

Figure S1. Phylogenetic tree of representative Pasteurellaceae with complete genomes based on 16S RNA sequences.

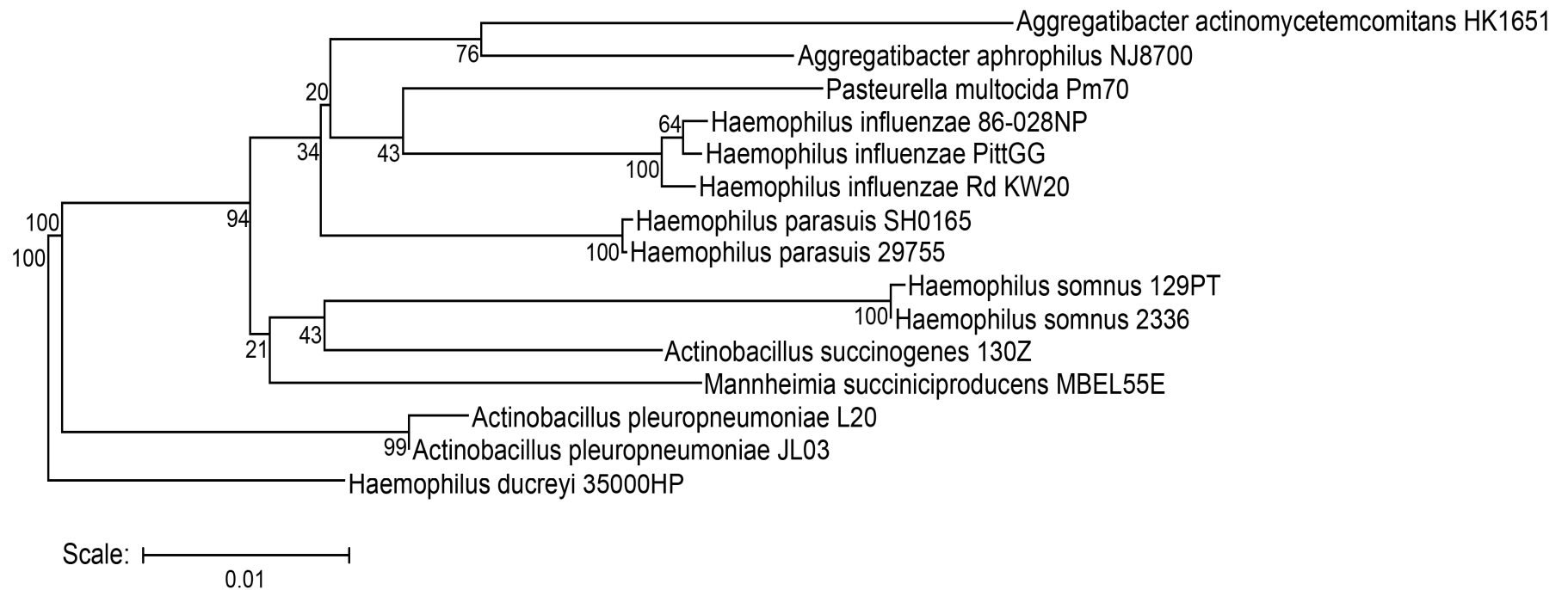


Figure S2. Hierarchical clusterings of Pasteurellaceae species according to COGS, PFAM, Enzymes, and TIGRfam classifications.

