Chipseq QC - aggregation plots and correlation between replicates

20/04/2016

Outline

Status samples

H3K4me1

H3K4me2

H3K4me3

H3K9ac

H3K9me3

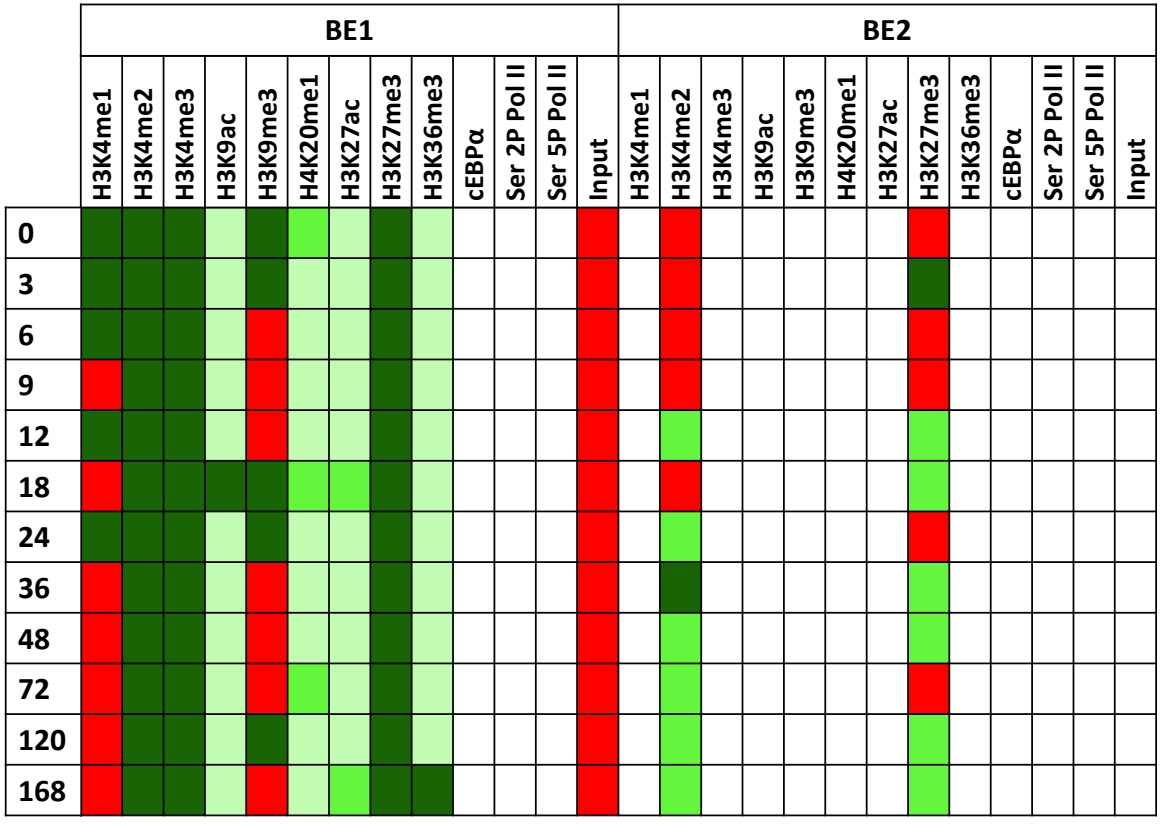
H3K27ac

H3K27me3

H3K36me3

Samples

ChIP update

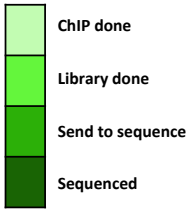


New samples sequenced:

