

Additional file 1

Description for all matrixes: The part of the matrix from the upper right corner shows differences in the number of deletions between sequence pairs; the part of the matrix from the lower left corner shows differences in the number of nucleotides between the sequence pairs. The green color indicates species pairs that differ in the lowest number of nucleotides or deletions, the red color the pairs with the highest number of nucleotide or deletion differences between sequences.

Table S1

A matrix showing the nucleotides and deletions differences between pairs of 16S rRNA gene sequences for *Streptococcus* species.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42		
<i>S_acidominus</i>	1	22	8	4	0	8	1	9	4	0	11	16	0	0	7	8	8	8	2	8	4	10	8	4	13	2	8	10	4	0	4	0	0	13	8	2	8	11	10	2	0	0		
<i>S_adiacens</i>	2	211		18	22	22	18	23	17	22	17	10	22	22	25	26	18	26	22	18	22	16	24	22	19	22	26	16	22	22	22	22	22	11	26	22	18	19	28	22	22	22		
<i>S_anginosus</i>	3	103	209		10	8	0	9	1	10	8	3	8	6	8	7	8	0	8	8	0	10	2	8	10	5	6	2	10	8	8	0	3	10	8	8	8	8	8					
<i>S_australis</i>	4	88	194	103		4	10	5	11	0	4	13	18	4	4	9	6	10	6	2	10	0	12	10	0	13	2	6	12	0	4	0	4	4	15	6	2	10	13	8	2	4	4	
<i>S_canis</i>	5	86	202	97	81		8	1	9	4	0	11	16	0	0	7	8	8	8	2	8	4	10	8	4	13	2	8	10	4	0	4	0	0	13	8	2	8	11	10	2	0	0	
<i>S_constellatus</i>	6	88	194	62	74	95		9	1	10	8	3	8	8	8	7	8	0	8	8	0	10	2	8	10	5	8	6	2	10	8	10	8	5	7	8	6	0	3	10	8	8	8	
<i>S_cremoris</i>	7	147	209	145	143	135	155		10	5	1	12	17	1	1	8	9	9	9	3	9	5	11	9	5	14	3	9	11	5	1	5	1	1	14	9	3	9	12	11	3	1	1	
<i>S_crucis</i>	8	98	219	90	119	89	111	153		11	9	2	7	9	9	8	9	1	9	9	1	11	3	9	11	4	9	9	1	11	9	11	9	9	6	9	9	1	2	11	9	9	9	
<i>S_cristatus</i>	9	78	197	82	40	83	81	136	96		4	13	18	4	4	9	6	10	6	2	10	0	12	10	0	13	2	6	12	0	4	0	4	4	15	6	2	10	13	8	2	4	4	
<i>S_difficilis</i>	10	64	198	108	82	55	88	125	107	84	11	16	0	0	7	8	8	8	2	8	4	10	8	4	13	2	8	10	4	0	4	0	0	13	8	2	8	11	10	2	0	0		
<i>S_downsi</i>	11	117	210	97	112	101	93	161	86	101	109	7	11	11	10	11	3	11	11	3	13	5	11	13	6	11	11	3	13	11	11	6	11	11	3	2	13	11	11	11				
<i>S_durans</i>	12	191	97	176	173	185	165	182	185	174	172	184	16	16	15	16	8	16	16	8	18	8	16	18	9	16	16	16	5	16	16	8	9	18	16	16	16	16						
<i>S_dygalactiae</i>	13	78	197	105	78	43	89	122	109	79	35	108	171		0	7	8	8	8	2	8	4	10	8	4	13	2	8	10	4	0	4	0	0	13	8	2	8	11	10	2	0	0	
<i>S_equi</i>	14	104	228	88	104	62	108	134	86	91	76	116	195	78		7	8	8	8	2	8	4	10	8	4	13	2	8	10	4	0	4	0	0	13	8	2	8	11	10	2	0	0	
<i>S_equinus</i>	15	83	207	89	79	91	85	139	103	66	91	99	180	90	95		7	7	7	7	7	9	9	7	9	12	7	7	9	9	7	7	14	7	7	7	10	9	7	7	7			
<i>S_galaliticus</i>	16	95	213	65	82	78	86	131	68	71	87	89	166	83	78	73		8	0	6	8	6	10	8	6	11	6	0	10	6	8	6	8	0	15	0	0	6	8	11	4	6	8	8
<i>S_gordononi</i>	17	88	197	62	53	83	59	153	92	48	91	91	167	89	101	80	74		8	8	0	10	2	8	10	5	8	8	2	10	6	10	8	8	0	3	10	8	8	8				
<i>S_infantis</i>	18	96	211	74	78	78	86	124	94	73	76	100	184	81	76	71	21	77		8	8	6	10	8	6	11	6	0	10	6	8	6	8	0	15	0	0	8	8	11	4	6	8	
<i>S_infantis</i>	19	88	197	99	25	84	76	139	112	35	84	106	171	74	99	77	75	53	80		8	2	10	8	2	13	0	6	10	2	2	2	2	13	6	0	8	11	8	0	2	2		
<i>S_intermedius</i>	20	90	203	48	76	82	23	154	101	74	96	88	175	93	99	89	81	44	80	81		10	2	8	10	5	8	6	2	10	6	10	8	7	8	0	3	10	8	8	8			
<i>S_mitis</i>	21	94	193	93	21	87	71	144	115	42	82	107	171	77	96	81	79	54	81	27	77		12	10	0	13	2	6	12	0	4	0	4	4	15	6	2	10	13	8	2	4	4	
<i>S_mutans</i>	22	122	217	96	112	119	107	152	104	98	119	99	194	121	107	106	99	84	93	107	102	108		8	12	5	10	10	2	12	10	12	10	10	7	10	10	2	5	12	10	10	10	
<i>S_oligoformans</i>	23	84	197	84	64	87	83	135	107	42	91	107	160	82	96	65	77	60	74	65	70	66	102		10	13	8	10	10	9	10	8	15	6	8	6	11	10	8	8	8	8		
<i>S_oralis</i>	24	88	192	94	18	84	72	141	114	41	79	105	168	73	97	80	78	49	78	24	74	8	106	65		13	2	6	12	0	4	0	4	4	15	6	2	10	13	8	2	4	4	
<i>S_ovis</i>	25	96	211	89	101	89	91	160	85	93	98	87	182	100	105	85	89	85	91	105	83	102	114	99	99		13	11	3	13	13	13	13	8	11	13	13	13	13	13	13	13	13	13
<i>S_parasanguinis</i>	26	70	188	87	50	78	76	131	99	49	76	105	160	68	90	70	73	64	73	48	78	48	110	62	43	96		6	10	2	2	2	2	2	13	6	0	6	11	8	0	2	2	
<i>S_pasteuriensis</i>	27	95	212	65	81	77	85	129	89	70	85	90	181	81	80	73	72	19	74	81	77	100	77	76	90	72		10	6	6	6	8	5	15	0	6	8	11	4	6	8	8		
<i>S_pluranimalium</i>	28	112	197	99	118	93	104	159	96	104	107	91	181	110	106	96	98	96	92	120	96	115	114	99	112	75	99	99		12	10	12	10	10	5	10	10	2	3	12	10	10	10	
<i>S_pneumoniae</i>	29	95	194	96	24	88	74	146	116	43	85	107	172	78	98	83	81	57	85	28	78	6	110	68	8	104	50	79	117		4	0	4	4	15	6	2	10	13	8	2	4	4	
<i>S_porcinus</i>	30	78	206	105	79	45	94	141	111	88	49	122	175	48	61	82	86	93	77	89	98	78	124	92	75	99	74	85	101	81		4	0	0	13	8	2	8	11	10	2	0	0	
<i>S_pseudopneumoniae</i>	31	92	191	93	21	87	69	144	116	41	82	105	178	77	96	79	77	53	81	24	72	5	108	65	5	99	47	77	113	6	78		4	4	15	6	2	10	13	8	2	4	4	
<i>S_pseudoporcini</i>	32	80	208	113	85	55	100	145	113	88	50	125	181	52	67	83	93	100	89	89	104	87	128	92	85	110	74	93	107	87	31	85		0	13	8	2	8	11	10	2	0	0	
<i>S_pyogenes</i>	33	84	200	102	84	27	94	132	91	81	51	100	179	37	69	90	75	84	85	119	87	83	85	70	73	92	86	57	86	62		13	8	2	8	11	10	2	0	0				
<i>S_saccharolyticus</i>	34	188	110	175	171	178	165	186	187	172	170	178	51	187	199	177	178	164	177	165	168	166	191	177	164	178	176	180	185	179	175	179	178	15	13	7	8	17	13	13	13			
<i>S_salivarius</i>	35	93	205	81	68	83	95	140	93	61	101																																	

Table S2

A matrix showing the nucleotides and deletions differences between pairs of 16S rRNA gene sequences for *Enterococcus* species.

