

Table S20

List of Transient Early Zygotic genes identified by SOM analysis, Blastoderm specific Zygotic genes

+ 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 65F2-65F2
CG8606 ID:43A5

+ unknown * 5e-10 FIP1_YEAST FIP1 PROTEIN FIP1 protein - yeast (Saccharom * 3e-16 contains similarity to S. cerevisiae FIP1 *
CG1078 2e-13 YAAA_SCHPO HYPOTHETICAL 37.3 [PRO_RICH // NLS_BP] CG1078 LD38592 82C2-82C2 dup:1/3 ID:97G11

+ 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
CG2916 ID:106A3

+ endopeptidase * hypothetical protein unip - mouse(aa) * Sad1p(aa) * putative protein(aa) * Contains similarity to Pfam domain:
CG7288 (UCH-1), Score=13.8, E-value=0.14, N= [UCH_2_3 // UCH-2] CG7288 LD30129 17E4-17E4 dup:1/3 ID:46G10

+ Bsg25D motor_protein * BSG2_DROME BLASTODERM SPECIFIC PROTEIN 25D bsg25D protein * 1e-05 contains similarity to
CG14025 kinesin (PFam: kinesin.hmm, score: 10.52 and 16.62) * 6e-1 CG14025 LD21844 25D2-25D2 dup:2/2 ID:83E8

+ enzyme * No definition line found(aa) * predicted secreted protein(aa) * 3e-06 predicted secreted protein * [NLS_BP] CG1745
CG1745 LD43003 10B15-10B15 dup:1/2 ID:101G12

+ transcription_factor_binding * 6e-06 DIP2_YEAST DOM34 INTERACTING PROTEIN DIP2 protein - y * 2e-06 similar to beta
transducin proteins containing TRP-ASP domains el * 6e-11 ap[WD40_REGION // WD_REPEATS // WD40] CG14722 LD21659 86F6-
CG14722 86F6 ID:43A8

CG1677 + CG1677 LD30482 ID:47A10

CG16901+ CG16901 ID:88G12

CG7269 + RNA_binding CG7269 dup:2/2 ID:106E3

+ 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
CG10417 LD27655 41D1-41D1 ID:86G1

CG9506 + protein_phosphatase * CG9506 LD27991 28D1-28D1 dup:1/2 ID:45C6

+ neur DNA_binding * finger protein neuralized - fruit fly (Drosophila melanogaster)(aa) * DMC3HC4ZF_2 neur * 3e-89 coded for by C.
CG11988 elegans cDNA yk27g3.5; coded for by C [zf-C3HC4 // ZF_RING] CG11988 LD45505 85C4-85C5 dup:1/2 ID:104C12

CG15634+ unknown * CG15634 LD42284 25A4-25A4 ID:101D10

+ transcription_factor * chromatin structural protein homolog Supt5hp(aa) * suppressor of Ty (S.cerevisiae) homolog(aa) * 9e-59
CG7626 SPT5_YEAST TRANSCRIPTION INITIATION PROTEIN CG7626 GH15359 56D7-56D7 dup:4/5 ID:67D10

+ unknown * PBK1 protein(aa) * 5e-11 predicted using Genefinder; Weak similarity to Mouse CSA-19 protei * 2e-16 PBK1 protein *
CG13096 7e-08 hypothetical protein [NLS_BP] CG13096 SD03546 29D1-29D1 ID:115H5

+ RNA_binding * LET 858(aa) * conserved hypothetical protein(aa) * BLASTX 7.4E-44 Caenorhabditis elegans Nucampholin (let-
CG12750 858) mRNA, complete cds.(dna) * BLASTX 3 [NLS_BP] CG12750 GH13383 36F7-36F7 dup:3/3 ID:40F2

CG4602 + CG4602 dup:3/4 ID:89H6

CG5175 + CG5175 ID:95H10
 CG9839 + unknown * [CYTOCHROME_C] CG9839 LD40589 85E9-85E9 ID:99F8
 CG1378 + tll steroid_hormone_receptor CG1378 tll dup:2/2 ID:8-31 cntrlBC1

