

Figure S3a: *Gammaproteobacteria: Gilliamella apicola*

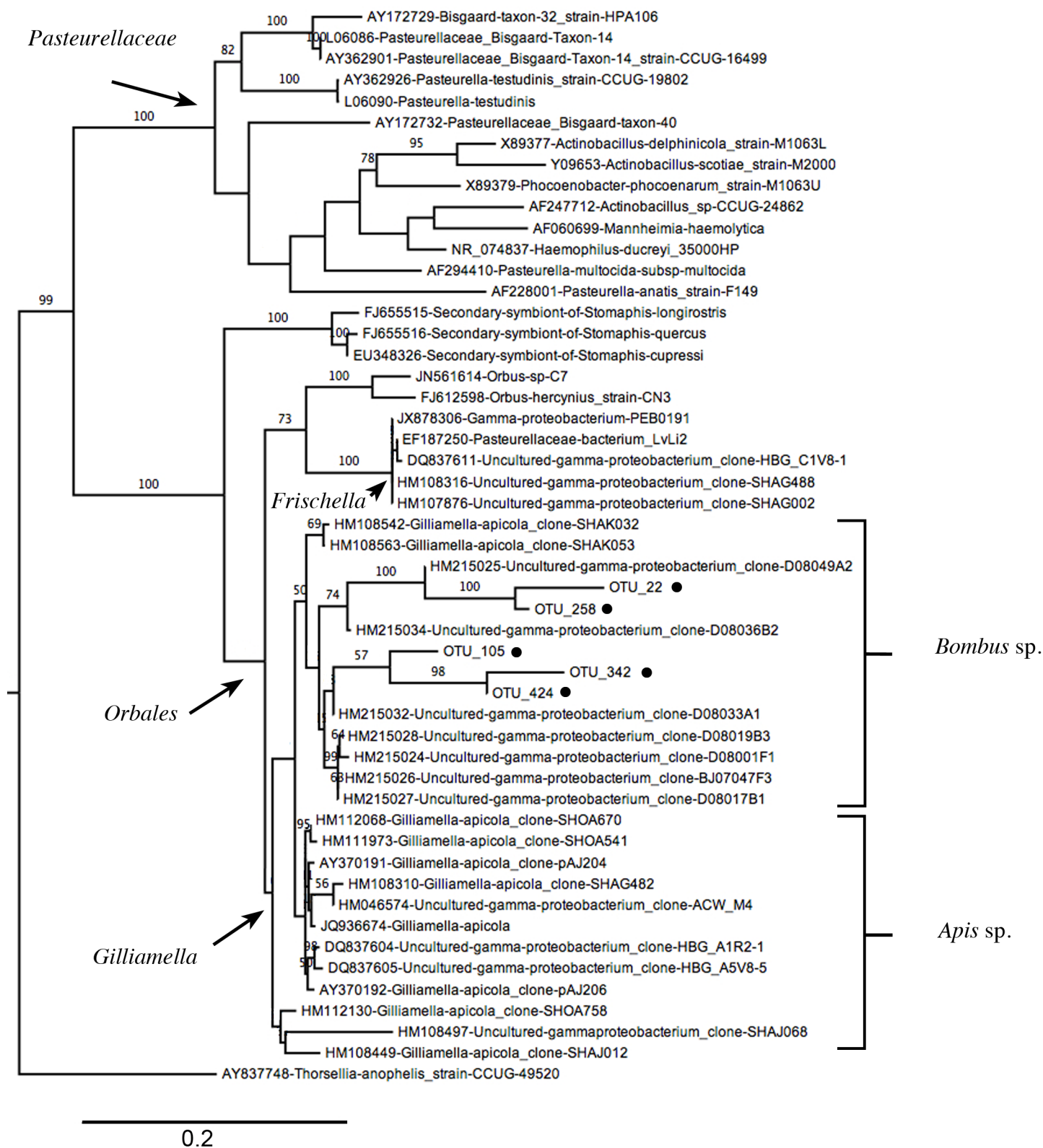


Figure S3a: Reads from high abundance (>1% in any sample) representative sequences of *Gilliamella* and closely related taxa reads from 454 dataset were aligned with near full length 16S rRNA sequences using RDP 2.2. Maximum likelihood trees were reconstructed by using RAxML with a GTRgamma base substitution model at 1000 iterations. Trees were visualized in FigTree 1.4. Characteristic bee related *Orbales* lineages are noted and OTU positions are marked ●.

Representative *Gammaproteobacterial* OTUs that clustered with lineages outside of Order *Orbales* not typically associated with bees are not shown. These lineages fell within several Orders including *Enterobacteriales*, *Pseudomonadales*, *Xanthomonadales*, *Legionellales*, and *Oceanospirillales*.

