

Table S25

male germline-list of genes from male germline cluster identified in hierarchical cluster (Fig. S7)

+ Cdic motor\_protein \* Cdic \* cytoplasmic dynein intermediate chain isoform DIC5b(aa) \* cytoplasmic dynein intermediate chain  
CG18000 isoform DIC3a(aa) \* 3e-83 cytoplasmic dynein CG18000 LD42953 19C1-19C1 dup:1/2 ID:101G10  
+ Cdlc2 motor\_protein \* 8kd dynein light chain(aa) \* Cdlc1 \* dynein light chain 5(aa) \* 1e-21 DYLL1\_YEAST DYNEIN LIGHT CHAIN 1,  
CG5450 CYTOPLASMIC dynein lig [Dynein\_light // DYNEIN\_LIGHT\_1] CG5450 LP02196 22A-22A ID:108A1  
+ DnaJ-60 chaperone \* dnaJ-like protein(aa) \* DMDNAJLP\_2 DnaJ-60 \* 3e-08 SCJ1\_YEAST SCJ1 PROTEIN SCJ1 protein - yeast  
CG12240 (Saccharomyce \* 1e-114 dnaJ-like protein [DnaJ // DNAJ\_2] CG12240 LP04971 60B9-60B9 dup:3/3 ID:109B12  
+ chaperone \* DMTIDT4M\_4 I(2)tid \* 1e-22 MDJ1\_YEAST MDJ1 PROTEIN PRECURSOR heat shock protein MDJ1 \* 2e-42 Tid56  
protein \* 2e-42 YLW5\_CAEEL HYPOTHETICAL 105.9 K[DnaJ\_CXXCXGXG // DNAJ\_1 // DnaJ // DNAJ] CG7387 LP05202 66B13-66B13  
CG7387 dup:1/2 ID:109C10  
+ Cyt-c1 electron\_transfer \* CYTOCHROME C(aa) \* 1e-32 pdb|1YCC| Cytochrome C (Isozyme 1) (Reduced) Saccharomyces cerevisia \*  
2e-58 CYC1\_DROME CYTOCHROME C-1 cytochrome c[CYTCHRMEDIA // cytochrome\_c // CYTOCHR] CG13263 LP05614 36A7-  
CG13263 36A7 dup:2/2 ID:109E5  
+ PpN58A protein\_phosphatase \* serine-threonine protein phosphatase(aa) \* PpN58A \* 1e-108 PP12\_YEAST SERINE/THREONINE  
PROTEIN PHOSPHATASE PP1-2 pho \* 1e-174 serine-threonine prot[PHOSPHO\_ESTER // STPHPTASE // SER\_THR\_] CG3245  
CG3245 SD01703 58B1-58B1 ID:113A9  
+ enzyme \* LONG-CHAIN-FATTY-ACID--COA LIGASE (LONG-CHAIN ACYL-COA SYNTHETASE 2) (LACS 2)(aa) \* 1e-83  
LCF2\_YEAST LONG-CHAIN-FATTY-ACID--COA LIGASE (LONG-CHAIN A [AMP\_BINDING // AMPBINDING // AMP-bindin] CG3961  
CG3961 SD02971 75E2-75E2 ID:114H10  
CG10192+ translation\_factor CG10192 SD03848 ID:116C4  
CG9531 + CG9531 SD04586 dup:3/3 ID:117E5  
CG2385 + CG2385 SD05054 dup:1/2 ID:118C5  
CG10589+ unknown \* [NLS\_BP] CG10589 GH01788 78A-78A ID:30F11  
CG12860+ unknown \* [NLS\_BP] CG12860 GH02210 51B11-51B11 ID:31A8  
+ enzyme \* hypothetical protein(aa) \* TUBULIN--TYROSINE LIGASE (TTL)(aa) \* Ybr094wp(aa) \* 2e-10 ORF2 [NLS\_BP] CG11201  
CG11201 GH02545 27A1-27A1 ID:31C9  
+ translation\_factor \* Eif4E \* 1e-23 IF4E\_YEAST EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA  
CG8023 CA \* 2e-56 IF4E\_DROME EUKARYOTIC TRANSLATION INITIATION [IF4E] CG8023 GH04024 66C-66C ID:32D6  
+ serpin \* serine protease inhibitor(aa) \* OVALBUMIN (PLAKALBUMIN) (ALLERGEN GAL D 2) (GAL D II)(aa) \* LEUKOCYTE  
CG9456 ELASTASE INHIBITOR (LEI) (LEUCOCYTE NEUTRAL P [serpin] CG9456 GH04125 42C8-42C8 dup:2/2 ID:32E4  
+ apoptosis\_inhibitor \* 2e-81 SINA\_DROME DEVELOPMENTAL PROTEIN SEVEN IN ABSENTIA devel \* 8e-67 seven-in-absentia  
CG13030 protein homologue-1 \* 2e-73 siah-1A protein - mouse siah-1A [ZF\_RING] CG13030 GH04279 73D1-73D1 ID:32F2  
+ unknown \* 1e-26 VP28\_YEAST VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS28 \* 3e-40 putative protein \* 3e-  
CG12770 76 inserted at base Both 5' and 3' ends of P elemen CG12770 GH04443 44A4-44A4 ID:32G10  
CG6405 + unknown \* CG6405 GH04442 33D5-33D5 ID:32G9

