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Code	Species	Collecting site (Commune,	Collecting method	Date of collection	Result CSP P.
2GEB0090	<i>An. maculatus</i>	Phuoc Binh, Vietnam	Human landing collection	12/11/2004	1
PY0643	<i>An. maculatus</i>	Pang Rolim, Cambodia	Human landing collection	19/05/2005	1
BY1130	<i>An. minimus</i>	Leutouch, Cambodia	Human landing collection	07/12/2005	1
4HZE0155	<i>An. maculatus</i>	Ma Noi, Vietnam	Human landing collection	03/11/2005	2
OZ0882	<i>An. barbirostris</i>	Prac, Cambodia	Human landing collection	28/08/2005	3
PY0291	<i>An. minimus</i>	Pang Rolim, Cambodia	Human landing collection	18/08/2005	1
OZ00698	<i>An. maculatus</i>	Prac, Cambodia	Human landing collection	26/08/2005	1
3HZG0069	<i>An. maculatus</i>	Ma Noi, Vietnam	Human landing collection	12/10/2005	1
6HZG0033	<i>An. minimus</i>	Ma Noi, Vietnam	Human landing collection	29/11/2006	2
4HZE0277	<i>An. maculatus</i>	Ma Noi, Vietnam	Human landing collection	07/11/2005	1
OZ0059	<i>An. barbirostris</i>	Prac, Cambodia	Human landing collection	21/05/2005	0
PZ0203	<i>An. maculatus</i>	O-Kting, Cambodia	Human landing collection	19/08/2005	0
ST	<i>An. stephensi</i>	Reared in laboratory,	-	-	-

Table 1. Characteristics of the samples analyzed through Next Generation Sequencing (NGS) in this study

Code	Species	Collecting site (Village, Country)	Collecting method	Date of collection	Result CSP <i>P.</i> <i>falciparum</i> ELISA
3B0820	<i>An.</i> <i>hyrcanus</i>	Kres, Ratanakiri, Cambodia	Human landing collection	08/08/2012	1
CC0481	<i>An.</i> <i>hyrcanus</i>	Klis, Ratanakiri, Cambodia	Human landing collection	12/08/2012	1
2C0145	<i>An.</i> <i>hyrcanus</i>	Klis, Ratanakiri, Cambodia	Human landing collection	16/06/2012	2
2C0153	<i>An.</i> <i>hyrcanus</i>	Klis, Ratanakiri, Cambodia	Human landing collection	16/06/2012	2
3C0446	<i>An.</i> <i>hyrcanus</i>	Klis, Ratanakari, Cambodia	Human landing collection	11/08/2012	2
3C0455	<i>An.</i> <i>hyrcanus</i>	Klis, Ratanakari, Cambodia	Human landing collection	22/06/2012	2

Table 2. Characteristics of the samples analyzed through Dynabeads® protein capture.

Primers*	Reference	Sequence (Forward)	Sequence (Reverse)
27F'/ 519R'	Lane, 1991 [56]	5'-AGAGTTTGATCMTGGCTCAG-3'	5'-GWATTACCGCGGCKGCTG-3'
356F'/1064R'	Winsley, 2012 [57]	5'-ACWCCTACGGGWGGCWGC-3'	5'-AYCTCACGRCACGAGCTGAC-3'
8F'/1492R'	Dojka, 1998 [60]	5'-AGAGTTTGATCCTTGGCTCAG-3'	5'-GCTACCTTGTTACGACTT-3'
Bakt_341F/Bakt_805R	Herlemann, 2011 [59]	5'-CCTACGGGNGGCWGCAG-3'	5'-ACHVGGGTATCTAATCC -3'
968F'/1381R'	Roudiere, 2011 [58]	5'-AACGCGAAGAACCTTAC-3'	5'-GGCCCGGGGAACGTATTCACC-3'

Table 3. Sets of primers used in the study.

