Table to compare 2n and 3n initial stage.

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| **Initial 2n** |  |  |  |  |
| **Trinity ID** | **UniProt ID** | **Protein name** | **Expression**  **LnFC** | **GO of interest** |
| TRINITY\_DN32354\_c0\_g1\_i2 | MSH5\_MOUSE | MutS protein homolog 5 | 6.92 | **GO:0030983:** Mismatched DNA binding.  **GO:0051026:** Chiasma assembly.  **GO:0006298:** Mismatch repair  **GO:0005524:** ATP binding  **GO:0030983:** Mismatched DNA binding.  **GO:0006298:** Mismatch repair. |
| TRINITY\_DN29394\_c2\_g1\_i3 | ATD1B\_DANRE | ATPase family AAA domain-containing protein 1-B | 7.48 | **GO:0006281:** DNA repair.  **GO:0006310:** DNA recombination |
| TRINITY\_DN34945\_c3\_g1\_i4 | PIAP\_PIG | Putative inhibitor of apoptosis | 6.65 | **GO:1990001:** Cysteine-type endopeptidase inhibitor activity involved in apoptotic process. |
| TRINITY\_DN28602\_c0\_g1\_i1 | NOX5\_HUMAN | NADPH oxidase 5 | 7.23 | **GO:0006915:** Apoptotic process.  **GO:0008283:** Cell proliferation.  **GO:0000910:** Cytokinesis |
| TRINITY\_DN34797\_c0\_g1\_i9 | NUP62\_HUMAN | Nuclear pore glycoprotein p62 | 9.83 | **GO:0043066:** negative regulation of apoptotic process.  **GO:0007080:** Mitotic metaphase plate congression.  **GO:0007077**: Mitotic nuclear envelope disassembly.  **GO:1903438**: Positive regulation of mitotic cytokinetic process.  **GO:0007283**: Spermatogenesis |
| TRINITY\_DN37351\_c1\_g1\_i10 | DRPR\_DROME | Protein draper | 6.79 | **GO:0043277:** Apoptotic cell clearance**.**  **GO:0006909:** Phagocytosis |
| TRINITY\_DN32906\_c1\_g2\_i1 | PPT1\_MACFA | Palmitoyl-protein thioesterase 1 | 8.1 | **GO:0043066:** Negative regulation of apoptotic process. |
| TRINITY\_DN36186\_c3\_g1\_i5 | STBPA\_DANRE | STAM-binding protein-like A | 7.2 | **GO:0000281:** Mitotic cytokinesis.7 **GO:0043524:** Negative regulation of neuron apoptotic process. |
| TRINITY\_DN29043\_c0\_g1\_i3 |  |  | 7.89 | **GO:1902236:** Negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway. |
| TRINITY\_DN33458\_c5\_g1\_i1 | IRF2\_CHICK | Interferon regulatory factor 2 | 8.75 | **GO:0006915:** Apoptotic process. |
| TRINITY\_DN37331\_c0\_g3\_i1 | DRPR\_DROME | Protein draper | 7.4 | **GO:0043277:** Apoptotic cell clearance.  **GO:0043652:** Engulfment of apoptotic cell |
| TRINITY\_DN34945\_c3\_g1\_i4 | PIAP\_PIG | Putative inhibitor of apoptosis | 6.6 | **GO:0043027:** Cysteine-type endopeptidase inhibitor activity involved in apoptotic process.  **GO:0060546:** Negative regulation of necroptotic process. |
| TRINITY\_DN34242\_c0\_g1\_i7 | IOD1\_FUNHE | Type I iodothyronine deiodinase | 8.2 | **GO:0055114:** Oxidation-reduction process |
| RINITY\_DN34652\_c0\_g1\_i6 | PDIP2\_MOUSE | Polymerase delta-interacting protein 2 | 7.03 | **GO:0016242**: Negative regulation of macroautophagy.  **GO:0045931:** Positive regulation of mitotic cell cycle.  **GO:0003677:** DNA binding. |
| TRINITY\_DN37022\_c0\_g1\_i1 | FLOT1\_DROME | Flotillin-1 | 12.21 | **GO:0007275:** Multicellular organism development. |
| TRINITY\_DN32497\_c0\_g2\_i1 | EXOS2\_BOVIN | Exosome complex component RRP4 | 5.3 | **GO:0030307:** Positive regulation of cell growth. |
| TRINITY\_DN37384\_c0\_g1\_i2 | MLC2\_DROME | Myosin-2 essential light chain | 13.15 | **GO:0030048:** Actin filament-based movement. |
| TRINITY\_DN35329\_c0\_g1\_i2 | PPR42\_XENLA | Protein phosphatase 1 regulatory subunit 42 | 8.4 | **GO:0015631:** Tubulin binding  **GO:0005515:** Protein binding |
