

| Lens Contig | Description | dorsal 1 |
|--------------------|---|-----------------|
| Contig_175 | 26s proteasome complex subunit dss1 | -0.833 |
| Contig_376 | 28s ribosomal protein mitochondrial-like | -1.584 |
| Contig_250 | 2-oxoisovalerate dehydrogenase subunit mitochondrial-like | -1.729 |
| Contig_459 | 3-hydroxybutyrate dehydrogenase type 2 | -3.468 |
| Contig_461 | 60s ribosomal protein l12-like | <missing> |
| Contig_287 | 60s ribosomal protein l9-like | -0.731 |
| Contig_300 | a chain crystal structures of transition state analogue inhibitors of inosine m | -2.110 |
| Contig_191 | acetyl- mitochondrial precursor | -0.331 |
| Contig_362 | acidic leucine-rich nuclear phosphoprotein 32 family member b | 0.302 |
| Contig_38 | actin related protein 2 3 subunit 41kda | 1.441 |
| Contig_439 | actin-related protein 6 | <missing> |
| Contig_186 | activating transcription factor 4 -iii | -0.912 |
| Contig_343 | acyl- oxidase palmitoyl | 1.774 |
| Contig_223 | adp atp translocase 1 | -1.386 |
| Contig_21 | adp-ribosylation factor 4 | -1.942 |
| Contig_390 | af465439_1beta i spectrin form betai sigma3 | -1.454 |
| Contig_215 | androgen-induced gene 1 | -0.154 |
| Contig_465 | annexin a6 | <missing> |
| Contig_206 | apoptosis-inducing factor 3-like | -0.220 |
| Contig_296 | arachidonate 5-lipoxygenase-activating | 0.908 |
| Contig_30 | arginine-rich mutated in early stage tumors | 0.844 |
| Contig_170 | atp synthase h+ transporting mitochondrial f0 complex subunit f variant 1 | -1.649 |
| Contig_66 | atp synthase lipid-binding mitochondrial precursor | -0.241 |
| Contig_315 | atp-dependent clp protease proteolytic mitochondrial-like | 1.427 |
| Contig_411 | atrial natriuretic factor precursor | 1.963 |
| Contig_398 | bat2 protein | -0.549 |
| Contig_450 | bccip homolog | <missing> |
| Contig_255 | bcl2-like 1 | -1.821 |
| Contig_345 | brix domain-containing protein 2 | 1.784 |
| Contig_463 | b-type natriuretic peptide | -3.493 |
| Contig_371 | cardiac tropomyosin | -2.373 |
| Contig_110 | catenin beta-1 | -2.047 |
| Contig_453 | cd79b antigen | <missing> |
| Contig_432 | cdkn2aip n-terminal-like protein | 3.448 |
| Contig_163 | cell cycle checkpoint protein rad1-like | -1.424 |
| Contig_164 | cell cycle checkpoint protein rad1-like | 1.350 |
| Contig_68 | cement precursor protein 3b variant 1 | -0.257 |
| Contig_242 | chromosome 11 open reading frame isoform cra_c | -1.579 |
| Contig_111 | chromosome 22 open reading frame 25 | -0.832 |
| Contig_193 | coagulation factor xi precursor | -1.161 |
| Contig_353 | coatomer subunit zeta-1 | -2.723 |
| Contig_347 | coiled-coil domain-containing protein 80 precursor | -0.516 |
| Contig_99 | collagen type i alpha 1 | 0.057 |
| Contig_457 | cop9 signalosome complex subunit 4 | <missing> |
| Contig_326 | copper metabolism domain containing 1 | <missing> |

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|------------|--|-----------|
| Contig_301 | c-type lectin domain family 2 member d-like | -2.323 |
| Contig_349 | cyclin-dependent kinase 7 | <missing> |
| Contig_231 | cysteine and glycine-rich protein 1 | -1.490 |
| Contig_257 | cysteine-rich protein 1 | -1.919 |
| Contig_352 | cytochrome b-c1 complex subunit mitochondrial-like | -2.592 |
| Contig_83 | cytochrome c oxidase subunit 2 | 0.850 |
| Contig_408 | cytochrome c oxidase subunit 3 | <missing> |
| Contig_271 | cytochrome c oxidase subunit iv isoform 1 | 0.333 |
| Contig_365 | cytochrome c oxidase subunit viia polypeptide 2 like | -1.407 |
| Contig_18 | cytochrome testis-specific | 1.540 |
| Contig_308 | cytoplasmic 1 (beta actin) | 1.376 |
| Contig_230 | cytoskeletal calmodulin and titin-interacting | -1.478 |
| Contig_444 | cytosolic phospholipase a2 gamma-like | <missing> |
| Contig_12 | d chain crystal structure of xenavidin | 3.088 |
| Contig_447 | dead (asp-glu-ala-as) box polypeptide 19b | -3.213 |
| Contig_91 | death-associated 1-a | -1.958 |
| Contig_162 | derlin-1-like isoform 1 | 1.427 |
| Contig_259 | dickkopf-related protein 3 precursor | -1.839 |
| Contig_281 | dna-directed dna polymerase delta 1 | -2.034 |
| Contig_44 | dnaj homolog subfamily a member 1 | -0.436 |
| Contig_29 | dynein light chain cytoplasmic | 0.895 |
| Contig_383 | electron-transfer- beta polypeptide | -1.303 |
| Contig_366 | elongation factor 1-beta | 0.903 |
| Contig_426 | envelope glycoprotein | -0.566 |
| Contig_10 | envelope protein syncytin-car1 | 1.081 |
| Contig_104 | envelope protein syncytin-car1 | 1.592 |
| Contig_25 | enzymatic polyprotein | -1.830 |
| Contig_417 | eri1 exoribonuclease 3 | -0.104 |
| Contig_336 | eukaryotic translation elongation factor 1 gamma | -0.340 |
| Contig_322 | eukaryotic translation initiation factor 2 alpha kinase 4 | -2.668 |
| Contig_151 | family with sequence similarity 32 member a variant 1 | 2.839 |
| Contig_324 | f-box lrr-repeat protein 8-like | -2.547 |
| Contig_360 | fibrinogen silencer-binding | 2.457 |
| Contig_50 | gaba receptor-associated 2 | -0.463 |
| Contig_33 | gamma-secretase subunit pen-2 | -1.737 |
| Contig_264 | gap junction gamma-1 protein | 0.119 |
| Contig_309 | gelsolin (finnish type) | -1.894 |
| Contig_407 | general transcription factor 12kda | -2.830 |
| Contig_214 | general transcription factor ii-i repeat domain-containing protein 2a | -0.170 |
| Contig_405 | glutathione peroxidase 1 | 2.209 |
| Contig_238 | glutathione peroxidase 4b | -1.635 |
| Contig_245 | glycerol-3-phosphate dehydrogenase 1b | -1.490 |
| Contig_316 | glycolipid transfer protein domain-containing protein 1-like | 1.564 |
| Contig_37 | guanosine-3 -bis 3 -pyrophosphohydrolase mesh1 | -1.697 |
| Contig_416 | guanylate binding protein 3 | <missing> |
| Contig_115 | hba1_plewa ame: full=hemoglobin subunit alpha-1 ame: full=alpha-1-globin | 0.640 |

