

Table S15

Maternal genes identified by SOM analysis, rapidly reinduced

Gene ID	mixed annotation (+ indicates sequence confirmation)
CG3566	+ electron_transfer * 3e-17 cytochrome b5 * 1e-18 Similarity to Human cytochrome b5 (SW:CYB5_HUMAN); cDNA EST EMBL:D * 5e-18 CYB5_MOUSE CYTOCHROME B5 * 7e-22 cytochrome b [CYTOCHROME_B5 // CYTOCHROME_B5_2 // NLS_] CG3566 GH05526 5E1-5E1 ID:33F10
CG4233	+ enzyme * similar to aspartate aminotransferase(aa) * 1e-99 aspartate aminotransferase cerevisiae, Peptide Partial, * 1e-157 similar to aspartate aminotransferase [aminotran_1 // AA_TRANSFER_CLASS_1 // T] CG4233 GH20337 22B8-22B8 dup:2/2 ID:72F2
CG5567	+ enzyme * 3e-40 4-nitrophenylphosphatase (EC 3.1.3.41) - yeast (Saccharomyces cerevisiae) * 6e-26 by content; 1-meth * 4e-52 contains similarity to 4-nitrophenylphosphatase CG5567 GH06744 75A4-75A4 ID:34G7
CG6770	+ unknown * 1E-178* 1e-105 inserted at base Both 5' and 3' ends of P element Inverse PCR * CG6770 GH05738 33B12-33B12 ID:33H4
CG3864	+ electron_transfer * thioredoxin(aa) * 8e-20 TRX1_YEAST THIOREDOXIN I (TR-I) thioredoxin I - yeast (Sacc * 1e-17 THIO_DROME THIOREDOXIN (DEADHEAD PROTEIN) thioredoxin-I [THIOREDOXIN // THIOREDOXIN_2 // thioered] CG3864 30C-30C2 ID:115A11
CG16882	+ BG:DS00180.8 cell_adhesion * DMTENA_3 Ten-a * DMC901PRT C901 * DMDELTA_4 DI * 3e-20 C901 protein [EGF_2] CG16882 GH07717 34E1-34E1 dup:3/4 ID:59H10
CG17608	+ fu12 enzyme * 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE(aa) * PUTATIVE 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE T06E8.1 (1- AGP ACYLTRANSFERASE) (1-AG [GLYCEROL_ACYLTRANS] CG17608 GH26888 29C4-29C4 ID:80F12
CG1721	+ Pglym78 enzyme * phosphoglyceromutase - fruit fly (Drosophila melanogaster)(aa) * DMPGLY_4 Pglym78 * 7e-48 pdb 4PGM A Chain A, Saccharomyces Cerevisiae Phosphoglycer [PGAM // PG_MUTASE] CG1721 GH13304 99A1-99A1 dup:2/2 ID:40E5
CG2789	+ receptor * 5e-14 cDNA EST comes from this gene; cDNA EST co * 3e-35 peripheral-type benzodiazepine receptor isoquinoline-binding protein - mouse * 1e-35 benzodiazepine CG2789 GH02075 21C6-21C6 dup:2/2 ID:30H12
CG5904	+ islet mitochondrial antigen CG5904 LP03542 ID:108F8
CG4600	+ enzyme * 3-KETOACYL-COA THIOLASE MITOCHONDRIAL (BETA-KETOTHIOLASE) (ACETYL-COA ACYLTRANSFERASE) (MITOCHONDRIAL 3-OXOACYL-COA THIOLASE)(aa) * 8e-54 pdb 1AFW A [thiolase // THIOLASE_1 // THIOLASE_2 //] CG4600 LD40538 33A1-33A1 dup:1/2 ID:99F6
CG4999	+ tumor_suppressor * 3e-09 /match=(desc;; /ma * 3e-16 predicted using Genefinder; Similarity to Human leukocyte surface * 4e-26 CD82_MOUSE CD82 ANTIGEN (INDUCIBLE MEMBRANE [transmembrane4 // TMFOUR // TM4_2] CG4999 GH11168 66E3-66E3 ID:38F10
CG12040	+ unknown similar to GTPase-activating (rhoGAP) like protein CRAL_TRIO CG12040 GH28696 dup:2/2 ID:82F6
CG8995	+ defense/immunity_protein * cuticular molt protein precursor(aa) * 2e-29 peptidoglycan recognition protein precursor * 2e-31 TNF superfamily, member (LTB)-like (peptidoglycan recognition protein) CG8995 GH01554 13F1-13F1 dup:2/2 ID:54E9
CG17822	+ transcription_factor CG17822 GH20378 ID:72F5
CG2171	+ Tpi enzyme * Chain A, Does The His12-Lys13 Pair Play A Role In The Adaptation Of Thermophilic Tims To High Temperatures ?(aa) * DMTPIG_2 Tpi * TRIOSEPHOSPHATE IS [TIM] CG2171 GH02005 99E-99E dup:1/3 ID:30H5
CG8861	+ unknown * CG8861 GH27383 85D7-85D7 ID:81C12

