

a) Ibarra



b) La Palma



c) Maltaraña



Fig. S1. Sampling sites located in Lerma-Chapala Basin. a) Ibarra ($20^{\circ}13' \text{ N } 102^{\circ}37' \text{ W}$, altitude 1530 m); b) La Palma ($20^{\circ}07' \text{ N } 102^{\circ} 39' \text{ O}$, altitude 1530 m) and c) Maltaraña ($20^{\circ}13' \text{ N } 102^{\circ}41' \text{ O}$, altitude 1528 m).

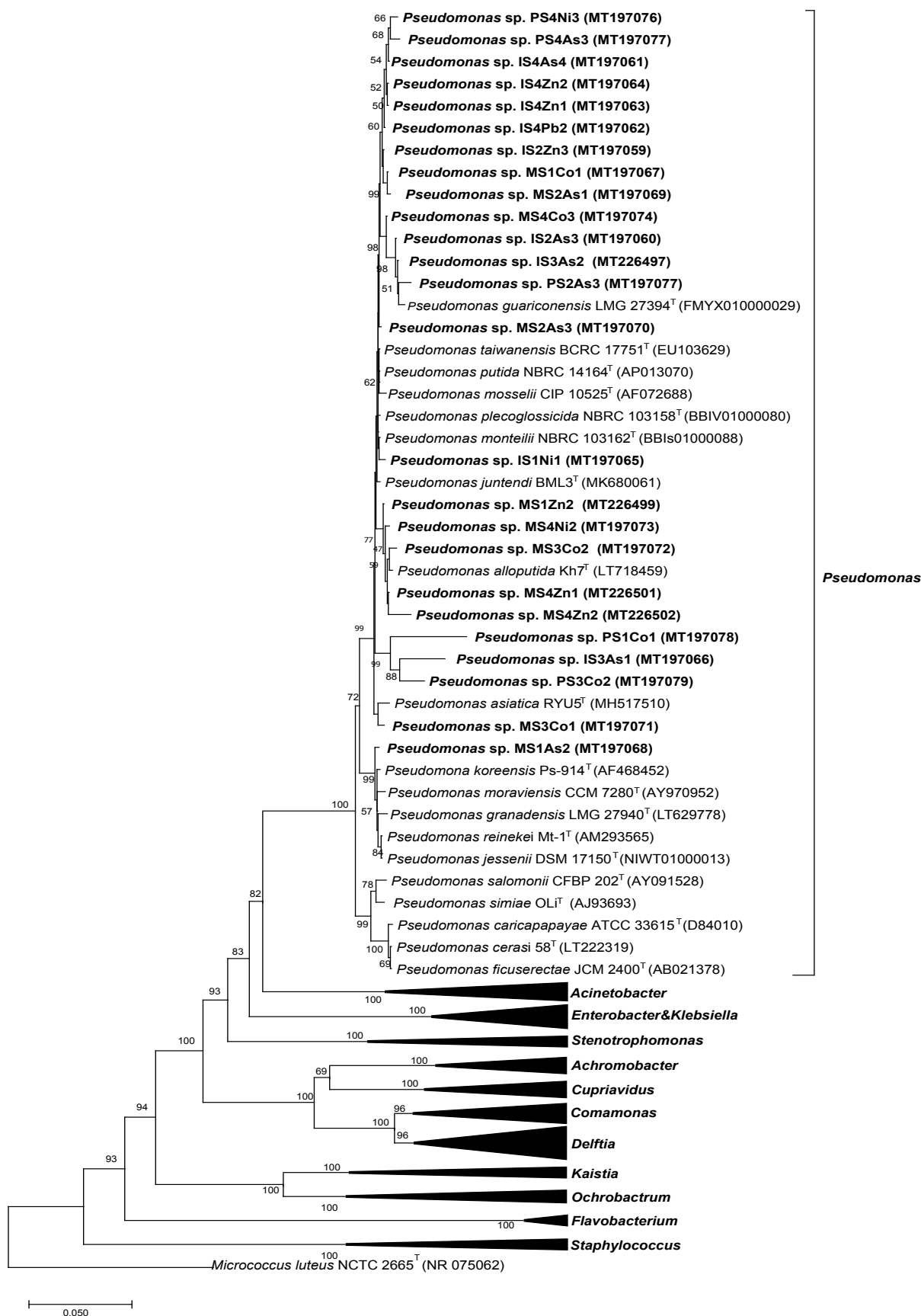


Fig. S2. Simplified neighbor joining (NJ) tree based on 16S rRNA gene sequences showing *Pseudomonas* relationships. Bootstrap values greater than 50% are shown at nodes as percentages of 1000 replicates. Scale Bar represents 0.050 changes per nucleotide position. GenBank accession numbers are given in parentheses.

