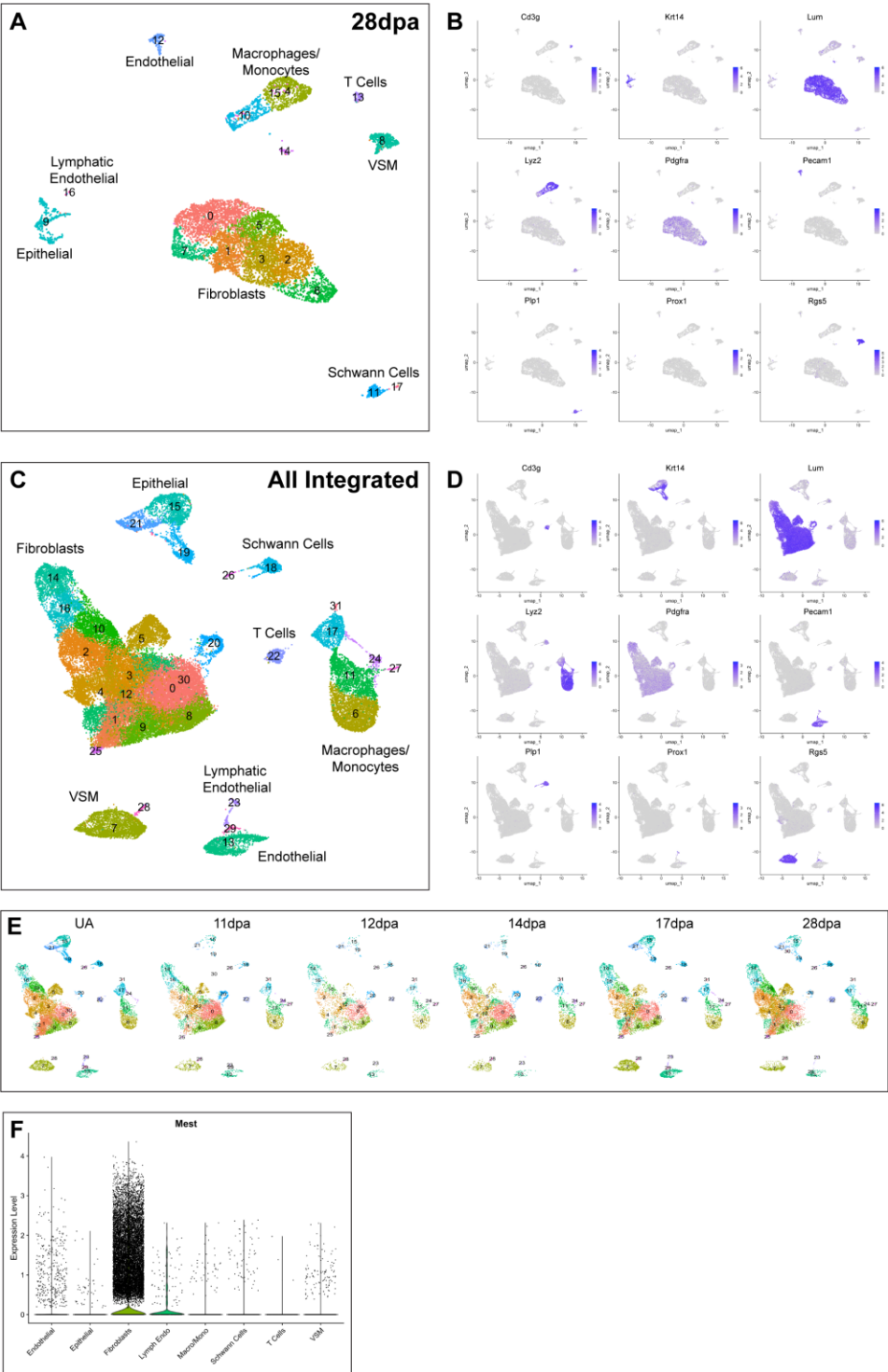
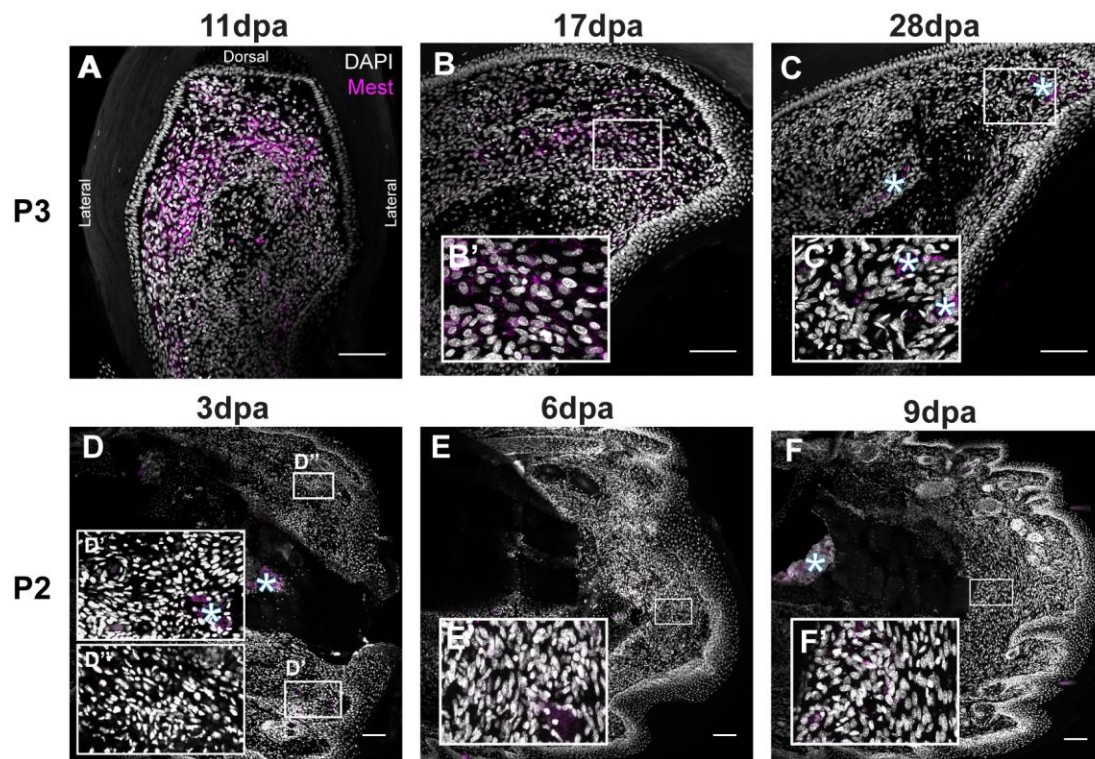


SUPPLEMENTARY INFORMATION

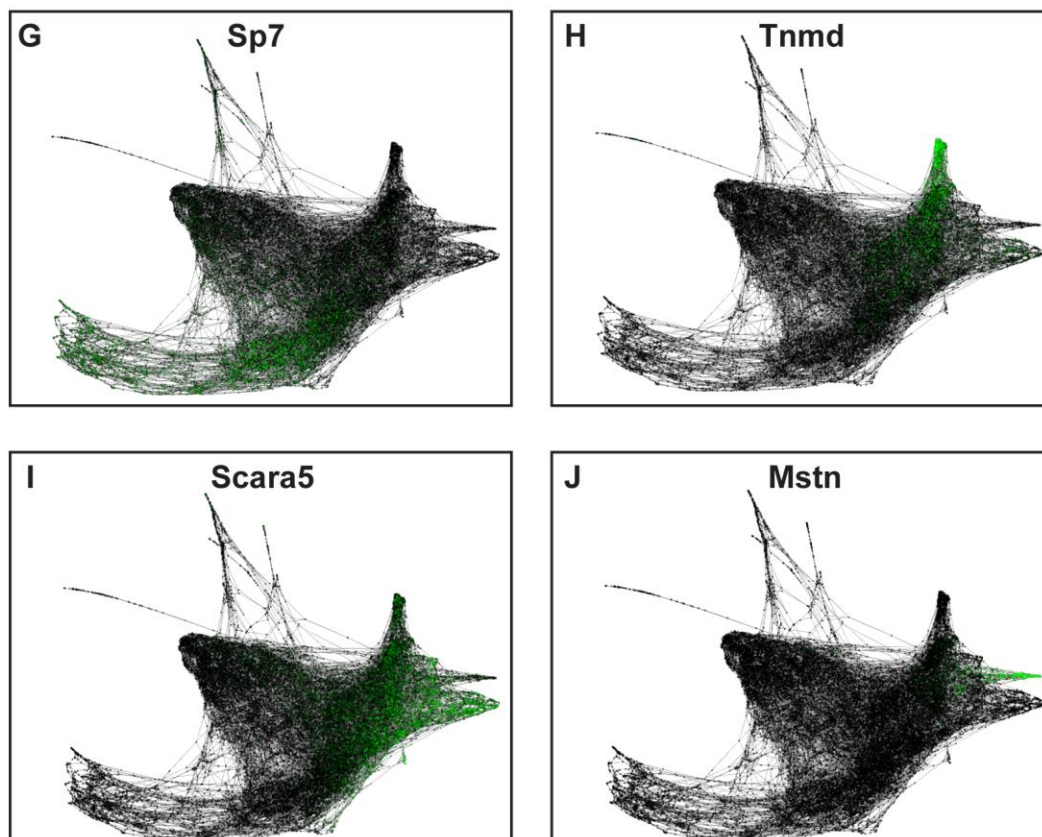


Supplementary Figure 1

Longitudinal regenerating digit tip scRNAseq analysis including 28dpa. (A) UMAP plot of cell clustering from 28dpa regenerated digit tip scRNAseq; (B) gene markers used to assign cluster identities. (C) UMAP plot of cell clustering from integrated UA, 11, 12, 14, 17, and 28dpa scRNAseq datasets; (D) gene markers used to assign cluster identities. (E) UMAP plots of integrated scRNAseq datasets, split by stage. (F) Violin plot of *Mest* expression by cell type.

