Supplementary Table S1. Biological processes enriched by differentially expressed genes at each physiological stage of *Octopus maya* oviducal glands.

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| **GO term** | **UniProt IDs** |
| **MAT24 upregulated** | |
| fat-soluble vitamin metabolic process | AL1A2\_HUMAN, CBR1\_PONAB, LRP2\_HUMAN |
| IMP biosynthetic process | PUR9\_CHICK, PUR6\_DROME, PUR4\_HUMAN |
| negative regulation of RNA splicing | PTBP1\_HUMAN, TRA2B\_RAT, ROA1\_DROME, SRSF4\_MOUSE, HNRPK\_CHICK |
| cellular biogenic amine metabolic process | KFA\_SALSA, KFA\_DANRE, SAT2\_BOVIN, SPEE\_HUMAN |
| cellular amine metabolic process | KFA\_SALSA, CSUP\_DROME, KFA\_DANRE, SAT2\_BOVIN, SPEE\_HUMAN |
| regulation of mRNA splicing, via spliceosome | PTBP1\_HUMAN, TRA2B\_RAT, ROA1\_DROME, SRSF4\_MOUSE, HNRPK\_CHICK, KHDR3\_RAT |
| extracellular structure organization | PRDX4\_MOUSE, CO1A2\_RAT, CO4A1\_CAEEL, FLNA\_DROME, COBA1\_HUMAN, PXDN\_DROME, CO3A1\_MOUSE, PPN\_DROME |
| alpha-amino acid metabolic process | PRDX4\_MOUSE, SERA\_MOUSE, PDIA1\_PONAB, SERB\_MOUSE, SPS1\_DROME, KFA\_SALSA, GCST\_HUMAN, KFA\_DANRE, PUR4\_HUMAN |
| nucleotide biosynthetic process | ANPRB\_BOVIN, KFA\_SALSA, KFA\_DANRE, DUT\_HUMAN, PUR9\_CHICK, PUR6\_DROME, PUR4\_HUMAN, TYSY\_MOUSE |
| DNA replication | CAF1B\_HUMAN, MCM7\_HUMAN, RFC5\_HUMAN, RFA2\_MOUSE, DUT\_HUMAN, PSF1\_BOVIN, MCM5A\_XENLA, MCM2\_XENTR, SETMR\_HUMAN |
| **FER24 upregulated** | |
| positive regulation of calcineurin-NFAT signaling cascade | SL9A1\_HUMAN, CIB1\_HUMAN, CIB1\_SHEEP |
| regulation of male germ cell proliferation | PRDX4\_MOUSE, CIB1\_HUMAN, CIB1\_SHEEP |
| positive regulation of cholesterol efflux | ABCAC\_HUMAN, ABCA1\_HUMAN, LRP1\_HUMAN |
| cell volume homeostasis | AQP4\_BOVIN, S12A2\_HUMAN, AQP\_DROME, CLCN3\_MOUSE, ANXA7\_BOVIN |
| water homeostasis | ABCAC\_HUMAN, AQP4\_BOVIN, AQP\_DROME, ANXA7\_BOVIN |
| hydrogen peroxide catabolic process | PXDN\_HUMAN, PXDN\_DROME, PERC\_AEDAE, PERC\_ANOGA |
| phagocytosis, engulfment | ABCA1\_HUMAN, GULP1\_HUMAN, CLCN3\_MOUSE, GULP1\_RAT |
| protein hydroxylation | PDIA1\_PONAB, P4HA2\_HUMAN, P4HA1\_CAEEL, P4HA3\_BOVIN |
| serine family amino acid biosynthetic process | GGT1\_RAT, SERB\_MOUSE, CBS\_RAT, AGT2\_BOVIN |
| retinoid metabolic process | RDH2\_RAT, RDH14\_MOUSE, AL1A2\_HUMAN, RDHE2\_HUMAN, LRP1\_HUMAN, LRP2\_HUMAN |
| muscle organ morphogenesis | TITIN\_MOUSE, TNNT\_DROME, TITIN\_HUMAN, COBA1\_HUMAN, CO3A1\_MOUSE |
| cellular hormone metabolic process | RDH2\_RAT, CP17A\_CHICK, RDH14\_MOUSE, AL1A2\_HUMAN, RDHE2\_HUMAN, ASMT\_BOVIN |
| positive regulation of cell-substrate adhesion | PTN\_RAT, VWC2\_MOUSE, CIB1\_HUMAN, NID1\_HUMAN, FLNA\_MOUSE, CIB1\_SHEEP |
| regulation of reproductive process | PRDX4\_MOUSE, CIB1\_HUMAN, AQP\_DROME, CIB1\_SHEEP, IF4G3\_MOUSE, ZAN\_MOUSE, ACH2\_CAEEL |
| cellular amino acid catabolic process | 3HIDH\_HUMAN, OAT\_HUMAN, FTCD\_CHICK, CBS\_RAT, ASGL1\_XENLA, IVD\_CAEEL, AGT2\_BOVIN, METK1\_HUMAN, AASS\_BOVIN |
