

Supplementary Table 1 – Information on the 16S rDNA nucleotide sequences of a selected group of bacterial isolates.

Isolate	Animal	Phenotypic Identification ¹	Nucleotide Sequence Length	Closest Reference Sequence Match	Query cover	E-value	Nucleotide Sequence Identity	Accession Number	Assigned Phylotype*
8	462	IX	1087	Pseudomonas plecoglossicida strain NBRC 103162 16S ribosomal RNA gene, partial sequence	99%	0.0	99%	NR_114226.1	<i>Pseudomonas</i>
9	467	VII	638	[Clostridium] bifermentans strain JCM 1386 16S ribosomal RNA gene, partial sequence	97%	0.0	99%	NR_113323.1	<i>Paraclostridium</i>
11	466	II	246	Enterococcus faecium strain NBRC 100486 16S ribosomal RNA gene, partial sequence	95%	0.0	99%	NR_113904.1	<i>Enterococcus</i>
22	462	I	1136	Staphylococcus saprophyticus subsp. bovis strain GTC 843 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_041324.1	<i>Staphylococcus</i>
29	462	V	582	Shigella sonnei strain CECT 4887 16S ribosomal RNA gene, partial sequence	99%	0.0	99%	NR_104826.1	<i>Enterobacteriaceae</i>
43	467	IX	1049	Clostridium baratii strain IP 2227 16S ribosomal RNA gene, complete sequence	100%	0.0	99%	NR_029229.1	<i>Clostridium baratii</i>

54	383	IX	710	[Eubacterium] tenue strain ATCC 25553 16S ribosomal RNA gene, partial sequence	99%	0.0	97%	NR_115794.1	<i>Paeniclostridium</i>
72	467	VII	1036	[Clostridium] sordellii strain JCM 3814 16S ribosomal RNA gene, partial sequence	100%	0.0	98%	NR_113140.1	<i>Peptostreptococcaceae</i>
79	399	VII	1095	Romboutsia lituseburensis strain ATCC 25759 16S ribosomal RNA gene, partial sequence	99%	0.0	98%	NR_118728.1	<i>Romboutsia</i>
84	462	VII	455	[Clostridium] bifermentans strain JCM 1386 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_113323.1	<i>Paraclostridium bifermentans</i>
91	501	IX	400	Bacillus anthracis strain SBS1 16S ribosomal RNA gene, partial sequence	87%	2,00E-149	99%	NR_118536.1	<i>Bacillus anthracis</i>
101	519	VII	617	[Clostridium] bifermentans strain JCM 1386 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_113323.1	<i>Paraclostridium bifermentans</i>
104	519	X	1001	Clostridium perfringens strain ATCC 13124 16S ribosomal RNA gene, complete sequence	99%	0.0	99%	NR_121697.1	<i>Clostridium perfringens</i>
116	636	II	600	Enterococcus faecalis strain NBRC 100480	100%	0.0	94%	NR_113901.1	<i>Enterococcaceae</i>

				16S ribosomal RNA gene, partial sequence					
117	636	VII	955	Clostridium tertium strain JCM 6289 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_113325.1	Clostridium tertium
131	516	VII	1018	[Clostridium] bifermentans strain JCM 1386 16S ribosomal RNA gene, partial sequence	99%	0.0	99%	NR_113323.1	Paraclostridium bifermentans
137	516	III	719	Stenotrophomonas maltophilia strain ATCC 13637 16S ribosomal RNA gene, partial sequence	100%	0.0	98%	NR_112030.1	Stenotrophomonas
147	501	VII	958	Bacillus thuringiensis strain NBRC 101235 16S ribosomal RNA gene, partial sequence	99%	0.0	98%	NR_112780.1	Bacillus
153	516	II	985	Enterococcus hirae strain ATCC 9790 16S ribosomal RNA gene, complete sequence	99%	0.0	99%	NR_075022.1	Enterococcus
170	396	IX	1062	Pseudomonas plecoglossicida strain NBRC 103162 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_114226.1	Pseudomonas
184	462	II	629	Pseudomonas alcaligenes strain IAM 12411 16S ribosomal	52%	3,00E-85	82%	NR_043419.1	Pseudomonadales

				RNA gene, complete sequence					
205	467	III	675	Hafnia alvei strain JCM 1666 16S ribosomal RNA gene, partial sequence	99%	0.0	99%	NR_112985.1	Hafniaceae
215	466	IX	966	Pseudomonas nitritireducens strain WZBFD3-5A2 16S ribosomal RNA, partial sequence	99%	0.0	99%	NR_133020.1	Pseudomonas
221	396	IX	400	Pseudomonas nitroreducens strain IAM1439 16S ribosomal RNA gene, complete sequence	96%	0.0	98%	NR_115611.1	Pseudomonas
224	467	IV	1046	Pseudomonas nitritireducens strain WZBFD3-5A2 16S ribosomal RNA, partial sequence	99%	0.0	99%	NR_133020.1	Pseudomonas
225	467	III	566	Ralstonia pickettii strain NBRC 102503 16S ribosomal RNA gene, partial sequence	100%	0.0	98%	NR_114126.1	Ralstonia
235	466	II	992	Enterococcus faecalis strain NBRC 100480 16S ribosomal RNA gene, partial sequence	99%	0.0	99%	NR_113901.1	Enterococcus faecalis
246	466	IX	474	Lysinibacillus sphaericus strain NBRC 15095 16S ribosomal	100%	0.0	98%	NR_112627.1	Lysinibacillus

				RNA gene, partial sequence					
248	462	IX	1014	Shigella boydii strain P288 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_104901.1	Enterobacteriaceae
260	462	VII	1032	Delftia lacustris strain 332 16S ribosomal RNA gene, partial sequence	99%	0.0	99%	NR_116495.1	Delftia
261	462	IV	773	Ralstonia pickettii strain NBRC 102503 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_114126.1	Ralstonia pickettii
271	396	IX	901	Pseudomonas nitritireducens strain WZBFD3-5A2 16S ribosomal RNA, partial sequence	97%	0.0	97%	NR_133020.1	Pseudomonas
293	505	IX	1043	Pseudomonas plecoglossicida strain NBRC 103162 16S ribosomal RNA gene, partial sequence	99%	0.0	99%	NR_114226.1	Pseudomonas
302	396	IX	1070	Bacillus anthracis strain ATCC 14578 16S ribosomal RNA gene, partial sequence	100%	0.0	98%	NR_041248.1	Bacillus
320	501	VII	1102	Bacillus thuringiensis strain NBRC 101235 16S ribosomal RNA gene, partial sequence	98%	0.0	99%	NR_112780.1	Bacillus

325	501	VII	656	Bacillus marcorestinum strain LQQ 16S ribosomal RNA gene, partial sequence	93%	0.0	92%	NR_117414.1	<i>Bacillaceae</i>
338	519	VII	965	Bacillus cereus ATCC 14579 16S ribosomal RNA (rrnA) gene, complete sequence	98%	0.0	99%	NR_074540.1	<i>Bacillus</i>
340	516	VII	937	Bacillus toyonensis strain BCT-7112 16S ribosomal RNA gene, complete sequence	100%	0.0	99%	NR_121761.1	<i>Bacillus</i>
344	516	II	248	Enterococcus faecalis strain NBRC 100480 16S ribosomal RNA gene, partial sequence	96%	2E-121	99%	NR_113901.1	<i>Enterococcus faecalis</i>
349	462	VII	1052	Shigella boydii strain P288 16S ribosomal RNA gene, partial sequence	99%	0.0	99%	NR_104901.1	<i>Enterobacteriaceae</i>
366	399	VII	1073	Enterococcus faecium strain DSM 20477 16S ribosomal RNA gene, complete sequence	99%	0.0	99%	NR_114742.1	<i>Enterococcus</i>
388	388	II	1050	Enterococcus hirae strain ATCC 9790 16S ribosomal RNA gene, complete sequence	100%	0.0	99%	NR_075022.1	<i>Enterococcus</i>
390	509	XI	303	Bacillus anthracis strain SBS1 16S ribosomal	94%	3,00E-116	99%	NR_118536.1	<i>Bacillus anthracis</i>