(*) Numbers represent the position in *Escherichia coli* genome

Parameter	Measure	Preferred outcome
Maximum score	Score of the longest matching sequence (one primer)	High scores represents high degree of similarity
Total score	Score of all sequences that matched in the target (both primers)	High scores represents high degree of similarity
Query coverage	Percentage of residues that match in the whole sequence	100%
e-value	Measure of the probability that the match is by chance	As low as possible
Maximum identity	Percentage of similar residues in the target sequence	100%

Table 4. BLAST parameters considered for *in silico* analysis of primers

Species	Number of sequences retrieved in BLAST	Kingdom
<i>Actinocymes sp.</i>	1	Fungi
<i>Arthrobacter sp.</i>	2	Prokarya
<i>Aspergillus fumigatus</i>	1	Fungi
<i>Boss grunniens mutus</i>	2	Eukarya
<i>Branchiostoma floridae</i>	1	Eukarya
<i>Capitella teleta</i>	1	Eukarya
<i>Columbia livia</i>	1	Eukarya
<i>Drosophilla mojavensis</i>	1	Eukarya
<i>Edhazardia aedis</i>	1	Fungi
<i>Enterococcus mundtii</i>	1	Prokarya
<i>Harpegnathos saltator</i>	1	Eukarya
<i>Hydra magnipapillata</i>	1	Eukarya
<i>Leucobacter sp.</i>	1	Prokarya
<i>Nematostella vectensis</i>	2	Eukarya
<i>Pelobacter cabinoculis</i>	1	Prokarya
<i>Streptococcus agalactiae</i>	54	Prokarya
<i>Streptomyces violaceusniger</i>	1	Prokarya
<i>Strongylocentrotus purpuratus</i>	1	Eukarya
<i>Thalassioria oceanica</i>	6	Eukarya
<i>Trichomonas vaginalis</i>	1	Prokarya
TOTAL	81	

Table 5. Number of sequences and species retrieved from BLAST analysis of *P. falciparum* CSP protein

	Lane, 1991	Winsley, 2012	Dojka, 1998	Herlemann	Roudiere, 2011
Variable Region amplified*	V4-V5 519-926	V6-V9 356-1064	V1-V9 1492-27	V3-V4 341-805	V6-V8 968-1381
Number of sequences (without initial cleaning)	7508	7470	5141	8813	7377
Number of genus (without initial cleaning)	1632	1618	1237	1735	1630
Number of sequences (both primers)	2175	7065	1625	8773	7186
Number of genus (both primers)	760	1516	637	1726	1550

Table 6. Number of sequences identified by each set of primers before and after preliminary cleaning through total and maximum scores.

(* Position in the genome of *Escherichia coli*).

	Lane	Winsley	Dojka	Herlemann	Roudiere
Lane	2175 (100%)	-	-	-	-
Winsley	2111 (97%)	7065 (100%)	-	-	-
Dojka	1392 (64%)	1554 (22%)	1624 (100%)	-	-
Herlemann	2168 (99,6%)	7052 (99,8%)	1620 (99,7%)	8773 (100%)	-
Roudiere	2136 (98%)	6952 (98%)	1592 (98%)	7165 (99,7%)	7186 (100%)

Table 7. Percentage of sequences identified by each set of primers.

	Winsley	Roudiere	Herlemann
	n= 6952	n= 6952	n= 6952
Parameters			
Maximum score*			
Mean	36,32666379	33,61911553	39,91793431
Standard deviation	3,180490861	1,517905869	2,584852636
Variance	10,11552212	2,304038227	6,681463149
Total score*			
Mean	62,83157591	66,14550562	73,05714492
Standard deviation	3,590461181	8,260854978	6,06303155
Variance	12,89141149	68,24172497	36,76035157
Query coverage*			
Mean	0,921623451	0,839128493	0,932712475
Standard deviation	0,053923561	0,048327885	0,050057046
Variance	0,00290775	0,002335584	0,002505708
E-value			
Mean	0,257281475	0,161755029	0,006434414
Standard deviation	0,819514449	3,587985345	0,023855992
Variance	0,671603931	12,87363883	0,000569108
Maximum identity*			
Mean	0,953422645	0,999698934	0,95678911
Standard deviation	0,016084971	0,00417961	0,019081205
Variance	0,000258726	1,74691E-05	0,000364092

Table 8. Statistical analysis showing the main parameters considered in BLAST search in three sets of primers without outliers restriction (*p<0,05).