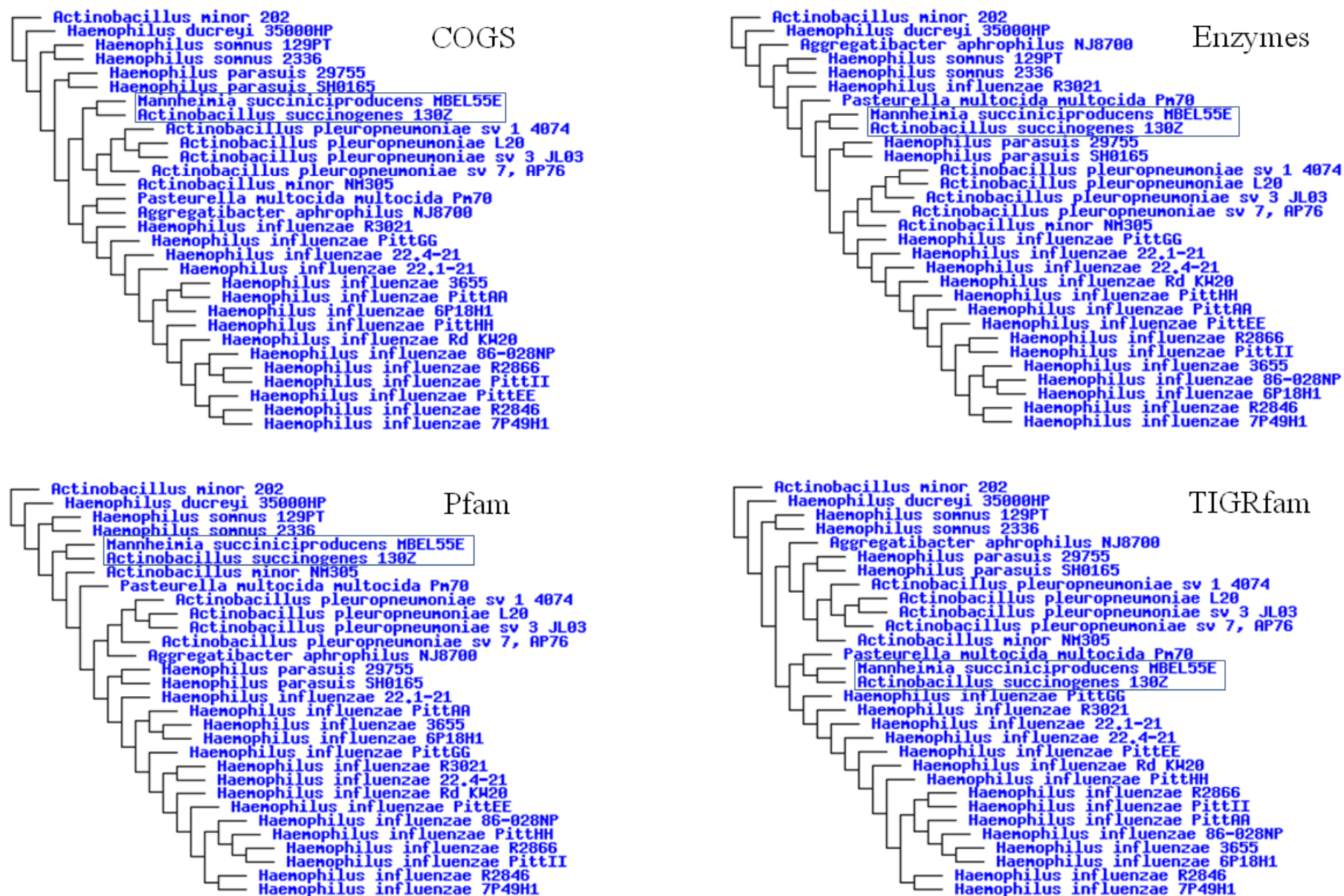


Figure S3. NUCmer and PROmer alignments of *A. succinogenes* and *M. succiniciproducens*, *P. multocida*, and *A. pleuropneumoniae* L20.

