

Table S22

List of early zygotic genes identified by SOM analysis, male germline

Gene ID mixed annotation (+ indicates sequence confirmation)

CG5048 + unknown * CG5048 GH27783 70F1-70F1 ID:81H2
CG1979 + BG:DS00464.1 transmembrane_receptor * unknown(aa) * * CG1979 GH19145 84C1-84C1 dup:1/2 ID:71C10
CG2267 + transcription_factor * CG2267 100A2-100A2 dup:2/2 ID:62F6
+ endopeptidase * 3e-11 TBP6_YEAST PROBABLE 26S PROTEASE SUBUNIT YTA6 (TAT-BINDING HOMOLOG 6) * 3e-08 MEI1_CAEEL MEIOTIC SPINDLE FORMATION PROTEIN MEI-1 mei-1 * 0.000 CG14183 GH08353 76E3-76E4 dup:3/3
CG14183 ID:60E12
CG4955 + RNA_binding * CG4955 GH27756 15D1-15D1 ID:81G7
+ enzyme * DMC103B4 * 1e-05 LYS2_YEAST AMINOADIPATE-SEMIALDEHYDE DEHYDROGENASE LARGE SUBUNIT (ALPHA-AMINOADI * 2e-53 /match=(desc:; /ma * 4e-75 similar to Arab [HELIX_LOOP_HELIX] CG12268 GH24480 95C13-95C13
CG12268 ID:77F5
+ chaperone * DMTIDT4M_4 I(2)tid * 1e-22 MDJ1_YEAST MDJ1 PROTEIN PRECURSOR heat shock protein MDJ1 * 2e-42 Tid56 protein * 2e-42 YLW5_CAEEL HYPOTHETICAL 105.9 K[DnaJ_CXXCXGXXG // DNAJ_1 // DnaJ // DNAJ] CG7387 LP05202
CG7387 66B13-66B13 dup:1/2 ID:109C10
CG3557 + unknown * CG3557 GH20409 23E4-23E4 ID:72F9
CG6186 + CG6186 dup:2/2 ID:32G1
CG7669 + unknown * [NLS_BP] CG7669 GH08407 91A-91A dup:1/2 ID:60F7
CG17450 + unknown * CG17450 GH25094 cyto_unknown ID:78C5
CG7742 + unknown * [TBC // RAB_GAP] CG7742 GH15768 25C9-25C9 ID:68A4
CG7366 + unknown * CG7366 GH02649 67E7-67E7 ID:55D4
+ unknown * 3e-80 YKL6_CAEEL HYPOTHETICAL 103.8 KD PROTEIN C03C10.6 IN CHROMOSOME III * E03A3.6 *
CG5237 E03A3.7 * [AA_TRNA_LIGASE_II_2 // PRO_RICH // CYTO] CG5237 GH01039 91F10-91F11 ID:54A4
CG7634 + unknown * [TPR_REPEAT] CG7634 GH12875 78E2-78E2 dup:2/2 ID:65A2
CG10934 + CG10934 GH26058 dup:2/3 ID:Farhad's BA12
CG9803 + unknown * [PRO_RICH] CG9803 GH03629 59D6-59D6 ID:56B1
+ enzyme * by content; by match; 2-match_description=4-NITROPHENYLPHOSPHATASE.; 2-match...(aa) * similar to N-acetyl-glucosamine catabolism(aa) * Similar to CG2077 GH05933 63B3-63B3 ID:58D8
CG2077 + DNA_binding * DMHMGDA_2 HmgD * HIGH MOBILITY GROUP PROTEIN Z (HMG-Z)(aa) * 2e-11 HMGD_DROME HIGH MOBILITY GROUP PROTEIN D (HMG-D) high mob * 2e-05 SSRP_CAEEL PROB [HIGHMOBLTY12 // HMG_box] CG7045
CG7045 GH21448 94B4-94B4 ID:73G1
CG5089 + unknown * [NLS_BP] CG5089 GH06435 53C8-53C9 dup:2/2 ID:58H4
+ enzyme * similar to pig tubulin-tyrosine ligase.(aa) * 1e-41 similar to tubulin tyrosine ligase; cDNA EST comes fro * 2e-55
CG16716 protein * 8e-16 TTL_BOVIN TUBULIN [NLS_BP] CG16716 GH01307 56D15-56E1 ID:54C7

CG13918+ unknown * CG13918 GH13002 62A-62A ID:65A12
 + enzyme * 5e-49 IDH1_YEAST ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT PRECURSOR (IS *
 CG3483 6e-57 IDHA_CAEEL PROBABLE ISOCITRATE DEHYDROGENASE (NAD), MIT [isodh] CG3483 GH13226 60D2-60D2 ID:65C9
 CG18396+ Mst98Cb unknown * CG18396 GH20038 98C2-98C2 ID:72C1
 + actin_binding * 1e-05 contains similarity to the kelch/MIPP family * 1e-06 Keap1 * 1e-07 The gene product is related to
 CG12423Drosophila melanogaster ri * 1e-06 kelch pro [BTB] CG12423 GH26310 cyto_unknown ID:79H3
 + transporter * 3e-19 nervous system antigen nerv * 5e-06 Similarity to Shrimp sodium/potassium-transporting ATPase beta
 CG11703cha * 7e-10 ATNB_MOUSE SODIUM/POTASSIUM-TRA CG11703 GH20514 91F10-91F10 ID:72G7
 CG3330 + unknown * CG3330 GH22851 97F8-97F8 ID:75D7
 CG9483 + unknown * CG9483 GH20208 29F3-29F3 ID:72D7
 CG7886 + signal_transduction * 2e-15 IP63 protein * * CG7886 GH12083 88C10-88C10 ID:64B9