| TRINITY\_DN31642\_c0\_g1\_i1 | GRB2A\_XENLA | Growth factor receptor-bound protein 2-A | 5.27 | **GO:0007143:** Female meiotic nuclear division. |
| TRINITY\_DN35559\_c0\_g3\_i1 | KDM8\_HUMAN | Lysine-specific demethylase 8 | 7.9 | **GO:0000086:** G2/M transition of mitotic cell cycle.  **GO:0070544:** Histone H3-K36 demethylation. |
| TRINITY\_DN37465\_c0\_g1\_i7 | ENS\_CHICK | Tensin | 10 | **GO:0003779:** Actin binding.  **GO:0005515:** Protein binding. |
| TRINITY\_DN36922\_c0\_g1\_i6 | P1M1\_HUMAN | AP-1 complex subunit mu-1 | 10.05 | **GO:0050690:** Regulation of defense response to virus by virus. |
| TRINITY\_DN30416\_c1\_g1\_i4 | BB4B\_MESAU | Tubulin beta-4B chain | 9.99 | **GO:0007017:** Microtubule-based process |
| TRINITY\_DN30336\_c0\_g1\_i3 | CENPT\_CHICK | Centromere protein T | 7.8 | **GO:0007049:** Cell cycle.  **GO:0051301:** Cell division.  **GO:1903394:** Protein localization to kinetochore involved in kinetochore. assembly |
| TRINITY\_DN34934\_c0\_g2\_i2 | HGL\_DROME | Glucose dehydrogenase [FAD, quinone] | 7.62 | **GO:0046693:** Sperm storage |
| TRINITY\_DN36174\_c0\_g1\_i1 | PUM3\_RAT | Pumilio homolog 3 | 8.4 | **GO:0006417:** Regulation of translation |
| TRINITY\_DN34500\_c0\_g2\_i9 | OSB11\_HUMAN | Oxysterol-binding protein-related protein 11 | 7.72 | **GO:0010890:** Positive regulation of sequestering of triglyceride. |
| TRINITY\_DN31108\_c0\_g1\_i3 | PATS1\_DICDI | Probable serine/threonine-protein kinase pats1 | 7.2 | **GO:0000281:** Mitotic cytokinesis.  **GO:0006470:** Protein dephosphorylation. |
| TRINITY\_DN37351\_c1\_g1\_i5 | FUCL5\_ANGJA | Fucolectin-5 | 8.03 | **GO:0010185:** Regulation of cellular defense response. |
| TRINITY\_DN30067\_c5\_g5\_i1 | FABP9\_HUMAN | Fatty acid-binding protein 9 | 7.07 | **GO:0001675:** Acrosome assembly.  **GO:0019433:** Triglyceride catabolic process. |
| TRINITY\_DN34319\_c0\_g2\_i1 | ZN207\_XENLA | BUB3-interacting and GLEBS motif-containing protein ZNF207 | 7.5 | **GO:0008608:** Attachment of spindle microtubules to kinetochore.  **GO:0051301:** Cell division  **GO:0001578:** Biological\_process^microtubule bundle formation.  **GO:0046785:** Microtubule polymerization.  **GO:0000070:** Mitotic sister chromatid segregation.  **GO:0090307:** Mitotic spindle assembly.  **GO:0007094**: Mitotic spindle assembly checkpoint.  **GO:0050821:** Protein stabilization.  **GO:0051983:** Regulation of chromosome segregation. |
| TRINITY\_DN35667\_c1\_g2\_i6 | CAD99\_DROME | Cadherin-99C | 10.23 | **GO:0007305:** Vitelline membrane formation involved in chorion-containing eggshell formation. |
| TRINITY\_DN33730\_c0\_g2\_i14 | NPHP1\_CANLF | Nephrocystin-1 | 9.4 | **GO:0007283:** Spermatogenesis**.** |
| TRINITY\_DN31394\_c0\_g1\_i1 | SPAT6\_MOUSE | Spermatogenesis-associated protein 6 | 8.3 | **GO:0007283:** Spermatogenesis**.** |
| TRINITY\_DN28889\_c0\_g1\_i2 | DMTA2\_XENTR | Doublesex- and mab-3-related transcription factor A2 | 7.9 | Sexual differentiation. |

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| **Initial 3n** |  |  |  |  |
| **Trinity ID** | **UniProt ID** | **Protein name** | **Expression**  **LnFC** | **GO of interest** |
| TRINITY\_DN37482\_c0\_g1\_i2 | XPC\_MOUSE | DNA repair protein complementing XP-C cells homolog | 9.33 | **GO:0006281:** DNA repair.  **GO:0070911:** Global genome nucleotide-excision repair.  **GO:0031573:** Intra-S DNA damage checkpoint.  **GO:0000715:** Nucleotide-excision repair, DNA damage recognition.  **GO:0000717:** Nucleotide-excision repair, DNA duplex unwinding  **GO:0006294:** nnucleotide-excision repair, preincision complex assembly.  **GO:1901990:** Regulation of mitotic cell cycle phase transition. |