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| Contig_26 | hbb1_tricr ame: full=hemoglobin subunit beta-1 ame: full=beta-1-globin am | 0.355 |
| Contig_1 | hbb2_tricr ame: full=hemoglobin subunit beta-2 ame: full=beta-2-globin am | -0.312 |
| Contig_85 | heat shock factor binding protein 1 | 0.744 |
| Contig_243 | heat shock protein beta-7 | -1.432 |
| Contig_305 | heparan sulfate 3-o-sulfotransferase 1 | 1.352 |
| Contig_100 | hepatitis b virus x-interacting protein homolog | -1.380 |
| Contig_425 | hig1 domain family member 2a | -3.175 |
| Contig_57 | hig1 domain member 1a | 1.318 |
| Contig_292 | high choriolytic enzyme 1 precursor | 0.824 |
| Contig_55 | high-mobility group nucleosome binding domain isoform cra_a | -0.249 |
| Contig_58 | histone (H2AFZ) | 0.350 |
| Contig_320 | histone-lysine n-methyltransferase setd2 | 1.903 |
| Contig_275 | hiv tat specific factor 1 | -2.055 |
| Contig_179 | homolog precursor (CutA) | -1.308 |
| Contig_286 | immunoglobulin m heavy chain constant region | 0.841 |
| Contig_310 | integrase core domain protein | 1.391 |
| Contig_280 | interferon-induced very large gtpase 1-like | 0.490 |
| Contig_370 | isocitrate dehydrogenase | -0.468 |
| Contig_272 | light tctex-type 1 | -1.996 |
| Contig_128 | line-1 element orf2 | -0.779 |
| Contig_386 | line-1 reverse transcriptase homolog | -3.308 |
| Contig_290 | l-isoaspartyl d-aspartyl protein carboxyl partial | 1.476 |
| Contig_298 | l-lactate dehydrogenase a chain | 1.317 |
| Contig_282 | loc100036815 protein | 0.593 |
| Contig_47 | low quality protein: neuroblast differentiation-associated protein ahnak-like | -0.581 |
| Contig_169 | lupus la protein | -0.713 |
| Contig_395 | lymphocyte cytosolic protein 1 (l-plastin) | 1.984 |
| Contig_258 | lysozyme g | 0.150 |
| Contig_20 | major vault protein | 0.362 |
| Contig_160 | methionine synthase reductase | -3.434 |
| Contig_328 | mgc89163 protein | 1.655 |
| Contig_218 | microfibril-associated glycoprotein 4-like | -1.490 |
| Contig_466 | microsomal glutathione s-transferase 3 | -3.370 |
| Contig_36 | middle subunit | 0.368 |
| Contig_48 | minor alpha-globin partial | -0.324 |
| Contig_49 | mitochondrial atp h+ transporting f1 complex beta subunit | 1.558 |
| Contig_78 | mitochondrial import receptor subunit tom22 homolog | <missing> |
| Contig_358 | mitochondrial inner membrane | -3.431 |
| Contig_86 | mitochondrial ribosomal protein s21 | 1.309 |
| Contig_325 | mmp18 protein | 1.558 |
| Contig_427 | multivesicular body subunit 12a-like | 2.311 |
| Contig_401 | muscle creatine kinase | -2.916 |
| Contig_126 | myelin p2 protein | -0.122 |
| Contig_95 | myelin p2 protein | -1.720 |
| Contig_241 | myeloid leukemia factor 1 | -1.625 |
| Contig_155 | myosin light polypeptide 6 | 0.449 |

