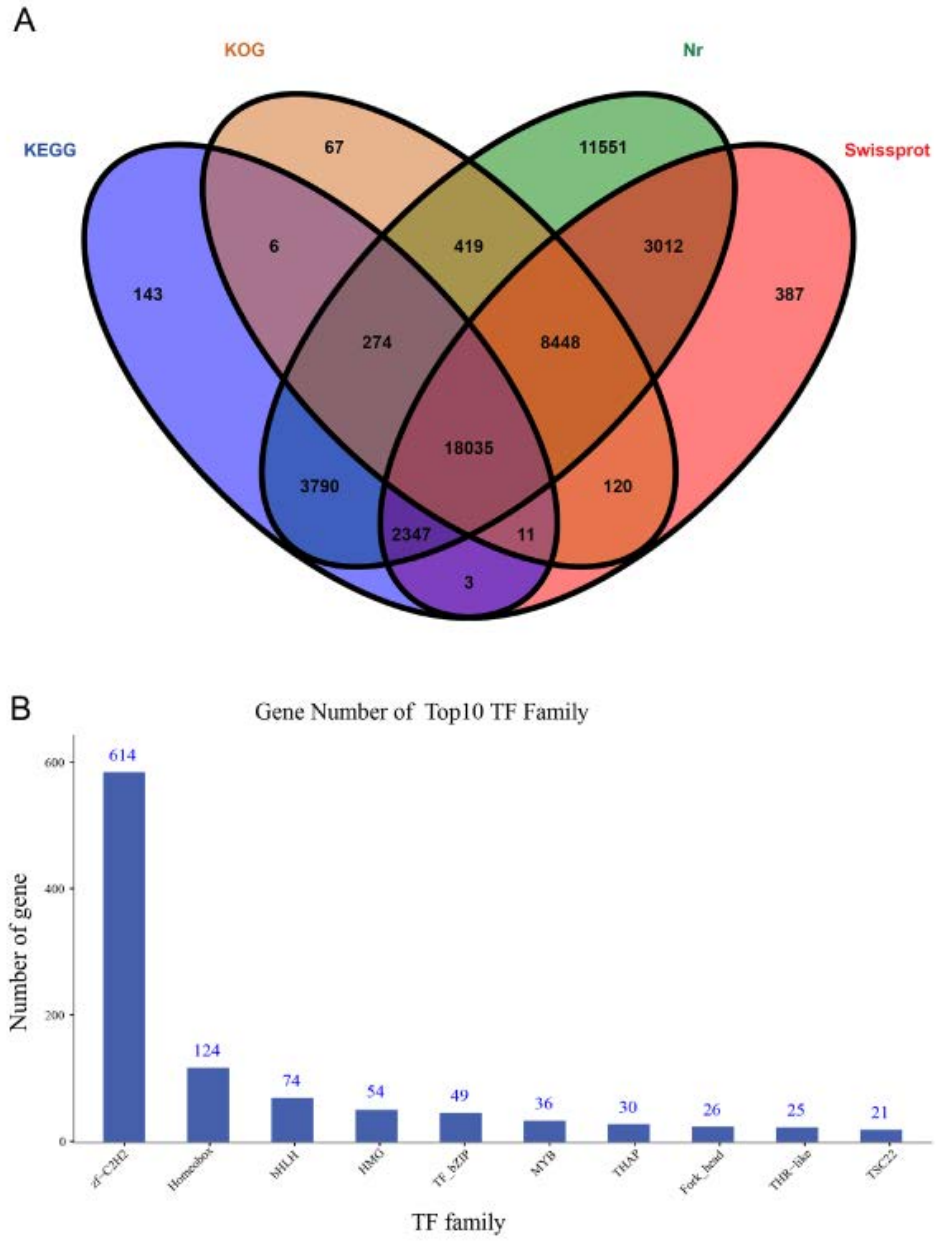

Fig S1. Annotation of unigenes.

(A) Venn diagram showing the basic annotation of the assembled unigenes. Sequence similarity searches against various protein database including non-redundant (nr) protein, SwissProt, Clusters of Orthologous Groups (COG/KOG) and Kyoto Encyclopedia of Genes and Genomes (KEGG) databases. (B) Transcription factors (TF) classification of the unigenes of amphioxus.

