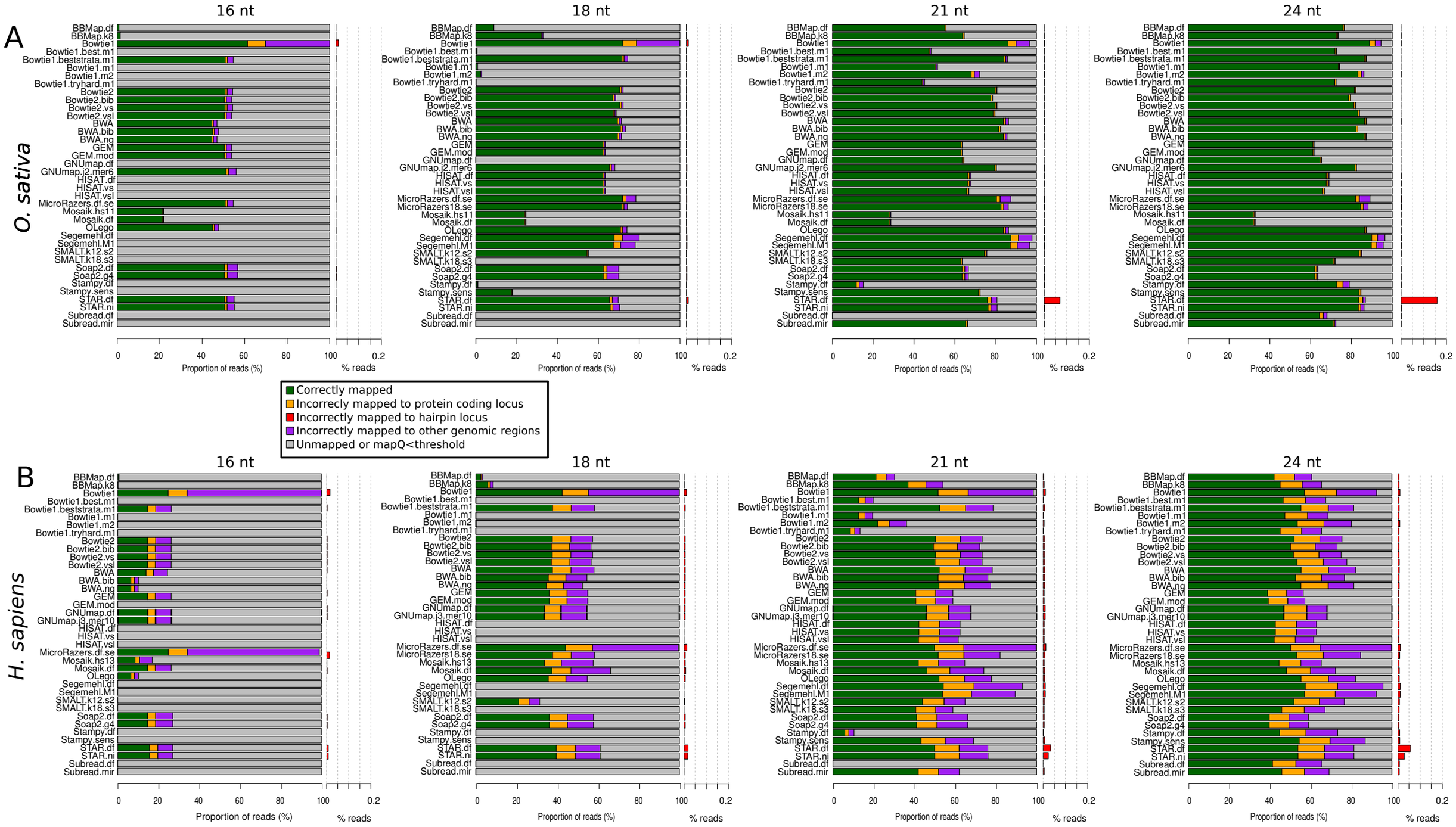

Supplementary Figure 4. Alignment of short simulated Illumina-like mRNA-derived sequences to the genome. For panels A and B, green bars denote correctly mapped reads, yellow bars denote incorrect mapping to protein coding locations, purple bars represent mapping to non-mRNA and non-hairpin loci and grey bars denote reads unmapped or below map quality threshold. Red bars denote incorrect mapping to hairpin loci, these are plotted on enlarged axes for visibility. Read mapping results at varying read lengths are shown for *O. sativa* (A) and *H. sapiens* (B).