				RNA gene, partial sequence					
456	516	OTHER	676	Rummeliibacillus stabekisii strain NBRC 104870 16S ribosomal RNA gene, partial sequence	98%	0.0	99%	NR_114270.1	<i>Rummeliibacillus stabekisii</i>
462	516	VIII	951	Rummeliibacillus stabekisii strain NBRC 104870 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_114270.1	<i>Rummeliibacillus stabekisii</i>
477	501	VIBRIUM	606	Ralstonia pickettii strain NBRC 102503 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_114126.1	<i>Ralstonia pickettii</i>
492	504	II	1094	Enterococcus faecium strain DSM 20477 16S ribosomal RNA gene, complete sequence	99%	0.0	99%	NR_114742.1	<i>Enterococcus</i>
499	504	OTHER	1027	Enterococcus faecium strain DSM 20477 16S ribosomal RNA gene, complete sequence	100%	0.0	99%	NR_114742.1	<i>Enterococcus</i>
505	508	II	950	Pseudomonas nitritireducens strain WZBFD3-5A2 16S ribosomal RNA, partial sequence	97%	0.0	97%	NR_133020.1	<i>Pseudomonas</i>
506	508	XI	1110	Carnobacterium gallinarum strain DSM 4847 16S ribosomal	99%	0.0	98%	NR_042093.1	<i>Carnobacterium</i>

				RNA gene, complete sequence					
509	508	IX	1150	Lysinibacillus fusiformis strain NBRC15717 16S ribosomal RNA gene, partial sequence	100%	0.0	98%	NR_112569.1	<i>Lysinibacillus</i>
531	505	V	122	Lysinibacillus alkaliphilus strain OMN17 16S ribosomal RNA, partial sequence	71%	3,00E-37	98%	NR_136779.1	<i>Lysinibacillus</i>
541	636	II	491	Enterococcus hirae strain LMG 6399 16S ribosomal RNA gene, complete sequence	99%	0.0	99%	NR_114783.2	<i>Enterococcus</i>
559	388	X	1004	Lysinibacillus fusiformis strain NBRC15717 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_112569.1	<i>Lysinibacillus fusiformis</i>
589	504	VII	401	Bacillus toyonensis strain BCT-7112 16S ribosomal RNA gene, complete sequence	99%	0.0	98%	NR_121761.1	<i>Bacillus</i>
596	508	VIII	500	Bacillus pumilus strain NRRL NRS-272 16S ribosomal RNA gene, partial sequence	100%	0.0	98%	NR_116191.1	<i>Bacillus</i>
611	466	II	974	Enterococcus faecium strain NBRC 100486 16S ribosomal RNA gene, partial sequence	100%	0.0	98%	NR_113904.1	<i>Enterococcus</i>

626	467	II	401	Enterococcus faecium strain DSM 20477 16S ribosomal RNA gene, complete sequence	100%	0.0	100%	NR_114742.1	<i>Enterococcus faecium</i>
627	467	OTHER	1047	Delftia lacustris strain 332 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_116495.1	<i>Delftia lacustris</i>
628	467	IX	856	Escherichia fergusonii strain ATCC 35469 16S ribosomal RNA gene, complete sequence	100%	0.0	99%	NR_074902.1	<i>Enterobacteriaceae</i>
629	467	OTHER	851	Pseudomonas nitroreducens strain NBRC 12694 16S ribosomal RNA gene, partial sequence	96%	0.0	98%	NR_113601.1	<i>Pseudomonas</i>
630	467	OTHER	410	Stenotrophomonas maltophilia strain NBRC 14161 16S ribosomal RNA gene, partial sequence	60%	5,00E-110	95%	NR_113648.1	<i>Xanthomonadaceae</i>
640	462	II	912	Enterococcus durans strain JCM 8725 16S ribosomal RNA gene, partial sequence	100%	0.0	98%	NR_113257.1	<i>Enterococcus</i>
665	383	IX	980	Pseudomonas nitritireducens strain WZBFD3-5A2 16S ribosomal RNA, partial sequence	99%	0.0	98%	NR_133020.1	<i>Pseudomonas</i>
670	467	IX	747	Delftia tsuruhatensis strain NBRC 16741 16S	100%	0.0	99%	NR_113870.1	<i>Delftia</i>

				ribosomal RNA gene, partial sequence					
680	502	V	224	Bacillus thuringiensis strain NBRC 101235 16S ribosomal RNA gene, partial sequence	99%	2,00E-111	99%	NR_112780.1	Bacillus
687	502	OTHER	408	Stenotrophomonas maltophilia strain ATCC 19861 16S ribosomal RNA gene, complete sequence	99%	0.0	96%	NR_040804.1	Stenotrophomonas
690	502	OTHER	584	Stenotrophomonas maltophilia strain ATCC 13637 16S ribosomal RNA gene, partial sequence	100%	0.0	97%	NR_112030.1	Stenotrophomonas
691	502	OTHER	740	Stenotrophomonas maltophilia strain ATCC 13637 16S ribosomal RNA gene, partial sequence	99%	0.0	98%	NR_112030.1	Stenotrophomonas
726	471	II	1133	Enterococcus hirae strain ATCC 9790 16S ribosomal RNA gene, complete sequence	99%	0.0	99%	NR_075022.1	Enterococcus
734	471	VII	1039	Bacillus toyonensis strain BCT-7112 16S ribosomal RNA gene, complete sequence	98%	0.0	99%	NR_121761.1	Bacillus
738	471	IV	1100	Ralstonia insidiosa strain AU2944 16S	100%	0.0	99%	NR_025242.1	Ralstonia insidiosa

				ribosomal RNA gene, partial sequence					
746	471	V	236	Rummeliibacillus stabekisii strain NBRC 104870 16S ribosomal RNA gene, partial sequence	95%	1E-114	99%	NR_114270.1	<i>Rummeliibacillus stabekisii</i>
747	471	V	400	Sporosarcina soli strain I80 16S ribosomal RNA gene, partial sequence	95%	0.0	98%	NR_043527.1	<i>Sporosarcina</i>
756	460	XI	678	Ralstonia pickettii strain NBRC 102503 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_114126.1	<i>Ralstonia pickettii</i>
794	399	IX	449	Staphylococcus saprophyticus strain ATCC 15305 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_115607.1	<i>Staphylococcus</i>
802	463	XI	668	Ralstonia insidiosa strain AU2944 16S ribosomal RNA gene, partial sequence	99%	0.0	99%	NR_025242.1	<i>Ralstonia insidiosa</i>
805	463	VII	360	Bacillus anthracis strain ATCC 14578 16S ribosomal RNA gene, partial sequence	97%	0.0	100%	NR_041248.1	<i>Bacillus anthracis</i>
837	508	V	752	Bacillus cereus ATCC 14579 16S ribosomal RNA (rrnA) gene, complete sequence	100%	0.0	99%	NR_074540.1	<i>Bacillus</i>

852	675	II	477	Pseudomonas nitritireducens strain WZBFD3-5A2 16S ribosomal RNA, partial sequence	84%	2E-160	92%	NR_133020.1	<i>Pseudomonadaceae</i>
864	471	VIII	968	Lysinibacillus sphaericus strain NBRC 15095 16S ribosomal RNA gene, partial sequence	99%	0.0	98%	NR_112627.1	<i>Lysinibacillus</i>
869	471	II	963	Enterococcus mundtii strain NBRC 100490 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_113906.1	<i>Enterococcus mundtii</i>
879	505	II	571	Lysinibacillus sphaericus strain NBRC 15095 16S ribosomal RNA gene, partial sequence	100%	0.0	98%	NR_112627.1	<i>Lysinibacillus</i>
889	504	VIII	1145	Lysinibacillus sphaericus strain NBRC 15095 16S ribosomal RNA gene, partial sequence	100%	0.0	98%	NR_112627.1	<i>Lysinibacillus</i>
915	516	II	252	Enterococcus faecalis strain NBRC 100480 16S ribosomal RNA gene, partial sequence	94%	1E-113	98%	NR_113901.1	<i>Enterococcus</i>
919	463	VI	220	Rummeliibacillus stabekisii strain NBRC 104870 16S ribosomal RNA gene, partial sequence	98%	3,00E-110	99%	NR_114270.1	<i>Rummeliibacillus stabekisii</i>

