Supplemental Table A1: Bacterial species identified by clinical microbiological and NGS methods

PtID	ClinDX	Chimera	NGS-DX											
			PathoScope			BLAST		SMRTPortal					BLAST	
		no.	Strain	RefSeq-ID	Abund	Similarity (%)	E-value	Strain	RefSeq-ID	Abund	Reads	Cov (X)	Similarity (%)	E-value
2	Moderate *Acinetobacter baumanii*	5	*Stenotrophomonas maltophila*	AB294553	83.1%		0.00E+00	*Acinetobacter baumannii*	X81660	53.1%	7933	4126.88		0.00E+00
			Acinetobacter baumanii	X81660	16.7%	86%		*Stenotrophomonas maltophilia*	AB294553	29.8%	3322	2311.87	86%	
			Acrhromobacter denitrificans	AJ278451	0.2%	85%		*Acinetobacter calcoaceticus*	AJ888983	3.0%	1090	231.65	97%	
								Achromobacter denitrificans	AJ278451	2.9%	551	222.29	83%	
								Stenotrophomonas pavanii	FJ748683	2.5%	349	191.13	86%	
								Achromobacter xylosoxidans	Y14908	1.6%	311	125.46	83%	
								Stenotrophomonas humi	AM403587	1.5%	307	113	85%	
			Other		0.0%			Other		5.7%				
6	Moderate *Pseudomonas aeruginosa*	43	*Pseudomonas otitidis*	AY953147	98.1%		0.00E+00	*Pseudomonas otitidis*	AY953147	73.2%	36327	27360		0.00E+00
			Shigella sonnei	FR870445	1.0%	86%		*Pseudomonas aeruginosa*	X06684	13.9%	10619	5198	97%	
			Enterobacter cancerogenus	Z96078	0.8%	86%		*Pseudomonas panipatensis*	EF424401	2.5%	2732	952	97%	
								Pseudomonas knackmussii	AF039489	2.0%	2554	748	97%	
								Pseudomona sdelhiensis	DQ339153	1.1%	1553	419	96%	
			Other		0.1%			Other		7.2%				
10	Abundant *Stenotrophomonas maltophilia*	0	*Stenotrophomonas maltophila*	AB294553	100.0%			*Stenotrophomonas maltophilia*	AB294553	83.6%	23353	16192		0.00E+00
								Stenotrophomonas pavanii	FJ748683	5.7%	2414	1111	99%	
								Stenotrophomonas humi	AM403587	4.0%	1983	773	98%	
								Pseudomonas hibiscicola	AB021405	5.7%	2414	367	99%	
								Pseudomonas beteli	AB021406	4.0%	1983	333	99%	
			Other		0.0%			Other		-3.0%				
12	Abundant *Pseudomonas aeruginosa*	22	*Acinetobacter baumanii*	X81660	84.6%		0.00E+00	Acinetobacter baumannii	X81660	56.0%	19033	13737		0.00E+00
			Pseudomonas otitidis	AY953147	14.3%	88%		Pseudomonas otitidis	AY953147	27.3%	8489	6702	88%	
			Enterococcus faecalis	AB012212	1.1%	81%		Pseudomonas aeruginosa	X06684	6.8%	2970	1679	87%	
								Acinetobacter calcoaceticus	AJ888983	2.1%	2289	519	97%	
								Pseudomonas knackmussii	AF039489	1.1%	622	260	87%	
			Other		0.0%			Other		6.7%				
14	Moderate yeast	0	*Stenotrophomonas maltophila*	AB294553	99.6%			*Stenotrophomonas maltophilia*	AB294553	84.6%	8359	5992		0.00E+00
			Phocaeicola abscessus	EU694176	0.3%	76%	2.00E-160	*Stenotrophomonas pavanii*	FJ748683	5.8%	744	413	99%	
			Achromobacter denitrificans	AJ278451	0.1%	85%	0.00E+00	*Stenotrophomonas humi*	AM403587	4.0%	861	284	98%	
								Pseudomonas hibiscicola	AB021405	1.9%	354	137	99%	
								Pseudomonas beteli	AB021406	1.4%	379	96	99%	
			Other		0.0%			Other		2.3%				
19	Moderate MRSA	1	*Lactobacillus rhamnosus*	D16552	48.3%		0.00E+00	*Enterobacter cancerogenus*	Z96078	14.8%	905	752		0.00E+00
			Enterobacter cancerogenus	Z96078	19.9%	79%		*Citrobacter braakii*	AF025368	14.3%	756	729	98%	
			Lactobacillus pontis	X76329	16.5%	92%		*Citrobacter murliniae*	AF025369	7.7%	462	390	98%	
			Lactobacillus gasseri	AF519171	7.2%	89%		*Enterobacter ludwigii*	AJ853891	6.5%	418	329	99%	
			Achromobacter denitrificans	AJ278451	3.6%	79%		*Escherichia vulneris*	AF530476	5.3%	400	270	98%	
			Other		4.6%			Other		51.5%				
43	Abundant *Pseudomonas aeruginosa*	40	*Pseudomonas otitidis*	AY953147	94.6%		0.00E+00	*Pseudomonas otitidis*	AY953147	74.8%	22045	16735		0.00E+00
			Gemella haemolysans	L14326	3.2%	81%		*Pseudomonas aeruginosa*	X06684	13.8%	5808	3097	97%	
			Staphylococcus aureus	L36472	2.1%	79%		*Pseudomonas panipatensis*	EF424401	2.1%	1327	478	97%	
								Pseudomonas knackmussii	AF039489	1.7%	1214	376	97%	
								Pseudomonas delhiensis	DQ339153	1.0%	755	221	96%	
			Other		0.1%			Other		6.6%				
48	Moderate MRSA	0	*Staphylococcus aureus*	L36472	98.3%			*Staphylococcus aureus*	L36472	59.1%	515	320		0.00E+00
			Veillonella parvula	AY995767	0.7%	81%	0.00E+00	*Veillonella parvula*	AY995767	11.1%	110	60	81%	
			Prevotella oulorum	L16472	0.5%	73%	2.00E-134	*Prevotella multiformis*	AB182483	8.8%	90	47	73%	5.00E-121
			Other		0.5%			Other		21.0%				
49	Abundant *Pseudomonas aeruginosa*	11	*Pseudomonas otitidis*	AY953147	90.0%		0.00E+00	*Pseudomonas otitidis*	AY953147	73.2%	2457	1971		0.00E+00
			Staphylococcus aureus	L36472	4.6%	79%		*Pseudomonas aeruginosa*	X06684	17.0%	829	457	97%	
			Shigella flexneri	X96963	4.4%	86%		*Pseudomonas panipatensis*	EF424401	2.8%	210	76	97%	

