

SUPPLEMENTARY MATERIAL


corresponding to:

**Transcriptome analysis of regeneration
during *Xenopus laevis* experimental twinning**

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TABLE S1

***XENOPUS LAEVIS* GENES UP-REGULATED BY SAGITTAL BISECTION AT STAGE 8 AND ALLOWED TO REGENERATE UNTIL STAGE 10.5**

Microsoft Excel Table is available for download at: <https://doi.org/10.1387/ijdb.190006ed>

Transcripts shown were up-regulated over two-fold from whole embryo controls in both left and right halves; to avoid wound-healing genes only transcripts that were higher in the dorsal or ventral halves by two-fold were selected; in all cases, transcripts in both sagittal halves had to be higher than the corresponding ventral or dorsal half; nine genes out of 16,672 genes with an average RPKM above 1 remained after these very stringent criteria, which are shown in [Table 1](#) of the main text. This table includes 16,672 genes.

TABLE S2

***XENOPUS LAEVIS* GENES UP-REGULATED BY SAGITTAL BISECTION AT STAGE 8 AND ALLOWED TO REGENERATE UNTIL STAGE 12**

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Transcripts shown were up-regulated over two-fold from whole embryo controls in both left and right halves; to avoid wound-healing genes only transcripts that were higher in the dorsal or ventral halves by two-fold were selected; in all cases, transcripts in both sagittal halves had to be higher than the corresponding ventral or dorsal half; twenty-five genes out of 15,595 genes with an average RPKM above 1 remained after these very stringent criteria, which are shown in [Table 2](#) of the main text. This table includes 15,595 genes.