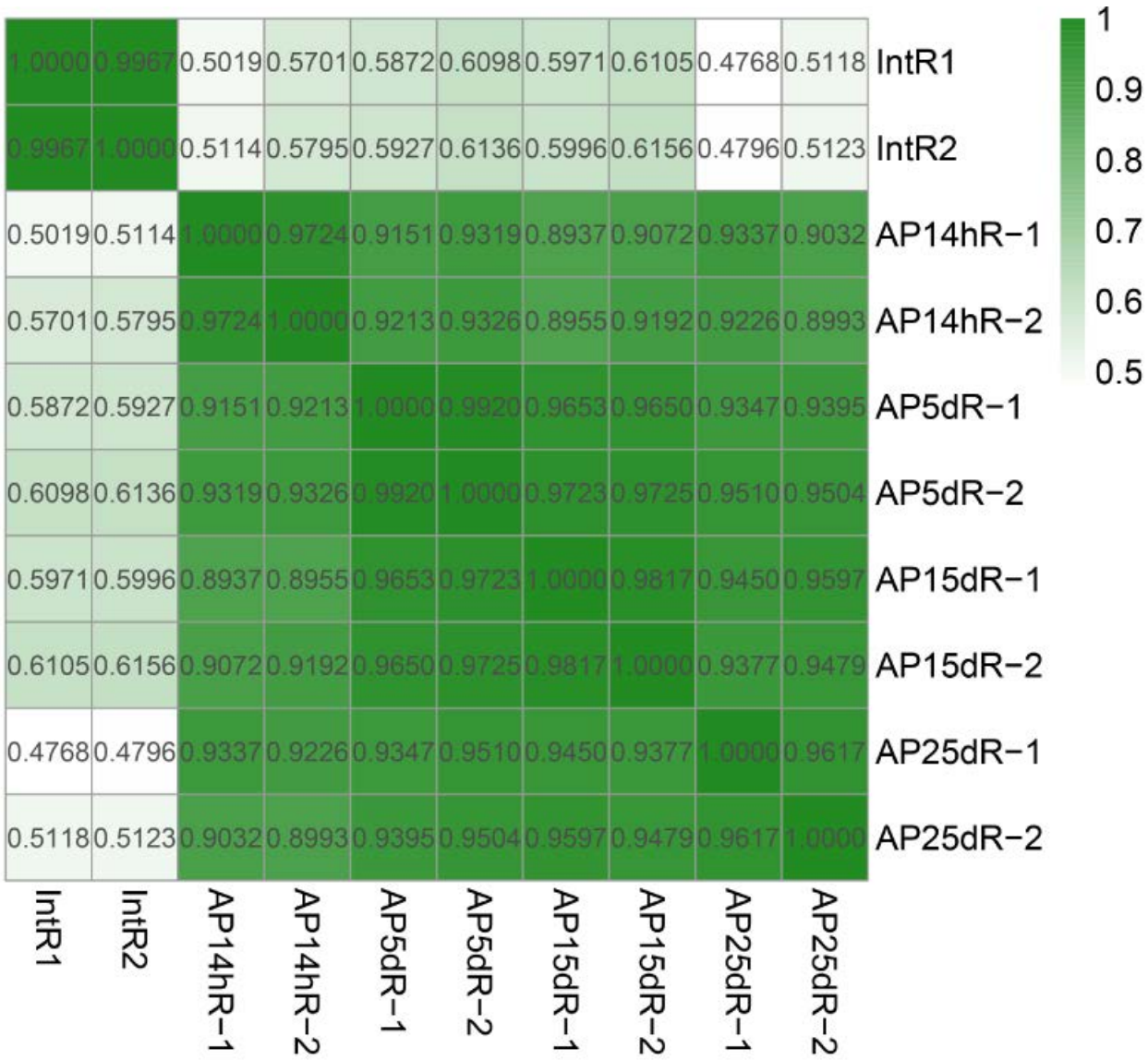

Fig S2. Heat map showing Pearson correlation between two samples.

Within a group, when the Pearson correlation between two samples is close to 1, it means that the two samples are highly related.

