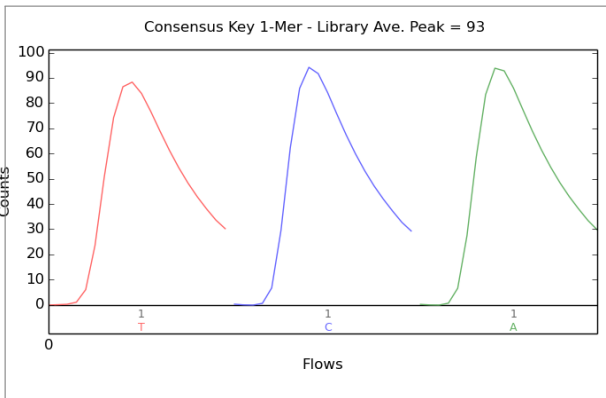
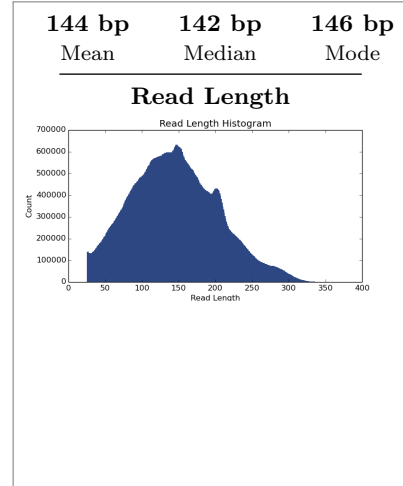
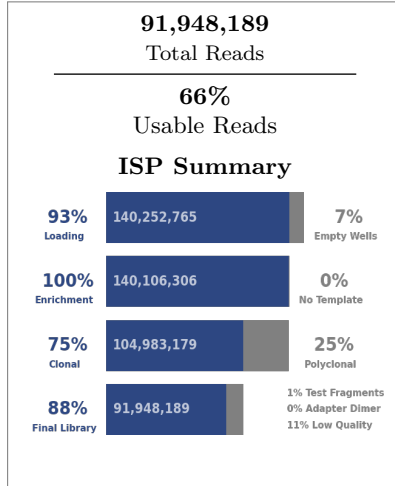
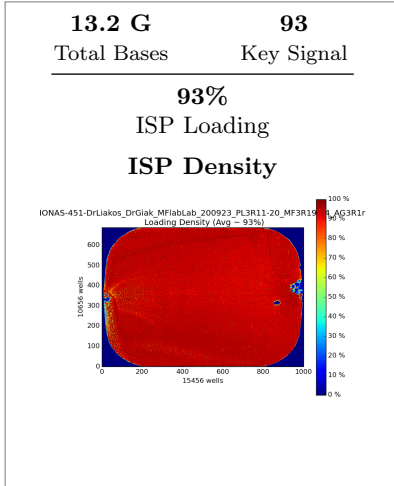


Run Summary



















Addressable Wells	151,539,288	
With ISPs	140,252,765	92.6%
Live	140,106,306	99.9%
Test Fragment	764,922	00.5%
Library	139,341,384	99.5%
Library ISPs	139,341,384	
Filtered: Polyclonal	35,123,127	25.2%
Filtered: Low Quality	12,199,738	08.8%
Filtered: Adapter Dimer	70,330	00.1%
Final Library ISPs	91,948,189	66.0%

