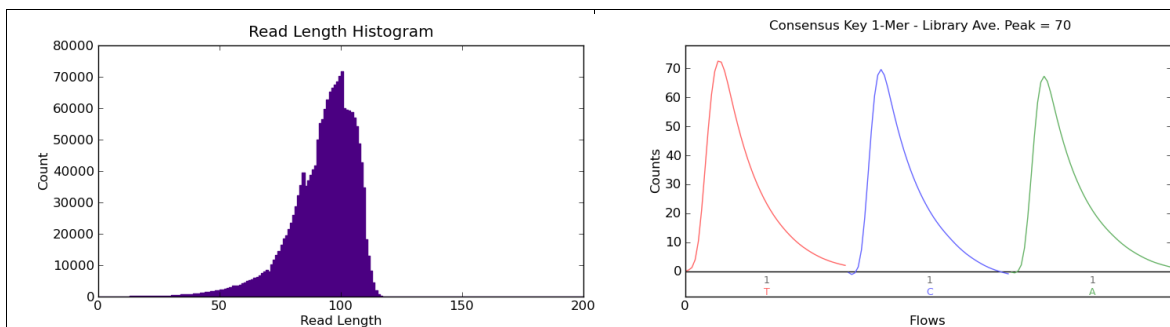


Report for Auto_SEQ-7_10

Library Summary

Based on Predicted Per-Base Quality Scores - Independent of Alignment

Total Number of Bases [Mbp]	169.92
▸ In Predicted Q17 Read Stretches [Mbp]	32.63
▸ In Predicted Q20 Read Stretches [Mbp]	14.70
Total Number of Reads	1,848,942
▸ At Least 50 bp Long	1,823,192
▸ At Least 100 bp Long	593,555
Mean Length [bp]	92
Longest Read [bp]	118



Reference Genome Information

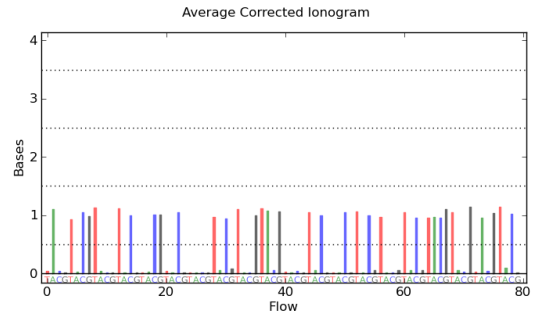
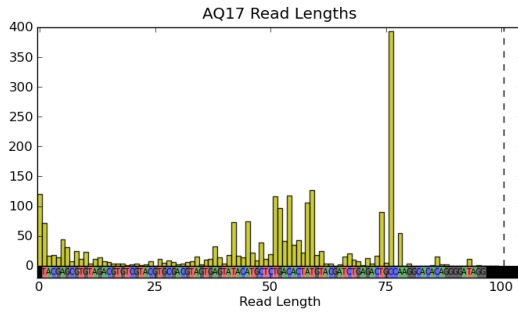
Genome Name	<i>Ecoli_O147_ref</i>
Genome Size	5,498,450 bases
Genome Version	1
Index Version	tmap-f2

Based on Full Library Alignment to Provided Reference

	AQ17	AQ20
Total Number of Bases [Mbp]	72.21	57.36
Total Number of Reads	1,190,459	1,101,669
▸ At Least 50 bp Long	797,530	499,611
▸ At Least 100 bp Long	119,659	84,727
Mean Length [bp]	61	52
Longest Alignment [bp]	118	118
Mean Coverage Depth	13.10x	10.40x
Percentage of Library Covered	94%	94%

TF Name	TF_C
TF Seq	TACGAGCGTGTAGACGTGTCGTACGTGCGACGTAGTGAGTATACATGCTC TGACACTATGTACGATCTGAGACTGCCAAGGCACACAGGGGATAGG
Num	2,319
Avg Q17 read length	49
50AQ17	1,446

