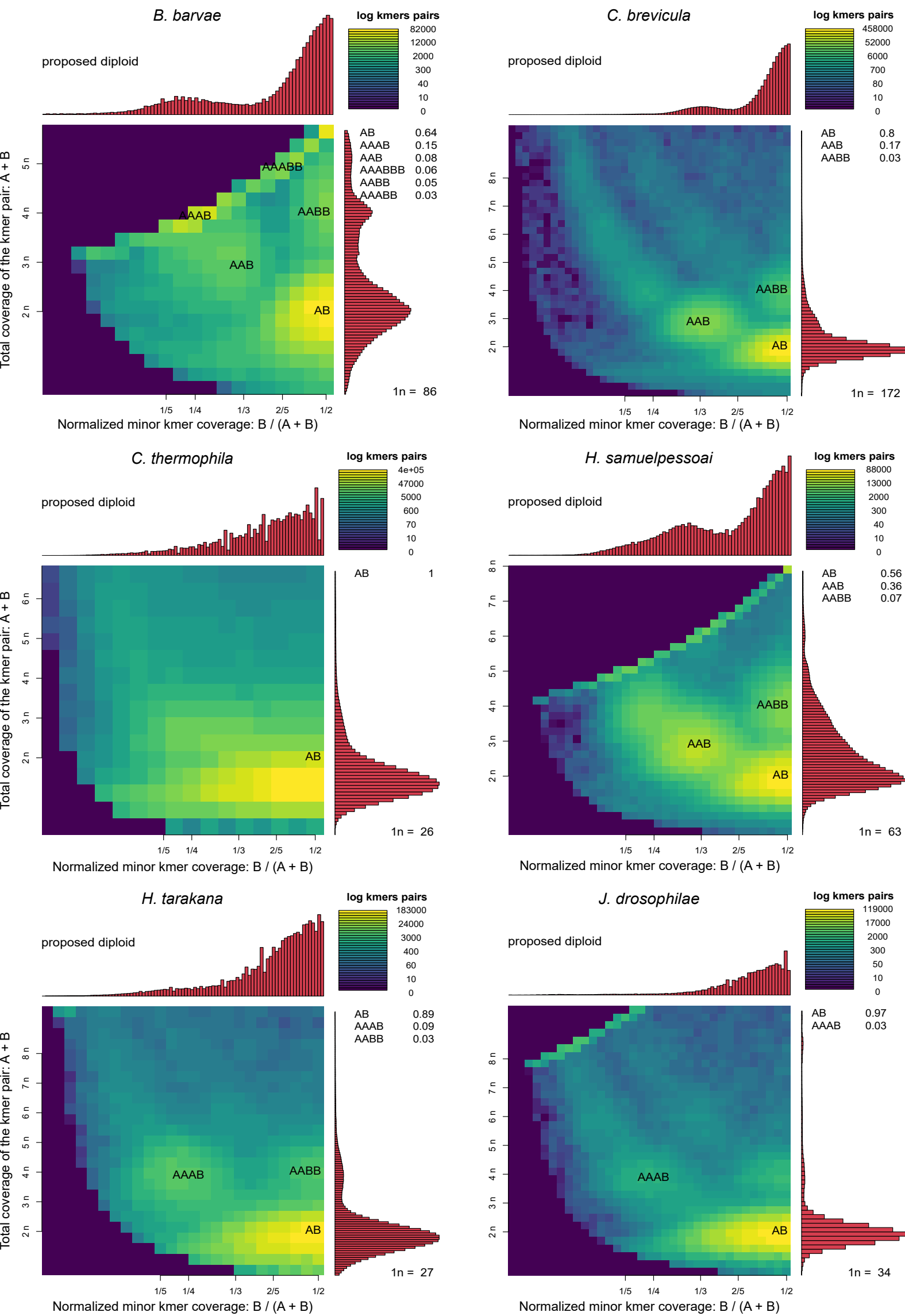
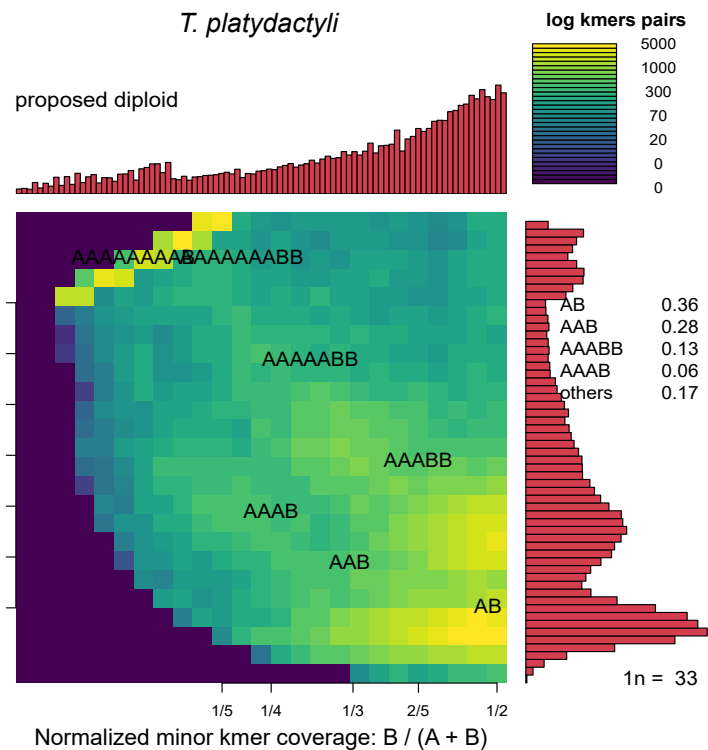
