VISTA plot of the *shh* genomic region (*Danio rerio* *shh* as reference sequence). Shuffle-LAGAN alignment (repeatmasker applied), visualized with mVISTA. The crossbar indicates the deduced *shh* gene structure (black: exons). Enhancer locations are indicated by grey bars as well as the putative *ar-E* CNE. Masked repeats are indicated by yellow bars. Conservation parameters were set as: Min Y: 50, min Id: 70, Min length: 60.