923	463	VIII	400	Lysinibacillus macroides strain LMG 18474 16S ribosomal RNA gene, partial sequence	72%	0%	97%	NR_114920.1	<i>Lysinibacillus</i>
928	502	VI	139	Geobacillus thermoglucosidasius strain R-35637 16S ribosomal RNA gene, partial sequence	61%	3,00E-28	92%	NR_116983.1	<i>Bacillaceae</i>
942	466	VI	447	Bacillus cereus ATCC 14579 16S ribosomal RNA (rrnA) gene, complete sequence	100%	0.0	100%	NR_074540.1	<i>Bacillus</i>
952	502	VI	412	Romboutsia lituseburensis strain ATCC 25759 16S ribosomal RNA gene, partial sequence	100%	0.0	98%	NR_118728.1	<i>Romboutsia</i>
953G	502	OTHER	801	Pseudomonas nitroreducens strain NBRC 12694 16S ribosomal RNA gene, partial sequence	99%	0.0	98%	NR_113601.1	<i>Pseudomonas</i>
953P	502	OTHER	650	Sporosarcina newyorkensis strain 6062 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_117567.1	<i>Sporosarcina newyorkensis</i>
956	502	V	312	Bacillus subtilis subsp. inaquosorum strain BGSC 3A28 16S	97%	4,00E-160	100%	NR_104873.1	<i>Bacillus</i>

				ribosomal RNA gene, partial sequence					
963	504	VI	396	Rummeliibacillus stabekisii strain NBRC 104870 16S ribosomal RNA gene, partial sequence	98%	0.0	99%	NR_114270.1	Rummeliibacillus stabekisii
966	463	II	630	Pseudomonas taiwanensis strain BCRC 17751 16S ribosomal RNA gene, partial sequence	61%	6,00E-106	85%	NR_116172.1	Pseudomonadales
978	471	VI	677	Bacillus toyonensis strain BCT-7112 16S ribosomal RNA gene, complete sequence	99%	0.0	99%	NR_121761.1	Bacillus
988	460	VIII	531	Pseudomonas nitroreducens strain NBRC 12694 16S ribosomal RNA gene, partial sequence	99%	0.0	98%	NR_113601.1	Pseudomonas
998	516	IX	637	Solibacillus silvestris strain HR3-23 16S ribosomal RNA gene, partial sequence	99%	0.0	99%	NR_028865.1	Solibacillus
1001	388	VIII	448	Lysinibacillus xylanilyticus strain XDB9 16S ribosomal RNA gene, partial sequence	93%	0.0	98%	NR_116698.1	Lysinibacillus
1004	388	VI	903	Psychrobacillus soli strain NHI-2 16S	89%	0.0	99%	NR_137244.1	Psychrobacillus soli

				ribosomal RNA, partial sequence					
1020	383	VII	86	Uncultured bacterium partial 16S rRNA gene, clone 1611_28_123	33%	3,00E-04	100%	LT173941.1	Enterobacteriaceae
1023	383	VII	400	Delftia tsuruhatensis strain NBRC 16741 16S ribosomal RNA gene, partial sequence	99%	0.0	99%	NR_113870.1	Delftia
1025	467	VII	870	Pseudomonas nitritireducens strain WZBFD3-5A2 16S ribosomal RNA, partial sequence	100%	0.0	99%	NR_133020.1	Pseudomonas
1029	467	II	300	Delftia tsuruhatensis strain NBRC 16741 16S ribosomal RNA gene, partial sequence	99%	4,00E-100	89%	NR_113870.1	Comamonadaceae
1040	467	V	655	Bacillus cereus ATCC 14579 16S ribosomal RNA (rrnA) gene, complete sequence	100%	0.0	99%	NR_074540.1	Bacillus
1042	462	V	681	Shigella boydii strain P288 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_104901.1	Enterobacteriaceae
1047	462	I	945	Enterococcus faecalis strain NBRC 100480 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_113901.1	Enterococcus faecalis
1048	462	I	1050	Enterobacter xiangfangensis strain	99%	0.0	99%	NR_126208.1	Enterobacteriaceae

				10-17 16S ribosomal RNA gene, partial sequence					
1071	466	VII	86	Delftia deserti strain YIM Y792 16S ribosomal RNA, partial sequence	91%	1,00E-35	100%	NR_136837.1	<i>Delftia</i>
1073	466	II	948	Bacillus anthracis strain ATCC 14578 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_041248.1	<i>Bacillus</i>
1110	388	II	356	Clostridium tertium strain JCM 6289 16S ribosomal RNA gene, partial sequence	100%	0.0	100%	NR_113325.1	<i>Clostridium tertium</i>
1120	508	VII	325	Clostridium tertium strain JCM 6289 16S ribosomal RNA gene, partial sequence	98%	5,00E-159	98%	NR_113325.1	<i>Clostridium</i>
1124	508	II	1085	Enterococcus faecium strain DSM 20477 16S ribosomal RNA gene, complete sequence	100%	0.0	99%	NR_114742.1	<i>Enterococcus</i>
1133	505	VII	1003	Enterococcus faecalis strain NBRC 100480 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_113901.1	<i>Enterococcus faecalis</i>
1153	388	V	400	Propionibacterium acnes strain ATCC 6919 16S ribosomal RNA, complete sequence	100%	0.0	99%	NR_040847.1	<i>Propionibacterium acnes</i>

1162	508	II	1005	Enterococcus faecium strain NBRC 100486 16S ribosomal RNA gene, partial sequence	98%	0.0	99%	NR_113904.1	<i>Enterococcus</i>
1164	508	VII	1026	Robinsoniella peoriensis strain PPC31 16S ribosomal RNA gene, complete sequence	100%	0.0	99%	NR_041882.1	<i>Robinsoniella peoriensis</i>
1185	516	IX	900	Enterococcus faecalis strain NBRC 100480 16S ribosomal RNA gene, partial sequence	100%	0.0	98%	NR_113901.1	<i>Enterococcus</i>
1188	471	IX	774	Pantoea eucrina strain LMG 2781 16S ribosomal RNA gene, partial sequence	97%	0.0	99%	NR_116246.1	<i>Pantoea eucrina</i>
1192	463	IX	337	Citrobacter koseri strain LMG 5519 16S ribosomal RNA gene, partial sequence	99%	5,00E-169	98%	NR_117751.1	<i>Enterobacteriaceae</i>
1202	504	VII	233	Clostridium tertium strain JCM 6289 16S ribosomal RNA gene, partial sequence	94%	2,00E-111	99%	NR_113325.1	<i>Clostridium tertium</i>
1295	501	II	826	Enterococcus faecium strain NBRC 100486 16S ribosomal RNA gene, partial sequence	99%	0.0	99%	NR_113904.1	<i>Enterococcus</i>
1319	501	II	224	Enterococcus faecium strain NBRC 100486 16S ribosomal RNA gene, partial sequence	98%	2,00E-112	100%	NR_113904.1	<i>Enterococcus</i>

1321	501	IX	1052	Clostridium septicum strain Pasteur III 16S ribosomal RNA gene, complete sequence	100%	0.0	98%	NR_026020.1	<i>Clostridium</i>
1340	519	IX	799	Pseudomonas nitroreducens strain NBRC 12694 16S ribosomal RNA gene, partial sequence	99%	0.0	99%	NR_113601.1	<i>Pseudomonas</i>
1343	519	X	323	Romboutsia sedimentorum strain LAM201 16S ribosomal RNA, partial sequence	90%	2,00E-132	96%	NR_134800.1	<i>Romboutsia</i>
1353	519	IV	220	Paenibacillus borealis strain KK19 16S ribosomal RNA gene, complete sequence	96%	2,00E-107	99%	NR_025299.1	<i>Paenibacillus borealis</i>
1359	502	IV	998	Enterococcus durans strain JCM 8725 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_113257.1	<i>Enterococcus</i>
1362	502	X	940	[Eubacterium] tenue strain ATCC 25553 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_115794.1	<i>Paeniclostridium tenue</i>
1368	460	X	843	Clostridium perfringens strain ATCC 13124 16S ribosomal RNA gene, complete sequence	99%	0.0	99%	NR_121697.1	<i>Clostridium perfringens</i>
1376	471	IV	1072	Bacillus kokeshiiformis strain MO-04 16S	99%	0.0	99%	NR_133975.1	<i>Bacillus kokeshiiformis</i>

				ribosomal RNA, partial sequence					
1377	516	VII	234	Clostridium tertium strain JCM 6289 16S ribosomal RNA gene, partial sequence	94%	1E-109	99%	NR_113325.1	Clostridium tertium
1381	509	VII	1037	Clostridium septicum strain Pasteur III 16S ribosomal RNA gene, complete sequence	100%	0.0	99%	NR_026020.1	Clostridium septicum
1388	463	VII	214	Clostridium perfringens strain JCM 1290 16S ribosomal RNA gene, partial sequence	98%	4,00E-103	98%	NR_113204.1	Clostridium
1393	675	VII	889	Clostridium perfringens strain JCM 1290 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_113204.1	Clostridium perfringens
1398	675	II	215	Enterococcus faecium strain NBRC 100486 16S ribosomal RNA gene, partial sequence	99%	1,00E-108	99%	NR_113904.1	Enterococcus
1404	463	VII	1074	Carnobacterium mobile strain DSM 4848 16S ribosomal RNA gene, partial sequence	99%	0.0	98%	NR_040926.1	Carnobacterium
1409	471	II	415	Enterococcus faecium strain NBRC 100486 16S ribosomal RNA gene, partial sequence	100%	0.0	99%	NR_113904.1	Enterococcus
1421	516	VII	774	[Clostridium] sordellii strain JCM 3814 16S	99%	0.0	98%	NR_113140.1	Paeniclostridium

ribosomal RNA gene,
partial sequence

¹Based on morphological (cell morphology, Gram, and endospore staining) and biochemical tests (catalase and oxidase tests).

