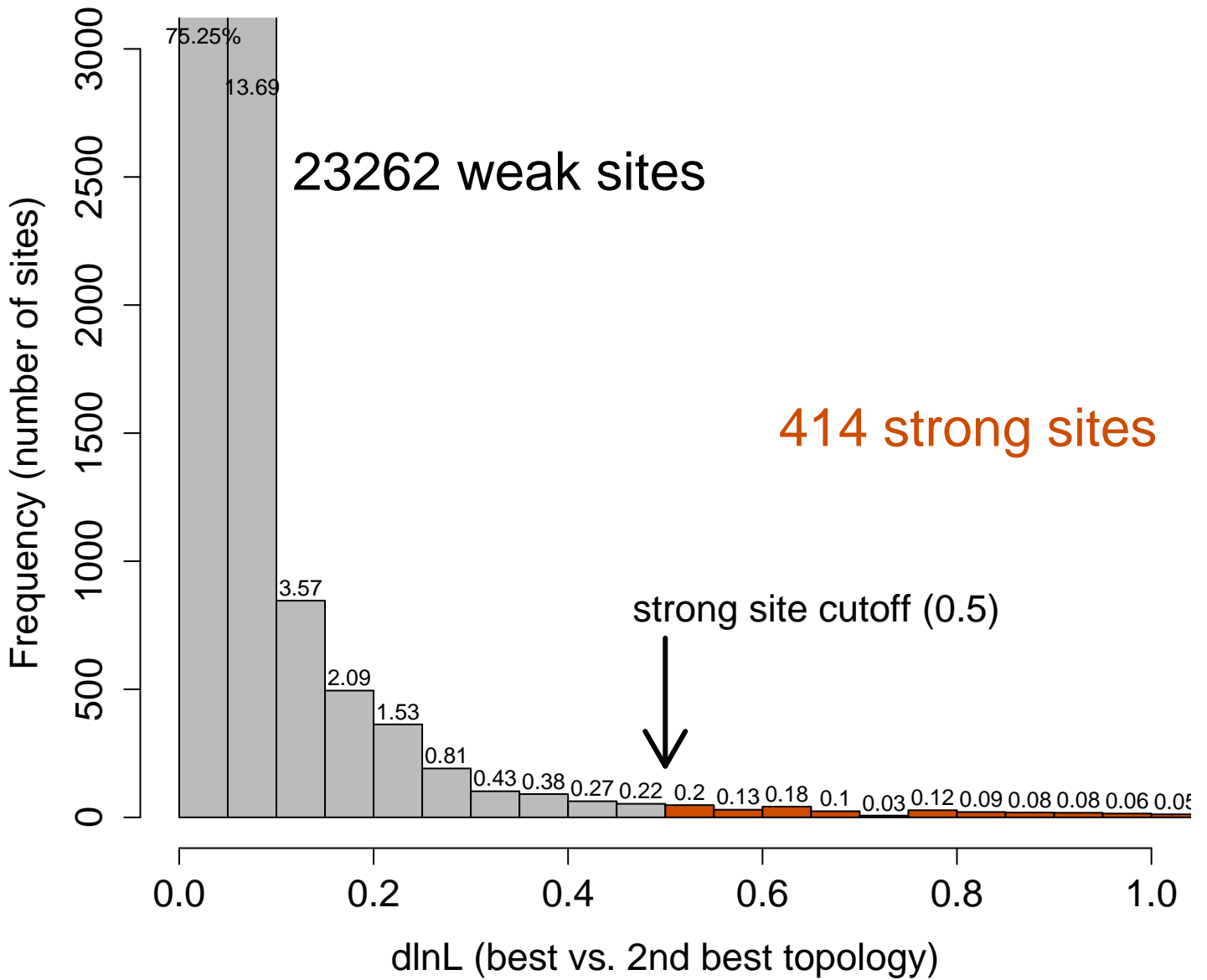


Histogram of sitewise lnL from Whelan D16 Opisthokont dataset

