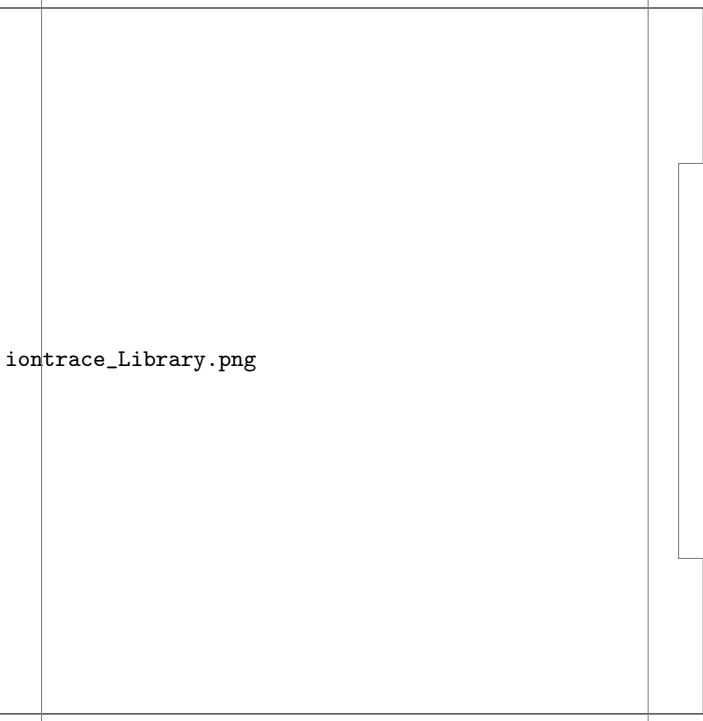
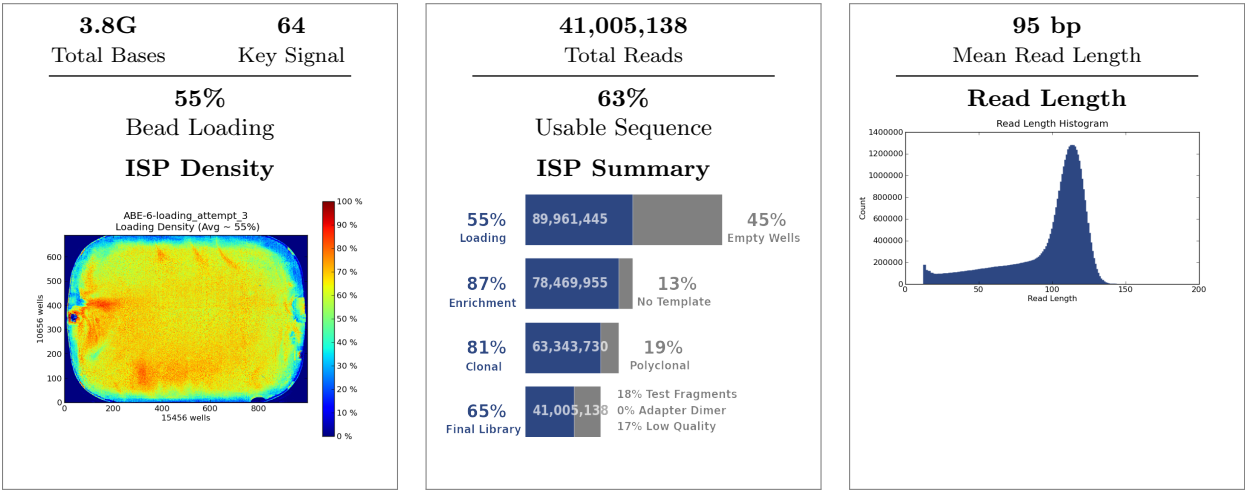
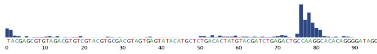