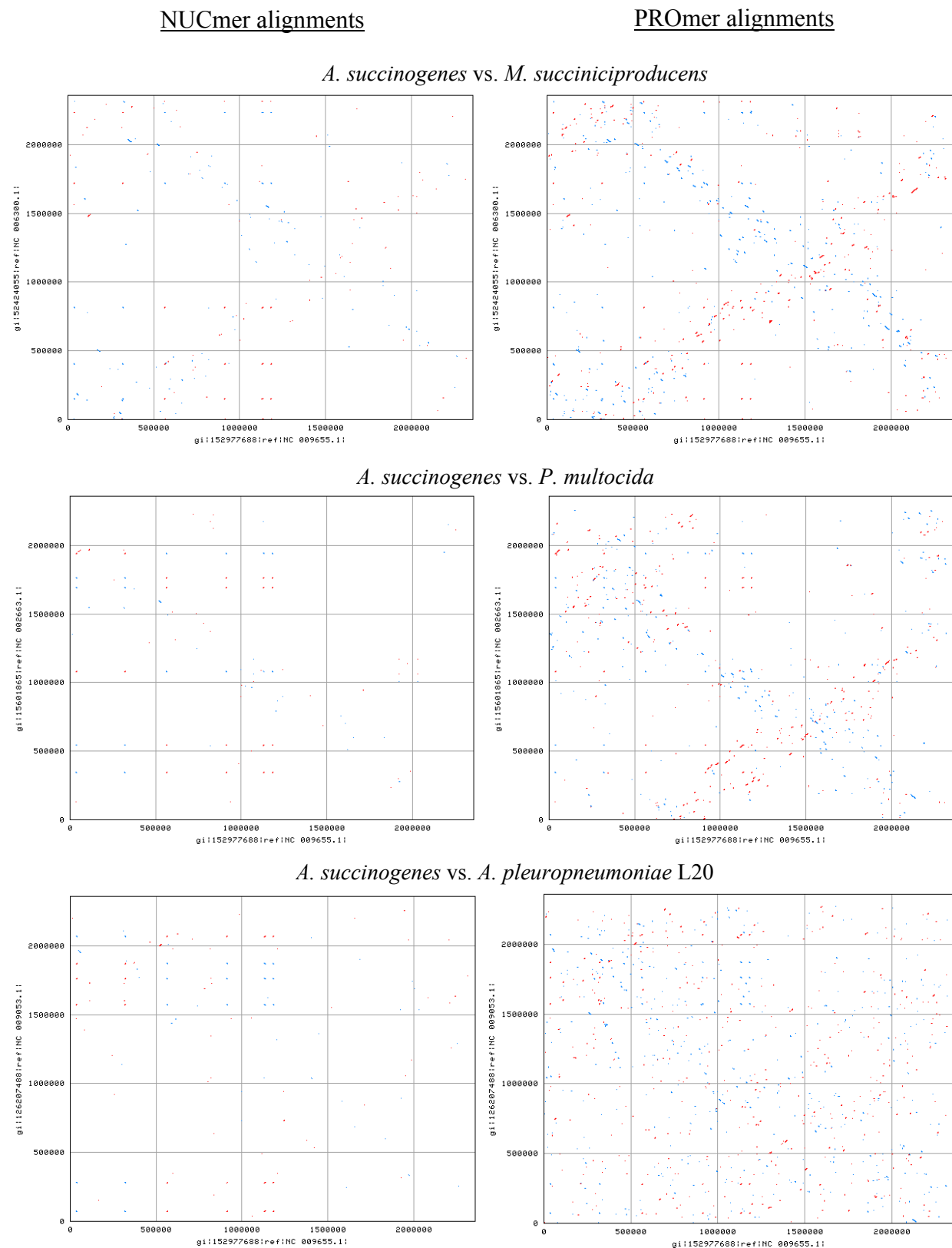
