

Table S26

female germline-List of genes identified as follows:

one-tailed t-test female vs tudor female ( $P < .01$  and female data > female tudor data)

genes in both male and female germline are excluded from this list

	+ Ote motor_protein * 1e-174 OTE_DROME OTEFIN otefin - fruit fly (Drosophila melanogaster * 1e-176 DMOTEDA_2 Ote * *
CG5581	CG5581 LD41911 55C3-55C4 ID:101A4 + BcDNA:LD06837 DNA_replication_factor * Similarity to Human activator KD subunit (SW:AC13_HUMAN); cDNA EST CEESG65F comes from this gene; cDNA EST yk267e6.5 comes from this gene; cDNA EST [RFC] CG6258 LD41983 32D4-32D4
CG6258	dup:2/2 ID:101B1 + Prat enzyme * AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR (GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE) (GPAT)(aa) * DMPRAT_2 Prat * 1e-55 PUR1_YE
CG2867	[Pribosyltran // PUR_PYR_PR_TRANSFER // ] CG2867 LD42113 84E1-84E1 dup:1/3 ID:101B11 + unknown * zinc finger protein(aa) * maf10(aa) * myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila)
CG1070	homolog); translocated to, 6(aa) * ALL1 fu [PHD] CG1070 LD42009 84C1-84C3 dup:1/3 ID:101B2 + unknown * similar to * conserved hypothetical protein, family(aa) * Yml080wp(aa) * hypothetical 35.8K protein (fis 5' -
CG3645	Escherichia coli(aa) [UPF0034 // FMN_ENZYMES] CG3645 LD42056 21B5-21B5 ID:101B8
CG4036	+ unknown * 5e-28 F09F7.7 gene product * [NLS_BP] CG4036 LD42289 32F1-32F1 dup:1/2 ID:101D11 + EG:39E1.1 unknown * 5e-33 YNJ2_YEAST HYPOTHETICAL 45.5 KD PROTEIN IN YPT53-RHO2 INTERGENIC REGION *
CG11596	/match=(desc:; /ma * 6e-54 Similarity with yeast hypothetical prote [NLS_BP] CG11596 LD42227 2B17-2B17 dup:2/2 ID:101D3 + osa DNA_binding * eyelid(aa) * eld * 3e-05 YM42_YEAST HYPOTHETICAL 162.7 KD PROTEIN IN SIP18-SPT21 INTERGENIC REGION * 2e-37 coded for by C. elegans cDNA yk7c8.5; co [ARID // PRO_RICH // ANTIFREEZE] CG7467 90C-
CG7467	90C dup:4/4 ID:101E12 + BcDNA:LD29892 unknown * 4e-09 YKT7_CAEEL HYPOTHETICAL 53.2 KD PROTEIN C07A9.7 IN CHROMOSOME III * 1e-05
CG8378	skm-BOP2 * 8e-52 inserted at base Both 5' and 3' ends of P element I [SET_DOMAIN] CG8378 48E10-48E10 dup:3/3 ID:101E8 + Pi3K21B signal_transduction * p60(aa) * DMPIK57 Pi3K21B * p60 p * 2e-08 similar to vav proto-oncogene [PI3KINASEP85 //
CG2699	SH2DOMAIN // SH2] CG2699 LD42724 21B7-21B7 dup:2/2 ID:101F10 + TH1 unknown * TH1(aa) * DMTH1X_3 TH1 * potential zinc-finger domains centered at aa and aa 364; kDa protein;
CG9984	putative(aa) * DMTH1X_3 TH1 CG9984 LD42626 14C4-14C4 ID:101F4 + Pabp2 RNA_binding * HYPOTHETICAL 29.0 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION(aa) * DMROX2Y_3 Rox2 *
CG2163	RNA binding protein(aa) * 3e-39 Similarity to Bovine Poly-A bind [RNP_1 // RBD // rrm] CG2163 LD42638 44A7-44A8 ID:101F6
CG15312	+ transmembrane_receptor * [ig] CG15312 LD42756 9B1-9B1 ID:101G1 + grp protein_kinase * 5e-08 Ssp31 protein kinase * 2e-54 Ser/Thr kinase * 5e-13 serine/threonine kinase * 7e-27 Chk1;
CG17161	checkpoint kinase [PROTEIN_KINASE_DOM // pkinase] CG17161 LD42896 36A6-36A7 ID:101G7 + BcDNA:GM10765 DNA_repair_protein * 5e-15 RA27_YEAST STRUCTURE SPECIFIC ENDONUCLEASE RAD27 hypothet * 2e-20 by match; 1-match_accession=SWISS-PROT:P397 * 5e-13 similar to the [53EXO_N_DOMAIN // 53EXO_I_DOMAIN // XPG]
CG10670	CG10670 LD43032 64C12-64C12 ID:101H3

+ cell\_cycle\_regulator \* pombe Cdc5-related protein(aa) \* similar to MYB transforming protein; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA [MYB\_1 // MYB\_2 // myb\_DNA-binding // MY] CG6905 LD43082 61C1-61C1  
 CG6905 dup:2/2 ID:102A1  
 + Chc transporter \* DMCHC\_2 Chc \* CLH\_YEAST CLATHRIN HEAVY CHAIN clathrin heavy chain - y \* CLH\_DROME  
 CLATHRIN HEAVY CHAIN clathrin heavy chain - fr \* CLH\_CAEEL PRO[RCC1\_2 // Clathrin\_repeat // CLATHRIN\_R] CG9012  
 CG9012 LD43101 13F3-13F3 dup:1/3 ID:102A3  
 + transcription\_factor \* C2H2 zinc finger protein(aa) \* anon-fe1E9 \* 2e-08 YJF6\_YEAST HYPOTHETICAL 98.9 KD ZINC  
 FINGER PROTEIN IN BTN1-PEP8 INTERGENIC REG \* 1e-0[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG11971 LD43103  
 CG11971 85C3-85C3 dup:1/4 ID:102A4  
 + 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-  
 CG7660 90C ID:102B3  
 + unknown \* 9e-56 cDNA EST comes from this gene; cDNA EST co \* \* [AROMATIC\_AA\_PERMEASE\_2] CG5262 LD43196  
 CG5262 77C1-77C1 ID:102B5  
 + Orc4 DNA\_replication\_factor \* 56-kDa subunit of recognition complex (ORC); Orc4p(aa) \* recognition complex subunit 4-  
 related protein Orp4p(aa) \* recognition complex, subunit (yea [ATP\_GTP\_A2 // ATP\_GTP\_A] CG2917 LD43280 60D16-60D16  
 CG2917 ID:102C1  
 + chaperone \* p58(aa) \* 4e-05 probable membrane protein YLR080w - yeast (Saccharomyces cerevisiae) \* 7e-84 Similarity to  
 CG6822 Xenopus P58 protein cDNA EST \* 1e-104 man CG6822 LD43551 66D5-66D5 ID:102D10  
 + unknown \* 1e-21 BC10\_HUMAN BLADDER CANCER KD PROTEIN 10kD protein \* 1E-136\* CG4867 LD43519 64E-64E  
 CG4867 ID:102D3  
 CG4497 + unknown \* [GRAM\_POS\_ANCHORING] CG4497 LD43863 27E4-27E4 ID:102F12  
 + unknown \* 6e-08 No definition line found \* 1e-13 signal peptidase:SUBUNIT=12kD \* 3E-97\* 1e-07 No definition line found  
 CG2310 [ATP\_GTP\_A] CG2310 LD43791 99B3-99B3 ID:102F8  
 CG5694 + unknown \* CG5694 LD44026 31B4-31B4 dup:1/2 ID:102G12  
 + BcDNA:GM13640 enzyme \* DNA primase, p58 subunit(aa) \* putative dna primase large subunit(aa) \* primase, polypeptide 2A  
 CG5553 (58kD)(aa) \* PROBABLE DNA PRIMASE LARGE SUBUNIT(aa) CG5553 LD44074 77B4-77B4 ID:102H6  
 + Tbp transcription\_factor \* Tbp \* TRANSCRIPTION INITIATION FACTOR TFIID (TATA-BOX FACTOR) (TATA SEQUENCE-  
 BINDING PROTEIN) (TBP) (TATA-BOX BINDING PROTEIN)(aa) \* 4e-80 TF2D\_YEAS [TFIID // TIFACTORIID // TBP] CG9874  
 CG9874 LD44083 57F8-57F8 dup:1/2 ID:102H7  
 + signal\_transduction \* Taf80 \* katanin p80 subunit(aa) \* 5e-07 YCW2\_YEAST HYPOTHETICAL 57.0 KD TRP-ASP  
 REPEATS CONTAINING PROTEIN IN CPR4-SSK2 \* 4e-09 transcription ini[GPROTEINBRPT // GPROTEINB // WD40\_REGIO]  
 CG9910 LD44201 14B11-14B11 ID:103A6  
 + unknown \* 8e-74 GPI3\_YEAST N-ACETYLGALUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN  
 CG6401 (GLCN \* 6e-92 similar to phosphatidylinositol biosynthetic protein; [Glycos\_transf\_1] CG6401 LD44262 54E7-54E7 ID:103B2  
 CG3995 + unknown \* [NLS\_BP] CG3995 89E12-89E12 dup:2/2 ID:103B9  
 CG5940 + 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  
 + pav motor\_protein \* 7e-35 YGW6\_YEAST PUTATIVE KINESIN-LIKE PROTEIN YGL216W hypoth \* PAV-KLP protein \* 5e-91  
 Similar to kinesin-like protein; coded for by C. elegans cDN [kinesin // KINESIN\_MOTOR\_DOMAIN1 // KIN] CG1258 64B4-64B4  
 dup:1/2 ID:103C2  
 CG1258  
 + function\_unknown \* Cdc23(aa) \*\* [NLS\_BP] CG9241 LD44370 39B4-39B4 dup:1/2 ID:103C3  
 + chaperone \* 5e-33 Similarity to Xenopus P58 protein cDNA EST \* 3e-78 GP36b glycoprotein \* 3e-83 coded for by C.  
 CG5510 elegans cDNA yk74e11.5; coded for by C. elegans CG5510 95E3-95E3 dup:2/2 ID:103C4  
 + hdc signal\_transduction \* cell cytoplasm ) map\_position:99F6-11 \* 4e-98 hdc protein - fruit fly (Drosophila melanogaster) (Z \*  
 CG15532 8e-11 similar to drosophila HCD protein \* 1e-10 CG15532 LD44381 99F-99F3 dup:2/3 ID:103C5  
 + motor\_protein \* Nijmegen breakage syndrome (nibrin)(aa) \* 2e-06 AMYH\_YEAST GLUCOAMYLASE S1/S2 PRECURSOR  
 (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPH \* 1e-08 predicted u [FHA\_DOMAIN // NLS\_BP // FHA] CG6754 LD44438 67C-  
 CG6754 67C dup:1/2 ID:103C9  
 + SPT4 enzyme \* 3e-13 SPT4\_YEAST TRANSCRIPTION INITIATION PROTEIN SPT4 SPT4 pro \* 6e-30 contains similarity to  
 CG12372 Saccharomyces cerevisiae Spt4 \* 7e-39 unknown \* 1e-39 CG12372 LD44495 49B5-49B5 ID:103D2  
 + unknown \* 1e-12 YKK4\_CAEEL HYPOTHETICAL 30.2 KD PROTEIN C02F5.4 IN CHROMOSOME III \*\* [NLS\_BP]  
 CG9018 CG9018 LD44521 62D3-62D3 dup:2/2 ID:103D5  
 + unknown \* 4e-14 YZG1\_CAEEL HYPOTHETICAL 28.7 KD PROTEIN F13E6.1 IN CHROMOSOME X \* 1e-13 D52 \* 7e-20  
 CG5174 tumor protein D52-like hD54+ins2 isoform \* 3e-14 CSPP28 CG5174 LD44733 55C11-55C11 dup:3/3 ID:103E10  
 + unknown \* F1N21.18(aa) \* HYPOTHETICAL 51.8 KD PROTEIN ZK632.11 IN CHROMOSOME III(aa) \* \* [ZF\_CCHC //  
 CG4622 PRO\_RICH // zf-CCHC // NLS\_B] CG4622 LD44757 60D5-60D5 dup:3/3 ID:103E12  
 + unknown \* BLASTX 4.0E-27 YER156C|Protein of unknown function(dna) \* HYPOTHETICAL 38.2 KD PROTEIN IN BEM2-  
 CG11980 NCB1 INTERGENIC REGION(aa) \* 6e-60 similar to Yeast h CG11980 LD44814 85C3-85C3 dup:2/2 ID:103F9  
 CG7347 + motor\_protein \* 8e-05 myosin heavy chain \*\* [PRO\_RICH] CG7347 LD44887 75B10-75B10 ID:103G1  
 + smid endopeptidase \* DMSMMIN\_2 smallminded \* smallminded(aa) \* 3e-68 AFG2\_YEAST AFG2 PROTEIN valosin-containing  
 CG8571 protein homolo \* smallminded [ENDOLAPTASE // AAA // ATP\_GTP\_A] CG8571 65F5-65F6 dup:2/2 ID:103G2  
 + unknown \* NY-REN-2 antigen(aa) \* 1e-27 hypothetical protein YDR374c - yeast (Saccharomyces cerevisiae) (U \* 9E-49\*  
 CG6422 Similarity to A. thaliana gene product F21M [PRO\_RICH] CG6422 LD44979 96B14-96B15 ID:103G8  
 + rdgBbetatransporter \* PHOSPHATIDYLINOSITOL TRANSFER PROTEIN BETA ISOFORM (PTDINS TRANSFER PROTEIN  
 BETA) (PTDINSTP) (PI-TP-BETA)(aa) \* BLASTX 3.1E-49 M.musculus mRNA for D [PITRANSFER] CG17818 LD44980 54E3-  
 CG17818 54E3 ID:103G9  
 + RNA\_binding \* spliceosome associated protein 145, SF3b subunit(aa) \* spliceosome associated protein-like(aa) \* BLASTX  
 CG3605 7.8E-75 Human spliceosome associated protei [NLS\_BP] CG3605 LD45152 23C4-23C4 ID:103H9  
 CG17469 + unknown \* 1E-123\* \* CG17469 LD45277 102E2-102E3 dup:2/2 ID:104B4  
 + snf RNA\_binding \* DMD25SNRN\_2 snf \* U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) (SEX  
 DETERMINATION PROTEIN SNF)(aa) \* 3e-05 YIS9\_YEAST HYPOTHETICAL 12.8 [RNP\_1 // RBD // rrm] CG4528 LD45302 4F1-  
 CG4528 4F2 dup:3/3 ID:104B7