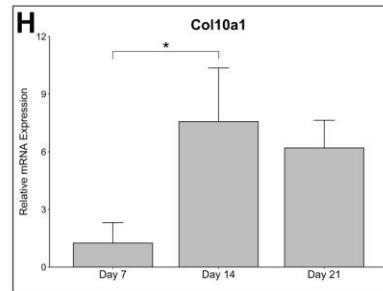
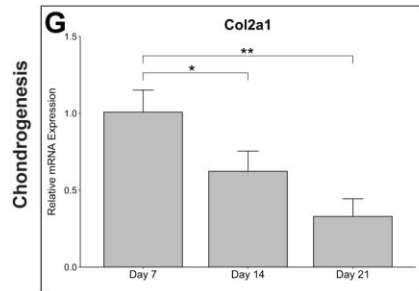
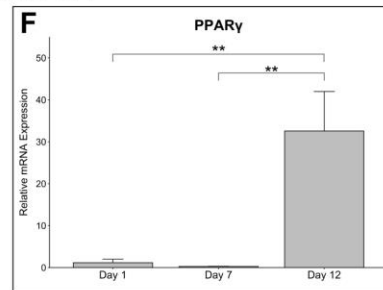
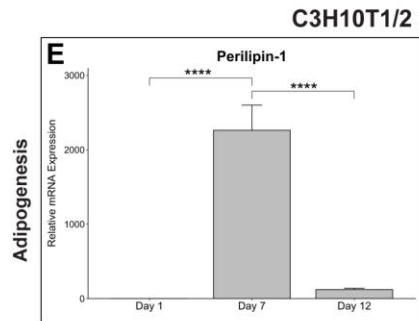
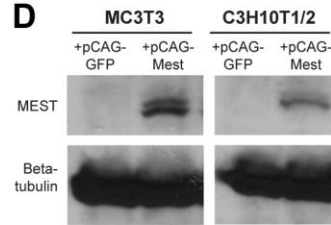
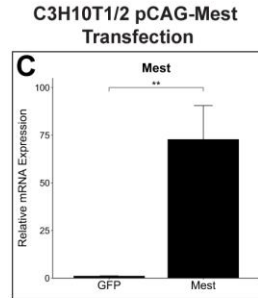
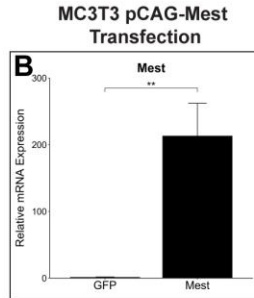
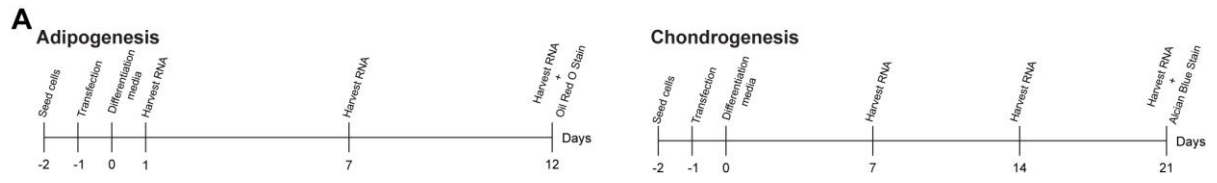


SPRING Trajectories

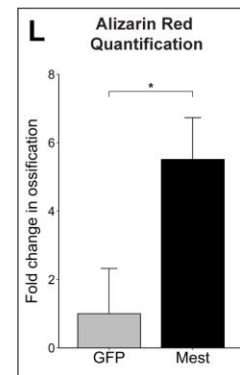
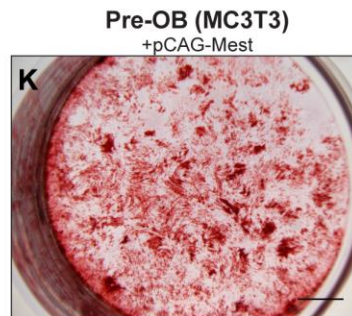
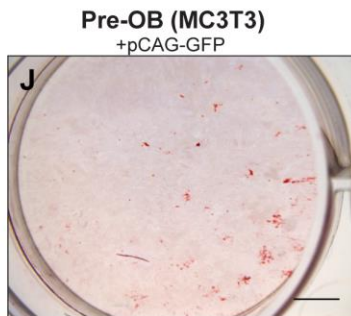
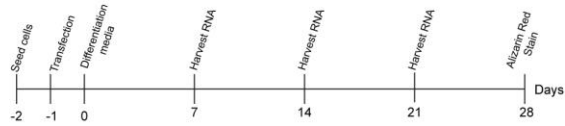


Supplementary Figure 2

Post-amputation Mest expression in distal P3 and proximal P2 digits. Mest RNA expression (magenta) in post-amputation digit sections visualized by HCR-RNA FISH, counterstained with DAPI (grayscale). (A-C) Regenerating P3 digits at (A) 11dpa, (B) 17dpa, and (C) 28dpa. (D-F) Mest expression in the P2 non-regenerating digit at (D) 3dpa, (E) 6dpa, and (F) 9dpa. The tissue orientation is distal to the right and dorsal to the top for all panels except (A) where dorsal is to the top and lateral is to the right and left. White boxes show locations of inset panels (B' - F'); all scale bars = 100µm. White asterisks denote blood vessel autofluorescence. (G-J) Computational trajectory plots of integrated fibroblasts with expression of the genes (G) *Sp7* (osteogenic), (H) *Tnmd* (ligaments and tendons), (I) *Scara5* (dermal), and (J) *Mstn* (myogenic and connective tissue) in green; plots generated using SPRING.

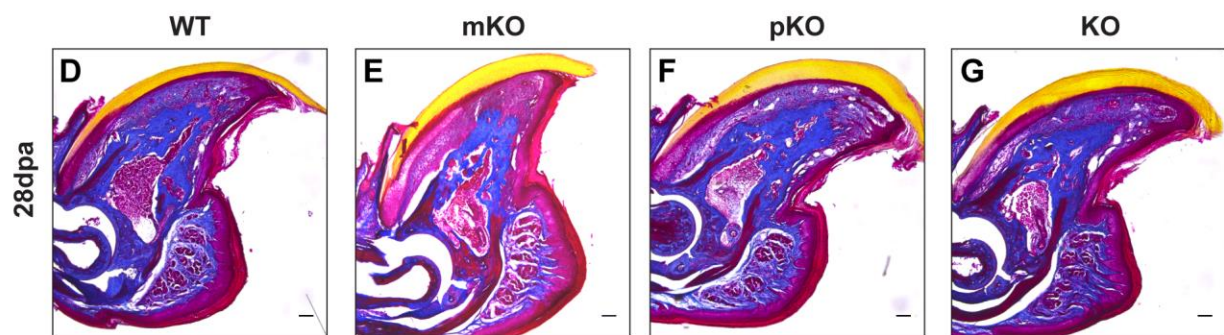
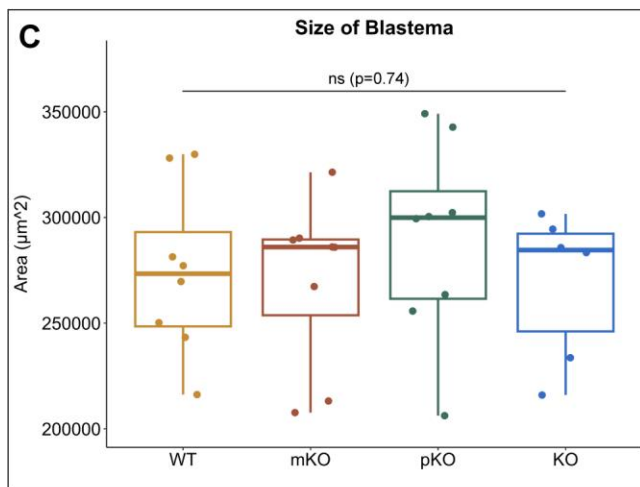
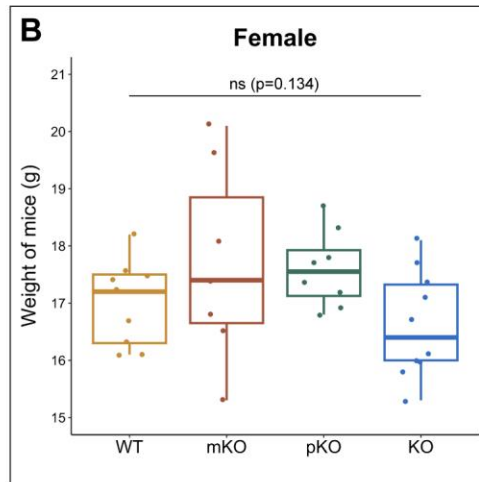
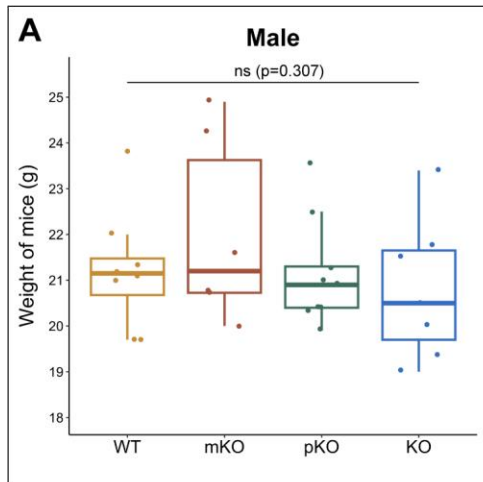


