 4 | 6 | diol metabolic process |
| **GO:0006749** | 0,006 | 5,198 | 2 | 6 | 13 | glutathione metabolic process |
| **GO:0043200** | 0,006 | 5,198 | 2 | 6 | 13 | response to amino acid stimulus |
| **GO:0042176** | 0,006 | 4,253 | 2 | 7 | 17 | regulation of protein catabolic process |
| **GO:0000910** | 0,007 | 2,573 | 6 | 13 | 44 | cytokinesis |
| **GO:0043523** | 0,008 | 3,227 | 4 | 9 | 26 | regulation of neuron apoptosis |
| **GO:0010243** | 0,008 | 2,624 | 6 | 12 | 40 | response to organic nitrogen |
| **GO:0006144** | 0,008 | 6,049 | 1 | 5 | 10 | purine base metabolic process |
| **GO:0010038** | 0,008 | 2,393 | 7 | 14 | 51 | response to metal ion |
| **GO:0009636** | 0,008 | 3,476 | 3 | 8 | 22 | response to toxin |
| **GO:0016055** | 0,009 | 4,545 | 2 | 6 | 14 | Wnt receptor signaling pathway |
| **GO:0006725** | 0,009 | 2,689 | 5 | 11 | 36 | cellular aromatic compound metabolic process |
| **GO:0044106** | 0,01 | 5,432 | 1 | 5 | 11 | cellular amine metabolic process |

## Genes in Cluster:

| Entrez Id | Symbol | description |
|---|---|---|
| 607306 | VPS4B | vacuolar protein sorting 4 homolog B (S. cerevisiae) |
| 474394 | RAB5B | RAB5B, member RAS oncogene family |
| 483970 | TXNL1 | thioredoxin-like 1 |
| 481459 | LOC481459 | similar to sequestosome 1 |

|  |  |  |
|---|---|---|
| 476242 | PCMT1 | protein-L-isoaspartate (D-aspartate) O-methyltransferase |
| 475043 | HRSP12 | heat-responsive protein 12 |
| 481486 | ALDH7A1 | aldehyde dehydrogenase 7 family, member A1 |
| 474844 | CSNK2B | casein kinase 2, beta polypeptide |
| 474847 | CLIC1 | chloride intracellular channel 1 |
| 481716 | VARS | valyl-tRNA synthetase |
| 484056 | EZR | ezrin |
| 475073 | NUDCD1 | NudC domain containing 1 |
| 484063 | ACAT2 | acetyl-CoA acetyltransferase 2 |
| 475081 | EIF3H | eukaryotic translation initiation factor 3, subunit H |
| 474484 | LOC474484 | similar to NHP2-like protein 1 (High mobility group-like nuclear protein 2 homolog 1) ([U4/U6.U5] tri-snRNP 15.5 kDa protein) (Sperm specific antigen 1) (Fertilization antigen 1) (FA-1) |
| 474487 | ACO2 | aconitase 2, mitochondrial |
| 482049 | NDRG1 | N-myc downstream regulated 1 |
| 475116 | TSTA3 | tissue specific transplantation antigen P35B |
| 607245 | PUF60 | poly-U binding splicing factor 60KDa |
| 475189 | COPG2 | coatomer protein complex, subunit gamma 2 |
| 474894 | GLO1 | glyoxalase I |
| 607816 | UBE2H | ubiquitin-conjugating enzyme E2H |
| 474712 | PSIP1 | PC4 and SFRS1 interacting protein 1 |
| 476318 | PSAT1 | phosphoserine aminotransferase 1 |
| 484161 | OSTF1 | osteoclast stimulating factor 1 |
| 482283 | CROT | carnitine O-octanoyltransferase |
| 474912 | POLR1C | polymerase (RNA) I polypeptide C, 30kDa |
| 403854 | TJP2 | tight junction protein 2 (zona occludens 2) |
| 474536 | TXNRD1 | thioredoxin reductase 1 |
| 609920 | CDK6 | cyclin-dependent kinase 6 |
| 476337 | LOC476337 | similar to D19Bwg1357e protein |
| 474928 | CD2AP | CD2-associated protein |
| 474759 | TLN1 | talin 1 |
| 611407 | PPAT | phosphoribosyl pyrophosphate amidotransferase |
| 494002 | MSH2 | mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli) |
| 474798 | LOC474798 | similar to Thioredoxin (ATL-derived factor) (ADF) (Surface associated sulphydryl protein) (SASP) |
| 475170 | GRSF1 | G-rich RNA sequence binding factor 1 |
| 474981 | PGM3 | phosphoglucomutase 3 |
| 403709 | ME1 | malic enzyme 1, NADP(+)-dependent, cytosolic |
| 474802 | PTGR1 | prostaglandin reductase 1 |
| 474609 | XPO1 | exportin 1 (CRM1 homolog, yeast) |
| 475499 | OGDH | oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) |
| 481396 | ACTR2 | ARP2 actin-related protein 2 homolog (yeast) |
| 475284 | SEPT7 | septin 7 |
| 475506 | NUP205 | nucleoporin 205kDa |
| 482401 | ANLN | anillin, actin binding protein |
| 606756 | ANXA4 | annexin A4 |
| 403487 | MTPN | myotrophin |
| 475293 | TES | testis derived transcript (3 LIM domains) |
| 474703 | PSMD5 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 |
| 482736 | ZYX | zyxin |
| 481945 | PREP | prolyl endopeptidase |
| 483817 | NAA15 | N(alpha)-acetyltransferase 15, NatA auxiliary subunit |
| 613007 | SNX3 | sorting nexin 3 |
| 476506 | ALDH1L1 | aldehyde dehydrogenase 1 family, member L1 |
| 483267 | NAMPT | nicotinamide phosphoribosyltransferase |
| 476094 | ANXA5 | annexin A5 |

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|---|---|---|
| 475897 | PMPCB | peptidase (mitochondrial processing) beta |
| 476425 | SAE1 | SUMO1 activating enzyme subunit 1 |
| 475896 | PSMC2 | proteasome (prosome, macropain) 26S subunit, ATPase, 2 |
| 607058 | LOC607058 | similar to SVH protein |
| 476434 | EML2 | echinoderm microtubule associated protein like 2 |
| 607116 | ESD | esterase D |
| 475156 | LOC475156 | similar to peroxiredoxin 1 |
| 477993 | RSU1 | Ras suppressor protein 1 |
| 477015 | PDCD6IP | programmed cell death 6 interacting protein |
| 474963 | SUMO2 | SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae) |
| 475913 | NUP85 | nucleoporin 85kDa |
| 478006 | NUDT5 | nudix (nucleoside diphosphate linked moiety X)-type motif 5 |
| 476449 | PAFAH1B3 | platelet-activating factor acetylhydrolase 1b, catalytic subunit 3 (29kDa) |
| 607809 | OXSR1 | oxidative-stress responsive 1 |
| 483322 | ACOX1 | acyl-CoA oxidase 1, palmitoyl |
| 476947 | UCHL3 | ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) |
| 476131 | MCM6 | minichromosome maintenance complex component 6 |
| 483343 | TK1 | thymidine kinase 1, soluble |
| 476456 | BLVRB | biliverdin reductase B (flavin reductase (NADPH)) |
| 476459 | PSMC4 | proteasome (prosome, macropain) 26S subunit, ATPase, 4 |
| 483345 | LGALS3BP | lectin, galactoside-binding, soluble, 3 binding protein |
| 483372 | PYCR1 | pyrroline-5-carboxylate reductase 1 |
| 476470 | PSMD8 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 8 |
| 476823 | RRM1 | ribonucleotide reductase M1 |
| 476552 | TRNT1 | tRNA nucleotidyl transferase, CCA-adding, 1 |
| 477297 | UFM1 | ubiquitin-fold modifier 1 |
| 482611 | LTA4H | leukotriene A4 hydrolase |
| 611746 | CAPNS1 | calpain, small subunit 1 |
| 608169 | FKBP1A | FK506 binding protein 1A, 12kDa |
| 477550 | LOC477550 | similar to poly(rC) binding protein 2 (predicted) |
| 482897 | ASAH1 | N-acylsphingosine amidohydrolase (acid ceramidase) 1 |
| 476490 | UBA2 | ubiquitin-like modifier activating enzyme 2 |
| 485383 | IPO7 | importin 7 |
| 477901 | COPS5 | COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis) |
| 485842 | CHMP4B | chromatin modifying protein 4B |
| 476499 | PDCD5 | programmed cell death 5 |
| 475454 | ABCE1 | ATP-binding cassette, sub-family E (OABP), member 1 |
| 483448 | OSBP | oxysterol binding protein |
| 607073 | ARF4 | ADP-ribosylation factor 4 |
| 486077 | CTSB | cathepsin B |
| 477610 | LIMA1 | LIM domain and actin binding 1 |
| 477213 | CPNE1 | copine I |
| 475781 | HK2 | hexokinase 2 |
| 478103 | GOT2 | glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) |
| 478111 | CIAPIN1 | cytokine induced apoptosis inhibitor 1 |
| 486559 | PRKAG1 | protein kinase, AMP-activated, gamma 1 non-catalytic subunit |
| 486107 | DPYSL2 | dihydropyrimidinase-like 2 |
| 479165 | LOC479165 | similar to Dihydrofolate reductase |
| 485866 | RPRD1B | regulation of nuclear pre-mRNA domain containing 1B |
| 477374 | PPP2R2A | protein phosphatase 2, regulatory subunit B, alpha |
| 483118 | SPR | sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) |
| 478453 | SEC31A | SEC31 homolog A (S. cerevisiae) |
| 478455 | COPS4 | COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis) |
| 478259 | IVD | isovaleryl-CoA dehydrogenase |

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|---|---|---|
| 483631 | ARHGAP1 | Rho GTPase activating protein 1 |
| 479173 | TBCA | tubulin folding cofactor A |
| 477501 | PEBP1 | phosphatidylethanolamine binding protein 1 |
| 478482 | PDLIM5 | PDZ and LIM domain 5 |
| 475998 | CARS | cysteinyl-tRNA synthetase |
| 478625 | NSUN2 | NOP2/Sun domain family, member 2 |
| 478148 | YARS | tyrosyl-tRNA synthetase |
| 477649 | DNM1L | dynamin 1-like |
| 478958 | UCHL5 | ubiquitin carboxyl-terminal hydrolase L5 |
| 477813 | GSTO1 | glutathione S-transferase omega 1 |
| 478424 | CSTB | cystatin B (stefin B) |
| 486880 | XPNPEP1 | X-prolyl aminopeptidase (aminopeptidase P) 1, soluble |
| 403532 | TNNT2 | troponin T type 2 (cardiac) |
| 478500 | PPA2 | pyrophosphatase (inorganic) 2 |
| 487893 | AIMP1 | aminoacyl tRNA synthetase complex-interacting multifunctional protein 1 |
| 609549 | PDCD6 | programmed cell death 6 |
| 475822 | ACP6 | acid phosphatase 6, lysophosphatidic |
| 478156 | FABP3 | fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor) |
| 611914 | SNRNP40 | small nuclear ribonucleoprotein 40kDa (U5) |
| 480242 | PRMT5 | protein arginine methyltransferase 5 |
| 477257 | CSE1L | CSE1 chromosome segregation 1-like (yeast) |
| 475191 | LOC475191 | similar to Glutathione S-transferase P (GST 7-7) (Chain 7) (GST class-pi) |
| 477262 | UBE2V1 | ubiquitin-conjugating enzyme E2 variant 1 |
| 483177 | SF3B4 | splicing factor 3b, subunit 4, 49kDa |
| 488622 | MNDA | myeloid cell nuclear differentiation antigen |
| 606979 | DCUN1D1 | DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae) |
| 479203 | TSNAX | translin-associated factor X |
| 480256 | PSME1 | proteasome (prosome, macropain) activator subunit 1 (PA28 alpha) |
| 480846 | PIR | pirin (iron-binding nuclear protein) |
| 485942 | RAE1 | RAE1 RNA export 1 homolog (S. pombe) |
| 480260 | IPO4 | importin 4 |
| 486344 | AP1B1 | adaptor-related protein complex 1, beta 1 subunit |
| 478250 | ACTC1 | actin, alpha, cardiac muscle 1 |
| 475101 | LOC475101 | similar to L-lactate dehydrogenase B chain (LDH-B) (LDH heart subunit) (LDH-H) |
| 487349 | NUDC | nuclear distribution gene C homolog (A. nidulans) |
| 477845 | SEC23IP | SEC23 interacting protein |
| 610113 | PEA15 | phosphoprotein enriched in astrocytes 15 |
| 477538 | SF3A1 | splicing factor 3a, subunit 1, 120kDa |
| 475846 | PIP5K1A | phosphatidylinositol-4-phosphate 5-kinase, type I, alpha |
| 478654 | PSMD2 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 2 |
| 488395 | GORASP2 | golgi reassembly stacking protein 2, 55kDa |
| 479050 | IQGAP1 | IQ motif containing GTPase activating protein 1 |
| 478595 | SNX4 | sorting nexin 4 |
| 480281 | SCFD1 | sec1 family domain containing 1 |
| 480478 | PSMC5 | proteasome (prosome, macropain) 26S subunit, ATPase, 5 |
| 477858 | OAT | ornithine aminotransferase |
| 478656 | POLR2H | polymerase (RNA) II (DNA directed) polypeptide H |
| 477430 | PPP1R7 | protein phosphatase 1, regulatory (inhibitor) subunit 7 |
| 478799 | LOC478799 | similar to histone aminotransferase 1 (predicted) |
| 488997 | CDK1 | cyclin-dependent kinase 1 |
| 484781 | MAP4 | microtubule-associated protein 4 |
| 480858 | PDHA1 | pyruvate dehydrogenase (lipoamide) alpha 1 |
| 612814 | PAK2 | p21 protein (Cdc42/Rac)-activated kinase 2 |
| 487373 | GALE | UDP-galactose-4-epimerase |

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|---|---|---|
| 478803 | OLA1 | Obg-like ATPase 1 |
| 487374 | LYPLA2 | lysophospholipase II |
| 490649 | CFL2 | cofilin 2 (muscle) |
| 480828 | ECHS1 | enoyl CoA hydratase, short chain, 1, mitochondrial |
| 482601 | LOC482601 | similar to malate dehydrogenase 2, NAD (mitochondrial) |
| 403979 | HSPB1 | heat shock 27kDa protein 1 |
| 478889 | IDH1 | isocitrate dehydrogenase 1 (NADP+), soluble |
| 479227 | HNRNPH3 | heterogeneous nuclear ribonucleoprotein H3 (2H9) |
| 483743 | DPF2 | D4, zinc and double PHD fingers family 2 |
| 479233 | VPS26A | vacuolar protein sorting 26 homolog A (S. pombe) |
| 607589 | DDT | D-dopachrome tautomerase |
| 479238 | PPA1 | pyrophosphatase (inorganic) 1 |
| 477558 | LOC477558 | similar to Glutathione S-transferase theta 2 (GST class-theta 2) |
| 479066 | IDH3A | isocitrate dehydrogenase 3 (NAD+) alpha |
| 477563 | RANBP1 | RAN binding protein 1 |
| 479444 | PPP2R1B | protein phosphatase 2, regulatory subunit A, beta |
| 480772 | UPP1 | uridine phosphorylase 1 |
| 609526 | DUT | deoxyuridine triphosphatase |
| 488784 | GRPEL1 | GrpE-like 1, mitochondrial (E. coli) |
| 479240 | PSAP | prosaposin |
| 486715 | LPCAT3 | lysophosphatidylcholine acyltransferase 3 |
| 476032 | PRDX5 | peroxiredoxin 5 |
| 480069 | PRDX6 | peroxiredoxin 6 |
| 486718 | USP5 | ubiquitin specific peptidase 5 (isopeptidase T) |
| 478907 | ARPC2 | actin related protein 2/3 complex, subunit 2, 34kDa |
| 490953 | VAT1 | vesicle amine transport protein 1 homolog (T. californica) |
| 479737 | MCM7 | minichromosome maintenance complex component 7 |
| 479246 | ANXA7 | annexin A7 |
| 478686 | PRKCI | protein kinase C, iota |
| 480325 | GNPNAT1 | glucosamine-phosphate N-acetyltransferase 1 |
| 478295 | COPS2 | COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis) |
| 612835 | SEC24C | SEC24 family, member C (S. cerevisiae) |
| 490342 | METTL13 | methyltransferase like 13 |
| 479744 | ARPC1B | actin related protein 2/3 complex, subunit 1B, 41kDa |
| 479081 | LAP3 | leucine aminopeptidase 3 |
| 610090 | PGLS | 6-phosphogluconolactonase |
| 477572 | UBE2L3 | ubiquitin-conjugating enzyme E2L 3 |
| 480084 | TIPRL | TIP41, TOR signaling pathway regulator-like (S. cerevisiae) |
| 479253 | ADK | adenosine kinase |
| 486736 | LOC486736 | similar to chromosome 12 open reading frame 5 |
| 609457 | RBM3 | RNA binding motif (RNP1, RRM) protein 3 |
| 403955 | RAC1 | ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1) |
| 487412 | RCC2 | regulator of chromosome condensation 2 |
| 607466 | PSMB6 | proteasome (prosome, macropain) subunit, beta type, 6 |
| 479107 | UGDH | UDP-glucose 6-dehydrogenase |
| 480525 | TOP2A | topoisomerase (DNA) II alpha 170kDa |
| 479270 | ANXA8 | annexin A8 |
| 476066 | CPSF7 | cleavage and polyadenylation specific factor 7, 59kDa |
| 611923 | SRP9 | signal recognition particle 9kDa |
| 607254 | LOC607254 | similar to EF hand domain containing 2 |
| 480364 | ARG2 | arginase, type II |
| 475298 | NAA38 | N(alpha)-acetyltransferase 38, NatC auxiliary subunit |
| 491924 | MSN | moesin |
| 480538 | NPEPPS | aminopeptidase puromycin sensitive |