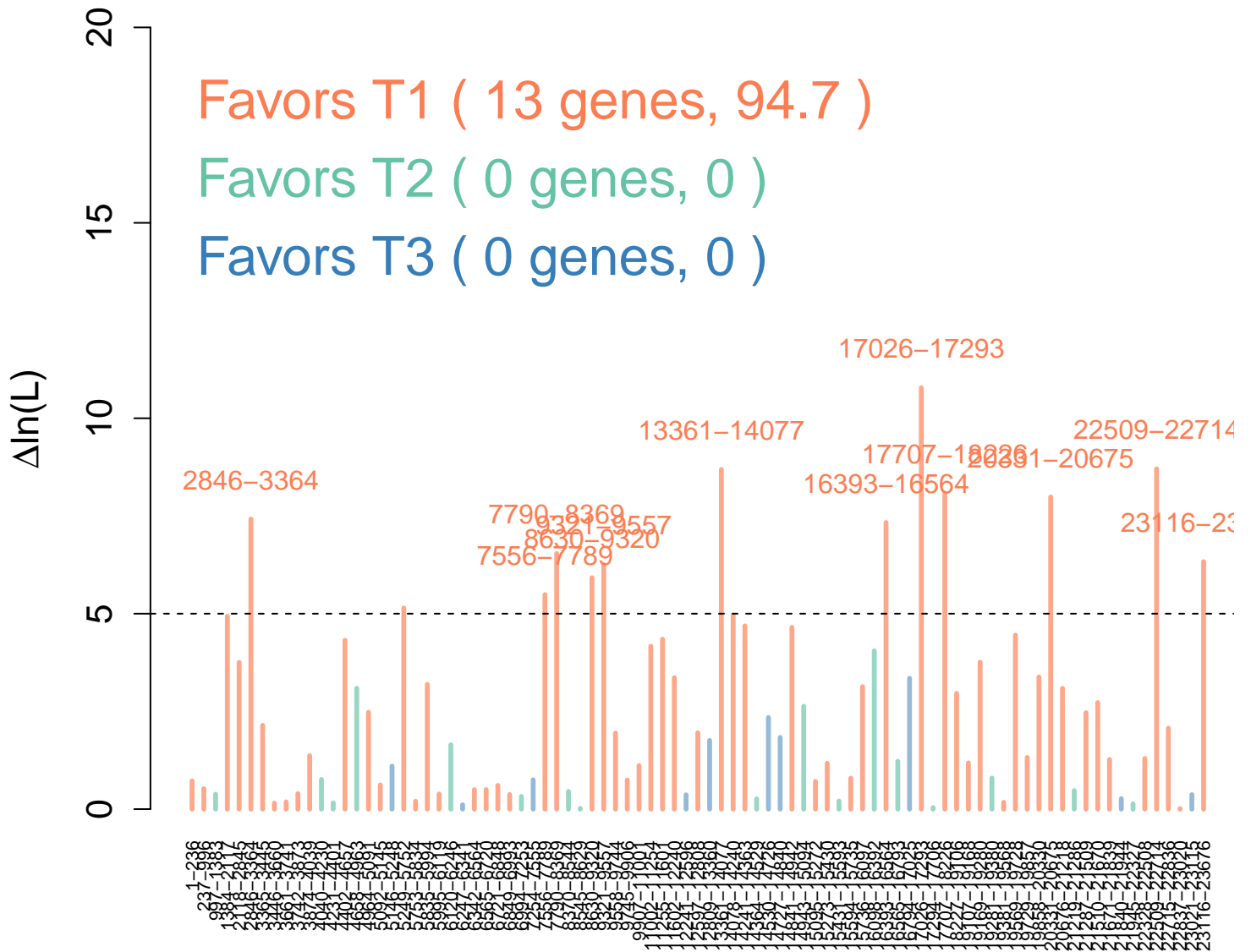


# RxML\_perSiteLLs.Whelan\_D16\_Opisthokonta\_gene\_1k.tab

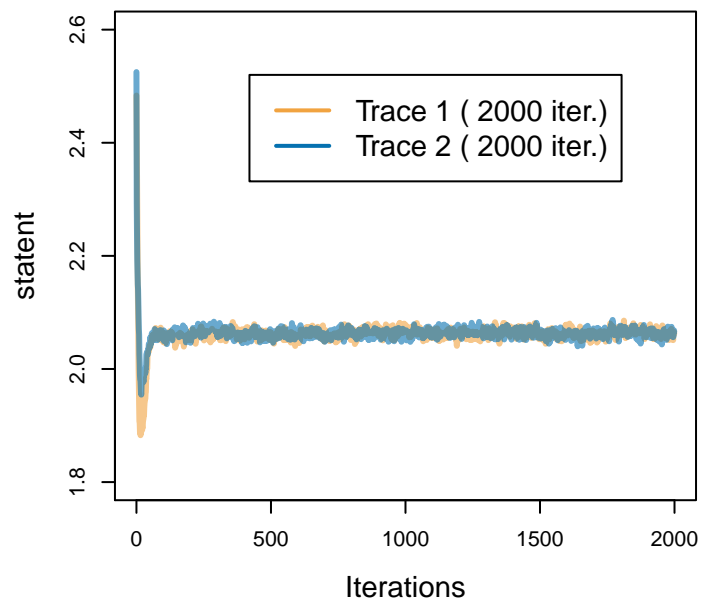