I Osteogenesis



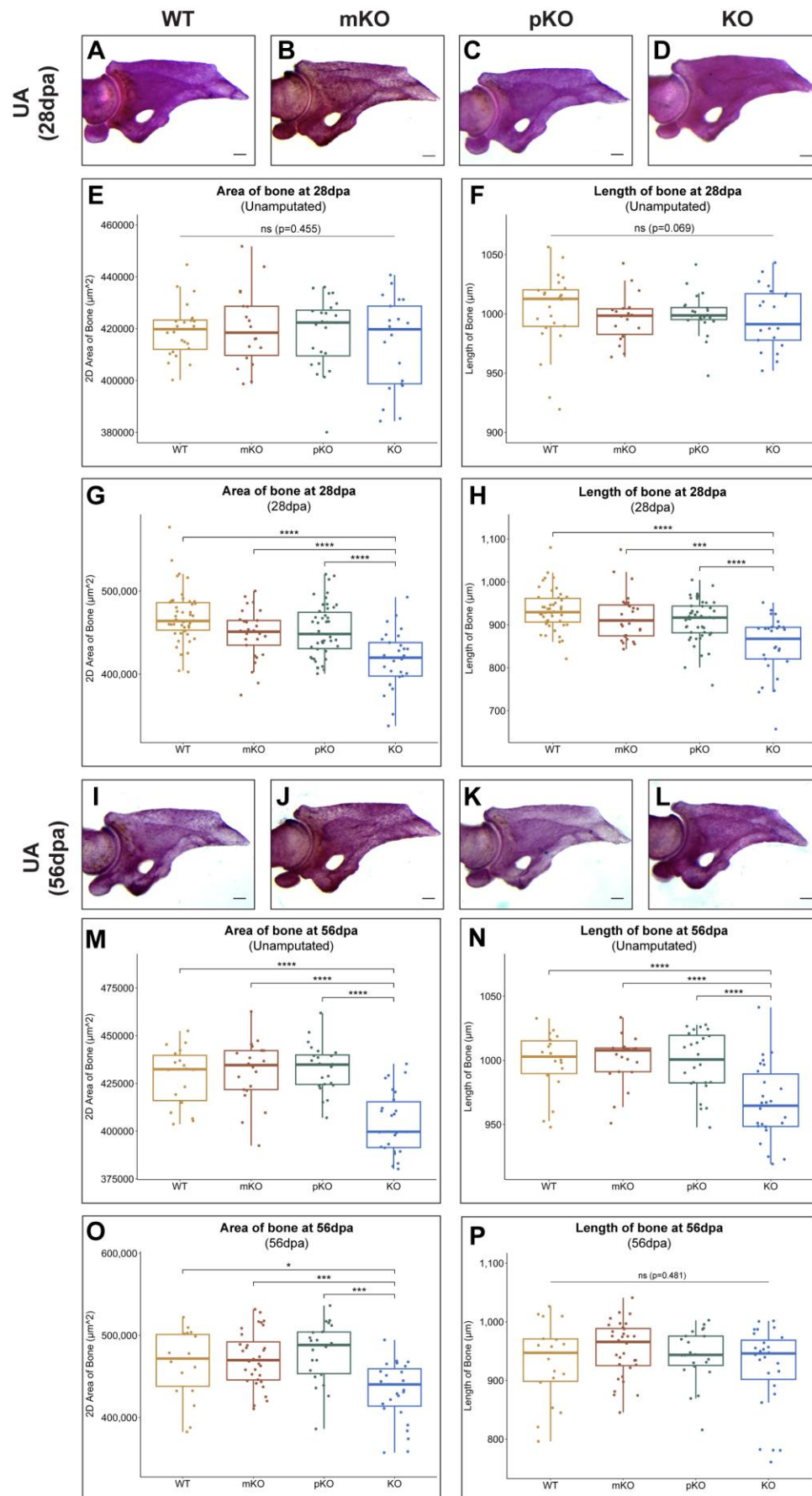
Supplementary Figure 3

In vitro Mest overexpression experiments. (A) In vitro (left) adipogenesis and (right) chondrogenesis experimental timelines. (B-C) Mest qPCR analysis of pCAG-GFP and pCAG-Mest transfected (B) MC3T3 and (C) C3H10T1/2 cells 24 hours post-transfection. (D) MEST protein and Beta-tubulin control western blot analysis of pCAG-GFP and pCAG-Mest transfected (left) MC3T3 and (right) C3H10T1/2 cells 48 hours post transfection. (E-F) qPCR analysis of adipogenic genes (E) Perilipin-1 and (F) PPAR γ of 1, 7, and 12dpi C3H10T1/2 cells transfected with GFP. (G-H) qPCR analysis of chondrogenic genes (G) Col2a1 and (H) Col10a1 of 7, 14, and 21dpi C3H10T1/2 cells transfected with GFP. (I) In vitro osteogenesis experimental timeline. (J-L) Alizarin Red stained wells of 28dpi (J) GFP and (K) Mest transfected MC3T3 cells for osteogenesis and (L) quantification of Alizarin Red staining. Scale bars = 250 μ m. Error bars are reported as standard deviation; (*) $p < 0.05$, (**) $p < 0.01$, (****) $p < 0.0001$.



Supplementary Figure 4

Extended data for Mest genetic cohorts. (A, B) Boxplot of weights of 8-10-week-old Mest knockout mice for (A) males and (B) females. (C) Boxplot of 12dpa blastema sizes across Mest genetic cohorts. All data was analyzed with one-way ANOVA and was not statistically significant (ns) for either the male or female cohorts for weight and for the size of blastemas ($p=0.307$, 0.134 , and 0.740 , respectively). Error bars are reported as standard deviation. (D-G) Masson trichrome histology of 28dpa regenerated digit sections from (D) WT, (E) mKO, (F) pKO, and (G) KO mice. Scale bars = $100\mu\text{m}$.



Supplementary Figure 5

Extended data for Alizarin Red stained whole-mount digits.

(A-D) Representative Alizarin Red stained unamputated contralateral digits for Mest genetic cohorts harvested at 28dpa. (E, F) Quantification of (E) 2D area of bone and (F) length of the P3 bone for unamputated, 28dpa digits. Data were not significant (ns) by one-way ANOVA ($p=0.455$ and 0.0694 , respectively). (G,H) Quantification of (G) 2D area and (H) length for amputated bones at 28dpa. (I-L) Representative Alizarin Red stained unamputated contralateral digits for Mest cohorts harvested at 56dpa. (M,N) Quantification of (M) 2D area of bone and (N) length of the P3 bone for the unamputated, 56dpa digits. (O,P) Quantification of (O) 2D area and (P) length of bone of amputated bones at 56dpa. All data was analyzed with one-way ANOVA followed by post-hoc t-test with Bonferroni correction. (*) $p < 0.05$, (***) $p < 0.001$, (****) $p < 0.0001$. Error bars are reported as standard deviation. Scale bars = $100\mu\text{m}$.

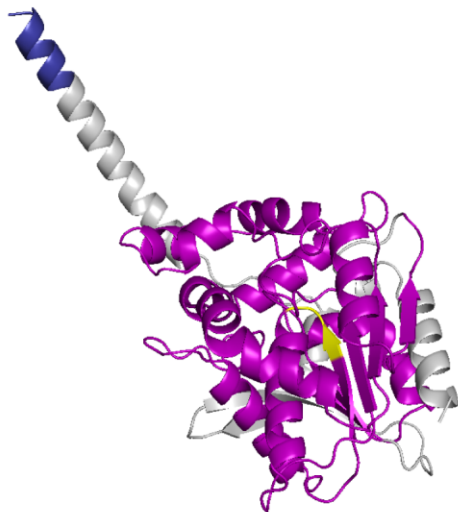
Supplementary Figure 6

Extended data for bisulfite sequencing of Mest cohorts. (A-B) Dot plots of methylated alleles only in (A) Exon1-5' and (B) Exon1-3'. One-way ANOVA analyzes indicated no significance in both datasets ($p=0.84$ and 0.616 , respectively). Error bars are reported as standard deviation. (C) Schematic of (top) CTCF and (bottom) ExonA amplicons for bisulfite sequencing; hand drawn using Adobe Illustrator. Gray bars indicate predicted methylated CpG position and black box indicates the location of exon A. (D-E) Graphs of methylation percentage at each predicted CpG position across all reads for each genotype in the (D) CTCF and (E) ExonA regions.

A

Mest211	1	MVRRD-----RLRRMREWWVQVGLLAVPLLAAYLHIPPQLSPALHSWKTSGKFFTYKGLRIFYQDSVGVVGSPEIVV	73
Mest210	1	-----MREWWVQVGLLAVPLLAAYLHIPPQLSPALHSWKTSGKFFTYKGLRIFYQDSVGVVGSPEIVV	64
Mest202	1	MYVLEprssslKAMQMREWWVQVGLLAVPLLAAYLHIPPQLSPALHSWKTSGKFFTYKGLRIFYQDSVGVVGSPEIVV	80
Mest211	74	LLHGFTSSYDWYKIWEGLTLRFHRVIALDFLGFGFSKPRPHQYSIFEQASIVESLLRHLGLQNRRLNLLSHDYGDIVA	153
Mest210	65	LLHGFTSSYDWYKIWEGLTLRFHRVIALDFLGFGFSKPRPHQYSIFEQASIVESLLRHLGLQNRRLNLLSHDYGDIVA	144
Mest202	81	LLHGFTSSYDWYKIWEGLTLRFHRVIALDFLGFGFSKPRPHQYSIFEQASIVESLLRHLGLQNRRLNLLSHDYGDIVA	160
Mest211	154	QELLYRYKQNRSGRLTIKSLCLSNGGIFPETHRPLLQKLLKGGVLSPILTRLMNFFVFSRGLTPVFGPYTRPTESELW	233
Mest210	145	QELLYRYKQNRSGRLTIKSLCLSNGGIFPETHRPLLQKLLKGGVLSPILTRLMNFFVFSRGLTPVFGPYTRPTESELW	224
Mest202	161	QELLYRYKQNRSGRLTIKSLCLSNGGIFPETHRPLLQKLLKGGVLSPILTRLMNFFVFSRGLTPVFGPYTRPTESELW	240
Mest211	234	DMWAVIRNNDGNLVIDSLLQYINQRKKFRRRWV GALASVSIPIHFIYGPLDPINPYEFLELYRKTLP RSTVSILDDHIS	313
Mest210	225	DMWAVIRNNDGNLVIDSLLQYINQRKKFRRRWV GALASVSIPIHFIYGPLDPINPYEFLELYRKTLP RSTVSILDDHIS	304
Mest202	241	DMWAVIRNNDGNLVIDSLLQYINQRKKFRRRWV GALASVSIPIHFIYGPLDPINPYEFLELYRKTLP RSTVSILDDHIS	320
Mest211	314	HYPQLEDPMGFLNAYMGFINSF	335
Mest210	305	HYPQLEDPMGFLNAYMGFINSF	326
Mest202	321	HYPQLEDPMGFLNAYMGFINSF	342

