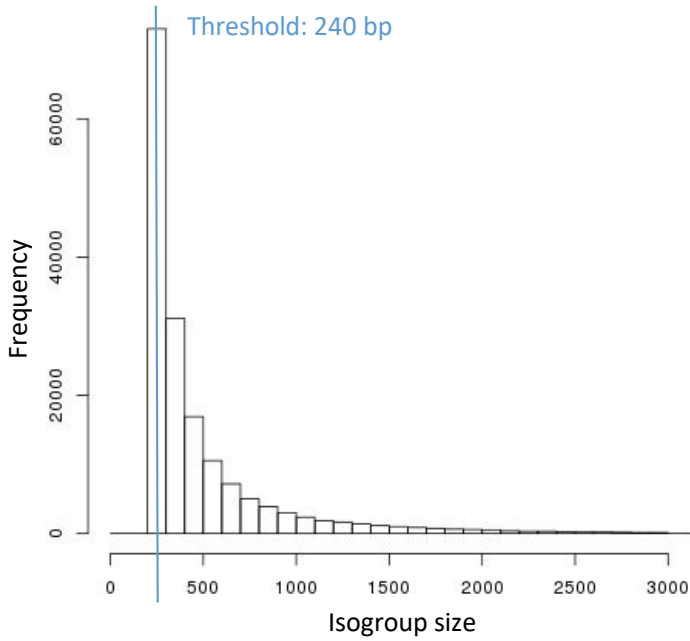
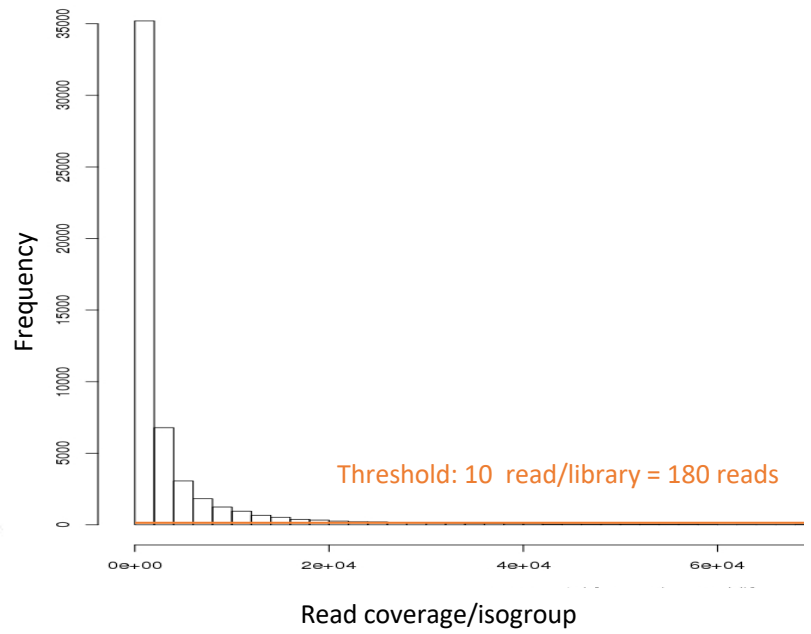


Supplementary File 2

A Size distribution of assembled isogroups before size/coverage filtering process

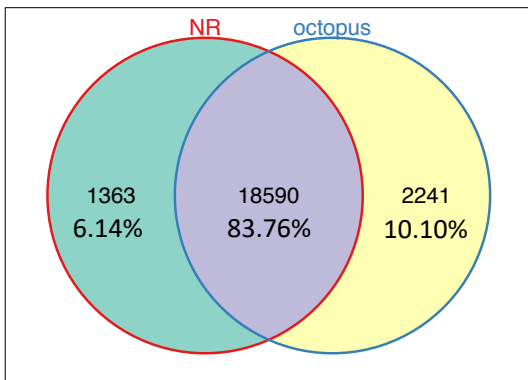


B Read coverage distribution of assembled isogroups before size/coverage filtering process



