

1) Project Information

Program	PLANT
PMO Project	Porphyra umbilicalis Spores –Single Cell
JGI Project ID	404785
Library(s)	IGAF
Libray Method	Illumina Std PE Unamplified

2) Read Statistics

Number of reads	7,256,406
Read type(s)	2x150, 2x150
Sequencing depth [†]	217x
File name(s)	2045.1.1737.ACTTGA.fastq.gz, 2045.2.1737.ACTTGA.fastq.gz

[†] A genome size of 5Mbp was assumed in this calculation.

3) Read QC Results

The following are the results of reads screened against comtaminants. Pairs of matching reads were removed from the dataset.

Description	Num Reads	Pct Reads
Input	7,256,406	100
Contam removed	24	0.0
Artifact removed	43,798	0.6
Normalized removed	3,955,294	54.5
Total removed	3,999,116	55.1
Total remaining	3,257,290	44.9

List of contaminants removed.

Description	Num Reads	Pct Reads
human_chr3	8	0.00
human_chr2	4	0.00
human_chrX	4	0.00
human_chr16	2	0.00
human_chr5	2	0.00
human_chr9	2	0.00
human_chr8	2	0.00
human_chr4	2	0.00

The following are the results of reads screened against potential reagent and process contaminants but were not removed from the dataset.

Description	Num Reads	Pct Reads
Input	7,256,406	100
Contam identified	7,194	0.1

List of contaminants identified.

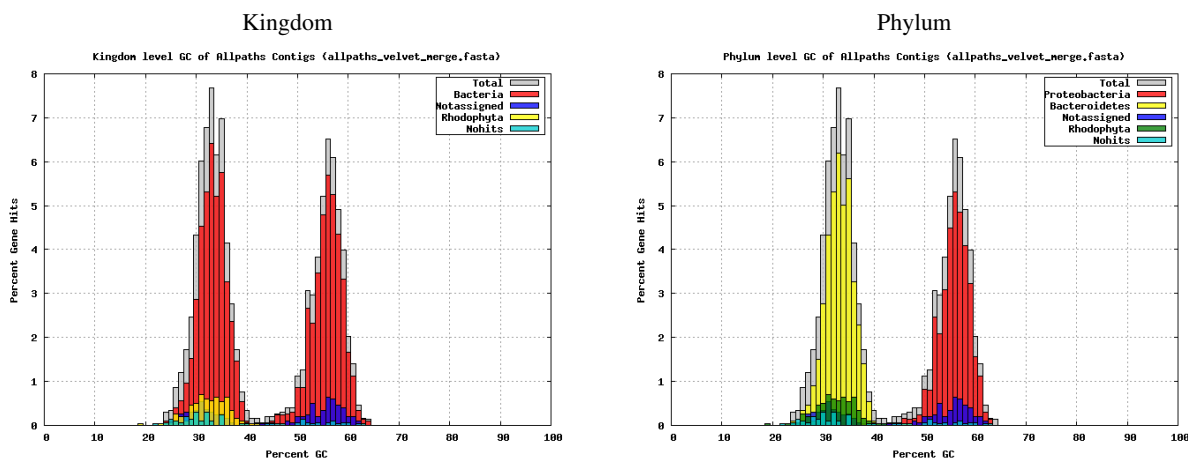
Description	Num Reads	Pct Reads
<i>Pseudomonas</i>	6,402	0.09
<i>Ralstonia</i>	786	0.01
<i>Cupriavidus</i>	6	0.00