+ signal\_transduction \* Plenty of SH3s; POSH(aa) \* 5e-09 hypothetical protein YHR016c - yeast (*Saccharomyces cerevisiae*)  
 (U1 \* 4e-05 DRK\_DROME PROTEIN E(SEV)2B (SH2-SH3 A[zf-C3HC4 // ZINC\_FINGER\_C3HC4 // P67PHO] CG4909 LD45365  
 CG4909 54D1-54D1 ID:104C3  
 + 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  
 CG4656 LD45535 94E-94E dup:2/2 ID:104D3  
 + endopeptidase \* autoantigen(aa) \* 1e-67 Ki antigen PA2 \* 3e-65 Ki nuclear autoantigen - human Ki nuclear autoantigen \*  
 CG1591 IGUP\_HUMAN INTERFERON GAMMA UP-REGULATED PR CG1591 LD45860 11D10-11D10 dup:2/2 ID:104F11  
 + unknown \* partner of Ral-binding protein 1(aa) \* 3e-09 PAN1\_YEAST PAN1 PROTEIN poly(A)-specific ribonuclease (EC \*  
 CG6192 6e-06 PAST-1 \* 3e-05 contain EF-hand-like c [EPS // PRO\_RICH // EF\_HAND\_2] CG6192 LD45769 32D3-32D4 ID:104F7  
 + DNAPol-alpha50 DNA\_replication\_factor \* DMDPRI\_2 DNAPol- agr;50 \* 8e-62 p48 DNA primase (AA 1-409) \* PRI1\_DROME  
 DNA PRIMASE SMALL SUBUNIT (DNA PRIMASE KD SUBUNIT) (DNA POLYMERAS \* 3e-64 N CG7108 LD46032 66C8-66C8  
 CG7108 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  
 CG7627 dup:2/4 ID:104H4  
 + ash2 transcription\_factor \* ash2 \* trithorax protein ASH2 \* 6e-83 Y17G7B.2a \* 1e-134 similar to *Drosophila ash2*  
 CG6677 [SPRY\_DOMAIN // NLS\_BP] CG6677 LD46053 96A17-96A17 ID:104H8  
 + BG:DS00004.12 unknown \* hypothetical 23.1kd-like protein(aa) \* 2e-17 YBF7\_YEAST HYPOTHETICAL 23.1 KD PROTEIN IN  
 CG1307 SHP1-PTC3 INTERGENIC REGION \* 9e-15 No definition line found CG1307 LD46144 84C4-84C4 ID:105A4  
 CG4949 + unknown \* [ATP\_GTP\_A] CG4949 LD46305 15D1-15D1 ID:105B10  
 CG4617 + DNA\_binding \* hypothetical protein(aa) \* 5e-16 HMGBCG protein \* \* [HMG] CG4617 LD46272 6F5-6F5 ID:105B7  
 + unknown \* 5e-69 YG4W\_YEAST HYPOTHETICAL 34.9 KD PROTEIN IN SMI1-PHO81 INTERGENIC REGION \* 2e-29  
 L2CC\_DROME L(2)37CC PROTEIN Cc protein - fruit fly (*Drosop* \* 3 [PROHIBITIN // Band\_7] CG15081 LD46344 55F2-55F2  
 CG15081 ID:105C4  
 + unknown \* 4e-41 protein \* 1e-09 putative protein \* coded for by *C. elegans* cDNA yk93e11.5; coded for by *C. elegans* cDNA  
 CG10473 yk103a11.5; \* [NLS\_BP] CG10473 LD46360 37B11-37B12 ID:105C7  
 + transcription\_factor \* zinc finger homeodomain enhancer-binding protein-1(aa) \* BLASTX 1.9E-18 *H.sapiens* OZF  
 mRNA.(dna) \* transcription factor RREB-1(aa) \* similar to Z[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG3941 LD46363  
 CG3941 59E3-59E3 ID:105C9  
 + receptor \* protein kinase C substrate 80K-H(aa) \* similar to Human protein kinase C substrate, 80KD protein, heavy chain,  
 CG6453 SWISS-PROT Accession Number \* similar [LDLRA\_2 // ER\_TARGET // EF\_HAND] CG6453 LD46533 36C4-36C4 ID:105D11  
 CG18177 + unknown \* CG18177 LD46538 67C-67C ID:105D12  
 + SelD enzyme \* SelD protein \* 2e-93 similar to AIR synthase related proteins *elegans* \* 1e-143 selenophosphate synthetase \*  
 CG8553 1e-159 SELD\_HUMAN SELENIDE,WATER DIKINAS [AIRS] CG8553 LD46437 50F-50F dup:1/2 ID:105D2  
 + transporter \* nucleoporin Nup153 homolog(aa) \* Ran/TC4-binding nucleopore protein(aa) \* NUCLEAR PORE COMPLEX  
 CG4453 PROTEIN NUP153 (NUCLEOPORIN NUP153) (153 KD NUCLEOPOR [zf-RanBP // ZF\_RANBP] CG4453 LD46585 14F2-14F2

dup:5/6 ID:105E3

+ unknown \* predicted using Genefinder; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this g CG12135 LD46621 8D10-8D10 dup:2/2 ID:105E7

CG12135 + msl-1 transcription\_factor \* MALE-SPECIFIC LETHAL-1 PROTEIN(aa) \* DMMSL1A\_2 msl-1 \* DMMSL1A\_2 msl-1 \* male-specific lethal-1 protein - fruit fly (Drosophila melanogaster) CG10385 LD46729 37A4-37A4 dup:4/4 ID:105F6

CG10385 + unknown \* HYPOTHETICAL 32.6 KD PROTEIN C1F3.04C IN CHROMOSOME I(aa) \* No definition line found(aa) \*

CG4338 Yor006cp(aa) \* 7e-49 YO06\_YEAST HYPOTHETICAL 35.7 KD PROT CG4338 LD46811 88E9-88E9 ID:105G2

+ \* 4e-10 similar to thyroglobulin and EF hand domains elega \* 8e-05 testican \* 6e-09 testican-3 \* 8e-05 EQST\_ACTEQ

CG2264 EQUISTATIN [thyroglobulin\_1 // THYROGLOBULIN\_1 // k] CG2264 46D8-46D9 dup:2/2 ID:106A12

+ cytoskeletal\_structural\_protein \* 1e-62 cell division cycle protein \* 1e-178 SEP2\_DROME SEPTIN septin \* 3e-82 CDC10 \* 1e-148 SEP2\_HUMAN SEPTIN HOMOLOG The gen [COPPER\_BLUE // GTP\_CDC // NLS\_BP // ATP] CG2916 LD47044 43F7-43F7 dup:1/2 ID:106A3

CG2916 + Actr13E cytoskeletal\_structural\_protein \* DMARP\_2 Actr13E \* 2e-45 ACT\_YEAST ACTIN actin - yeast (Saccharomyces cerevisiae) \* ACTU\_DROME ACTIN-LIKE PROTEIN 13E actin-related protein \* 1e-70 [actin] CG11678 LD47054 13E15-13E16 ID:106A4

CG11678 + ribosomal\_protein \* ACIDIC RIBOSOMAL PROTEIN P0 HOMOLOG (L10E)(aa) \* coded for by C. elegans cDNA CEESN26F; coded for by C. elegans cDNA CEESI89F; similar to 60S acidi [Ribosomal\_L10] CG1381 LD47064 46E3-46E3 ID:106A5

CG1381 + unknown \* CGI-67 protein(aa) \* Similarity to S. Pombe BEM1/BUD5 suppressor; cDNA EST comes from this gene; cDNA EST yk482d4.3 comes from this gene; cDNA EST y [ESTERASE] CG11935 LD47093 96B19-96B19 ID:106A6

CG11935 + unknown \* clot.672(dna) \* 7e-07 YEQ8\_YEAST HYPOTHETICAL 58.0 KD PEPTIDASE IN PTP3-ILV1 INTERGENIC REGION \* 5e-08 similar to the peptidase family M24B \* 3e-12 CG11367 LD47277 79F2-79F2 dup:2/2 ID:106B10

CG11367 + chaperone \* 2e-11 SCJ1\_YEAST SCJ1 PROTEIN SCJ1 protein - yeast (Saccharomyce \* 6e-11 Tid(56) protein - fruit fly (Drosophila melanogaster) \* 2e-07 similar to DN [DNAJ\_1 // DnaJ // DNAJ\_2] CG8448 LD47190 52F8-52F9 dup:1/2 ID:106B3

CG8448 + enzyme \* VITELLOGENIN II PRECURSOR (YOLK PROTEIN 2)(aa) \* lipoprotein lipase precursor(aa) \* Chain A, Triacylglycerol LipaseCOLIPASE COMPLEX(aa) \* TRIACYLGL [TAGLIPASE // ESTERASE // lipase // LIPA] CG5966 LD47264 5C10-5D1 ID:106B8

CG5966 + chaperone \* similar to chaperonins cpn60 and TCP-1 (Pfam: cpn60\_TCP1.hmm, score: 416.20 and 102.94)(aa) \* Component of Chaperonin Containing T-complex subunit s [TCP1\_2 // TCP1\_3 // TCOMPLEXTCP1 // CHA] CG8351 LD47396 85E9-85E9 ID:106C10

CG8351 + unknown \* calcium-regulated heat stable protein CRHSP-24(aa) \* calcium-regulated heat stable protein CRHSP-24(aa) \* RNA-binding protein PIPPin - rat PIPPin pr [CSD] CG9705 LD47312 73C-73C ID:106C2

CG9705 + Gbp signal\_transduction \* striatin, calmodulin-binding protein(aa) \* WD-40-family-member \* 3e-16 SFL2 gene product (AA 1-669) \* 2e-19 transcription initiation factor IID-as[GPROTEINBRPT // WD40\_REGION // WD\_REPEA] CG5519 LD47390 55C13-55C13 ID:106C9

CG5519 + dah unknown \* dystrobrevin(aa) \* similar to the kDa Torpedo acetylcholine receptor-associated protein; similar to rat apodystrophin-3, PIR Accession Number \* dah [ZF\_ZZ // ZZ] CG6157 LD47411 13C1-13C1 ID:106D2

CG6157

+ unknown \* hypothetical protein(aa) \* HSPC039 protein(aa) \* 2e-11 LAS1\_YEAST LAS1 PROTEIN LAS1 protein - yeast  
 CG6316 (Saccharomyc \* CG6316 LD47413 70E1-70E1 ID:106D3  
 + transcription\_factor \* 8e-33 cDNA EST yk416a1.3 comes from this gene; cDNA EST yk466h2.3 comes \* 1e-13 hypothetical  
 CG7845 protein \* [NLS\_BP // WD40] CG7845 LD47540 42A5-42A6 dup:2/2 ID:106E12  
 CG7269 + RNA\_binding CG7269 dup:2/2 ID:106E3  
 + unknown \* 2e-16 YKJ2\_CAEEL HYPOTHETICAL 36.9 KD PROTEIN C02D5.2 IN CHROMOSOME III \* 1e-05  
 INIP\_HUMAN GAMMA-INTERFERON-INDUCIBLE PROTEIN IP-30 PRECURSOR \* 4e-1 CG9796 LD47508 87E10-87E10  
 CG9796 dup:3/3 ID:106E4  
 + Dbp45A RNA\_binding \* DMDBP45A\_18 Dbp45A \* probable ATP-dependent RNA helicase Dbp45A - fruit fly (Drosophila  
 melanogaster)(aa) \* 1e-77 DBP8\_YEAST PROBABLE ATP-DEPEND[helicase\_C // ALDEHYDE\_DEHYDR\_CYS // HE] CG12759  
 CG12759 LD47509 45A11-45A11 dup:3/3 ID:106E5  
 + signal\_transduction \* 1e-71 YG4C\_YEAST HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN  
 PMT6-PCT1 \* 7e-09 Lis1 homolog \* 8e-08 YKY4\_CAEEL HYPOTHETICAL[GPROTEINBRPT // WD40\_REGION // WD\_REPEA]  
 CG11887 CG11887 LD47515 47B1-47B1 dup:3/3 ID:106E6  
 CG2182 + unknown \* [NLS\_BP] CG2182 LD47517 83B7-83B7 dup:3/3 ID:106E7  
 + 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  
 CG4535 LD47530 30E1-30E1 dup:2/2 ID:106E9  
 + signal\_transduction \* Ylr222cp(aa) \* WD repeat protein(aa) \* coatomer alpha subunit(aa) \* BLASTX 2.6E-32  
 YLR222C[Protein of unknown function, has beta-transducin (WD-[GPROTEINBRPT // WD40\_REGION // WD\_REPEA] CG1671  
 CG1671 LD47550 46B13-46B14 ID:106F3  
 + transcription\_factor\_binding \* hypothetical protein(aa) \* 2e-05 serine-threonine kinase receptor-associated protein \* 2e-05  
 CG5632 WD-40 repeat protein \* 3e-05 DMEST6P\_15 Est-P [WD40\_REGION // WD40] CG5632 LD47568 68F8-68F8 dup:1/2 ID:106F8  
 + stg protein\_tyrosine\_phosphatase \* DMCDC25\_2 stg \* 3e-21 MPIP\_YEAST M-PHASE INDUCER PHOSPHATASE (MITOSIS  
 INITIATION PROTEIN MIH1) (MITOT \* cdc25 protein - fruit fly (D[Rhodanese // RHODANESE // MPIPHPTASE] CG1395  
 CG1395 LD47579 99A5-99A6 dup:3/3 ID:106F9  
 CG18543 + unknown \* CG18543 LD47919 66C12-66C12 ID:107B1  
 + enzyme \* 1e-19 FAT2\_YEAST PEROXISOMAL-COENZYME A SYNTHETASE probable AMP \* 3e-11 acetyl-CoA  
 CG5568 synthetase - fruit fly (Drosophila melanogaster) \* 9e-40 similar [AMP-binding] CG5568 LD47944 64F3-64F3 ID:107B6  
 + unknown \* Kelch-repeat protein, similar to Kel1 and Kel2; Kel3p(aa) \* 2e-32 hypothetical protein YPL263c - yeast  
 CG4069 (Saccharomyces cerevisiae) \* 9e-06 host cell [NLS\_BP] CG4069 LD47970 69C4-69C4 ID:107B8  
 + unknown \* 5e-17 probable membrane protein YLR418c - yeast (Saccharomyces cerevisiae) \* 1e-10 unknown conserved  
 CG11990 hypothetical protein \* [DDC\_GAD\_HDC\_YDC] CG11990 LD47989 85C5-85C5 dup:3/3 ID:107B9  
 + unknown \* 5e-20 YNZ5\_YEAST HYPOTHETICAL 17.1 KD PROTEIN IN SIP3-MRPL30 INTERGENIC REGION \* 3e-12  
 CG3800 RNA helicase \* 2e-25 cellular nucleic acid binding protein cl [ZF\_CCHC // zf-CCHC] CG3800 LD48005 59B6-59B6 ID:107C1  
 + signal\_transduction \* BIOTINIDASE PRECURSOR(aa) \* Vanin-1(aa) \* Vanin 1(aa) \* 1e-19 Vanin-1 [NITRIL\_CHT\_3 //  
 CG3648 CN\_hydrolase] CG3648 LP03005 5D5-5D6 ID:108C12

+ enzyme \* 1e-152 Naglu \* 1e-153 N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB) \* 1e-113 alpha-N-  
 CG13397 acetylglucosaminidase \* alpha-N-acetylglucosaminida CG13397 LP03571 29C1-29C1 ID:108F10  
 + enzyme \* RNA polymerase 1-1 (40 kDa subunit)(aa) \* 5e-75 RPC5\_YEAST DNA-DIRECTED RNA POLYMERASES I AND  
 CG3756 III KD POLYPEPTIDE (AC40) \* 9e-22 RNA polymerase II p3 CG3756 LP03982 25B-25B ID:108H3  
 CG11169 + unknown \* CG11169 LP04006 60A1-60A2 ID:108H6  
 + pbl signal\_transduction \* ect2 oncogene(aa) \* 4e-05 regulatory protein CLS4 - yeast (Saccharomyces cerevisiae) \* 3e-08  
 /match=(desc:; /ma \* 1e-30 similar to transf[GRF\_DBL // BRCT\_DOMAIN // G\_PROTEIN\_REC] CG8114 SD01796 66A18-66A20  
 CG8114 dup:2/4 ID:113B7  
 + enzyme \* similar to aspartyl-tRNA synthetase; cDNA EST yk250e3.3 comes from this gene(aa) \* 2e-40 SYDM\_YEAST  
 ASPARTYL-TRNA SYNTHETASE, MITOCHONDRIAL (ASPARTA [tRNA-synt\_2 // TRNASYNTHLYS // TRNASYNT] CG17938  
 CG17938 SD02215 36A10-36A10 ID:113G1  
 + 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  
 CG1763 10C5-10C6 ID:113H6  
 + signal\_transduction \* beta2-chimerin, cerebellar - human(aa) \* beta2-chimerin, cerebellar - rat (fragment)(aa) \* 2e-07  
 BEM2\_YEAST GTPASE ACTIVATING PROTEIN BEM2/IP[RHO\_GAP // RhoGAP // DAG\_PE\_BINDING\_DOM] CG3208 SD02309  
 CG3208 5A8-5A8 dup:1/3 ID:113H7  
 + ligand\_binding\_or\_carrier \* chromatin assembly factor I (150 kDa)(aa) \* chromatin assembly factor I p150 chain - human \*  
 CG12109 [NLS\_BP] CG12109 SD02526 7F4-7F5 dup:1/2 ID:114C7  
 CG9484 + hyd enzyme hyperplastic discs HECT, PABP, UBA CG9484 SD02820 ID:114F11  
 + I(2)not transmembrane\_receptor \* DMNOTB\_2 I(2)not \* Not22(aa) \* putative Dol-P-Man dependent alpha(1-3)  
 CG4084 mannosyltransferase involved in the biosynthesis of the lipid-linked oligosac CG4084 SD03142 59F5-59F5 ID:115C6  
 + unknown \* 3e-55 hypothetical protein YOL124c - yeast (Saccharomyces cerevisiae) ( \* 3e-51 hypothetcal protein \*  
 Y724\_METTH HYPOTHETICAL PROTEIN MTH724 methyl [N6\_MTASE // N12N6MTFRASE] CG1074 SD03208 82C1-82C1  
 CG1074 ID:115D7  
 + unknown \* PBK1 protein(aa) \* 5e-11 predicted using Genefinder; Weak similarity to Mouse CSA-19 protei \* 2e-16 PBK1  
 CG13096 protein \* 7e-08 hypothetical protein [NLS\_BP] CG13096 SD03546 29D1-29D1 ID:115H5  
 + esc transcription\_factor \* DMESCOMBS\_4 esc \* 3e-08 YCW2\_YEAST HYPOTHETICAL 57.0 KD TRP-ASP REPEATS  
 CONTAINING PROTEIN IN CPR4-SSK2 \* extra sex combs protein - fruit fly (Dr[GPROTEINBRPT // RCC1\_2 // WD40\_REGION /]  
 CG14941 CG14941 SD03549 33B1-33B2 ID:115H6  
 CG6665 + unknown \* HSPC012(aa) \* \* [NLS\_BP] CG6665 SD03555 53E6-53E6 ID:115H7  
 CG8887 + transcription\_factor CG8887 SD03724 dup:2/2 ID:116B2.2  
 CG9127 + SD03765  
 + ppan unknown \* Peter Pan(aa) \* 4e-35 SSF1\_YEAST SSF1 PROTEIN SSF1 protein - yeast (Saccharomyc \* 1e-53 contains  
 CG5786 similarity to human RNA-binding protein FUS/TLS \* 1 [NLS\_BP] CG5786 SD03871 95F1-95F1 dup:1/3 ID:116C10  
 CG6033 + CG6033 SD04091 ID:116F10.2

