

Supplemental Table 2. Significantly over-represented gene ontology terms identified for intervals of time during limb regeneration.

0-1 DPA

Category	Term	Count	Genes	Prob
GOTERM_BP_FAT	GO:0030574~collagen catabolic process	8	MMP10, PRTN3, MMP8, MMP19, MMP3, MMP13, MMP2, MMP1 ZFAND5, CCK, PTGS2, ENPP2, TNFRSF12A, ARF6, ZEB2, CDH2, CAPZB, TGFB1, TPM3, NRCAM, CTTNBP2, BDNF, OVOL2, CXCR4, SFTPD, TEK2, IL1B, B3GNT2, PPAP2A, NR2F2, THBS1, CEACAM1, SCG2, IL8, LMX1B, ARID5B, NR4A2, CCNL2, PLAUR, LSP1, NDEL1, ITGA6, ID1,	0.0018827
GOTERM_BP_FAT	GO:0006928~cell motion	39	BTG1, HBEGF, FOXC1, NGFR LDLR, PTGS2, RHOQ, FOXO1, BCL2L1, MMP3, VGF, TGFB1, CCNE1, CTTNBP2, FOS, GOT1, BCHE, HMOX1, IL1B, PCSK9, THBS1, RNF14, MAT2A, GATM, CRYAB, SOCS1, NR4A2, FBP1,	0.00235216
GOTERM_BP_FAT	GO:0009719~response to endogenous stimulus	35	RCAN1, NR4A3, MMP13, ADIPOQ, JUNB, DDIT3, LEP, SDC1, DUSP1, SLC25A36, VLDLR BMP2, CCK, GATM, PTGS2, HSD17B2, NR4A2, ADIPOQ, DDIT3, TGFB1, LEP, CCNE1, FOS,	0.00249722
GOTERM_BP_FAT	GO:0009991~response to extracellular stimulus	23	SSTR2, DUSP1, ITGA6, BCHE, HMOX1, LIPG, IL1B, PCSK9, HSPA5, KLF4, VLDLR PTGS2, AIF1, PRTN3, NFKBIA, FOXO1, BCL2L1, MXI1, SESN1, TGFB1, TIMP1, CTTNBP2, BDNF, OVOL2, CCL3L1, HMOX1, SERPINE1, SFTPD, IL1B, PPAP2A, THBS1, NRG1, FGF1, MYC,	0.00768026
GOTERM_BP_FAT	GO:0042127~regulation of cell proliferation	46	SCG2, ODC1, CDC6, BMP2, IL8, KLF10, GJB6, MYCN, PTHLH, ADRB2, SSTR2, ID2, EREG, BTG1, F3, BTG3, TGIF1, MDM2, HBEGF, ADAMTS1, NGFR, PRKRIR, KLF4 TNFRSF6B, CRYAB, NFKBIA, FOXO1, BCL2L1, CITED2, BDNF, SQSTM1, HMOX1, F3, TNFAIP8,	0.03651238
GOTERM_BP_FAT	GO:0006916~anti-apoptosis	21	MPO, IL1B, NAIP, FOXC1, HSPA5, NGFR, NRG1, THBS1, MYC, GSTP1 TCEANC, RBM15B, ZNF530, SNIP1, SPI1, FOXO1, RHOQ, ZEB2, TGFB1, YBX1, CITED2, FOS, CCNE1, HOXC8, ZNF182, ZNF300, HMOX1, LRRFIP1, NR2F2, NFIL3, MYC, ZNF180, ALX1, BATF3, EGR1, ZFP36, ARID5B, ZNF543, TLE3, ZNF792, SPEN, ECSIT, HMGA1, JUNB, DDIT3, ZNF3, MYCN, ADRB2, PRDM9, NAB1, TGIF1, MDM2, FOXC1, CREM, TFCP2L1, ZNF510, ZNF367, NFKBIA, ZFP36L2, TSC22D2, OVOL2, SQSTM1, XBP1, JUNB, MYOG, ZNF268, VEZF1, RNF14, BMP2, NFE2, LMX1B, ZNF567, KLF10, LMCD1, NR4A2, NR4A1, NR4A3, ADNP2,	0.01566257
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	78	SALL4, ID2, ID1, ETS2, CSRNP1, ZNF214, ZNF418, HIF3A, HIVEP2, KLF4	0.02475392
GOTERM_BP_FAT	GO:0051094~positive regulation of developmental process	22	BMP2, PDLIM7, TNFRSF12A, KLF10, PLXNB2, JUNB, TGFB1, LEP, NRCAM, CCNE1, BDNF, ADRB2, NDEL1, ID2, BTG1, F3, JUNB, TGIF1, IL1B, NGFR, THBS1, NRG1 SPI1, NFKBIA, RHOQ, FOXO1, TGFB1, CITED2, CCNE1, FOS, OVOL2, SQSTM1, HMOX1, IL1B, MYOG, NR2F2, THBS1, MYC, RNF14, ALX1, EGR1, BMP2, HSP90AA1, NFE2, LMX1B, NR4A2, NR4A1, GRHL3, NR4A3, HMGA1, JUNB, DDIT3, PTHLH, ADRB2, SALL4, EREG, ETS2, CSRNP1,	0.04305954
GOTERM_BP_FAT	GO:0031328~positive regulation of cellular biosynthetic process	40	FOXC1, AREG, KLF2, KLF4	0.04310444
GOTERM_BP_FAT	GO:0031667~response to nutrient levels	20	BMP2, CCK, GATM, PTGS2, HSD17B2, ADIPOQ, DDIT3, TGFB1, LEP, CCNE1, SSTR2, DUSP1, BCHE, HMOX1, LIPG, IL1B, PCSK9, HSPA5, KLF4, VLDLR	0.02720872