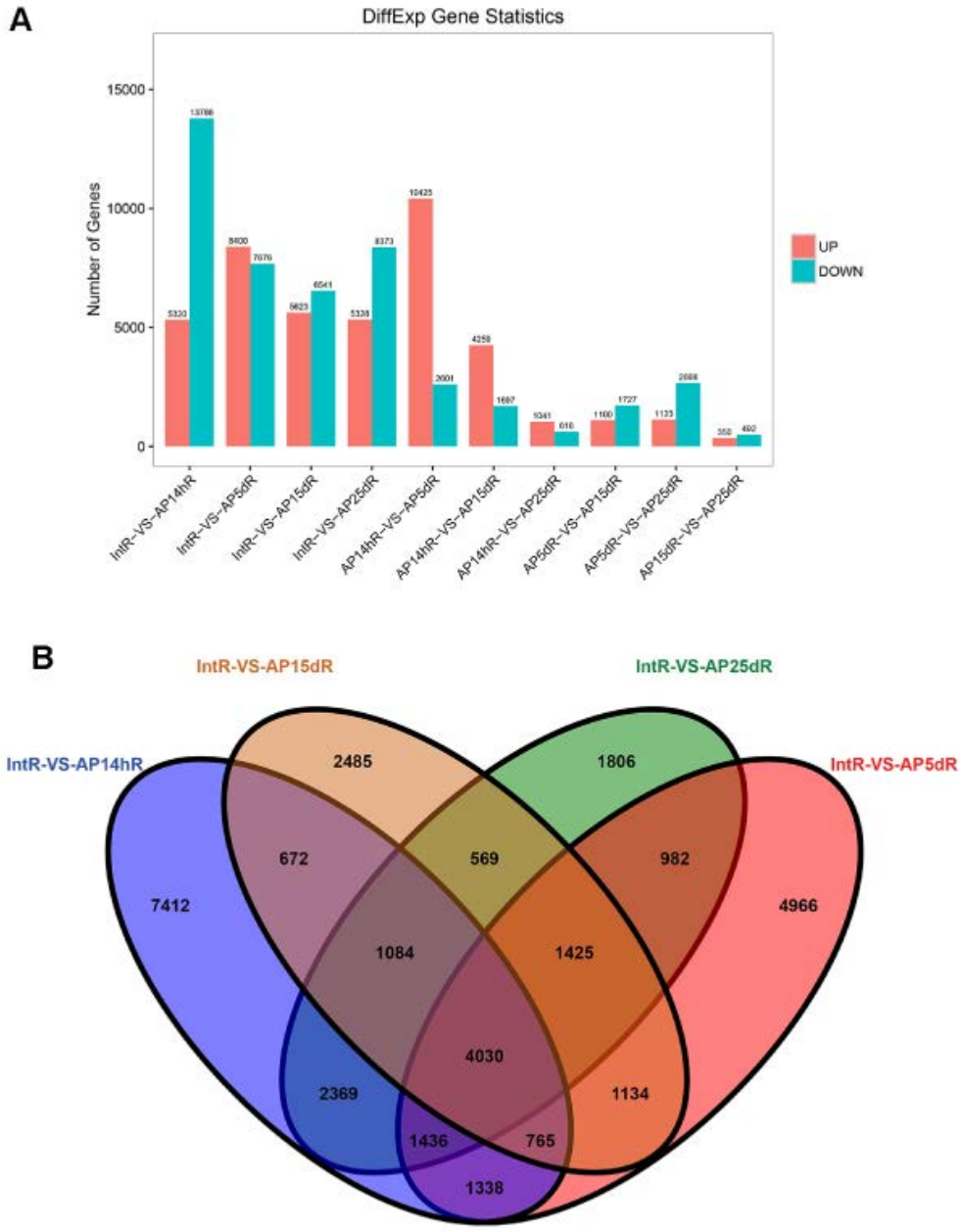

Fig S3. Statistics of differentially-expressed genes between different regeneration stages.

(A) Bar graph shows the up-regulated and down-regulated gene numbers between two different tissues. (B) Venn diagram shows DEGs shared by different regenerative stages respective to the intact tail. IntR means intact tail, and AP14hR, AP5dR, AP15dR and AP25dR mean tail regenerates at 14 h, 5 d, 15 d and 25 d post-amputation respectively.