+ alpha-Adaptin transporter \* highly similar to alpha-adaptin (rat and mouse)(aa) \* DMALPADPT\_2 agr;-Adaptin \* adaptor-related  
 CG4260 protein complex AP-2, alpha subunit(aa) \* ALPHA-AD CG4260 SD04083 21C2-21C2 dup:2/3 ID:116F9  
 CG13647 + CG13647 SD04105 dup:2/2 ID:116G2.2  
 + transcription\_factor \* 1e-10 YJF6\_YEAST HYPOTHETICAL 98.9 KD ZINC FINGER PROTEIN IN BTN1-PEP8  
 INTERGENIC REG \* 7e-12 Kr-h \* 1e-05 similar to Zinc finger, C2H2 type[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG13620  
 CG13620 96A13-96A14 dup:3/3 ID:116H5.2  
 CG10245 + cytochrome\_P450 CG10245 SD04231 dup:2/2 ID:117A1.2  
 CG8948 + signal\_transduction SD04454  
 CG5366 + transcription factor SD04454  
 CG6562 + enzyme SD04710  
 CG8151 + CG8151 SD04652 ID:117F3  
 + protein\_kinase \* protein(aa) \* cdc2-like protein kinase(aa) \* 3e-65 CTK1\_YEAST CTD KINASE ALPHA SUBUNIT (CTD  
 KINASE KD SUBUNIT) (CTDK-I ALPHA SUB \* 6e-69 posi[PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM] CG7597  
 CG7597 SD04681 78E1-78E1 dup:2/3 ID:117F7.2  
 + ligand\_binding\_or\_carrier \* 7e-07 YT67\_CAEEL HYPOTHETICAL CALCIUM-BINDING PROTEIN IN CHROMOSOME X \*  
 5e-08 CATR\_MOUSE CALTRACTIN (CENTRIN) caltractin - mouse \* 2e-07 ce[EF\_HAND // efhand // EF\_HAND\_2] CG10641  
 CG10641 SD04693 37B8-37B9 dup:3/3 ID:117F9.2  
 + unknown \* 1e-28 weak similarity to chromosomal replicator initiator protein DNAA ( \* similar to a C.elegans protein encoded  
 CG11943 in cosmid \* CG11943 SD04935 19A3-19A3 dup:3/7 ID:118A12  
 CG15618 + CG15618 SD04871 dup:1/4 ID:118A3  
 CG3353 + CG3353 dup:1/6 ID:118A7  
 + Mcm6 DNA\_replication\_factor Minichromosome maintenance 6, chromatin binding involved in pre-replicative complex  
 CG4039 formation MCM, MCM\_1, MCM\_2 CG4039 SD04977 dup:3/3 ID:118B11  
 108000000+ GTP\_binding 108000000 SD05004 ID:118C1  
 CG6556 + CG6556 SD05024 dup:1/8 ID:118C3  
 + enzyme \* protease(aa) \* 1e-95 TyB protein - yeast (Saccharomyces cerevisiae) retrotransposon Ty3-2 \* 2e-95 gag, pol and  
 CG2485 env protein precursor \* hypothetical [rvt // NLS\_BP] CG2485 SD05236 10B1-10B1 dup:4/7 ID:118D11  
 CG3715 + CG3715 SD05206 dup:2/2 ID:118D4.2  
 CG7143 + DNA\_repair\_protein CG7143 SD05329 dup:2/2 ID:118F3  
 CG6339 + motor\_protein CG6339 SD05424 ID:118G5  
 CG7110 + unknown \* [NLS\_BP] CG7110 SD05480 34B7-34B7 dup:2/3 ID:118H1  
 CG14045 + CG14045 SD05785 dup:2/2 ID:119D8.2  
 CG7518 + unknown \* [MYB\_1 // PRO\_RICH // NLS\_BP // ANTIFREE] CG7518 SD05989 87D9-87D9 dup:5/6 ID:119F12.2  
 CG1553 + CG1553 SD06318 dup:4/5 ID:119G2.2  
 CG1371 + \* contains similarity to human Pm5 protein(aa) \* Pm5 protein - human(aa) \* pM5 (3' partial)(aa) \* 2e-81 contains similarity



to human Pm5 protein CG1371 46D9-46E1 dup:3/3 ID:119G3.2

CG3075 + transcription\_factor CG3075 SD06336 dup:2/2 ID:119G4.2

CG12204 + CG12204 SD06362 dup:2/2 ID:119G7.2

CG9799 + CG9799 SD06427 dup:3/3 ID:119H4.2

CG4817 + DNA\_binding CG4817 SD06504 dup:2/2 ID:119H6.2

CG18273 + CG18273 SD06521 dup:2/2 ID:119H9.2

CG12101 + chaperone CG12101 SD06594 dup:1/2 ID:120A4.2

CG11844 + unknown CG11844 SD06613 dup:1/2 ID:120A6.2

+ transcription\_factor \* GASTRULA ZINC FINGER PROTEIN XFG20-1 (XLCGF20.1)(aa) \* ovo \* ZINC FINGER PROTEIN

CG10462 186(aa) \* DMC115C2 [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG10462 SD07008 38A2-38A2 dup:1/3 ID:120E2.2

CG13185 + CG13185 SD07158 dup:1/3 ID:120G1.2

+ unknown \* 2e-83 inserted at base 5' end of P element Inverse PCR \* 1e-124 inserted at base Both 5' and 3' ends of P

CG2765 element Inverse PCR \* CG2765 SD07219 60E5-60E5 dup:3/5 ID:120G10.2

CG4510 + CG4510 SD09607 dup:1/2 ID:124A6.2

+ Hsc70Cb chaperone \* 1e-121 HS78\_YEAST HEAT SHOCK PROTEIN HOMOLOG SSE1 heat shock pr \* heatshock protein

cognate 70Cb \* 1e-160 YLA4\_CAEEL HYPOTHETICAL 86.9 KD PROTEIN C3 [HEATSHOCK70 // HSP70 // HSP70\_3] CG6603

CG6603 SD09792 70C11-70C11 dup:1/4 ID:124C5.2

CG11100 + CG11100 dup:1/4 ID:124D5.2

CG6501 + unknown CG6501 SD10213 dup:1/2 ID:124H5.2

CG6939 + CG6939 SD10541 dup:1/2 ID:125D1.2

+ structural\_protein \* unknown(aa) \* Allele: hi4(aa) \* gene is related to S.cerevisiae NIC96 gene.(aa) \* 7e-24 NI96\_YEAST

CG7262 KD NUCLEOPORIN-INTERACTING COMPONENT nucle CG7262 GH01087 88D8-88D8 ID:30A8

+ DNA\_binding \* ISWI PROTEIN (IMITATION SWI PROTEIN) (NUCLEOSOME REMODELING FACTOR KD SUBUNIT)

(NURF-140) (CHRAK KD SUBUNIT)(aa) \* DMISWI\_6 lswi \* 8e-94 YAB9\_YEAST [helicase\_C // SNF2\_N] CG5899 GH01406

CG5899 33A1-33A1 ID:30C10

+ Mer actin\_binding \* merlin \* 1e-105 coded for by C. elegans cDNA yk167f5.5; coded for by C. elegans cDNA yk130f8.5; \* 1e-

135 MERL\_MOUSE MERLIN (SCHWANNOMIN) merlin - mo [Band\_41 // BAND41 // ERM // ERMFAMILY] CG14228 GH01330

CG14228 18E1-18E1 ID:30C2

+ dim-7 unknown \* RanBP7(aa) \* 1e-73 NMD5\_YEAST NONSENSE-MEDIATED MRNA DECAY PROTEIN NMD5 \* 8E-26\*

CG7935 RanBP7/importin [IBN\_NT] CG7935 GH01576 66B9-67E3 dup:3/3 ID:30E1

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

+ transcription\_factor \* pleiomorphic adenoma gene-like 2; PLAG-like 2(aa) \* DMZFH1\_2 zfh1 \* 1e-06 ZFH1\_DROME ZINC-

FINGER PROTEIN (ZINC-FINGER HOMEODOMAIN PROTEIN [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG12744

CG12744 GH03826 46C1-46C1 dup:1/2 ID:32C5

+ unknown \* HSPC015(aa) \* 8e-45 hypothetical protein YOR173w - yeast (Saccharomyces cerevisiae) ( \* hypothetical protein  
 CG2091 YLR270w - yeast (Saccharomyces cerevisiae) CG2091 GH04919 83C-83C ID:33C2  
 + 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 ID:33F10  
 + EG:22E5.3 enzyme \* RNA 3'-terminal phosphate cyclase(aa) \* 1e-10 RTC1\_YEAST RNA 3'-TERMINAL PHOSPHATE  
 CG4061 CYCLASE (RNA-3'-PHOSPHATE CYCLASE) (RNA CY \* /match=(desc;; /ma \* [RCT] CG4061 GH05410 2C7-2C7 ID:33F4  
 + unknown \* zinc-finger protein MCG4(aa) \* 3e-53 zinc-finger protein MCG4 \* unknown \* [ZF\_RING] CG5382 GH05689  
 CG5382 94A15-94A15 ID:33G12  
 + unknown \* R12B2.2 gene product(aa) \* basic-leucine zipper nuclear factor(aa) \* basic-leucine zipper nuclear factor \*  
 CG9356 CG9356 GH05665 85D15-85D15 ID:33G8  
 CG10139 + unknown \* CG10139 GH05836 51B9-51B9 ID:34A1  
 + unknown \* 9e-30 inserted at base Both 5' and 3' ends of P element Inverse PCR \* \* CG3570 GH09390 60D8-60D8  
 CG3570 dup:1/3 ID:37A3  
 + Cct5 chaperone \* 1e-179 chaperonin TCP1 epsilon - yeast (Saccharomyces cerevisiae) \* 7e-63 TCPA\_DROME T-COMPLEX  
 PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA) \* [TCP1\_1 // TCP1\_3 // TCOMPLEXTCP1 // CHA] CG8439  
 CG8439 GH10122 48F1-48F1 ID:37F2  
 + protein\_kinase \* DMDFR2\_2 btl \* 3e-43 ABL\_DROME TYROSINE-PROTEIN KINASE DASH/ABL protein-tyrosine \* 7e-41  
 Tyrosine-protein kinase ABL-1; cDNA EST comes from th[PROTEIN\_KINASE\_TYR // TYRKINASE // PROT] CG17309 GH10267  
 CG17309 86E18-86E19 dup:1/2 ID:37G1  
 + T-cp1 chaperone \* DMTCP1\_2 T-cp1 \* T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA)(aa) \* 1e-  
 178 T complex protein (put.); putative \* similar to T-complex [TCP1\_1 // TCP1\_2 // TCP1\_3 // TCOMPLEXT] CG5374 GH10347  
 CG5374 94B4-94B4 ID:37H1  
 none + none GH10657 ID:38B12  
 + unknown \* 1e-45 YABC\_ECOLI HYPOTHETICAL 34.9 KD PROTEIN IN FRUR-FTSL INTERGENIC REGION (ORFB) >g \*  
 CG14683 1E-170\* hypothetical protein \* hypothetical protein CG14683 GH10770 86C2-86C2 ID:38C10  
 + endopeptidase \* DMSMMIN\_2 smallminded \* hypothetical protein(aa) \* 3e-40 AFG2\_YEAST AFG2 PROTEIN valosin-  
 CG5977 containing protein homolo \* 6E-37 [AAA // ATP\_GTP\_A] CG5977 GH11184 95D5-95D5 ID:38F12  
 + TfiIEalpha transcription\_factor \* 6e-23 T2EA\_YEAST TRANSCRIPTION INITIATION FACTOR IIE, ALPHA SUBUNIT (TFIIE-  
 CG10415 ALPHA) (TRA \* TFIIE large subunit \* 7e-35 cDNA EST yk210d12.5 comes from CG10415 GH11150 68C13-68C13 ID:38F9  
 + transporter \* Contains similarity to equilibrative nucleoside transporter from Homo sapiens. ESTs and come from this  
 CG11045 gene.(aa) \* NBMPR-insensitive nucleoside tr [DERENTRNSPT] CG11045 GH12067 26E2-26E2 ID:39D11  
 + BcDNA:GH12174 DNA\_binding \* 1e-05 eyelid \* 6e-45 YP83\_CAEEL HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN  
 CHROMOSOME II \* 5e-06 FMO5\_MOUSE DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FO [ARID] CG3274 GH12174  
 CG3274 42B2-42B3 dup:4/4 ID:39E10  
 + unknown \* 2e-10 YEA3\_YEAST HYPOTHETICAL 14.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION \* 7e-28  
 CG6302 prefoldin subunit \* 2e-68 I(3)j9B4 I(3)j9B4 inserted at base Bo CG6302 GH12095 70E1-70E1 dup:2/2 ID:39E2

