

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	6,729,702
Read type(s)	2x150, 2x150
Sequencing depth [†]	201x
File name(s)	2045.1.1737.CGATGT.fastq.gz, 2045.2.1737.CGATGT.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	6,729,702	100
Contam removed	6,310	0.1
Artifact removed	55,674	0.8
Normalized removed	6,452,306	95.9
Total removed	6,514,290	96.8
Total remaining	215,412	3.2

List of contaminants removed.

Description	Num Reads	Pct Reads
human_chr2	539	0.01
human_chr1	528	0.01
human_chr4	463	0.01
human_chr3	431	0.01
human_chr5	431	0.01
human_chr6	422	0.01
human_chr7	338	0.01
human_chr10	336	0.00
human_chrX	332	0.00

human_chr8	320	0.00
human_chr11	285	0.00
human_chr12	282	0.00
human_chr9	267	0.00
human_chr14	230	0.00
human_chr15	204	0.00
human_chr13	202	0.00
human_chr16	167	0.00
human_chr18	162	0.00
human_chr17	162	0.00
human_chr20	136	0.00
human_chr19	113	0.00
human_chr21	69	0.00
human_chr22	54	0.00
human_chrY	12	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	6,729,702	100
Contam identified	206	0.0

List of contaminants identified.

Description	Num Reads	Pct Reads
<i>Pseudomonas</i>	146	0.00
<i>Ralstonia</i>	56	0.00
<i>Delftia</i>	4	0.00

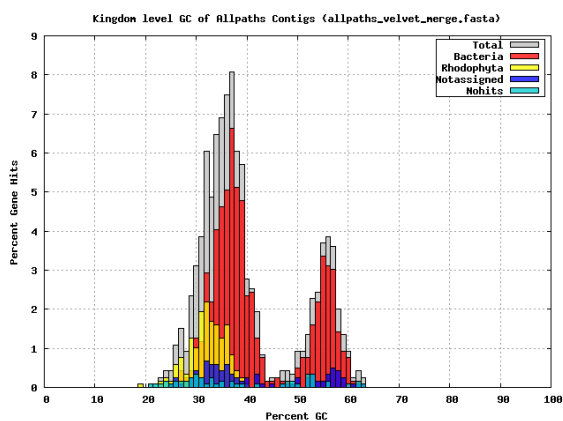
4) Assembly Statistics

Assembly method	Velvet/Allpaths hybrid
Scaffold total	302
Contig total	302
Scaffold sequence length	1.0 MB
Contig sequence length	1.0 MB (0.0% gap)
Scaffold N/L50	24 / 9.9 KB
Contig N/L50	24 / 9.9 KB
Number of scaffolds >50 KB	1
Pct of genome in scaffolds >50 KB	14.6

