

Table S13

Maternal genes identified by SOM analysis, gradual decline

Gene ID mixed annotation (+ indicates sequence confirmation)

+ unknown * 5e-08 No definition line found * 5e-16 PSD-95/SAP90-associated protein-2 * 1e-16 PSD-95 binding protein * 1e-171
CG8390 inserted at base Unknown 5' end of [NLS_BP] CG8390 LD44824 41E5-41E5 ID:103F11
+ CDC45L DNA_replication_factor * CDC45L * 2e-31 Cdc45p: assembles into a complex with Cdc46p/Mcm5p * CDC45L * 1e-30
CG3658 predicted using Genefinder; cDNA EST yk307h3.3 comes from this ge CG3658 LD35753 1E1-1E1 ID:95D1
CG7143 + DNA_repair_protein CG7143 SD05329 dup:2/2 ID:118F3
+ Rfc40 DNA_replication_factor * 3e-99 RFC4_YEAST ACTIVATOR KD SUBUNIT (REPLICATION FACTOR C KD SUBUNIT) *
AC14_DROME ACTIVATOR KD SUBUNIT (REPLICATION FACTOR C KD SUBUNIT) (A1 * 1 [ATP_GTP_A] CG14999 LD40483
CG14999 64A10-64A10 dup:2/2 ID:99E11
CG9924 + actin_binding CG9924 LD28030 dup:2/2 ID:87B2
+ transmembrane_receptor * HYPOTHETICAL PROTEIN * cysteine-rich protein (intestinal)(aa) * 4e-09 MLP2_DROME MUSCLE
LIM PROTEIN MLP84B muscle L * 4e-18 gene product [LIM_DOMAIN_1 // LIM // LIM_DOMAIN_2 //] CG4656 LD45535 94E-94E
CG4656 dup:2/2 ID:104D3
+ motor_protein * 8e-08 /motif=(desc: * 7e-11 contains similarity to a C3HC4-class zinc finger * 1e-20 mTRIP * 3e-20 hTRIP [zf-
CG5140 C3HC4 // NLS_BP // ZF_RING] CG5140 GH03577 55B9-55B9 ID:56A7
+ Orc4 DNA_replication_factor * 56-kDa subunit of recognition complex (ORC); Orc4p(aa) * recognition complex subunit 4-related
CG2917 protein Orp4p(aa) * recognition complex, subunit (yea [ATP_GTP_A2 // ATP_GTP_A] CG2917 LD43280 60D16-60D16 ID:102C1
+ transcription_factor_binding * WD-repeat protein(aa) * 3e-05 YGA3_YEAST HYPOTHETICAL 62.8 KD TRP-ASP REPEATS
CONTAINING PROTEIN IN PMC1-TFG2 * 1e-07 Method: conceptual translation [WD40_REGION // WD40] CG11330 LD43270 26F5-
CG11330 26F6 ID:102B11
CG6407 + signal_transduction CG6407 dup:3/3 ID:87H5
CG17678 + CG17678 dup:2/2 ID:89B3
CG6311 + unknown * CG6311 LD37618 74D2-74D2 dup:1/2 ID:96H12
+ protein_phosphatase * myotubularin related protein 1(aa) * 3e-14 YJ80_YEAST HYPOTHETICAL 80.2 KD PROTEIN IN CPA2-
CG5026 NNF1 INTERGENIC REGION * 2e-19 SET domain binding factor CG5026 LD48015 66E5-66E5 ID:107C5
+ nod motor_protein * DMKINLA_3 nod * KINESIN-LIKE PROTEIN NOD(aa) * 4e-19 Cin8p kinesin-related * 9e-46 similar to Kinesin
motor domain; cDNA EST yk256h1.3 comes from t [kinesin // KINESIN_MOTOR_DOMAIN1 // KIN] CG1763 SD02282 10C5-10C6
CG1763 ID:113H6
+ RpA-70 DNA_replication_factor * DMRPA1_3 RpA-70 * REPLICATION PROTEIN A KD DNA-BINDING SUBUNIT (RP-A) (RF-A)
(REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) CG9633 LD40420 84F-84F dup:4/4
CG9633 ID:99E5
+ unknown * 5e-70 weak similarity to HSP90 * 1e-05 YXAQ_BACSU HYPOTHETICAL 37.5 KD PROTEIN IN GNTR-HTPG
CG2982 INTERGENIC REGION * CG2982 LD40453 4B5-4B5 dup:2/2 ID:99E8
CG4947 + unknown * queuine trna-ribosyltransferase(aa) * 7e-98 TGT_CAEEL PUTATIVE QUEUINE TRNA-RIBOSYLTRANSFERASE