+ CBP calcium\_binding \* CBP \* sarcoplasmic calcium-binding protein(aa) \* 1e-161 sarcoplasmic calcium-binding protein \* 4e-23  
 SCP\_PERVT SARCOPLASMIC CALCIUM-BINDING PROTEIN [EF\_HAND // NLS\_BP // efhand // EF\_HAND\_] CG1435  
 CG1435 GH12350 7A4-7A4 ID:39F9  
 + ribosomal\_protein \* similar to Ribosomal protein L7Ae; cDNA EST comes from this gene(aa) \* 2e-18 NHP2\_YEAST HIGH  
 MOBILITY GROUP-LIKE NUCLEAR PROTEIN hi \* 2e-27 similar [Ribosomal\_L7Ae // L7ARS6FAMILY // NUCLE] CG5258  
 CG5258 GH14757 70F6-70F6 ID:41G10  
 + signal\_transduction \* predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain);  
 cDNA EST comes from this gene; cDNA EST comes from thi [ArfGap // ZF\_GCS // REVINTRACTNG] CG8243 GH15285 44F9-  
 CG8243 44F9 ID:42C5  
 + signal\_transduction \* serine/threonine kinase with Dbl- and pleckstrin homology domains(aa) \* actin-filament binding  
 protein Frabin(aa) \* 5e-12 ROM1\_YEAST RHO1 GDP-GTP E [GRF\_DBL // RhoGEF // PRO\_RICH // NLS\_BP] CG8606 LD21492  
 CG8606 65F2-65F2 ID:43A5  
 CG11993 + Mst85C unknown \* CG11993 LD21554 85C6-85C6 ID:43A6  
 CG3510 + CycB cell\_cycle\_regulator G2/MITOTIC-SPECIFIC CYCLIN B CYCLINS, cyclin CG3510 dup:2/4 ID:43B3  
 + DNA\_binding \* SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1(aa) \*  
 CG7055 BAF57(aa) \* 1e-08 HMG1-related DNA-binding [HMG // HMG\_box // PRO\_RICH] CG7055 LD22182 8C17-8D1 ID:43B5  
 CG17252 + BCL7-like CG17252 LD22180 dup:2/2 ID:43B6  
 + Mcm2 DNA\_replication\_factor \* BLASTX 4.1E-84 Homo sapiens mRNA for DNA replication licensing factor (huMCM2),  
 complete cds.(dna) \* BLASTX 4.1E-84 Homo sapiens mRNA for DNA replic [MCM // MCM\_1 // MCM\_2] CG7538 LD22409 84F-  
 CG7538 84F dup:1/2 ID:43C3  
 + RNA\_binding \* mus308 \* contains ATP-GTP binding motif; similar to Saccharomyces cerevisiae antiviral protein SKI2,  
 corresponds to Swiss-Prot Accession Number \* RNA [HELICASE // DEAD // ATP\_GTP\_A] CG10210 LD23303 95B9-95B9 dup:6/8  
 CG10210 ID:43E10  
 + signal\_transduction G-protein beta-subunit 6 GPROTEINBRPT, RCC1\_2, WD40, WD40\_REGION,] CG3004 LD23129  
 CG3004 dup:3/3 ID:43E6  
 + TfiIFbeta transcription\_factor \* TfiIF bgr; \* TRANSCRIPTION INITIATION FACTOR IIF, BETA SUBUNIT (TFIIF-BETA)(aa) \* 6e-  
 CG6538 05 T2FB\_YEAST TRANSCRIPTION INITIATION FACTOR IIF, BETA SUBUNIT CG6538 LD23340 86C4-86C4 dup:1/2 ID:43F2  
 + Mat1 transcription\_factor CDK7/cyclin H assembly factor NLS\_BP, ZF\_RING, ZINC\_FINGER\_C3HC4, zf-C] CG7614 LD23429  
 CG7614 ID:43F4  
 + dbe unknown \* DMDRIBBLE dbe \* dribble(aa) \* 9e-98 YCF9\_YEAST HYPOTHETICAL 37.2 KD PROTEIN IN CHA1-PRD1  
 CG4258 INTERGENIC REGION \* 5e-88 similar to human REV interacting CG4258 LD24634 21E3-21E3 ID:43G5  
 + chaperone \* FK506-binding protein 6(aa) \* FK506-binding protein - Arabidopsis thaliana(aa) \* FKBP (FK506 binding protein)  
 CG4735 13; peptidylprolyl cis-trans isomerase [FKBP // FKBP\_PPIASE\_3 // TPR\_REPEAT] CG4735 LD24746 60A4-60A4 ID:43G6  
 + Dom transcription\_factor \* DOMINA protein (WHN-homologue)(aa) \* 1e-12 FKH2\_YEAST FORK HEAD PROTEIN  
 HOMOLOG FKH2 protein - y \* 4e-16 SLP1\_DROME FORK HEAD DOMAIN TRANSCRIPTION F [Fork\_head // FORKHEAD]  
 CG4029 CG4029 LD24749 86A2-86A3 ID:43G7  
 CG9967 + CG9967 LD25280 dup:1/2 ID:43H7

+ huckebein transcription\_factor specific RNA polymerase II transcription factor ZINC\_FINGER\_C2H2, ZINC\_FINGER\_C2H2\_2, zf] CG9768 LD25709 dup:2/3 ID:44B3  
 + endopeptidase serine proteinase [Anopheles gambiae] CHYMOTRYPSIN, TRYPSIN\_CATAL, TRYPSIN\_HIS] CG11836 LD25830 dup:2/2 ID:44B8  
 + RNA\_binding \* son3 protein - human (fragment)(aa) \* SON DNA binding protein(aa) \* Pad-1(aa) \* similar to RNA binding proteins(aa) [RBD // rrm // NLS\_BP] CG16788 LD26185 85D25-85D25 ID:44C10  
 + PEK protein\_kinase \* 8e-30 protein kinase GCN2 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) \* 2e-24 eIF-2alpha kinase \* 2e-55 similar to serine/threonine kinase (2 do [Bacterial\_PQQ // PROTEIN\_KINASE\_ST // P] CG2087 LD25978 83A8-83A8 ID:44C5  
 + unknown \* 9e-61 inserted at base Both 5' and 3' ends of P element Inverse PCR \* [SAM\_DOMAIN] CG8572 LD26045 65F5-65F5 dup:2/2 ID:44C6  
 + signal\_transduction \* Polyadenylation Factor I subunit; Pfs2p(aa) \* 3e-17 alpha-COP (Z466 \* 3e-18 lissencephaly-1 \* 3e-15 SEL-10 [GPROTEINBRPT // WD40\_REGION // WD40] CG1109 LD26389 83B7-83B7 dup:2/3 ID:44D6  
 + CHROMO\_2, chromo CG18622 LD26416 dup:2/3 ID:44D9  
 + Sr-CII cell\_adhesion Scavenger receptor class C, type II MAM, MAM\_2, SOMATOMEDIN\_B, Somatomedin\_B] CG8856 LD26673 dup:3/3 ID:44E10  
 + cdc2 protein\_kinase \* CDK5 kinase(aa) \* DMCDC2\_2 cdc2 \* 1e-101 CC28\_YEAST CELL DIVISION CONTROL PROTEIN protein kinase \* 1e-174 CC2\_DROME CELL DIVISION CONTROL PROT[PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM] CG5363 LD26702 31D11-31D11 dup:3/3 ID:44E11  
 + CG11504 LD26477 dup:3/3 ID:44E2  
 + ligand\_binding\_or\_carrier \* 4e-05 fizzy-related protein \* 1e-05 transducin (beta)-like transducin (beta) like pr \* 1e-05 CG16892 hypothetical protein \* 5e-07 DMRNAFRP fzr CG16892 LD26813 8D7-8D8 dup:2/2 ID:44F4  
 + unknown unknown protein CIT987SK\_2A8\_1 [Homo sapiens] CG5222 LD26912 dup:1/2 ID:44F9  
 + transcription\_factor \* 9e-06 Z33A\_HUMAN ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (HA09 \* 8e-05 zinc finger protein XFDL \* 3e-05 DMDROSOPH\_4 wdn \* zinc finger:[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG11906 LD27134 56C7-56C8 ID:44G9  
 + chaperone \* DMNINAA\_7 ninaA \* DMCYP1\_2 Cyp1 \* 5e-23 CYPC\_YEAST PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C PRECURSOR (PPIASE) (ROTAMASE) ( \* 1e-20 CYPH\_DROME PEPTIDYL [pro\_isomerase // CSA\_PPIASE\_2 // WD40\_R] CG3511 LD27277 60D5-60D5 dup:1/2 ID:44H8  
 + enb signal\_transduction \* map\_position:56B5 \* clot.396(dna)\* 1e-124 Abl substrate ena (enabled) - fruit fly (Drosophila melanogaster) \* 6e-39 neural variant mena+ protein [WH1 // PRO\_RICH // RANBP1\_WASP] CG15112 LD27343 56B5-56B5 dup:3/5 ID:45A1  
 + transcription\_factor similar to crol protein ZINC\_FINGER\_C2H2, ZINC\_FINGER\_C2H2\_2, z] CG2678 LD27553 dup:1/2 ID:45A10  
 + unknown \* CG18608 LD27570 56A-56A dup:1/2 ID:45A11  
 + actin\_binding \* has homology to the Dictyostelium and human actin-binding protein coronin; Crn1p(aa) \* coronin-1(aa) \* 3e-76 CORO\_YEAST CORONIN-LIKE PROTEIN hypothe [WD40\_REGION // ARGINASE\_2 // WD\_REPEATS] CG9446 42C8-42C8

dup:3/3 ID:45B2

CG7825 + Rad17 DNA\_repair\_protein DNA repair protein ATP\_GTP\_A, ATP\_GTP\_A2, RFC CG7825 LD27993 ID:45C7  
CG10018 + DNA\_repair\_protein homology to mouse and human SNM1 protein NLS\_BP CG10018 LD28027 dup:1/2 ID:45C8  
+ unknown \* 1e-106 probable membrane protein YPL217c - yeast (Saccharomyces cerevisiae) \* 2e-11 No definition line  
CG7728 found \* 1E-152\* 1e-100 conserved hypothetical [NLS\_BP // ATP\_GTP\_A] CG7728 LD28182 73E3-73E4 dup:3/3 ID:45D11  
CG6994 + cytoskeletal\_structural\_protein CG6994 LD28101 dup:2/2 ID:45D5  
+ enzyme \* nudix (nucleoside diphosphate linked moiety X)-type motif 3(aa) \* 7e-40 diphosphoinositol polyphosphate  
CG6391 phosphohydrolase (A \* [MUTT // mutT] CG6391 LD28241 67F4-67F4 dup:3/4 ID:45E3  
CG8783 + unknown Conserved gene telomeric to alpha globin cluster [Homo sapiens] CG8783 LD28428 dup:2/3 ID:45F2  
CG14657 + unknown CG14657 LD28447 ID:45F4  
CG4300 + unknown spermine synthase SAM\_BIND CG4300 LD28457 ID:45F5  
+ sgg protein\_kinase \* DMSGG46\_2 sgg \* 5e-98 MDS1\_YEAST SERINE/THREONINE-PROTEIN KINASE MDS1/RIM11 pr \*  
zeste-white 3-A - fruit fly (Drosophila melanogaster) \* 1e-141 pred [PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM] CG2621  
CG2621 3B2-3B3 dup:1/2 ID:45G9  
+ unknown \* phosphatidylinositol glycan, class B(aa) \* 2e-29 YGO2\_YEAST HYPOTHETICAL 72.6 KD PROTEIN IN MRF1-  
CG12006 SEC27 INTERGENIC REGION \* 5e-08 coded for by C. ele CG12006 64C4-64C4 dup:2/2 ID:45H10  
CG10640 + CG10640 dup:4/4 ID:45H8  
CG4916 + RNA\_binding CG4916 dup:2/2 ID:46C4  
+ transporter \* ATP-DEPENDENT RNA HELICASE GLH-1(aa) \* 1e-08 EAST\_DROME SERINE PROTEASE EASTER  
CG3820 PRECURSOR serine protein \* 6e-22 similar to nucleoporin; cDNA EST com CG3820 LD29808 59B4-59B4 dup:3/4 ID:46E7  
+ endopeptidase \* hypothetical protein unp - mouse(aa) \* Sad1p(aa) \* putative protein(aa) \* Contains similarity to Pfam  
CG7288 domain: (UCH-1), Score=13.8, E-value=0.14, N= [UCH\_2\_3 // UCH-2] CG7288 LD30129 17E4-17E4 dup:1/3 ID:46G10  
CG3309 + unknown \* 3e-62 No definition line found \* No definition line found \* CG3309 LD30005 4F2-4F2 dup:1/2 ID:46G3  
CG17681 + unknown \* CG17681 LD30009 36E-36E ID:46G4  
+ transcription\_factor\_binding \* 4e-71 YER2\_YEAST HYPOTHETICAL 62.3 KD PROTEIN IN PTP3-ILV1 INTERGENIC  
REGION \* 9e-94 Similarity to Yeast hypothetical protein YER2 (SW:YER2\_YEAS[WD40\_REGION // WD\_REPEATS // WD40]  
CG2260 CG2260 LD30339 7D11-7D11 ID:46H10  
+ Transcription factor IIA L transcription\_factor general RNA polymerase II transcription factor, PHOSPHOPANTETHEINE  
CG5930 CG5930 LD30231 dup:2/2 ID:46H2  
CG9949 + SEVEN IN ABSENTIA DNA binding ubiquitin-dependent protein degradation ZF\_RING CG9949 LD30265 ID:46H3  
CG14005 + unknown \* CG14005 LD30293 26A2-26A2 dup:2/3 ID:46H6  
CG1677 + CG1677 LD30482 ID:47A10  
+ translation\_factor \* 1e-85 NAT1\_YEAST N-TERMINAL ACETYLTRANSFERASE (AMINO-TERMINAL, ALPHA-AMINO,  
ACETYLTR \* 1e-123 N-terminal acetyltransferase \* O-linked GlcNAc tran[TPR\_REGION // TPR\_REPEAT // NLS\_BP] CG12202  
CG12202 LD30511 18C8-18D1 dup:3/6 ID:47B1

+ transcription\_factor \* general transcription factor IIH, polypeptide (52kD subunit)(aa) \* TFIIH subunit Tfb2; has homology to  
 CG7764 CAK and human IIH subunits; Tfb2p(aa) \* 9e-71 CG7764 LD30622 71D3-71D4 ID:47B11  
 CG9231 + \* 2e-14 pIL2 hypothetical protein - rat (fragment) growth and trans \* \* CG9231 76B9-76B9 dup:2/2 ID:47B12  
 CG3508 + unknown \* HMBA-inducible(aa) \* 3e-11 HIS1 protein \* [NLS\_BP] CG3508 LD30520 88C11-88C11 ID:47B4  
 + FK506-bp1 ligand\_binding\_or\_carrier \* DMFKBP39\_2 FK506-bp1 \* KD FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-  
 PROLYL CIS-TRANS ISOMERASE) (PPIASE)(aa) \* 7e-24 hypothetical protein YLR4[FKBP // FKBP\_PPIASE\_2 //  
 CG6226 FKBP\_PPIASE\_3] CG6226 LD30817 90E1-90E1 ID:47C12  
 + msl-3 tumor\_suppressor \* MALE-SPECIFIC LETHAL-3 PROTEIN(aa) \* DMMSL3\_2 msl-3 \* 7e-08 hypothetical protein \*  
 CG8631 DMMSL3\_2 msl-3 CG8631 LD30726 65E5-65E5 dup:1/2 ID:47C5  
 + unknown \* 2e-34 hypothetical protein YPR131c - yeast (Saccharomyces cerevisiae) ( \* 8e-20 contains similarity to N-  
 CG14222 terminal acetyltransferase complex subunit [Acetyltransf] CG14222 LD30731 18D9-18D9 dup:1/2 ID:47C6  
 + transcription\_factor \* with similarity to Homo sapiens TAFII55 encoded by Genbank Accession Number and C. elegans  
 CG2670 unknown protein encoded by Genbank Accession Number \* an CG2670 LD30980 84E1-84E1 ID:47D11  
 + Mcm3 DNA\_replication\_factor \* Mcm3 \* DNA replication factor MCM3(aa) \* 1e-168 MCM3\_YEAST MINICHROMOSOME  
 CG4206 MAINTENANCE PROTEIN minichrom \* MCM3 [MCM // MCM\_1 // MCM\_2] CG4206 LD30950 4F2-4F2 ID:47D8  
 + protein\_phosphatase \* 4e-25 PVH1\_YEAST PROTEIN-TYROSINE PHOSPHATASE YVH1 (PTPASE YVH1) \* 8e-13  
 puckered protein \* 1e-14 predicted using Genefinder; similar to D[PTS\_HPR\_SER // DSPc // TYR\_PHOSPHATASE\_] CG14211  
 CG14211 LD31102 18D9-18D9 dup:2/2 ID:47E10  
 + tos DNA\_repair\_protein \* DMTOSCAP1\_2 tos \* Tosca(aa) \* 7e-47 EXO1\_YEAST EXONUCLEASE I (EXO I) (DHS1  
 CG10387 PROTEIN) DHS1 pr \* Tosca [53EXO\_N\_DOMAIN // 53EXO\_I\_DOMAIN // XPG] CG10387 LD31018 37A4-37A4 dup:2/2 ID:47E5  
 + unknown \* 7e-05 YHOB\_DROME TRANSPOSABLE ELEMENT HOBO KD HYPOTHETICAL PROTEIN \* 9e-05  
 CG17153 transposase \* 7e-05 ORF1 \* Hermes transposase CG17153 LD31163 68F3-68F3 ID:47F2  
 + ligand\_binding\_or\_carrier \* 3e-51 ARF1\_YEAST ADP-RIBOSYLATION FACTOR ADP-ribosylation fac \* 3e-49  
 ARF1\_DROME ADP-RIBOSYLATION FACTOR ADP-ribosylation fac \* 1e-52 ARFL\_CA[arf // SAR1GTPBP // RASTRNSFRMNG]  
 CG7197 CG7197 LD31204 66C5-66C5 dup:2/5 ID:47F5  
 CG8440 + signal\_transduction CG8440 ID:47F8  
 + motor\_protein \* coded for by C. elegans cDNA yk38d7.3; coded for by C. elegans cDNA cm06h5; coded for by C. elegans  
 CG12301 cDNA yk38d7.5(aa) \* Yml093wp(aa) \* 5e-33 YMJ3\_Y [NLS\_BP] CG12301 LD31322 71D4-71D4 dup:1/2 ID:47G3  
 CG8149 + motor\_protein \* CG8149 LD31448 86C1-86C1 ID:47G6  
 + \* contains weak similarity to HIV P17 matrix protein \* 7e-13 RL1\_SERMA 50S RIBOSOMAL PROTEIN L1 ribosomal  
 CG7494 protein L1 - S \* RL1\_HAEDU 50S RIBOSOMAL P [Ribosomal\_L1] CG7494 84F9-84F9 dup:2/2 ID:47H12  
 + msi RNA\_binding \* DMMUSASH\_3 msi \* 9e-41 NAB4\_YEAST NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN  
 NAB4 \* musashi \* 2e-31 heterogeneous ribonuclear particel protein homol [RNP\_1 // RBD // rrm // ANTIFREEZEI] CG5099  
 CG5099 LD31631 96E5-99B9 ID:47H3  
 + enzyme \* PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE PRECURSOR (LYSYL HYDROXYLASE)  
 (LH)(aa) \* PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE PRECURSOR ( [GLYC\_TRANS //  
 CG6199 HTH\_LYSR\_FAMILY] CG6199 LD31687 68A8-68A8 dup:3/4 ID:47H7