BE1:
H3K4me1: all samples
H3K9me3: all samples

BE2:
H3K4me2: 5 more
H3K27me3: 6 more

Input



Outline

Status samples

H3K4me1

Mapping stats

Aggregation plots

NRF and FRiP

H3K4me2

H3K4me3

H3K9ac

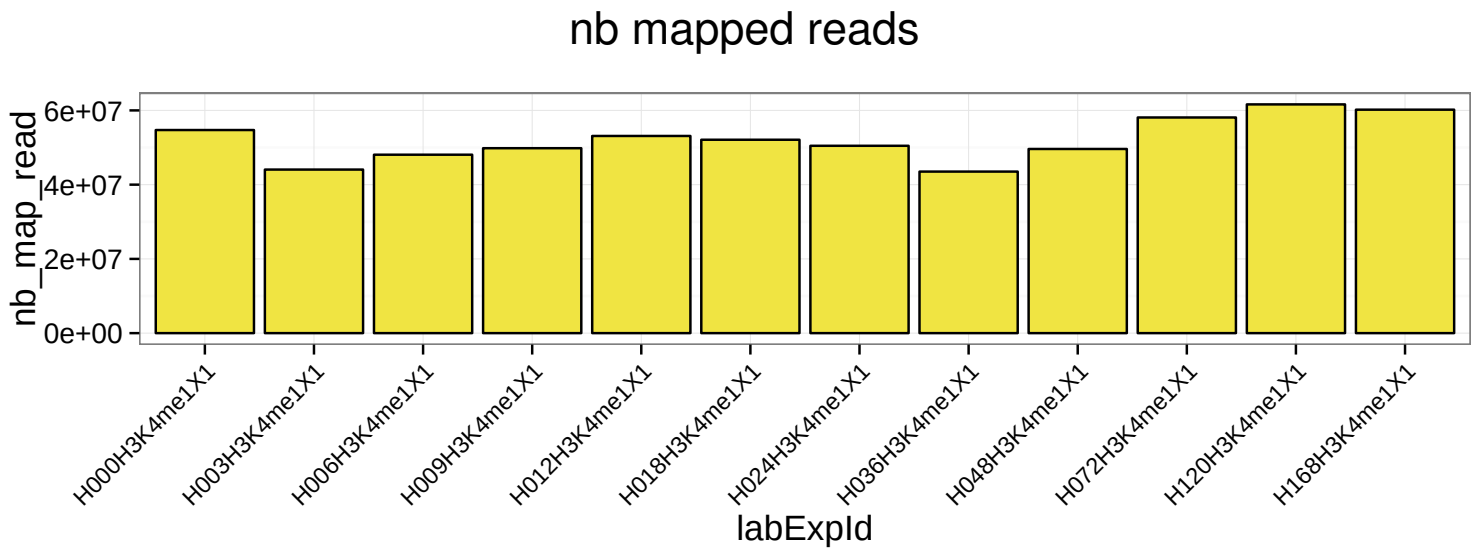
H3K9me3

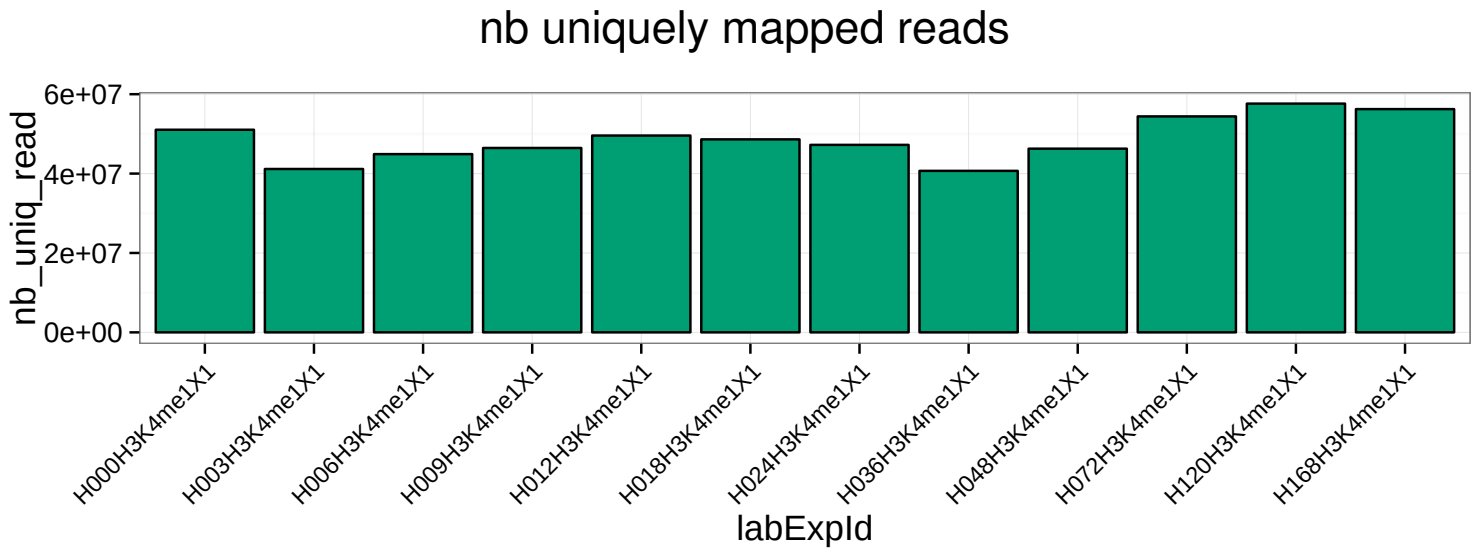
H3K27ac

H3K27me3

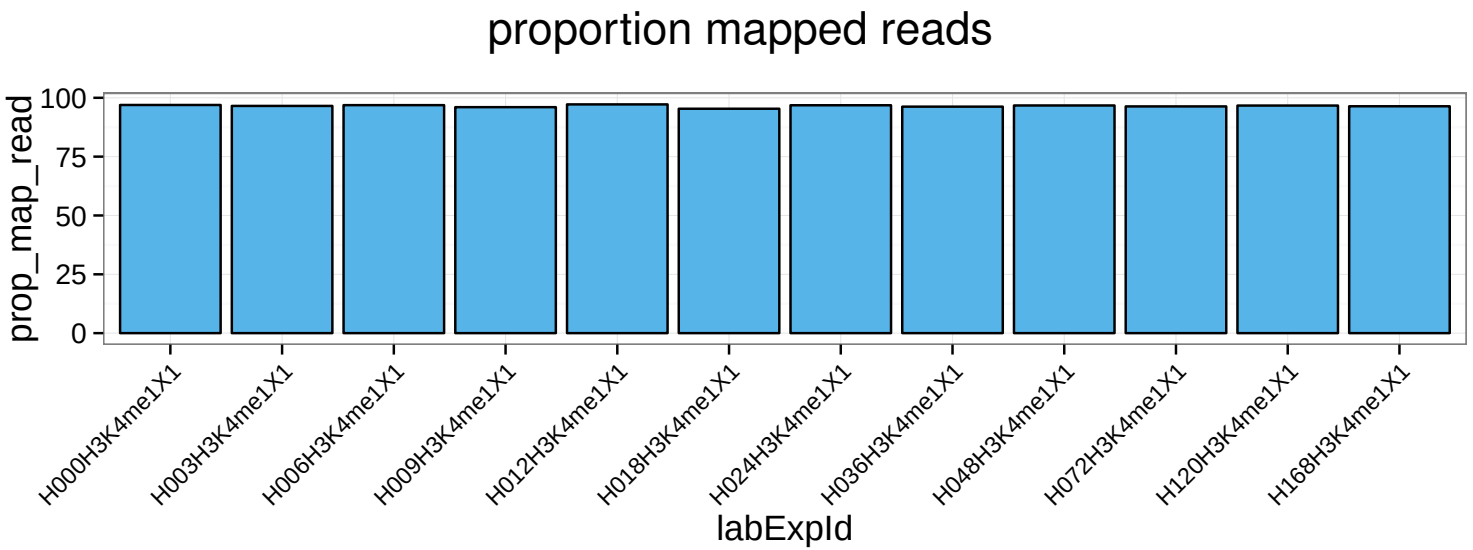
H3K36me3

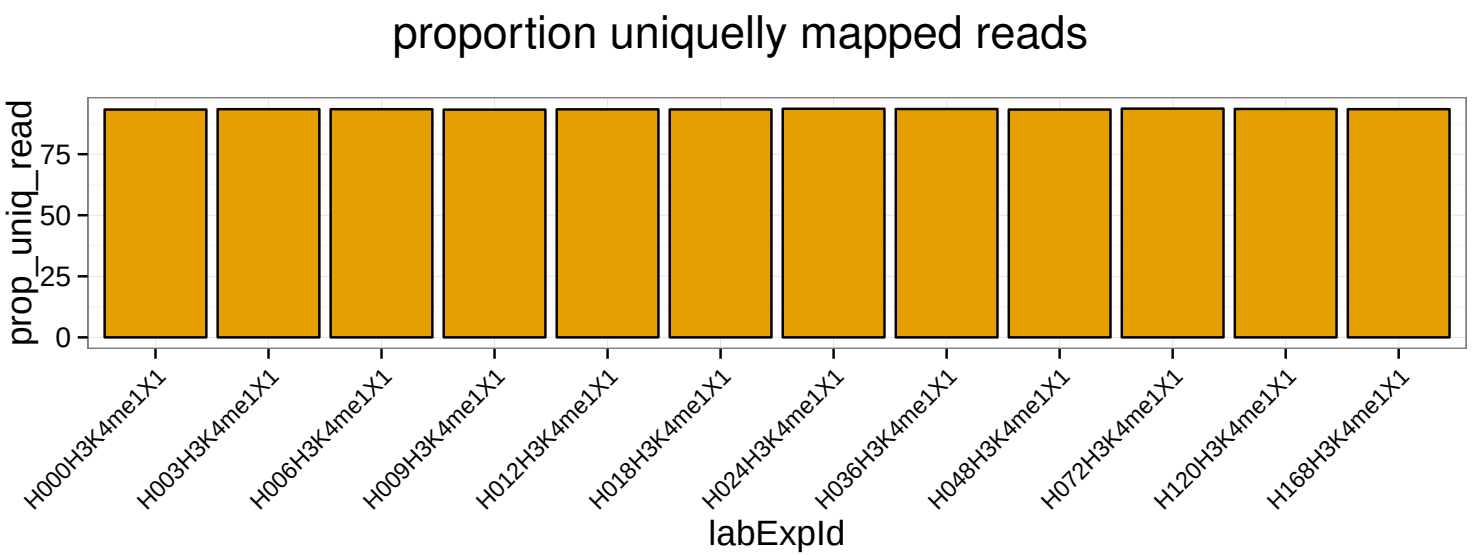
H3K4me1 - mapping stats





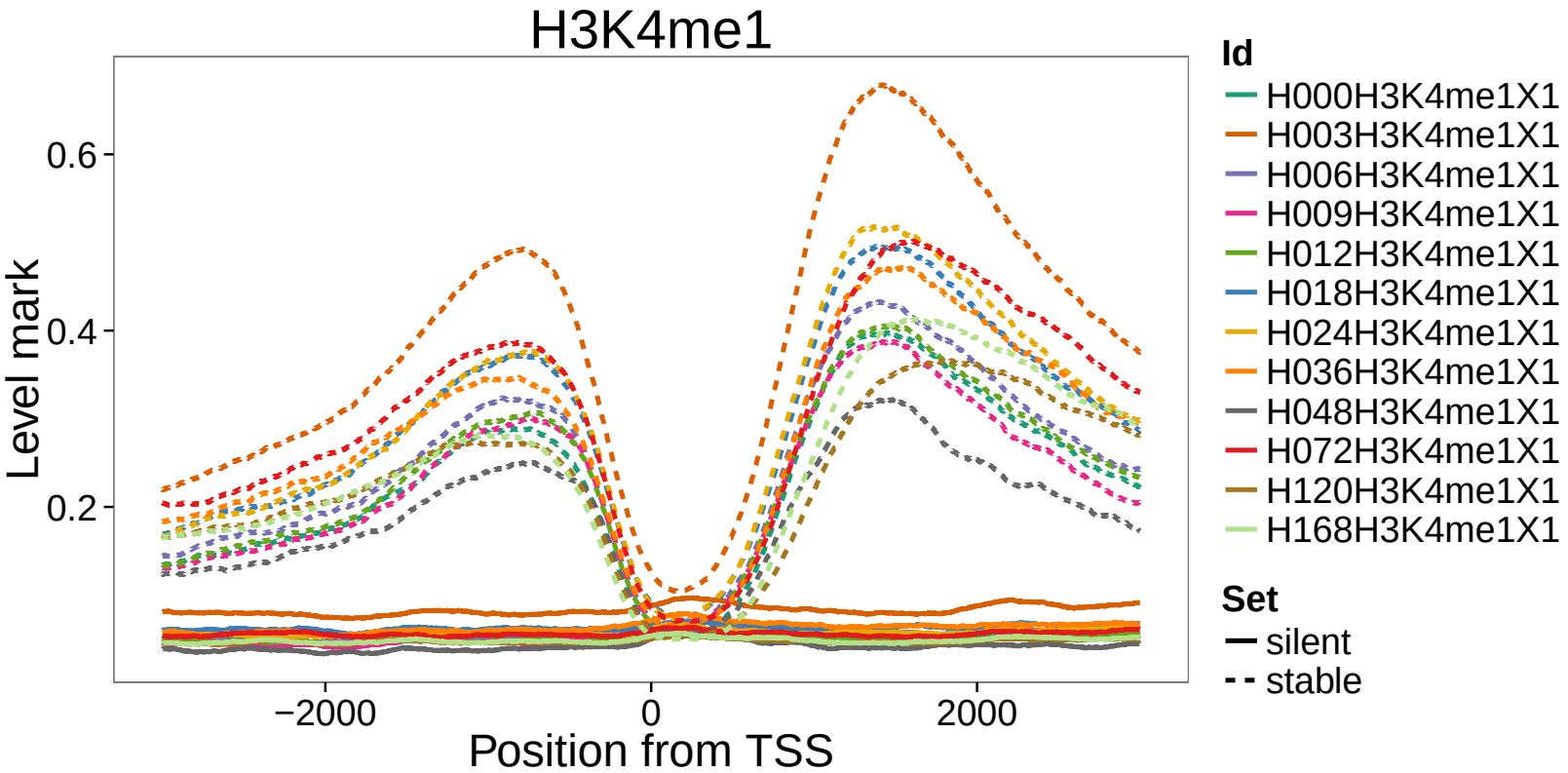
H3K4me1 - mapping stats





H3K4me1

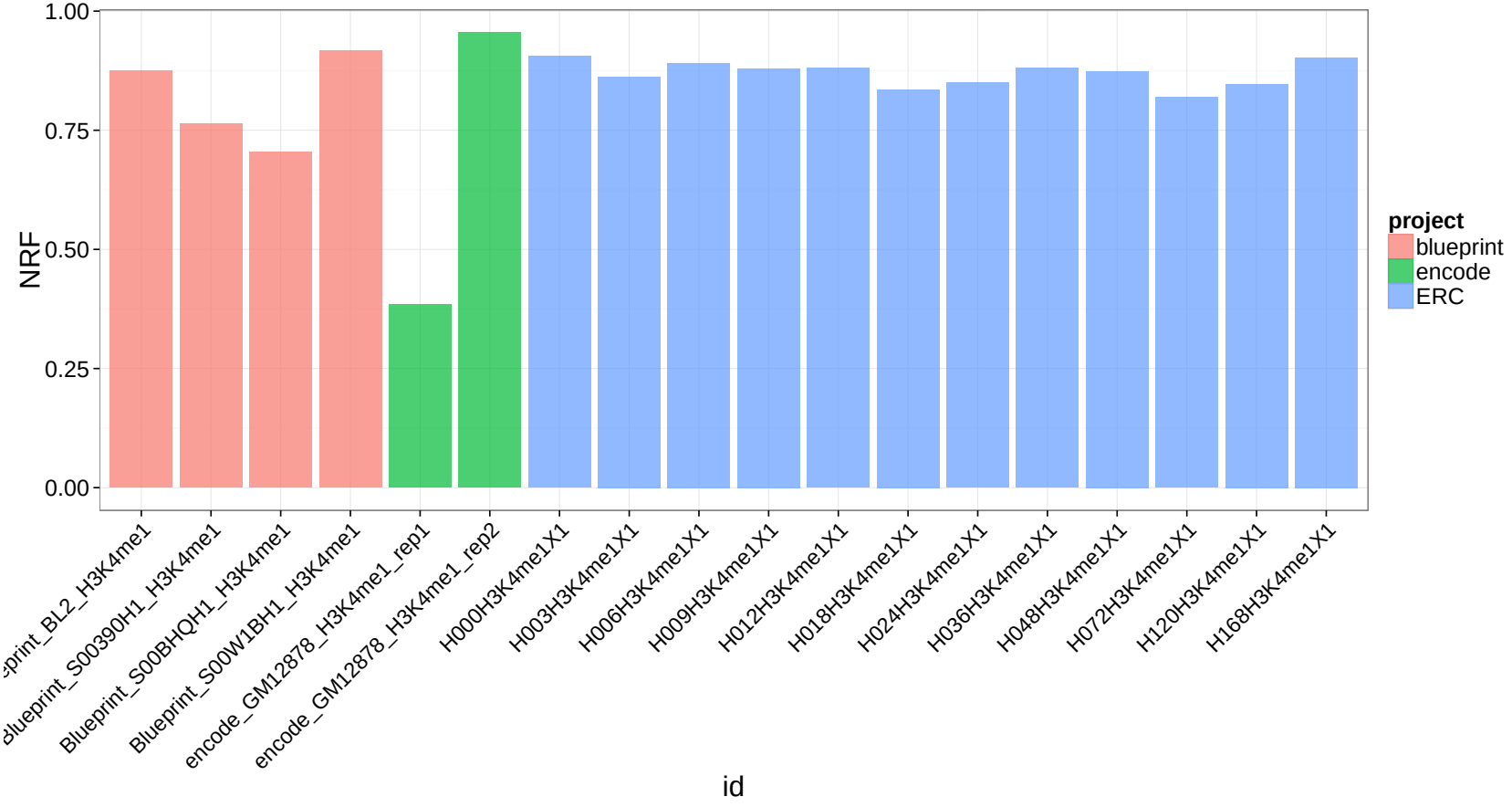
- 1000 silent genes
- 1000 stable genes (lowest CV)
- gencode v24



