

1. Read Statistics

Illumina Std PE Statistics

File name	ZHYX.bbqc.fq.gz.fastq
Number of reads	28,766,796
Sequencing depth [†]	863X
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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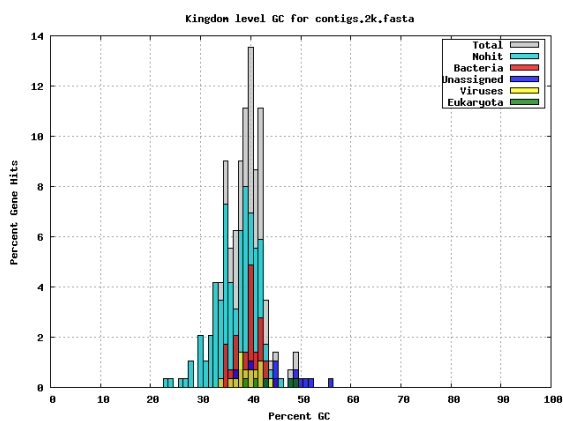
3. Unscreened Assembly Statistics

Assembly method	SPAdes
Scaffold total	29
Contig total	29
Scaffold sequence length	214.0 kb
Contig sequence length	214.0 kb (0.0% gap)
Scaffold N/L50	3/21.5 kb
Contig N/L50	3/21.5 kb
Largest Contig	53.3 kb
Number of scaffolds >50 kb	1
Pct of genome in scaffolds >50 kb	24.9
Pct of reads assembled	30.1