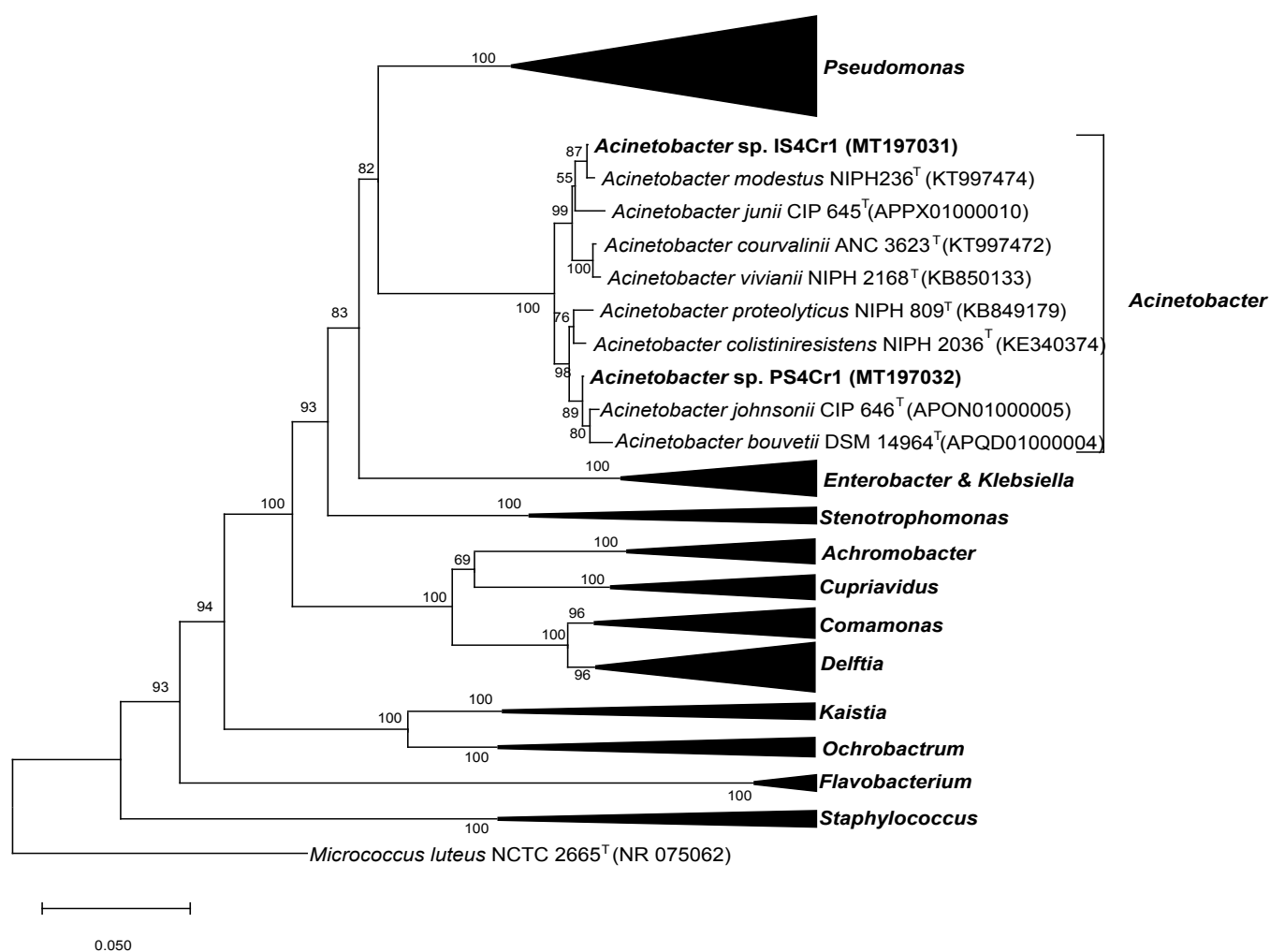


Fig. S3. Simplified neighbor joining (NJ) tree based on 16S rRNA gene sequences showing *Acinetobacter* relationships. Bootstrap values greater than 50% are shown at nodes as percentages of 1000 replicates. Scale Bar represents 0.050 changes per nucleotide position. GenBank accession numbers are given in parentheses.