	1	2	3	4	5	6	7	8	9
E._avium	1		0	0	3	3	3	3	0
E._casseliflavus	2	22		0	3	3	3	3	0
E._cecorum	3	59	53		3	3	3	3	0
E._durans	4	22	34	71		0	0	0	3
E._faecium	5	24	35	74	7		0	0	3
E._faecalis	6	66	62	90	59	55		0	3
E._hirae	7	20	34	71	5	7	56		3
E._porcinus	8	27	35	75	16	14	63	13	
E._raffinosus	9	5	20	59	23	25	67	21	26

Table S3

A matrix showing the nucleotides and deletions differences between pairs of *sodA* gene sequences for *Streptococcus* species.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42		
<i>S_acidominimus</i>	1		9	0	0	0	0	17	0	0	0	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>S_adiacens</i>	2	162		9	9	9	9	14	9	9	9	0	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9		
<i>S_anginosus</i>	3	104	135		0	0	0	1	0	0	0	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
<i>S_australis</i>	4	103	141	96		0	0	1	0	0	0	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
<i>S_canis</i>	5	113	193	115	120		0	17	0	0	0	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
<i>S_constellatus</i>	6	105	152	53	93	122		1	0	0	0	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
<i>S_cremoris</i>	7	157	169	146	156	157	159		17	17	17	14	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17						
<i>S_crucis</i>	8	105	174	116	110	98	123	163		0	0	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
<i>S_cristatus</i>	9	93	151	91	52	117	86	159	109		0	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
<i>S_difficilis</i>	10	98	168	103	109	102	100	155	103	104		9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
<i>S_downsi</i>	11	110	172	115	114	101	121	164	62	112	103	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
<i>S_durans</i>	12	165	138	156	147	155	153	176	155	151	160	161	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9						
<i>S_dysgalactiae</i>	13	119	158	113	122	30	118	16	103	120	102	107	154	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
<i>S_equi</i>	14	124	166	122	123	71	130	165	114	120	115	107	160	78		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
<i>S_equinus</i>	15	85	172	117	120	114	115	167	101	114	91	97	167	115	128		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
<i>S_galolyticus</i>	16	111	148	99	106	106	97	159	117	104	103	117	153	110	114	124		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
<i>S_gordonii</i>	17	98	138	79	71	115	72	149	105	67	93	118	146	119	129	102	103		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
<i>S_infantis</i>	18	116	162	107	106	97	107	165	106	105	103	113	159	115	112	76	104		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
<i>S_infantis</i>	19	99	153	95	34	120	91	165	105	54	109	114	151	121	124	113	115	73	108		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
<i>S_intermedius</i>	20	107	152	64	96	123	38	151	120	88	104	130	158	125	130	122	102	70	108	89		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
<i>S_mitis</i>	21	97	145	90	29	116	84	155	106	49	105	115	145	117	126	106	101	66	103	24	83		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
<i>S_mutans</i>	22	101	168	111	113	82	110	154	96	110	93	100	165	88	106	97	93	107	97	115	111	107		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
<i>S_oligoflamentans</i>	23	96	150	90	56	123	92	158	117	32	109	119	182	127	129	118	108	74	113	85	96	60	116		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
<i>S_oralis</i>	24	93	153	90	28	122	90	160	104	49	105	113	148	123	127	110	108	72	105	15	91	22	116	60		0	0	0	0	0	0	0	0	0	0	0	0	0	0					
<i>S_ovis</i>	25	85	157	93	90	111	101	159	105	88	90	111	162	108	113	90	106	87	107	85	103	84	107	90	88		0	0	0	0	0	0	0	0	0	0	0	0	0					
<i>S_parasanguinis</i>	26	99	151	91	49	111	81	150	102	54	95	114	148	117	122	107	106	64	94	53	83	43	106	63	48	95		0	0	0	0	0	0	0	0	0	0	0	0	0				
<i>S_pasteuriensis</i>	27	108	154	104	111	107	98	164	113	105	103	113	149	110	117	120	16	102	74	113	107	102	96	109	111	107		0	0	0	0	0	0	0	0	0	0	0	0					
<i>S_pluranimalium</i>	28	112	150	111	104	97	121	153	105	106	96	98	148	92	109	111	113	114	108	108	125	104	102	115	111	101	105	116		0	0	0	0	0	0	0	0	0	0	0				
<i>S_pneumoniae</i>	29	92	145	92	34	113	88	154	105	47	105	111	150	115	124	103	106	66	106	25	90	13	109	60	26	84	48	107	98		0	0	0	0	0	0	0	0	0	0	0			
<i>S_porcinus</i>	30	112	169	113	123	93	105	142	110	111	100	111	162	92	110	109	107	110	114	121	107	111	94	120	119	110	117	111	106	117	111	106	117		0	0	0	0	0	0	0			
<i>S_pseudoporcinus</i>	31	93	147	93	38	114	89	153	106	49	106	112	157	117	125	104	108	67	108	27	91	15	110	62	28	86	49	109	99	2	118		0	0	0	0	0	0	0					
<i>S_pyogenes</i>	32	109	168	117	116	90	109	152	104	108	101	112	170	88	102	107	111	113	110	116	111	113	93	117	119	104	116	114	112	118	27	119		0	0	0	0	0	0	0				
<i>S_saccharolyticus</i>	33	118	169	114	123	31	119	168	102	121	103	106	155	4	179	114	111	126	96	122	126	118	124	109	118	111	93	114	93	116	88		0	0	0	0	0	0	0					
<i>S_salivarius</i>	34	149	125	149	147	155	152	162	147	143	146	161	98	156	165	153	161	137	159	145	144	142	158	146	142	157	136	161	145	144	158	145	162	157		0	0	0	0	0	0	0		
<i>S_sanguinis</i>	35	97	151	105	86	96	100	159	95	96	93	99	156	94	109	106	88	89	88	92	105	84	82	102	90	84	101	92	96	88	102	90	97	95	162		0	0	0	0	0	0		
<i>S_simensis</i>	36	104	149	90	82	122	77	159	106	80	93	113	150	123	125	118	103	57	117	83	85	77	103	80	82	104	71	106	115	82	121	83	121	124	150	103		0	0	0	0	0	0	
<i>S_sobrinus</i>	37	104	163	80	84	125	79	169																																				

Table S4

A matrix showing the nucleotides and deletions differences between pairs of *sodA* gene sequences for *Enterococcus* species.

	1	2	3	4	5	6	7	8	9
E_avium	1		0	0	0	0	0	0	0
E_casseliflavus	2	96		0	0	0	0	0	0
E_cecorum	3	119	114		0	0	0	0	0
E_durans	4	112	98	121		0	0	0	0
E_faecium	5	99	77	106	95		0	0	0
E_faecalis	6	97	75	106	94	5		0	0
E_hirae	7	96	80	105	62	78	80		0
E_porcinus	8	118	105	113	70	99	100	60	
E_raffinosus	9	52	84	124	100	94	93	90	114

Table S5

A matrix showing the nucleotides and deletions differences between pairs of *tuf* gene sequences for *Streptococcus* species.

Table S6

A matrix showing the nucleotides and deletions differences between pairs of *tuf* gene sequences for *Enterococcus* species.

	1	2	3	4	5	6	7	8	9
E._avium	1		0	0	0	0	0	0	0
E._casseliflavus	2	70		0	0	0	0	0	0
E._cecorum	3	71	76		0	0	0	0	0
E._durans	4	80	75	72		0	0	0	0
E._faecium	5	86	71	75	28		0	0	0
E._faecalis	6	69	73	75	89	93		0	0
E._hirae	7	80	73	70	10	26	87		0
E._porcinus	8	107	99	99	57	72	114	57	
E._raffinosus	9	19	73	72	81	83	74	82	104

Table S7

A matrix showing the nucleotides and deletions differences between pairs of *rpoB* gene sequences for *Streptococcus* species.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42															
<i>S. acidominimus</i>	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0														
<i>S. adjacens</i>	2	172		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0															
<i>S. anginosus</i>	3	113	172		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0															
<i>S. australis</i>	4	91	168	103		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0															
<i>S. canis</i>	5	109	160	108	99		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0															
<i>S. constellatus</i>	6	110	173	58	109	112		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0															
<i>S. crenoris</i>	7	134	140	148	133	132	153		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0															
<i>S. cricellii</i>	8	113	178	132	122	114	140	156		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																
<i>S. cristatus</i>	9	97	175	104	78	91	106	136	112		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																
<i>S. difficile</i>	10	113	168	105	100	84	113	127	123	119		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																
<i>S. downsi</i>	11	117	180	138	129	111	139	167	70	115	130		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																	
<i>S. durans</i>	12	153	123	149	148	140	149	139	154	141	142	163		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																	
<i>S. dysgalactiae</i>	13	107	161	93	86	47	103	136	108	94	96	107	144		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																
<i>S. equi</i>	14	121	180	120	119	95	117	154	112	108	104	118	154	90		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																	
<i>S. equinus</i>	15	103	163	111	96	87	111	148	129	97	103	129	157	97	115		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																	
<i>S. galiloticus</i>	16	108	168	88	76	82	94	127	121	84	99	123	139	75	104	104		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																	
<i>S. gordoni</i>	17	100	177	110	88	100	113	141	111	69	109	117	154	91	103	96	97		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																		
<i>S. infantarius</i>	18	102	155	96	72	77	106	122	116	90	98	118	139	79	115	97	46	108		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																		
<i>S. infantis</i>	19	101	179	111	51	103	113	135	123	71	110	118	151	94	115	94	90	91	82		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																		
<i>S. intermedius</i>	20	116	179	77	118	127	81	151	135	112	116	147	155	121	131	122	102	120	104	122		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																		
<i>S. mitis</i>	21	89	179	103	48	98	101	126	118	70	100	120	141	89	119	93	80	87	80	37	122		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																	
<i>S. mutans</i>	22	116	161	114	110	101	121	145	118	115	98	123	154	92	92	101	109	111	105	113	127	113		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																	
<i>S. oligolementans</i>	23	102	179	109	71	91	107	140	126	53	119	122	150	84	110	99	90	66	98	72	124	65	120		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																
<i>S. oralis</i>	24	102	166	112	47	94	102	135	121	76	110	122	148	86	107	99	84	83	80	33	119	43	109	63		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0													
<i>S. ovis</i>	25	99	181	119	92	107	111	151	114	93	106	119	164	106	110	94	102	98	106	97	120	96	118	100	97		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0													
<i>S. parasanguinis</i>	26	101	177	96	90	96	92	138	128	82	105	130	142	96	112	97	82	82	85	92	99	86	128	92	84	90		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0												
<i>S. pasteurianus</i>	27	109	163	87	77	83	93	125	123	85	96	122	140	76	106	103	3	98	43	89	99	81	106	91	85	104	79		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0											
<i>S. pluranimulatum</i>	28	102	166	108	88	73	115	130	115	103	91	123	142	75	91	95	84	89	82	103	104	114	97	90	106	97	104	98	84		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
<i>S. pneumoniae</i>	29	92	169	110	50	97	107	128	121	74	104	120	143	88	114	91	83	93	77	39	123	32	110	69	39	100	82	89	90		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
<i>S. porcinus</i>	30	108	157	124	97	97	129	124	118	111	106	124	142	104	116	117	87	112	88	112	126	106	108	113	102	113	108	89	100	104		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
<i>S. pseudopneumoniae</i>	31	91	163	107	43	100	103	128	124	75	101	126	139	90	114	98	78	92	78	36	124	26	106	69	37	97	88	79	96	37	105		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
<i>S. pseudoporcinus</i>	32	100	158	117	101	93	122	120	119	99	96	117	148	97	114	107	93	105	102	106	121	106	104	104	102	105	108	94	96	98	76	106		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
<i>S. pyogenes</i>	33	120	174	97	96	63	103	148	110	98	103	112	147	39	88	106	75	103	84	104	121	98	100	98	95	108	104	77	83	97	102	103	101		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
<i>S. saharolyticus</i>	34	158	121	165	165	144	173	153	169	165	159	166	188	98	150	166	165	148	167	146	168	173	171	167	168	165	181	164	150	151	164	143	170	156	157		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
<i>S. salivarius</i>	35	93	154	92	67	73	92	131	112	76	85	112	140	71	91	88	55	90	59	75	102	81	64	90	67	56	66	69	93	72	94	72	151		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
<i>S. sanguinis</i>	36	96	182	110	95	108	114	140	117	74	111	120	160	106	116	98	100	61	109	99	112	101	123	72	97	91	91	101	114	96	117	106	98	113	170	92		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
<i>S. sinensis</i>	37	98	177	113	92	107	111	143	115	70	115	120	147	103	120	97	102	61	112	89	117	86	127	66	93	85	86	105	124	98	114	99	100	104	178	94	47		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>S. sobrinus</i>	38	112	182	139	116	112	135	150	73	100	124																																														

Table S8

A matrix showing the nucleotides and deletions differences between pairs of *rpoB* gene sequences for *Enterococcus* species.