+ motor\_protein \* 7e-15 cytoplasmic dynein intermediate chain isoform DIC2b \* 7e-15 similar to the beta transducin family \* 3e-14  
 CG9313 cytoplasmic dynein intermediate chain [NLS\_BP // WD40] CG9313 GH05829 57B14-57B14 ID:33H12  
 CG5538 + unknown \* [NLS\_BP] CG5538 87C-87C dup:1/3 ID:34G11  
 + cytoskeletal\_structural\_protein \* hypothetical protein(aa) \* BRCA1 associated protein(aa) \* HYPOTHETICAL 141.2 KD PROTEIN  
 EEED8.9 IN CHROMOSOME II(aa) \* HYPOTHETICAL[zf-C3HC4 // SPEC\_REPEAT // ZF\_UBP // ZF] CG5555 GH07062 91F6-91F7 dup:1/2  
 CG5555 ID:35A7  
 CG8701 + unknown \* CG8701 GH07855 44B9-44B9 ID:35G4  
 + motor\_protein \* very strong similarity to C. elegans myosin heavy chain B \* 6e-09 MYS1\_YEAST MYOSIN-1 ISOFORM (TYPE II  
 CG6059 MYOSIN) myosin heavy \* 1e-12 nonmuscle myosin [PEROXIDASE\_3] CG6059 GH07888 97E8-97E8 dup:1/2 ID:35G7  
 + motor\_protein \* signaling molecule(aa) \* contains similarity to Mus musculus tumor susceptibility protein TSG101 \* tumor  
 CG9712 susceptibility protein TSG101(aa) \* 4e-11 [TPR\_REPEAT] CG9712 GH09529 73C4-73C4 ID:37B1  
 + cmp44E unknown \* map\_position:44E3-4 \* HYPOTHETICAL PROTEIN \* HYPOTHETICAL 96.7 KD PROTEIN C32D5.3 IN  
 CG8739 CHROMOSOME II(aa) CG8739 GH09667 44E1-44E1 dup:1/3 ID:37C1  
 CG3074 + endopeptidase similar to cysteine protease Peptidase\_C1, THIOL\_PROTEASE\_HIS CG3074 GH10620 dup:1/3 ID:38B6  
 CG9133 + unknown \* CG9133 GH10732 61F4-61F4 dup:1/3 ID:38C6  
 CG6456 + unknown \* 9e-07 prepro-APGWamide \* APGWamide \* [NLS\_BP] CG6456 GH11008 74B-74B dup:2/2 ID:38E7  
 CG17567 + unknown \* 1E-78\* \* CG17567 GH11551 37C-37C ID:39A10  
 CG12907 + unknown \* 1E-145\* \* [PRO\_RICH // NLS\_BP] CG12907 GH11521 47A-47A ID:39A8  
 + \* 1e-29 cDNA EST yk428d5.3 comes from this gene; cDNA EST yk428d5.5 comes \* 3e-12 conserved hypothetical secreted  
 CG13865 protein pylori \* putative pylori \* c CG13865 cyto\_unknown dup:3/3 ID:39B1  
 CG3825 + unknown \* CG3825 GH11727 60A14-60A14 dup:1/3 ID:39C1  
 + unknown \* HSPC017(aa) \* 5e-35 YOY9\_CAEEL PUTATIVE UBIQUINONE BIOSYNTHESIS METHYLTRANSFERASE ZK652.9 \*  
 CG12162 4e-17 apaG protein \* APAG\_ECOLI APAG PROTEIN apaG prote CG12162 GH11824 83A8-83A9 ID:39C7  
 CG9284 + unknown \* CG9284 GH11908 58A2-58A2 ID:39D1  
 CG1146 + unknown \* CG1146 GH12037 62E6-62E6 ID:39D9  
 CG10841 + unknown \* CG10841 GH12158 87F6-87F6 dup:2/2 ID:39E9  
 + peptidase \* PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III(aa) \* Chain A, Bovine Lens Leucine Aminopeptidase  
 CG4750 Complexed With L-Leucine Phosphonic Acid(aa) \* [Peptidase\_M17] CG4750 GH12543 53C-53C ID:39G10  
 + transporter \* similar to ADP/ATP translocase(aa) \* 2e-17 probable membrane protein YPL134c - yeast (Saccharomyces  
 CG4995 cerevisiae) \* 1e-32 colt \* 1e-58 similar to mito [mito\_carr // MITOCARRIER // MITOCH\_CARR] CG4995 GH13054 31D8-31D8 ID:40C11  
 CG6306 + unknown \* CG6306 GH12946 17B1-17B1 ID:40C7  
 + peptidase \* Chain A, Bovine Lens Leucine Aminopeptidase Complexed With L-Leucine Phosphonic Acid(aa) \* 6e-20  
 YOJ6\_CAEEL PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROM [LAMNOPPTDASE // Peptidase\_M17] CG6372 GH13022 68C1-  
 CG6372 68C1 dup:2/2 ID:40C9  
 + RNA\_binding \* 3e-16 RNA-binding protein cabeza - fruit fly (Drosophila melanogaster) ( \* 4e-14 EWS\_MOUSE RNA-BINDING  
 CG14718 PROTEIN EWS RNA-binding protein E \* 2e-15 TLS [RBD // zf-RanBP // rrm // ZF\_RANBP] CG14718 GH13594 86F1-86F1 ID:40G5

+ protein\_kinase \* serine/threonine protein kinase; Cdc7p(aa) \* protein kinase Cdc7(aa) \* DMSTPK Pk61C \* HsCdc7(aa)  
 CG5790 [PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM] CG5790 GH13884 36F-36F ID:41A7  
 + enzyme \* C. elegans glyceraldehyde 3-phosphate dehydrogenase \* GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE II  
 (GAPDH II)(aa) \* GLYCERALDEHYDE 3-PHOSPHATE DEHYDR [G3PDHDRGNASE // gpdh // GAPDH] CG9010 GH13901 53E6-53E6  
 CG9010 ID:41A8  
 CG7251 + unknown \* [NLS\_BP] CG7251 GH13914 27D1-27D1 ID:41A9  
 CG7131 + unknown \* CG7131 GH14048 90F7-90F7 ID:41B9  
 + electron\_transfer \* 9e-06 PDI\_YEAST PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) / DOLICHYL-  
 DIPHOSPHOOLIGOS \* 2e-08 PDI\_DROME PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) [THIOREDOXIN //  
 CG3315 THIOREDOXIN\_2 // thioed] CG3315 GH14562 4F2-4F2 ID:41F1  
 CG8136 + unknown \* CG8136 GH14973 85B2-85B2 dup:1/2 ID:42A2  
 + enzyme \* DMUBCD2\_2 UbcD2 \* similar to Ubiquitin-conjugating enzymes; cDNA EST comes from this gene(aa) \* ubiquitin-  
 conjugating enzyme(aa) \* 6e-12 UBCC\_YEAST [CRYSTALLIN\_BETAGAMMA // UQ\_con // UBIQU] CG7220 GH15032 47B7-47B7  
 CG7220 ID:42A5  
 CG2149 + unknown \* [NLS\_BP] CG2149 GH15120 44B9-44B9 dup:1/2 ID:42B2  
 CG2127 + unknown \* [EF\_HAND // NLS\_BP] CG2127 GH15271 44B9-44B9 ID:42C3  
 + unknown \* 3e-80 YKL6\_CAEEL HYPOTHETICAL 103.8 KD PROTEIN C03C10.6 IN CHROMOSOME III \* E03A3.6 \* E03A3.7 \*  
 CG5237 [AA\_TRNA\_LIGASE\_II\_2 // PRO\_RICH // CYTO] CG5237 GH01039 91F10-91F11 ID:54A4  
 + enzyme \* similar to pig tubulin-tyrosine ligase.(aa) \* 1e-41 similar to tubulin tyrosine ligase; cDNA EST comes fro \* 2e-55 protein \*  
 CG16716 8e-16 TTL\_BOVIN TUBULIN [NLS\_BP] CG16716 GH01307 56D15-56E1 ID:54C7  
 CG7366 + unknown \* CG7366 GH02649 67E7-67E7 ID:55D4  
 + unknown \* 2e-22 YKQ5\_YEAST HYPOTHETICAL 105.7 KD PROTEIN IN TPK3-PIR1 INTERGENIC REGION \* 6e-36 Mcd4p  
 CG6790 homolog \* 1e-18 hypothetical protein \* unknown protein CG6790 GH02677 86E15-86E15 ID:55D6  
 + Chi DNA\_binding \* neural src interacting protein, long form; NSIP long form(aa) \* Nuclear LIM interactor(aa) \* short form of CHIP(aa)  
 CG3924 \* CHIP(aa) [NLS\_BP] CG3924 GH02919 60B1-60B1 dup:3/4 ID:55E11  
 CG4714 + unknown \* 6e-05 centromere protein E CENTROMERIC \* 6e-05 CENP-E protein \* CG4714 GH03085 50A1-50A1 ID:55F11  
 + unknown \* 2e-17 FMR2 protein \* 1e-17 X mental retardation X ment \* lymphoid nuclear protein related to AF4 \* [HMGI\_Y //  
 CG8817 NLS\_BP] CG8817 GH03237 23C1-23C1 dup:1/2 ID:55G11  
 + transcription\_factor \* LTG19 - human(aa) \* BLASTX 1.2E-10 Caenorhabditis elegans cosmid ZK354.(dna) \* 1e-11 YNK7\_YEAST  
 CG4913 HYPOTHETICAL 26.0 KD PROTEIN IN CYB5-LEU4 INTERGENIC [NLS\_BP] CG4913 GH03493 90E1-90E1 dup:1/2 ID:55H10  
 CG9803 + unknown \* [PRO\_RICH] CG9803 GH03629 59D6-59D6 ID:56B1  
 CG3124 + unknown \* CG3124 GH03736 59D4-59D4 ID:56B12  
 CG9861 + DNA\_binding \* [NLS\_BP] CG9861 GH03827 59D6-59D6 ID:56C11  
 + BcDNA:GH07626 enzyme \* p270(aa) \* Similar to polyketide synthase.(aa) \* FK506 polyketide synthase(aa) \* [adh\_zinc //  
 CG3523 Thioesterase // ACP\_DOMAIN ] CG3523 GH03816 23D-23D dup:4/9 ID:56C9  
 CG6541 + Mst33A unknown \* [NLS\_BP] CG6541 GH04277 33A3-33A3 ID:56G4