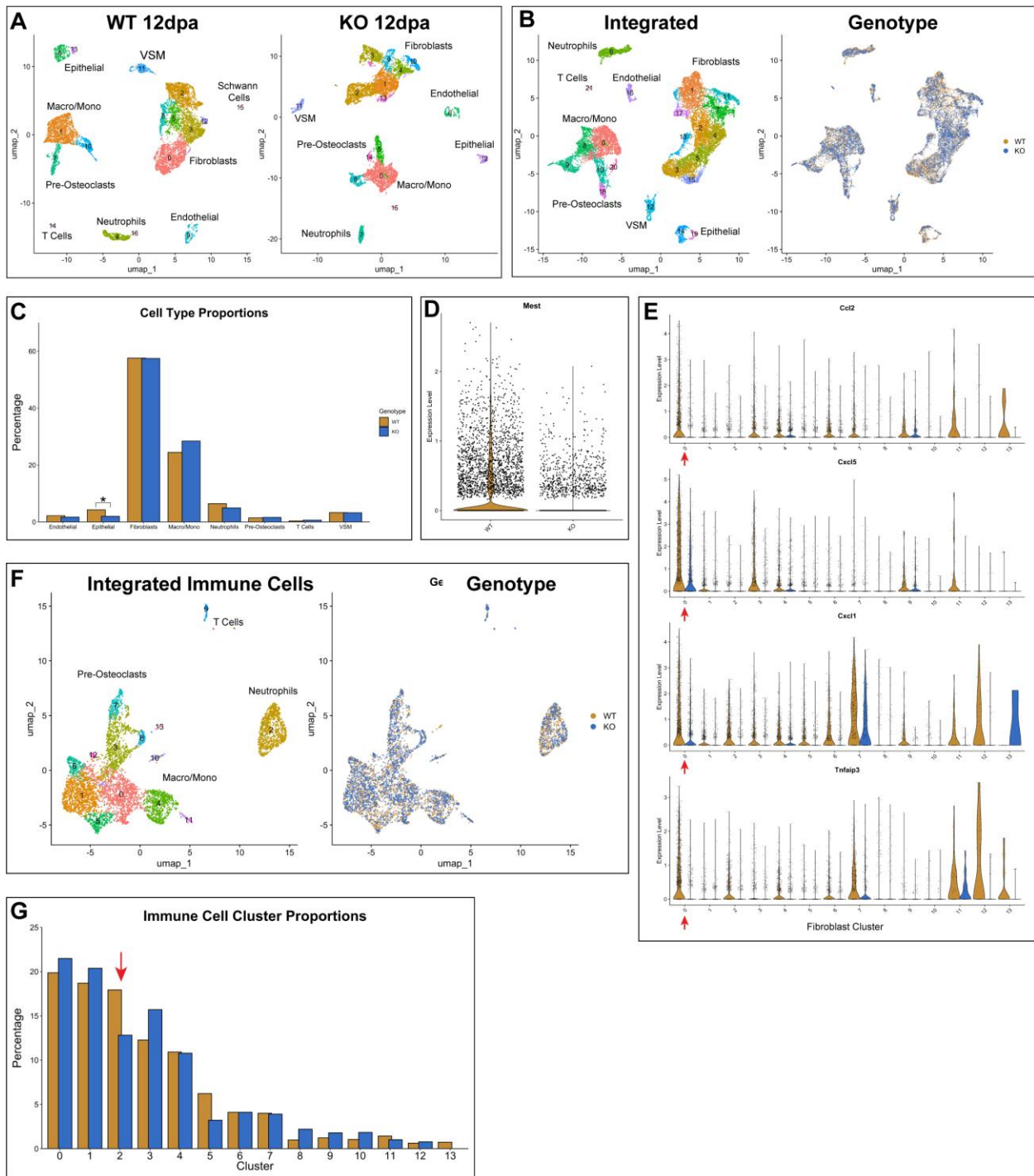
B



Dark Blue = N-terminus region specific to Mest211
Magenta = alpha/beta hydrolase domain
Yellow = Ser-His-Asp catalytic triad

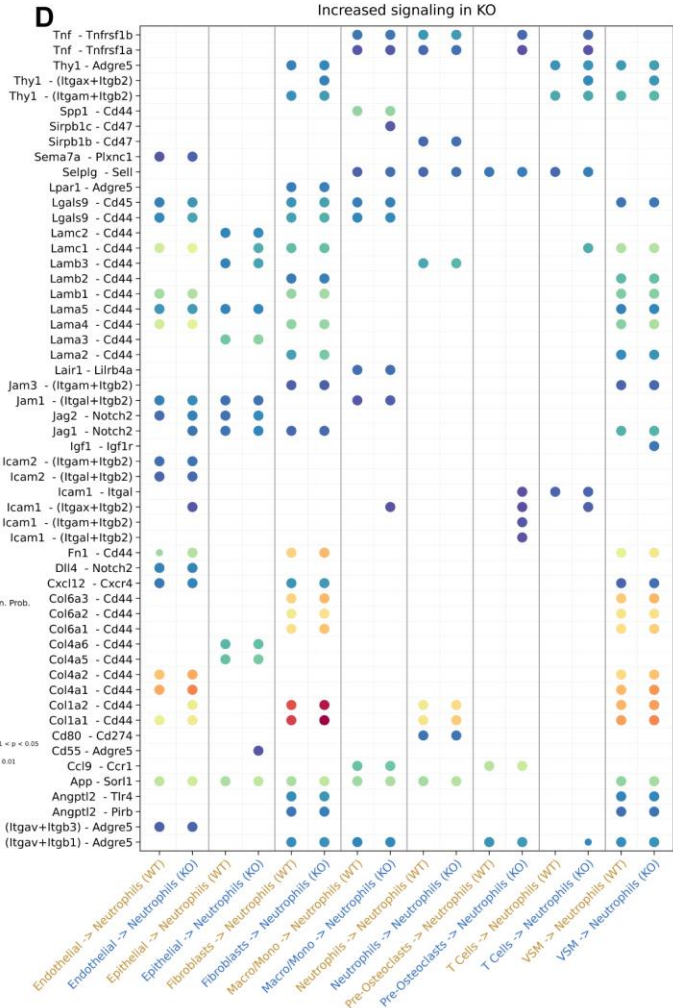
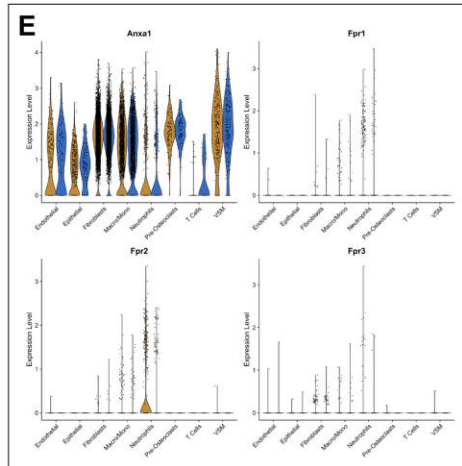
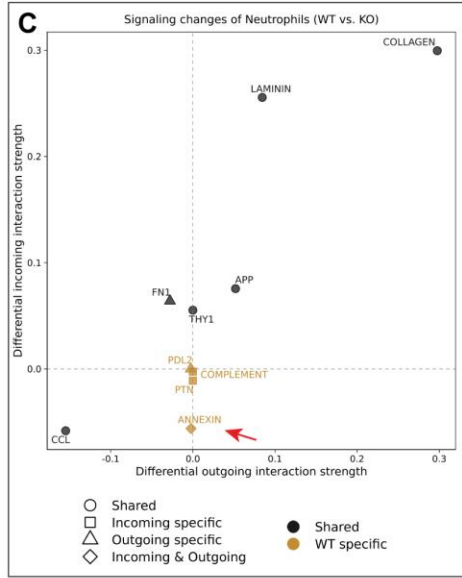
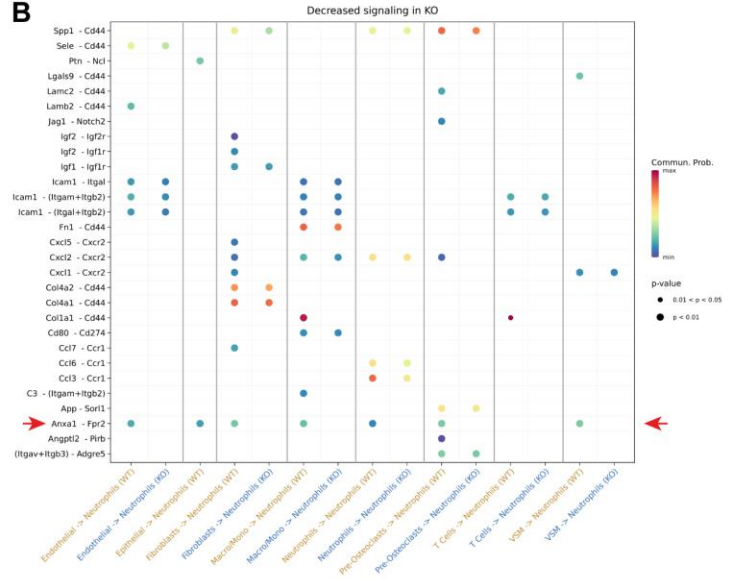
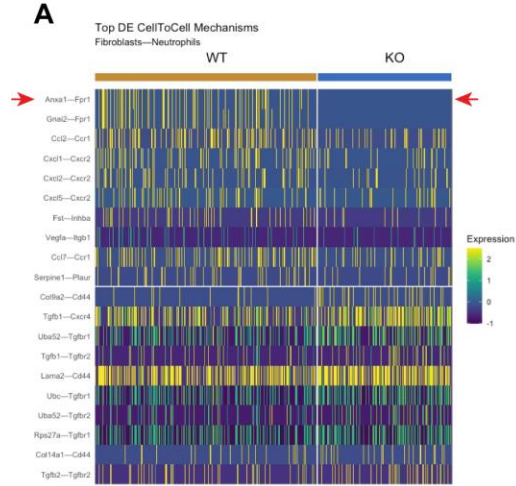
Supplementary Figure 7

Protein alignment for Mest variants. (A) Protein sequence alignment for Mest211, 210 and 202 variants with 100% identical amino acids in red font. (B) AlphaFold predicted structure of Mest211 based on #Q07646 with the follow features colored: dark blue = N-terminal amino acids 1-9 specific to Mest211, magenta=alpha/beta hydrolase domain, and yellow = Ser-His-Asp catalytic triad.



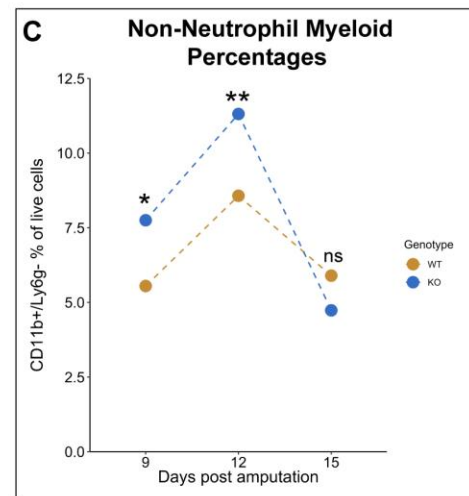
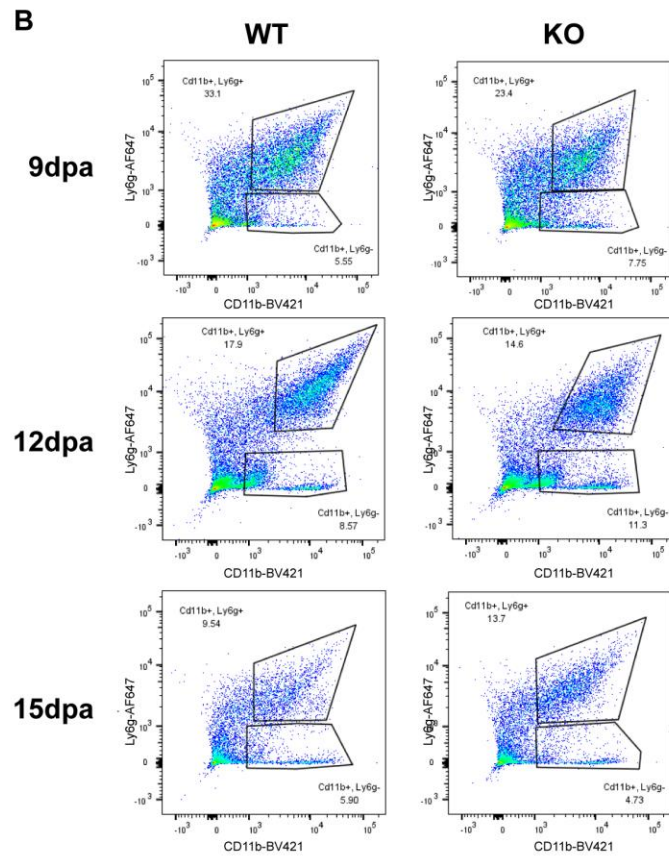
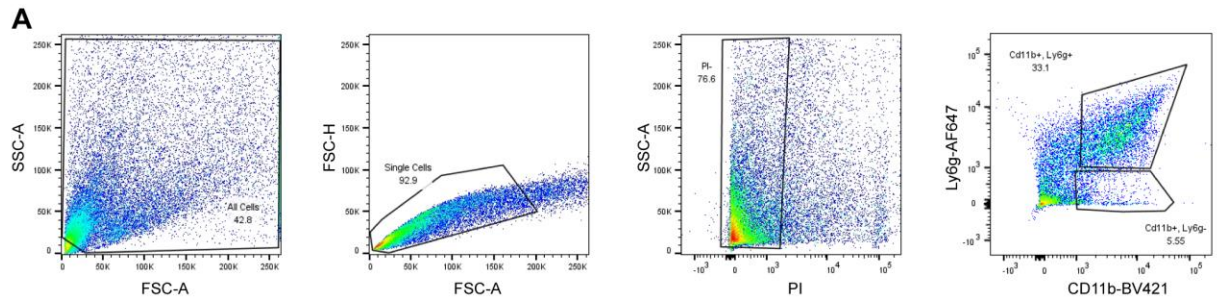
Supplementary Figure 8