Graphs

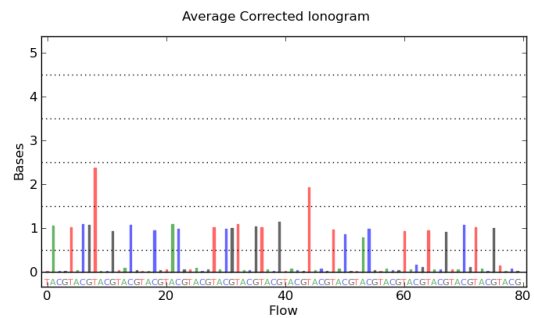
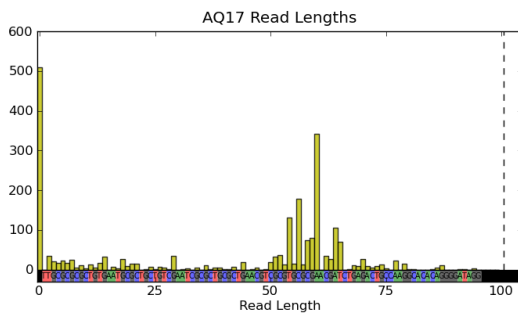


Test Fragment - TF_D

Quality Metrics

TF Name	TF_D
TF Seq	TTGCGCGCTGTGAATGCGCTGCTGTGCGAATCGCGCTGCGCTGAACGTC GCGTGCGCGAACGATCTGAGACTGCCAAGGCACACAGGGGATAGG
Num	2,290
Avg Q17 read length	39
50AQ17	1,334

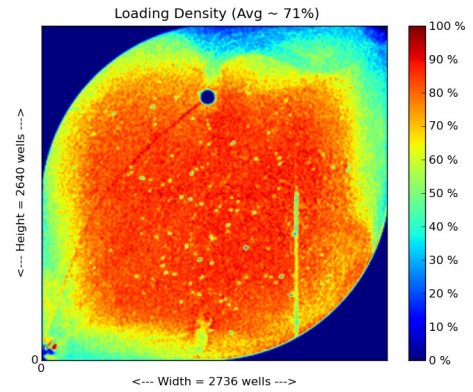
Graphs



Ion Sphere™ Particle (ISP) Identification Summary

	Count	Percentage
Total Addressable Wells	6,337,656	
▸ Wells with ISPs	4,519,469	71%
▸ Live ISPs	4,018,585	89%
▸ Test Fragment ISPs	10,163	<1%
▸ Library ISPs	4,008,422	100%

	Count	Percentage
Library ISPs / Percent Enrichment	4,008,422	89%
▸ Filtered: Too short	106	<1%
▸ Filtered: Keypass failure	128,833	3%
▸ Filtered: Mixed / Polyclonal	270,253	7%
▸ Filtered: Poor Signal Profile	1,760,228	44%
▸ Final Library Reads	1,849,002	46%



Report Information

Analysis Info

Run Name	R_2011_06_29_10_53_41_user_SEQ-7
Run Date	2011-06-29 10:53:41
Analysis Name	Auto_SEQ-7_10
Analysis Date	2011-07-01
Analysis Cycles	65
Project	RUN_DU_E.coli_01.07.2011
Sample	sample1
Library	ecoliO147
PGM	SEQ
Chip Check	Passed
Chip Type	"316D"
Notes	
Flow Order	TACGTACGTCTGAGCATCGATCGATGTACAGC

Software Version

Host	JF1QWP1
Analysis	1.40-2
Alignment	1.42-0
Dbreports	1.95-5
Tmap	0.0.19-1
Docs	1.15-1
Tsconfig	1.3-10
Referencelibrary	1.6-1

File Links

Library Sequence (SFF)
Library Sequence (FASTQ)
Library Alignments (SAM)
Library Alignments (BAM)
Library Alignments (BAM Index)
Test Fragments (SFF)
PDF of this Report
Analysis Log File