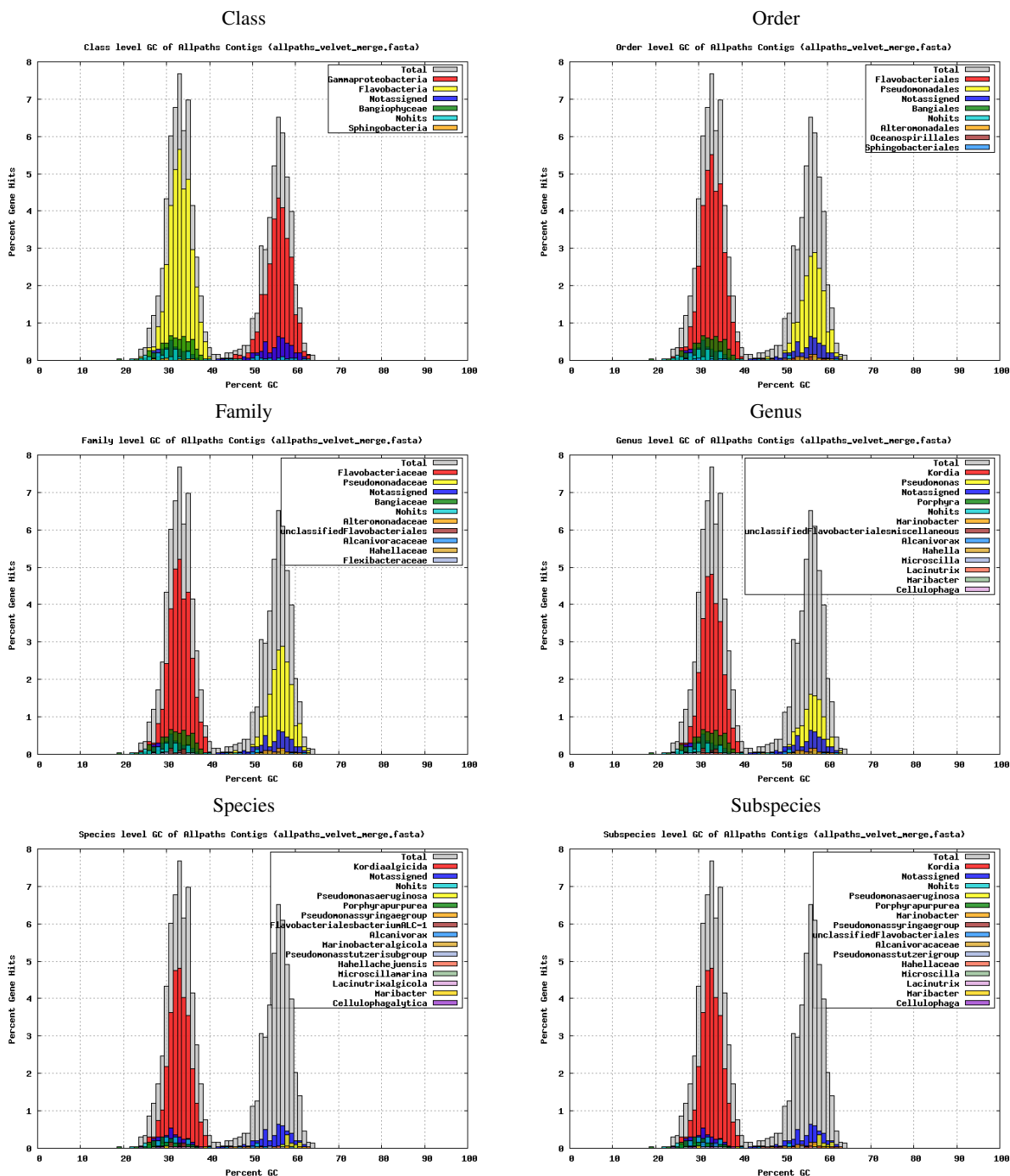
4) Assembly Statistics

Assembly method	Velvet/Allpaths hybrid
Scaffold total	3,908
Contig total	3,908
Scaffold sequence length	17.4 MB
Contig sequence length	17.4 MB (0.0% gap)
Scaffold N/L50	92 / 34.3 KB
Contig N/L50	92 / 34.3 KB
Number of scaffolds >50 KB	64
Pct of genome in scaffolds >50 KB	43.6