Figure S3b: *Betaproteobacteria: Snodgrassella alvi*

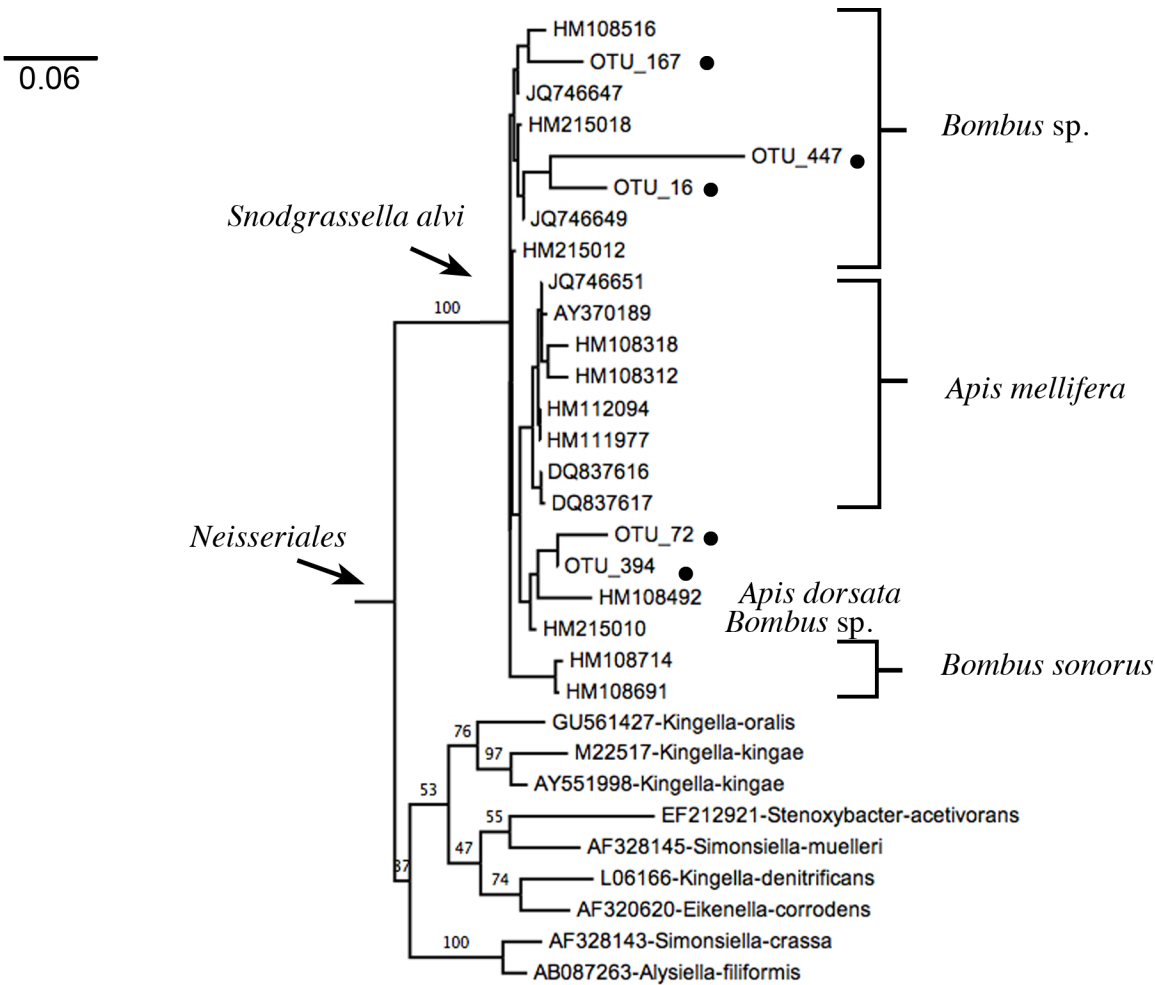


Figure S3b: Reads from high abundance (>1% in any sample) representative sequences of *Snodgrassella* reads from 454 dataset were aligned with near full length 16S rRNA sequences using RDP 2.2. Maximum likelihood trees were reconstructed by using RAxML with a GTRgamma base substitution model at 1000 iterations. Trees were visualized in FigTree 1.4. Characteristic bee related *Betaproteobacterial* lineage are noted and OTU positions are marked ●.

Representative *Betaproteobacterial* OTUs that clustered with lineages outside of *Snodgrassella* not typically associated with bees are not shown. These lineages fell within the Order *Burkholderiales*.