² Phylotype assignment based on information from top three best matches displaying the higher nucleotide pairwise identity, using taxonomic threshold similarity values as discussed in Material and Methods chapter.

Supplementary Table 2 – Relative abundances, at the bacterial genus level, of each taxon in culturomics¹ and microbial profiling² approaches.

Taxon ³	Culturomics	Microbial profiling	Taxon ³	Female C	Male C	Female MP	Male MP	Taxon ³	Non-adults C	Adults C	Non-adults MP	Adults MP
<i>Bacillus</i>	16	0	<i>Bacillus</i>	14	19	0	0	<i>Bacillus</i>	17	16	0	0
<i>Blautia</i>	0	7	<i>Blautia</i>	0	0	8	6	<i>Blautia</i>	0	0	6	7
<i>Carnobacterium</i>	3	4	<i>Carnobacterium</i>	4	2	6	0	<i>Carnobacterium</i>	2	3	0	5
<i>Clostridioides</i>	0	25	<i>Clostridioides</i>	0	0	27	23	<i>Clostridioides</i>	0	0	37	22
<i>Clostridium</i>	5	19	<i>Clostridium</i>	6	5	18	19	<i>Clostridium</i>	11	4	18	19
<i>Collinsella</i>	0	5	<i>Collinsella</i>	0	0	5	5	<i>Collinsella</i>	0	0	3	5
<i>Delftia</i>	3	0	<i>Delftia</i>	1	4	0	0	<i>Delftia</i>	0	3	0	0
<i>Enterococcus</i>	34	1	<i>Enterococcus</i>	36	33	2	0	<i>Enterococcus</i>	29	36	0	1
<i>Escherichia</i>	0	2	<i>Escherichia</i>	0	0	3	1	<i>Escherichia</i>	0	0	3	2
<i>Fusobacterium</i>	0	2	<i>Fusobacterium</i>	0	0	1	3	<i>Fusobacterium</i>	0	0	0	3
<i>Lactobacillus</i>	0	4	<i>Lactobacillus</i>	0	0	6	1	<i>Lactobacillus</i>	0	0	0	4
<i>Lysinibacillus</i>	4	0	<i>Lysinibacillus</i>	5	3	0	0	<i>Lysinibacillus</i>	6	3	0	0
<i>Paeniclostridium</i>	1	7	<i>Paeniclostridium</i>	0	2	7	7	<i>Paeniclostridium</i>	2	1	4	8
<i>Paraclostridium</i>	1	5	<i>Paraclostridium</i>	1	1	5	5	<i>Paraclostridium</i>	0	2	3	5
<i>Pseudomonas</i>	10	0	<i>Pseudomonas</i>	12	9	0	0	<i>Pseudomonas</i>	9	11	0	0
<i>Ralstonia</i>	5	0	<i>Ralstonia</i>	3	7	0	0	<i>Ralstonia</i>	5	5	0	0
<i>Rummellibacillus</i>	4	0	<i>Romboutsia</i>	1	1	0	3	<i>Romboutsia</i>	2	1	0	2
<i>Sporosarcina</i>	0	3	<i>Rummellibacillus</i>	2	6	0	0	<i>Rummellibacillus</i>	9	3	0	0
Others (<2%)	14	17	<i>Sporosarcina</i>	0	1	0	7	<i>Sporosarcina</i>	2	0	0	4
			<i>Stenotrophomonas</i>	1	2	0	0	Others (<2%)	9	13	16	13
			Others (<2%)	15	7	12	16					

¹the relative abundances (%) were calculated based on the differentiation information obtained by Random Amplification of Polymorphic DNA (RAPD) and 16S rRNA gene sequencing; the isolates within each RAPD cluster were considered to belong to the same genus of the isolate(s) within that cluster that was(were) subject to molecular identification; calculations were made by dividing the number of differentiated strains within each cluster by the total number of differentiated strains using RAPD.

²the relative abundances (%) were calculated based on the taxonomical classification of OTU and the total number of obtained OTU reads.

³taxon representativity was based on the relative abundance of groups (%).

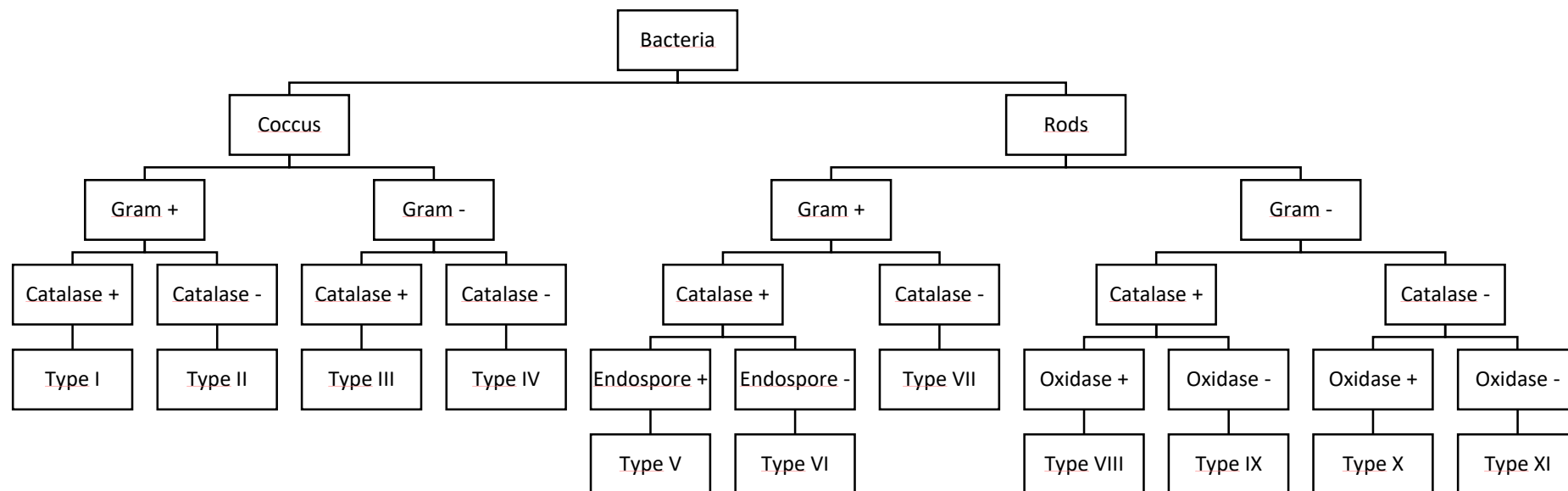
Supplementary Table 3 – Information on the ITS nucleotide sequences of a selected group of fungi isolates.

Isolate	Animal	Phenotypic Identification ¹	Nucleotide Sequence Length	Closest Reference Sequence Match	Query cover	E-value	Nucleotide Sequence Identity	Accession Number	Assigned Phylotype ²
1205	471	XIII	400	Pseudozyma sp. JS1231 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 26S rRNA gene (partial), isolate 1231	80%	5,00E-134	94%	AM176740.1	<i>Pseudozyma</i>
1206	675	XIII	400	Mucor circinelloides strain S032IMR 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	100%	0.0	99%	KU198340.1	<i>Mucor circinelloides</i>
1212	509	XII	459	Cryptococcus albidus var. kuetzingii culture-collection CBS:6086 large subunit ribosomal RNA gene, partial sequence	98%	0.0	99%	KY106964.1	<i>Cryptococcus albidus/</i> <i>Naganishia albida</i>
1213	463	XII	400	Cryptococcus albidus var. kuetzingii strain YM26709 26S ribosomal RNA gene, partial sequence	62%	1,00E-105	95%	KY463404.1	<i>Cryptococcus albidus/</i> <i>Naganishia albida</i>
1331	460	XIII	400	Penicillium citreonigrum strain SFCF20120912-25 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	90%	2,00E-163	96%	KF313080.1	<i>Penicillium</i>

