

# First 10X Chromium run

Sequenced on HiSeq X, analyzed with LongRanger on Irma

Sample requirements: 5 ng/ $\mu$ L in 30  $\mu$ L. Only 2 ng is used per run.

Well	Sample	Reads (M)	Median insert size (bp)	Mean depth	Average input molecule length (kb)	SNPs phased	Longest phase block (Mb)	N50 phase block (Mb)
1	User sample 1	627	301	26	51	0,983	8,6	2,0
2	User sample 2	698	296	28	23	0,981	4,3	0,5
3	User sample 3	769	274	22	7	<b>0,908</b>	<b>0,7</b>	0,1
4	User sample 4	795	323	34	36	0,958	5,4	1,0
5	User sample 5	748	333	31	35	0,984	6,3	0,9
6	GM12878 A	670	299	28	<b>105</b>	<b>0,955</b>	<b>31,3</b>	8,2
7	GM12878 B	632	311	26	<b>70</b>	<b>0,955</b>	<b>22,2</b>	4,0
8	10X control	577	300	26	63	0,909	0,4	0,6
Ref 1	NA12878	844	340	35	73	0,99	18,0	3,4
Ref 2	HCC1954N	84	211	72	80	0,973	1,0	0,1

Supernova N50 13.16 Mb  
Longest scaffold - 56.2 Mb  
Number of scaffolds – 67 355  
( $\geq$  10 kb - 3097)

## Conclusions:

Successful first run

Input length strongly affect the results

DNA extraction method matters

We extracted the best! (Wells 6 & 7)