| TRINITY\_DN25833\_c0\_g1\_i3 | CASP3\_PANTR | Caspase-3 | 8.65 | **GO:0004861:** Cyclin-dependent protein serine/threonine kinase inhibitor activity.  **GO:0008656:** Cysteine-type endopeptidase activator activity involved in apoptotic process.  **GO:0006309:** Apoptotic DNA fragmentation.  **GO:0006915:** Apoptotic process.  **GO:0097190**: Apoptotic signaling pathway.  **GO:0006974:** Cellular response to DNA damage stimulus.  **GO:0097194:** Execution phase of apoptosis.  **GO:0045736**: Negative regulation of cyclin-dependent protein serine/threonine kinase activity.  **GO:0006508:** Proteolysis. |
| TRINITY\_DN36539\_c0\_g1\_i | MYO6\_CHICK | Unconventional myosin-VI | 9.79 | **GO:0030330:** DNA damage response, signal transduction by p53 class mediator.  **GO:0006897:** Endocytosis. |
| TRINITY\_DN35761\_c0\_g1\_i7 | RA51C\_CRIGR | DNA repair protein RAD51 homolog 3 | 7.01 | **GO:0006310:** DNA recombination  **GO:0006281:** DNA repair.  **GO:0000724:** Double-strand break repair via homologous recombination.  **GO:0010971:** Positive regulation of G2/M transition of mitotic cell cycle.  **GO:0007062:** Sister chromatid cohesion. |
| TRINITY\_DN31588\_c0\_g1\_i5 | DFFA\_MOUSE | DNA fragmentation factor subunit alpha | 6.60 | **GO:0043065:** Positive regulation of apoptotic process.  **GO:0006915:** Apoptotic process |
| TRINITY\_DN36926\_c0\_g1\_i4 | TMF1\_HUMAN | TATA element modulatory factor | 8.13 |  |
| TRINITY\_DN35612\_c1\_g1\_i10 | ATG4D\_MOUSE | Cysteine protease ATG4D | 4.52 | **GO:0006915:** Apoptotic process.  **GO:0000045**: Autophagosome assembly  **GO:0006914**: Autophagy  **GO:0000422**: Autophagy of mitochondrion  **GO:0044804**: Autophagy of nucleus. |
| TRINITY\_DN35168\_c6\_g1\_i1 | PRUN2\_PONAB | Protein prune homolog 2 | 9.5 | **GO:0006915:** Apoptotic process. |
| TRINITY\_DN32329\_c0\_g1\_i1 | TNB\_CHICK | Methylthioribulose-1-phosphate dehydratase | 9.5 | **GO:0006915:** Apoptotic process. |
| TRINITY\_DN29108\_c1\_g2\_i6 | MBL\_DROME | Protein muscleblind | 6.10 | **GO:0006915:** Apoptotic process. |
| TRINITY\_DN33077\_c0\_g2\_i3 | TNR5\_PIG | Tumor necrosis factor receptor superfamily member 5 | 8.04 | **GO:0097190:** Apoptotic signaling pathway**.**  **GO:2000353:** Positive regulation of endothelial cell apoptotic process.  **GO:0042981:** Regulation of apoptotic process. |
| TRINITY\_DN37198\_c1\_g1\_i2 | FBW1B\_MOUSE | F-box/WD repeat-containing protein 11 | 6.11 | **GO:0007049:** Cell cycle.  **GO:0045862:** Positive regulation of proteolysis. |
| TRINITY\_DN32092\_c5\_g1\_i4 | DOLK\_MOUSE | Dolichol kinase | 7.4 | **GO:0004168:** Dolichol kinase activity  **GO:0006486:** Protein glycosylation |
| TRINITY\_DN36926\_c0\_g1\_i4 | TMF1\_HUMAN | TATA element modulatory factor | 8.13 | **GO:0043066:** Negative regulation of apoptotic process  **GO:0001819:** Positive regulation of cytokine production.  **GO:0061136:** Regulation of proteasomal protein catabolic process**.**  **GO:0007289:** Spermatid nucleus differentiation. |
| TRINITY\_DN34453\_c0\_g1\_i2 | CMTR1\_DANRE | Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1 | 8.24 | **GO:0032259:** Methylation |
| TRINITY\_DN32289\_c0\_g1\_i3 | SPNS1\_DANRE | Protein spinster homolog 1 | 8.03 | **GO:0006914:** Autophagy |