	1	2	3	4	5	6	7	8	9
E._avium	1	0	0	0	0	0	0	0	0
E._casseliflavus	2	118		0	0	0	0	0	0
E._cecorum	3	113	110		0	0	0	0	0
E._durans	4	108	98	98		0	0	0	0
E._faecium	5	114	99	101	62		0	0	0
E._faecalis	6	103	94	94	99	92		0	0
E._hirae	7	116	115	94	69	71	104		0
E._porcinus	8	114	113	94	83	77	83	71	
E._raffinosus	9	64	102	113	103	118	92	117	109

Table S9

A matrix showing the nucleotides and deletions differences between pairs of 16S-23S rRNA region sequences for *Streptococcus* species.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	
<i>S._adomininus</i>	1		425	111	244	279	170	287	235	236	287	236	322	279	167	258	262	247	270	240	217	240	182	235	238	283	237	262	290	240	182	242	168	150	405	269	223	242	250	390	241	274	290
<i>S._adjacens</i>	2	1065		372	241	274	301	266	564	269	274	479	143	274	384	547	215	244	219	239	256	237	359	256	237	298	244	213	275	237	455	237	417	39	42	216	248	251	371	343	238	329	273
<i>S._anginosus</i>	3	415	991		167	259	79	234	292	159	268	301	287	258	86	343	203	152	206	163	128	169	101	158	165	260	162	201	261	167	188	165	153	119	346	294	186	149	319	385	164	253	287
<i>S._australis</i>	4	495	830	391		157	94	95	435	30	159	352	166	157	223	492	58	35	60	4	51	10	202	29	6	163	13	59	184	19	332	8	294	262	219	55	39	38	282	28	9	204	184
<i>S._canis</i>	5	570	870	519	392		209	202	414	165	14	363	107		264	451	139	158	129	153	180	159	257	160	155	108	158	135	39	157	289	155	203	147	242	136	160	161	227	195	152	65	17
<i>S._constellatus</i>	6	456	905	248	292	474		161	355	90	213	268	202	208	155	406	128	81	132	90	53	96	132	91	92	265	89	128	210	96	252	94	222	180	275	129	101	82	260	328	91	238	28
<i>S._cremoris</i>	7	814	951	740	588	682	666		434	101	204	355	177	204	282	439	123	110	125	91	122	93	263	100	93	220	94	121	213	95	292	93	259	303	244	126	92	109	269	303	92	207	211
<i>S._cristatus</i>	8	717	1209	714	784	782	753	983		441	416	115	421	412	258	251	403	428	403	433	263	442	437	400	426	407	399	439	183	437	239	277	524	400	430	433	241	525	432	363	471		
<i>S._difficilis</i>	9	456	841	349	178	407	272	592	782		169	350	182	165	219	466	72	23	72	26	47	32	209	5	28	161	28	70	176	32	324	30	292	260	235	69	23	12	272	274	25	204	177
<i>S._downei</i>	10	574	893	549	382	211	482	683	793	404		267	199	14	268	457	145	164	135	155	182	161	263	164	157	104	160	141	33	159	271	157	209	153	242	138	162	165	231	197	154	71	6
<i>S._duranus</i>	11	694	1124	678	662	719	640	915	419	656	710		356	361	281	266	328	341	328	350	325	356	270	351	354	327	343	332	348	356	204	354	268	300	449	301	341	342	146	458	349	320	319
<i>S._dysgalactiae</i>	12	923	573	848	680	751	775	797	1067	712	738	965		187	278	430	138	165	136	162	177	162	258	178	162	219	187	136	182	162	334	162	298	115	135	171	172	250	284	161	234	199	
<i>S._equi</i>	13	563	891	538	381	101	482	660	798	408	175	729	743		266	451	141	160	131	153	180	159	257	160	155	108	156	137	39	157	267	155	205	145	242	136	160	161	225	195	152	67	16
<i>S._equinus</i>	14	556	1000	423	500	493	501	770	697	504	521	692	860	529		355	199	228	195	221	206	225	93	220	221	272	197	297	225	180	229	159	120	360	206	228	227	331	397	220	281	267	
<i>S._galolyticus</i>	15	595	1194	643	714	728	712	966	817	712	740	781	1047	721	723	462	481	482	488	453	486	378	483	486	457	485	462	452	486	198	488	258	319	531	459	473	476	328	324	487	404	484	
<i>S._gordonii</i>	16	542	851	432	293	361	395	601	745	305	363	651	700	371	439	711	71	10	56	85	62	184	73	58	149	53	4	146	62	306	62	268	246	195	19	75	80	238	259	55	176	148	
<i>S._infantis</i>	17	478	854	331	174	402	273	625	764	132	394	636	689	403	495	725	298	71	31	36	37	101	24	33	156	34	71	161	37	321	35	293	265	218	72	38	15	253	277	30	199	167	
<i>S._infantis</i>	18	553	838	445	281	352	399	589	748	299	336	659	698	358	437	706	81	301	58	89	64	192	71	60	141	55	10	138	64	304	64	266	238	191	17	77	78	236	259	57	170	138	
<i>S._intermedius</i>	20	477	855	270	239	427	157	626	770	224	444	645	732	446	511	733	333	195	335	240	49	175	46	45	164	44	83	183	47	307	49	271	230	94	54	37	267	285	48	217	168		
<i>S._mitis</i>	21	501	827	386	52	397	294	584	779	182	385	660	678	383	490	712	294	186	291	58	248	296	31	4	165	17	60	168	47	334	4	296	264	215	61	41	40	282	277	9	206	168	
<i>S._mutans</i>	22	665	1002	510	548	638	537	823	740	544	637	709	892	645	514	847	531	523	535	542	540	555		201	202	265	197	188	248	206	220	204	190	164	335	195	209	194	292	394	197	270	269
<i>S._oligoflamentans</i>	23	464	844	357	190	405	285	589	797	49	405	669	718	404	507	710	314	151	305	192	226	202	554	27	160	30	69	175	29	318	27	287	255	232	68	22	9	273	277	24	199	167	
<i>S._oralis</i>	24	492	829	388	49	384	293	587	783	178	380	655	678	370	487	705	292	179	285	53	239	27	553	197		163	15	56	184	4	330	6	292	260	215	57	37	36	280	274	1	202	162
<i>S._ovis</i>	25	567	877	520	373	352	455	708	739	386	374	647	761	356	549	651	388	374	388	374	415	379	642	393	378		154	147	97	163	319	161	257	201	264	142	150	151	229	161	160	143	113
<i>S._parasanguinis</i>	26	486	853	381	156	384	299	574	754	210	385	654	680	379	477	715	266	222	270	154	234	166	557	221	166	381	51	165	19	321	17	291	257	220	52	34	37	257	27	12	201	163	
<i>S._pasteurianus</i>	27	543	844	431	285	359	393	597	751	300	358	659	689	367	442	708	28	297	59	280	331	289	537	312	285	391	267	144	60	304	60	266	242	193	15	73	76	242	256	53	178	144	
<i>S._planitimum</i>	28	585	861	541	432	271	493	706	764	416	275	688	759	281	545	747	377	406	363	431	449	427	634	410	353	408	378		168	294	166	234	176	241	141	171	168	212	204	161	40		
<i>S._pneumoniae</i>	29	502	850	385	63	394	299	589	784	188	387	661	681	387	486	717	296	189	297	62	249	22	558	207	35	381	179	291	433	332	2	284	262	215	61	39	38	262	277	9	204	164	
<i>S._porcinus</i>	30	580	1088	551	622	428	598	847	760	610	502	728	945	455	541	633	593	614	577	624	626	614	605	610	612	587	554	613	330	64	130	425	307	319	300	264	408	377	210	274			
<i>S._pseudopneumoniae</i>	31	503	828	385	57	394	291	587	780	183	384	657	683	383	488	717	295	56	248	18	556	202	33	375	167	291	429	20	610		292	269</td											

Table S10

A matrix showing the nucleotides and deletions differences between pairs of 16S-23S rRNA region sequences for *Enterococcus* species.

	1	2	3	4	5	6	7	8	9
E._avium	1	55	77	148	160	47	149	135	29
E._casseliflavus	2	238		62	115	125	28	116	102
E._cecorum	3	333	294		159	167	58	156	142
E._durans	4	332	280	416		70	115	55	35
E._faecium	5	336	279	416	204		123	17	37
E._faecalis	6	289	261	354	333	307		110	96
E._hirae	7	349	295	431	104	180	348		22
E._porcinus	8	341	271	418	114	193	336	103	
E._raffinosus	9	62	199	307	294	295	252	309	302

Table S11

The length of 16S-23S rRNA region, 16S rRNA gene, intergenic spacer region and 23S rRNA region for all *Streptococcus* and *Enterococcus* species.