+ dib cytochrome\_P450 \* 2e-17 cytochrome P-450 - fruit fly (Drosophila melanogaster) (fragment) \* 1e-10 YS45\_CAEEL PUTATIVE CYTOCHROME P450 ZK177.5 IN CHROMOSOME II \* 3e-30 [EP450II // p450 // P450 // MITP450 // C] CG12028 GH04745 64A5-64A5  
CG12028 ID:57C3

CG9686 + unknown \* CG9686 GH05060 9A2-9A2 dup:2/2 ID:57E11  
+ CaMKI protein\_kinase \* CaMKI \* calcium/calmodulin dependent protein kinase I(aa) \* 1e-28 KCC1\_YEAST  
CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE I \* 5e-17 Contains si[PROTEIN\_KINASE\_ST // TYRKINASE // PROTE]

CG1495 CG1495 GH04968 102B7-102B7 dup:7/7 ID:57E2

CG15867 + unknown CG15867 GH05072 ID:57F2

none + none GH05253 ID:57G7  
+ cli unknown \* DMABSNTI\_3 cli \* DEVELOPMENTAL PROTEIN EYES ABSENT (PROTEIN CLIFT)(aa) \* EYES ABSENT HOMOLOG

CG9554 1(aa) \* eyes absent homolog 1(aa) [PHOSPHOPANTETHEINE] CG9554 GH05272 26D11-26E1 ID:57G8  
+ transcription\_factor\_binding \* oxidoreductase(aa) \* 3e-20 YULF\_BACSU HYPOTHETICAL 36.5 KD PROTEIN IN GBSA-TLPB  
INTERGENIC REGION \* YMO1\_RHIME HYPOTHETICAL 36.4 KD PROTEIN IN MOC [GFO\_IDH\_MocA] CG13280 GH05468 36A9-  
CG13280 36A10 dup:2/2 ID:57H11

CG9136 + CG9136 GH05420 ID:57H7

CG14008 + unknown \* 1E-109\*\* CG14008 GH05437 25F3-25F3 ID:57H8  
+ BcDNA:GH12504 transmembrane\_receptor \* 3e-07 microtubule binding protein D-CLIP-190 \* 1e-06 DYNA\_MOUSE DYNACTIN, KD  
ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP- \* 1e-06 DYNA\_HUMAN CG9808 GH05455 85B3-85B4 dup:3/4  
CG9808 ID:57H9  
+ sm RNA\_binding \* DMSMOOTH\_2 sm \* 4e-20 homologous to human hnRNP L \* 5e-22 DMSMOOTH\_2 sm \* [RBD] CG9218  
CG9218 GH05823 56D11-56E1 dup:1/2 ID:58C12  
+ chaperone \* DMHSP60\_2 Hsp60 \* CHAPERONIN HOMOLOG HSP60 PRECURSOR (HEAT SHOCK PROTEIN 60) (HSP-60)(aa)  
\* MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYT [CHAPERONINS\_CPN60 // TCOMPLEXTCP1 // CH]

CG2830 CG2830 GH05807 21D1-21D1 ID:58C8  
+ enzyme \* by content; by match; 2-match\_description=4-NITROPHENYLPHOSPHATASE.; 2-match...(aa) \* similar to N-acetyl-  
CG2077 glucosamine catabolism(aa) \* Similar to CG2077 GH05933 63B3-63B3 ID:58D8  
+ cell\_adhesion \* sdk \* DMNRGAA\_3 Nrg \* fra \* 8e-23 LAR\_DROME PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR  
CG8619 (PROTEIN-TYROSINE-PHOSPHAT [ig // FNTYPEIII // fn3] CG8619 GH06134 65E7-65E7 dup:2/2 ID:58F1  
+ transcription\_factor \* 6e-06 TF3A\_YEAST TRANSCRIPTION FACTOR IIIA (TFIIIA) transcriptio \* 2e-11 zinc finger motif protein \*  
CG10631 5e-09 similar to Zinc finger, C2H2 typ[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG10631 GH06278 38A2-38A dup:1/3 ID:58G1  
+ transporter \* organic anion transporter-K2(aa) \* solute carrier family (prostaglandin transporter), member 2(aa) \* SODIUM-  
CG3380 INDEPENDENT ORGANIC ANION TRANSPORTER (O CG3380 GH06385 58D1-58D1 dup:1/2 ID:58G11  
+ EG:BACN32G11.3 unknown \* BACN32G11.f \* 1e-29 L130\_HUMAN KD LEUCINE-RICH PROTEIN (LRP 130) (GP130) le \* leucine-rich  
CG14786 protein - human leucine-rich protein sa \* BACN32G11.l CG14786 GH06301 2B1-2B1 ID:58G4

