**SUPPLEMENTARY Tables**

**Table 1. List of various filtered genes involved in different biological processes (BP), molecular functions (MF) and cellular components (CC) in HF bull spermatozoa**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Category** | **Term** | **Count** | **%** | **P-value** | **Genes involved** |
|  | **Biological process** |
| GOTERM\_BP\_DIRECT | GO:0015986~ATP synthesis coupled proton transport | 3 | 3.48 | 0.004 | ATP8, ATP6, ATP6V0A2 |
| GOTERM\_BP\_DIRECT | GO:0007605~sensory perception of sound | 3 | 3.48 | 0.07 | ATP8B1, STRC, CCDC50 |
| GOTERM\_BP\_DIRECT | GO:0006958~complement activation, classical pathway | 2 | 2.32 | 0.07 | C7, CD46 |
|  | **Cellular components** |
| GOTERM\_CC\_DIRECT | GO:0005654~nucleoplasm | 12 | 13.95 | 0.03 | PNN, SH3RF2, NEIL3, ANXA1, VWA5A, RBBP6, SHOC2, NDRG2, CCDC174, SF3B1, GIMAP8, BPTF |
| GOTERM\_CC\_DIRECT | GO:0016324~apical plasma membrane | 7 | 8.13 | 7.99E-05 | ABCC2, ANXA1, C15H11ORF34, ATP8B1, SLC30A5, ADRB2, SLC17A3 |
| GOTERM\_CC\_DIRECT | GO:0048471~perinuclear region of cytoplasm | 7 | 8.13 | 0.01 | PICK1, PTPRM, STX4, NDRG2, TYR, ATP9A, SLC17A3 |
| GOTERM\_CC\_DIRECT | GO:0005794~Golgi apparatus | 6 | 6.97 | 0.08 | ARHGAP21, ST6GALNAC2, ATP8B1, SLC30A5, NDRG2, EAPP |
| GOTERM\_CC\_DIRECT | GO:0005925~focal adhesion | 5 | 5.81 | 0.05 | AKAP12, ANXA1, ATP6V0A2, MYH9, CD46 |
| GOTERM\_CC\_DIRECT | GO:0070469~respiratory chain | 2 | 2.32 | 0.06 | ND3, ND5 |
| GOTERM\_CC\_DIRECT | GO:0005753~mitochondrial proton-transporting ATP synthase complex | 2 | 2.32 | 0.08 | ATP8, ATP6 |
|  | **Molecular functions** |
| GOTERM\_MF\_DIRECT | GO:0008270~zinc ion binding | 10 | 11.62 | 0.02 | SH3RF2, NEIL3, MKRN1, LTN1, CHD5, RBBP6, BAZ2B, BAZ1A, ADAMTS20, BPTF |
| GOTERM\_MF\_DIRECT | GO:0044822~poly(A) RNA binding | 9 | 10.46 | 0.03 | PNN, ZNF207, CISD2, MYH9, RBBP6, SSRP1, RRP1B, WDR43, EIF1 |
| GOTERM\_MF\_DIRECT | GO:0000287~magnesium ion binding | 4 | 4.65 | 0.04 | ATP8B1, HACL1, ENO4, ATP9A |
| GOTERM\_MF\_DIRECT | GO:0008514~organic anion transmembrane transporter activity | 2 | 2.32 | 0.04 | ABCC2, SLC17A3 |
| GOTERM\_MF\_DIRECT | GO:0004012~phospholipid-translocating ATPase activity | 2 | 2.32 | 0.06 | ATP8B1, ATP9A |
| GOTERM\_MF\_DIRECT | GO:0015078~hydrogen ion transmembrane transporter activity | 2 | 2.32 | 0.08 | ATP8, ATP6 |
| GOTERM\_MF\_DIRECT | GO:0016887~ATPase activity | 3 | 3.48 | 0.08 | DNAH10, ATP8, ATP6 |