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|---|---|---|
| 612089 | HDGF | hepatoma-derived growth factor |
| 610314 | RBM25 | RNA binding motif protein 25 |
| 490779 | ALDH6A1 | aldehyde dehydrogenase 6 family, member A1 |
| 480129 | FDPS | farnesyl diphosphate synthase |
| 609803 | RARS | arginyl-tRNA synthetase |
| 476695 | FARSA | phenylalanyl-tRNA synthetase, alpha subunit |
| 403892 | SULT1A1 | sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1 |
| 480955 | OGT | O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase) |
| 491969 | LOC491969 | similar to CG7519-PA |
| 480135 | UBAP2L | ubiquitin associated protein 2-like |
| 480566 | SCPEP1 | serine carboxypeptidase 1 |
| 478355 | KIF23 | kinesin family member 23 |
| 612322 | LOC612322 | similar to S100 calcium binding protein A14 |
| 403787 | S100A4 | S100 calcium binding protein A4 |
| 492015 | CSTF2 | cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa |
| 480143 | S100A6 | S100 calcium binding protein A6 |
| 490465 | KATNAL2 | katanin p60 subunit A-like 2 |
| 403713 | ATOX1 | ATX1 antioxidant protein 1 homolog (yeast) |
| 611273 | MRPL4 | mitochondrial ribosomal protein L4 |
| 480435 | WARS | tryptophanyl-tRNA synthetase |
| 484963 | PIN1 | peptidylprolyl cis/trans isomerase, NIMA-interacting 1 |
| 490508 | PSMA8 | proteasome (prosome, macropain) subunit, alpha type, 8 |
| 489536 | SHMT1 | serine hydroxymethyltransferase 1 (soluble) |
| 489547 | MAP2K3 | mitogen-activated protein kinase kinase 3 |
| 479545 | PGM1 | phosphoglucomutase 1 |
| 492128 | UTP14A | UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast) |
| 608647 | NAPG | N-ethylmaleimide-sensitive factor attachment protein, gamma |
| 479548 | DOCK7 | dedicator of cytokinesis 7 |
| 479370 | TARS | threonyl-tRNA synthetase |
| 442945 | HPRT1 | hypoxanthine phosphoribosyltransferase 1 |
| 479854 | USP7 | ubiquitin specific peptidase 7 (herpes virus-associated) |
| 485039 | SH3GL1 | SH3-domain GRB2-like 1 |
| 480640 | GLOD4 | glyoxalase domain containing 4 |
| 490021 | PPL | periplakin |
| 610939 | LOC610939 | similar to LSM5 homolog, U6 small nuclear RNA associated |
| 490032 | TRAP1 | TNF receptor-associated protein 1 |
| 491221 | TAX1BP3 | Tax1 (human T-cell leukemia virus type I) binding protein 3 |
| 485067 | SGTA | small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha |
| 489622 | LRRC47 | leucine rich repeat containing 47 |
| 481084 | FLNA | filamin A, alpha |
| 479589 | ACOT7 | acyl-CoA thioesterase 7 |
| 481088 | G6PD | glucose-6-phosphate dehydrogenase |
| 479595 | PARK7 | parkinson protein 7 |
| 490124 | SARS | seryl-tRNA synthetase |
| 479615 | APRT | adenine phosphoribosyltransferase |
| 489680 | LOC489680 | similar to coactosin-like 1 |
| 609752 | HSBP1 | heat shock factor binding protein 1 |
| 479937 | CNN3 | calponin 3, acidic |
| 480712 | AK1 | adenylate kinase 1 |
| 479654 | GLG1 | golgi glycoprotein 1 |
| 609251 | LOC609251 | similar to niban protein |
| 479656 | AARS | alanyl-tRNA synthetase |
| 479658 | DDX19A | DEAD (Asp-Glu-Ala-As) box polypeptide 19A |
| 610935 | NQO1 | NAD(P)H dehydrogenase, quinone 1 |

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|---|---|---|
| 480741 | NDUFA8 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa |
| 479681 | NUTF2 | nuclear transport factor 2 |
| 490207 | ACADM | acyl-CoA dehydrogenase, C-4 to C-12 straight chain |
| 479693 | LOC479693 | similar to Dynein light intermediate chain 2, cytosolic (LIC53/55) (LIC-2) |
| 479991 | CTH | cystathionase (cystathionine gamma-lyase) |
| 403954 | RHOA | ras homolog gene family, member A |
| 403686 | HMGN2 | non-histone chromosomal protein HMG-17 |
| 478123 | NUDT21 | nudix (nucleoside diphosphate linked moiety X)-type motif 21 |
| 479731 | SRRT | serrate RNA effector molecule homolog (Arabidopsis) |
| 610164 | CBR1 | carbonyl reductase 1 |
| 474939 | GSTA4 | glutathione S-transferase A4 |
| 476177 | SERPINB5 | serpin peptidase inhibitor, clade B (ovalbumin), member 5 |
| 483402 | RNH1 | ribonuclease/angiogenin inhibitor 1 |
| 476022 | CFL1 | cofilin 1 (non-muscle) |

## Cluster 2

### Enriched Terms:

| Gene to GO BP Conditional test for over-representation GOBPID | Pvalue | OddsRatio | ExpCount | Count | Size | Term |
|---|---|---|---|---|---|---|
| **GO:0031397** | 0 | 10,836 | 6 | 25 | 37 | negative regulation of protein ubiquitination |
| **GO:0051352** | 0 | 11,318 | 6 | 24 | 35 | negative regulation of ligase activity |
| **GO:0051436** | 0 | 11,318 | 6 | 24 | 35 | negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle |
| **GO:0051437** | 0 | 9,996 | 7 | 25 | 38 | positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle |
| **GO:0051351** | 0 | 9,029 | 7 | 26 | 41 | positive regulation of ligase activity |
| **GO:0051438** | 0 | 8,459 | 7 | 26 | 42 | regulation of ubiquitin-protein ligase activity |
| **GO:0032446** | 0 | 5,462 | 12 | 35 | 69 | protein modification by small protein conjugation |
| **GO:0031145** | 0 | 9,564 | 6 | 24 | 37 | anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process |
| **GO:0031398** | 0 | 7,956 | 7 | 26 | 43 | positive regulation of protein ubiquitination |
| **GO:0006511** | 0 | 4,923 | 13 | 37 | 77 | ubiquitin-dependent protein catabolic process |
| **GO:0044257** | 0 | 4,6 | 14 | 38 | 82 | cellular protein catabolic process |
| **GO:0043632** | 0 | 4,682 | 14 | 37 | 79 | modification-dependent macromolecule catabolic process |
| **GO:0048523** | 0 | 2,389 | 56 | 95 | 327 | negative regulation of cellular process |
| **GO:0010498** | 0 | 5,404 | 10 | 29 | 57 | proteasomal protein catabolic process |
| **GO:0032270** | 0 | 4,221 | 13 | 33 | 74 | positive regulation of cellular protein metabolic process |
| **GO:0044092** | 0 | 4,184 | 12 | 32 | 72 | negative regulation of molecular function |
| **GO:0048522** | 0 | 2,185 | 58 | 94 | 341 | positive regulation of cellular process |
| **GO:0031399** | 0 | 3,363 | 18 | 40 | 103 | regulation of protein modification process |
| **GO:0032269** | 0 | 4,146 | 12 | 31 | 70 | negative regulation of cellular protein metabolic process |
| **GO:0009057** | 0 | 3,08 | 21 | 45 | 123 | macromolecule catabolic process |
| **GO:0044093** | 0 | 3 | 21 | 44 | 122 | positive regulation of molecular function |
| **GO:0050790** | 0 | 2,636 | 25 | 48 | 145 | regulation of catalytic activity |
| **GO:0051246** | 0 | 2,484 | 28 | 52 | 164 | regulation of protein metabolic process |
| **GO:0006508** | 0 | 2,525 | 26 | 48 | 149 | proteolysis |
| **GO:0022402** | 0 | 2,585 | 23 | 44 | 138 | cell cycle process |
| **GO:0031323** | 0 | 1,883 | 65 | 95 | 378 | regulation of cellular metabolic process |
| **GO:0010604** | 0 | 2,482 | 23 | 43 | 134 | positive regulation of macromolecule metabolic process |
| **GO:0043412** | 0 | 2 | 47 | 73 | 272 | macromolecule modification |
| **GO:0009056** | 0 | 5,86 | 4 | 14 | 27 | catabolic process |
| **GO:0000278** | 0 | 3,223 | 11 | 25 | 68 | mitotic cell cycle |

| | | | | | | |
|---|---|---|---|---|---|---|
| **GO:0010605** | 0 | 2,158 | 26 | 45 | 154 | negative regulation of macromolecule metabolic process |
| **GO:0050789** | 0 | 1,666 | 126 | 155 | 789 | regulation of biological process |
| **GO:0012501** | 0 | 1,945 | 36 | 57 | 212 | programmed cell death |
| **GO:0019320** | 0 | 4,378 | 5 | 14 | 30 | hexose catabolic process |
| **GO:0032271** | 0 | 4,378 | 5 | 14 | 30 | regulation of protein polymerization |
| **GO:0006606** | 0 | 3,648 | 7 | 16 | 38 | protein import into nucleus |
| **GO:0044087** | 0 | 3,058 | 9 | 20 | 53 | regulation of cellular component biogenesis |
| **GO:0046164** | 0 | 4,118 | 5 | 14 | 31 | alcohol catabolic process |
| **GO:0007015** | 0 | 2,948 | 10 | 21 | 57 | actin filament organization |
| **GO:0033365** | 0 | 2,59 | 13 | 25 | 74 | protein localization to organelle |
| **GO:0007346** | 0 | 3,886 | 5 | 14 | 32 | regulation of mitotic cell cycle |
| **GO:0006096** | 0 | 4,971 | 4 | 11 | 22 | glycolysis |
| **GO:0016265** | 0 | 1,814 | 38 | 57 | 222 | death |
| **GO:0071822** | 0,001 | 1,86 | 32 | 49 | 186 | protein complex subunit organization |
| **GO:0044275** | 0,001 | 3,409 | 6 | 15 | 37 | cellular carbohydrate catabolic process |
| **GO:0030216** | 0,001 | 8,628 | 2 | 7 | 11 | keratinocyte differentiation |
| **GO:0006458** | 0,001 | 6,586 | 2 | 8 | 14 | 'de novo' protein folding |
| **GO:0051086** | 0,001 | Inf | 1 | 4 | 4 | chaperone mediated protein folding independent of cofactor |
| **GO:0070271** | 0,001 | 1,813 | 30 | 45 | 173 | protein complex biogenesis |
| **GO:0072521** | 0,001 | 2,17 | 15 | 27 | 90 | purine-containing compound metabolic process |
| **GO:0006413** | 0,002 | 3,233 | 6 | 13 | 33 | translational initiation |
| **GO:0044248** | 0,002 | 1,649 | 41 | 58 | 241 | cellular catabolic process |
| **GO:0009124** | 0,002 | 3,636 | 4 | 11 | 26 | nucleoside monophosphate biosynthetic process |
| **GO:0009117** | 0,002 | 1,96 | 20 | 32 | 115 | nucleotide metabolic process |
| **GO:0051533** | 0,002 | 12,264 | 1 | 5 | 7 | positive regulation of NFAT protein import into nucleus |
| **GO:0048610** | 0,002 | 2,054 | 17 | 28 | 97 | cellular process involved in reproduction |
| **GO:0016044** | 0,002 | 1,666 | 38 | 54 | 222 | cellular membrane organization |
| **GO:0008064** | 0,002 | 3,31 | 5 | 12 | 30 | regulation of actin polymerization or depolymerization |
| **GO:0000279** | 0,002 | 1,813 | 26 | 39 | 149 | M phase |
| **GO:0006974** | 0,003 | 2,1 | 15 | 25 | 85 | response to DNA damage stimulus |
| **GO:0044267** | 0,003 | 1,529 | 61 | 79 | 385 | cellular protein metabolic process |
| **GO:0016192** | 0,003 | 1,604 | 43 | 59 | 250 | vesicle-mediated transport |
| **GO:0042981** | 0,003 | 1,723 | 30 | 44 | 175 | regulation of apoptosis |
| **GO:0001821** | 0,004 | 19,574 | 1 | 4 | 5 | histamine secretion |
| **GO:0002349** | 0,004 | 19,574 | 1 | 4 | 5 | histamine production involved in inflammatory response |
| **GO:0002553** | 0,004 | 19,574 | 1 | 4 | 5 | histamine secretion by mast cell |
| **GO:0008633** | 0,004 | 19,574 | 1 | 4 | 5 | activation of pro-apoptotic gene products |
| **GO:0035094** | 0,004 | 19,574 | 1 | 4 | 5 | response to nicotine |
| **GO:0035308** | 0,004 | 19,574 | 1 | 4 | 5 | negative regulation of protein dephosphorylation |
| **GO:0046822** | 0,004 | 3,533 | 4 | 10 | 24 | regulation of nucleocytoplasmic transport |
| **GO:0006164** | 0,004 | 2,367 | 10 | 18 | 56 | purine nucleotide biosynthetic process |
| **GO:0010941** | 0,004 | 1,684 | 31 | 45 | 182 | regulation of cell death |
| **GO:0034621** | 0,004 | 1,684 | 31 | 45 | 182 | cellular macromolecular complex subunit organization |

