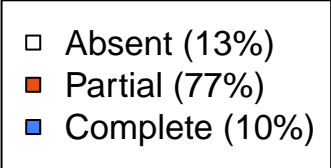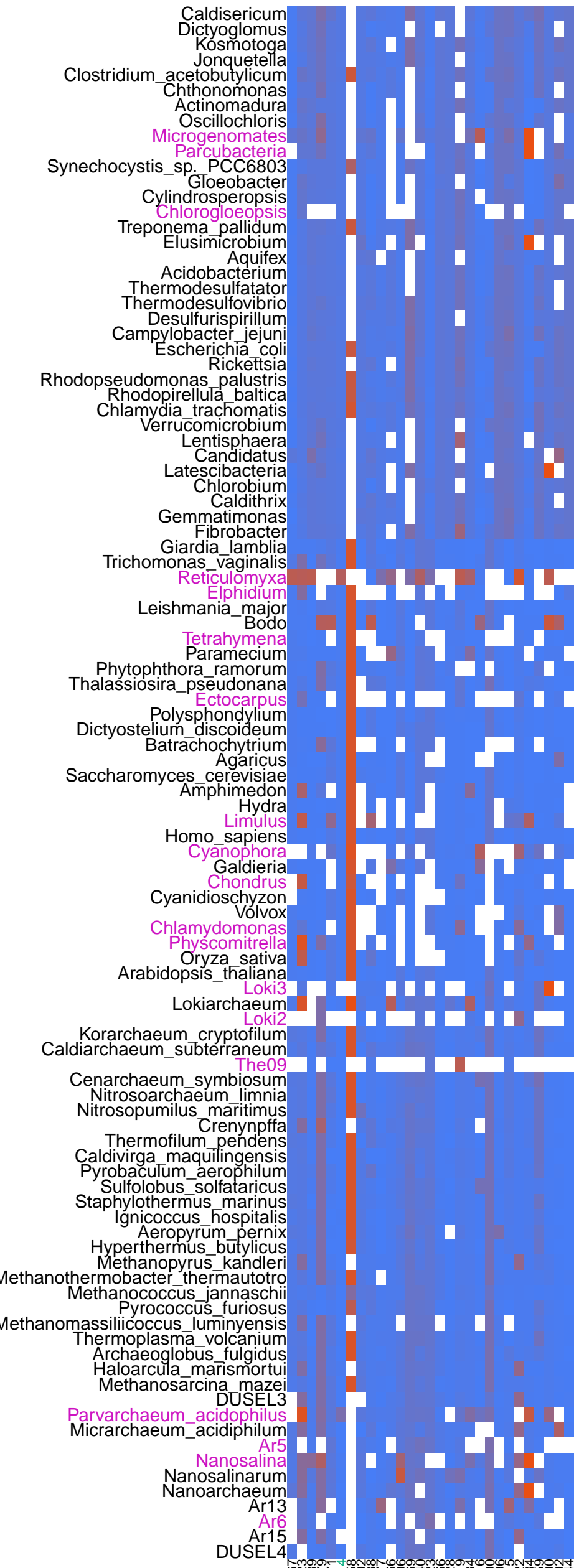n taxa = 102   betts2018_alignment_102_matrix.

Gene partitions (n = 29)

Absent (13%)
Partial (77%)
Complete (10%)