

Table S1. Consensus sequence of the *tuf* gene for *Staphylococcus* spp.

atgagagataaattgaaataactttaytaagaataggagagattaataatggcwaagaaaattygaycgycwcwwwarmmcatgcc
aatatyggdacwatyyggwcacgtgaccayggtaaacdacwttaamagcdgcwatygchacwgtwwtrkdaarmrttcyggtgay
dsdvwwgcwcrwtcwtaygmymwratyrayarygcddcwgaagaaamagarcgtggtatyacwatyaabacdckwcayatygart
ayvmwacrvnwmwcgctactaygc当地caygtwgaytgyccwgwcaygckgactaygtkaadaayatgatyachggkkcdgcnc
aatggayggghgskathtrgtwgtwtcwgchgayggccaatgccwcaaackcgtgarcAYATYYDTTATCWCFTAAYGT
WGGWGTDCNCNGCDYTWTGTATTYTTAAAYAAAGYTGAYMWRGTWGACGAYGAAGAAYTAYTAGAATT
AGTWGAAATGGAAGTWCCTGAYYTAYTAWSHGAATAYGAYTWYCCWGGHAYGAYRYNCCWRTWATKY
TGGWTCWGCYTDAAGCDYTWAARGCGWHVMVVHYWHGARVVAACHTNDGAMYTAATGVAH
BHDGTWGAYDMNTWYATYCCAACWCCRGAACGYGAYTSWGAARCMATTCRTGATGCCDRTWGARGAY
GTWTTCTCAATHACWGGTCGYGGTACWGTWGYDACPGBCGTGTGAAACGTGGDCAARTYAMWGTYGGY
GMHGARRTHGAAATYATYGGWHTNNMHGANVrdwBHNNNAARACWACDTWACWGGYGTWGRATGT
TYCGTAARTTRYTRGAYTWYGCTGAAGCTGGHAYAAYATYGGTCDTTATTACGTGGBRTHKDCGTGAHGA
HRTHHMHCYTGGWCAAGTWHTAGCDRMNCCHGGHWSWATYAcddcayacwrrvtyamwkcdgahgtwtayg
twttatcwaagahaagggyggcgtcwyacdccdtctcdswaaytaycgcycrcarttytayttccgtacwacwgaytaacwggyg
twrthmvhytacmagaaggghryhgaaatggtwatgcctggbgayaayrthraaatravnhtwgarytrathkcwmmwatgcdatyg
aagayggwacdcgbttypcwatcgtcgtgarggyggmcgtacwgtwggwtcaggygtgtwwcwnhhakhnwnvmngctaa

Table S2. *In silico* analysis of *tuf* gene fragments. *S.*, *Staphylococcus*.

