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Supplemental Information

Heart Regeneration in the Mexican Cavefish

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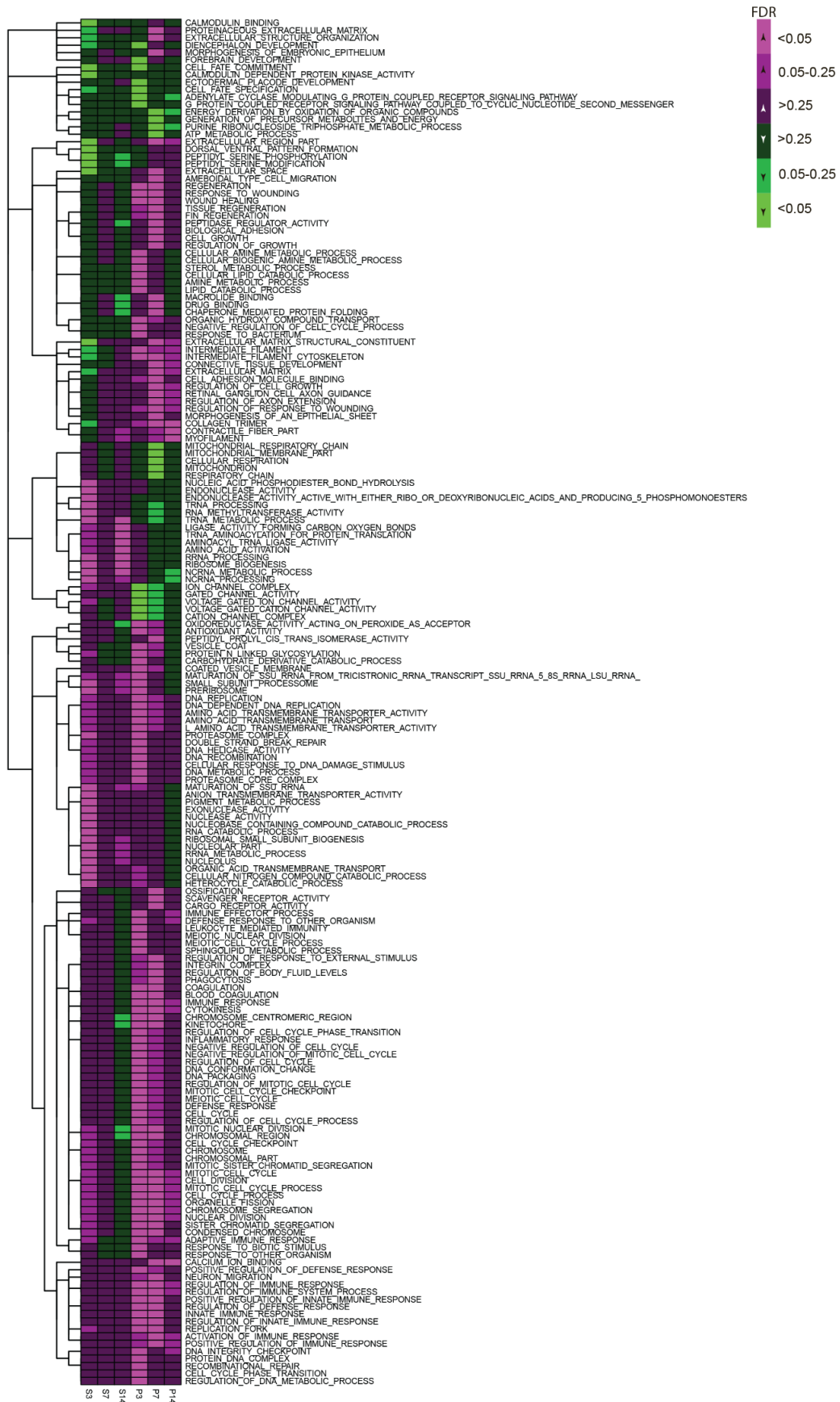


Figure S1. RNA sequencing GO term analysis, related to Figure 3. Heatmap of signed FDR values for all GO terms significantly different (FDR < 0.05) between sham and at least one time point per population by pre-ranked GSEA. S, surface; P, Pachón; FDR, false discovery rate.