+ cell_adhesion * 2e-09 SLIT_DROME SLIT PROTEIN PRECURSOR slit protein precurs * 2e-06 coded for by C. elegans cDNA
 CG17667 yk133e1.5; coded for by C. elegans cDNA yk133d4.5 [LRR] CG17667 LD45603 69E1-69E2 dup:2/2 ID:104E3
 CG18525+ unknown * CG18525 GH14439 88E7-88E7 dup:2/2 ID:41E4
 + peptidase * 1e-112 APE2_YEAST AMINOPEPTIDASE II (YSCII) aminopeptidase yscII * 1e-110 Similarity to Human aminopeptidase
 N (SW:AMPN_HUMAN); cDNA EST EMB * 1e-16 [ALADIPTASE // Peptidase_M1 // ZINC_PROT] CG8775 GH12821 87E6-87E6 dup:2/2
 CG8775 ID:40B8
 + Eno enzyme * DMENOLAS_2 Eno * 1e-154 phosphopyruvate hydratase (EC 4.2.1.11) - yeast (Saccharomyces cerevisiae) >g *
 CG17654 ENO_DROME ENOLASE (2-PHOSPHOGLYCERATE DEHYD [ENOLASE // enolase] CG17654 GH01942 22F3-22F3 ID:55A2
 + enzyme * 5e-19 VIT1_DROME VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1) vitell * 6e-23 pancreatic lipase related protein *
 CG17292 3e-25 pancreatic lipase-related protei [TAGLIPASE // ESTERASE // lipase] CG17292 GH01208 29B3-29B3 ID:54B11
 CG10373+ unknown * gene product(aa) * 6e-19 gene product * 2e-23 JWA protein * JM4 CG10373 GH05842 37A4-37A4 ID:58D2
 + chaperone * 1e-13 gene product * 1e-09 disulfide-like protein prote * [THIOREDOXIN_2] CG11790 GH08893 96B15-96B15 dup:1/2
 CG11790 ID:61B4
 CG1927 + BcDNA:GH11112 unknown * CG1927 GH11112 62B11-62B11 ID:38F4
 + BEAF-32 DNA_binding * boundary element-associated factor, 32k - fruit fly (Drosophila melanogaster)(aa) * 1e-146 DMBEAF32A_2
 CG10159 BEAF-32 * boundary element associated factor [NLS_BP] CG10159 GH10592 51C3-51C3 ID:38B2
 + Thiolaseenzyme * Thiolase * thiolase(aa) * 3e-37 THIL_YEAST ACETYL-COA ACETYLTRANSFERASE (ACETOACETYL-COA
 CG4581 THIOLASE) * 1e-140 YKA3_CAEEL HYPOTHETICAL 47.9 KD PROTEIN [thiolase] CG4581 GH13256 60A6-60A6 dup:2/2 ID:40E2