DROSOPHILA CHIP-SEQ UPDATE

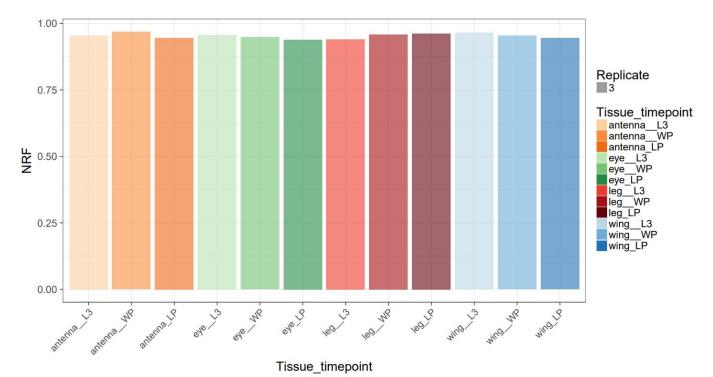
Sílvia, Cecilia, Marina 11/07/2018

OVERVIEW

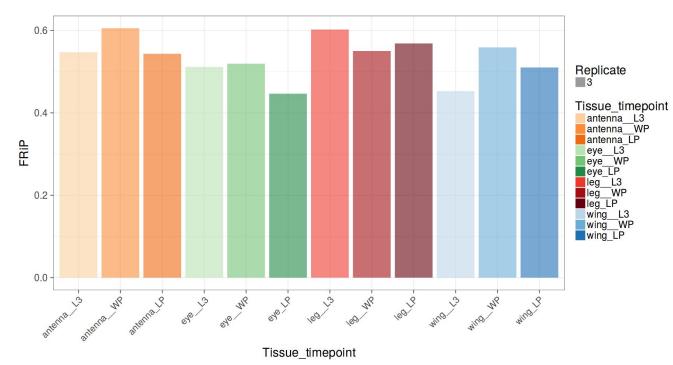
- H3K9me3: QC and results
- H4K20me1: QC and results
- Quantile normalization
- ChIP protocol trial in low input human cells:
 - Protocol
 - Trial
 - QC and results