CG5571 + \* [G\_PROTEIN\_RECEPTOR] CG5571 77B6-77B6 dup:1/2 ID:58H1

CG3748 + unknown \* CG3748 GH06504 30B-30B ID:58H11

CG5089 + unknown \* [NLS\_BP] CG5089 GH06435 53C8-53C9 dup:2/2 ID:58H4  
 CG7557 + unknown \* [ATP\_GTP\_A] CG7557 GH07076 68C3-68C3 ID:59C11  
 CG6761 + unknown \* CG6761 GH07092 67B12-67B12 ID:59D1  
 + transporter \* 9e-43 hypothetical protein YLR348c - yeast (*Saccharomyces cerevisiae*) (U \* 1e-74 Oxoglutarate/malate carrier  
 CG4323 protein - *Caenorhabditis elegans* \* 8e-2 [mito\_carr // MITOCARRIER // MITOCH\_CARR] CG4323 GH07093 92E7-92E7 ID:59D2  
 + peptidase \* alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13,  
 p150)(aa) \* 8e-98 AAP1\_YEAST ALANINE/ARGININE [ALADIPTASE // Peptidase\_M1 // HEMOPEXIN] CG11955 GH07390 99A5-99A5  
 CG11955 dup:2/3 ID:59F7  
 + enzyme \* DMADHA1\_9 Adh \* DMSCU scu \* 7e-17 SP19\_YEAST SPORULATION PROTEIN SPS19 (SPORULATION-SPECIFIC  
 PROTEIN SPX19) \* 4e-05 3-hydroxyacyl-CoA dehydrogenase [CPSASE\_2 // adh\_short\_C2 // GDHRDH // a] CG2907 GH07691 83B6-  
 CG2907 83B6 ID:59H8  
 CG3092 + unknown \* CG3092 GH07743 59D-59D dup:1/2 ID:60A5  
 CG6332 + unknown \* [NLS\_BP] CG6332 GH07879 93F14-93F14 dup:1/2 ID:60B8  
 + endopeptidase \* coded for by *C. elegans* cDNA CEESC71F; similar to the S25B family of peptidases(aa) \* PROTEASOME  
 COMPONENT C7-I (MACROPAIN SUBUNIT C7-I) (MULTI[PROTEASOME\_B // PROTEASOME\_PROTEASE // ] CG17302 GH07971  
 CG17302 23A3-23A3 dup:1/3 ID:60C10  
 CG11018+ unknown \* [DNA\_LIGASE\_A1] CG11018 GH07940 56E2-56E2 dup:1/2 ID:60C2  
 + endopeptidase \* 3e-11 TBP6\_YEAST PROBABLE 26S PROTEASE SUBUNIT YTA6 (TAT-BINDING HOMOLOG 6) \* 3e-08  
 CG14183 MEI1\_CAEEL MEIOTIC SPINDLE FORMATION PROTEIN MEI-1 mei-1 \* 0.000 CG14183 GH08353 76E3-76E4 dup:3/3 ID:60E12  
 + enzyme \* SUCCINYL-COA SYNTHETASE ALPHA CHAIN (SCS-ALPHA)(aa) \* DMSUCCOAA Scs agr; \* 9e-77 SUCA\_YEAST  
 PROBABLE SUCCINYL-COA LIGASE (GDP-FORMING), ALPHA-CHAIN [SUCCINYL\_COA\_LIG\_2 // ligase-CoA // SUC] CG6255  
 CG6255 GH08383 92A6-92A6 dup:2/4 ID:60F3  
 CG7669 + unknown \* [NLS\_BP] CG7669 GH08407 91A-91A dup:1/2 ID:60F7  
 CG11656+ unknown \* CG11656 GH08448 87D9-87D9 dup:1/2 ID:60F9  
 CG6304 + unknown \* [NLS\_BP] CG6304 GH09088 36A14-36A14 dup:2/3 ID:61D2  
 CG8508 + unknown \* CG8508 GH09161 87E2-87E2 dup:1/2 ID:61D9  
 + endopeptidase \* TRYPSIN DELTA PRECURSOR(aa) \* Ser12 \* Ser6 \* Dvtry-1 trypsin precursor(aa) [trypsin // CHYMOTRYPSIN //  
 CG4653 TRYPSIN\_HIS ] CG4653 GH09333 15A1-15A1 ID:61F1  
 + enzyme \* DMCATHPO\_2 Cat \* CATALASE(aa) \* 1e-110 CATA\_YEAST CATALASE A catalase (EC 1.11.1.6), peroxisomal - \* 1e-  
 CG9314 158 catalase (EC 1.11.1.6) - *Caenorhabditis* [CATALASE // catalase // CATALASE\_1] CG9314 GH09387 29E4-29E4 dup:1/2 ID:61F8  
 CG4891 + BG:DS04095.1 unknown \* CG4891 GH09478 35F1-35F1 dup:1/2 ID:61G1  
 + enzyme \* 7e-62 SYWM\_YEAST TRYPTOPHANYL-TRNA SYNTHETASE, MITOCHONDRIAL (TRYPTOPHAN--TRNA LIGASE) \*  
 1e-60 SYWM\_CAEEL PROBABLE TRYPTOPHANYL-TRNA SYNTHETASE, MIT [TRNASYNTHTRP // tRNA-synt\_1b // AA\_TRNA]  
 CG7441 CG7441 GH09538 75A4-75A4 dup:1/3 ID:61G8  
 CG11074+ unknown \* [NLS\_BP] CG11074 GH09884 42F2-42F2 ID:62A8  
 CG6128 + enzyme \* alpha-L-fucosidase(aa) \* fucosidase, alpha-L- 1, tissue(aa) \* 8e-28 hypothetical protein YIL106w - yeast

(Saccharomyces cerevisiae) \* 4e-73 FUCO\_CAE [Alpha\_L\_fucos // GLHYDRLASE29] CG6128 GH09976 68C4-68C5 ID:62B4  
 + chaperone \* 5e-06 YB05\_YEAST HYPOTHETICAL 44.1 KD PROTEIN IN RPB5-CDC28 INTERGENIC REGION \* 1e-10  
 CG6980 Hsp70/Hsp90 organizing protein homolog \* 1e-08 coded for by C. [TPR\_REGION] CG6980 GH10293 98E1-98E1 ID:62D2  
 CG6130 + unknown \* CG6130 GH10346 90E4-90E4 ID:62D6  
 + motor\_protein \* 2e-05 cellular myosin heavy chain \* 8e-07 myosin heavy chain, neuronal - rat \* 1e-05 Klp68D \* myosin heavy  
 CG4681 chain IIb CG4681 GH10544 60D6-60D6 dup:2/2 ID:62E11  
 CG2267 + transcription\_factor \* CG2267 100A2-100A2 dup:2/2 ID:62F6  
 + acj6 DNA\_binding \* DMIPOU\_2 acj6 \* POU domain transcription factor(aa) \* INHIBITORY POU PROTEIN (I-POU) (ABNORMAL  
 CHEMOSENSORY JUMP PROTEIN)(aa) \* 1e-152 PP12\_YEAST SE [HOMEBOX\_1 // homeobox // HOMEBOX\_2 //] CG9151  
 CG9151 GH10637 13C1-13C4 ID:62F9  
 + unknown \* 1e-36 predicted using Genefinder; Similarity to Human leukocyte surface \* 7e-22 CD63\_MOUSE CD63 ANTIGEN  
 CG10742 CD63/ME491 antigen homolog - mou \* 3e-44 tet [transmembrane4 // TMFOUR // TM4\_2] CG10742 GH10778 3A9-3A9 dup:1/2 ID:62G10  
 + metabolism \* xylulokinase (H. influenzae) homolog(aa) \* xylulose kinase(aa) \* xylulokinase(aa) \* HYPOTHETICAL 60.3 KD  
 CG3544 PROTEIN R08D7.7 IN CHROMOSOME III(aa) [FGGY] CG3544 GH10780 21E1-21E1 ID:62G11  
 CG17564 + unknown \* 7E-86\* \* CG17564 GH10882 37D3-37D3 ID:62H12  
 + enzyme \* intermediate chain 1(aa) \* nm23-H7(aa) \* NUCLEOSIDE DIPHOSPHATE KINASE (NDK) (NDP KINASE)(aa) \* 1e-06  
 CG8362 type nucleoside diphosphate kinase NM23-H6 CG8362 GH10857 85E4-85E4 ID:62H9  
 + transcription\_factor \* scrt \* Similarity to Drosophila scratch neuronal zinc-finger transcription factor \* 9e-05 RIM1 \* 7e-73 neuron  
 CG12605 specific zinc finger transcription[zf-C2H2 // ZINC\_FINGER\_C2H2 // ATP\_GTP\_] CG12605 GH11439 64A1-64A1 ID:63D10  
 CG18418 + unknown \* CG18418 GH11346 65A10-65A10 ID:63D4  
 CG6441 + unknown \* CG6441 GH11511 28A1-28A1 dup:2/2 ID:63E3  
 + cytoskeletal\_structural\_protein \* DMTUBA1\_2 agr;Tub84B \* 1e-117 TBA1\_YEAST TUBULIN ALPHA-1 CHAIN tubulin alpha-1  
 CG7794 chain \* 1e-132 TBA1\_DROME TUBULIN ALPHA-1 CHAIN tubulin alpha-1 chain [tubulin] CG7794 GH11574 90D2-90D2 ID:63F2  
 CG3306 + unknown \* CG3306 GH11578 67B9-67B9 ID:63F3  
 CG1324 + unknown \* [ATP\_GTP\_A] CG1324 GH11587 19E3-19E3 ID:63F6  
 CG16959 + unknown \* [EGF\_2] CG16959 GH11627 71B2-71B2 dup:2/2 ID:63F7  
 + RNA\_binding \* putative RNA-binding protein(aa) \* Wbscr1(aa) \* 7e-05 NSR1\_YEAST NUCLEAR LOCALIZATION SEQUENCE  
 BINDING PROTEIN (P67) \* 2e-13 RNA recognition motif-t [RNP\_1 // RBD // rrm // NLS\_BP] CG1340 GH11731 100A-100A dup:2/2  
 CG1340 ID:63G10  
 CG14355 + unknown \* CG14355 GH11706 88A12-88B1 ID:63G5  
 CG11404 + unknown \* CG11404 GH11730 79E-79E ID:63G9  
 CG7886 + signal\_transduction \* 2e-15 IP63 protein \* \* CG7886 GH12083 88C10-88C10 ID:64B9  
 CG11146 + signal\_transduction Shb=Src homology 2 protein ANTIFREEZE1, SH2 CG11146 ID:64F5  
 CG3982 + unknown \* CG3982 GH12755 67B3-67B3 dup:2/2 ID:64G10  
 + RNA\_binding \* BLASTX 2.0E-34 Arabidopsis thaliana Col-O putative RNA helicase A mRNA, complete cds.(dna) \* DMMLE\_2 mle  
 CG9323 \* 1e-79 hypothetical protein YLR419w - yeas [PROTEIN\_SPLICING // G\_PROTEIN\_RECEPTOR ] CG9323 GH12763 38E5-38E5

