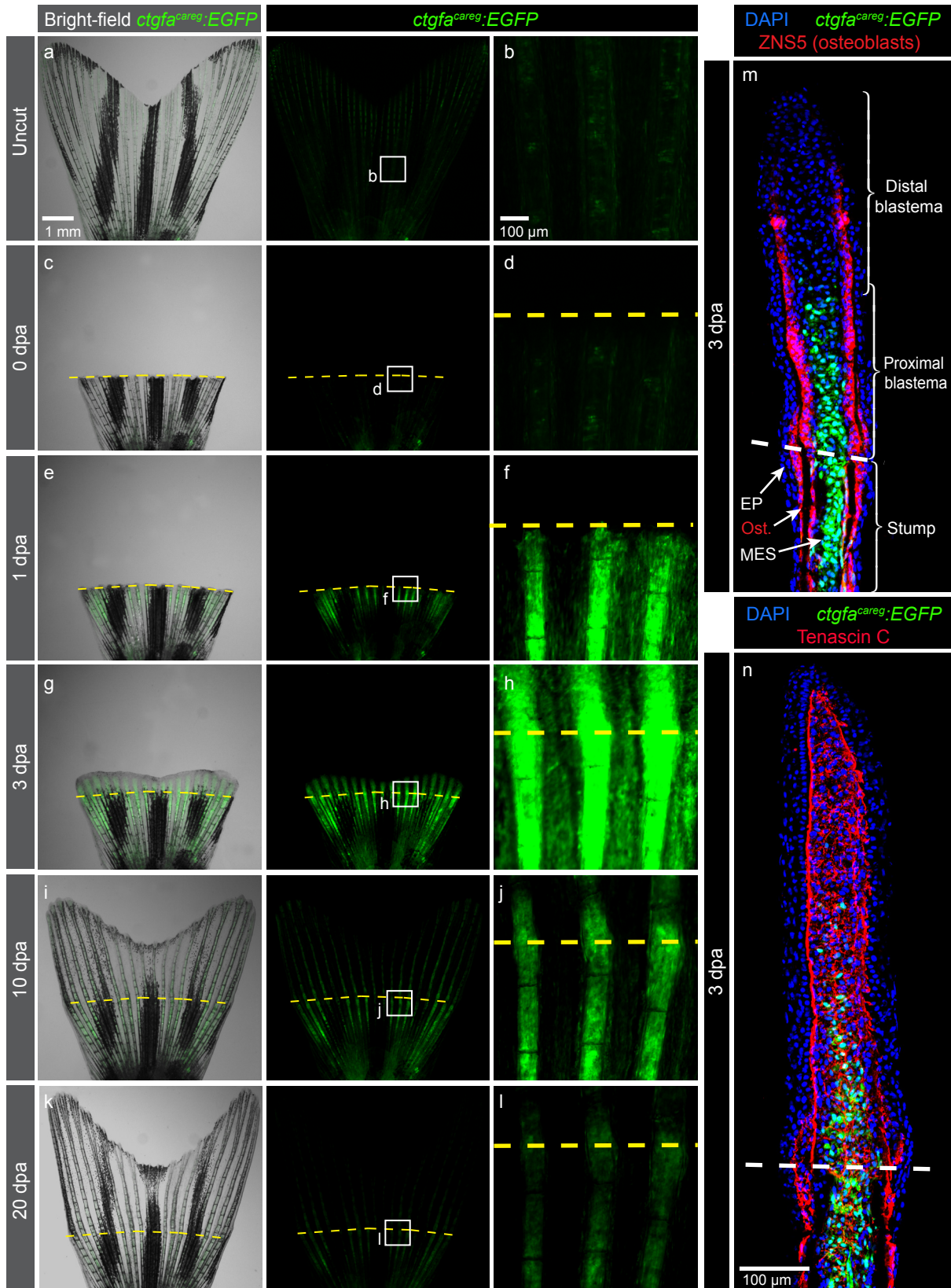


Supplementary Figure 1. The *ctgfa^{careg}:EGFP* transgenic reporter is transiently activated in the peri-injured myocardium during heart regeneration.

(a-h) Immunofluorescence staining of *ctgfa^{careg}:EGFP* transversal heart sections with antibodies against GFP (green) and embCMHC (red) at different time points after cryoinjury. The intact myocardium is detected by F-actin staining (Phalloidin, blue). (a-b) In uninjured ventricle, *ctgfa^{careg}:EGFP* is expressed in a fine layer in the subcortical myocardium. No embCMHC is observed. (c-d) At 4 dpci, *ctgfa^{careg}:EGFP* is induced in trabecular fascicles abutting the post-infarcted area, a subset of which also displays embCMHC expression. (e-f) At 7 dpci, *ctgfa^{careg}:EGFP* expression is maintained at the injury border covering embCMHC+ CMs. (g-h) At 30 dpci, *ctgfa^{careg}:EGFP* is reduced to a small margin around the remaining fibrotic tissue. (i) Quantification of *ctgfa^{careg}:EGFP*⁺ and embCMHC⁺ area within 100 μ m from the injury border. N \geq 8.

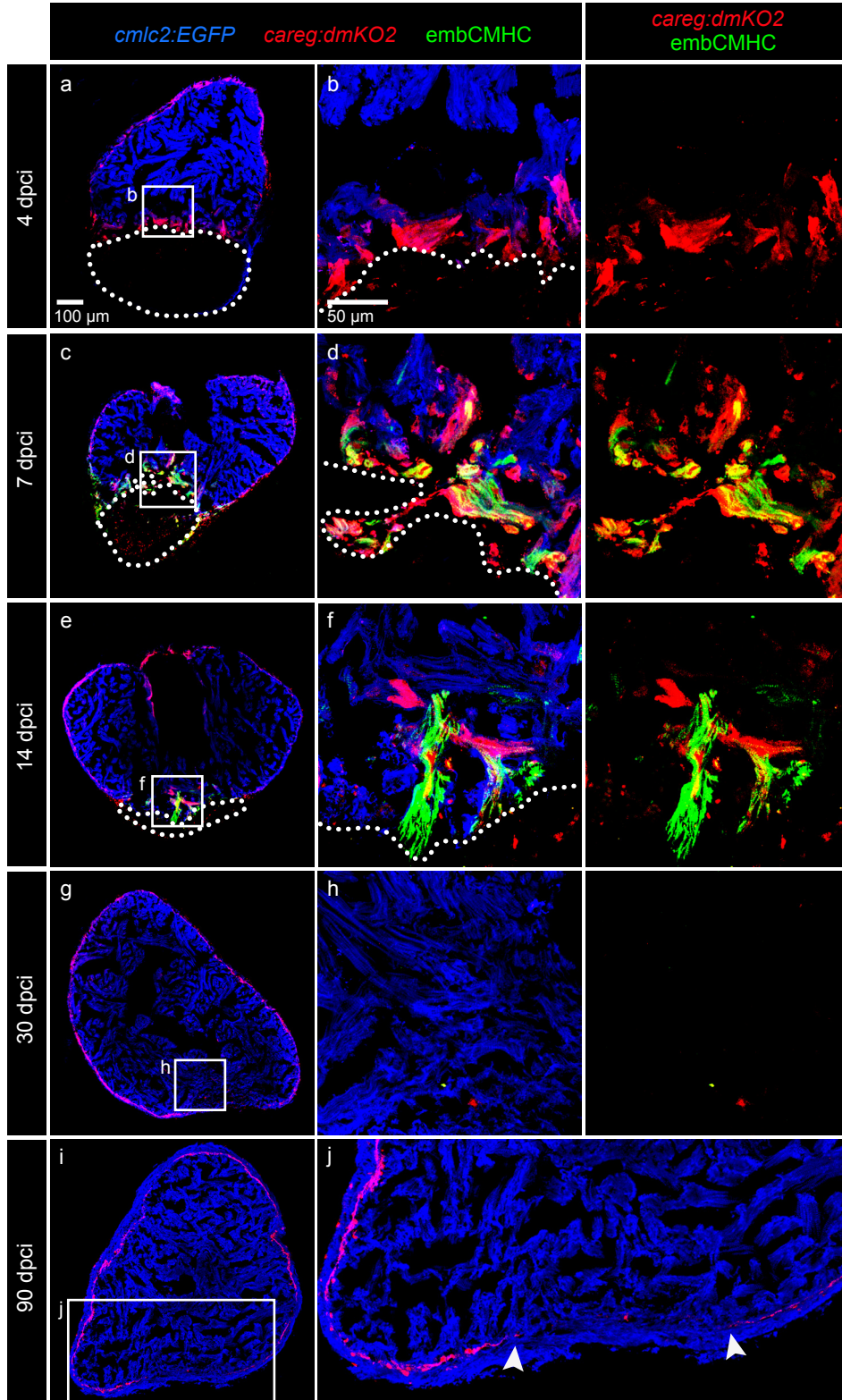
Post-infarcted ventricle is encircled with a dotted line. The same rules apply to all subsequent figures.