Species	16S-23S rRNA region length (bp)	16S rRNA gene length (bp)	Intergenic spacer region length (bp)	23S rRNA gene length (bp)
<i>Streptococcus acidominimus</i>	4486	1523	468	2495
<i>Streptococcus adjacens</i>	4251	1525	218	2508
<i>Streptococcus anginosus</i>	4411	1531	387	2493
<i>Streptococcus australis</i>	4254	1521	240	2493
<i>Streptococcus canis</i>	4301	1524	283	2494
<i>Streptococcus constellatus</i>	4340	1531	315	2494
<i>Streptococcus cremoris</i>	4317	1522	300	2495
<i>Streptococcus criceti</i>	4649	1532	625	2492
<i>Streptococcus cristatus</i>	4260	1522	248	2490
<i>Streptococcus difficile</i>	4295	1524	277	2494
<i>Streptococcus downei</i>	4564	1533	538	2493
<i>Streptococcus durans</i>	4366	1535	326	2505
<i>Streptococcus dysgalactiae</i>	4301	1524	283	2494
<i>Streptococcus equi</i>	4429	1524	414	2491
<i>Streptococcus equinus</i>	4732	1531	708	2493
<i>Streptococcus gallolyticus</i>	4284	1524	270	2490
<i>Streptococcus gordonii</i>	4267	1532	243	2492
<i>Streptococcus infantarius</i>	4284	1524	269	2491
<i>Streptococcus infantis</i>	4258	1523	242	2493
<i>Streptococcus intermedius</i>	4291	1531	267	2493
<i>Streptococcus mitis</i>	4258	1521	244	2493
<i>Streptococcus mutans</i>	4408	1532	384	2492
<i>Streptococcus oligofermentans</i>	4263	1524	249	2490
<i>Streptococcus oralis</i>	4256	1522	242	2492
<i>Streptococcus ovis</i>	4295	1533	265	2497
<i>Streptococcus parasanguinis</i>	4261	1523	245	2493
<i>Streptococcus pasteurianus</i>	4284	1524	268	2492
<i>Streptococcus pluranimalium</i>	4304	1534	276	2494
<i>Streptococcus pneumoniae</i>	4258	1521	244	2493
<i>Streptococcus porcinus</i>	4558	1524	538	2496
<i>Streptococcus pseudopneumoniae</i>	4260	1521	244	2495
<i>Streptococcus pseudoporcinus</i>	4498	1524	478	2496
<i>Streptococcus pyogenes</i>	4436	1524	418	2494
<i>Streptococcus saccharolyticus</i>	4263	1533	224	2506
<i>Streptococcus salivarius</i>	4283	1523	269	2491
<i>Streptococcus sanguinis</i>	4275	1523	260	2492
<i>Streptococcus sinensis</i>	4270	1532	248	2490
<i>Streptococcus sobrinus</i>	4424	1532	403	2489

Species	16S-23S rRNA region length (bp)	16S rRNA gene length (bp)	Intergenic spacer region length (bp)	23S rRNA gene length (bp)
<i>Streptococcus suis</i>	4420	1524	401	2495
<i>Streptococcus tigurinus</i>	4259	1524	242	2493
<i>Streptococcus uberis</i>	4352	1524	336	2492
<i>Streptococcus urinalis</i>	4292	1524	273	2495
<i>Enterococcus avium</i>	4273	1540	231	2502
<i>Enterococcus casseliflavus</i>	4266	1541	220	2505
<i>Enterococcus cecorum</i>	4224	1540	182	2502
<i>Enterococcus durans</i>	4313	1541	268	2504
<i>Enterococcus faecium</i>	4381	1541	335	2505
<i>Enterococcus faecalis</i>	4262	1542	217	2503
<i>Enterococcus hirae</i>	4366	1541	321	2504
<i>Enterococcus porcinus</i>	4346	1541	301	2504
<i>Enterococcus raffinosus</i>	4258	1540	215	2503

Table S12

The intraspecies polymorphism of 16S-23S rRNA region sequence within *Streptococcus* and *Enterococcus* genera^a.

Species	The lowest intraspecies nucleotide difference compared to GenBank sequences	The highest intraspecies nucleotide difference compared to GenBank sequences	Amount of complete genome sequences/genome assembly/ 16S-23S rRNA region (GenBank)
<i>Streptococcus acidominimus</i>	-	-	0/1
<i>Streptococcus anginosus</i>	0 (0%)	49 (1.11%)	6/1
<i>Streptococcus australis</i>	111 (2.6%)	111 (2.6%)	0/1
<i>Streptococcus canis</i>	3 (0.07%)	3 (0.07%)	0/1
<i>Streptococcus constellatus</i>	0 (0%)	18 (0.41%)	3/0
<i>Streptococcus cremoris</i>	0 (0%)	18 (0.42%)	14/0
<i>Streptococcus criceti</i>	0 (0%)	1 (0.02%)	0/0/3
<i>Streptococcus durans</i>	0 (0%)	73 (2.74%)	3/0
<i>Streptococcus dysgalactiae</i>	0 (0%)	39 (0.91%)	6/7
<i>Streptococcus equi</i>	0 (0%)	67 (1.51%)	6/9
<i>Streptococcus equinus</i>	-	-	0/4
<i>Streptococcus gallolyticus</i>	0 (0%)	7 (0.16%)	5/1
<i>Streptococcus gordonii</i>	0 (0%)	21 (0.49%)	5/3
<i>Streptococcus infantarius</i>	0 (0%)	40 (0.93%)	2/0
<i>Streptococcus intermedius</i>	0 (0%)	20 (0.47%)	6/1
<i>Streptococcus mitis</i>	0 (0%)	37 (0.87%)	5/0
<i>Streptococcus mutans</i>	0 (0%)	20 (0.45%)	9/2/3
<i>Streptococcus oligofermentans</i>	0 (0%)	4 (0.09%)	1/2
<i>Streptococcus oralis</i>	0 (0%)	55 (1.29%)	4/1
<i>Streptococcus parasanguinis</i>	0 (0%)	40 (0.94%)	2/0
<i>Streptococcus pasteurianus</i>	0 (0%)	2 (0.05%)	2/1
<i>Streptococcus pluranimalium</i>	0 (0%)	16 (0.37%)	2/0
<i>Streptococcus pneumoniae</i>	0 (0%)	496 (11.65%)	52/83
<i>Streptococcus porcinus</i>	0 (0%)	0 (0%)	0/1
<i>Streptococcus pseudopneumoniae</i>	16 (0.4%)	16 (0.4%)	1/0
<i>Streptococcus pseudoporcinius</i>	0 (0%)	0 (0%)	0/1
<i>Streptococcus pyogenes</i>	0 (0%)	98 (2.2%)	136/65
<i>Streptococcus salivarius</i>	0 (0%)	33 (0.77%)	9/2
<i>Streptococcus sanguinis</i>	7 (0.16%)	31 (0.72%)	1/5
<i>Streptococcus sobrinus</i>	0 (0%)	15 (0.34%)	4/2
<i>Streptococcus suis</i>	0 (0%)	58 (1.31%)	43/2
<i>Streptococcus tigurinus</i>	38 (0.9%)	38 (0.9%)	1/0
<i>Streptococcus uberis</i>	0 (0%)	5 (0.11%)	2/2
<i>Streptococcus urinalis</i>	0 (0%)	0 (0%)	0/1
<i>Enterococcus casseliflavus</i>	1 (0.02%)	4 (0.09%)	2/0
<i>Enterococcus cecorum</i>	1 (0.02%)	28 (0.66%)	6/1

Species	The lowest intraspecies nucleotide difference compared to GenBank sequences	The highest intraspecies nucleotide difference compared to GenBank sequences	Amount of complete genome sequences/genome assembly/ 16S-23S rRNA region (GenBank)
<i>Enterococcus durans</i>	0 (0%)	42 (0.97%)	3/0
<i>Enterococcus faecium</i>	0 (0%)	102 (2.33%)	70/58
<i>Enterococcus faecalis</i>	0 (0%)	17 (0.4%)	31/1
<i>Enterococcus hirae</i>	0 (0%)	71 (2.67%)	3/1

^a For species not included in a Table (*Streptococcus adjacens*, *Streptococcus cristatus*, *Streptococcus difficile*, *Streptococcus downei*, *Streptococcus infantis*, *Streptococcus ovis*, *Streptococcus saccharolyticus*, *Streptococcus sinensis*, *Enterococcus avium*, *Enterococcus porcinus*, *Enterococcus raffinosus*), there are no reference genomes available.

Figure S1

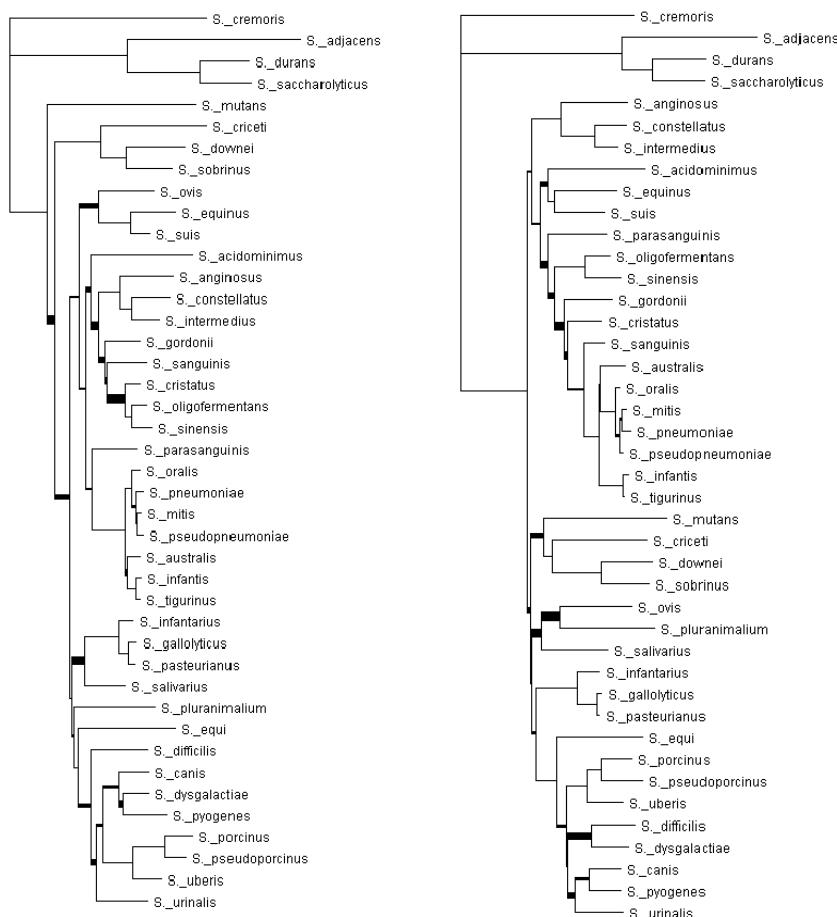
The comparison between phylogenetic trees based on 16S-23S rRNA region and 16S rRNA, *rpoB*, *sodA* and *tuf* genes for both *Streptococcus* and *Enterococcus* species.

