

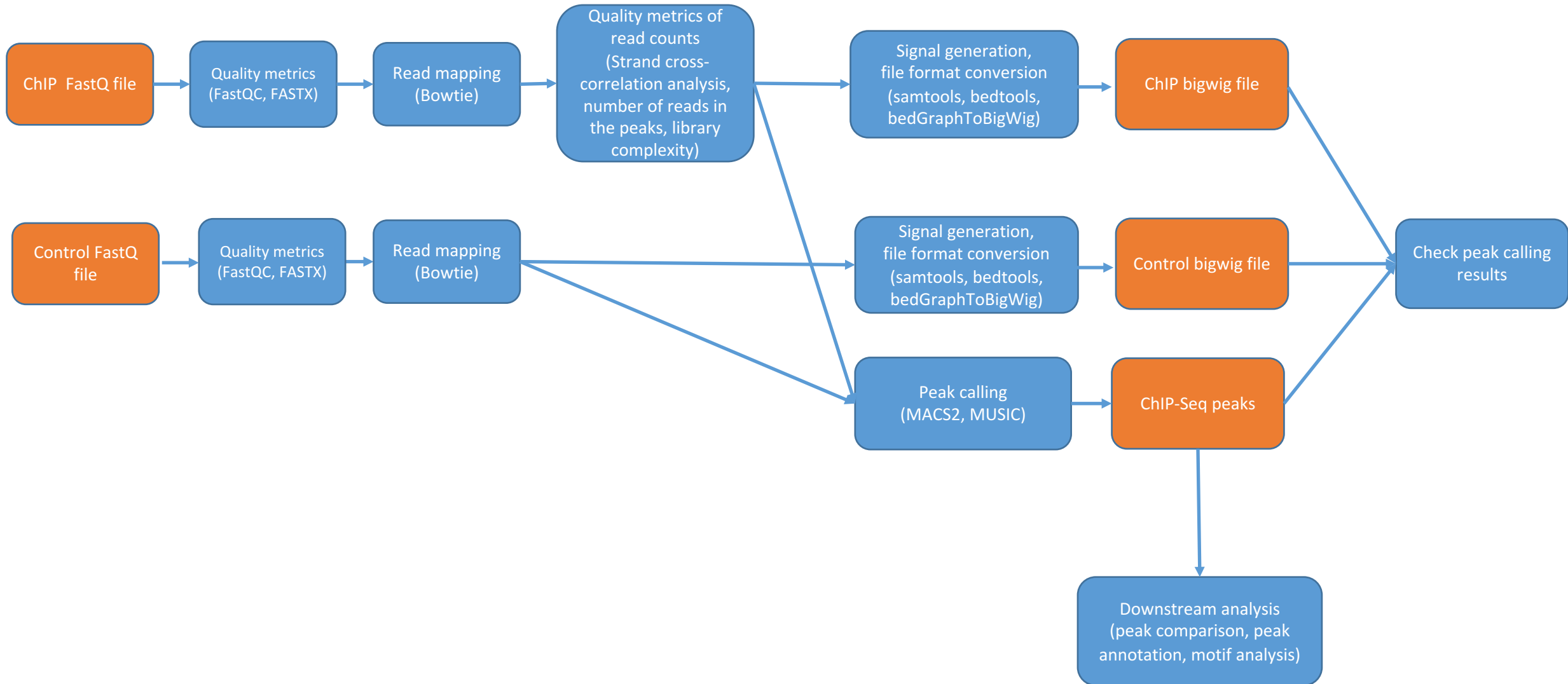
iPSc ChIP-Seq results updates

Shuang Liu
Gerstein Lab
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iPSc ChIP-seq datasets Fetal 320

FileName	ID	Clone #	Stage	CellType	Passage	TD	Mark
54	320	N/A	Fetal	brain FR CP	N/A	N/A	INPUT
55	320	N/A	Fetal	brain FR CP	N/A	N/A	H3K4me3
56	320	7	Fetal	DIF	20	11	H3K27ac
57	320	N/A	Fetal	brain FR SVZ\VZ	N/A	N/A	H3K27ac
58	320	13	Fetal	DIF	16	0	INPUT
59	320	7	Fetal	DIF	21	30	H3K4me3
60	320	13	Fetal	DIF	16	30	INPUT
61	320	7	Fetal	DIF	21	0	INPUT
62	320	13	Fetal	DIF	19	11	INPUT
63	320	13	Fetal	DIF	16	30	H3K27ac
64	320	7	Fetal	DIF	21	0	H3K4me3
65	320	N/A	Fetal	brain FR CP	N/A	N/A	H3K27ac
66	320	7	Fetal	DIF	20	11	INPUT
67	320	N/A	Fetal	brain FR SVZ\VZ	N/A	N/A	H3K4me3
68	320	13	Fetal	DIF	19	11	H3K27ac
69	320	7	Fetal	DIF	21	30	H3K27ac
70	320	7	Fetal	DIF	21	0	H3K27ac
71	320	13	Fetal	DIF	16	0	H3K27ac
72	320	7	Fetal	DIF	21	30	INPUT
73	320	7	Fetal	DIF	20	11	H3K4me3
74	320	13	Fetal	DIF	19	11	H3K4me3
75	320	13	Fetal	DIF	16	0	H3K4me3
76	320	13	Fetal	DIF	16	30	H3K4me3
77	320	N/A	Fetal	brain FR SVZ\VZ	N/A	N/A	INPUT

