

1. Read Statistics

Illumina Std PE Statistics

File name	ZHZG.bbqc.fq.gz.fastq
Number of reads	30,227,690
Sequencing depth [†]	901X
Read type	2x149 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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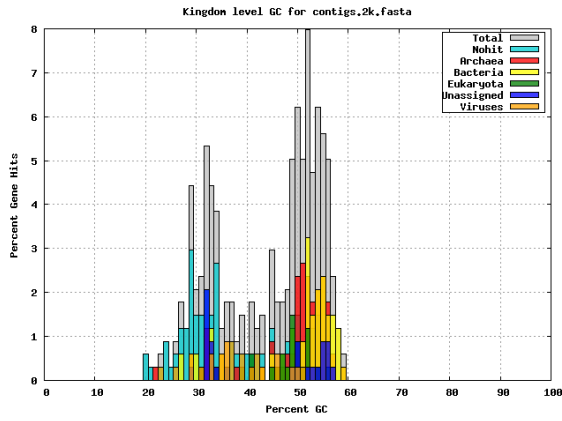
3. Unscreened Assembly Statistics

Assembly method	SPAdes
Scaffold total	54
Contig total	55
Scaffold sequence length	292.6 kb
Contig sequence length	292.5 kb (0.0% gap)
Scaffold N/L50	11/6.2 kb
Contig N/L50	11/6.2 kb
Largest Contig	33.3 kb
Number of scaffolds >50 kb	0
Pct of genome in scaffolds >50 kb	0.0
Pct of reads assembled	31.3

