

Table S12

Strict Maternal

Gene ID mixed annotation (+ indicates sequence confirmation)

+ enzyme * 1e-98 PERO_DROME PEROXIDASE PRECURSOR myeloperoxidase (EC 1.11. * 6e-87 similar to eosinophil peroxidase and myelo-peroxydase * 2e-65 PERT_MOUSE THY [ANPEROXIDASE // PEROXIDASE_3] CG7660 LD43174 90C-90C ID:102B3

+ CycA cell_cycle_regulator * cell cycle regulator cyclin) map_position:68E1-2 * DMCYCA_3 CycA * G2/MITOTIC-SPECIFIC CYCLIN A(aa) * 2e-27 CG23_YEAST G2/MITOTIC-SPECIFIC[cyclin // HELIX_LOOP_HELIX // CYCLINS] CG5940 LD44443 68D4-68D4 dup:2/2 ID:103C10

+ DNAPol-alpha50 DNA_replication_factor * DMDPRI_2 DNAPol- agr;50 * 8e-62 p48 DNA primase (AA 1-409) * PRI1_DROME DNA CG7108 PRIMASE SMALL SUBUNIT (DNA PRIMASE KD SUBUNIT) (DNA POLYMERAS * 3e-64 N CG7108 LD46032 66C8-66C8 ID:104H2

+ transporter * cystic fibrosis transmembrane conductance regulator(aa) * DMMDR49_2 Mdr49 * canalicular multispecific organic anion transporter (ABC superfamily)(a[ATP_GTP_A2 // ABC_TRANSPORTER // ABC_tr] CG7627 LD46040 29B2-29B2 dup:2/4 ID:104H4

+ unknown * 5e-14 /match=(desc: * 6e-43 weak similarity to drosophila tyrosine kinase ele * 5e-23 The gene is expressed ubiquitously.; The protein * 1e-20 caffe [PAP_ASSOCIATED // PAP_CORE // PAP // PR] CG15737 LD47659 10F5-10F6 dup:1/2 ID:106G9

+ unknown * cDNA EST comes from this gene; cDNA EST comes from this gene(aa) * huntingtin interacting protein HYPE(aa) * 9e- CG9523 84 cDNA EST comes from this gene; c [TPR_REGION // TPR_REPEAT] CG9523 LD47713 26D3-26D3 ID:106H2

+ enzyme * 1e-19 FAT2_YEAST PEROXISOMAL-COENZYME A SYNTHETASE probable AMP * 3e-11 acetyl-CoA synthetase - CG5568 fruit fly (Drosophila melanogaster) * 9e-40 similar [AMP-binding] CG5568 LD47944 64F3-64F3 ID:107B6

+ unknown * 5e-20 YNZ5_YEAST HYPOTHETICAL 17.1 KD PROTEIN IN SIP3-MRPL30 INTERGENIC REGION * 3e-12 RNA CG3800 helicase * 2e-25 cellular nucleic acid binding protein cl [ZF_CCHC // zf-CCHC] CG3800 LD48005 59B6-59B6 ID:107C1

+ CycB cell_cycle_regulator G2/MITOTIC-SPECIFIC CYCLIN B CYCLINS, cyclin CG3510 dup:2/4 ID:43B3

+ chaperone * FK506-binding protein 6(aa) * FK506-binding protein - Arabidopsis thaliana(aa) * FKBP (FK506 binding protein) 13; CG4735 peptidylprolyl cis-trans isomerase [FKBP // FKBP_PPIASE_3 // TPR_REPEAT] CG4735 LD24746 60A4-60A4 ID:43G6

+ aret RNA_binding * aret * 8e-06 polyadenylate-binding protein * 1e-148 testis-specific RNP-type RNA binding protein * 2e-29 elav- CG6319 type ribonucleoprotein coded [RBD // HUDSXL RNA // rrm] CG6319 33D-33D4 dup:3/3 ID:44D5

+ smg * cloned by ability to arrest the cell cycle when expressed in the fission yeast Schizosaccharomyces pombe(aa) * 1e-124 cloned CG5263 by ability to arrest th CG5263 66F1-66F1 dup:1/5 ID:46A10

+ RNA_binding CG4916 dup:2/2 ID:46C4

+ unknown * CG7730 LD31138 73E4-73E4 dup:2/2 ID:47E12

+ tos DNA_repair_protein * DMTOSCAP1_2 tos * Tosca(aa) * 7e-47 EXO1_YEAST EXONUCLEASE I (EXO I) (DHS1 PROTEIN) CG10387 DHS1 pr * Tosca [53EXO_N_DOMAIN // 53EXO_I_DOMAIN // XPG] CG10387 LD31018 37A4-37A4 dup:2/2 ID:47E5

+ yin transporter * opt1 long(aa) * 8e-17 PTR2_YEAST PEPTIDE TRANSPORTER PTR2 (PEPTIDE PERMEASE PTR2) * 8e-74 high- CG2913 affinity peptide transporter * 2e-06 cAMP inducible p [PTR2 // PTR2_1 // PTR2_2] CG2913 GH27264 4A1-4A1 dup:2/2 ID:81B12

CG17018+ unknown CG17018 LD26456 dup:1/2 ID:85F2
 CG9925 + unknown * [PRO_RICH] CG9925 LD26515 88A4-88A4 dup:2/3 ID:85F6
 CG4790 + unknown * CG4790 LD27288 5C8-5C9 ID:86D8
 CG8180 + unknown * 1E-178* * [ANTIFREEZEI] CG8180 LD38554 52A4-52A4 dup:1/2 ID:97G8
 + transcription_factor * 0.00000000006* 9e-25 YMB4_CAEEL HYPOTHETICAL 104.4 KD PROTEIN F54G8.4 IN CHROMOSOME
 CG1624 III * 4e-13 TIF1 protein - mouse TIF1 isoform Pepti * 8e-24 brai [NHL] CG1624 LD39167 43C5-43C7 ID:98D2
 + unknown * 5e-40 prediabetic NOD sera-reactive autoantigen muscul * 5e-10 IVR-like protein * IVR-like protein * [TPR_REGION //
 CG14444TPR_REPEAT] CG14444 LD39177 6C1-6C1 dup:3/3 ID:98D4
 CG14764+ unknown * CG14764 LD39211 43F6-43F6 ID:98D5
 + fs(1)Ya cell_cycle_regulator * mitosis initiation protein fs(1)Ya - fruit fly (Drosophila melanogaster)(aa) * FSYA_DROME MITOSIS
 CG2707 INITIATION PROTEIN FS(1)YA fs(1)Ya prote * DMFS1Y [ZINC_FINGER_C2H2] CG2707 LD40381 3B6-3B6 dup:2/2 ID:99E2
 CG18543+ unknown * CG18543 LD47919 66C12-66C12 ID:107B1
 + swa RNA_binding * SWA_DROME SWALLOW PROTEIN gene swallow protein - fruit fl * DMSWAL_3 swa * * [NLS_BP] CG3429
 CG3429 LD21771 5E6-5E7 dup:2/2 ID:83E6
 + CycJ cell_cycle_regulator * CycJ * 4e-11 CG22_YEAST G2/MITOTIC-SPECIFIC CYCLIN cyclin B2 - yeast * cyclin J * 3e-05 Similar
 CG10308to cyclin [cyclin // HELIX_LOOP_HELIX // NLS_BP] CG10308 GH04281 63D2-63D2 ID:56G5