

Riggs Supplemental Table ST5. Note that gene ontology (GO) categories overlapped (OVRLP), but the specific genes in those categories in IPS and OF were sometimes distinct

| IPS GO | # IPS genes | IPSC Genes in category | IPS GOP | OF GO | # OF genes | OF Genes in category | OF GOP | OVRLP GO | # IPS genes | IPSC Genes in category | IPS GOP | # OF genes | OF Genes in category | OF GOP | # shared genes | IPSC/OF shared Genes in category | SHRDGOP |
|--|-------------|---|----------|--------------------------------------|------------|---|----------|--|-------------|---|----------|------------|---|----------|----------------|--|----------|
| positive regulation of transcription | 11 | EGR1, ATF4, ETS1, SMARCD3, GATA6, EBF3, SOX9, SMARCA1, GLI2, SRF, WT1 | 1.50E-04 | muscle protein | 19 | MYL6, ACTC1, ACTA1, TNNC2, ACTA2, MYH5, MYL1, MYLPF, TPM2, MYH8, TNN1, TPM4, MYL9, TNN2, TNNT3, TNNT1, MYBPB, CAPN22, MB | 1.26E-20 | skeletal system development | 7 | OSR2, TGFBR1, EDN1, PRRX1, DLK1, SOX9, GLC2 | 3.44E-03 | 11 | IBSP, WNT5A, CTGF, TBX4, CYTL1, FOXC2, SP7, COL2A1, MYOG, GJA5, TGFBI2 | 1.45E-02 | | | |
| positive regulation of gene expression | 11 | EGR1, ATF4, ETS1, SMARCD3, GATA6, EBF3, SOX9, SMARCA1, GLI2, SRF, WT1 | 1.86E-04 | contractile fiber | 18 | CDK5R1, ACTC1, ACTA1, TCAP, CRYAB, ACTA2, MYH3, ANKR2, PDLM3, ACTN3, ACTN2, ACTN3, TPM2, TNM, MYH8, CSRP3, ITGB1BP2, AIP2A1 | 1.50E-13 | blood vessel development | 6 | TGFBR1, EDN1, PRRX1, MEIS1, SRF, WT1 | 8.41E-03 | 10 | RTN4, EMCN, HEY1, CTGF, ITGAV, BAX, TBX4, FOXC2, GJA5, TGFBI2 | 1.50E-02 | | | |
| positive regulation of cell differentiation | 7 | LPL, ADAMTS9, ETS1, GATA6, JAG1, GLI2, SRF | 2.78E-04 | muscle organ development | 22 | MYL6, MYOD1, ACTC1, ACTA1, CRYAB, TNC, PDLM3, RXRG, MYLPF, FKBP1A, TRIM72, TAGLN2, TNM, CSRP3, TGB1, TNN1, TGFBI2, DNER, FOXC2, MYOG, CHRNA1 | 4.50E-13 | vasculature development | 6 | TGFBR1, EDN1, PRRX1, MEIS1, SRF, WT1 | 9.28E-03 | 10 | RTN4, EMCN, HEY1, CTGF, ITGAV, BAX, TBX4, FOXC2, GJA5, TGFBI2 | 1.72E-02 | | | |
| positive regulation of nitrogen compound metabolic process | 11 | EGR1, ATF4, ETS1, SMARCD3, GATA6, EBF3, SOX9, SMARCA1, GLI2, SRF, WT1 | 3.40E-04 | striated muscle tissue development | 19 | MYL6, MYOD1, ACTC1, ACTA1, TNC, PDLM3, RXRG, MYLPF, FKBP1A, TNM, CSRP3, ITGB1, TNN1, TGFBI2, DNER, VGLL2, FOXC2, MYOG, CHRNA1 | 1.15E-12 | heart development | 7 | SMARCD3, GATA6, TGFBR1, EDN1, SOX9, GLI2, SRF | 9.98E-04 | 15 | ACTC1, ALPK3, TCAP, PDLM3, COL2A1, FKBP1A, TNM, GJA5, ITGB1, CSRP3, TNN1, TGFBI2, NPBP, FOXC2, MB | 1.12E-05 | | | |
