



ParaC Pan-genome 1. Maximum Likelihood radial phylogeny derived from 61,451 non-repetitive core SNPs within the Para C Lineage plus Birkenhead. Internal branch numbers are indicated in black (BR_XXX) while internal nodes for major sub-lineages are indicated by cyan rounded rectangles. Other numbers refer to gain or loss of genomic islands (42 for GI042, etc.) or plasmids (P1xx) in the accessory genome coloured according to the key (see ParaC Pan-genome 4).