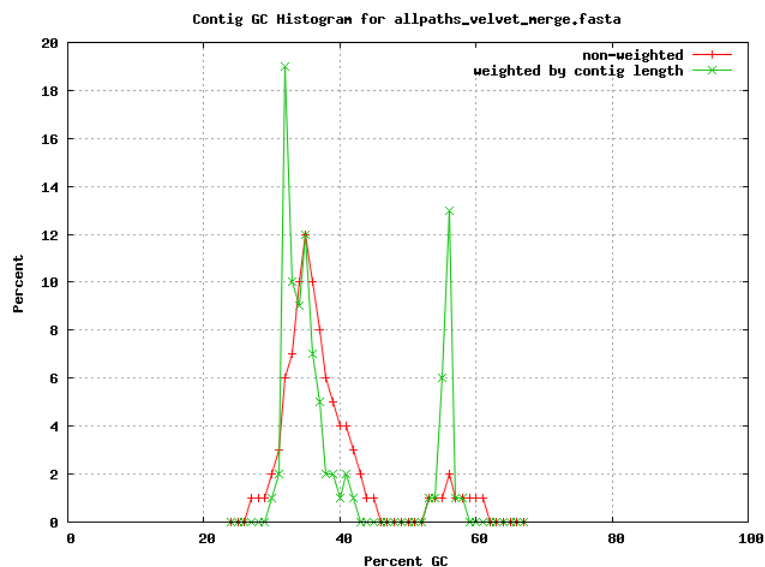
5) Assembly QC Results

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





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



List of contigs and average percent GC, grouped in bins of 5:

Pct GC Bin	Contig Name
20	NODE-unique.2546.length.720, NODE-unique.3269.length.580, NODE-unique.3338.length.570
25	NODE-unique.263.length.10611, NODE-unique.481.length.4471, NODE-unique.494.length.4339, NODE-unique.530.length.3793, NODE-unique.544.length.3609, NODE-unique.630.length.2945, NODE-unique.659.length.2797, NODE-unique.694.length.2620, NODE-unique.697.length.2604, NODE-unique.718.length.2530, NODE-unique.732.length.2501, NODE-unique.748.length.2447, NODE-unique.752.length.2436, NODE-unique.834.length.2209, NODE-unique.838.length.2189, NODE-unique.941.length.1901, NODE-unique.996.length.1797, NODE-unique.1027.length.1740, NODE-unique.1050.length.1703, NODE-unique.1130.length.1570, NODE-unique.1138.length.1564, NODE-unique.1161.length.1532, NODE-unique.1202.length.1475, NODE-unique.1225.length.1451, NODE-unique.1289.length.1368, NODE-unique.1290.length.1367, NODE-unique.1324.length.1338, NODE-unique.1333.length.1332, NODE-unique.1372.length.1297, NODE-unique.1378.length.1291, NODE-unique.1396.length.1278, NODE-unique.1403.length.1275, NODE-unique.1443.length.1247, NODE-unique.1493.length.1203, NODE-unique.1512.length.1190, NODE-unique.1514.length.1188, NODE-unique.1519.length.1184, NODE-unique.1527.length.1178, NODE-unique.1565.length.1150, NODE-unique.1616.length.1127, NODE-unique.1630.length.1121, NODE-unique.1647.length.1109, NODE-unique.1654.length.1106, NODE-unique.1684.length.1089, NODE-unique.1695.length.1085, NODE-unique.1701.length.1083, NODE-unique.1729.length.1070, NODE-unique.1764.length.1048, NODE-unique.1776.length.1043, NODE-unique.1786.length.1040, NODE-unique.1810.length.1027, NODE-unique.1852.length.996, NODE-unique.1860.length.992, NODE-unique.1862.length.991, NODE-unique.1884.length.975, NODE-unique.1914.length.959, NODE-unique.1938.length.942, NODE-unique.1942.length.941, NODE-unique.1945.length.940, NODE-unique.1961.length.931, NODE-unique.1970.length.925, NODE-unique.1980.length.917, NODE-unique.1992.length.912, NODE-unique.1998.length.910, NODE-unique.2001.length.910, NODE-unique.2016.length.900, NODE-unique.2044.length.890, NODE-unique.2049.length.886, NODE-unique.2054.length.885, NODE-unique.2067.length.881, NODE-unique.2096.length.865, NODE-unique.2160.length.838, NODE-unique.2162.length.835, NODE-unique.2168.length.834, NODE-unique.2242.length.808, NODE-unique.2253.length.804, NODE-unique.2268.length.796, NODE-unique.2273.length.794, NODE-unique.2279.length.793, NODE-unique.2297.length.788, NODE-unique.2311.length.782, NODE-unique.2319.length.779, NODE-unique.2338.length.774, NODE-unique.2404.length.756, NODE-unique.2501.length.734, NODE-unique.2503.length.732, NODE-unique.2517.length.728, NODE-unique.2524.length.727, NODE-unique.2541.length.720, NODE-unique.2566.length.715, NODE-unique.2629.length.700, NODE-unique.2646.length.696, NODE-unique.2653.length.695, NODE-unique.2655.length.694, NODE-unique.2676.length.689, NODE-unique.2693.length.685, NODE-unique.2715.length.679, NODE-unique.2716.length.679, NODE-unique.2765.length.665, NODE-unique.2778.length.663, NODE-unique.2790.length.660, NODE-unique.2803.length.657, NODE-unique.2835.length.651, NODE-unique.2855.length.648, NODE-unique.2884.length.644, NODE-unique.2893.length.643, NODE-unique.2925.length.637, NODE-unique.2949.length.632, NODE-unique.2961.length.631, NODE-unique.2998.length.625, NODE-unique.3062.length.612, NODE-unique.3074.length.611, NODE-unique.3109.length.606, NODE-unique.3144.length.599, NODE-unique.3152.length.598, NODE-unique.3186.length.593, NODE-unique.3205.length.589, NODE-unique.3227.length.585, NODE-unique.3279.length.578, NODE-unique.3299.length.575, NODE-unique.3306.length.574, NODE-unique.3340.length.569, NODE-unique.3353.length.567, NODE-unique.3360.length.566, NODE-unique.3365.length.566, NODE-unique.3366.length.566, NODE-unique.3372.length.565, NODE-unique.3379.length.564, NODE-unique.3406.length.560, NODE-unique.3480.length.551, NODE-unique.3504.length.548, NODE-unique.3558.length.542, NODE-unique.3566.length.540, NODE-unique.3580.length.538, NODE-unique.3581.length.538,

