

Supplementary figures

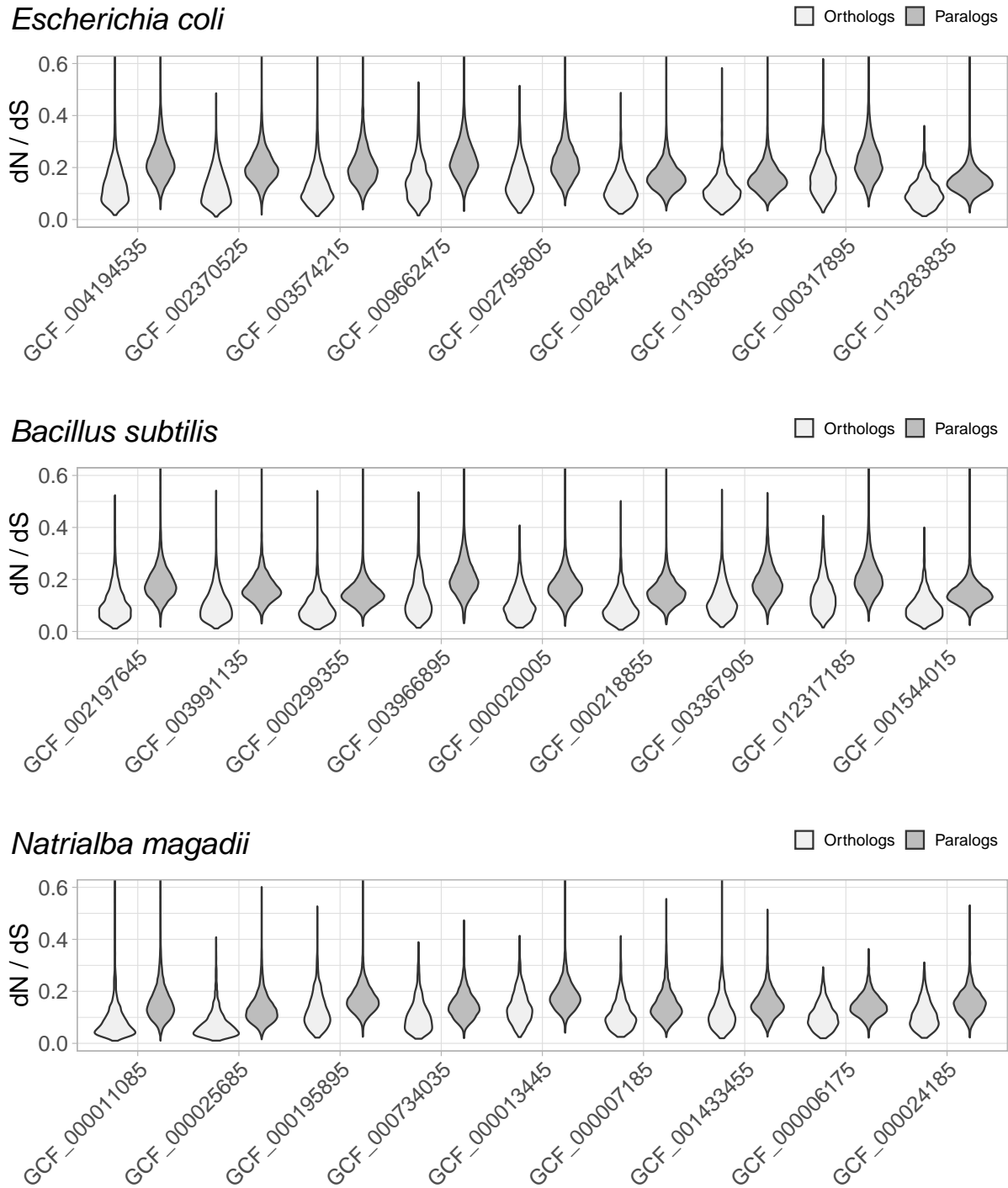


Figure S1: Full dN/dS results obtained with InParanoid as a working definition of orthology.