| extracellular structure organization | CR3L2\_DANRE, FLNA\_DROME, MMP13\_RABIT, PXDN\_HUMAN, TENX\_HUMAN, PPN\_DROME, PRDX4\_MOUSE, CO1A2\_RAT, COBA1\_HUMAN, LRP1\_HUMAN, NID1\_HUMAN, PXDN\_DROME, SPTCA\_DROME, CO3A1\_MOUSE |
| extracellular matrix organization | PRDX4\_MOUSE, CR3L2\_DANRE, CO1A2\_RAT, COBA1\_HUMAN, LRP1\_HUMAN, NID1\_HUMAN, MMP13\_RABIT, PXDN\_HUMAN, PXDN\_DROME, TENX\_HUMAN, CO3A1\_MOUSE, PPN\_DROME |
| reactive oxygen species metabolic process | RGN\_RAT, PRDX4\_MOUSE, CBS\_RAT, PXDN\_HUMAN, CLCN3\_MOUSE, PXDN\_DROME, PERC\_AEDAE, AGT2\_BOVIN, PERC\_ANOGA |
| glycosylation | B3GN5\_PIG, MGT4B\_DANRE, GCNT1\_MOUSE, TMM59\_MOUSE, ALG8\_HUMAN, BRE4\_CAEBR, PMGT1\_HUMAN, D19L1\_HUMAN, FUCT1\_MOUSE, GALT9\_CAEEL, FUCTA\_DROME, STT3A\_BOVIN, GOGA2\_RAT, EDEM2\_HUMAN, LRP2\_HUMAN |
| glycoprotein metabolic process | B3GN5\_PIG, MGT4B\_DANRE, GCNT1\_MOUSE, TMM59\_MOUSE, ALG8\_HUMAN, BRE4\_CAEBR, PMGT1\_HUMAN, D19L1\_HUMAN, CANT1\_HUMAN, G3ST2\_MOUSE, GALT9\_CAEEL, COBA1\_HUMAN, FUCTA\_DROME, STT3A\_BOVIN, GOGA2\_RAT, EDEM2\_HUMAN, LRP2\_HUMAN |
| **SEN24 upregulated** | |
| regulation of microvillus organization | PLSI\_BOVIN, RPGP1\_MOUSE, USH1C\_HUMAN |
| cellular hormone metabolic process | RDH11\_MOUSE, CP17A\_CHICK, RDHE2\_HUMAN, RISC\_MOUSE, RDH14\_HUMAN, S5A1\_RAT |
| retinoid metabolic process | RDH11\_MOUSE, RDHE2\_HUMAN, RISC\_MOUSE, RDH14\_HUMAN |
| iron ion homeostasis | TRFM\_RABIT, MFRN2\_HUMAN, SFXN1\_PIG, NRAM2\_RAT, STEA4\_HUMAN |
| transition metal ion transport | TRFM\_RABIT, MFRN2\_HUMAN, P3C2A\_MOUSE, SFXN1\_PIG, NRAM2\_RAT, STEA4\_HUMAN |
| hormone metabolic process | RDH11\_MOUSE, CP17A\_CHICK, RDHE2\_HUMAN, RISC\_MOUSE, DUOX2\_RAT, RDH14\_HUMAN, S5A1\_RAT |
| cellular response to growth factor stimulus | FSTL3\_HUMAN, ATS7\_MOUSE, RPGP1\_MOUSE, S5A1\_RAT, KCP\_HUMAN, CD109\_MOUSE, PTPRK\_HUMAN, PTN\_RAT, CD63\_RAT, RAB14\_PONAB, COR1B\_HUMAN, DOK5\_HUMAN, CASP3\_PIG, NRP1A\_DANRE |
| lipid metabolic process | THAS\_RAT, SAP\_BOVIN, PLD3\_XENLA, P3C2A\_MOUSE, SCD5\_BOVIN, RISC\_MOUSE, S14L2\_RAT, PTPM1\_RAT, PTPM1\_DROME, S5A1\_RAT, PLBL2\_HUMAN, SERC1\_MOUSE, RDH11\_MOUSE, CP17A\_CHICK, RDHE2\_HUMAN, GDPD5\_HUMAN, PK3CB\_MOUSE, OCTC\_MOUSE, FABG\_THEMA, RDH14\_HUMAN, SAP3\_MACFA |
| **FER24 vs FER-TD** | |
| extracellular matrix disassembly | TRFM\_RABIT, MMP19\_HUMAN |
| plasma membrane organization | PLSI\_BOVIN, SPTCB\_DROME, TMED2\_CRIGR |
| regulation of cell adhesion | TRFM\_RABIT, VWC2\_MOUSE, LEG3\_RABIT |
| single-organism membrane organization | PLSI\_BOVIN, GOSR1\_MOUSE, SPTCB\_DROME, TMED2\_CRIGR |
| signaling | MYOM1\_APLCA, PTBP1\_HUMAN, VWC2\_MOUSE, DLGP1\_DANRE, TSN18\_MOUSE, CAR9\_ARATH, SPTCB\_DROME, ABR\_XENLA, LEG3\_RABIT, NEC1\_HUMAN |

IDs of the gene products are shown within each gene ontology (GO) term. MAT: mated, FER: fertilization, SEN: senescence, 24: control treatment at 24 °C, TD: heat-shock treatment with temperature decrease.