	Winsley	Roudiere	Herlemann
	n= 6297	n= 6297	n= 6297
Parameters			
Maximum score*			
Mean	37,24179768	33,59518818	40,63439733
Standard deviation	1,1169617	1,289592858	1,133057459
Variance	1,247603438	1,663049738	1,283819206
Total score*			
Mean	63,73771637	65,72779101	74,0307448
Standard deviation	2,006671909	7,827855456	5,328920794
Variance	4,026732152	61,27532104	28,39739682
Query coverage*			
Mean	0,937033508	0,837905352	0,946898523
Standard deviation	0,018198114	0,044327365	0,018202224
Variance	0,000331171	0,001964915	0,000331321
E-value*			
Mean	0,011765285	0,039977546	0,001150945
Standard deviation	0,076843506	0,112095309	0,007160862
Variance	0,005904924	0,012565358	5,12779E-05
Maximum identity*			
Mean	0,949161505	0,999906305	0,952837859
Standard deviation	0,007755727	0,002248805	0,014402434
Variance	6,01513E-05	5,05713E-06	0,00020743

Table 9. Statistical analysis showing the main parameters considered in BLAST search in three sets of primers with outliers restriction

(*p<0,05)

Index Number	Sample ID	Index 1 (17)	Index 2 (15)	% Reads Identified (PF)
1	STHT	TAAGGCGA	TAGATCGC	1.3216
2	STABD	CGTACTAG	TAGATCGC	2.0526
3	2GEB0090HT	AGGCAGAA	TAGATCGC	2.8306
4	2GEB0090ABD	TCCTGAGC	TAGATCGC	1.34
5	PY0463HT	GGACTCCT	TAGATCGC	4.558
6	PY0463ABD	TAGGCATG	TAGATCGC	1.8123
7	BY01130HT	TAAGGCGA	CTCTCTAT	5.9499
8	BY01130ABD	CGTACTAG	CTCTCTAT	3.3225
9	4HZG0155HT	AGGCAGAA	CTCTCTAT	2.5178
10	4HZG0155ABD	TCCTGAGC	CTCTCTAT	2.7865
11	OZ0882HT	GGACTCCT	CTCTCTAT	6.8821
12	OZ0882ABD	TAGGCATG	CTCTCTAT	3.0175
13	PY0291HT	TAAGGCGA	TATCCTCT	6.2882
14	PY0291ABD	CGTACTAG	TATCCTCT	2.9265
15	OZ0698HT	AGGCAGAA	TATCCTCT	4.7724
16	OZ0698ABD	TCCTGAGC	TATCCTCT	1.9317
17	3HZG0069HT	GGACTCCT	TATCCTCT	3.2416
18	3HZG0069ABD	TAGGCATG	TATCCTCT	8.0952
19	6HZG0033HT	TAAGGCGA	AGAGTAGA	3.6967
20	6HZG0033ABD	CGTACTAG	AGAGTAGA	2.0918
21	4HZE277HT	AGGCAGAA	AGAGTAGA	4.3592
22	4HZE277ABD	TCCTGAGC	AGAGTAGA	1.912
23	OZ0059HT	GGACTCCT	AGAGTAGA	4.969
24	PZ0203ABD	TAGGCATG	AGAGTAGA	2.121

Table 10. Summary of indexes in each sample identified through Illumina® Sequencing.

Genus
[Cellvibrio]
Acidovorax
Acinetobacter
Alicyclophilus
Alkanindiges
Amycolatopsis
Arthrobacter
Asticcacaulis
Azohydromonas
Azomonas
Azotobacter
Bacillus
Blastobacter
Bradyrhizobium
Buttiauxella
Candidatus
Catenulispora
Caulobacter
Cellvibrio
Chromohalobacter
Collimonas
Comamonas
Corynebacterium
Diaphorobacter
Ehrlichia
Enterobacter
Enterococcus
Erwinia
Escherichia
Giesbergeria
Gordonia
Hydrogenophaga
Hyphomicrobium
Isopterocola
Klebsiella
Kluyvera
Lactobacillus
Lactococcus
Luteimonas
Marinobacter
Marinomonas
Methylobacterium

Microbacterium
Micrococcus
Moraxella
Mycobacterium
Nitrobacter
Oligotropha
Pantoea
Pelomonas
Perlucidibaca
Propionibacterium
Pseudacidovorax
Pseudomonas
Pseudoxanthomonas
Psychrobacter
Ramlibacter
Rhodococcus
Rickettsia
Rothia
Rubrivivax
Saccharothrix
Shigella
Sphingomonas
Staphylococcus
Stenotrophomonas
Streptococcus
Streptomyces
Thioalkalivibrio
Variovorax
Xanthomonas
Xylella
Zymobacter
Total Number of genera: 73

Table 11. Common core of genus identified through Next Generation Sequencing in all five groups.

