

Supplementary Table S1. Feature of the sequenced draft genomes assembled with SPAdes and quality checked with Quast.

Isolate	Total length (bp)	#Contigs	N50	L50	ST	G+C content (%)	CDSs (bp)	Accession number
CFS1154	4542213	50	199872	8	1	56.7	4446777	JAWLKX000000000
CFS1155	4556805	39	260217	7	1	56.69	4455968	JAWLKW000000000
CFS1156	4640775	61	232291	7	1	56.69	4509936	JAWLSK000000000
CFS1157	4641177	66	211383	8	1	56.7	4542177	JAWLSJ000000000
CFS1158	4612695	66	211383	8	1	56.7	4583034	JAWLKV000000000
CFS1159	4609363	65	195298	7	1	56.69	4547080	JAWLKU000000000
CFS1160	4542966	46	203518	7	1	56.76	4463582	JAWLKT000000000
CFS1161	4621986	361	230205	61	1	56.35	4612327	JAWLSI000000000
CFS1169	4572077	173	651609	24	1	56.6	4502144	JAWLSH000000000
CFS1297	4531883	44	166921	8	4	56.67	4504511	JAWLKN000000000
CFS1304	4420999	40	267914	7	99	57.05	4356816	JAWLKO000000000
CFS1322	4621902	51	265761	6	4	56.7	4564789	JAWLKQ000000000
CFS1328	4614795	56	224690	8	4	56.49	4609599	JAWLKP000000000
CFS1362	4603160	86	253680	7	99	56.76	4569007	JAWLKM000000000
CFS1370	4425465	20	601557	3	99	57.06	4225455	JAWLKL000000000
CFS1377	4508875	49	152844	9	4	56.69	4448610	JAWLKK000000000
CFS2786	4748603	212	222391	8	1	56.59	4698933	JAWLKS000000000
CFS2788	4652879	85	222391	8	1	56.6	4632748	JAWLKR000000000