H3K4me1 - NRF

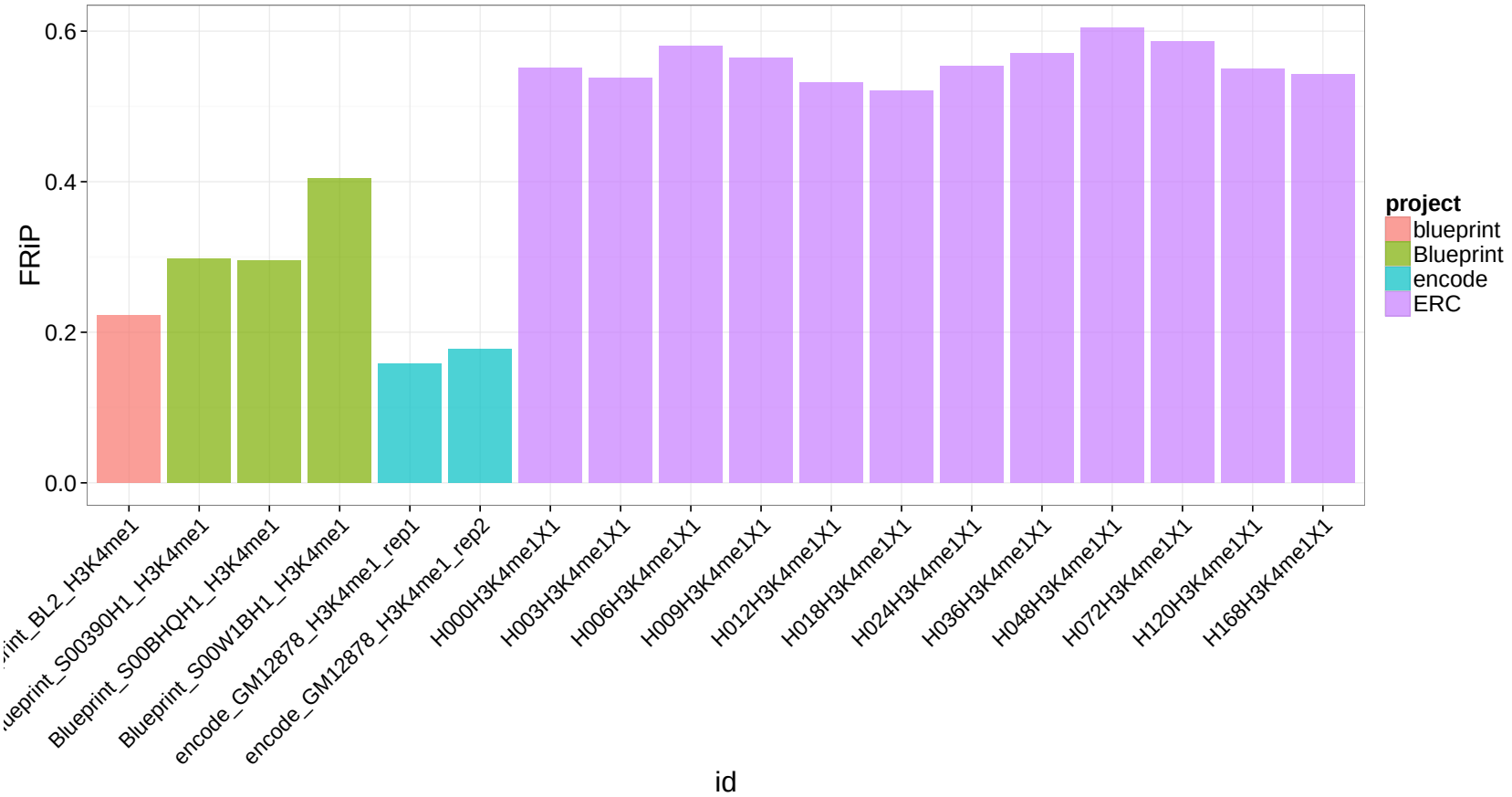
NRF: nonredundant fraction

NRF= nb unique start positions of uniquely mappable reads/nb uniquely mappable reads

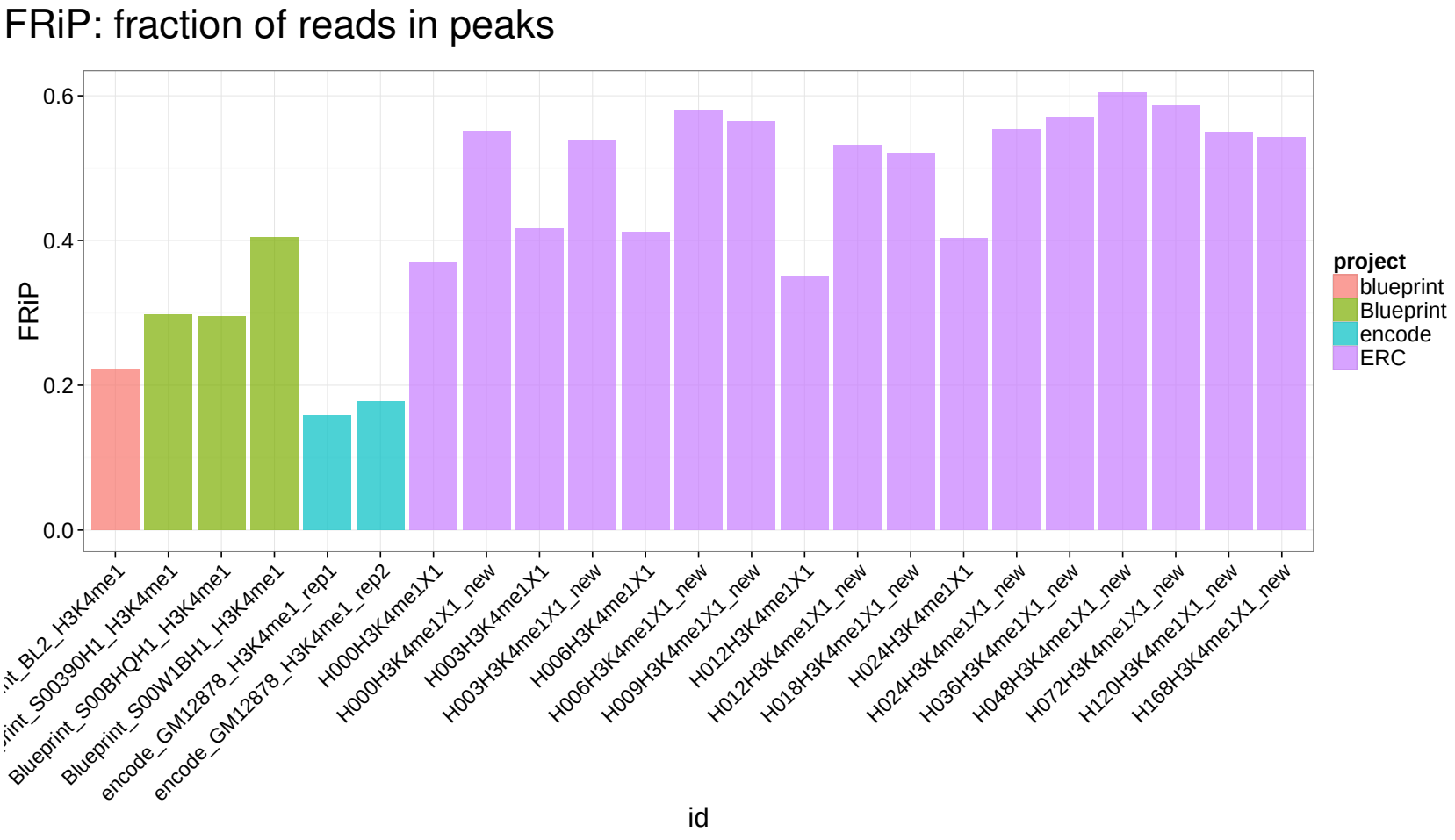


H3K4me1 - FRiP

FRiP: fraction of reads in peaks



H3K4me1 - FRiP (compare old VS new input)



H3K4me1 - 36h: problem sequencing

1. due to bubbles in the flowcell (lane 6) approx. 15% of the reads have lower quality.
2. for sample 13387 we do not reach the requested 40 M good quality reads
3. Please let us know if you need more reads.

Outline

Status samples

H3K4me1

H3K4me2

- Mapping stats
- Aggregation plots
- Correlation between replicates
- NRF and FRiP

