

Additional File 3

Prokaryotic intrageneric genome signature comparisons. In these matrices; the 16S rDNA sequence identity is given in the top-right half, and the δ^* (x1000) are given in the lower left part. Note that comparisons are intrageneric, except for the E. coli/Shigella/Salmonella group (which consists of multiple genera) and the Bacillus cereus cluster, which is considered one species.

Prokaryotic species

	1	2	3	4	5					
1. Mycobacterium avium subsp. paratuberculosis K-10		98.3	97	98.3	98.3					
2. Mycobacterium bovis AF2122/97	30.3		97.2	100	100					
3. Mycobacterium leprae TN	68.3	48.4		97.2	97.2					
4. Mycobacterium tuberculosis CDC1551	30.1	0.3	48.6		100					
5. Mycobacterium tuberculosis H37Rv	30.1	0.4	48.5	0.5						
	1	2	3	4	5					
1. Rickettsia bellii RML369-C		99.1	99.4	98.2	97.8					
2. Rickettsia conorii str. Malish 7	37.2		99.3	98.4	98					
3. Rickettsia felis URRWX Cal 2	39.2	11.6		98.3	97.9					
4. Rickettsia prowazekii str. Madrid E	42.8	58.5	65.0		98.8					
5. Rickettsia typhi str. Wilmington	50.4	66.6	74.0	10.2						
	1	2	3	4	5	6	7	8	9	10
1. Chlamydia muridarum Nigg		98.4	98.6	95.8	95.9	95.7	94.5	94.4	94.4	94.5
2. Chlamydia trachomatis A/HAR13	25.2		99.9	95.4	95.5	95.1	94	94	93.9	94
3. Chlamydia trachomatis D/UW3/CX	25.2	0.5		95.5	95.7	95.3	94.2	94.1	94	94.2
4. Chlamydia philae abortus S26/3	40.7	40.5	40.8		99.5	98.4	95.5	95.5	95.4	95.5
5. Chlamydia philae GPIC	29.0	27.7	27.9	19.7		98.8	95.5	95.4	95.3	95.5
6. Chlamydia felis Fe/C56	24.0	32.4	32.7	22.2	16.9		95.1	95.1	95	95.1
7. Chlamydia pneumoniae AR39	27.8	18.4	18.8	38.0	28.9	35.5		99.9	99.9	100
8. Chlamydia pneumoniae CWL029	27.8	18.4	18.8	38.0	28.9	35.5	0.1		99.8	99.9
9. Chlamydia pneumoniae J138	27.8	18.3	18.7	38.0	28.7	35.5	0.2	0.2		99.9

10. CpneumoniaeTW183	27.8	18.4	18.8	37.9	28.8	35.4	0.2	0.2	0.3				
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	1	2	3	4	5								
1. LactobacillusacidophilusNCFM		92	86.1	86.7	86.1								
2. LactobacillusjohnsoniiNCC533	34.5		89.6	89	88.1								
3. LactobacillusplantarumWCFS1	83.4	111.3		92.9	90.6								
4. Lactobacillussakeisubsp.sakei23K	75.5	98.1	33.0		90.6								
5. Lactobacillussalivariussubsp.salivariusUCC118	41.3	33.3	105.1	97.6									