Extended data for Mest scRNAseq. (A) UMAP plots of (left) Mest-WT and (right) KO 12dpa blastemas colored by Seurat clusters with major cell types labeled. (B) UMAP plot of integrated WT and KO 12dpa blastemas colored by (left) Seurat clusters with major cell types labeled and (right) genotype. (C) Cell type proportions in Mest-WT versus KO datasets. (D) Violin plot of Mest expression in integrated fibroblasts. (E) Expression of Ccl2, Cxcl5, Cxcl1, and Tnfaip3 (the top 4 DEGs in WT fibroblasts) across all fibroblast subpopulations, split by genotype. Cluster 0 is indicated by a red arrow in each graph. (F) UMAP plots of integrated immune cells colored by (left) Seurat clusters and (right) genotype. (G) Cluster proportions in the immune cell subpopulations; red arrow points to cluster 2 neutrophils. Differential proportion analysis was performed for both (C) and (G) and all genotypic comparisons were non-significant, except for the epithelial population in (C).



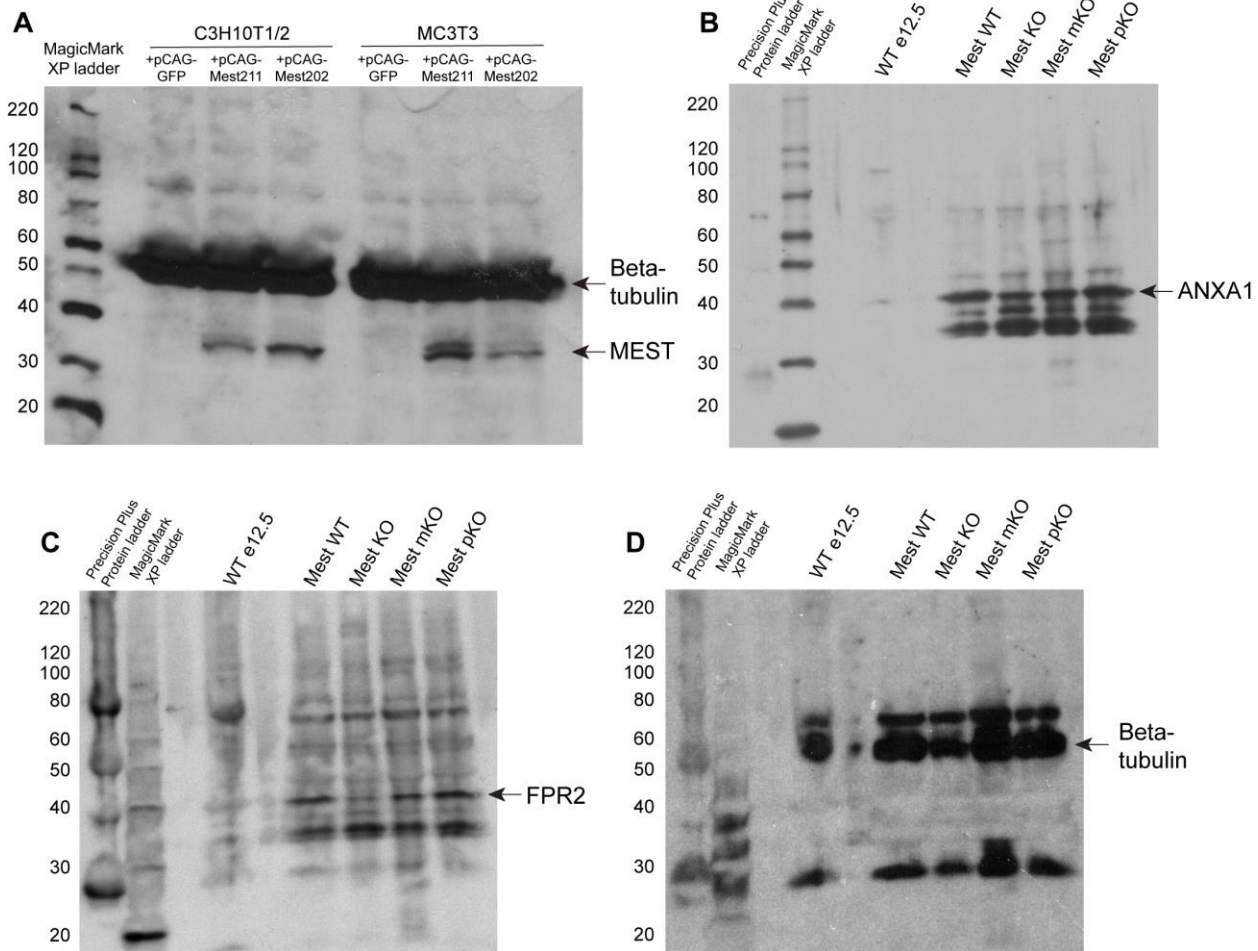
Supplementary Figure 9

Extended data for Mest scRNAseq cell-cell communication analysis. (A) Heatmap of differential ligand-receptor interactions between fibroblasts and neutrophils in the Mest-WT and KO blastemas generated by NICHES analysis. (B, D) Dot plot of ligand-receptor interactions (B) downregulated and (D) upregulated in KO blastemas compared with Mest-WT, with neutrophils as the receiving cell type. (C) Differential strength in signaling pathways with neutrophils as receiving cell type, negative X- and Y-values indicate upregulated in WT blastema while positive X- and Y-values indicate upregulated in KO blastema. Graphs (B-D) were generated using CellChat. Red arrows in (A-C) point to Anxa1 signaling. (E) Violin plots of Anxa1, Fpr1, Fpr2, and Fpr3 expression in Mest-WT vs KO blastemas by cell type.



Supplementary Figure 10

FACS analysis of neutrophils in wildtype and knockout tissue (A) Sample gating strategy to quantify number of neutrophils and non-neutrophil myeloid cells. (B) CD11b-BV421 versus Ly6g-AF647 plots for WT and KO tissues at 9, 12, and 15dpa indicating the quantified regions for CD11b⁺/Ly6g⁺ double-positive and CD11b⁺/Ly6g⁻ cells. (C) Quantification of Mest-WT and KO non-neutrophil myeloid cells at 9, 12, and 15dpa by flow cytometry. Percentages were calculated for CD11b⁺/Ly6g⁻ cells out of all PI⁻ cells. (*) $p < 0.05$, (**) $p < 0.01$ and ns=not significant.



Supplementary Figure 11

Original Western blots. (A) Full image of anti-MEST and anti-Beta-tubulin blot shown in Supplementary Figure 3D. Arrows indicate Beta-tubulin and MEST bands. (B) Full image of anti-ANXA1 Western blot shown in Figure 6H. Arrow indicates ANXA1 band. (C-D) Full images of same Western membrane used in (B), stripped and re-probed for (C) FPR2, then (D) Beta-tubulin. Arrows indicate bands for FPR2 in (C) and Beta-tubulin in (D). All molecular weight ladders and samples used are indicated above each membrane.

Supplementary Table 1. Primers

Genotyping primers:	
Mest-F-Genotype	AATATGAGGATGTCTACACAACCTCTTAA
Mest-R-Genotype	ACTCCAGCTTTAATTTGGCAGT
qPCR primers:	
GAPDH-F	AAGAGGGGATGCTGCCCTTAC
GAPDH-R	CCATTTTGTCTACGGGACGA
Mest-Total-F	AAGCCATGTAAAAGCACAACTATCTC
Mest-Total-R	CCTACAAAGGCCTACGCATCTT
Mest211-F	GCGGCATGGGATAATGC
Mest211-R	CTACTTGGACCCACCACTCT
Mest210-F	GGGTAGAGAGAAAAAGTGTGGAA
Mest210-R	CCTCTAAGGAACAGCGACTTC
Mest202-F	CCCTGTGATCCGCAATCCT
Mest202-R	ACTACTGTCTGCATTTGGGCTATG
Perilipin-1-F	GGCCTGGACGACAAAACC
Perilipin-1-R	CAGGATGGGCTCCATGAC
PPAR γ -F	CCAGAGCATGGTGCCTTCGCT
PPAR γ -R	CAGCAACCATTGGGTCAGCTC
Col2a1-F	AGGGGTACCAGGTTCTCCATC
Col2a1-R	CTGCTCATCGCCGCGGTCCGA
Col10a1-F	ATGCCTTGTTCTCCTCTTACTGGA
Col10a1-R	CTTTCTGCTGCTAATGTTCTTGACC
Runx2-F	TCCACAAGGACAGAGTCAGATTAC
Runx2-R	TGGCTCAGATAGGAGGGGTA
Bisulfite PCR primers:	
CTCF-F	TGTTATTTTATATTTTTTGTAATAGGTGG
CTCF-R	CAAATAAAACCTATCCTACATACAAAAC
ExonA-F	GGTTAGGAGGTAATTTAAATTATTTGTT
ExonA-R	CACACATTATCTCATTTACTACTCAC
Exon1-5'-F	ATTTGGGGTTTAGGATTAGAGATTTATA
Exon1-5'-R	AAAAAAAACCTACTACRCCTAAAAAAA
Exon1-3'-F	AGTTGTTGTTTGTGTTTGTGTTGT
Exon1-3' -R	CCTTTAAATAAAAATTTTACCTCCC