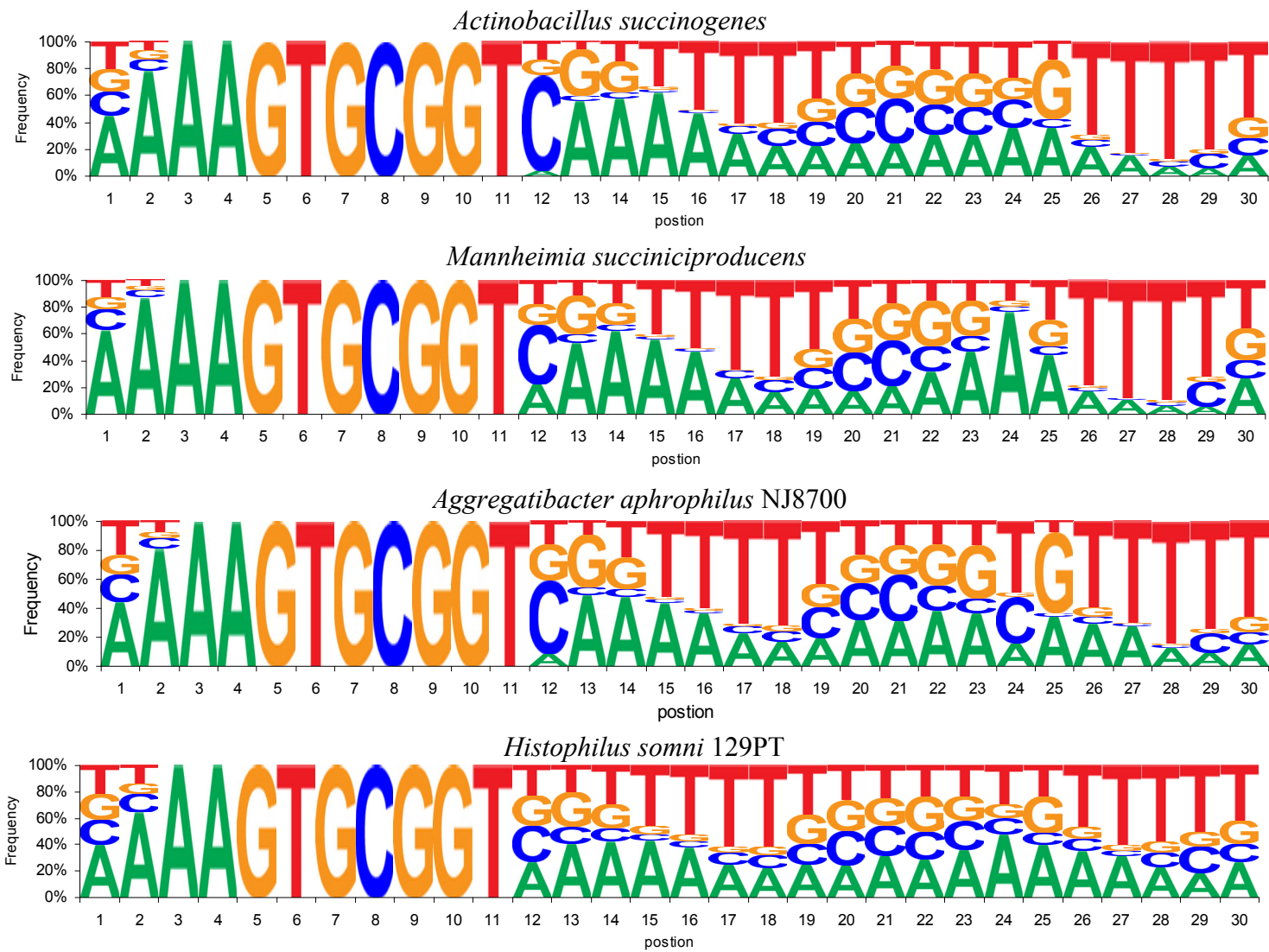