+ translation\_factor \* translation repressor NAT1(aa) \* eukaryotic protein synthesis initiation factor(aa) \* 2e-19 IF41\_YEAST  
 CG3845 EUKARYOTIC INITIATION FACTOR 4F SUBUNIT P150 CG3845 LD32057 49E1-49E1 dup:1/2 ID:48A10  
 + transcription\_factor \* 1e-11 AZF1\_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin \* 4e-20 CROL BETA \*  
 2e-08 similar to Zinc finger, C2H2 type (4 domains); cDNA EST \*[ZF\_MATRIN // zf-C2H2 // ZINC\_FINGER\_C2H] CG17806  
 CG17806 LD32088 93B1-93B1 ID:48A11  
 CG5995 + unknown \* CG5995 LD31910 97F3-97F4 dup:1/2 ID:48A2  
 + enzyme \* cystathionine beta-synthetase; CBS(aa) \* BLASTX 8.7E-06 CYS4[Cystathionine beta-synthase (beta-CTase),  
 CG1753 converts serine and homocysteine to cystathi [CBS // SNF4\_REP // S\_T\_dehydratase // C] CG1753 LD32051 19E6-19E6 ID:48A9  
 + 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  
 CG8975 48D8-48D8 ID:48D10  
 + enzyme \* similar to Transketolase; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes  
 CG8199 from this gene; cDNA EST comes from this gene [E1\_dehydrog // NLS\_BP] CG8199 LD32808 85D25-85D25 dup:2/2 ID:48D12  
 + signal\_transduction \* protein(aa) \* BLASTX 4.9E-08 Mus musculus TDAG51 (TDAG51) mRNA, complete cds.(dna) \*  
 BLASTX 7.3E-13 Rattus PSD-95/SAP90-related gene (chapsyn isoform) [GUANYLATE\_KINASE\_2 // PDZ // NLS\_BP] CG6509  
 CG6509 LD32687 33A2-33A2 ID:48D7  
 + motor\_protein \* ARX(aa) \* 1e-58 UBA2\_YEAST UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-  
 INTERACTING PROTEIN \* 2e-28 ubiquitin activating enzyme \* 1e-67 simila[UBA\_NAD // ThiF\_family // NAD\_BINDING /] CG7528  
 CG7528 LD33023 67E3-67E3 dup:5/5 ID:48E10  
 + transcription\_factor \* 4e-05 stwl \* 5e-13 inserted at base 5' end of P element Inverse PCR \* CG7745 LD32860 47E6-47E6  
 CG7745 dup:2/2 ID:48E2  
 + nop5 unknown \* nucleolar protein NOP5/NOP58(aa) \* 1e-100 NOP5\_YEAST NUCLEOLAR PROTEIN NOP5 hypothetical  
 CG10206 protein \* 1e-119 contains similarity to S. cerevisiae Prp31 [NLS\_BP] CG10206 LD32943 27C-27C dup:2/2 ID:48E7  
 + unknown \* Yjr072cp(aa) \* ATP(GTP)-binding protein(aa) \* HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN  
 CG3704 CHROMOSOME III(aa) \* putative protein(aa) [ATP\_GTP\_A] CG3704 LD33276 1D1-1D1 ID:48G10  
 + unknown \* Ygl101wp(aa) \* unknown protein(aa) \* 2e-27 YB92\_YEAST HYPOTHETICAL 27.6 KD PROTEIN IN THI2-ALG7  
 CG11050 INTERGENIC REGION \* 3e-15 No definition line found CG11050 LD33330 26F1-26F1 ID:48G12  
 + 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  
 + unknown \* protein(aa) \* SSXT PROTEIN (SYNOVIAL SARCOMA, TRANSLOCATED TO X CHROMOSOME) (SYT  
 PROTEIN)(aa) \* synovial sarcoma, translocated to X chromosome(aa) \* [PRO\_RICH] CG10555 LD33241 7E2-7E3 dup:2/2  
 CG10555 ID:48G6  
 + unknown \* hypothetical protein(aa) \* 4e-25 YMO9\_YEAST HYPOTHETICAL 20.9 KD PROTEIN IN PLB1-HXT2  
 CG8000 INTERGENIC REGION \* 9e-21 Closely related to Arabidopsis thal [NLS\_BP] CG8000 LD33361 67E4-67E4 ID:48H2  
 + enzyme \* 1e-10 FMS1\_YEAST FMS1 PROTEIN FMS1 protein - yeast (Saccharom \* 6e-11 Cs protein \* 8e-33 No definition  
 CG7737 line found \* 2e-13 protein [ADXRDTASE // AMINEOXDASEF // NAD\_BINDING] CG7737 LD33764 47D6-47D7 dup:1/2 ID:49A10  
 CG7357 + transcription\_factor \* transcription factor 17(aa) \* zinc finger protein(aa) \* RENAL TRANSCRIPTION FACTOR KID-1

(TRANSCRIPTION FACTOR 17)(aa) \* crol [zf-C2H2 // ZINC\_FINGER\_C2H2\_2] CG7357 LD33778 93B1-93B1 ID:49A11

CG15736 + transcription\_factor \* CG15736 LD33780 11A4-11A4 ID:49A12

+ enzyme \* SUMO-1 activating enzyme subunit 1(aa) \* Similar to ubiquitin activating proteins; Aos1p(aa) \* 6e-30

RH31\_YEAST DNA DAMAGE TOLERANCE PROTEIN RHC31 ( [UBA\_NAD // ThiF\_family] CG12276 LD33652 87B15-87B15

CG12276 ID:49A3

+ unknown \* similar to the postsynaptic membrane 43K protein from Xenopus \* LGN protein(aa) \* 4e-13 C10A gene product

CG5692 \* 2e-29 hypothetical protein [TPR\_REGION // TPR\_REPEAT // NLS\_BP] CG5692 LD33695 98A3-98A3 ID:49A6

+ RNA\_binding \* DMRM62RH\_2 Rm62 \* RNA helicase(aa) \* mitochondrial DEAD box protein(aa) \* VASA PROTEIN(aa)

CG7878 [helicase\_C // KH-domain // KH\_DOMAIN //] CG7878 LD33749 84F1-84F1 ID:49A7

+ unknown \* 3e-47 YKT6\_YEAST HYPOTHETICAL 22.7 KD PROTEIN IN PAS1-MST1 INTERGENIC REGION \* 7e-53

YMP8\_CAEEL HYPOTHETICAL 82.6 KD PROTEIN IN CHROMOSOME III \* 1e- [SYNAPTOBREVIN // synaptobrevin] CG1515

CG1515 LD34211 7C8-7C8 ID:49C12

+ unknown \* Ydl060wp(aa) \* No definition line found(aa) \* 8e-91 hypothetical protein YDL060w - yeast (Saccharomyces

CG7338 cerevisiae) \* 0.00000000006 [NLS\_BP] CG7338 LD34093 78D-78D dup:2/4 ID:49C5

+ unknown \* RRM3/PIF1 helicase homolog(aa) \* PIF1(aa) \* putative helicase(aa) \* DNA helicase homolog(aa) [NLS\_BP //

CG3238 ATP\_GTP\_A] CG3238 LD34105 25A3-25A3 ID:49C6

+ pelo unknown \* pelo \* 9e-61 DOM34 protein - yeast (Saccharomyces cerevisiae) (X77 \* PELO\_DROME PELOTA PROTEIN

CG3959 pelota \* 1e-120 YNU6\_CAEEL HYPOTHETICAL 42.9 KD PROT CG3959 LD34262 30C6-30C7 ID:49D2

+ cell\_cycle\_regulator \* DMUNKNOWN anon-DM192 \* unknown product(aa) \* 4e-05 CC27\_YEAST CELL DIVISION

CONTROL PROTEIN cell division \* 1e-139 unknown product [TPR\_REGION // TPR\_REPEAT // TPR] CG4050 57C2-57C2

CG4050 dup:3/4 ID:49D5

+ motor\_protein \* 7e-09 by content; 1-meth \* 2e-07 homeotic most like HMPB\_DROME: homeotic proboscipedia protein \* 9e-

07 Williams-Beuren syndrome deletion transcript [PHD // NLS\_BP // ATP\_GTP\_A] CG8677 LD34730 39C1-39C1 dup:5/5

CG8677 ID:49E10

+ TfiIS transcription\_factor \* 2e-20 DST1 DNA strand transferase alpha \* 1e-124 TFS2\_DROME TRANSCRIPTION

ELONGATION FACTOR S-II (RNA POLYMERASE II ELONGATION FA \* 3e-42 TFS2\_CAEEL [TFIIS] CG3710 LD34766 35C1-

CG3710 35C1 ID:49F1

+ unknown \* apoptosis specific protein(aa) \* 1e-05 APG5\_YEAST AUTOPHAGY PROTEIN APG5 Apg5 protein - yeast \* 6e-

CG1643 13 apoptosis specific protein homologue \* dJ134E1 CG1643 LD34980 7A4-7A4 ID:49F10

+ DNA\_binding \* zinc finger protein (RING finger, C3HC4 type)(aa) \* 4e-34 YL23\_YEAST HYPOTHETICAL 29.7 KD

PROTEIN IN REC102-SFH1 INTERGENIC REGION \* 5e-65 similar t [ZF\_CCCH // zf-C3HC4 // ZINC\_FINGER\_C3HC] CG4973

CG4973 LD35003 92C4-92C4 ID:49F12

+ DNA\_binding \* DNA helicase(aa) \* HYPOTHETICAL 175.7 KD PROTEIN C05C10.2 IN CHROMOSOME II(aa) \* DNA

CG6967 helicase A; Hcs1p(aa) \* hypothetical helicase(aa) [ATP\_GTP\_A] CG6967 LD34829 53F5-53F6 ID:49F6

CG9754 + unknown \* [NLS\_BP] CG9754 LD34845 57D4-57D4 ID:49F8

+ motor\_protein \* HYPOTHETICAL 25.4 KD PROTEIN F53F4.3 IN CHROMOSOME V(aa) \* 3e-12 YNO8\_YEAST

CG11242 HYPOTHETICAL 28.4 KD PROTEIN IN RPC8-MFA2 INTERGENIC REGION \* 9e-07 kine [CAP\_GLY\_2 // CAP\_GLY] CG11242



LD35048 56D9-56D9 dup:2/2 ID:49G2

CG15217 + transmembrane\_receptor \* CG15217 GH01875 40C2-40C2 ID:54H7  
+ RNA-directed\_DNA\_polymerase\_group\_II\_intron\_encoded \* reverse transcriptase - fruit fly (*Drosophila melanogaster*)(aa)  
\* SPAC3G9.15c; len:230aa; similarity: to YLR051C, Q120 35, unclassified protein, (21 [NLS\_BP] CG1142 GH02295 85A1-85A1

CG1142 ID:55B7  
+ unknown \* molybdenum cofactor biosynthesis protein E isolog(aa) \* molybdenum cofactor synthesis 2(aa) \* 8e-28 similar to

CG10238 molybdenum cofactor biosynthesis pro CG10238 GH02855 96B20-96B20 dup:2/2 ID:55E4  
+ Pkc53E protein\_kinase \* DMPKC53E\_2 inaC \* DMPKCR\_2 Pkc53E \* 3e-85 protein kinase C-like protein (PKC1) \*  
KPC1\_DROME PROTEIN KINASE C, BRAIN ISOZYME (PKC) (DPKC53E(BR)) [DAG\_PE\_BINDING\_DOMAIN //

CG6622 PROTEIN\_KINASE] CG6622 GH03188 53E3-53E ID:55G8  
+ SMC2 DNA\_binding \* 1e-179 SMC2\_YEAST CHROMOSOME SEGREGATION PROTEIN SMC2 (DA-BOX PROTEIN SMC2)  
\* 3e-69 Cap \* 1e-136 mitotic chromosome and X-chromosome associated MIX- [ATP\_GTP\_A] CG10212 GH03364 51D1-51D1

CG10212 ID:55H8  
+ CycJ cell\_cycle\_regulator \* CycJ \* 4e-11 CG22\_YEAST G2/MITOTIC-SPECIFIC CYCLIN cyclin B2 - yeast \* cyclin J \* 3e-05

CG10308 Similar to cyclin [cyclin // HELIX\_LOOP\_HELIX // NLS\_BP] CG10308 GH04281 63D2-63D2 ID:56G5  
+ enzyme \* ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (PROTEIN 9) (SUBUNIT C)(aa) \* 5e-12 ATP  
synthase (EC 3.6.1.-) c chain - *Caenorhabditis elegans* \* 3e- [ATPASE\_C // ATPASEC // ATP-synt\_C] CG1746 GH04827 100B9-

CG1746 100B9 ID:57C6

CG4571 + unknown \* CG4571 GH05034 6D6-6D7 dup:4/4 ID:57E8  
+ unknown \* weakly similar to *S. cerevisiae* hypothetical 24.1 kd protein in APN1 3' \* 2e-05 YKL7\_YEAST 24.1 KD PROTEIN

CG16817 IN VMA12-APN1 INTERGENIC REGION \* 3e-06 CG16817 GH05808 85E4-85E4 ID:58C9  
+ Lrr47 actin\_binding \* LRR47 protein - fruit fly (*Drosophila melanogaster*)(aa) \* DMLRR47\_3 Lrr47 \* 2e-05 predicted using

CG6098 Genefinder; Similarity to Glucose-repressible alco [LRR // LEURICHRPT] CG6098 GH06740 31E6-31E6 ID:59B11

CG14732 + unknown \* CG14732 GH07457 87A6-87A6 dup:2/2 ID:59F10  
+ enzyme \* DIHYDROFOLATE REDUCTASE(aa) \* 6e-10 hypothetical protein YOR280c - yeast (*Saccharomyces cerevisiae*)

CG5412 \* 6e-31 Similarity to *S.pombe* dihydrofolate redu CG5412 GH07367 92E11-92E11 ID:59F2  
+ fl(2)d unknown \* FL(2)D protein(aa) \* 1e-08 gene predicted from cDNA with a complete coding sequence \* 2e-16 FKBP12

CG6315 interacting protein \* 3e-39 inserted at base Bot [TROPOMYOSIN] CG6315 GH08722 50C12-50C12 dup:3/4 ID:60H8  
+ unknown \* coded for by *C. elegans* cDNA cm16h1; coded for by *C. elegans* cDNA yk13a7.5; coded for by *C. elegans* cDNA

CG8919 yk13a7.3; similar to *S. cerevisiae* SAC3 pro [RBD] CG8919 GH09410 15E1-15E1 dup:2/3 ID:61F10  
+ enzyme \* 6e-42 soluble guanylyl cyclase beta subunit \* 3e-78 similar to guanylate cyclase; cDNA EST yk355b5.3 comes  
from this g \* 9e-47 soluble guanylate cyc [GUANYLATE\_CYCLASES // guanylate\_cyc // ] CG14886 GH09958 89C6-89C6 dup:2/2