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|------------|----------------------------|-----------|
| Contig_35 | myosin light polypeptide 6 | 0.568 |
| Contig_101 | ---NA--- | -0.076 |
| Contig_102 | ---NA--- | -0.349 |
| Contig_103 | ---NA--- | -0.696 |
| Contig_105 | ---NA--- | -0.230 |
| Contig_106 | ---NA--- | -0.677 |
| Contig_107 | ---NA--- | -0.259 |
| Contig_108 | ---NA--- | 0.089 |
| Contig_11 | ---NA--- | 2.086 |
| Contig_112 | ---NA--- | -0.204 |
| Contig_113 | ---NA--- | -0.354 |
| Contig_116 | ---NA--- | 0.266 |
| Contig_117 | ---NA--- | -0.466 |
| Contig_118 | ---NA--- | -1.388 |
| Contig_119 | ---NA--- | -0.797 |
| Contig_120 | ---NA--- | -0.593 |
| Contig_121 | ---NA--- | 1.371 |
| Contig_123 | ---NA--- | <missing> |
| Contig_127 | ---NA--- | -0.434 |
| Contig_129 | ---NA--- | -0.549 |
| Contig_13 | ---NA--- | -0.362 |
| Contig_130 | ---NA--- | -0.049 |
| Contig_131 | ---NA--- | <missing> |
| Contig_132 | ---NA--- | -0.253 |
| Contig_133 | ---NA--- | -0.280 |
| Contig_134 | ---NA--- | -0.551 |
| Contig_135 | ---NA--- | -2.613 |
| Contig_136 | ---NA--- | -1.622 |
| Contig_137 | ---NA--- | -0.538 |
| Contig_139 | ---NA--- | -1.933 |
| Contig_141 | ---NA--- | -0.401 |
| Contig_142 | ---NA--- | 2.358 |
| Contig_143 | ---NA--- | 2.152 |
| Contig_144 | ---NA--- | 1.615 |
| Contig_145 | ---NA--- | -1.636 |
| Contig_146 | ---NA--- | -2.018 |
| Contig_147 | ---NA--- | -0.275 |
| Contig_148 | ---NA--- | -0.298 |
| Contig_149 | ---NA--- | -0.515 |
| Contig_15 | ---NA--- | -0.316 |
| Contig_150 | ---NA--- | -0.429 |
| Contig_156 | ---NA--- | -0.266 |
| Contig_157 | ---NA--- | 0.377 |
| Contig_158 | ---NA--- | <missing> |
| Contig_159 | ---NA--- | 0.731 |
| Contig_161 | ---NA--- | 1.867 |

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| Contig_166 | ---NA--- | -1.519 |
| Contig_167 | ---NA--- | -1.475 |
| Contig_168 | ---NA--- | -1.363 |
| Contig_17 | ---NA--- | -1.480 |
| Contig_174 | ---NA--- | -0.387 |
| Contig_176 | ---NA--- | -0.875 |
| Contig_177 | ---NA--- | 0.233 |
| Contig_181 | ---NA--- | -0.315 |
| Contig_182 | ---NA--- | -0.878 |
| Contig_183 | ---NA--- | -0.301 |
| Contig_184 | ---NA--- | -0.316 |
| Contig_188 | ---NA--- | -0.234 |
| Contig_189 | ---NA--- | -0.366 |
| Contig_19 | ---NA--- | -0.679 |
| Contig_190 | ---NA--- | -0.360 |
| Contig_192 | ---NA--- | -0.855 |
| Contig_194 | ---NA--- | -1.297 |
| Contig_195 | ---NA--- | -0.299 |
| Contig_196 | ---NA--- | -0.297 |
| Contig_197 | ---NA--- | -0.245 |
| Contig_200 | ---NA--- | -0.273 |
| Contig_201 | ---NA--- | -1.284 |
| Contig_203 | ---NA--- | -0.400 |
| Contig_204 | ---NA--- | -0.810 |
| Contig_205 | ---NA--- | -0.230 |
| Contig_208 | ---NA--- | -1.097 |
| Contig_209 | ---NA--- | -0.399 |
| Contig_210 | ---NA--- | -0.244 |
| Contig_211 | ---NA--- | -0.325 |
| Contig_212 | ---NA--- | -0.145 |
| Contig_213 | ---NA--- | -1.355 |
| Contig_217 | ---NA--- | -0.760 |
| Contig_221 | ---NA--- | -1.386 |
| Contig_222 | ---NA--- | -0.075 |
| Contig_224 | ---NA--- | -0.059 |
| Contig_225 | ---NA--- | -1.362 |
| Contig_226 | ---NA--- | -1.327 |
| Contig_227 | ---NA--- | -0.401 |
| Contig_228 | ---NA--- | -0.187 |
| Contig_23 | ---NA--- | -0.217 |
| Contig_233 | ---NA--- | -1.455 |
| Contig_235 | ---NA--- | -0.326 |
| Contig_237 | ---NA--- | -0.322 |
| Contig_244 | ---NA--- | -1.405 |
| Contig_246 | ---NA--- | -0.041 |
| Contig_251 | ---NA--- | -1.656 |

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|------------|----------|-----------|
| Contig_252 | ---NA--- | -1.812 |
| Contig_253 | ---NA--- | -1.743 |
| Contig_254 | ---NA--- | -0.451 |
| Contig_256 | ---NA--- | -1.731 |
| Contig_262 | ---NA--- | -1.830 |
| Contig_266 | ---NA--- | -0.440 |
| Contig_268 | ---NA--- | -0.441 |
| Contig_269 | ---NA--- | -0.441 |
| Contig_273 | ---NA--- | -2.034 |
| Contig_276 | ---NA--- | 0.483 |
| Contig_279 | ---NA--- | 0.558 |
| Contig_28 | ---NA--- | 0.701 |
| Contig_283 | ---NA--- | -2.081 |
| Contig_284 | ---NA--- | -1.907 |
| Contig_288 | ---NA--- | 0.619 |
| Contig_291 | ---NA--- | -2.392 |
| Contig_293 | ---NA--- | 0.830 |
| Contig_294 | ---NA--- | 1.334 |
| Contig_297 | ---NA--- | 1.313 |
| Contig_306 | ---NA--- | 1.346 |
| Contig_312 | ---NA--- | -0.493 |
| Contig_313 | ---NA--- | 1.564 |
| Contig_314 | ---NA--- | -2.378 |
| Contig_317 | ---NA--- | 1.412 |
| Contig_321 | ---NA--- | <missing> |
| Contig_330 | ---NA--- | -1.392 |
| Contig_331 | ---NA--- | 1.302 |
| Contig_332 | ---NA--- | 1.726 |
| Contig_333 | ---NA--- | 1.299 |
| Contig_334 | ---NA--- | 1.734 |
| Contig_339 | ---NA--- | <missing> |
| Contig_341 | ---NA--- | <missing> |
| Contig_342 | ---NA--- | -0.687 |
| Contig_348 | ---NA--- | 1.605 |
| Contig_354 | ---NA--- | -0.644 |
| Contig_355 | ---NA--- | -0.695 |
| Contig_359 | ---NA--- | -0.686 |
| Contig_361 | ---NA--- | 1.558 |
| Contig_363 | ---NA--- | -0.473 |
| Contig_367 | ---NA--- | -1.837 |
| Contig_368 | ---NA--- | 2.596 |
| Contig_372 | ---NA--- | -1.348 |
| Contig_373 | ---NA--- | <missing> |
| Contig_377 | ---NA--- | -0.016 |
| Contig_379 | ---NA--- | -0.992 |
| Contig_380 | ---NA--- | 1.415 |