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|---|---|---|---|---|---|---|
| **GO:0007010** | 0,004 | 1,663 | 33 | 47 | 197 | cytoskeleton organization |
| **GO:0033043** | 0,004 | 2,101 | 13 | 23 | 78 | regulation of organelle organization |
| **GO:0034654** | 0,004 | 2,122 | 13 | 22 | 74 | nucleobase-containing biosynthetic process |
| **GO:0046686** | 0,004 | 2,975 | 5 | 12 | 32 | response to cadmium ion |
| **GO:0009161** | 0,005 | 4,921 | 2 | 7 | 14 | ribonucleoside monophosphate metabolic process |
| **GO:0031109** | 0,005 | 4,921 | 2 | 7 | 14 | microtubule polymerization or depolymerization |
| **GO:0051494** | 0,005 | 5,985 | 2 | 6 | 11 | negative regulation of cytoskeleton organization |
| **GO:0006183** | 0,005 | Inf | 1 | 3 | 3 | GTP biosynthetic process |
| **GO:0009220** | 0,005 | Inf | 1 | 3 | 3 | pyrimidine ribonucleotide biosynthetic process |
| **GO:0045138** | 0,005 | Inf | 1 | 3 | 3 | tail tip morphogenesis |
| **GO:0048566** | 0,005 | Inf | 1 | 3 | 3 | embryonic digestive tract development |
| **GO:0021761** | 0,005 | 8,171 | 1 | 5 | 8 | limbic system development |
| **GO:0007052** | 0,005 | 2,009 | 14 | 24 | 84 | mitotic spindle organization |
| **GO:0043624** | 0,005 | 3,295 | 4 | 10 | 25 | cellular protein complex disassembly |
| **GO:0030041** | 0,006 | 4,003 | 3 | 8 | 18 | actin filament polymerization |
| **GO:0010035** | 0,006 | 1,799 | 21 | 32 | 122 | response to inorganic substance |
| **GO:0051234** | 0,006 | 1,395 | 100 | 120 | 585 | establishment of localization |
| **GO:0009119** | 0,006 | 3,942 | 3 | 8 | 18 | ribonucleoside metabolic process |
| **GO:0031333** | 0,006 | 3,942 | 3 | 8 | 18 | negative regulation of protein complex assembly |
| **GO:0018130** | 0,006 | 1,975 | 15 | 24 | 85 | heterocycle biosynthetic process |
| **GO:0009150** | 0,007 | 2,156 | 11 | 19 | 63 | purine ribonucleotide metabolic process |
| **GO:0006006** | 0,007 | 2,342 | 9 | 16 | 50 | glucose metabolic process |
| **GO:0008360** | 0,007 | 3,415 | 4 | 9 | 22 | regulation of cell shape |
| **GO:0009314** | 0,007 | 2,405 | 8 | 15 | 46 | response to radiation |
| **GO:0007030** | 0,007 | 4,303 | 3 | 7 | 15 | Golgi organization |
| **GO:0042990** | 0,007 | 4,303 | 3 | 7 | 15 | regulation of transcription factor import into nucleus |
| **GO:0051650** | 0,007 | 4,303 | 3 | 7 | 15 | establishment of vesicle localization |
| **GO:0032984** | 0,008 | 3,087 | 4 | 10 | 26 | macromolecular complex disassembly |
| **GO:0043627** | 0,008 | 2,863 | 5 | 11 | 30 | response to estrogen stimulus |
| **GO:0043623** | 0,008 | 1,989 | 13 | 22 | 78 | cellular protein complex assembly |
| **GO:0007017** | 0,008 | 1,675 | 26 | 37 | 149 | microtubule-based process |
| **GO:0009260** | 0,009 | 2,419 | 7 | 14 | 43 | ribonucleotide biosynthetic process |
| **GO:0051707** | 0,009 | 1,966 | 13 | 22 | 78 | response to other organism |
| **GO:0009168** | 0,009 | 4,909 | 2 | 6 | 12 | purine ribonucleoside monophosphate biosynthetic process |
| **GO:0030837** | 0,009 | 4,909 | 2 | 6 | 12 | negative regulation of actin filament polymerization |
| **GO:0080090** | 0,009 | 1,596 | 32 | 44 | 201 | regulation of primary metabolic process |
| **GO:0048513** | 0,009 | 1,393 | 81 | 98 | 470 | organ development |
| **GO:0050793** | 0,009 | 1,672 | 25 | 36 | 145 | regulation of developmental process |
| **GO:0009408** | 0,009 | 2,395 | 7 | 14 | 43 | response to heat |
| **GO:0006000** | 0,01 | 9,781 | 1 | 4 | 6 | fructose metabolic process |
| **GO:0007021** | 0,01 | 9,781 | 1 | 4 | 6 | tubulin complex assembly |
| **GO:0030435** | 0,01 | 9,781 | 1 | 4 | 6 | sporulation resulting in formation of a cellular spore |
| **GO:0051220** | 0,01 | 9,781 | 1 | 4 | 6 | cytoplasmic sequestering of protein |
| **GO:0032535** | 0,01 | 2,477 | 7 | 13 | 39 | regulation of cellular component size |
| **GO:0006733** | 0,01 | 3,169 | 4 | 9 | 23 | oxidoreduction coenzyme metabolic process |

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|---|---|---|---|---|---|---|
| **GO:0046496** | 0,01 | 3,169 | 4 | 9 | 23 | nicotinamide nucleotide metabolic process |
| **GO:0072524** | 0,01 | 3,169 | 4 | 9 | 23 | pyridine-containing compound metabolic process |
| **GO:0002275** | 0,01 | 6,124 | 2 | 5 | 9 | myeloid cell activation involved in immune response |
| **GO:0002444** | 0,01 | 6,124 | 2 | 5 | 9 | myeloid leukocyte mediated immunity |
| **GO:0043299** | 0,01 | 6,124 | 2 | 5 | 9 | leukocyte degranulation |
| **GO:0048205** | 0,01 | 6,124 | 2 | 5 | 9 | COPI coating of Golgi vesicle |

## Genes in cluster:

| Entrez Id | Symbol | description |
|---|---|---|
| **474393** | DGKA | diacylglycerol kinase, alpha 80kDa |
| **612760** | PTGES3 | prostaglandin E synthase 3 (cytosolic) |
| **476200** | RNMT | RNA (guanine-7-) methyltransferase |
| **474414** | MARS | methionyl-tRNA synthetase |
| **474415** | DCTN2 | dynactin 2 (p50) |
| **474437** | CAND1 | cullin-associated and neddylation-dissociated 1 |
| **474441** | CPSF6 | cleavage and polyadenylation specific factor 6, 68kDa |
| **474445** | CCT2 | chaperonin containing TCP1, subunit 2 (beta) |
| **474839** | DDX39B | DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B |
| **474840** | ATP6V1G2 | ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G2 |
| **474657** | SNX2 | sorting nexin 2 |
| **474842** | BAG6 | BCL2-associated athanogene 6 |
| **475864** | YWHAZ | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide |
| **403612** | HSP70 | heat shock protein 70 |
| **475070** | EIF3E | eukaryotic translation initiation factor 3, subunit E |
| **484064** | TCP1 | t-complex 1 |
| **608479** | LOC608479 | similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) |
| **474667** | HINT1 | histidine triad nucleotide binding protein 1 |
| **474474** | TTLL12 | tubulin tyrosine ligase-like family, member 12 |
| **474680** | HSPA4 | heat shock 70kDa protein 4 |
| **474682** | SKP1 | S-phase kinase-associated protein 1 |
| **403608** | PPP2CA | protein phosphatase 2, catalytic subunit, alpha isozyme |
| **474685** | DDX46 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 46 |
| **483608** | LOC483608 | similar to heat shock 70kD protein binding protein |
| **474499** | ADSL | adenylosuccinate lyase |
| **442946** | HMGA1 | high mobility group AT-hook 1 |
| **475115** | EEF1D | eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) |
| **476309** | HNRNPK | heterogeneous nuclear ribonucleoprotein K |
| **476312** | UBQLN1 | ubiquilin 1 |
| **474513** | LOC474513 | similar to eukaryotic translation initiation factor 3 subunit 6 interacting protein |
| **482263** | TNPO3 | transportin 3 |
| **608665** | EIF3D | eukaryotic translation initiation factor 3, subunit D |
| **475132** | PSMA4 | proteasome (prosome, macropain) subunit, alpha type, 4 |
| **476322** | ANXA1 | annexin A1 |
| **476323** | ALDH1A1 | aldehyde dehydrogenase 1 family, member A1 |
| **475220** | SRI | sorcin |
| **481590** | VCP | valosin containing protein |
| **474919** | HSP90AB1 | heat shock protein 90kDa alpha (cytosolic), class B member 1 |
| **475240** | ASNS | asparagine synthetase (glutamine-hydrolyzing) |
| **475150** | PAICS | phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase |

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|---|---|---|
| **609822** | GCLC | glutamate-cysteine ligase, catalytic subunit |
| **484221** | UBE2M | ubiquitin-conjugating enzyme E2M |
| **475250** | BZW2 | basic leucine zipper and W2 domains 2 |
| **474584** | CALM2 | calmodulin 2 (phosphorylase kinase, delta) |
| **403506** | EEF1A1 | eukaryotic translation elongation factor 1 alpha 1 |
| **474585** | MSH6 | mutS homolog 6 (E. coli) |
| **403743** | SPTBN1 | spectrin, beta, non-erythrocytic 1 |
| **476400** | ETFB | electron-transfer-flavoprotein, beta polypeptide |
| **607412** | DBNL | drebrin-like |
| **475260** | HNRNPA2B1 | heterogeneous nuclear ribonucleoprotein A2/B1 |
| **482015** | CBX3 | chromobox homolog 3 |
| **475317** | CAP1 | CAP, adenylate cyclase-associated protein 1 (yeast) |
| **482271** | CCT4 | chaperonin containing TCP1, subunit 4 (delta) |
| **475268** | GARS | glycyl-tRNA synthetase |
| **474614** | MDH1 | malate dehydrogenase 1, NAD (soluble) |
| **475326** | SF3A3 | splicing factor 3a, subunit 3, 60kDa |
| **478521** | LOC478521 | similar to 14-3-3 protein theta (14-3-3 protein tau) |
| **482476** | THRAP3 | thyroid hormone receptor associated protein 3 |
| **484370** | NUP62 | nucleoporin 62kDa |
| **475870** | PSMA2 | proteasome (prosome, macropain) subunit, alpha type, 2 |
| **475338** | PSMB2 | proteasome (prosome, macropain) subunit, beta type, 2 |
| **475346** | VPS35 | vacuolar protein sorting 35 homolog (S. cerevisiae) |
| **476418** | RUVBL2 | RuvB-like 2 (E. coli) |
| **475035** | HDAC2 | histone deacetylase 2 |
| **475529** | LUC7L2 | LUC7-like 2 (S. cerevisiae) |
| **475040** | PSMB1 | proteasome (prosome, macropain) subunit, beta type, 1 |
| **476512** | RUVBL1 | RuvB-like 1 (E. coli) |
| **476517** | COPG | coatomer protein complex, subunit gamma |
| **476909** | KPNA3 | karyopherin alpha 3 (importin alpha 4) |
| **403936** | VASP | vasodilator-stimulated phosphoprotein |
| **475373** | NASP | nuclear autoantigenic sperm protein (histone-binding) |
| **477991** | VIM | vimentin |
| **476924** | TPT1 | tumor protein, translationally-controlled 1 |
| **483299** | SLC9A3R1 | solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1 |
| **477999** | SEPHS1 | selenophosphate synthetase 1 |
| **483312** | GRB2 | growth factor receptor-bound protein 2 |
| **477951** | LOC477951 | similar to suppressor of G2 allele of SKP1 |
| **476115** | DBI | diazepam binding inhibitor (GABA receptor modulator, acyl-CoA binding protein) |
| **475703** | PPM1G | protein phosphatase, Mg2+/Mn2+ dependent, 1G |
| **403702** | ACTR3 | ARP3 actin-related protein 3 homolog (yeast) |
| **476454** | SNRPA | small nuclear ribonucleoprotein polypeptide A |
| **476132** | DARS | aspartyl-tRNA synthetase |
| **483339** | SEPT9 | septin 9 |
| **403818** | GDI2 | GDP dissociation inhibitor 2 |
| **475391** | EBNA1BP2 | EBNA1 binding protein 2 |
| **482558** | APEX1 | APEX nuclease (multifunctional DNA repair enzyme) 1 |
| **475393** | PNP | purine nucleoside phosphorylase |
| **478019** | PFKP | phosphofructokinase, platelet |
| **476462** | SUPT5H | suppressor of Ty 5 homolog (S. cerevisiae) |
| **403809** | RRBP1 | ribosome binding protein 1 homolog 180kDa (dog) |
| **485528** | IPO5 | importin 5 |
| **475715** | DPY30 | dpy-30 homolog (C. elegans) |
| **403580** | ACTB | actin, beta |
| **484526** | ACTN4 | actinin, alpha 4 |

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|---|---|---|
| **476468** | EIF3K | eukaryotic translation initiation factor 3, subunit K |
| **475924** | ARHGDIA | Rho GDP dissociation inhibitor (GDI) alpha |
| **475926** | DCXR | dicarbonyl/L-xylulose reductase |
| **483378** | FASN | fatty acid synthase |
| **477166** | PCNA | proliferating cell nuclear antigen |
| **476784** | LOC476784 | similar to ubiquitin-conjugating enzyme E2N |
| **475934** | PSMD13 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 |
| **483048** | EML4 | echinoderm microtubule associated protein like 4 |
| **607013** | LOC607013 | similar to Coatomer zeta-1 subunit (Zeta-1 coat protein) (Zeta-1 COP) |
| **477322** | HSPH1 | heat shock 105kDa/110kDa protein 1 |
| **475937** | TALDO1 | transaldolase 1 |
| **477177** | IDH3B | isocitrate dehydrogenase 3 (NAD+) beta |
| **442976** | RAN | RAN, member RAS oncogene family |
| **483413** | API5 | apoptosis inhibitor 5 |
| **607950** | SKIV2L2 | superkiller viralicidic activity 2-like 2 (S. cerevisiae) |
| **608575** | COMMD9 | COMM domain containing 9 |
| **484700** | PSMD6 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 6 |
| **476840** | LOC476840 | similar to eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa |
| **486953** | ATP6V1H | ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H |
| **477600** | EIF4B | eukaryotic translation initiation factor 4B |
| **486788** | IFIT5 | interferon-induced protein with tetratricopeptide repeats 5 |
| **475208** | LOC475208 | similar to Microtubule-associated protein RP/EB family member 1 (APC-binding protein EB1) (End-binding protein 1) (EB1) |
| **475950** | EIF3M | eukaryotic translation initiation factor 3, subunit M |
| **477768** | IDE | insulin-degrading enzyme |
| **477449** | RILPL1 | Rab interacting lysosomal protein-like 1 |
| **477198** | AHCY | adenosylhomocysteinase |
| **490977** | KRT17 | keratin 17 |
| **484713** | FLNB | filamin B, beta |
| **476854** | EIF4G2 | eukaryotic translation initiation factor 4 gamma, 2 |
| **475767** | USP39 | ubiquitin specific peptidase 39 |
| **612329** | LSM6 | LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae) |
| **475770** | MAT2A | methionine adenosyltransferase II, alpha |
| **483082** | CAPG | capping protein (actin filament), gelsolin-like |
| **475968** | TIMM10 | translocase of inner mitochondrial membrane 10 homolog (yeast) |
| **479148** | CAST | calpastatin |
| **613005** | LOC613005 | similar to thymosin, beta 10 |
| **477463** | DIABLO | diablo, IAP-binding mitochondrial protein |
| **478093** | TNPO1 | transportin 1 |
| **477914** | TCEB1 | transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C) |
| **476719** | LOC476719 | similar to Fructose-bisphosphate aldolase A (Muscle-type aldolase) (Lung cancer antigen NY-LU-1) |
| **477216** | RBM39 | RNA binding motif protein 39 |
| **478429** | G3BP2 | GTPase activating protein (SH3 domain) binding protein 2 |
| **476866** | COPB1 | coatomer protein complex, subunit beta 1 |
| **478430** | USO1 | USO1 vesicle docking protein homolog (yeast) |
| **477474** | ARPC3 | actin related protein 2/3 complex, subunit 3, 21kDa |
| **476867** | PSMA1 | proteasome (prosome, macropain) subunit, alpha type, 1 |
| **477477** | VPS29 | vacuolar protein sorting 29 homolog (S. cerevisiae) |
| **477116** | MBNL1 | muscleblind-like (Drosophila) |
| **476588** | TKT | transketolase |
| **478399** | CCT8 | chaperonin containing TCP1, subunit 8 (theta) |
| **475481** | PPID | peptidylprolyl isomerase D |
| **475980** | PSMC3 | proteasome (prosome, macropain) 26S subunit, ATPase, 3 |
| **474591** | ARF1 | ADP-ribosylation factor 1 |

