

1. Read Statistics

Illumina Std PE Statistics

File name	AAUAN.15M.bbqc.fq.gz.fastq
Number of reads	100,086
Sequencing depth [†]	3X
Read type	2x150 bp

[†] A genome size of 5.0 Mbp was assumed in this calculation.

2. Screened Assembly QC Results

GC vs coverage based on GC of NCBI nt and Greengenes 16S rRNA gene hits to the assembly using megablast, shown for different taxonomic levels.

No hits found.

Estimated genome recovery derived from analysis of universal single-copy genes detected in final assembly.

HMM	Pct Recovered
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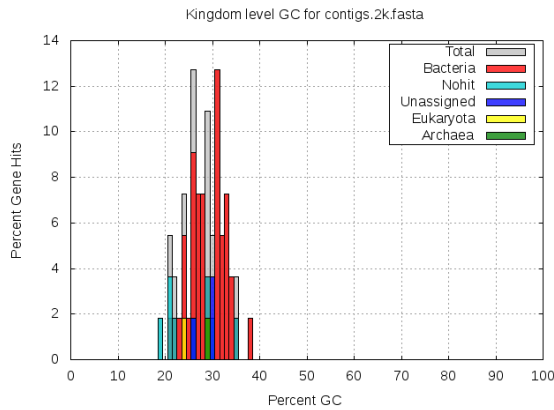
3. Unscreened Assembly Statistics

Assembly method	SPAdes
Scaffold total	4
Contig total	4
Scaffold sequence length	45.6 kb
Contig sequence length	45.6 kb (0.0% gap)
Scaffold N/L50	1/25.2 kb
Contig N/L50	1/25.2 kb
Largest Contig	25.2 kb
Number of scaffolds >50 kb	0
Pct of genome in scaffolds >50 kb	0.0
Pct of reads assembled	96.2

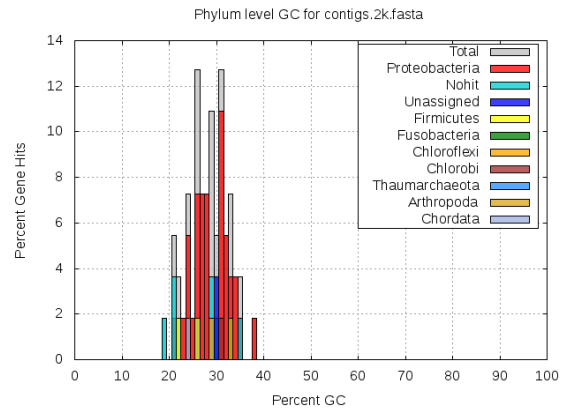
4. Unscreened Assembly QC Results

GC histogram of the predicted genes on each contig, overlaid with GC of hits based on LAST, shown for different taxonomic levels.

