

1) Project Information

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

2) Read Statistics

Number of reads	5,032,144
Read type(s)	2x150, 2x150
Sequencing depth [†]	150x
File name(s)	2045.1.1737.ACAGTG.fastq.gz, 2045.2.1737.ACAGTG.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 contaminants. Pairs of matching reads were removed from the dataset.

Description	Num Reads	Pct Reads
Input	5,032,144	100
Artifact removed	24,610	0.5
Normalized removed	3,864,538	76.8
Total removed	3,889,148	77.3
Total remaining	1,142,996	22.7

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	5,032,144	100
Contam identified	712	0.0

List of contaminants identified.

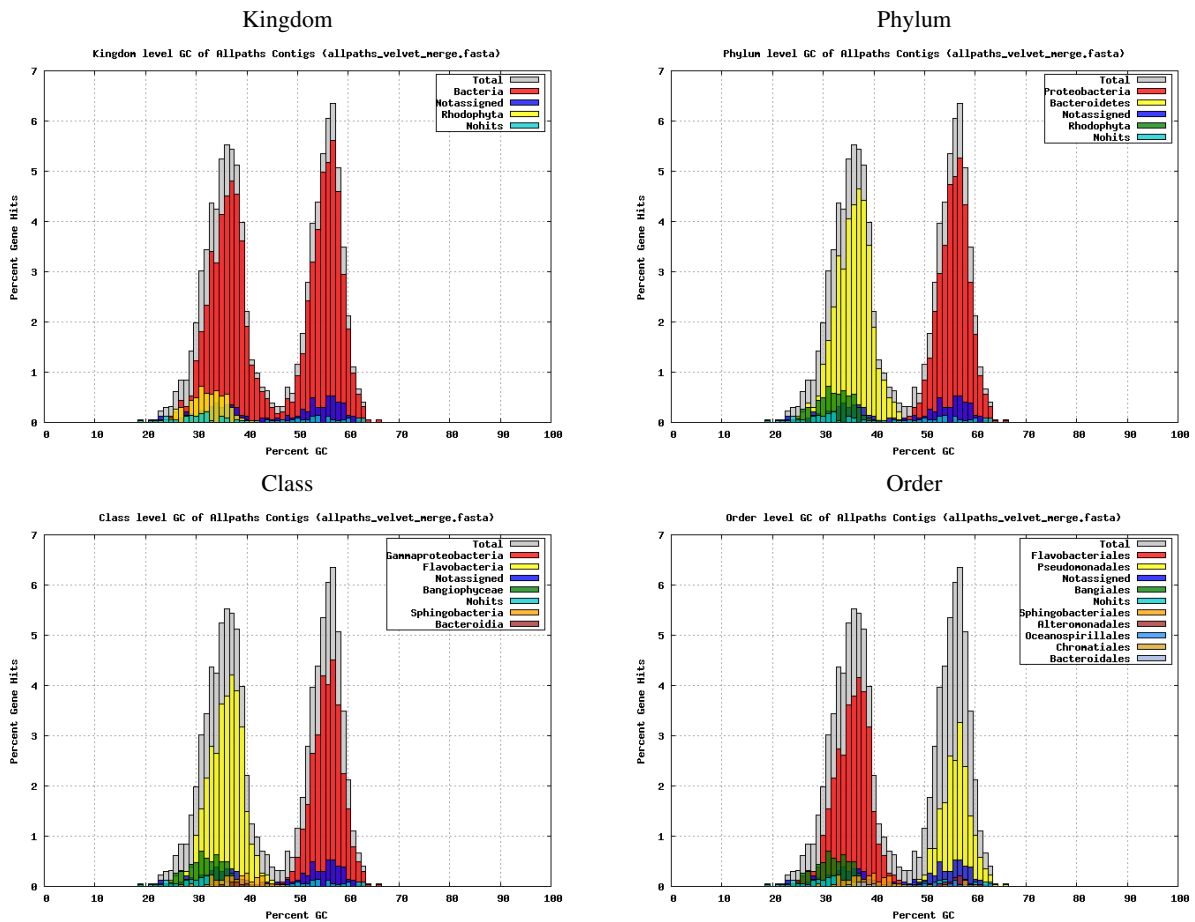
Description	Num Reads	Pct Reads
<i>Ralstonia</i>	378	0.01
<i>Pseudomonas</i>	334	0.01