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|---|---|---|
| **477123** | GMPS | guanine monphosphate synthetase |
| **478447** | ANXA3 | annexin A3 |
| **477786** | PGAM1 | phosphoglycerate mutase 1 (brain) |
| **478119** | NUP93 | nucleoporin 93kDa |
| **478406** | SON | SON DNA binding protein |
| **487948** | LOC487948 | similar to coproporphyrinogen oxidase |
| **476882** | LDHA | lactate dehydrogenase A |
| **487740** | GART | phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase |
| **488192** | SERPINB9 | serpin peptidase inhibitor, clade B (ovalbumin), member 9 |
| **486122** | LOC486122 | similar to p30 DBC protein |
| **487954** | TFG | TRK-fused gene |
| **477237** | YWHAB | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide |
| **478717** | EEF1E1 | eukaryotic translation elongation factor 1 epsilon 1 |
| **486600** | TWF1 | twinfilin, actin-binding protein, homolog 1 (Drosophila) |
| **478765** | PSMD14 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 14 |
| **483662** | CTSD | cathepsin D |
| **609496** | NOLC1 | nucleolar and coiled-body phosphoprotein 1 |
| **607890** | LOC607890 | similar to D-3-phosphoglycerate dehydrogenase (3-PGDH) |
| **606873** | CCT5 | chaperonin containing TCP1, subunit 5 (epsilon) |
| **486137** | ATP6V1B2 | ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B2 |
| **606787** | LOC606787 | similar to T-complex protein 1, zeta subunit (TCP-1-zeta) (CCT-zeta) (CCT-zeta-1) |
| **403791** | ACTR1A | ARP1 actin-related protein 1 homolog A, centractin alpha (yeast) |
| **483670** | NAP1L4 | nucleosome assembly protein 1-like 4 |
| **609233** | LOC609233 | similar to dynein, cytoplasmic, light peptide |
| **478145** | AK2 | adenylate kinase 2 |
| **610283** | CTTN | cortactin |
| **478149** | RBBP4 | retinoblastoma binding protein 4 |
| **478957** | TROVE2 | TROVE domain family, member 2 |
| **607102** | SNRPA1 | small nuclear ribonucleoprotein polypeptide A' |
| **478422** | U2AF1 | U2 small nuclear RNA auxiliary factor 1 |
| **480004** | IPO9 | importin 9 |
| **478152** | EIF3I | eukaryotic translation initiation factor 3, subunit I |
| **487981** | ATP6V1A | ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A |
| **477403** | CAB39 | calcium binding protein 39 |
| **612989** | GLTP | glycolipid transfer protein |
| **487316** | KHDRBS1 | KH domain containing, RNA binding, signal transduction associated 1 |
| **478962** | EPRS | glutamyl-prolyl-tRNA synthetase |
| **608525** | BPNT1 | 3'(2'), 5'-bisphosphate nucleotidase 1 |
| **480459** | PRKAR1A | protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1) |
| **480246** | PSMB5 | proteasome (prosome, macropain) subunit, beta type, 5 |
| **480465** | PSMD12 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 |
| **490611** | PABPN1 | poly(A) binding protein, nuclear 1 |
| **486633** | BCAT1 | branched chain amino-acid transaminase 1, cytosolic |
| **476007** | CORO1B | coronin, actin binding protein, 1B |
| **480469** | KPNA2 | karyopherin alpha 2 (RAG cohort 1, importin alpha 1) |
| **403609** | PPP1CA | protein phosphatase 1, catalytic subunit, alpha isozyme |
| **479406** | HSPA8 | heat shock 70kDa protein 8 |
| **475834** | ANP32E | acidic (leucine-rich) nuclear phosphoprotein 32 family, member E |
| **487332** | RCC1 | regulator of chromosome condensation 1 |
| **610210** | TAGLN2 | transgelin 2 |
| **476628** | QARS | glutaminyl-tRNA synthetase |
| **478865** | BZW1 | basic leucine zipper and W2 domains 1 |
| **476630** | IMPDH2 | IMP (inosine 5'-monophosphate) dehydrogenase 2 |
| **480258** | PSME2 | proteasome (prosome, macropain) activator subunit 2 (PA28 beta) |

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|---|---|---|
| **607749** | EIF4H | eukaryotic translation initiation factor 4H |
| **486914** | EIF3A | eukaryotic translation initiation factor 3, subunit A |
| **484774** | PRKAR2A | protein kinase, cAMP-dependent, regulatory, type II, alpha |
| **488336** | cOR2W9 | cOR2W9 olfactory receptor family 2 subfamily W-like |
| **487351** | SFN | stratifin |
| **478593** | UMPS | uridine monophosphate synthetase |
| **610639** | RBM14 | RNA binding motif protein 14 |
| **478787** | SSB | Sjogren syndrome antigen B (autoantigen La) |
| **404305** | PSMA7 | proteasome (prosome, macropain) subunit, alpha type, 7 |
| **479415** | ARCN1 | archain 1 |
| **477284** | ADRM1 | adhesion regulating molecule 1 |
| **480854** | RBBP7 | retinoblastoma binding protein 7 |
| **475848** | PSMB4 | proteasome (prosome, macropain) subunit, beta type, 4 |
| **478175** | STMN1 | stathmin 1 |
| **480479** | DDX42 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 42 |
| **487367** | CLIC4 | chloride intracellular channel 4 |
| **475852** | LOC475852 | similar to Calgizzarin (S100 calcium-binding protein A11) (S100C protein) (MLN 70) |
| **478185** | SRRM1 | serine/arginine repetitive matrix 1 |
| **487886** | SEPT2 | septin 2 |
| **476015** | SF3B2 | splicing factor 3b, subunit 2, 145kDa |
| **476640** | SMARCC1 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1 |
| **477691** | DDX47 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 47 |
| **479425** | PAFAH1B2 | platelet-activating factor acetylhydrolase 1b, catalytic subunit 2 (30kDa) |
| **477869** | GLRX3 | glutaredoxin 3 |
| **480037** | ARPC5 | actin related protein 2/3 complex, subunit 5, 16kDa |
| **478881** | EEF1B2 | eukaryotic translation elongation factor 1 beta 2 |
| **480290** | PSMA6 | proteasome (prosome, macropain) subunit, alpha type, 6 |
| **475857** | CAPZA1 | capping protein (actin filament) muscle Z-line, alpha 1 |
| **608979** | UCK2 | uridine-cytidine kinase 2 |
| **490921** | NSF | N-ethylmaleimide-sensitive factor |
| **489818** | YWHAG | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide |
| **487532** | EIF3J | eukaryotic translation initiation factor 3, subunit J |
| **484785** | CCDC12 | coiled-coil domain containing 12 |
| **488118** | EIF4A2 | eukaryotic translation initiation factor 4A2 |
| **480045** | TPR | translocated promoter region (to activated MET oncogene) |
| **479433** | ZW10 | ZW10, kinetochore associated, homolog (Drosophila) |
| **480048** | PLA2G4A | phospholipase A2, group IVA (cytosolic, calcium-dependent) |
| **480295** | SEC23A | Sec23 homolog A (S. cerevisiae) |
| **481417** | PCBP1 | poly(rC) binding protein 1 |
| **479441** | CRYAB | crystallin, alpha B |
| **479068** | WDR61 | WD repeat domain 61 |
| **476031** | SF1 | splicing factor 1 |
| **488513** | ATIC | 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase |
| **480062** | CACYBP | calcyclin binding protein |
| **476033** | TRMT112 | tRNA methyltransferase 11-2 homolog (S. cerevisiae) |
| **477711** | TPI1 | triosephosphate isomerase 1 |
| **474837** | STIP1 | stress-induced-phosphoprotein 1 |
| **480512** | PSME3 | proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki) |
| **476039** | OTUB1 | OTU domain, ubiquitin aldehyde binding 1 |
| **478522** | PSMC6 | proteasome (prosome, macropain) 26S subunit, ATPase, 6 |
| **480896** | UBA1 | ubiquitin-like modifier activating enzyme 1 |
| **403581** | PPIA | peptidylprolyl isomerase A (cyclophilin A) |
| **480329** | MAPK1IP1L | mitogen-activated protein kinase 1 interacting protein 1-like |
| **404021** | LGALS3 | lectin, galactoside-binding, soluble, 3 |

| | | |
|---|---|---|
| **489861** | PDAP1 | PDGFA associated protein 1 |
| **478209** | CAPZB | capping protein (actin filament) muscle Z-line, beta |
| **480338** | PSMA3 | proteasome (prosome, macropain) subunit, alpha type, 3 |
| **478922** | DNPEP | aspartyl aminopeptidase |
| **477575** | MAPK1 | mitogen-activated protein kinase 1 |
| **611070** | WDR1 | WD repeat domain 1 |
| **477726** | FKBP4 | FK506 binding protein 4, 59kDa |
| **477584** | ATAD1 | ATPase family, AAA domain containing 1 |
| **476055** | UBXN1 | UBX domain protein 1 |
| **479259** | ANXA11 | annexin A11 |
| **609879** | TPM4 | tropomyosin 4 |
| **476570** | LOC476570 | similar to Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma) |
| **480352** | MTHFD1 | methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase |
| **480921** | GSPT2 | G1 to S phase transition 2 |
| **477736** | LOC477736 | similar to cat eye syndrome chromosome region, candidate 5 isoform 2 precursor |
| **478926** | FARSB | phenylalanyl-tRNA synthetase, beta subunit |
| **477740** | ATP6V1E1 | ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E1 |
| **476067** | DDB1 | damage-specific DNA binding protein 1, 127kDa |
| **491018** | PSMD3 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 |
| **476689** | DDX39A | DEAD (Asp-Glu-Ala-Asp) box polypeptide 39A |
| **480118** | CAPN2 | calpain 2, (m/II) large subunit |
| **479766** | EIF3B | eukaryotic translation initiation factor 3, subunit B |
| **611552** | PRPF19 | PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae) |
| **480369** | ACTN1 | actinin, alpha 1 |
| **608624** | LASP1 | LIM and SH3 protein 1 |
| **480371** | ERH | enhancer of rudimentary homolog (Drosophila) |
| **474987** | LOC474987 | similar to Proteasome subunit beta type 3 (Proteasome theta chain) (Proteasome chain 13) (Proteasome component C10-II) |
| **479485** | EIF4A1 | eukaryotic translation initiation factor 4A1 |
| **491042** | KPNB1 | karyopherin (importin) beta 1 |
| **612240** | CTBP1 | C-terminal binding protein 1 |
| **478236** | PGD | phosphogluconate dehydrogenase |
| **476790** | LOC476790 | similar to chaperonin containing TCP1, subunit 3 isoform c |
| **479795** | EIF3C | eukaryotic translation initiation factor 3, subunit C |
| **484926** | PRDX2 | peroxiredoxin 2 |
| **480402** | AHSA1 | AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast) |
| **480964** | PGK1 | phosphoglycerate kinase 1 |
| **478347** | MAP2K1 | mitogen-activated protein kinase kinase 1 |
| **480559** | NME2 | non-metastatic cells 2, protein (NM23B) expressed in |
| **403534** | ANP32A | acidic (leucine-rich) nuclear phosphoprotein 32 family, member A |
| **480979** | HNRNPK | heterogeneous nuclear ribonucleoprotein K |
| **478703** | PSMC1 | proteasome (prosome, macropain) 26S subunit, ATPase, 1 |
| **480986** | TIMM8A | translocase of inner mitochondrial membrane 8 homolog A (yeast) |
| **489167** | LOC489167 | similar to CG9590-PA |
| **403874** | PKM2 | pyruvate kinase, muscle |
| **480151** | LOC480151 | similar to CG14299-PA, isoform A |
| **480989** | HNRNPH2 | heterogeneous nuclear ribonucleoprotein H2 (H') |
| **484955** | CDC37 | cell division cycle 37 homolog (S. cerevisiae) |
| **480595** | AATF | apoptosis antagonizing transcription factor |
| **612971** | EIF3G | eukaryotic translation initiation factor 3, subunit G |
| **480437** | LOC480437 | similar to dynein, cytoplasmic, heavy polypeptide 1 |
| **491130** | ACACA | acetyl-CoA carboxylase alpha |
| **491146** | CCT6B | chaperonin containing TCP1, subunit 6B (zeta 2) |
| **480182** | USP14 | ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase) |

| | | |
|---|---|---|
| **480610** | PSMD11 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 |
| **479528** | COPS3 | COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis) |
| **476725** | HNRNPM | heterogeneous nuclear ribonucleoprotein M |
| **479344** | HMGCS1 | 3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble) |
| **485022** | KHSRP | KH-type splicing regulatory protein |
| **480622** | ALDOC | aldolase C, fructose-bisphosphate |
| **479846** | GSPT1 | G1 to S phase transition 1 |
| **480631** | NUFIP2 | nuclear fragile X mental retardation protein interacting protein 2 |
| **481063** | RBMX | RNA binding motif protein, X-linked |
| **480645** | YWHAE | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide |
| **476744** | EEF2 | eukaryotic translation elongation factor 2 |
| **491201** | LOC491201 | similar to CG7338-PA |
| **609638** | SRRM2 | serine/arginine repetitive matrix 2 |
| **479575** | ISG15 | ISG15 ubiquitin-like modifier |
| **479873** | TCEB2 | transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B) |
| **612188** | SF3A2 | splicing factor 3a, subunit 2, 66kDa |
| **611128** | HN1L | hematological and neurological expressed 1-like |
| **403819** | GDI1 | GDP dissociation inhibitor 1 |
| **479597** | ENO1 | enolase 1, (alpha) |
| **490123** | PSMA5 | proteasome (prosome, macropain) subunit, alpha type, 5 |
| **479625** | USP10 | ubiquitin specific peptidase 10 |
| **403484** | SPTAN1 | spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) |
| **479644** | KARS | lysyl-tRNA synthetase |
| **612856** | ARPC5L | actin related protein 2/3 complex, subunit 5-like |
| **479671** | PSMD7 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 |
| **490201** | FUBP1 | far upstream element (FUSE) binding protein 1 |
| **476166** | CNDP2 | CNDP dipeptidase 2 (metallopeptidase M20 family) |
| **476767** | NME1 | non-metastatic cells 1, protein (NM23A) expressed in |
| **476540** | ARPC4 | actin related protein 2/3 complex, subunit 4, 20kDa |
| **478680** | KPNA4 | karyopherin alpha 4 (importin alpha 3) |
| **488473** | CASP8 | caspase 8, apoptosis-related cysteine peptidase |
| **477928** | CA2 | carbonic anhydrase II |

# Cluster 3

## Enriched Terms:

| Gene to GO BP Conditional test for over-representation GOBPID | Pvalue | OddsRatio | ExpCount | Count | Size | Term |
|---|---|---|---|---|---|---|
| **GO:0006414** | 0 | 4,073 | 5 | 16 | 79 | translational elongation |
| **GO:0006270** | 0 | 29,847 | 0 | 4 | 6 | DNA-dependent DNA replication initiation |
| **GO:0000003** | 0,001 | 1,955 | 28 | 43 | 427 | reproduction |
| **GO:0042303** | 0,001 | 4,306 | 3 | 9 | 42 | molting cycle |
| **GO:0018996** | 0,001 | 4,175 | 3 | 9 | 42 | molting cycle, collagen and cuticulin-based cuticle |
| **GO:0010467** | 0,001 | 1,814 | 36 | 51 | 551 | gene expression |
| **GO:0006892** | 0,002 | 5,648 | 1 | 6 | 22 | post-Golgi vesicle-mediated transport |
| **GO:0042274** | 0,002 | 5,648 | 1 | 6 | 22 | ribosomal small subunit biogenesis |
| **GO:0009059** | 0,003 | 1,813 | 25 | 38 | 390 | macromolecule biosynthetic process |
| **GO:0033572** | 0,004 | Inf | 0 | 2 | 2 | transferrin transport |
| **GO:0051304** | 0,004 | Inf | 0 | 2 | 2 | chromosome separation |
| **GO:0007017** | 0,006 | 2,156 | 10 | 18 | 149 | microtubule-based process |
| **GO:0030855** | 0,008 | 4,093 | 2 | 6 | 28 | epithelial cell differentiation |
| **GO:0022404** | 0,008 | 6,606 | 1 | 4 | 13 | molting cycle process |
| **GO:0033205** | 0,008 | 11,086 | 0 | 3 | 7 | cell cycle cytokinesis |
| **GO:0035017** | 0,008 | 11,086 | 0 | 3 | 7 | cuticle pattern formation |

