

Table S14

Maternal genes identified by SOM analysis, core germline

Gene ID mixed annotation (+ indicates sequence confirmation)

+ 26/29kD-proteinase * 26,29kDa proteinase(aa) * 8e-61 cysteine proteinase cysteine * 1e-56 predicted using Genefinder; similar to
CG8947 cathepsin-like protease; cD * 2e-61 cath [THIOL_PROTEASE_CYS // PAPAIN // Peptida] CG8947 70C9-70C9 dup:1/2 ID:61C5
+ enzyme * 3-phosphoglycerate dehydrogenase(aa) * similar to D-3-Phosphoglycerate dehydrogenase; cDNA EST comes from this
CG6287 gene; cDNA EST comes from this gene; [2-Hacid_DH // D_2_HYDROXYACID_DH_1 // A] CG6287 GH03305 32D5-32D5 ID:31H4
+ motor_protein * 7e-09 by content; 1-meth * 2e-07 homeotic most like HMPB_DROME: homeotic proboscipedia protein * 9e-07 Williams-
CG8677 Beuren syndrome deletion transcript [PHD // NLS_BP // ATP_GTP_A] CG8677 LD34730 39C1-39C1 dup:5/5 ID:49E10
CG5194 + unknown * CG5194 LD39537 66F1-66F1 ID:98F8
+ Hsp27 chaperone * DMHSP27G_3 Hsp27 * 1e-118 HS27_DROME HEAT SHOCK PROTEIN heat shock protein - f * 3e-13 Contains
similarity to Pfam domain: (HSP20), Score=130.7, * 2 [TONB_DEPENDENT_REC_1 // HSP20 // ACRYST] CG4466 GM13686 67B2-67B2
CG4466 ID:83A12
+ enzyme * 1e-31 pdb|1SDY|A Saccharomyces cerevisiae Saccharomyces cerevisiae * 1e-34 SODC_DROME SUPEROXIDE
DISMUTASE (CU-ZN) superoxide dismuta * 5e-38 SODE_C [CUZNDISMUTASE // SOD_CU_ZN_1 // SOD_CU_Z] CG9027 47F6-47F7
CG9027 ID:76F8
+ motor_protein * 6e-23 ARP5_YEAST ACTIN-LIKE PROTEIN ARP5 probable nuclear pro * 2e-12 ACTU_DROME ACTIN-LIKE
CG12321 PROTEIN 13E actin-related protein * 6e-11 similar to Act CG12321 LP02120 90E6-90E6 ID:107H11
+ glutathione_transferase * predicted using Genefinder; similar to Glutathione S-transferases.(aa) * 2e-11 YKJ3_CAEEEL
CG6662 HYPOTHETICAL 42.8 KD PROTEIN C02D5.3 IN CHROMOSOME III * 7 [GST] CG6662 66D5-66D5 dup:2/2 ID:40H2
CG9578 + CG9578 ID:83D8
+ Sptr enzyme * sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)(aa) * ORF 7(aa) * similar to glucose 1-
CG12117 dehydrogenase(aa) * sepiapterin reductase; [GDHRDH // adh_short] CG12117 GH04031 7E7-7E7 ID:32D8
CG9828 + chaperone DnaJ homolog 2 DNAJPROTEIN CG9828 LD27049 dup:2/2 ID:86B6
CG4449 + unknown * CG4449 LP06117 97B1-94E9 ID:109G2
+ Prosalpha1 unknown * endopeptidase multicatalytic endopeptidase) cell 26S proteasome) map_position:54B3-5 * 20S proteasome subunit
CG18495 alpha1(aa) * endopeptidase multicata CG18495 SD02332 43F-43F dup:2/2 ID:114A1
CG2604 + unknown CG2604 SD10384 dup:1/2 ID:125B2.2
+ enzyme * 1e-43 CCR4_YEAST GLUCOSE-REPRESSIBLE ALCOHOL DEHYDROGENASE TRANSCRIPTIONAL EFFECTOR (C * 2e-
CG5534 07 ANGEL * 3e-86 predicted using Genefinder; Similarity CG5534 GH27503 95E6-95E6 dup:2/2 ID:81E4
+ electron_transfer * 1e-11 C05E11.1 gene product * 2e-07 hypothetical protein * 3e-45 inserted at base Both 5' and 3' ends of P element
CG8735 Inverse PCR * [CYTOCHROME_C] CG8735 LD34731 44D-44D2 dup:3/3 ID:49E11
+ * EPIDIDYMAL SECRETORY PROTEIN E1 PRECURSOR (CE1)(aa) * 4e-22 epididymal secretory protein * 9e-23 EP1_HUMAN
CG7291 EPIDIDYMAL SECRETORY PROTEIN E1 PRECURSOR CG7291 22B8-22B8 dup:2/3 ID:88D3
+ peptidase * PROBABLE CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP)(aa) * leucine aminopeptidase(aa) *
CG7340 PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III([LAMNOPPTDASE // RCC1_2 // Peptidase_M17] CG7340 LD34492 87D7-

88E1 ID:49D12

+ ligand_binding_or_carrier * Pen * 1e-107 IMA1_YEAST IMPORTIN ALPHA SUBUNIT (KARYOPHERIN ALPHA SUBUNIT) (SERINE-RICH RNA P * overgrown hematopoietic organs-31 tumor suppressor O [ARM_REPEAT // Armadillo_seg] CG4799 LP03126 31A1-31A1

CG4799 ID:108D10

CG18218+ CG18218 SD07272 dup:1/4 ID:120H6.2

+ enzyme * 3e-55 probable membrane protein YPR066w - yeast (*Saccharomyces cerevisiae*) * 3e-21 ubiquitin activating enzyme * 1e-

CG13343111 coded for by *C. elegans* cDNA [UBA_NAD // ThiF_family // NAD_BINDING /] CG13343 LD47462 50C14-50C14 ID:106D10

+ exu RNA_binding * Exuperantia (exu) protein - fruit fly (*Drosophila melanogaster*)(aa) * exu * 1e-158 exuperantia protein - fruit fly

CG8994 (*Drosophila virilis*) * exu [LECTIN_LEGUME_BETA] CG8994 LD26657 57B2-57B2 ID:85G4

CG8592 + stil unknown * 1e-171 STAND STILL (Y * 1e-173 stil * * [NLS_BP] CG8592 GH06596 49B2-49B2 ID:59A10

+ Uch endopeptidase * DMUBICTHG_3 Uch * 3e-19 UBL1_YEAST UBIQUITIN CARBOXYL-TERMINAL HYDROLASE YUH1 (UBIQUITIN THIOLESTERASE) * 1e-130 UBL_DROME UBIQUITIN CARBOXYL-TERMIN [UCH // UCH_1 // UBCTHYDRLASE] CG4265 GH02396 23D1-

CG4265 23D1 dup:1/2 ID:31B8