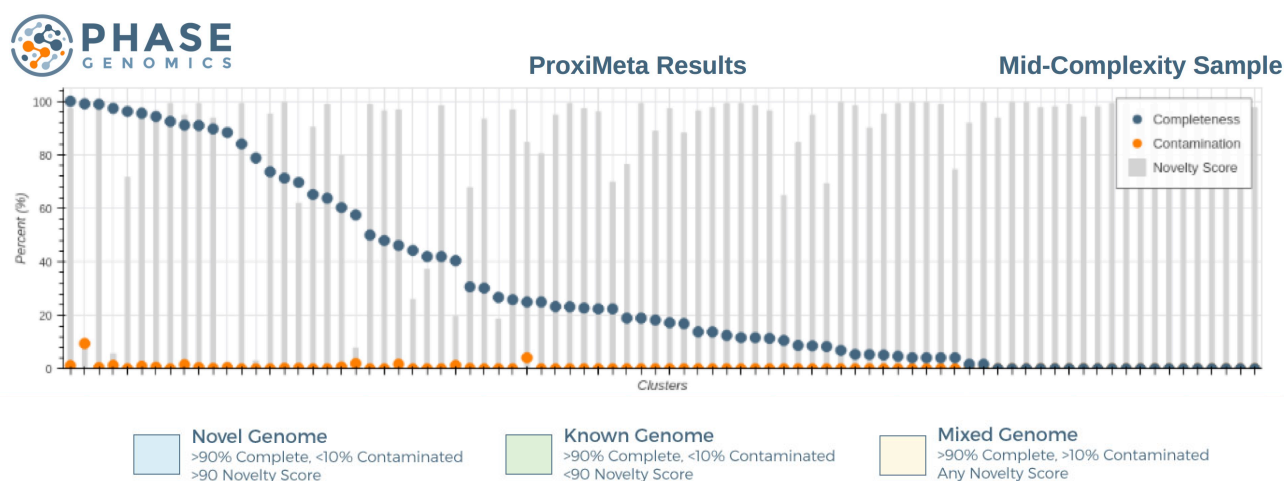


ProxiMeta™ Hi-C Metagenome Deconvolution

SAMPLE REPORT

After deconvolution, ProxiMeta™ Hi-C estimates the completeness of each genome assembly, the level of contamination/mis-clustering, and abundance of each organism in the sample. It also compares each assembled genome to a global database in order to find each genome's identity or, in the case of novel genomes, its closest taxonomic group.



Cluster ID	Top Reference	Novelty Score	Completeness (%)	Contamination (%)	Abundance (%)	GC (%)	Genome Size	Num Contigs	Contig N50
clusters.46	<i>p__Proteobacteria</i>	97.23	100.00	1.22	0.52	64.82	3,896,639	51	99,072
clusters.14	<i>Pseudoxanthomonas suwonensis</i> J42	9.69	99.02	9.47	1.26	68.66	4,208,291	147	78,620
clusters.9	<i>p__Bacteroidetes</i>	99.20	98.89	0.49	0.35	41.46	2,982,618	39	169,127
clusters.61	<i>Allicycliphilus</i> sp. CRZ1	5.67	97.37	1.31	1.29	69.33	3,370,190	58	157,009
clusters.33	<i>Castellaniella defragrans</i> 65Phen	71.64	96.21	0.03	1.42	66.77	2,890,307	79	53,648
clusters.24	<i>c__Betaproteobacteria</i>	97.62	95.50	0.98	0.53	49.94	2,672,098	120	32,251
clusters.3	<i>o__Rhizobiales</i>	96.06	94.30	0.63	0.42	64.89	3,767,809	42	136,004
clusters.6	<i>k__Bacteria</i>	99.20	92.47	0.00	1.58	47.41	2,014,927	27	98,566
clusters.15	<i>c__Betaproteobacteria</i>	94.90	91.09	1.57	1.52	64.53	2,959,056	118	33,099
clusters.12	<i>p__Bacteroidetes</i>	99.20	90.95	0.48	0.97	48.19	4,850,982	56	101,163
clusters.50	<i>o__Rhizobiales</i>	93.75	89.67	0.19	0.52	63.23	4,633,035	190	33,187
clusters.5	<i>Achromobacter xylosoxidans</i>	2.59	88.33	0.47	1.12	65.00	6,110,034	102	112,383
clusters.11	<i>f__Flavobacteriaceae</i>	99.20	84.05	0.00	0.54	37.34	2,020,106	17	137,099
clusters.10	<i>Paracoccus pantotrophus</i> J40	3.02	78.79	0.00	1.49	67.93	3,180,337	43	85,551
clusters.17	<i>o__Burkholderiales</i>	95.29	73.64	0.00	1.50	67.06	2,343,750	51	55,520
clusters.38	<i>p__Bacteroidetes</i>	99.60	71.27	0.24	0.82	49.67	3,938,850	21	217,726
clusters.0	<i>Cupriavidus</i> sp. HPC L	61.90	69.69	0.23	1.51	68.17	2,876,256	26	584,347
clusters.2	<i>k__Bacteria</i>	90.37	65.17	0.00	1.48	68.30	4,226,780	21	231,655