Species grown	Tuf32/900			Tuf108/408			Tuf387/765			Tuf216/522		
	Proposed species	Sequence identity (%)	Accession number	Proposed species	Sequence identity (%)	Accession number	Proposed species	Sequence identity (%)	Accession number	Proposed species	Sequence identity (%)	Accession number
<i>S. arlettae</i>	<i>S. saprophyticus</i>	94	CP022093.2	sequence could not be retrieved			<i>S. arlettae</i>	100	EU652781.1	<i>S. kloosi</i>	96	CP027846.1
<i>S. auricularis</i>	<i>S. auricularis</i>	99	LS483491.1	<i>S. auricularis</i>	100	LS483491.1	<i>S. auricularis</i>	100	LS483491.1	<i>S. auricularis</i>	100	LS483491.1
<i>S. carnosus</i>	<i>S. carnosus</i>	100	AM295250.1	<i>S. condimenti</i>	100	CP018776.1	<i>S. carnosus</i>	100	CP016760.1	<i>S. kloosi</i>	96	CP027846.1
<i>S. chromogenes</i>	<i>S. hyicus</i>	97	LS483304.1	<i>S. hyicus</i>	97	LS483304.1	<i>S. chromogenes</i>	100	EU652790.1	<i>S. hyicus</i>	97	LS483304.1
<i>S. cohnii</i>	<i>S. cohnii</i>	100	CP033735.1	<i>S. cohnii</i>	100	CP033735.1	<i>S. cohnii</i>	100	CP033735.1	<i>S. cohnii</i>	100	CP033735.1
<i>S. epidermidis</i>	<i>S. epidermidis</i>	99	CP034115.1	<i>S. epidermidis</i>	100	CP034115.1	<i>S. epidermidis</i>	100	CP034115.1	<i>S. epidermidis</i>	100	CP034115.1
<i>S. equorum</i>	<i>S. equorum</i>	100	CP013980.1	<i>S. equorum</i>	100	CP013980.1	<i>S. equorum</i>	100	CP013980.1	<i>S. equorum</i>	100	CP013980.1
<i>S. fleuretti</i>	<i>S. sciuri</i>	97	CP020377.1	<i>S. sciuri</i>	98	CP020377.1	<i>S. fleuretti</i>	100	EU652798.1	<i>S. sciuri</i>	98	CP020377.1
<i>S. haemolyticus</i>	<i>S. haemolyticus</i>	99	LT963441.1	<i>S. hominis</i>	98	CP020618.1	<i>S. hominis</i>	98	CP014107.1	<i>S. hominis</i>	98	CP020618.1
<i>S. hominis</i>	<i>S. hominis</i>	100	LT963442.1	<i>S. hominis</i>	100	LT963442.1	<i>S. hominis</i>	100	CP033732.1	<i>S. hominis</i>	100	LT963442.1
<i>S. lugdunensis</i>	<i>S. lugdunensis</i>	100	CP020769.1	<i>S. lugdunensis</i>	100	LS483312.1	<i>S. lugdunensis</i>	100	LS483482.1	<i>S. lugdunensis</i>	100	LS483312.1
<i>S. pasteurii</i>	<i>S. pasteurii</i>	100	CP017463.1	<i>S. pasteurii</i>	100	CP017463.1	<i>S. pasteurii</i>	100	CP017463.1	<i>S. pasteurii</i>	100	CP017463.1
<i>S. saprophyticus</i>	<i>S. saprophyticus</i>	100	CP022093.2	<i>S. saprophyticus</i>	100	CP022093.2	<i>S. saprophyticus</i>	100	LT963436.1	<i>S. saprophyticus</i>	100	CP022093.2
<i>S. sciuri</i>	<i>S. sciuri</i>	99	CP020377.1	<i>S. sciuri</i>	100	CP020377.1	<i>S. sciuri</i>	100	CP020377.1	<i>S. sciuri</i>	99	CP020377.1
<i>S. simulans</i>	<i>S. simulans</i>	99	CP015642.1	<i>S. simulans</i>	99	CP015642.1	<i>S. simulans</i>	100	CP015642.1	<i>S. simulans</i>	100	CP015642.1
<i>S. succinus</i>	<i>S. succinus</i>	100	CP018199.1	<i>S. succinus</i>	100	CP018199.1	<i>S. succinus</i>	100	CP018199.1	<i>S. succinus</i>	100	CP018199.1
<i>S. warneri</i>	<i>S. warneri</i>	99	CP003668.1	<i>S. warneri</i>	100	CP003668.1	<i>S. warneri</i>	100	CP003668.1	<i>S. warneri</i>	100	CP003668.1
<i>S. xylosus</i>	<i>S. xylosus</i>	100	CP008724.1	Sequence could not be retrieved			<i>S. xylosus</i>	100	CP008724.1	<i>S. xylosus</i>	100	CP008724.1

Table S4. Estimates of the average evolutionary divergence over sequence pairs within *Staphylococcus* species. Cases for which it was not possible to estimate evolutionary distances, due to the presence of a single sequence in the database, are denoted with na (non-applicable).