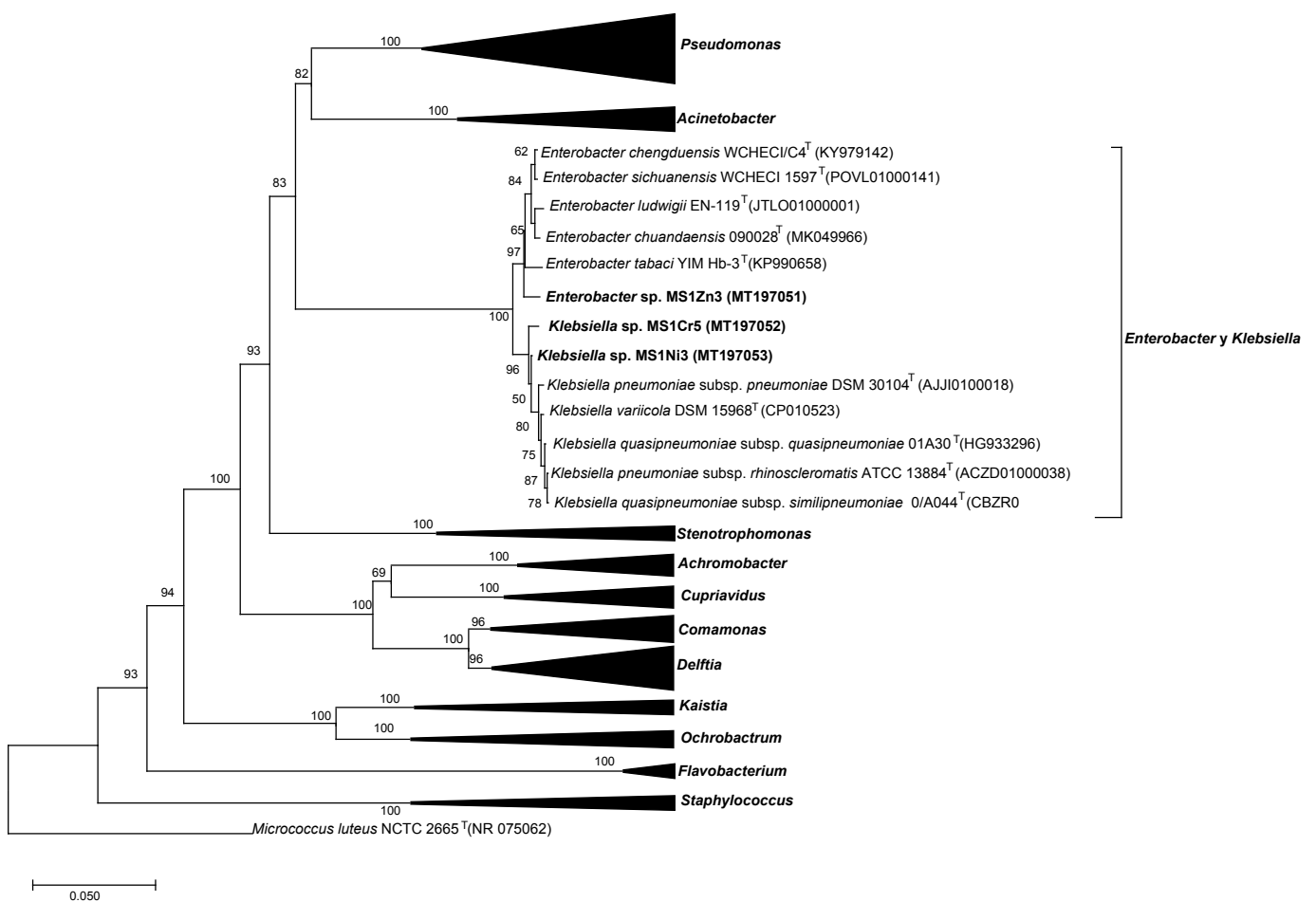


Fig. S4. Simplified neighbor joining (NJ) tree inferred with 16S rRNA gene sequences showing *Enterobacter*, *Klebsiella* and *Stenotrophomonas* relationships. Bootstrap values greater than 50% are shown at nodes as percentages of 1000 replicates. Scale Bar represents 0.05 changes per nucleotide position. GenBank accession numbers are given in parentheses.