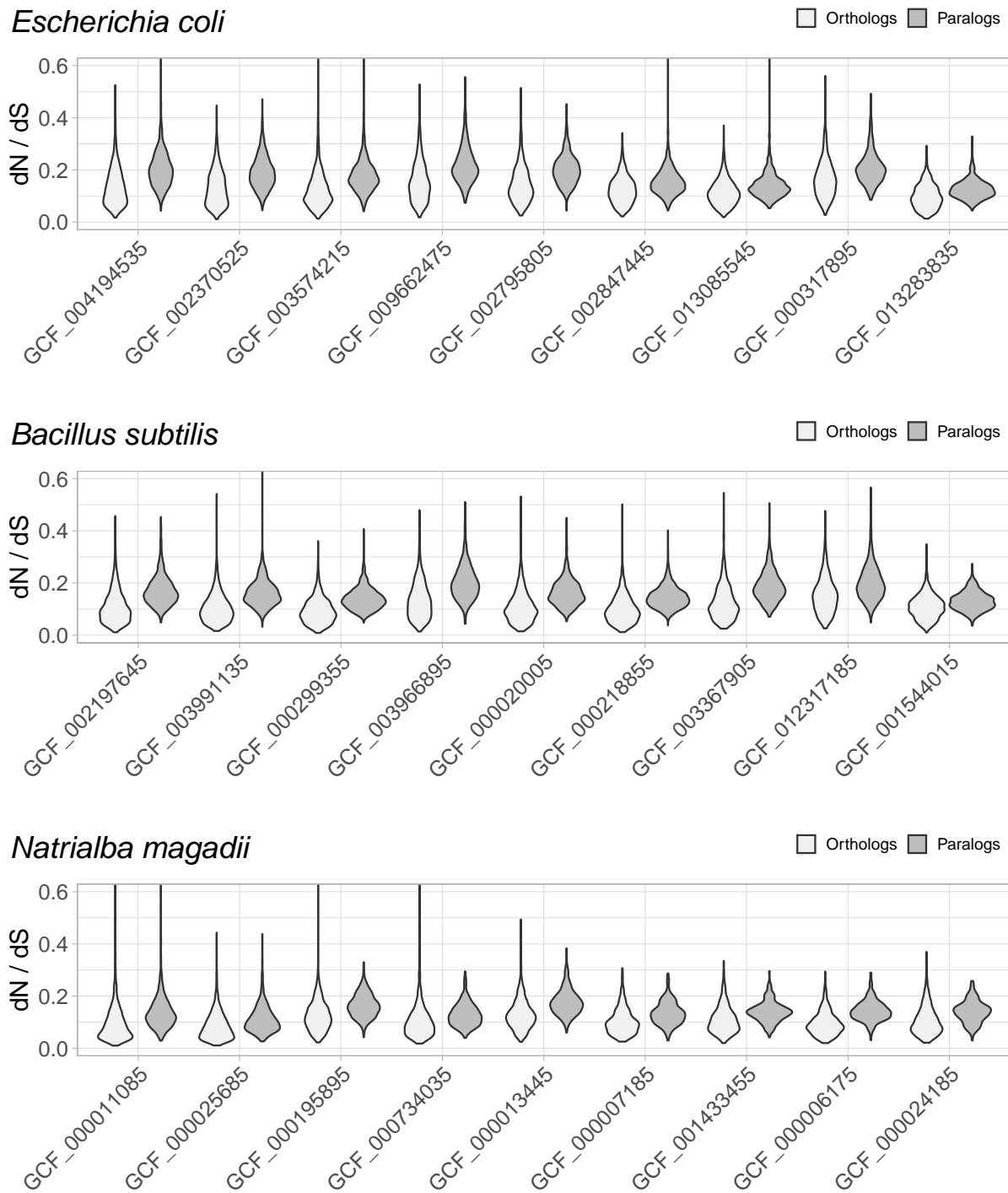


Figure S2: Full dN/dS results obtained with the Orthologous Matrix (OMA) working definition of orthology.