Supplementary Figure 2. Peri-injury tissue of the fin stump transiently induces *ctgfa^{careg}:EGFP* expression

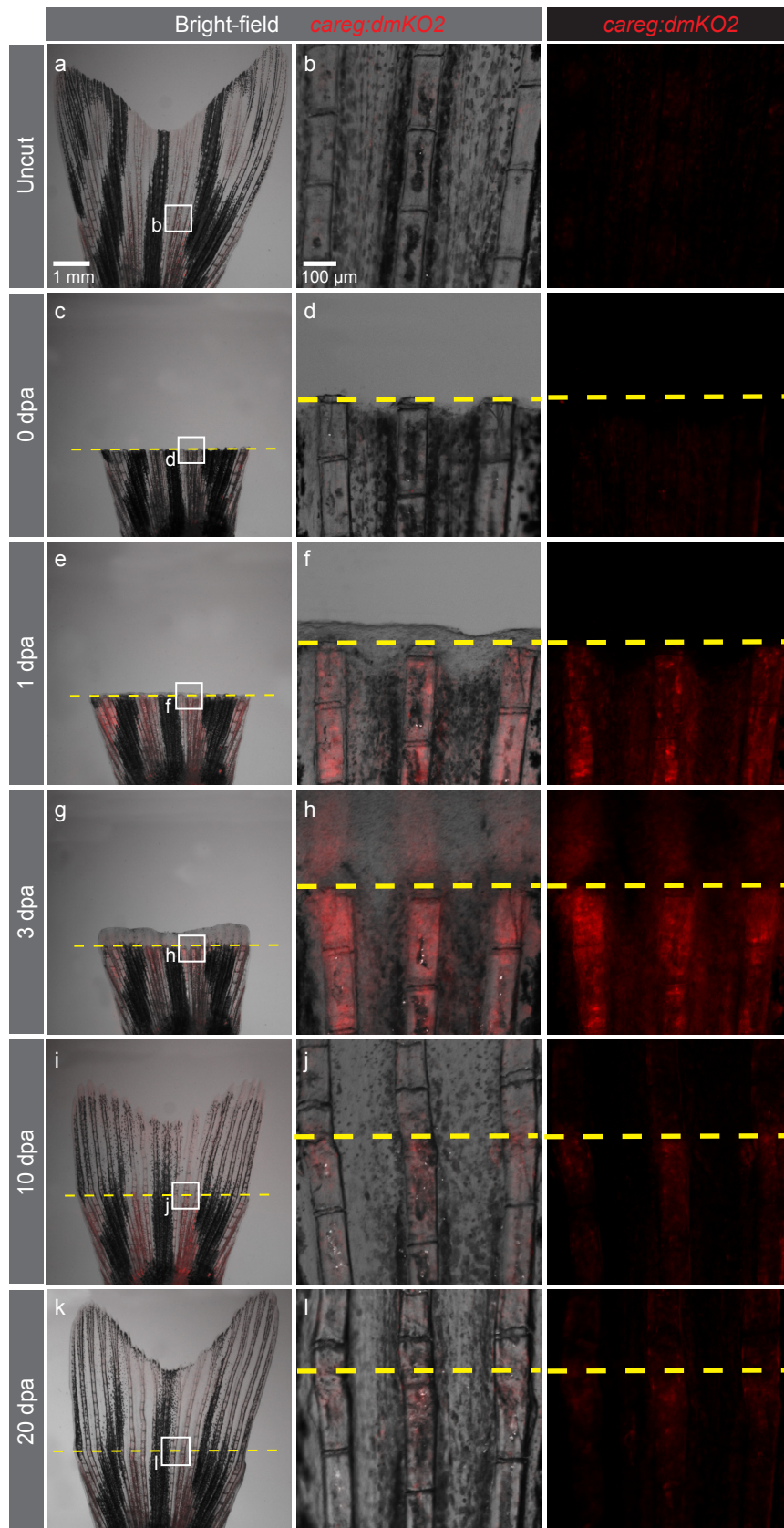
(a-l) Live imaging of *ctgfa^{careg}:EGFP* fins at different days post-amputation (dpa). Higher magnifications of framed areas show the region of the amputation plane (yellow dashed line). N=4.

(m-n) Immunofluorescence staining of longitudinal *ctgfa^{careg}:EGFP* fin sections at 3 dpa. EP, epidermis; Ost, osteoblasts; MES, mesenchyme. (m) *ctgfa^{careg}:EGFP* is detected in the stump mesenchyme and osteoblasts (red) below the amputation plane (dashed line), and in the proximal blastema. (n) The mesenchyme of the regenerating fin abundantly expresses Tenascin C, a tissue remodelling extracellular protein. N≥4.



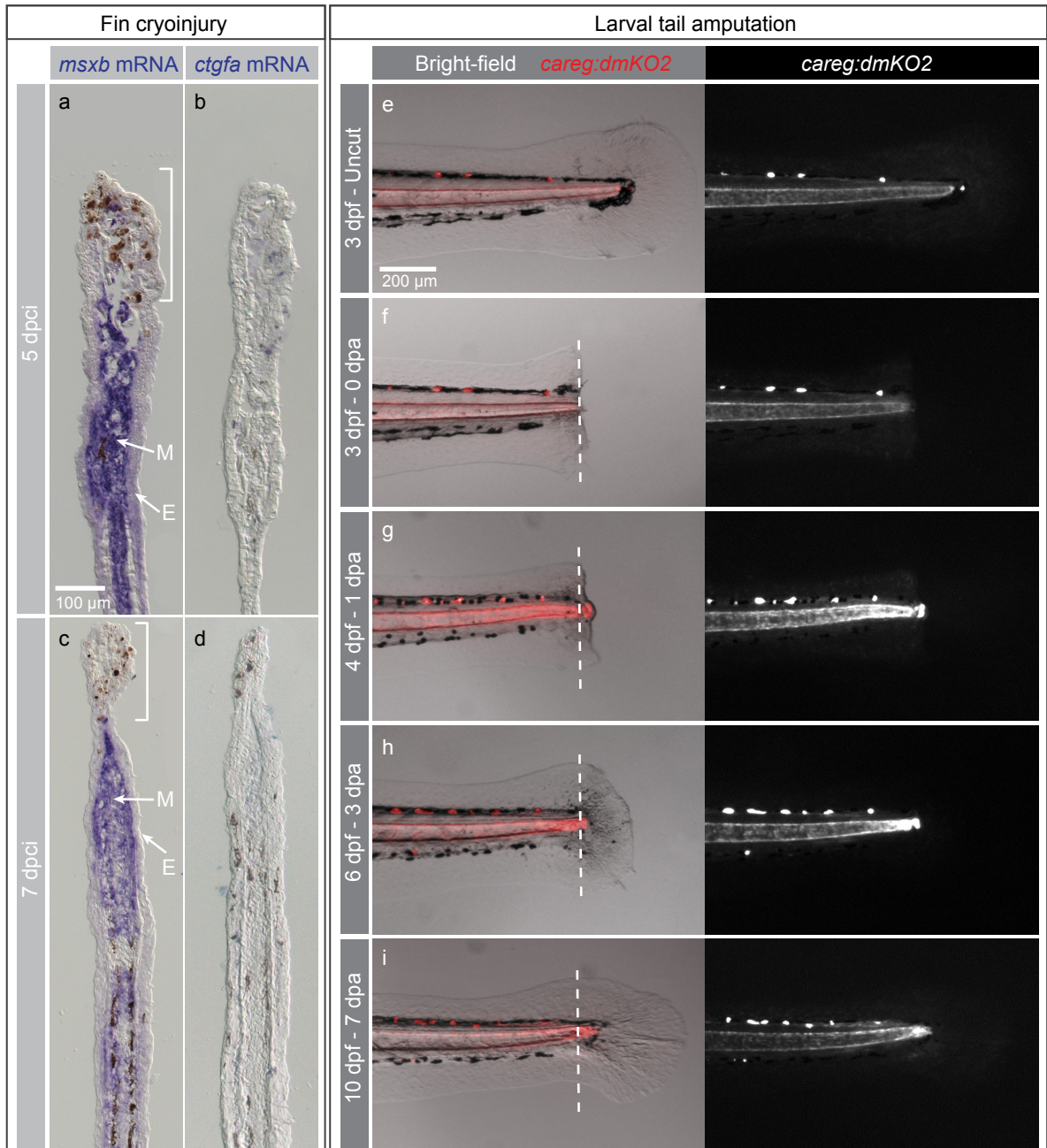
Supplementary Figure 3. *careg:dmKO2* is transiently expressed in the peri-injured myocardium during heart regeneration.