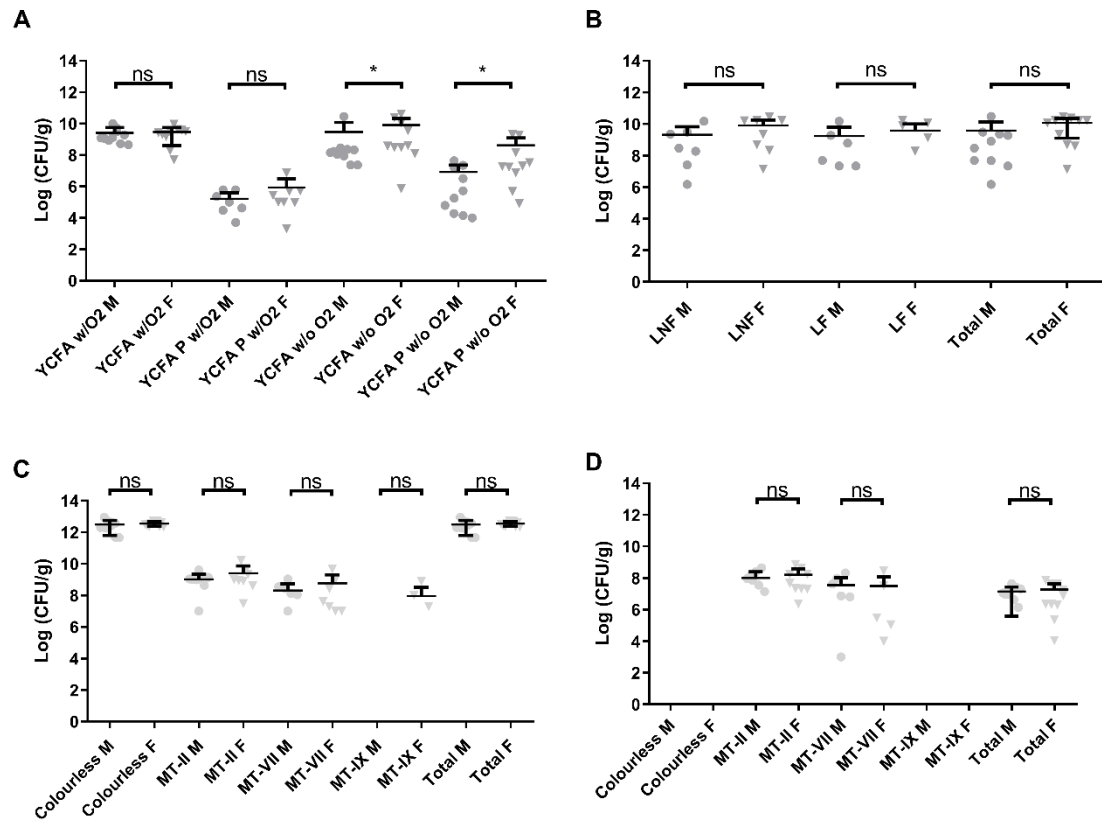
1334	463	XIII	482	Penicillium amaliae strain CV401 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	100%	0.0	99%	JX091440.1	<i>Penicillium amaliae</i>
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¹Based on morphological (hyphal septation and spores color, morphology, and septation, cell morphology, and division) tests.

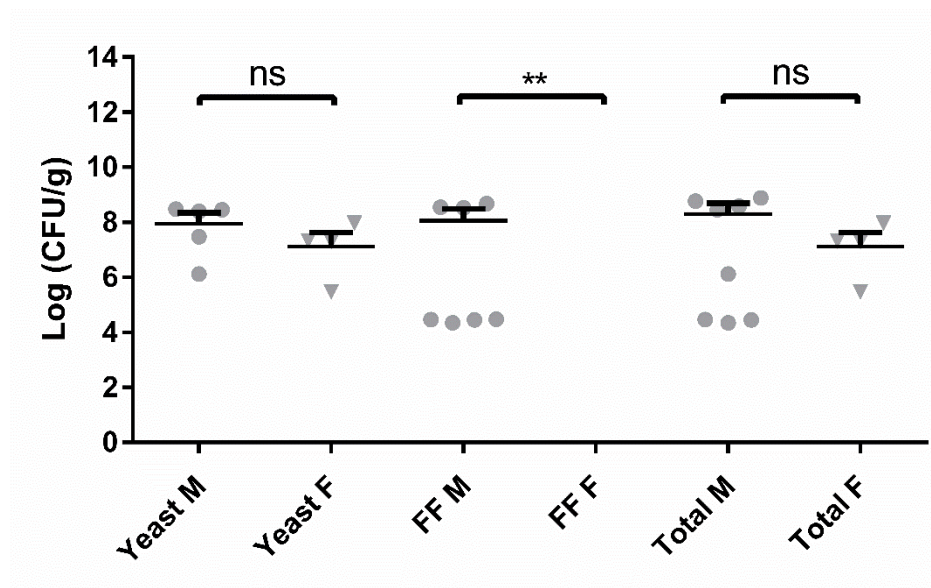
² Phylotype assignment based on information from top three best matches displaying the higher nucleotide pairwise identity, using taxonomic threshold similarity values as discussed in Material and Methods chapter.



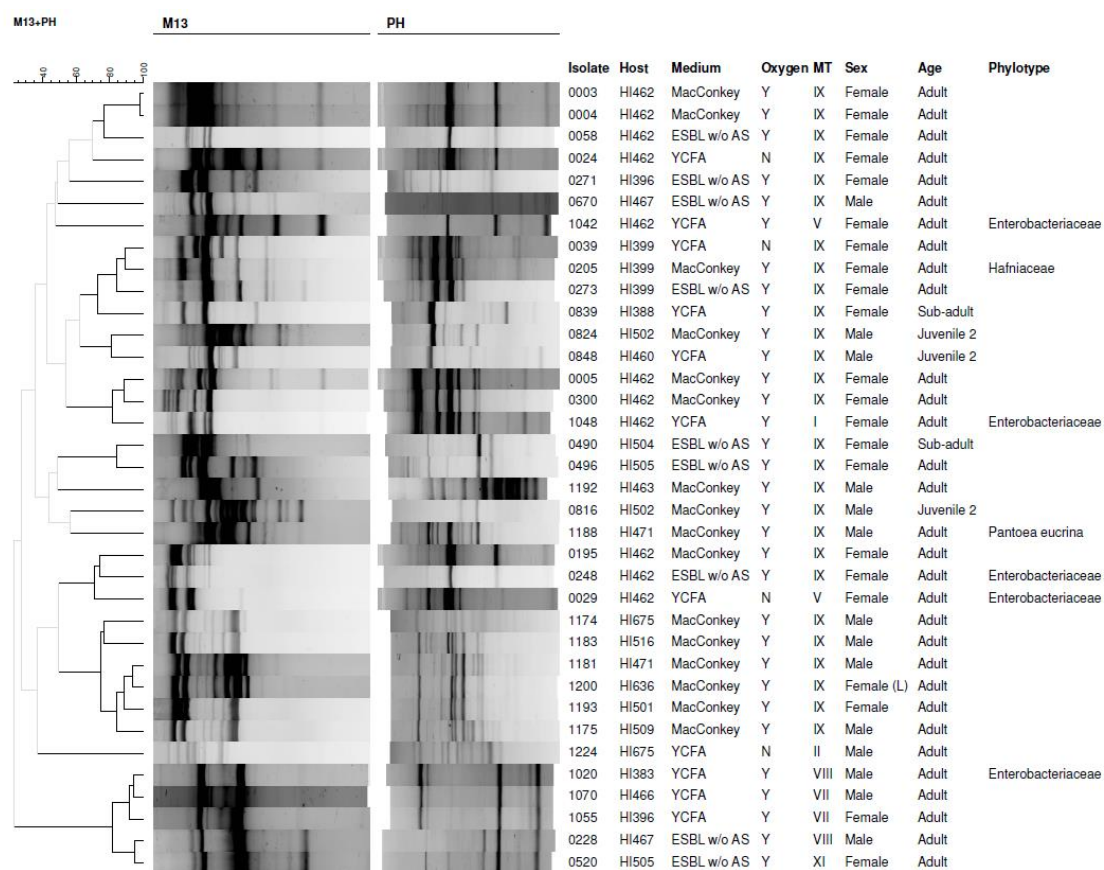
Supplementary Figure 1 – Flowchart used for differentiation of the purified bacterial isolates into different morpho-physiological types (from [25]).