ID:64G12

+ protein\_phosphatase \* DMPP1A1\_2 Pp1 agr;-96A \* serine-threonine protein phosphatase(aa) \* type 1-related protein phosphatase(aa) \* 1e-110 PP12\_YEAST SERINE/THREONINE PR[PHOSPHO\_ESTER // STPHPHTASE // SER\_THR\_] CG10138  
CG10138 GH12873 58B9-58B9 ID:65A1  
CG13918+ unknown \* CG13918 GH13002 62A-62A ID:65A12  
CG7634 + unknown \* [TPR\_REPEAT] CG7634 GH12875 78E2-78E2 dup:2/2 ID:65A2  
+ unknown \* FLAGELLAR RADIAL SPOKE PROTEIN 4(aa) \* radial spokehead(aa) \* 9e-13 predicted using Genefinder; similar to  
CG3121 Sugar transporter; cDNA EST \* 5e-55 radia [ER\_TARGET] CG3121 GH13165 60A16-60A16 dup:1/2 ID:65C3  
CG2209 + unknown \* CG2209 GH13175 11D3-11D3 ID:65C5  
+ enzyme \* 5e-49 IDH1\_YEAST ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT PRECURSOR (IS \* 6e-57  
CG3483 IDHA\_CAEEL PROBABLE ISOCITRATE DEHYDROGENASE (NAD), MIT [isodh] CG3483 GH13226 60D2-60D2 ID:65C9  
+ \* ribokinase(aa) \* ribokinase RbsK(aa) \* DMC115C2 \* 1e-71 /match=(desc;; /ma [pfkB // PRO\_RICH // RIBOKINASE] CG17010  
CG17010 33D3-33D3 dup:2/2 ID:65D12  
+ enzyme \* 1-PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (P5C DEHYDROGENASE)(aa) \* UNKNOWN(aa) \* Similar to  
CG6670 aldehyde dehydrogenase; coded for by C. elegans cDNA cm1 [aldedh // NLS\_BP] CG6670 GH13449 93F-93F10 dup:2/2 ID:65D9  
+ cytoskeletal\_structural\_protein \* 2e-47 dystrophin \* 1e-117 unnamed protein product \* 1e-143 dystrobrevin dystrobrevin \* 1e-143  
CG8529 dystrobrevin B [ZF\_ZZ // ZZ // CYTOCHROME\_C] CG8529 GH13689 49A6-49A7 dup:2/2 ID:65E12  
CG1314 + unknown \* CG1314 GH13802 19E4-19E4 ID:65F10  
+ structural\_protein \* 8e-30 YLS5\_CAEEL HYPOTHETICAL 55.1 KD PROTEIN F09G8.5 IN CHROMOSOME III \* 2e-07 B7 \* 6e-36  
CG14995 chromosome open reading frame 28.3 KD PROTEIN C21OR \* 8e- [LRR] CG14995 GH13848 64A7-64A8 dup:3/3 ID:65F12  
+ signal\_transduction \* cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene;  
CG8683 cDNA EST comes from this gene; cDNA EST comes from thi CG8683 GH13975 28E5-28E6 dup:2/3 ID:65G12  
CG3372 + unknown \* CG3372 GH14065 60C1-60C1 ID:65H8  
+ DNA\_binding \* component of CCR4 transcriptional complex; Caf17p(aa) \* putative protein(aa) \* Similarity to S.pombe  
CG8043 hypothetical protein C21E11.07 (SW:YAL7\_SCHPO CG8043 GH14121 85B-85B ID:66A7  
+ translation\_factor \* HYPOTHETICAL 64.2 KD PROTEIN R08D7.3 IN CHROMOSOME III(aa) \* UNKNOWN(aa) \* eIF3 p66(aa) \*  
CG4810 9e-98 putative elongation initiation factor subunit CG4810 GH14470 87B5-87B5 ID:66D7  
+ enzyme\_activator \* 2e-40 inserted at base Both 5' and 3' ends of P element Inverse PCR \* \* [EF\_HAND\_2] CG3565 GH14476  
CG3565 60D8-60D8 ID:66D8  
+ endopeptidase \* phosphate regulator(aa) \* endothelin converting enzyme, ECE=putative zinc-binding metalloprotease aortic  
CG6265 endothelial cells, Peptide, \* Similarity t CG6265 GH14576 97E2-97E3 dup:2/2 ID:66E8  
CG9469 + unknown \* [PRO\_RICH // NLS\_BP // ATP\_GTP\_A] CG9469 GH14660 42E1-42E1 dup:2/3 ID:66F10  
CG1394 + unknown \* CG1394 GH14622 10A11-10A11 ID:66F4  
CG12699+ unknown \* CG12699 GH14656 54B7-54B7 ID:66F9  
+ enzyme \* Ac76E \* type VIII adenylyl cyclase - human(aa) \* Ac35C \* ADENYLATE CYCLASE, TYPE VIII (ATP  
CG5983 PYROPHOSPHATE-LYASE) (CA(2+)/CALMODULIN ACTIVATED ADENYLY [guanylate\_cyc // GUANYLATE\_CYCLASES\_2] CG5983