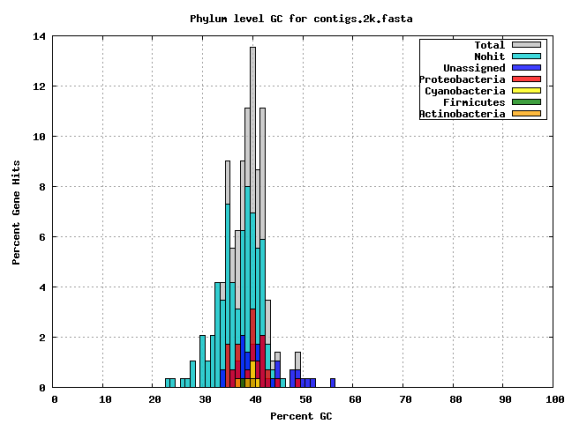
4. Unscreened Assembly QC Results

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

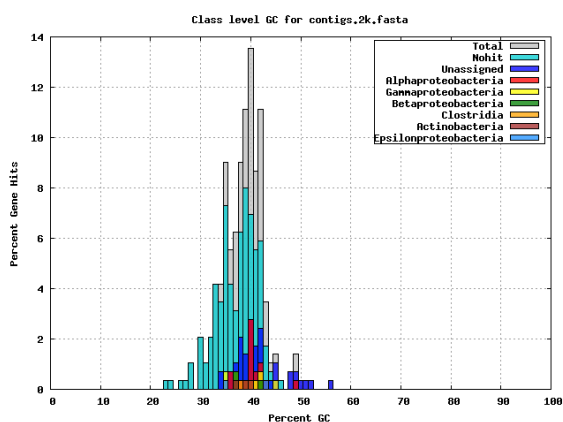
Kingdom



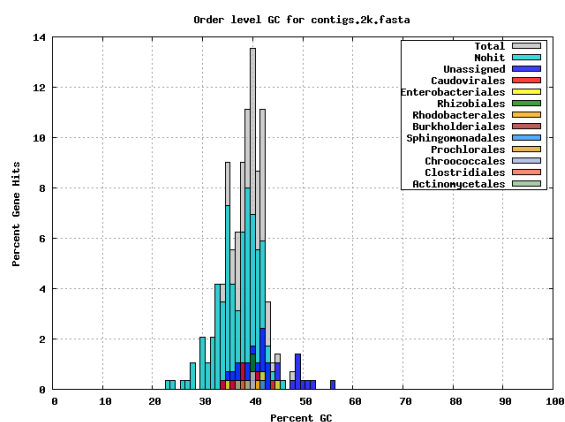
Phylum



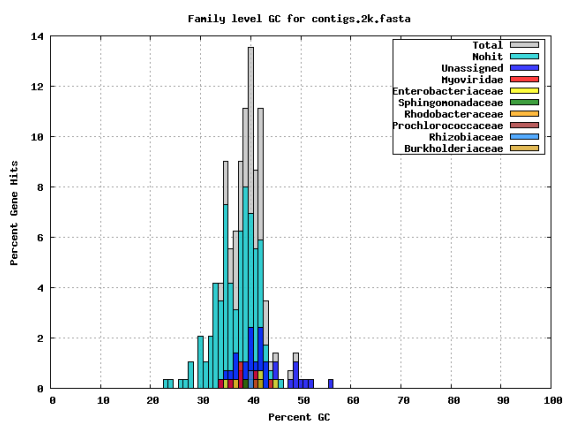