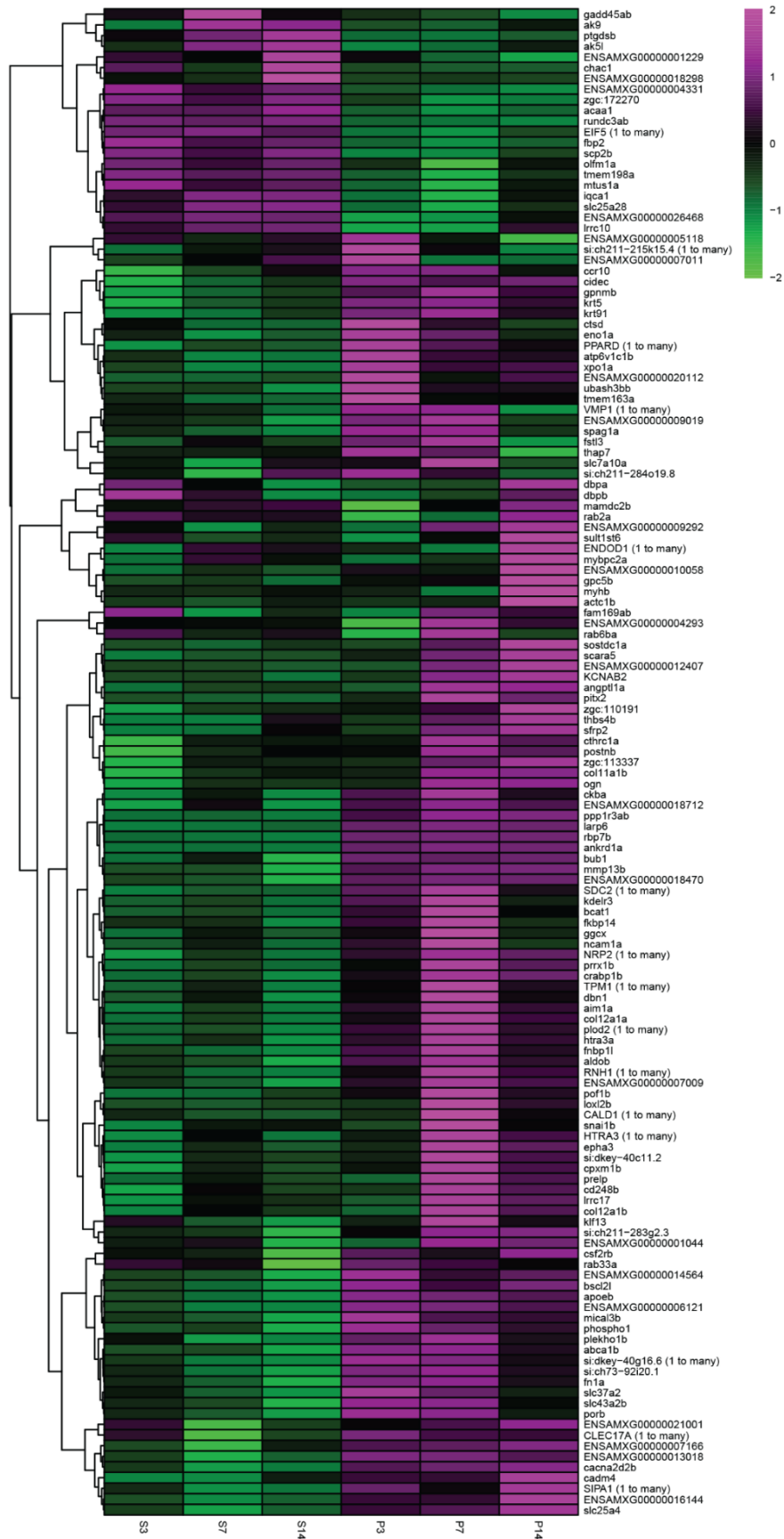


Figure S2. RNA sequencing analysis, related to Figure 3. Heatmap of row-normalised expression values for 141 genes with differential kinetics over the different time points clustered by Pearson correlation. Values are log₂ fold change relative to sham. S, surface; P, Pachón.

Gene	Forward primer sequence (5'- 3')	Reverse primer sequence (5'- 3')
<i>caveolin</i>	CAACGAGAGAGACCCACGAC	AGTCATCCAACCTGACCAAC
<i>ckba</i>	CTTCCCAACGTGAGCAAACA	TGAGAACCCCAGACGGTCA
<i>lrrc10</i>	TCCCAACCTGAAAACCTACAT	AGTCATCCAACCTGACCAAC
<i>snai1b</i>	GCGCTAAAGATGCACATCCG	GTGAGGACAGGAGAACGGAC
<i>sfrp2</i>	AAGACGACAGTGAGATGGTGG	CGCCGTTTCAGCTTGTATATGG
<i>xpo1a</i>	CAGGAGGCATTTTGTTTCAGGTG	CGCCAATCATATAACCCACTGC
<i>rpl13a</i> (housekeeping)	TCTGGAGGACTGTAAGAGGTATGC	AGACGCACAATCTTGAGAGCAG
<i>18s</i> (housekeeping)	CGGAGGTTCTGAAGACGATCA	GGAACCCAAAGACTCGTGGT

Table S1. QPCR primer sequences, related to methods section 'Quantitative PCR'.