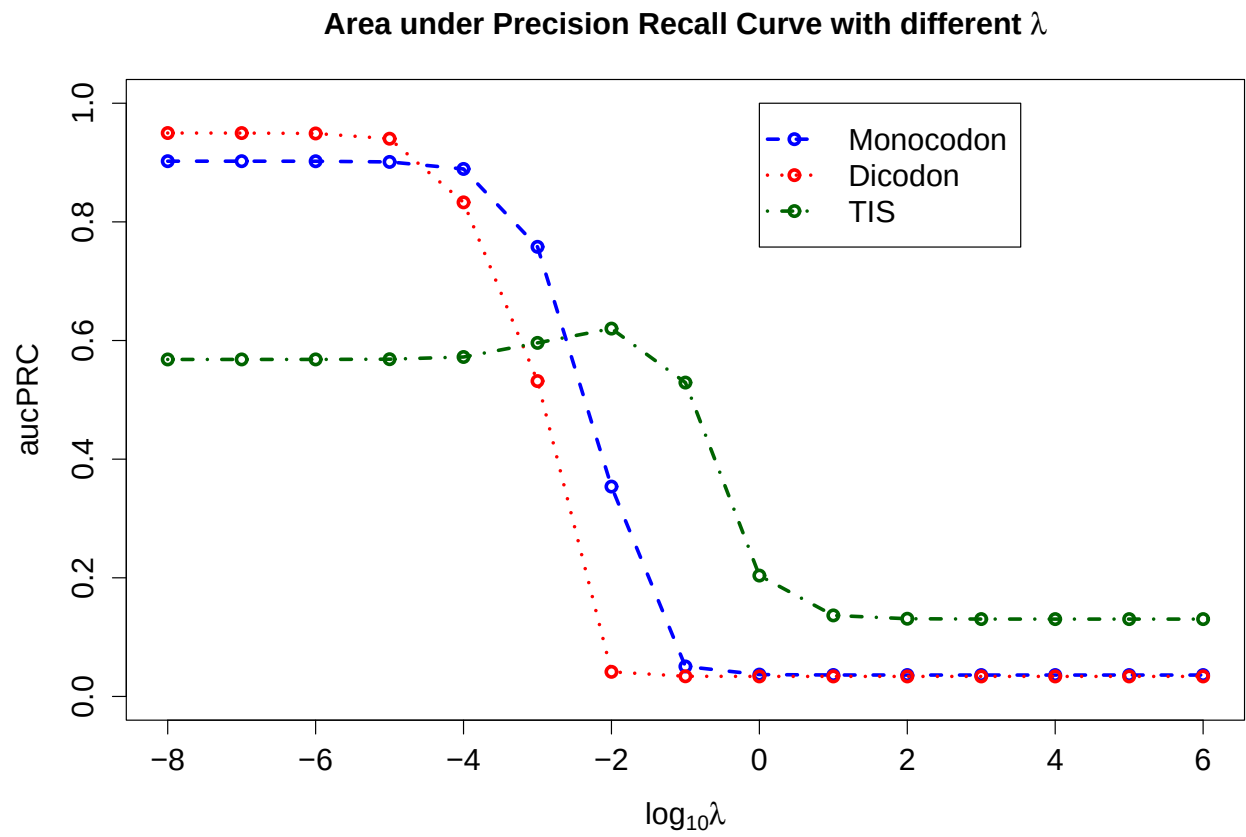
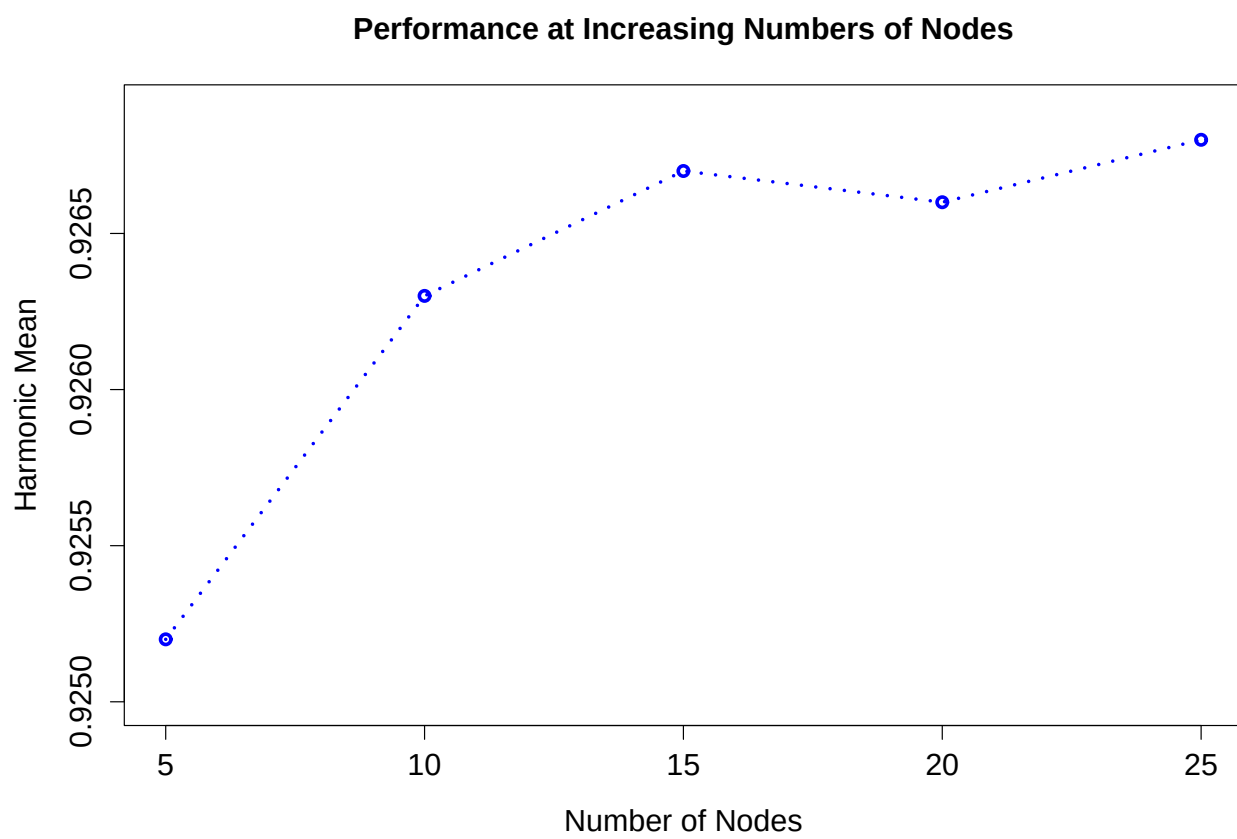