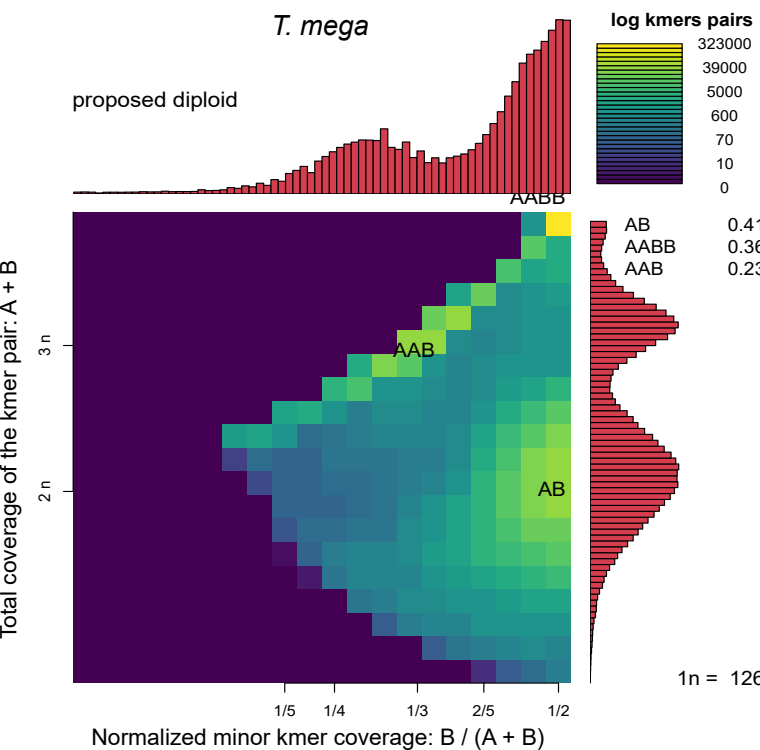
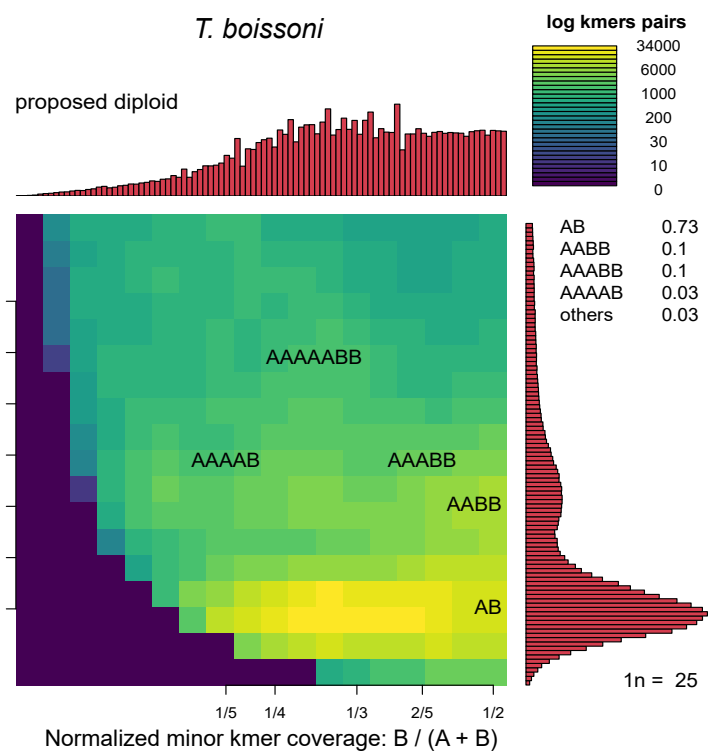