Class



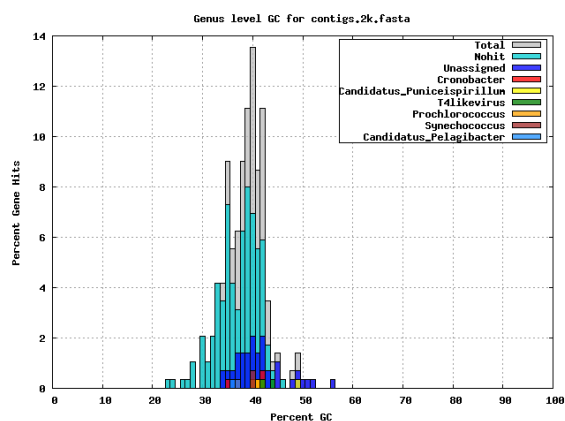
Order

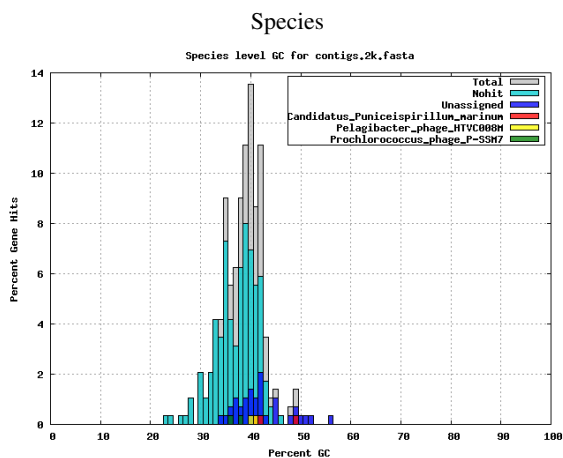


Family

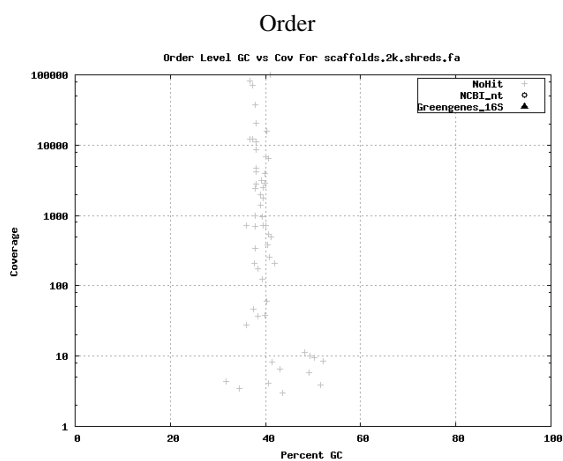
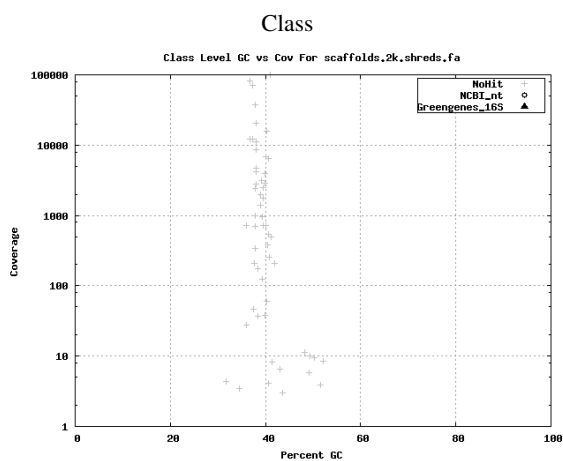
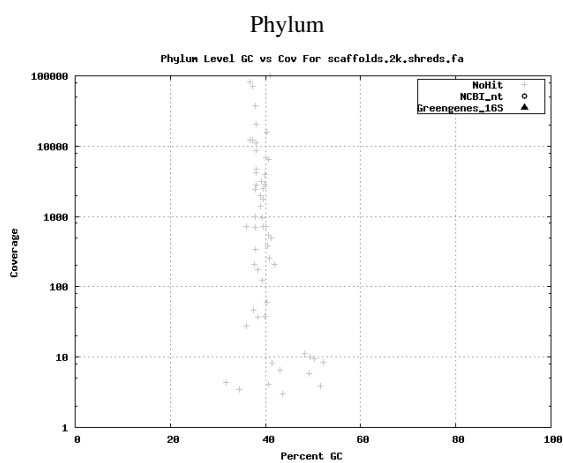
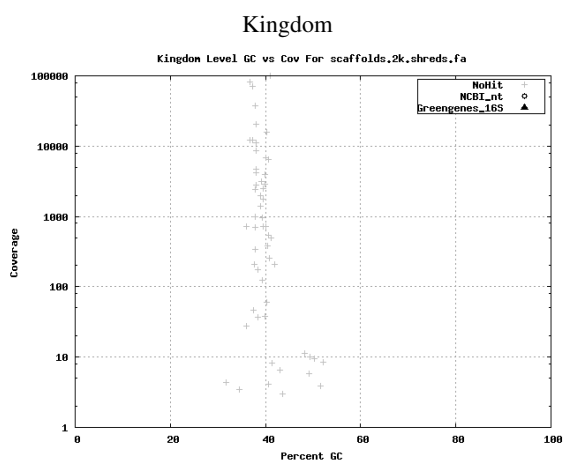