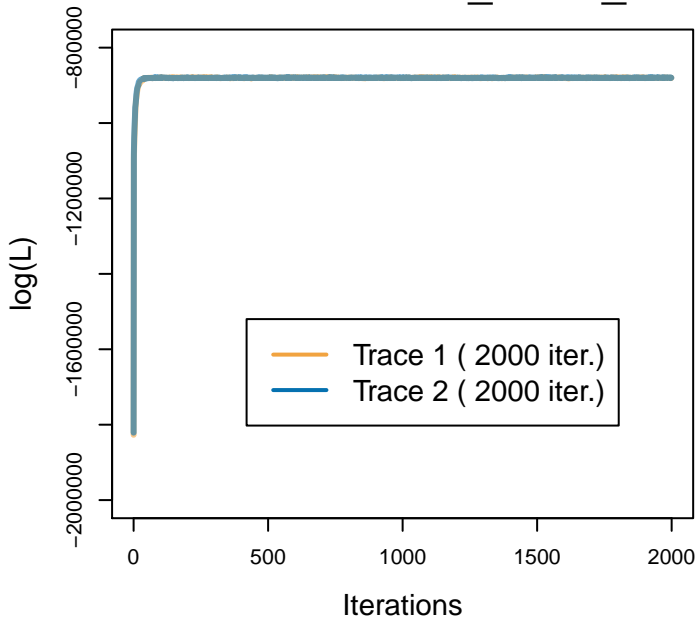
Favors T1 ( 13 genes, 94.7 )

Favors T2 ( 0 genes, 0 )