ChIP-Seq analysis pipeline

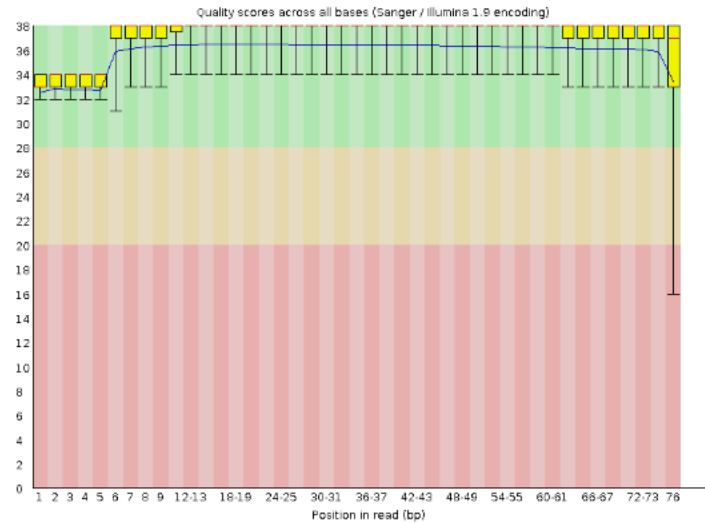


FASTQC

Basic Statistics

Measure	Value
Filename	Fetal.320.7.56.DIF.11.H3K27ac.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	81965672
Sequences flagged as poor quality	0
Sequence length	76
%GC	45