(a-j) Immunofluorescence staining of *careg:dmKO2;cmlc2:EGFP* heart sections labelled with antibodies against GFP (cardiac cells, blue) and embCMHC (green) at different time points after cryoinjury. N=4. (a-b) At 4 dpci, *careg:dmKO2*⁺ CMs emerge along the wound margin. (c-f) At 7 and 14 dpci, a large proportion of *careg:dmKO2*⁺ CMs activates the expression of embCMHC. (g-h) At 30 dpci, *careg:dmKO2* expression declines in the trabecular myocardium, but the primordial layer was not fully restored in the regenerated part of the ventricle. (i-j) At 90 dpci, the myocardium is completely regenerated, but the expression of *careg:dmKO2* is not completely reestablished in the subcortical region. The arrowheads indicate the position of the gap in the subcorical layer.



Supplementary Figure 4. *careg:dmKO2* is transiently expressed in the peri-injured stump during fin regeneration.

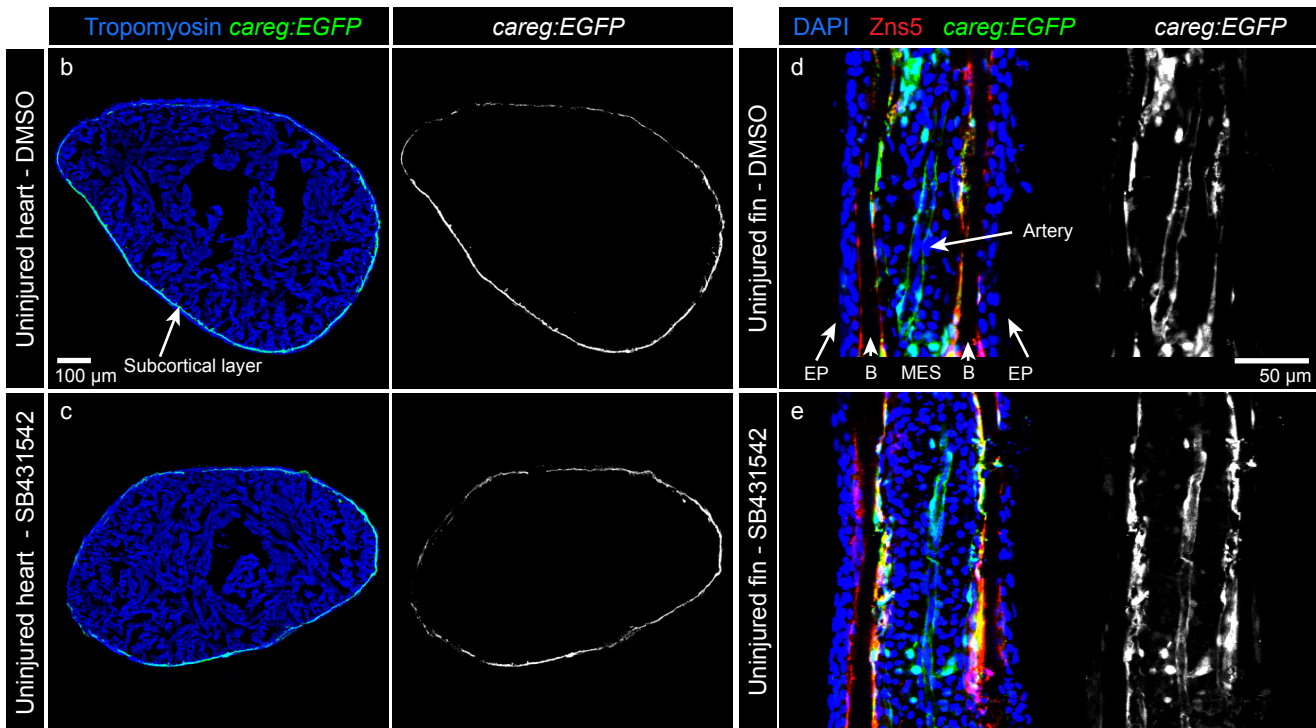
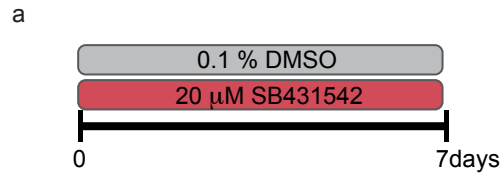
(a-l) Live-imaging of *careg:dmKO2* fins at different days post-amputation (dpa). Higher magnifications of framed areas show the region of the amputation plane (yellow dashed line). N=4.



Supplementary Figure 5. The *careg* reporter is activated in other injury models of tissue regeneration in zebrafish.

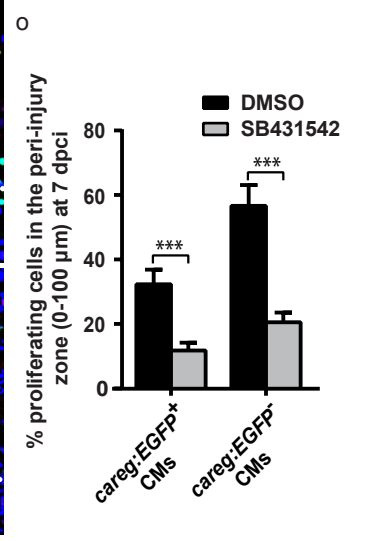
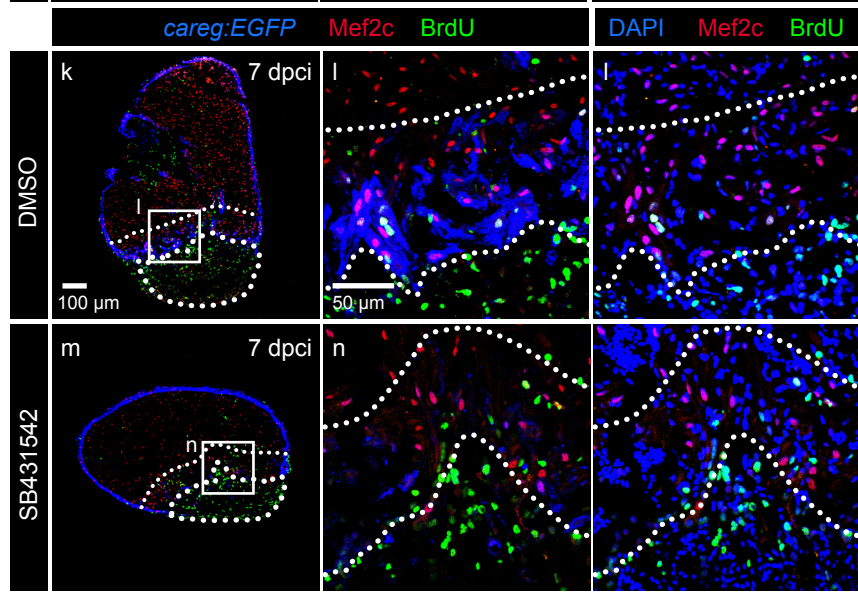
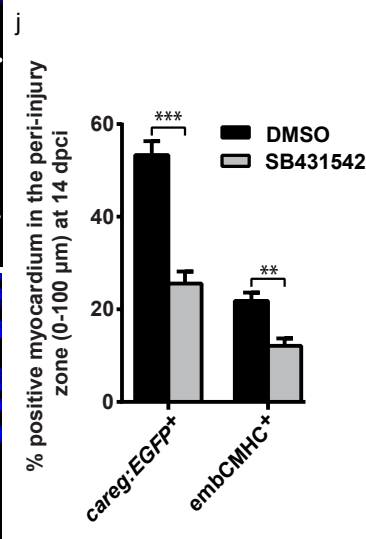
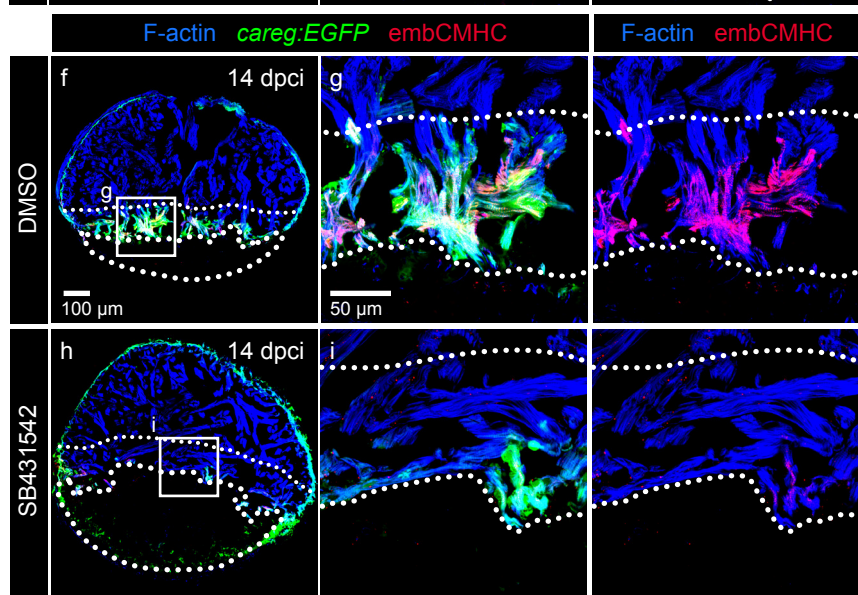
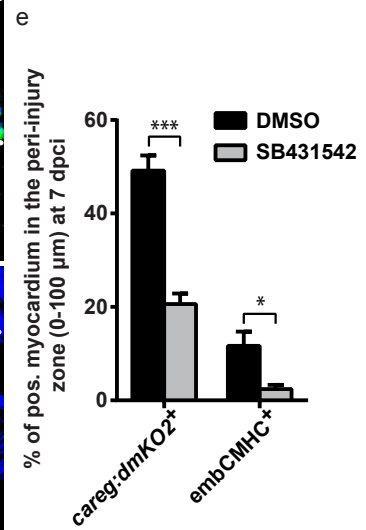
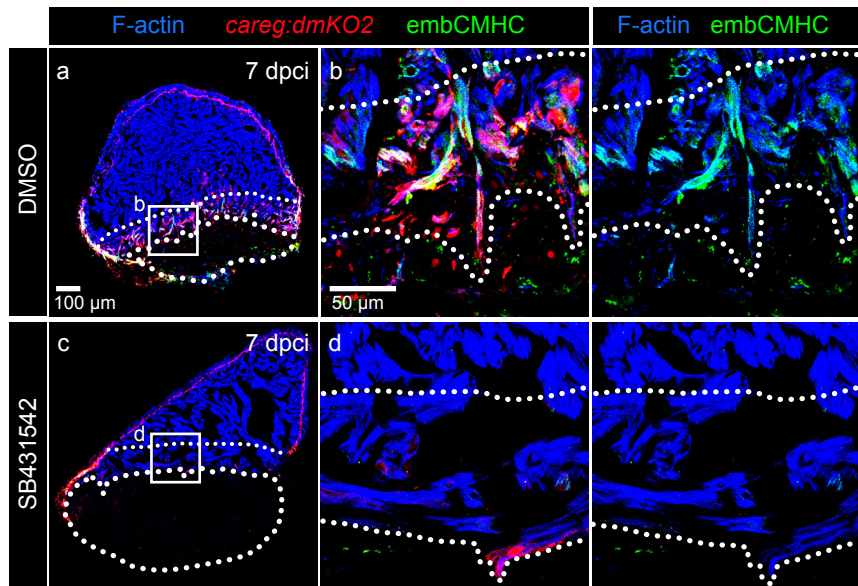
(a-d) In-situ hybridization (purple) on longitudinal fin sections reveals that, as in the amputation model, the endogenous *ctgfa* gene is not upregulated in the regenerating fin after cryoinjury. (a, c) A probe against a blastema marker, *msxb*, was used as a positive control to detect the activated mesenchyme. (b, d) A *ctgfa* probe does not label the regenerating fin tissues. M, mesenchyme; E, epidermis. Brackets indicate the damaged tissue remaining at the tip of the cryoinjured stump. N=3.