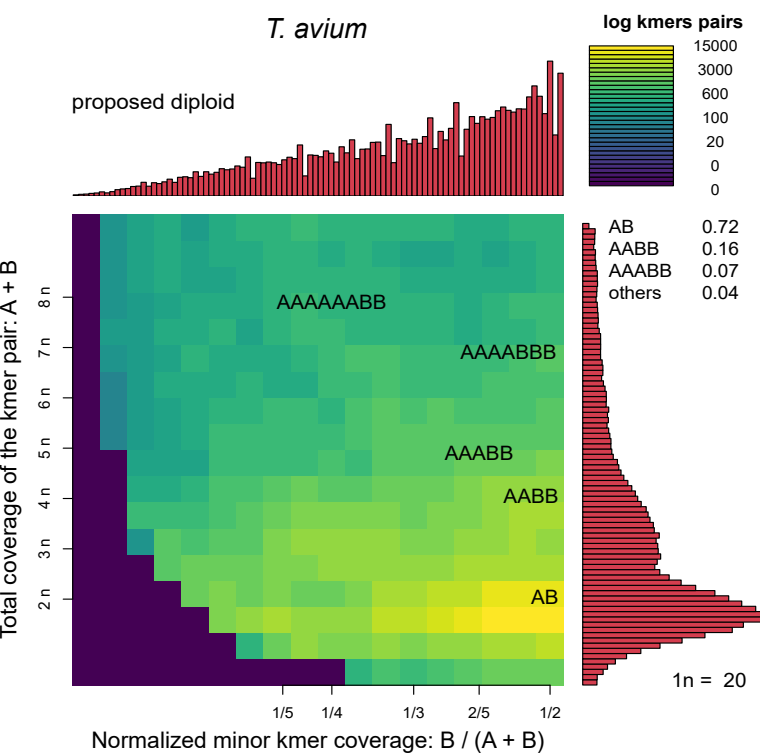
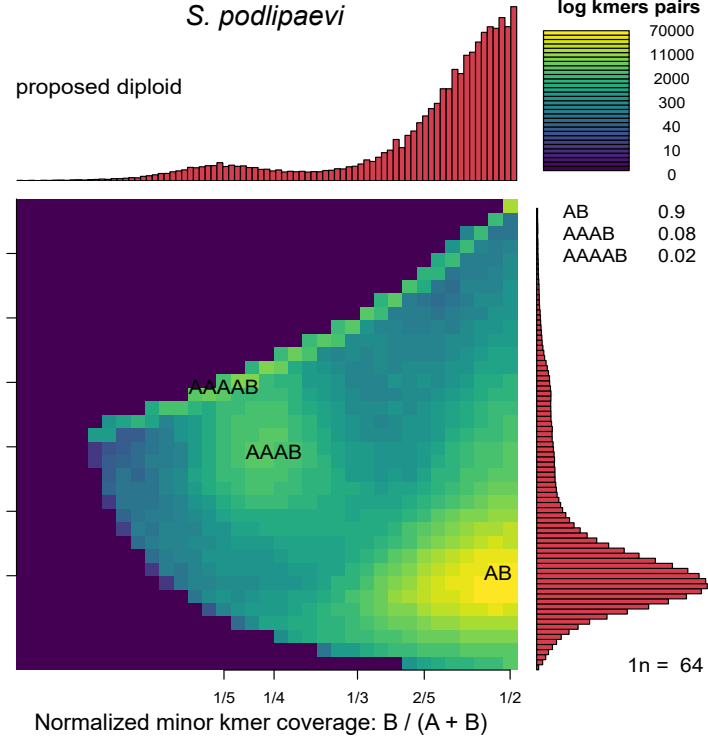
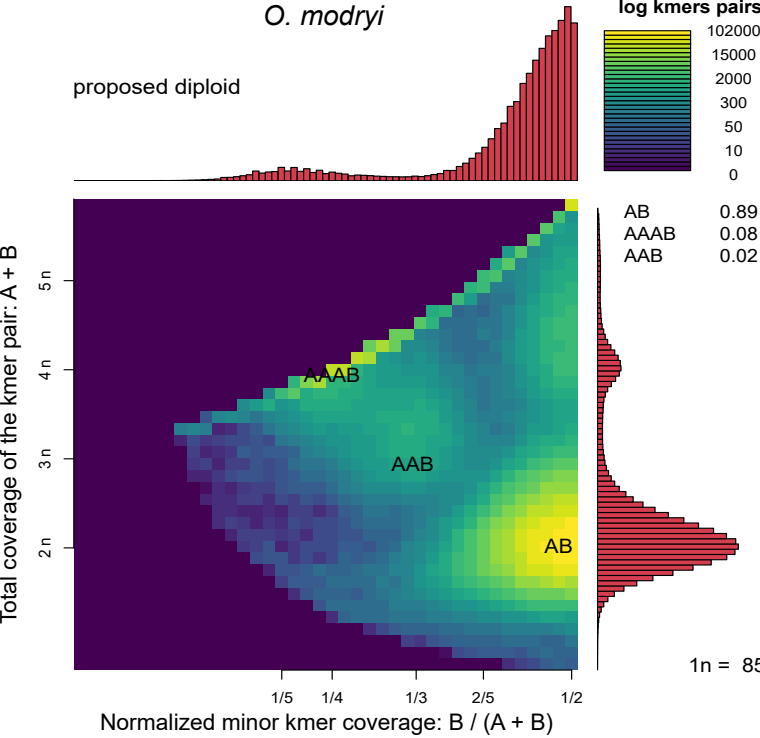