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|------------|----------|-----------|
| Contig_381 | ---NA--- | -0.469 |
| Contig_384 | ---NA--- | -0.556 |
| Contig_385 | ---NA--- | -0.760 |
| Contig_387 | ---NA--- | -1.313 |
| Contig_388 | ---NA--- | -0.404 |
| Contig_389 | ---NA--- | -2.941 |
| Contig_39 | ---NA--- | -0.600 |
| Contig_392 | ---NA--- | 3.035 |
| Contig_393 | ---NA--- | -0.029 |
| Contig_394 | ---NA--- | -3.360 |
| Contig_4 | ---NA--- | -0.559 |
| Contig_400 | ---NA--- | -2.852 |
| Contig_403 | ---NA--- | 2.679 |
| Contig_41 | ---NA--- | <missing> |
| Contig_410 | ---NA--- | <missing> |
| Contig_412 | ---NA--- | <missing> |
| Contig_413 | ---NA--- | 2.449 |
| Contig_419 | ---NA--- | -0.092 |
| Contig_420 | ---NA--- | -1.379 |
| Contig_421 | ---NA--- | -0.116 |
| Contig_422 | ---NA--- | -0.623 |
| Contig_424 | ---NA--- | -3.160 |
| Contig_429 | ---NA--- | -0.575 |
| Contig_43 | ---NA--- | -0.431 |
| Contig_431 | ---NA--- | -0.558 |
| Contig_433 | ---NA--- | 3.244 |
| Contig_436 | ---NA--- | 3.248 |
| Contig_437 | ---NA--- | <missing> |
| Contig_438 | ---NA--- | <missing> |
| Contig_440 | ---NA--- | -3.414 |
| Contig_442 | ---NA--- | <missing> |
| Contig_445 | ---NA--- | <missing> |
| Contig_448 | ---NA--- | -3.229 |
| Contig_45 | ---NA--- | -1.226 |
| Contig_451 | ---NA--- | <missing> |
| Contig_452 | ---NA--- | <missing> |
| Contig_458 | ---NA--- | -2.817 |
| Contig_460 | ---NA--- | <missing> |
| Contig_462 | ---NA--- | -0.676 |
| Contig_467 | ---NA--- | -3.636 |
| Contig_51 | ---NA--- | 0.460 |
| Contig_52 | ---NA--- | -0.991 |
| Contig_59 | ---NA--- | 2.121 |
| Contig_6 | ---NA--- | 1.558 |
| Contig_64 | ---NA--- | -0.163 |
| Contig_67 | ---NA--- | -0.414 |

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|------------|---|-----------|
| Contig_69 | ---NA--- | -0.479 |
| Contig_71 | ---NA--- | -0.270 |
| Contig_72 | ---NA--- | -0.007 |
| Contig_73 | ---NA--- | -0.669 |
| Contig_75 | ---NA--- | <missing> |
| Contig_77 | ---NA--- | -0.019 |
| Contig_79 | ---NA--- | <missing> |
| Contig_80 | ---NA--- | -2.449 |
| Contig_81 | ---NA--- | -2.922 |
| Contig_82 | ---NA--- | -1.954 |
| Contig_84 | ---NA--- | 2.925 |
| Contig_87 | ---NA--- | <missing> |
| Contig_88 | ---NA--- | 1.950 |
| Contig_89 | ---NA--- | 0.851 |
| Contig_9 | ---NA--- | -0.403 |
| Contig_92 | ---NA--- | <missing> |
| Contig_93 | ---NA--- | -0.579 |
| Contig_94 | ---NA--- | -0.400 |
| Contig_96 | ---NA--- | -0.362 |
| Contig_449 | na+ +-adenosine triphosphatase | -0.633 |
| Contig_270 | nadh dehydrogenase | -1.986 |
| Contig_74 | nadh dehydrogenase | 2.593 |
| Contig_2 | nadh dehydrogenase subunit 5 | -0.066 |
| Contig_98 | nedd8 ultimate buster 1 isoform 2 | -2.730 |
| Contig_138 | neurofilament heavy polypeptide | 1.880 |
| Contig_7 | non-histone chromosomal protein hmg-17 | 0.675 |
| Contig_285 | nuak family snf1-like kinase 1-like | -2.167 |
| Contig_446 | nuclear cap binding protein subunit 20kda | -3.179 |
| Contig_289 | orf2 | -0.469 |
| Contig_344 | orf2 | -3.352 |
| Contig_236 | orf2-encoded protein | -0.028 |
| Contig_391 | origin recognition complex subunit 2 | 0.142 |
| Contig_180 | otu domain containing 6b | -0.373 |
| Contig_418 | parvalbumin gene 1 | -1.379 |
| Contig_318 | pdz and lim domain protein 3-like isoform 2 | -0.479 |
| Contig_60 | peroxiredoxin 6 | -0.267 |
| Contig_247 | peroxiredoxin- mitochondrial-like | 0.846 |
| Contig_40 | peroxiredoxin-1 | 2.135 |
| Contig_16 | phosphogluconate dehydrogenase | 2.086 |
| Contig_219 | phospholipid transfer protein precursor | -1.506 |
| Contig_423 | phosphatidylinositol phosphatase ptpaq-like | -0.632 |
| Contig_70 | piggybac transposase uribo1 | -0.460 |
| Contig_274 | piggybac transposase uribo2 | -0.444 |
| Contig_232 | pl-5283 protein | -1.417 |
| Contig_187 | polyprotein | -0.319 |
| Contig_240 | potassium channel tetramerisation domain containing 5 | -1.549 |

