

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	6,666,908
Read type(s)	2x150, 2x150
Sequencing depth [†]	200x
File name(s)	2045.1.1737.GCCAAT.fastq.gz, 2045.2.1737.GCCAAT.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	6,666,908	100
Contam removed	26	0.0
Artifact removed	31,412	0.5
Normalized removed	4,057,028	60.9
Total removed	4,088,466	61.3
Total remaining	2,578,442	38.7

List of contaminants removed.

Description	Num Reads	Pct Reads
human_chr7	6	0.00
human_chr2	6	0.00
human_chrX	5	0.00
human_chr9	4	0.00
human_chr15	3	0.00
human_chr5	2	0.00
human_chr11	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	6,666,908	100
Contam identified	1,472	0.0

List of contaminants identified.

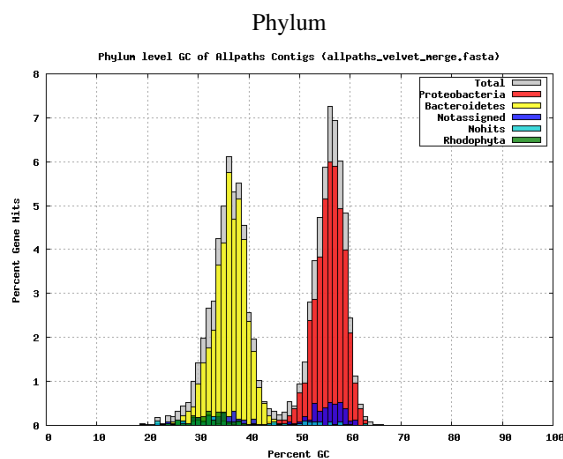
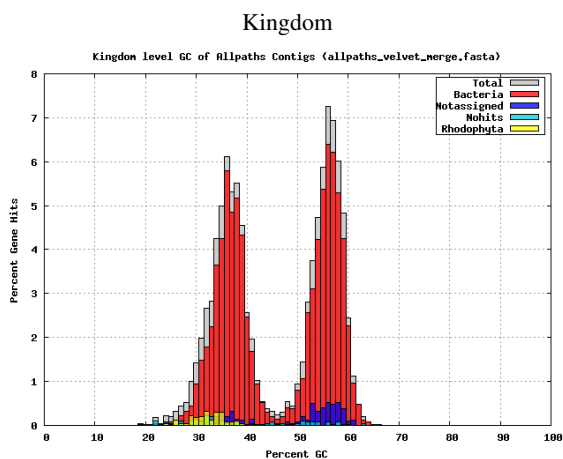
Description	Num Reads	Pct Reads
<i>Ralstonia</i>	1,020	0.02
<i>Pseudomonas</i>	450	0.01
<i>Cupriavidus</i>	2	0.00

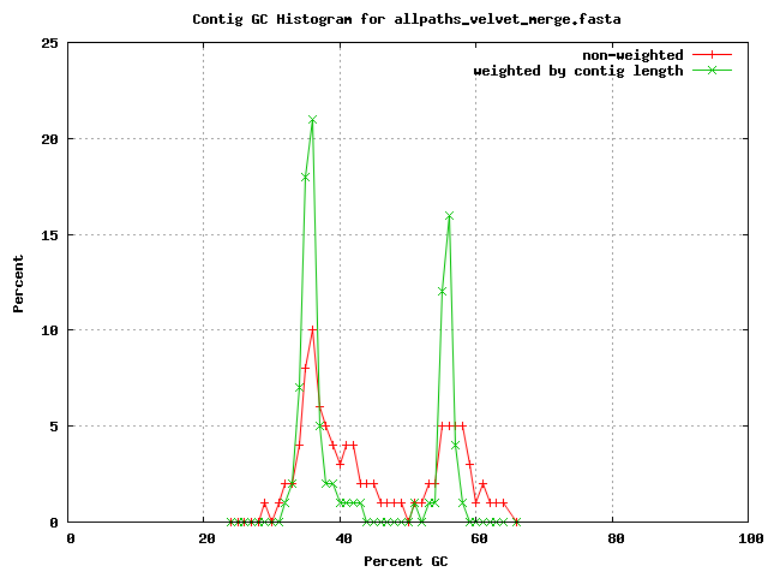
4) Assembly Statistics

Assembly method	Velvet/Allpaths hybrid
Scaffold total	985
Contig total	985
Scaffold sequence length	10.4 MB
Contig sequence length	10.4 MB (0.0% gap)
Scaffold N/L50	62 / 47.7 KB
Contig N/L50	62 / 47.7 KB
Number of scaffolds >50 KB	56
Pct of genome in scaffolds >50 KB	47.3

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.