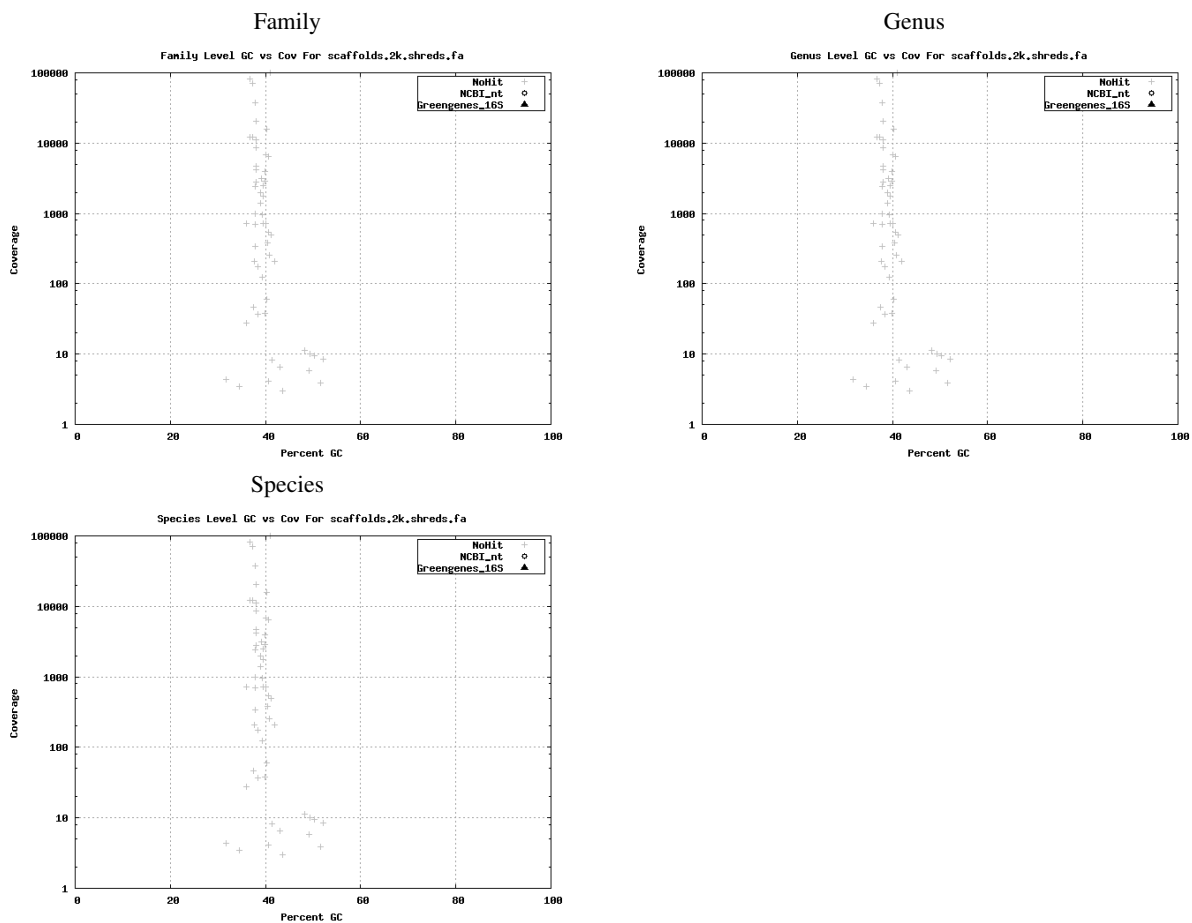
Genus



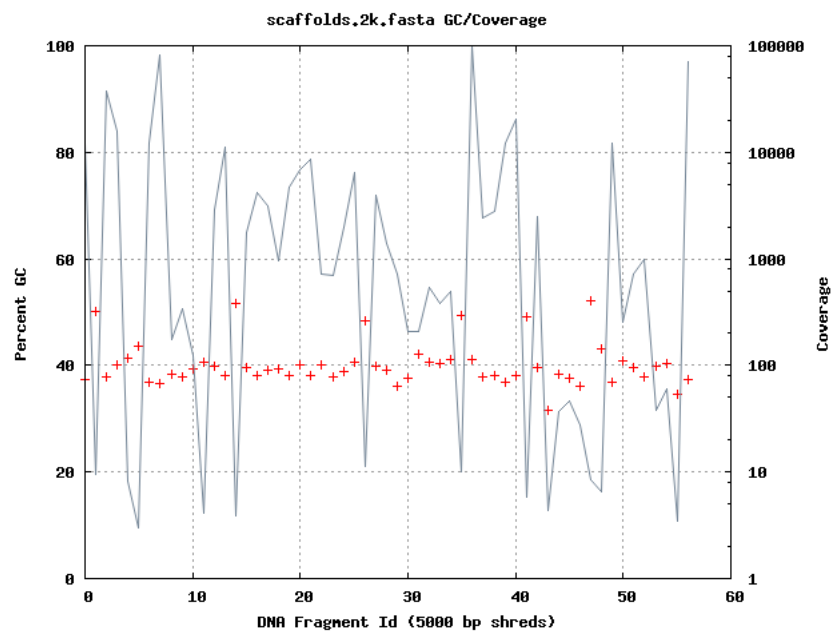


GC vs coverage based on GC of NCBI nt and Greengenes 16S rRNA gene hits to the assembly using megablast, shown for different taxonomic levels.