(e-i) Live-imaging of the larval tail of *careg:dmKO2* fish at different days post-fertilization (dpf) and post-amputation. The transgenic reporter is constitutively expressed in the notochord. After amputation (dashed line), the expression of *careg:dmKO2* is markedly upregulated at the tip of the regenerating tail. N=6.



Supplementary Figure 6. Treatment of uninjured organs with the inhibitor of TGF β /Activin- β signalling does not affect the homeostatic expression of *careg:EGFP*.

(a) Experimental design. Uninjured fish were treated with the inhibitor of TGF β /Activin- β (20 μ M SB431542) for 7 days. (b-c) Immunofluorescence staining of uninjured ventricles after 7 days of SB431542 treatment. The expression of *careg:EGFP* in the subcortical layer is similar in control and treated fish. (d-e) Longitudinal sections of rays in uninjured fins. Osteoblasts are marked with Zns5 antibody (red). They cover the surface of acellular bone matrix. In both control and treated specimens, *careg:EGFP* is expressed in intraray osteoblasts, in a few scattered MES and the artery. EP, epidermis; MES, mesenchyme; B, acellular bones. N=4.



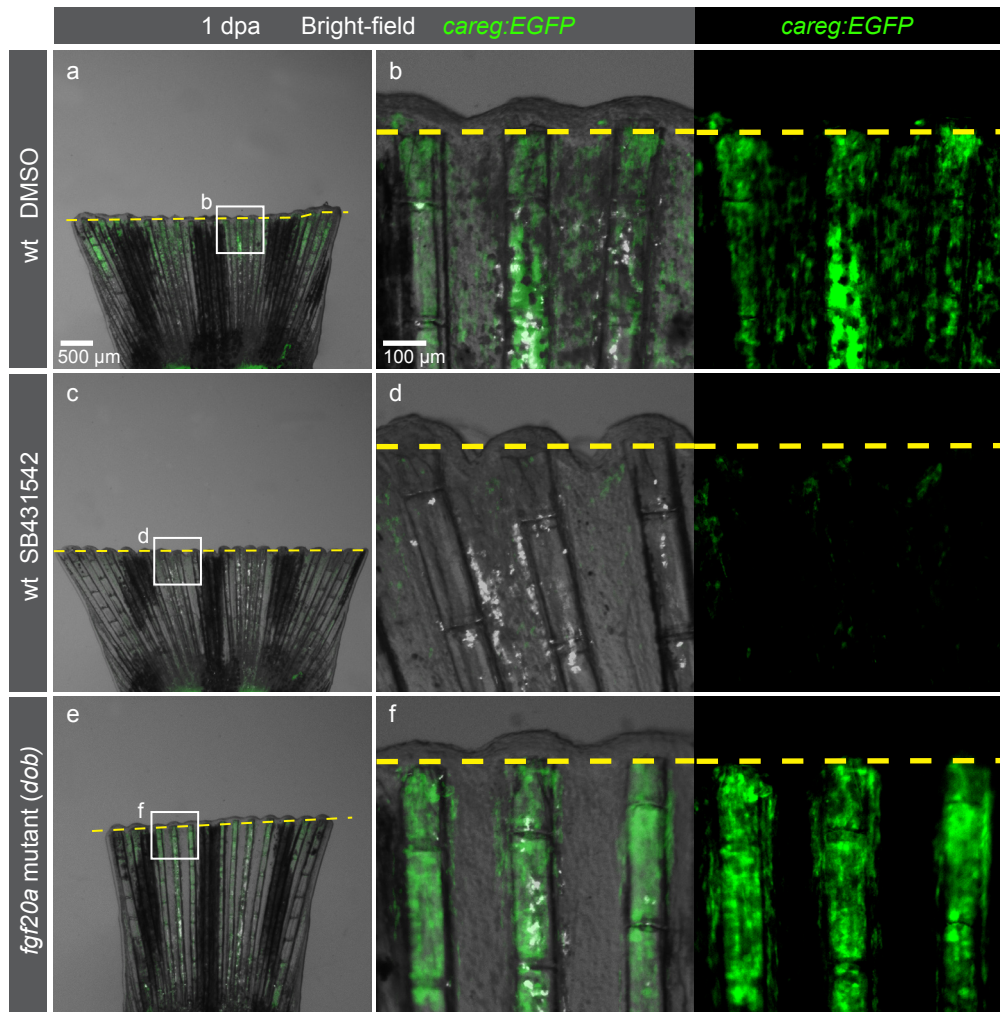
Supplementary Figure 7. The inhibition of TGF β /Activin- β signaling suppresses CM dedifferentiation and proliferation at the injury-abutting zone during heart regeneration.

(a-d, f-i) Immunofluorescence staining of ventricles at 7 dpci (a-d) or 14 dpci (f-i) treated with DMSO or 20 μ M SB431542 labelled with antibodies against fluorescent proteins and embCMHC. The intact myocardium is detected by F-actin staining (blue). The upper dotted lines indicate the 100 μ m-thick margin of the myocardium along the injury border.

(e, j) Percentage of positive myocardium for the *careg* reporter or embCMHC in a 100 μ m-wide margin of the regenerating myocardium in control or SB431542-treated hearts. $N \geq 5$. *** $p < 0.0001$, ** $p < 0.01$, * $p < 0.05$; unpaired t-test. Error bars correspond to standard error of the mean (SEM).

