**Table S3 GO functional enrichment analysis interpretation**

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **ONTOLOGY** | **ID** | **Description** | **GeneRatio** | **BgRatio** | **pvalue** | **p.adjust** | **qvalue** | **geneID** | **Count** |
| BP | GO:0003012 | muscle system process | 38/274 | 467/18866 | 5.48E-18 | 8.75E-15 | 7.08E-15 | ACTA2/MYL9/HSPB6/CACNA1H/RGS4/MYLK/SMTN/GNAO1/KCNMA1/CASQ2/ATP1A2/MYOC/CHRNA3/SGCA/SORBS1/TMOD1/MYOCD/ACTG2/GUCY1A1/FLNA/TPM2/HAND2/LMOD1/CACNA2D1/DMD/TACR2/CALD1/CNN1/CACNA1C/CRYAB/DES/MYH11/PI16/PPP1R12B/SYNM/PLN/SGCD/CAV1 | 38 |
| BP | GO:0006936 | muscle contraction | 34/274 | 362/18866 | 4.37E-18 | 8.75E-15 | 7.08E-15 | ACTA2/MYL9/HSPB6/CACNA1H/MYLK/SMTN/GNAO1/KCNMA1/CASQ2/ATP1A2/CHRNA3/SGCA/SORBS1/TMOD1/MYOCD/ACTG2/GUCY1A1/FLNA/TPM2/LMOD1/CACNA2D1/DMD/TACR2/CALD1/CNN1/CACNA1C/CRYAB/DES/MYH11/PPP1R12B/SYNM/PLN/SGCD/CAV1 | 34 |
| BP | GO:0007517 | muscle organ development | 28/274 | 407/18866 | 9.91E-12 | 1.05E-08 | 8.54E-09 | CACNA1H/RGS4/DCN/LAMA2/MYLK/SMTN/ITGA7/SVIL/SMYD1/ELN/GREM1/SGCA/BVES/MYOCD/GLI1/FHL1/MEOX2/DMD/SPEG/JPH2/CRYAB/PI16/ASB2/CFL2/SGCD/TAGLN/POPDC2/CAV1 | 28 |
| BP | GO:0043062 | extracellular structure organization | 26/274 | 396/18866 | 1.58E-10 | 1.01E-07 | 8.15E-08 | CTSG/ADAMTS8/DCN/LAMA2/ITGA9/ITGA7/CCDC80/DDR2/ELN/GREM1/SMOC2/COL10A1/COL14A1/CYP1B1/TNC/ITGA8/ELANE/ABI3BP/MFAP4/DPT/MYH11/SFRP2/JAM2/TNXB/PHLDB2/CAV1 | 26 |
| BP | GO:0030198 | extracellular matrix organization | 26/274 | 395/18866 | 1.49E-10 | 1.01E-07 | 8.15E-08 | CTSG/ADAMTS8/DCN/LAMA2/ITGA9/ITGA7/CCDC80/DDR2/ELN/GREM1/SMOC2/COL10A1/COL14A1/CYP1B1/TNC/ITGA8/ELANE/ABI3BP/MFAP4/DPT/MYH11/SFRP2/JAM2/TNXB/PHLDB2/CAV1 | 26 |
| BP | GO:0042692 | muscle cell differentiation | 25/274 | 390/18866 | 5.95E-10 | 3.17E-07 | 2.56E-07 | CACNA1H/PGM5/RGS4/SMYD1/CASQ2/GREM1/BOC/RBPMS2/BVES/TMOD1/MYOCD/LDB3/CSRP1/ITGA8/LMOD1/DMD/SPEG/MYH11/PI16/TMEM119/JAM2/FLNC/CFL2/SGCD/POPDC2 | 25 |
| BP | GO:0060537 | muscle tissue development | 23/274 | 409/18866 | 3.47E-08 | 1.11E-05 | 8.97E-06 | PGM5/RGS4/DCN/MYLK/SVIL/SMYD1/ELN/GREM1/BVES/MYOCD/GLI1/CSRP1/ITGA8/MEOX2/JPH2/MYH11/PI16/ASB2/CFL2/PLN/SGCD/POPDC2/CAV1 | 23 |
| BP | GO:0051146 | striated muscle cell differentiation | 21/274 | 295/18866 | 2.34E-09 | 9.34E-07 | 7.56E-07 | CACNA1H/PGM5/RGS4/SMYD1/CASQ2/GREM1/BVES/TMOD1/MYOCD/LDB3/CSRP1/LMOD1/DMD/MYH11/PI16/TMEM119/JAM2/FLNC/CFL2/SGCD/POPDC2 | 21 |