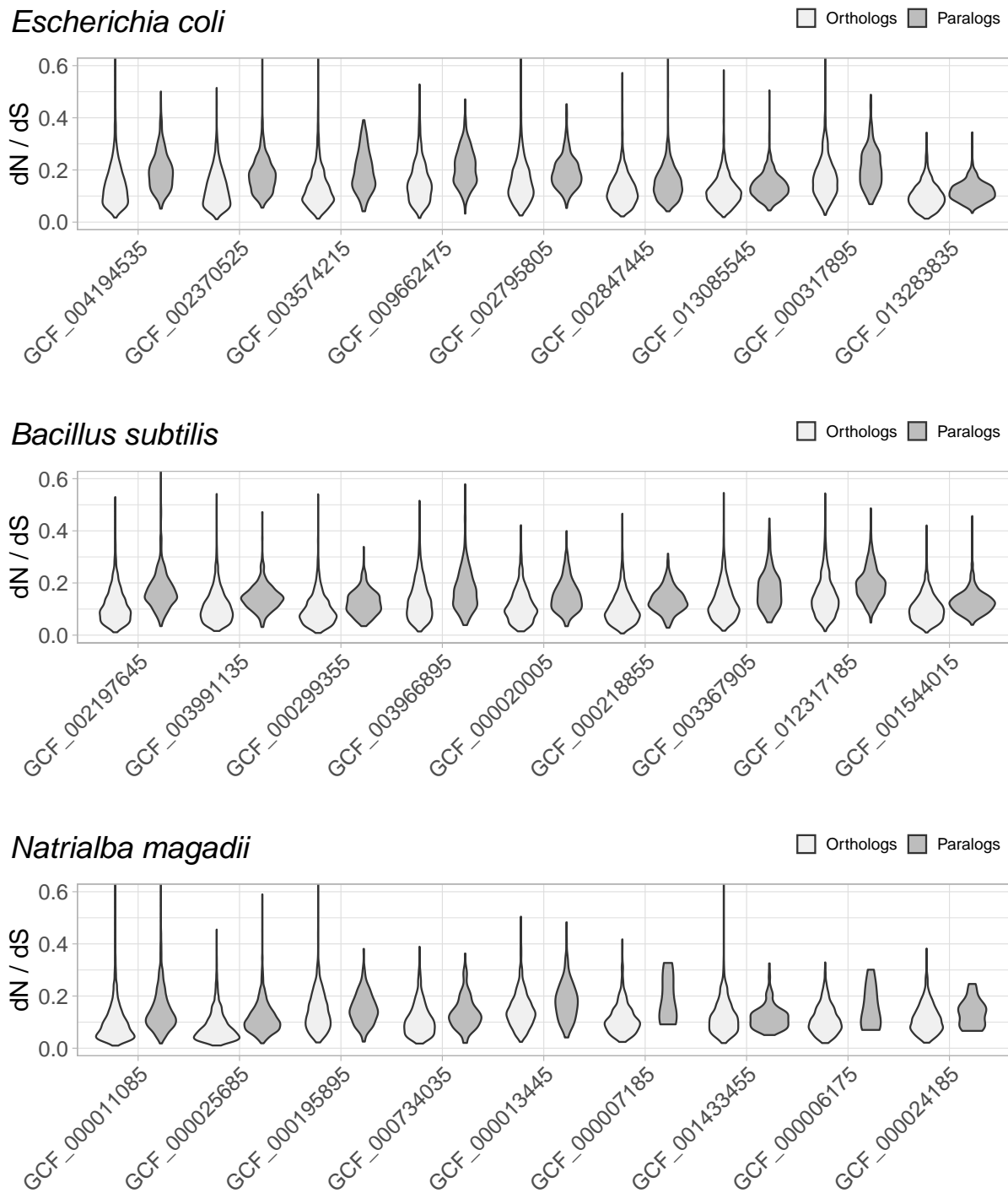


Figure S3: Full dN/dS results obtained with the OrthoFinder working definition of orthology.