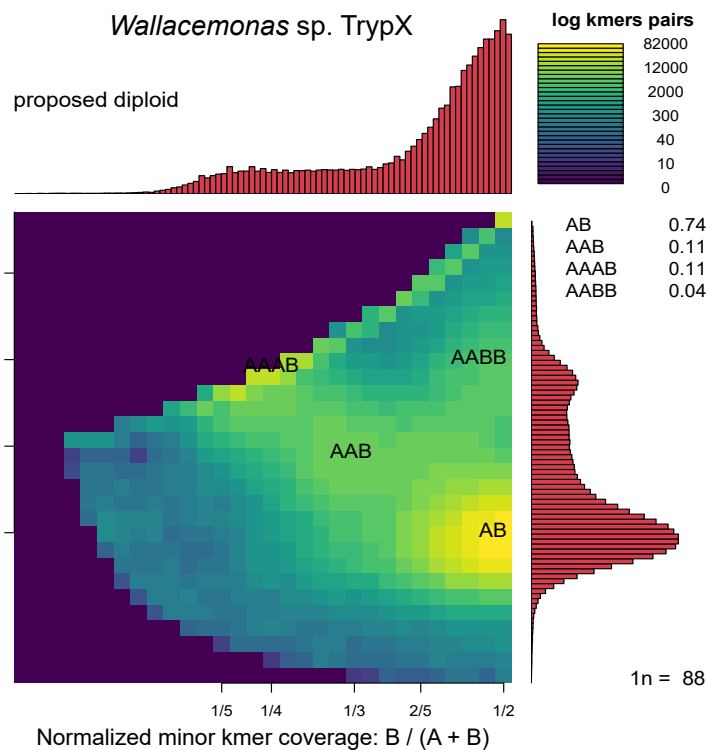
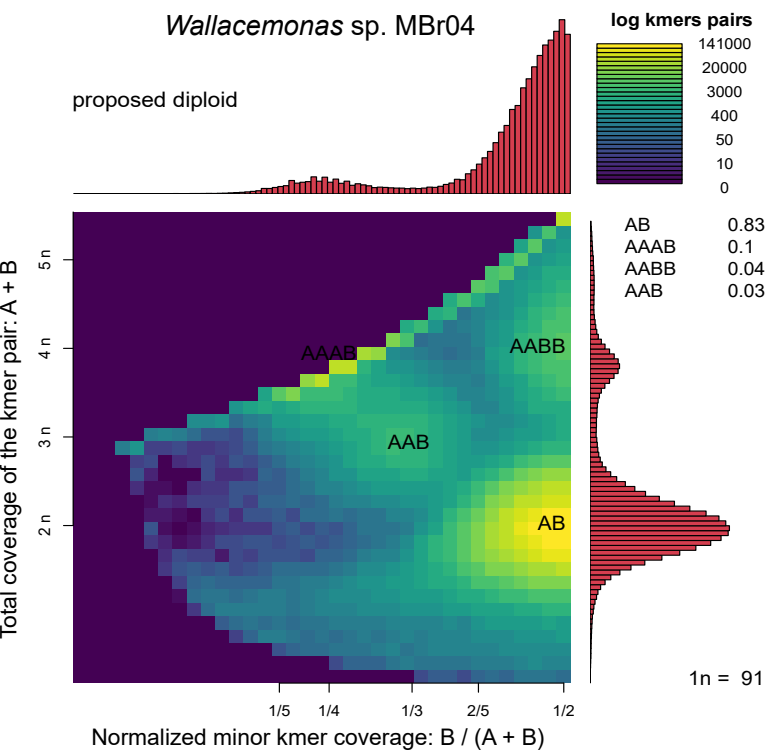
