

Report for Arachne assembly of *galdieria*

Assembly started on: Thu Oct 13 19:50:16 2005.
Thu Oct 13 21:46:47 2005.

Data: /usr/local/genome/data/galdieria
Run: /usr/local/genome/data/galdieria/Build_2005-10-13-A
This file: /usr/local/genome/data/galdieria/Build_2005-10-13-A/assembly.ps

1 Read Statistics

Initial Read Processing							
library	input reads	excluded by config file	excluded by base quality	excluded by vector or bacterial host sequence	other exclusion	total excluded	total remaining
MSU_GTTSF-BAC-Bam	2304	0	700	0	0	700	1604
MSU_GTTSF-BAC-Hind	2304	0	627	0	0	627	1677
MSU_GTTSF-Fosmid	7296	0	1479	0	0	1479	5817
MSU_GTTSF-GC	2880	0	744	0	0	744	2136
MSU_GTTSF-GS0	157304	768	23168	29	1	23966	133338
MSU_GTTSF-GS2	63744	3264	5020	23	0	8307	55437
total	235832	4032	31738	52	1	35823	200009

Non-Excluded Read Statistics							
library	number of reads	trimmed read length mean \pm st. dev.	genomic coverage by trimmed read bases	genomic coverage by trimmed read bases of qual \geq 20	fraction paired	fraction assembled	fraction assembled along with partner
MSU_GTTSF-BAC-Bam	1604	602 \pm 166	0.06X	0.05X	89.7%	94.1%	82.3%
MSU_GTTSF-BAC-Hind	1677	588 \pm 190	0.06X	0.05X	86.2%	89.5%	74.5%
MSU_GTTSF-Fosmid	5817	593 \pm 166	0.22X	0.18X	88.4%	88.4%	71.7%
MSU_GTTSF-GC	2136	601 \pm 224	0.08X	0.07X	92.6%	92.3%	83.4%
MSU_GTTSF-GS0	133338	700 \pm 181	5.83X	5.38X	93.1%	94.9%	87.0%
MSU_GTTSF-GS2	55437	741 \pm 174	2.57X	2.36X	95.9%	94.2%	88.6%
total	200009	705 \pm 182	8.82X	8.10X	93.6%	94.4%	86.8%

Genomic coverage was computed relative to a genome size of 16000000, as specified in the file genome.size.

2 Contig Statistics

- There are 1079 contigs, of lengths: 304861, 294127, 223188, 206028, 191799, 181017, 177836, 174205, 169763, 159123, 154406, 154036, 153558, 150233, 138705, ..., 517, 507, 469, 464, 424.
- Total contig length: 14357686 bases.
- Average contig length:
 - mean = 13306 bases;

- length-weighted mean = 86739 bases;
- length-weighted median (N50) = 80518 bases.

3 Supercontig Statistics

- There are 894 supercontigs, of lengths: 374968, 364776, 334351, 325379, 305035, 298641, 293734, 285644, 282925, 273291, 245434, 243541, 238216, 226412, 216452, ..., 517, 507, 469, 464, 424.
- Total supercontig length: 14932726 bases.
- Average supercontig length:
 - mean = 16703 bases;
 - length-weighted mean = 159859 bases;
 - length-weighted median (N50) = 158738 bases.