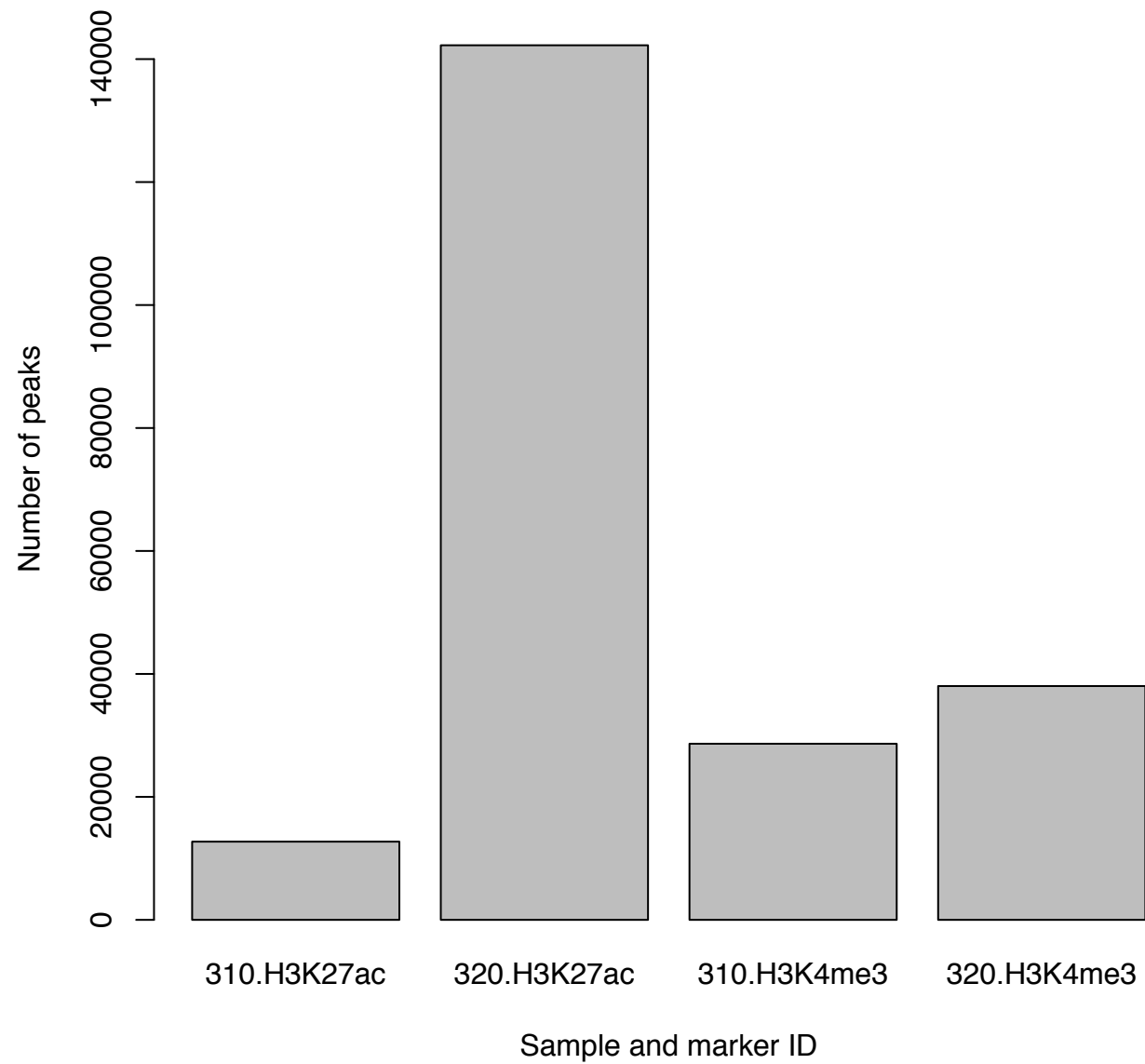
Per base sequence quality



Alignment using bowtie2

File name	Alignment results
Fetal.320.54.CP.INPUT	59267502 reads; of these: 59267502 (100.00%) were unpaired; of these: 1857631 (3.13%) aligned 0 times 44097974 (74.40%) aligned exactly 1 time 13311897 (22.46%) aligned >1 times 96.87% overall alignment rate
Fetal.320.55.CP.H3K4me3	60316388 reads; of these: 60316388 (100.00%) were unpaired; of these: 926117 (1.54%) aligned 0 times 53150914 (88.12%) aligned exactly 1 time 6239357 (10.34%) aligned >1 times 98.46% overall alignment rate
Fetal.320.65.CP.H3K27ac	50537812 reads; of these: 50537812 (100.00%) were unpaired; of these: 462400 (0.91%) aligned 0 times 44431985 (87.92%) aligned exactly 1 time 5643427 (11.17%) aligned >1 times 99.09% overall alignment rate