Sample	Description	Max score	Total	Query cover	E value	Max ident	Accession Number
2HGEB0090 (Head/Thorax)	<i>Limnesia sp.</i> AP-2010 voucher MZSPAC 00007 18S ribosomal RNA gene, partial sequence	2314	2314	95%	0.0	91%	HM070346.1
2HGEB0090 Abdomen	<i>Microsporidium sp.</i> 3 NR-2013 small subunit ribosomal RNA gene, partial sequence	1860	1860	100%	0.0	96%	JX839890.1
Nosema Positive control	<i>Brachiola algerae</i> 16S rRNA gene, ITS1 and 23S rRNA gene, strain Undeen	1910	1910	100%	0.0	96%	AM422905.1

Table 12. Identification of Microsporidia in PCR positive samples through sequencing of 18s rDNA.

Result Type	Spot Label	Protein Name	Accession Number	Protein MW	Peptide Count	Protein Score
Mascot	Light protein	actin [Mortierella minutissima]	gi 209402327	30039,19922	5	126
Mascot	Light protein	beta-actin, partial [Macaca fuscata]	gi 6636344	29544,92969	5	124
Mascot	Light protein	actin [Dissophora decumbens]	gi 12697220	30046,32031	5	123
Mascot	Light protein	actin [Psychroteuthis glacialis]	gi 8895917	29169,60938	5	122
Mascot	Light protein	beta-actin [Sparus aurata]	gi 14485767	31854,84961	5	121
Mascot	Light protein	unnamed protein product [Homo sapiens]	gi 194376310	38950,30078	5	121
Mascot	Light protein	beta-actin [Paralichthys olivaceus]	gi 158668333	11692,69043	4	121
Mascot	Light protein	PREDICTED: beta-actin-like protein 2 isoform 2 [Ceratotherium simum simum]	gi 478497115	37091,48828	5	121
Mascot	Light protein	PREDICTED: beta-actin-like protein 2 isoform X2 [Sorex araneus]	gi 505801926	37370,71094	5	120
Mascot	Light protein	actin [Coprinopsis cinerea okayama7#130]	gi 169865532	41928,07813	5	120
Mascot	Light protein	actin 1 [Auricularia delicata TFB-10046 SS5]	gi 393228332	41968,08984	5	120
Mascot	Light protein	Actin [Wallemia ichthyophaga EXF-994]	gi 505756334	41973,12891	5	119
Mascot	Light protein	beta-actin [Myodes glareolus]	gi 311222955	39265,73828	5	119
Mascot	Light protein	Actin [Crassostrea gigas]	gi 405974534	42066,85156	5	119
Mascot	Light protein	beta-actin [Hypophthalmichthys molitrix]	gi 10442727	42053,83984	5	119
Mascot	Light protein	PREDICTED: actin, cytoplasmic-like [Maylandia zebra]	gi 499050836	45894,92188	5	119
Mascot	Light protein	muscle actin [Strongylocentrotus purpuratus]	gi 187282496	42052,78125	5	119
Mascot	Light protein	B-actin [Pagrus major]	gi 6693629	42097,96094	5	119
Mascot	Light protein	cytoplasmic actin [Seriopora hystrix]	gi 303306184	42003,89063	5	119
Mascot	Light protein	actin [Aedes aegypti]	gi 157106887	42159,96094	5	119
Mascot	Light protein	actin [Cotinusa sp. CJV-2008]	gi 187968772	26840,50977	4	118
Mascot	Light protein	beta actin-1 [Rachycentron canadum]	gi 319893880	42076,85156	5	118