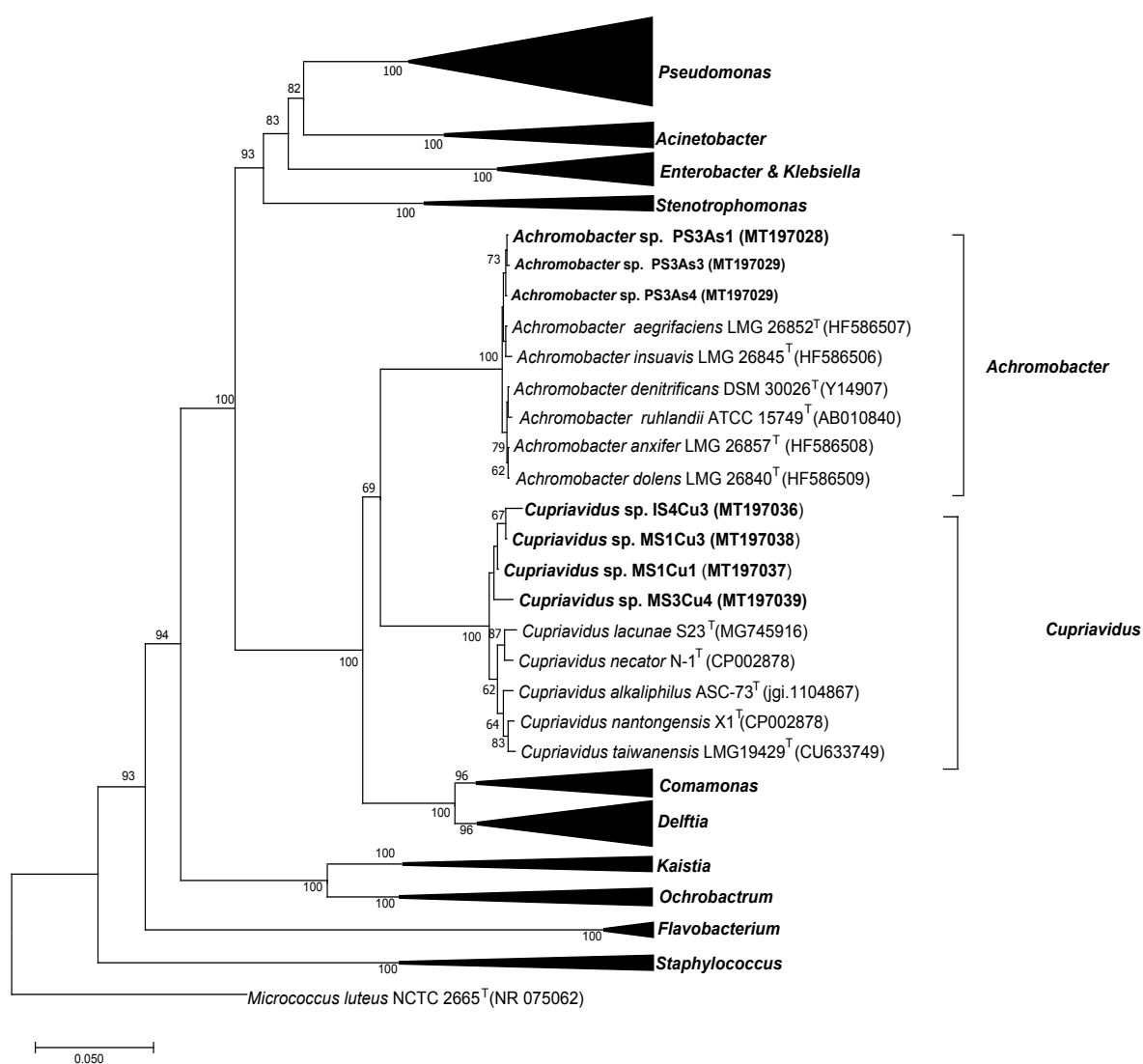


Fig. S5. Simplified neighbor joining (NJ) tree based on 16S rRNA gene sequences showing *Achromonbacter* and *Cupriavidus* relationships. Bootstrap values greater than 50% are shown at nodes as percentages of 1000 replicates. Scale Bar represents 0.050 changes per nucleotide position. GenBank accession numbers are given in parentheses.