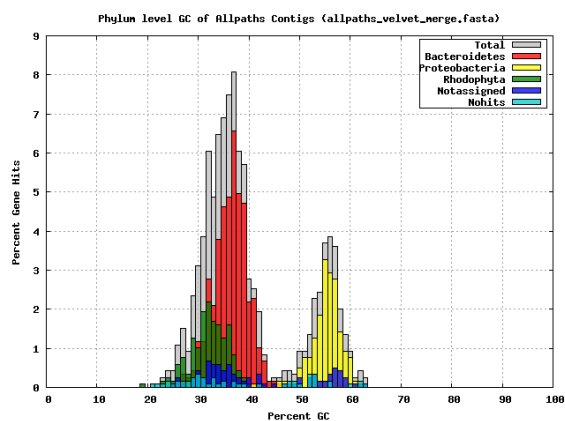
5) Assembly QC Results

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

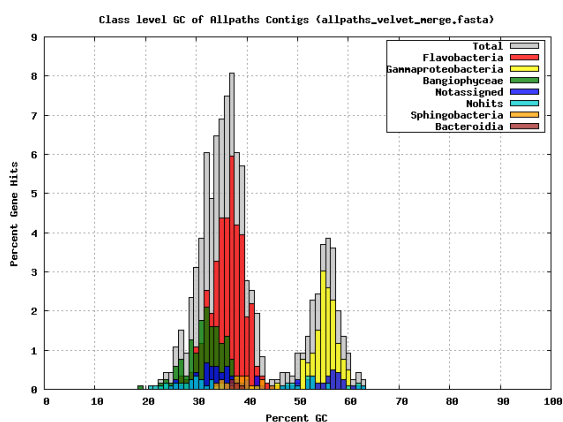
Kingdom



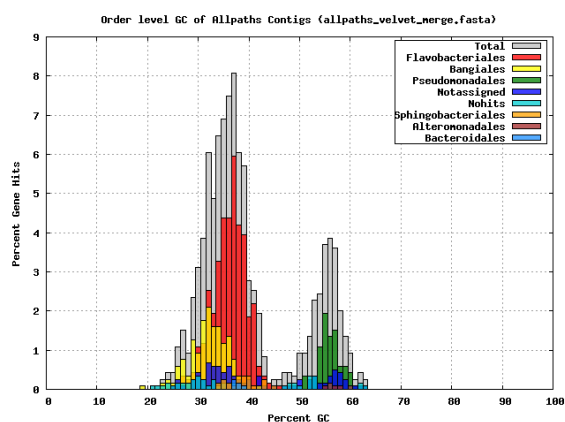
Phylum



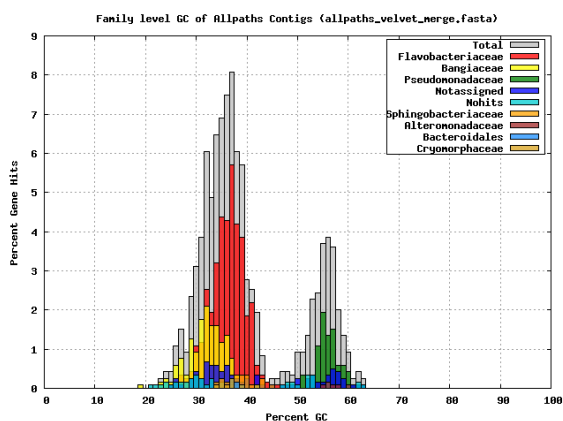
Class



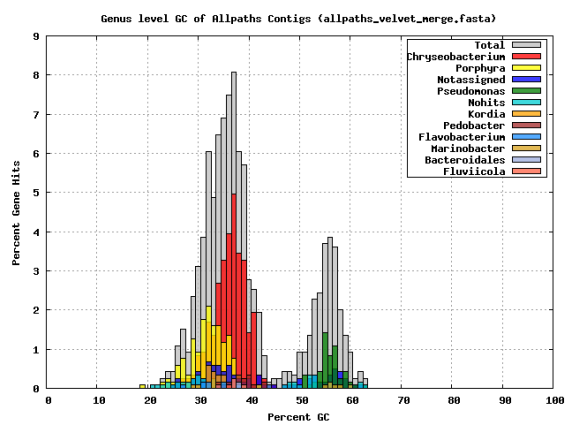
Order

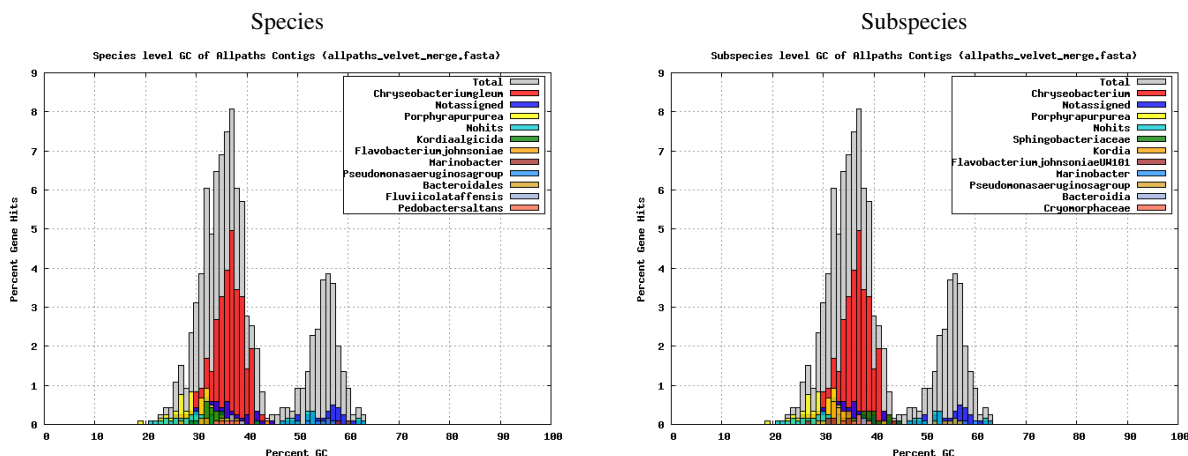


Family

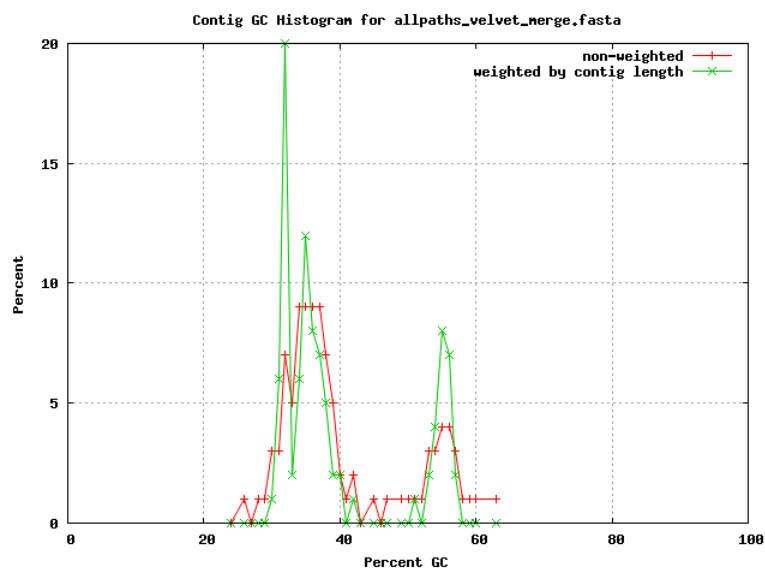


Genus





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
20	NODE-unique_302.length_501
25	NODE-unique_110.length_1925, NODE-unique_168.length_1181, NODE-unique_169.length_1170, NODE-unique_176.length_1119, NODE-unique_245.length_591, NODE-unique_282.length_526, NODE-unique_294.length_510, NODE-unique_300.length_503
30	NODE-unique_1.length_149266, NODE-unique_2.length_29218, NODE-unique_5.length_20758, NODE-unique_16.length_13258, NODE-unique_21.length_11137, NODE-unique_28.length_7878, NODE-unique_31.length_7192, NODE-unique_34.length_6554, NODE-unique_37.length_5913, NODE-unique_45.length_5208, NODE-unique_49.length_4303, NODE-unique_51.length_4229, NODE-unique_55.length_3931, NODE-unique_57.length_3772, NODE-unique_64.length_3242, NODE-unique_75.length_2774, NODE-unique_76.length_2768, NODE-unique_81.length_2559, NODE-unique_83.length_2498, NODE-unique_89.length_2309, NODE-unique_90.length_2306, NODE-unique_91.length_2290, NODE-unique_94.length_2268, NODE-unique_96.length_2213, NODE-unique_102.length_2065, NODE-unique_107.length_1957, NODE-unique_109.length_1934, NODE-unique_116.length_1820, NODE-unique_122.length_1655, NODE-unique_127.length_1615, NODE-unique_134.length_1482, NODE-unique_139.length_1449, NODE-unique_141.length_1442, NODE-unique_145.length_1417, NODE-unique_153.length_1289, NODE-unique_154.length_1280, NODE-unique_157.length_1244, NODE-unique_158.length_1233, NODE-unique_165.length_1200, NODE-unique_166.length_1191, NODE-unique_171.length_1135, NODE-unique_177.length_1113, NODE-unique_179.length_1106, NODE-unique_186.length_1072, NODE-unique_191.length_1044, NODE-unique_198.length_979, NODE-unique_200.length_900, NODE-unique_201.length_895,

