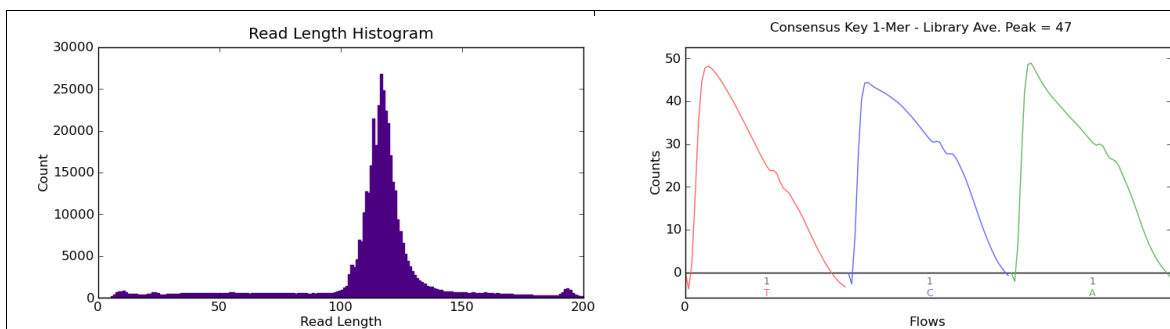


Report for Auto_EBI-16_18

Library Summary

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

Total Number of Bases [Mbp]	47.87
▶ Number of Q17 Bases [Mbp]	31.45
▶ Number of Q20 Bases [Mbp]	25.15
Total Number of Reads	424,958
Mean Length [bp]	113
Longest Read [bp]	202



Reference Genome Information

There was an alignment error. For details see the [Report Log](#)

alignmentQC returned with error code: 2

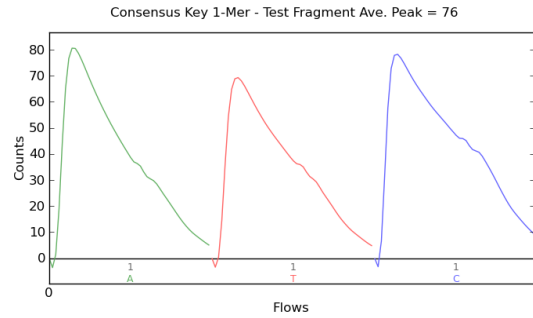
Unable to process alignment for genome, because the **none** reference library was not found.

Read Alignment Distribution

Test Fragment Report

Test Fragment Summary

Test Fragment	Percent (50AQ17 / Num)
TF_A	71%
TF_D	78%

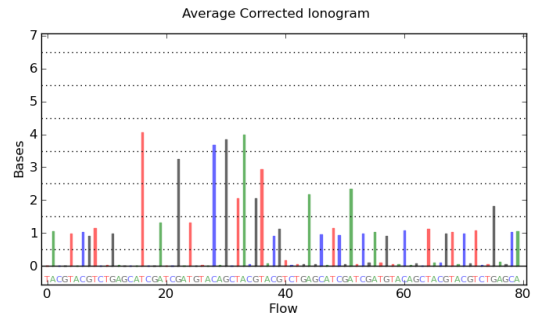
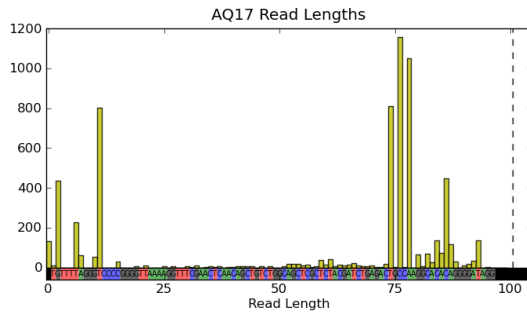


Test Fragment - TF_A

Quality Metrics

TF Name	TF_A
TF Seq	TGTTTTAGGGTCCCCGGGGTTAAAGGTTTCGAACTCAACAGCTGTCTGG CAGCTCGCTCTACGATCTGAGACTGCCAAGGCACACAGGGGATAGG
Num	6,373
Avg Q17 read length	58
50AQ17	4,515