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|------------|---|-----------|
| Contig_464 | potassium voltage-gated channel subfamily g member 4 | <missing> |
| Contig_346 | PREDICTED: hypothetical protein LOC100551521 [Anolis carolinensis] | <missing> |
| Contig_56 | PREDICTED: hypothetical protein LOC100565863 [Anolis carolinensis] | 1.768 |
| Contig_340 | PREDICTED: hypothetical protein LOC325517 [Danio rerio] | -2.707 |
| Contig_199 | programmed cell death 1 ligand 1-like | -2.259 |
| Contig_302 | proline arginine-rich end leucine-rich repeat protein | -0.470 |
| Contig_97 | proteasome maturation protein | <missing> |
| Contig_261 | proteasome subunit beta type-1-a | -1.960 |
| Contig_27 | protein (hypothetical) | 2.638 |
| Contig_369 | protein mis18-beta-like | -1.370 |
| Contig_435 | protein mitochondrial (preY) | -3.288 |
| Contig_22 | protein s100-a13 | 0.462 |
| Contig_295 | protein uxt-like | 1.334 |
| Contig_249 | puromycin-sensitive aminopeptidase | -1.730 |
| Contig_311 | pyruvate muscle | 1.372 |
| Contig_299 | receptor activity modifying protein 1 | -2.103 |
| Contig_396 | receptor-type tyrosine-protein phosphatase epsilon | 2.004 |
| Contig_409 | redox-regulatory protein fam213a isoform 1 precursor | <missing> |
| Contig_356 | regulator of g-protein signaling 18 | 1.817 |
| Contig_267 | retrotransposon-like family member (retr-1)- partial | 0.264 |
| Contig_173 | reverse transcriptase | -0.828 |
| Contig_414 | reverse transcriptase | -3.875 |
| Contig_172 | reverse transcriptase and intron maturase | -0.873 |
| Contig_122 | reverse transcriptase-like protein | -1.407 |
| Contig_263 | reverse transcriptase-like protein | -1.726 |
| Contig_382 | rho gtpase-activating protein 24 | -2.180 |
| Contig_109 | ribosomal protein l14 | 1.639 |
| Contig_434 | ribosomal protein s3a | <missing> |
| Contig_374 | ribosomal protein s8 | <missing> |
| Contig_456 | riddle 4 | 2.091 |
| Contig_430 | riken cdna isoform cra_a | 2.253 |
| Contig_3 | rrna intron-encoded endonuclease | -2.616 |
| Contig_31 | rtf1 protein | 2.083 |
| Contig_364 | sec62 protein | 0.845 |
| Contig_415 | selenoprotein 1 precursor | -0.596 |
| Contig_443 | serine threonine-protein phosphatase 2a catalytic subunit alpha isoform | <missing> |
| Contig_303 | serpin b6 | 1.346 |
| Contig_248 | set and mynd domain containing 1 | -1.685 |
| Contig_32 | sh3 domain-binding glutamic acid-rich-like protein 3 | 0.386 |
| Contig_406 | slu7 protein | -0.680 |
| Contig_125 | small edrk-rich factor 2 | 0.470 |
| Contig_441 | small nuclear ribonucleoprotein-associated protein b | <missing> |
| Contig_54 | soluble type ii il-1 receptor precursor | 1.916 |
| Contig_404 | solute carrier family 48 (heme transporter) member 1b | -2.829 |
| Contig_455 | sphingolipid delta -desaturase des1 | 2.071 |
| Contig_220 | spindle and kinetochore-associated protein 2 isoform 1 | -1.538 |