H3K4me3

H3K9ac

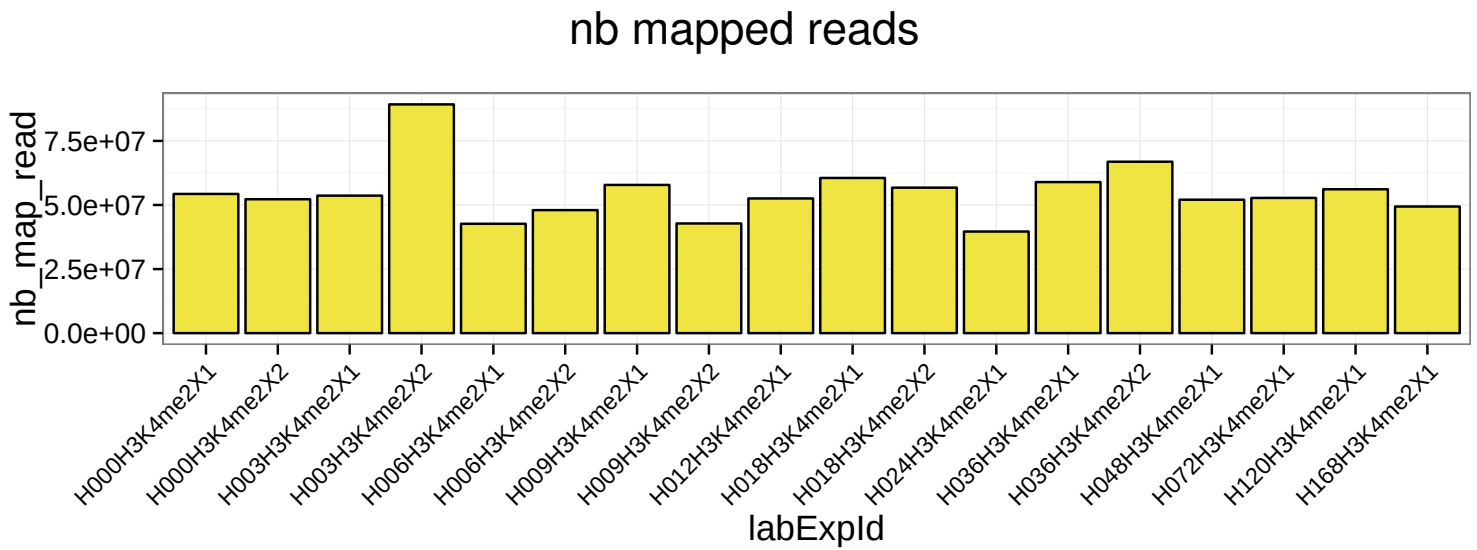
H3K9me3

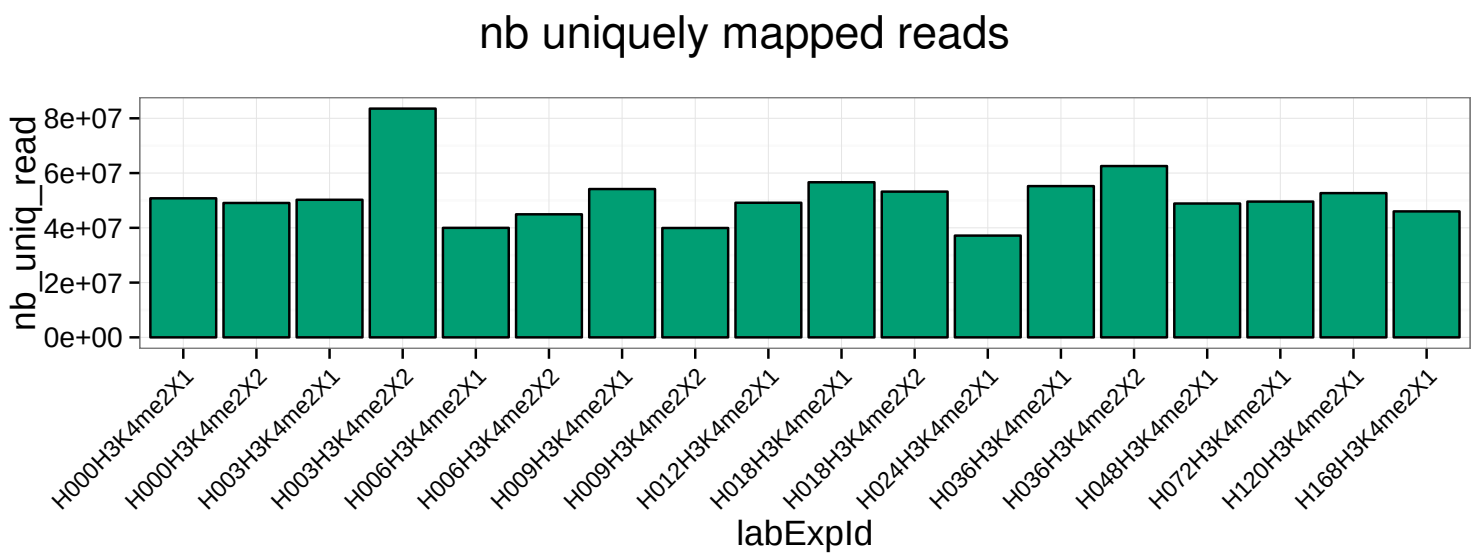
H3K27ac

H3K27me3

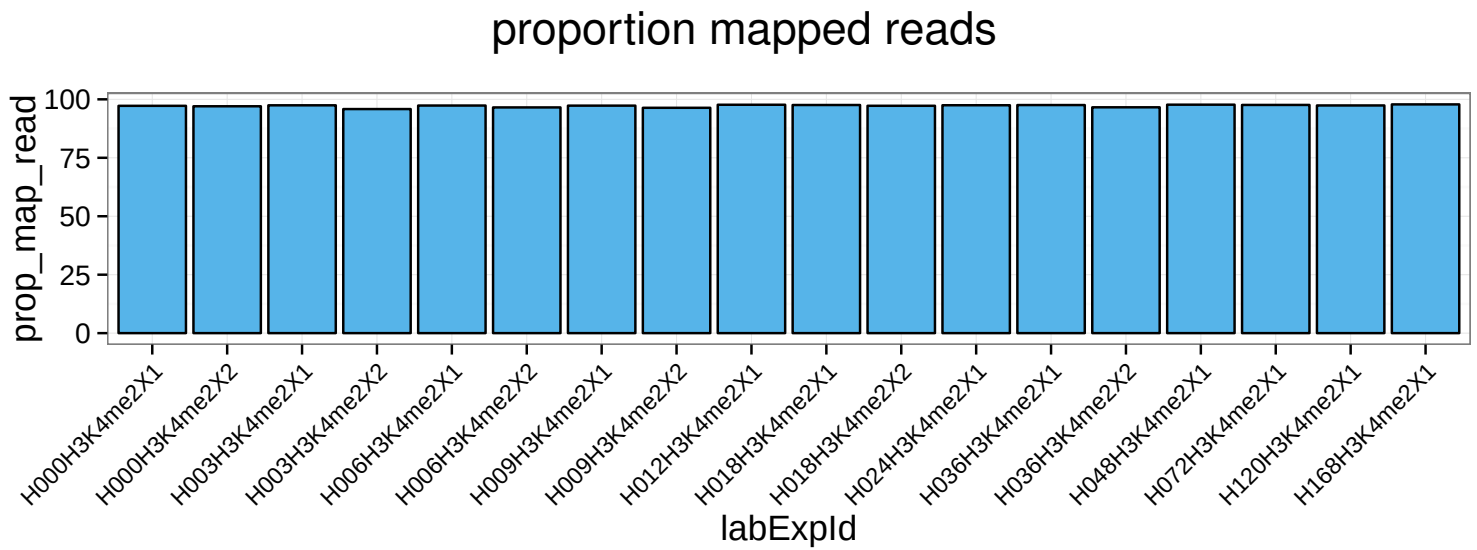
H3K36me3

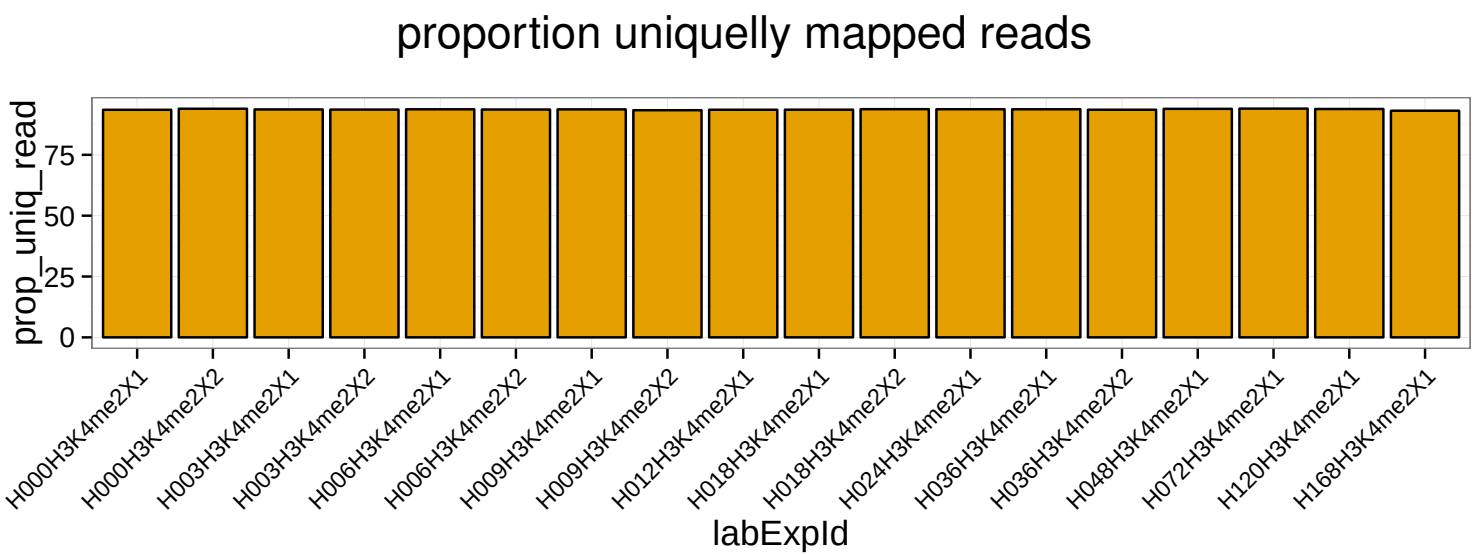
H3K4me2 - mapping stats





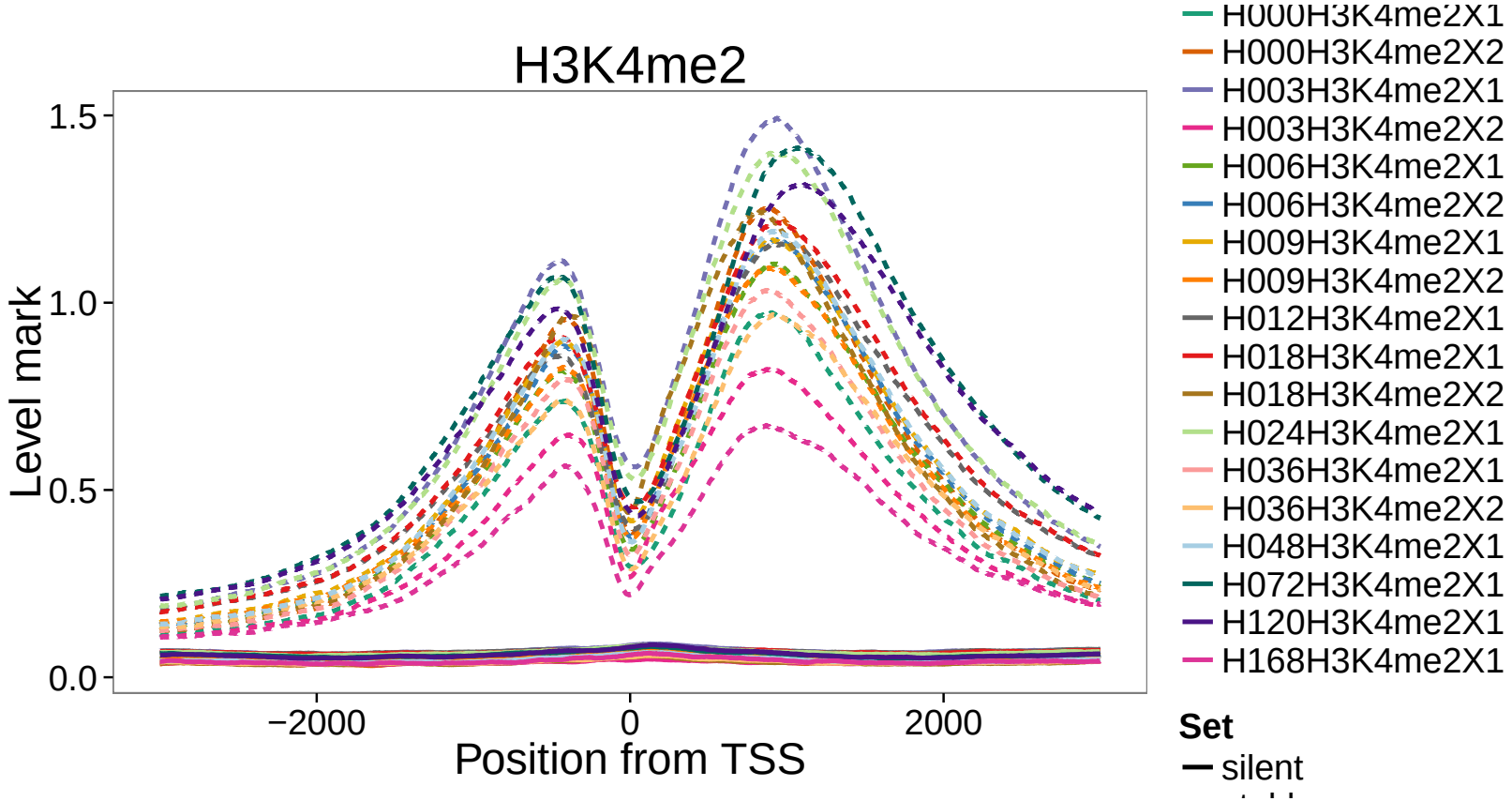
H3K4me2 - mapping stats