List of Early Zygotic genes identified by SOM analysis, induced then maintained

Gene ID mixed annotation (+ indicates sequence confirmation)
 + endopeptidase * 5e-32 Similarity to human placental protein * 2e-42 glucocorticoid-sensitive T cell-specific protein - mouse * 5e-
 CG2145 41 placental protein (serine protease) CG2145 GH10845 10A1-10A1 dup:2/2 ID:38D4
 + Mipp1 protein_phosphatase * multiple inositol polyphosphate phosphatase 1; MIPP1(aa) * Mipp1 * 1e-22 multiple inositol
 CG4123 polyphosphate phosphatase * 2e-23 multiple inositol polyp [acid_phosphatase] CG4123 GH04949 77A1-77A1 dup:4/7 ID:33C7
 + unknown * dJ413H6.1.1 (hamster Androgen-dependent Expressed Protein LIKE PUTATIVE protein) (isoform 1)(aa) * androgen-
 CG3625 regulated protein FAR-17 - golden hamster CG3625 GH04039 21B5-21B5 dup:2/2 ID:56E6
 + cell_adhesion * 2e-11 CHAO_DROME CHAOPTIN PRECURSOR (PHOTORECEPTOR CELL-SPECIFIC MEMBRANE
 PROTEIN) * 3e-06 Similarity to Rat insulin-like growth factor binding protein [LRR // LEURICHRPT // NLS_BP] CG15658 GH22922 57C7-
 CG15658 57C7 dup:2/2 ID:75E6
 + 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 CHROMOSOME CG7780 GH10876 90D-90D ID:38D8
 + transporter * 2e-50 Na(+)-dependent inorganic phosphate cotransporter mela * 7e-54 YLD2_CAEEL HYPOTHETICAL 52.7 KD
 CG15095 PROTEIN C38C10.2 IN CHROMOSOME III * 2e-45 NPT1 [sugar_tr] CG15095 GH11849 55F1-55F1 ID:39C9
 CG15319+ CG15319 SD03263 ID:115D11
 CG13868+ unknown * 0.0000000000000008 * CG13868 SD03066 56F17-57A dup:4/4 ID:115B4
 + weak homology to leucine carboxyl methyltransferase [Homo sapiens] and receptor protein kinase-like protein [Arabidopsis
 CG14768 thaliana] CG14768 GH21888 ID:74C2
 + Phas1 translation_factor * 2e-16 PHAS-II * 4e-16 eukaryotic translation initiation factor 4E binding protein * 1e-14 insulin-stimulated
 CG8846 phosphoprotein PHAS-I - rat PHAS-I * in CG8846 HL08053 25A3-25A3 ID:83D4
 + protein_phosphatase * similar to glycogen-binding subunit protein phosphatase-1(aa) * smooth muscle protein phosphatase type
 CG9619 1-binding subunit(aa) * protein phosphatase CG9619 GH27769 76A4-76A5 ID:81G10
 + enzyme * 1e-05 GCST_YEAST AMINOMETHYLTRANSFERASE PRECURSOR (GLYCINE CLEAVAGE SYSTEM T PROTEIN) *
 1e-10 partial CDS, * 4e-08 sarcosine oxidase * sarcosine dehydrogenase [FAD_Gly3P_dh // NAD_BINDING] CG6385 GH19226 54E7-54E8
 CG6385 ID:71D6
 CG11347+ unknown * [NLS_BP] CG11347 GH28550 64B11-64B11 dup:2/2 ID:82E4
 + enzyme * 1e-107 ecto-5'-nucleotidase * 1e-105 5' nucleotidase (CD73) 5'-NUCLEOTID * 1e-132 putative 5'-nucleotidase * 3e-08
 CG4827 inserted at base 5' end of P element [PHOSPHO_ESTER // 5_nucleotidase // 5_NU] CG4827 LP01562 54C6-54C6 ID:107F5
 CG10521+ NetB cell_adhesion * extracellular extracellular) map_position:12F1 * NetB * 1e-170 NETB_DROME NETRIN-B PRECURSOR