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PtID	ClinDX	Chimera	NGS-DX											
			PathoScope			BLAST		SMRTPortal					BLAST	
		no.	Strain	RefSeq-ID	Abund	Similarity (%)	E-value	Strain	RefSeq-ID	Abund	Reads	Cov (X)	Similarity (%)	E-value
			Other		1.0%			Other		7.0%				
50	Moderate Enterobacter aerogenes	0	*Raoultella ornithinolytica*	U78182	92.2%			*Raoultella ornithinolytica*	X87276	41.5%	520	430		0.00E+00
			Streptococcus sanginosus	AF104678	3.7%	78%	0.00E+00	*Enterobacter aerogenes*	U78182	17.0%	241	177	99%	
			Prevotella melaninogenica	CP002122	2.2%	74%	7.00E-126	*Citrobacter murliniae*	AB004750	14.7%	61	152	98%	
			Other		1.9%			Other		26.8%				
53	Abundant *Enterobacter aerogenes*	4	*Enterobacter aerogenes*	AB004750	100.0%			*Citrobacter murliniae*	U78182	37.4%	10161	8620		0.00E+00
								Raoultella ornithinolytica	AB004750	16.3%	4911	3765	99%	
								Enterobacter aerogenes	AF025369	13.1%	3860	3007	98%	
			Other		0.0%			Other		33.2%				
54	Few *Pseudomonas aeruginosa*	28	*Pseudomonas otitidis*	AY953147	100.0%			*Pseudomonas otitidis*	AY953147	79.0%	313	219		0.00E+00
								Pseudomonas aeruginosa	X06684	21.0%	123	57	97%	
			Other		100.0%			Other		0.0%				
61	Moderate oropharyngeal flora	1	*Achromobacter denitrificans*	AJ278451	58.7%		0.00E+00	*Achromobacter denitrificans*	AJ278451	46.2%	2933	1611		0.00E+00
			Enterococcus duras	AJ276354	35.6%	78%		*Achromobacter xylosoxidans*	Y14908	19.1%	1285	667	99%	
			Pseudomonas migulae	AF074383	3.7%	84%		*Achromobacter insolitus*	AY170847	7.0%	510	243	99%	
			Stenotrophomonas maltophila	AB294553	1.3%	85%		*Achromobacter spanius*	AY170848	6.3%	405	219	99%	
			Other		0.7%			Other		21.4%				
64	Moderate *Pseudomonas aeruginosa*, Few *Acinetobacter baumanii*	9	*Prevotella melaninogenica*	CP002122	79.6%			*Prevotella melaninogenica*	AY995767	61.1%	15173	9188		
			Lactobacillus gasseri	AF519171	9.3%	76%	1.00E-170	*Acinetobacter baumannii*	CP002122	10.0%	2578	1499	76%	1.00E-160
			Acinetobacter baumannii	X81660	6.6%	76%	1.00E-160	*Pseudomonas otitidis*	FJ545434	7.0%	1542	1055	74%	2.00E-159
			Veillonella parvula	AY995767	2.5%	74%	5.00E-135	*Veillonella parvula*	AY953147	4.5%	1240	677	74%	4.00E-135
			Pseudomonas otitidis	AY953147	1.5%	74%	2.00E-159	*Prevotella scopos*	X81660	1.6%	881	234	98%	0.00E+00
			Other		0.5%			Other		15.9%				