Mascot	Light protein	beta actin variant [Homo sapiens]	gi 62897409	42037,83984	5	118
Mascot	Light protein	actin [Stylophora pistillata]	gi 38176182	41919,96094	5	118
Mascot	Light protein	RecName: Full=Actin, cytoskeletal 1B; AltName: Full=Actin, cytoskeletal 1B; Flags: Precursor	gi 1703130	42137,85156	5	118
Mascot	Light protein	beta actin variant [Homo sapiens]	gi 62897625	42079,89844	5	118
Mascot	Light protein	hypothetical protein BRAFLDRAFT_125401 [Branchiostoma floridae]	gi 260785919	42115,87891	5	118
Mascot	Light protein	predicted protein [Nematostella vectensis]	gi 156388857	42052,80859	5	118
Mascot	Light protein	actin A2 [Haliotis iris]	gi 60391982	41944,91016	5	118
Mascot	Light protein	PREDICTED: beta-actin-like protein 2-like [Saimiri boliviensis boliviensis]	gi 403267534	42279,07031	5	118
Mascot	Light protein	actin [Chtenopteryx sicula]	gi 8895853	29099,80078	4	118
Mascot	Light protein	PREDICTED: beta-actin-like protein 2 [Papio anubis]	gi 402871595	42304,12891	5	117
Mascot	Light protein	PREDICTED: beta-actin-like protein 2 isoform X1 [Sorex araneus]	gi 505801923	42149,01172	5	117
Mascot	Light protein	PREDICTED: beta-actin-like protein 2 [Felis catus]	gi 410948613	42245,98047	5	117
Mascot	Light protein	actin [Octopoteuthis nielsenii]	gi 8895901	29087,75977	4	117
Mascot	Light protein	beta-actin [Felis catus]	gi 11191964	32308,26953	4	117
Mascot	Light protein	PREDICTED: actin, cytoplasmic 1-like [Oryzias latipes]	gi 432875503	41776,76172	5	117
Mascot	Light protein	PREDICTED: beta-actin-like protein 2 isoform 1 [Ceratottherium simum simum]	gi 478497113	41869,78906	5	117
Mascot	Light protein	actin [Sepia officinalis]	gi 8895795	29082,66992	4	117
Mascot	Light protein	actin [Leptosphaeria maculans 'brassicae' group]	gi 55982464	31498,94922	4	117
Mascot	Light protein	beta-actin [Anthopleura elegantissima]	gi 84873373	15109,38965	4	116
Mascot	Light protein	actin [Gamsiella multidivariata]	gi 12697246	30100,26953	4	116
Mascot	Heavy protein	AGAP010147-PA [Anopheles gambiae str. PEST]	gi 158299190	225142,625	20	96,40000 153
Mascot	Heavy protein	hypothetical protein BTF1_30707 [Bacillus thuringiensis HD-789]	gi 434379306	268250,4688	28	86,69999 695
Mascot	Heavy protein	GK16602 [Drosophila willistoni]	gi 195428968	508156,8438	32	86,59999 847
Mascot	Heavy protein	myosin heavy chain variant C [Bombyx mandarina]	gi 234204034	105087,8672	12	86,30000 305

Mascot	Heavy protein	muscle myosin heavy chain [Drosophila melanogaster]	gi 2546936	135749,7813	14	85,69999 695
Mascot	Heavy protein	muscle myosin heavy chain [Drosophila melanogaster]	gi 2546938	138692,2188	14	85
Mascot	Heavy protein	myosin heavy chain, isoform N [Drosophila melanogaster]	gi 281365095	223795,4531	18	83,69999 695
Mascot	Heavy protein	myosin heavy chain [Drosophila melanogaster]	gi 157892	225457,1719	18	83,40000 153
Mascot	Heavy protein	myosin heavy chain, isoform H [Drosophila melanogaster]	gi 28574239	225485,1875	18	83,30000 305
Mascot	Heavy protein	PREDICTED: myosin heavy chain, muscle-like isoform X18 [Ceratitis capitata]	gi 498961155	223631,875	18	83,30000 305
Mascot	Heavy protein	G117055 [Drosophila mojavensis]	gi 195114526	248683,5156	17	83,09999 847
Mascot	Heavy protein	PREDICTED: myosin heavy chain, muscle-like isoform X4 [Ceratitis capitata]	gi 498961069	225240,6875	18	83
Mascot	Heavy protein	PREDICTED: myosin heavy chain, muscle-like isoform X5 [Ceratitis capitata]	gi 498961076	225201,6563	18	82,5
Mascot	Heavy protein	PREDICTED: myosin heavy chain, muscle-like isoform X11 [Ceratitis capitata]	gi 498961113	225181,8906	18	82,19999 695
Mascot	Heavy protein	GK18232 [Drosophila willistoni]	gi 195436762	247887,125	17	81,80000 305
Mascot	Heavy protein	PREDICTED: myosin heavy chain, muscle-like isoform X1 [Ceratitis capitata]	gi 498961051	225083,5781	18	81,40000 153
Mascot	Heavy protein	PREDICTED: myosin heavy chain, muscle-like isoform X15 [Ceratitis capitata]	gi 498961137	225328,9844	18	81,19999 695
Mascot	Heavy protein	myosin heavy chain, isoform M [Drosophila melanogaster]	gi 24584716	222356,2344	17	81,09999 847
Mascot	Heavy protein	myosin heavy chain, isoform P [Drosophila melanogaster]	gi 281365099	223709,9688	17	81
Mascot	Heavy protein	PREDICTED: myosin heavy chain, muscle-like isoform X3 [Ceratitis capitata]	gi 498961063	225173,5625	18	80,90000 153
Mascot	Heavy protein	myosin heavy chain, isoform L [Drosophila melanogaster]	gi 24584714	222365,2031	17	80,80000 305
Mascot	Heavy protein	myosin heavy chain [Drosophila melanogaster]	gi 157891	225371,6875	17	80,59999 847
Mascot	Heavy protein	myosin heavy chain, isoform S [Drosophila melanogaster]	gi 386769712	225571,1875	17	80,09999 847
Mascot	Heavy protein	myosin heavy chain, isoform F [Drosophila melanogaster]	gi 24584700	225303,0781	17	79,30000 305
Mascot	Heavy protein	phosphoglucosamine mutase [Fusobacterium sp. 2_1_31]	gi 496069830	50070,10938	13	79
Mascot	Heavy protein	myosin heavy chain, isoform R [Drosophila melanogaster]	gi 386769710	225100,9219	16	78,90000 153
Mascot	Heavy protein	myosin heavy chain [Bombyx mandarina]	gi 229472621	96070,88281	10	78,40000 153
Mascot	Heavy protein	PREDICTED: myosin heavy chain, muscle-like isoform X17 [Ceratitis capitata]	gi 498961149	225076,8438	17	77,19999 695