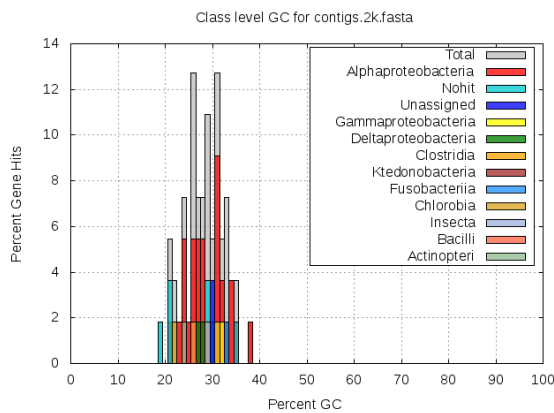
Kingdom



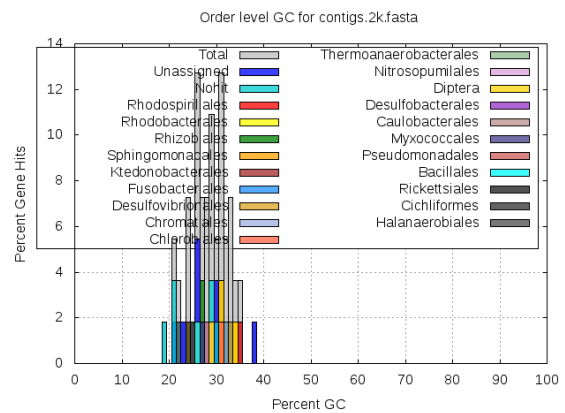
Phylum



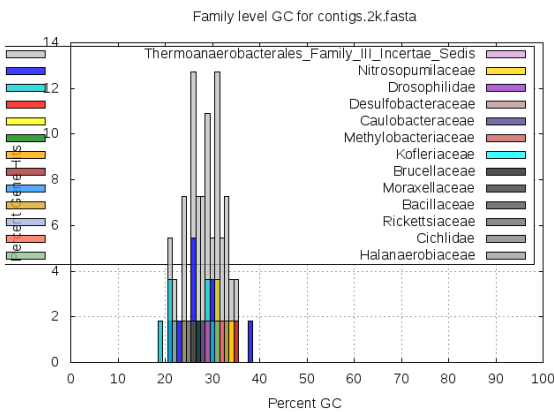
Class



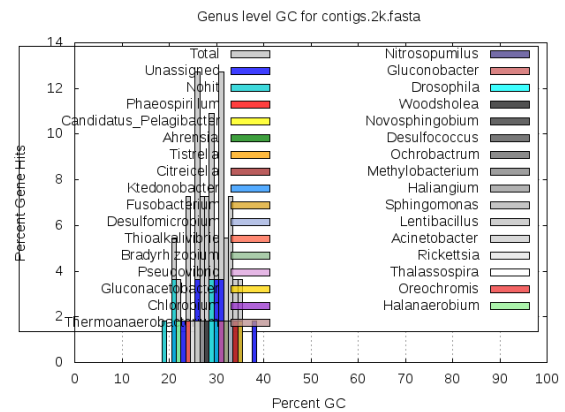
Order



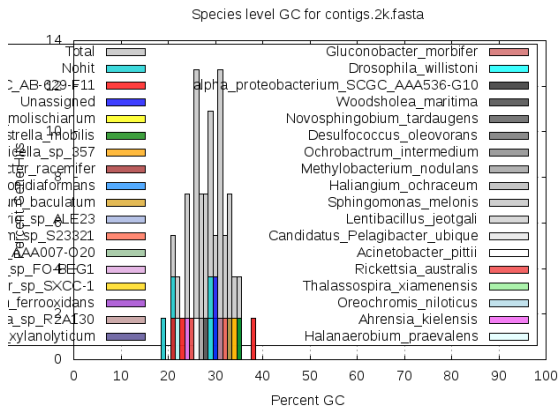
Family



Genus

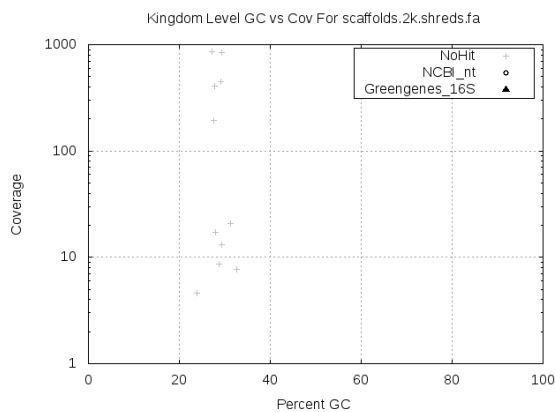


Species

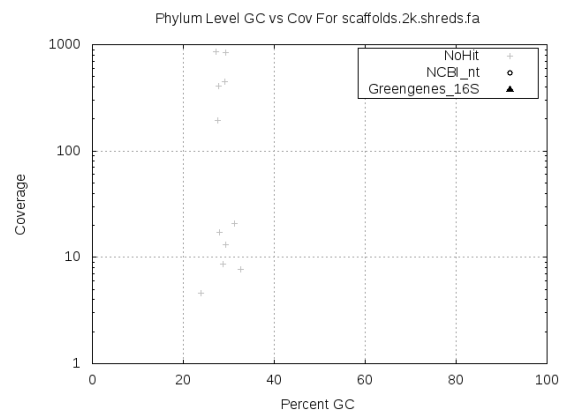


GC vs coverage based on GC of NCBI nt and Greengenes 16S rRNA gene hits to the assembly using megablast, shown for different taxonomic levels.