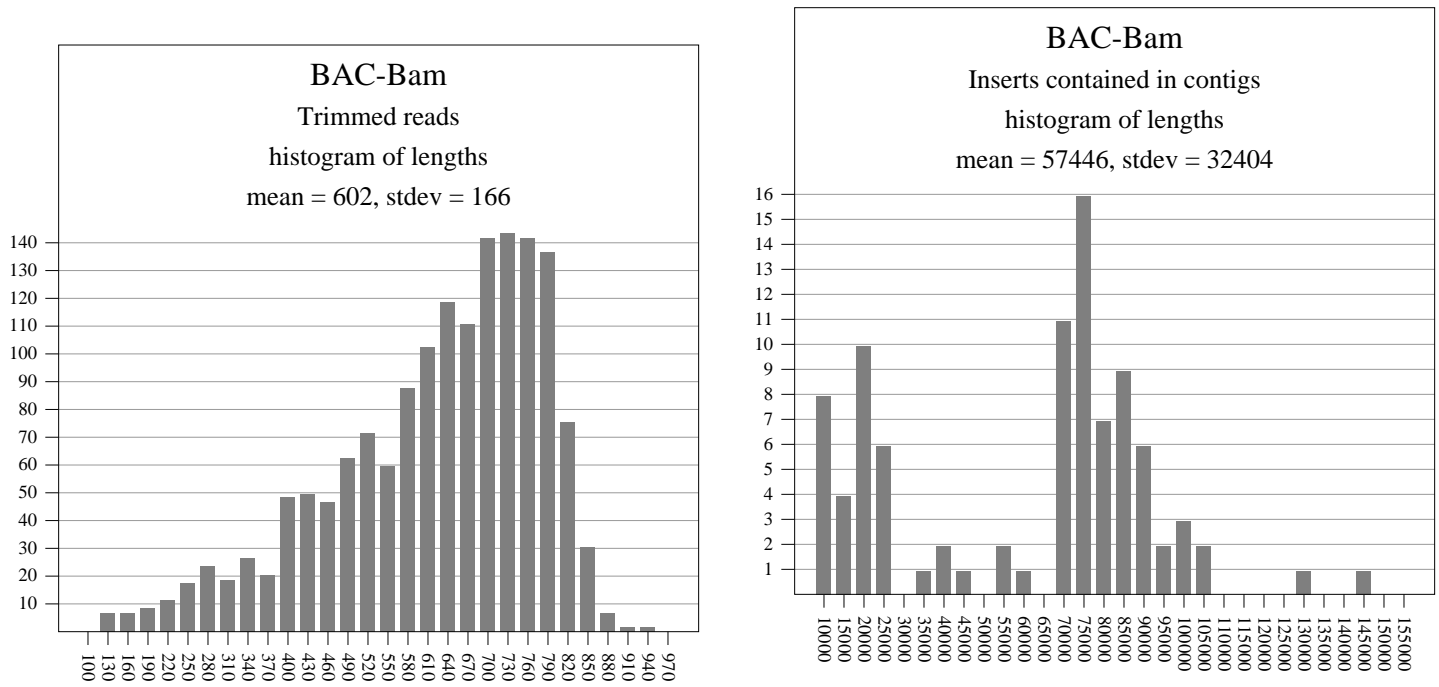
4 Contig Coverage Statistics

- Coverage of genome: (total length of included sequence)/(genome size), where the genome size is taken to be 16000000 (the value given in the file genome.size). Coverage may be exaggerated by overlaps between included sequence. (Technical note. Where we include gaps, we do not include gaps reported as negative. This could introduce a slight inconsistency between the “coverage of genome” for “all contigs and all gaps” and the total supercontig length, as reported in the previous section.)

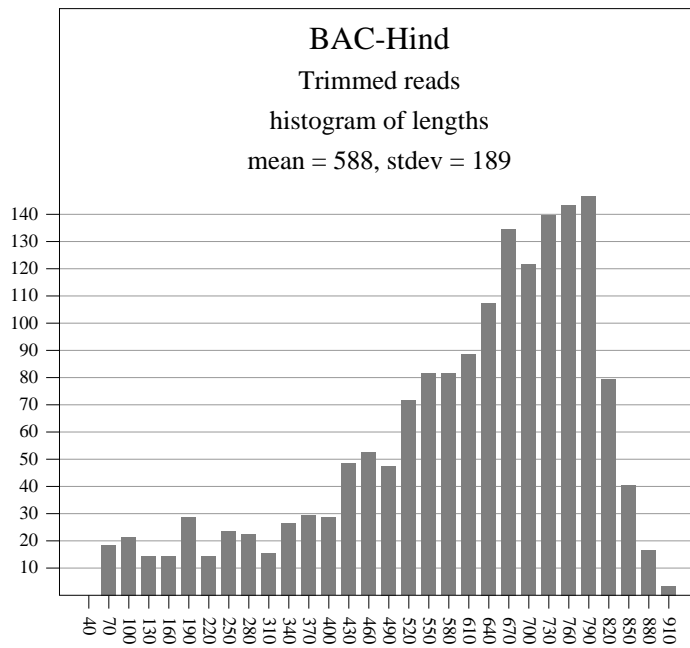
Coverage Statistics		
sequence included	contigs	coverage of genome
contigs \geq 512 kb	0	0.00%
contigs \geq 256 kb	2	3.74%
contigs \geq 128 kb	23	24.35%
contigs \geq 64 kb	70	51.35%
contigs \geq 32 kb	103	60.97%
contigs \geq 16 kb	148	67.20%
contigs \geq 8 kb	253	74.22%
contigs \geq 4 kb	473	81.89%
contigs \geq 2 kb	753	87.02%
contigs \geq 1 kb	1009	89.38%
all contigs	1079	89.74%
all contigs, and gaps \leq 100 b	1079	89.74%
all contigs, and gaps \leq 200 b	1079	89.75%
all contigs, and gaps \leq 400 b	1079	89.78%
all contigs, and gaps \leq 800 b	1079	89.81%
all contigs, and gaps \leq 1600 b	1079	89.86%
all contigs, and gaps \leq 3200 b	1079	89.97%
all contigs, and gaps \leq 6400 b	1079	90.28%
all contigs, and gaps \leq 12800 b	1079	91.41%
all contigs, and gaps \leq 25600 b	1079	92.81%
all contigs and all gaps	1079	93.54%