The thicker branches reflect a low topological score and result from different positions on the compared trees.

Streptococcus

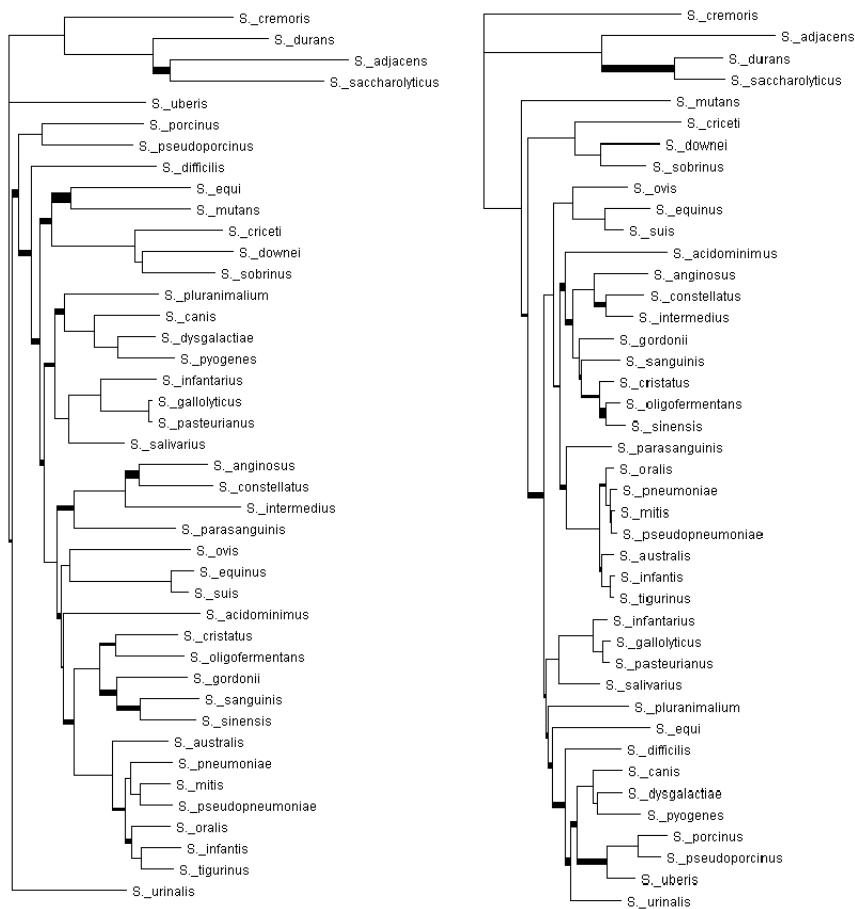
16S rRNA gene vs 16S-23S rRNA region

Overall topological score = 72.4 %



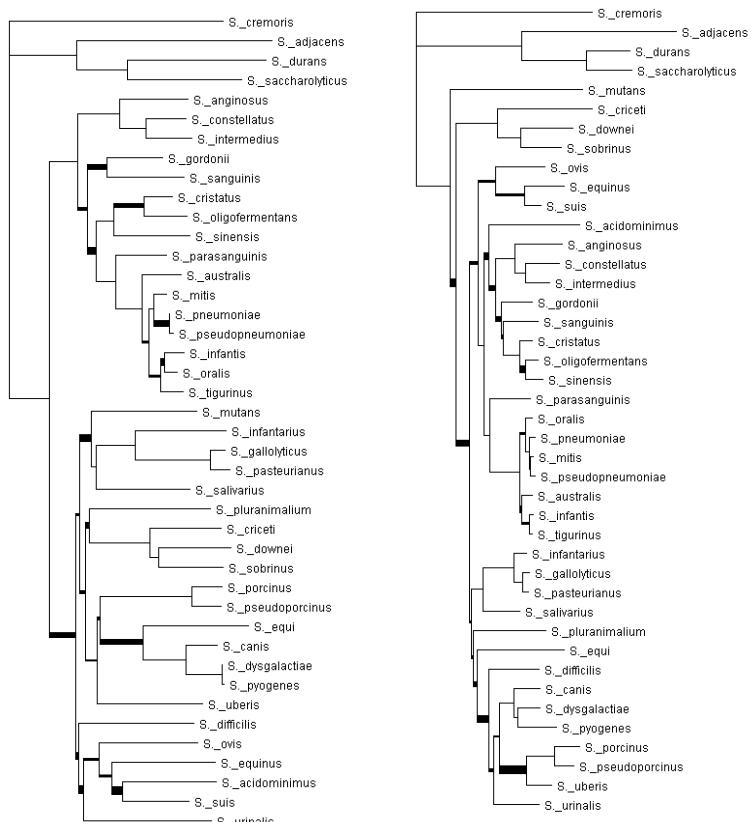
rpoB gene vs 16S-23S rRNA region

Overall topological score = 71.6 %



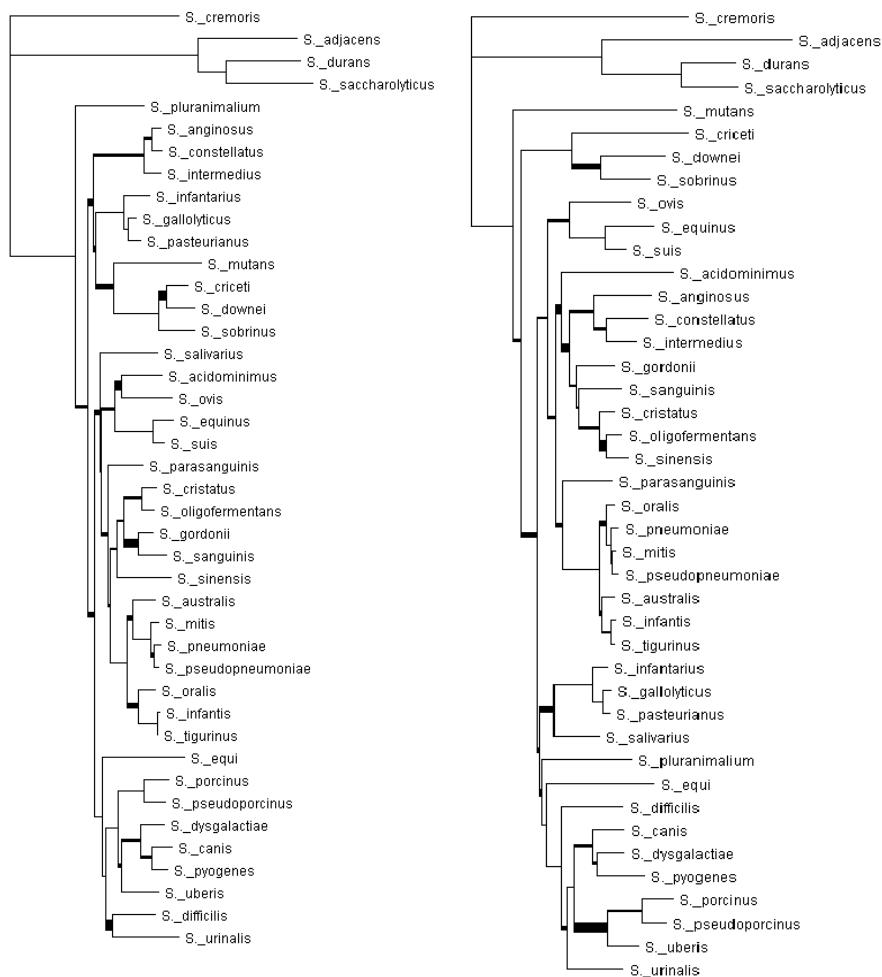
sodA gene vs 16S-23S rRNA region

Overall topological score = 70.4 %



tuf gene vs 16S-23S rRNA region

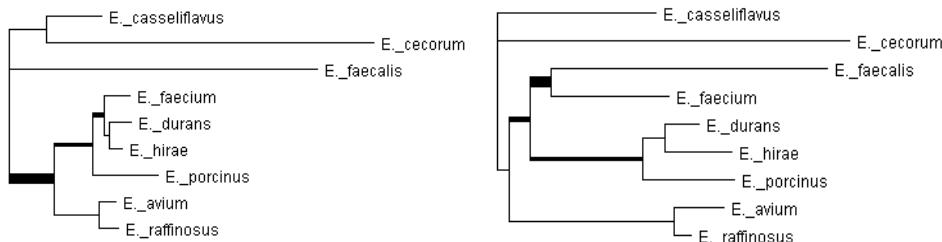
Overall topological score = 70 %



Enterococcus