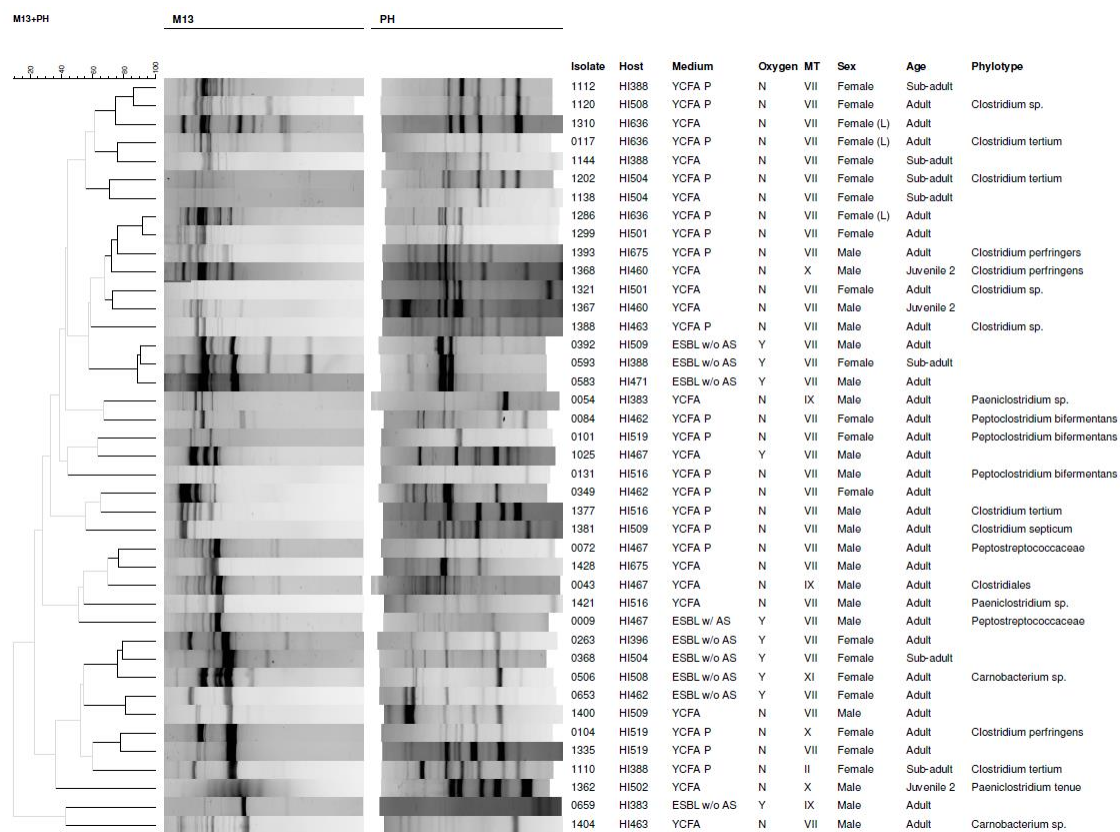
Supplementary Figure 2 — Microbial load (expressed as Log CFU/mL) of mongoose cultivable bacteria grown in selective and non-selective media. (A) Comparison among four different media/conditions: YCFA incubated under aerobiosis (YCFA w/O2), YCFA supplemented with sodium taurocholate and incubated under aerobiosis (YCFA P w/O2), YCFA incubated under anaerobiosis (YCFA w/o O2), and YCFA supplemented with sodium taurocholate and incubated under anaerobiosis (YCFA P w/o O2). (B) Comparison among lactose non-fermenting (LNF) bacteria and lactose-fermenting (LF) bacteria in MacConkey medium. (C/D) Comparison between Extended-spectrum beta-lactamases (ESBL) Chromogenic medium (C) without (ESBL w/o AS) and (D) with (ESBL w/ AS) ESBL antibiotic supplement with the results presented by colony color/type. Results from male (M), female (F), and in total (T) are presented. Horizontal bars represent the mean and error bars represent the standard deviation from 10 (male and female) and 20 (total) independent values. Statistical analysis was performed using a Mann-Whitney test ($\alpha=0.05$). ns – non-significant ($p\text{-value} \geq 0.05$); * - significant ($p\text{-value} < 0.05$).



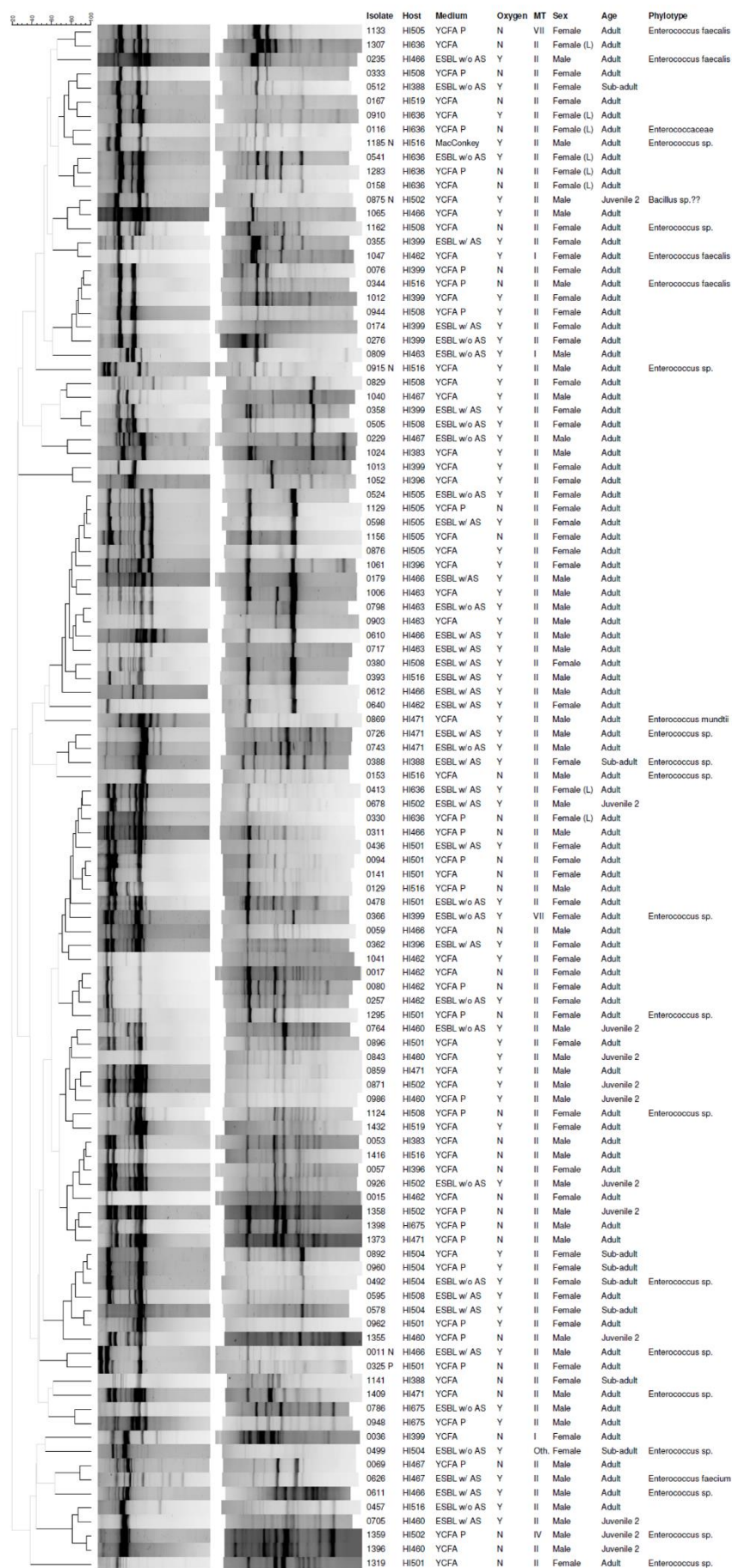
Supplementary Figure 3 – Comparison of microbial load (expressed as Log CFU/g) between male and female individuals in Potato Dextrose Agar medium with chloramphenicol (PDA w/ CHLO). Results from yeast and filamentous fungi (FF) are presented. Horizontal bars represent the mean and error bars represent the standard deviation from 10 independent values. Statistical analysis was performed using a Mann-Whitney test ($\alpha=0.05$); ns – non-significant (p-value ≥ 0.05), ** - very significant (p-value=0.001 to 0.01).



