



Figure S1. Genetic diversity of koala *Chlamydia pecorum* polymorphic membrane proteins (*pmp*). Mid-point rooted approximate maximum likelihood tree, constructed using GTR+G nucleotide substitution model using FastTree 2.1.11 as implemented in Geneious Prime, from the koala strains *pmp* genes alignment. Support values (using 1,000 resamples) are displayed on the nodes, and scale represent the rate of nucleotide substitution per site. Each koala strain is denoted by colours outlined in the legend, and locus tag in Mc/Marbar_2018 is displayed next to the corresponding clade.