## Genes in cluster:

| Entrez Id | Symbol | description |
|---|---|---|
| **474396** | PA2G4 | proliferation-associated 2G4, 38kDa |
| **607631** | NARS | asparaginyl-tRNA synthetase |
| **474408** | NACA | nascent polypeptide-associated complex alpha subunit |
| **476206** | RPS12 | ribosomal protein S12 |
| **474826** | ABCF1 | ATP-binding cassette, sub-family F (GCN20), member 1 |
| **474663** | LMNB1 | lamin B1 |
| **474696** | LOC474696 | similar to eukaryotic translation termination factor 1 (predicted) |
| **474508** | DDX17 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 17 |
| **482083** | PLEC | plectin |
| **474519** | TXN2 | thioredoxin 2 |
| **474722** | RPS6 | ribosomal protein S6 |
| **475199** | ATP6V1F | ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F |
| **481280** | MYH9 | myosin, heavy chain 9, non-muscle |
| **475204** | SND1 | staphylococcal nuclease and tudor domain containing 1 |
| **610519** | MCM5 | minichromosome maintenance complex component 5 |
| **474576** | LOC474576 | similar to DnaJ homolog subfamily A member 1 (Heat shock 40 kDa protein 4) (DnaJ protein homolog 2) (HSJ-2) (HSDJ) |
| **474740** | SMU1 | smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans) |
| **481839** | MCM3 | minichromosome maintenance complex component 3 |
| **403944** | SRP72 | signal recognition particle 72kDa |
| **474556** | EIF5B | eukaryotic translation initiation factor 5B |
| **474765** | CLTA | clathrin, light chain A |
| **476378** | RPL28 | ribosomal protein L28 |

| | | |
|---|---|---|
| **475321** | MACF1 | microtubule-actin crosslinking factor 1 |
| **475649** | RPS7 | ribosomal protein S7 |
| **482963** | RRM2 | ribonucleotide reductase M2 |
| **476411** | PRMT1 | protein arginine methyltransferase 1 |
| **475671** | DDX1 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 1 |
| **475682** | LOC475682 | similar to splicing factor 3B, 14 kDa subunit |
| **612058** | GRWD1 | glutamate-rich WD repeat containing 1 |
| **484622** | MCM2 | minichromosome maintenance complex component 2 |
| **477968** | KIF5B | kinesin family member 5B |
| **476111** | MKI67IP | MKI67 (FHA domain) interacting nucleolar phosphoprotein |
| **483009** | CAD | carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase |
| **475540** | LOC475540 | similar to testis-specific histone 2b |
| **403952** | SRP68 | signal recognition particle 68kDa |
| **477029** | RPSA | ribosomal protein SA |
| **607653** | SEC13 | SEC13 homolog (S. cerevisiae) |
| **476460** | FBL | fibrillarin |
| **474964** | HNRNPCL1 | heterogeneous nuclear ribonucleoprotein C-like 1 |
| **475719** | TTC27 | tetratricopeptide repeat domain 27 |
| **475721** | LOC475721 | similar to CG5913-PA |
| **607948** | LOC607948 | similar to THO complex subunit 4 (Tho4) (Ally of AML-1 and LEF-1) (Transcriptional coactivator Aly/REF) (bZIP enhancing factor BEF) |
| **475429** | METAP2 | methionyl aminopeptidase 2 |
| **483399** | PKP3 | plakophilin 3 |
| **477871** | MCM4 | minichromosome maintenance complex component 4 |
| **485806** | SNRPB | small nuclear ribonucleoprotein polypeptides B and B1 |
| **477879** | TCEA1 | transcription elongation factor A (SII), 1 |
| **477887** | RPS20 | ribosomal protein S20 |
| **477757** | HNRNPF | heterogeneous nuclear ribonucleoprotein F |
| **477601** | KRT18 | keratin 18 |
| **486513** | KRT8 | keratin 8 |
| **477602** | KRT7 | keratin 7 |
| **609784** | VAMP8 | vesicle-associated membrane protein 8 (endobrevin) |
| **478864** | LOC478864 | similar to 60S ribosomal protein L21 |
| **477309** | LOC477309 | similar to Transcription factor BTF3 homolog 3 |
| **478254** | LOC478254 | similar to CG5913-PA |
| **477224** | CTNNBL1 | catenin, beta like 1 |
| **488448** | GLS | glutaminase |
| **488207** | DSP | desmoplakin |
| **487314** | KPNA6 | karyopherin alpha 6 (importin alpha 7) |
| **475816** | SEC22B | SEC22 vesicle trafficking protein homolog B (S. cerevisiae) (gene/pseudogene) |
| **478504** | PAPSS1 | 3'-phosphoadenosine 5'-phosphosulfate synthase 1 |
| **480311** | RPL36AL | ribosomal protein L36a-like |
| **478642** | FXR1 | fragile X mental retardation, autosomal homolog 1 |
| **476855** | PRPS2 | phosphoribosyl pyrophosphate synthetase 2 |
| **442955** | EPB41 | erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked) |
| **480472** | DDX5 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 |
| **478165** | ATPIF1 | ATPase inhibitory factor 1 |
| **610764** | CAMK2D | calcium/calmodulin-dependent protein kinase II delta |
| **475838** | GOLPH3L | golgi phosphoprotein 3-like |
| **477274** | VAPB | VAMP (vesicle-associated membrane protein)-associated protein B and C |
| **479071** | LOC479071 | similar to Probable ATP-dependent RNA helicase DDX6 (DEAD-box protein 6) (ATP-dependent RNA helicase p54) (Oncogene RCK) |
| **477856** | ACADSB | acyl-CoA dehydrogenase, short/branched chain |
| **485959** | RPS21 | ribosomal protein S21 |
| **486663** | STRAP | serine/threonine kinase receptor associated protein |

| | | |
|---|---|---|
| **477857** | BUB3 | budding uninhibited by benzimidazoles 3 homolog (yeast) |
| **477431** | HDLBP | high density lipoprotein binding protein |
| **611715** | EIF1AX | eukaryotic translation initiation factor 1A, X-linked |
| **479230** | CCAR1 | cell division cycle and apoptosis regulator 1 |
| **480306** | FKBP3 | FK506 binding protein 3, 25kDa |
| **479237** | SAR1A | SAR1 homolog A (S. cerevisiae) |
| **480886** | DDX3X | DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked |
| **479733** | GNB2 | guanine nucleotide binding protein (G protein), beta polypeptide 2 |
| **478831** | ZC3H15 | zinc finger CCCH-type containing 15 |
| **476663** | COPE | coatomer protein complex, subunit epsilon |
| **479969** | LOC479969 | similar to Protein C14orf166 |
| **477714** | CHD4 | chromodomain helicase DNA binding protein 4 |
| **490966** | PTRF | polymerase I and transcript release factor |
| **480332** | KTN1 | kinectin 1 (kinesin receptor) |
| **478918** | TUBA4A | tubulin, alpha 4a |
| **610636** | TUBA3C | tubulin, alpha 3c |
| **489450** | C1QBP | complement component 1, q subcomponent binding protein |
| **476053** | HNRNPUL2 | heterogeneous nuclear ribonucleoprotein U-like 2 |
| **607852** | ACLY | ATP citrate lyase |
| **480100** | HNRNPU | heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) |
| **480522** | JUP | junction plakoglobin |
| **489468** | EIF5A | eukaryotic translation initiation factor 5A |
| **403682** | RPL19 | ribosomal protein L19 |
| **488856** | DHX15 | DEAH (Asp-Glu-Ala-His) box polypeptide 15 |
| **403683** | RPL23 | ribosomal protein L23 |
| **490754** | SRSF5 | serine/arginine-rich splicing factor 5 |
| **403435** | ANXA2 | annexin A2 |
| **479282** | NOP16 | NOP16 nucleolar protein homolog (yeast) |
| **480124** | LMNA | lamin A/C |
| **475722** | LOC475722 | similar to nucleophosmin 1 |
| **490449** | RPS27 | ribosomal protein S27 |
| **480578** | CLTC | clathrin, heavy chain (Hc) |
| **484949** | DNM2 | dynamin 2 |
| **479322** | G3BP1 | GTPase activating protein (SH3 domain) binding protein 1 |
| **403690** | RPS14 | ribosomal protein S14 |
| **480440** | TNFAIP2 | tumor necrosis factor, alpha-induced protein 2 |
| **480442** | EIF5 | eukaryotic translation initiation factor 5 |
| **480193** | MYL12B | myosin, light chain 12B, regulatory |
| **479535** | SERBP1 | SERPINE1 mRNA binding protein 1 |
| **476799** | RPL23A | ribosomal protein L23a |
| **485028** | SAFB | scaffold attachment factor B |
| **480213** | TUBB6 | tubulin, beta 6 |
| **481079** | NSDHL | NAD(P) dependent steroid dehydrogenase-like |
| **489591** | CDK11A | cyclin-dependent kinase 11A |
| **492246** | HCFC1 | host cell factor C1 (VP16-accessory protein) |
| **491231** | TUBB2C | tubulin, beta 2C |
| **480674** | EDF1 | endothelial differentiation-related factor 1 |
| **479949** | RPL5 | ribosomal protein L5 |
| **479666** | AP1G1 | adaptor-related protein complex 1, gamma 1 subunit |
| **489733** | NOB1 | NIN1/RPN12 binding protein 1 homolog (S. cerevisiae) |
| **489738** | CIRH1A | cirrhosis, autosomal recessive 1A (cirhin) |
| **475851** | S100A10 | S100 calcium binding protein A10 |
| **480818** | GNB2L1 | guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 |
| **487554** | TMOD3 | tropomodulin 3 (ubiquitous) |

# Cluster 4

## Enriched Terms:

| Gene to GO BP Conditional test for over-representation GOBPID | Pvalue | OddsRatio | ExpCount | Count | Size | Term |
|---|---|---|---|---|---|---|
| **GO:0071824** | 0 | 5,528 | 4 | 15 | 35 | protein-DNA complex subunit organization |
| **GO:0006334** | 0 | 6,35 | 4 | 13 | 28 | nucleosome assembly |
| **GO:0046942** | 0 | 5,836 | 3 | 12 | 27 | carboxylic acid transport |
| **GO:0006333** | 0 | 4,409 | 5 | 15 | 40 | chromatin assembly or disassembly |
| **GO:0055085** | 0 | 3,545 | 7 | 18 | 57 | transmembrane transport |
| **GO:0006323** | 0 | 3,663 | 6 | 15 | 45 | DNA packaging |
| **GO:0006200** | 0 | 10,051 | 2 | 7 | 12 | ATP catabolic process |
| **GO:0006172** | 0 | Inf | 1 | 4 | 4 | ADP biosynthetic process |
| **GO:0009136** | 0 | Inf | 1 | 4 | 4 | purine nucleoside diphosphate biosynthetic process |
| **GO:0009188** | 0 | Inf | 1 | 4 | 4 | ribonucleoside diphosphate biosynthetic process |
| **GO:0006820** | 0 | 7,374 | 2 | 8 | 16 | anion transport |
| **GO:0022904** | 0 | 5,168 | 3 | 10 | 24 | respiratory electron transport chain |
| **GO:0009206** | 0 | 4,153 | 4 | 12 | 33 | purine ribonucleoside triphosphate biosynthetic process |
| **GO:0015992** | 0 | 5,409 | 3 | 9 | 21 | proton transport |
| **GO:0015711** | 0 | 10,728 | 1 | 6 | 10 | organic anion transport |
| **GO:0051234** | 0,001 | 1,627 | 73 | 96 | 585 | establishment of localization |
| **GO:0006839** | 0,001 | 3,787 | 4 | 12 | 35 | mitochondrial transport |
| **GO:0009142** | 0,001 | 3,787 | 4 | 12 | 35 | nucleoside triphosphate biosynthetic process |
| **GO:0015980** | 0,001 | 3,002 | 7 | 16 | 55 | energy derivation by oxidation of organic compounds |
| **GO:0008203** | 0,001 | 5,751 | 2 | 8 | 18 | cholesterol metabolic process |
| **GO:0034220** | 0,001 | 3,982 | 4 | 11 | 31 | ion transmembrane transport |
| **GO:0009179** | 0,001 | 28,414 | 1 | 4 | 5 | purine ribonucleoside diphosphate metabolic process |
| **GO:0019233** | 0,001 | 28,414 | 1 | 4 | 5 | sensory perception of pain |
| **GO:0033555** | 0,001 | 11,876 | 1 | 5 | 8 | multicellular organismal response to stress |
| **GO:0040008** | 0,001 | 1,861 | 25 | 40 | 203 | regulation of growth |
| **GO:0040010** | 0,002 | 1,98 | 19 | 31 | 148 | positive regulation of growth rate |
| **GO:0009853** | 0,002 | Inf | 0 | 3 | 3 | photorespiration |
| **GO:0015800** | 0,002 | 8,902 | 1 | 5 | 9 | acidic amino acid transport |
| **GO:0006119** | 0,003 | 4,416 | 3 | 8 | 21 | oxidative phosphorylation |
| **GO:0051240** | 0,003 | 2,748 | 6 | 14 | 51 | positive regulation of multicellular organismal process |

| | | | | | | |
|---|---|---|---|---|---|---|
| **GO:0015986** | 0,003 | 5,01 | 2 | 7 | 17 | ATP synthesis coupled proton transport |
| **GO:0014911** | 0,003 | 14,198 | 1 | 4 | 6 | positive regulation of smooth muscle cell migration |
| **GO:0015837** | 0,003 | 3,806 | 3 | 9 | 26 | amine transport |
| **GO:0030001** | 0,004 | 3,101 | 5 | 11 | 37 | metal ion transport |
| **GO:0030155** | 0,004 | 4,552 | 2 | 7 | 18 | regulation of cell adhesion |
| **GO:0006816** | 0,005 | 3,822 | 3 | 8 | 23 | calcium ion transport |
| **GO:0007568** | 0,006 | 1,961 | 14 | 24 | 114 | aging |
| **GO:0019915** | 0,006 | 4,17 | 2 | 7 | 19 | lipid storage |
| **GO:0006814** | 0,006 | 9,46 | 1 | 4 | 7 | sodium ion transport |
| **GO:0019218** | 0,006 | 9,46 | 1 | 4 | 7 | regulation of steroid metabolic process |
| **GO:0051276** | 0,007 | 1,99 | 13 | 22 | 103 | chromosome organization |
| **GO:0009199** | 0,007 | 2,54 | 6 | 13 | 50 | ribonucleoside triphosphate metabolic process |
| **GO:0016126** | 0,007 | 4,754 | 2 | 6 | 15 | sterol biosynthetic process |
| **GO:0001662** | 0,007 | 21,219 | 1 | 3 | 4 | behavioral fear response |
| **GO:0006971** | 0,007 | 21,219 | 1 | 3 | 4 | hypotonic response |
| **GO:0046513** | 0,007 | 21,219 | 1 | 3 | 4 | ceramide biosynthetic process |
| **GO:0001817** | 0,007 | 5,927 | 1 | 5 | 11 | regulation of cytokine production |
| **GO:0008610** | 0,008 | 2,234 | 9 | 16 | 68 | lipid biosynthetic process |
| **GO:0022610** | 0,008 | 2,234 | 9 | 16 | 68 | biological adhesion |
| **GO:0009144** | 0,008 | 2,471 | 6 | 13 | 51 | purine nucleoside triphosphate metabolic process |
| **GO:0016049** | 0,008 | 2,874 | 4 | 10 | 35 | cell growth |
| **GO:0006812** | 0,009 | 3,752 | 3 | 7 | 21 | cation transport |