Species	Number of nucleotide differences
<i>Staphylococcus agnetis</i>	1
<i>Staphylococcus argensis</i>	na
<i>Staphylococcus argenteus</i>	1
<i>Staphylococcus arlettae</i>	0
<i>Staphylococcus aureus</i>	3
<i>Staphylococcus auricularis</i>	4
<i>Staphylococcus capititis</i>	0
<i>Staphylococcus caprae</i>	0
<i>Staphylococcus carnosus</i>	0
<i>Staphylococcus chromogenes</i>	3
<i>Staphylococcus cohnii</i>	14
<i>Staphylococcus condimenti</i>	0
<i>Staphylococcus delphini</i>	0
<i>Staphylococcus devriesei</i>	3
<i>Staphylococcus edaphicus</i>	na
<i>Staphylococcus epidermidis</i>	1
<i>Staphylococcus equorum</i>	4
<i>Staphylococcus felis</i>	2
<i>Staphylococcus fleurettii</i>	0
<i>Staphylococcus gallinarum</i>	6
<i>Staphylococcus haemolyticus</i>	3
<i>Staphylococcus hominis</i>	6
<i>Staphylococcus hyicus</i>	1
<i>Staphylococcus intermedius</i>	na
<i>Staphylococcus kloosii</i>	0
<i>Staphylococcus lento</i>	4
<i>Staphylococcus lugdunensis</i>	2
<i>Staphylococcus lutrae</i>	na
<i>Staphylococcus massiliensis</i>	na
<i>Staphylococcus microti</i>	0
<i>Staphylococcus muscae</i>	na
<i>Staphylococcus nepalensis</i>	1
<i>Staphylococcus pasteurii</i>	0
<i>Staphylococcus petrasii</i>	11
<i>Staphylococcus pettenkoferi</i>	3
<i>Staphylococcus pseudintermedius</i>	1
<i>Staphylococcus rostri</i>	na
<i>Staphylococcus saprophyticus</i>	7
<i>Staphylococcus schleiferi</i>	1
<i>Staphylococcus schweitzeri</i>	na

<i>Staphylococcus sciuri</i>	5
<i>Staphylococcus simiae</i>	na
<i>Staphylococcus simulans</i>	1
<i>Staphylococcus stepanovicii</i>	na
<i>Staphylococcus succinus</i>	4
<i>Staphylococcus vitulinus</i>	1
<i>Staphylococcus warneri</i>	3
<i>Staphylococcus xylosus</i>	11

Table S5. Comparison of expected and observed relative abundance of staphylococcal species for mock communities M1, M2, and M3, and amplicon-based mock communities R1, R2, R3, R4, and R5 based on amplicon sequencing results with primer pair Tuf387/765

Species	R1		R2		R3		R4		R5		M1		M2		M3	
	Expected abundance (%)	Observed abundance (%)														
<i>Staphylococcus carnosus</i>	9,53	9,89	10,66	11,50	8,48	9,28	9,12	11,72	8,01	10,96	12,91	25,84	0,05	0,06	32,74	35,83
<i>Staphylococcus epidermidis</i>	12,30	12,62	13,76	12,38	10,94	10,76	11,78	11,36	10,34	9,95	10,25	6,94	0,02	0,03	0,04	0,02
<i>Staphylococcus equorum</i>	8,44	10,38	9,43	8,34	7,50	7,70	8,07	9,50	7,09	8,60	10,25	6,51	13,34	9,11	0,26	0,05
<i>Staphylococcus haemolyticus</i>	0,00	0,00	0,00	0,00	11,08	9,86	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
<i>Staphylococcus hominis</i>	10,55	6,41	0,00	0,00	9,38	6,78	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
<i>Staphylococcus lugdunensis</i>	15,04	14,03	16,81	17,21	13,37	13,12	14,39	15,20	12,64	13,22	0,00	0,00	0,00	0,00	0,00	0,00
<i>Staphylococcus pasteuri</i>	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	12,21	8,72	0,00	0,00	0,00	0,00	0,00	0,00
<i>Staphylococcus saprophyticus</i>	10,47	8,04	11,70	8,27	9,31	7,27	10,02	7,78	8,80	7,21	40,82	16,68	53,09	19,75	1,64	0,27
<i>Staphylococcus sciuri</i>	6,41	7,91	7,16	9,22	5,70	6,86	6,13	7,33	5,38	6,36	0,00	0,00	0,00	0,00	0,00	0,00
<i>Staphylococcus succinus</i>	14,26	11,13	15,94	11,64	12,68	9,40	13,64	10,02	11,98	9,35	0,00	0,00	0,00	0,00	0,00	0,00
<i>Staphylococcus warneri</i>	0,00	0,00	0,00	0,00	0,00	0,00	14,39	7,65	12,64	7,51	0,00	0,00	0,00	0,00	0,00	0,00
<i>Staphylococcus xylosus</i>	13,01	11,80	14,54	12,09	11,57	10,68	12,45	11,43	10,93	11,17	25,76	28,80	33,50	43,26	65,32	62,72