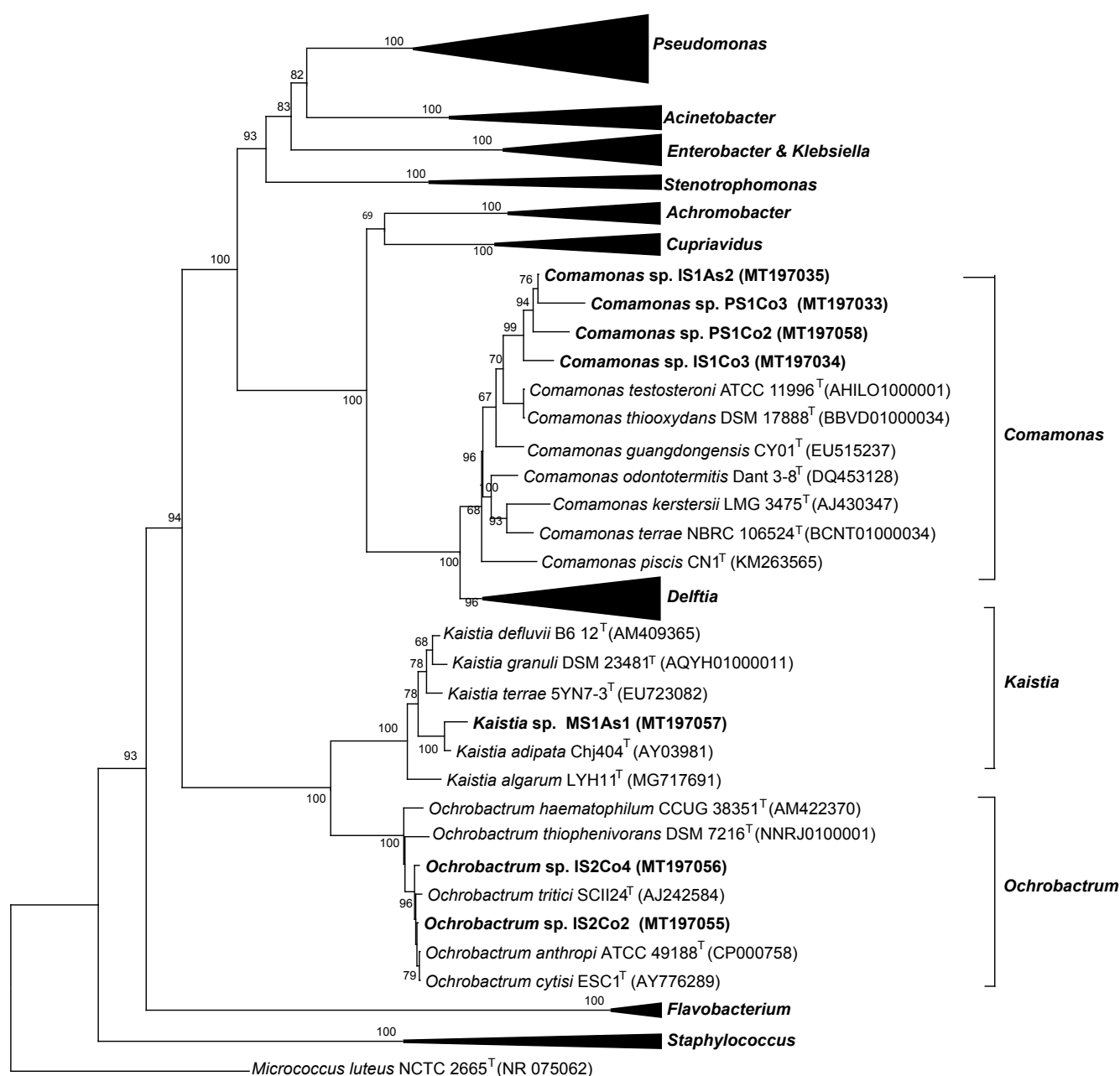


Fig. S7. Simplified neighbor joining (NJ) tree based on 16S rRNA gene sequences showing *Comamonas*, *Kaistia* and *Ochrobactrum* relationships. Bootstrap values greater than 50% are shown at nodes as percentages of 1000 replicates. Scale Bar represents 0.050 changes per nucleotide position. GenBank accession numbers are given in parentheses.