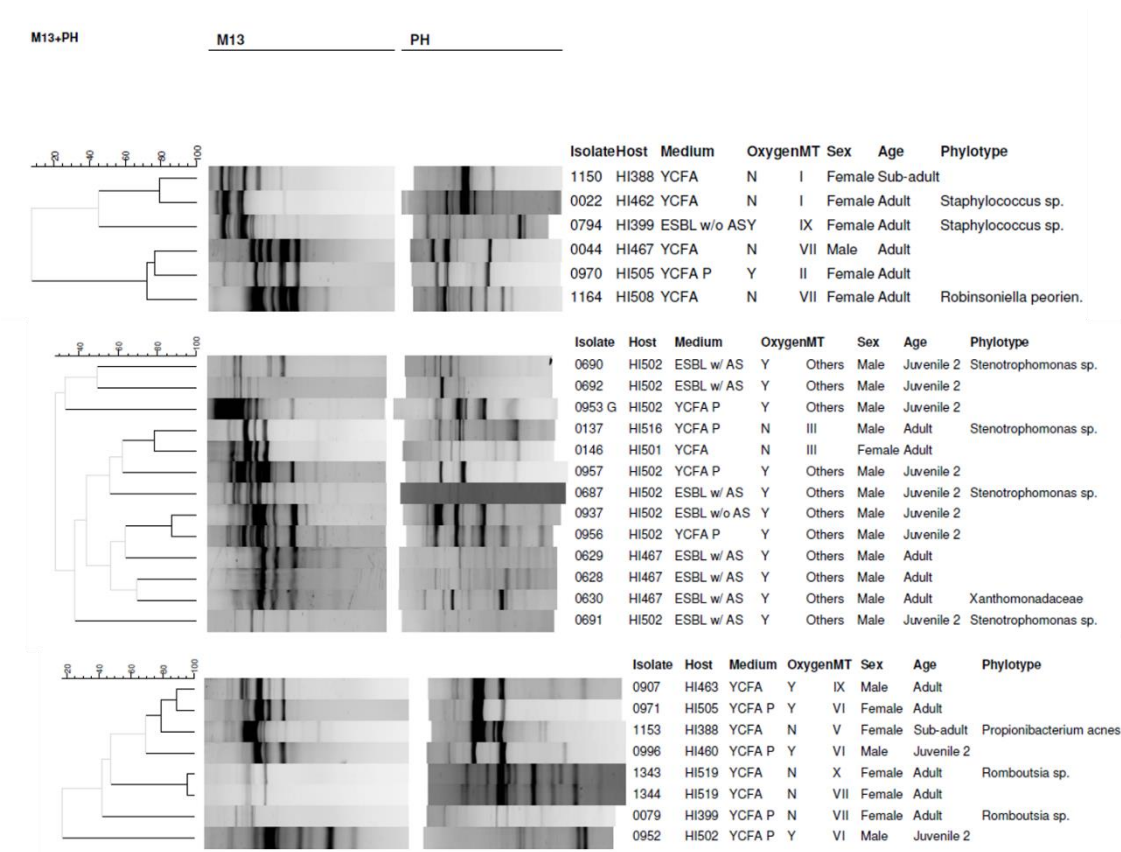
Supplementary Figure 4 – Bacterial isolates identification and differentiation by a hierarchical numerical analysis. The PCR fingerprints obtained for M13 and PH were integrated, similarity was calculated by Pearson correlation coefficient and clustering was performed with UPGMA. The scale corresponds to global percentage of similarity. Cut-off value for cluster formation at 70% similarity. N – No; Y – Yes; (L) – Lactating.



Supplementary Figure 4 (Continuation)

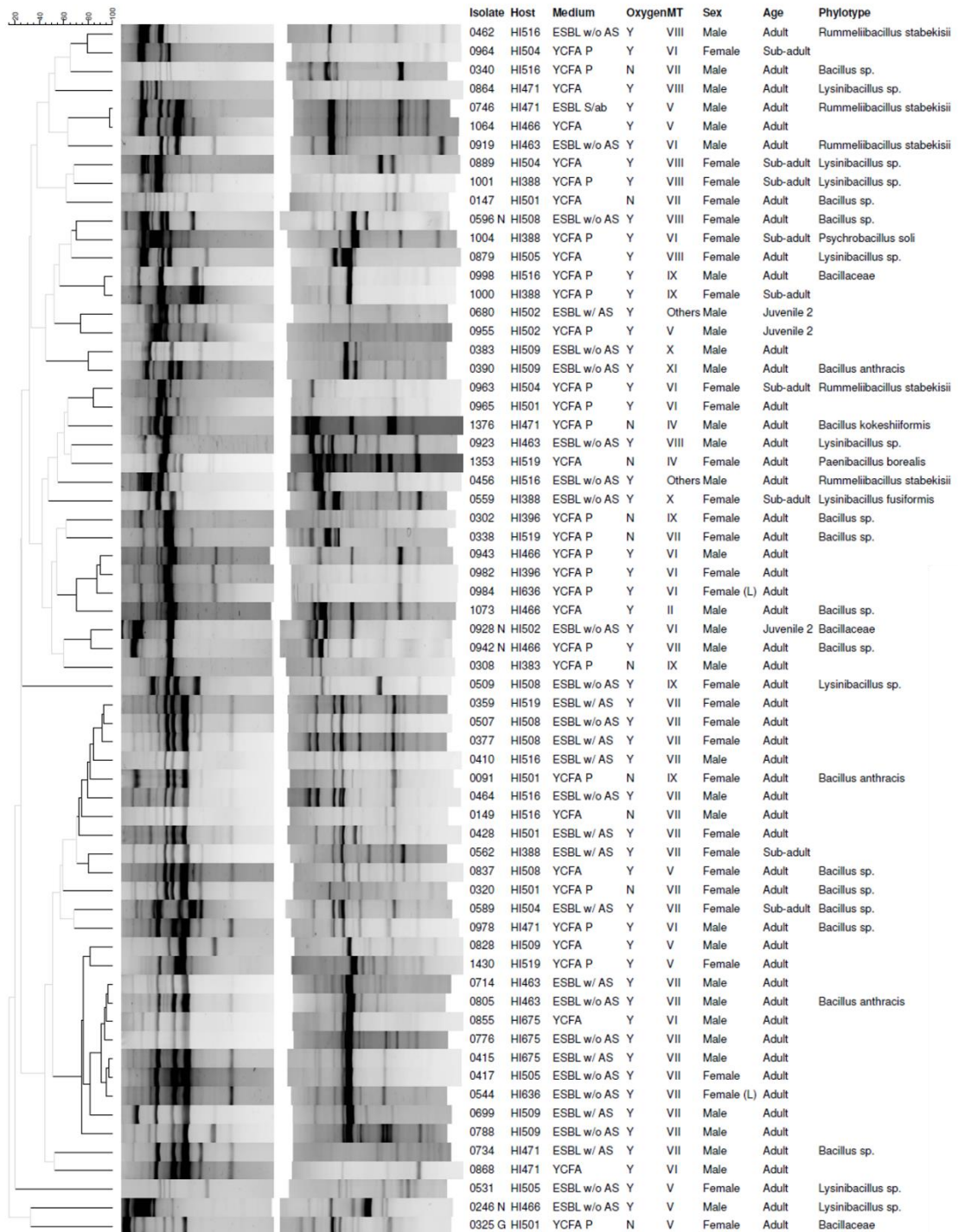


10 Supplementary Figure 4 (Continuation)



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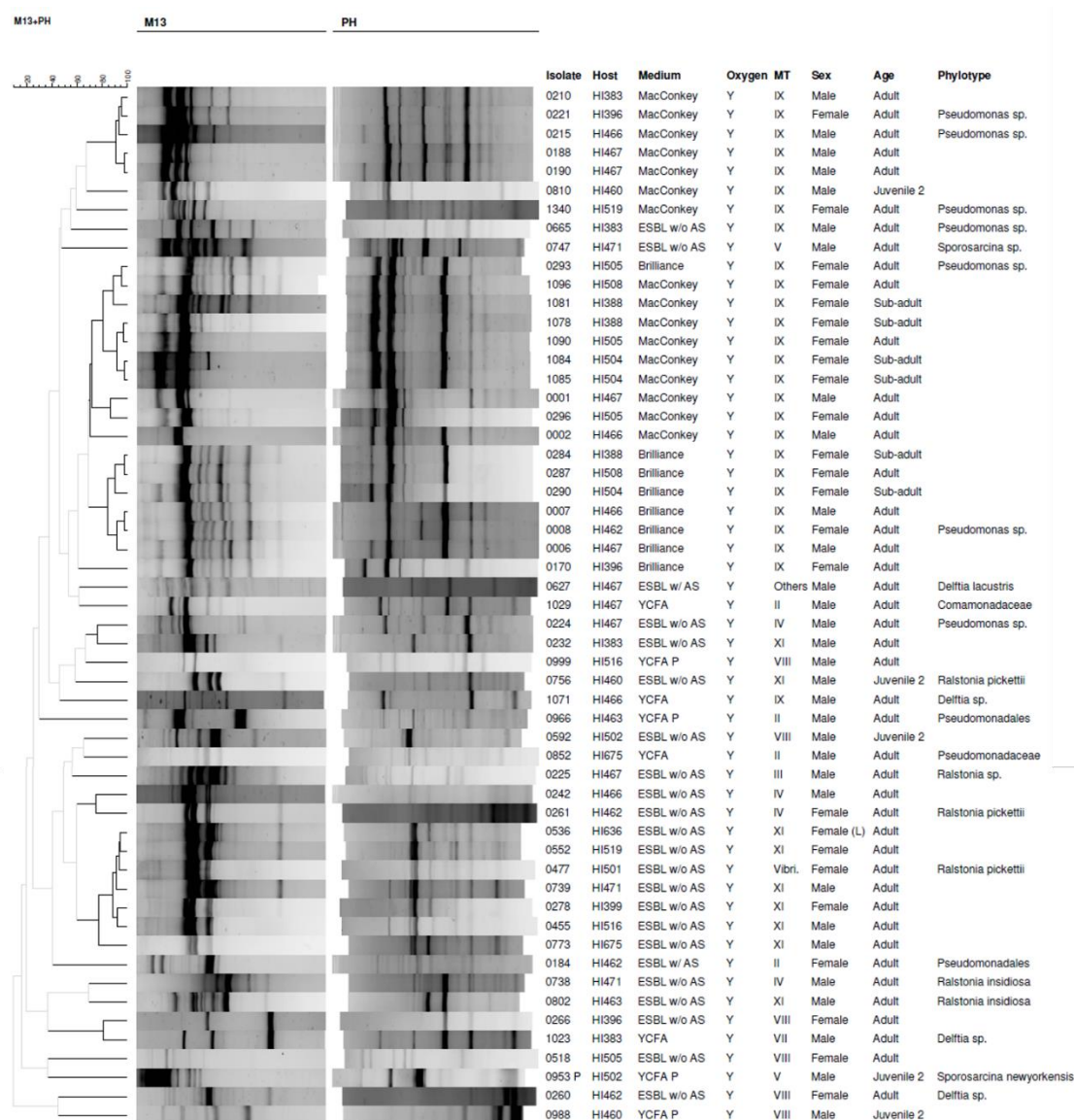
12 Supplementary Figure 4 (Continuation)