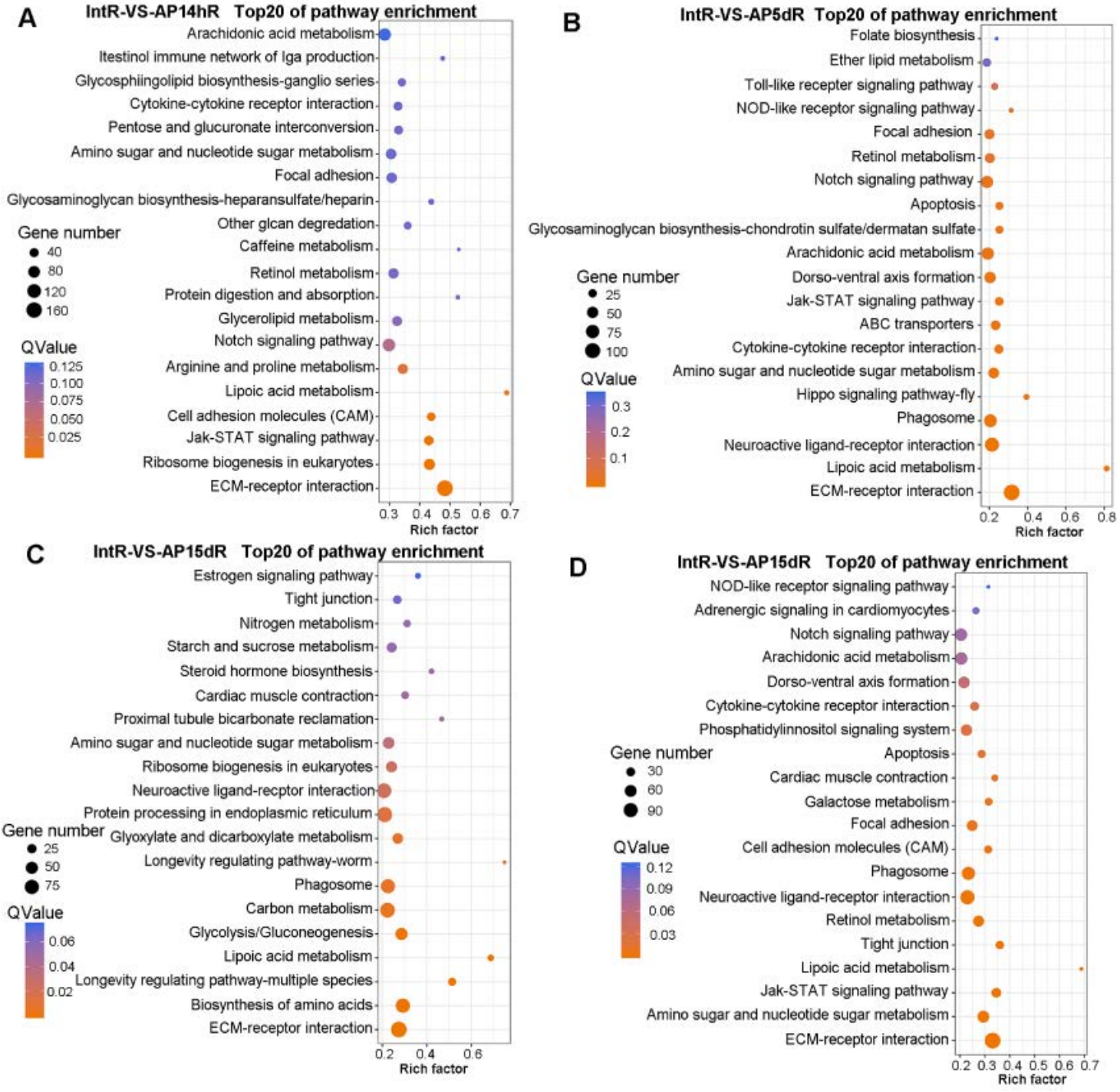

Fig S4. KEGG analysis of DEGs of tail regenerates at different regenerative stages, compared to intact tails.

(A) Top 20 pathways by enrichment of DEGs of tail regenerates at 14 h post-amputation. (B) Top 20 pathways by enrichment of DEGs of tail regenerates at 5 d post-amputation. (C) Top 20 pathways by enrichment of DEGs of tail regenerates at 15 days post-amputation. (D) Top 20 pathways by enrichment of DEGs of tail regenerates at 25 d post-amputation. Rich Factor is the ratio of differentially expressed gene numbers annotated in this pathway terms to all gene numbers annotated in this pathway term. Q value means corrected P value, $Q < 0.05$ as significantly enriched.