67	Few oropharyngeal flora	0	*Obesumbacterium proteus*	AJ233422	54.2%		0.00E+00	*Acinetobacter baumannii*	X81660	45.1%	9	6		0.00E+00
			Achromobacter denitrificans	AJ278451	31.4%	82%		*Bacteroides intestinalis*	AB214328	13.4%	3	2	77%	
			Pseudomonas otitidis	AY953147	10.8%	86%		*Lactobacillus gasseri*	AF519171	9.5%	5	1	80%	
			Streptococcus mitis	AF003929	3.5%	78%		*Prevotella melaninogenica*	CP002122	8.9%	6	1	76%	1.00E-163
			Other		0.1%			Other		23.1%				
70	Abundant oropharyngeal flora	6	*Neisseria cinerea*	ACDY02000019	96.4%		0.00E+00	*Neisseria cinerea*	ACDY02000019	62.0%	15690	10515		0.00E+00
			Streptococcus mitis	AF003929	1.8%	78%		*Neisseria sicca*	ACKO02000016	14.4%	5200	2448	97%	
			Corynebacterium pseudodiphtheriticum	AJ439343	1.6%	79%		*Corynebacterium pseudodiphtheriticum*	AJ439343	7.1%	2262	1202	79%	
								Neisseria flavescens	L06168	3.8%	2158	645	97%	
								Streptococcus mitis	AF003929	2.5%	704	430	78%	
			Other		0.1%			Other		10.2%				
71	Abundant MRSA	3	*Staphylococcus aureus*	L36472	99.8%		0.00E+00	*Staphylococcus aureus*	L36472	80.2%	13572	8890		0.00E+00
			Enterococcus faecalis	AB012212	0.2%	89%		*Staphylococcus aureus*	D83355	5.3%	951	592	99%	
								Staphylococcus simiae	AY727530	4.6%	1009	512	99%	
								Enterococcus faecalis	AB012212	4.4%	823	490	89%	
			Other		0.0%			Other		5.4%				
73	Abundant *Aeromonas hydrophilia*, Abundant *Pantoea species*	20	*Aeromonas punctata*	X60408	92.5%			*Serratia grimesii*	AJ233430	12.4%	3109	2792		
			Serratia grimesii	AJ233430	2.1%	91%	0.00E+00	*Dysgonomonas capnocytophagoides*	U41355	9.8%	4321	2192	74%	2.00E-126
			Streptococcus salivarius	AY188352	1.6%	78%		*Yersinia entomophaga*	DQ400782	9.3%	2887	2085	96%	0.00E+00
			Dysgonomonas capnocytophagoides	U41355	1.5%	76%	1.00E-162	*Aeromonas punctata*	X60408	5.7%	1596	1274	91%	
			Pseudomonas extremaustralis	AJ583501	1.0%	89%	0.00E+00	*Aeromonas hydrophila*	FR870443	5.3%	2697	1193	91%	
			Stenotrophomonas maltophilia	AB294553	1.0%	86%		*Hafnia paralvei*	FM179943	5.3%	1678	1192	98%	
			Other		0.3%			Other		52.3%				
75	Moderate yeast	0	*Pseudomonas otitidis*	AY953147	99%		0.00E+00	*Pseudomonas otitidis*	AY953147	0.834	695	539		0.00E+00
			Achromobacter denitrificans	AJ278451	1.0%	84%		*Pseudomonas aeruginosa*	X06684	12.0%	167	78	97%	
								Pseudomonas panipatensis	EF424401	2.9%	53	19	97%	
								Pseudomonas knackmussii	AF039489	1.7%	55	11	97%	
			Other		0.0%			Other		0.0%				