H3K9ME3

NRF(non redundancy fraction): >0.8

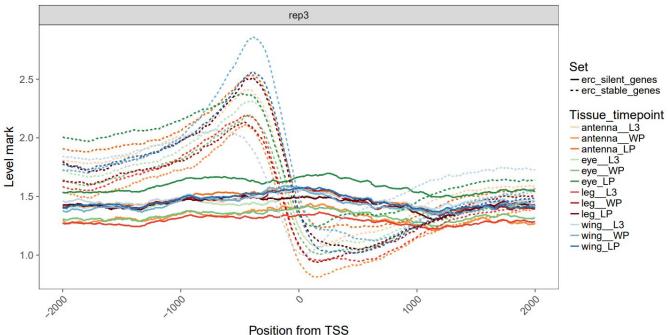


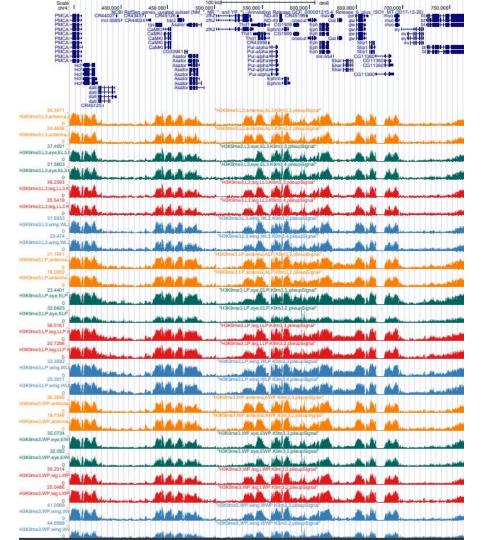
FRiP(fraction of reads in peaks): >0.8



Aggregation plot

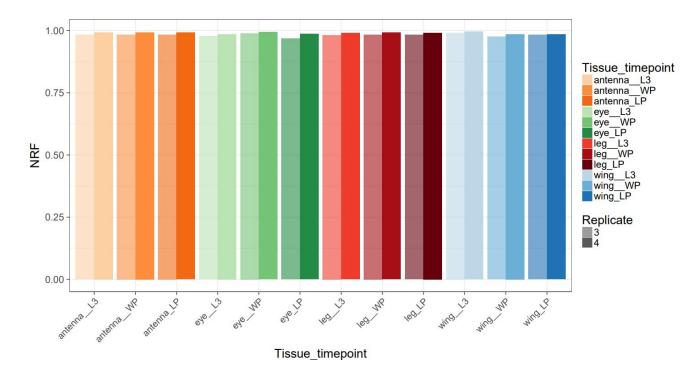
H3K9me3



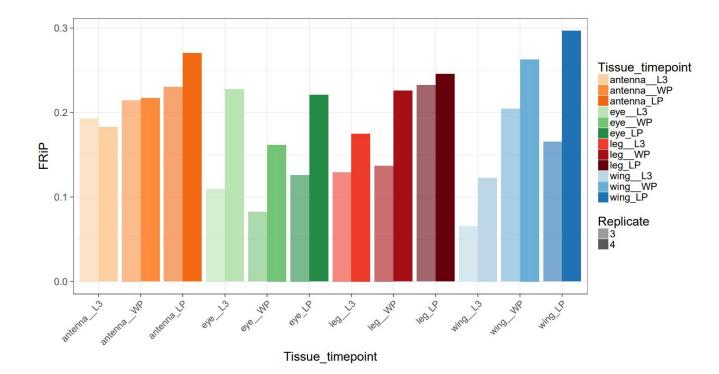


H4K20ME1

NRF(non redundancy fraction): >0.8

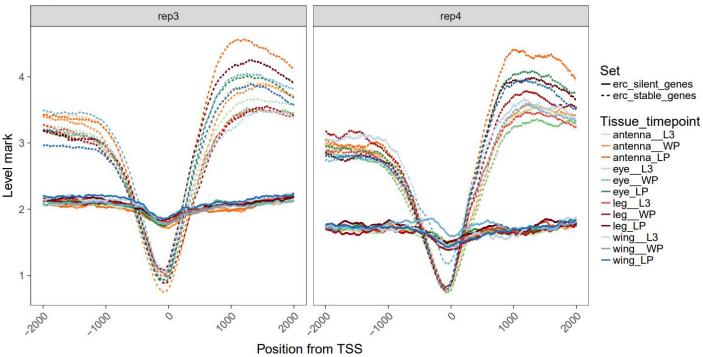


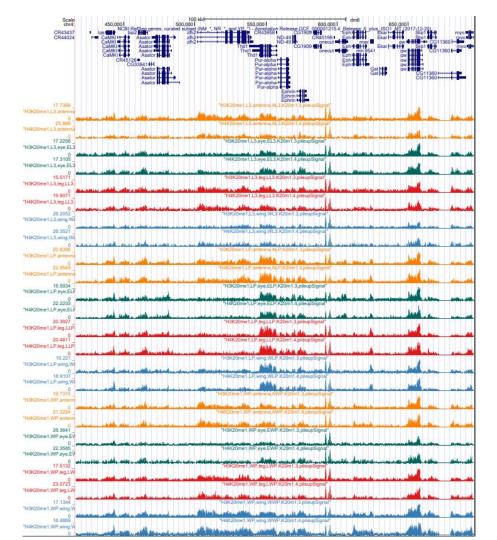
FRiP(fraction of reads in peaks): >0.8



Aggregation plot

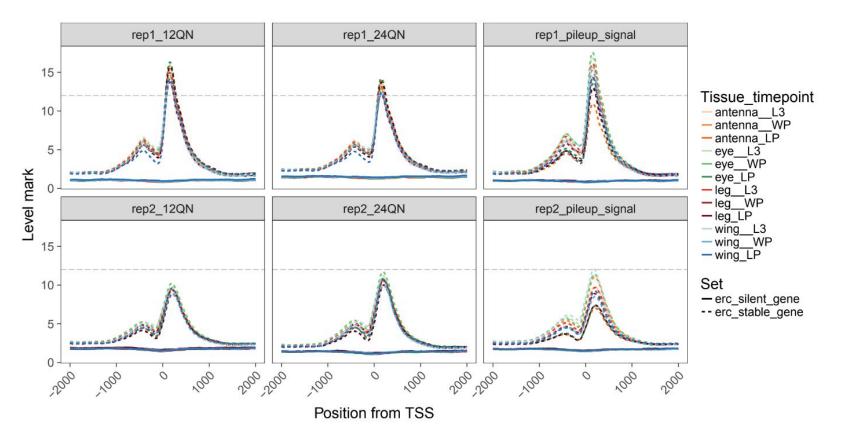
H4K20me1





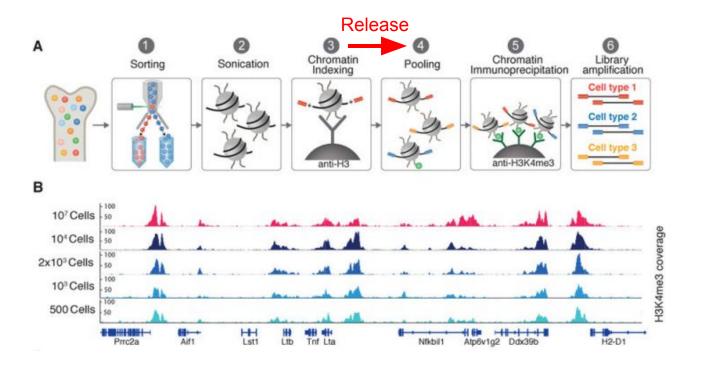
QUANTILE NORMALIZATION TEST

QUANTILE NORMALIZATION TEST: H3K27AC