Supplementary Table 2. Differentially expressed genes upregulated in scRNAseq Mest-WT fibroblasts

gene	avg_log2FC	p_val_adj
Ccl2	2.34156423	8.31E-54
Cxcl5	1.98077639	1.47E-36
Cxcl1	1.95148461	7.87E-100
Tnfaip3	1.91003983	1.29E-72
Mest	1.76395879	3.21E-75
Cxcl2	1.59974693	2.10E-74
Gm26771	1.47109463	1.00E-33
Nr4a1	1.43910062	1.38E-40
Nfkbia	1.42959324	4.01E-121
Zfp36	1.39327038	6.81E-68
Dio2	1.38824246	1.85E-25
Nfkb1	1.35876783	2.75E-34
Ier3	1.32744243	5.24E-82
Ptgs2	1.28631537	4.15E-21
Ccl7	1.27844535	1.47E-20
Ddx3y	1.21368016	1.31E-80
Pde10a	1.17373904	1.45E-31
Eif2s3y	1.13980406	5.25E-69
Slpi	1.12664099	4.41E-39
Serpina3n	1.1173895	2.77E-28
Mt2	1.10528856	3.52E-59
Nfkbiz	1.08716752	2.97E-77
Sfrp2	1.07993783	2.01E-42
Angptl4	1.01276328	8.40E-33
Dusp1	0.99915841	2.17E-37
Cebpd	0.9990948	1.89E-20
Maff	0.99549165	1.77E-16
Chl1	0.9738698	4.57E-19
Ndr1	0.95801991	2.53E-40
Birc3	0.94343215	1.27E-14
Pnrc1	0.93198878	1.22E-25
Hspb1	0.93105983	9.10E-19
Phlda1	0.92565355	1.61E-12
Uty	0.92034308	1.54E-55

Plpp3	0.91927962	2.57E-29
Ddit4	0.91759515	2.18E-24
Gem	0.91206775	3.26E-48
Nr4a2	0.89771788	1.58E-30
Irf1	0.88708871	2.19E-31
Rcan1	0.88254913	8.16E-28
Pappa2	0.87704629	0.00202526
Egr1	0.87572491	1.86E-54
Arrdc3	0.87329321	2.94E-11
Hspa1b	0.87150305	9.72E-65
Nfil3	0.86941835	1.47E-16
Adamts1	0.86394997	1.19E-12
Junb	0.84822771	1.93E-71
Cebpb	0.84454004	4.25E-59
Ntrk2	0.84403564	1.31E-18
Cfb	0.83207384	2.10E-13
Fosb	0.83118495	1.11E-16
March3	0.82889961	6.70E-11
Cadm2	0.78914276	0.000808
Zfp36l1	0.78857663	3.78E-37
Sdc4	0.78014257	1.16E-73
Rspo4	0.77704207	4.02E-09
Sik1	0.75977479	8.01E-16
Hk2	0.7593632	1.10E-15
Hspa1a	0.75857196	8.13E-57
Pim1	0.74465993	1.66E-16
Klf9	0.74267027	9.79E-34
Tnfaip2	0.73671805	2.37E-34
Btg2	0.73374366	1.33E-27
Hivep1	0.73006277	2.14E-14
Tiparp	0.72806166	7.90E-06
Rbpms	0.72473835	2.17E-26
Schip1	0.72383564	0.00235524
Ackr3	0.72129156	6.00E-11
Ifrd1	0.71918814	4.16E-36
Sod3	0.71809612	2.66E-97
Slc6a17	0.71708275	1.17E-12
Tgif1	0.71648015	3.31E-09
Mt1	0.70387384	2.83E-53

Tnfsf11	0.70219356	2.31E-18
Il11	0.69897883	9.51E-11
Glis3	0.69808464	9.91E-66
Cdkn1a	0.69331898	1.46E-12
Ier2	0.69249101	4.95E-32
Igf2	0.68101283	0.00027552
Rorb	0.67999956	5.47E-18
Sh3rf3	0.6793746	5.42E-07
Jun	0.67656001	1.15E-32
Gadd45b	0.67044861	4.25E-23
Ets2	0.66916533	2.59E-16
Dapk1	0.66844784	0.00345154
Sox5	0.66612425	1.70E-07
Igf2bp2	0.65610912	5.19E-09
Tnfrsf11b	0.65447818	0.00182813
Lncpint	0.64490747	3.77E-24
Man1a	0.64282503	5.10E-13
Apoe	0.64277737	0.00023825
Steap4	0.64255647	5.33E-12
Glul	0.63932723	6.47E-06
Hspa4l	0.63529061	0.00053848
Ptger4	0.63165589	2.56E-09
Spp1	0.62805469	3.41E-15
Bcl3	0.62612089	5.98E-13
Btaf1	0.62409228	8.49E-50
Ern1	0.62021302	6.69E-07
Nfatc1	0.61885638	5.25E-13
Mxd1	0.61751919	1.02E-09
Fos	0.6175066	4.18E-24
Cxcl14	0.61740227	9.05E-21
Cdh13	0.61597944	0.00268987
Pfkfb3	0.61259018	7.12E-06
Crim1	0.61176009	0.0009021
Btg1	0.60919064	1.18E-49
Pitpnc1	0.60839758	2.38E-22
Slc16a1	0.6072917	6.93E-19
Hipk2	0.60264817	1.05E-09
Cmip	0.59877163	1.43E-39
Gfpt2	0.5983172	0.028104

Serping1	0.59502007	2.29E-30
Slc4a4	0.5906213	8.29E-05
Mgst1	0.58989248	8.29E-08
St3gal1	0.58974132	1.05E-09
Aff1	0.58905681	1.93E-26
Pde1a	0.58271423	5.00E-15

Supplementary Table 3. Differentially expressed genes upregulated in scRNAseq Mest-KO fibroblasts

gene	avg_log2FC	p_val_adj
Matn3	-1.0851626	2.82E-55
Sept4	-1.0217861	2.71E-43
Npr3	-0.9667224	1.05E-38
Bcl11b	-0.9657123	3.66E-48
Lsp1	-0.903422	1.44E-76
Sorbs2	-0.8152891	2.06E-25
Ecm2	-0.7955849	5.36E-34
Itm2a	-0.7941606	5.82E-64
Lepr	-0.7495048	1.55E-19
Omd	-0.7381966	1.42E-88
Dlx6	-0.73436	3.04E-29
Col8a2	-0.6880018	2.62E-62
Ogn	-0.6796653	2.14E-47
Cdh10	-0.6789679	4.96E-33
Hacd4	-0.6767732	4.56E-48
Fndc1	-0.6711159	5.59E-74
Pdlim2	-0.6014694	3.78E-71
Cdkn2b	-0.5976389	5.54E-18
Gas2	-0.5959082	1.56E-23
Fat3	-0.5907015	3.88E-13
Dlx5	-0.5868251	9.34E-31

**Supplementary Table 4. Differentially expressed genes for scRNAseq Mest-WT and KO
integrated fibroblasts cluster-0**

gene	avg_log2FC	p_val_adj
Cyp2f2	6.34080912	0
Lcn2	5.65710861	0
Dio3	5.43277833	0
Nrg2	4.81359999	0
Sfrp2	4.77934049	0
Dio2	4.68736639	0
Gm26771	4.63641059	0
Apod	4.60650856	0
Cck	4.56405487	3.53E-197
Hhex	4.55570143	0
Pappa2	4.54854018	0
Dio3os	4.4685892	0
Apoc1	4.46386155	0
C4b	4.40418619	0
Steap4	4.39910113	0
Tnxb	4.37973759	0
Slco2a1	4.33919485	0
Lrg1	4.24875927	0
Ccn3	4.2186837	0
Vipr2	4.20443238	0
Rspo4	4.19626175	0
Rspo1	4.19050236	0
Gpm6a	4.16929537	0
C3	4.07785118	0
Corin	4.07070636	0
Gm26512	4.03487965	0
Ramp2	4.02241096	0
Serpina3n	3.96859527	0
Zcchc18	3.93960051	0
Apoe	3.92401807	0
Cntn5	3.82567051	0
Scara5	3.8242697	0
Sorcs3	3.81151283	0
Ntrk2	3.75273996	0

Cntn1	3.70973028	0
Epha5	3.69113101	0
Shisal1	3.68209453	9.99E-244
Susd2	3.67330143	6.77E-209
Trf	3.66091695	5.52E-125
Nrg3	3.65243197	0
Cfb	3.62162299	0
Plpp3	3.51654181	0
Mgst1	3.5162599	0
Procr	3.505636	0
Emx2	3.50086002	1.67E-290
a	3.49031241	0
Rarres2	3.45806947	0
Prxl2a	3.45626398	0
Fbxo2	3.42935784	1.10E-240
Ntrk3	3.42796389	0
Hspb1	3.3561184	0
Fos	3.35322755	0
Pcdh10	3.33578345	1.30E-238
Cxcl5	3.30899532	3.16E-177
Icam1	3.2882509	0
Cebpd	3.28086759	0
Entpd2	3.24550033	0
Efemp1	3.18688395	0
Nr4a1	3.17747904	0
Dusp1	3.16652227	0
Wif1	3.15197592	0
Ifitm1	3.14799256	0
Syt13	3.08748364	0
Prelp	3.07716464	0
Tst	3.04654326	2.07E-260
Maob	3.04374672	0
Calcl	3.04269749	9.95E-246
Egfem1	3.03294006	0
Csrnp1	3.01766371	2.86E-151
Igf2	3.00591208	0
Cybrd1	2.96877471	0
Snhg11	2.96757921	7.71E-251
Rgs6	2.9668774	0

Klhl32	2.96665456	2.32E-257
Orm1	2.96071605	9.91E-146
Ptger4	2.95014067	0
Frmpd4	2.93166212	0
Gstm1	2.91508403	0
Isyna1	2.88718629	2.42E-157
Hsd11b1	2.86704166	4.47E-106
Gstt1	2.85016109	4.73E-293
Ackr4	2.84966298	3.74E-234
Rspo3	2.84436876	0
Igfbp5	2.83323038	0
Clu	2.83145027	0
Zfp36	2.8304276	2.68E-234
Plxdc1	2.82987453	0
Tnmd	2.80726868	0
Chl1	2.80516577	0
Cxcl12	2.80393595	0
Nog	2.79260156	4.58E-194
Sema3a	2.77145576	0
Dach1	2.75028485	0
Gsta4	2.74646137	0
Slc5a3	2.71154011	8.14E-185
Spock1	2.68510964	0
Cadm2	2.67729085	0
Gch1	2.67095098	1.11E-108
Gng8	2.66962851	1.36E-188
Gna14	2.65349756	0
Alx3	2.65092722	1.64E-165
Emx2os	2.64855272	1.19E-179
Rorb	2.64454768	0
Dcn	2.63732683	0
Pcp4l1	2.63134256	2.50E-99
9330159F19Rik	2.61004214	6.43E-196
Gda	2.60597569	3.79E-209
Steap1	2.58779607	0
Nr4a3	2.56091033	3.70E-177
Draxin	2.55761982	4.52E-186
Dapk1	2.55565902	6.21E-218
Kitl	2.54485434	6.57E-145

