

Table S19

List of Early Zygotic genes that are 10-fold induced

Gene ID mixed annotation (+ indicates sequence confirmation)

CG15634+ unknown \* CG15634 LD42284 25A4-25A4 ID:101D10  
 CG4702 + unknown \* CG4702 LD43816 88A1-88A1 ID:102F9  
 CG6234 + motor\_protein \* 1e-06 TRFA \*\* CG6234 LP04345 87C6-87C6 dup:1/2 ID:108H11  
 CG14766+ unknown CG14766 LP04033 ID:108H9  
 CG13868+ unknown \* 0.0000000000000008\* \* CG13868 SD03066 56F17-57A dup:4/4 ID:115B4  
 CG15319+ CG15319 SD03263 ID:115D11  
 CG9366 + enzyme CG9366 SD05212 ID:118D6  
 + enzyme \* lysine ketoglutarate reductase/saccharopine dehydrogenase(aa) \* similar to saccharopine dehydrogenases(aa) \*  
 CG7144 lysine-ketoglutarate reductase /sacch CG7144 SD05742 28C9-28D dup:2/2 ID:119D4  
 CG3879 + transporter CG3879 SD10012 dup:1/3 ID:124E12.2  
 CG15009+ CG15009 SD10052 dup:1/2 ID:124F9.2  
 CG5370 + endopeptidase CG5370 SD10530 dup:1/2 ID:125C11.2  
 + metabolism \* 1e-47 PNPH\_YEAST PROBABLE PURINE NUCLEOSIDE PHOSPHORYLASE (INOSINE PHOSPHORYLASE)  
 CG16758(PN \* 3e-51 similar to purine nucleoside phosphorylases \* 4e-73 pu [Mtap\_PNP] CG16758 GH04159 62E6-62E6 dup:5/5 ID:32E5  
 + Mipp1 protein\_phosphatase \* multiple inositol polyphosphate phosphatase 1; MIPP1(aa) \* Mipp1 \* 1e-22 multiple inositol  
 CG4123 polyphosphate phosphatase \* 2e-23 multiple inositol polyp [acid\_phosphat] CG4123 GH04949 77A1-77A1 dup:4/7 ID:33C7  
 + ubiquitin-protein\_ligase ubiquitin-conjugating enzyme E2B (RAD6 homolog) UBIQUITIN\_CONJUGAT\_2 CG10536 GH10432  
 CG10536ID:37H11  
 + endopeptidase \* 5e-32 Similarity to human placental protein \* 2e-42 glucocorticoid-sensitive T cell-specific protein - mouse \*  
 CG2145 5e-41 placental protein (serine prote CG2145 GH10845 10A1-10A1 dup:2/2 ID:38D4  
 + enzyme \* DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)(aa) \* 2e-48  
 CG7780 YKU5\_CAEEL HYPOTHETICAL 41.5 KD PROTEIN C07B5.5 IN CHROMOSOM CG7780 GH10876 90D-90D ID:38D8  
 CG3624 + cell\_adhesion \* [ig] CG3624 GH11432 58D7-58D7 dup:2/2 ID:38H12  
 + transporter \* 2e-50 Na(+)-dependent inorganic phosphate cotransporter mela \* 7e-54 YLD2\_CAEEL HYPOTHETICAL 52.7  
 CG15095KD PROTEIN C38C10.2 IN CHROMOSOME III \* 2e-45 NPT1 [sugar\_tr] CG15095 GH11849 55F1-55F1 ID:39C9  
 CG7563 + calpain CG7563 dup:1/4 ID:46C8  
 CG17506+ unknown smilarity to indora CG17506 GH02266 ID:55B6  
 + Cyt-b5 electron\_transfer \* CYBR\_DROME PROTEIN TU-36B (CYTOCHROME B5-RELATED PROTEIN) \* 9e-66 CYBR\_DROVI  
 CYTOCHROME B5 RELATED PROTEIN cytochrome b5 \* DMTU36B\_4 Cyt-b5 \* delta [CYTOCHROME\_B5\_2 // heme\_1] CG13279  
 CG13279GH03691 36A9-36A9 ID:56B5  
 + unknown \* dJ413H6.1.1 (hamster Androgen-dependent Expressed Protein LIKE PUTATIVE protein) (isoform 1)(aa) \*  
 CG3625 androgen-regulated protein FAR-17 - golden hamst CG3625 GH04039 21B5-21B5 dup:2/2 ID:56E6