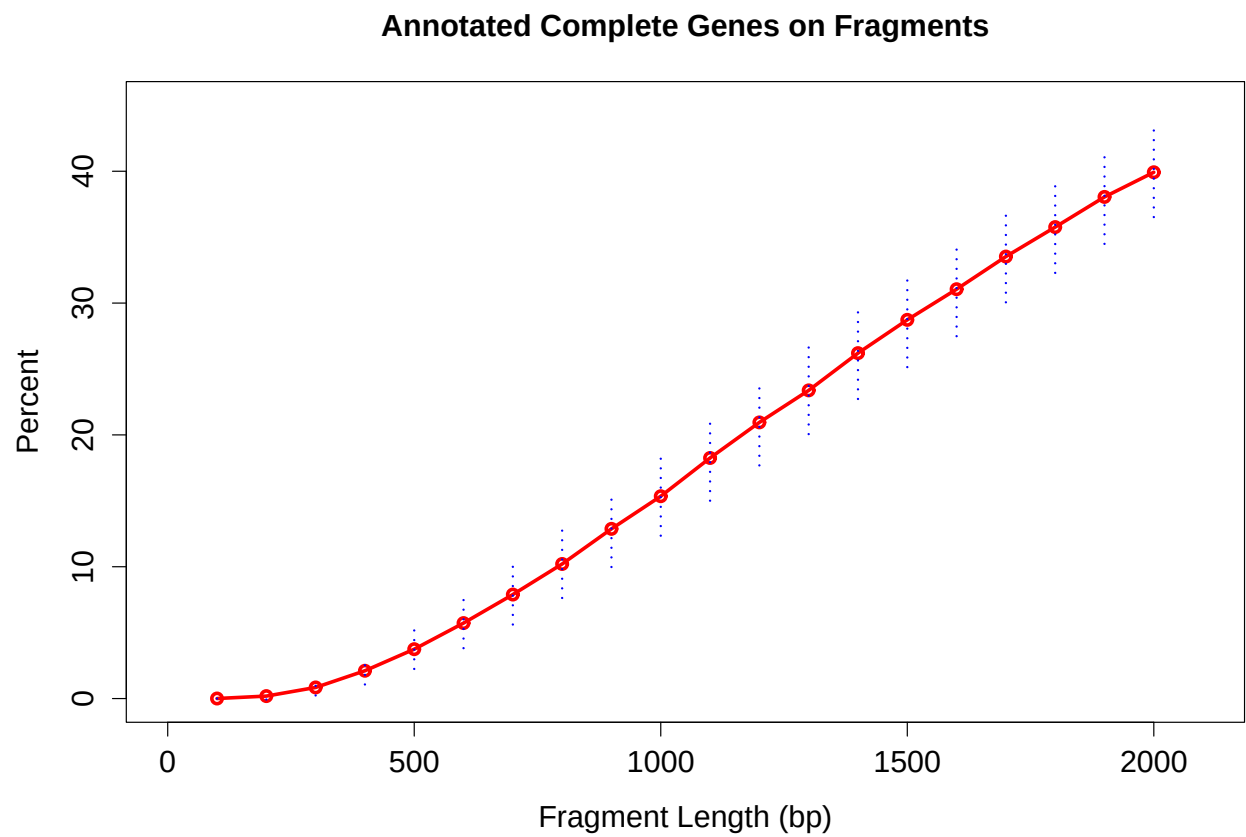
Additional file 2 — Supplementary figures
Supplementary Figure 1: Discriminant validation



Supplementary Figure 2: Neural network performance



Supplementary Figure 3: Mean and standard deviation of the percentage of complete genes within all annotated genes per fragment averaged over all test-species fragments (with a 5-fold genome coverage, according to GenBank annotation).



Supplementary Figure 4: Gene prediction performance on fragments ranging from 5000 to 60000 bp length (sampled to a 5-fold genomes coverage).