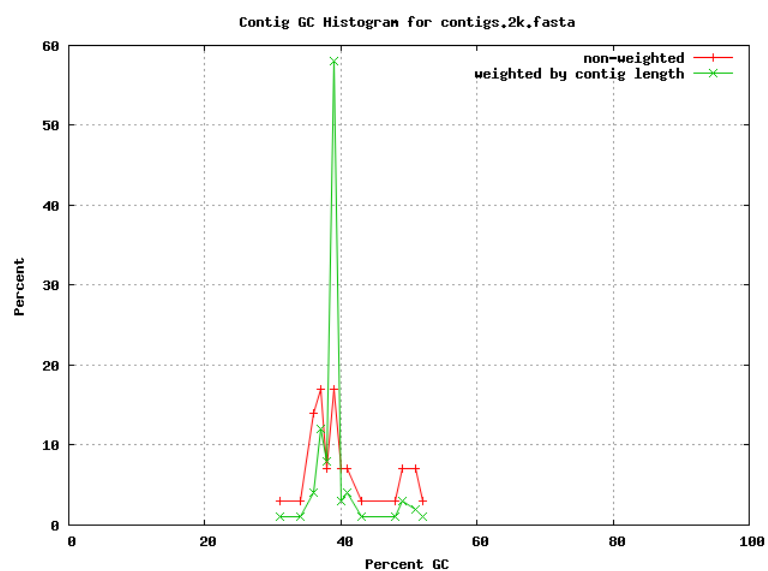




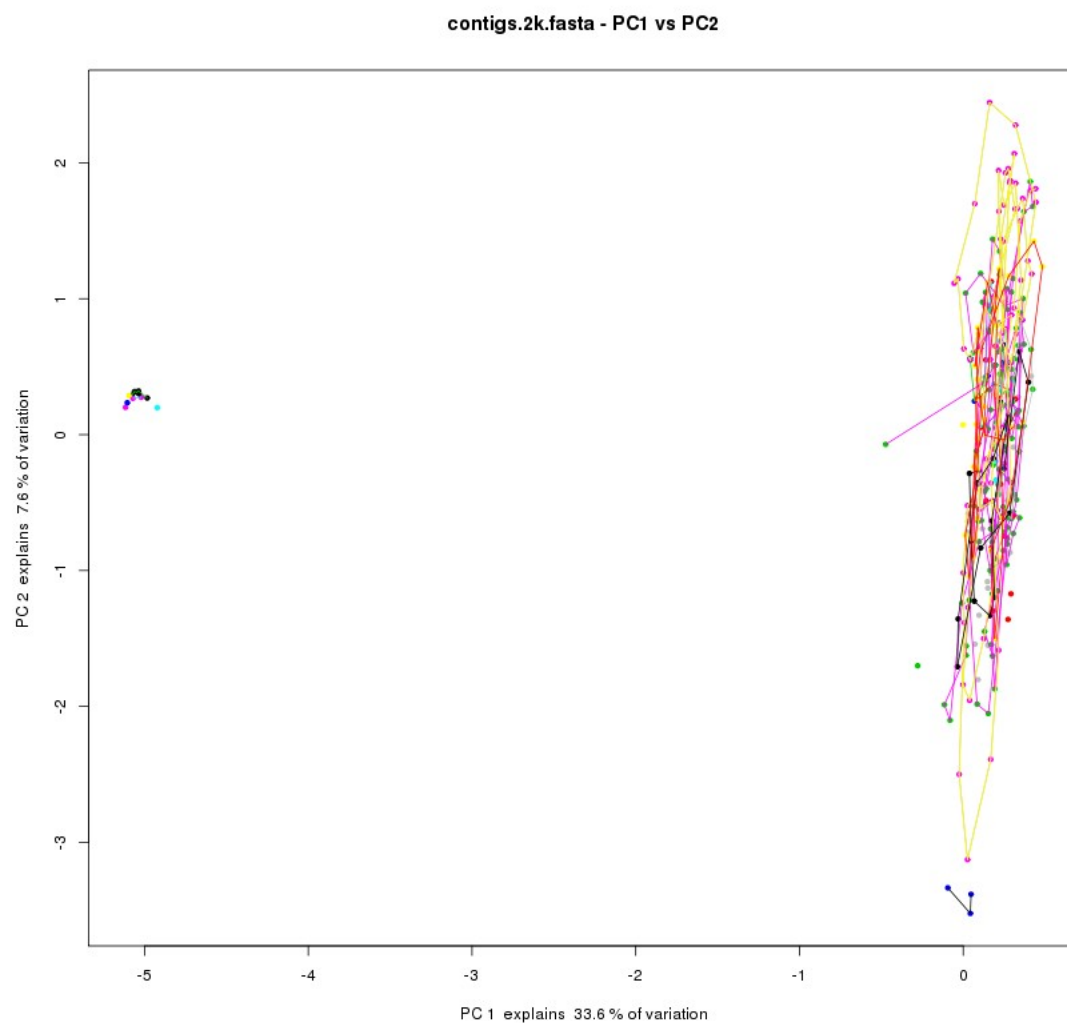
Coverage vs GC. Scaffolds were shredded into non-overlapping 5 kb fragments and the GC of each shred was plotted as a point, colored by scaffold id. Coverage was calculated by mapping the fragment library to the final assembly and plotted as connected points.



