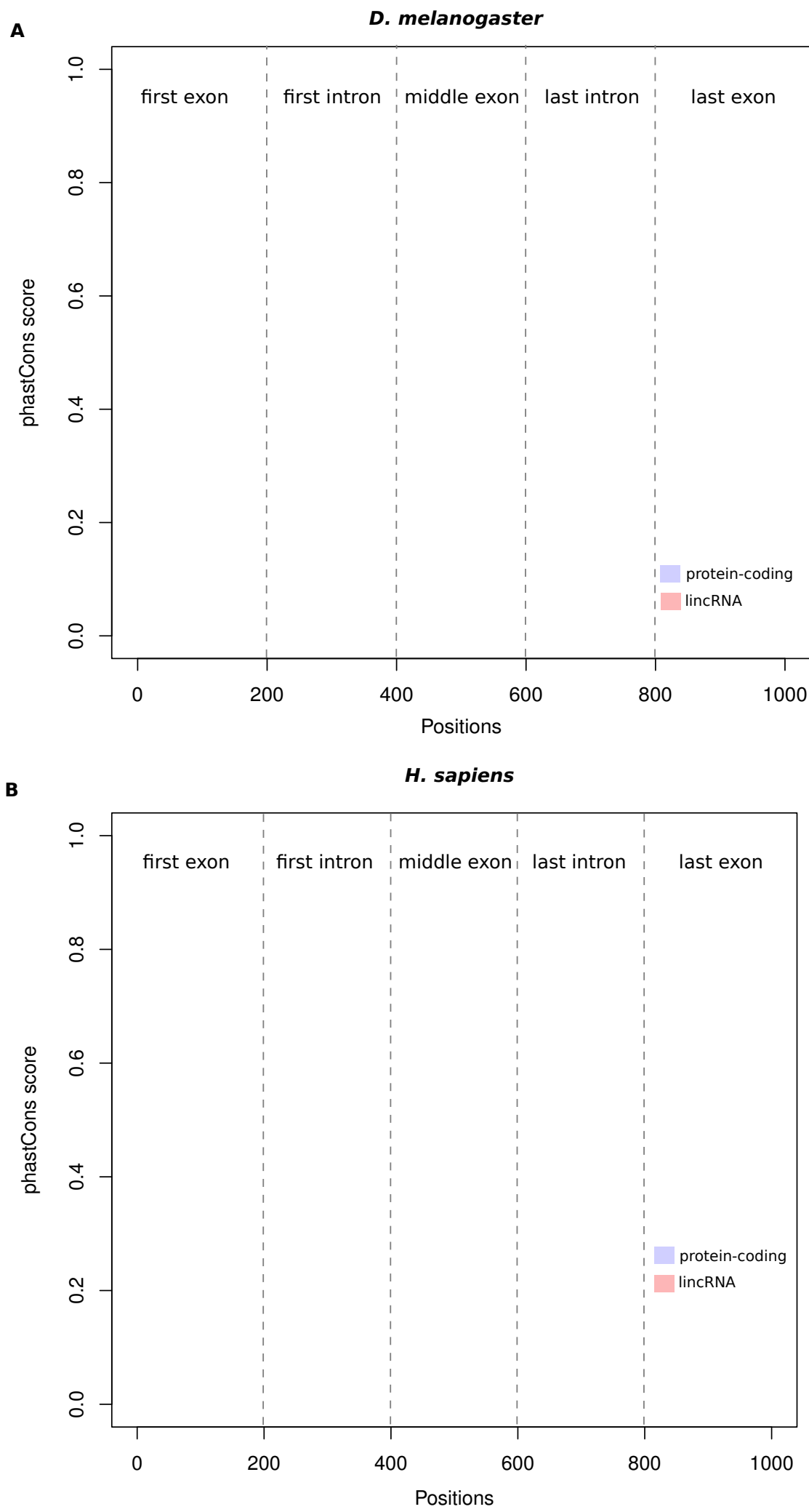


Figure: Average phastCons scores across protein-coding (blue) and lincRNAs (red) gene models in *D. melanogaster* (A) and human (B, C). Two hundred evenly spaced nucleotides were randomly sampled per feature. The grey lines represent the 95% confidence intervals computed over 1000 resampling.



c

H. sapiens