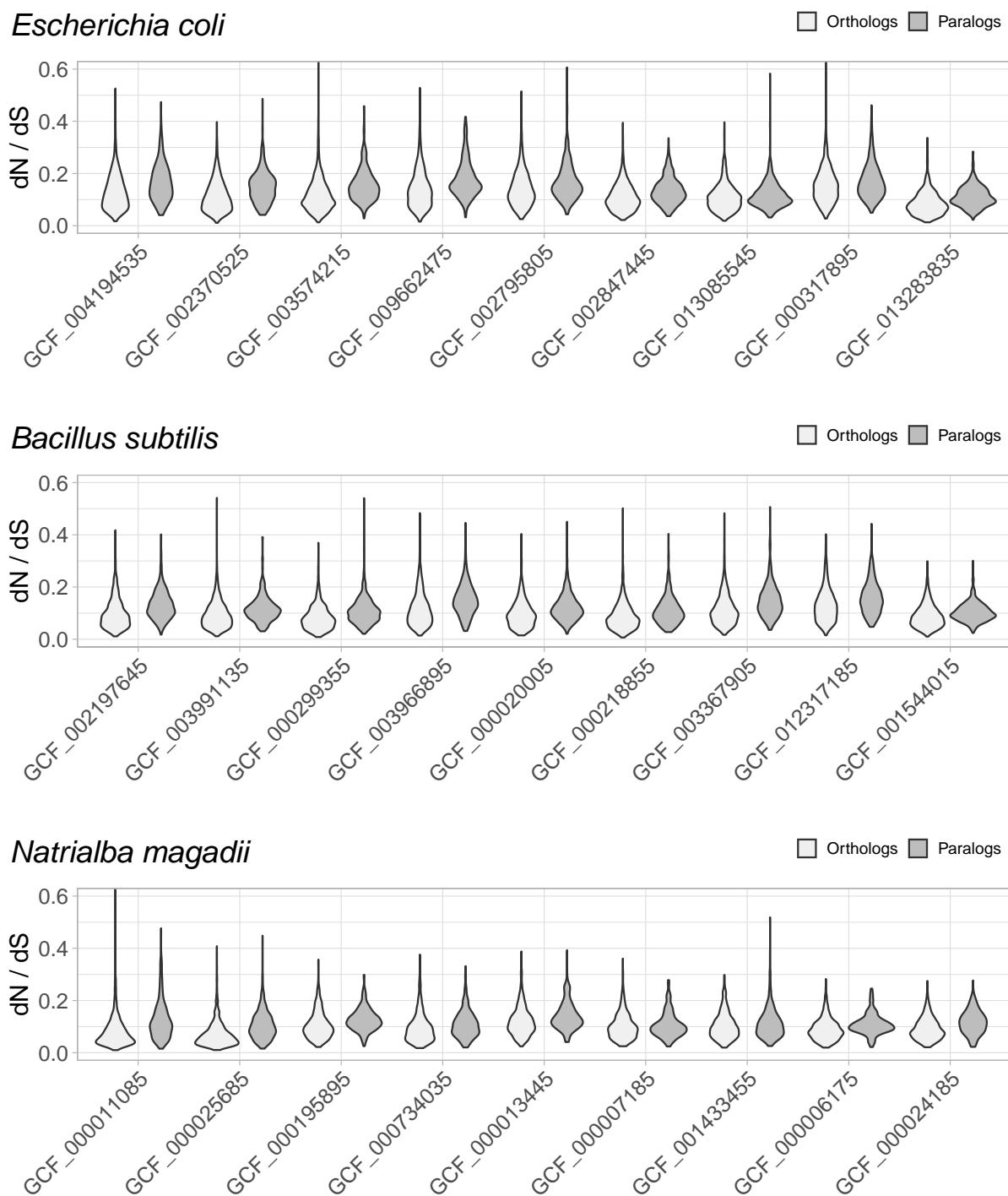


Figure S4: Full dN/dS results obtained with the ProteinOrtho working definition of orthology.