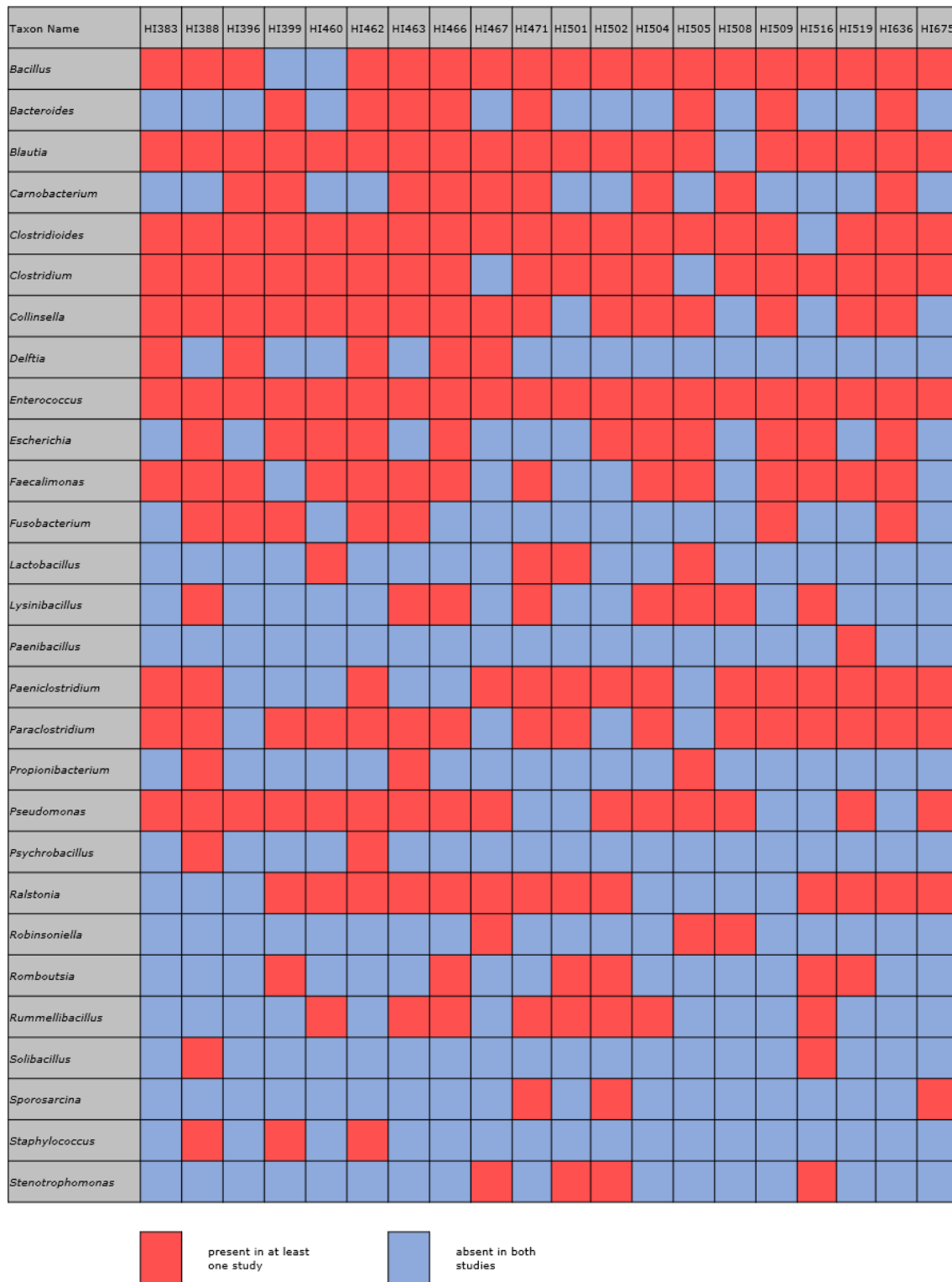


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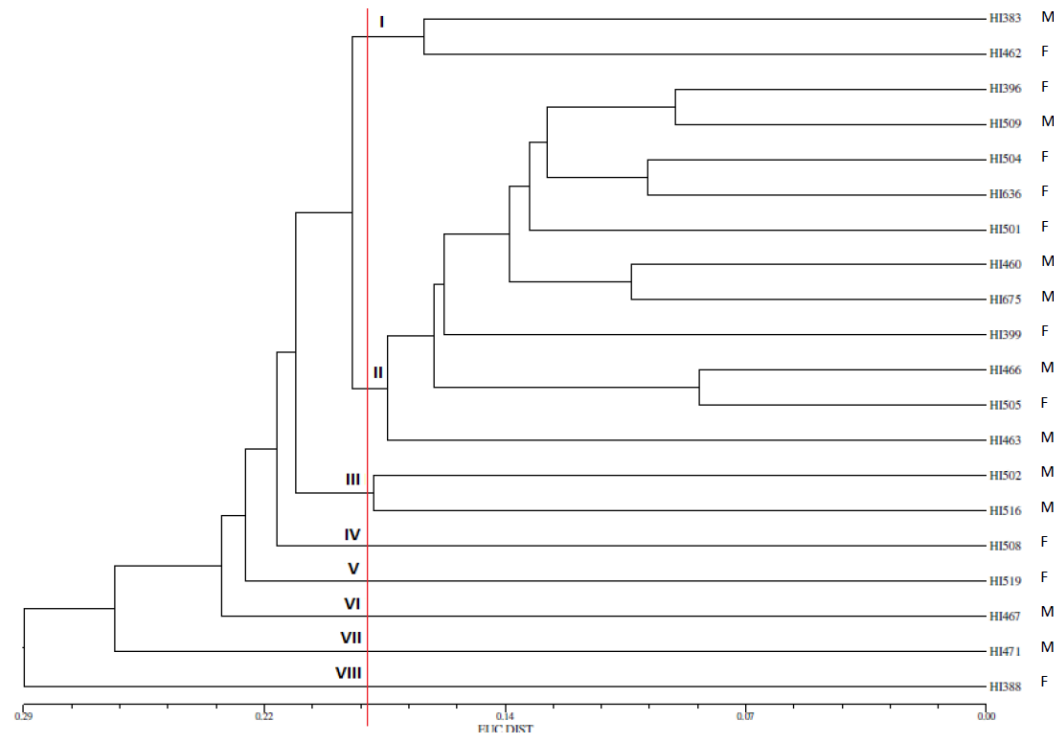
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Supplementary Figure 4 (Continuation)





Supplementary Figure 6: Genera distribution per faecal sample.



Supplementary Figure 7 – Dendrogram representing the relationship between the Egyptian mongoose specimens in terms of microbiota. The 20 specimens were clustered using the normalized Euclidean distance derived from the projection matrix of the PCA obtained from the microbiota data and clustered using UPGMA. The cut-off value was determined at 0.18 of normalized Euclidean distance, producing 8 clusters, 5 of them single member clusters. M – Male; F- Female.