

Table S30

male somatic genes identified as follows:

two-way ANOVA (sex as independent factor,  $P < 0.001$ , wt male data > wt female data) and female tudor vs male tudor (one-tailed T-test,  $P < 0.01$ ) and male tudor data must be 2X female tudor data

+ qua actin\_binding \* qua \* QUA1\_DROME VILLIN-LIKE PROTEIN QUAIL villin homolog qua \* 9e-18 similar to gelsolin; cDNA EST comes from this gene \* 3e-71 putative actin-bin [GELS // GELSOLIN] CG6433 LD42165 36C4-36C4 ID:101C8  
 + unknown \* predicted using Genefinder; similar to GNS1/SUR4 family; cDNA EST comes from this gene(aa) \* CGI-88 protein(aa) \* 9e-15 SUR4\_YEAST SUR4 PROTEIN (SRE CG5326 LP03255 94B5-94B5 dup:2/2 ID:108E4  
 CG7821 + CG7821 SD05678 ID:119C2  
 CG3879 + transporter CG3879 SD10012 dup:1/3 ID:124E12.2  
 + signal\_transduction \* TOM1(aa) \* 2e-17 YHQ8\_YEAST HYPOTHETICAL 64.3 KD PROTEIN IN CDC12-ERP5 INTERGENIC REGION \* 2e-62 weak similarity to yeast hypothetical protein in C [VHS // HRS\_DOMAIN] CG3529 GH05942 67B4-67B4 ID:34A11  
 CG18284 + unknown \* CG18284 GH10507 31F5-31F5 ID:38A9  
 + Acp36DE signal\_transduction \* 36DE accessory gland protein(aa) \* 1e-156 accessory gland protein Acp36DE \* 1e-124 Acp36DE \* CG7157 CG7157 GH11288 36F6-36F6 ID:38G8  
 + Ugt35b enzyme \* antennal-enriched UDP-glycosyltransferase melanogas \* 3e-31 similar to UDP-glucuronosyltransferase \* 5e-62 UDB5\_MOUSE UDP-GLUCURONOSYLTRANSFERASE 2B [UDPGT] CG6649 GH11333 86D5-86D5 ID:38H1  
 + OstStt3 enzyme \* STT3\_YEAST OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT STT3 \* STT3\_CAEEL OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG \* STT3\_MOUSE OLIGOSACCHARYL [ATPASE\_ALPHA\_BETA] CG7748 GH13452 98F6-98F6 ID:40F6  
 + ligand\_binding\_or\_carrier \* DMC30B8 \* ALPHA-TOCOPHEROL TRANSFER PROTEIN (ALPHA-TTP)(aa) \* alpha tocopherol transfer protein(aa) \* 62D9.a(aa) [CRETINALDHBP // CRAL\_TRIO] CG2663 GH15295 83A6-83A6 ID:42C7  
 + ligand\_binding\_or\_carrier \* 2e-13 62D9.a \* 2e-25 retinaldehyde-binding protein C \* 2e-15 DMC30B8 \* /match=(desc;; /ma CG10657[CRETINALDHBP // CRAL\_TRIO] CG10657 LD32330 69C2-69C2 dup:2/2 ID:48B10  
 + unknown \* MALE STERILITY PROTEIN 2(aa) \* DMC103B4 \* male sterility 2-like protein(aa) \* /match=(desc;; /match=(desc:(aa) CG10096 CG10096 GH01346 87B13-87B14 ID:54C10  
 + enzyme \* 2e-07 CN1C\_RAT CALCIUM/CALMODULIN-DEPENDENT 3',5'-CYCLIC NUCLEOTIDE PHOSPHODIESTERASE \* \* [kazal CG14942// KAZAL] CG14942 GH01602 33B2-33B2 dup:2/2 ID:54F6  
 + endopeptidase \* COAGULATION FACTOR XII PRECURSOR (HAGEMAN FACTOR) (HAF)(aa) \* Chain A, Coagulation Factor Xa-Trypsin Chimera Inhibited With D-Phe-Pro-Arg-Chlorometh [trypsin // TRYPSIN\_CATAL] CG6069 GH04903 97A4-97A5 ID:57D5  
 CG6761 + unknown \* CG6761 GH07092 67B12-67B12 ID:59D1  
 CG2267 + transcription\_factor \* CG2267 100A2-100A2 dup:2/2 ID:62F6  
 + transporter \* HYPOTHETICAL 48.6 KD PROTEIN IN CHROMOSOME II(aa) \* DMORCT2\_2 Orct \* solute carrier family (organic cation transporter), member 1(aa) \* 1e-42 putati [sugar\_tr] CG7342 GH13557 92A11-94D3 dup:2/2 ID:65E3  
 + unknown \* 3e-07 serine rich protein \* SERA\_ENTHI SERINE-RICH KD ANTIGEN PROTEIN (SHEHP) (SREHP) \* merozoite protein CG17022 Bb-1 - Babesia bovis (fragment) \* CG17022 GH13755 30B10-30B10 ID:65F5