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|------------|---|-----------|
| Contig_198 | splicing arginine serine-rich 3 | 0.958 |
| Contig_278 | spondin extracellular matrix protein | -2.051 |
| Contig_24 | stathmin 1 oncoprotein isoform cra_a | -0.173 |
| Contig_124 | stress-induced-phosphoprotein 1 | -2.387 |
| Contig_76 | stromelysin-1 2-a | -0.135 |
| Contig_350 | succinate dehydrogenase | -2.540 |
| Contig_265 | sulfotransferase 1 family member d1 | -1.946 |
| Contig_277 | suppression of tumorigenicity isoform a | -0.452 |
| Contig_335 | surfeit 2 | <missing> |
| Contig_323 | svil protein | 1.778 |
| Contig_8 | t-cell receptor beta chain ana 11 | -1.014 |
| Contig_165 | tetraspanin-3 isoform 1 | 0.807 |
| Contig_229 | tf-b protein | -0.173 |
| Contig_357 | thap domain-containing protein 9-like | 1.441 |
| Contig_307 | thioredoxin | 1.378 |
| Contig_397 | thymocyte nuclear protein 1 | -2.778 |
| Contig_65 | tmsb4x protein | 1.110 |
| Contig_319 | transaldolase 1 | 1.519 |
| Contig_153 | transcription factor btf3 homolog 4 | 2.422 |
| Contig_5 | transducin -like 3 | 0.359 |
| Contig_114 | transgelin 2 | -0.012 |
| Contig_14 | transgelin 2 | 0.038 |
| Contig_178 | translation elongation factor 1 | -0.964 |
| Contig_34 | translation initiation factor eif-2b subunit gamma isoform 1 | 0.718 |
| Contig_351 | translation initiation factor if- mitochondrial-like | -2.591 |
| Contig_304 | translocator protein | 1.365 |
| Contig_239 | transmembrane protein 11 | -1.574 |
| Contig_207 | transmembrane protein 205 | -0.297 |
| Contig_375 | transposase | -0.208 |
| Contig_329 | triadin | -2.386 |
| Contig_402 | trm112-like protein | -2.862 |
| Contig_152 | troponin cardiac muscle | -0.839 |
| Contig_185 | truncated integrase | -0.359 |
| Contig_154 | tubb6 | 1.864 |
| Contig_378 | tumor susceptibility gene 101 | -3.311 |
| Contig_42 | type 1 tumor necrosis factor receptor shedding aminopeptidase regulator | -0.360 |
| Contig_260 | ubiquinol-cytochrome c reductase binding protein | -1.886 |
| Contig_216 | ubiquitin carboxyl-terminal hydrolase 16-like isoform 1 | -1.356 |
| Contig_454 | uhrf1-binding protein 1-like | <missing> |
| Contig_140 | unnamed protein product [Mus musculus] | -0.459 |
| Contig_61 | unnamed protein product [Rickettsia rickettsii str. Hino] | -3.018 |
| Contig_62 | unnamed protein product [Rickettsia rickettsii str. Hino] | -3.153 |
| Contig_63 | unnamed protein product [Rickettsia rickettsii str. Hino] | -2.749 |
| Contig_90 | upf0197 transmembrane protein c11orf10 homolog | -2.352 |
| Contig_171 | upf0708 protein c6orf162 homolog | -2.407 |
| Contig_338 | vacuolar protein sorting-associated protein 29 | <missing> |

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| Contig_202 | vascular endothelial growth factor receptor 1 | -1.314 |
| Contig_327 | versican core protein precursor | -2.759 |
| Contig_399 | v-ha-ras harvey rat sarcoma viral oncogene homolog | -0.613 |
| Contig_53 | wd repeat-containing protein 1 | 0.802 |
| Contig_46 | zinc finger bed domain-containing protein 6 | -0.418 |
| Contig_234 | zinc finger protein | -0.967 |
| Contig_337 | zinc finger protein 354a | -2.774 |
| Contig_428 | zinc finger protein 394-like | 2.434 |

| dorsal 3 | dorsal 5 | ventral 1 | ventral 3 | ventral 5 | ESTID (Newtomics) |
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| 1.617 | 1.293 | 1.158 | 1.624 | 1.627 | 48827###48857###49077###48569###4! |
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| 0.608 | 1.085 | -0.496 | 0.111 | 1.157 | 49389###49068##48968###48588##4! |
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| 0.104 | -1.330 | -0.666 | -0.615 | 1.574 | 49157 |
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| 0.358 | -2.421 | -0.484 | -0.703 | 1.887 | 48891 |
| -0.054 | -1.515 | -0.374 | -0.356 | 1.164 | 49114 |
| -0.410 | -0.755 | <missing> | <missing> | 0.036 | 49165 |
| -0.221 | 0.125 | -1.959 | -0.249 | -0.550 | 49117 |
| -0.061 | 0.434 | 1.350 | 0.142 | 0.026 | 49050 |
| 0.476 | -0.339 | -0.052 | -0.189 | 0.498 | 49230##49245 |
| <missing> | <missing> | <missing> | 0.374 | -0.441 | 48874 |
| 0.054 | 0.017 | <missing> | <missing> | <missing> | 49061 |
| 0.377 | 0.383 | 1.329 | 0.611 | -0.056 | 49039 |
| -0.086 | -0.317 | <missing> | <missing> | 0.020 | 48966 |
| -0.265 | 0.065 | 1.379 | 0.023 | -0.542 | 48962 |
| 0.075 | 0.113 | -0.364 | <missing> | 0.210 | 49069 |
| 0.633 | 1.015 | 0.117 | 0.809 | 0.067 | 48940 |
| -0.422 | -0.266 | -0.530 | <missing> | <missing> | 49306 |
| -0.459 | -1.296 | -0.760 | -0.712 | 0.992 | 49383 |
| 1.214 | 1.729 | 1.961 | 1.636 | 1.708 | 48813 |
| <missing> | -0.956 | <missing> | <missing> | <missing> | 49108 |
| 0.196 | 0.237 | <missing> | <missing> | 0.607 | 49118 |
| 0.752 | 0.449 | 2.106 | <missing> | 0.669 | 49127 |
| 0.844 | <missing> | <missing> | <missing> | <missing> | 49305 |
| 0.252 | 0.111 | -0.212 | 0.064 | -0.025 | 48547 |
| 0.828 | 0.755 | <missing> | <missing> | 0.803 | 49268 |
| 1.365 | 2.272 | 1.079 | 1.603 | 0.885 | 48853 |
| -0.103 | -0.173 | <missing> | <missing> | 0.484 | 49060 |
| 0.066 | -0.952 | -1.600 | <missing> | 0.220 | 48949 |
| <missing> | -0.631 | -1.801 | -1.865 | <missing> | 49086 |
| -0.375 | -1.547 | -0.025 | -0.243 | -1.307 | 48553 |
| -0.026 | -0.286 | <missing> | -0.301 | -0.127 | 49322 |
| -0.043 | -2.222 | 0.104 | 0.754 | 1.245 | 48974 |
| -0.431 | -3.013 | -0.630 | -0.717 | 2.090 | 49001 |
| -0.115 | -1.949 | -0.302 | 0.596 | 1.185 | 49223 |
| 0.022 | -0.187 | -2.107 | <missing> | 0.056 | 49130 |
| -0.648 | -1.465 | -0.059 | -0.213 | 0.222 | 49096 |
| <missing> | 0.245 | -0.125 | -0.020 | <missing> | 49156 |
| -0.090 | <missing> | <missing> | <missing> | 0.018 | 48577 |
| -1.058 | -1.869 | <missing> | -1.142 | <missing> | 49391 |
| <missing> | -0.324 | 2.343 | <missing> | 0.326 | 48567 |
| 0.195 | -2.107 | -0.714 | -0.451 | 2.098 | 48563 |
| -0.221 | -1.488 | -0.153 | -0.628 | 1.820 | 49207 |
| 1.690 | 0.776 | 1.892 | 2.061 | 1.819 | 49217 |

