

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	7,340,824
Read type(s)	2x150, 2x150
Sequencing depth [†]	220x
File name(s)	2045.1.1737.TAGCTT.fastq.gz, 2045.2.1737.TAGCTT.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 comtaninants. Pairs of matching reads were removed from the dataset.

Description	Num Reads	Pct Reads
Input	7,340,824	100
Contam removed	2,912	0.0
Artifact removed	48,404	0.7
Normalized removed	5,960,030	81.2
Total removed	6,011,346	81.9
Total remaining	1,329,478	18.1

List of contaminants removed.

Description	Num Reads	Pct Reads
human_chr22	2,855	0.04
human_chr3	28	0.00
human_chr15	26	0.00
human_chr2	10	0.00
human_chr1	6	0.00
human_chr7	6	0.00
human_chr4	6	0.00
human_chr20	4	0.00
human_chr13	2	0.00

human_chr5	2	0.00
human_chrX	2	0.00
human_chr8	2	0.00
human_chr9	1	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	7,340,824	100
Contam identified	1,154	0.0

List of contaminants identified.

Description	Num Reads	Pct Reads
<i>Pseudomonas</i>	586	0.01
<i>Ralstonia</i>	566	0.01
<i>Delftia</i>	2	0.00

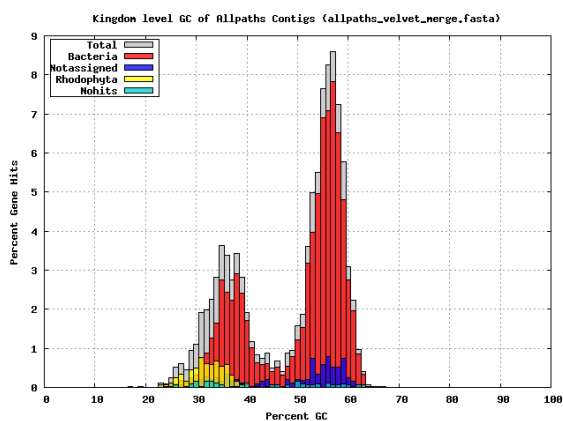
4) Assembly Statistics

Assembly method	Velvet/Allpaths hybrid
Scaffold total	1,206
Contig total	1,206
Scaffold sequence length	6.4 MB
Contig sequence length	6.4 MB (0.0% gap)
Scaffold N/L50	94 / 17.5 KB
Contig N/L50	94 / 17.5 KB
Number of scaffolds >50 KB	13
Pct of genome in scaffolds >50 KB	16.1