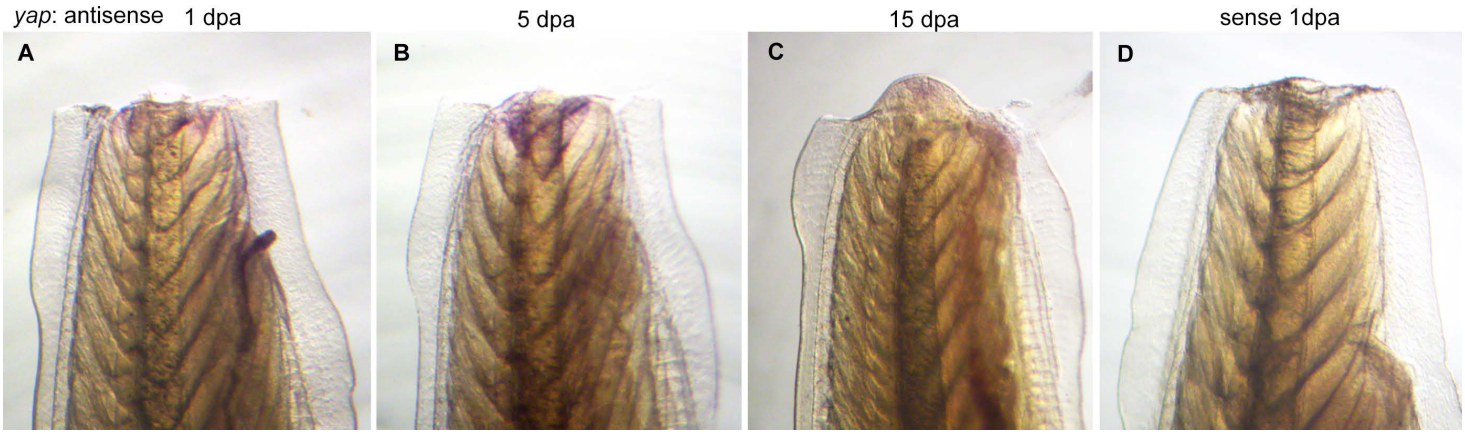

Fig S5. Whole-mount *in situ* hybridization analysis of *yap* expression during tail regeneration process.

(A-C) tail regenerates at 1 day, 5 days and 15 days post-amputation respectively, hybridized with antisense probes. (D) tail regenerate at 1 day post-amputation, hybridized with the sense probes. The blue represents positive staining for *yap* expression. All panels are tail regenerates with distal at the top.