| negative regulation of cellular biosynthetic process | 10 | EGR1, EDN1, ZFP238, PRRX1, RBM9, SOX9, GLI2, PKA, WT1, TWIST2 | 3.44E-04 | muscle tissue development | 19 | MYL6, MYOD1, ACTC1, ACTA1, TNC, PDLM3, RXRG, MYLPF, FKBP1A, TNM, CSRP3, ITGB1, TNN1, TGFBI2, DNER, VGLL2, FOXC2, MYOG, CHRNA1 | 3.81E-12 | positive regulation of macromolecule biosynthetic process | 11 | EGR1, ATF4, ETS1, SMARCD3, GATA6, EBF3, SOX9, SMARCA1, GLI2, SRF, WT1 | 3.61E-04 | 15 | MYO1, EGR2, SOX11, RXRG, CYTL1, MED6, HES1, FOS, INHBA, GATA3, C10TNF2, VGLL2, FOXC2, MYOG, SERTAD1 | 3.97E-02 | | | |
| positive regulation of macromolecule metabolic process | 11 | EGR1, ATF4, ETS1, SMARCD3, GATA6, EBF3, SOX9, SMARCA1, GLI2, SRF, WT1 | 3.63E-04 | cytoskeleton | 44 | MYL6, LOR, NDN, MYL1, AKAP12, PDLM3, TNM, TPM2, TPM4, GTSE1, DSTN, MYL9, PRR22, MECOM, CALM, TUBA1A, LM003, EMD, NEFM, ACTB, NES, ACTC1, ACTA1, ACTA2, MYH3, MYLPF, ACTN1, ACTN2, TMSB11, TMSB12, TMSB13, TMSB14, RAPSN, LASP1, NMN1, SH3KBP1, WDR1, TGFBI1, MAPRE1 | 6.24E-08 | positive regulation of gene expression | 11 | EGR1, ATF4, ETS1, SMARCD3, GATA6, EBF3, SOX9, SMARCA1, GLI2, SRF, WT1 | 1.86E-04 | 14 | MYO1, EGR2, SOX11, RXRG, CYTL1, MED6, HES1, FOS, INHBA, GATA3, VGLL2, FOXC2, MYOG, SERTAD1 | 4.39E-02 | | | |
| negative regulation of biosynthetic process | 10 | EGR1, EDN1, ZFP238, PRRX1, RBM9, SOX9, GLI2, PKA, WT1, TWIST2 | 3.68E-04 | skeletal muscle tissue development | 11 | MYL6, MYOD1, ACTA1, DNER, TNC, RXRG, PDLM3, MYLPF, VGLL2, MYOG, CHRNA1 | 1.67E-07 | positive regulation of transcription | 11 | EGR1, ATF4, ETS1, SMARCD3, GATA6, EBF3, SOX9, SMARCA1, GLI2, SRF, WT1 | 1.50E-04 | 14 | MYO1, EGR2, SOX11, RXRG, CYTL1, MED6, HES1, FOS, INHBA, GATA3, VGLL2, FOXC2, MYOG, SERTAD1 | 3.68E-02 | | | |
| epithelium development | 8 | AGPAT6, GPC3, GATA6, JAG1, FZD2, SOX9, GLI2, WT1 | 4.77E-04 | skeletal muscle organ development | 11 | MYL6, MYOD1, ACTA1, DNER, TNC, RXRG, PDLM3, MYLPF, VGLL2, MYOG, CHRNA1 | 2.17E-07 | positive regulation of transcription from RNA polymerase II promoter | 8 | EGR1, ATF4, ETS1, GATA6, SOX9, GLI2, SRF, WT1 | 2.40E-03 | 13 | MYO1, EGR2, SOX11, RXRG, CYTL1, MED6, HES1, INHBA, FOS, GATA3, VGLL2, FOXC2, MYOG | 1.09E-02 | | | |
| positive regulation of developmental process | 7 | LPL, ADAMTS9, ETS1, GATA6, JAG1, GLI2, SRF | 8.06E-04 | striated muscle cell differentiation | 11 | MYO1, ACTC1, TCAP, ACTA1, DNER, TNC, MYOG, TNM, CAPN2, CHRNA1, ITGB1 | 1.25E-06 | blood vessel morphogenesis | 6 | TGFBR1, EDN1, PRRX1, MEIS1, SRF, WT1 | 3.51E-03 | 9 | RTN4, EMCN, HEY1, CTGF, ITGAV, BAX, TBX4, FOXC2, TGFBI2 | 1.29E-02 | | | |