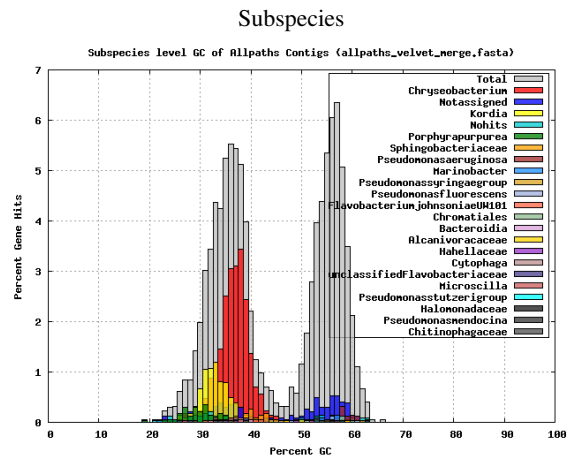
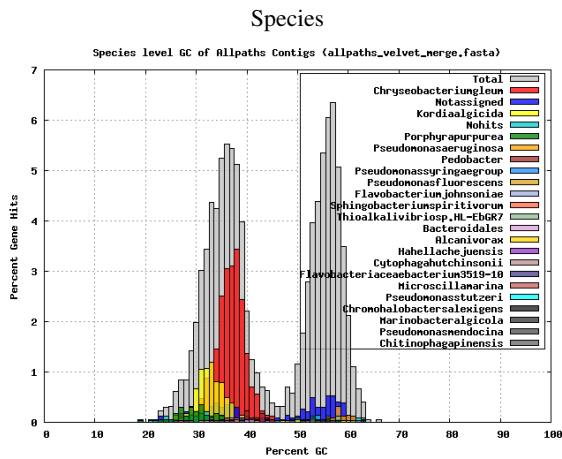
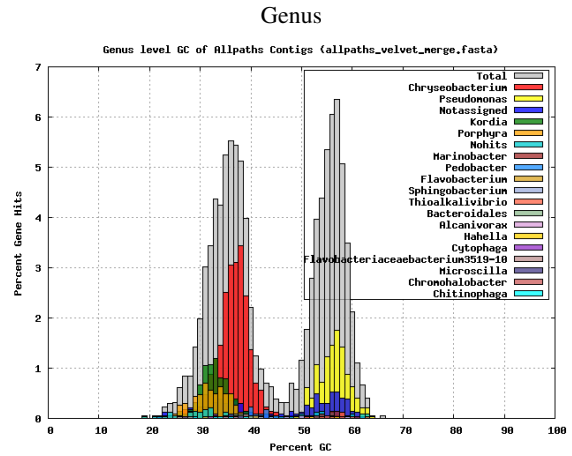
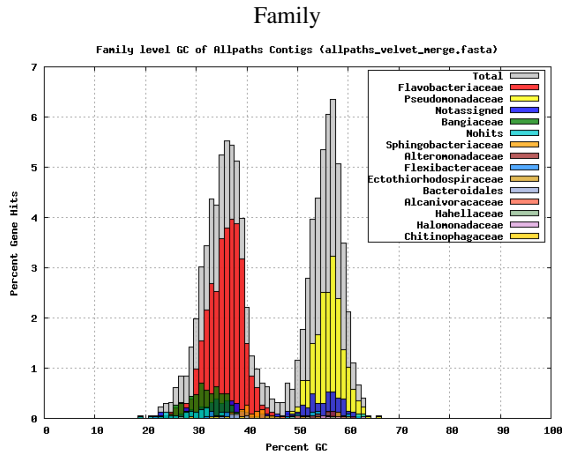
4) Assembly Statistics

Assembly method	Velvet/Allpaths hybrid
Scaffold total	1,280
Contig total	1,280
Scaffold sequence length	5.9 MB
Contig sequence length	5.9 MB (0.0% gap)
Scaffold N/L50	121 / 12.3 KB
Contig N/L50	121 / 12.3 KB
Number of scaffolds >50 KB	6
Pct of genome in scaffolds >50 KB	8.1