| | | | | | |
|------------------|------------------|------------------|------------------|--------|------------------------------------|
| 0.427 | -2.418 | -0.417 | -0.644 | 2.081 | 48899 |
| 0.207 | -1.547 | -0.166 | -0.744 | 2.138 | 48628 |
| 0.229 <missing> | | -1.814 | 0.216 | 2.461 | 49192 |
| 0.296 | -3.298 | -2.479 | -2.345 | 2.125 | 49619 |
| 0.252 | -1.626 | -0.675 | -0.839 <missing> | | 49329 |
| 0.616 | -2.947 | -0.408 | -0.556 | 1.805 | 48852 |
| -0.051 | 0.259 | 1.634 | 0.056 | -0.247 | 48859 |
| -0.144 | 0.062 | 0.170 <missing> | | -0.822 | 48847 |
| -1.545 | -0.991 | -0.024 | -1.514 | -1.326 | 49385 |
| 1.097 | 0.311 | 0.543 | 0.424 | -0.225 | 49215 |
| -1.097 | -1.119 <missing> | <missing> | | -0.544 | 48620 |
| <missing> | -0.053 | -1.784 <missing> | <missing> | | 49179 |
| -0.051 | -0.954 <missing> | | -1.739 | 1.060 | 48868 |
| -0.063 | 0.190 | 1.985 <missing> | | -0.410 | 48615 |
| 0.315 | -2.501 | -0.865 | -0.530 | 1.091 | 48759###48763###48738###48806###4! |
| -0.556 | -2.154 | 1.367 <missing> | <missing> | | 48951 |
| 0.229 | -1.423 | -0.226 | 0.797 | 1.804 | 48545 |
| 0.585 | -1.418 | -0.495 | 0.159 | 1.210 | 48929 |
| 0.222 | -3.063 | -0.820 | -0.737 | 1.982 | 48613 |
| -1.226 | -1.403 | -0.701 | -0.806 | -1.106 | 49142 |
| -0.063 | 0.439 | 0.069 | 0.265 | 0.051 | 49049 |
| <missing> | <missing> | -0.085 <missing> | <missing> | | 48845 |
| 0.639 | -1.431 | -0.181 | -0.122 | 1.015 | 49083###49278###49240###49244###4! |
| -0.992 | -3.936 | -3.475 | -4.088 | -0.085 | 48581 |
| -0.900 | -0.771 | 0.226 | -1.618 | -1.772 | 48541 |
| 0.958 | 1.862 | 0.279 | 0.451 | 1.295 | 49537###49400###49515 |
| -0.278 | 0.027 <missing> | <missing> | <missing> | | 49324 |
| <missing> | 1.046 | 0.364 | 0.892 | -0.388 | 49394 |
| -0.020 | -2.055 | 0.755 | -0.657 | 1.103 | 48988 |
| -0.236 | -0.566 | 1.451 <missing> | | 0.398 | 49091 |
| 0.051 | -1.758 | -0.307 | -0.516 | 1.287 | 49013 |
| -0.408 | -0.038 | 2.131 | -0.222 | -0.950 | 48564 |
| 0.208 | -1.661 | 0.089 | -0.060 | 1.742 | 48978 |
| -0.172 <missing> | <missing> | <missing> | <missing> | | 49104 |
| -0.071 | -2.734 | 0.019 | -0.911 | -0.395 | 48627 |
| -0.719 | -1.394 | -0.347 | -0.711 | -0.511 | 49216###49377###49026###48829 |
| 0.494 | 0.276 | 1.690 | 1.035 | 0.141 | 49139 |
| 1.849 | 2.650 | 2.017 | 2.094 | 1.780 | 49167###49075###48894###48942###4! |
| 1.282 | 0.923 | 1.656 | 1.502 | 0.966 | 48582###49444 |
| -1.147 | -2.469 | -2.235 | -1.949 | -0.373 | 49045 |
| -0.239 <missing> | | -1.974 | -1.946 | 1.734 | 49078 |
| 0.344 | -2.794 | -0.557 | -0.833 | 2.061 | 49430 |
| 0.512 <missing> | | -1.975 | -2.302 | 3.033 | 49229 |
| -0.376 | -0.006 | -0.196 | 0.110 | 0.051 | 48590 |
| 0.233 | -2.179 | -0.804 | -0.774 | 0.742 | 49470 |
| 0.316 <missing> | <missing> | <missing> | | -0.197 | 48544 |