Steap2	2.54229319	0
Trpm3	2.53227928	0
Stxbp6	2.51429478	0
Wdr17	2.50825812	0
Wfdc1	2.49653105	1.74E-271
Ccl2	2.47518727	1.86E-41
Cygb	2.45899354	0
Ccdc74a	2.45835715	1.57E-152
Fst	2.44930957	0
Ly6c1	2.44874445	0
Pde10a	2.44363192	1.53E-222
Fosb	2.43760147	1.20E-229
Lbp	2.42973937	0
Hfe	2.42618833	5.04E-289
Ptger3	2.41743584	3.25E-203
Cfap69	2.40663523	0
Tox3	2.39982738	1.80E-198
Hey2	2.3967081	5.06E-148
C130021I20Rik	2.39632451	7.40E-266
Lmx1b	2.39618546	0
Add3	2.39583156	0
Il34	2.37684923	2.14E-158
Calml4	2.36807343	1.05E-102
Btg2	2.36798278	0
Cxadr	2.3566763	0
Nr4a2	2.3549928	5.67E-246
Lamc3	2.34628445	2.62E-191
Maff	2.33461091	1.91E-145
Cxcl14	2.33342659	0
Serping1	2.33016048	0
Ptgs2	2.32693391	1.80E-70
Flrt3	2.28625505	3.75E-153
Pnrc1	2.28607636	7.67E-297
Tshz2	2.26386964	0
Hspa1a	2.25664503	0
Junb	2.24915588	0
Ccdc3	2.24523285	4.12E-261
Enpp2	2.2367081	0
Rgs2	2.23470259	1.05E-95

Adh7	2.22335812	8.98E-89
Sik1	2.21379477	1.24E-248
S100a1	2.19123508	0
Hspa1b	2.18859523	0
Gpm6b	2.18858975	0
Csmd3	2.18099325	8.25E-155
Gm19522	2.18062862	1.80E-116
C1s1	2.17499384	0
Mapk13	2.16148544	1.34E-97
Atf3	2.16070537	3.87E-41
Gem	2.16030782	2.78E-259
Ly6a	2.16005082	0
Gfra1	2.15643466	3.85E-133
Fgf2	2.143934	5.08E-214
Olfml1	2.13336579	4.01E-159
Nr3c2	2.11810255	4.24E-226
Selenop	2.10607419	1.41E-278
Ednra	2.10125124	0
Ntng1	2.09338891	2.36E-216
C1ra	2.09225382	0
B3galt1	2.09222241	1.05E-295
Gm2a	2.08687109	5.58E-194
Ptprz1	2.08573721	2.35E-161
Dpep1	2.07873678	7.82E-253
Rab40b	2.06990332	4.07E-132
Masp1	2.06969016	0
Sfrp1	2.05756797	1.01E-156
Capn1	2.05145259	5.76E-128
Tnfrsf11b	2.05115969	1.14E-239
Shox2	2.04874791	1.97E-138
Txnip	2.04526533	0
Igfbp4	2.04345324	0
Rom1	2.037574	1.90E-118
Sybu	2.02881173	6.25E-250
Sgip1	2.02630488	0
Scara3	2.01502406	0
B3gnt5	2.00914722	5.09E-70
Pear1	2.00337578	4.09E-115
Adam33	2.00288684	2.72E-238

Grina	1.99711815	1.07E-205
Klf4	1.99566586	2.48E-125
Nfkbia	1.98570099	3.22E-219
Cyb5a	1.98139207	0
Thsd4	1.98118084	5.28E-143
Kctd1	1.97336123	0
Cyp26b1	1.95984373	3.07E-185
Trabd2b	1.95021818	7.43E-288
Sat1	1.94537858	0
Glul	1.94524232	5.42E-209
Inpp4b	1.94426141	8.35E-64
Man1a	1.94255827	0
Gldn	1.94022075	0
Bambi	1.93639993	6.94E-232
Rnf180	1.9357463	2.17E-116
Mllt3	1.92441982	0
Daam2	1.92184498	1.92E-284
Dnajc6	1.92162752	7.68E-68
Meg3	1.91582216	1.35E-246
Plscr4	1.91265185	8.47E-275
Tmem204	1.91132635	3.89E-53
Chd5	1.89676832	5.56E-95
Cx3cl1	1.89576612	3.20E-120
Cebpb	1.88156623	0
Cpne8	1.88127773	0
Nos1ap	1.87858333	5.46E-63
Prr16	1.87852459	0
Sned1	1.87572807	0
Tnfaip3	1.86149707	7.99E-60
Vdr	1.8443144	2.70E-74
Ndufa4l2	1.83960939	0
Cxcl1	1.81758656	2.94E-37
Rsph9	1.8127073	1.33E-52
Nfil3	1.80706139	4.87E-78
Slc6a6	1.80619749	0
Hs3st1	1.80326163	1.16E-60
Bcl2	1.80032218	2.40E-192
Tmem132c	1.79960991	1.66E-193
Igf1	1.7989712	2.40E-164

Tmod2	1.79100423	2.35E-189
Hs3st3a1	1.79067645	2.03E-90
Grk5	1.78813942	2.67E-213
Pcdh17	1.78352751	3.71E-122
Ppp1r15a	1.77537133	1.55E-165
Flywch2	1.77091028	1.85E-86
Id4	1.76282666	8.89E-48
Pltp	1.76224675	5.12E-193
Ism1	1.76209621	1.44E-82
Sall1	1.75599235	1.92E-78
C630043F03Rik	1.75479315	1.81E-95
Fth1	1.75044212	0
Col23a1	1.74649145	0
Gadd45b	1.74630964	5.92E-135
Dab2	1.7406871	2.00E-285
Acvrl1	1.73663013	1.14E-113
Rab6b	1.72925811	3.92E-55
Birc3	1.72845567	1.28E-85
Gm26532	1.72745051	4.12E-72
Emc9	1.72417366	2.34E-50
Hpse2	1.71431449	3.05E-266
Klhl29	1.70691802	2.46E-110
Twist1	1.70657878	0
Fgfr3	1.69994541	3.64E-89
Prxl2b	1.69849308	1.52E-113
Gm5089	1.6968869	3.80E-184
Sp9	1.69056196	6.31E-65
Pitx1	1.68858503	1.09E-196
Pink1	1.68836255	8.79E-183
Ier2	1.68258838	7.44E-165
Vcan	1.6805148	0
Egr1	1.67996058	6.83E-117
Ar	1.67443267	9.38E-109
Nkd2	1.67366396	9.71E-190
Slc16a1	1.66913481	3.36E-152
Inhbb	1.65962727	8.87E-153
Dpt	1.65787365	4.05E-257
Cd302	1.65568508	0
Gfpt2	1.65126909	1.57E-133

Svep1	1.64996428	0
Ahr	1.64710209	5.31E-161
Hsph1	1.64296406	4.91E-154
Slc6a17	1.64009048	4.71E-143
Sema3b	1.63760548	2.29E-71
Chst2	1.63445418	1.23E-86
Adgra2	1.62792708	3.03E-283
Zfp36l1	1.62315463	4.92E-198
Aff2	1.62224723	2.29E-171
Cdc14a	1.621645	2.00E-98
St6galnac5	1.61923786	2.12E-66
Psen2	1.61496141	4.08E-83
Ssbp2	1.61054341	1.10E-285
Magi1	1.60929688	7.91E-150
Rgs17	1.60810421	1.24E-59
Sdc4	1.6068473	0
Zic2	1.60675524	2.01E-107
Prex2	1.60219917	6.00E-89
Arrdc3	1.5993865	1.94E-82
Dnajb1	1.59484737	3.37E-44
2200002D01Rik	1.59421995	2.99E-49
Pde4b	1.59369154	3.75E-219
Serpine2	1.59088314	0
Ecscr	1.58668973	1.05E-67
Cdc42ep4	1.57894965	3.29E-70
Abhd14b	1.57803468	5.42E-73
Bag3	1.57776877	2.13E-185
Cox4i2	1.57758863	3.07E-86
Il11ra1	1.57142648	0
Mir99ahg	1.57010482	0
Igfbp6	1.56874983	1.34E-44
Ptgis	1.5680595	2.04E-301
Galt	1.56640575	1.81E-52
Mxi1	1.55940603	1.42E-106
S100a4	1.55622326	0
Pde1a	1.5553975	2.74E-208
Ifi27	1.55424365	0
2310010J17Rik	1.55421453	3.37E-86
Atoh8	1.55027166	7.44E-37

Cdkn1c	1.54714775	4.98E-89
Epha7	1.54569947	8.70E-92
Celf2	1.54549605	4.66E-91
Tspyl4	1.54536161	4.66E-43
Ndrgr1	1.54218826	4.30E-200
Slc16a2	1.54042355	0
Ccl7	1.53591196	0.01798001
Ifrd1	1.53276911	3.28E-226
Bmp4	1.53055584	2.10E-211
Crabp2	1.52888192	1.83E-70
Efnb2	1.52774047	6.36E-222
Tmem176a	1.52721234	0
1500009L16Rik	1.52620055	4.75E-38
Irf1	1.5257205	5.94E-109
Hebp1	1.52057668	4.55E-106
Crlf1	1.51781108	0
Msx1	1.51579043	0
Igfbp2	1.5130004	3.09E-122
Phyh	1.51072471	8.83E-109
Pde5a	1.50940132	7.03E-99
Reck	1.50773565	4.68E-163
Bmp2	1.50724807	1.53E-95
Ddx3y	1.50087661	7.17E-30
Tmem158	1.49726815	3.84E-84
Chp1	1.49638628	9.02E-205
Olfr1	1.4949342	1.14E-171
Zfp423	1.48863702	6.86E-74
Lgals3	1.48632122	0
Id2	1.48313185	6.94E-193
Cd248	1.47370961	1.18E-246
Pim3	1.46553429	7.08E-22
Angptl4	1.46347146	9.41E-48
Kctd8	1.45586449	5.37E-236
Mtm1	1.45174718	2.27E-63
Klf9	1.44777964	1.48E-141
Mill2	1.44497284	3.66E-71
Layn	1.44453586	2.87E-110
Nol3	1.44408476	1.11E-66
Mvb12b	1.44202353	3.95E-63

