

Figure S1. *Elizabethkingia miricola* species specific phylogenomic analysis. Maximum likelihood midpoint-rooted phylogeny was reconstructed using 135,087 biallelic, orthologous single-nucleotide polymorphisms identified among the 18 genomes. Correctly speciated *E. miricola* strains are coloured orange, incorrectly speciated *Elizabethkingia meningoseptica* coloured blue and *Elizabethkingia anophelis* genomes generated in this study coloured black. Bootstrap support <0.80 is shown.

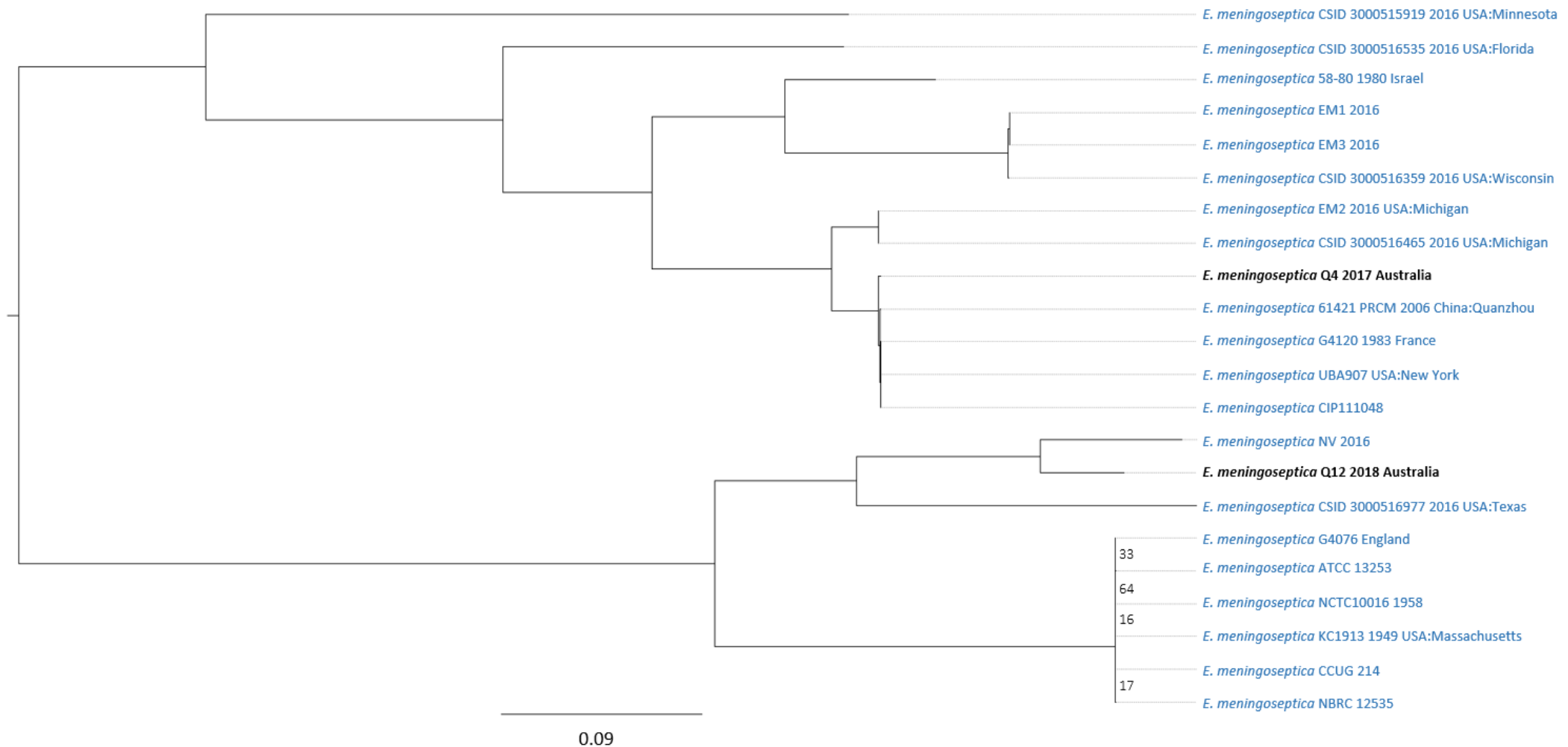


Figure S2. *Elizabethkingia meningoseptica* species specific phylogenomic analysis. Maximum likelihood midpoint-rooted phylogeny was reconstructed using 61,500 biallelic, orthologous single-nucleotide polymorphisms identified among the 22 genomes. Reference *Elizabethkingia meningoseptica* strains are coloured blue with strains generated in this study coloured black. Bootstrap support <0.8 is shown.