5 Library by Library Statistics

5.1 Center MSU_GTSF - library BAC-Bam

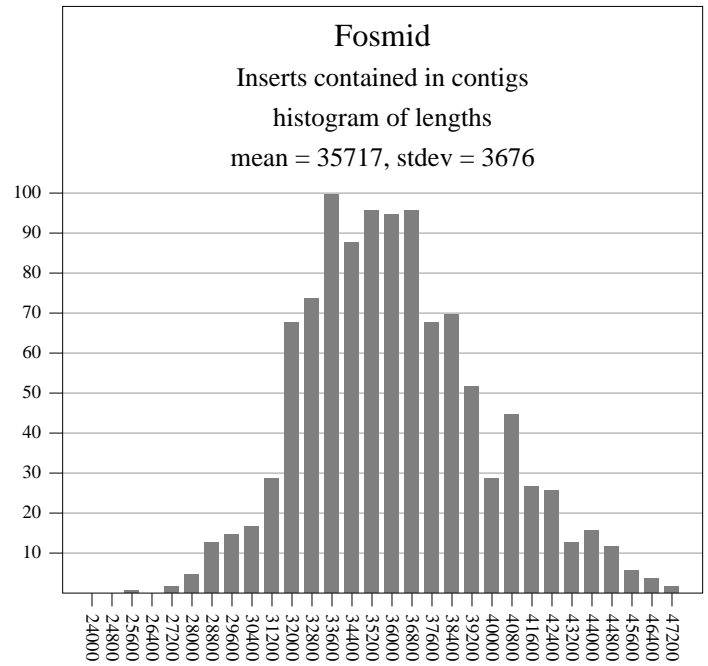
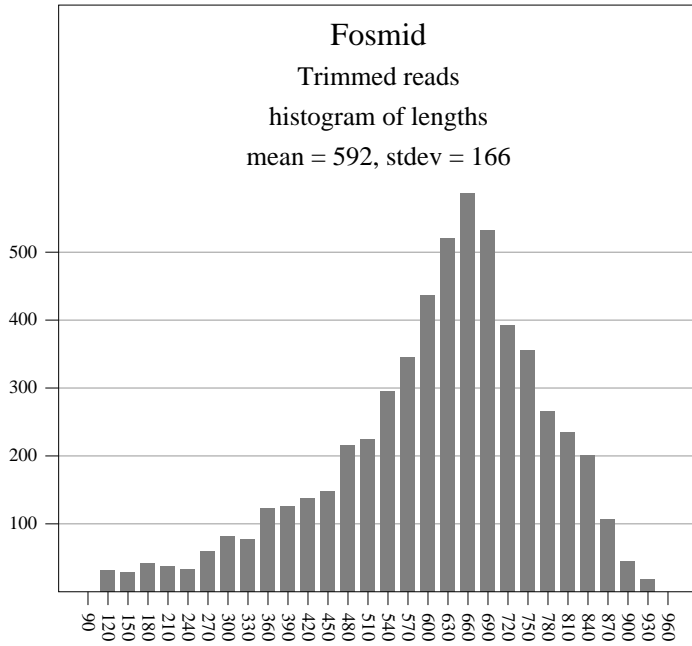