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|-----------|------------------|------------------|-----------------|--------|-----------------------------------|
| -0.603 | -0.717 | -2.418 | -0.972 | -0.034 | 48835 |
| 0.079 | 1.566 | 0.184 <missing> | | 0.473 | 48922 |
| 2.374 | 2.687 | 1.132 | 2.612 | 1.518 | 48933###49403 |
| -0.115 | 0.503 | -0.072 <missing> | | -0.542 | 49368 |
| <missing> | -0.335 <missing> | <missing> | | 0.307 | 49058 |
| 0.009 | -1.425 | -0.710 | -0.694 | 1.375 | 48591 |
| -0.120 | 1.697 <missing> | <missing> | | -0.805 | 48890 |
| -0.420 | -1.229 | -0.661 | -0.904 | -0.205 | 49113 |
| 1.466 | 0.824 | 1.646 | 1.922 | 0.198 | 49048###49062###48865 |
| -0.049 | 0.271 <missing> | <missing> | <missing> | | 49214 |
| <missing> | <missing> | <missing> | <missing> | -0.393 | 49299 |
| 0.047 | 0.437 | 2.059 | -0.092 | -0.833 | 49390###48583###49009 |
| 0.182 | 0.690 | 0.066 | 0.483 | -0.466 | 49359 |
| -0.219 | 0.138 <missing> | | -0.499 | 0.686 | 49259 |
| 1.714 | 1.711 | 1.444 | 1.905 | 1.771 | 49169 |
| 0.222 | -0.317 <missing> | <missing> | | 0.160 | 49325 |
| <missing> | -0.309 <missing> | <missing> | <missing> | | 49242 |
| 0.451 | 1.472 | 0.295 <missing> | | 0.311 | 48930 |
| -0.129 | 0.285 | -0.147 <missing> | | -0.271 | 49196 |
| 0.074 | -0.413 | 1.441 <missing> | | 0.047 | 48888 |
| -0.193 | -4.018 | -0.490 | -0.839 | 2.728 | 48608 |
| -0.101 | -0.712 <missing> | <missing> | <missing> | | 48887 |
| -0.392 | -1.814 | -0.615 | -0.653 | 1.093 | 48622 |
| 0.001 | -1.774 | -0.663 <missing> | | 1.529 | 49134 |
| -0.265 | -0.832 <missing> | <missing> | | 0.976 | 48779 |
| -0.332 | -0.084 | -0.522 | -0.308 | -0.709 | 49145 |
| 0.560 | 1.057 | -0.421 | 0.210 | -1.231 | 48996 |
| 0.080 | 1.607 <missing> | | 0.462 <missing> | | 48994 |
| 0.033 | 1.913 | 0.198 <missing> | <missing> | | 48941 |
| 0.415 | 0.617 | 1.951 | 0.644 | 0.852 | 49533 |
| 0.096 | 0.266 | -0.295 | 0.203 <missing> | | 49150 |
| -1.091 | -4.300 | -2.213 | -2.082 | -1.003 | 48957###48595###48811###49152###4 |
| 0.658 | -0.376 | 0.455 | 0.336 | -0.289 | 48967###48606 |
| 0.725 | 0.244 | 1.394 | 1.016 | 0.612 | 49021 |
| -0.610 | -1.393 | -0.363 | -0.263 | -0.342 | 48846 |
| -0.906 | -0.214 | 2.650 | -0.289 | -0.175 | 48557 |
| 0.168 | 0.626 <missing> | | 0.240 | -0.050 | 48603 |
| -0.132 | 0.538 <missing> | <missing> | <missing> | | 48556 |
| 0.857 | 1.555 | 0.557 | 0.962 | 0.783 | 49258###48898 |
| -0.220 | -1.305 | -0.472 | -0.633 | 0.013 | 48782 |
| 0.466 | 1.308 | 0.438 | 0.704 | -0.511 | 48864 |
| -0.611 | 2.076 <missing> | <missing> | <missing> | | 48713 |
| 2.501 | 2.701 | 1.100 | 2.550 | 1.896 | 48889###48998###49224 |
| -0.155 | -0.178 <missing> | | -0.490 | 0.289 | 49395 |
| 0.077 | 0.118 <missing> | <missing> | | 0.047 | 49343 |
| <missing> | 0.047 | -0.004 | -0.142 | -0.058 | 49072 |

| | | | | | |
|-----------|-----------|-----------|-----------|--------|---------------|
| <missing> | -0.179 | <missing> | <missing> | 0.136 | 48555 |
| 0.491 | <missing> | <missing> | <missing> | 0.324 | 49132 |
| -0.297 | -1.365 | -0.175 | -0.451 | 0.916 | 48648 |
| 0.678 | 0.444 | 1.449 | 1.295 | 0.391 | 48649###49371 |
| 0.590 | -2.196 | -0.618 | -0.424 | 2.850 | 49315###49200 |
| -0.163 | <missing> | -2.423 | <missing> | 2.937 | 49384 |
| 0.135 | 1.077 | <missing> | <missing> | -0.105 | 49093 |
| -0.579 | -0.248 | <missing> | <missing> | -0.730 | 49138 |

9133##49335

Please note:

Researchers can use ESTID column to search in the newtomics database (<http://newtomics.mpi-bn.mpg.de>) in order to find more information about the ESTs including annotation to other databases, if peptides have been identified and expression to other tissues that regenerate, such as heart. If more than one ESTID corresponds to the Lens Contig then the ESTIDs are separated by ##. Researchers **cannot** use Lens contig column since it does not reference to the database and contigs were named only for assembly purposes.

9213##48866##48883##49339##48542##49174##49128##49161##49388

9052

9228

9596##49590##49548##49274##49463##49527

8936

9528##49549##49488

9255##48798##48650##48754##48669##48667##48727##48747##48658##48635##48656

8597##48562

8823##48696##48719##48768##48777##48709##48684##48736##48693

9288##48755##49261##49248##49302##49237##48840##48750##48801##49253##49283##49284

8772##48593##49539

8906##48786##49443##49411##49308##48904##49178##48749##48748##49109##48821##49521;

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