CG14886 ID:62B2  
+ signal\_transduction \* protein(aa) \* 1e-31 Sec7p \* 2e-76 similar to *S. cerevisiae* protein transport protein SEC7 \* 1e-38

CG10577 cytohesin [SEC7 // Sec7 // NLS\_BP] CG10577 GH10594 78B1-78B1 dup:1/2 ID:62F7  
+ unknown \* 6e-05 transducer \* 6e-05 chemotactic transducer \* [VWA\_DOMAIN] CG16868 GH11109 56F16-56F16 dup:1/2

CG16868 ID:63B9

+ Sin3A transcription\_factor \* 3e-58 SIN3\_YEAST PAIRED AMPHIPATHIC HELIX PROTEIN regulatory \* transcription factor \*  
 2e-31 cDNA EST comes from this gene; cDNA EST co \* 1e-135 co-r [ATPASE\_ALPHA\_BETA // NLS\_BP] CG8815 GH11769  
 CG8815 49B2-49B3 dup:1/2 ID:63G12  
 + Nacalphaunknown \* 4e-13 EGD2\_YEAST EGD2 PROTEIN EGD2 protein - yeast (Saccharomyc \* 5e-73 alpha NAC \* 1e-34  
 CG8759 alpha NAC/1.9.2. protein alpha-NAC, non-musc \* 1e-34 Nasce CG8759 GH11940 49C2-49C2 dup:2/2 ID:63H12  
 CG10286 + unknown \* CG10286 GH12023 83E6-83E6 dup:1/2 ID:64A12  
 + unknown \* 1e-10 cDNA EST yk471b2.5 comes from this gene; cDNA EST yk471b2.3 come \* \* CG4742 GH12140 15A5-  
 CG4742 15A5 ID:64C2  
 + \* membrane-type metalloproteinase precursor(aa) \* MATRIX METALLOPROTEINASE-14 PRECURSOR (MMP-14)  
 (MEMBRANE-TYPE MATRIX METALLOPROTEINASE 1) (MT-MMP 1) [Peptidase\_M10 // hemopexin // ZINC\_PROT] CG1794  
 CG1794 45F6-46A1 dup:4/5 ID:64E7  
 + unknown \* Mob1p-like protein; Mob2p(aa) \* partial CDS(aa) \* cDNA EST yk373c2.5 comes from this gene; cDNA EST  
 CG11711 yk361f7.5 comes from this gene(aa) \* putative m CG11711 GH13236 68C5-68C7 dup:1/3 ID:65C10  
 + endopeptidase \* INSULIN-DEGRADING ENZYME (INSULYSIN) (INSULINASE) (INSULIN PROTEASE)(aa) \* DMD1DE\_2  
 Ide \* 2e-63 STE23 protein - yeast (Saccharomyces cerevisiae) Ste [Peptidase\_M16 // INSULINASE] CG2025 GH13968 10F2-  
 CG2025 10F2 ID:65G10  
 none + none GH14469 ID:66D6  
 + chaperone \* similar to chaperonins cpn60 and TCP-1 (Pfam: cpn60\_TCP1.hmm, score: 416.20 and 102.94)(aa) \*  
 Cytoplasmic chaperonin subunit gamma; Cct3p(aa) \* chap [TCP1\_1 // TCP1\_2 // TCP1\_3 // TCOMPLEX] CG7033 GH15038  
 CG7033 8C13-8C13 dup:2/2 ID:67B3  
 + motor\_protein \* receptor-associated protein(aa) \* 9e-14 predicted using Genefinder; Similarity to Human alpha-2-  
 CG8507 macroglobu \* 2e-16 heparin binding protein \* 5e-18 CG8507 GH16343 86D1-86D1 dup:3/3 ID:68E5  
 + RNA\_binding \* pit \* 2e-78 SPB4\_YEAST ATP-DEPENDENT RRNA HELICASE SPB4 RNA helicase S \* 2e-69 helicase  
 pitchoune \* 8e-87 YOQ2\_CAEEL PUTATIVE ATP-DEPENDENT RNA HELI [helicase\_C // HELICASE // DEAD // NLS\_B] CG9630  
 CG9630 GH16590 84F-84F ID:68G6  
 CG12022 + unknown \* CG12022 GH18574 62E1-62E1 ID:70G8  
 + transcription\_factor \* DMC95B7 \* zinc finger protein (myeloid-specific retinoic acid- responsive)(aa) \* /motif=(desc;;  
 /motif=(desc;; /motif=(desc;; /match=(desc:(aa) \* [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG1233 GH18779 61C1-61C1  
 CG1233 ID:70H12  
 CG3342 + unknown \* 1e-05 protein \* \* CG3342 GH18625 6A4-6A4 ID:70H2  
 + sec10 motor\_protein \* BLASTX 1.7E-36 Human brain secretory protein hSec10p (HSEC10) mRNA, complete cds.(dna) \* 1e-  
 CG6159 110 C33H5.9 gene product \* 1e-157 brain secretory protei CG6159 GH19049 95E1-95E1 ID:71B10  
 CG4186 + CG4186 77E4-77E5 ID:71H2  
 + transporter \* sodium-dependent multi-vitamin transporter(aa) \* anon-100EF-D3 \* 1e-83 unknown \* 3e-50 Similarity to  
 Salmonella sodium/proline symporter (SW:PUTP\_SA [SSF // NA\_SOLUTE\_SYMP\_3] CG8451 GH19970 28F1-28F3 dup:1/2  
 CG8451 ID:72B4

CG10209 + unknown \* [PRO\_RICH] CG10209 GH20077 51D1-51D1 ID:72C8  
+ unknown \* 1e-37 cDNA EST comes from this gene; cDNA EST co \* 3e-49 protein \* predicted protein dJ257A7.2 \*

CG10860 [NLS\_BP] CG10860 GH21062 64C1-64C1 dup:3/3 ID:73D7  
+ ribosomal\_protein \* ribosome recycling factor(aa) \* RRF\_HAEIN RIBOSOME RECYCLING FACTOR (RIBOSOME  
RELEASING FACTOR) (RRF) \* RRF\_CLOPE RIBOSOME RECYCLING FACTOR (RIBOS CG4447 GH21184 67B1-67B1  
CG4447 dup:2/2 ID:73E11  
+ mu2 unknown \* mutator 2(aa) \* mutator \* 4e-06 Pax transcription activation domain interacting protein PTIP \* CG1960

CG1960 GH21591 62B11-62B11 dup:2/2 ID:73H6  
+ ligand\_binding\_or\_carrier \* 4e-59 62D9.a \* 1e-09 cellular retinaldehyde-binding protein; CRALBP \* 3e-14 tocopherol (alpha)  
CG3091 transfer protein (ataxia (Friedreich-like) with \* 3e- [CRAL\_TRIO] CG3091 GH21689 2F1-2F1 ID:74A6  
+ enzyme \* AMIDASE(aa) \* 2e-05 DUR1\_YEAST UREA AMIDOLYASE UREA CARBOXYLASE ; ALLOPHANATE  
HYDROLASE \* 2e-12 similar to amidases \* 1e-24 Glu-tRNA amidotransferas [Amidase] CG5191 GH21739 92E10-92E11 dup:1/3  
CG5191 ID:74A9  
+ unknown \* BLASTX 7.1E-06 Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 4.(dna) \* \*

CG10341 [PRO\_RICH] CG10341 GH23387 37A4-37A4 ID:76B9

CG13773 + enzyme \* 4e-10 match to \* 3e-06 hypothetical protein \* [NLS\_BP] CG13773 GH23590 27C3-27C3 ID:76D12  
+ unknown \* growth factor-responsive protein, vascular smooth muscle - rat(aa) \* 3e-47 Weak similarity with apoptosis protein

CG1114 RP-8; cDNA EST \* SM-20 \* CG1114 GH23732 83A1-83A1 ID:76F11  
+ transcription\_factor \* zinc finger protein 37(aa) \* hkb \* 2e-17 AZF1\_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN

CG8367 AZF1 fin \* 4e-47 zinc finger motif protein [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG8367 GH24215 50E4-50E4 ID:77C11  
+ 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  
CG1605 dup:3/3 ID:77E5  
+ unknown \* 1e-149 inserted at base Unknown 5' end of P element Plasmid rescue \* \* [NLS\_BP] CG7682 GH24605 91A2-  
CG7682 91A2 ID:77G5  
+ unknown \* hypothetical 43.2 kDa protein(aa) \* predicted using Genefinder; Similarity to Yeast hypothetical protein YAE2  
CG7011 (SW:YAE2\_YEAST); cDNA EST comes from t CG7011 GH25868 71B3-71B3 dup:2/2 ID:79C6

CG16724 + tra CG16724 tra dup:2/2 ID:8-31 cntrlBA5

CG9019 + dsf steroid\_hormone\_receptor CG9019 dsf dup:2/2 ID:8-31 cntrlBG1  
+ apt RNA\_binding \* apt \* apontic \* 1e-07 inserted at base 5' end of P element Inverse PCR \* tracheae defective protein

CG5393 [MYB\_3] CG5393 apt 59F1-59F1 dup:2/2 ID:8-31 cntrlBH8

CG10965 + unknown \* CG10965 GH26991 7D21-7D21 ID:80H1  
+ unknown \* 3e-12 YKJ5\_YEAST 32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION \* 1e-64 YS19\_CAEEL

CG15084 HYPOTHETICAL 42.1 KD PROTEIN IN CHROMOSOME III \* 1e-17 unknown \* CG15084 GH26994 55F4-55F4 ID:80H2  
+ yin transporter \* opt1 long(aa) \* 8e-17 PTR2\_YEAST PEPTIDE TRANSPORTER PTR2 (PEPTIDE PERMEASE PTR2) \* 8e-  
74 high-affinity peptide transporter \* 2e-06 cAMP inducible p [PTR2 // PTR2\_1 // PTR2\_2] CG2913 GH27264 4A1-4A1 dup:2/2  
CG2913 ID:81B12

CG8861 + unknown \* CG8861 GH27383 85D7-85D7 ID:81C12  
+ enzyme \* threonyl-tRNA synthetase(aa) \* threonyl-tRNA synthetase (aa 1-734) \* SYTC\_CAEEL PROBABLE THREONYL-  
TRNA SYNTHETASE, CYTOPLASMIC (THREONINE--TRNA LIG [TRNASYNTHTHR // tRNA-synt\_2b // AA\_TRNA] CG5353

CG5353 GH27773 33C1-33C1 ID:81G11  
+ enzyme \* G4 nucleic acid binding protein, involved in tRNA aminoacylation; Arc1p(aa) \* PROBABLE METHIONYL-TRNA

CG8235 SYNTHETASE (METHIONINE--TRNA LIGASE) (METRS)(a CG8235 GH27932 44F9-44F9 ID:82A6  
+ Elf translation\_factor \* Elf \* elongation factor alpha-like factor(aa) \* 1e-141 GST1 \* elongation factor alpha-like factor

CG6382 [ELONGATNFCT // GTP\_EFTU // EFACTOR\_GTP ] CG6382 GM14684 33E-33E dup:1/2 ID:83C5  
+ chaperone \* HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR(aa) \* DNAJ PROTEIN  
HOMOLOG (DROJ1)(aa) \* 1e-06 SCJ1\_YEAST SCJ1 PROTEIN SCJ1 protein [DnaJ // DNAJ\_2] CG9089 LD21896 15B4-15B4  
CG9089 dup:2/2 ID:83E11  
+ 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  
+ Bsg25D motor\_protein \* BSG2\_DROME BLASTODERM SPECIFIC PROTEIN 25D bsg25D protein \* 1e-05 contains similarity

CG14025 to kinesin (PFam: kinesin.hmm, score: 10.52 and 16.62) \* 6e-1 CG14025 LD21844 25D2-25D2 dup:2/2 ID:83E8  
+ Crk signal\_transduction \* v-crk avian sarcoma virus CT10 oncogene homolog(aa) \* CRK protein(aa) \* 3e-10 SEM5\_CAEEL  
SEX MUSCLE ABNORMAL PROTEIN sem-5 protein - \* 2e-63 CRK\_MOU [SH2DOMAIN // SH2 // SH3DOMAIN // SH3] CG1587

CG1587 LD22148 102A1-102A1 ID:83F5  
+ CycE cell\_cycle\_regulator \* DMRNACE\_2 CycE \* 4e-20 CGS5\_YEAST S-PHASE ENTRY CYCLIN cyclin B5 - yeast (Sacc \*  
CG1E\_DROME G1/S-SPECIFIC CYCLIN E cyclin E type I - frui \* 5e-37 c [cyclin // CYCLINS // ATP\_GTP\_A] CG3938 LD22682

CG3938 35D5-35D6 dup:2/2 ID:83G5  
+ par-6 ion\_channel \* PAR-6(aa) \* PAR-6(aa) \* PAR-6(aa) \* dJ850H21.2 (novel protein containing a PDZ (DHR, GLGF)

CG5884 domain)(aa) [PDZ // ATP\_GTP\_A] CG5884 LD22757 16C5-16C5 ID:83G6  
+ MRG15 DNA\_binding \* MRG15(aa) \* MORF-related gene 15(aa) \* 4e-19 hypothetical protein YPR023c - yeast

CG6363 (Saccharomyces cerevisiae) \* 4e-10 predicted using Genefinder; cDN [NLS\_BP] CG6363 LD22902 88E9-88E10 dup:2/2 ID:83H4  
+ knrl steroid\_hormone\_receptor \* ZYGOTIC GAP PROTEIN KNIRPS(aa) \* DMKNR1\_2 knrl \* KNIRPS-RELATED PROTEIN(aa)  
\* 1e-09 contains similarity to C4-type zinc fingers [STROIDFINGER // zf-C4 // NUCLEAR\_RECEPT] CG4761 LD23140 77D1-

CG4761 77D4 ID:84A4  
+ RNA\_binding \* 4e-55 SUV3\_YEAST MITOCHONDRIAL ATP-DEPENDENT RNA HELICASE SUV3 PRECURSOR \* 1e-151

CG9791 Similarity to Yeast ATP-dependent RNA helicase (SW:SUV3\_YEAST); cD [helicase\_C] CG9791 LD23445 82A5-82A5 ID:84B12

CG6712 + unknown NLS\_BP CG6712 LD23405 dup:2/2 ID:84B8  
+ La RNA\_binding \* LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)(aa) \* La \*  
LUPUS LA PROTEIN (SJOGREN SYNDROME TYPE B ANTIGEN (SS-B)) (LA RIBONUCL [RNP\_1 // RBD // rrm // NLS\_BP //

CG10922 LUPUSL] CG10922 LD24519 38C7-38C7 ID:84C12

CG11403 + DNA\_repair\_protein CG11403 LD24267 dup:2/2 ID:84C8  
+ transcription\_factor \* 8e-11 YGJ6\_YEAST HYPOTHETICAL 31.3 KD HOMEBOX PROTEIN IN PRP20-VPS45

CG8819 INTERGENIC REGI \* 6e-13 homothorax dorsotonal \* 4e-08 CEH-25 homeobox protein [HOMEBOX\_2 // NLS\_BP] CG8819

LD25085 49A10-49A10 ID:84D12

CG2446 + unknown \* 1e-133 inserted at base Both 5' and 3' ends of P element Inverse PCR \* 1e-133 inserted at base Both 5' and 3' ends of P element Inverse PCR \* CG2446 LD24866 10D4-10D5 dup:2/2 ID:84D4

CG6854 + enzyme \* 1e-171 CTP synthase (EC 6.3.4.2) URA8 - yeast (*Saccharomyces cerevisiae*) \* 1e-147 similar to CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP \* [GATase // GATASE\_TYPE\_I]) CG6854 LD25005 71B2-71B2 dup:2/6 ID:84D5

CG10390 + transcription\_factor \* TATA box binding protein (TBP)-associated factor, RNA polymerase II, E, 70/85kD(aa) \* TAFII60(aa) \* 8e-48 transcription factor TFIID \* 2e-15 contain CG10390 LD25013 83B2-83B2 ID:84D6