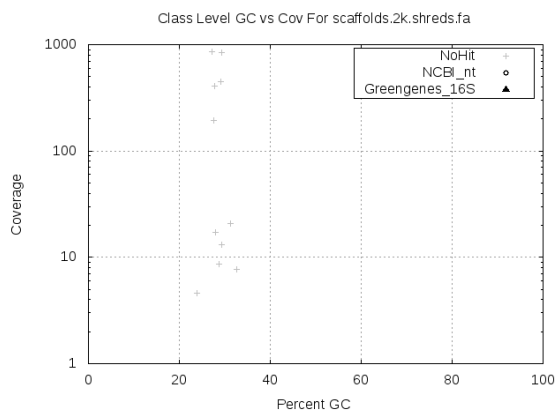
Kingdom



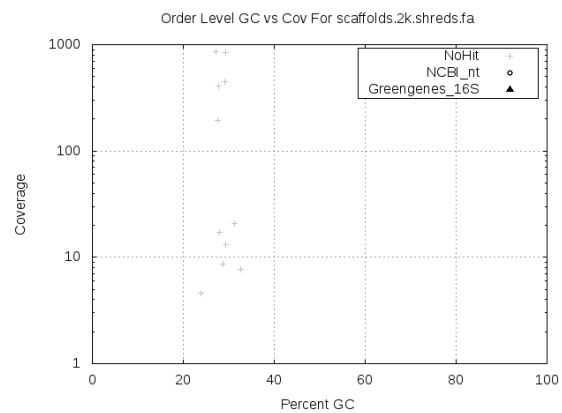
Phylum

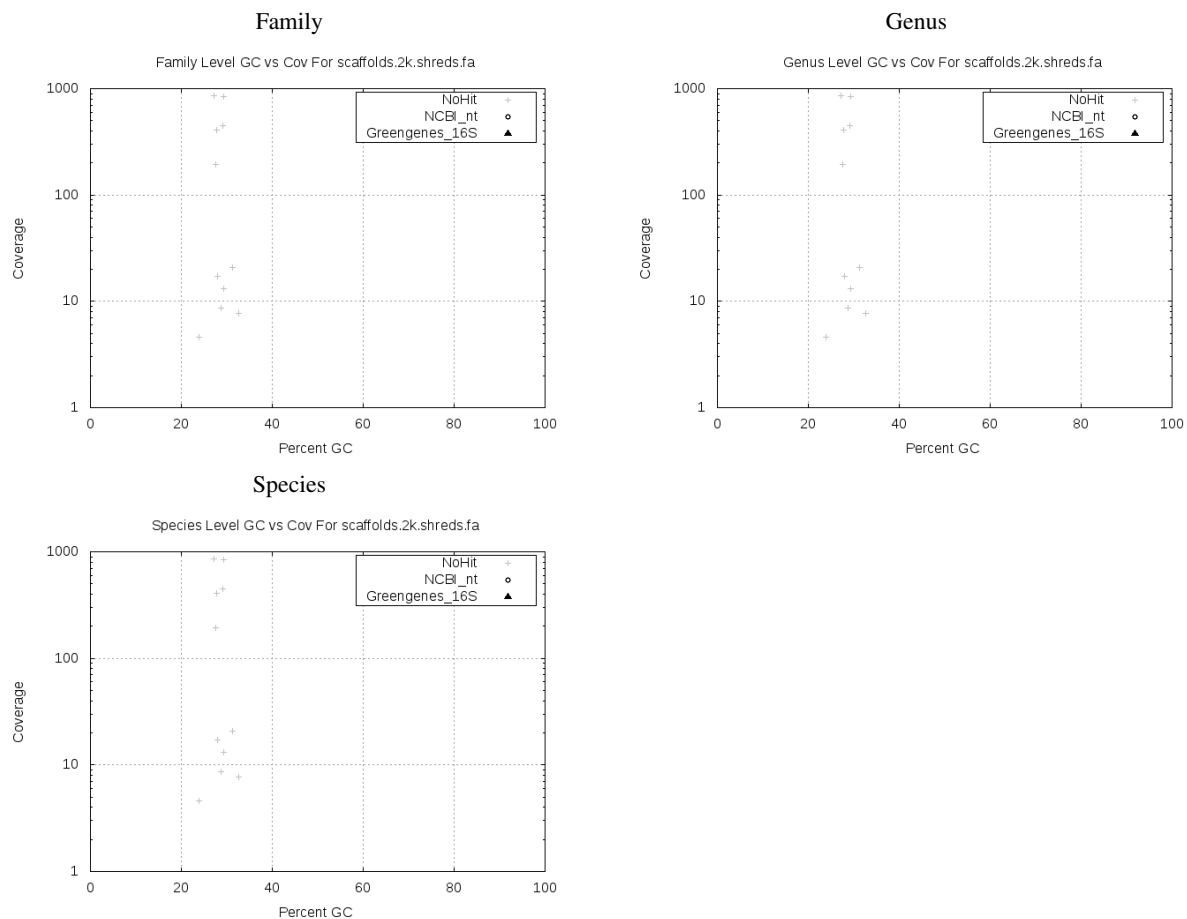


Class

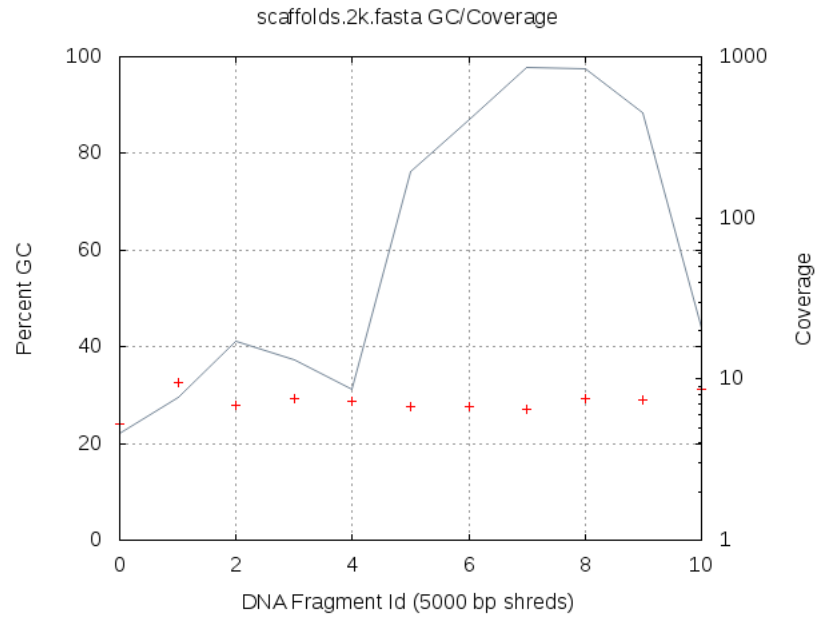


Order

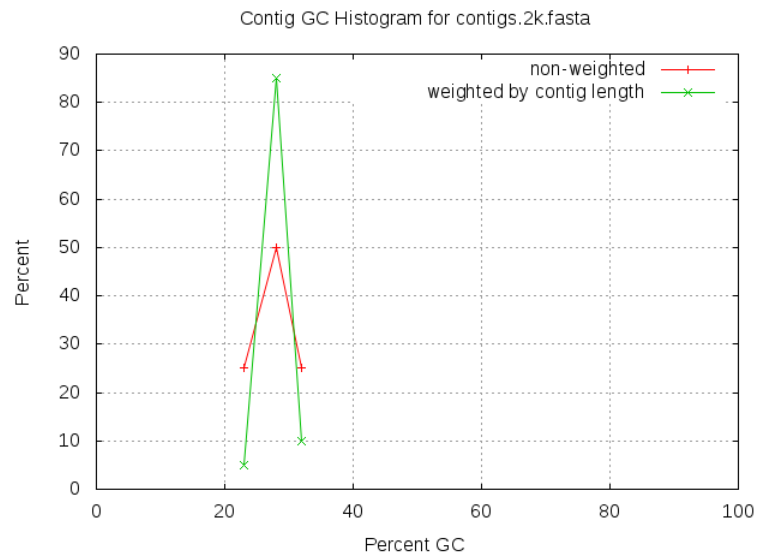




Coverage vs GC. Scaffolds were shredded into non-overlapping 5 kb fragments and the GC of each shred was plotted as a point, colored by scaffold id. Coverage was calculated by mapping the fragment library to the final assembly and plotted as connected points.



GC histogram of the contigs, including contig length weighted distribution.