	NODE-unique.204.length.843, NODE-unique.205.length.827, NODE-unique.206.length.794, NODE-unique.207.length.775, NODE-unique.211.length.747, NODE-unique.214.length.704, NODE-unique.215.length.701, NODE-unique.220.length.680, NODE-unique.223.length.668, NODE-unique.227.length.652, NODE-unique.229.length.636, NODE-unique.233.length.617, NODE-unique.235.length.608, NODE-unique.237.length.607, NODE-unique.238.length.602, NODE-unique.242.length.595, NODE-unique.244.length.592, NODE-unique.247.length.589, NODE-unique.256.length.570, NODE-unique.257.length.569, NODE-unique.260.length.564, NODE-unique.261.length.562, NODE-unique.262.length.560, NODE-unique.263.length.557, NODE-unique.270.length.540, NODE-unique.271.length.540, NODE-unique.276.length.533, NODE-unique.279.length.527, NODE-unique.286.length.523, NODE-unique.287.length.522, NODE-unique.288.length.520, NODE-unique.289.length.519, NODE-unique.296.length.509, NODE-unique.298.length.508
35	NODE-unique.6.length.20495, NODE-unique.7.length.18025, NODE-unique.8.length.17394, NODE-unique.10.length.16329, NODE-unique.12.length.15817, NODE-unique.15.length.13992, NODE-unique.17.length.12217, NODE-unique.18.length.11516, NODE-unique.19.length.11405, NODE-unique.22.length.10484, NODE-unique.23.length.9939, NODE-unique.26.length.9186, NODE-unique.27.length.7928, NODE-unique.30.length.7698, NODE-unique.32.length.6986, NODE-unique.35.length.6015, NODE-unique.43.length.5504, NODE-unique.47.length.4386, NODE-unique.50.length.4240, NODE-unique.52.length.4165, NODE-unique.53.length.4135, NODE-unique.54.length.4087, NODE-unique.60.length.3453, NODE-unique.62.length.3315, NODE-unique.65.length.3227, NODE-unique.66.length.3206, NODE-unique.67.length.3185, NODE-unique.68.length.3174, NODE-unique.70.length.2956, NODE-unique.71.length.2882, NODE-unique.72.length.2865, NODE-unique.74.length.2776, NODE-unique.79.length.2620, NODE-unique.80.length.2610, NODE-unique.84.length.2482, NODE-unique.85.length.2436, NODE-unique.86.length.2381, NODE-unique.87.length.2331, NODE-unique.92.length.2290, NODE-unique.93.length.2276, NODE-unique.95.length.2220, NODE-unique.98.length.2142, NODE-unique.101.length.2074, NODE-unique.103.length.2052, NODE-unique.104.length.2001, NODE-unique.105.length.1994, NODE-unique.108.length.1950, NODE-unique.111.length.1892, NODE-unique.112.length.1891, NODE-unique.113.length.1849, NODE-unique.114.length.1847, NODE-unique.115.length.1834, NODE-unique.118.length.1788, NODE-unique.119.length.1686, NODE-unique.125.length.1637, NODE-unique.126.length.1632, NODE-unique.128.length.1581, NODE-unique.130.length.1549, NODE-unique.132.length.1535, NODE-unique.133.length.1496, NODE-unique.135.length.1482, NODE-unique.136.length.1467, NODE-unique.138.length.1458, NODE-unique.142.length.1431, NODE-unique.143.length.1431, NODE-unique.146.length.1407, NODE-unique.147.length.1403, NODE-unique.148.length.1387, NODE-unique.149.length.1383, NODE-unique.150.length.1360, NODE-unique.152.length.1312, NODE-unique.155.length.1267, NODE-unique.156.length.1260, NODE-unique.167.length.1185, NODE-unique.170.length.1169, NODE-unique.174.length.1130, NODE-unique.175.length.1119, NODE-unique.182.length.1093, NODE-unique.183.length.1090, NODE-unique.184.length.1077, NODE-unique.185.length.1074, NODE-unique.189.length.1051, NODE-unique.192.length.1042, NODE-unique.195.length.1015, NODE-unique.197.length.981, NODE-unique.199.length.904, NODE-unique.209.length.761, NODE-unique.213.length.714, NODE-unique.217.length.692, NODE-unique.219.length.683, NODE-unique.221.length.679, NODE-unique.224.length.665, NODE-unique.225.length.660, NODE-unique.226.length.654