| BP | GO:0090257 | regulation of muscle system process | 20/274 | 256/18866 | 1.14E-09 | 5.21E-07 | 4.22E-07 | MYL9/HSPB6/RGS4/KCNMA1/CASQ2/ATP1A2/CHRNA3/SGCA/MYOCD/GUCY1A1/FLNA/HAND2/DMD/TACR2/CNN1/CACNA1C/PI16/PPP1R12B/PLN/CAV1 | 20 |
| BP | GO:0006937 | regulation of muscle contraction | 16/274 | 173/18866 | 4.96E-09 | 1.76E-06 | 1.42E-06 | MYL9/HSPB6/KCNMA1/CASQ2/ATP1A2/CHRNA3/MYOCD/GUCY1A1/FLNA/DMD/TACR2/CNN1/CACNA1C/PPP1R12B/PLN/CAV1 | 16 |
| CC | GO:0062023 | collagen-containing extracellular matrix | 42/289 | 427/19559 | 1.28E-22 | 3.85E-20 | 2.91E-20 | CTSG/OMD/ADAMTS8/DCN/LAMA2/CCDC80/HMCN1/SSC5D/SRPX/ELN/GREM1/MYOC/OGN/CLC/SMOC2/S100A7/SERPINF1/COL10A1/TGFB1I1/COL14A1/PODN/TNC/NTN1/ANGPTL1/PRELP/ELANE/SPARCL1/ABI3BP/MFAP4/FGL2/DPT/THBS4/ITIH5/EFEMP1/ASPN/SFRP2/MMRN1/CILP/TNXB/GPC3/SFRP1/MGP | 42 |
| CC | GO:0043292 | contractile fiber | 32/289 | 238/19559 | 1.55E-21 | 2.34E-19 | 1.77E-19 | SYNC/ACTA2/MYL9/PGM5/PALLD/SVIL/CASQ2/PDLIM3/TMOD1/LDB3/SYNPO2/NEXN/FLNA/CSRP1/TPM2/LMOD1/DMD/FERMT2/ABCC9/CALD1/ARHGEF25/JPH2/CACNA1C/CRYAB/FBXL22/DES/MYH11/FLNC/PPP1R12B/SYNM/CFL2/AHNAK2 | 32 |
| CC | GO:0030016 | myofibril | 30/289 | 227/19559 | 4.97E-20 | 4.99E-18 | 3.77E-18 | SYNC/MYL9/PGM5/PALLD/SVIL/CASQ2/PDLIM3/TMOD1/LDB3/SYNPO2/NEXN/FLNA/CSRP1/TPM2/LMOD1/DMD/FERMT2/ABCC9/CALD1/ARHGEF25/JPH2/CACNA1C/CRYAB/FBXL22/DES/FLNC/PPP1R12B/SYNM/CFL2/AHNAK2 | 30 |
| CC | GO:0030055 | cell-substrate junction | 27/289 | 423/19559 | 1.97E-10 | 7.42E-09 | 5.60E-09 | TNS1/PGM5/PALLD/SVIL/DDR2/DIXDC1/LIMS2/S100A7/TGFB1I1/SORBS1/SYNPO2/NEXN/FLNA/FHL1/CSRP1/TNC/ITGA8/ALOX15B/DMD/FERMT2/LAYN/CNN1/FLNC/ITGBL1/PHLDB2/NFASC/CAV1 | 27 |
| CC | GO:0030017 | sarcomere | 27/289 | 207/19559 | 5.56E-18 | 4.18E-16 | 3.16E-16 | SYNC/MYL9/PGM5/PALLD/CASQ2/PDLIM3/TMOD1/LDB3/SYNPO2/NEXN/FLNA/CSRP1/TPM2/LMOD1/DMD/FERMT2/ABCC9/ARHGEF25/JPH2/CACNA1C/CRYAB/FBXL22/DES/FLNC/PPP1R12B/CFL2/AHNAK2 | 27 |
| CC | GO:0005925 | focal adhesion | 26/289 | 415/19559 | 6.48E-10 | 2.17E-08 | 1.64E-08 | TNS1/PGM5/PALLD/SVIL/DDR2/DIXDC1/LIMS2/S100A7/TGFB1I1/SORBS1/SYNPO2/NEXN/FLNA/FHL1/CSRP1/TNC/ITGA8/ALOX15B/FERMT2/LAYN/CNN1/FLNC/ITGBL1/PHLDB2/NFASC/CAV1 | 26 |
| CC | GO:0031674 | I band | 22/289 | 140/19559 | 1.29E-16 | 7.78E-15 | 5.88E-15 | SYNC/MYL9/PGM5/PALLD/CASQ2/PDLIM3/LDB3/SYNPO2/NEXN/FLNA/CSRP1/DMD/FERMT2/JPH2/CACNA1C/CRYAB/FBXL22/DES/FLNC/PPP1R12B/CFL2/AHNAK2 | 22 |
| CC | GO:0030018 | Z disc | 21/289 | 128/19559 | 2.62E-16 | 1.31E-14 | 9.92E-15 | SYNC/MYL9/PGM5/PALLD/CASQ2/PDLIM3/LDB3/SYNPO2/NEXN/FLNA/CSRP1/DMD/JPH2/CACNA1C/CRYAB/FBXL22/DES/FLNC/PPP1R12B/CFL2/AHNAK2 | 21 |