+ BG:DS02780.1 cell\_adhesion \* Toll protein(aa) \* 9e-05 cell-surface molecule connectin - fruit fly (*Drosophila melanogaster*) \* 2e-  
 CG5888 06 predicted using Genefinder; Similarity to Dr [LRR] CG5888 GH08155 35F12-36A1 dup:1/2 ID:60D6  
 + cell\_adhesion \* DMARTAN\_7 trn \* kek1 \* tartan protein(aa) \* 5e-16 CYAA\_YEAST ADENYLATE CYCLASE (ATP  
 CG11280 PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE) [LRR // LEURICHRPT // LRRCT] CG11280 GH10871 69F5-69F5 ID:62H10  
 + grh transcription\_factor \* DMELF1\_2 grh \* transcription factor NTF1 - fruit fly (*Drosophila melanogaster*) (fragment) \* 1e-22  
 CG5058 alpha-globin transcription factor CP2 - mouse \* 9e [NLS\_BP] CG5058 GH11672 54F1-54F4 ID:63G1  
 + 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  
 + bnb unknown \* DMBNBR\_2 bnb \* 1e-148 BNB\_DROME BANGLES AND BEADS PROTEIN bangles and \* GAP-43-related  
 CG7088 protein - fruit fly (*Drosophila melanogaster*) \* bnb gene prod CG7088 GH12078 17D6-17D6 ID:64B8  
 + unknown \* 6e-05 transmembrane protein \* 2e-12 Similarity to *C.elegans* cuticulin (SW:CUT1\_CAEEL) \* 7e-07 DMDUSKY\_1  
 CG3541 dy \* similar to cuticlin CG3541 GH12163 60D7-60D8 dup:1/2 ID:64C4  
 + Pka-C3 protein\_kinase \* PROTEIN KINASE DC2(aa) \* DMDC2\_2 Pka-C3 \* 5e-88 cAMP-dependent protein kinase subunit (put.);  
 CG6117 putative \* 2e-99 KAPC\_CAEEL CAMP-DEPENDENT PROTEIN KIN CG6117 GH13608 72B1-72B2 dup:3/3 ID:65E5  
 + transporter \* K05B2.5 gene product(aa) \* 1e-13 YKW1\_YEAST HYPOTHETICAL 52.3 KD PROTEIN IN FRE2 5'REGION \*  
 CG8468 2e-82 /match=(desc;; /ma \* 1e-40 predicted using Genefin CG8468 GH16148 50E-50E7 dup:2/5 ID:68C9  
 + weak homology to leucine carboxyl methyltransferase [*Homo sapiens*] and receptor protein kinase-like protein [*Arabidopsis*  
 CG14768 *thaliana*] CG14768 GH21888 ID:74C2  
 + cell\_adhesion \* 2e-11 CHAO\_DROME CHAOPTIN PRECURSOR (PHOTORECEPTOR CELL-SPECIFIC MEMBRANE  
 PROTEIN) \* 3e-06 Simiarity to Rat insulin-like growth factor binding prote [LRR // LEURICHRPT // NLS\_BP] CG15658 GH22922  
 CG15658 57C7-57C7 dup:2/2 ID:75E6  
 + 18w cell\_adhesion \* DMWHEELER\_2 18w \* 5e-15 CYAA\_YEAST ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE)  
 CG8896 (ADENYLYL CYCLASE) \* leucine-rich motif (LRR) protein homology to int CG8896 GH23463 56F9-56F9 dup:1/4 ID:76C9  
 CG11440+ wunen \* similarity to phosphatidic acid phosphatase PA\_PHOSPHATASE CG11440 ID:77F12  
 + bib transporter \* pore-forming protein MIP family(aa) \* NEUROGENIC PROTEIN BIG BRAIN(aa) \* 1e-07 YFF4\_YEAST  
 HYPOTHETICAL 70.5 KD PROTEIN IN AGP3-DAK3 INTERGENIC REG[MINTRINSICP // MIP // PRO\_RICH] CG4722 big brain  
 CG4722 30F4-30F5 dup:2/3 ID:8-31 cntrlBB5  
 CG1378 + tll steroid\_hormone\_receptor CG1378 tll dup:2/2 ID:8-31 cntrlBC1  
 CG1374 + tsh transcription\_factor CG1374 tsh dup:3/3 ID:8-31 cntrlBD3  
 + inv transcription\_factor \* SEGMENTATION POLARITY PROTEIN ENGRAILED(aa) \* DMINVR\_2 inv \* INVECTED  
 PROTEIN(aa) \* 2e-29 HM16\_CAEEL HOMEBOX PROTEIN ENGRAILED-LIKE CEH-16 homology CG17835 inv 47F17-48A  
 CG17835 dup:3/4 ID:8-31 cntrlBD4  
 + pros transcription\_factor \* DMPROS\_3 pros \* PRO\_DROME PROTEIN PROSPERO homeotic protein prospero - f \* 4e-58  
 HM26\_CAEEL HOMEBOX PROTEIN CEH-26 K12H4.1 protein - *Caen* \* 2e-50 [PRO\_RICH] CG17228 pros p'3' 3211 86E2-86E2  
 CG17228 dup:4/4 ID:8-31 cntrlBD7  
 CG1028 + Antp transcription\_factor \* DMANTPG5\_7 Antp \* 1e-159 HMAN\_DROME HOMEOTIC ANTENNAPEDIA PROTEIN homeotic

