

JGI assembly of 1023773 OYCP KBS Corn C4 is complete.

The assembled contigs stats are as follows:

A C G T N GC GC_stdev
 Base Content 0.1845 0.3156 0.3155 0.1844 0.0005 0.6311 0.0831

Main genome scaffold total: 882876
 Main genome contig total: 882876
 Main genome scaffold sequence total: 395.304 MB
 Main genome contig sequence total: 395.124 MB 0.045% gap
 Main genome scaffold N/L50: 237882/425
 Main genome contig N/L50: 237562/425
 Max scaffold length: 133.921 KB
 Max contig length: 133.9 KB
 Number of scaffolds > 50 KB: 2
 % main genome in scaffolds > 50 KB: 0.05%

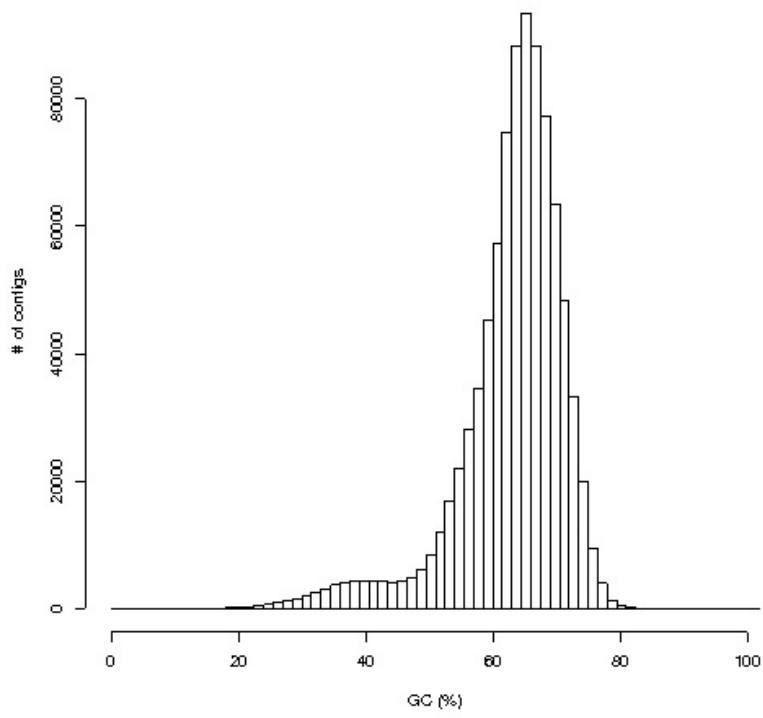
Minimum Scaffold Length	Number of Scaffolds	Number of Contigs	Total Scaffold Length	Total Contig Length	Scaffold Contig Coverage
All	882,876	882,876	395,303,618	395,124,322	99.95%
100	882,876	882,876	395,303,618	395,124,322	99.95%
250	828,015	828,015	381,822,079	381,642,928	99.95%
500	163,003	163,003	163,582,114	163,464,086	99.93%
1 KB	36,514	36,514	80,742,564	80,686,253	99.93%
2.5 KB	7,575	7,575	39,089,397	39,063,964	99.93%
5 KB	2,339	2,339	21,403,663	21,390,769	99.94%
10 KB	660	660	10,043,681	10,038,497	99.95%
25 KB	41	41	1,414,879	1,414,430	99.97%
50 KB	2	2	185,362	185,341	99.99%
100 KB	1	1	133,921	133,900	99.98%

Read stats are as follows:

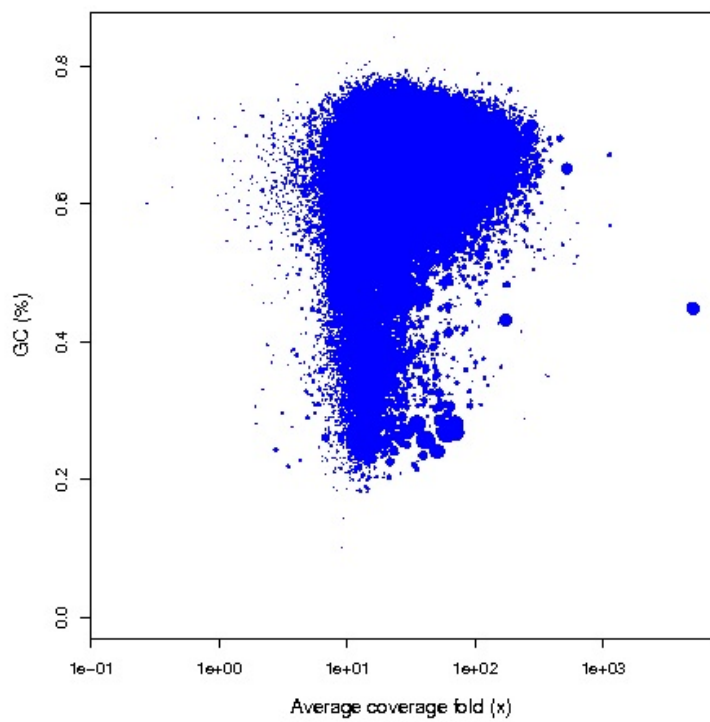
369167106 + 0 in total (QC-passed reads + QC-failed reads)
 0 + 0 duplicates
 75255050 + 0 mapped (20.39%:-nan%)
 359012504 + 0 paired in sequencing
 179506252 + 0 read1
 179506252 + 0 read2
 50257092 + 0 properly paired (14.00%:-nan%)
 60136596 + 0 with itself and mate mapped
 13209908 + 0 singletons (3.68%:-nan%)
 9848260 + 0 with mate mapped to a different chr
 9848260 + 0 with mate mapped to a different chr (mapQ>=5)

If you have any questions, please let us know: Brian Foster bfoster@lbl.gov, Alex Copeland accopeland@lbl.gov

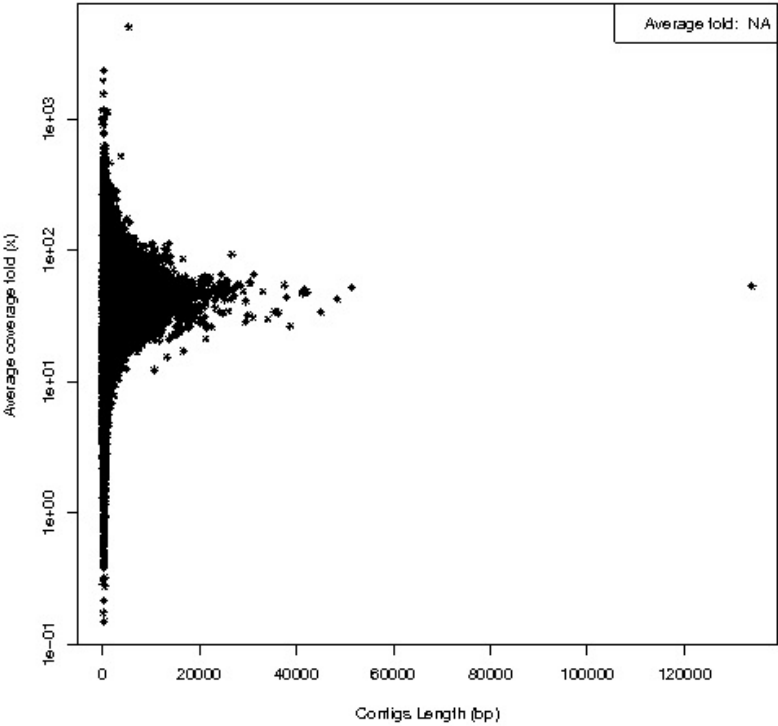
GC Histogram for contigs



Contigs average fold coverage vs. GC



Contigs average fold coverage vs. Contigs Length



Contigs Coverage vs. Contigs Length