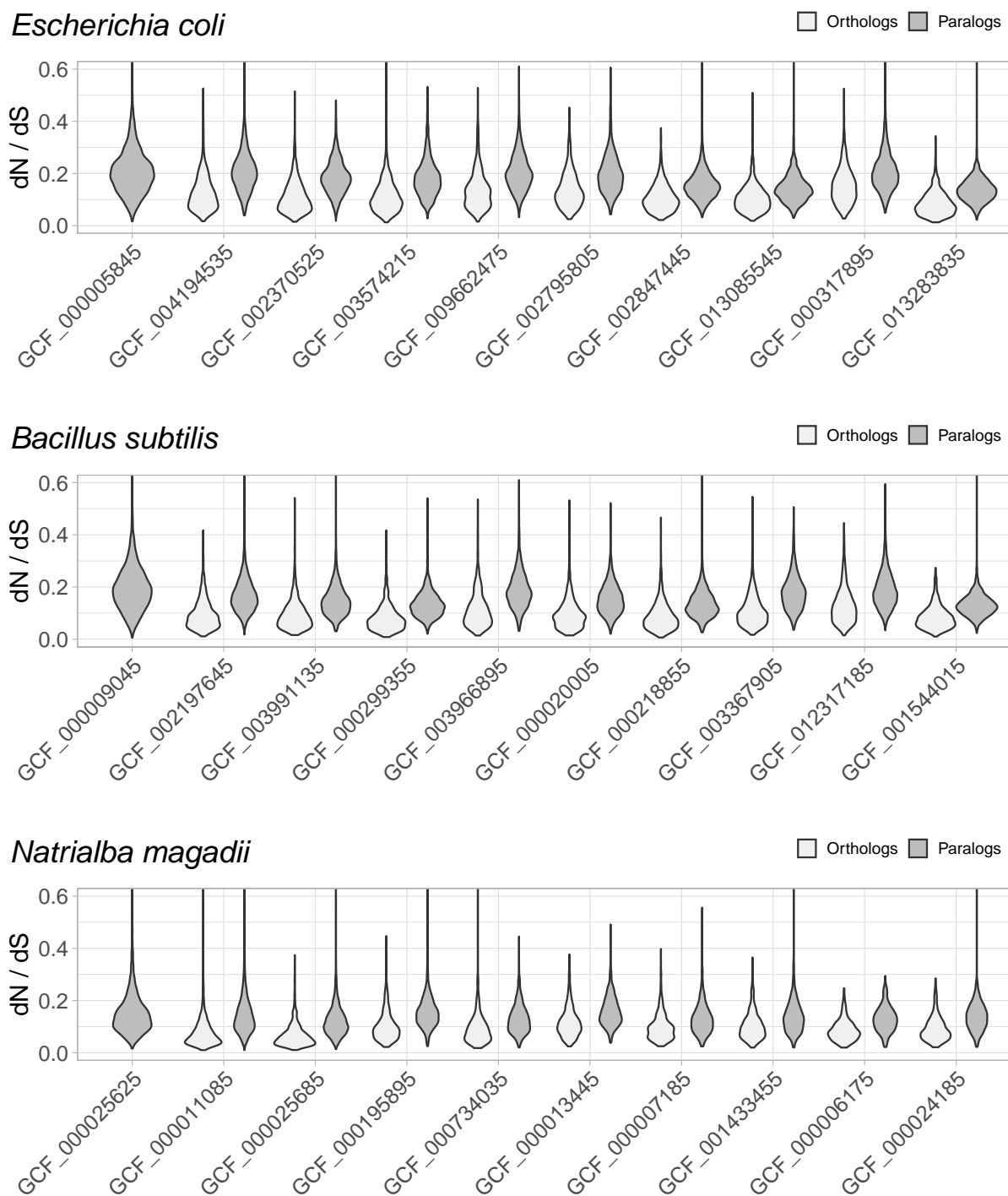


Figure S5: Full dN/dS results obtained with alignments covering at least 80% of both proteins.