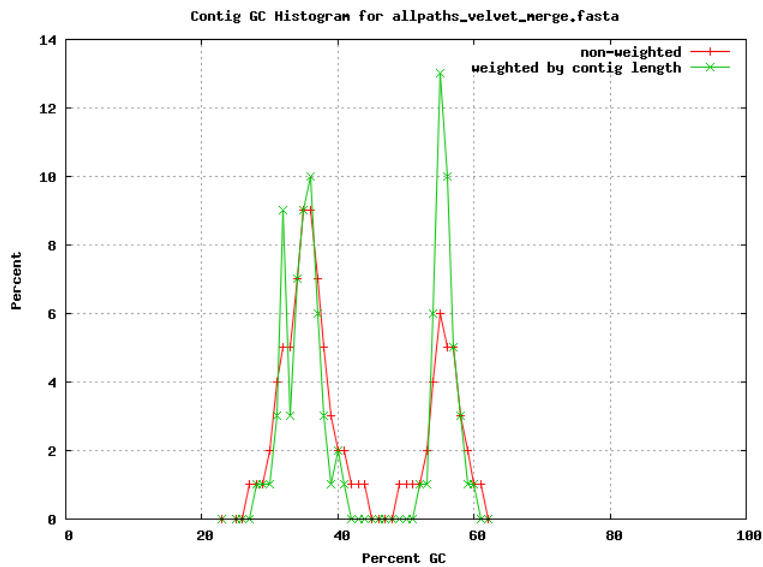
5) Assembly QC Results

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





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.1277.length.502
25	NODE-unique.74.length.16163, NODE-unique.195.length.8456, NODE-unique.370.length.3369, NODE-unique.398.length.3103, NODE-unique.410.length.2958, NODE-unique.414.length.2944, NODE-unique.444.length.2634, NODE-unique.446.length.2622, NODE-unique.455.length.2549, NODE-unique.519.length.2195, NODE-unique.522.length.2187, NODE-unique.523.length.2183, NODE-unique.627.length.1689, NODE-unique.674.length.1559, NODE-unique.675.length.1557, NODE-unique.697.length.1520, NODE-unique.716.length.1482, NODE-unique.724.length.1462, NODE-unique.725.length.1456, NODE-unique.730.length.1448, NODE-unique.735.length.1434, NODE-unique.748.length.1412, NODE-unique.754.length.1393, NODE-unique.783.length.1346, NODE-unique.784.length.1341, NODE-unique.834.length.1245, NODE-unique.844.length.1225, NODE-unique.850.length.1205, NODE-unique.868.length.1172, NODE-unique.890.length.1136, NODE-unique.900.length.1130, NODE-unique.935.length.1082, NODE-unique.963.length.1042, NODE-unique.972.length.1036, NODE-unique.974.length.1036, NODE-unique.1009.length.997, NODE-unique.1012.length.960, NODE-unique.1019.length.897, NODE-unique.1024.length.875, NODE-unique.1039.length.806, NODE-unique.1042.length.797, NODE-unique.1049.length.772, NODE-unique.1061.length.729, NODE-unique.1067.length.714, NODE-unique.1071.length.708, NODE-unique.1075.length.692, NODE-unique.1076.length.691, NODE-unique.1093.length.655, NODE-unique.1101.length.637, NODE-unique.1107.length.626, NODE-unique.1115.length.617, NODE-unique.1141.length.590, NODE-unique.1143.length.588, NODE-unique.1158.length.576, NODE-unique.1161.length.574, NODE-unique.1207.length.543, NODE-unique.1217.length.532, NODE-unique.1229.length.524, NODE-unique.1261.length.509, NODE-unique.1268.length.505, NODE-unique.1273.length.504
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	NODE-unique.609.length.1737, NODE-unique.612.length.1721, NODE-unique.613.length.1720, NODE-unique.615.length.1715, NODE-unique.630.length.1674, NODE-unique.635.length.1663, NODE-unique.637.length.1662, NODE-unique.638.length.1658, NODE-unique.640.length.1654, NODE-unique.645.length.1643, NODE-unique.652.length.1622, NODE-unique.656.length.1604, NODE-unique.658.length.1594, NODE-unique.661.length.1591, NODE-unique.664.length.1583, NODE-unique.668.length.1575, NODE-unique.670.length.1569, NODE-unique.678.length.1551, NODE-unique.680.length.1548, NODE-unique.684.length.1537, NODE-unique.688.length.1534, NODE-unique.690.length.1531, NODE-unique.695.length.1523, NODE-unique.696.length.1522, NODE-unique.704.length.1506, NODE-unique.705.length.1505, NODE-unique.712.length.1487, NODE-unique.719.length.1469, NODE-unique.722.length.1467, NODE-unique.726.length.1454, NODE-unique.734.length.1436, NODE-unique.743.length.1418, NODE-unique.750.length.1411, NODE-unique.752.length.1410, NODE-unique.757.length.1389, NODE-unique.767.length.1373, NODE-unique.780.length.1352, NODE-unique.785.length.1339, NODE-unique.787.length.1336, NODE-unique.790.length.1331, NODE-unique.797.length.1310, NODE-unique.801.length.1309, NODE-unique.808.length.1297, NODE-unique.809.length.1296, NODE-unique.810.length.1290, NODE-unique.812.length.1286, NODE-unique.815.length.1279, NODE-unique.818.length.1274, NODE-unique.819.length.1273, NODE-unique.820.length.1273, NODE-unique.821.length.1272, NODE-unique.831.length.1254, NODE-unique.839.length.1238, NODE-unique.840.length.1237, NODE-unique.859.length.1185, NODE-unique.862.length.1182, NODE-unique.867.length.1174, NODE-unique.872.length.1168, NODE-unique.873.length.1168, NODE-unique.880.length.1156, NODE-unique.881.length.1154, NODE-unique.889.length.1139, NODE-unique.901.length.1130, NODE-unique.904.length.1126, NODE-unique.908.length.1123, NODE-unique.915.length.1115, NODE-unique.918.length.1108, NODE-unique.920.length.1107, NODE-unique.921.length.1104, NODE-unique.930.length.1088, NODE-unique.937.length.1076, NODE-unique.940.length.1074, NODE-unique.944.length.1071, NODE-unique.946.length.1068, NODE-unique.954.length.1059, NODE-unique.956.length.1052, NODE-unique.964.length.1041, NODE-unique.966.length.1041, NODE-unique.969.length.1039, NODE-unique.977.length.1033, NODE-unique.979.length.1032, NODE-unique.985.length.1022, NODE-unique.990.length.1016, NODE-unique.991.length.1014, NODE-unique.994.length.1009, NODE-unique.1018.length.900, NODE-unique.1021.length.878, NODE-unique.1030.length.858, NODE-unique.1057.length.744, NODE-unique.1065.length.715, NODE-unique.1072.length.707, NODE-unique.1080.length.678, NODE-unique.1082.length.674, NODE-unique.1086.length.662, NODE-unique.1092.length.655, NODE-unique.1117.length.612, NODE-unique.1127.length.598, NODE-unique.1129.length.595, NODE-unique.1135.length.592, NODE-unique.1137.length.591, NODE-unique.1138.length.591, NODE-unique.1151.length.583, NODE-unique.1179.length.563, NODE-unique.1193.length.551, NODE-unique.1201.length.546, NODE-unique.1202.length.546, NODE-unique.1206.length.543, NODE-unique.1227.length.525, NODE-unique.1233.length.524, NODE-unique.1234.length.524, NODE-unique.1237.length.523, NODE-unique.1240.length.520, NODE-unique.1243.length.519, NODE-unique.1263.length.508, NODE-unique.1274.length.504
60	NODE-unique.152.length.10387, NODE-unique.223.length.7179, NODE-unique.404.length.2987, NODE-unique.426.length.2820, NODE-unique.441.length.2650, NODE-unique.459.length.2516, NODE-unique.494.length.2306, NODE-unique.539.length.2074, NODE-unique.621.length.1700, NODE-unique.623.length.1693, NODE-unique.660.length.1592, NODE-unique.685.length.1536, NODE-unique.710.length.1489, NODE-unique.788.length.1336, NODE-unique.794.length.1317, NODE-unique.841.length.1234, NODE-unique.854.length.1195, NODE-unique.968.length.1040, NODE-unique.1011.length.962, NODE-unique.1029.length.858, NODE-unique.1059.length.731, NODE-unique.1106.length.631, NODE-unique.1162.length.574, NODE-unique.1262.length.508

