

Table S21

List of early zygotic genes identified by SOM analysis, reinduced.

Gene ID mixed annotation (+ indicates sequence confirmation)

CG4889 + Wg signal\_transduction CG4889 Wg dup:2/2 ID:8-31 cntrlBE8  
CG6234 + motor\_protein \* 1e-06 TRFA \*\* CG6234 LP04345 87C6-87C6 dup:1/2 ID:108H11  
CG9885 + dpp signal\_transduction CG9885 dpp dup:2/2 ID:8-31 cntrlBE9  
+ Ama cell\_adhesion \* DMAMA\_5 Ama \* Immunoglobulin-C2-type-domain protein \* 1e-15 hemicentin precursor \* 3e-19 cell adhesion  
CG2198 molecule (AA - 681) is 1st base in codon [ig] CG2198 LD39923 84D1-84D1 ID:99A4  
+ BG:DS02780.1 cell\_adhesion \* Toll protein(aa) \* 9e-05 cell-surface molecule connectin - fruit fly (Drosophila melanogaster) \* 2e-06  
CG5888 predicted using Genefinder; Similarity to Dr [LRR] CG5888 GH08155 35F12-36A1 dup:1/2 ID:60D6  
+ 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 dup:4/4  
CG17228 ID:8-31 cntrlBD7  
+ bnb unknown \* DMBNBR\_2 bnb \* 1e-148 BNB\_DROME BANGLES AND BEADS PROTEIN bangles and \* GAP-43-related protein -  
CG7088 fruit fly (Drosophila melanogaster) \* bnb gene prod CG7088 GH12078 17D6-17D6 ID:64B8  
+ 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  
+ 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  
CG1133 + opa transcription\_factor CG1133 opa dup:4/4 ID:8-31 cntrlBH4  
+ sli cell\_adhesion \* DMSLIT\_2 sli \* slit protein(aa) \* 2e-35 contains similarity to multiple EGF-like domains \* neurogenic extracellular slit  
CG8355 protein [LRR // LRRNT // EGF\_1 // EGF // LEURICH] CG8355 LD39407 52D4-52D7 dup:2/2 ID:98E11  
CG7434 + RpL22 ribosomal\_protein Ribosomal protein L22 60S subunit ANTIFREEZE1 CG7434 SD02522 ID:114C6  
CG17348 + drl CG17348 drl dup:2/2 ID:8-31 cntrlBC8  
CG15427 + cell\_adhesion CG15427 LD28224 dup:1/2 ID:87D1  
+ BG:DS09218.3 chaperone \* 8e-19 ERP5\_CAEEL PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR \* 4e-21 protein  
CG4455 disulfide isomerase-related protein \* 9e-21 ERP5\_RAT PROBABLE PRO CG4455 LD33101 35F10-35F10 dup:2/3 ID:48F10  
+ unknown \* 3e-21 hypothetical protein YOR289w - yeast (Saccharomyces cerevisiae) \* 1e-43 R166.3 \* 3e-45 unknown protein \*  
CG5902 Y810\_METJA HYPOTHETICAL PROTEIN hypo CG5902 97F1-97F1 dup:1/6 ID:98G6  
+ unknown \* tight junction protein (zona occludens 1)(aa) \* TIGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1)(aa) \*  
CG11782 1e-05 ZO-1 MDCK \* [NLS\_BP] CG11782 LD44404 85B4-85B4 ID:103C6  
+ shg cell\_adhesion \* DMDACHSOU\_2 ds \* EPITHELIAL-CADHERIN PRECURSOR (E-CADHERIN) (LIVER CELL ADHESION  
MOLECULE) (L-CAM)(aa) \* DE-cadherin(aa) \* DMDEC\_1 shg [EGF\_1 // EGF\_2 // LAM\_G\_DOMAIN // Cadhe] CG3722 LP01248 57B19-  
CG3722 57B20 ID:107D10  
CG4609 + fax failed axon connections protein CG4609 LD28084 dup:2/2 ID:45D1