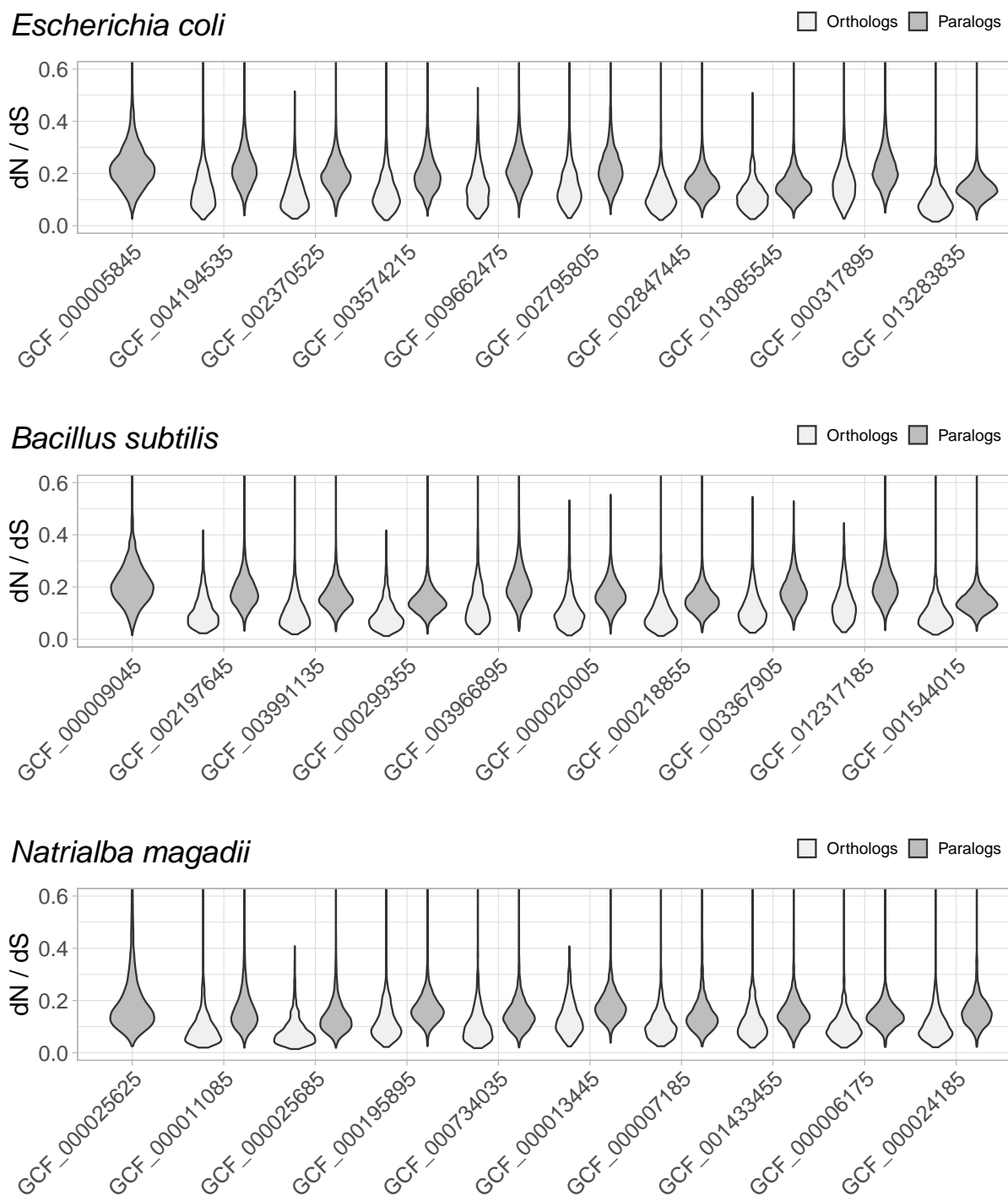


Figure S6: Full dN/dS results obtained with proteins no more that 70% identical.

