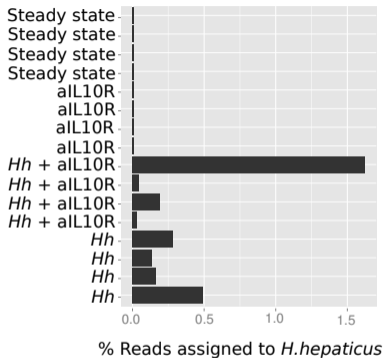


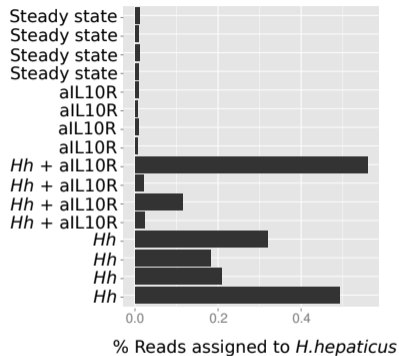
a

DNA-seq



b

RNA-seq



**Supplementary Figure S4** Proportion of alignments assigned to *Helicobacter hepaticus* using the lowest common ancestor approach for (a) metagenomic and (b) metatranscriptomic data.