+ transporter \* transmembrane transporter - electric ray (*Discopyge ommata*)(aa) \* 1e-09 HXT3\_YEAST LOW-AFFINITY GLUCOSE  
 TRANSPORTER HXT3 hexose t \* 2e-14 putative o [SUGAR\_TRANSPORT\_1 // SUGAR\_TRANSPORT\_2 ] CG3168 GH13883 6C9-6C10  
 CG3168 ID:65G5  
 + receptor \* LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (LDL RECEPTOR 1)(aa) \* low density lipoprotein receptor-  
 related protein 7(aa) \* LDL receptor member LR3(a [LDLRA\_2 // LDLRECEPTOR // EGF // EGF\_2 ] CG8909 GH14506 13F10-13F12  
 CG8909 ID:66D12  
 + ion\_channel \* 7e-59 DrosGluCl \* 1e-48 Contains similarity to Pfam domain: (neur\_chan), Score=39 \* 7e-67 glycine receptor subunit  
 CG14723 alpha \* 8e-68 glycine receptor al [neur\_chan // NEUROTR\_ION\_CHANNEL // NRI] CG14723 GH14445 86F9-86F9 ID:66D2  
 CG8420 + \* [ER\_TARGET] CG8420 85D2-85D3 dup:3/3 ID:67F12  
 CG12558 + endopeptidase \* [TRYPSIN\_CATAL] CG12558 GH15905 98E3-98E3 ID:68B5  
 CG16820 + unknown \* CG16820 GH15921 34A11-34A11 dup:2/2 ID:68B9  
 CG9520 + unknown CG9520 dup:5/5 ID:70E7  
 + BcDNA:GH02439 unknown \* 1e-59 cDNA EST comes from this gene; cDNA EST co \* 7e-33 cytoplasmic protein Ndr1 \* 5e-32 RTP nickel-  
 CG2082 specific inductio \* 2e-25 development-related p CG2082 GH19206 83C-83C dup:2/2 ID:71D3  
 + signal\_transduction \* HYPOTHETICAL 128.6 KD PROTEIN IN CHROMOSOME III(aa) \* 2e-07 melanog \* 2e-96 protein \* 2e-09  
 CG8110 DMC132E8 CG8110 GH19969 66A20-66A21 ID:72B3  
 + receptor \* 3e-10 tolloid related-1 \* 5e-17 similar to CUB domain (2 domains), Low-density lipoprotein recepto \* 8e-15 BMP1\_MOUSE  
 CG5449 BONE MORPHOGENETIC PROTEIN PRE [LDLRA\_2 // CUB // ldl\_recept\_a // PRO\_R] CG5449 GH21941 94A3-94A3 ID:74C9  
 + prd transcription\_factor \* SEGMENTATION PROTEIN PAIRED(aa) \* DMPRD\_5 prd \* 3e-58 similar to 'Paired box' domain, homeobox  
 protein (paired subfamily \* 2e-87 PAX3\_MOUSE PAIRE[PAX // HOMEBOX\_1 // homeobox // HOMEOB] CG6716 GH22686 33B14-33B14  
 CG6716 ID:75B4  
 + electron\_transfer \* GEC-3(aa) \* 3e-43 coded for by C. elegans cDNA yk51h9.5; coded for by C. elegans cDNA yk117c2.5; c \* 1e-64  
 CG17843 quiescin Q6 quiescin \* 2e-66 GEC-3 [THIOREDOXIN\_2] CG17843 GH22889 96B6-96B6 dup:2/2 ID:75E2  
 + enzyme \* DMGLDY01\_11 Gld \* 1e-101 DHGL\_DROME GLUCOSE DEHYDROGENASE (ACCEPTOR) PRECURSOR glu \* 6e-68  
 CG9519 similar to choline dehydrogenase; cDNA EST yk346d5.5 come [GMC\_oxred // GMC\_OXRED\_2] CG9519 13A1-13A1 dup:2/2 ID:76E9  
 + endopeptidase \* DMSTUBBLE\_1 Sb \* zgr;Try \* 2e-22 TRYI\_DROME TRYPSIN IOTA PRECURSOR iota trypsin \* 2e-15 kallikrein  
 CG9898 [trypsin // CHYMOTRYPSIN // TRYPSIN\_CATA] CG9898 GH23641 59B8-59B8 ID:76F1  
 CG11440 + wunen \* similarity to phosphatidic acid phosphatase PA\_PHOSPHATASE CG11440 ID:77F12  
 CG7178 + CG7178 dup:2/2 ID:77H12  
 CG2956 + twist transcription\_factor CG2956 twist dup:3/5 ID:8-31 cntrlBG3  
 + enzyme \* CGI-82 protein(aa) \* 1e-16 YM71\_YEAST HYPOTHETICAL OXIDOREDUCTASE IN MRPL44-MTF1 INTERGENIC REGION  
 CG7675 \* 0.000000000002 \* 6e-42 predicted using Genefinde [GDHRDH // adh\_short] CG7675 GH26851 91A2-91A2 dup:2/4 ID:80F8  
 + \* similar to Arabidopsis thaliana male sterility protein \* 4e-47 /match=(desc;; /ma \* 6e-30 male sterility 2-like protein \* 4e-49  
 CG2858 DMC103B4 CG2858 60E5-60E5 dup:1/2 ID:96C7