Graphs

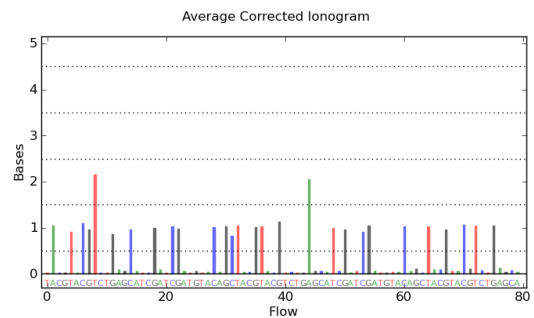
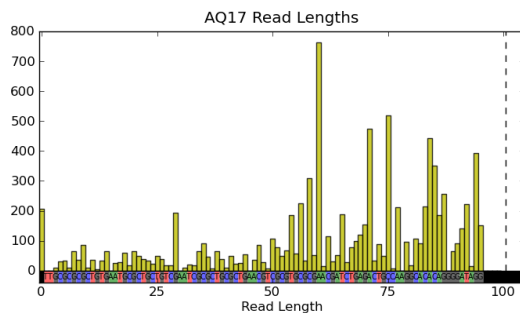


Test Fragment - TF_D

Quality Metrics

TF Name	TF_D
TF Seq	TTGCGCGGCTGTGAATGCGCTGCTGTGCGAATCGCGCTGGCTGAACGTC CGCTGCGGAACGATCTGAGACTGCCAAGGCACACAGGGGATAGG
Num	9,006
Avg Q17 read length	63
50AQ17	7,037

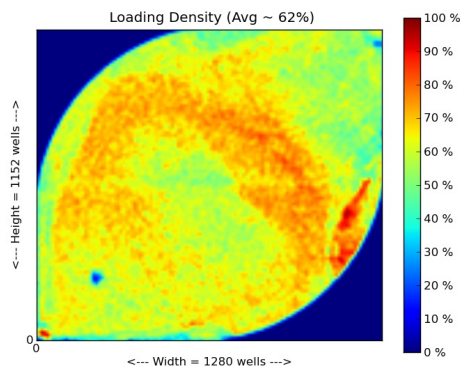
Graphs



Ion Sphere™ Particle (ISP) Identification Summary

	Count	Percentage
Total Addressable Wells	1,262,519	
▸ Wells with ISPs	802,349	64%
▸ Live ISPs	698,328	87%
▸ Test Fragment ISPs	16,193	2%
▸ Library ISPs	682,135	98%

	Count	Percentage
Library ISPs / Percent Enrichment	682,135	87%
▸ Filtered: Too short	30,491	4%
▸ Filtered: Keypass failure	42,557	6%
▸ Filtered: Mixed / Polyclonal	21,678	3%
▸ Filtered: Low Signal	9,983	1%
▸ Filtered: Poor Signal Profile	151,812	22%
▸ Filtered: 3' Adapter trim	386	<1%
▸ Filtered: 3' Quality trim	0	<1%
▸ Final Library Reads	424,958	62%



Report Information

Analysis Info

Run Name	R_2011_08_24_14_17_38_user_EBI-16
Run Date	2011-08-24 14:17:38
Analysis Name	Auto_EBI-16_18
Analysis Date	2011-08-24
Analysis Cycles	65
Project	EBI_PCR1
Sample	EBI.moscow.sample.run2
Library	none
PGM	EBI
Chip Check	Passed
Chip Type	"314R"
Notes	
Flow Order	TACGTACGTCTGAGCATCGATCGATGTACAGC
Library Key	TCAG

Software Version

Host	G8L4DQ1
Analysis	1.52-13
Alignment	1.47-6
Dbreports	1.106-18
Tmap	0.0.28-1
Docs	1.28-3
Tsconfig	1.5-10
Referencelibrary	1.6-2

File Links

Library Sequence (SFF)
Library Sequence (FASTQ)
Full Library Alignments (BAM)
Library Alignments (BAM Index)
Test Fragments (SFF)
PDF of this Report
Customer Support Archive

Plugin Summary

 **Select Plugins To Run**

 **Refresh Plugin Status**