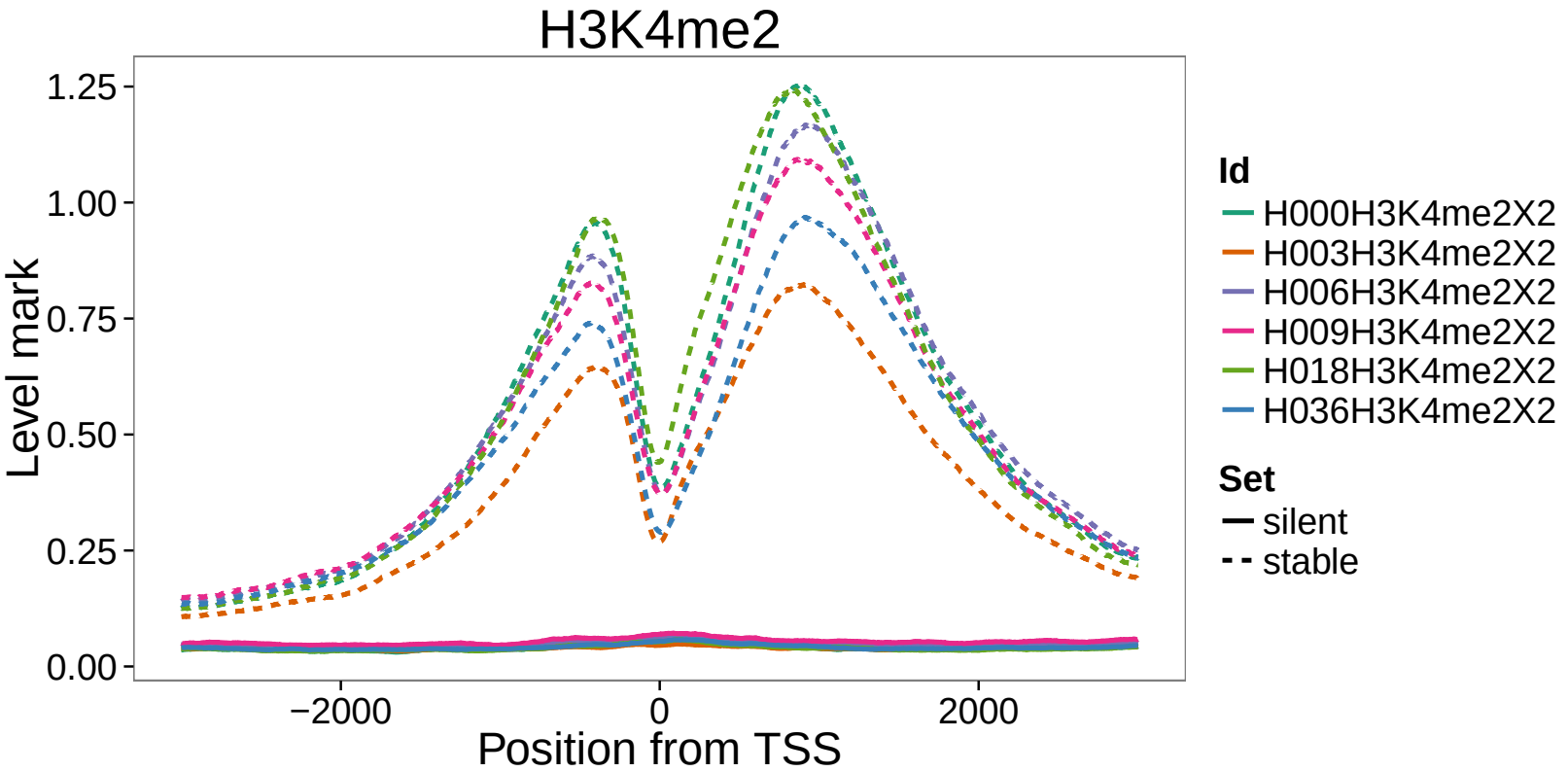
H3K4me2 - all sequenced samples

- 1000 silent genes
- 1000 stable genes (lowest CV)
- gencode v24

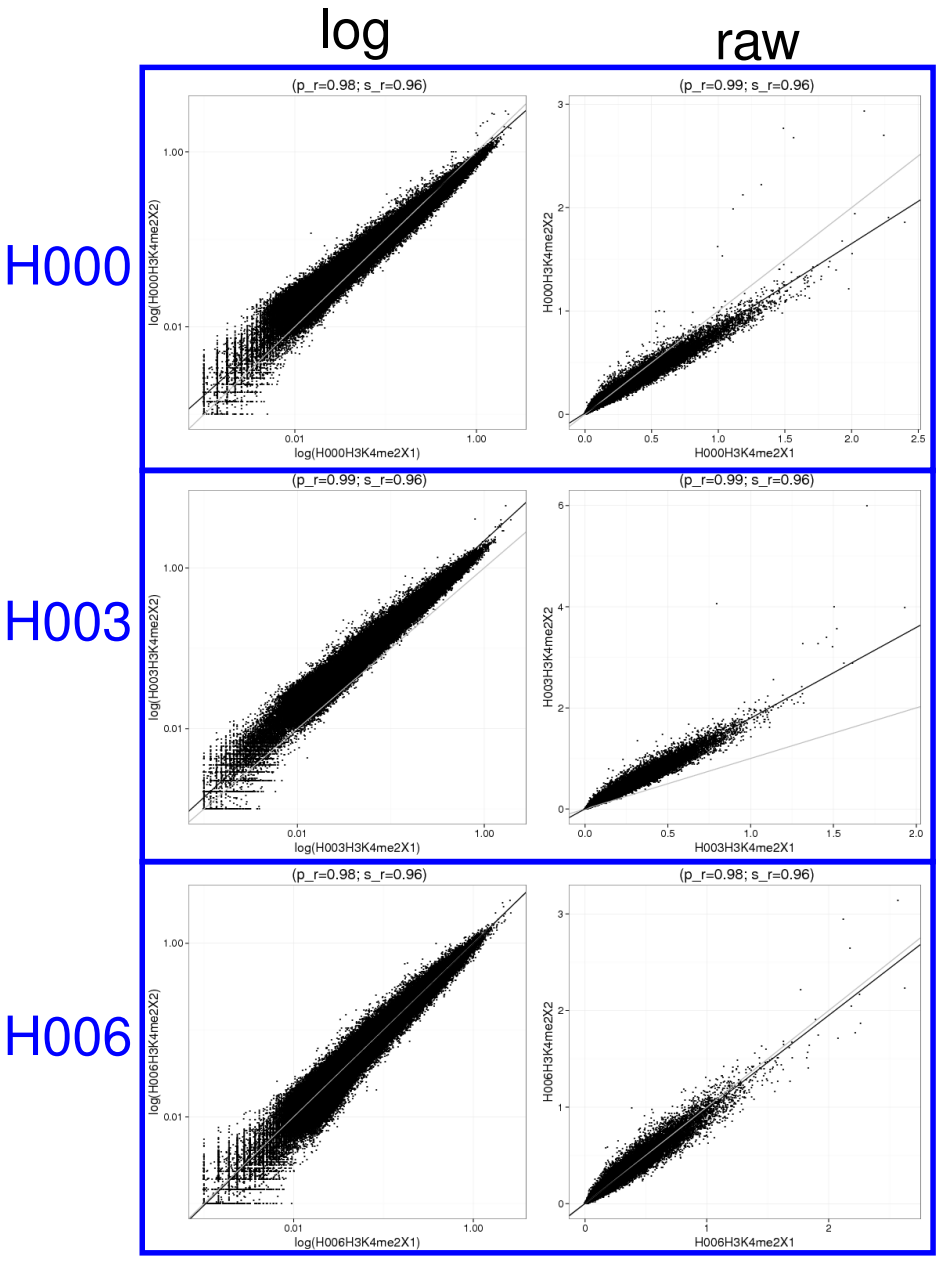


H3K4me2 - second replicate only

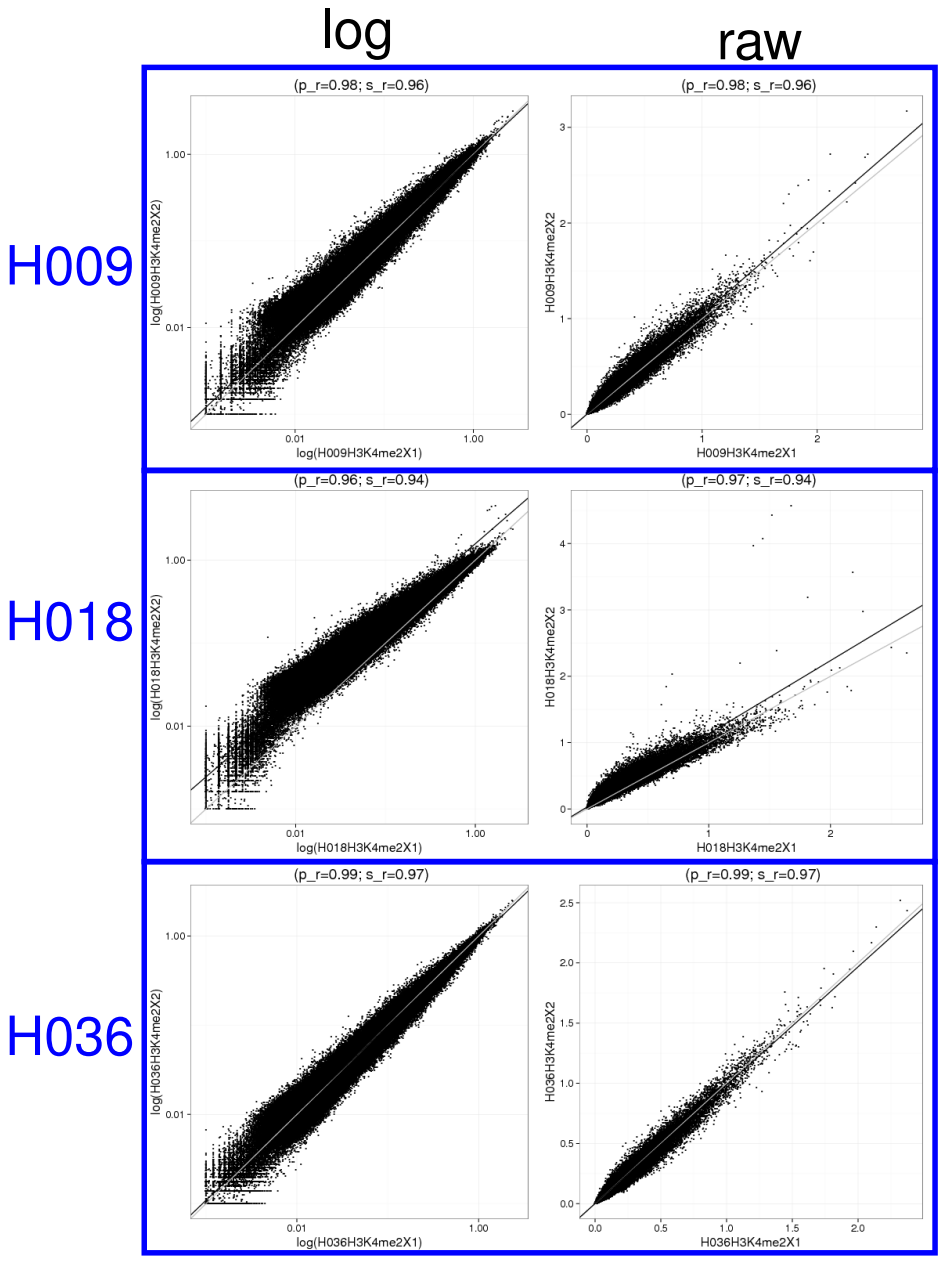
- 1000 silent genes
- 1000 stable genes (lowest CV)
- gencode v24