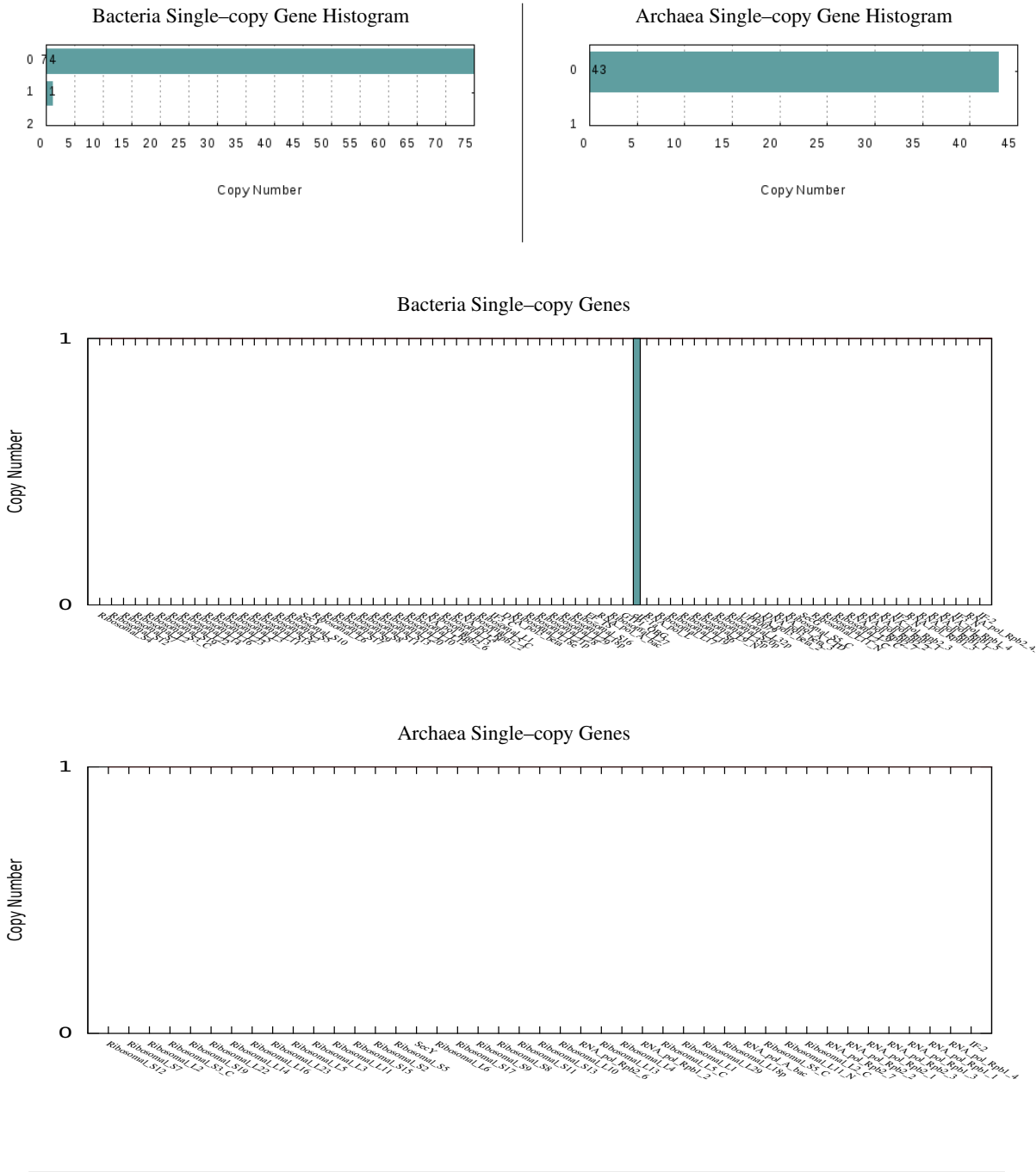


Principal component analysis of tetramer frequencies of contigs. Detectable variations are highlighted in color.

Insufficient number of contigs with length ≥ 2000 bp. Minimum number required is 10 to run tetramer analysis.

Estimated genome recovery derived from analysis of universal single-copy genes detected in final assembly.

HMM	Pct Recovered
archaea	0 %
bacteria	1.48 %



Bacteria Single-copy Genes

A dot plot showing the copy number for individual bacterial single-copy genes. The y-axis is labeled 'Copy Number' and ranges from 0 to 1. The x-axis lists 100 genes. A single vertical line at copy number 1 indicates that all genes have a copy number of 1.

Archaea Single-copy Genes

A dot plot showing the copy number for individual archaeal single-copy genes. The y-axis is labeled 'Copy Number' and ranges from 0 to 1. The x-axis lists 20 genes. No vertical lines are present, indicating a copy number of 0 for all genes.