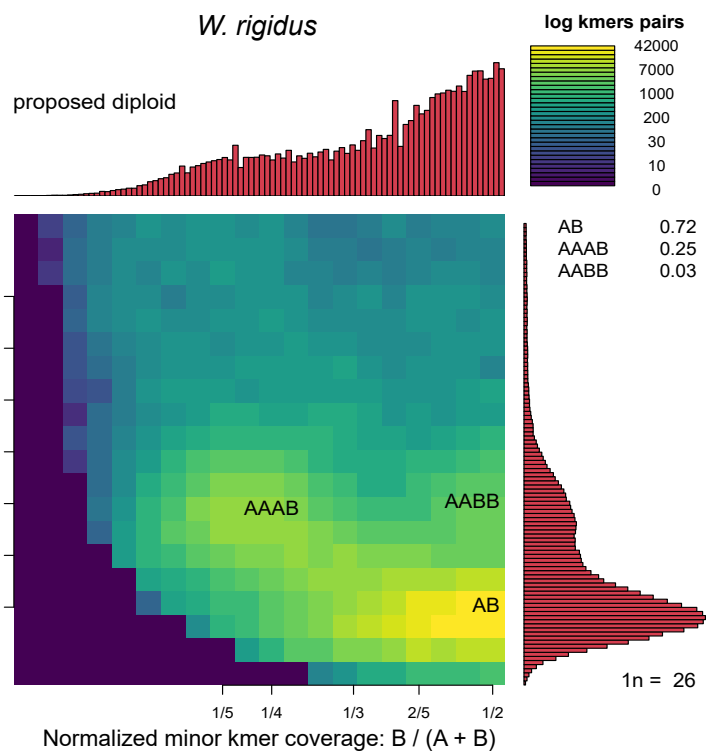
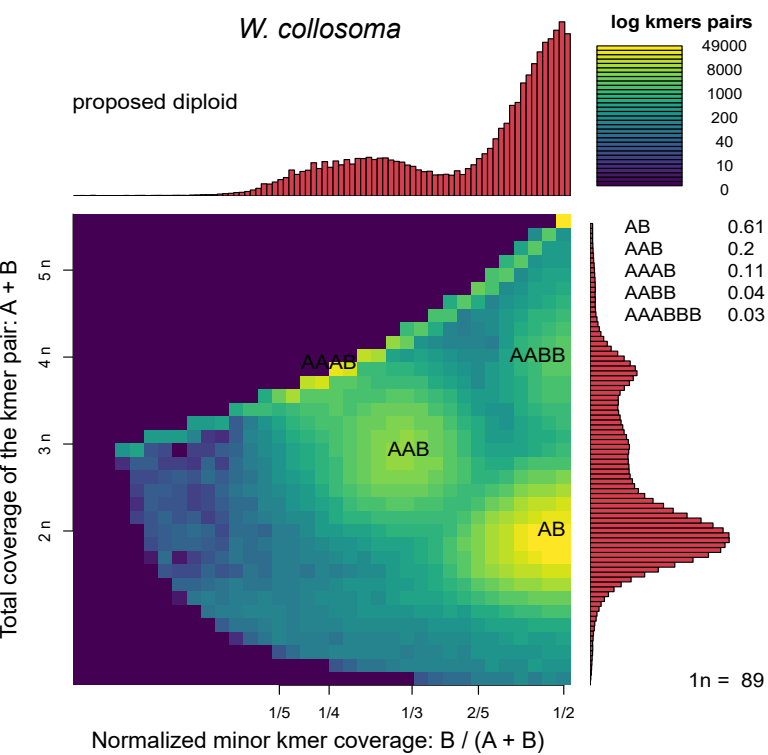