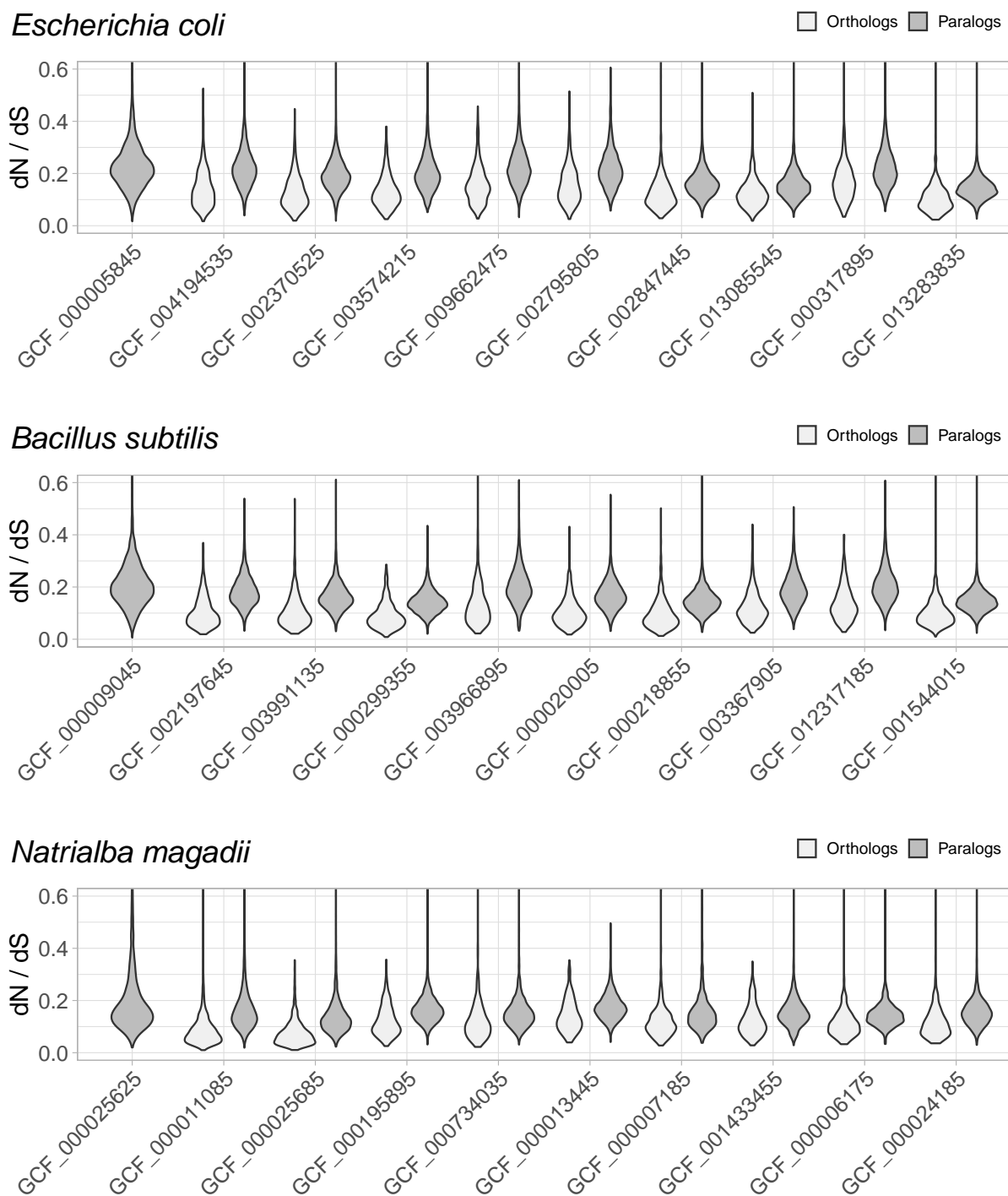
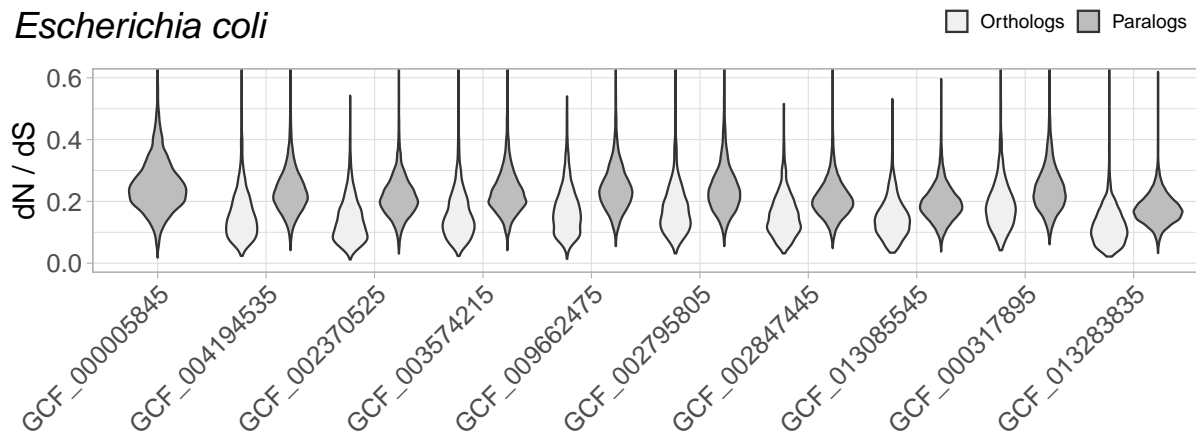
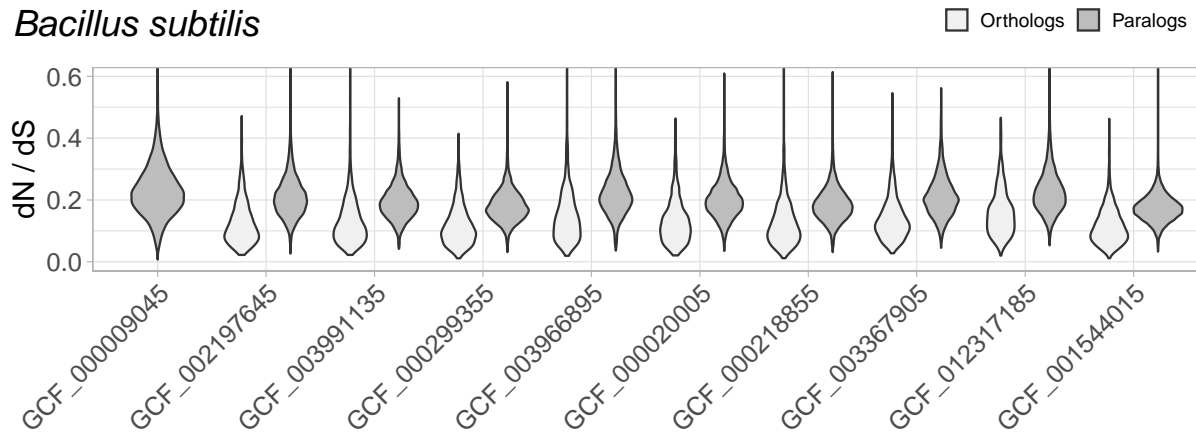