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

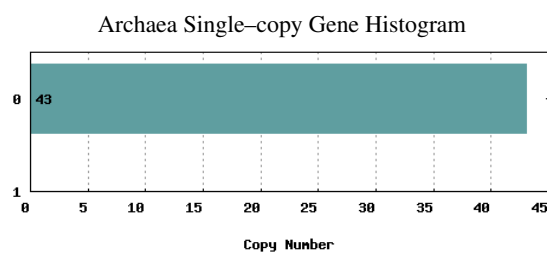
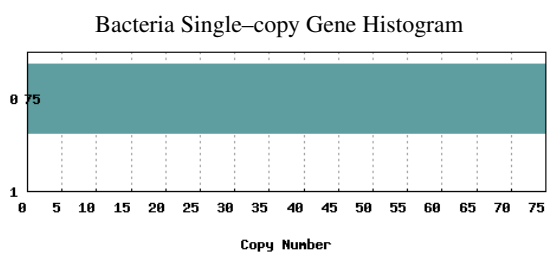


Principal component analysis of tetramer frequencies of contigs. Detectable variations are highlighted in color.



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

HMM	Pct Recovered
archaea	0 %
bacteria	0 %



Copy Number

1

0

RPL10A, RPL11, RPL12, RPL13, RPL14, RPL15, RPL16, RPL17, RPL18, RPL19, RPL20, RPL21, RPL22, RPL23, RPL24, RPL25, RPL26, RPL27, RPL28, RPL29, RPL30, RPL31, RPL32, RPL33, RPL34, RPL35, RPL36, RPL37, RPL38, RPL39, RPL40, RPL41, RPL42, RPL43, RPL44, RPL45, RPL46, RPL47, RPL48, RPL49, RPL50, RPL51, RPL52, RPL53, RPL54, RPL55, RPL56, RPL57, RPL58, RPL59, RPL60, RPL61, RPL62, RPL63, RPL64, RPL65, RPL66, RPL67, RPL68, RPL69, RPL70, RPL71, RPL72, RPL73, RPL74, RPL75, RPL76, RPL77, RPL78, RPL79, RPL80, RPL81, RPL82, RPL83, RPL84, RPL85, RPL86, RPL87, RPL88, RPL89, RPL90, RPL91, RPL92, RPL93, RPL94, RPL95, RPL96, RPL97, RPL98, RPL99, RPL100

[illegible]