# Coevolving gene pairs shared between Humans and Choanos

## Apoptosis / Cell Death

• THYN1 (NP\_001032382.1) and DELE1 (NP\_001136075.1)

• THYN1 encodes a protein that is highly conserved among

vertebrates and plant species and may be involved in the induction

of apoptosis. DELE1 is an extrinsic apoptotic signaling pathway via death domain receptors; and regulation of cysteine-type endopeptidase activity involved in apoptotic process

## Flagellum related

• CFAP418 (NP\_808880.1) and DALRD3 (XP\_005265326.1)

• CFAP418 is a cilia- and flagella-associated protein. DALRD3 has unknown function but preferential expression of this gene in testis suggests a role of this gene in spermatogenesis

## Metal homeostasis

• TMEM203 (NP\_444273.1) and TATDN3 (NP\_001139643.1)

• TMEM203 is predicted to enable metal ion binding activity and nuclease activity. TATDN3 is predicted to enable metal ion binding activity and nuclease activity.

## Glycosylation

• ALG14 (NP\_659425.1) and PIGQ (NP\_683721.1)

• Both are implicated in Congenital Disorders of Glycosylation

• <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7827962/>

## Cell cycle and DNA replication / repair

• ACTR1B (NP\_005726.1) and MAD2L1BP (NP\_001003690.1)

• ACTR1B (actin-related protein 1B) encodes a subunit of dynactin, which is involved in many processes including spindle formation. MAD2L1BP (MAD2L1 binding protein) interacts with MAD2 and interacts with the spindle checkpoint.

• GPI (NP\_001276718.1) and CDKN3 (NP\_005183.2)

• Both are co-expressed in small-cell lung cancer cells

• <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3631177/>

• PIR (NP\_001018119.1) and CENPV (NP\_859067.2)

• CENPV is involved in regulation of chromosome organization. Acts upstream of or within ameboidal-type cell migration. Located in several cellular components, including midbody; nucleus; and spindle midzone

• PIR protein may act as a transcriptional cofactor and be involved in the regulation of DNA transcription and replication

• RNF168 (NP\_689830.2) and CDKN3 (NP\_005183.2)

• RNF168 involved in DNA double-strand break (DSB) repair

• CDKN3 is a cyclin-dependent kinase inhibitor, and has been shown to interact with, and dephosphorylate CDK2 kinase, thus prevent the activation of CDK2 kinase

• CENPV (NP\_859067.2) and SMC5 (NP\_055925.2)

• CENPV is involved in pericentric heterochromatin assembly; positive regulation of cytokinesis; and regulation of chromosome organization

• SMC5 is involved in several processes, including DNA recombination; cellular senescence; and positive regulation of maintenance of mitotic sister chromatid cohesion

• CENPV (NP\_859067.2) and CEP20 (NP\_001291428.1)

• CEP20 is a centrosomal protein located in centriolar satellite and nucleoplasm

• CENPV (NP\_859067.2) and MKI67 (NP\_002408.3)

• NKI67 Involved in regulation of chromosome segregation and regulation of mitotic nuclear division

## Peri-implantation

• EIF4E3 (NP\_001128123.1) and TMEM218 (XP\_024304152.1)

• Both genes show similar expression dynamics during peri-implantation, the 3 to 9 days prior to the end of the menstrual cycle

• <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8967306/>

## Postsynaptic density complex

• PPP5C (XP\_016882424.1) and PSMD10 (NP\_002805.1)

• both are part of the postsynaptic density protein complex <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1785339/>

• The postsynaptic density protein complex is associated with postsynaptic membranes of excitatory synapses

## Lipid metabolism

• NDUFS3 (NP\_004542.1) RPP14 (NP\_001092253.1)

• both are involved in PLIN2-associated lipid metabolism and lipid droplet biology

• <https://www.biorxiv.org/content/10.1101/2022.08.27.505556v1.full.pdf>

• BDH2 (XP\_006714337.1) and CYP51A1 (NP\_000777.1)

• both involved in lipid-related processes

## Testis

• TEX9 (NP\_001382425.1) and EFHB (NP\_653316.3)

• both have a biased expression in Testis

• CCDC112 (NP\_001035530.1) and CCDC86 (NP\_077003.1)