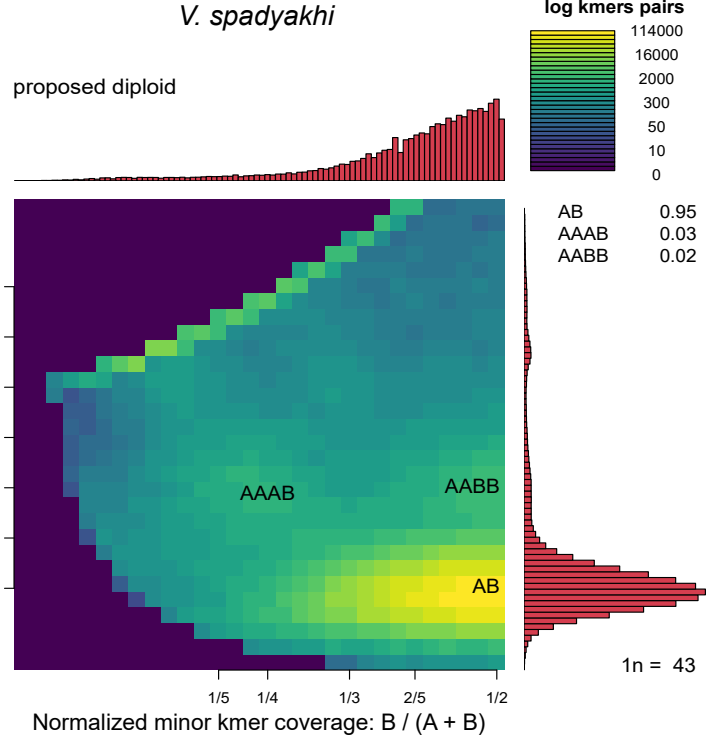
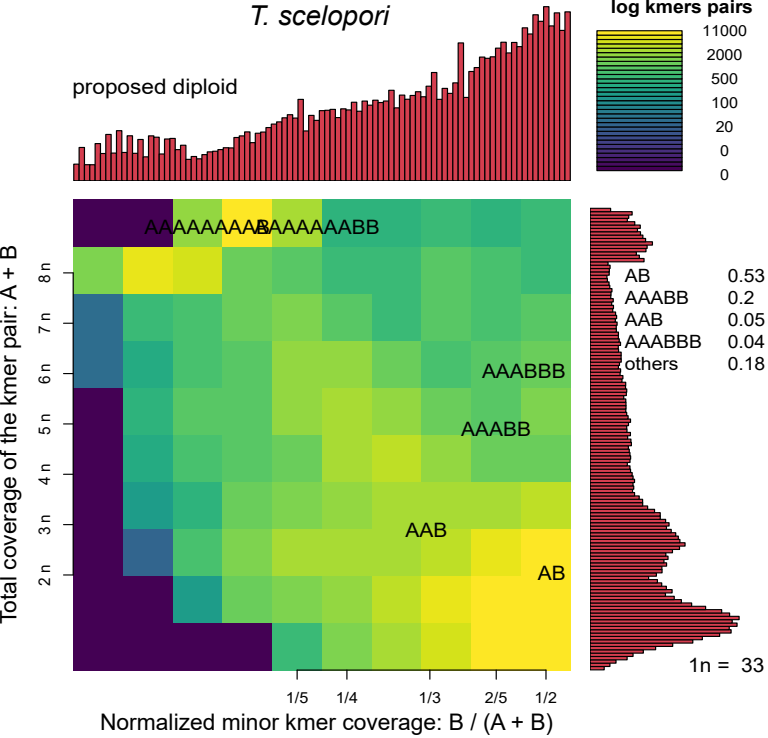