GH14744 36A2-36A2 ID:66G6  
 CG9137 + unknown \* CG9137 GH14903 61F4-61F4 ID:66H10  
 CG18314+ unknown \* CG18314 GH14918 64B9-64B9 dup:1/3 ID:66H11  
 + And ligand\_binding\_or\_carrier \* similar to calmodulin-like protein.(aa) \* Homo sapiens(aa) \* CALMODULIN(aa) \* Eip63F-1 [efhand //  
 CG17769 EF\_HAND\_2] CG17769 GH15245 99D1-99D1 ID:67D2  
 CG1999 + unknown \* CG1999 GH15272 7A4-7A4 ID:67D3  
 + EG:66A1.3 unknown \* by match; LD Drosophila melanogaster embryo BlueScript Drosophila melanogaster cDNA clone 5prime.; 1-  
 CG12184 match\_species=Drosophil...(aa) \* map\_position:4 [PRO\_RICH] CG12184 GH15731 4C6-4C6 dup:1/2 ID:67H9  
 + motor\_protein \* 6e-31 tektin \* 3e-54 testicular tektin B1-like protein \* 4e-52 tektin B1 \* tektin A1 - sea urchin (Strongylocentrotus  
 CG3085 purpuratus) [TEKTIN] CG3085 GH15825 59C3-59C3 dup:2/4 ID:68A12  
 CG7742 + unknown \* [TBC // RAB\_GAP] CG7742 GH15768 25C9-25C9 ID:68A4  
 + enzyme \* Chain A, Crystal Structure Of Recombinant Human Brain Hexokinase Type I Complexed With Glucose And Glucose-6-  
 CG5443 Phosphate(aa) \* hexokinase-like protei [HEXOKINASES // hexokinase // HEXOKINASE] CG5443 GH15883 100A5-97B2 ID:68B3  
 CG14891+ unknown \* CG14891 GH16156 92A1-92A1 ID:68C12  
 CG17349+ unknown \* E04F6.2 gene product(aa) \* 1E-130\* CG17349 GH16267 37D6-37D7 ID:68D11  
 + BG:DS02252.2 cytoskeletal\_structural\_protein \* 2e-48 tektin \* 2e-34 testicular tektin B1-like protein \* 3e-59 tektin A1 - sea urchin  
 CG4767 (Strongylocentrotus purpuratus) \* tektin C1 [TEKTIN] CG4767 GH16413 35E-35E ID:68F2  
 none + none GH16763 ID:68H11  
 CG8278 + enzyme \* 1e-05 cyclophilin Dicyc-2 \* \* [PRENYLATION] CG8278 GH17930 44F2-44F2 ID:70A2  
 CG4983 + DNA\_repair\_protein \* CG4983 GH17939 33A5-33A5 ID:70A4  
 CG3492 + chaperone \* [CSA\_PPIASE\_2 // PRENYLATION] CG3492 GH18016 60D2-60D2 ID:70B2  
 CG6614 + unknown \* [TPR\_REGION // NLS\_BP // ATP\_GTP\_A] CG6614 GH18077 33A5-33A5 ID:70C2  
 CG18568+ unknown \* CG18568 GH18325 50C21-50C21 dup:2/2 ID:70E3  
 + serpin \* 2e-30 Similar to serine protease inhibitor \* 1e-33 serine proteinase inhibitor \* 5e-42 SCC2\_HUMAN SQUAMOUS CELL  
 CG7722 CARCINOMA ANTIGEN (SCCA-2) (LEUPIN) [serpin // SERPIN] CG7722 GH18514 47C7-47C7 dup:2/4 ID:70F12  
 CG8838 + unknown \* [NLS\_BP // ATP\_GTP\_A] CG8838 GH18521 25A1-25A1 ID:70G2  
 CG15891+ unknown \* CG15891 GH18658 5E1-5E1 ID:70H6  
 + unknown \* T03G11.3 gene product(aa) \* CGI-62 protein(aa) \* 1e-16 T03G11.3 gene product \* CG10999 GH18838 83C3-83C3  
 CG10999 dup:1/2 ID:71A3  
 CG16783+ signal\_transduction fizzy-related protein FIZZY\_DOMAIN, WD40 CG16783 ID:71B5  
 CG1979 + BG:DS00464.1 transmembrane\_receptor \* unknown(aa) \* \* CG1979 GH19145 84C1-84C1 dup:1/2 ID:71C10  
 + BcDNA:GH02439 unknown \* 1e-59 cDNA EST comes from this gene; cDNA EST co \* 7e-33 cytoplasmic protein Ndr1 \* 5e-32 RTP  
 CG2082 nickel-specific inductio \* 2e-25 development-related p CG2082 GH19206 83C-83C dup:2/2 ID:71D3  
 + transporter \* mitochondrial carrier protein-like; similar to \* 4e-13 probable membrane protein YPR011c - yeast (Saccharomyces  
 CG2616 cerevisiae) \* 6e-11 colt \* 3e-61 YQ [mito\_carr // MITOCH\_CARRIER] CG2616 GH19222 84D10-84D10 ID:71D5



CG9130 + unknown \* CG9130 GH19274 61F4-61F4 dup:2/3 ID:71D9  
 CG2854 + unknown \* CG2854 GH19593 2F4-2F4 ID:71G3  
 + unknown \* 1e-24 YLS5\_CAEEL HYPOTHETICAL 55.1 KD PROTEIN F09G8.5 IN CHROMOSOME III \* 2e-25 c21ORF-  
 CG15208HumF09G8.5 \* 5e-08 outer arm dynein light chain reinhar \* 2e- CG15208 GH19655 9F12-9F12 ID:71G8  
 + enzyme \* citrate synthase(aa) \* CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR(aa) \* PROBABLE CITRATE  
 SYNTHASE, MITOCHONDRIAL PRECURSOR(aa) \* citrate synthase. Nu [citrate\_synt // CITRATE\_SYNTHASE // CIT] CG14740  
 CG14740GH19789 87B1-87B1 ID:71H12  
 + Ea2t2 neurotransmitter\_transporter \* EXCITATORY AMINO ACID TRANSPORTER (SEAAT1)(aa) \* glutamate transporter 2B(aa) \*  
 CeGlt-2(aa) \* predicted using Genefinder; Similari[SDF // EDTRANSPORT // NA\_DICARBOXYL\_SYMP] CG3159 GH19729 21D1-21D1  
 CG3159 dup:2/4 ID:71H5  
 CG18396+ Mst98Cb unknown \* CG18396 GH20038 98C2-98C2 ID:72C1  
 CG9483 + unknown \* CG9483 GH20208 29F3-29F3 ID:72D7  
 + alpha-Est6 enzyme \* agr;-Est6 \* enzyme carboxyesterase ) map\_position:84D4 \* alpha esterase(aa) \* agr;-Est7 [ESTERASE //  
 CG1108 COesterase] CG1108 GH20431 84D5-84D5 ID:72F11  
 + enzyme \* Yjr105wp(aa) \* 9e-49 ADK\_YEAST PUTATIVE ADENOSINE KINASE ribokinase homolog \* 2e-78 Similarity to Human  
 adenosine kinase cDNA EST EMBL:Z1 \* 2e-50 AD [ADENOKINASE // MITOCH\_CARRIER // HELIX\_] CG3809 GH20396 87B5-87B5  
 CG3809 ID:72F8  
 CG3557 + unknown \* CG3557 GH20409 23E4-23E4 ID:72F9  
 + chaperone \* KD CHAPERONIN, CHLOROPLAST PRECURSOR (PROTEIN CPN10) (PROTEIN GROES)(aa) \* chaperonin  
 10(aa) \* 6e-17 CH10\_YEAST KD HEAT SHOCK PROTEIN, MITOCHONDRIA [CHAPERONIN10 // cpn10] CG9920 GH20473 88A10-  
 CG9920 88A10 ID:72G3  
 + transporter \* 3e-19 nervous system antigen nerv \* 5e-06 Similarity to Shrimp sodium/potassium-transporting ATPase beta cha \*  
 CG117037e-10 ATNB\_MOUSE SODIUM/POTASSIUM-TRA CG11703 GH20514 91F10-91F10 ID:72G7  
 CG14021+ unknown \* CG14021 GH20612 25D5-25D6 dup:2/2 ID:72H2  
 + enzyme \* UNKNOWN(aa) \* 7e-63 PUT2\_YEAST DELTA-1-PYRROLINE-5-CARBOXYLATE DEHYDROGENASE PRECURSOR  
 CG6661 (P5C DEHYDROG \* 8e-11 alternatively spliced form; /prediction [aldedh] CG6661 GH20963 70C11-70C11 ID:73C5  
 CG2750 + enzyme \* No definition line found(aa) \* \* [ATP\_GTP\_A] CG2750 GH20980 11A7-11A7 ID:73C8  
 + transporter \* 2e-28 YG5F\_YEAST PUTATIVE MITOCHONDRIAL CARRIER YGR257C hypot \* 1e-52 YQ51\_CAEEL PUTATIVE  
 MITOCHONDRIAL CARRIER C16C10.1 (Z \* 1e-53 mitochondrial ca [mito\_carr // MITOCH\_CARRIER] CG14208 GH21048 18D8-18D8  
 CG14208ID:73D5  
 CG10752+ unknown \* CG10752 GH21086 69E8-69E8 ID:73D8  
 + enzyme \* similar to tubulin tyrosine ligase; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes  
 CG8918 from this gene; cDNA EST comes fro CG8918 GH21352 15E5-15E5 ID:73F10  
 + structural\_protein \* 6e-22 NSP1\_YEAST NUCLEOPORIN NSP1 (NUCLEAR PORE PROTEIN NSP1) (NUCLEOSKELETAL-LIKE  
 CG8086 PRO \* 5e-08 C. elegans DNA-directed RNA polymerase II large subun CG8086 GH21437 29A1-29A1 dup:3/4 ID:73F12  
 CG7045 + DNA\_binding \* DMHMGDA\_2 HmgD \* HIGH MOBILITY GROUP PROTEIN Z (HMG-Z)(aa) \* 2e-11 HMGD\_DROME HIGH