, NODE-unique.231.length.635, NODE-unique.234.length.614, NODE-unique.243.length.594, NODE-unique.246.length.590, NODE-unique.251.length.585, NODE-unique.258.length.567, NODE-unique.264.length.556, NODE-unique.266.length.553, NODE-unique.267.length.547, NODE-unique.269.length.542, NODE-unique.272.length.540, NODE-unique.273.length.539, NODE-unique.275.length.537, NODE-unique.283.length.525, NODE-unique.284.length.525, NODE-unique.285.length.524, NODE-unique.290.length.519, NODE-unique.293.length.517, NODE-unique.297.length.509, NODE-unique.301.length.502
40	NODE-unique.9.length.16661, NODE-unique.100.length.2088, NODE-unique.137.length.1467, NODE-unique.144.length.1427, NODE-unique.159.length.1231, NODE-unique.164.length.1202, NODE-unique.187.length.1071, NODE-unique.194.length.1028, NODE-unique.196.length.1004, NODE-unique.203.length.849, NODE-unique.212.length.720, NODE-unique.216.length.698, NODE-unique.240.length.599, NODE-unique.250.length.587, NODE-unique.278.length.527, NODE-unique.280.length.526, NODE-unique.281.length.526
45	NODE-unique.121.length.1661, NODE-unique.140.length.1445, NODE-unique.210.length.753, NODE-unique.222.length.673, NODE-unique.232.length.621, NODE-unique.277.length.529, NODE-unique.295.length.510
50	NODE-unique.11.length.15990, NODE-unique.14.length.14139, NODE-unique.41.length.5548, NODE-unique.56.length.3888, NODE-unique.59.length.3586, NODE-unique.61.length.3446, NODE-unique.73.length.2800, NODE-unique.77.length.2706, NODE-unique.106.length.1967, NODE-unique.117.length.1793, NODE-unique.160.length.1223, NODE-unique.161.length.1221, NODE-unique.163.length.1211, NODE-unique.172.length.1135, NODE-unique.181.length.1098, NODE-unique.190.length.1046, NODE-unique.202.length.878, NODE-unique.208.length.770, NODE-unique.218.length.685, NODE-unique.236.length.608, NODE-unique.248.length.588, NODE-unique.249.length.587, NODE-unique.252.length.577, NODE-unique.253.length.574, NODE-unique.254.length.573, NODE-unique.259.length.565, NODE-unique.274.length.537, NODE-unique.291.length.518
55	NODE-unique.3.length.27433, NODE-unique.4.length.24885, NODE-unique.13.length.14563, NODE-unique.20.length.11213, NODE-unique.24.length.9868, NODE-unique.25.length.9242, NODE-unique.29.length.7867, NODE-unique.33.length.6806, NODE-unique.36.length.5985, NODE-unique.38.length.5764, NODE-unique.39.length.5746, NODE-unique.40.length.5631, NODE-unique.42.length.5525, NODE-unique.44.length.5462, NODE-unique.46.length.4784, NODE-unique.48.length.4380, NODE-unique.58.length.3600, NODE-unique.63.length.3283, NODE-unique.69.length.2964, NODE-unique.78.length.2657, NODE-unique.82.length.2507, NODE-unique.97.length.2144, NODE-unique.99.length.2112, NODE-unique.120.length.1668,

	NODE-unique_123_length_1646, NODE-unique_129_length_1580, NODE-unique_131_length_1546, NODE-unique_151_length_1355, NODE-unique_162_length_1213, NODE-unique_178_length_1106, NODE-unique_180_length_1103, NODE-unique_188_length_1056, NODE-unique_193_length_1037, NODE-unique_228_length_647, NODE-unique_230_length_636, NODE-unique_239_length_600, NODE-unique_241_length_598, NODE-unique_255_length_573, NODE-unique_265_length_553, NODE-unique_299_length_508
60	NODE-unique_88_length_2316, NODE-unique_124_length_1640, NODE-unique_173_length_1132, NODE-unique_268_length_545, NODE-unique_292_length_517

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

Organism	Pct Align	Pct Id	Contig Name
<i>Pseudomonas putida_KT2440_chromosome,_complete_genome_5s,_16s,_23s_masked</i>	0	100	NODE-unique_29_length_7867
<i>Pseudomonas stutzeri_A1501,_complete_genome_5s,_16s,_23s_masked</i>	2	100	NODE-unique_56_length_3888