**Table. 2. List of enriched pathways of novel and filtered genes in HF bull spermatozoa**

|  |  |
| --- | --- |
|  | **Enriched pathways of the novel genes** |
| **Pathway** | **Count** | **P-value** | **Genes Involved** |
| bta04024:cAMP signalling pathway | 25 | 2.14E-10 | GRIA1, OXTR, ADCY3, ADCY2, ATP1A1, PIK3CB, HTR4, GLI3, MAPK9, AKT3, CNGA1, PDE4B, RAC2, PLCE1, PRKACB, CAMK2G, VAV3, PPP1R12A, PDE4D, NPY1R, ATP2B2, MAPK10, PIK3CA, PDE3A, CFTR |
| bta04080:Neuroactive ligand-receptor interaction | 24 | 1.36E-05 | GRIA1, PTGFR, GABRA1, LHCGR, OXTR, THRB, GZMA, NPY2R, NPY1R, GRIK4, OPRM1, GRIK2, HTR2A, HTR4, ADRA1A, TAAR1, RXFP1, P2RX7, GLRA1, MC3R, GRM5, CYSLTR1, GABRR1, C3AR1 |
| bta04510:Focal adhesion | 23 | 1.14E-07 | VAV3, COL27A1, PPP1R12A, SHC3, ACTN2, LAMA4, CAV1, LAMA3, ACTN4, PIK3CB, MYLK, MAPK10, MAPK9, COL1A2, PIK3CA, PDGFD, AKT3, COL5A2, RAC2, FLNB, FYN, TLN2, ITGA9 |
| bta04020:Calcium signaling pathway | 22 | 1.36E-08 | PTGFR, LHCGR, OXTR, ADCY3, PHKB, ATP2B2, ADCY2, HTR2A, HTR4, ADRA1A, RYR3, MYLK, P2RX7, PPP3CA, GNA14, GRM5, CYSLTR1, PTK2B, PLCE1, PLCB1, CAMK2G, PRKACB |
| bta04010:MAPK signaling pathway | 20 | 3.21E-06 | CACNA2D3, STK4, NGF, TGFBR1, MAPK10, PPP3CA, MAPK9, PPM1A, RPS6KA3, CACNB2, IL1B, NTF3, AKT3, RAC2, RAPGEF2, FLNB, PRKACB, HSPA1A, MAP3K5 |
| bta00230:Purine metabolism | 18 | 1.15E-06 | ENTPD2, GDA, PDE4D, ENTPD6, AK2, ADK, AK3, ADCY3, ADCY2, FHIT, PAPSS2, POLE2, POLR2D, POLE3, PDE4B, PDE3A, PDE6C, PDE7B |
| bta04015:Rap1 signaling pathway | 18 | 1.73E-06 | MAGI1, RALB, INSR, ADCY3, ADCY2, PIK3CB, NGF, PIK3CA, PDGFD, AKT3, RAC2, RAPGEF2, PLCE1, TEK, TLN2, PRKD1, PLCB1, SKAP1 |
| bta04310:Wnt signaling pathway | 17 | 8.36E-07 | FZD2, WNT5B, TCF7, PRICKLE2, WNT8B, DKK2, LRP6, MAPK10, PPP3CA, MAPK9, DAAM1, RAC2, BTRC, PLCB1, CAMK2G, PRKACB, SKP1 |
| bta04141:Protein processing in endoplasmic reticulum | 17 | 5.38E-06 | ERO1A, TUSC3, UBE2D2, NGLY1, SEL1L, UBE4B, UBE2J1, MAPK10, MAPK9, DNAJC1, PLAA, UGGT1, SIL1, HSPA1A, SKP1, MAP3K5 |
| bta05202:Transcriptional misregulation in cancer | 16 | 3.82E-05 | ATF1, EYA1, ZBTB16, PBX3, TMPRSS2, ETV1, MLLT1, MLLT3, UNC13D, ETV5, RUNX2, FLI1, FUT8, NR4A3, NCOR1, RUNX1T1 |
|  | **Enriched pathways of genes which are novel and filtered** |
| bta00190:Oxidative phosphorylation | 5 | 0.001 | ATP8, ATP6, ATP6V0A2, ND3, ND5 |
| bta05012:Parkinson's disease | 4 | 0.02 | ATP8, ATP6, ND3, ND5 |
| bta01100:Metabolic pathways | 9 | 0.09 | ATP8, SI, ATP6, ATP6V0A2, IDNK, TYR, IDO2, ND3, ND5 |

**Table 3: List of various filtered genes involved in different biological processes (BP), molecular functions (MF) and cellular components (CC) in LF bull spermatozoa**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Category** | **Term** | **Count** | **%** | **P-Value** | **Genes involved** |
|  | **Biological Process** |
| GOTERM\_BP\_DIRECT | GO:0006412~translation | 7 | 11.47 | 3.85E-05 | RPS17, RPS28, COA1, RPS29, RPL14, RPL13, RPS27A |
| GOTERM\_BP\_DIRECT | GO:0000028~ribosomal small subunit assembly | 2 | 3.27 | 0.05 | RPS17, RPS28 |
| GOTERM\_BP\_DIRECT | GO:0032870~cellular response to hormone stimulus | 2 | 3.27 | 0.08 | NCOA3, JUNB |
|  | **Molecular function** |
| GOTERM\_MF\_DIRECT | GO:0003735~structural constituent of ribosome | 7 | 11.47 | 1.31E-04 | RPS17, RPS28, COA1, RPS29, RPL14, RPL13, RPS27A |
| GOTERM\_MF\_DIRECT | GO:0005509~calcium ion binding | 7 | 11.47 | 0.02 | CABP4, MGP, ITSN1, OIT3, SULF1, TPT1, FBN1 |
| GOTERM\_MF\_DIRECT | GO:0044822~poly(A) RNA binding | 8 | 13.11 | 0.04 | RPS28, DDX5, RPL14, RACK1, RPL13, RPS27A, PPIA, HNRNPA0 |
| GOTERM\_MF\_DIRECT | GO:0001540~beta-amyloid binding | 2 | 3.27 | 0.09 | CD74, SORL1 |
|  | **Cellular Component** |
| GOTERM\_CC\_DIRECT | GO:0022627~cytosolic small ribosomal subunit | 4 | 6.55 | 3.44E-04 | RPS17, RPS28, RPS29, RPS27A |
| GOTERM\_CC\_DIRECT | GO:0070062~extracellular exosome | 17 | 27.86 | 0.001 | CD74, DDX5, NCOA3, SORL1, CD2AP, RPS28, RPS29, NEU1, RPL14, RACK1, ECHDC1, PSME1, BOLA-DRA, PROM1, RPS27A, UTRN, PPIA |
| GOTERM\_CC\_DIRECT | GO:0005615~extracellular space | 9 | 14.75 | 0.01 | LTB, RPS27A, SULF1, PROM1, SORL1, PPIA, TPT1, FBN1, LYZL6 |
| GOTERM\_CC\_DIRECT | GO:0022625~cytosolic large ribosomal subunit | 3 | 4.91 | 0.02 | COA1, RPL14, RPL13 |
| GOTERM\_CC\_DIRECT | GO:0005771~multivesicular body | 2 | 3.27 | 0.05 | CD74, TPT1 |
| GOTERM\_CC\_DIRECT | GO:0042613~MHC class II protein complex | 2 | 3.27 | 0.06 | CD74, BOLA-DRA |
| GOTERM\_CC\_DIRECT | GO:0031941~filamentous actin | 2 | 3.27 | 0.08 | TMSB10, CD2AP |
| GOTERM\_CC\_DIRECT | GO:0016020~membrane | 7 | 11.47 | 0.09 | DDX5, NEU1, RPL14, RPL13, LTB, RPS27A, PPIA |