MOBILITY GROUP PROTEIN D (HMG-D) high mob \* 2e-05 SSRP\_CAEEL PROB [HIGHMOBLTY12 // HMG\_box] CG7045 GH21448 94B4-94B4 ID:73G1

CG6652 + motor\_protein \* 6e-13 unknown \*\* [NLS\_BP] CG6652 GH21622 73E4-73E4 dup:2/2 ID:73H9

+ corto nucleic\_acid\_binding \* corto \* CENTROSOMAL AND CHROMOSOMAL FACTOR (CCF) (CHROMOCENTROSOMIN)(aa) \* CP-

CG2530 1(aa) \* inserted at base Both 5' and 3' ends of P element Inverse PCR CG2530 GH21787 82F5-82F5 ID:74B1

+ unknown \* POLYPOSIS LOCUS PROTEIN (TB2 PROTEIN)(aa) \* pathogenicity protein(aa) \* 2e-09 YSV4\_CAEEL

CG5539 HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III (U CG5539 GH21788 60A2-60A2 ID:74B2

+ unknown \* /match=(desc:; /match=(desc:(aa) \* 4e-77 /match=(desc:; /ma \* 7e-06 No definition line found \* No definition line found

CG7135 CG7135 GH21891 16F7-16F7 dup:1/2 ID:74C3

+ enzyme \* 1e-151 GLS1\_CAEEL PUTATIVE GLUTAMINASE DH11.1 (GLS) (L-GLUTAMINE AMIDOHYDROLASE) \* 1e-170

protein \* 1e-171 GLSK\_RAT GLUTAMINASE, KIDNEY ISOFORM PREC [ANK\_REP // ank // ANK\_REP\_REGION] CG8772 GH22838

CG8772 49B8-49B8 dup:2/2 ID:75D1

CG3330 + unknown \* CG3330 GH22851 97F8-97F8 ID:75D7

+ enzyme \* PHOSPHOMANNOMUTASE (PMM)(aa) \* 2e-91 YM8L\_YEAST HYPOTHETICAL 71.1 KD PROTEIN IN DSK2-CAT8

CG10202 INTERGENIC REGION \* 1e-114 similar to Phosphoglucomutase a [PGM\_PMM // PGMPMM] CG10202 GH22984 51C5-51C5 ID:75F1

+ unknown \* hypothetical protein gs1.1.27.1(aa) \* 6e-26 hypothetical protein YPL020c - yeast (Saccharomyces cerevisiae) ( \* 1e-29

CG11023 YRW3\_CAEEL HYPOTHETICAL 75.7 K CG11023 GH23213 21A3-21A3 dup:1/2 ID:75H9

+ cytoskeletal\_structural\_protein \* p60 katanin(aa) \* katanin p60 subunit(aa) \* 4e-42 CC48\_YEAST CELL DIVISION CONTROL

CG1193 PROTEIN cell divisi \* 3e-43 transitional endoplasmic reticulum A [AAA // NLS\_BP // ATP\_GTP\_A] CG1193 GH23455 83C-83C ID:76C7

+ rha motor\_protein \* RADHA protein(aa) \* 1e-10 similar to C. elegans UNC-89 and titins \* 3e-07 ORF 73, contains large complex

CG11908 repeat CR sarcoma-associated herpesv \* YL CG11908 GH23783 96D-96D ID:76G7

+ enzyme \* CYSTEINYL-TRNA SYNTHETASE (CYSTEINE--TRNA LIGASE) (CYSRS)(aa) \* 5e-52 YNY7\_YEAST PUTATIVE

CYSTEINYL-TRNA SYNTHETASE C29E6.06C (CYSTEINE--TRNA LIGASE [TRNASYNTHCYS // tRNA-synt\_1e] CG8257 GH24360

CG8257 50E2-50E2 dup:3/3 ID:77E7

CG10750 + unknown \* CG10750 GH24871 37D3-37D3 dup:1/3 ID:78A7

CG17450 + unknown \* CG17450 GH25094 cyto\_unknown ID:78C5

+ ftz-f1 steroid hormone receptor steroid receptor beta FTZ-F1 [Drosophila melanogaster] NUCLEAR\_RECEPTOR, STRDHORMONER,

CG4059 STROIDFI] CG4059 GH25189 dup:3/3 ID:78D6

+ Cyp4d21 cytochrome\_P450 \* DMC152A3 \* Cyp4e2 \* DMCYP4D2\_12 Cyp4d2 \* 1e-112 cytochrome P450 cytochrome P4 CG6730

CG6730 GH25251 28A6-28B1 dup:2/2 ID:78E3

CG6470 + transcription\_factor \* [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG6470 GH25257 17B5-17B5 dup:2/2 ID:78E4

+ Ork1 ion\_channel \* potassium channel, subfamily K, member (TASK-2); TASK-2(aa) \* two P domain potassium channel ORK1(aa) \*

CG1615 Ork1 \* BLASTX 8.1E-08 Mus musculus TREK-1 K [CHANNEL\_PORE\_K] CG1615 GH25390 9F8-9F10 ID:78F2

CG1835 + unknown \* [NLS\_BP] CG1835 GH25431 19E2-19E2 ID:78F5

none + none GH25455 ID:78F8

CG1540 + cell\_adhesion \* similar to the BPTI/Kunitz family of inhibitors; most similar to tissue factor pathway inhibitor precursor (TFPI)(aa) \*