Figure S7: Full dN/dS results obtained with proteins within usual codon usage.

Escherichia coli



Bacillus subtilis



Natrialba magadii

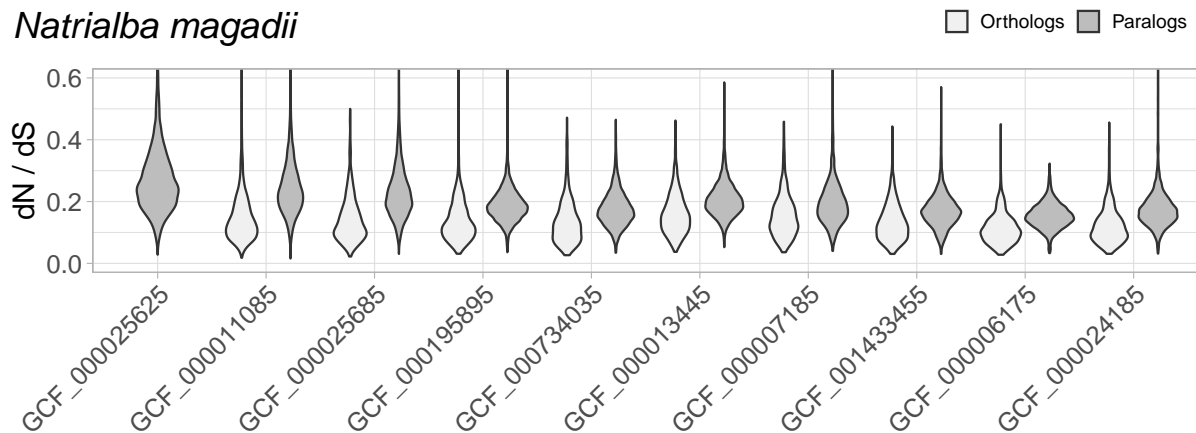


Figure S8: Full dN/dS results using Muse and Gaut's estimate of background codon frequencies.