**Table 4: List of enriched pathways of novel and filtered genes in LF bull spermatozoa**

|  |  |
| --- | --- |
|  | **Enriched pathways of the novel genes**  |
| Pathway | Count | P-Value | Genes Involved |
| bta03010:Ribosome | 47 | 2.44E-54 | RPL4, RPL5, RPL3, RPL32, RPL34, RPLP1, RPLP0, RPL8, RPS15, RPS14, RPS17, RPS16, RPL18A, RPL14, RPS3, RPLP2, RPL35, RPL13, RPS2, RPL37, RPL18, RPS27A, RPS11, RPS10, RPL19, RPS12, RPS9, RPS7, RPL21, RPS8, RPL23, RPS5, RPL35A, RPL13A, RPSA, RPL3L, RPS26, RPS25, RPS28, RPS27, RPL27A, RPL37A, FAU, RPL28, UBA52, RPS24, RPS23 |
| bta04810:Regulation of actin cytoskeleton | 18 | 7.94E-11 | APC2, CYFIP2, ITGA2, ARPC1A, PXN, ARPC4, ACTB, ACTG1, FGF16, MRAS, DIAPH3, ARPC2, TMSB4X, ITGA8, PIP4K2A, ITGA7, PFN1, SOS1 |
| bta04144:Endocytosis | 16 | 4.39E-08 | ARFGEF1, HSPA8, RAB5C, ARPC1A, CLTC, CLTA, NEDD4L, WWP1, ARPC4, AP2B1, STAM, JSP.1, GRK5, ARPC2, DNAJC6, IL2RA |
| bta03040:Spliceosome | 10 | 1.34E-05 | HSPA8, PRPF38B, DDX5, TRA2A, HNRNPU, PRPF40A, SRSF5, RBMX, LSM4, SRSF7 |
| bta04120:Ubiquitin mediated proteolysis | 10 | 1.84E-07 | UBE2Q2, UBE2E3, SYVN1, HUWE1, NEDD4L, WWP1, TRIM37, TRIM32, BIRC3, PIAS1 |
| bta05414:Dilated cardiomyopathy | 9 | 2.64E-06 | CACNB4, TPM3, ITGA2, ITGA8, ITGA7, ACTB, ADCY6, SGCG, ACTG1 |
| bta05412:Arrhythmogenic right ventricular cardiomyopathy (ARVC) | 8 | 3.22E-06 | GJA1, CACNB4, ITGA2, ITGA8, ITGA7, ACTB, SGCG, ACTG1 |
| bta05100:Bacterial invasion of epithelial cells | 8 | 3.22E-06 | ARPC2, ARPC1A, PXN, CLTC, CLTA, ARPC4, ACTB, ACTG1 |
| bta05410:Hypertrophic cardiomyopathy (HCM) | 8 | 1.36E-05 | CACNB4, TPM3, ITGA2, ITGA8, ITGA7, ACTB, SGCG, ACTG1 |
| bta05132:Salmonella infection | 8 | 0.0002 | ARPC2, PKN3, ARPC1A, ARPC4, PKN1, PFN1, ACTB, ACTG1 |
|  | **Enriched pathways of genes which are novel and filtered** |
| bta03010:Ribosome | 6 | 5.30E-05 | RPS17, RPS28, RPS29, RPL14, RPL13, RPS27A |
| bta04612:Antigen processing and presentation | 3 | 0.02 | CD74, PSME1, BOLA-DRA |