## Genes in cluster:

| Entrey Id | Symbol | description |
|---|---|---|
| **476186** | LMAN1 | lectin, mannose-binding, 1 |
| **474397** | ESYT1 | extended synaptotagmin-like protein 1 |
| **403669** | ATP5B | ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide |
| **474630** | HSD17B4 | hydroxysteroid (17-beta) dehydrogenase 4 |
| **483987** | STX7 | syntaxin 7 |
| **607458** | SHMT2 | serine hydroxymethyltransferase 2 (mitochondrial) |
| **481436** | TMED7 | transmembrane emp24 protein transport domain containing 7 |
| **474644** | NHP2 | NHP2 ribonucleoprotein homolog (yeast) |
| **481455** | HNRNPH1 | heterogeneous nuclear ribonucleoprotein H1 (H) |
| **403908** | CANX | calnexin |
| **608981** | RAP1B | RAP1B, member of RAS oncogene family |
| **474448** | TSPAN8 | tetraspanin 8 |
| **481991** | LOC481991 | similar to small nuclear ribonucleoprotein D2 |
| **474475** | TSPO | translocator protein (18kDa) |
| **474479** | CYB5R3 | cytochrome b5 reductase 3 |
| **474681** | VDAC1 | voltage-dependent anion channel 1 |
| **403935** | ANXA13 | annexin A13 |
| **608021** | SQLE | squalene epoxidase |
| **481514** | H2AFY | H2A histone family, member Y |
| **481746** | ITPR3 | inositol 1,4,5-trisphosphate receptor, type 3 |
| **474697** | HSPA9 | heat shock 70kDa protein 9 (mortalin) |

| | | |
|---|---|---|
| **476303** | GOLM1 | golgi membrane protein 1 |
| **610117** | TOMM22 | translocase of outer mitochondrial membrane 22 homolog (yeast) |
| **482252** | PODXL | podocalyxin-like |
| **403687** | SRSF3 | serine/arginine-rich splicing factor 3 |
| **475121** | LOC475121 | similar to cytochrome c-1 |
| **609079** | TOMM6 | translocase of outer mitochondrial membrane 6 homolog (yeast) |
| **474526** | PWP1 | PWP1 homolog (S. cerevisiae) |
| **612937** | TMEM33 | transmembrane protein 33 |
| **475225** | LOC475225 | similar to Cytochrome P450 51A1 (CYPLI) (P450LI) (Sterol 14-alpha demethylase) (Lanosterol 14-alpha demethylase) (LDM) (P450-14DM) (P45014DM) |
| **476333** | DOCK8 | dedicator of cytokinesis 8 |
| **475140** | OCIAD1 | OCIA domain containing 1 |
| **474755** | STOML2 | stomatin (EPB72)-like 2 |
| **484192** | SPTLC1 | serine palmitoyltransferase, long chain base subunit 1 |
| **610138** | SLC25A13 | solute carrier family 25, member 13 (citrin) |
| **474567** | COX5B | cytochrome c oxidase polypeptide Vb |
| **474572** | LRPPRC | leucine-rich PPR-motif containing |
| **481360** | EPCAM | epithelial cell adhesion molecule |
| **611134** | LOC611134 | similar to cytochrome c oxidase, subunit 7a 3 |
| **474598** | RTN4 | reticulon 4 |
| **474978** | BCKDHB | branched chain keto acid dehydrogenase E1, beta polypeptide |
| **484356** | LOC484356 | hypothetical LOC484356 |
| **482460** | ZMPSTE24 | zinc metallopeptidase (STE24 homolog, S. cerevisiae) |
| **482464** | PABPC4 | poly(A) binding protein, cytoplasmic 4 (inducible form) |
| **475501** | LOC475501 | similar to H2A histone family, member V isoform 5 |
| **482691** | TBRG4 | transforming growth factor beta regulator 4 |
| **403774** | RAB1A | RAB1A, member RAS oncogene family |
| **481418** | PCYOX1 | prenylcysteine oxidase 1 |
| **403980** | CAV1 | caveolin 1, caveolae protein, 22kDa |
| **482966** | NOL10 | nucleolar protein 10 |
| **404017** | SEC61G | Sec61 gamma subunit |
| **612336** | LOC612336 | similar to Protein FAM3C precursor (Protein GS3786) |
| **475875** | RALA | v-ral simian leukemia viral oncogene homolog A (ras related) |
| **476413** | RRAS | related RAS viral (r-ras) oncogene homolog |
| **474818** | RAB14 | RAB14, member RAS oncogene family |
| **612719** | STOM | stomatin |
| **477956** | ITGB1 | integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) |
| **476084** | PGRMC2 | progesterone receptor membrane component 2 |
| **475524** | LOC475524 | similar to single-stranded DNA binding protein 1 isoform 1 |
| **482764** | AGK | acylglycerol kinase |
| **475029** | RPF2 | ribosome production factor 2 homolog (S. cerevisiae) |
| **485119** | ENDOD1 | endonuclease domain containing 1 |
| **476516** | RPN1 | ribophorin I |
| **404007** | RAB7A | RAB7A, member RAS oncogene family |
| **484425** | SLC1A5 | solute carrier family 1 (neutral amino acid transporter), member 5 |
| **403958** | RAB10 | RAB10, member RAS oncogene family |
| **476101** | UGGT1 | UDP-glucose glycoprotein glucosyltransferase 1 |
| **475687** | HADHA | hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit |
| **476519** | ACAD9 | acyl-CoA dehydrogenase family, member 9 |
| **477002** | ACSS1 | acyl-CoA synthetase short-chain family member 1 |
| **477988** | YME1L1 | YME1-like 1 (S. cerevisiae) |
| **484637** | TMEM43 | transmembrane protein 43 |

| | | |
|---|---|---|
| **485448** | SUCLA2 | succinate-CoA ligase, ADP-forming, beta subunit |
| **611055** | TOMM40 | translocase of outer mitochondrial membrane 40 homolog (yeast) |
| **474433** | LOC474433 | similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d isoform a |
| **476794** | NDUFC2 | NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa |
| **483318** | ITGB4 | integrin, beta 4 |
| **475916** | H3F3B | H3 histone, family 3B (H3.3B) |
| **484473** | CEACAM28 | carcinoembryonic antigen-related cell adhesion molecule 28 |
| **478009** | ATP5C1 | ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1 |
| **476130** | UBXN4 | UBX domain protein 4 |
| **612817** | SRSF2 | serine/arginine-rich splicing factor 2 |
| **477032** | CTNNB1 | catenin (cadherin-associated protein), beta 1, 88kDa |
| **482533** | ELOVL1 | ELOVL fatty acid elongase 1 |
| **485187** | SERPINH1 | serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1) |
| **476461** | TIMM50 | translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae) |
| **475462** | VDAC3 | voltage-dependent anion channel 3 |
| **612874** | SUPT16H | suppressor of Ty 16 homolog (S. cerevisiae) |
| **608330** | RAB6A | RAB6A, member RAS oncogene family |
| **485637** | SLC4A7 | solute carrier family 4, sodium bicarbonate cotransporter, member 7 |
| **612944** | ARL8B | ADP-ribosylation factor-like 8B |
| **608030** | MRPL12 | mitochondrial ribosomal protein L12 |
| **607518** | ERLIN2 | ER lipid raft associated 2 |
| **475593** | MAK16 | MAK16 homolog (S. cerevisiae) |
| **477175** | MRPS26 | mitochondrial ribosomal protein S26 |
| **477072** | TF | transferrin |
| **476559** | ARL6IP5 | ADP-ribosylation-like factor 6 interacting protein 5 |
| **475436** | SLC25A3 | solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3 |
| **475939** | HSD17B12 | hydroxysteroid (17-beta) dehydrogenase 12 |
| **486776** | TIMM23 | translocase of inner mitochondrial membrane 23 homolog (yeast) |
| **612644** | LOC612644 | similar to cytochrome c oxidase, subunit VIb polypeptide 1 |
| **403474** | CAT | catalase |
| **477185** | CSNK2A1 | casein kinase 2, alpha 1 polypeptide |
| **431686** | ATP4A | ATPase, H+/K+ exchanging, alpha polypeptide |
| **404009** | RAB2A | RAB2A, member RAS oncogene family |
| **486970** | YTHDF3 | YTH domain family, member 3 |
| **486978** | RRS1 | RRS1 ribosome biogenesis regulator homolog (S. cerevisiae) |
| **479137** | REEP5 | receptor accessory protein 5 |
| **477347** | PSPC1 | paraspeckle component 1 |
| **475764** | IMMT | inner membrane protein, mitochondrial |
| **475630** | SLC25A4 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4 |
| **477088** | COPB2 | coatomer protein complex, subunit beta 2 (beta prime) |
| **477098** | ATP1B3 | ATPase, Na+/K+ transporting, beta 3 polypeptide |
| **607472** | MYOF | myoferlin |
| **483489** | CTNND1 | catenin (cadherin-associated protein), delta 1 |
| **607299** | NOP10 | NOP10 ribonucleoprotein homolog (yeast) |
| **477362** | FDFT1 | farnesyl-diphosphate farnesyltransferase 1 |
| **477103** | U2SURP | U2 snRNP-associated SURP domain containing |
| **477210** | EIF6 | eukaryotic translation initiation factor 6 |
| **476372** | LOC476372 | similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2 |
| **475978** | NDUFS3 | NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase) |
| **403878** | ATP2A2 | ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 |

| | | |
|---|---|---|
| **475979** | CELF1 | CUGBP, Elav-like family member 1 |
| **475480** | ETFDH | electron-transferring-flavoprotein dehydrogenase |
| **477223** | RPN2 | ribophorin II |
| **612786** | TM9SF3 | transmembrane 9 superfamily member 3 |
| **608951** | FKBP11 | FK506 binding protein 11, 19 kDa |
| **477124** | SSR3 | signal sequence receptor, gamma (translocon-associated protein gamma) |
| **608725** | RRP12 | ribosomal RNA processing 12 homolog (S. cerevisiae) |
| **479172** | SCAMP1 | secretory carrier membrane protein 1 |
| **478059** | LOC478059 | similar to F26E4.12 |
| **478755** | GPD2 | glycerol-3-phosphate dehydrogenase 2 (mitochondrial) |
| **488199** | PRPF4B | PRP4 pre-mRNA processing factor 4 homolog B (yeast) |
| **403951** | SSR1 | signal sequence receptor, alpha |
| **478410** | LOC478410 | similar to ATP synthase O subunit, mitochondrial precursor (Oligomycin sensitivity conferral protein) (OSCP) |
| **403992** | ATP1A1 | ATPase, Na+/K+ transporting, alpha 1 polypeptide |
| **486848** | SFXN3 | sideroflexin 3 |
| **478552** | CD47 | CD47 molecule |
| **488289** | LOC488289 | similar to Histone H2A.1 |
| **442957** | GNAI2 | guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2 |
| **403583** | CPT1A | carnitine palmitoyltransferase 1A (liver) |
| **610084** | CISD2 | CDGSH iron sulfur domain 2 |
| **486308** | TRPV4 | transient receptor potential cation channel, subfamily V, member 4 |
| **488456** | SF3B1 | splicing factor 3b, subunit 1, 155kDa |
| **479192** | HEATR1 | HEAT repeat containing 1 |
| **488264** | LOC488264 | similar to Histone H1.2 (H1d) |
| **477660** | MRPS35 | mitochondrial ribosomal protein S35 |
| **480830** | SLC25A6 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6 |
| **483166** | LOC483166 | similar to germinal histone H4 gene |
| **476004** | NDUFV1 | NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa |
| **486317** | DAO | D-amino-acid oxidase |
| **611089** | LOC611089 | similar to H2B histone family, member F |
| **483175** | LOC483175 | similar to histone H2A |
| **477264** | DPM1 | dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit |
| **477841** | TIAL1 | TIA1 cytotoxic granule-associated RNA binding protein-like 1 |
| **479212** | CISD1 | CDGSH iron sulfur domain 1 |
| **489372** | LOC489372 | similar to Histone H2A.x (H2a/x) |
| **608244** | NDUFA10 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa |
| **478974** | F11R | F11 receptor |
| **476012** | MRPL11 | mitochondrial ribosomal protein L11 |
| **478798** | SLC25A12 | solute carrier family 25 (mitochondrial carrier, Aralar), member 12 |
| **403703** | TFRC | transferrin receptor (p90, CD71) |
| **611961** | BANF1 | barrier to autointegration factor 1 |
| **480032** | DHX9 | DEAH (Asp-Glu-Ala-His) box polypeptide 9 |
| **478192** | HNRNPR | heterogeneous nuclear ribonucleoprotein R |
| **478880** | NDUFS1 | NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase) |
| **478663** | TRA2B | transformer 2 beta homolog (Drosophila) |
| **403728** | ZONAB | Y-box protein ZONAB-A |
| **480866** | EIF2S3 | eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa |
| **477695** | LOC477695 | similar to mago-nashi homolog |
| **489816** | POR | P450 (cytochrome) oxidoreductase |
| **478992** | TMCO1 | transmembrane and coiled-coil domains 1 |
| **488421** | AGPS | alkylglycerone phosphate synthase |

| | | |
|---|---|---|
| **491408** | RAB18 | RAB18, member RAS oncogene family |
| **476891** | DDX21 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 21 |
| **479728** | FIS1 | fission 1 (mitochondrial outer membrane) homolog (S. cerevisiae) |
| **477700** | M6PR | mannose-6-phosphate receptor (cation dependent) |
| **483747** | MRPL49 | mitochondrial ribosomal protein L49 |
| **489406** | DLAT | dihydrolipoamide S-acetyltransferase |
| **476659** | NDUFA13 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13 |
| **489042** | MCU | mitochondrial calcium uniporter |
| **488437** | ITGAV | integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) |
| **610791** | TMX1 | thioredoxin-related transmembrane protein 1 |
| **488807** | LETM1 | leucine zipper-EF-hand containing transmembrane protein 1 |
| **404012** | DDOST | dolichyl-diphosphooligosaccharide--protein glycosyltransferase |
| **476043** | RTN3 | reticulon 3 |
| **476044** | ATL3 | atlastin GTPase 3 |
| **487406** | MRTO4 | mRNA turnover 4 homolog (S. cerevisiae) |
| **611024** | LOC611024 | similar to 3-beta-hydroxysteroid-delta(8),delta(7)-isomerase (Cholestenol delta-isomerase) (Delta8-delta7 sterol isomerase) (D8-D7 sterol isomerase) (Emopamil-binding protein) |
| **612432** | LOC612432 | similar to CG2943-PA |
| **403966** | ATP1B1 | ATPase, Na+/K+ transporting, beta 1 polypeptide |
| **489442** | MYBBP1A | MYB binding protein (P160) 1a |
| **477718** | NDUFA9 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa |
| **480086** | BRP44 | brain protein 44 |
| **479255** | VDAC2 | voltage-dependent anion channel 2 |
| **483777** | SLC3A2 | solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 |
| **607694** | CNP | 2',3'-cyclic nucleotide 3' phosphodiesterase |
| **403773** | RAB8A | RAB8A, member RAS oncogene family |
| **478217** | SDHB | succinate dehydrogenase complex, subunit B, iron sulfur (Ip) |
| **479470** | SLC25A11 | solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11 |
| **479261** | LOC479261 | similar to R53.5 |
| **403423** | RBM47 | RNA binding motif protein 47 |
| **489463** | ACADVL | acyl-CoA dehydrogenase, very long chain |
| **490385** | PARP1 | poly (ADP-ribose) polymerase 1 |
| **480928** | SMC1A | structural maintenance of chromosomes 1A |
| **489477** | MPDU1 | mannose-P-dolichol utilization defect 1 |
| **606860** | LOC606860 | similar to Cytochrome c oxidase polypeptide VIc-2 |
| **489102** | FAF2 | Fas associated factor family member 2 |
| **489109** | SFXN1 | sideroflexin 1 |
| **479778** | LOC479778 | similar to fusion (involved in t(12;16) in malignant liposarcoma) (predicted) |
| **480547** | PHB | prohibitin |
| **480127** | DAP3 | death associated protein 3 |
| **491074** | LOC491074 | similar to integrin alpha 3 isoform b, precursor |
| **480388** | DLST | dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) |
| **610559** | TMED10 | transmembrane emp24-like trafficking protein 10 (yeast) |
| **491080** | LOC491080 | similar to CG3408-PA |
| **478337** | PPIB | peptidylprolyl isomerase B (cyclophilin B) |
| **480403** | SPTLC2 | serine palmitoyltransferase, long chain base subunit 2 |
| **491103** | TRIM25 | tripartite motif containing 25 |
| **475148** | MSI2 | musashi homolog 2 (Drosophila) |
| **609693** | SRSF1 | serine/arginine-rich splicing factor 1 |
| **490458** | LOC490458 | similar to S100 calcium binding protein A16 |
| **480149** | ATP5A1 | ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle |

| | | |
|---|---|---|
| **479815** | UQCRC2 | ubiquinol-cytochrome c reductase core protein II |
| **478370** | LOC478370 | similar to Cytochrome c oxidase polypeptide Va, mitochondrial precursor |
| **481018** | ACSL4 | acyl-CoA synthetase long-chain family member 4 |
| **610134** | ETFA | electron-transfer-flavoprotein, alpha polypeptide |
| **489992** | NOMO2 | NODAL modulator 2 |
| **490532** | YES1 | v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 |
| **481029** | PGRMC1 | progesterone receptor membrane component 1 |
| **489208** | ITGA2 | integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) |
| **480204** | NDUFV2 | NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa |
| **480208** | VAPA | VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa |
| **481048** | AIFM1 | apoptosis-inducing factor, mitochondrion-associated, 1 |
| **480626** | SDF2 | stromal cell-derived factor 2 |
| **479365** | LOC479365 | similar to Brix domain containing protein 2 (Ribosome biogenesis protein Brix) |
| **489573** | DHCR24 | 24-dehydrocholesterol reductase |
| **481073** | HMGB3 | high mobility group box 3 |
| **480646** | MYO1C | myosin IC |
| **479864** | HMOX2 | heme oxygenase (decycling) 2 |
| **480651** | PRPF8 | PRP8 pre-mRNA processing factor 8 homolog (S. cerevisiae) |
| **481080** | BCAP31 | B-cell receptor-associated protein 31 |
| **479568** | ATAD3B | ATPase family, AAA domain containing 3B |
| **485062** | NCLN | nicalin |
| **481082** | SSR4 | signal sequence receptor, delta |
| **491203** | LOC491203 | similar to Putative eukaryotic translation initiation factor 3 subunit (eIF-3) |
| **492244** | L1CAM | L1 cell adhesion molecule |
| **476756** | ATP5D | ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit |
| **612784** | DNAJC11 | DnaJ (Hsp40) homolog, subfamily C, member 11 |
| **476758** | LOC476758 | similar to basigin isoform 1 |
| **479901** | ATP5F1 | ATP synthase, H+ transporting, mitochondrial Fo complex, subunit B1 |
| **479623** | LOC479623 | similar to Cytochrome c oxidase subunit IV isoform 1, mitochondrial precursor (COX IV-1) (Cytochrome c oxidase polypeptide IV) |
| **611922** | SLC25A24 | solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24 |
| **479633** | GCSH | glycine cleavage system protein H (aminomethyl carrier) |
| **490153** | F3 | coagulation factor III (thromboplastin, tissue factor) |
| **479939** | ABCD3 | ATP-binding cassette, sub-family D (ALD), member 3 |
| **612406** | ZNF326 | zinc finger protein 326 |
| **610942** | LOC610942 | similar to cytochrome b5 outer mitochondrial membrane precursor |
| **483035** | CEBPZ | CCAAT/enhancer binding protein (C/EBP), zeta |
| **608348** | SLC25A1 | solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1 |
| **488273** | LOC488273 | similar to Histone H1.5 (Histone H1a) |
| **488258** | LOC488258 | similar to Histone H1.2 (H1d) |
| **483167** | LOC483167 | similar to H3 histone, family 2 isoform 2 |
| **483168** | LOC483168 | similar to Histone H2A.o (H2A/o) (H2A.2) (H2a-615) |
| **475214** | NDUFA5 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa |
| **608656** | LOC608656 | similar to oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) isoform 1 precursor |
| **610569** | RPS27L | ribosomal protein S27-like |