Supplemental Table A1: Bacterial species identified by clinical microbiological and NGS methods

PtID	ClinDX	Chimera	NGS-DX											
			PathoScope			BLAST		SMRTPortal					BLAST	
		no.	Strain	RefSeq-ID	Abund	Similarity (%)	E-value	Strain	RefSeq-ID	Abund	Reads	Cov (X)	Similarity (%)	E-value
77	Few *Moraxella catarrhalis*, Few oropharyngeal flora	1	*Staphylococcus aureus*	L36472	79.5%		0.00E+00	*Streptococcus mitis*	AF003929	12.1%	188	55		0.00E+00
			Streptococcus mitis	AF003929	13.5%	86%		*Moraxella catarrhalis*	AF005185	9.5%	182	43	79%	
			Moraxella catarrhalis	AF005185	2.3%	79%		*Shewanella donghaensis*	AY326275	5.7%	611	26	78%	
			Corynebacterium accolens	AJ439346	1.1%	79%		*Desulfovibrio piger*	AF192152	5.7%	693	26	79%	
			Other		3.6%			Other		67.0%				
78	Few *Enterobacter aerogenes*	12	*Streptococcus mitis*	AF003929	75.1%		0.00E+00	*Streptococcus mitis*	AF003929	16.4%	3277	2050		0.00E+00
			Haemophilus influenzae	M35019	4.8%	77%		*Corynebacterium accolens*	AJ439346	14.3%	3159	1788	79%	
			Streptococcus anginosus	AF104678	3.9%	93%		*Neisseria cinerea*	ACDY02000019	8.5%	1567	1058	78%	
			Gemella haemolysans	L14326	3.5%	85%		*Streptococcus anginosus*	AF104678	6.4%	1494	799	93%	
			Streptococcus intermedius	AF104671	3.4%	95%		*Prevotellamela ninogenica*	CP002122	4.1%	1080	508	76%	6.00E-166
			Corynebacterium accolens	AJ439346	2.6%	79%		*Streptococcus pneumoniae*	AF003930	3.6%	902	456	99%	0.00E+00
			Staphylococcus epidermidis	D83363	2.2%	85%		*Streptococcus intermedius*	AF104671	3.5%	727	433	95%	
			Neisseria flavescens	L06168	2.0%	78%		*Haemophilus parainfluenzae*	AY362908	3.2%	822	406	79%	
			Neisseria sicca	ACKO02000016	1.2%	80%		*Haemophilus pittmaniae*	AJ290755	2.8%	394	355	77%	
			Other		1.3%			Other		37.2%				
80	Few oropharyngeal flora	0	*Achromobacter denitrificans*	AJ278451	96.7%		0.00E+00	*Achromobacter denitrificans*	AJ278451	41.3%	357	253		0.00E+00
			Pseudomonas otitidis	AY953147	1.5%	84%		*Achromobacter xylosoxidans*	Y14908	13.6%	143	84	94%	
			Streptococcus pneumoniae	AF003930	1.2%	78%		*Pseudomonas otitidis*	AY953147	5.9%	48	36	84%	
								Achromobacter insolitus	AY170847	4.3%	54	27	99%	
			Other		0.6%			Other		34.9%				
83	Few *Enterobacter cloacae*		*Enterobacter ludwigii*	AJ853891	80.2%		0.00E+00	*Enterobacter ludwigii*	AJ853891	40.8%	5495	4471		0.00E+00
			Veillonella parvula	AY995767	6.1%	79%		*Acinetobacter guillouiae*	X81659	12.8%	1834	1400	85%	
			Acinetobacter guillouiae	X81659	5.7%	85%		*Porphyromonas catoniae*	X82823	5.4%	903	596	76%	6.00E-166
			Enterococcus faecalis	AB012212	2.6%	78%		*Actinomyces odontolyticus*	AJ234040	5.4%	736	594	79%	0.00E+00
			Streptococcus pneumoniae	AF003930	2.0%	77%		*Veillonella parvula*	AY995767	5.1%	876	558	79%	
			Klebsiella pneumoniae	X87276	1.9%	98%		*Acinetobacter bereziniae*	Z93443	4.8%	911	522	85%	
			Lautropia mirabilis	AEQP01000026	1.1%	83%		*Abiotrophia defectiva*	D50541	2.8%	436	309	78%	
			Other		0.5%			Other		23.0%				
85	Moderate MSSA		*Lactobacillus gasseri*	AF519171	54.8%		0.00E+00	*Streptococcus salivarius*	AY188352	46.2%	1710	1148		
			Streptococcus salivarius	AY188352	35.6%	85%		*Streptococcus mitis*	AF003929	11.0%	369	274	95%	0.00E+00
			Gemella morbillorum	L14327	4.6%	85%		*Prevotella histicola*	EU126661	6.6%	250	164	76%	3.00E-154
			Streptococcus mutans	AY188348	2.6%	86%		*Streptococcus vestibularis*	AY188353	5.0%	285	123	99%	0.00E+00
			Other		2.4%			Other		31.2%				
86	Abundant MSSA		*Staphylococcus aureus*	L36472	47.9%		0.00E+00	*Haemophilus influenzae*	M35019	56.2%	6829	3879		0.00E+00
			Haemophilus influenzae	M35019	27.5%	78%		*Streptococcus mitis*	AF003929	13.0%	1778	900	77%	
			Streptococcus pneumoniae	AF003930	22.4%	85%		*Streptococcus pneumoniae*	AF003930	11.6%	1300	804	78%	
			Raoultella ornithinolytica	U78182	1.6%	79%		*Haemophilus aegyptius*	AY362905	6.2%	1031	431	99%	
								Streptococcus pseudopneumoniae	AY612844	5.8%	773	399	78%	
								Staphylococcus aureus	L36472	1.6%	200	113	78%	
			Other		0.6%			Other		5.5%				
89	Moderate *Klebsiella pneumoniae*, Moderate *Providencia stuartii*		*Streptococcus agalactiae*	AB023574	72.2%		0.00E+00	*Streptococcus agalactiae*	AB023574	66.8%	22695	15220		0.00E+00
			Lactobacillus gasseri	AF519171	11.4%	87%		*Klebsiella pneumoniae*	X87276	13.5%	4181	3069	78%	
			Streptococcus anginosus	AF104678	7.5%	93%		*Streptococcus anginosus*	AF104678	8.8%	3184	1999	93%	
			Klebsiella pneumoniae	X87276	6.5%	78%		*Klebsiella pneumoniae*	AF130982	1.7%	694	388	78%	
								Enterococcusfaecalis	AB012212	1.6%	641	356	89%	