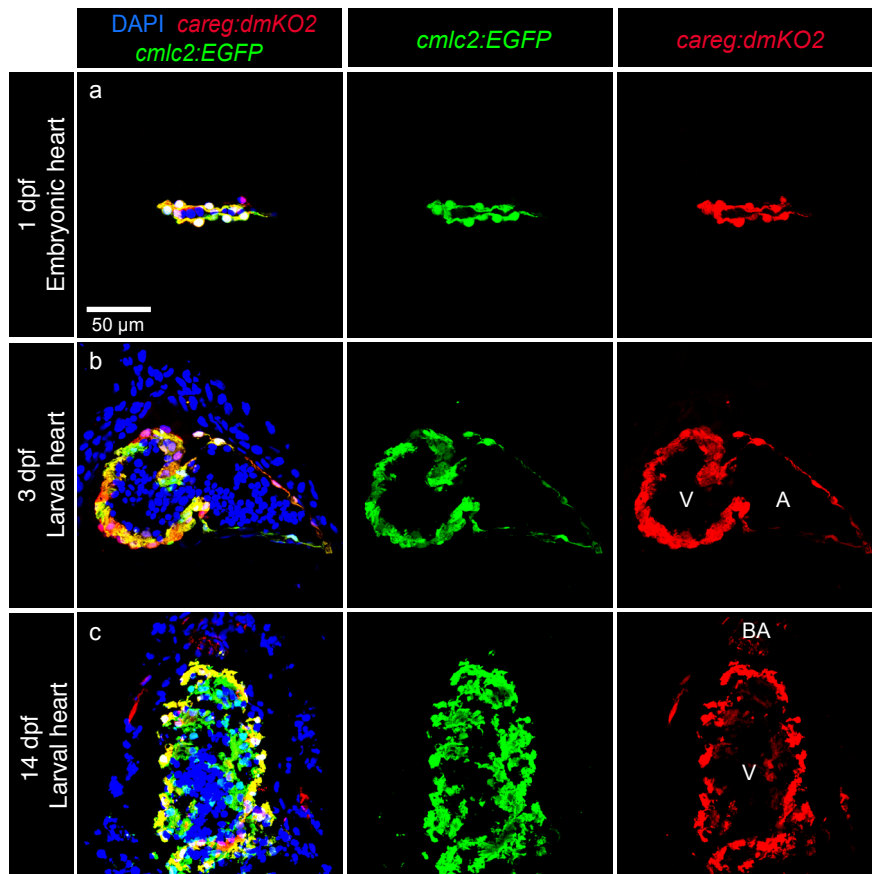
(k-n) Immunofluorescence staining of *careg:EGFP* ventricle at 7 dpci treated with DMSO or 20 μ M SB431542 labelled with antibodies against GFP (blue), Mef2c (cardiac nuclei, red) and BrdU (green).

(o) Percentage of BrdU+ CMs in a 100 μ m-wide margin of the regenerating myocardium in control or SB431542-treated hearts. $N \geq 5$. *** $p < 0.0001$; unpaired t-test. Error bars correspond to standard error of the mean (SEM).



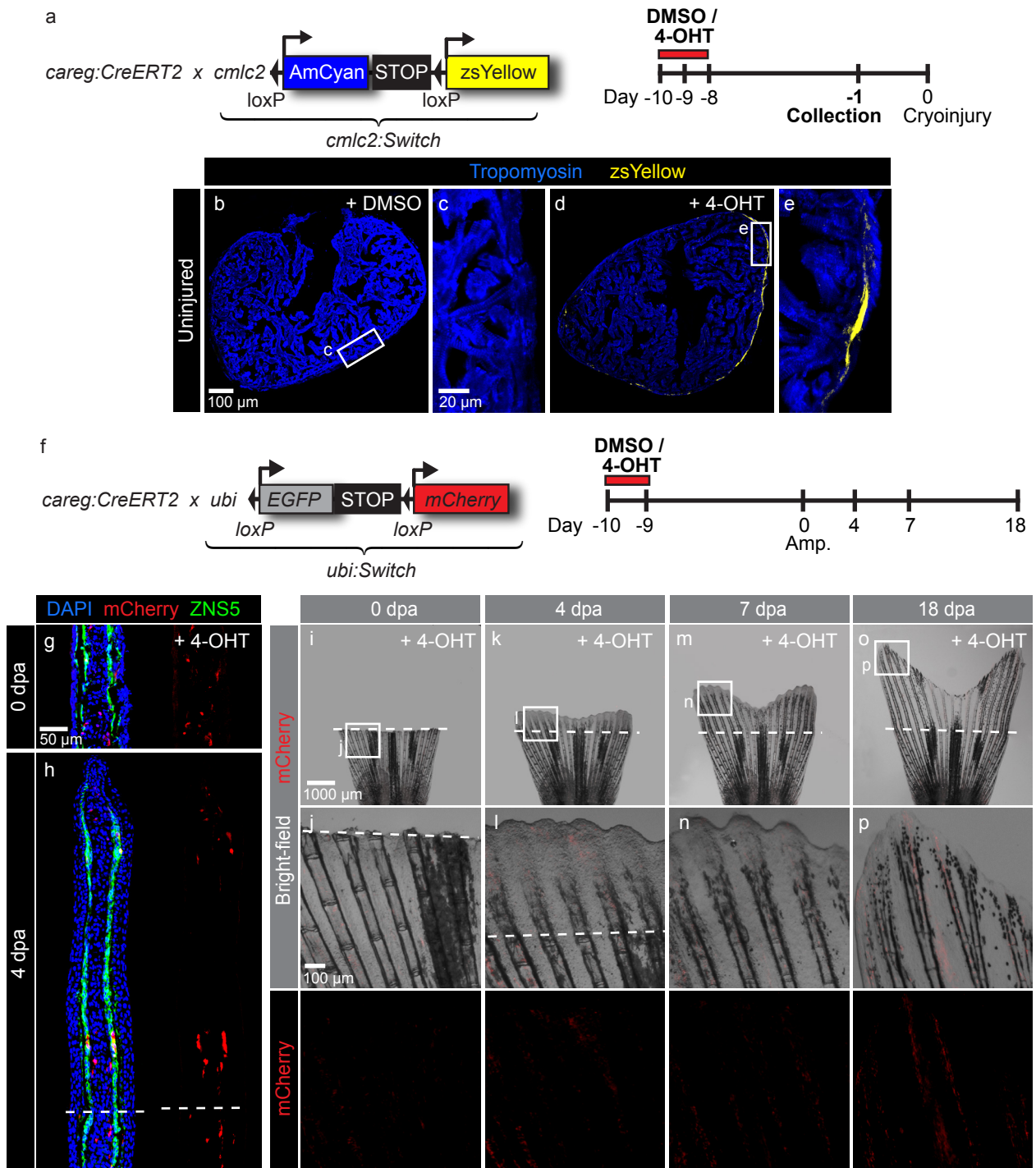
Supplementary Figure 8. Despite an absence of the regenerative outgrowth, *dob* mutant fins normally induce *careg:EGFP* in the amputation-activated stump.

(a-f) Live-imaging of *careg:EGFP* fins at 1 dpa in a wild-type (wt) background treated with DMSO or SB431542, and in the *fgf20a* (*dob*) mutant background. *careg:EGFP* expression is suppressed in the stump by the inhibition of TGF β /Activin- β signaling, but it remains normal in *fgf20a* mutant fins. N=4.



Supplementary Figure 9. Developmental dynamics of *careg:dmKO2* expression in the zebrafish heart.

(a-c) Longitudinal sections of *careg:dmKO2;cmhc2:EGFP* transgenic hearts at different time points during development, labelled with DAPI (nuclei, blue) and antibodies against GFP (green, cardiac cells) and KO2 (red). (a, b) *careg:dmKO2* is expressed in all embryonic cardiomyocytes at 1 and 3 dpf. (c) At 14 dpf, *careg:dmKO2* is maintained in the outer compact layer of the ventricle, whereas it is downregulated in the trabecular myocardium. *careg:dmKO2* is also expressed in the bulbus arteriosus. $N \geq 5$. dpf, days post-fertilization; V, ventricle; BA, bulbus arteriosus; A, atrium.



Supplementary Figure 10. Control experiments for *careg* lineage tracing analysis of heart and fin regeneration.

(a) Schematic representation of the transgenic strains and the experimental design for lineage tracing of *careg*-expressing primordial CMs during ventricle regeneration. (b-e) Immunostaining of uninjured ventricles treated with DMSO or 4-OHT using Tropomyosin (blue). Exposure to 4-OHT for 2 days is sufficient to label primordial CMs with zsYellow, as analysed at 7 days after the treatment (-1 day). (f) Schematic representation of the transgenic strains and the experimental design for lineage tracing of *careg*-expressing cells during fin regeneration. (g, h) Longitudinal fin sections at 0 and 4 dpa immunostaining for mCherry (red) and Zns5 (green). Exposure to 4-OHT for 1 day results in labelling of a few osteoblasts. (i-p) Live imaging of fins at different dpa after treatment with 4-OHT reveals only a few mCherry labelled cells in the stump and the regenerate. $N \geq 4$.