(TRNA-GUANINE TRANSGLYCOSYLA * TGT_BACSU QUEUINE TR CG4947 LP01967 21F1-21F1 ID:107H4
 + transcription_factor * DMSUHW_6 su(Hw) * crol * zf43C * 7e-08 zinc finger 30C [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN]
 CG7101 CG7101 GH24178 17E1-17E1 ID:77C7
 CG13773+ enzyme * 4e-10 match to * 3e-06 hypothetical protein * [NLS_BP] CG13773 GH23590 27C3-27C3 ID:76D12
 CG4300 + unknown spermine synthase SAM_BIND CG4300 LD28457 ID:45F5
 CG11329+ unknown * 1e-16 inserted at base 5' end of P element Inverse PCR * * CG11329 LD26217 26F6-26F6 ID:44C11
 + lic protein_kinase (licorn) stress activated MAP kinase kinase 3 [Drosophila melanogaster] PROTEIN_KINASE_DOM,
 CG12244 PROTEIN_KINASE_ST, p] CG12244 SD04985 ID:118B12
 + az2 transcription_factor * zf43C * 2e-09 AZF1_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin * putative zinc finger
 protein * 3e-09 similar to Zinc finger, C2H2 type (3 do [SERPIN // zf-C2H2 // ZINC_FINGER_C2H2] CG1605 43D3-43D3 dup:3/3
 CG1605 ID:77E5
 + Lrr47 actin_binding * LRR47 protein - fruit fly (Drosophila melanogaster)(aa) * DMLRR47_3 Lrr47 * 2e-05 predicted using Genefinder;
 CG6098 Similarity to Glucose-repressible alco [LRR // LEURICHRPT] CG6098 GH06740 31E6-31E6 ID:59B11
 + motor_protein * kda paraneoplastic cerebellar degeneration-associated antigen Peptide, * MYOSIN HEAVY CHAIN D (MHC
 CG1962 D)(aa) * CLIP-190 * 7e-05 microtubule binding pro [NLS_BP] CG1962 38E-38E dup:3/5 ID:48G3
 CG11403+ DNA_repair_protein CG11403 LD24267 dup:2/2 ID:84C8
 CG10346+ chaperone * CG10346 37A4-37A4 dup:1/3 ID:87G7
 + TfiIS transcription_factor * 2e-20 DST1 DNA strand transferase alpha * 1e-124 TFS2_DROME TRANSCRIPTION ELONGATION
 CG3710 FACTOR S-II (RNA POLYMERASE II ELONGATION FA * 3e-42 TFS2_CAEEL [TFIIS] CG3710 LD34766 35C1-35C1 ID:49F1
 + unknown * BLASTX 4.0E-27 YER156C[Protein of unknown function(dna) * HYPOTHETICAL 38.2 KD PROTEIN IN BEM2-NCB1
 CG11980 INTERGENIC REGION(aa) * 6e-60 similar to Yeast h CG11980 LD44814 85C3-85C3 dup:2/2 ID:103F9
 CG10018+ DNA_repair_protein homology to mouse and human SNM1 protein NLS_BP CG10018 LD28027 dup:1/2 ID:45C8
 + Rbf cell_cycle_regulator * DMRBFPRTN_2 Rbf * EST comes from the 3' UTR m * 3e-24 similar to retinoblastoma proteins * 1e-84
 CG7413 RBL1_MOUSE RETINOBLASTOMA-LIKE PROTEIN (107 KD RETI CG7413 GH05946 1C2-1C2 ID:58D10
 CG3273 + unknown * CG3273 GH05256 42B3-42B3 dup:2/2 ID:33E8
 + bcd transcription_factor * DNA-binding-protein,transcription-factor(aa) * DMBCDG_3 bcd * 1e-125 bcd protein * 8e-52 homeotic
 CG1034 protein bicoid - fruit fly (Drosophila ps[RNP_1 // HOMEBOX_1 // homeobox // HOME] CG1034 LD27003 84D1-84D1 dup:1/2 ID:86A8
 + RnrS enzyme * 1e-113 RIR2_YEAST RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE R *
 1e-107 RIR2_DROME PROBABLE RIBONUCLEOSIDE-DIPHOSPHATE REDUCTA [RIBORED_SMALL] CG8975 LD32770 48D8-48D8
 CG8975 ID:48D10
 + transcription_factor * 5e-87 inserted at base 5' end of P element Inverse PCR * * [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN]
 CG8961 CG8961 LD32631 53F5-53F5 ID:48D3
 + dah unknown * dystrobrevin(aa) * similar to the kDa Torpedo acetylcholine receptor-associated protein; similar to rat apodystrophin-
 CG6157 3, PIR Accession Number * dah [ZF_ZZ // ZZ] CG6157 LD47411 13C1-13C1 ID:106D2
 + transcription_factor * 7e-10 AZF1_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin * 2e-37 transcription factor
 CG3445 YY1 homolog * 1e-14 contains similarity to C2H2-type z[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG3445 67B4-67B4 dup:3/4