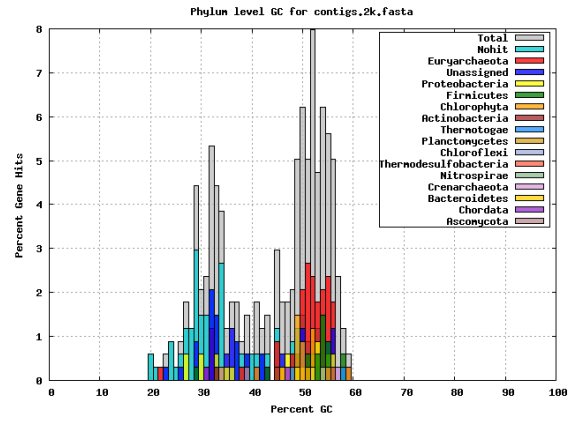
4. Unscreened Assembly QC Results

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

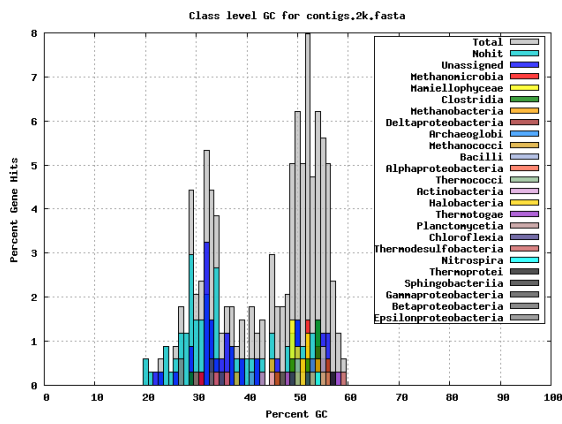
Kingdom



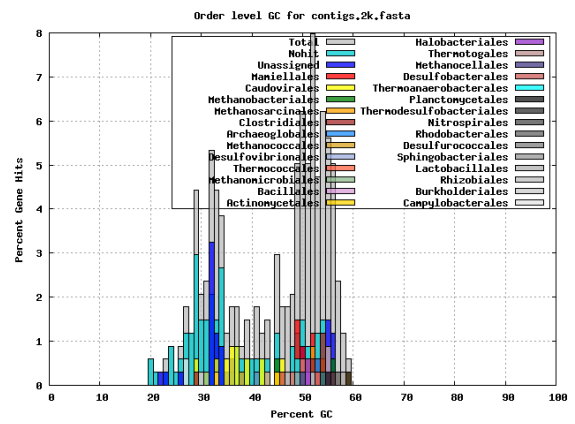
Phylum



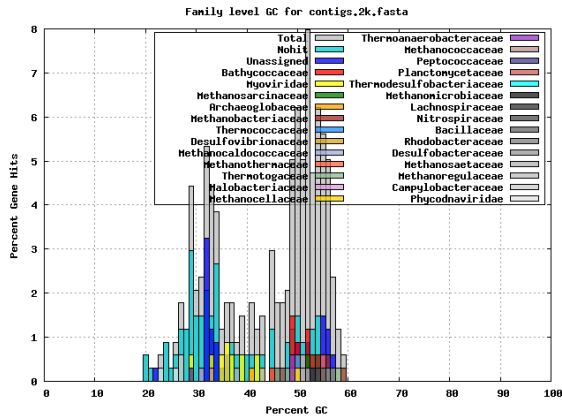
