

Supporting Table S5. Distinctive properties of major scaffold clusters. Percentages are based on taxonomic classifications of all predicted protein tophit matches to Genbank nr, as determined using the DarkHorse algorithm at a filter threshold setting of 0.05, including only alignments covering at least 70% of both query and target sequences with an e-value of 1e-5 or better.

group	pct G+C	pct reads 0.1 filt	avg read depth	pct Halo- quadrataum	pct Nano- haloarchaea	pct Halo- rabdus	pct Halo- ferax	pct Halo- rubrum	pct Salini- bacter	pct LYS	pct THR	pct ALA	pct GLU
Haloquadratum	48	20%	8.6	79%	0%	2%	1%	1%	0%	2.3	7.5	9.0	7.7
HQX50	50	20%	2.5	44%	1%	5%	7%	2%	0%	1.4	4.3	5.6	4.8
Halonotius HN4	61	59%	3.8	10%	1%	12%	15%	12%	0%	1.7	6.5	10.1	7.2
Halonotius HN6	63	81%	4.6	9%	0%	12%	17%	12%	0%	1.7	6.2	9.9	7.2
Nanosalina J07AB43	43	94%	6.4	1%	60%	3%	1%	2%	0%	6.0	5.0	5.8	10.5
Nanosalinarum J07AB56	56	91%	4.7	1%	53%	4%	0%	1%	0%	4.0	5.3	7.1	10.2
HX5	60	21%	2.9	5%	1%	28%	2%	3%	0%	1.4	6.3	9.8	6.1
HX64	64	24%	3.6	5%	1%	27%	3%	4%	0%	1.3	6.6	9.4	7.9
HB67	67	33%	2.9	10%	1%	12%	14%	8%	0%	1.3	7.5	11.4	7.7
Halorubrum	60	25%	2.4	7%	0%	7%	14%	32%	0%	0.9	3.1	4.9	3.7
Salinibacter	66	44%	2.2	0%	0%	0%	0%	0%	92%	0.8	2.7	4.4	3.0