

**Review Plan:** BoteroExperimentalEvolution003A\_2L\_HCT  
**Report:** BoteroExperimentalEvolution003A\_2L\_HCT\_p2

Application

**Application Group:** DNA  
**Sample Grouping:**  
**Target Technique:**   Generic Sequencing  
**Sample Set:**

Kits

**Sample Preparation Kit:**  
**Library Kit:** Ion Xpress Plus Fragment Library Kit  
**Library Key:** TCAG  
**3' Adapter:** ATCACCGACTGCCCATAGAGAGGCTGAGAC  
**Flow Order:** TACGTACGTCTGAGCATCGATCGATGTACAGC  
**Template Kit:** Ion PI Hi-Q Chef Kit  
**Templating Size:** 200  
**Templating Protocol:** (use instrument default)  
**Sequencing Kit:** Ion PI Hi-Q Sequencing 200 Kit  
**Control Sequence:**  
**Library Read Length:**   236  
**Flows:** 520  
**Chip Type:** Ion PI™ Chip  
**Barcode Set:** HCT\_barcode\_set\_PU  
**Mark as PCR Duplicates:** False  
**Base Calibration Mode:**   Default Calibration  
**Enable Realignment:**      False

Monitoring

**Bead Loading (%)**        ≤ 30  
**Key Signal (1-100)**     ≤ 30  
**Usable Sequence (%)** ≤ 30

Reference

**Reference Library:**  
**Target Regions:**  
**Hotspot Regions:**

Plugins & Output

**Plugins:**  
**Projects:**   BoteroExperimentalEvolution  
**Uploaders:**

Notes

LIMS Meta Data

Plan Meta Data:

**TS version when created:** 5.2.2  
**Plan created via:**           GUI

Barcodes & Samples

Sample Tube Label: 00378062  
Chip ID:

Barcode ID	Sequence	Sample Name	DNA/RNA
IonXpress_017	TCTATTCGTC	BC17	DNA
IonXpress_018	AGGCAATTGC	BC18	DNA
IonXpress_019	TTAGTCGGAC	BC19	DNA
IonXpress_020	CAGATCCATC	BC20	DNA
IonXpress_021	TCGCAATTAC	BC21	DNA
IonXpress_022	TTCGAGACGC	BC22	DNA
IonXpress_023	TGCCACGAAC	BC23	DNA
IonXpress_024	AACCTCATTC	BC24	DNA
IonXpress_025	CGTCAGATAC	BC25	DNA

Analysis Parameters Used (Custom)

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 --mixed-first-flow 12 --mixed-last-flow 120
Pre-BaseCaller Args for calibration:	BaseCaller --barcode-filter 0.01 --barcode-filter-minreads 10 --phasing-residual-filter=2.0 --max-phasing-levels 2
Calibration Args:	Calibration
BaseCaller Args:	BaseCaller --barcode-filter 0.01 --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

History

Date	User
Aug. 4, 2017,	ionuser
Created Planned Run: BoteroExperimentalEvolution003A_HCT (397)	
2:08 p.m.	

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irOptions	0
projects	BoteroExperimentalEvolution
isSameRefInfoPerSample	True
irVersion	None

Aug.  
4,  
2017, ionuser Updated Planned Run: BoteroExperimentalEvolution003A\_HCT (397).  
2:09  
p.m.

Parameter	Old Value
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Aug.  
7,  
2017, ionuser samplesTable  
2:31  
p.m.

[illegible]

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isSameRefInfoPerSample True on

Parameter	Old Value	
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Aug.  
8,  
2017, ionuser  
8:31  
a.m.

Updated Planned Run: BoteroExperimentalEvolution003A\_2L\_HCT (397).

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isSameRefInfoPerSample True

on

Parameter	Old Value	New Value
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platform		PROTON
storageHost		localhost
expName		R_2017_08_08_09_44_54_user_sn247770187-267-BoteroExperimentalEvolution003A_2L_HCT
sequencekitbarcode		20071
usePreBeadfind	True	
reverse_primer	None	Ion Kit
cycles	0	16
seqKitBarcode		20071

Aug.  
8,  
2017, system  
9:53  
a.m.

Updated Planned Run from explog: BoteroExperimentalEvolution003A\_2L\_HCT (397).

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[illegible]

Aug.  
8,  
2017, ionuser samplesTable  
1:35  
p.m.

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isSameRefInfoPerSample True on

Aug.  
8,  
2017, ionuser Updated Run: BoteroExperimentalEvolution003A\_2L\_HCT (397).  
1:35  
p.m.

Parameter	Old Value
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Aug.  
8,  
2017, 1:36  
p.m.

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```

x

View Plugin Configuration

isSameRefInfoPerSample True on

Aug.  
8,  
2017, ionuser Updated Run: BoteroExperimentalEvolution003A\_2L\_HCT (397).  
1:36  
p.m.

[Close](#)