CG10267 + transcription\_factor CG10267 dup:2/2 ID:84E4

CG2275 + Jra transcription\_factor \* DMJUN\_2 Jra \* 1e-139 AP1\_DROME TRANSCRIPTION FACTOR JUN (DJUN) (DJRA) (JUN-RELATED ANTIGEN) (AP-1) >g \* 1e-07 similar to BZIP protein; cDNA[LEUZIPPRJUN // B\_ZIP // bZIP // BZIP\_BA] CG2275 LD25202 46E2-46E2 dup:2/2 ID:84E7

CG3297 + mnd transporter \* minidisks(aa) \* 1e-23 MUP1\_YEAST HIGH AFFINITY METHIONINE PERMEASE methionine \* 1e-105 strong similarity to Schistosoma amino acid permease \* 1e-120 [aa\_permeases // AMINO\_ACID\_PERMEASE\_2] CG3297 LD25378 71A2-71A3 ID:84F8

CG5776 + endopeptidase \* Tat-binding protein-1(aa) \* 1e-112 AFG2\_YEAST AFG2 PROTEIN valosin-containing protein homolo \* 1e-60 smallminded \* 3e-97 TER1\_CAEEL TRANSITIONAL END [AAA // ATP\_GTP\_A] CG5776 LD25466 33F2-33F2 ID:84G1

CG10545 + Gbeta13Fsignal\_transduction \* HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHROMOSOME V(aa) \* Miller-Dieker lissencephaly gene(aa) \* HYPOTHETICAL WD-REPEAT[GPROTEINBRPT // GPROTEINB // WD40\_REGIO] CG10545 LD25526 13F5-13F5 ID:84G4

CG18145 + unknown \* mitochondrial and cytoplasmic fumarase (fumarate hydratase); Fum1p \* FUMARATE HYDRATASE, MITOCHONDRIAL PRECURSOR (FUMARASE) \* Contains similarity to CG18145 31B-31B dup:2/2 ID:85C2

CG2158 + structural\_protein \* 7e-06 bK217C2.1 (Rat RTP60 (nuclear pore complex protein Npap60) isolog) \* 4e-11 RTP60 \* [Ran\_BP1 // RAN\_BP1 // RANBP1\_WASP] CG2158 LD26583 44A7-44A7 dup:3/3 ID:85F12

CG17018 + unknown CG17018 LD26456 dup:1/2 ID:85F2

CG9925 + unknown \* [PRO\_RICH] CG9925 LD26515 88A4-88A4 dup:2/3 ID:85F6

CG12234 + unknown exportin CG12234 LD26789 dup:1/2 ID:85G12

CG7824 + unknown \* unknown(aa) \* 2e-14 unknown \* \* [PPASE // NLS\_BP] CG7824 LD26655 99C6-99C7 ID:85G3

CG14100 + unknown \* 6e-11 hypothetical protein \* hypothetical protein \* YG73\_SYNY3 HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE \* [SpoU\_methylase] CG14100 LD26903 76B9-76B9 dup:1/2 ID:85H9

CG9201 + unknown \* [THIOREDOXIN] CG9201 LD26971 13D2-13D2 ID:86A3

CG1034 + bcd transcription\_factor \* DNA-binding-protein,transcription-factor(aa) \* DMBCDG\_3 bcd \* 1e-125 bcd protein \* 8e-52 homeotic protein bicoid - fruit fly (*Drosophila* ps[RNP\_1 // HOMEBOX\_1 // homeobox // HOME] CG1034 LD27003 84D1-84D1 dup:1/2 ID:86A8

CG5452 + dnk enzyme \* 1e-145 deoxynucleoside kinase \* 2e-31 DCK\_MOUSE DEOXYCYTIDINE KINASE (DCK) deoxycytidine kina \* 1e-49 thymidine kinase \* 2e-30 DCK\_RAT DEOXYCYTIDINE [ATP\_GTP\_A] CG5452 94A3-94A3 dup:2/2 ID:86C1

+ enzyme \* *Drosophila melanogaster* P lethal line *Drosophila melanogaster* genomic Sequence recovered from 5' end of P element, genomic survey sequence(dna) \* IS [tRNA-synt\_1 // AA\_TRNA\_LIGASE\_I // TRNA] CG11471 LD27166 79E2-79E2  
 CG11471 dup:1/2 ID:86C7  
 CG7396 + unknown \* [PPASE // NLS\_BP] CG7396 LD27215 71E1-71E1 dup:2/2 ID:86D3  
 CG4790 + unknown \* CG4790 LD27288 5C8-5C9 ID:86D8  
 + unknown \* O1(aa) \* 2e-31 predicted protein of unknown function thal \* \* [NLS\_BP] CG6066 LD27582 97E8-97E8  
 CG6066 ID:86F10  
 + unknown \* predicted using Genefinder; Similarity in 3' end to Human protein cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from CG9986 LD27564 98D4-98D4 ID:86F8  
 CG9986 + protein\_phosphatase \* PROTEIN PHOSPHATASE 2C GAMMA ISOFORM (PP2C-GAMMA) (FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 13) (FIN13)(aa) \* PROTEIN PHOSPHATASE 2C GAMMA ISOFORM [PP2C\_1 // PP2C // PP2C\_2] CG10417 LD27655 41D1-41D1 ID:86G1  
 CG10417 + Ckl1alpha protein\_kinase \* 1e-103 KC21\_YEAST CASEIN KINASE II, ALPHA CHAIN (CK II) casein ki \* KC2A\_DROME CASEIN KINASE II, ALPHA CHAIN (CK II) casein kina \* 1e-151 KC2A\_CAE[PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM]  
 CG17520 CG17520 LD27706 cyto\_unknown ID:86G9  
 + transcription\_factor \* CROL ALPHA(aa) \* zinc finger protein 207(aa) \* predicted using Genefinder; similar to Zinc finger, C2H2 type; cDNA EST comes from this gene; cDNA E CG17912 LD27810 36A7-36A8 dup:3/3 ID:86H6  
 CG17912 + zimp nucleic\_acid\_binding \* map\_position:45A4-8 \* Zimp-A(aa) \* 2e-19 NFI1\_YEAST NFI1 PROTEIN NFI1 protein - yeast  
 CG8068 (Saccharom \* 6e-43 cDNA EST comes from this gene; cDNA EST co CG8068 LD27861 45A13-45B1 dup:1/5 ID:87A1  
 CG8068 + sl enzyme \* 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) gamma-D - fruit fly (*Drosophila melanogaster*)(aa) \* DMCS\_2 sl \* phospholipa [PHPHLIPASEC // SH2DOMAIN // C2 // PIPLC] CG4200 LD27939 14B18-14C1  
 CG4200 ID:87A7  
 + receptor \* 4e-16 VT11\_YEAST VESICLE TRANSPORT V-SNARE PROTEIN VT11 proba \* 3e-27 cDNA EST yk433f11.3  
 CG3279 comes from this gene; cDNA EST yk433f11.5 come \* 3e-32 put CG3279 LD27967 61C9-61C9 dup:1/3 ID:87A9  
 CG3279 + enzyme\_activator \* 1e-29 YQK1\_CAEEL HYPOTHETICAL 55.9 KD PROTEIN C56G2.1 IN CHROMOSOME III (U \* 6e-32  
 CG3249 AKAP121 \* 9e-33 A kinase anchor protein, 149kD \* 9e-35 A-kinase a [TUDOR] CG3249 LD28079 4F8-4F9 dup:2/3 ID:87B11  
 CG9924 + actin\_binding CG9924 LD28030 dup:2/2 ID:87B2  
 CG9924 + unknown \* \* 1e-05 HR12\_MOUSE HEAT-RESPONSIVE PROTEIN heat-responsive prot \* 7e-05 UK14\_HUMAN 14.5 KD  
 CG1578 TRANSLATIONAL INHIBITOR PROTEIN (P14.5) (UK114 ANTIGEN H [UPF0076 // PROTEIN\_KINASE\_ATP] CG1578 LD28359  
 CG1578 10E3-10E4 dup:4/5 ID:87D12  
 CG7275 + signal\_transduction transducin (beta) like 1 protein GPROTEINBRPT, WD40 CG7275 LD28275 dup:2/3 ID:87D5  
 CG7275 + G\_protein\_linked\_receptor \* Dfz2(aa) \* 1e-32 transmembrane receptor \* 2e-60 transmembrane receptor \* 1e-43 frizzled  
 CG4626 (*Drosophila*) homolog frizzled homo [Fz // FRIZZLED] CG4626 LD28410 6F5-6F5 dup:2/2 ID:87E9  
 CG17033 + CG17033 ID:87H8  
 CG1218 + CG1218 ID:87H9  
 CG12132 + unknown \* 7e-30 C34G6.1 gene product \* CG12132 8D8-8D8 dup:1/3 ID:88C6

CG11177 + CG11177 ID:88C8  
 CG8116 + unknown \* 1e-108 inserted at base 3' end of P element Inverse PCR \*\* CG8116 85B2-85B2 dup:1/2 ID:88D7  
 CG13849 + unknown CG13849 dup:2/2 ID:88E12  
 CG17138 + CG17138 dup:2/2 ID:88G10  
 CG16901 + CG16901 ID:88G12  
 + structural\_protein \* 0.000000000006\* 2e-06 nonmuscle myosin-II heavy chain \* 2e-07 Identity to myosin heavy chain C  
 CG12702 (SW:MYSC\_CAEEL); cDNA EST EMBL:M8 \* 0.0000001 CG12702 18F1-18F2 dup:1/3 ID:88G4  
 + P34-ARC actin\_binding PROBABLE ARP (actin related protein) 2/3 COMPLEX 34 KDA SUBUNIT CG10954 LD29815 dup:2/3  
 CG10954 ID:89C2  
 + transcription\_factor \* 4e-30 alternatively spliced form \* 4e-07 BAC1\_MOUSE TRANSCRIPTION REGULATOR PROTEIN  
 CG8924 BACH1 (BTB AND CNC HOMOLOG 1) \* 2e-07 actin binding protein MAYV [BTB] CG8924 LD29820 13F14-13F14 ID:89C4  
 + Nop60B enzyme \* CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5 (CENTROMERE-BINDING FACTOR 5)  
 (NUCLEOLAR PROTEIN CBF5)(aa) \* major low affinity kDa Centromere/microtubu CG3333 LD30073 60B10-60B10 dup:4/4  
 CG3333 ID:89E9  
 CG12050 + unknown unknown protein [Arabidopsis thaliana] NLS\_BP, WD40\_REGION CG12050 LD30416 dup:2/2 ID:89H12  
 + ribosomal\_protein \* cDNA EST yk433f11.3 comes from this gene; cDNA EST yk433f11.5 comes from this gene(aa) \* 9e-05  
 CG5108 YJ83\_YEAST PUTATIVE 40S RIBOSOMAL PROTEIN YJR113C pro [Ribosomal\_S7] CG5108 LD35371 31D11-31D11 ID:95A3  
 + actin\_binding \* erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)(aa) \* DMP41A\_4 cora \* 2e-55 product  
 of alternative splicing; homologue to membra [BAND\_41\_1 // Band\_41 // BAND41 // BAND\_] CG9764 LD35542 89A1-89A1  
 CG9764 ID:95B4  
 + E2f transcription\_factor \* E2f \* E2F \* 1e-19 predicted using Genefinder; cDNA EST comes from this \* 5e-35 E2F3\_MOUSE  
 CG6376 TRANSCRIPTION FACTOR E2F3 (E2F-3) transcripti [NLS\_BP] CG6376 LD35741 93F1-93F1 dup:2/3 ID:95C12  
 + unknown \* BLASTX 1.2E-22 Human YL-1 mRNA for YL-1 protein (nuclear protein with DNA-binding ability), complete  
 CG4621 cds.(dna) \* transcription factor-like 1(aa) \* t [NLS\_BP] CG4621 LD35676 34A3-34A3 ID:95C3  
 CG7705 + unknown \* CG7705 LD35690 91B7-91B8 ID:95C5  
 + Arp66B cytoskeletal\_structural\_protein \* DMACTR66B\_2 Arp66B \* 1e-126 ARP3\_YEAST ACTIN-LIKE PROTEIN ARP3 actin  
 homolog YJR065 \* ARP3\_DROME ACTIN-LIKE PROTEIN (ACTIN-LIKE PROTEIN 66B) (ACTIN [ACTINS\_ACT\_LIKE // actin]  
 CG7558 CG7558 LD35711 66B8-66B8 ID:95C9  
 + unknown \* 8e-73 YIJ1\_YEAST HYPOTHETICAL 84.0 KD PROTEIN IN SGA1-KTR7 INTERGENIC REGION \* 1e-119  
 CG3735 dJ434O14.5 (novel PUTATIVE protein similar to YIL091C yeast hy CG3735 LD35854 60A11-60A11 ID:95D10  
 + Bub1 enzyme \* Bub1 \* 4e-75 hypothetical protein YLR419w - yeast (Saccharomyces cerevisiae) (U \* DDX9\_CAEEL  
 PROBABLE ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HEL [PROTEIN\_KINASE\_ST // pkinase // PROTEIN]  
 CG7838 CG7838 LD35813 42A1-42A1 ID:95D5  
 + defense/immunity\_protein \* 1e-101 inserted at base Both 5' and 3' ends of P element Inverse PCR \*\* CG8187 LD35843  
 CG8187 52A10-52A10 ID:95D8  
 CG3594 + RNA\_binding \* 8e-06 hypothetical protein YPR112c - yeast (Saccharomyces cerevisiae) (U \* 1e-05 similar to RNA

recognition motif. (aka RRM, RBD, or RNP domain); c [RBD // rrm // NLS\_BP] CG3594 LD36016 60D15-60D15 dup:2/2 ID:95E12  
+ unknown \* dimethylase(aa) \* 2e-97 DIM1\_YEAST DIMETHYLADENOSINE TRANSFERASE (S-ADENOSYLMETHIONINE-6-N', N'-ADENOSY \* 4e-99 YQN1\_CAEEL HYPOTHETICAL 34.1 KD PROT [RrnaAD // RRNA\_A\_DIMETH // SAM\_BIND]

CG11837 CG11837 LD35950 98F9-98F9 dup:2/2 ID:95E6  
+ motor\_protein \* 6e-08 F35D11.11 gene product \* YL17\_CAEEL HYPOTHETICAL 131.5 KD PROTEIN C02F12.7 IN

CG17081 CHROMOSOME X ( \* [NLS\_BP] CG17081 LD35990 71B2-71B2 dup:3/3 ID:95E9

CG1943 + unknown \* CG1943 LD36048 84C1-84C1 ID:95F5

CG4454 + unknown \* CG4454 LD36125 32A1-32A1 dup:2/3 ID:95G2  
+ unknown \* HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III(aa) \* similar to Zinc finger, C3HC4 type

CG15814 (RING finger); cDNA EST EMBL:D7 \* [zf-C3HC4 // ZF\_RING] CG15814 16D6-16D6 dup:3/3 ID:95H12

CG1918 + \* [PHOSPHOPANTETHEINE // ANTIFREEZE] CG1918 43F4-43F4 ID:96A9  
+ Dlc90F motor\_protein \* Tctex protein(aa) \* DMTCTEXPR\_2 Tctex \* 1e-61 Tctex protein \* 7e-14 predicted using Genefinder;

CG12363 cDNA EST yk460f12.5 comes from this ge CG12363 LD36705 90F7-90F7 ID:96B11  
+ 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

CG4831 32E4-32E4 ID:96D1  
+ thr unknown \* three rows protein \* thr \* THR\_DROME THREE ROWS PROTEIN chromosome disjunction prot [NLS\_BP]

CG5785 CG5785 LD37031 54F5-54F6 dup:2/2 ID:96D10

CG13626 + unknown \* 1e-05 No definition line found \* [T\_SNARE] CG13626 LD37002 96A14-96A14 ID:96D6

CG6144 + unknown \* predicted using Genefinder(aa) \* \* CG6144 LD37206 31E4-31E4 dup:2/2 ID:96E12  
+ cell\_cycle\_regulator \* cut4+(aa) \* subunit of ubiquitin- protein ligase; Apc1p(aa) \* predicted using Genefinder; cDNA EST

CG9198 comes from this gene; cDNA EST comes from this g [APC\_SEN3\_REPEAT] CG9198 LD37115 13D1-13D2 dup:2/2 ID:96E2

CG5541 + unknown \* [C\_TYPE\_LLECTIN\_1] CG5541 LD37145 13A8-13A8 dup:3/3 ID:96E6