Notes: PLiakos-12-3RNAs.MFlab-6-3RNAs_Agiak-1rerun

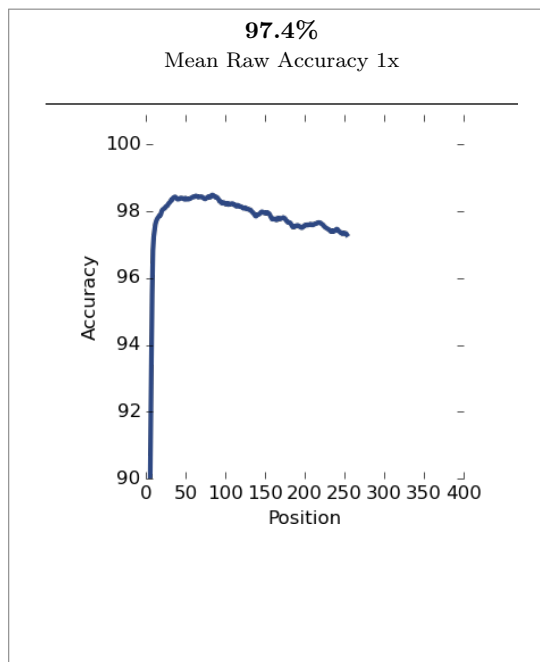
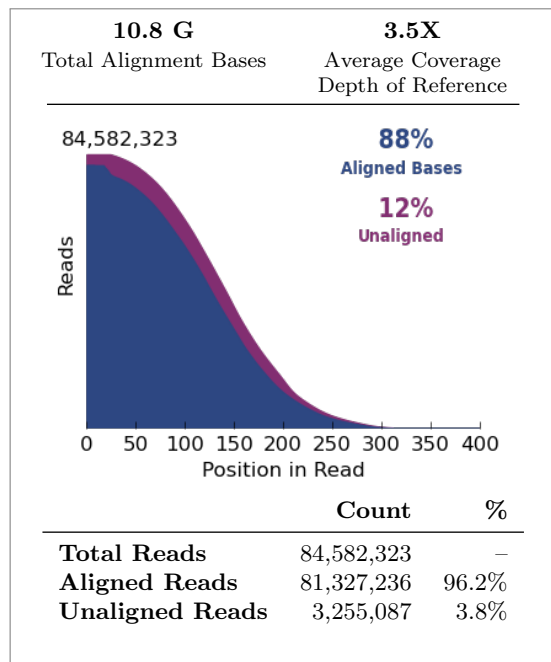
Barcode Name	Sample	Bases	$\geq Q20$	Reads	Mean Read Length	Read Length Histogram
No barcode	none	1,007,621,946	782,884,612	7,108,451	141 bp	
IonXpress.011	AG3R1r.G1	670,735,496	536,947,801	4,580,864	146 bp	
IonXpress.031	MF3R23_Prox1-542,919,959 2	437,076,443	437,076,443	4,033,312	134 bp	
IonXpress.032	MF3R24_Prox1-908,383,359 new2	726,611,613	726,611,613	6,162,115	147 bp	
IonXpress.033	PL3R11_N-nonTarg- ctrl	669,343,638	534,646,783	4,722,342	141 bp	
IonXpress.034	PL3R12_N-Reptin1	612,764,919	488,558,252	4,343,597	141 bp	

Run Report for Auto_user_IONAS-451-DrLiakos_DrGiak_MFlabLab_200923_PL3R11-20_MF3R19-24_AG3R1r_664

IonXpress_035	PL3R13_H-nonTarg-ctr1	879,657,578	697,970,095	5,827,783	150 bp	
IonXpress_036	PL3R14_H-Reptin1	317,354,844	256,366,742	2,228,208	142 bp	
IonXpress_037	PL3R15_H-HIF2a-1	293,282,383	233,930,615	2,059,393	142 bp	
IonXpress_038	PL3R16_H-HIF2aReptin1	580,666,840	466,299,293	3,976,916	146 bp	
IonXpress_039	PL3R17_N-norTarg-ctr2	504,285,869	403,371,452	3,403,855	148 bp	
IonXpress_040	PL3R18_N-Reptin2	1,094,329,607	872,809,141	7,449,848	146 bp	
IonXpress_041	PL3R19_H-nonTarg-ctr2	405,706,371	325,664,377	2,854,644	142 bp	
IonXpress_042	PL3R20_H-Reptin2	725,385,620	584,459,111	4,741,856	152 bp	
IonXpress_043	PL3R21_H-HIF2a-2	371,457,795	296,585,361	2,535,385	146 bp	
IonXpress_044	PL3R22_H-HIF2aReptin2	1,189,362,865	956,821,165	8,061,140	147 bp	
IonXpress_045	MF3R19_GFP1	554,722,321	449,420,049	4,153,057	133 bp	
IonXpress_046	MF3R20_GFP2	685,738,412	553,924,172	4,833,253	141 bp	
IonXpress_047	MF3R21_GFPn662	450,337	463,338,784	3,859,458	147 bp	
IonXpress_048	MF3R22_Prox1	660,900,037	533,248,167	4,755,297	138 bp	

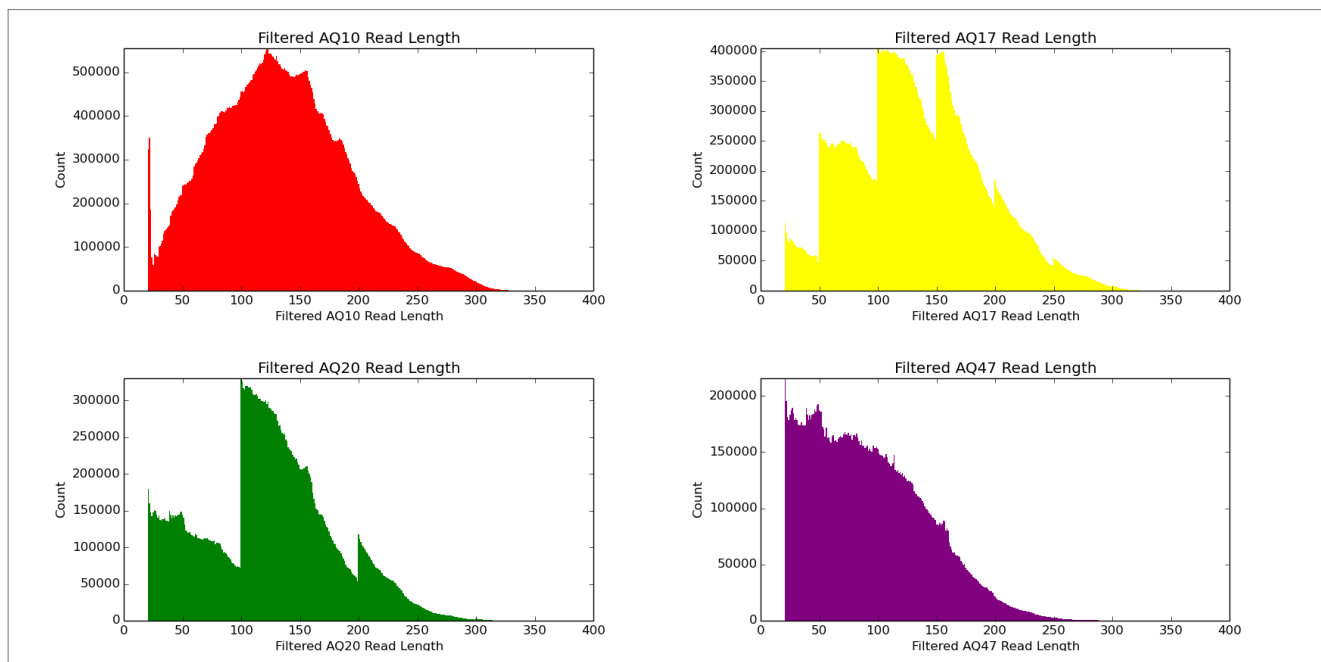
Test Fragment	Reads	Percent 50AQ17	Read Length Histogram
TF_C	453,794	90	
TF_1	248,217	92	