Figure S3d: *Lactobacillus* (Firm-4, Firm-5)

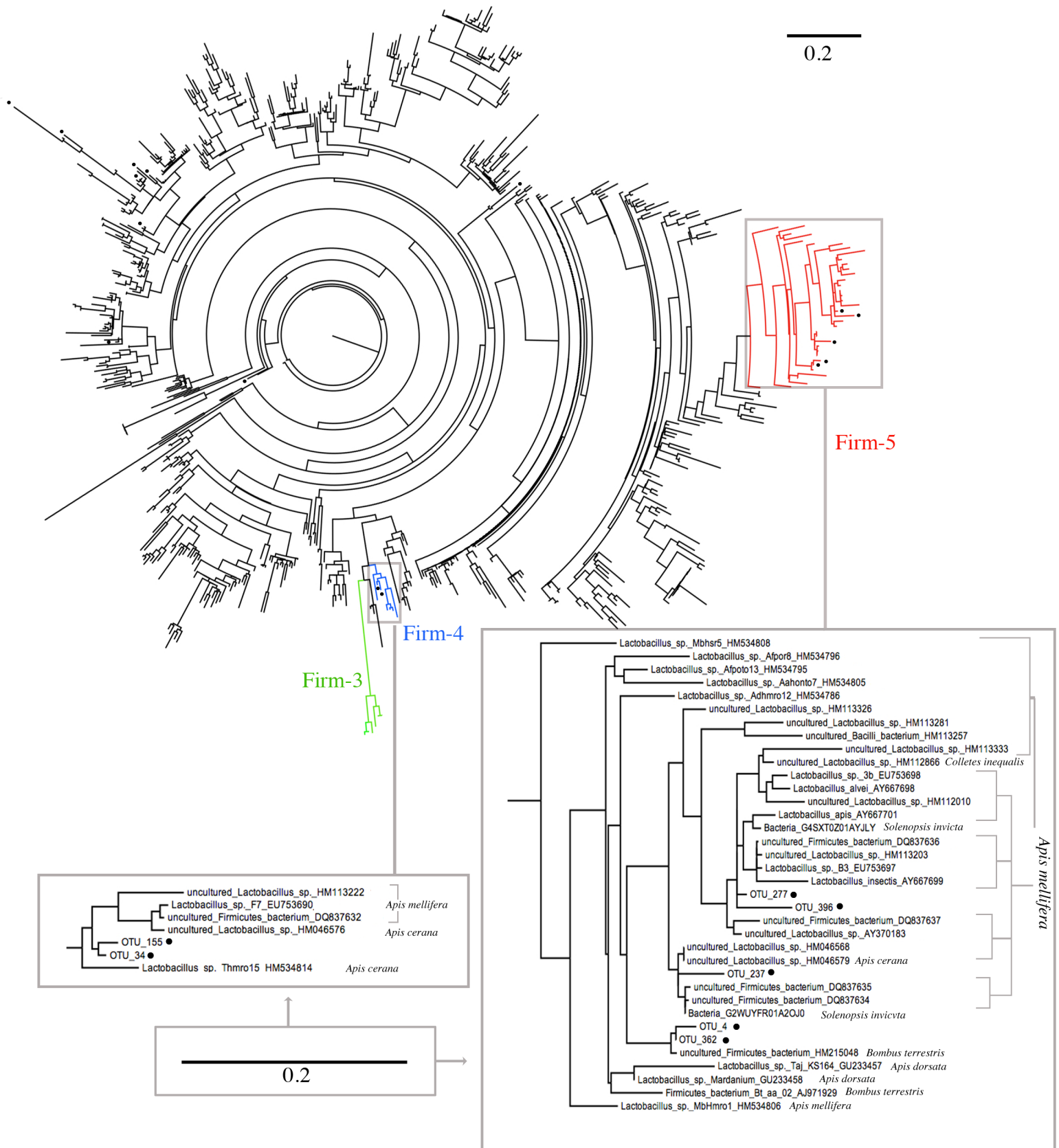


Figure S3d: Reads from high abundance (>1% in any sample) representative sequences of *Lactobacillus* binned reads from the 454 dataset were aligned to a previously reconstructed 16S rRNA *Lactobacillus* alignment (McFrederick et al, 2013) via the pyNAST aligner in Qiime (Caporaso et al., 2010a). Maximum likelihood trees were reconstructed by using RAXML with a GTRgamma base substitution model at 1000 iterations. Trees were visualized in FigTree 1.4. Characteristic bee related Firm-4 and Firm-5 lineages are noted and OTU positions are marked ●.