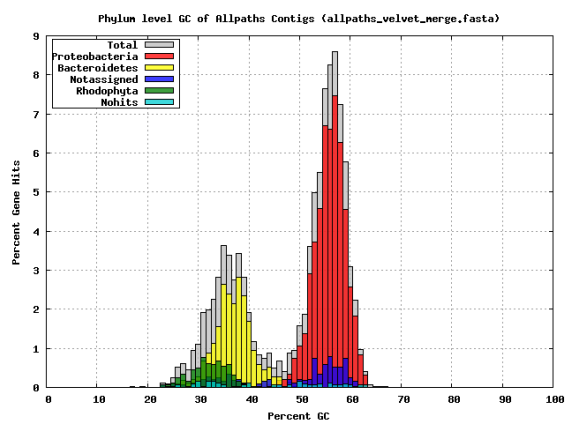
5) Assembly QC Results

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

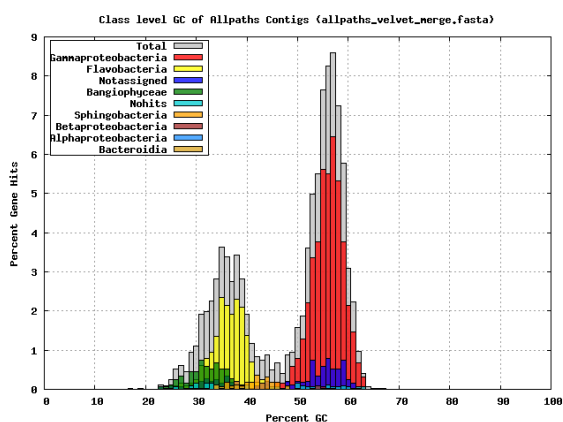
Kingdom



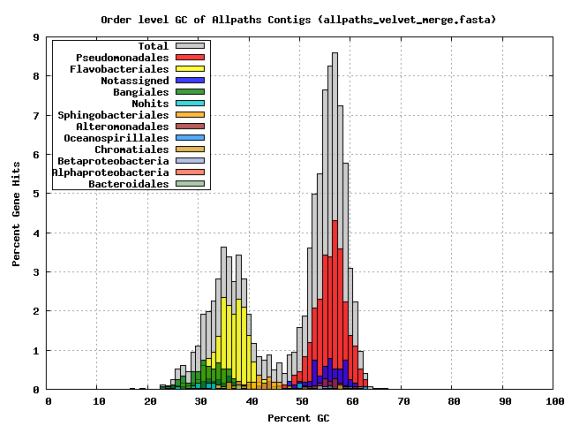
Phylum



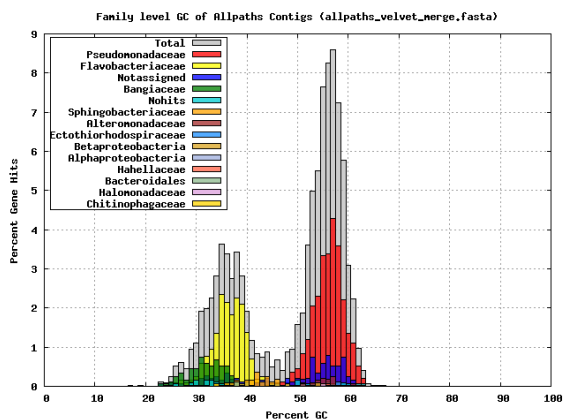
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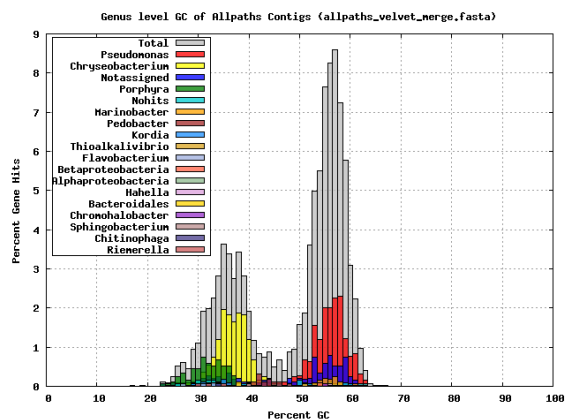
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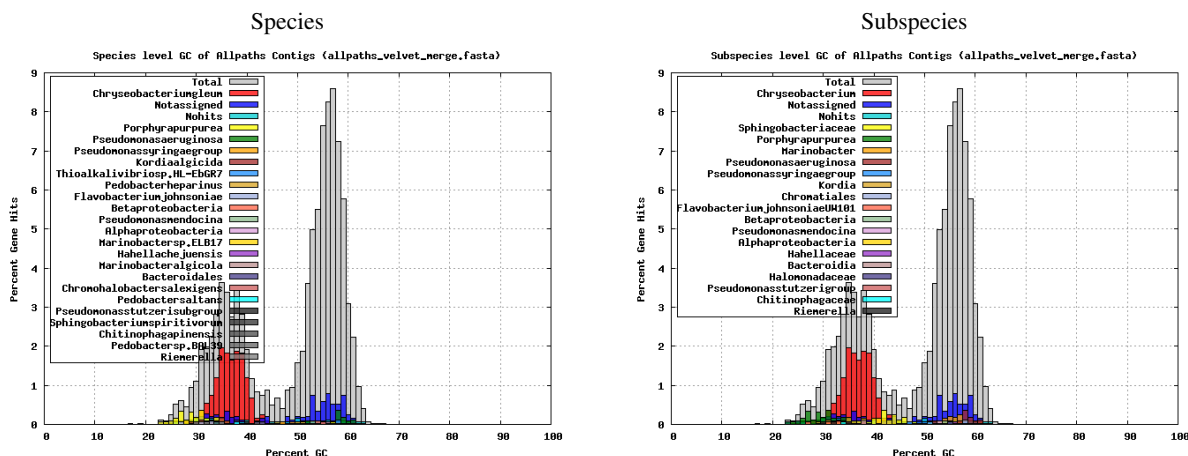