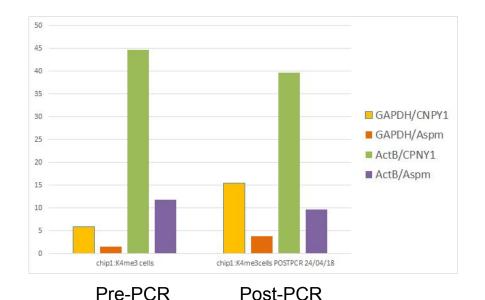


CHIP PROTOCOL TRIAL: LOW INPUT HUMAN CELLS

ICHIP PROTOCOL FROM LARA-ASTIASO ET AL. 2014

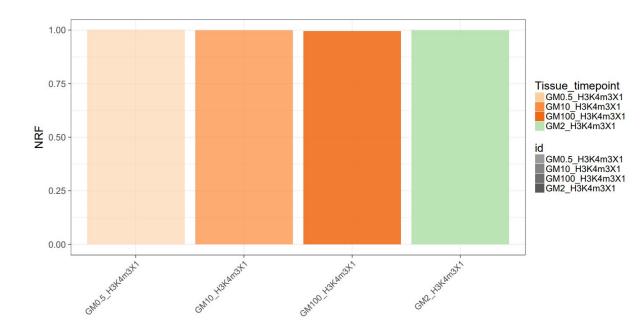


qPCR: Chip against H3K4me3 in a pool of 100.000, 10.000, 2.000 and 500 cells

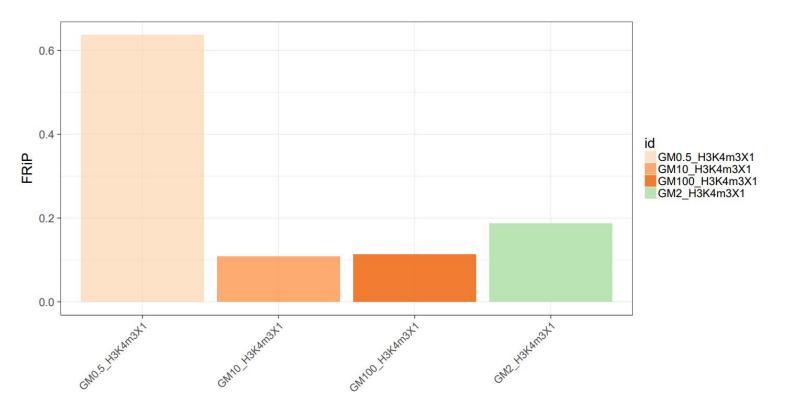


Positive regions: GAPDH and ActB Negative regions: CPNY1 and Aspm

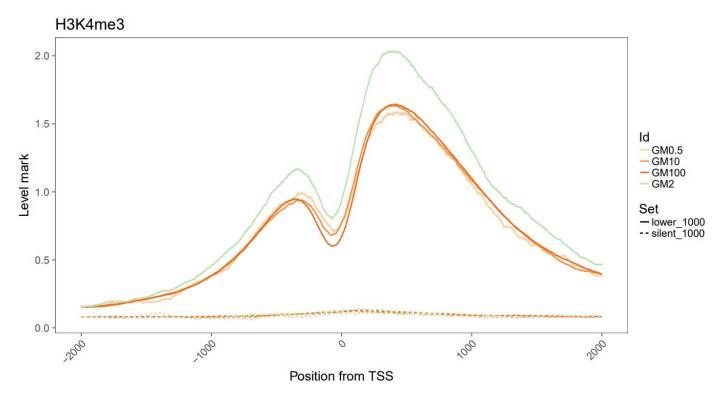
NRF(non redundancy fraction): >0.8



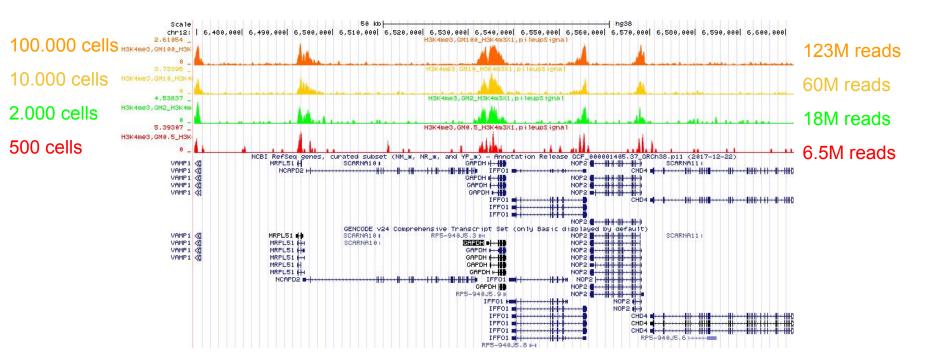
FRiP(fraction of reads in peaks): >0.8



Aggregation plot



Chip against H3K4me3 in 100.000, 10.000, 2.000 and 500 cells Run in 1 lane (200 million reads)



EXTRA SLIDES

