

Table S17

Maternal genes 10-fold degraded

Gene ID mixed annotation (+ indicates sequence confirmation)

+ qua actin\_binding \* qua \* QUA1\_DROME VILLIN-LIKE PROTEIN QUAIL villin homolog qua \* 9e-18 similar to gelsolin; cDNA EST comes from this gene \* 3e-71 putative actin-bin [GELS // GELSOLIN] CG6433 LD42165 36C4-36C4 ID:101C8

+ 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

CG17469+ unknown \* 1E-123\* \* CG17469 LD45277 102E2-102E3 dup:2/2 ID:104B4

+ chaperone \* FK506-binding protein FKBP51(aa) \* 6e-20 FKBP\_YEAST FK506-BINDING PROTEIN (FKBP) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (P \* 6e-24 FKB2\_DROME KD FK50 [TPR\_REGION // FKBP // FKBP\_PPIASE\_1 // ] CG4535 LD47530 30E1-30E1

CG4535 dup:2/2 ID:106E9

CG18543+ unknown \* CG18543 LD47919 66C12-66C12 ID:107B1

+ unknown \* 5e-20 YNZ5\_YEAST HYPOTHETICAL 17.1 KD PROTEIN IN SIP3-MRPL30 INTERGENIC REGION \* 3e-12 RNA helicase \* 2e-25 cellular nucleic acid binding protein cl [ZF\_CCHC // zf-CCHC] CG3800 LD48005 59B6-59B6 ID:107C1

CG5904 + islet mitochondrial antigen CG5904 LP03542 ID:108F8

+ 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 // thioired] CG3864 30C-30C2 ID:115A11

+ receptor \* 5e-14 cDNA EST comes from this gene; cDNA EST co \* 3e-35 peripheral-type benzodiazepine receptor isoquinoline-binding protein - mouse \* 1e-35 benzod CG2789 GH02075 21C6-21C6 dup:2/2 ID:30H12

+ 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 // UBCTHYDLASE] CG4265 GH02396 23D1-23D1 dup:1/2 ID:31B8

+ enzyme \* 3-phosphoglycerate dehydrogenase(aa) \* similar to D-3-Phosphoglycerate dehydrogenase; cDNA EST comes from this gene; cDNA EST comes from this gene; [2-Hacid\_DH // D\_2\_HYDROXYACID\_DH\_1 // A] CG6287 GH03305 32D5-32D5 ID:31H4

+ 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

CG3566 ID:33F10

+ unknown \* 1E-178\* 1e-105 inserted at base Both 5' and 3' ends of P element Inverse PCR \* CG6770 GH05738 33B12-33B12

CG6770 ID:33H4

+ 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-nitrophe CG5567 GH06744 75A4-75A4 ID:34G7

+ BEAF-32 DNA\_binding \* boundary element-associated factor, 32k - fruit fly (Drosophila melanogaster)(aa) \* 1e-146 DMBEAF32A\_2 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 THIOLASE) \* 1e-140 YKA3\_CAEEL HYPOTHETICAL 47.9 KD PROTEIN [thiolase] CG4581 GH13256 60A6-60A6 dup:2/2 ID:40E2

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  
 + aret RNA\_binding \* aret \* 8e-06 polyadenylate-binding protein \* 1e-148 testis-specific RNP-type RNA binding protein \* 2e-29 elav-type  
 CG6319 ribonucleoprotein coded [RBD // HUDSXL RNA // rrm] CG6319 33D-33D4 dup:3/3 ID:44D5  
 + unknown \* 1e-07 ADRP\_MOUSE ADIPOSE DIFFERENTIATION-RELATED PROTEIN (ADRP) \* \* [ATP\_GTP\_A] CG9057 13A11-  
 CG9057 13A11 dup:2/2 ID:46D11  
 + 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  
 + structural\_protein \* Similarity to Yeast YIP1 protein cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST  
 CG3652 comes from this gene; cDNA EST comes from t CG3652 GH04132 24F1-24F1 dup:2/3 ID:56F4  
 + BG:DS00180.8 cell\_adhesion \* DMTENA\_3 Ten-a \* DMC901PRT C901 \* DMDELTA\_4 DI \* 3e-20 C901 protein [EGF\_2] CG16882  
 CG16882 GH07717 34E1-34E1 dup:3/4 ID:59H10  
 + ligand\_binding\_or\_carrier \* DMC30B8 \* retinaldehyde-binding protein 1(aa) \* tocopherol (alpha) transfer protein (ataxia (Friedreich-like)  
 CG10237 with vitamin E deficiency)(aa) \* 62D[CRETINALDHBP // CRAL\_TRIO] CG10237 GH08711 37E3-37E3 dup:2/3 ID:60H5  
 CG12024 + signal\_transduction \* 5e-25 BAW protein \* \* [NLS\_BP] CG12024 GH08896 62E3-62E3 dup:1/2 ID:61B6  
 + 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 // PAPAINE // Peptida] CG8947 70C9-70C9 dup:1/2 ID:61C5  
 + Nacalphan unknown \* 4e-13 EGD2\_YEAST EGD2 PROTEIN EGD2 protein - yeast (Saccharomyc \* 5e-73 alpha NAC \* 1e-34 alpha  
 CG8759 NAC/1.9.2. protein alpha-NAC, non-musc \* 1e-34 Nasce CG8759 GH11940 49C2-49C2 dup:2/2 ID:63H12  
 + motor\_protein \* receptor-associated protein(aa) \* 9e-14 predicted using Genefinder; Similarity to Human alpha-2-macroglobu \* 2e-16  
 CG8507 heparin binding protein \* 5e-18 CG8507 GH16343 86D1-86D1 dup:3/3 ID:68E5  
 + enzyme \* similar to aspartate aminotransferase(aa) \* 1e-99 aspartate aminotransferase cerevisiae, Peptide Partial, \* 1e-157 similar to  
 CG4233 aspartate aminotransfe [aminotran\_1 // AA\_TRANSFER\_CLASS\_1 // T] CG4233 GH20337 22B8-22B8 dup:2/2 ID:72F2  
 + 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-  
 CG17608 29C4 ID:80F12  
 + 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  
 + 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  
 + 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  
 CG8180 + unknown \* 1E-178 \* [ANTIFREEZEI] CG8180 LD38554 52A4-52A4 dup:1/2 ID:97G8  
 + unknown \* 5e-40 prediabetic NOD sera-reactive autoantigen muscul \* 5e-10 IVR-like protein \* IVR-like protein \* [TPR\_REGION //  
 CG14444 TPR\_REPEAT] CG14444 LD39177 6C1-6C1 dup:3/3 ID:98D4  
 CG5194 + unknown \* CG5194 LD39537 66F1-66F1 ID:98F8  
 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