Netrin-B melanog * 3e-67 UNC6_CAEEL UNC-6 PROTEIN P[laminin_EGF // EGFLAMININ // EGF_LAM //] CG10521 GH10173 12F1-12F3 dup:1/2 ID:62C5

CG9503

+ peptidase * 5e-10 carboxypeptidase s * 3e-90 Similarity to Human aminoacylase-1 (SW:ACY1_HUMAN) * 1e-109 aminoacylase AMINOACYLASE-1 (N-A * 1e-103 ACY1_PIG AMIN [ARGE_DAPE_CPG2_1 // ARGE_DAPE_CPG2_2] CG6465 GH04054 86C2-86C2

CG6465 dup:2/2 ID:56E8

+ unknown * predicted using Genefinder; cDNA EST yk268h6.5 comes from this gene; cDNA EST yk465f2.5 comes from this gene;

CG10512 cDNA EST yk393g7.5 comes from this gen CG10512 GH06154 78C3-78C4 ID:58F3

+ enzyme * acid phosphatase (EC 3.1.3.2) Acph-1 precursor, lysosomal - fruit fly (Drosophila melanogaster)(aa) * acid

CG6656 phosphatase-1(aa) * PUTATIVE ACID PHOSPH [acid_phosphat] CG6656 GH06011 93F-93F dup:3/3 ID:58E4

+ unknown * 8e-21 ERP6_YEAST ERP6 PROTEIN PRECURSOR probable membrane pro * 9e-39 similar to emp24/gp25L/p24

CG9443 family * 8e-72 associated to apparatus * 2e-51 G25L [EMP24_GP25L] CG9443 SD01878 85E4-85E5 dup:1/2 ID:113C5

CG11388+ unknown * CG11388 GH22974 60B1-60B1 dup:2/2 ID:75E11

+ transcription_factor * ORFveg132; similar to Caenorhabditis elegans ORF F59B10.1 encoded by EMBL Accession Number *

CG3328 protein(aa) * 2e-70 similarity to a transmembranous of [CASPASE_HIS] CG3328 GH24458 60B9-60B10 dup:3/3 ID:77E12

CG17676+ CG17676|unknown|CT39055 ID:82H3

+ unknown * glycine-, glutamate-, thienylcyclohexylpiperidine-binding protein(aa) * 1e-59 protein * 1E-170* CG10137 37F1-37F1

CG10137 ID:77F4

CG2467 + unknown * [PRO_RICH // NLS_BP] CG2467 GH09980 10F7-10F8 dup:2/2 ID:62B5

+ HmgZ DNA_binding * 2e-07 cerevisiae mitochondrial protein gene, complete gene produc * 5e-42 HMGZ_DROME HIGH MOBILITY

CG17921 GROUP PROTEIN Z (HMG-Z) high mob * 2e-11 SSRP_CAE [HMG // HMG_box // NLS_BP] CG17921 GH14749 57F8-57F9 ID:41G9

CG18437+ unknown * CG18437 GH15426 98A6-98A6 dup:2/2 ID:67E2

+ transporter * solute carrier family (sodium/chloride transporters), member 3(aa) * BUMETANIDE-SENSITIVE SODIUM-(POTASSIUM)-CHLORIDE COTRANSPORTER (NA-K-CL SYMPORT [AMINO_ACID_PERMEASE_2] CG4357 GH07280 69B-69B2

CG4357 dup:7/8 ID:59E7

CG3246 + unknown * CG3246 25A3-25A3 dup:2/2 ID:74E11

CG11960+ unknown * [NLS_BP] CG11960 GH14769 56D8-56D8 dup:1/2 ID:66G8

+ endopeptidase * 2e-11 similar to Zinc-binding metalloprotease; cDNA EST come * 3e-14 NEP_MOUSE NEPRILYSIN (NEUTRAL ENDOPEPTIDASE) (NEP) (ENKEPHALINASE) (CD10) * 2e[NEPRILYSIN // PRENYLATION // ZINC_PROTE] CG3239 GH24674 5A1-

CG3239 5A1 dup:1/3 ID:77G12