Alignment Summary (*aligned to Homo sapiens*)



	Alignment Quality		
	AQ17	AQ20	Perfect
Total Number of Bases [Mbp]	6.88 G	4.12 G	2.1 G
Mean Length [bp]	134	123	92
Longest Alignment [bp]	359	350	336
Mean Coverage Depth	2.2	1.3	0.7

Run Report for Auto_user_IONAS-451-DrLiakos_DrGiak_MFlabLab_200923_PL3R11-20_MF3R19-24_AG3R1r_664



Analysis Details

Run Name	R.2020_09_23_15_51_52_user_IONAS-451-DrLiakos_DrGiak_MFlabLab_200923_PL3R11-20_MF3R19-24_AG3R1r
Run Date	Sept. 23, 2020, 3:53 p.m.
Run Flows	520
Projects	DrGiakountis_3RNAseq , MFlab_3RNAseq , DrLiakos_3RNAseq
Samples	PL3R20_H-Reptin2, PL3R11_N-nonTarg-ctr1, PL3R21_H-HIF2a-2, MF3R21_GFPnew2, AG3R1r_G1, PL3R17_N-norTarg-ctr2, PL3R13_H-nonTarg-ctr1, MF3R19_GFP1, PL3R19_H-nonTarg-ctr2, PL3R16_H-HIF2aReptin1, MF3R20_GFP2, PL3R14_H-Reptin1, PL3R18_N-Reptin2, MF3R22_Prox1-1, MF3R23_Prox1-2, MF3R24_Prox1-new2, PL3R15_H-HIF2a-1, PL3R12_N-Reptin1, PL3R22_H-HIF2aReptin2
Reference	
Instrument	IONAS
Operation Mode	Customer mode
Flow Order	TACGTACGTCTGAGCATCGATCGATGTACAGC
Library Key	TCAG
TF Key	ATCG
Chip Barcode	
Chip Check	Passed
Chip Type	P1.1.17
Chip Data	tiled
Chip Lot Number	QVS135
Chip Wafer	10
Barcode Set	IonXpress
Analysis Name	Auto_user_IONAS-451-DrLiakos_DrGiak_MFlabLab_200923_PL3R11-20_MF3R19-24_AG3R1r_664
Analysis Date	Sept. 24, 2020, 4:52 a.m.
Analysis Flows	0
runID	L9Y4H
BeadFind Args	justBeadFind -args-json /opt/ion/config/args_P1.1.17_beadfind.json
Analysis Args	Analysis -args-json /opt/ion/config/args_P1.1.17_analysis.json
Pre-BaseCaller	BaseCaller -trim-qual-cutoff 15 -barcode-filter-minreads 10 -phasing-residual-filter=2.0 -max-phasing-levels 2
Calibration Args	Calibration
BaseCaller Args	BaseCaller -trim-qual-cutoff 15 -barcode-filter-minreads 10 -phasing-residual-filter=2.0 -max-phasing-levels 2 -num-unfiltered 1000 -barcode-filter-postpone 1
Alignment Args	tmap mapall ... stage1 map4
IonStats Args	ionstats alignment
Analysis Parameters	default

Chef Summary

Ion Chef was not used for this run |

Software Version

Torrent_Suite	5.12.1
host	FW7DQV1
ion-analysis	5.12.27-1
ion-dbreports	5.12.60-1
ion-gpu	5.12.1-1
ion-pipeline	5.12.17-1
ion-torrentpy	5.12.21-1
ion-torrentr	5.12.23-1
Script	2.1.46
LiveView	2514
DataCollect	3738
OIA	51206
OS	35
Graphics	134