protein \* 7e-23 DNA-binding protein mab5 \* 5e-34 HXB7\_MOUSE HOMEBOX PROT CG1028 ANTP 84B-84D11 dup:3/3 ID:8-31  
 cntrlBE12  
 CG4889 + Wg signal\_transduction CG4889 Wg dup:2/2 ID:8-31 cntrlBE8  
 CG9885 + dpp signal\_transduction CG9885 dpp dup:2/2 ID:8-31 cntrlBE9  
 + tup transcription\_factor \* isl \* LIM homeobox protein(aa) \* LIM homeobox protein \* 4e-30 CeLIM-7 contains similarity to L  
 CG10619[LIM\_DOMAIN\_1 // HOMEBOX\_1 // homeobox ] CG10619 islet 37B5-37B5 dup:3/3 ID:8-31 cntrlBF7  
 CG7902 + Bap transcription\_factor CG7902 Bap dup:6/6 ID:8-31 cntrlBH11  
 CG1133 + opa transcription\_factor CG1133 opa dup:4/4 ID:8-31 cntrlBH4  
 CG10630+ RNA\_binding \* CG10630 GH28067 64E-64E ID:82B10  
 + unknown \* 5e-05 XIAP associated factor-1 (ZAP-1) \* 6e-09 SINA\_DROME DEVELOPMENTAL PROTEIN SEVEN IN  
 CG16745ABSENTIA devel \* 1e-07 seven-in-absentia protein homologue- [ZF\_TRAF] CG16745 GH28844 63B5-63B5 ID:82H4  
 + Phas1 translation\_factor \* 2e-16 PHAS-II \* 4e-16 eukaryotic translation initiation factor 4E binding protein \* 1e-14 insulin-  
 CG8846 stimulated phosphoprotein PHAS-I - rat PHAS-I \* in CG8846 HL08053 25A3-25A3 ID:83D4  
 + BG:DS05899.1 enzyme \* protein(aa) \* fadD15(aa) \* putative long chain fatty acid coA ligase(aa) \* protein(aa) [AMP-binding]  
 CG4500 CG4500 LD28132 34E4-34E4 ID:87C8  
 + transcription\_factor \* fruitless protein(aa) \* fruitless class I male isoform(aa) \* 3e-21 LOLS\_DROME LOLA PROTEIN, SHORT  
 ISOFORM (LONGITUDINALS LACKING PROTEIN) \* 2e-06 co [BTB // HTH\_FIS\_FAMILY // NLS\_BP] CG7230 56C-56C dup:6/10  
 CG7230 ID:89H5  
 + \* 2e-45 sulfate permease \* 1e-27 Similar to sulfate transporter. \* 9e-33 DTD\_MOUSE SULFATE TRANSPORTER  
 (DIASTROPHIC DYSPLASIA PROTEIN HOMOLOG) (ST-OB) [Sulfate\_transp // SUGAR\_TRANSPORT\_2] CG5002 54E7-54E7  
 CG5002 ID:97G9  
 + Ama cell\_adhesion \* DMAMA\_5 Ama \* Immunoglobulin-C2-type-domain protein \* 1e-15 hemicentin precursor \* 3e-19 cell  
 CG2198 adhesion molecule (AA - 681) is 1st base in codon [ig] CG2198 LD39923 84D1-84D1 ID:99A4  
 CG15288+ CG15288 ck01592 ID:Farhad's BE4