

Table S29

female somatic genes identified as follows:

two-ANOVA (sex as independent factor, $P < .001$, wt female data > wt male data) and female tudor vs male tudor (one-tailed T-test, $P < .01$) and female tudor data must be 2X male tudor data

+ unknown * Similar to a C.elegans protein encoded in cosmid C27F2 * RW1 protein(aa) * $3e-57$ coded for by C. elegans
CG8370 cDNA yk86c6.3; coded for by C. elegans cDNA [NLS_BP] CG8370 LD47858 52E1-52E1 dup:2/2 ID:107A9
+ ligand_binding_or_carrier * retinaldehyde-binding protein 1(aa) * ALPHA-TOCOPHEROL TRANSFER PROTEIN (ALPHA-TTP)(aa) * $8e-07$ SC14_YEAST SEC14 CYTOSOLIC FACTOR (PHOSPHATIDYLINOSI [CRETINALDHBP // CRAL_TRIO] CG5958
CG5958 LP02316 27F7-27F7 ID:108A6
+ Cyp1 chaperone * DMCYP1_2 Cyp1 * $1e-63$ CYPH_YEAST PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) * $2e-93$ CYPH_DROME PEPTIDYL-PROLYL CIS-TRANS[pro_isomerase // CSA_PPIASE_1 // CG9916
CG9916 CSA_PP] CG9916 LP04479 14B15-14B15 dup:1/2 ID:109A7
+ Pgk protein_kinase * 3-phosphoglycerate kinase; Pgk1p(aa) * DMPGKG_2 Pgk * PHOSPHOGLYCERATE KINASE(aa) * $1e-136$ PGK_YEAST PHOSPHOGLYCERATE KINASE 3-phosphoglycerate kina [PGK // PGLYCERATE_KINASE // PHGLYCKINAS]
CG3127 CG3127 23A7-23A7 dup:2/3 ID:109G12
CG10652+ CG10652 ID:35A1
+ ribosomal_protein * Similar to 40S ribosomal protein S29; coded for by C. elegans cDNA cm10c2; coded for by C. elegans cDNA yk61d8.5; coded for by C. elegans cDNA yk10 [RIBOSOMAL_S14 // Ribosomal_S14] CG8495 GH07263 86D1-86D1 dup:1/2
CG8495 ID:35C1
+ ribosomal_protein * ribosomal protein L10a(aa) * 60S RIBOSOMAL PROTEIN L10A (CSA-19)(aa) * 60S RIBOSOMAL PROTEIN L10A(aa) * $2e-06$ predicted using Genefinder; Weak simil [Ribosomal_L1] CG7283 GH13356 68D3-68D3 dup:3/3
CG7283 ID:40E11
CG18525+ unknown * CG18525 GH14439 88E7-88E7 dup:2/2 ID:41E4
+ RpL7 ribosomal_protein RL7_DROME 60S RIBOSOMAL PROTEIN L7 CG4897 Ribosomal_L30, THIOL_PROTEASE_HIS
CG4897 ID:60C3
+ enzyme * spermidine synthase(aa) * SPERMIDINE SYNTHASE (PUTRESCINE AMINOPROPYLTRANSFERASE) (SPDSY)(aa) * $1e-77$ SPEE_YEAST SPERMIDINE SYNTHASE (PUTRESCINE AMI [SAM_BIND // ATP_GTP_A] CG8327
CG8327 GH08387 85E2-85E2 dup:2/3 ID:60F4
CG8403 + SP2353 cell_adhesion agrin-like ATP_GTP_A, EGF, EGF_1, EGF_2, LAM_G_DOMA] CG8403 GH09608 dup:1/3 ID:61G12
+ gbb signal_transduction * DM60AP * 60A PROTEIN PRECURSOR(aa) * $9e-17$ contains similarity to the TGF-beta family of growth factors e * $3e-52$ BMP7_MOUSE BONE MORPHOGENETIC PROT [TGFB_propeptide] CG5562 GH12092 60A5-60A5
CG5562 ID:64B10
+ RpP2 ribosomal_protein * DMRP21C_2 RpP2 * 60S ACIDIC RIBOSOMAL PROTEIN P1 (RP21C) (ACIDIC RIBOSOMAL PROTEIN RPA2)(aa) * $5e-14$ acidic ribosomal protein P1.e.A, cytosolic - ye [60s_ribosomal // RIBOSOMALP2] CG4087 GH13422
CG4087 21C2-21C2 dup:3/3 ID:65D7
CG6117 + Pka-C3 protein_kinase * PROTEIN KINASE DC2(aa) * DMDC2_2 Pka-C3 * $5e-88$ cAMP-dependent protein kinase subunit (put.);