Figure S4: Comparison of nucleotide frequencies in Pasteurellaceae uptake signal sequences.

A. Uptake signal sequence version 1



B. Uptake signal sequence version 2

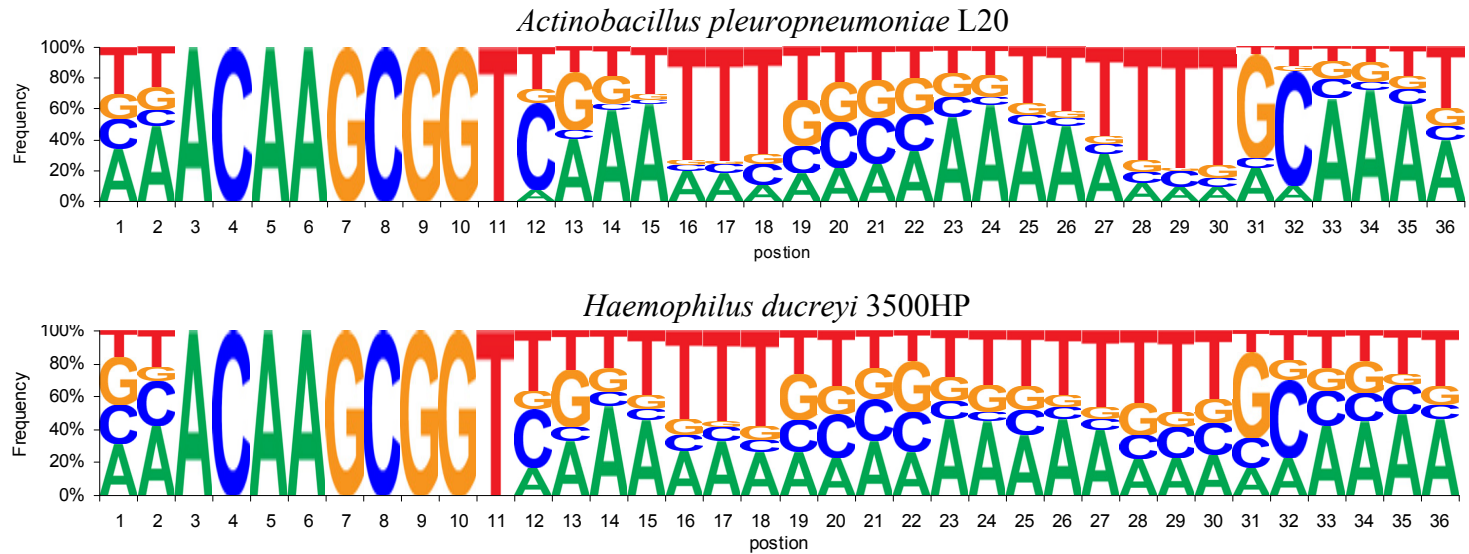


Figure S5: *A. succinogenes* has incomplete pathways for assimilatory sulfate reduction (A) and methionine synthesis (B).