similar to Kunitz/Bovine [ig // EGF\_1 // BPTI\_KUNITZ // Kunitz\_BP] CG1540 GH25513 98D2-98D2 dup:1/3 ID:78G5  
 + \* Chain B, \* 305aa long hypothetical \* lysosomal \* PUTATIVE N4-(BETA-N-ACETYLGLUCOSAMINYL)-L-ASPARAGINASE  
 CG1827 PRECURSOR (GLYCOSYLASPARAGINASE) (ASPARTYL [Asparaginase\_2] CG1827 45F4-45F4 dup:2/2 ID:79B3  
 + ligand\_binding\_or\_carrier \* GTP binding protein, almost identical to Gsp1p; Gsp2p(aa) \* 3e-70 GSP2\_YEAST GTP-BINDING  
 NUCLEAR PROTEIN GSP2/CNR2 GTP-bind \* 3e-23 rab11 \* 6e[ras // GTPRANTC4 // ATP\_GTP\_A // RASTRN] CG7815 GH25818  
 CG7815 75F9-75F9 ID:79B9  
 + enzyme \* 1e-19 probable membrane protein YLR070c - yeast (Saccharomyces cerevisiae) \* 8e-40 sorbitol dehydrogenase \* 5e-39  
 CG4836 similar to sorbitol dehydrogenase; [adh\_zinc // NLS\_BP] CG4836 GH25858 92C-92C dup:1/4 ID:79C3  
 CG17470+ unknown \* CG17470 GH26094 38E-38E dup:2/2 ID:79E10  
 + enzyme\_activator \* HYPOTHETICAL 45.1 KD PROTEIN IN IMP2-DNA43 INTERGENIC REGION(aa) \* phosphotyrosyl  
 CG8509 phosphatase activator(aa) \* similar to phosphotyrosyl phosphatase CG8509 GH26069 13F1-13F1 dup:2/2 ID:79E2  
 + unknown \* hypothetical protein(aa) \* Hrt2p(aa) \* F31D4.2(aa) \* hypothetical protein(aa) [NLS\_BP] CG11475 GH26080 58C1-  
 CG11475 58C1 dup:2/2 ID:79E5  
 + transcription\_factor \* segmentation protein hairy - fruit fly (Drosophila melanogaster)(aa) \* DMHAIRG\_5 h \* 3e-07 lin-22 \* 2e-18  
 CG10446 HES1\_MOUSE TRANSCRIPTION FACTOR HES-1 (HAI [HLH // HELIX\_LOOP\_HELIX\_2] CG10446 37B10-37B10 dup:2/2 ID:79F1  
 + transporter \* aquaporin 2(aa) \* 1e-07 YFF4\_YEAST HYPOTHETICAL 70.5 KD PROTEIN IN AGP3-DAK3 INTERGENIC REGION  
 CG5398 \* 8e-05 BIB\_DROME NEUROGENIC PROTEIN BIG BRAIN bib pr [MINTRINSICP // MIP] CG5398 GH26134 59F1-59F1 ID:79F5  
 CG12136+ unknown \* [AA\_TRNA\_LIGASE\_I // NLS\_BP] CG12136 GH26280 8D10-8D10 ID:79G11  
 + actin\_binding \* 1e-05 contains similarity to the kelch/MIPP family \* 1e-06 Keap1 \* 1e-07 The gene product is related to Drosophila  
 CG12423 melanogaster ri \* 1e-06 kelch pro [BTB] CG12423 GH26310 cyto\_unknown ID:79H3  
 + unknown \* contains similarity to E. coli cation transport protein \* 6e-16 YEZ3\_YEAST HYPOTHETICAL 26.3 KD PROTEIN IN  
 CG10365 RAD4-CHD1 INTERGENIC REGION \* 3e-22 cont CG10365 GH26317 95B5-95B5 ID:79H4  
 + motor\_protein \* BACR37P7.j(aa) \* MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) LINKER HISTONE  
 CG9392 PROTEINS ALPHA, BETA, DELTA AND \* \* CG9392 GH26462 76C1-76C1 ID:80B3  
 CG5755 + transporter \* TB1(aa) \* \* [mito\_carr] CG5755 GH26696 36E-36E ID:80D7  
 CG4669 + unknown \* [PRO\_RICH] CG4669 GH26702 64D1-64D1 ID:80D8  
 CG5758 + unknown \* CG5758 GH26746 36E-36E dup:2/2 ID:80E5  
 + ion\_channel \* Vdac \* DMMITPORN\_2 porin \* 1e-09 POR2\_YEAST OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN  
 (VOLTAGE-DEPENDENT ANION \* 3e-66 voltage dependent anion-sele [Euk\_porin // EUKARYTPORIN] CG17137 GH26967 32B3-32B3  
 CG17137 ID:80G10  
 + unknown \* 2e-11 cDNA EST CEMSB78F comes from this gene; cDNA EST yk293d9.3 comes \* 2e-10 Unknown \* CG12118  
 CG12118 GH27430 8D2-8D2 dup:3/4 ID:81D8  
 CG14735+ unknown \* CG14735 GH27720 87A10-87A10 ID:81G2  
 CG8813 + transcription\_factor \* CG8813 GH27752 23B5-23B5 dup:1/2 ID:81G5  
 CG4955 + RNA\_binding \* CG4955 GH27756 15D1-15D1 ID:81G7  
 CG15360+ unknown \* CG15360 GH27779 22B3-22B3 ID:81H1

CG5048 + unknown \* CG5048 GH27783 70F1-70F1 ID:81H2  
 + RNA\_binding \* protein(aa) \* 2e-49 ovarian protein - fruit fly (*Drosophila melanogaster*) s \* 8e-75 YLF1\_CAEEL HYPOTHETICAL  
 42.4 KD PROTEIN C40H1.1 IN CHROMOSOME II [RNP\_1 // RBD // PFKB\_KINASES\_1 // rrm] CG5735 GH28038 66E4-66E4 dup:2/3  
 CG5735 ID:82B7  
 + ligand\_binding\_or\_carrier \* 16k antigen precursor - nematode (*Onchocerca volvulus*)(aa) \* phosphatidylethanolamine binding  
 CG6180 protein Ovd1 - nematode (*Onchocerca volvulus*) (fragmen [PBP] CG6180 33F2-33F2 dup:1/2 ID:82C12  
 + RNA\_binding \* hypothetical protein(aa) \* heterogeneous nuclear ribonucleoprotein R(aa) \* 1e-08 RN15\_YEAST MRNA 3'-END  
 CG17838 PROCESSING PROTEIN RNA15 RNA15 pro \* 6e-16 p [RBD // rrm // NLS\_BP] CG17838 GH28335 92F10-92F10 dup:2/5 ID:82C6  
 + enzyme \* phosphoglyceromutase - fruit fly (*Drosophila melanogaster*)(aa) \* DMPGLY\_4 Pglym78 \* 3e-72 PMG1\_YEAST  
 CG17645 PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE 1 [PGAM // PG\_MUTASE] CG17645 GH28416 87B7-87B7 ID:82D6  
 + unknown \* protein(aa) \* 5e-16 SSM4\_YEAST SSM4 PROTEIN SSM4 protein - yeast (*Saccharomy* \* 2e-08 predicted using  
 CG1317 Genefinder \* 2e-37 putative protein [PRO\_RICH] CG1317 GH28722 62E-62E ID:82F10  
 + peptidase \* leucyl aminopeptidase - like protein (partial)(aa) \* 1e-103 leucine aminopeptidase \* 1e-105 AMPL\_BOVIN CYTOSOL  
 AMINOPEPTIDASE (LEUCINE AMINOPEPTIDAS [LAMNOPPTDASE // CRYSTALLIN\_BETAGAMMA //] CG8040 GH28719 67D12-  
 CG8040 67D13 dup:3/3 ID:82F9  
 CG17884+ Snap25 synaptosome-associated\_protein Synapse protein 25 CG17884 GH28821 ID:82G10  
 CG8006 + unknown \* CG8006 GH28769 67E7-67E7 ID:82G2  
 + enzyme \* 7e-52 DEOC\_CAEEL PUTATIVE DEOXYRIBOSE-PHOSPHATE ALDOLASE (PHOSPHODEOXYRIBOALDOLASE) ( \*  
 CG8525 9e-69 CGI-26 protein \* 1e-26 2-deoxyribose 5-phosphate aldol CG8525 LD25963 49A4-49A5 ID:85B10  
 CG2061 + BcDNA:LD28247 G protein-coupled receptor 69A CRYSTALLIN\_BETAGAMMA CG2061 LD28247 dup:2/3 ID:87D2  
 CG16972+ motor\_protein \* [NLS\_BP] CG16972 LD28380 34A9-34A9 dup:4/4 ID:87E5  
 + Sdic motor\_protein \* Sdic \* DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTERMEDIATE  
 CG9580 CHAIN)(aa) \* axonemal dynein intermediate chain Sdic(aa) \* 4e- [WD40] CG9580 LD35918 19C1-19C1 dup:2/2 ID:95E4  
 + unknown \* hypothetical protein(aa) \* Hrt2p(aa) \* F31D4.2(aa) \* hypothetical protein(aa) CG2921 LD38241 58C1-58C1 dup:2/2  
 CG2921 ID:97E5  
 CG10934+ CG10934 GH26058 dup:2/3 ID:Farhad's BA12