GOTERM_BP_FAT	GO:0001944~vasculature development	22	ZFAND5, IL8, TNFRSF12A, TIPARP, MMP19, FOXO1, CDH2, MMP2, JUNB, CITED2, EREG, CXCR4, ID1, HMOX1, IL1B, FOXC1, NR2F2, VEZF1, THBS1, CEACAM1, CYR61, SCG2	0.02727271
GOTERM_BP_FAT	GO:0042330~taxis	12	CXCL14, IL8, ENPP2, CXCR4, CMKLR1, CCL3L1, SFTPD, IL1B, CCNL2, CYR61, PLAUR, SCG2	0.03676292

2-3 DPA

Category	Term	Count	Genes	
GOTERM_BP_FAT	GO:0007049~cell cycle	56	KIF23, MAD1L1, MAEA, TUBB2B, PTTG1, CCNE2, KIF2C, MLL5, CDCA8, CUL5, MCM7, DDX11, INCENP, TARDBP, PSMD1, VPS4B, CCNA2, STAG2, CDC7, CDC6, RBL1, CDC5L, MCM3, ESCO2, VASH1, NCAPD3, MCM6, UHRF1, SASS6, MAD2L1, CKS1B, HAUS6, BLM, NEK3, LRRCC1, ANLN, CEP55, CCNG2, NIPBL, NCAPG2, PPP3CA, TFDP1, MSH6, MSH2, NASP, ATR, TET2, SMC2, CDC25A, SMC4, MAPK12, ZNF318, CHAF1A, CHAF1B, MYH10, UBE2E1	5.51E-07
GOTERM_BP_FAT	GO:0000279~M phase	27	NCAPD3, CDC25A, SMC4, MAD2L1, ZNF318	5.88E-04
GOTERM_BP_FAT	GO:0051276~chromosome organization	31	PTGES3, SMARCA1, ENY2, BLM, CBX1, TRRAP, PTTG1, MLL5, CDCA8, NIPBL, DDX11, NCAPG2, MSH6, NFE2, HIST1H1B, MSH2, NASP, RBL1, SMC2, NCAPD3, SMC4, MAD2L1, BAZ1B, SMARCE1, BPTF, SMARCA5, CHAF1A, RBM14, SMARCA2, CHAF1B, UBE2E1	0.00200607
GOTERM_BP_FAT	GO:0006259~DNA metabolic process	37	PTGES3, BLM, POLA2, PTTG1, MCM10, DNASE1L3, TK1, CCNE2, MLL5, MCM7, POLE2, CTGF, ORC6L, FEN1, CDC7, MSH6, CDC6, RAD51AP1, MSH2, NASP, PPFIBP2, TOPBP1, ATR, MCM3, MCM4, ORC1L, MCM5, CDC25A, ESCO2, MCM6, UHRF1, RRM2, RRM1, PCNA, CHAF1A, RBM14, CHAF1B	1.15E-04

9-10 DPA

Category	Term	Count	Genes	
GOTERM_CC_FAT	GO:0031012~extracellular matrix	15	COL4A2, COL4A1, CILP, HSPG2, OLFML2A, LAMA2, LAMA4, COL6A3, COL6A2, COL6A1, RELN, COL29A1, LAMB1, LOXL1, DST	5.77E-06
GOTERM_CC_FAT	GO:0005576~extracellular region	25	MMRN1, BDNF, HTRA1, COL6A3, COL6A2, IL1B, COL6A1, PTX3, LAMB1, LOXL1, ADAM28, COL4A2, COL4A1, CILP, HSPG2, OLFML2A, LAMA2, PTHLH, PROM1, LAMA4, TNFSF10, CLEC3B, RELN, COL29A1, DST	1.95E-04
GOTERM_CC_FAT	GO:0005604~basement membrane	7	LAMA2, LAMA4, COL4A2, COL4A1, HSPG2, LAMB1, DST	5.37E-04

18-20 DPA

GOTERM_BP_FAT	GO:0051789~response to protein stimulus	9	EGR1, FOS, HSP90AA1, MAP1B, ITGA2, NR3C1, SETD2, VARS, CYR61	0.0019629
---------------	---	---	--	-----------

22-24 DPA

Category	Term	Count	Genes	
GOTERM_BP_FAT	GO:0008203~cholesterol metabolic process	10	LDLR, CYP51A1, SQLE, INSIG1, HMGCS1, FDPS, MVK, LSS, PMVK, FDFT1	7.38E-07
GOTERM_BP_FAT	GO:0008202~steroid metabolic process	12	LDLR, CYP51A1, SQLE, INSIG1, HMGCS1, FDPS, MVK, LSS, PMVK, SC5DL, SC4MOL, FDFT1	8.32E-07