Supplementary Data 1. The complete list of transcription factor (TF) binding sites within the careg sequence that were predicted with MatInspector (Genomatix)

Selected TF binding sites are schematically represented in Fig. 3c.

Seq. name	Accession no.	Gene symbol	GeneID	Matrix	Family	Detailed Family Information	Matrix	Detailed Matrix Information	Tissue	Opt.
Start position	End position	Anchor position	Strand	Core sim.	Matrix sim.	Mat. sim. - opt.	Evidence #	Evidence	Sequence	
TempSeq_FZX4oauC				V\$TEAF	TEA/ATTS	DNA binding domain factors	V\$TEAD.01	"TEA domain-containing factors,		
transcriptional enhancer factors 1,3,4,5" "Cardiovascular System										
Embryonic Structures										
Heart										
Muscle, Skeletal										
Muscles										
Myocardium										
Urogenital System"	0.9	2	14	8	-	1	0.991	0.091	0	gaaCATTcctcat
TempSeq_FZX4oauC				V\$TALE	TALE	homeodomain class recognizing TG motifs	V\$TGIF.01	TG-interacting factor belonging to		
TALE class of homeodomain factors "Bone Marrow Cells										
Embryonic Structures										
Hematopoietic System										
Nervous System										
Neurons"	1	98	114	106	-	1	0.999	-0.001	0	tgtctggctGTCAaggc
TempSeq_FZX4oauC				V\$ZF11	C2H2	zinc finger transcription factors 11	V\$ZBTB3.01	Zinc finger and BTB domain containing 3		
0.95	103	113	108	+	1	0.994	0.044	0	gacaGCCAgac	
TempSeq_FZX4oauC				V\$ETSF	Human and murine	ETS1 factors	V\$ETV1.02	Ets variant 1	"Antibody-Producing Cells	
Blood Cells										
Bone Marrow Cells										
Breast										
Central Nervous System										
Endocrine System										
Germ Cells										
Hematopoietic System										
Immune System										
Leukocytes										
Myeloid Cells										
Nervous System										
Phagocytes										
Prostate										
Spinal Cord										
Testis										
Urogenital System"	0.96	123	143	133	+	1	0.99	0.03	0	cctgaccaGGAAGtgacttaa
TempSeq_FZX4oauC				V\$FKHD	Fork head	domain factors	V\$FOXP1_ES.01	"Alternative splicing variant of FOXP1, activated in		
ESCs" "Blood Cells										
Brain										
Breast										
Cartilage										
Central Nervous System										
Connective Tissue										
Ear										
Endocrine System										
Eye										
Immune System										
Islets of Langerhans										
Leukocytes										
Liver										
Lung										
Lymphocytes										
Muscle, Skeletal										
Muscles										
Nervous System										
Ovary										
Pancreas										
Pituitary Gland										
Prostate										
Testis										
Thymus Gland										
Thyroid Gland										
Urogenital System"	1	143	159	151	+	1	0.993	-0.007	0	aaaacacAACAtgggat
TempSeq_FZX4oauC				V\$IKRS	Ikaros	zinc finger family	V\$IK2.01	"Ikaros 2, potential regulator of lymphocyte differentiation"		
"Antibody-Producing Cells										
Blood Cells										
Bone Marrow Cells										

Hematopoietic System
Immune System
Leukocytes
Lymphocytes
Thymus Gland" 0.98 155 167 161 - 1 0.996 0.016 0 atttGGGAatccc
TempSeq_FZX4oauC V\$SORY SOX/SRY-sex/testis determinig and related HMG box factors V\$SOX5.01 Sox-5 "Bone and
Bones
Cartilage
Connective Tissue
Embryonic Structures
Endocrine System
Leydig Cells
Nervous System
Neuroglia
Skeleton
Testis
Thyroid Gland
Urogenital System" 0.87 243 265 254 - 1 0.996 0.126 0 gcctaaCAATaaggataacaaaa
TempSeq_FZX4oauC V\$MYT1 MYT1 C2HC zinc finger protein V\$MYT1.02 MyT1 zinc finger transcription factor involved in
primary neurogenesis "Central Nervous System
Nervous System
Neuroglia
Neurons" 0.88 397 409 403 + 1 0.992 0.112 0 agaAAGTtttgca
TempSeq_FZX4oauC V\$MEF3 MEF3 binding sites V\$SIX.01 "Binding sites for Six1, Six4 and Six5" "Brain
Central Nervous System
Ear
Embryonic Structures
Endocrine System
Eye
Kidney
Muscle, Skeletal
Muscles
Nervous System
Pituitary Gland
Urogenital System" 0.89 495 507 501 - 1 0.997 0.107 0 tgcTCAGgttact
TempSeq_FZX4oauC V\$NKXH NKX homeodomain factors V\$NKX25.05 Homeodomain factor Nkx-2.5/Csx "Cardiovascular
System
Central Nervous System
Digestive System
Embryonic Structures
Endocrine System
Heart
Islets of Langerhans
Lung
Muscles
Myocardium
Nervous System
Pancreas
Prostate
Respiratory System
Spinal Cord
Thyroid Gland
Urogenital System" 0.97 498 516 507 - 1 0.994 0.024 0 taatTGAGtgctcaggtt
TempSeq_FZX4oauC V\$SMAD Vertebrate SMAD family of transcription factors V\$SMAD3.01 Smad3 transcription factor involved
in TGF-beta signaling "Embryonic Structures
Kidney
Urogenital System" 0.99 532 542 537 - 1 0.996 0.006 0 tctGTCTggac
TempSeq_FZX4oauC V\$CART Cart-1 (cartilage homeoprotein 1) V\$S8.01 Binding site for S8 type homeodomains "Adrenal
Glands
Bone and Bones
Brain
Cardiovascular System
Central Nervous System
Connective Tissue
Digestive System
Embryonic Structures
Endocrine System
Eye
Heart
Immune System

Islets of Langerhans
 Muscle, Skeletal
 Muscles
 Myeloid Cells
 Nervous System
 Neurons
 Nose
 Pancreas
 Phagocytes
 Pituitary Gland
 Skeleton
 Spinal Cord" 0.97 555 575 565 + 1 0.995 0.025 0 tggtgTAATtgcgcagctatg
 TempSeq_FZX4oauC V\$ZF11 C2H2 zinc finger transcription factors 11 V\$ZBTB3.01 Zinc finger and BTB domain containing 3
 0.95 589 599 594 + 1 0.992 0.042 0 ggcaGCCAgat
 TempSeq_FZX4oauC V\$SIX3 Sine oculis homeobox homolog 3 V\$SIX3.03 SIX3 / SIXdomain (SD) and Homeodomain (HD)
 transcription factor "Brain
 Central Nervous System
 Embryonic Structures
 Endocrine System
 Eye
 Nervous System
 Pituitary Gland" 1 588 608 598 - 1 0.996 -0.004 0 agagtggTAATctggctgcca
 TempSeq_FZX4oauC V\$CDXF Vertebrate caudal related homeodomain protein V\$CDX2.03 Caudal type homeobox transcription
 factor 2 "Digestive System
 Embryonic Structures" 0.91 641 659 650 - 1 0.99 0.08 0 gaggctgtTATtgttctc
 TempSeq_FZX4oauC V\$SORY SOX/SRY-sex/testis determinig and related HMG box factors V\$SOX5.02 SRY-related HMG-
 box gene 5 "Bone and Bones
 Cartilage
 Connective Tissue
 Embryonic Structures
 Endocrine System
 Leydig Cells
 Nervous System
 Neuroglia
 Skeleton
 Testis
 Thyroid Gland
 Urogenital System" 0.87 640 662 651 + 1 0.997 0.127 0 agagaACAAtaacagctccaa
 TempSeq_FZX4oauC V\$ZFHX Two-handed zinc finger homeodomain transcription factors V\$ZEB1.01 "Zinc finger E-box
 binding homeobox 1 (AREB6, DELTAEF1)" Embryonic Structures 0.98 676 688 682 + 1 0.991 0.011 0 cacccACCTgcct
 TempSeq_FZX4oauC V\$TCFF TCF11 transcription factor V\$TCF11.01 TCF11/LCR-F1/Nrf1 homodimers 1 732 738
 735 + 1 0.998 -0.002 0 GTCAtgt
 TempSeq_FZX4oauC V\$TALE TALE homeodomain class recognizing TG motifs V\$TGIF.01 TG-interacting factor belonging to
 TALE class of homeodomain factors "Bone Marrow Cells
 Embryonic Structures
 Hematopoietic System
 Nervous System
 Neurons" 1 753 769 761 + 1 0.998 -0.002 0 gtgactctGTCAacag
 TempSeq_FZX4oauC V\$ESRR Estrogen-related receptors V\$ESRRA.02 Estrogen-related receptor alpha (secondary DNA binding
 preference) "Connective Tissue
 Digestive System
 Embryonic Structures
 Liver
 Muscle, Skeletal
 Muscles" 0.9 823 845 834 - 1 0.996 0.096 0 tattcactgagaggGGTCaaagg
 TempSeq_FZX4oauC V\$FKHD Fork head domain factors V\$HNF3.01 "Hepatocyte nuclear factor 3 (alpha, beta) (FOXA1,
 FOXA2)" "Blood Cells
 Brain
 Breast
 Cartilage
 Central Nervous System
 Connective Tissue
 Ear
 Endocrine System
 Eye
 Immune System
 Islets of Langerhans
 Leukocytes
 Liver
 Lung