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

Organism	Pct Align	Pct Id	Contig Name
<i>Pseudomonas fluorescens</i> .Pf-5.chromosome,.complete.genome.5s,.16s,.23s.masked	0	100	NODE-unique.12.length.40218
	0	100	NODE-unique.154.length.10298
<i>Pseudomonas mendocina</i> .ymp,.complete.genome.5s,.16s,.23s.masked	0	100	NODE-unique.203.length.8267
	0	98	NODE-unique.77.length.15792
<i>Pseudomonas putida</i> .KT2440.chromosome,.complete.genome.5s,.16s,.23s.masked	0	100	NODE-unique.106.length.13759
	0	98	NODE-unique.29.length.30059
<i>Pseudomonas stutzeri</i> .A1501,.complete.genome.5s,.16s,.23s.masked	6	100	NODE-unique.771.length.1367
	4	100	NODE-unique.540.length.2066
	0	98	NODE-unique.39.length.25627
<i>Pseudomonas syringae</i> .pv.phaseolicola.1448A.chromosome,.complete.genome.5s,.16s,.23s.masked	0	98	NODE-unique.21.length.33348
<i>Pseudomonas syringae</i> .pv.tomato.str.DC3000,.complete.genome.5s,.16s,.23s.masked	0	98	NODE-unique.69.length.16553