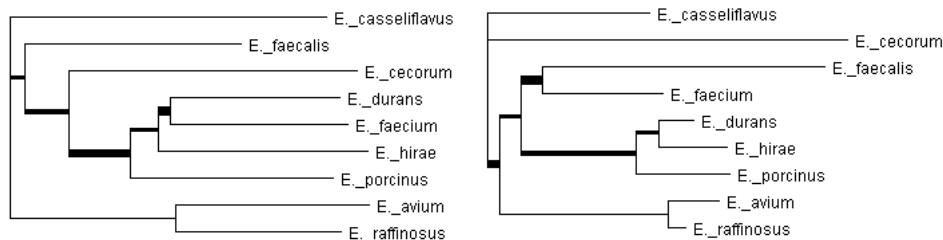
16S rRNA gene vs 16S-23S rRNA region

Overall topological score = 76.7 %



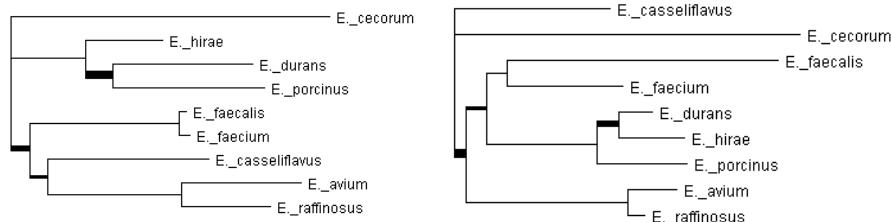
rpoB gene vs 16S-23S rRNA region

Overall topological score = 62.5 %



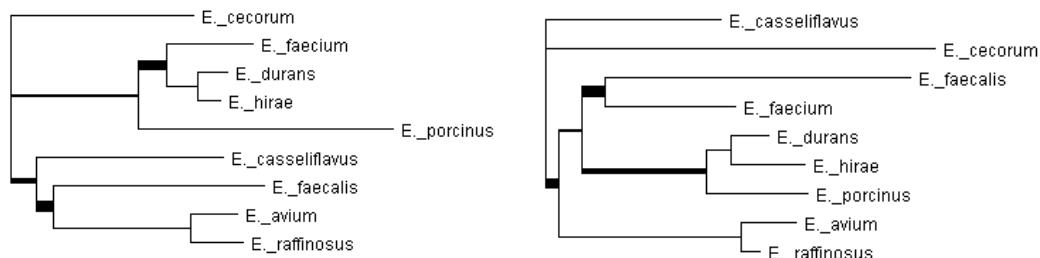
sodA gene vs 16S-23S rRNA region

Overall topological score = 75.6 %



tuf gene vs 16S-23S rRNA region

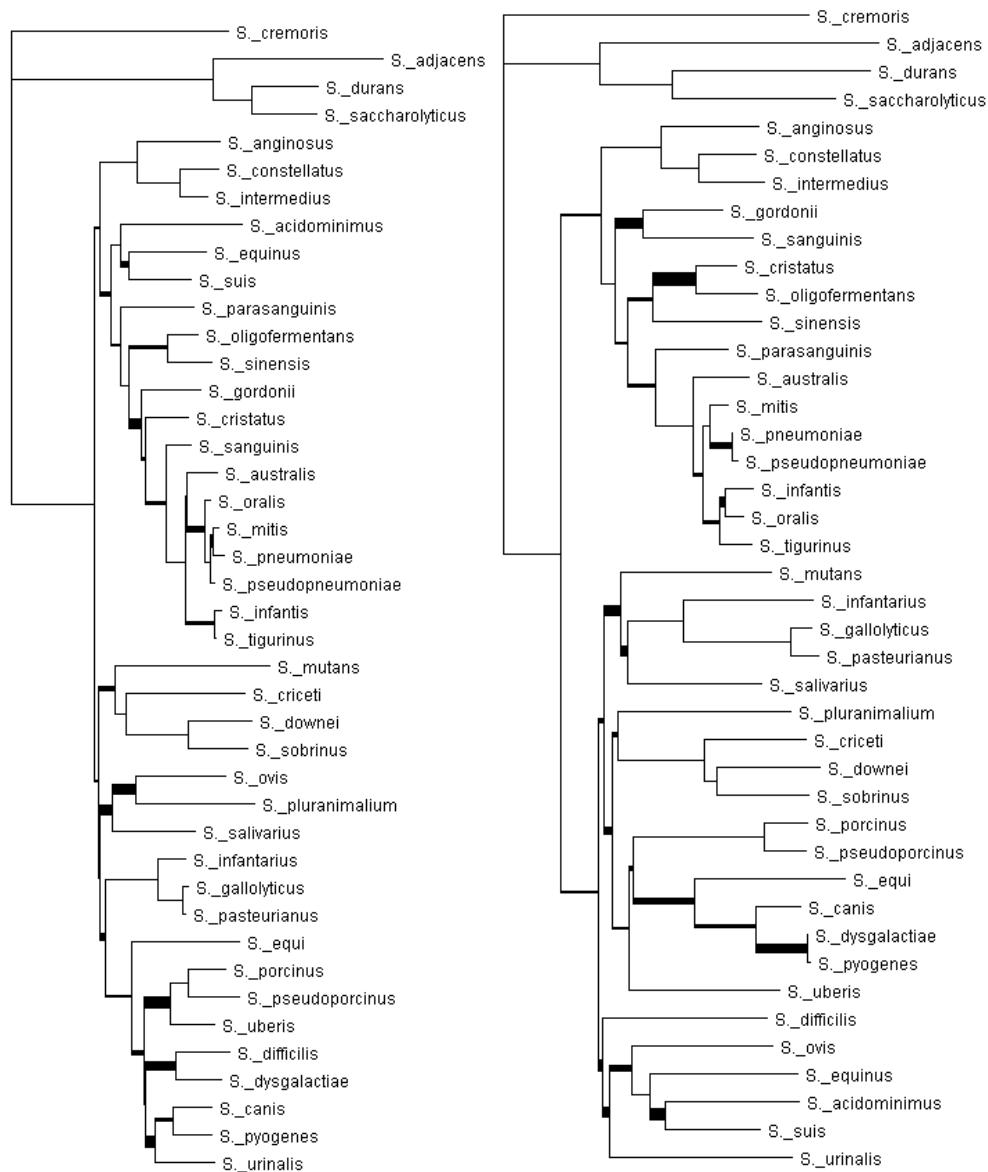
Overall topological score = 66.4 %



Streptococcus

16S rRNA gene vs *sodA* gene

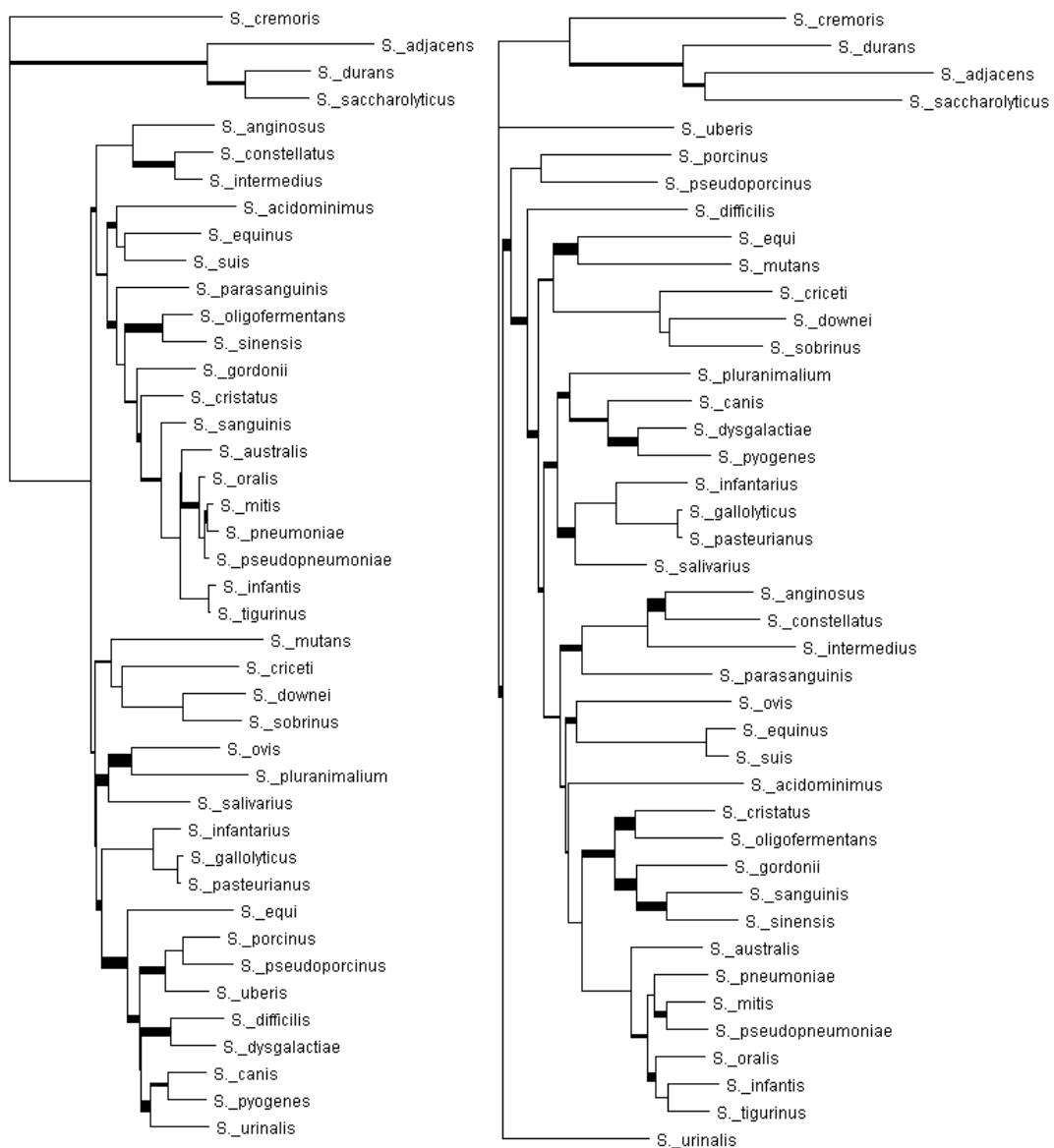
Overall topological score = 66.5 %



Streptococcus