Lymphocytes
 Muscle, Skeletal
 Muscles
 Nervous System
 Ovary
 Pancreas
 Pituitary Gland
 Prostate
 Testis
 Thymus Gland
 Thyroid Gland
 Urogenital System" 0.98 875 891 883 - 1 0.999 0.019 0 ggacggcAAACagaact
 TempSeq_FZX4oauC V\$TCFF TCF11 transcription factor V\$TCF11.01 TCF11/LCR-F1/Nrf1 homodimers 1 920 926
 923 + 1 0.994 -0.006 0 GTCAtca
 TempSeq_FZX4oauC V\$ABDB Abdominal-B type homeodomain transcription factors V\$HOXC10.01 Homeobox C10/ Hox-3iota
 "Bone Marrow Cells
 Bone and Bones
 Central Nervous System
 Connective Tissue
 Embryonic Structures
 Hematopoietic System
 Integumentary System
 Nervous System
 Prostate
 Skeleton
 Spinal Cord
 Urogenital System" 0.83 999 1015 1007 - 1 0.996 0.166 0 tgatgtcgTAAAatggt
 TempSeq_FZX4oauC V\$TALE TALE homeodomain class recognizing TG motifs V\$TGIF.01 TG-interacting factor belonging to
 TALE class of homeodomain factors "Bone Marrow Cells
 Embryonic Structures
 Hematopoietic System
 Nervous System
 Neurons" 1 1184 1200 1192 - 1 0.997 -0.003 0 aactttaatGTCAcgt
 TempSeq_FZX4oauC V\$FKHD Fork head domain factors V\$HFH3.01 "HNF-3/Fkh Homolog 3 (FOXI1, Freac-6)" "Blood Cells
 Brain
 Breast
 Cartilage
 Central Nervous System
 Connective Tissue
 Ear
 Endocrine System
 Eye
 Immune System
 Islets of Langerhans
 Leukocytes
 Liver
 Lung
 Lymphocytes
 Muscle, Skeletal
 Muscles
 Nervous System
 Ovary
 Pancreas
 Pituitary Gland
 Prostate
 Testis
 Thymus Gland
 Thyroid Gland
 Urogenital System" 0.97 1330 1346 1338 - 1 0.992 0.022 0 gctaaatAAACataact
 TempSeq_FZX4oauC V\$HAML Human acute myelogenous leukemia factors V\$AML1.01 AML1/CBFA2 Runt domain binding
 site "Bone Marrow Cells
 Bone and Bones
 Cartilage
 Connective Tissue
 Hematopoietic System
 Skeleton" 0.93 1373 1387 1380 - 1 0.991 0.061 0 ttctGTGGtcaagca
 TempSeq_FZX4oauC V\$SORRY SOX/SRY-sex/testis determinig and related HMG box factors V\$SOX5.01 Sox-5 "Bone and
 Bones
 Cartilage
 Connective Tissue

Embryonic Structures
 Endocrine System
 Leydig Cells
 Nervous System
 Neuroglia
 Skeleton
 Testis
 Thyroid Gland
 Urogenital System" 0.87 1406 1428 1417 - 1 0.992 0.122 0 cattaaCAATgtgctctgcgtgt
 TempSeq_FZX4oauC V\$TCFF TCF11 transcription factor V\$TCF11.01 TCF11/LCR-F1/Nrf1 homodimers 1 1480
 1486 1483 - 1 0.993 -0.007 0 GTCAtac
 TempSeq_FZX4oauC V\$CDXF Vertebrate caudal related homeodomain protein V\$CDX2.03 Caudal type homeobox transcription
 factor 2 "Digestive System
 Embryonic Structures" 0.91 1490 1508 1499 - 1 0.99 0.08 0 ttagggTTATtgagcta
 TempSeq_FZX4oauC V\$GATA GATA binding factors V\$GATA1.02 GATA-binding factor 1 "Blood Cells
 Bone Marrow Cells
 Bone and Bones
 Cardiovascular System
 Connective Tissue
 Embryonic Structures
 Erythrocytes
 Heart
 Hematopoietic System
 Immune System
 Leukocytes
 Lymphocytes
 Muscles
 Myocardium
 Skeleton" 1 1559 1571 1565 + 1 0.997 -0.003 0 gcaaGATTaggaa
 TempSeq_FZX4oauC V\$CART Cart-1 (cartilage homeoprotein 1) V\$S8.01 Binding site for S8 type homeodomains "Adrenal
 Glands
 Bone and Bones
 Brain
 Cardiovascular System
 Central Nervous System
 Connective Tissue
 Digestive System
 Embryonic Structures
 Endocrine System
 Eye
 Heart
 Immune System
 Islets of Langerhans
 Muscle, Skeletal
 Muscles
 Myeloid Cells
 Nervous System
 Neurons
 Nose
 Pancreas
 Phagocytes
 Pituitary Gland
 Skeleton
 Spinal Cord" 0.97 1612 1632 1622 - 1 0.997 0.027 0 gttaTAATtaagattatc
 TempSeq_FZX4oauC V\$CART Cart-1 (cartilage homeoprotein 1) V\$S8.01 Binding site for S8 type homeodomains "Adrenal
 Glands
 Bone and Bones
 Brain
 Cardiovascular System
 Central Nervous System
 Connective Tissue
 Digestive System
 Embryonic Structures
 Endocrine System
 Eye
 Heart
 Immune System
 Islets of Langerhans
 Muscle, Skeletal
 Muscles

Myeloid Cells
 Nervous System
 Neurons
 Nose
 Pancreas
 Phagocytes
 Pituitary Gland
 Skeleton
 Spinal Cord" 0.97 1617 1637 1627 + 1 0.992 0.022 0 tatctTAATtataaacaggaa
 TempSeq_FZX4oauC V\$ETSF Human and murine ETS1 factors V\$ERG.02 v-ets erythroblastosis virus E26 oncogene homolog
 "Antibody-Producing Cells
 Blood Cells
 Bone Marrow Cells
 Breast
 Central Nervous System
 Endocrine System
 Germ Cells
 Hematopoietic System
 Immune System
 Leukocytes
 Myeloid Cells
 Nervous System
 Phagocytes
 Prostate
 Spinal Cord
 Testis
 Urogenital System" 0.93 1626 1646 1636 + 1 0.991 0.061 0 tataacaGGAAataagccac
 TempSeq_FZX4oauC V\$SORY SOX/SRY-sex/testis determinig and related HMG box factors V\$SOX5.01 Sox-5 "Bone and
 Bones
 Cartilage
 Connective Tissue
 Embryonic Structures
 Endocrine System
 Leydig Cells
 Nervous System
 Neuroglia
 Skeleton
 Testis
 Thyroid Gland
 Urogenital System" 0.87 1661 1683 1672 - 1 0.992 0.122 0 gggtaaCAATatagagaccaatt
 TempSeq_FZX4oauC V\$NKXH NKX homeodomain factors V\$NKX25.05 Homeodomain factor Nkx-2.5/Csx "Cardiovascular
 System
 Central Nervous System
 Digestive System
 Embryonic Structures
 Endocrine System
 Heart
 Islets of Langerhans
 Lung
 Muscles
 Myocardium
 Nervous System
 Pancreas
 Prostate
 Respiratory System
 Spinal Cord
 Thyroid Gland
 Urogenital System" 0.97 1677 1695 1686 - 1 0.994 0.024 0 ttttTGAGtgggggtaac
 TempSeq_FZX4oauC V\$TCFF TCF11 transcription factor V\$TCF11.01 TCF11/LCR-F1/Nrf1 homodimers 1 1791
 1797 1794 + 1 0.994 -0.006 0 GTCAtga
 TempSeq_FZX4oauC V\$AP1R MAF and AP1 related factors V\$MARE.01 "Maf response elements, half sites" "Antibody-
 Producing Cells
 Blood Cells
 Blood Platelets
 Bone Marrow Cells
 Digestive System
 Ear
 Endocrine System
 Eye
 Hematopoietic System