	1	2	3	4	5	6	7	8	9	10	11	12	13
1. Mycoplasmacapricolumsubsp.capricolumATCC27343		79.2	77.7	79	79	79	81.6	99.3	75.6	77.7	79.9	80.1	75
2. MycoplasmagenitaliumG37	80.4		89.7	73.5	73.5	73.5	76.2	78.8	83.1	89.7	76.3	77.5	82.6
3. Mycoplasmahyopneumoniae232	81.3	109.1		72.6	72.7	72.6	76.2	77.5	82.2	98.1	75.7	75.9	81.2
4. Mycoplasmahyopneumoniae7448	177.9	170.1	185.6		99.8	99.8	86.7	78.7	70	72.4	85.8	85.7	70.5
5. MycoplasmahyopneumoniaeJ	175.8	167.8	183.6	3.5		99.9	86.7	78.7	70	72.4	85.8	85.6	70.5
6. MycoplasmahyopneumoniaeJ	174.9	166.6	182.8	4.1	1.3		86.7	78.7	70	72.3	85.9	85.7	70.7
7. Mycoplasmamobile163K	77.2	121.3	79.3	127.9	125.7	124.4		81.2	74	75.9	86.8	85.9	73.4
8. Mycoplasmamycooidessubsp.mycoidesSCstr.PG1	18.1	67.2	71.0	181.0	178.8	177.5	74.5		75.4	77.4	79.9	79.8	74.9
9. MycoplasmapenetransHF-2	45.4	84.8	78.3	210.7	208.5	207.2	99.0	41.1		82.2	72.8	74	86.9
10. MycoplasmapneumoniaeM129	148.5	107.7	87.6	153.8	151.8	151.0	148.0	142.4	153.9		75.4	75.2	81.6
11. MycoplasmapulmonisUABCTIP	56.7	127.6	96.4	156.3	154.2	153.1	44.7	67.4	87.8	161.3		87.8	72
12. Mycoplasmasyoviae53	106.1	94.4	137.8	134.8	132.5	132.6	118.5	113.6	147.8	142.6	109.6		73.3
13. Ureaplasmaparvumserovar3str.ATCC700970	105.0	103.3	117.2	137.4	134.5	134.4	127.6	102.7	117.8	121.4	149.2	118.3	

	1	2	3	4	5	6	7	8	9	10	11	12	13
1. Staphylococcus aureus RF122		99.9	99.9	99.9	99.9	99.9	99.8	99.8	99.9	98.5	98.6	98.4	97.8
2. Staphylococcus aureus subsp. aureus COL	2.8		100	100	100	99.9	99.9	99.9	100	98.5	98.7	98.5	97.8
3. Staphylococcus aureus subsp. aureus MRSA252	2.9	1.6		100	100	99.9	99.9	99.9	100	98.5	98.7	98.5	97.8
4. Staphylococcus aureus subsp. aureus MSSA476	2.3	1.1	1.1		100	99.9	99.9	99.9	100	98.5	98.7	98.5	97.8
5. Staphylococcus aureus subsp. aureus MW2	2.6	0.9	1.4	0.4		99.9	99.9	99.9	100	98.5	98.7	98.5	97.8
6. Staphylococcus aureus subsp. aureus Mu50	3.0	2.0	1.2	1.4	1.6		99.8	99.8	99.9	98.5	98.6	98.4	97.8
7. Staphylococcus aureus subsp. aureus N315	2.7	1.4	1.3	0.8	0.9	1.1		99.7	99.9	98.5	98.7	98.3	97.7
8. Staphylococcus aureus subsp. aureus NCTC8325	2.6	1.0	1.2	0.8	0.8	1.2	1.0		99.9	98.4	98.6	98.3	97.7

9. <i>Staphylococcus aureus</i> subsp. <i>aureus</i> USA300	3.0	1.2	0.8	1.2	1.1	1.4	1.2	1.0		98.5	98.7	98.5	97.8
10. <i>Staphylococcus epidermidis</i> ATCC12228	41.9	41.7	40.5	41.4	41.5	40.5	40.9	41.4	40.6		99.8	98.5	97.8
11. <i>Staphylococcus epidermidis</i> RP62A	43.9	43.7	42.5	43.4	43.5	42.5	42.9	43.4	42.6	3.0		98.6	97.7
12. <i>Staphylococcus haemolyticus</i> JCSC1435	30.7	30.5	29.4	30.2	30.3	29.3	29.6	30.2	29.6	13.8	14.8		98.7
13. <i>Staphylococcus saprophyticus</i> ATCC15305	12.3	13.0	12.3	12.6	12.7	12.4	12.3	12.8	97.9	32.0	33.9	26.5	