16S rRNA gene vs *rpoB* gene

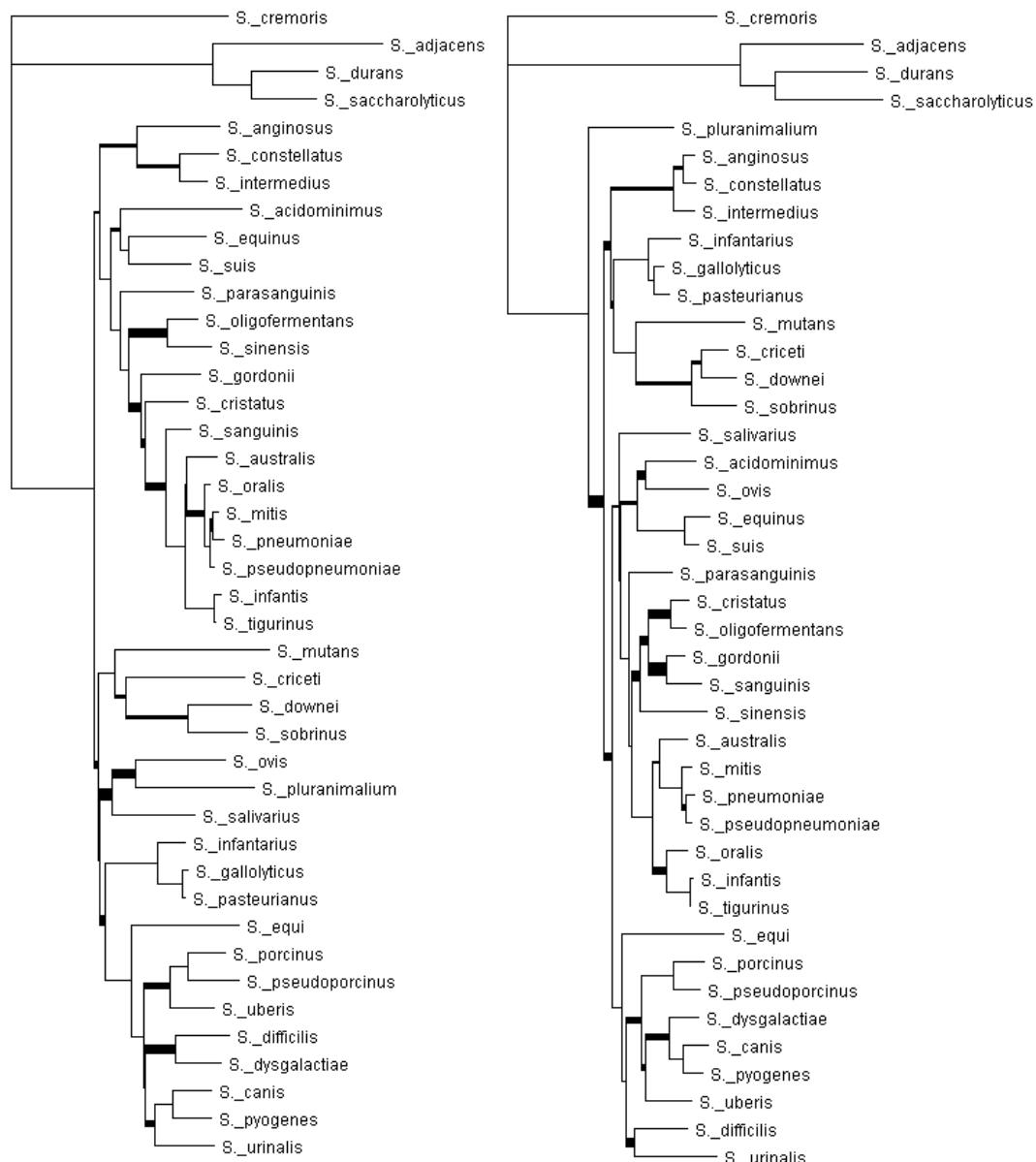
Overall topological score = 61.7 %



Streptococcus

16S rRNA gene vs *tuf* gene

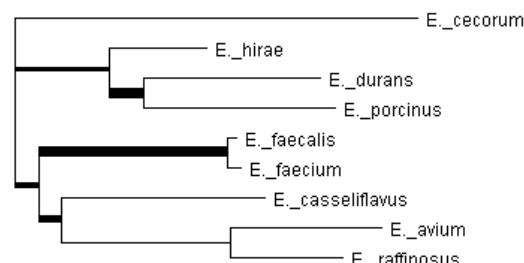
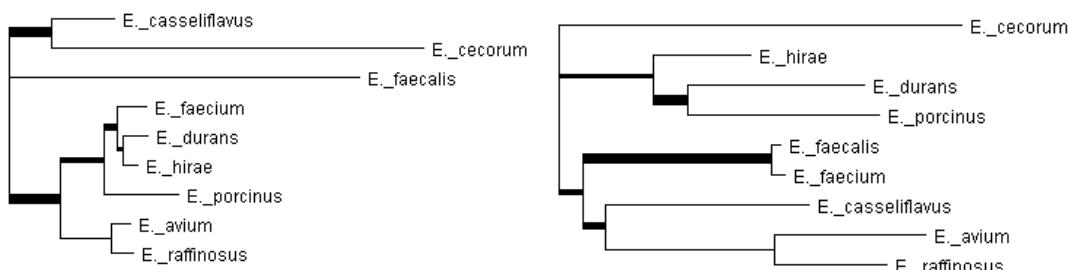
Overall topological score = 69.1 %



Enterococcus

16S rRNA gene vs *sodA* gene

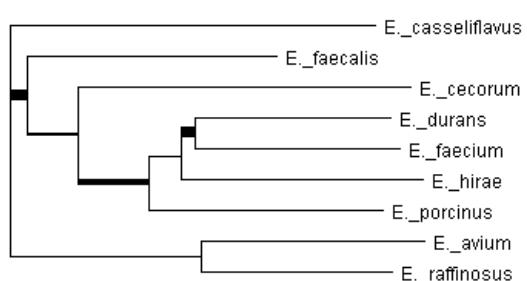
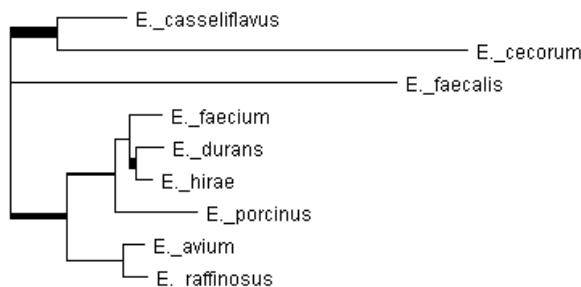
Overall topological score = 56.4 %



Enterococcus

16S rRNA gene vs *rpoB* gene

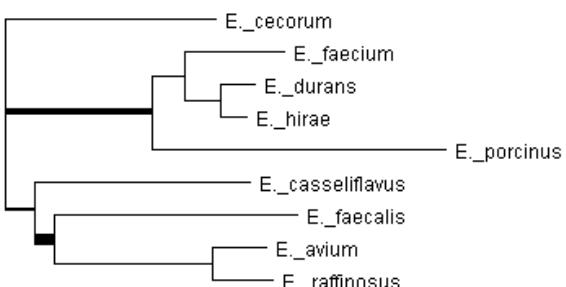
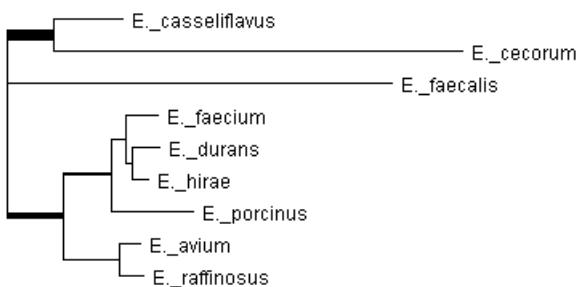
Overall topological score = 67.0 %