Zbtb4	1.44095412	5.10E-133
Irak3	1.44055675	6.40E-42
Npdc1	1.43844387	3.57E-158
C1qtnf2	1.4370771	2.41E-62
St3gal1	1.43450627	4.28E-103
Cd81	1.43017447	0
Jun	1.42935511	3.09E-105
Lefty1	1.42887347	3.57E-45
Prkar1b	1.42745338	2.59E-46
Rerg	1.41980777	4.40E-107
Hsd17b4	1.41346813	9.26E-216
Naaa	1.41102862	4.33E-34
Lmbrd1	1.41082822	2.77E-140
Alx4	1.4084423	3.06E-166
Nfkb1	1.39849891	3.10E-49
Tfap2b	1.39829195	3.52E-177
Ccn1	1.39636353	9.84E-56
Mcub	1.39565005	3.63E-146
Pnp	1.39222615	4.37E-233
Klf2	1.38858763	9.39E-11
St6galnac3	1.38297695	3.84E-122
Cd151	1.38192702	7.28E-125
Ndrg2	1.3810225	4.28E-33
Tmem176b	1.3762319	0
9530026P05Rik	1.36990262	1.39E-69
Nfkbiz	1.36683473	1.40E-71
Gpc3	1.36560936	2.48E-67
Zbtb20	1.36214526	0
Ids	1.35875347	1.26E-128
Irs2	1.35155468	1.16E-37
Gas6	1.34801259	2.47E-133
Thy1	1.34466586	0
Wnt11	1.33925066	7.43E-31
Flot1	1.3321775	1.88E-167
Lgals3bp	1.33003767	3.43E-72
Sema6d	1.32698501	1.74E-66
Pmp22	1.32489097	0
Pgpep1	1.32457355	1.66E-23
Ier3	1.32331911	1.54E-86

Ccnl1	1.32308141	4.92E-106
Gja1	1.32065617	3.13E-231
Smim1	1.3200819	4.31E-41
Pbxip1	1.31558477	1.55E-178
Vcam1	1.31468289	8.25E-220
Gabbr1	1.31324329	3.35E-76
Agtrap	1.31316155	2.31E-35
Fcgrt	1.31301453	1.73E-238
Fxyd1	1.3129196	3.62E-246
Tcea3	1.31290432	3.80E-36
Pitpnm2	1.31245587	1.53E-33
Usp2	1.30902706	7.13E-32
Abcb1a	1.30615968	1.62E-25
Mrps6	1.29882578	2.25E-74
Lysmd2	1.29562339	8.28E-74
Hes1	1.29254646	5.88E-97
Adamts1	1.29248701	9.60E-35
Tmem159	1.28998263	2.68E-109
Acp2	1.2807492	5.63E-48
Enc1	1.28037627	1.65E-35
Scn7a	1.27872945	3.69E-74
Asap3	1.27835861	1.20E-63
Crim1	1.27458111	4.22E-63
Isg20	1.27360726	1.73E-26
Dnaja4	1.27345767	3.11E-24
Adi1	1.27196773	1.32E-29
Ggt7	1.26950117	1.73E-44
Zic5	1.26657976	2.81E-56
Zfp703	1.25867561	1.72E-75
Pdpn	1.25781312	9.07E-147
Sirpa	1.25611298	1.03E-81
Hspb8	1.25562057	8.87E-41
Vegfa	1.25350615	2.32E-89
H2-D1	1.25248255	2.62E-196
Cgnl1	1.25227752	7.73E-67
Npr2	1.25087415	1.96E-60
Sh3bp5	1.2498673	1.72E-64
Slc22a17	1.24593566	6.99E-59
Ophn1	1.24164442	3.49E-103

Ppp2r5b	1.24053785	1.67E-23
Tsc22d3	1.24005387	1.62E-28
Vegfc	1.23920727	5.02E-117
Lum	1.23778883	0
Ror1	1.23606656	2.11E-141
Lgals9	1.23570106	3.14E-114
Nfia	1.23494661	3.88E-195
Rnase4	1.23484786	0
Slc9a3r2	1.22971007	1.19E-26
Rab4a	1.22898886	2.85E-20
Insyn1	1.22795599	4.58E-23
Dync2li1	1.22750825	2.13E-38
Btbd3	1.22744045	1.90E-36
Csad	1.2265231	3.29E-88
Ptx3	1.22644165	9.53E-46
Bmp7	1.22457094	3.42E-30
Rnf220	1.2240137	2.52E-50
Hs3st3b1	1.22390771	3.17E-38
Prnp	1.22379159	1.93E-298
Boc	1.22315475	2.25E-50
Acyp1	1.22167512	1.08E-29
Rab30	1.21968377	4.88E-69
Mkx	1.21593279	1.14E-121
Ctsf	1.21472435	1.39E-27
Ltbp1	1.21138866	7.97E-214
Pcsk5	1.21012352	1.72E-82
Coq10b	1.2087778	5.66E-85
Bmyc	1.20849662	8.43E-52
Pcdh18	1.20844649	2.23E-73
Mocs2	1.20748134	3.30E-216
Jund	1.20307432	8.33E-148
Ccnd3	1.20152036	3.17E-144
Apbb1ip	1.19804198	5.73E-63
Aldh3a2	1.19694049	4.01E-38
Fhit	1.19565781	1.77E-45
Cacna1g	1.19064465	1.81E-121
Sertad1	1.18655539	3.47E-34
Tgoln1	1.1857298	1.61E-155
Tnfrsf1a	1.18240804	9.31E-198

Id1	1.18126198	4.25E-67
Sat2	1.17958516	1.10E-25
Fbxo6	1.17429043	2.34E-19
Stard5	1.17388283	2.02E-78
Rnf167	1.17343458	3.51E-20
Tcp11l2	1.17222943	1.39E-25
Acvr1b	1.16858549	2.52E-24
Id3	1.16767127	2.06E-179
Castor1	1.16605805	1.18E-33
Hexim1	1.16604152	9.86E-60
Tiparp	1.15731349	1.19E-19
Dnajb4	1.15627614	3.74E-76
Scube1	1.15458547	2.57E-64
Cib2	1.15397754	5.47E-45
Pon2	1.15119065	2.94E-129
Nkd1	1.14968566	1.48E-100
Arrdc4	1.14765649	2.73E-55
Mettl26	1.14374289	2.06E-12
Dipk2a	1.14294143	2.41E-108
Ssc5d	1.14275021	1.28E-37
Pdgfra	1.14023241	0
Fosl2	1.13901527	1.32E-77
Map1lc3a	1.13428334	0
Dcun1d3	1.13291952	1.32E-33
Ltbp3	1.12956812	7.61E-131
Dcun1d4	1.12851947	4.58E-09
Lrp1	1.12828015	0
Gaa	1.12811381	5.92E-49
Abca1	1.12045498	3.81E-76
Igfbp7	1.11783896	0
Ubc	1.11260448	1.30E-214
Gclc	1.11176962	7.40E-28
Dnajb9	1.1103562	1.38E-57
Vamp2	1.10907155	5.87E-54
Tmem205	1.10565261	4.68E-59
Runx1t1	1.10518077	7.27E-147
Gim1	1.10311072	4.87E-143
Tmem38b	1.10130761	2.85E-15
Scamp1	1.09841825	1.88E-62

Prps2	1.09838904	1.37E-19
Wwtr1	1.09596703	6.03E-297
Blvrb	1.09204446	3.50E-143
Emilin2	1.09063874	1.71E-66
Smarca1	1.08644842	1.18E-22
Cdkn1b	1.08595445	5.42E-91
Col8a1	1.08468477	1.05E-05
Hgsnat	1.08073426	8.66E-109
Cpq	1.07987096	7.70E-153
Cachd1	1.07943896	9.71E-166
Gm45338	1.07887586	8.57E-39
Pgm2l1	1.0782045	9.00E-10
Arhgap29	1.07700363	9.21E-39
Ncoa7	1.07507022	3.74E-92
S100a16	1.07484969	4.98E-181
Dnajb2	1.07469076	9.19E-17
Cmtm6	1.0735663	6.32E-28
Il16	1.07289648	5.09E-39
Fas	1.07127376	3.70E-34
Mr1	1.07101136	1.70E-13
Stk40	1.06963562	2.26E-27
Tmem63a	1.06766866	7.97E-57
Fuom	1.0674642	2.15E-20
Slc48a1	1.06623653	3.88E-71
Gnptg	1.0627977	1.10E-19
Rsrp1	1.06254621	8.25E-234
Tnfrsf8	1.0625362	2.06E-63
Tmem45a	1.05955767	1.90E-122
Plpbbp	1.05792431	2.02E-36
Dhrs7	1.05695619	1.36E-66
Arsk	1.0566031	7.81E-14
Cox6b2	1.05575274	1.17E-07
Stat5a	1.05502505	5.04E-23
Hivep1	1.0546933	2.62E-10
Mir22hg	1.05467845	2.61E-53
Erlin2	1.05320759	6.64E-13
Pqlc3	1.0527826	1.29E-24
Usp53	1.05277927	1.59E-12
Gabarapl1	1.05219217	4.49E-19

Sod3	1.05036079	2.68E-185
Aldh2	1.04974323	5.06E-155
Ilvbl	1.04966336	1.75E-12
Pros1	1.04946643	7.76E-183
Cdon	1.04701632	2.75E-166
Cbx4	1.04560092	2.46E-33
Il1rap	1.04498431	4.49E-32
Ankrd12	1.04332774	2.34E-137
Hapln1	1.04229937	1.78E-106
Mxd1	1.04148878	1.23E-26
Gstm5	1.04108021	1.12E-159
S100a13	1.04062214	5.91E-217
Crebrf	1.03803853	2.11E-73
Adgrl2	1.03708214	2.46E-157
Lpar4	1.03694462	1.50E-14
Thsd7a	1.0357309	8.42E-112
Akap7	1.03517874	2.56E-26
Glis3	1.03317379	1.71E-169
Bphl	1.03213408	3.29E-20
Uty	1.03116822	7.86E-16
Snx15	1.02484702	1.03E-28
Ephx1	1.02350637	2.36E-15
Atg2a	1.02104606	2.56E-10
Nsg1	1.01976021	7.02E-204
Rhou	1.01742842	5.81E-21
Itgb8	1.01640647	9.37E-21
Dcaf11	1.01633398	3.24E-25
Zhx1	1.01403627	2.77E-31
Tcn2	1.01120929	4.64E-53
Plpp2	1.01109485	5.49E-29
Paxx	1.00969694	3.90E-27
Etfrf1	1.00781633	5.76E-10
Mt2	1.00703671	8.12E-10
Cltb	1.00509255	7.15E-121