

Additional file 34. Bacterial strains used in the phylogenomic analyses.

Strain	GenBank Accession no.	Genome size (Mb)	GC%	Protein
<i>M. agalactiae</i>	NC_013948.1	1.01	29.6	813
<i>M. agalactiae</i> PG2	NC_009497.1	0.88	29.7	742
<i>M. arthritidis</i> 158L3-1	NC_011025.1	0.82	30.7	631
<i>M. bovis</i> PG45	NC_014760.1	1.00	29.3	765
<i>M. bovis</i> Hubei-1	NC_015725.1	0.95	29.3	801
<i>M. capricolum</i> subsp. <i>capricolum</i> ATCC 27343	NC_007633.1	1.01	23.8	812
<i>M. conjunctivae</i> HRC/581	NC_012806.1	0.85	28.6	692
<i>M. crocodyli</i> MP145	NC_014014.1	0.93	27	689
<i>M. fermentans</i> M64	NC_014921.1	1.12	26.9	1,050
<i>M. fermentans</i> JER	NC_014552.1	0.98	26.9	797
<i>M. flocculare</i>		0.76	28.9	585
<i>M. gallisepticum</i> str. R(low)	NC_004829.2	1.01	31.5	763
<i>M. genitalium</i> G37	NC_000908.2	0.58	31.7	475
<i>M. haemofelis</i> str. Langford 1	NC_014970.1	1.15	38.9	1,545
<i>M. hominis</i> ATCC 23114	NC_013511.1	0.67	27.1	523
<i>M. hyopneumoniae</i> 232	NC_006360.1	0.89	28.6	691
<i>M. hyopneumoniae</i> 7422		0.89	28.4	692
<i>M. hyopneumoniae</i> 7448	NC_007332.1	0.92	28.5	657
<i>M. hyopneumoniae</i> J	NC_007295.1	0.9	28.5	657
<i>M. hyorhinae</i> HUB-1	NC_014448.1	0.84	25.9	658

<i>M. leachii</i> PG50	NC_014751.1	1.01	23.8	905
<i>M. mobile</i> 163K	NC_006908.1	0.78	25	633
<i>M. mycoides</i> subsp. Capri LC str. 95010	NC_015431.1	1.16	23.8	1,017
<i>M. mycoides</i> subsp. <i>mycoides</i> SC str. PG1	NC_005364.2	1.21	24	1,017
<i>M. penetrans</i> HF-2	NC_004432.1	1.36	25.7	1,037
<i>M. pneumoniae</i> M129	NC_000912.1	0.82	40	689
<i>M. pulmonis</i> UAB CTIP	NC_002771.1	0.96	26.6	782
<i>M. putrefaciens</i> KS1	NC_015946.1	0.83	26.9	650
<i>M. suis</i> KI3806	NC_015153.1	0.71	31.1	794
<i>M. suis</i> str. Illinois	NC_015155.1	0.74	31.1	845
<i>M. synoviae</i> 53	NC_007294.1	0.8	28.5	659
<i>Streptococcus pyogenes</i> M1 GAS	NC_002737	1.85	38.5	1,696