Immune System
 Islets of Langerhans
 Liver
 Pancreas" 0.97 1848 1870 1859 - 1 0.995 0.025 0 tttgtctgTCAGcaacctctcat
 TempSeq_FZX4oauC V\$TALE TALE homeodomain class recognizing TG motifs V\$TGIF.01 TG-interacting factor belonging to
 TALE class of homeodomain factors "Bone Marrow Cells
 Embryonic Structures
 Hematopoietic System
 Nervous System
 Neurons" 1 1856 1872 1864 - 1 0.998 -0.002 0 gctttgtctGTCAgcaa
 TempSeq_FZX4oauC V\$SORY SOX/SRY-sex/testis determinig and related HMG box factors V\$SOX6.01 SRY (sex determining
 region Y)-box 6 "Bone and Bones
 Cartilage
 Connective Tissue
 Embryonic Structures
 Endocrine System
 Leydig Cells
 Nervous System
 Neuroglia
 Skeleton
 Testis
 Thyroid Gland
 Urogenital System" 0.97 1861 1883 1872 + 1 0.993 0.023 0 gacagACAAagcatattacaatc
 TempSeq_FZX4oauC V\$SRFF Serum response element binding factor V\$SRF.05 Serum response factor "Cardiovascular System
 Heart
 Muscle, Smooth
 Muscles
 Myocardium" 0.8 1985 2003 1994 + 1 0.992 0.192 0 attcccatatAAGGcaagt
 TempSeq_FZX4oauC V\$MZF1 Myeloid zinc finger 1 factors V\$MZF1.01 Myeloid zinc finger protein MZF1 "Blood Cells
 Bone Marrow Cells
 Hematopoietic System
 Immune System
 Leukocytes
 Myeloid Cells" 0.99 2145 2155 2150 + 1 0.992 0.002 0 gaGGGGagtct
 TempSeq_FZX4oauC V\$BRAC "Brachyury gene, mesoderm developmental factor" V\$TBX20.01 T-box transcription factor TBX20
 "Blood Cells
 Brain
 Breast
 Cardiovascular System
 Central Nervous System
 Ear
 Embryonic Structures
 Endocrine System
 Heart
 Immune System
 Leukocytes
 Lymphocytes
 Muscles
 Myocardium
 Nervous System
 Parathyroid Glands
 Pituitary Gland" 1 2259 2287 2273 - 1 0.991 -0.009 0 ttacagtcAGGTgtggtatggtctatt
 TempSeq_FZX4oauC V\$CART Cart-1 (cartilage homeoprotein 1) V\$S8.01 Binding site for S8 type homeodomains "Adrenal
 Glands
 Bone and Bones
 Brain
 Cardiovascular System
 Central Nervous System
 Connective Tissue
 Digestive System
 Embryonic Structures
 Endocrine System
 Eye
 Heart
 Immune System
 Islets of Langerhans
 Muscle, Skeletal
 Muscles
 Myeloid Cells
 Nervous System

Neurons
 Nose
 Pancreas
 Phagocytes
 Pituitary Gland
 Skeleton
 Spinal Cord" 0.97 2320 2340 2330 - 1 0.992 0.022 0 ttctTAATtatatacttca
 TempSeq_FZX4oauC V\$CART Cart-1 (cartilage homeoprotein 1) V\$S8.01 Binding site for S8 type homeodomains "Adrenal Glands
 Bone and Bones
 Brain
 Cardiovascular System
 Central Nervous System
 Connective Tissue
 Digestive System
 Embryonic Structures
 Endocrine System
 Eye
 Heart
 Immune System
 Islets of Langerhans
 Muscle, Skeletal
 Muscles
 Myeloid Cells
 Nervous System
 Neurons
 Nose
 Pancreas
 Phagocytes
 Pituitary Gland
 Skeleton
 Spinal Cord" 0.97 2325 2345 2335 + 1 0.997 0.027 0 gtataTAATtaaagaaaaaca
 TempSeq_FZX4oauC V\$TCFF TCF11 transcription factor V\$TCF11.01 TCF11/LCR-F1/Nrf1 homodimers 1 2485
 2491 2488 - 1 0.998 -0.002 0 GTCAtgt
 TempSeq_FZX4oauC V\$TALE TALE homeodomain class recognizing TG motifs V\$TGIF.01 TG-interacting factor belonging to
 TALE class of homeodomain factors "Bone Marrow Cells
 Embryonic Structures
 Hematopoietic System
 Nervous System
 Neurons" 1 2515 2531 2523 + 1 0.998 -0.002 0 ccaaattatGTCAttac
 TempSeq_FZX4oauC V\$TCFF TCF11 transcription factor V\$TCF11.01 TCF11/LCR-F1/Nrf1 homodimers 1 2524
 2530 2527 + 1 0.996 -0.004 0 GTCAtta
 TempSeq_FZX4oauC V\$TALE TALE homeodomain class recognizing TG motifs V\$TGIF.01 TG-interacting factor belonging to
 TALE class of homeodomain factors "Bone Marrow Cells
 Embryonic Structures
 Hematopoietic System
 Nervous System
 Neurons" 1 2715 2731 2723 + 1 0.998 -0.002 0 aacagaattGTCActta
 TempSeq_FZX4oauC V\$HNF6 One cut homeodomain factor HNF6 V\$HNF6.02 Liver enriched Cut - Homeodomain transcription
 factor HNF6 (ONECUT1) "Digestive System
 Embryonic Structures
 Endocrine System
 Islets of Langerhans
 Liver
 Pancreas" 0.86 2771 2787 2779 - 1 0.998 0.138 0 atcataaatCAATaatc
 TempSeq_FZX4oauC V\$HOXC HOX - PBX complexes V\$MEIS1.03 Meis homeobox 1 "Bone Marrow Cells
 Bone and Bones
 Brain
 Central Nervous System
 Connective Tissue
 Ear
 Embryonic Structures
 Hematopoietic System
 Immune System
 Lung
 Nervous System
 Phagocytes
 Respiratory System
 Skeleton
 Spinal Cord

Thymus Gland"	0.85	2773	2789	2781	+	1	0.99	0.14	0	ttattGATTtatgatca					
TempSeq_FZX4oauC										V\$GATA	GATA binding factors	V\$GATA1.02 GATA-binding factor 1 "Blood Cells			
Bone Marrow Cells															
Bone and Bones															
Cardiovascular System															
Connective Tissue															
Embryonic Structures															
Erythrocytes															
Heart															
Hematopoietic System															
Immune System															
Leukocytes															
Lymphocytes															
Muscles															
Myocardium															
Skeleton" 1	2794	2806	2800	-	1	0.997	-0.003	0	tgatGATTtagcag						
TempSeq_FZX4oauC										V\$AP1R	MAF and AP1 related factors	V\$MARE.01 "Maf response elements, half sites" "Antibody-Producing			
Cells															
Blood Cells															
Blood Platelets															
Bone Marrow Cells															
Digestive System															
Ear															
Endocrine System															
Eye															
Hematopoietic System															
Immune System															
Islets of Langerhans															
Liver															
Pancreas" 0.97	2832	2854	2843	+	1	0.995	0.025	0	gccaaaagTCAGcattattaatt						
TempSeq_FZX4oauC										V\$RUSHSWI/SNF related nucleophosphoproteins with a RING finger DNA binding motif	V\$SMARCA3.02				
"SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3"										0.98	2931	2941	2936	+	1
0.993	0.013	0	ctgcACTTtta												
TempSeq_FZX4oauC										V\$TALE	TALE homeodomain class recognizing TG motifs	V\$TGIF.01	TG-interacting factor belonging to		
TALE class of homeodomain factors													"Bone Marrow Cells		
Embryonic Structures															
Hematopoietic System															
Nervous System															
Neurons" 1	2948	2964	2956	-	1	0.998	-0.002	0	tctgggctGTCAcata						
TempSeq_FZX4oauC										V\$MZF1	Myeloid zinc finger 1 factors	V\$MZF1.01	Myeloid zinc finger protein MZF1 "Blood Cells		
Bone Marrow Cells															
Hematopoietic System															
Immune System															
Leukocytes															
Myeloid Cells"	0.99	3004	3014	3009	+	1	0.992	0.002	0	gaGGGGagtgg					
TempSeq_FZX4oauC										V\$NKXH	NKX homeodomain factors	V\$NKX21.01	NK2 homeobox 1 (Thyroid transcription factor 1)		
"Cardiovascular System															
Central Nervous System															
Digestive System															
Embryonic Structures															
Endocrine System															
Heart															
Islets of Langerhans															
Lung															
Muscles															
Myocardium															
Nervous System															
Pancreas															
Prostate															
Respiratory System															
Spinal Cord															
Thyroid Gland															
Urogenital System" 1	3143	3161	3152	-	1	0.99	-0.01	0	ggctTGGAggttctgatt						