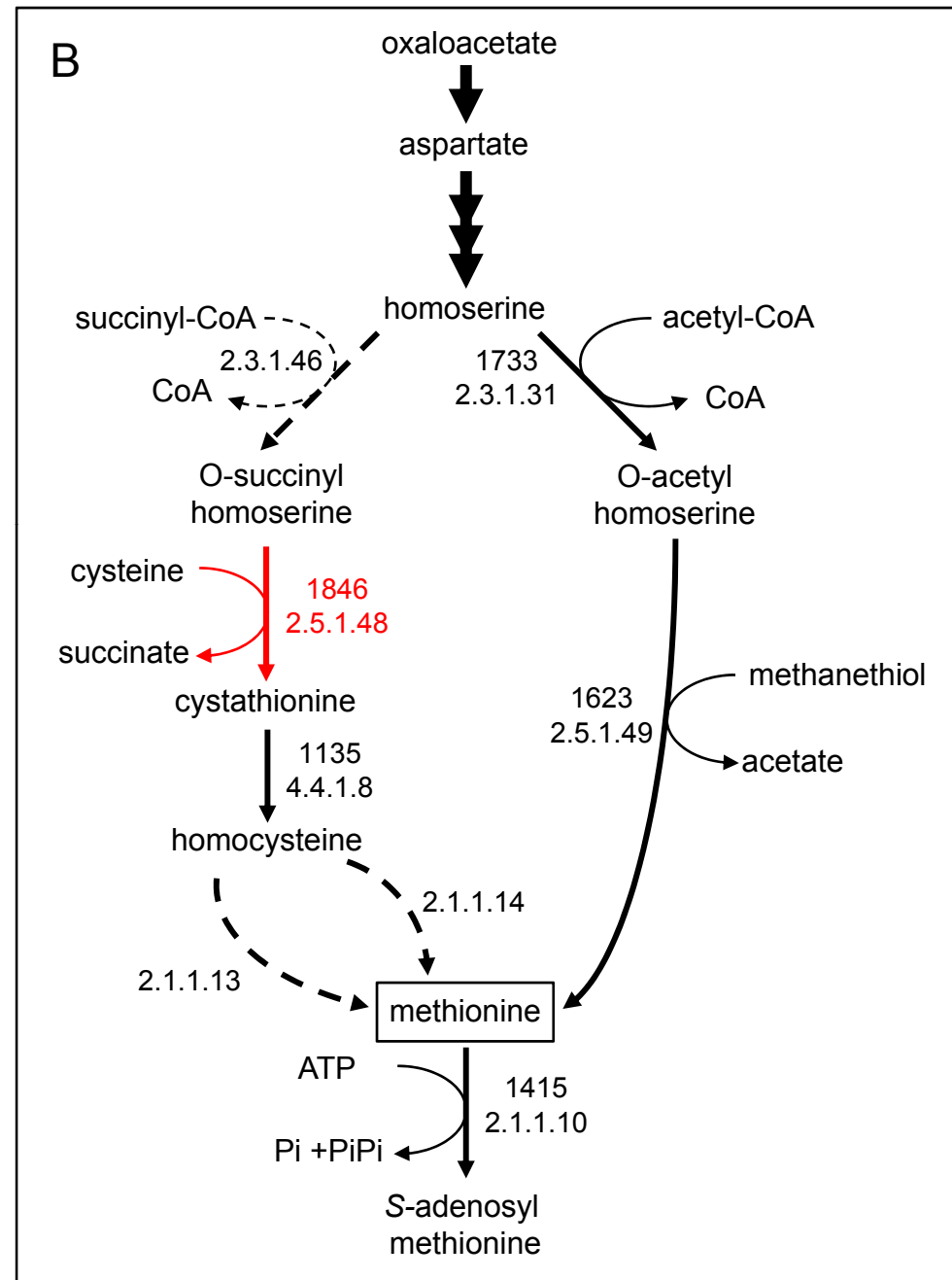
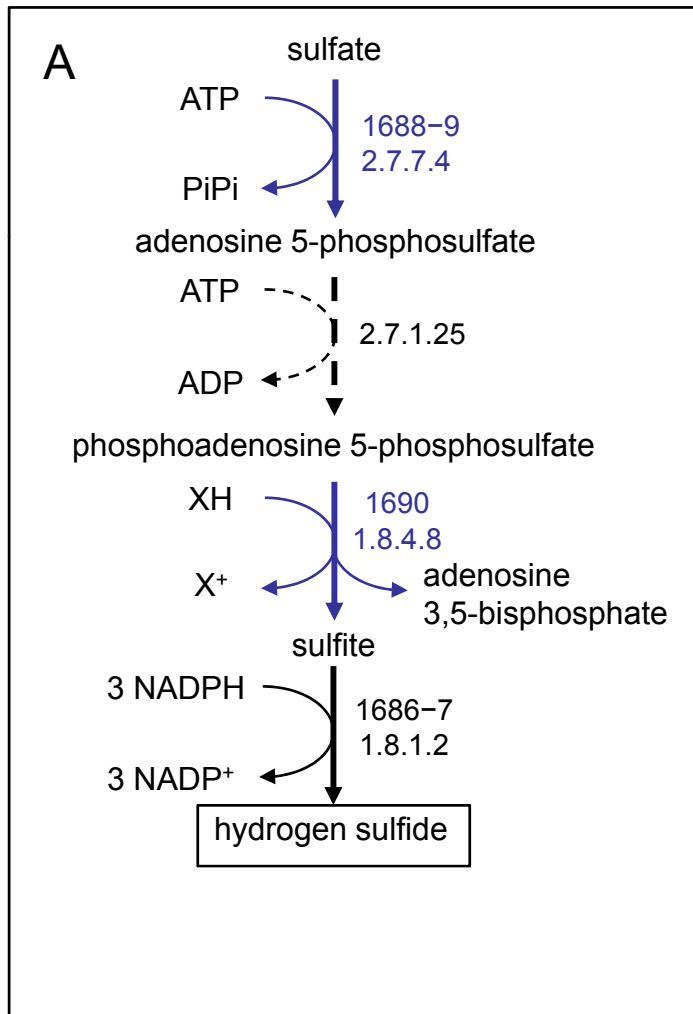


Figure S6. *A. succinogenes* has incomplete pathways for biotin, nicotinic acid, pantothenic acid, and pyridoxine synthesis.