| heart development | 7 | SMARCD3, GATA6, TGFBR1, EDN1, SOX9, GLI2, SRF | 9.98E-04 | striated muscle cell development | 9 | ACTC1, TCAP, ACTA1, DNER, TNC, MYOG, TNM, CHRNA1, ITGB1 | 1.79E-06 | positive regulation of RNA metabolic process | 9 | EGR1, ATF4, ETS1, GATA6, SOX9, SMARCA1, GLI2, SRF, WT1 | 1.36E-03 | 13 | MYO1, EGR2, SOX11, RXRG, CYTL1, MED6, HES1, INHBA, FOS, GATA3, VGLL2, FOXC2, MYOG | 3.25E-02 | | | |
| skeletal system development | 7 | OSR2, TGFBR1, EDN1, PRRX1, DLK1, SOX9, GLI2 | 3.44E-03 | muscle cell differentiation | 12 | MYO1, ACTC1, TCAP, ACTA1, LGALS1, DNER, TNC, MYOG, TNM, CAPN2, CHRNA1, ITGB1 | 2.20E-06 | skeletal system development | 6 | | | | | | 6 | PDLIM7, TGFBI3, FHL2, IGF2, HOXD10, IGFBP5 | 5.75E-04 |
| blood vessel morphogenesis | 6 | TGFBR1, EDN1, PRRX1, MEIS1, SRF, WT1 | 3.51E-03 | myosin complex | 8 | MYL6, MYH5, MYL1, MYBPB, MYLPF, TNM, MYH8, MYL9 | 5.39E-05 | ossification | 4 | | | | | | 4 | PDLIM7, FHL2, IGF2, IGFBP5 | 2.12E-03 |

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|--|---|---|----------|---|----|--|----------|--|---|----------------------------|----------|
| morphogenesis of a branching structure | 5 | GPC3, EDN1, SOX9, GLI2, SRF | 3.92E-03 | regulation of cell growth | 9 | RTN4, E124, NDN, CTGF, TRO, ESM1, DCUN1D3, SERTAD1, TGFB2 | 9.62E-05 | bone development | 4 | POLIM7, FHL2, IGF2, IGFBP5 | 2.88E-03 |
| chondate embryonic development | 8 | OSR2, GATA6, TGFBR1, EDN1, PRRX1, DLK1, GLI2, SRF | 5.83E-03 | tissue morphogenesis | 13 | WNT5A, ACTC1, TNC, FST, TBX4, FZD3, FKBP1A, TNN1, TGFB2, PFN1, CD44, FOXC2, TGFB11 | 3.78E-04 | osteoblast differentiation | 3 | FHL2, IGF2, IGFBP5 | 5.77E-03 |
| regulation of cell proliferation | 9 | IRS2, OSR2, GPC3, EDN1, PRRX1, FGF21, SOX9, GLI2, H19 | 6.28E-03 | regulation of apoptosis | 20 | IRAK2, CDK5R1, CD3G, COL2A1, INHA, PMAIP1, BCL2L1, CAPIP1, HRAS1, TGFB2, E124, CDKN1A, BAX, PPP2CB, FOXC2, NGFRAP1, DCUN1D3, PHLD3, ERCC1, TRAF4 | 1.13E-03 | sarcolemma | 3 | CACNA2D1, DES, TGFb3 | 8.78E-03 |
| urogenital system development | 5 | GPC3, TGFBR1, SOX9, GLI2, WT1 | 6.78E-03 | regulation of programmed cell death | 20 | IRAK2, CDK5R1, CD3G, COL2A1, INHA, PMAIP1, BCL2L1, CAPIP1, HRAS1, TGFB2, E124, CDKN1A, BAX, PPP2CB, FOXC2, NGFRAP1, DCUN1D3, PHLD3, ERCC1, TRAF4 | 1.31E-03 | glycerophospholipid metabolic process | 3 | SERINC2, SH3GLB1, FABP3 | 1.92E-02 |
| blood vessel development | 6 | TGFBR1, EDN1, PRRX1, MEIS1, SRF, WT1 | 8.41E-03 | regulation of cell death | 20 | IRAK2, CDK5R1, CD3G, COL2A1, INHA, PMAIP1, BCL2L1, CAPIP1, HRAS1, TGFB2, E124, CDKN1A, BAX, PPP2CB, FOXC2, NGFRAP1, DCUN1D3, PHLD3, ERCC1, TRAF4 | 1.39E-03 | branching morphogenesis of a tube | 3 | EDNRA, FLT1, ILK | 2.13E-02 |