H3K4me2 - correlation between replicates mean of 10kb windows



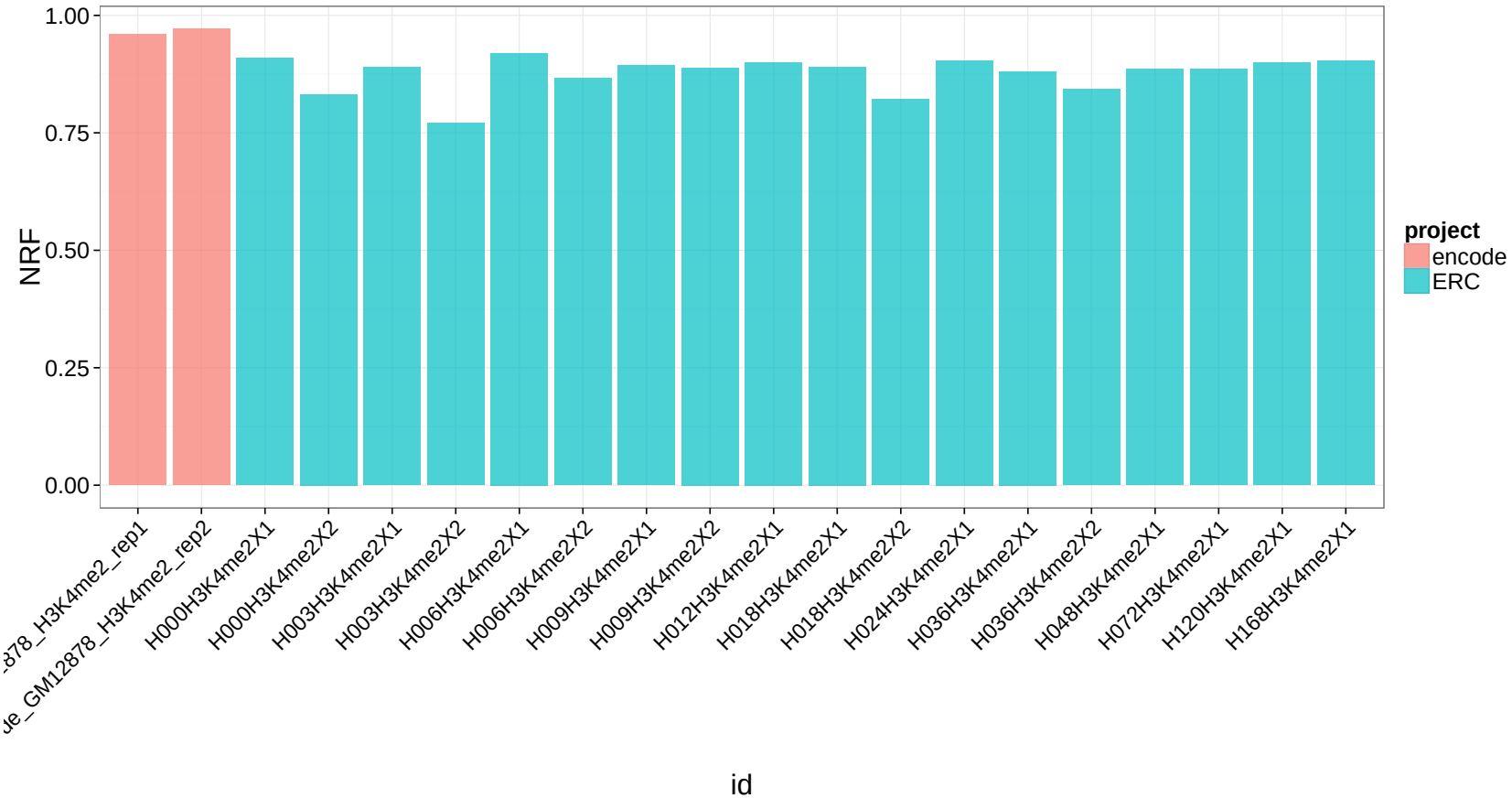
H3K4me2 - correlation between replicates mean of 10kb windows



H3K4me2 - NRF

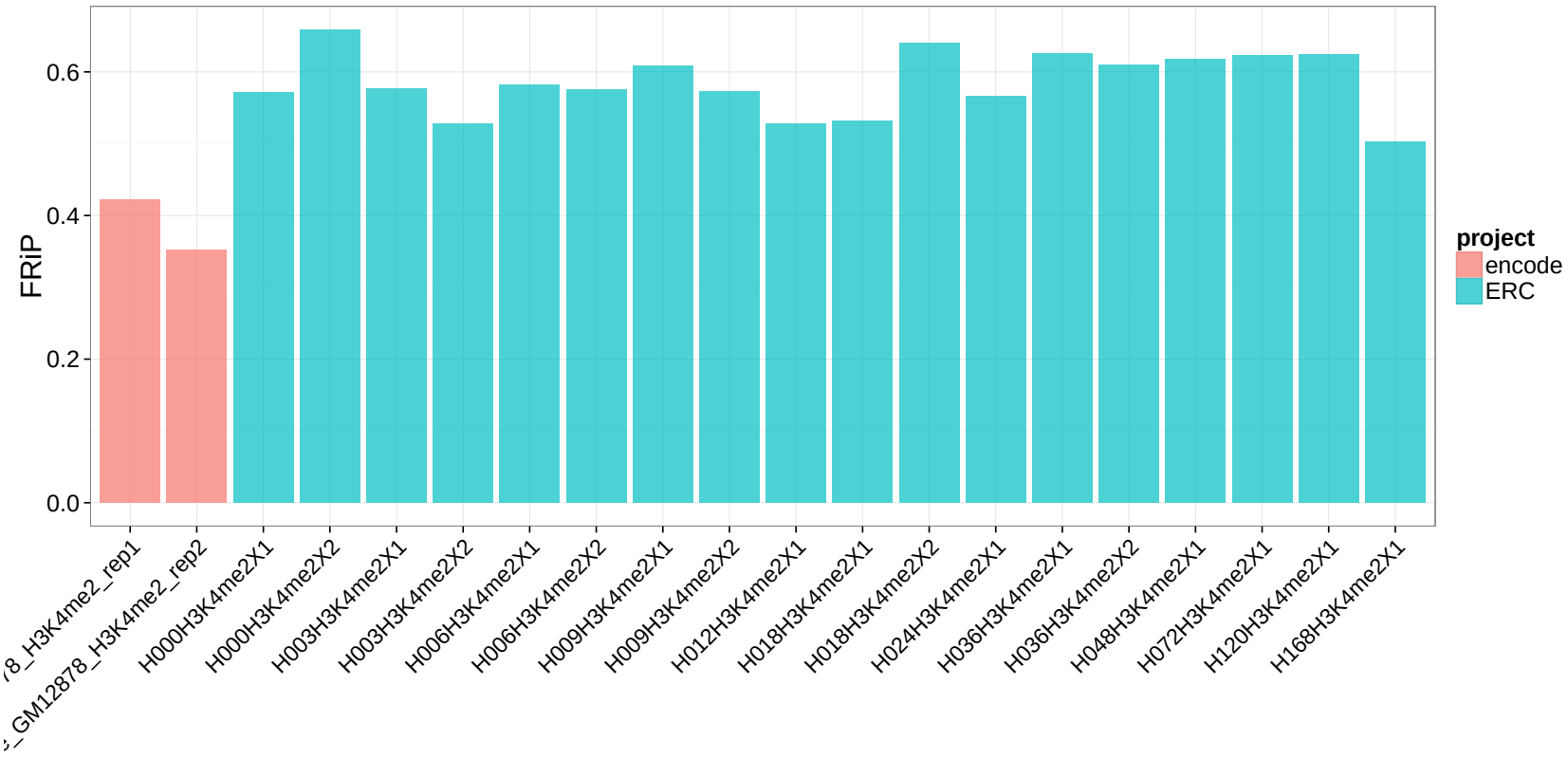
NRF: nonredundant fraction

NRF= nb unique start positions of uniquely mappable reads/nb uniquely mappable reads