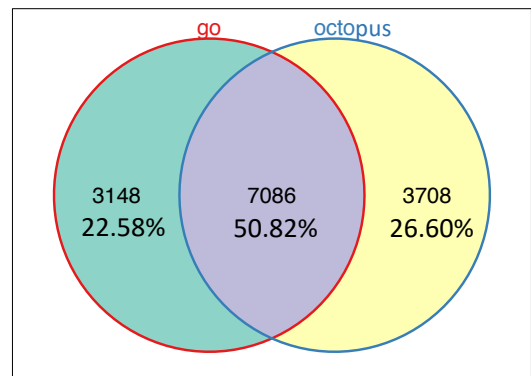
C Comparison between two BLAST procedures

Number of isogroups with BLAST results
(22 194/53719 = 41.3% of total transcripts)



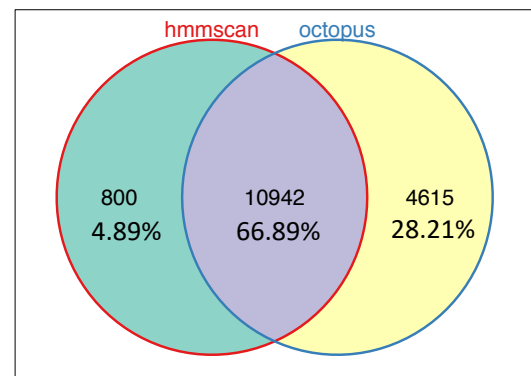
NR = BLAST result against nr
octopus = BLAST result against the *Octopus bimaculoides* transcriptome

Number of isogroups with GO annotation
(13 942 = 62.8% of BLASTed transcripts)



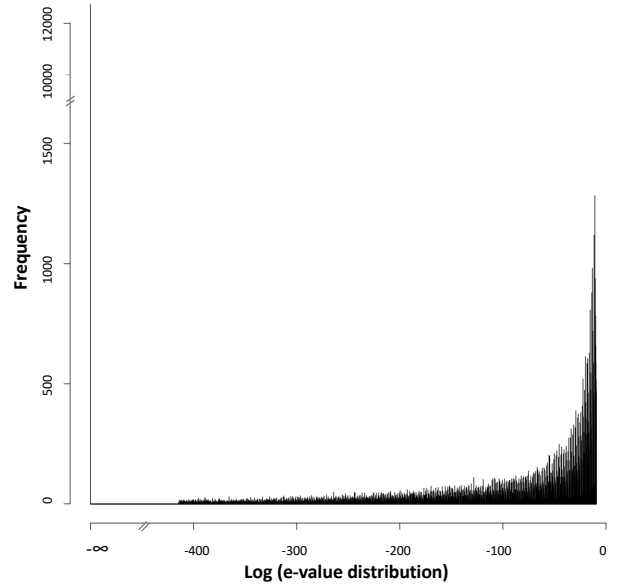
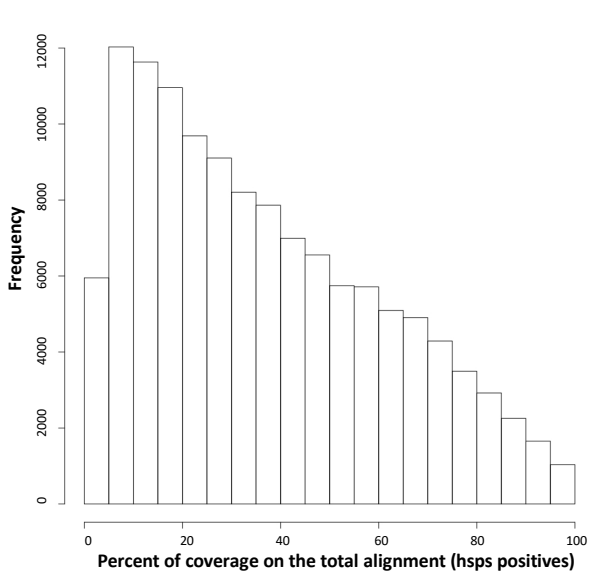
go = GO annotation via Blast2go from nr BLAST
octopus = GO annotation from the *Octopus bimaculoides* annotation

Number of isogroups with PFAM annotation
(16357 = 73.7% of BLASTed transcripts)



hmmscan = prediction of PFAM motifs on predicted ORFs
octopus = PFAM terms from the *Octopus bimaculoides* annotation

D Sequence similarity and e-value distribution from the BLASTs against nr and against the *Octopus* transcriptome



E Species distribution from the BLAST against nr