Additional file 7. Genome ploidy estimation based on the analysis of heterozygous k -mer pairs. Total coverage of k -mer pairs and normalized minor k -mer coverage are plotted on Y and X axes, respectively.



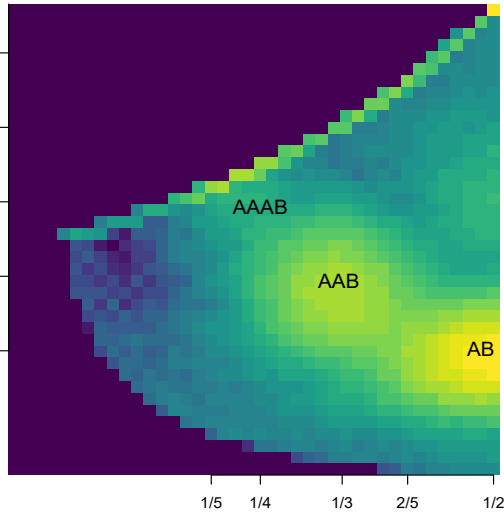




Wallacemonas sp. Wsd

proposed diploid

Total coverage of the kmer pair: A + B



AB	0.6
AAAB	0.35
AAAB	0.02
others	0.02

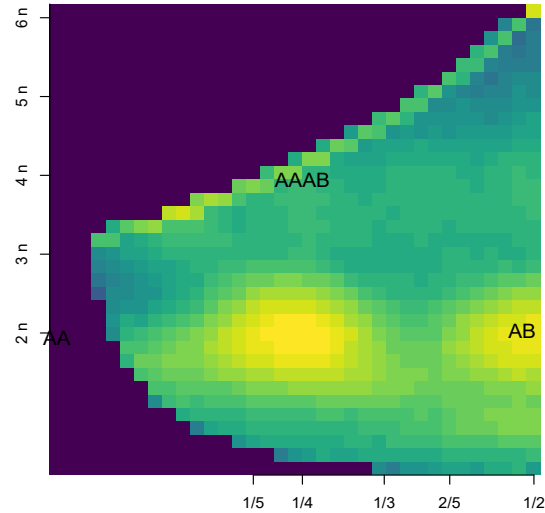
1n = 76

Normalized minor kmer coverage: B / (A + B)

Wallacemonas sp. 195SL

proposed diploid

Total coverage of the kmer pair: A + B



AA	0.7
AB	0.26
AAAB	0.03

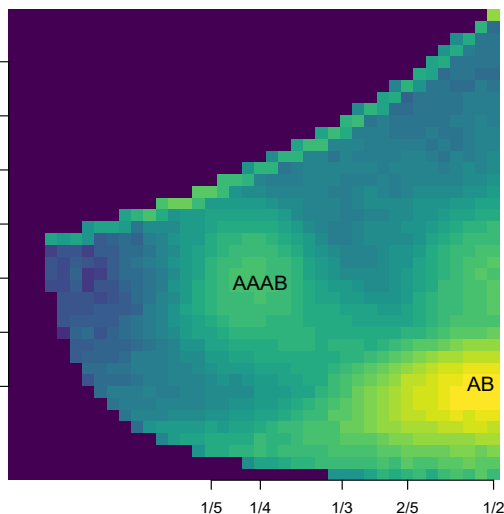
1n = 81

Normalized minor kmer coverage: B / (A + B)

Z. costaricensis

proposed diploid

Total coverage of the kmer pair: A + B



AB	0.95
AAAB	0.05

1n = 56

Normalized minor kmer coverage: B / (A + B)