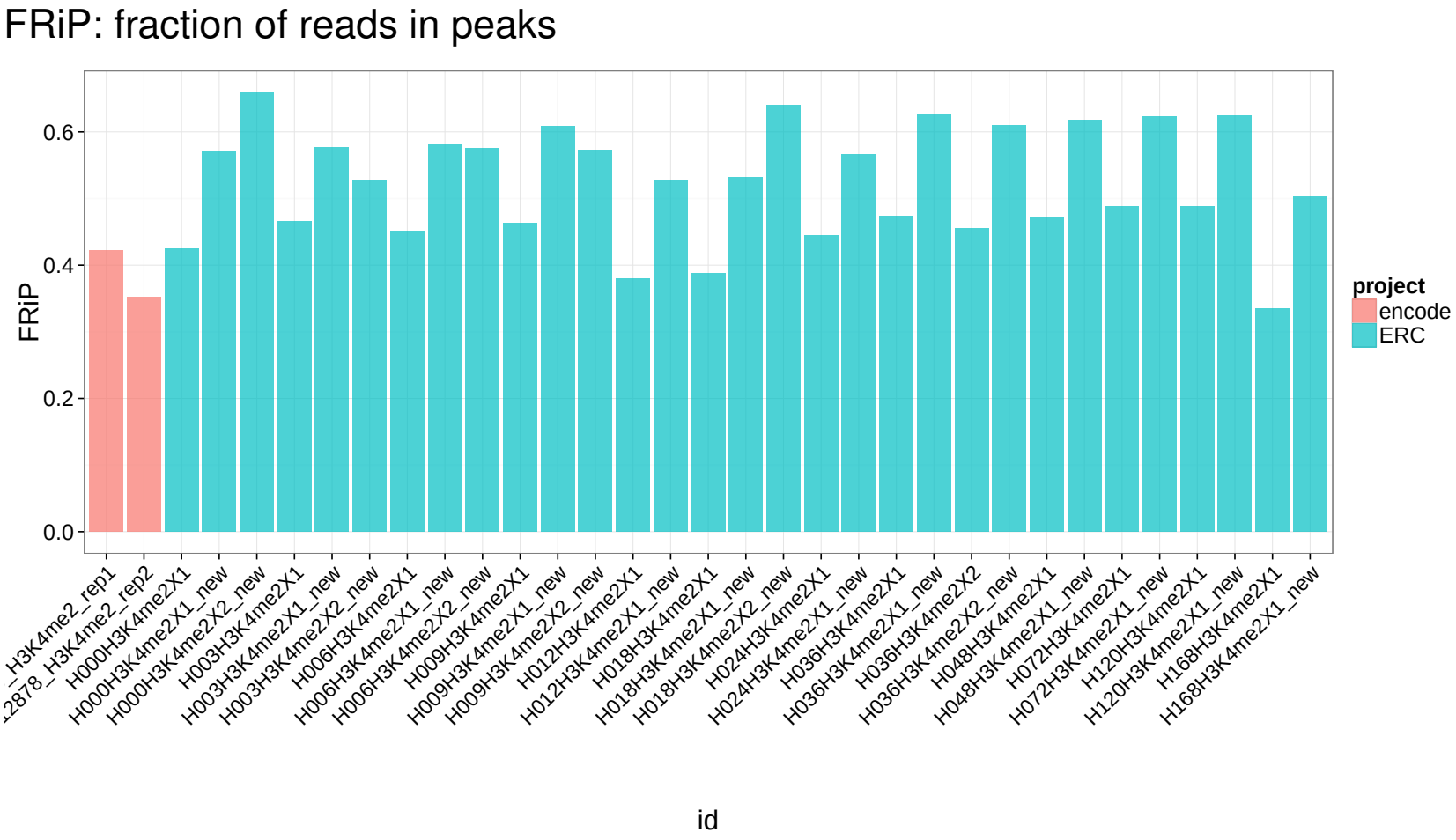


H3K4me2 - FRiP

FRiP: fraction of reads in peaks



H3K4me2 - FRiP (compare old VS new inputs)