Fetal Brain FR CP ChIP-seq peaks by MACS2



iPSc ChIP-seq datasets Reference brain

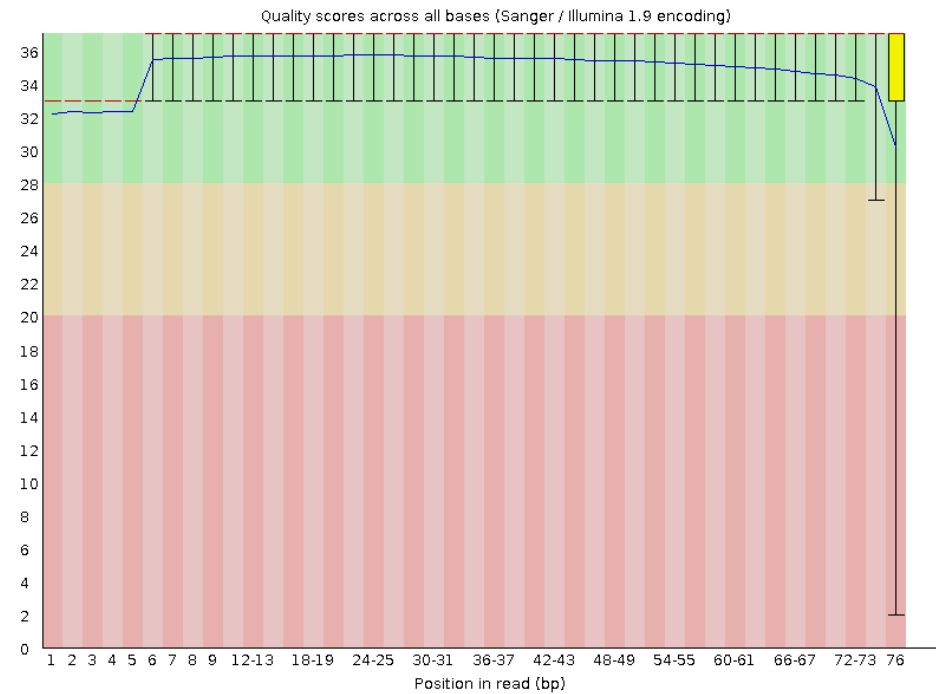
FileName	ID	Clone #	Stage	CellType	Passage	TD	Mark	CellFraction
94	HSB277 Sinai sorted	N/A	Adult	Ref brain	N/A	N/A	INPUT	NeuN-
95	HSB277 Sinai sorted	N/A	Adult	Ref brain	N/A	N/A	H3K4me3	NeuN+
96	HSB277 Sinai sorted	N/A	Adult	Ref brain	N/A	N/A	H3K4me3	NeuN-
97	HSB277 Yale sorted	N/A	Adult	Ref brain	N/A	N/A	INPUT	NeuN+
98	HSB277 Yale sorted	N/A	Adult	Ref brain	N/A	N/A	H3K27ac	NeuN+
99	HSB277 Yale sorted	N/A	Adult	Ref brain	N/A	N/A	H3K27ac	NeuN-
100	HSB 181	N/A	Adult	Ref brain	N/A	N/A	INPUT	NeuN+
101	HSB 181	N/A	Adult	Ref brain	N/A	N/A	H3K4me3	NeuN+
102	HSB 189	N/A	Adult	Ref brain	N/A	N/A	H3K4me3	NeuN+
103	HSB 106	N/A	Adult	Ref brain	N/A	N/A	H3K27ac	NeuN-
104	HSB 189	N/A	Adult	Ref brain	N/A	N/A	INPUT	NeuN+
105	HSB 181	N/A	Adult	Ref brain	N/A	N/A	H3K4me3	NeuN-
106	HSB 106	N/A	Adult	Ref brain	N/A	N/A	H3K4me3	NeuN-
107	HSB 181	N/A	Adult	Ref brain	N/A	N/A	H3K27ac	NeuN-
108	HSB 106	N/A	Adult	Ref brain	N/A	N/A	INPUT	NeuN-
109	HSB 189	N/A	Adult	Ref brain	N/A	N/A	H3K27ac	NeuN+
110	HSB 189	N/A	Adult	Ref brain	N/A	N/A	H3K4me3	NeuN-
111	HSB 181	N/A	Adult	Ref brain	N/A	N/A	H3K27ac	NeuN+
112	HSB 181	N/A	Adult	Ref brain	N/A	N/A	INPUT	NeuN-
113	HSB 106	N/A	Adult	Ref brain	N/A	N/A	H3K27ac	NeuN+
114	HSB 189	N/A	Adult	Ref brain	N/A	N/A	H3K27ac	NeuN-
115	HSB 106	N/A	Adult	Ref brain	N/A	N/A	H3K4me3	NeuN+
116	HSB 106	N/A	Adult	Ref brain	N/A	N/A	INPUT	NeuN+
117	HSB 189	N/A	Adult	Ref brain	N/A	N/A	INPUT	NeuN-

FASTQC

Basic Statistics

Measure	Value
Filename	HSB277_Yale.98.NeuN+.H3K27ac.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	37294186
Sequences flagged as poor quality	0
Sequence length	76
%GC	41

Per base sequence quality



Alignment using bowtie2

File name	Alignment results
HSB277_Sinai.94.NeuN-.INPUT	52895193 reads; of these: 52895193 (100.00%) were unpaired; of these: 1222292 (2.31%) aligned 0 times 44883391 (84.85%) aligned exactly 1 time 6789510 (12.84%) aligned >1 times 97.69% overall alignment rate
HSB277_Sinai.96.NeuN-.H3K4me3	49980569 reads; of these: 49980569 (100.00%) were unpaired; of these: 1391228 (2.78%) aligned 0 times 41245649 (82.52%) aligned exactly 1 time 7343692 (14.69%) aligned >1 times 97.22% overall alignment rate
HSB277_Yale.97.NeuN+.INPUT	37995271 reads; of these: 37995271 (100.00%) were unpaired; of these: 1364216 (3.59%) aligned 0 times 29205417 (76.87%) aligned exactly 1 time 7425638 (19.54%) aligned >1 times 96.41% overall alignment rate
HSB277_Yale.98.NeuN+.H3K27ac	37084139 reads; of these: 37084139 (100.00%) were unpaired; of these: 1736224 (4.68%) aligned 0 times 27824607 (75.03%) aligned exactly 1 time 7523308 (20.29%) aligned >1 times 95.32% overall alignment rate

Adult brain CHIP-seq peaks by MACS2