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1. <i>Streptococcusagalactiae</i> 2603V/R		99.9	99.9	93.2	95	95.2	97.1	97	97.1	97.1	97.1	97	97.1	93.7	93.7
2. <i>Streptococcusagalactiae</i> A909	1.3		99.9	93.1	95.1	95.1	97.2	97.1	97.2	97.2	97.2	97.1	97.2	93.8	93.8
3. <i>Streptococcusagalactiae</i> NEM316	3.4	3.9		93.1	94.9	95.1	97	96.9	97	97	97	96.9	97	93.6	93.6
5. <i>Streptococcusmutans</i> UA159	37.1	37.2	36.7		93.7	93.8	93.3	93.2	93.3	93.3	93.3	93.3	93.3	94.4	94.4
4. <i>Streptococcus pneumoniae</i> R6	39.2	40.0	36.5	44.9		99.8	94.8	94.7	94.8	94.8	94.8	94.7	94.8	95.1	95.1
6. <i>Streptococcus pneumoniae</i> TIGR4	39.1	40.5	36.7	45.5	2.3		94.6	94.5	94.6	94.6	94.6	94.5	94.6	94.9	94.9
7. <i>Streptococcus pyogenes</i> M1GAS	23.2	23.7	22.7	24.1	37.0	36.9		99.9	100	100	100	99.9	100	95.1	95.1
9. <i>Streptococcus pyogenes</i> MGAS10394	22.5	23.1	21.4	25.0	36.2	36.0	1.3		99.9	99.9	99.9	99.9	99.9	95.2	95.2
12. <i>Streptococcus pyogenes</i> MGAS315	23.3	23.8	22.8	25.4	38.9	37.8	2.7	2.9		100	100	99.9	100	95.1	95.1
13. <i>Streptococcus pyogenes</i> MGAS5005	22.8	23.4	22.5	23.5	36.7	36.6	0.7	1.5	2.7		100	99.9	100	95.1	95.1
14. <i>Streptococcus pyogenes</i> MGAS6180	22.3	22.4	21.0	25.4	35.6	36.3	2.3	1.4	3.8	2.5		99.9	100	95.1	95.1
15. <i>Streptococcus pyogenes</i> MGAS8232	23.2	23.7	22.6	24.7	37.8	36.8	2.0	2.2	1.1	1.8	3.2		99.9	95.1	95.1
17. <i>Streptococcus pyogenes</i> SSI-1	23.7	24.3	23.3	25.0	39.0	37.9	2.5	3.0	0.4	2.5	4.0	1.2		95.1	95.1
18. <i>Streptococcus thermophilus</i> CNRZ1066	25.4	26.6	24.2	46.3	22.0	21.8	31.0	29.9	31.0	30.8	30.4	30.7	31.4		100
19. <i>Streptococcus thermophilus</i> LMG18311	25.7	26.8	24.5	47.0	22.5	21.9	31.7	30.5	31.3	31.5	31.0	31.0	31.6	0.9	

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1. <i>Escherichia coli</i> CFT073		99.4	99.4	99.4	98.8	99.4	96.6	97	97.5	97.5	97.5	98.6	98.9	98.8	98.6	99.5
2. <i>Escherichia coli</i> K12	7.7		99.9	99.9	99	100	96.8	97.2	97.7	97.7	97.6	98.6	99.1	98.9	98.8	99.6
3. <i>Escherichia coli</i> O157:H7 EDL933	3.3	6.6		100	99	99.9	96.8	97.2	97.7	97.7	97.6	98.6	99.1	98.9	98.8	99.6
4. <i>Escherichia coli</i> O157:H7 str. Sakai	3.2	7.1	0.6		99	99.9	96.8	97.2	97.7	97.7	97.6	98.6	99.1	98.9	98.8	99.6
5. <i>Escherichia coli</i> UTI89	2.8	4.9	4.0	4.2		99	97.4	97.8	97.1	97.1	97.1	99.2	99	99.5	99.4	99
6. <i>Escherichia coli</i> W3110 DNA	7.6	0.3	6.4	6.9	4.7		96.8	97.2	97.7	97.7	97.6	98.6	99.1	98.9	98.8	99.6
7. <i>Salmonella enterica</i> subsp. <i>enterica</i> ...	42.5	35.2	41.5	41.9	40.1	35.4		99.6	99	99	99	97.4	96.7	97.3	97.6	96.8
8. <i>Salmonella enterica</i> subsp. <i>enterica</i> (2)	44.1	36.7	43.1	43.5	41.6	36.9	1.6		99.3	99.3	99.2	97.8	97.1	97.6	98	97.2
9. <i>Salmonella enterica</i> subsp. <i>enterica</i> (3)	40.4	33.5	39.4	39.7	37.9	33.7	2.2	3.7		100	99.7	97.1	97.2	97	97.3	97.7