Run Summary

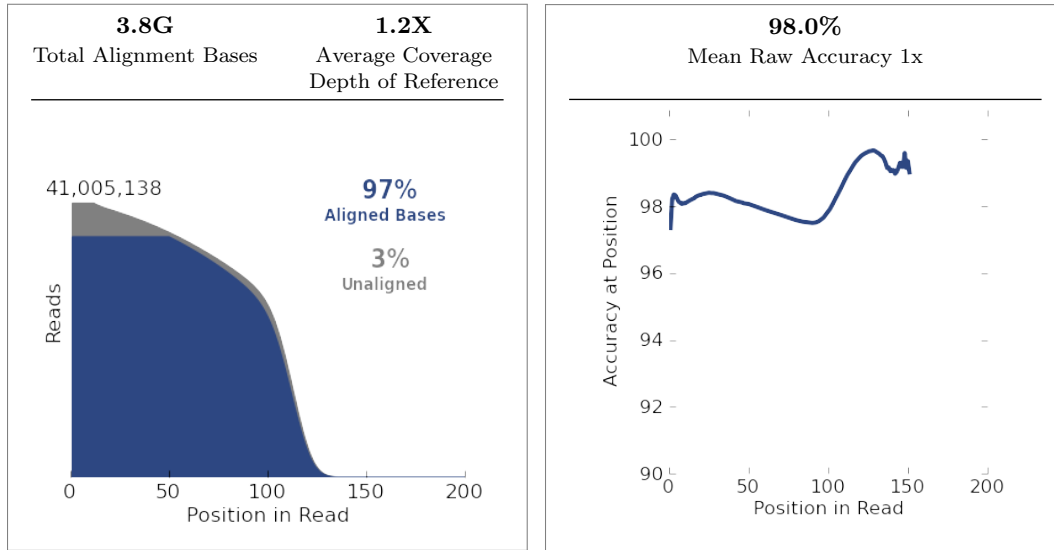


Addressable Wells	164,699,136	
With ISPs	89,961,445	54.6%
Live	78,469,955	87.2%
Test Fragment	13,143,523	16.7%
Library	65,326,432	83.3%

Library ISPs	65,326,432	
Filtered: Polyclonal	15,126,225	23.2%
Filtered: Low Quality	9,194,878	14.1%
Filtered: Primer Dimer	191	00.0%
Final Library ISPs	41,005,138	62.8%

Test Fragment	Reads	Percent 50AQ17	Read Length Histogram
TF_C	11,381,988	75%	

Alignment Summary (*aligned to Human genome build 19*)



	AQ17	AQ20	Perfect
Total Number of Bases [Mbp]	3G	2.4G	2G
Mean Length [bp]	89	78	68
Longest Alignment [bp]	173	173	173
Mean Coverage Depth	1.0	0.8	0.7

Filtered_Alignments_Q10.png

Filtered_Alignments_Q17.png

Filtered_Alignments_Q20.png

Filtered_Alignments_Q47.png

Analysis Details

Run Name	R.2013.04.19_06.58.42_user_ABE-6-loading_attempt_3
Run Date	April 19, 2013, 6:58 a.m.
Run Flows	260
Projects	SampleData
Sample	Control
Library	hg19
PGM	Aber-Proton
Flow Order	TACGTACGTCTGAGCATCGATCGATGTACAGC
Library Key	TCAG
TF Key	ATCG
Chip Check	Passed
Chip Type	900
Chip Data	tilted
Barcode Set	
Analysis Name	Auto_user_ABE-6-loading_attempt_3_7
Analysis Date	April 20, 2013, 3:24 a.m.
Analysis Flows	0
runID	8NI6Q

Software Version

Torrent_Suite	3.4.1
host	HJQS3V1
ion-alignment	3.4.3-1
ion-analysis	3.4.7-1
ion-dbreports	3.4.26-1
ion-gpu	3.0.0-1
ion-pipeline	3.4.16-1
ion-plugins	3.4.19-1
ion-protonupdates	3.4.4
ion-torrentr	3.4.5-1
LiveView	126
DataCollect	201
OIA	15
OS	10
Graphics	26