Class



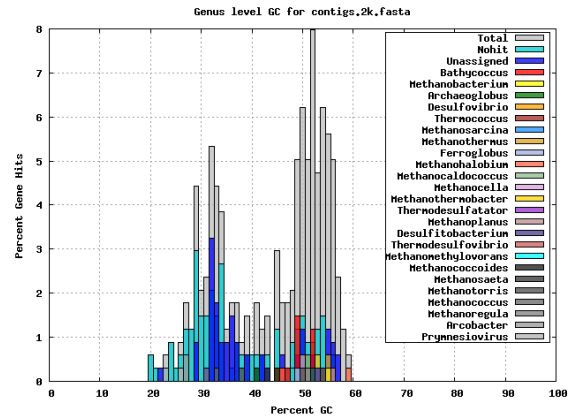
Order

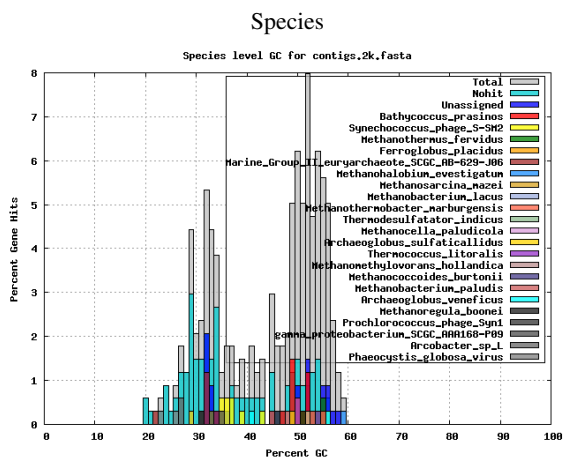


Family

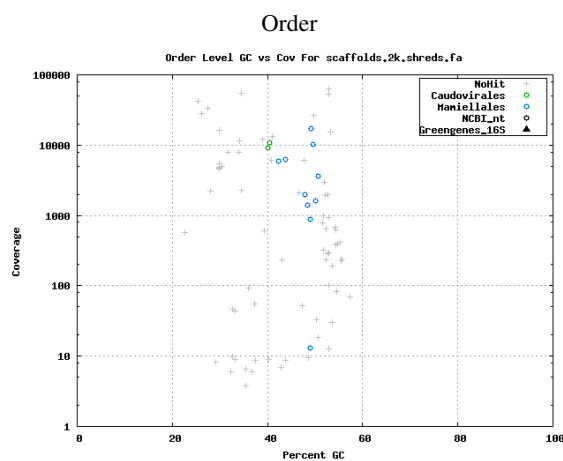
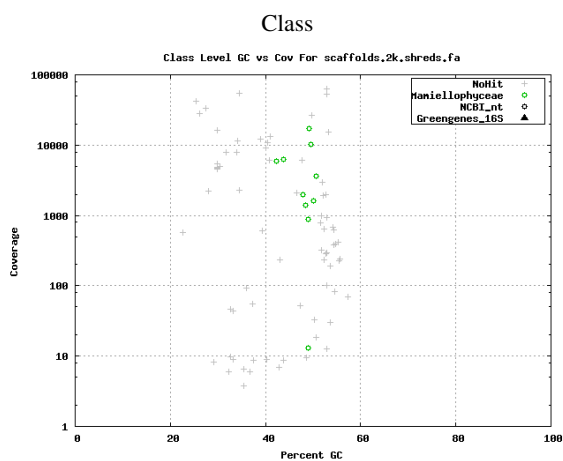
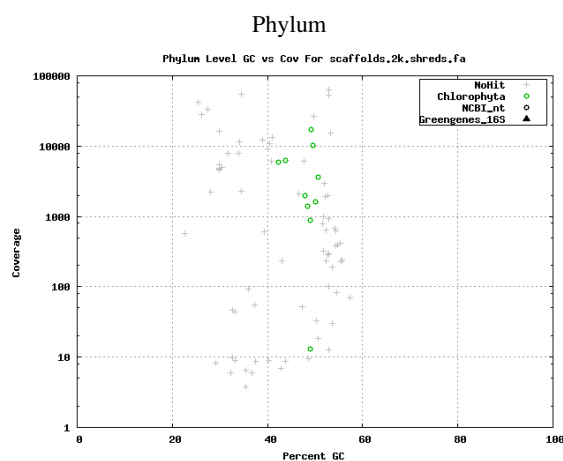
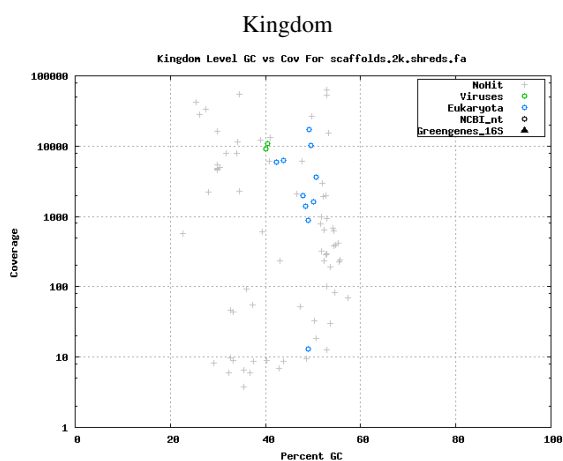