5.2 Center MSU_GTSF - library BAC-Hind

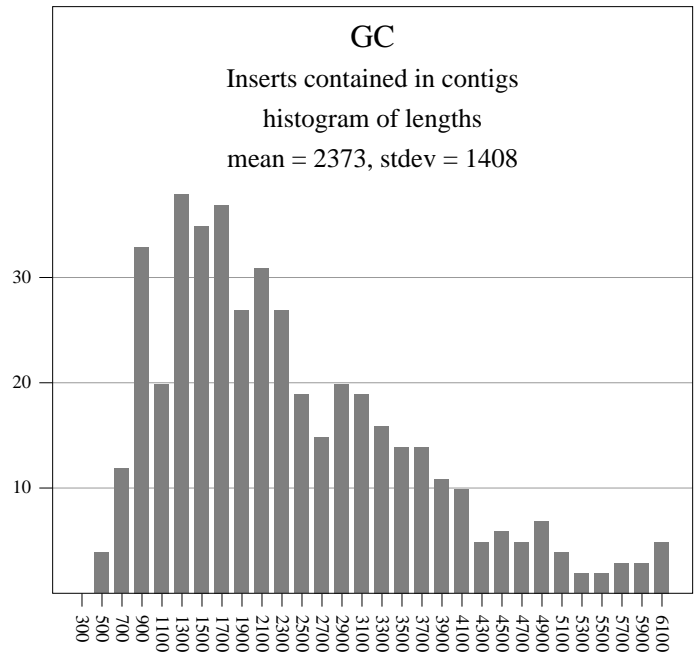
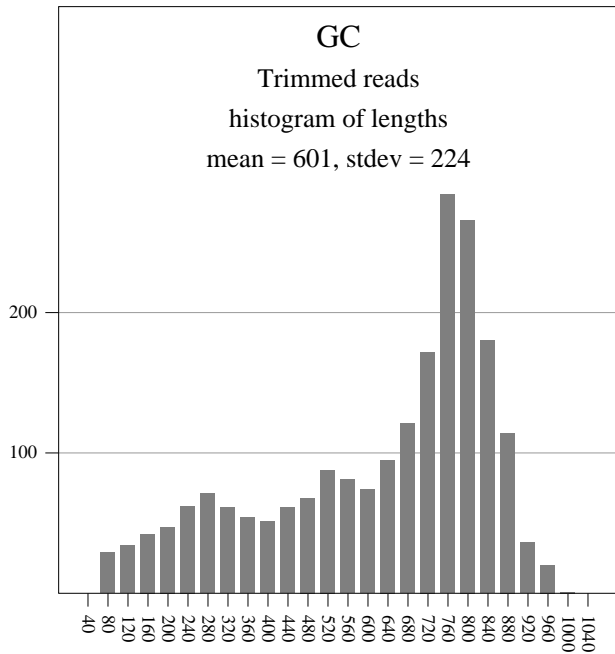


A meaningful insert lengths histogram could not be produced.

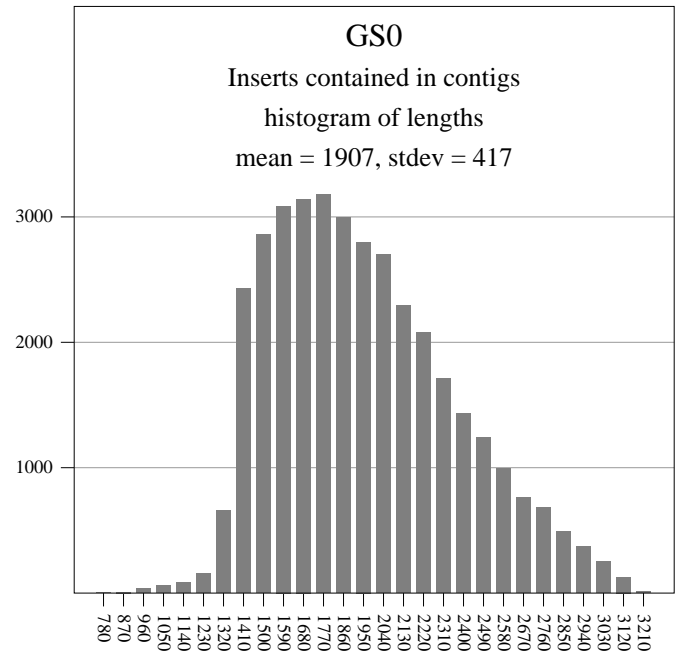
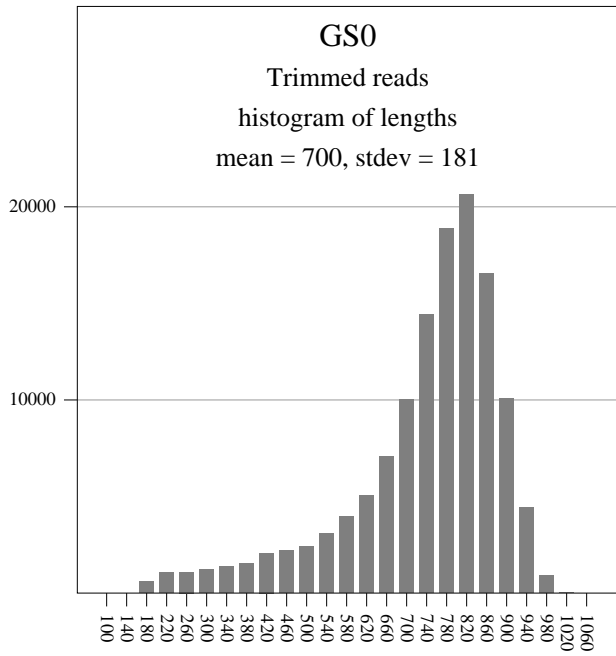
5.3 Center MSU_GTSF - library Fosmid



5.4 Center MSU_GTSF - library GC



5.5 Center MSU_GTSF - library GS0



5.6 Center MSU_GTSF - library GS2