putative * 2e-99 KAPC_CAEEL CAMP-DEPENDENT PROTEIN KIN CG6117 GH13608 72B1-72B2 dup:3/3 ID:65E5
 CG8332 + CG8332 dup:3/5 ID:66D9
 + Flo-2 unknown * 1e-176 flotillin-2 * 1e-114 epidermal surface antigen * 1e-114 flotillin epidermal surface antigen - human * 1e-
 CG11547 114 growth-associated protein [NLS_BP] CG11547 GH22754 13A3-13A4 ID:75C4
 + transporter * retinal rod Na/Ca+K exchanger(aa) * Na/Ca,K-exchanger(aa) * 2e-06 probable membrane protein YDL206w -
 CG1090 yeast (*Saccharomyces cerevisiae*) * 1e-05 Na/C CG1090 GH23040 82B1-82B1 ID:75G4
 CG2985 + YP1 CG2985 dup:1/5 ID:75H3
 + defense/immunity_protein * similar to rat autoimmune target protein p69 * 1e-39 similar to rat autoimmune target protein p69
 CG10566 * 5e-67 ICAp69 * 1e-64 diabetes mellitus type I au CG10566 GH23156 78B4-78C1 ID:75H6
 CG13787 + It has been mapped cytologically to 28A1 CG13787 GH23165 ID:75H7
 CG3868 + signal_transduction * 2e-07 antifreeze glycopeptide AFGP polypeptide precursor * * CG3868 GH23259 70D7-70D7 ID:76A2
 CG17012 + *Caenorhabditis elegans* 'similar to peptidase family S1 (trypsin family)' EMBL:U58751 CG17012 ID:79G7
 + dco protein_kinase * serin/threonin-kinase(aa) * dbt * Ckl agr; * DMDG2CD5_3 for [PROTEIN_KINASE_ST //
 CG2048 PROTEIN_KINASE_DOM] CG2048 LD27173 100B-100B ID:86C9
 + transporter * 2e-14 aquaporin * 5e-22 BIB_DROME NEUROGENIC PROTEIN BIG BRAIN bib protein - frui * 6e-22 similar to
 CG7777 MIP transmembrane protein; cDNA EST yk459g7.3 c [MINTRINSICP // MIP] CG7777 LD27313 47F13-47F13 ID:86D9
 + Qm ribosomal_protein 60S RIBOSOMAL PROTEIN L10 (QM PROTEIN HOMOLOG) RIBOSOMAL_L10E, Ribosomal_L10e
 CG17521 CG17521 ID:87H3
 + unknown * rap55(aa) * 2e-07 SCD6_YEAST SCD6 PROTEIN SCD6 protein - yeast (*Saccharom* * 2e-19 predicted using
 CG10686 Genefinder; cDNA EST yk343c12.5 comes from this * CG10686 69C3-69C3 dup:1/3 ID:88A5
 CG5821 + RNA_binding CG5821 ID:88A7
 + sop ribosomal_protein * Ribosomal protein S2 (S4) (rp12) (YS5); Rps2p(aa) * sop * 2e-73 RS4_YEAST 40S RIBOSOMAL
 PROTEIN S4 (OMNIPOTENT SUPPRESSOR PROTEIN SUP44) (RP12) (* 1 [Ribosomal_S5 // RIBOSOMAL_S5] CG5920 33A1-
 CG5920 33A1 dup:1/2 ID:88A8
 + RpS3 * Ribosomal protein S3 (rp13) (YS3); Rps3p(aa) * 40S RIBOSOMAL PROTEIN S3(aa) * DMRPS3_2 RpS3 * 8e-82
 RS3_YEAST 40S RIBOSOMAL PROTEIN S3 (YS3) (RP13) [KH-domain // RIBOSOMAL_S3 // Ribosomal_] CG6779 94F1-94F1
 CG6779 dup:2/2 ID:89B9
 + enzyme * acyl-CoA oxidase (EC 1.3.3.6), peroxisomal - human(aa) * 6e-52 CAO_YEAST ACYL-COENZYME A OXIDASE
 CG9709 (ACYL-COA OXIDASE) ac * 1e-111 similar to ACYL-COEN CG9709 LD30186 57D12-57D12 dup:2/2 ID:89F10
 CG6141 + RpL9 ribosomal_protein 60S RIBOSOMAL PROTEIN L9 RIBOSOMAL_L6_2, Ribosomal_L6 CG6141 ID:98F7