# Cluster 5

## Enriched Terms:

| Gene to GO BP Conditional test for over-representation GOBPID | Pvalue | OddsRatio | ExpCount | Count | Size | Term |
|---|---|---|---|---|---|---|
| **GO:0043436** | 0 | 2,601 | 13 | 28 | 181 | oxoacid metabolic process |
| **GO:0055114** | 0 | 2,555 | 13 | 26 | 169 | oxidation-reduction process |
| **GO:0006105** | 0 | 25,632 | 0 | 4 | 6 | succinate metabolic process |
| **GO:0002520** | 0,001 | 3,102 | 6 | 15 | 80 | immune system development |
| **GO:0048878** | 0,001 | 3,005 | 6 | 15 | 82 | chemical homeostasis |
| **GO:0040027** | 0,001 | 17,078 | 1 | 4 | 7 | negative regulation of vulval development |
| **GO:0061062** | 0,001 | 17,078 | 1 | 4 | 7 | regulation of nematode larval development |
| **GO:0043648** | 0,001 | 6,658 | 1 | 6 | 18 | dicarboxylic acid metabolic process |
| **GO:0065008** | 0,001 | 1,917 | 24 | 38 | 322 | regulation of biological quality |
| **GO:0032496** | 0,002 | 5,05 | 2 | 7 | 25 | response to lipopolysaccharide |
| **GO:0032787** | 0,002 | 2,783 | 6 | 14 | 81 | monocarboxylic acid metabolic process |
| **GO:0006084** | 0,002 | 4,781 | 2 | 7 | 26 | acetyl-CoA metabolic process |
| **GO:0051186** | 0,005 | 2,679 | 5 | 12 | 71 | cofactor metabolic process |
| **GO:0045454** | 0,005 | 4,551 | 2 | 6 | 23 | cell redox homeostasis |
| **GO:0050804** | 0,005 | 4,551 | 2 | 6 | 23 | regulation of synaptic transmission |
| **GO:0001837** | 0,005 | Inf | 0 | 2 | 2 | epithelial to mesenchymal transition |
| **GO:0048147** | 0,005 | Inf | 0 | 2 | 2 | negative regulation of fibroblast proliferation |
| **GO:0051588** | 0,005 | Inf | 0 | 2 | 2 | regulation of neurotransmitter transport |
| **GO:2000300** | 0,005 | Inf | 0 | 2 | 2 | regulation of synaptic vesicle exocytosis |
| **GO:0007399** | 0,006 | 1,867 | 17 | 27 | 225 | nervous system development |
| **GO:0006091** | 0,006 | 2,486 | 6 | 13 | 82 | generation of precursor metabolites and energy |
| **GO:0006457** | 0,006 | 2,722 | 5 | 11 | 64 | protein folding |
| **GO:0030097** | 0,006 | 2,588 | 5 | 12 | 73 | hemopoiesis |
| **GO:0006099** | 0,006 | 5,349 | 1 | 5 | 17 | tricarboxylic acid cycle |
| **GO:0030866** | 0,006 | 7,303 | 1 | 4 | 11 | cortical actin cytoskeleton organization |
| **GO:0048581** | 0,006 | 7,303 | 1 | 4 | 11 | negative regulation of post-embryonic development |
| **GO:0022904** | 0,007 | 4,296 | 2 | 6 | 24 | respiratory electron transport chain |
| **GO:0002562** | 0,007 | 12,715 | 0 | 3 | 6 | somatic diversification of immune receptors via germline recombination within a single locus |
| **GO:0006664** | 0,007 | 12,715 | 0 | 3 | 6 | glycolipid metabolic process |
| **GO:0055072** | 0,007 | 12,715 | 0 | 3 | 6 | iron ion homeostasis |
| **GO:0008406** | 0,008 | 4,068 | 2 | 6 | 25 | gonad development |
| **GO:0045333** | 0,009 | 4,743 | 1 | 5 | 19 | cellular respiration |
| **GO:0006873** | 0,01 | 2,525 | 5 | 11 | 68 | cellular ion homeostasis |

## Genes in cluster:

| Entrez Id | Symbol | description |
|---|---|---|
| **474403** | CS | citrate synthase |

| | | |
|---|---|---|
| **607115** | CNPY2 | canopy 2 homolog (zebrafish) |
| **610360** | FECH | ferrochelatase |
| **476198** | ME2 | malic enzyme 2, NAD(+)-dependent, mitochondrial |
| **481134** | TSFM | Ts translation elongation factor, mitochondrial |
| **442965** | UTRN | utrophin |
| **476245** | MTHFD1L | methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like |
| **481489** | PRRC1 | proline-rich coiled-coil 1 |
| **476258** | SOD2 | superoxide dismutase 2, mitochondrial |
| **607061** | TRABD | TraB domain containing |
| **474473** | SAMM50 | sorting and assembly machinery component 50 homolog (S. cerevisiae) |
| **481226** | NAGA | N-acetylgalactosaminidase, alpha- |
| **481234** | CHADL | chondroadherin-like |
| **481524** | HNRNPA0 | heterogeneous nuclear ribonucleoprotein A0 |
| **474700** | MATR3 | matrin 3 |
| **475201** | CALU | calumenin |
| **608746** | TOM1 | target of myb1 (chicken) |
| **481576** | ACO1 | aconitase 1, soluble |
| **481582** | NOL6 | nucleolar protein family 6 (RNA-associated) |
| **484188** | ERMP1 | endoplasmic reticulum metallopeptidase 1 |
| **403689** | TRIM28 | tripartite motif containing 28 |
| **482343** | MACC1 | metastasis associated in colon cancer 1 |
| **404018** | SEC61B | Sec61 beta subunit |
| **481884** | MYO6 | myosin VI |
| **482355** | GPNMB | glycoprotein (transmembrane) nmb |
| **481376** | PNPT1 | polyribonucleotide nucleotidyltransferase 1 |
| **479610** | HIBADH | 3-hydroxyisobutyrate dehydrogenase |
| **403550** | ALB | albumin |
| **610135** | LOC610135 | similar to small nuclear ribonucleoprotein polypeptide G |
| **503863** | CAPZA2 | capping protein (actin filament) muscle Z-line, alpha 2 |
| **475668** | PDIA6 | protein disulfide isomerase family A, member 6 |
| **475518** | GSTK1 | glutathione S-transferase kappa 1 |
| **484388** | SNRNP70 | small nuclear ribonucleoprotein 70kDa (U1) |
| **403978** | DLD | dihydrolipoamide dehydrogenase |
| **403523** | BAX | BCL2-associated X protein |
| **484391** | NUCB1 | nucleobindin 1 |
| **484417** | EHD2 | EH-domain containing 2 |
| **612960** | NAPA | N-ethylmaleimide-sensitive factor attachment protein, alpha |
| **476773** | CHORDC1 | cysteine and histidine-rich domain (CHORD) containing 1 |
| **475374** | LOC475374 | similar to Alcohol dehydrogenase [NADP+] (Aldehyde reductase) (Aldo-keto reductase family 1 member A1) |
| **477023** | ACAA1 | acetyl-CoA acyltransferase 1 |
| **485604** | ENTPD3 | ectonucleoside triphosphate diphosphohydrolase 3 |
| **475713** | WDR43 | WD repeat domain 43 |
| **476152** | PRPF40A | PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae) |
| **483369** | P4HB | prolyl 4-hydroxylase, beta polypeptide |
| **477294** | MRPS31 | mitochondrial ribosomal protein S31 |
| **475730** | SRSF7 | serine/arginine-rich splicing factor 7 |
| **482609** | SNRPF | small nuclear ribonucleoprotein polypeptide F |
| **476831** | PRKCDBP | protein kinase C, delta binding protein |
| **482618** | TMPO | thymopoietin |
| **403170** | HMGB1 | high mobility group box 1 |
| **476562** | SUCLG2 | succinate-CoA ligase, GDP-forming, beta subunit |
| **475742** | SNRNP200 | small nuclear ribonucleoprotein 200kDa (U5) |
| **477597** | PFDN5 | prefoldin subunit 5 |
| **476574** | PDHB | pyruvate dehydrogenase (lipoamide) beta |

| | | |
|---|---|---|
| **485385** | SWAP70 | SWAP switching B-cell complex 70kDa subunit |
| **404019** | HSP90B1 | heat shock protein 90kDa beta (Grp94), member 1 |
| **488888** | LOC488888 | hypothetical LOC488888 |
| **476503** | LOC476503 | similar to ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 |
| **486068** | HMGB2 | high mobility group box 2 |
| **475775** | SUCLG1 | succinate-CoA ligase, alpha subunit |
| **477781** | ALDH18A1 | aldehyde dehydrogenase 18 family, member A1 |
| **477482** | ERP29 | endoplasmic reticulum protein 29 |
| **477488** | PTPN11 | protein tyrosine phosphatase, non-receptor type 11 |
| **487050** | CDH17 | cadherin 17, LI cadherin (liver-intestine) |
| **607040** | HIBCH | 3-hydroxyisobutyryl-CoA hydrolase |
| **478934** | SNRPE | small nuclear ribonucleoprotein polypeptide E |
| **479700** | GBAS | glioblastoma amplified sequence |
| **608421** | MANF | mesencephalic astrocyte-derived neurotrophic factor |
| **488246** | ALDH5A1 | aldehyde dehydrogenase 5 family, member A1 |
| **610883** | ACOT13 | acyl-CoA thioesterase 13 |
| **489293** | SRPR | signal recognition particle receptor (docking protein) |
| **490236** | RNPEP | arginyl aminopeptidase (aminopeptidase B) |
| **403739** | COL17A1 | collagen, type XVII, alpha 1 |
| **403486** | PPP3CA | protein phosphatase 3, catalytic subunit, alpha isozyme |
| **607017** | SBDS | Shwachman-Bodian-Diamond syndrome |
| **478854** | HSPD1 | heat shock 60kDa protein 1 (chaperonin) |
| **478855** | LOC478855 | similar to heat shock 10kDa protein 1 (chaperonin 10) |
| **487993** | POGLUT1 | protein O-glucosyltransferase 1 |
| **478634** | SDHA | succinate dehydrogenase complex, subunit A, flavoprotein (Fp) |
| **478963** | IARS2 | isoleucyl-tRNA synthetase 2, mitochondrial |
| **478506** | HADH | hydroxyacyl-CoA dehydrogenase |
| **479714** | GTF2I | general transcription factor IIi |
| **480255** | PCK2 | phosphoenolpyruvate carboxykinase 2 (mitochondrial) |
| **479043** | IDH2 | isocitrate dehydrogenase 2 (NADP+), mitochondrial |
| **477839** | LOC477839 | similar to Thioredoxin-dependent peroxide reductase, mitochondrial precursor (Peroxiredoxin 3) (Antioxidant protein 1) (AOP-1) (MER5 protein homolog) (HBC189) (PRX III) |
| **479410** | HYOU1 | hypoxia up-regulated 1 |
| **480971** | LOC480971 | similar to Ewing sarcoma breakpoint region 1 isoform EWS |
| **477686** | EPS8 | epidermal growth factor receptor pathway substrate 8 |
| **488648** | PFDN2 | prefoldin subunit 2 |
| **488664** | UAP1 | UDP-N-acteylglucosamine pyrophosphorylase 1 |
| **478279** | PDIA3 | protein disulfide isomerase family A, member 3 |
| **491776** | PRDX4 | peroxiredoxin 4 |
| **480864** | ACOT9 | acyl-CoA thioesterase 9 |
| **607482** | BCR | breakpoint cluster region |
| **477554** | LOC477554 | similar to small nuclear ribonucleoprotein D3 |
| **403907** | PNN | pinin, desmosome associated protein |
| **491830** | MID1IP1 | MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish)) |
| **490935** | EFTUD2 | elongation factor Tu GTP binding domain containing 2 |
| **479446** | RDX | radixin |
| **489421** | ACAT1 | acetyl-CoA acetyltransferase 1 |
| **403934** | CDC42 | cell division cycle 42 (GTP binding protein, 25kDa) |
| **490691** | ERO1L | ERO1-like (S. cerevisiae) |
| **607705** | ATP6V0A1 | ATPase, H+ transporting, lysosomal V0 subunit a1 |
| **477715** | NCAPD2 | non-SMC condensin I complex, subunit D2 |
| **478210** | AKR7A2 | aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase) |
| **490967** | STAT3 | signal transducer and activator of transcription 3 (acute-phase response factor) |
| **483780** | NXF1 | nuclear RNA export factor 1 |
| **403941** | RAB5C | RAB5C, member RAS oncogene family |

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|---|---|---|
| **479752** | AIMP2 | aminoacyl tRNA synthetase complex-interacting multifunctional protein 2 |
| **480092** | FH | fumarate hydratase |
| **483784** | GANAB | glucosidase, alpha; neutral AB |
| **490975** | FKBP10 | FK506 binding protein 10, 65 kDa |
| **403674** | EIF1 | eukaryotic translation initiation factor 1 |
| **487421** | EPHA2 | EPH receptor A2 |
| **480112** | PYCR2 | pyrroline-5-carboxylate reductase family, member 2 |
| **479116** | PGM2 | phosphoglucomutase 2 |
| **480930** | HSD17B10 | hydroxysteroid (17-beta) dehydrogenase 10 |
| **480130** | MTX1 | metaxin 1 |
| **490789** | EIF2B2 | eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa |
| **476694** | CALR | calreticulin |
| **476699** | ASNA1 | arsA arsenite transporter, ATP-binding, homolog 1 (bacterial) |
| **479796** | TUFM | Tu translation elongation factor, mitochondrial |
| **490810** | LOC490810 | similar to CG33071-PC, isoform C |
| **479313** | CLINT1 | clathrin interactor 1 |
| **484941** | PRKCSH | protein kinase C substrate 80K-H |
| **476708** | RAB3D | RAB3D, member RAS oncogene family |
| **479805** | NDUFAB1 | NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa |
| **611211** | AP1M2 | adaptor-related protein complex 1, mu 2 subunit |
| **490500** | DSG2 | desmoglein 2 |
| **480605** | AP2B1 | adaptor-related protein complex 2, beta 1 subunit |
| **480178** | SNRPD1 | small nuclear ribonucleoprotein D1 polypeptide 16kDa |
| **479331** | CSNK1A1 | casein kinase 1, alpha 1 |
| **491142** | NLE1 | notchless homolog 1 (Drosophila) |
| **403880** | STXBP2 | syntaxin binding protein 2 |
| **485005** | TIMM44 | translocase of inner mitochondrial membrane 44 homolog (yeast) |
| **481037** | LAMP2 | lysosomal-associated membrane protein 2 |
| **481038** | MCTS1 | malignant T cell amplified sequence 1 |
| **611425** | LONP1 | lon peptidase 1, mitochondrial |
| **480635** | BLMH | bleomycin hydrolase |
| **489585** | CPT2 | carnitine palmitoyltransferase 2 |
| **479564** | SCP2 | sterol carrier protein 2 |
| **479880** | RNPS1 | RNA binding protein S1, serine-rich domain |
| **611859** | POLR2E | polymerase (RNA) II (DNA directed) polypeptide E, 25kDa |
| **480677** | PMPCA | peptidase (mitochondrial processing) alpha |
| **611810** | GNAI3 | guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3 |
| **479659** | SF3B3 | splicing factor 3b, subunit 3, 130kDa |
| **480726** | HSPA5 | heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa) |
| **479685** | ATP6V0D1 | ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d1 |
| **490679** | ARF6 | ADP-ribosylation factor 6 |
| **488269** | LOC488269 | similar to Histone H1.4 (Histone H1b) |
| **476018** | DRAP1 | DR1-associated protein 1 (negative cofactor 2 alpha) |