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

Pct GC Bin	Contig Name
20	NODE-unique_982.length_503
25	NODE-unique_283.length_5290, NODE-unique_320.length_3594, NODE-unique_347.length_2884, NODE-unique_366.length_2553, NODE-unique_411.length_1885, NODE-unique_459.length_1513, NODE-unique_492.length_1347, NODE-unique_566.length_1047, NODE-unique_623.length_882, NODE-unique_773.length_650, NODE-unique_775.length_649, NODE-unique_923.length_534, NODE-unique_937.length_526, NODE-unique_967.length_511
30	NODE-unique_10.length_123529, NODE-unique_17.length_100524, NODE-unique_19.length_95835, NODE-unique_27.length_77411, NODE-unique_58.length_49488, NODE-unique_77.length_41163, NODE-unique_84.length_37773, NODE-unique_94.length_34591, NODE-unique_103.length_31187, NODE-unique_118.length_27461, NODE-unique_120.length_27262, NODE-unique_125.length_26212, NODE-unique_132.length_23505, NODE-unique_133.length_23142, NODE-unique_143.length_21087, NODE-unique_152.length_18255, NODE-unique_161.length_17294, NODE-unique_170.length_16072, NODE-unique_172.length_15881, NODE-unique_181.length_14851, NODE-unique_187.length_13841, NODE-unique_188.length_13794, NODE-unique_193.length_13173, NODE-unique_207.length_11914, NODE-unique_226.length_9882, NODE-unique_227.length_9776, NODE-unique_241.length_8806, NODE-unique_244.length_8672, NODE-unique_251.length_8160, NODE-unique_261.length_6916, NODE-unique_275.length_6341, NODE-unique_277.length_5987, NODE-unique_280.length_5466, NODE-unique_282.length_5337, NODE-unique_284.length_5255, NODE-unique_292.length_5012, NODE-unique_298.length_4759, NODE-unique_302.length_4389, NODE-unique_318.length_3766, NODE-unique_334.length_3135, NODE-unique_337.length_3100, NODE-unique_344.length_2942, NODE-unique_345.length_2941, NODE-unique_351.length_2810, NODE-unique_364.length_2594, NODE-unique_365.length_2558, NODE-unique_380.length_2314, NODE-unique_407.length_1993, NODE-unique_422.length_1768, NODE-unique_436.length_1668, NODE-unique_437.length_1667, NODE-unique_450.length_1571, NODE-unique_455.length_1527, NODE-unique_470.length_1464, NODE-unique_475.length_1437, NODE-unique_477.length_1429, NODE-unique_488.length_1372, NODE-unique_490.length_1364, NODE-unique_491.length_1348, NODE-unique_497.length_1319, NODE-unique_529.length_1140, NODE-unique_531.length_1135, NODE-unique_539.length_1109, NODE-unique_554.length_1078, NODE-unique_587.length_960, NODE-unique_596.length_942, NODE-unique_610.length_907, NODE-unique_615.length_900, NODE-unique_633.length_855, NODE-unique_634.length_855, NODE-unique_639.length_843, NODE-unique_689.length_748, NODE-unique_698.length_729, NODE-unique_703.length_724, NODE-unique_709.length_716, NODE-unique_733.length_688, NODE-unique_736.length_686, NODE-unique_738.length_684, NODE-unique_747.length_677, NODE-unique_778.length_646, NODE-unique_795.length_628, NODE-unique_837.length_592, NODE-unique_845.length_583, NODE-unique_858.length_577, NODE-unique_863.length_571, NODE-unique_871.length_565, NODE-unique_895.length_549, NODE-unique_915.length_539, NODE-unique_918.length_537, NODE-unique_931.length_530, NODE-unique_939.length_525, NODE-unique_946.length_521, NODE-unique_973.length_507
35	NODE-unique_7.length_133456, NODE-unique_8.length_130535, NODE-unique_11.length_118491, NODE-unique_18.length_97202, NODE-unique_21.length_93118, NODE-unique_23.length_91908, NODE-unique_24.length_90873, NODE-unique_25.length_89362, NODE-unique_26.length_82541, NODE-unique_28.length_76689, NODE-unique_29.length_70976, NODE-unique_33.length_65984, NODE-unique_34.length_65883, NODE-unique_35.length_65754, NODE-unique_36.length_65059, NODE-unique_37.length_65038, NODE-unique_39.length_62884, NODE-unique_42.length_61192, NODE-unique_43.length_60431, NODE-unique_44.length_60083, NODE-unique_45.length_59074, NODE-unique_46.length_58498, NODE-unique_47.length_57602, NODE-unique_50.length_55850, NODE-unique_51.length_55217, NODE-unique_52.length_55031, NODE-unique_53.length_54512,

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65	NODE-unique.930.length.530, NODE-unique.933.length.529

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.6.length.134407
<i>Pseudomonas fluorescens</i> .Pf-5.chromosome, complete_genome_5s, _16s, _23s_masked	0	100	NODE-unique.5.length.145353
	0	100	NODE-unique.70.length.43465
<i>Pseudomonas mendocina</i> .ymp, complete_genome_5s, _16s, _23s_masked	5	98	NODE-unique.468.length.1471
	0	100	NODE-unique.4.length.149877
	0	98	NODE-unique.2.length.158754
<i>Pseudomonas putida</i> .GB-1, complete_genome_5s, _16s, _23s_masked	0	100	NODE-unique.16.length.111145
<i>Pseudomonas putida</i> .KT2440.chromosome, complete_genome_5s, _16s, _23s_masked	0	100	NODE-unique.40.length.62703
	0	98	NODE-unique.49.length.55870
<i>Pseudomonas putida</i> .W619.chromosome, complete_genome_5s, _16s, _23s_masked	20	99	NODE-unique.629.length.859
<i>Pseudomonas stutzeri</i> .A1501, complete_genome_5s, _16s, _23s_masked	1	100	NODE-unique.281.length.5364
	0	98	NODE-unique.12.length.117488

<i>Pseudomonas_syringae_pv._phaseolicola_1448A_chromosome,_complete_genome_5s,_16s,_23s_masked</i>	0	98	NODE-unique_13_length_114880
<i>Pseudomonas_syringae_pv._tomato_str._DC3000,_complete_genome_5s,_16s,_23s_masked</i>	0	98	NODE-unique_3_length_152450