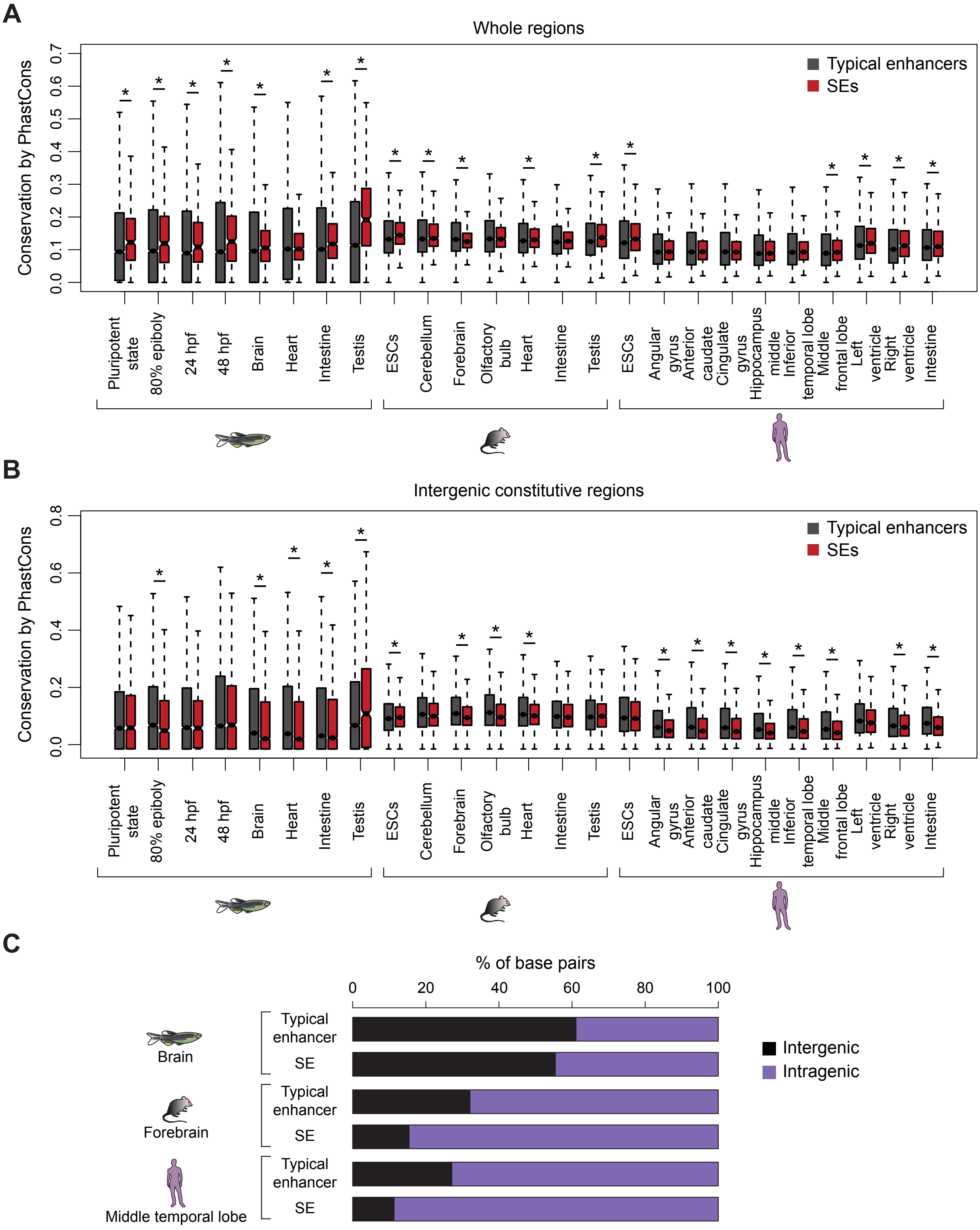

Supplemental Figure S5. Sequence conservation of typical enhancers and SEs. (A) Box plots depicting the average sequence conservation of whole typical enhancers and SEs in the indicated zebrafish, mouse and human cells and tissues (x-axis). The y-axis shows sequence conservation calculated by PhastCons. The box bounds the interquartile range divided by the median and the notch approximates a 95% confidence interval for the median. Observed significant differences in conservation between typical enhancers and SEs are denoted with an asterisk (p-value ≤ 1.3×10^{-3}) based on Wilcoxon rank-sum analyses. (B) Box plots depicting average sequence conservation of intergenic constitutive regions of typical enhancers and SEs in the indicated zebrafish, mouse and human cells and tissues (x-axis). The y-axis shows sequence conservation calculated by PhastCons. Box bounds and notch as in (A). Observed significant differences in conservation between constitutive regions of typical enhancers and SEs are denoted with an asterisk (p-value ≤ 0.01) based on Wilcoxon rank-sum analyses. (C) Distribution of constitutive typical enhancer and SE regions relative to RefSeq gene annotations in representative brain datasets of zebrafish, mouse and human. The percentages of intergenic (black) and intragenic (purple) sequences overlapping with typical enhancers and SEs are shown in the x-axis.