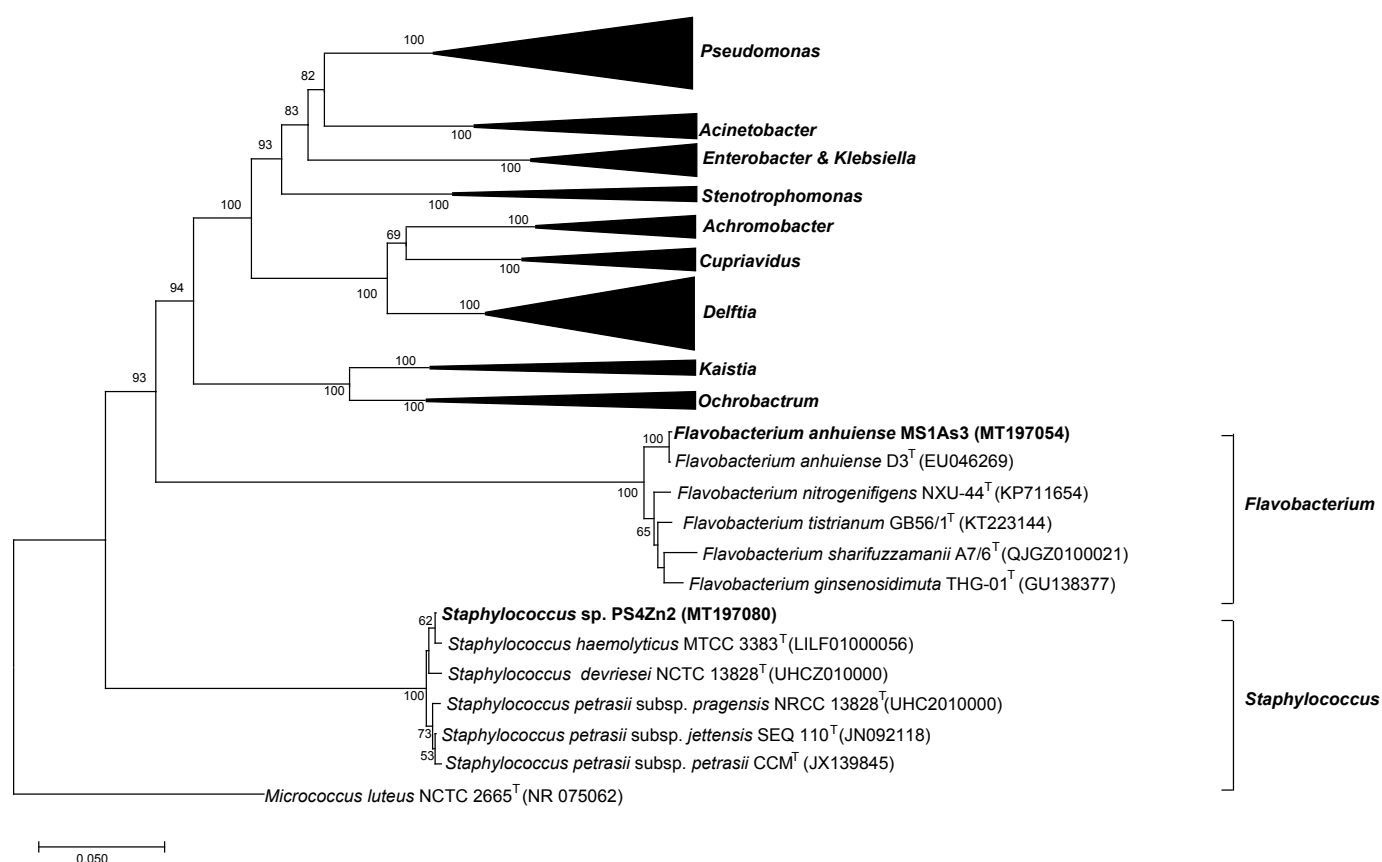


Fig. S8. Simplified neighbor joining (NJ) tree based on 16S rRNA gene sequences showing *Flavobacterium* and *Staphylococcus* relationships. Bootstrap values greater than 50% are shown at nodes as percentages of 1000 replicates. Scale Bar represents 0.050 changes per nucleotide position. GenBank accession numbers are given in parentheses.