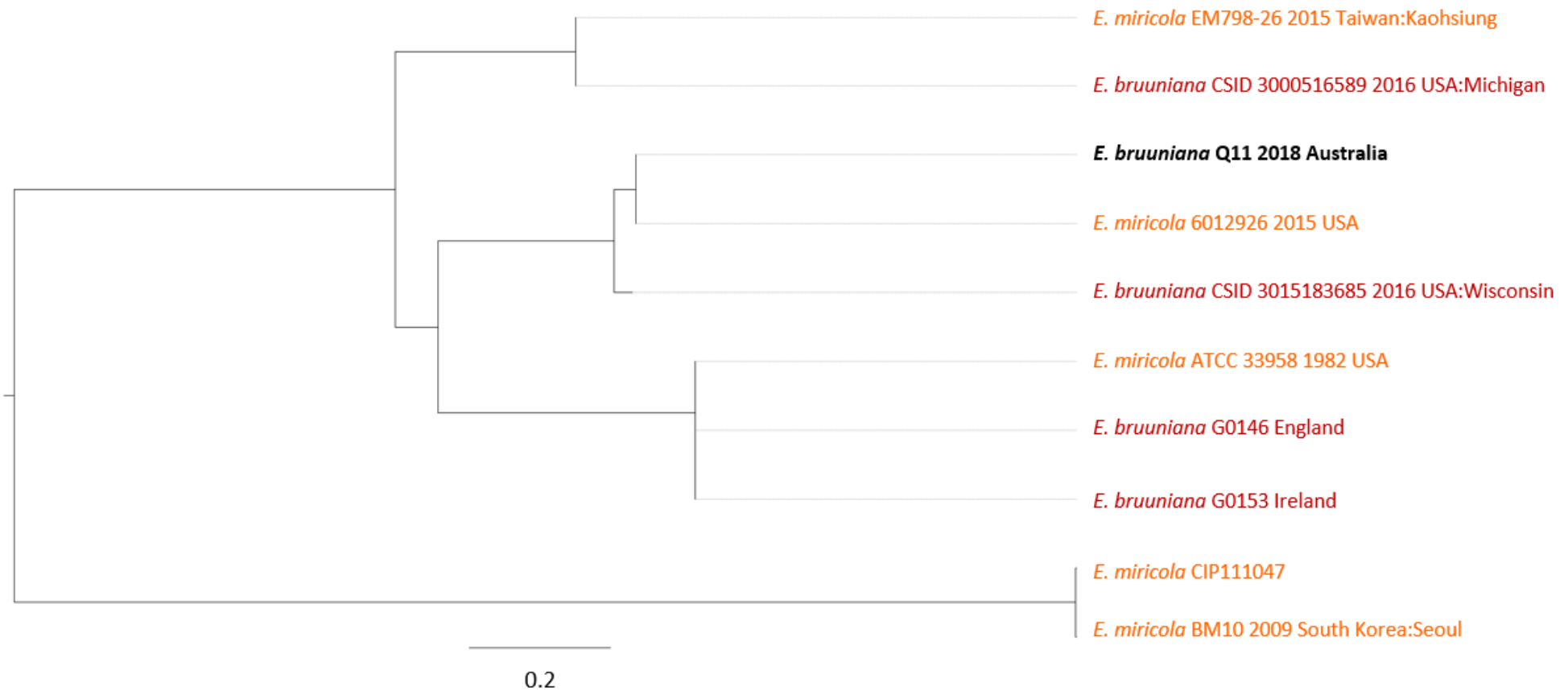


Figure S3. *Elizabethkingia bruuniana* species specific phylogenomic analysis. Maximum likelihood midpoint-rooted phylogeny was reconstructed using 82,680 biallelic, orthologous single-nucleotide polymorphisms identified among the 10 genomes. Correctly speciated *Elizabethkingia bruuniana* strains are coloured red, incorrectly speciated *Elizabethkingia miricola* strains are coloured orange and genomes generated in this study are coloured black. Bootstrap support is 100 for all branches.