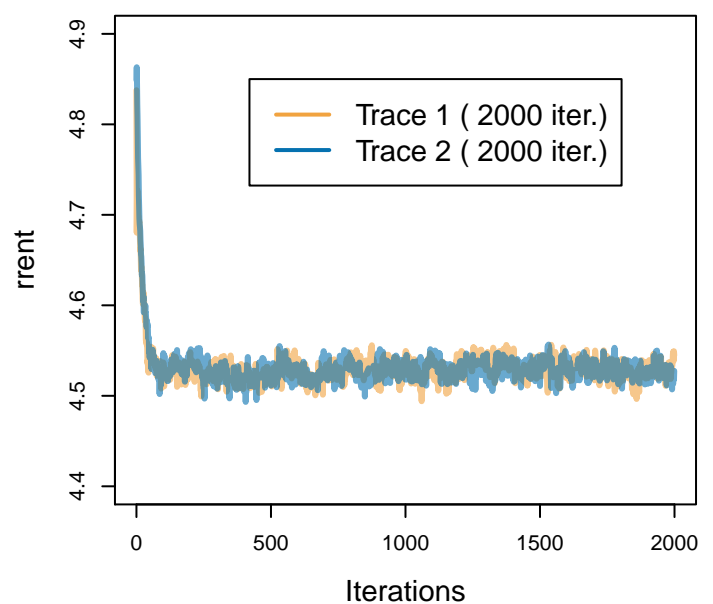
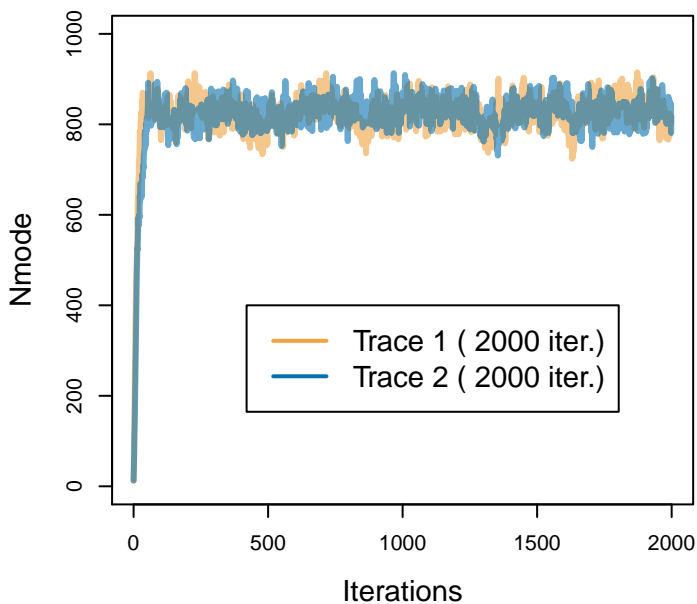
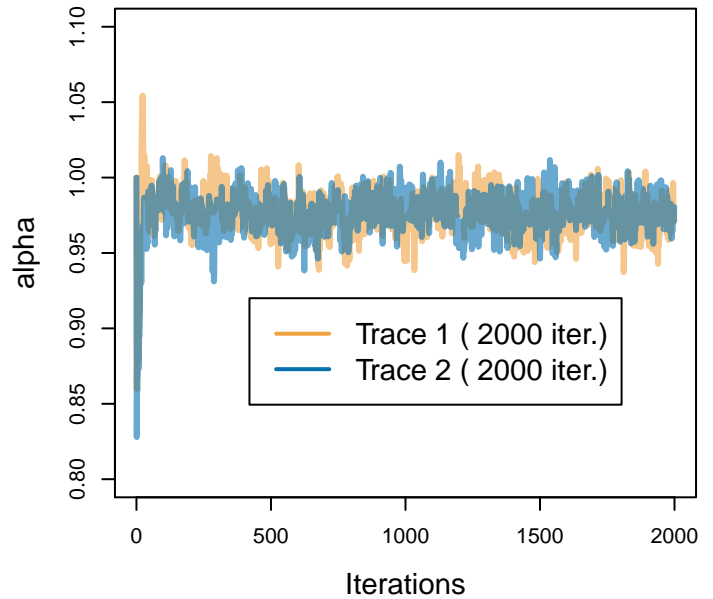
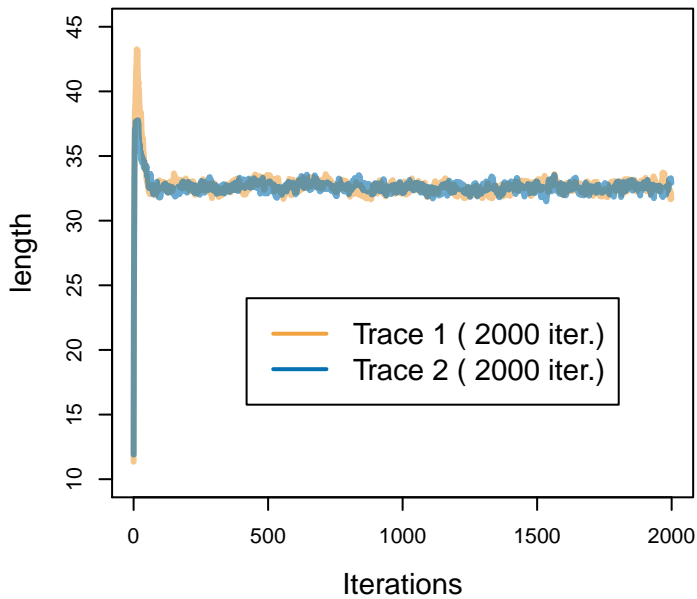
Favors T3 ( 0 genes, 0 )



