

Table S1

Taxonomic distance analysis for AMD metagenome scaffolds assignment to draft genome assemblies generated for five strains in the AMD metagenome project.

Method	Measure	Population					Taxonomic Distance	
		T (404)	L1 (417)	L2 (126)	F1 (172)	F2 (64)	Micro average	Macro average
PPS SS	Assigned	404	410	118	172	64	--	--
	Const_n_scaff	0.83	0.91	0.76	0.98	0.95	0.89	0.89
	Const_n_bp	0.89	0.94	0.95	0.99	0.99	0.94	0.95
	Tax dist	2.82	1.60	1.73	3.72	3.83	2.11	2.74
PPS G	Assigned	403	414	126	172	64	--	--
	Const_n_scaff	0.81	0.38	0.29	0.97	0.91	0.63	0.67
	Const_n_bp	0.86	0.38	0.11	0.99	0.98	0.62	0.66
	Tax dist	2.96	8.01	7.56	4.46	3.70	4.97	5.34
BLASTN	Assigned	403	416	126	172	64	--	--
	Const_n_scaff	0.13	0.16	0.05	0.07	0.08	0.12	0.10
	Const_n_bp	0.08	0.11	0.01	0.02	0.02	0.05	0.05
	Tax dist	5.65	11.18	11.45	7.97	6.64	7.90	8.58
MEGAN	Assigned	377	306	89	164	63	--	--
	Const_n_scaff	0.38	0.67	0.61	0.24	0.25	0.22	0.43
	Const_n_bp	0.33	0.65	0.57	0.19	0.12	0.37	0.37
	Tax dist	4.16	6.91	6.62	6.98	5.81	3.55	6.09
NBC	Assigned	403	413	126	172	63	--	--
	Const_n_scaff	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	Const_n_bp	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	Tax dist	11.35	10.97	10.65	14.85	13.63	12.40	12.29