# Cluster 6

## Enriched Terms:

| Gene to GO BP Conditional test for over-representation GOBPID | Pvalue | OddsRatio | ExpCount | Count | Size | Term |
|---|---|---|---|---|---|---|
| **GO:0006414** | 0 | 23,644 | 7 | 48 | 79 | translational elongation |
| **GO:0009059** | 0 | 7,008 | 16 | 57 | 211 | macromolecule biosynthetic process |
| **GO:0000022** | 0 | 14,465 | 3 | 20 | 37 | mitotic spindle elongation |
| **GO:0044260** | 0 | 3,342 | 71 | 112 | 857 | cellular macromolecule metabolic process |
| **GO:0044249** | 0 | 3,437 | 28 | 59 | 361 | cellular biosynthetic process |
| **GO:0019538** | 0 | 2,864 | 50 | 86 | 589 | protein metabolic process |
| **GO:0071843** | 0 | 5,065 | 8 | 27 | 94 | cellular component biogenesis at cellular level |
| **GO:0006364** | 0 | 7,713 | 3 | 15 | 38 | rRNA processing |
| **GO:0007051** | 0 | 4,144 | 8 | 24 | 95 | spindle organization |
| **GO:0006396** | 0 | 2,627 | 18 | 36 | 209 | RNA processing |
| **GO:0007017** | 0 | 2,835 | 13 | 28 | 149 | microtubule-based process |
| **GO:0043487** | 0 | 13,202 | 1 | 7 | 13 | regulation of RNA stability |
| **GO:0042254** | 0 | 8,336 | 2 | 8 | 20 | ribosome biogenesis |
| **GO:0008152** | 0 | 2,178 | 112 | 132 | 1326 | metabolic process |
| **GO:0048255** | 0 | 13,498 | 1 | 6 | 11 | mRNA stabilization |
| **GO:0070925** | 0 | 7,567 | 2 | 8 | 20 | organelle assembly |
| **GO:0042273** | 0 | 11,242 | 1 | 6 | 12 | ribosomal large subunit biogenesis |
| **GO:0034660** | 0 | 3,161 | 6 | 16 | 75 | ncRNA metabolic process |
| **GO:0000028** | 0,001 | 22,245 | 1 | 4 | 6 | ribosomal small subunit assembly |
| **GO:0006417** | 0,001 | 4,07 | 3 | 10 | 38 | regulation of translation |
| **GO:0090304** | 0,001 | 1,751 | 39 | 56 | 465 | nucleic acid metabolic process |
| **GO:0010556** | 0,001 | 2,103 | 15 | 27 | 180 | regulation of macromolecule biosynthetic process |
| **GO:0022403** | 0,002 | 2,13 | 14 | 25 | 164 | cell cycle phase |
| **GO:0031326** | 0,002 | 1,965 | 17 | 29 | 205 | regulation of cellular biosynthetic process |
| **GO:0007010** | 0,004 | 1,88 | 19 | 30 | 220 | cytoskeleton organization |
| **GO:0010468** | 0,004 | 1,821 | 21 | 33 | 250 | regulation of gene expression |
| **GO:0071826** | 0,004 | 3,392 | 3 | 9 | 39 | ribonucleoprotein complex subunit organization |
| **GO:0000291** | 0,007 | Inf | 0 | 2 | 2 | nuclear-transcribed mRNA catabolic process, exonucleolytic |
| **GO:0006412** | 0,007 | 2,63 | 5 | 11 | 83 | translation |
| **GO:0006402** | 0,008 | 5,062 | 1 | 5 | 16 | mRNA catabolic process |
| **GO:0042157** | 0,01 | 11,045 | 1 | 3 | 6 | lipoprotein metabolic process |

## Genes in cluster:

| Entrez Id | Symbol | description |
|---|---|---|
| **478509** | LOC478509 | similar to ribosomal protein L34 |
| **490572** | LOC490572 | similar to myosin, light polypeptide 6, alkali, smooth muscle and non-muscle |
| **474830** | TUBB | tubulin, beta |
| **612751** | PABPC1 | poly(A) binding protein, cytoplasmic 1 |
| **476328** | LOC476328 | similar to 60S ribosomal protein L29 (Cell surface heparin binding protein HIP) |
| **474672** | P4HA2 | prolyl 4-hydroxylase, alpha polypeptide II |

| | | |
|---|---|---|
| **403685** | RPS18 | ribosomal protein S18 |
| **609684** | LOC609684 | similar to breast cancer membrane protein 101 |
| **474877** | LOC474877 | similar to 40S ribosomal protein S10 |
| **481774** | LOC481774 | similar to U1 small nuclear ribonucleoprotein C (U1 snRNP protein C) (U1C protein) (U1-C) |
| **607574** | CHCHD3 | coiled-coil-helix-coiled-coil-helix domain containing 3 |
| **474698** | LOC474698 | similar to catenin (cadherin-associated protein), alpha 1, 102kDa |
| **474656** | LOC474656 | similar to ribosomal protein L10a |
| **474504** | LOC474504 | similar to 60S ribosomal protein L3 (L4) |
| **474887** | SRPK1 | SRSF protein kinase 1 |
| **482266** | FLNC | filamin C, gamma |
| **475203** | RBM28 | RNA binding motif protein 28 |
| **475130** | RPL8 | ribosomal protein L8 |
| **474524** | LOC474524 | similar to CG9987-PA |
| **403855** | PON2 | paraoxonase 2 |
| **481543** | LOC481543 | similar to ribosomal protein L31 |
| **476366** | RPS5 | ribosomal protein S5 |
| **482437** | SLC2A1 | solute carrier family 2 (facilitated glucose transporter), member 1 |
| **476387** | RPS9 | ribosomal protein S9 |
| **479350** | LOC479350 | similar to ribosomal protein L37 |
| **403684** | RPS11 | ribosomal protein S11 |
| **442938** | FLT3LG | fms-related tyrosine kinase 3 ligand |
| **476422** | RPL18 | ribosomal protein L18 |
| **475889** | SYPL1 | synaptophysin-like 1 |
| **484627** | LOC484627 | similar to H1 histone family, member X |
| **608089** | LOC608089 | similar to Adipocyte plasma membrane-associated protein (BSCv protein) |
| **476780** | PICALM | phosphatidylinositol binding clathrin assembly protein |
| **476523** | MRPS25 | mitochondrial ribosomal protein S25 |
| **475381** | RPS8 | ribosomal protein S8 |
| **475410** | LOC475410 | similar to 60S ribosomal protein L32 |
| **476120** | DDX18 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 |
| **476450** | RPS19 | ribosomal protein S19 |
| **477031** | LOC477031 | similar to ribosomal protein L14 |
| **478018** | PITRM1 | pitrilysin metallopeptidase 1 |
| **476804** | RPS3 | ribosomal protein S3 |
| **485628** | STT3B | STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae) |
| **476463** | RPS16 | ribosomal protein S16 |
| **478021** | GTPBP4 | GTP binding protein 4 |
| **475922** | EIF4A3 | eukaryotic translation initiation factor 4A3 |
| **476466** | HNRNPL | heterogeneous nuclear ribonucleoprotein L |
| **477046** | RPL15 | ribosomal protein L15 |
| **483038** | CYP1B1 | cytochrome P450, family 1, subfamily B, polypeptide 1 |
| **475044** | LOC475044 | similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP) |
| **612871** | NOP56 | NOP56 ribonucleoprotein homolog (yeast) |
| **475942** | PDHX | pyruvate dehydrogenase complex, component X |
| **476842** | LOC476842 | similar to ribosomal protein L27a |
| **607420** | CAPRIN1 | cell cycle associated protein 1 |
| **477760** | BMS1 | BMS1 homolog, ribosome assembly protein (yeast) |
| **478067** | NDUFAF2 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 2 |
| **486246** | DDX55 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 55 |
| **485845** | RALY | RNA binding protein, autoantigenic (hnRNP-associated with lethal yellow homolog (mouse)) |
| **477197** | EIF2S2 | eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa |
| **403677** | RPS3A | ribosomal protein S3A |
| **477912** | RPL7 | ribosomal protein L7 |
| **479257** | LOC479257 | similar to ribosomal protein S24 isoform 3 |

| | | |
|---|---|---|
| **442971** | CLU | clusterin |
| **477112** | EIF2A | eukaryotic translation initiation factor 2A, 65kDa |
| **612261** | MRPL53 | mitochondrial ribosomal protein L53 |
| **608138** | TUBA1C | tubulin, alpha 1c |
| **479159** | RPS23 | ribosomal protein S23 |
| **480235** | LOC480235 | similar to ribosomal protein S13 |
| **487034** | CPNE3 | copine III |
| **403691** | RPL6 | Ribosomal protein L6 |
| **476976** | HNRPDL | heterogeneous nuclear ribonucleoprotein D-like |
| **486112** | STC1 | stanniocalcin 1 |
| **488443** | WDR75 | WD repeat domain 75 |
| **478701** | TUBB2A | tubulin, beta 2A |
| **477944** | LOC477944 | similar to ubiquinol-cytochrome c reductase binding protein |
| **475805** | BCAS2 | breast carcinoma amplified sequence 2 |
| **475991** | RPLP2 | ribosomal protein, large, P2 |
| **478547** | RPL24 | ribosomal protein L24 |
| **475807** | CSDE1 | cold shock domain containing E1, RNA-binding |
| **477801** | NPM3 | nucleophosmin/nucleoplasmin 3 |
| **479011** | YBX1 | Y box binding protein 1 |
| **477505** | GCN1L1 | GCN1 general control of amino-acid synthesis 1-like 1 (yeast) |
| **477510** | SRSF9 | serine/arginine-rich splicing factor 9 |
| **486886** | SMC3 | structural maintenance of chromosomes 3 |
| **489300** | STT3A | STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae) |
| **608445** | NCL | nucleolin |
| **476824** | LOC476824 | similar to NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial precursor (Complex I-23KD) (CI-23KD) (TYKY subunit) |
| **478158** | PUM1 | pumilio homolog 1 (Drosophila) |
| **477258** | STAU1 | staufen, RNA binding protein, homolog 1 (Drosophila) |
| **478161** | YTHDF2 | YTH domain family, member 2 |
| **608455** | UQCRC1 | ubiquinol-cytochrome c reductase core protein I |
| **610648** | RBM4 | RNA binding motif protein 4 |
| **479412** | RPS25 | ribosomal protein S25 |
| **607667** | NOP58 | NOP58 ribonucleoprotein homolog (yeast) |
| **478876** | WDR12 | WD repeat domain 12 |
| **478973** | COPA | coatomer protein complex, subunit alpha |
| **478597** | RPL35A | ribosomal protein L35a |
| **478981** | NDUFS2 | NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase) |
| **610762** | RAB1B | RAB1B, member RAS oncogene family |
| **403681** | RPS17 | ribosomal protein S17 |
| **478662** | IGF2BP2 | insulin-like growth factor 2 mRNA binding protein 2 |
| **608074** | HNRNPA3 | heterogeneous nuclear ribonucleoprotein A3 |
| **478664** | DNAJB11 | DnaJ (Hsp40) homolog, subfamily B, member 11 |
| **403788** | ITGB3 | integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) |
| **442942** | PTGS2 | prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) |
| **480751** | RPL30 | ribosomal protein L30 |
| **480494** | NMT1 | N-myristoyltransferase 1 |
| **479886** | RPS2 | ribosomal protein S2 |
| **479234** | HK1 | hexokinase 1 |
| **483748** | FAU | Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed |
| **610596** | RPS29 | ribosomal protein S29 |
| **480503** | UBTF | upstream binding transcription factor, RNA polymerase I |
| **478828** | NCKAP1 | NCK-associated protein 1 |
| **478904** | RPL37A | ribosomal protein L37a |
| **476664** | UPF1 | UPF1 regulator of nonsense transcripts homolog (yeast) |
| **403688** | RPL27 | ribosomal protein L27 |

| | | |
|---|---|---|
| **489047** | DNAJC9 | DnaJ (Hsp40) homolog, subfamily C, member 9 |
| **611645** | NOP2 | NOP2 nucleolar protein homolog (yeast) |
| **476637** | LOC476637 | similar to ribosomal protein L18a |
| **478213** | TAS1R2 | taste receptor, type 1, member 2 |
| **479109** | RPL9 | ribosomal protein L9 |
| **480361** | EIF2S1 | eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa |
| **478325** | MYO1E | myosin IE |
| **491064** | IGF2BP1 | insulin-like growth factor 2 mRNA binding protein 1 |
| **489409** | LOC489409 | similar to secretory carrier membrane protein 3 isoform 1 |
| **476525** | LOC476525 | similar to 60S ribosomal protein L26 (Silica-induced gene 20 protein) (SIG-20) |
| **607081** | LOC607081 | similar to non-POU domain containing, octamer-binding |
| **403893** | RPS4Y1 | ribosomal protein S4, Y-linked 1 |
| **478348** | LOC478348 | similar to ribosomal protein L4 |
| **480139** | ILF2 | interleukin enhancer binding factor 2, 45kDa |
| **478356** | RPLP1 | ribosomal protein, large, P1 |
| **612929** | LARP1 | La ribonucleoprotein domain family, member 1 |
| **403678** | RPL7A | Ribosomal protein L7a |
| **484950** | ILF3 | interleukin enhancer binding factor 3, 90kDa |
| **610121** | INTS2 | integrator complex subunit 2 |
| **610402** | HNF1B | HNF1 homeobox B |
| **490868** | CDC42BPB | CDC42 binding protein kinase beta (DMPK-like) |
| **480466** | LOC480466 | similar to ELAV-like protein 1 (Hu-antigen R) (HuR) |
| **491153** | MYO1D | myosin ID |
| **492093** | SLC25A5 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 |
| **485010** | RPS28 | ribosomal protein S28 |
| **611619** | RAB11B | RAB11B, member RAS oncogene family |
| **479347** | OXCT1 | 3-oxoacid CoA transferase 1 |
| **479360** | NUP155 | nucleoporin 155kDa |
| **490560** | AFG3L2 | AFG3 ATPase family gene 3-like 2 (S. cerevisiae) |
| **479847** | RSL1D1 | ribosomal L1 domain containing 1 |
| **479283** | LOC479283 | similar to Activated RNA polymerase II transcriptional coactivator p15 (Positive cofactor 4) (PC4) (p14) |
| **475077** | RPL17 | ribosomal protein L17 |
| **403912** | GNB1 | guanine nucleotide binding protein (G protein), beta polypeptide 1 |
| **479569** | MRPL20 | mitochondrial ribosomal protein L20 |
| **403914** | GNA11 | guanine nucleotide binding protein (G protein), alpha 11 (Gq class) |
| **485070** | LMNB2 | lamin B2 |
| **490064** | TBL3 | transducin (beta)-like 3 |
| **479887** | NDUFB10 | NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa |
| **476755** | CIRBP | cold inducible RNA binding protein |
| **481085** | RPL10 | ribosomal protein L10 |
| **479587** | RPL22 | ribosomal protein L22 |
| **485097** | PTBP1 | polypyrimidine tract binding protein 1 |
| **608025** | TUBB3 | tubulin, beta 3 |
| **479612** | RPL13 | ribosomal protein L13 |
| **479929** | DBT | dihydrolipoamide branched chain transacylase E2 |
| **476346** | RPL12 | ribosomal protein L12 |
| **479947** | TMED5 | transmembrane emp24 protein transport domain containing 5 |
| **480729** | RPL35 | ribosomal protein L35 |
| **442858** | CDH1 | cadherin 1, type 1, E-cadherin (epithelial) |
| **489745** | ESRP2 | epithelial splicing regulatory protein 2 |
| **475827** | RBM8A | RNA binding motif protein 8A |
| **476753** | RPS15 | ribosomal protein S15 |
| **474599** | RPS27A | ribosomal protein S27a |
| **476738** | RPL36 | ribosomal protein L36 |

|  |  |  |
|---|---|---|
| **478450** | HNRNPD | heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa) |
| **478576** | LOC478576 | similar to ribosomal protein S15a |