CG8825 + unknown \* 3e-18 Contains similarity to Pfam domain: (PLDc), Score=13.8, \* \* CG8825 LD37277 23D4-23D4 ID:96F12  
+ unknown \* kDa silk protein(aa) \* VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR

CG7103 PERMEABILITY FACTOR) (VPF)(aa) \* platelet-derived growth facto CG7103 LD37208 17E1-17E2 dup:2/9 ID:96F2  
+ transporter \* 4e-09 maltose permease - Bacillus stearothermophilus maltose pe \* transcription factor IIE - African clawed

CG7334 frog \* TfIIIE&agr; CG7334 LD37218 68C13-68C13 ID:96F3  
+ fs(1)K10DNA\_binding \* regulatory protein K10, oocyte-specific - fruit fly (Drosophila melanogaster)(aa) \* DMK10G\_4 fs(1)K10 \*

CG3218 4e-58 K10\_DROME DNA-BINDING PROTEIN K10 \* 62 [PRO\_RICH] CG3218 LD37240 2F1-2F1 ID:96F7  
+ unknown \* 8e-08 predicted using Genefinder; similar to WW domain \* 1e-07 inserted at base Both 5' and 3' ends of P

CG8949 element Inverse PCR \* [WW\_rsp5\_WWP // WW\_DOMAIN\_1 // NLS\_BP //] CG8949 15D1-15D1 ID:96G10  
+ function\_unknown \* 2e-05 hypothetical protein YDL115c - yeast (Saccharomyces cerevisiae) \* 5e-09 hypothetical protein \*

CG10528 2e-43 inserted at base 5' end of P element Inve CG10528 LD37329 38A-38A4 dup:1/3 ID:96G3  
+ unknown \* No definition line found(aa) \* 3e-40 hypothetical protein YER007c-a - yeast (Saccharomyces cerevisiae) \* 3e-58

CG5941 No definition line found \* 3e-39 hypo CG5941 LD37358 5D1-5D1 ID:96G7



CG6311 + unknown \* CG6311 LD37618 74D2-74D2 dup:1/2 ID:96H12  
+ enzyme \* protein(aa) \* 3e-37 PAN2\_YEAST PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN2  
(PAB1P-DEPE \* 4e-59 YPO4\_CAEEL HYPOTHETICAL 127.2 KD PROTEIN [UCH\_2\_3 // Exonuclease] CG8232 LD37466 44F9-  
CG8232 44F11 dup:1/4 ID:96H2  
+ RNA\_binding \* \* 3e-33 cDNA EST yk500a3.3 comes from this gene; cDNA EST yk500a3.5 comes \* 2e-64 inserted at base  
CG2503 Unknown 5' end of P element Plasmid rescue \* CG2503 LD37523 82E1-82E1 ID:96H6  
CG10978 + \* 2e-14 cDNA EST yk448c11.3 comes from this gene; cDNA EST com \* \* CG10978 83C-83C dup:2/4 ID:97A5  
CG2669 + unknown \* [NLS\_BP] CG2669 LD38047 83A4-83A5 ID:97C12  
+ unknown \* member of major facilitator superfamily; Cdc91p(aa) \* 6e-41 CC91\_YEAST CELL DIVISION CONTROL  
CG13089 PROTEIN cell divisio \* 4e-13 similar to cell division c CG13089 LD37974 29D1-29D1 ID:97C4  
+ transcription\_factor \* Cys2/His2 zinc finger protein(aa) \* ovo \* fruit fly STS clone SP6(dna) \* zinc finger protein NY-REN-21  
CG4639 antigen(aa) [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG4639 LD38072 94E-94E ID:97D4  
CG8928 + unknown \* CG8928 LD38104 13F14-13F14 ID:97D7  
+ transcription\_factor \* DMPLYCMB\_2 Pcl \* BLASTX 2.1E-16 element DNA-binding protein(dna) \* polycomblake nuclear  
CG5109 protein [PHD // PRO\_RICH] CG5109 LD38218 55B5-55B7 dup:3/3 ID:97E2  
+ su(f) DNA\_binding \* 2e-47 RN14\_YEAST MRNA 3'-END PROCESSING PROTEIN RNA14 RNA14 p \* SUF\_DROME  
SUPPRESSOR OF FORKED PROTEIN gene su(f) protein \* cleavage stimulation fa [NLS\_BP] CG17170 LD38348 cyto\_unknown  
CG17170 ID:97F2  
CG8180 + unknown \* 1E-178 \* \* [ANTIFREEZEI] CG8180 LD38554 52A4-52A4 dup:1/2 ID:97G8  
+ unknown \* weak similarity to ATP/GTP-binding site motif A \* 2e-40 weak similarity to ATP/GTP-binding site motif A elega \*  
CG5924 1e-63 POM1 chabaudi \* [ATP\_GTP\_A] CG5924 LD38710 33A1-33A1 dup:1/2 ID:97H9  
+ ubiquitin \* 2e-11 ubiquitin-like protein DSK2 - yeast (Saccharomyces cerevisiae) \* 1e-76 similar to Ubiquitin family; cDNA  
CG14224 EST comes from this \* 1E-61 \* 1e-58 pu [UBA // ubiquitin // UBIQUITIN\_2] CG14224 LD38919 18D13-18D13 dup:3/4 ID:98B11  
+ motor\_protein \* rabaptin-4(aa) \* CLIP-190 \* weak similarity to rodlike tail domain of myosin heavy chain(aa) \* 8e-17  
CG4030 NUF1\_YEAST NUF1 PROTEIN (SPINDLE POLY BODY SPA CG4030 LD38884 57C-57C ID:98B6  
+ chromatin\_binding \* hypothetical protein - human (fragment)(aa) \* UVB-resistance protein UVR8(aa) \* 8e-06 RCC\_YEAST  
REGULATOR OF CHROMOSOME CONDENSATION (PRP20 [RCC1 // RCC1\_2 // GRF\_RCC // RCCNDNSATI] CG6678  
CG6678 LD39062 93F10-93F10 dup:2/2 ID:98C4  
+ transcription\_factor\_binding \* Ydr324cp(aa) \* 1e-25 hypothetical protein YDR324c - yeast (Saccharomyces cerevisiae) (U \*  
CG5018 3e-29 hypothetical protein \* 7e-05 DMENHSPA\_3 gro [WD40\_REGION] CG5018 LD39110 72D11-72D12 ID:98C8  
+ unknown \* 5e-40 prediabetic NOD sera-reactive autoantigen muscul \* 5e-10 IVR-like protein \* IVR-like protein \*  
CG14444 [TPR\_REGION // TPR\_REPEAT] CG14444 LD39177 6C1-6C1 dup:3/3 ID:98D4  
CG14764 + unknown \* CG14764 LD39211 43F6-43F6 ID:98D5  
+ asf1 cell\_cycle\_regulator \* involved in silencing; Asf1p(aa) \* Similarity with yeast anti-silencing protein I (Swiss Prot accession  
CG9383 number cDNA EST comes from this gene; cDNA CG9383 LD39377 76C1-76C1 dup:2/2 ID:98E8  
CG1896 + unknown \* [NLS\_BP] CG1896 LD39576 100E2-100E2 dup:2/2 ID:98F12

+ mod DNA\_binding \* DNA-BINDING PROTEIN MODULO(aa) \* DMLA9\_4 mod \* 3e-05 Similarity to Human spliceosome-associated protein SAP62 (PIR Acc. \* 5e-05 NUCL\_MOUSE NUCLEOLIN [RBD // rrm // NLS\_BP // ATP\_GTP\_A] CG2050 100F5-100F5 dup:3/3 ID:98F9  
 CG2050 + BcDNA:LD27873 actin\_binding \* 1e-06 RNA-binding protein \* 1e-06 NAB2\_YEAST NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2 \* 3e-88 inserted at base Both 5' and 3' ends of P eleme [NLS\_BP] CG5720 95F-98B1 dup:5/8 ID:98G12  
 CG5720 + transporter \* minidisks(aa) \* 3e-26 MUP1\_YEAST HIGH AFFINITY METHIONINE PERMEASE methionine \* 1e-110 Similarity to Human membrane protein E16 (SW:E16\_HUMAN); cDNA [aa\_permeases // AMINO\_ACID\_PERMEASE\_2] CG12317 LD39658 33B12-33B13 ID:98G7  
 CG12317 + EG:95B7.7 transcription\_factor \* /motif=(desc;; /motif=(desc;; /motif=(desc;; /match=(desc:(aa) \* /motif=(desc;; /motif=(desc;; /motif=(de \* 3e-29 similar to Zinc finger, C2H2 type[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG2712 LD39664 3B6-3B6 ID:98G8  
 CG2712 + Dp transcription\_factor \* DMDPRTF\_2 Dp \* transcription factor \* 6e-59 similar to transcription factor DP-1; cDNA EST comes f \* 5e-72 TDP1\_MOUSE TRANSCRIPTION FACTOR DP-1 (E2F CG4654 LD39905 49F13-49F13 dup:2/2 ID:99A2  
 CG4654 + enzyme \* putative serine protease-like protein(aa) \* weakly similar to human placental protein precursor (SP:PP11\_HUMAN)(aa) \* placental protein (serine pro CG3303 LD39912 89A13-89B1 ID:99A3  
 CG3303 + motor\_protein \* 8e-22 putative \* 4e-19 microtubule binding protein D-CLIP-190 \* 3e-36 predicted using Genefinder \* 1e-10 rho/rac-interacting citron kinase [SPEC\_REPEAT // NLS\_BP // CYTOCHROME\_C] CG12734 LD40094 63B13-63B13 dup:2/2 ID:99B10  
 CG12734 + \* similar to S. cerevisiae nitrogen permease regulator \* G21 protein(aa) \* homologous to yeast nitrogen permease (candidate tumor suppressor)(aa) \* 3e CG9104 15A11-15B1 dup:1/2 ID:99C3  
 CG9104 CG9866 + unknown \* CG9866 LD40170 22E-22E ID:99C4  
 CG9866 + unknown \* ilvB (bacterial acetolactate synthase)-like(aa) \* BLASTX 4.8E-22 YEL020C|Protein with similarity to oxalyl-CoA decarboxylase from Oxalobacter formig [TPP\_enzymes // TPP\_ENZYMES] CG11208 LD40177 56F14-56F14 ID:99C5  
 CG11208 + gammaTub23C cytoskeletal\_structural\_protein \* similar to Tubulin (2 domains); cDNA EST CEMSG51F comes from this gene(aa) \* gamma-tubulin 3(aa) \* TUBULIN ALPHA-4 CHAIN(aa) \* DMTUBA4\_2 agr;Tub67C [TUBULIN // tubulin] CG3157 LD40196 23C2-23C2 ID:99C6  
 CG3157 CG8374 + dmt unknown \* [NLS\_BP] CG8374 LD40216 85E5-85E5 ID:99C7  
 CG8374 CG13840 + CG13840 LD40283 ID:99D4  
 CG13840 + 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 64A10-64A10 dup:2/2 ID:99E11  
 CG14999 + fs(1)Ya cell\_cycle\_regulator \* mitosis initiation protein fs(1)Ya - fruit fly (Drosophila melanogaster)(aa) \* FSYA\_DROME MITOSIS INITIATION PROTEIN FS(1)YA fs(1)Ya prote \* DMFS1Y [ZINC\_FINGER\_C2H2] CG2707 LD40381 3B6-3B6 dup:2/2 ID:99E2  
 CG2707 + 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  
 CG9633

dup:4/4 ID:99E5

+ unknown \* 5e-70 weak similarity to HSP90 \* 1e-05 YXAA\_BACSU HYPOTHETICAL 37.5 KD PROTEIN IN GNTR-HTPG

CG2982 INTERGENIC REGION \* CG2982 LD40453 4B5-4B5 dup:2/2 ID:99E8

+ M(2)21ABenzyme \* 1e-88 METK\_YEAST S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE 1) \* 1e-142 METK\_DROME S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE

CG2674 [ADOMET\_SYNTHETASE\_1 // ADOMET\_SYNTHETAS] CG2674 LD40460 21B-21B dup:2/2 ID:99E9

+ RNA\_binding \* DMB52\_2 B52 \* ASF/SF2 homolog(aa) \* nuclear phosphoprotein SRp55 - fruit fly (Drosophila melanogaster)(aa) \* dJ862K6.2.1 (splicing factor, (SRP55-1) [RBD // rrm] CG6987 LD40489 89B21-89B21 dup:2/3 ID:99F1

CG6987 + DNA\_binding \* 9e-09 ssrp2 \* 4e-09 contains similiarity to HMG boxes \* 3e-19 mitochondrial transcription factor A \* 6e-27

CG4217 transcription factor 6-like (mitochondria [HMG // HMG\_box // NLS\_BP] CG4217 LD40493 92E11-92E11 ID:99F2

+ signal\_transduction \* Caf1 \* Nle \* Taf80 \* 5e-13 T2D4\_YEAST TRANSCRIPTION INITIATION FACTOR TFIID KD

CG6724 SUBUNIT (TAFII-90) [GPROTEINBRPT // WD40\_REGION // WD\_REPEA] CG6724 LD40657 32A5-32A5 ID:99G1

+ RNA\_binding \* Bub3 \* WD-40 repeat protein(aa) \* HYPOTHETICAL 41.4 KD TRP-ASP REPEATS CONTAINING PROTEIN F10G8.3 IN CHROMOSOME I(aa) \* HYPOTHETICAL RAE1-LIKE PROTE [GPROTEINBRPT // WD40\_REGION // WD\_REPEA]

CG9862 CG9862 LD40776 57F6-57F6 ID:99G12

+ unknown \* HYPOTHETICAL 96.2 KD PROTEIN C08B11.4 IN CHROMOSOME II(aa) \* predicted using Genefinder(aa) \*

CG8185 3e-05 /match=(desc: \* 7e-38 cDNA EST comes from this CG8185 LD40680 52A9-52A10 dup:1/2 ID:99G3

+ RNA\_binding \* 1e-89 ROK1\_YEAST ATP-DEPENDENT RNA HELICASE ROK1 ATP-dependen \* 1e-41 VASA\_DROME VASA PROTEIN vasa mel \* 1e-81 similar to ATP dependent RNA helicase [helicase\_C // HELICASE // DEAD // NLS\_B] CG5589

CG5589 LD40692 75A2-75A2 dup:1/3 ID:99G4

+ unknown \* hypothetical protein(aa) \* 6e-71 inserted at base Both 5' and 3' ends of P element Inverse PCR \* [NLS\_BP]

CG2162 CG2162 LD40717 63B4-63B5 dup:2/2 ID:99G7

+ enzyme \* Yjr084wp(aa) \* acyl-protein thioesterase(aa) \* 1e-22 probable membrane protein YLR118c - yeast

CG7351 (Saccharomyces cerevisiae) \* 3e-67 YPI7\_CAEEL HYPOTH [TNF\_1] CG7351 LD40777 68C10-68C10 dup:2/3 ID:99H1

+ unknown \* 7e-41 SS72\_YEAST SSU72 PROTEIN hypothetical protein YNL222w - \* 7e-57 coded for by C. elegans cDNA

CG14216 yk10c10.3; coded for by C. elegans cDNA yk37e8.3; CG14216 LD40846 18D12-18D12 ID:99H10

+ \* BLASTX 2.3E-13 TRA1|Homolog of human TR-AP which associates with a domain of c-Myc essential for cellular

CG2905 transformation(dna) \* predicted using Gen [PI3\_4\_KINASE\_3] CG2905 41A1-41A1 ID:99H3

+ sec23 unknown \* COPII protein, homolog of s. cerevisiae SEC23p(aa) \* SC23\_YEAST PROTEIN TRANSPORT PROTEIN

CG1250 SEC23 protein transpo \* S23A\_MOUSE PROTEIN TRANSPORT PRO CG1250 LD40826 83B6-83B6 dup:3/4 ID:99H8

CG13398 + CG13398 SNT ID:Farhad's BA7

CG3411 + CG3411 dSRF dup:1/2 ID:Path + CtrlL1 + kras113

CG3375 + CG3375 stumps dup:1/4 ID:Path + CtrlL1 + kras115

CG3619 + cell\_adhesion CG3619 Delta dup:2/4 ID:Path + CtrlL1 + kras195

CG8049 + protein\_kinase CG8049 Tec29 dup:3/3 ID:Path + CtrlL1 + kras350