| embryonic skeletal system development | 4 | OSR2, TGFBR1, PRRX1, DLK1 | 8.97E-03 | skeletal muscle fiber development | 5 | ACTA1, DNER, TNC, MYOG, CHRNA1 | 1.50E-03 | myofibril | 3 | DES, POLIM5, ANKRD1 | 2.39E-02 |
| vasculature development | 6 | TGFBR1, EDN1, PRRX1, MEIS1, SRF, WT1 | 9.28E-03 | cardiac muscle tissue morphogenesis | 4 | ACTC1, FOXC2, FKBP1A, TNNT1 | 2.60E-03 | tube development | 4 | EDNRA, FLT1, ILK, TGFb3 | 2.58E-02 |
| neural crest cell development | 3 | EDNRB, EDN1, SOX9 | 1.25E-02 | muscle tissue morphogenesis | 4 | ACTC1, FOXC2, FKBP1A, TNNT1 | 2.60E-03 | morphogenesis of a branching structure | 3 | EDNRA, FLT1, ILK | 3.68E-02 |
| neural crest cell differentiation | 3 | EDNRB, EDN1, SOX9 | 1.25E-02 | muscle fiber development | 5 | ACTA1, DNER, TNC, MYOG, CHRNA1 | 2.85E-03 | glycerolipid metabolic process | 3 | SERINC2, SH3GLB1, FABP3 | 3.90E-02 |
| mesenchymal cell development | 3 | EDNRB, EDN1, SOX9 | 2.44E-02 | positive regulation of neuron apoptosis | 4 | CDK5R1, BAX, PMAIP1, TGFB2 | 3.06E-03 | angiogenesis | 3 | EDNRA, VEGFC, FLT1 | 4.12E-02 |
| mesenchymal cell differentiation | 3 | EDNRB, EDN1, SOX9 | 2.63E-02 | development of primary sexual characteristics | 7 | WNT5A, BAX, FST, BCL2L1, VGF, ERCC1, GJB2 | 5.87E-03 | | | | |
| mesenchyme development | 3 | EDNRB, EDN1, SOX9 | 2.73E-02 | positive regulation of programmed cell death | 11 | CDKN1A, CDK5R1, E124, BAX, NGFRAP1, BCL2L1, PMAIP1, INHA, DCUN1D3, PHLD3, TGFB2 | 6.14E-03 | | | | |

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|---|---|---------------------------------|----------|------------------------------------|----|--|----------|--|
| skeletal system morphogenesis | 4 | OSR2, TGFBR1, PRRX1, SOX9 | 2.94E-02 | negative regulation of cell growth | 5 | RTN4, E124, TRO, DCUN1D3, SERTAD1 | 6.18E-03 | |
| embryonic organ development | 5 | OSR2, TGFBR1, EDN1, PRRX1, GLI2 | 3.56E-02 | apoptosis | 16 | IRAK2, ACTC1, PMAIP1, BCL2L1, CIAPIN1, TGFBR2, TNFRSF1B, BAX, SH3KBP1, NGFRAP1, POCO5, PHLDA3, TRAF4, PHLDA1, CIB1, PEG3 | 6.59E-03 | |
| embryonic skeletal system morphogenesis | 3 | OSR2, TGFBR1, PRRX1 | 4.30E-02 | regulation of blood vessel size | 5 | ACTA2, NPPB, FOXC2, NPPA, TES | 6.66E-03 | |
| sensory organ development | 5 | EDN1, PRRX1, JAG1, MEIS1, WT1 | 4.34E-02 | programmed cell death | 16 | IRAK2, ACTC1, PMAIP1, BCL2L1, CIAPIN1, TGFBR2, TNFRSF1B, BAX, SH3KBP1, NGFRAP1, POCO5, PHLDA3, TRAF4, PHLDA1, CIB1, PEG3 | 7.67E-03 | |
| | | | | induction of apoptosis | 7 | E124, BAX, NGFRAP1, PMAIP1, INHA, PHLDA3, TGFBR2 | 4.79E-02 | |
| | | | | induction of programmed cell death | 7 | E124, BAX, NGFRAP1, PMAIP1, INHA, PHLDA3, TGFBR2 | 4.79E-02 | |