| CC | GO:0042383 | sarcolemma | 17/289 | 135/19559 | 1.61E-11 | 6.92E-10 | 5.23E-10 | SYNC/PGM5/LAMA2/ATP1A2/SGCA/BVES/CACNA2D1/DMD/SLC2A4/CACNA1C/DES/FLNC/SYNM/AHNAK2/SGCD/POPDC2/CAV1 | 17 |
| CC | GO:0032432 | actin filament bundle | 10/289 | 76/19559 | 1.72E-07 | 5.16E-06 | 3.90E-06 | MYL9/PGM5/PALLD/MYLK/PDLIM3/SORBS1/LDB3/SYNPO2/FERMT2/CRYAB | 10 |
| MF | GO:0003779 | actin binding | 28/267 | 437/18352 | 5.36E-11 | 8.14E-09 | 7.37E-09 | TNS1/PALLD/MYLK/SMTN/SVIL/KCNMA1/DIXDC1/MAP1B/PDLIM3/SORBS1/TMOD1/LDB3/SYNPO2/CAP2/NEXN/FLNA/TPM2/LMOD1/DMD/FERMT2/CALD1/CNN1/MYH11/FLNC/MAP1A/CFL2/DAAM2/TAGLN | 28 |
| MF | GO:0005539 | glycosaminoglycan binding | 21/267 | 232/18352 | 2.83E-11 | 6.44E-09 | 5.83E-09 | CTSG/ADAMTS8/DCN/MPO/CCDC80/SMOC2/NRP2/GREM2/PRELP/ELANE/REG3A/ABI3BP/THBS4/LAYN/RSPO3/SELP/TNXB/SLIT2/DPYSL3/SFRP1/SLIT3 | 21 |
| MF | GO:0005201 | extracellular matrix structural constituent | 21/267 | 169/18352 | 5.73E-14 | 2.61E-11 | 2.36E-11 | DCN/LAMA2/HMCN1/SRPX/ELN/OGN/COL10A1/COL14A1/PODN/TNC/PRELP/ABI3BP/MFAP4/FGL2/DPT/EFEMP1/ASPN/MMRN1/CILP/TNXB/MGP | 21 |
| MF | GO:1901681 | sulfur compound binding | 18/267 | 262/18352 | 5.88E-08 | 4.47E-06 | 4.04E-06 | CTSG/ADAMTS8/MPO/CCDC80/SMOC2/NRP2/GREM2/PRELP/ELANE/ABI3BP/THBS4/RSPO3/SELP/TNXB/SLIT2/DPYSL3/SFRP1/SLIT3 | 18 |
| MF | GO:0008201 | heparin binding | 17/267 | 169/18352 | 4.47E-10 | 5.10E-08 | 4.62E-08 | CTSG/ADAMTS8/MPO/CCDC80/SMOC2/NRP2/GREM2/PRELP/ELANE/ABI3BP/THBS4/RSPO3/SELP/TNXB/SLIT2/SFRP1/SLIT3 | 17 |
| MF | GO:0008307 | structural constituent of muscle | 9/267 | 43/18352 | 9.34E-09 | 8.52E-07 | 7.71E-07 | MYL9/SMTN/PDLIM3/NEXN/CSRP1/TPM2/DMD/MYH11/SYNM | 9 |
| MF | GO:0005518 | collagen binding | 8/267 | 70/18352 | 7.82E-06 | 0.000446 | 0.0004036 | DCN/ITGA9/DDR2/COL14A1/PODN/SPARCL1/ABI3BP/ASPN | 8 |
| MF | GO:0004714 | transmembrane receptor protein tyrosine kinase activity | 8/267 | 61/18352 | 2.73E-06 | 0.000178 | 0.0001611 | EPHA7/ROR2/DDR2/EPHA3/NRP2/EFEMP1/ERBB2/PDGFRL | 8 |
| MF | GO:0042805 | actinin binding | 6/267 | 36/18352 | 1.21E-05 | 0.0006133 | 0.000555 | PALLD/PDLIM3/LDB3/SYNPO2/CSRP1/CACNA1C | 6 |
| MF | GO:0030021 | extracellular matrix structural constituent conferring compression resistance | 5/267 | 22/18352 | 1.35E-05 | 0.0006156 | 0.0005571 | DCN/OGN/PODN/PRELP/ASPN | 5 |

GO, Gene Ontology; BP, biological processes;CC, Cellular components; MF, molecular functions.