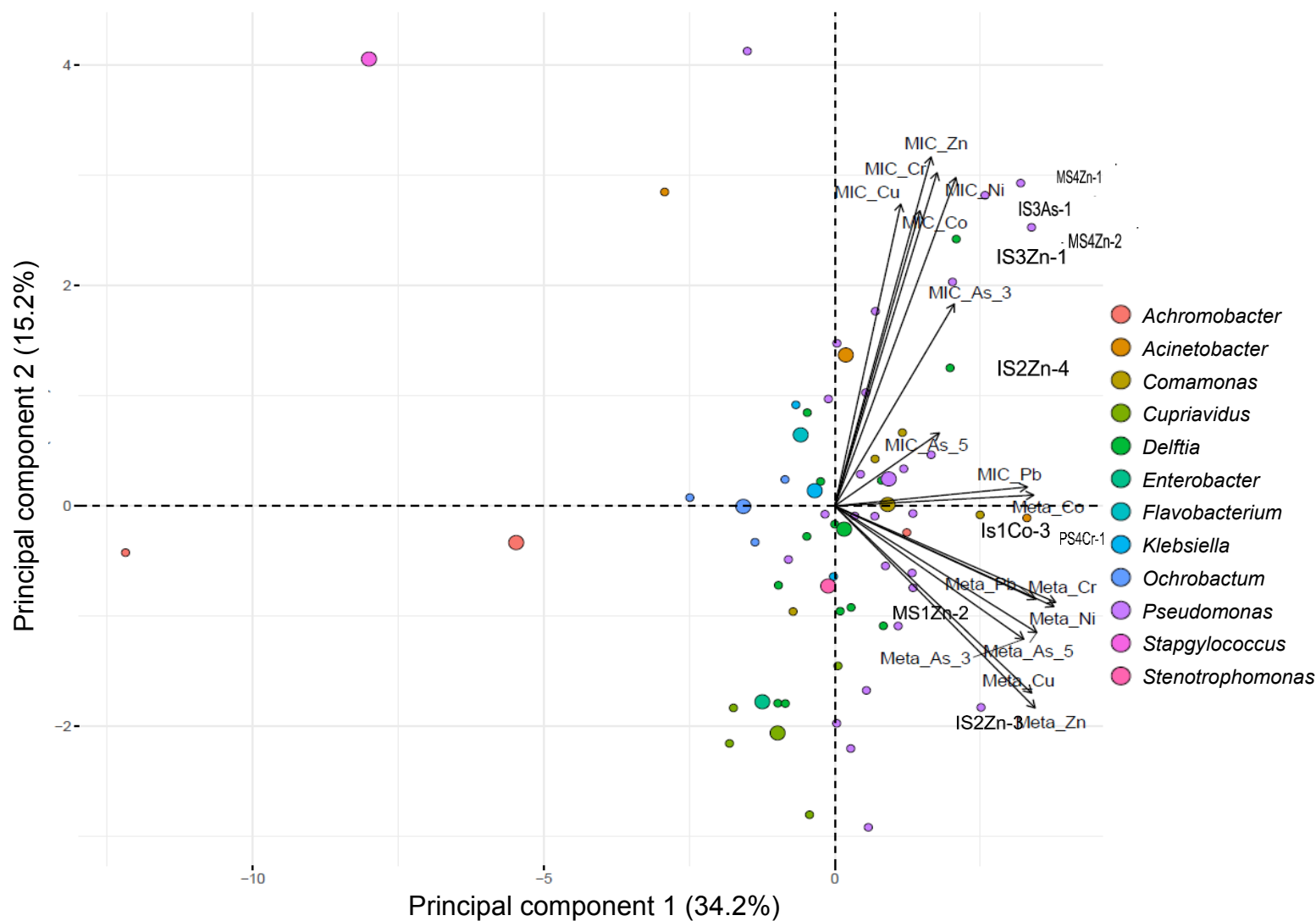


Fig. S9. PCA-biplot of the relation between metallophores production and MIC showing the distribution of the strains in relation with each of the metals for which the metallophores were produced. Also showed the MIC for each metals tested