

Table 1. Bacterial MAGs recovered from ISS metagenomic samples treated with PMA

Sample*	Species Identified	NCBI Accession # of type strain	Type strain	ANI with type strain (%)	CheckM completeness (%)	CheckM contamination (%)	Contig count	DNA size (bp)	Contigs N50 (bp)	Mean Coverage (x)	Identified pipeline (MetaSPAdes and MetaWRAP)
F1-2P	<i>Enterobacter bugandensis</i>	NZ_LT992502.1	EB-247	98.62	99.37	0.33	18	4,677,674	306,406	447	Yes
F1-2P	<i>Klebsiella quasipneumoniae</i>	CCDF00000000.1	01A030	96.60	99.40	0.29	26	5,139,708	343,051	116	MetaWRAP
F1-4P	<i>Staphylococcus aureus</i>	NZ_CP035101.1	ATCC 12600	98.25	90.81	4.7	974	2,813,949	5,100	12	MetaSPAdes
F1-5P	<i>Pantoea brenneri</i>	MLFN00000000.1	LMG 24534	99.13	100.00	1.95	139	5,160,744	122,775	165	Yes
F1-7P	<i>Methylobacterium ajmalii</i>	GCF_016613415.1	IF7SW-B2	99.98	100.00	0.47	135	6,457,840	103,728	118	MetaWRAP
F1-8P	<i>Microbacterium aurum</i>	NZ_BCWI00000000.1	NBRC 15708	95.95	94.11	3.78	349	3,384,148	14,218	13	Yes
F2-1P	<i>Acinetobacter pittii</i>	BBST00000000.1/	DSM 25618	98.26	100.00	1.78	150	5,633,218	89,240	37	MetaSPAdes
F2-1P	<i>Kocuria palustris</i>	NZ_JAFBCR00000000.1	DSM 11925	98.87	100.00	3.44	105	4,785,551	127,675	22	MetaSPAdes
F2-2P	<i>Staphylococcus saprophyticus</i>	PPRA00000000.1/	CCUG 38042	99.62	99.44	8.4	127	2,775,084	486,110	39	MetaSPAdes
F2-5P	<i>Paenibacillus polymyxa</i>	NZ_CP049783.1	DSM 36	98.34	99.56	0.12	292	5,630,072	34,896	8	Yes
F2-5P	<i>Pantoea brenneri</i>	MLFN00000000.1	LMG 24534	99.13	100.00	0.22	86	5,013,168	153,890	231	Yes
F2-7P	<i>Bacillus velezensis</i>	LHCC00000000.1/	KCTC 13012	98.05	90.39	1.65	654	3,288,500	6,166	9	MetaWRAP
F2-7P	<i>Methylobacterium ajmalii</i>	GCF_016613415.1	IF7SW-B2	99.98	100.00	0.94	182	6,808,664	83,968	42	Yes
F2-7P	<i>Sphingomonas sanguinis</i>	BCTY00000000	NBRC 13937	99.71	99.42	1.48	73	4,484,914	218,858	121	Yes
F2-7P	<i>Staphylococcus saprophyticus</i>	NC_007350.1	ATCC 15305	99.55	98.89	1.02	243	2,532,577	17,062	33	MetaWRAP
F2-8P	<i>Methylobacterium extorquens</i>	NZ_LT962688.1	TK 0001	96.57	98.28	0.63	359	5,572,757	24,891	14	MetaWRAP
F2-8P	<i>Paenibacillus polymyxa</i>	NZ_CP049783.1	DSM 36	98.30	99.85	0	51	5,763,874	670,748	143	Yes
F2-8P	<i>Staphylococcus aureus</i>	NZ_CP035101.1	ATCC 12600	97.48	97.46	0.38	220	2,568,938	19,819	16	Yes
F3-1P	<i>Kalamiella piersonii</i>	NZ_RARB00000000.1	IIIF1SW-P2	99.99	89.69	0.38	168	4,802,117	61,466	50	Yes
F3-2P	<i>Cutibacterium acnes</i>	NZ_CP023676.1	ATCC 6919	99.74	91.36	2.54	370	2,311,212	8,625	126	MetaWRAP
F3-2P	<i>Staphylococcus saprophyticus</i>	NC_007350.1	ATCC 15305	99.33	96.57	0.00	186	2,582,173	21,246	696	Yes
F3-3P	<i>Klebsiella pneumoniae</i>	JOOW00000000	ATCC 13883	96.55	89.66	0.46	93	5,141,666	140,190	50	MetaSPAdes
F3-3P	<i>Klebsiella quasipneumoniae</i>	NZ_CP012252.1	01A030	96.59	98.47	0.54	167	5,021,601	47,004	506	MetaWRAP
F3-3P	<i>Staphylococcus saprophyticus</i>	NC_007350.1	ATCC 15305	99.52	82.39	0.28	551	1,830,596	3,691	57	MetaWRAP
F3-4P	<i>Pantoea dispersa</i>	NZ_SCKT00000000.1	DSM 30073	98.00	99.33	0.16	100	4,618,120	73,915	480	Yes
F3-4P	<i>Pantoea dispersa</i>	NZ_SCKT00000000.1	DSM 30073	97.89	92.92	0.38	60	4,944,646	138,933	50	Yes
F3-5P	<i>Kalamiella piersonii</i>	NZ_RARB00000000.1	IIIF1SW-P2	99.98	88.94	0	107	4,802,460	94,185	50	Yes
F3-7P	<i>Kalamiella piersonii</i>	NZ_RARB00000000.1	IIIF1SW-P2	99.98	87.70	0.34	146	4,656,932	59,699	50	Yes
F3-7P	<i>Klebsiella aerogenes</i>	NC_015663.1	KCTC 2190	98.52	90.49	0.59	451	4,261,436	12,705	71	MetaWRAP
F3-8P	<i>Kalamiella piersonii</i>	NZ_RARB00000000.1	IIIF1SW-P2	99.98	89.38	0.16	152	4,749,371	57,018	50	Yes

*key to samples: F1, F2, F3: Flight 1, 2, and 3. The numerals after flight numbers denote location from where sampled. P is PMA-treated. Descriptions of the locations were published in detail in Singh et al. (2018).