Mascot	Heavy protein	PREDICTED: myosin heavy chain, muscle-like isoform X20 [Ceratitis capitata]	gi 498961167	223476,0781	17	77,09999 847
Mascot	Heavy protein	GH11564 [Drosophila grimshawi]	gi 195035369	248462,1406	18	77,09999 847
Mascot	Heavy protein	RecName: Full=Myosin heavy chain, muscle	gi 110825729	225411,0313	16	76,90000 153
Mascot	Heavy protein	PREDICTED: myosin heavy chain, muscle-like isoform X19 [Ceratitis capitata]	gi 498961161	223626,2031	17	76,5
Mascot	Heavy protein	PREDICTED: myosin heavy chain, muscle-like isoform X10 [Ceratitis capitata]	gi 498961107	225174,875	17	76,40000 153
Mascot	Heavy protein	myosin heavy chain [Bombyx mori]	gi 197322818	96130,85938	10	76,30000 305
Mascot	Heavy protein	PREDICTED: myosin heavy chain, muscle-like isoform X9 [Ceratitis capitata]	gi 498961101	225325,0156	17	75,80000 305

Table 13. Sequences retrieved by MALDI TOF/TOF analysis from both proteins isolated from Coomassie blue staining.

Red letters indicate sequences present in the Circumsporozoite Protein of *P. falciparum* BLAST analysis.

Sequence	Number of repeats	Position in Pf CSP
NANP	43	134-137; 142-145; 150-153; 154-209; 214-317
NVDP	3	138-141; 146-149; 210-213
NDPN	1	332-335

Table 14. Position of repetitions recognized by monoclonal antibodies in *P. falciparum* CSP.

Genera described in [97]	Genera in this study		
	FBABD	FPHT	TN
Acinetobacter	YES	YES	YES
Aeromonas	YES	YES	YES
Asaia	YES	YES	YES
Bacillus	YES	YES	YES
Cellvibrio	YES	YES	YES
Chromobacterium	NO	NO	NO
Chryseobacterium	YES	YES	YES
Citrobacter	YES	YES	YES
Corynebacterium	YES	YES	YES
Cronobacter	YES	YES	YES
Diaphorobacter	YES	YES	YES
Diplorickettsia	NO	NO	NO
Elizabethkingia	YES	YES	NO
Enhydrobacter	YES	YES	YES
Enterobacter	YES	YES	YES
Escherichia	YES	YES	YES
Gluconacetobacter	YES	YES	YES
Kluyvera	YES	YES	YES
Microbacterium	YES	YES	YES
Moraxella	YES	YES	YES
Nitrincola	YES	YES	YES
Pantoea	YES	YES	YES
Pseudomonas	YES	YES	YES
Psychrobacter	YES	YES	YES
Raoultella	YES	YES	YES
Riemerella	YES	YES	YES
Serratia	YES	YES	YES
Shewanella	YES	YES	YES
Sphingomonas	YES	YES	YES
Staphylococcus	YES	YES	YES
Stenotrophomonas	YES	YES	YES

Table 15. Comparison between the microbiota description in [97] and the present study.