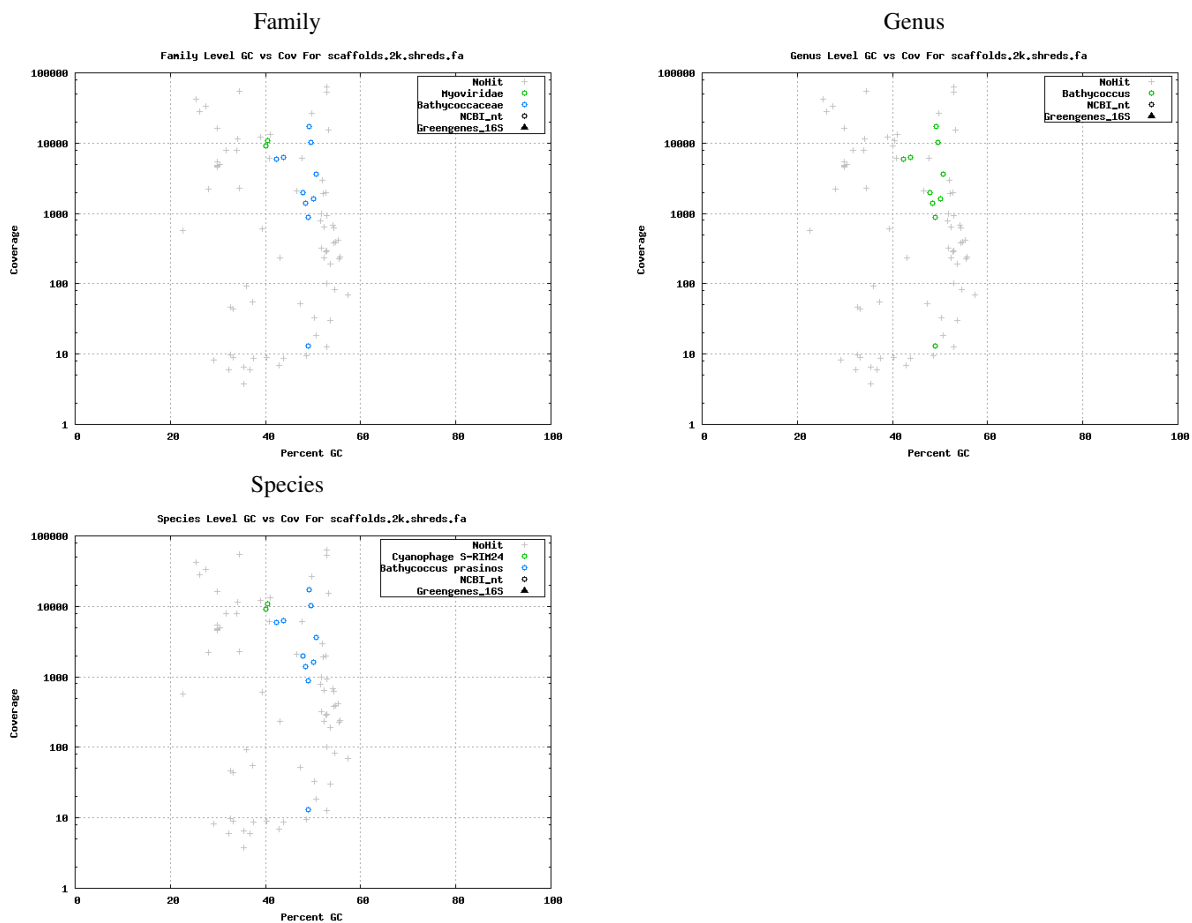
Genus



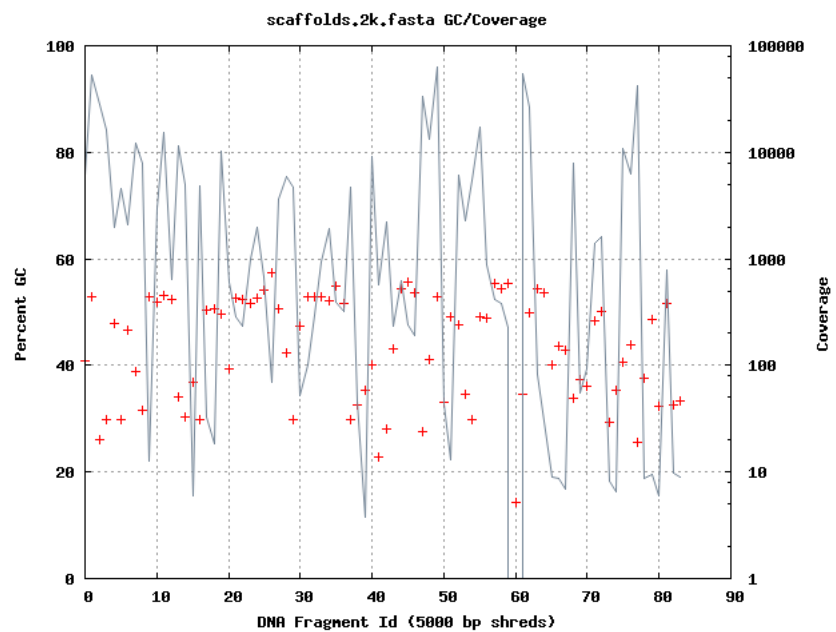


GC vs coverage based on GC of NCBI nt and Greengenes 16S rRNA gene hits to the assembly using megablast, shown for different taxonomic levels.

