



Supplementary Figure 2. Real-time PCR analysis of targeted genes in the zebrafish caudal fin. Changes in mRNA levels in targeted genes are shown in days of recovery following amputation in controls (clear bars) or days of recovery following inhibitor washout as described for **Figure 4** (black bars), or at baseline before fin clip (gray bars). All mRNA levels have been standardized with β-actin transcript levels. **(a)**. *vegfr1* **(b)**. *semaphorin3aa* **(c)**. *ephrinB2a* **(d)**. baseline levels in amputated caudal fins. Standard abbreviations are used as follows: *n* = number of experimental replicates (pool of fins); *N* = Number of fins used; * = significantly different from control (*: $P \leq 0.05$, **: $P \leq 0.01$, ***: $P \leq 0.001$); #: significantly different from unclipped fin (#: $P \leq 0.05$, ##: $P \leq 0.01$, ###: $P \leq 0.001$). Error bars indicate standard deviations.