ID:56G10

CG3918 + NLS_BP, ZF_CCHC CG3918 ID:56H5
+ unknown * androgen-induced prostate proliferative shutoff associated protein(aa) * protein(aa) * 1e-28 unknown * 6e-40 cDNA
CG17509 EST comes from this gene elegan CG17509 GH12788 48E2-48E2 dup:3/3 ID:64H3
+ Orc2 DNA_replication_factor * recognition complex, subunit (yeast homolog)-like(aa) * ORIGIN RECOGNITION COMPLEX
PROTEIN, SUBUNIT (XORC2)(aa) * Orc2 * ORIGIN RECOGNITION COMPLE[ALDOKETO_REDUCTASE_3 // SUBTILASE_ASP]
CG3041 CG3041 GH13824 88A4-88A4 ID:40H11
+ TfiIEalpha transcription_factor * 6e-23 T2EA_YEAST TRANSCRIPTION INITIATION FACTOR IIE, ALPHA SUBUNIT (TFIIE-ALPHA)
CG10415 (TRA * TFIIE large subunit * 7e-35 cDNA EST yk210d12.5 comes from CG10415 GH11150 68C13-68C13 ID:38F9
CG11484 + transcription_factor_binding * [UBA] CG11484 LD47780 102D1-102D3 ID:106H12
CG7825 + Rad17 DNA_repair_protein DNA repair protein ATP_GTP_A, ATP_GTP_A2, RFC CG7825 LD27993 ID:45C7
+ ial protein_kinase * Ipl1/aur serine/threonine kinase(aa) * 2e-68 IPL1_YEAST SERINE/THREONINE-PROTEIN KINASE IPL1
probable * 1e-75 protein kinase (EC 2.7.1.37) aurora - [PROTEIN_KINASE_ST // TYRKINASE // PROTE] CG6620 32B4-32B4 dup:4/5
CG6620 ID:98E9
+ DNA_binding * protein(aa) * 3e-65 YEZ9_YEAST PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC
CG15835 REGION > * 2e-26 Similarity to Human XE169 protein (SW:X CG15835 LD33386 43F5-43F5 ID:48H3
+ motor_protein * Mklp1 * kinesin motor protein KIFC3(aa) * 2e-20 NUF1_YEAST NUF1 PROTEIN (SPINDLE POLY BODY
SPACER PROTEIN SPC110) * 4e-30 microtubule binding prote [kinesin // KINESIN_MOTOR_DOMAIN1 // KIN] CG4831 LD36932 32E4-
CG4831 32E4 ID:96D1
+ E2f2 transcription_factor * E2f2 * 1e-174 E2F-like transcription factor (E2F2) * 7e-14 predicted using Genefinder; cDNA EST comes
CG1071 from this * 3e-18 E2F5_MOUSE TRANSCRIPTION FAC CG1071 GH13089 39B3-39B3 ID:40D1
CG3510 + CycB cell_cycle_regulator G2/MITOTIC-SPECIFIC CYCLIN B CYCLINS, cyclin CG3510 dup:2/4 ID:43B3
CG7730 + unknown * CG7730 LD31138 73E4-73E4 dup:2/2 ID:47E12