Enterococcus

16S rRNA gene vs *tuf* gene

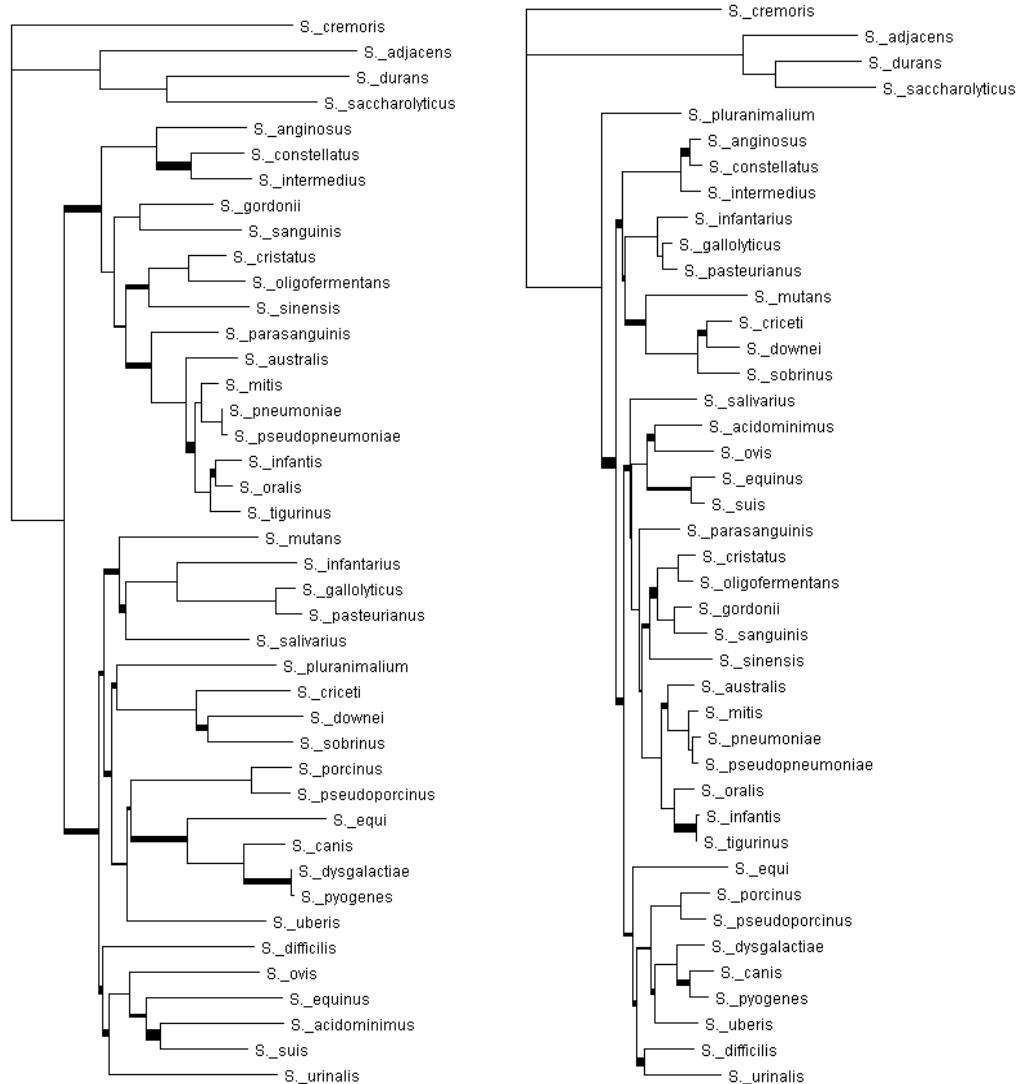
Overall topological score = 78.9 %



Streptococcus

tuf gene vs *sodA* gene

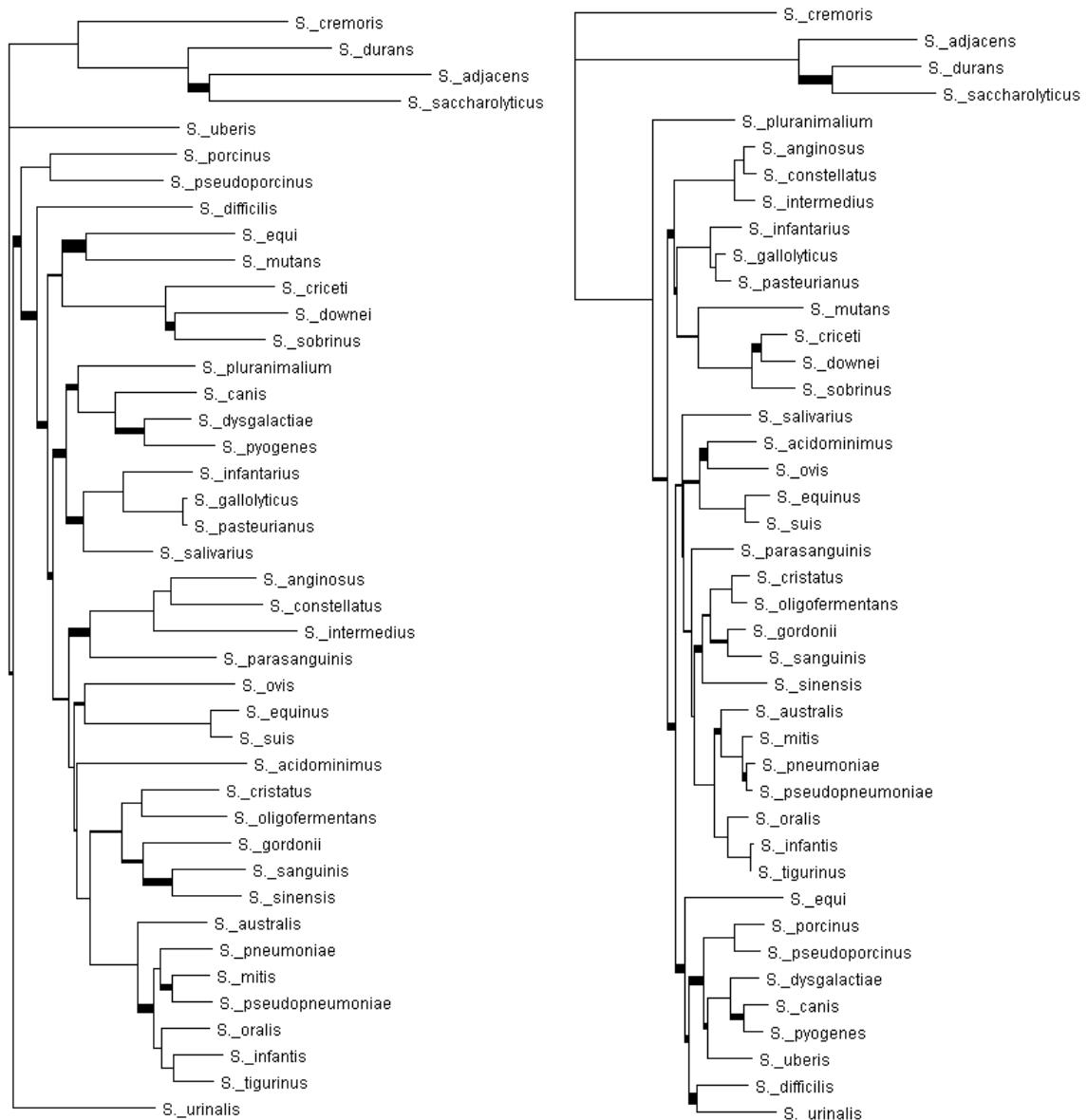
Overall topological score = 70.4 %



Streptococcus

rpoB gene vs *tuf* gene

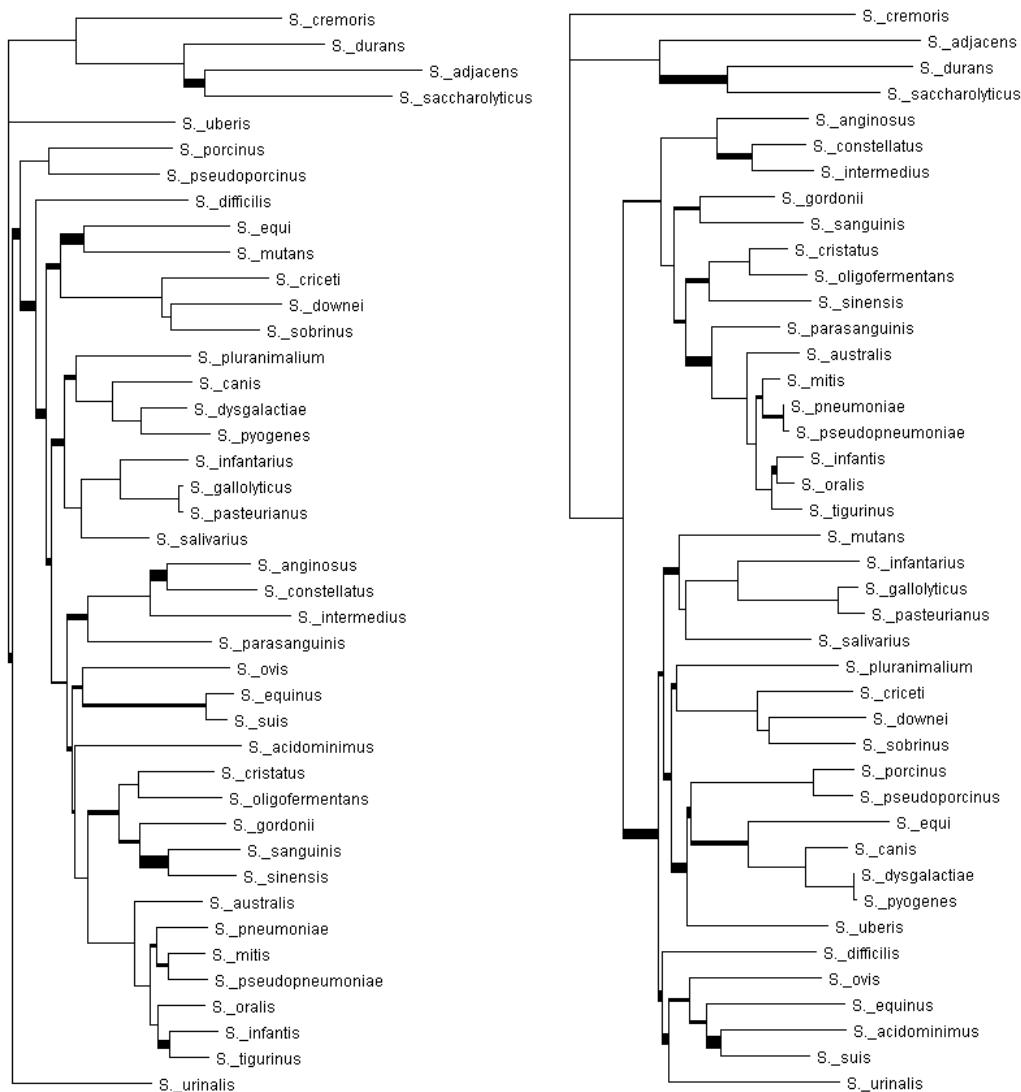
Overall topological score = 70.3 %



Streptococcus

rpoB gene vs *sodA* gene

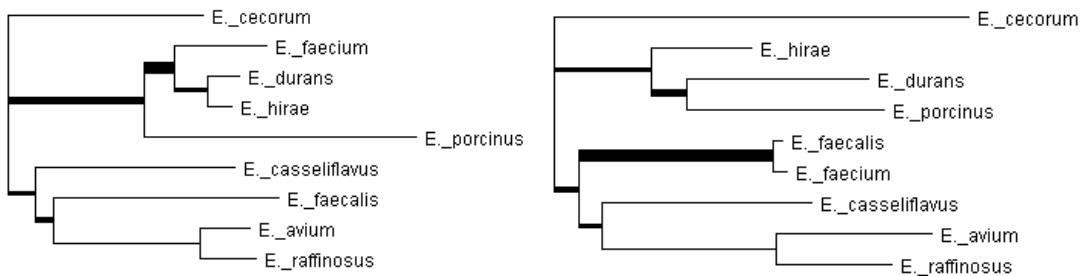
Overall topological score = 67.3 %



Enterococcus

tuf gene vs *sodA* gene

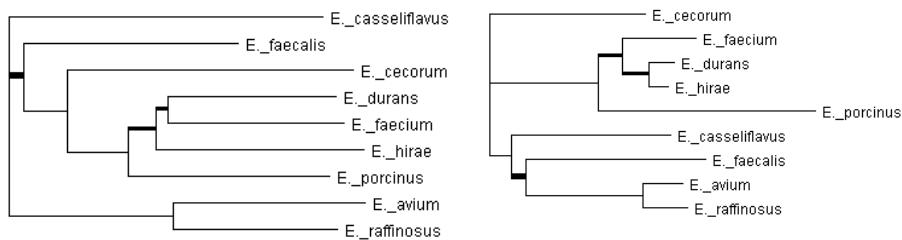
Overall topological score = 62.8 %



Enterococcus

rpoB gene vs *tuf* gene

Overall topological score = 80.6 %



Enterococcus

rpoB gene vs *sodA* gene

Overall topological score = 68.9 %