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65	NODE-unique.1505.length.1193, NODE-unique.1553.length.1156, NODE-unique.2202.length.822, NODE-unique.2467.length.740, NODE-unique.2488.length.737, NODE-unique.2695.length.684, NODE-unique.2763.length.666, NODE-unique.3662.length.530, NODE-unique.3749.length.520, NODE-unique.3864.length.504

List of the top contig megablast hits against potential reagent and process contaminants.

Organism	Pct Align	Pct Id	Contig Name
<i>Pseudomonas aeruginosa</i> .LESB58,complete_genome_5s, _16s,_23s_masked	0	100	NODE-unique.11.length.163454
<i>Pseudomonas aeruginosa</i> .PA7,complete_genome_5s,_16 s,_23s_masked	5	99	NODE-unique.24.length.117042
<i>Pseudomonas fluorescens</i> .Pf-5.chromosome,complete_ genome_5s,_16s,_23s_masked	0	100	NODE-unique.12.length.157918
	0	100	NODE-unique.85.length.36584
<i>Pseudomonas mendocina</i> .ymp,complete_genome_5s,_16s ,_23s_masked	0	100	NODE-unique.18.length.150145
	0	98	NODE-unique.183.length.17849
	0	98	NODE-unique.19.length.142520
<i>Pseudomonas putida</i> .GB-1,complete_genome_5s,_16s,_ 23s_masked	0	100	NODE-unique.26.length.114463
<i>Pseudomonas putida</i> .KT2440.chromosome,complete_gen ome_5s,_16s,_23s_masked	0	100	NODE-unique.48.length.62637
	0	98	NODE-unique.15.length.153114
<i>Pseudomonas putida</i> .W619.chromosome,complete_genom e_5s,_16s,_23s_masked	3	99	NODE-unique.214.length.14181
<i>Pseudomonas stutzeri</i> .A1501,complete_genome_5s,_16 s,_23s_masked	69	98	NODE-unique.1120.length.1589
	56	98	NODE-unique.689.length.2642
	0	100	NODE-unique.3.length.298280
	0	98	NODE-unique.65.length.47603
<i>Pseudomonas syringae</i> .pv.phaseolicola.1448A.chromo some,complete_genome_5s,_16s,_23s_masked	0	98	NODE-unique.21.length.130242