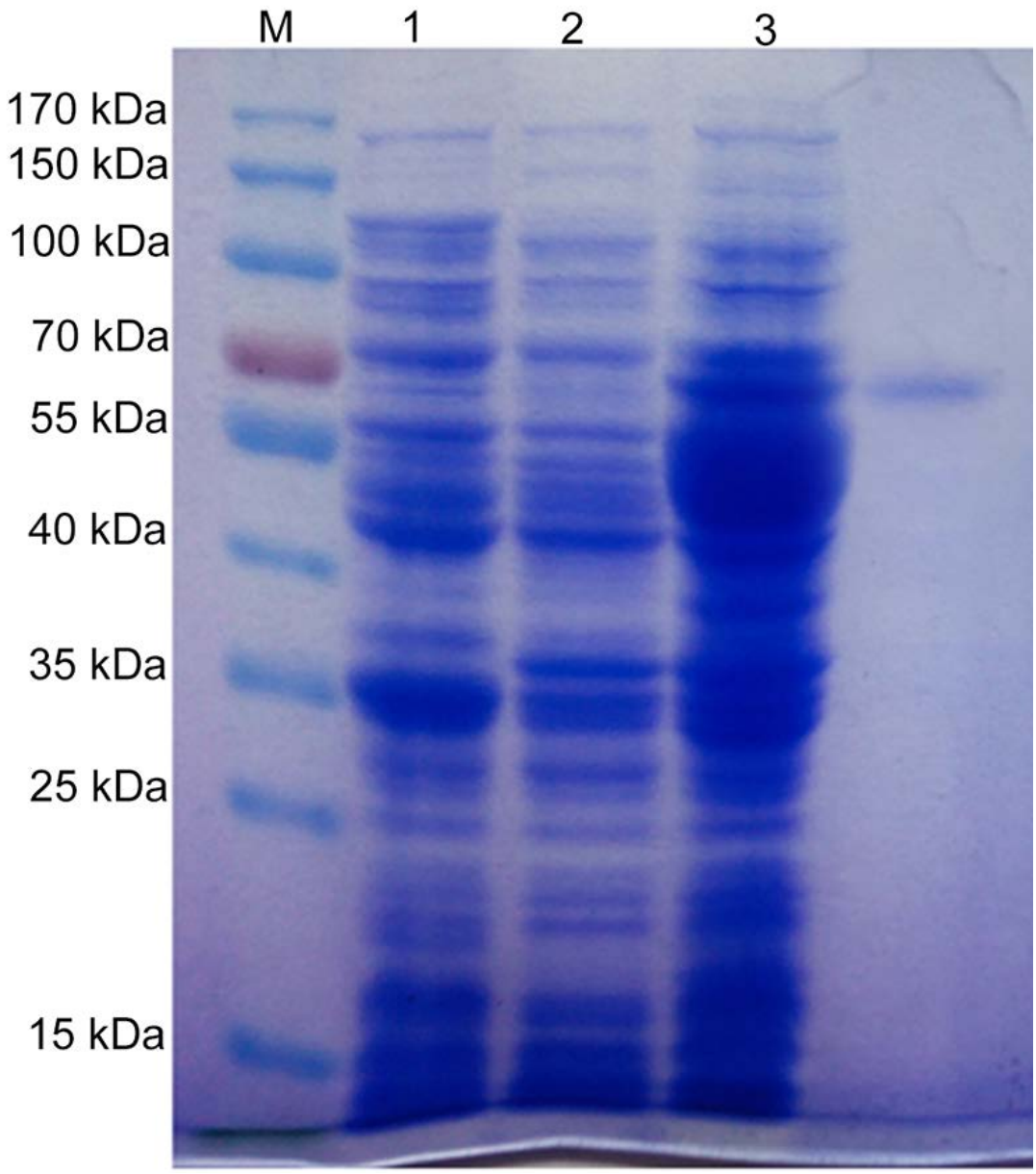

Fig S6. SDS-PAGE analysis of the expression and purification of recombinant BMP2/4 from *E. coli* cells.

Lane M, molecular mass standards; lane 1, extracts from *E. coli* BL21 containing pET32a empty vector; lane 2, extracts from *E. coli* BL21 containing pET32a/BMP2/4 before induction; lane 3, total cellular extracts from IPTG-induced E. coli BL21 containing pET32a/BMP2/4; lane 4, recombinant BMP2/4 purified on NiNTA resin column.

