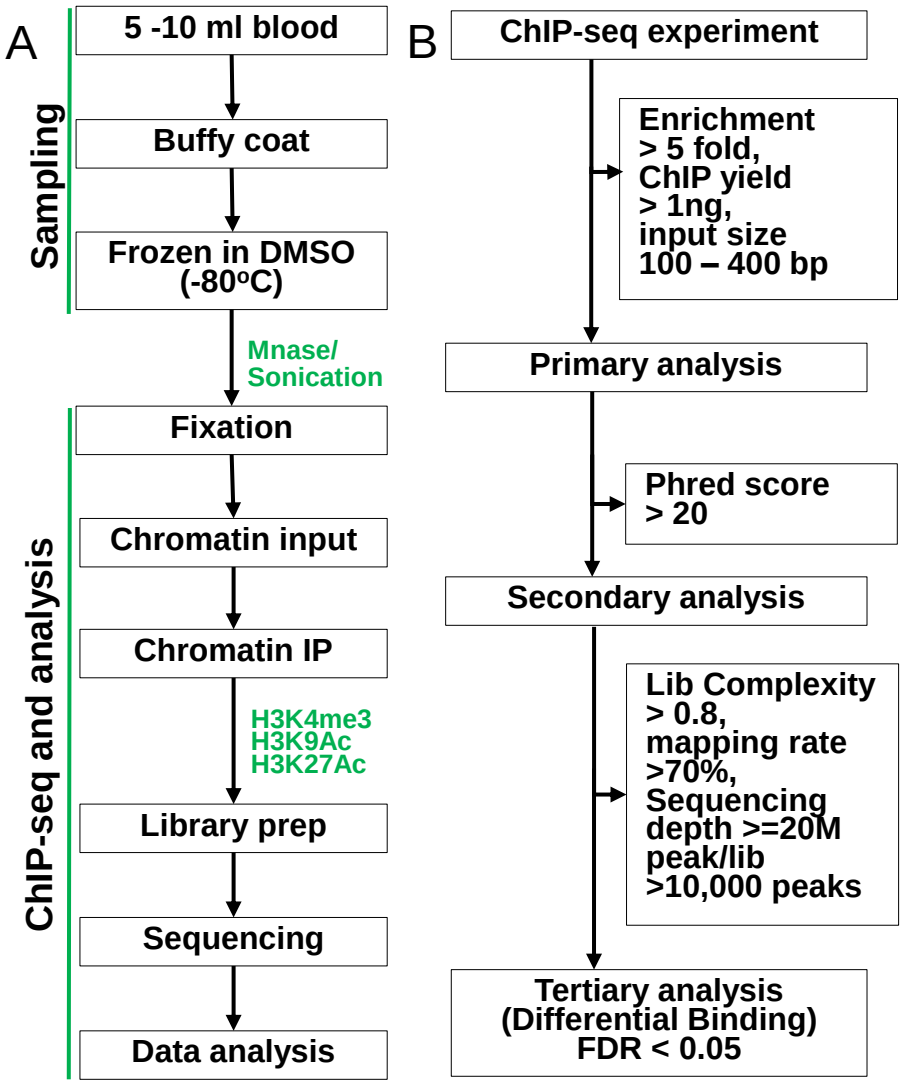
A
Sampling
5 -10 ml blood
Buffy coat
Frozen in DMSO
(-80ºC)
Mnase/
Sonication
ChIP-seq and analysis
Fixation
Chromatin input
Chromatin IP
H3K4me3
H3K9Ac
H3K27Ac
Library prep
Sequencing
Data analysis
B
ChIP-seq experiment
Enrichment
> 5 fold,
ChIP yield
> 1ng,
input size
100 – 400 bp
Primary analysis
Phred score
> 20
Secondary analysis
Lib Complexity
> 0.8,
mapping rate
>70%,
Sequencing
depth >=20M
peak/lib
>10,000 peaks
Tertiary analysis
(Differential Binding)
FDR < 0.05