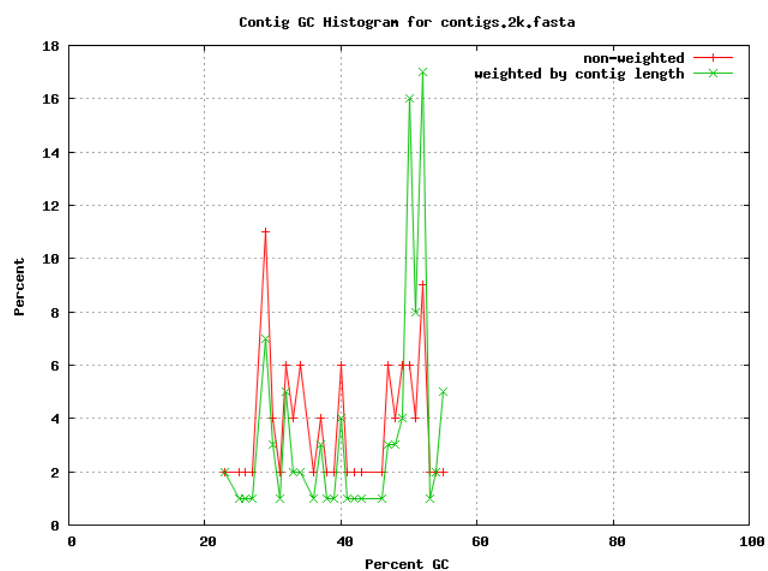




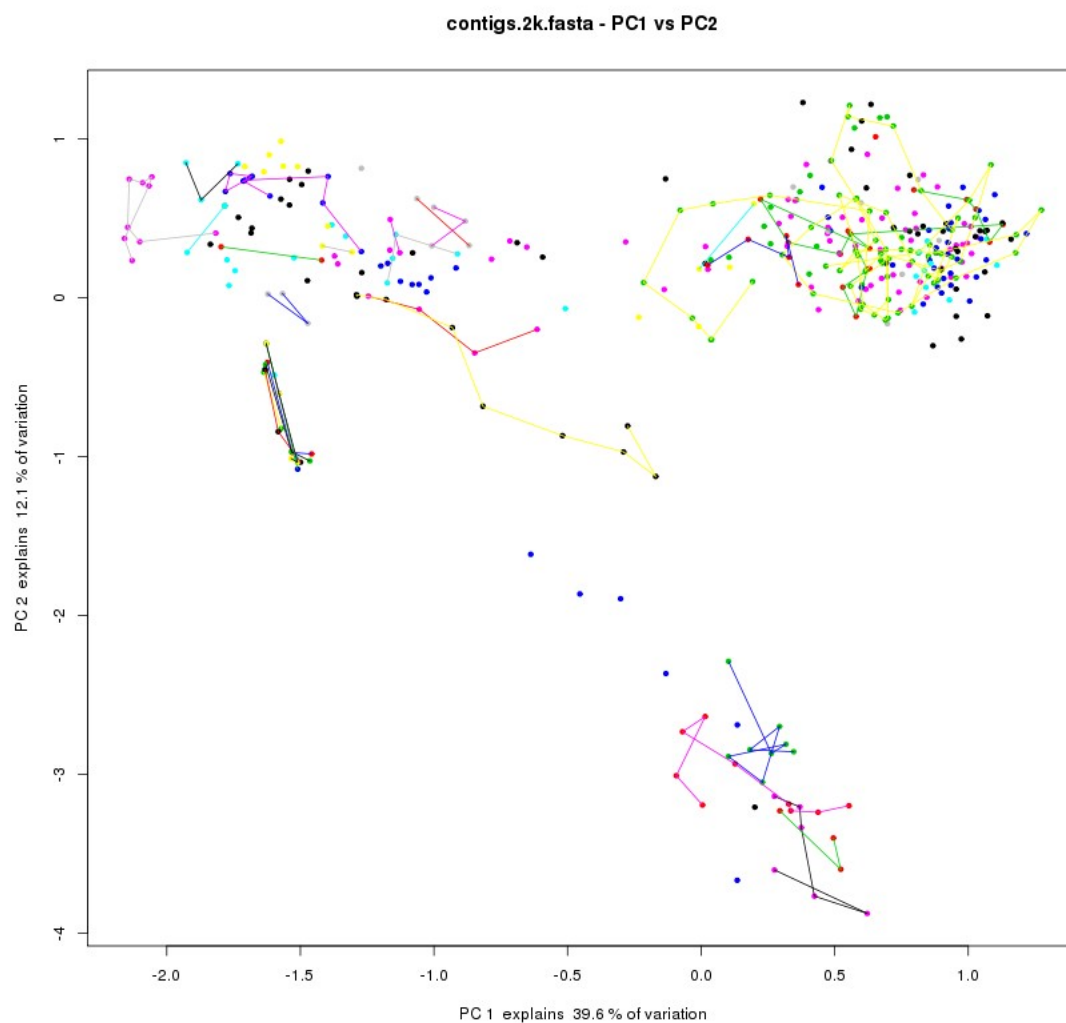
Coverage vs GC. Scaffolds were shredded into non-overlapping 5 kb fragments and the GC of each shred was plotted as a point, colored by scaffold id. Coverage was calculated by mapping the fragment library to the final assembly and plotted as connected points.



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

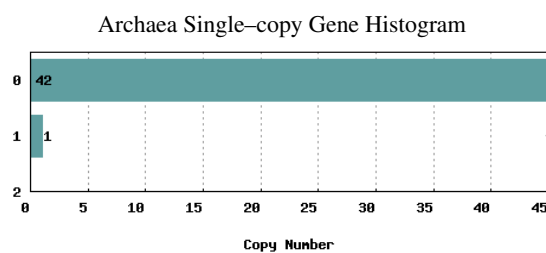
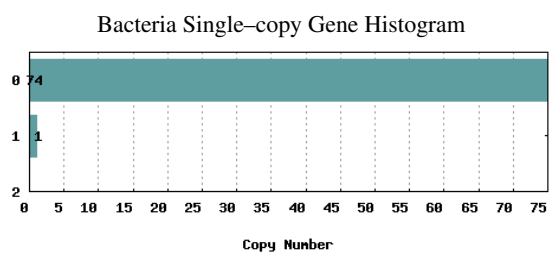


Principal component analysis of tetramer frequencies of contigs. Detectable variations are highlighted in color.



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

HMM	Pct Recovered
archaea	2.58 %
bacteria	1.48 %



Horizontal bar chart showing the number of copies for various genes. The y-axis is labeled 'Copy Number' and ranges from 0 to 1. The x-axis lists numerous gene names. The bars are colored in a light blue/teal shade. The gene names are rotated 90 degrees for readability. The chart shows that most genes have a copy number of 1, while a few have a copy number of 0.

[illegible]