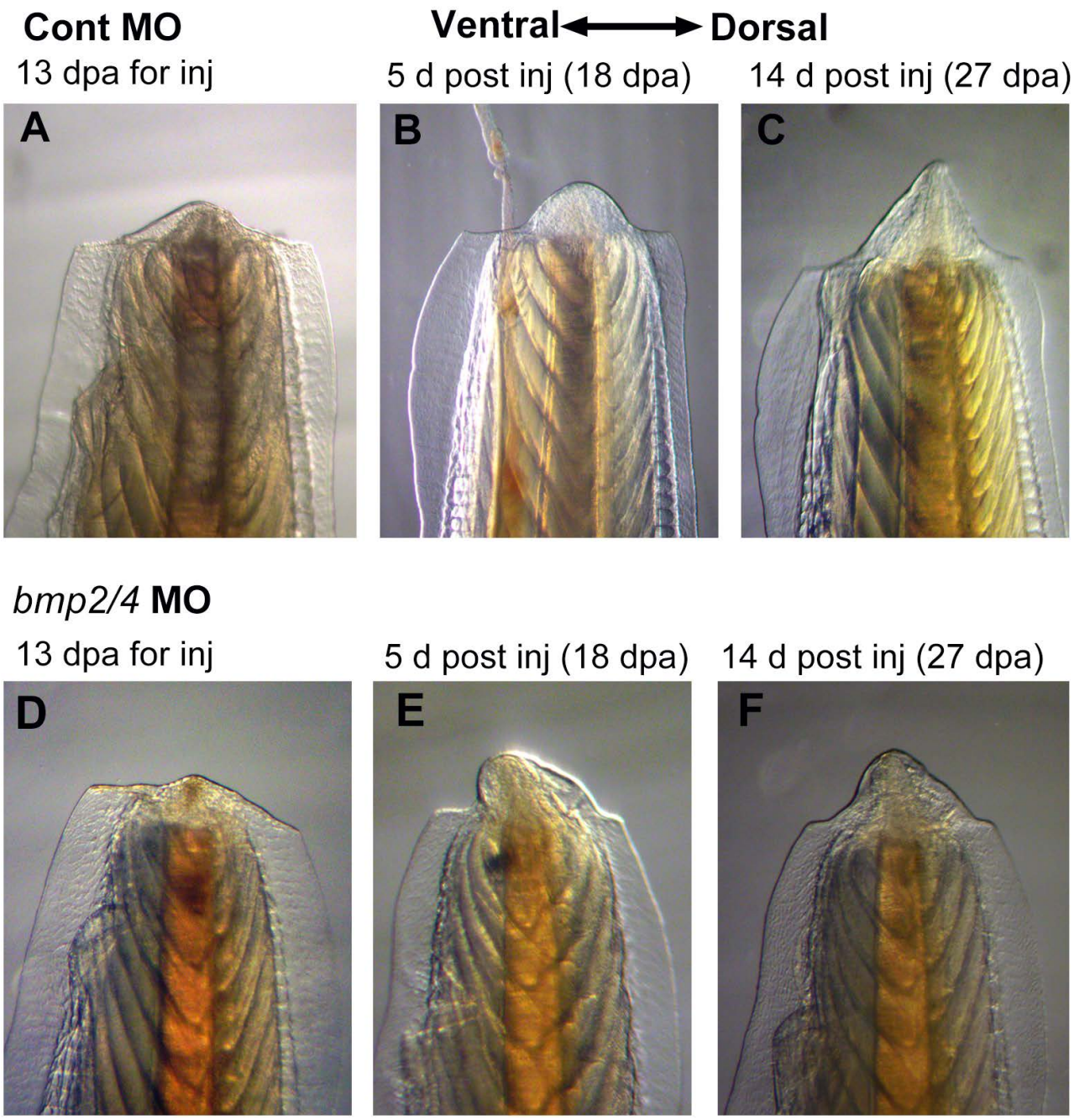

Fig. S7. vivo-morpholino mediated BMP2/4 knockdown disturbed the patterning of the regenerative blastema.

(A-C) tail regenerates at different time points post injection of control MO. (D-F) Tail regenerates at different time points post injection of BMP2/4 MO. The BMP2/4 MO caused the tail blastema to grow and fold toward ventral side of the body, compare to the controls. dpa means days post-amputation. d post inj means days post-injection.