• both are expressed in the Testis

• both have coiled-coil domains

## mRNA processing

• ZC3H3 (XP\_016868737.1) and GEMIN7 (NP\_001007270.1)

• both involved in mRNA processing

## Ribosomal

• DHX30 (XP\_011531792.1) and RPL8 (NP\_000964.1)

• DHX30 is a DEAD box protein and is implicated in a number of cellular processes involving alteration of RNA secondary structure such as translation initiation, nuclear and mitochondrial splicing, and ribosome and spliceosome assembly

• RPL8 encodes a ribosomal protein that is a component of the 60S subunit

• RPP14 (NP\_001092253.1) and YJU2B (NP\_001307490.1)

• RPP14 encodes a subunit of ribonuclease P and has 3' to 5' exoribonuclease activity

• YJU2B is part of U2-type spliceosomal complex and post-mRNA release spliceosomal complex

## Transcription

• MED27 (XP\_016870818.1) and CTDSPL2 (NP\_057480.2)

• MED27 is part of numerous factors that, along with co-activators, direct transcriptional initiation by the RNA polymerase II apparatus. The protein encoded by this gene is a subunit of the CRSP (cofactor required for SP1 activation) complex

• CTDSPL2 helps enables RNA polymerase II CTD heptapeptide repeat phosphatase activity

• MED27 (XP\_016870818.1) and DHX29 (NP\_061903.2)

• DHX29 encoded protein functions in translation initiation, and is specifically required for ribosomal scanning across stable mRNA secondary structures during initiation codon selection

## Translation

• DRG1 (NP\_004138.1) and ETF1 (NP\_004721.1)

• DRG1 is part of polysome, ensembles of two or more consecutive ribosomes that translate mRNA into proteins

• ETF1 encoded protein plays an essential role in directing termination of mRNA translation from the termination codons UAA, UAG and UGA. This protein is a component of the SURF complex which promotes degradation of prematurely terminated mRNAs via the mechanism of nonsense-mediated mRNA decay (NMD)

## Mitochondrial

• MRPS14 (NP\_071383.1) and COA5 (NP\_001008216.1)

• COA5 encodes a subunit of a large oligomeric complex associated with the mitochondrial inner membrane, and required for the assembly of the cytochrome c oxidase complex

• MRPS14 encodes a 28S subunit protein that belongs to the mitochondrial ribosomal protein S14P family

• NDUFA12 (NP\_061326.1) and SARM1 (NP\_055892.2)

• NDUFA12 encodes a protein which is part of mitochondrial complex 1, part of the oxidative phosphorylation system in mitochondria

• SARM1 is located in mitochondrion

• NDUFA2 (NP\_002479.1) and PIN4 (NP\_006214.3)

• NDUFA2 encodes a protein that is a subunit of the hydrophobic protein fraction of the NADH:ubiquinone oxidoreductase (complex 1), the first enzyme complex in the electron transport chain located in the inner mitochondrial membrane, and may be involved in regulating complex I activity or its assembly via assistance in redox processes

• PIN4 may play an additional role in the mitochondria

• UQCR10 (NP\_037519.2) and ACSS3 (NP\_078836.1)

• ACSS3 is located in mitochondrial matrix

• UQCR10 is a part of the UCRC, a subunit of mitochondrial complex III

• NDUFAF8 (NP\_001340331.1) and MRPL21 (XP\_005273880.1)

• NDUFAF8 is involved in mitochondrial respiratory chain complex I assembly and located in mitochondrion

• MRPL21 stands for mitochondrial ribosomal protein L21

## Transport

• TRAPPC12 (NP\_001308031.1) and SSR4 (NP\_001191455.1)

• TRAPPC12 is involved in several processes, including endoplasmic reticulum to Golgi vesicle-mediated transport; positive regulation of protein localization to kinetochore; and regulation of kinetochore assembly

• SSR4 encodes the delta subunit of the translocon-associated protein complex which is involved in translocating proteins across the endoplasmic reticulum membrane

## Interesting

• TAF13 (NP\_005636.1) and HYPK (NP\_057484.4)

• TAF13 initiates transcription whereas HYPK is associated with apoptosis