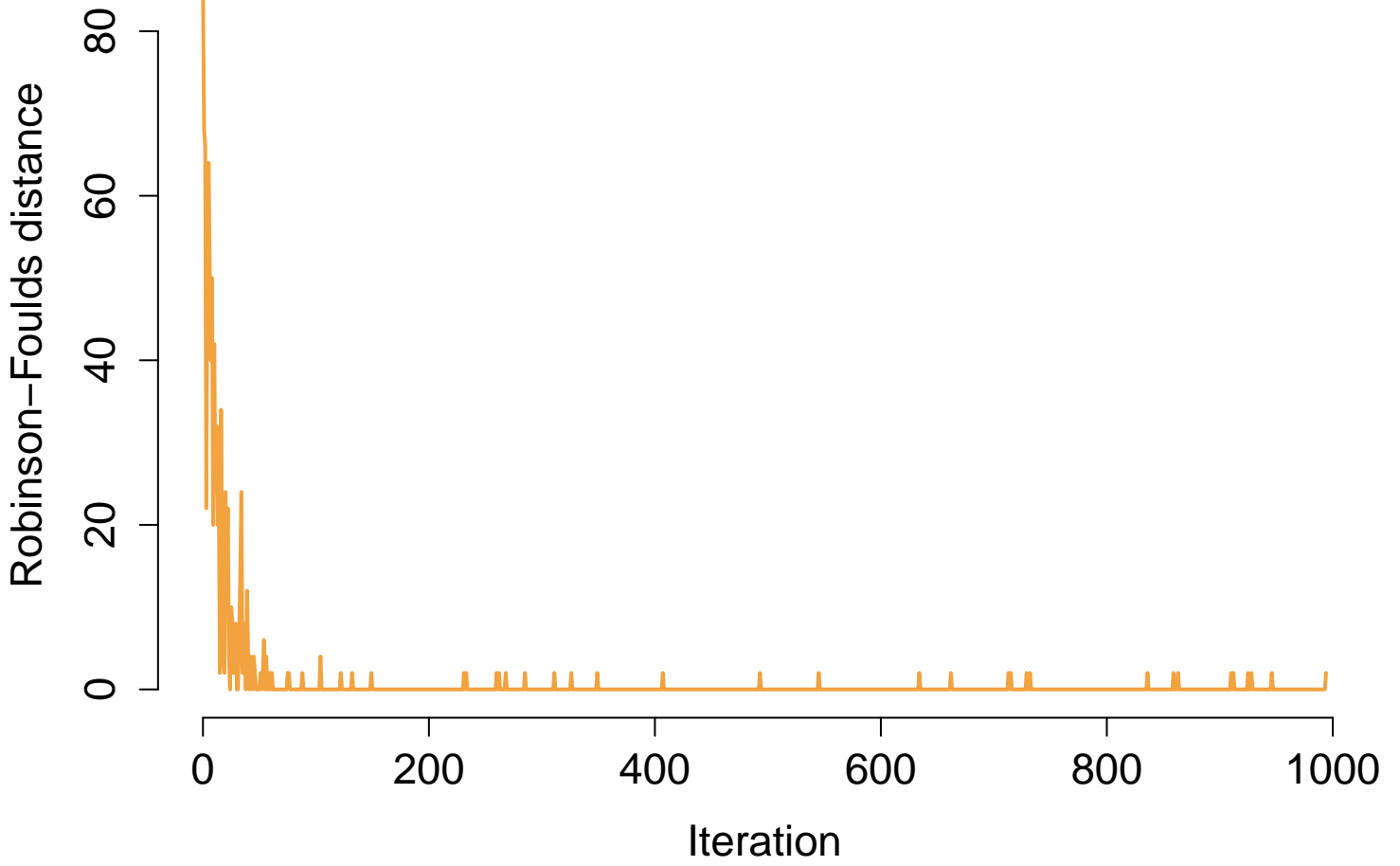
# Weak dataset d16\_chain\_01.trace + d16\_chain\_02.trace



## Final iterations = 2000



**Weak D16 dataset Chain 1**



**Weak D16 dataset Chain 2**