"Table S1: Bacterial species identified by clinical microbiological and NGS methods"

Supplemental Table A1: Bacterial species identified by clinical microbiological and NGS methods

PtID	ClinDX	Chimera	NGS-DX											
			PathoScope			BLAST		SMRTPortal					BLAST	
		no.	Strain	RefSeq-ID	Abund	Similarity (%)	E-value	Strain	RefSeq-ID	Abund	Reads	Cov (X)	Similarity (%)	E-value
								Klebsiella pneumoniae	Y17657	1.2%	451	271	78%	
			Other		2.3%			Other		6.5%				
90	Standard culture negative		*Lactobacillus gasseri*	AF519171	41.5%		0.00E+00	*Enterobacter cancerogenus*	Z96078	14.1%	479	397		0.00E+00
			Lactobacillus rhamnosus	D16552	38.9%	89%		*Citrobacter braakii*	AF025368	13.0%	402	368	98%	
			Enterobacter cancerogenus	Z96078	4.4%	81%		*Citrobacter murliniae*	AF025369	8.1%	263	228	98%	
			Pseudomonas otitidis	AY953147	3.3%	81%		*Enterobacter ludwigii*	AJ853891	7.2%	262	204	99%	
			Streptococcus anginosus	AF104678	2.5%	86%		*Citrobacter werkmanii*	AF025373	5.6%	273	158	98%	
			Streptococcus agalactiae	AB023574	2.5%	87%		*Escherichia vulneris*	AF530476	5.0%	205	142	98%	
			Streptococcus pneumoniae	AF003930	2.3%	85%		*Lactobacillus rhamnosus*	D16552	4.5%	176	126	79%	
			Shigella flexneri	X96963	2.2%	81%		*Citrobacter freundii*	AJ233408	3.9%	130	109	98%	
			Haemophilus influenzae	M35019	1.1%	79%		*Haemophilus influenzae*	M35019	3.8%	160	108	87%	
			Achromobacter denitrificans	AJ278451	1.0%	79%		*Salmonella enterica*	AE006468	3.2%	141	90	97%	
			Other		0.4%			Other		31.6%				

Average CHIMERA /sample 9

Average (No. Reads/Cov per sample) 2739 1662