| TRINITY\_DN30802\_c0\_g1\_i2 | TRIM9\_BOVIN | E3 ubiquitin-protein ligase TRIM9 | 8.19 | **GO:0043161:** Proteasome-mediated ubiquitin-dependent protein catabolic process. |
| TRINITY\_DN35007\_c0\_g1\_i10 | MCN1\_MOUSE | Hemicentin-1 | 8.84 | **GO:0007049:** Cell cycle  **GO:0051301:** Cell division |
| TRINITY\_DN29159\_c0\_g1\_i3 | SYB\_APLCA | Synaptobrevin | 6.41 | **O:0006887:** Exocytosis  **GO:0006623:** Protein targeting to vacuole  **GO:0007033:** Vacuole organization  **GO:0006906:** Vesicle fusion  **GO:0016192:** Vesicle-mediated transport |
| TRINITY\_DN37053\_c0\_g1\_i3 | NUF2B\_XENLA | Kinetochore protein Nuf2-B | 7.4 | **GO:0051301:** Cell division  **GO:0000278:** Mitotic cell cycle  **GO:0000278:** Mitotic cell cycle |
| TRINITY\_DN30732\_c0\_g1\_i4 | Y8948\_DICDI | Putative methyltransferase | 8.4 | **GO:0008168:** Methyltransferase activity.  **GO:0008152:** Metabolic process. |
| TRINITY\_DN35865\_c1\_g2\_i2 | TYSY\_MOUSE | Thymidylate synthase | 8.38 | **GO:0034097:** Response to cytokine. |
| TRINITY\_DN32329\_c0\_g1\_i1 | MTNB\_CHICK | Methylthioribulose-1-phosphate dehydratase | 9.5 | **GO:0006915:** Apoptotic process. |
| TRINITY\_DN33730\_c0\_g2\_i14 | NPHP1\_CANLF | Nephrocystin-1 | 9.10 | **GO:0007283:** Spermatogenesis. |
| TRINITY\_DN34548\_c0\_g1\_i5 | SLP1\_SCHPO | WD repeat-containing protein slp1 | 9.35 | **GO:0051301:** cell division  **GO:0034613:** cellular protein localization  **GO:0000070:** mitotic sister chromatid segregation  **GO:1905188:** positive regulation of metaphase/anaphase transition of meiosis I  **GO:1905191:** Positive regulation of metaphase/anaphase transition of meiosis II  **GO:0005515:** Protein binding |
| TRINITY\_DN34648\_c0\_g2\_i8 | RELN\_CHICK | Reelin | 8 | **GO:0045860:** Positive regulation of protein kinase activity. |
| TRINITY\_DN33077\_c0\_g2\_i3 | TNR5\_PIG | Tumor necrosis factor receptor superfamily member 5 | 8.0406298309 | **GO:0097190:** apoptotic signaling pathway  **GO:2000353:** positive regulation of endothelial cell apoptotic process`  **GO:0048304:** positive regulation of isotype switching to IgG isotypes  **GO:0043406:** positive regulation of MAP kinase activity  **GO:0090037:** positive regulation of protein kinase C signaling  **GO:0042981:** regulation of apoptotic process |
| TRINITY\_DN31588\_c0\_g1\_i5 | DFFA\_MOUSE | DNA fragmentation factor subunit alpha | 6.60 | **GO:0043065:** positive regulation of apoptotic process  **GO:0070242:** thymocyte apoptotic process  **GO:0006915:** apoptotic process |
| TRINITY\_DN36918\_c0\_g1\_i2 | HEM\_DROME | Membrane-associated protein Hem | 9.06 | **GO:0006909:** phagocytosis |
| TRINITY\_DN37209\_c0\_g1\_i3 | IFT56\_HUMAN | Intraflagellar transport protein 56 | 10.13 | **GO:0007286:** Spermatid development |
| TRINITY\_DN37621\_c1\_g2\_i2 | LCP2\_MOUSE | Lymphocyte cytosolic protein 2 | 9.47 | **GO:0045860:** positive regulation of protein kinase activity |
| TRINITY\_DN29611\_c1\_g1\_i2 | RAB14\_PONAB | Ras-related protein Rab-14 | 6.15 | **GO:0090382:** phagosome maturation |
| TRINITY\_DN28829\_c0\_g1\_i2 | TPRGL\_HUMAN | Tumor protein p63-regulated gene 1-like protein | 7.42 | **GO:0008021^cellular\_component^synaptic vesicle`GO:0030672^cellular\_component^synaptic vesicle membrane** |
| TRINITY\_DN25996\_c0\_g2\_i11 | RI2\_ARATH | Probable E3 ubiquitin-protein ligase ARI2 | 6.4 | **GO:0042787^biological\_process^protein ubiquitination involved in ubiquitin-dependent protein catabolic process** |