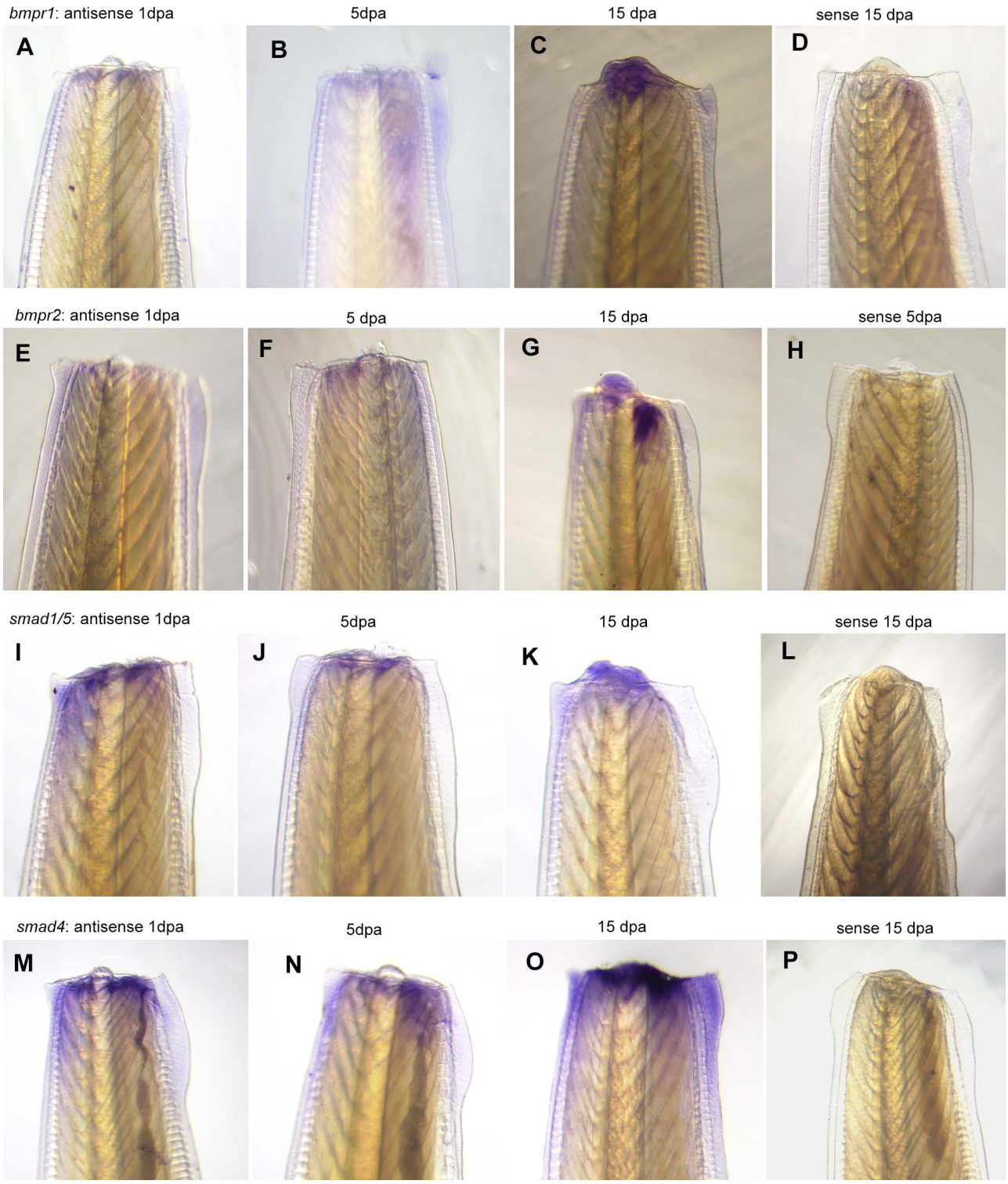

Fig. S8. Whole-mount *in situ* hybridization analysis of expression patterns of BMP signaling related genes during tail regeneration process.

(A-D) expression of *bmpr*1 during tail regeneration process. (E-H) expression of *bmpr*2 during tail regeneration process. (I-L) expression of *smad1/5* during tail regeneration process. (M-P) expression of *smad4* during tail regeneration process. All the four BMP signaling genes were specifically expressed in wound region at wound healing stage, and their expressions were also specially detected in the newly formed blastema at blastemal stage. (D, H, L and P) Controls for the genes respectively, and no positive staining signals were detected. dpa means days post-amputation.

Table S1. Assignment of Unigenes into TF families

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Table S2. Description of DEGs at early wound healing stage (14 hpa), compared to intact tail.

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Table S3. Description of DEGs at late wound healing stage (5 dpa), compared to intact tail.

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Table S4. Description of DEGs at early blastema stage (15 dpa), compared to intact tail.

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Table S5. Description of DEGs at late blastema stage (25 dpa), compared to intact tail.

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Table S6. Biological processes classification in GO enrichment of up-regulated DEGs at early wound healing stage (14 hpa), compared to intact tail.

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Table S7. Biological processes classification in GO enrichment of up-regulated DEGs at late wound healing stage (5 dpa), compared to intact tail.

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Table S8. Description of the genes listed in Fig. 4A.

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Table S9. Biological processes classification in GO enrichment of up-regulated DEGs at early blastemal stage (15 dpa), compared to intact tail.

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Table S10. Biological processes classification in GO enrichment of up-regulated DEGs at late blastemal stage (25 dpa), compared to intact tail.

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Table S11. Description of the genes listed in Fig. 4B.

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Table S12. KEGG classification of up-regulated DEGs at early wound healing stage (14 hpa), compared to intact tail.

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Table S13. KEGG classification of up-regulated DEGs at late wound healing stage (5 dpa), compared to intact tail.

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Table S14. KEGG classification of up-regulated DEGs at early blastemal stage (15 dpa), compared to intact tail.

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Table S15. KEGG classification of up-regulated DEGs at late blastemal stage (25 dpa), compared to intact tail.

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