Family

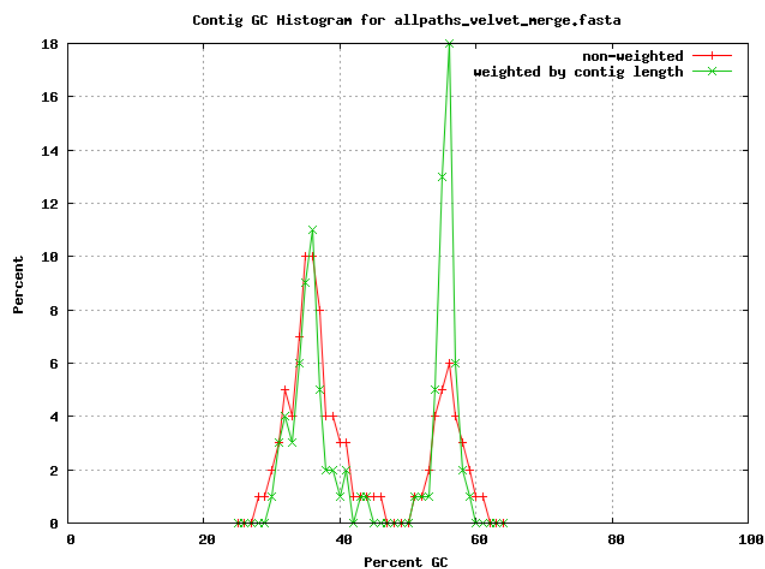


Genus





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
25	NODE-unique_394_length_2789, NODE-unique_409_length_2631, NODE-unique_460_length_2194, NODE-unique_532_length_1822, NODE-unique_597_length_1571, NODE-unique_662_length_1370, NODE-unique_728_length_1253, NODE-unique_735_length_1235, NODE-unique_751_length_1214, NODE-unique_787_length_1158, NODE-unique_827_length_1103, NODE-unique_832_length_1096, NODE-unique_951_length_744, NODE-unique_984_length_674, NODE-unique_1010_length_621, NODE-unique_1049_length_583, NODE-unique_1057_length_577, NODE-unique_1083_length_559, NODE-unique_1095_length_553, NODE-unique_1112_length_545, NODE-unique_1118_length_540, NODE-unique_1121_length_539, NODE-unique_1125_length_537, NODE-unique_1130_length_535, NODE-unique_1156_length_523, NODE-unique_1158_length_522, NODE-unique_1164_length_520, NODE-unique_1184_length_507, NODE-unique_1186_length_506, NODE-unique_1199_length_503
30	NODE-unique_1_length_151150, NODE-unique_21_length_40555, NODE-unique_29_length_33651, NODE-unique_41_length_29219, NODE-unique_42_length_28963, NODE-unique_48_length_26927, NODE-unique_64_length_21655, NODE-unique_75_length_20236, NODE-unique_81_length_19648, NODE-unique_91_length_17775, NODE-unique_99_length_17024, NODE-unique_115_length_14863, NODE-unique_118_length_14708, NODE-unique_125_length_14024, NODE-unique_132_length_13292, NODE-unique_135_length_13001, NODE-unique_137_length_12772, NODE-unique_141_length_12331, NODE-unique_142_length_12118, NODE-unique_147_length_11643, NODE-unique_156_length_11072, NODE-unique_167_length_10100, NODE-unique_172_length_9824, NODE-unique_178_length_9360, NODE-unique_181_length_9163, NODE-unique_188_length_8760, NODE-unique_194_length_8429, NODE-unique_195_length_8388, NODE-unique_201_length_8123, NODE-unique_202_length_8073,

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60	NODE-unique.215.length.7500, NODE-unique.329.length.3771, NODE-unique.336.length.3647, NODE-unique.380.length.2952, NODE-unique.427.length.2422, NODE-unique.484.length.2059, NODE-unique.541.length.1769, NODE-unique.571.length.1663, NODE-unique.577.length.1648, NODE-unique.590.length.1592, NODE-unique.624.length.1479, NODE-unique.708.length.1292, NODE-unique.709.length.1292, NODE-unique.752.length.1213, NODE-unique.801.length.1144, NODE-unique.812.length.1130, NODE-unique.818.length.1115, NODE-unique.831.length.1099, NODE-unique.886.length.1046, NODE-unique.889.length.1040, NODE-unique.907.length.1011, NODE-unique.923.length.982, NODE-unique.1001.length.638, NODE-unique.1052.length.580, NODE-unique.1082.length.559, NODE-unique.1109.length.547, NODE-unique.1179.length.511,

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_35_length_30948
<i>Pseudomonas entomophila</i> L48 chromosome, complete genome 5s, 16s, 23s masked	15	100	NODE-unique_1206_length_501
<i>Pseudomonas fluorescens</i> Pf-5 chromosome, complete genome 5s, 16s, 23s masked	0	100	NODE-unique_53_length_24570
<i>Pseudomonas mendocina</i> ymp, complete genome 5s, 16s, 23s masked	0	100	NODE-unique_24_length_35454
<i>Pseudomonas putida</i> KT2440 chromosome, complete genome 5s, 16s, 23s masked	0	100	NODE-unique_17_length_46373
<i>Pseudomonas stutzeri</i> A1501, complete genome 5s, 16s, 23s masked	0	98	NODE-unique_9_length_62824
<i>Pseudomonas syringae</i> pv. phaseolicola 1448A chromosome, complete genome 5s, 16s, 23s masked	0	98	NODE-unique_28_length_33931
<i>Pseudomonas syringae</i> pv. tomato str. DC3000, complete genome 5s, 16s, 23s masked	1	100	NODE-unique_266_length_5427
<i>Pseudomonas syringae</i> pv. phaseolicola 1448A chromosome, complete genome 5s, 16s, 23s masked	0	98	NODE-unique_36_length_30914
<i>Pseudomonas syringae</i> pv. tomato str. DC3000, complete genome 5s, 16s, 23s masked	0	98	NODE-unique_13_length_51539
<i>Pseudomonas syringae</i> pv. tomato str. DC3000, complete genome 5s, 16s, 23s masked	0	98	NODE-unique_32_length_32324