Outline

Status samples

H3K4me1

H3K4me2

H3K4me3
- Mapping stats
- Aggregation plots
- NRF and FRiP

H3K9ac

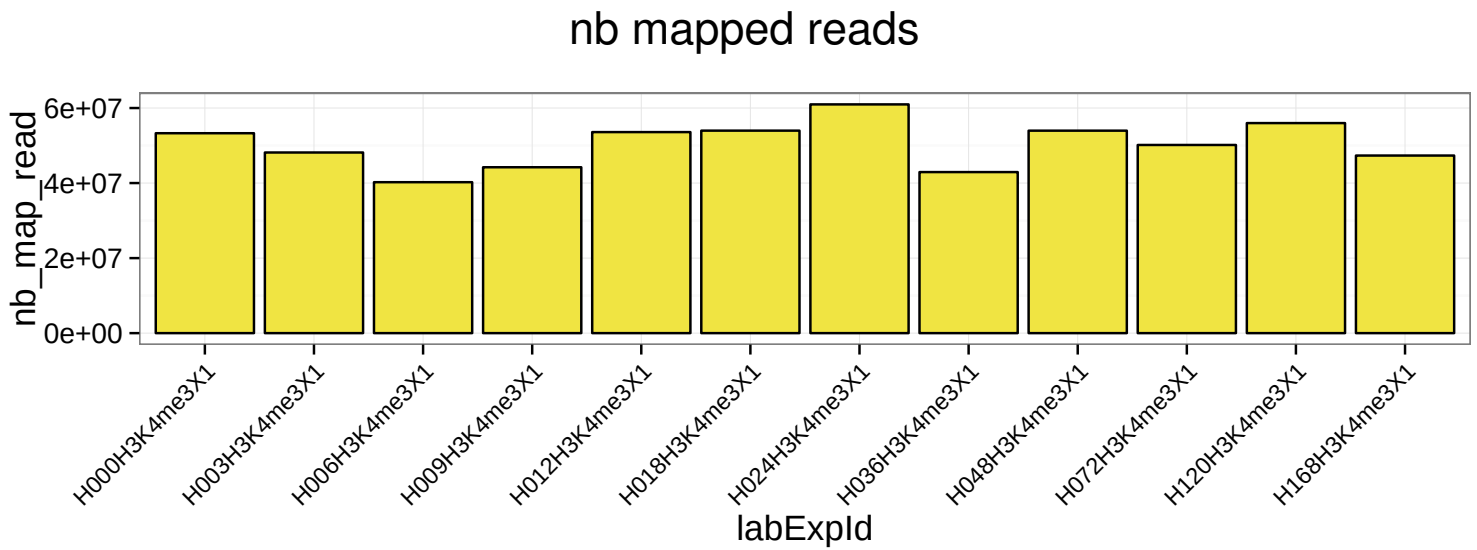
H3K9me3

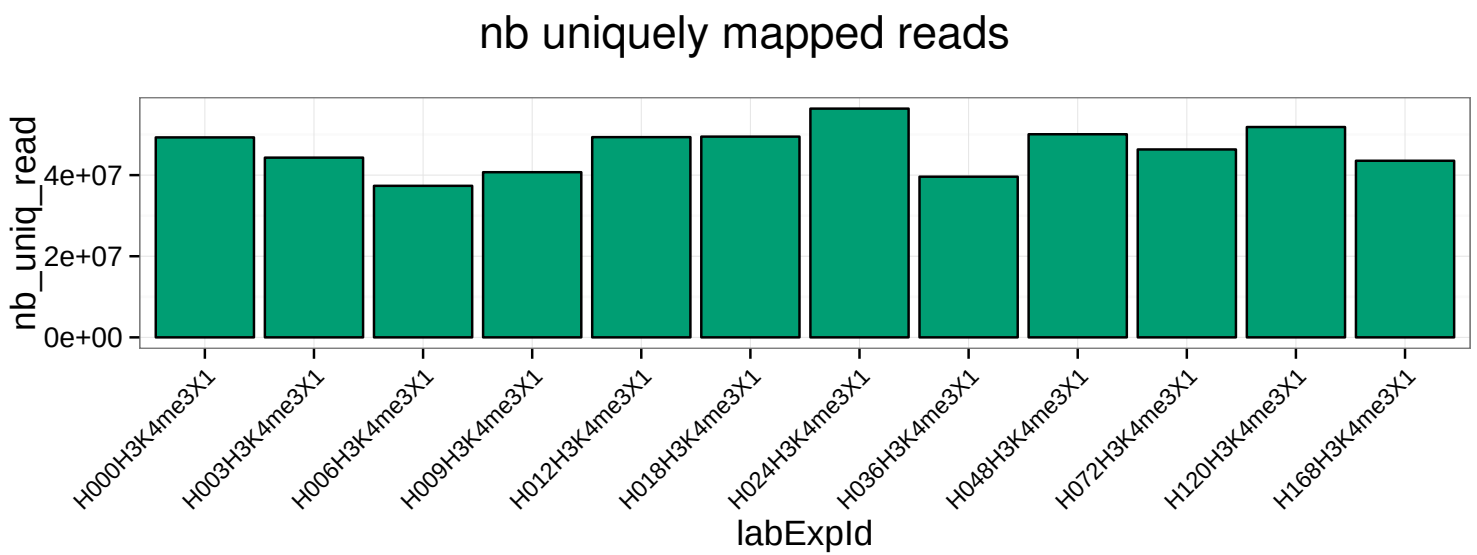
H3K27ac

H3K27me3

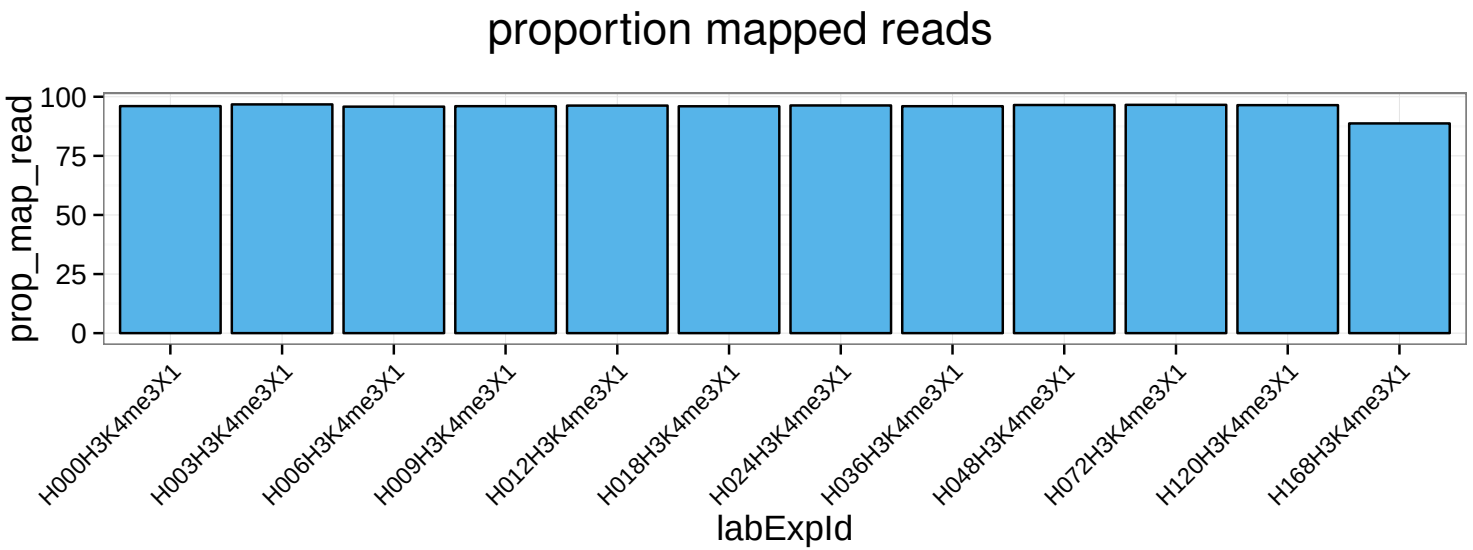
H3K36me3

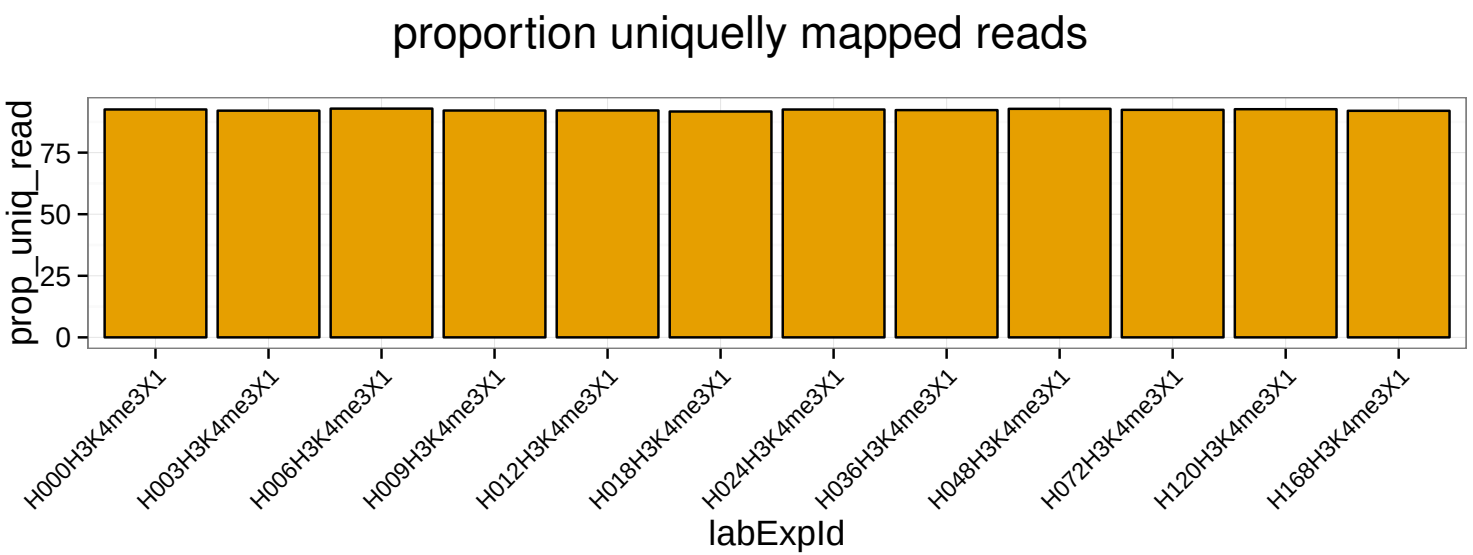
H3K4me3 - mapping stats





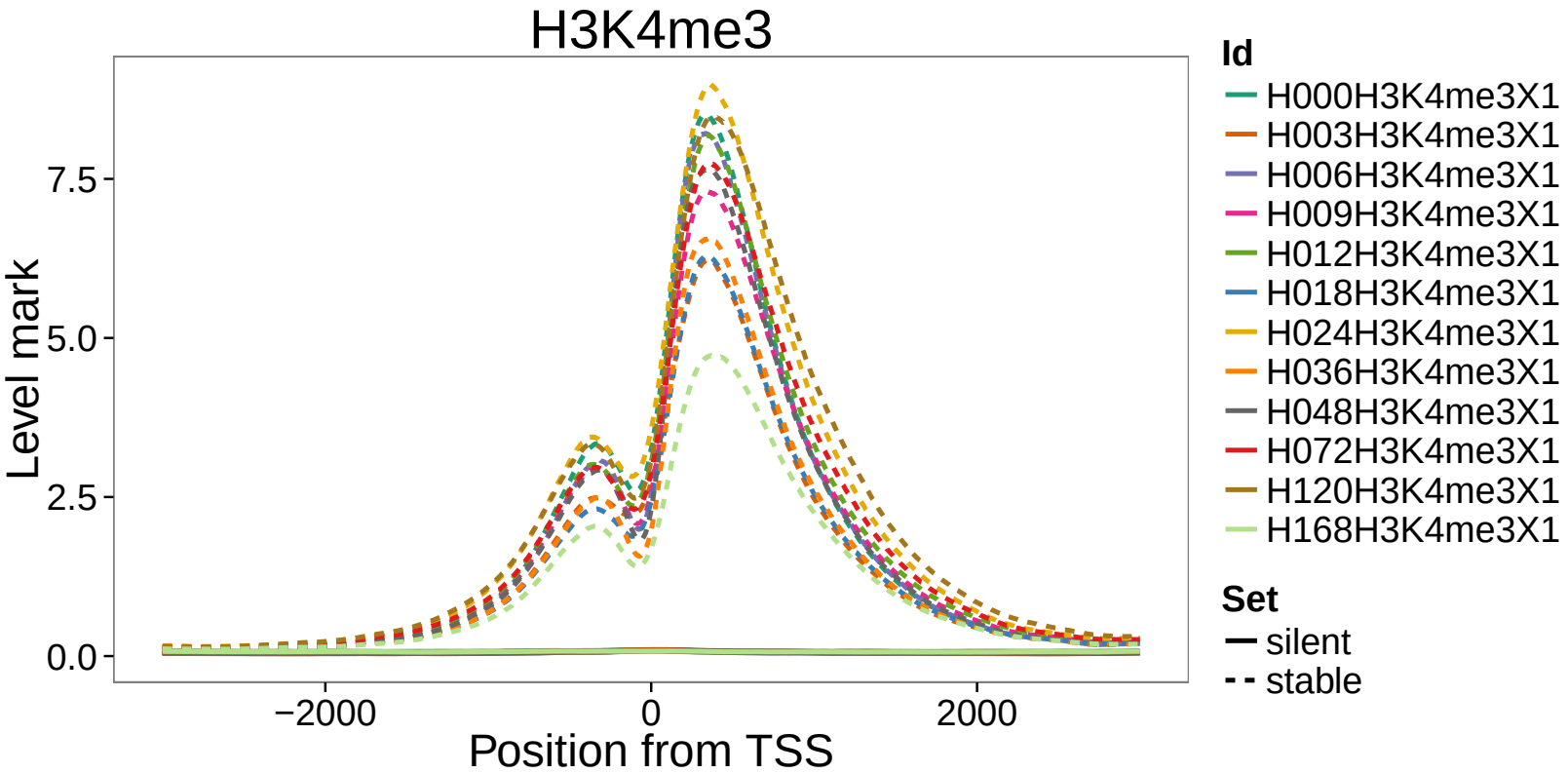
H3K4me3 - mapping stats





H3K4me3

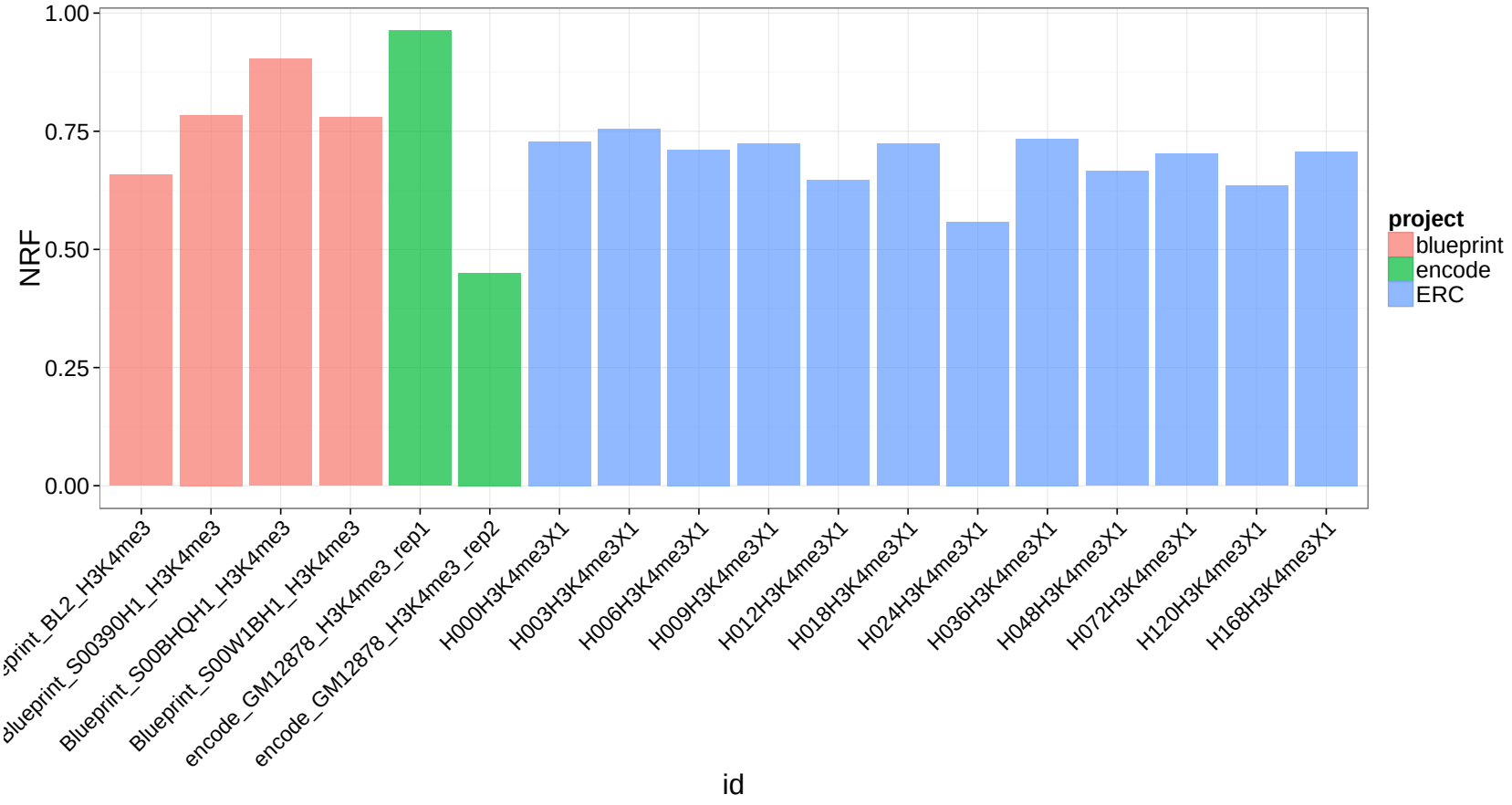
- 1000 silent genes
- 1000 stable genes (lowest CV)
- gencode v24



H3K4me3 - NRF

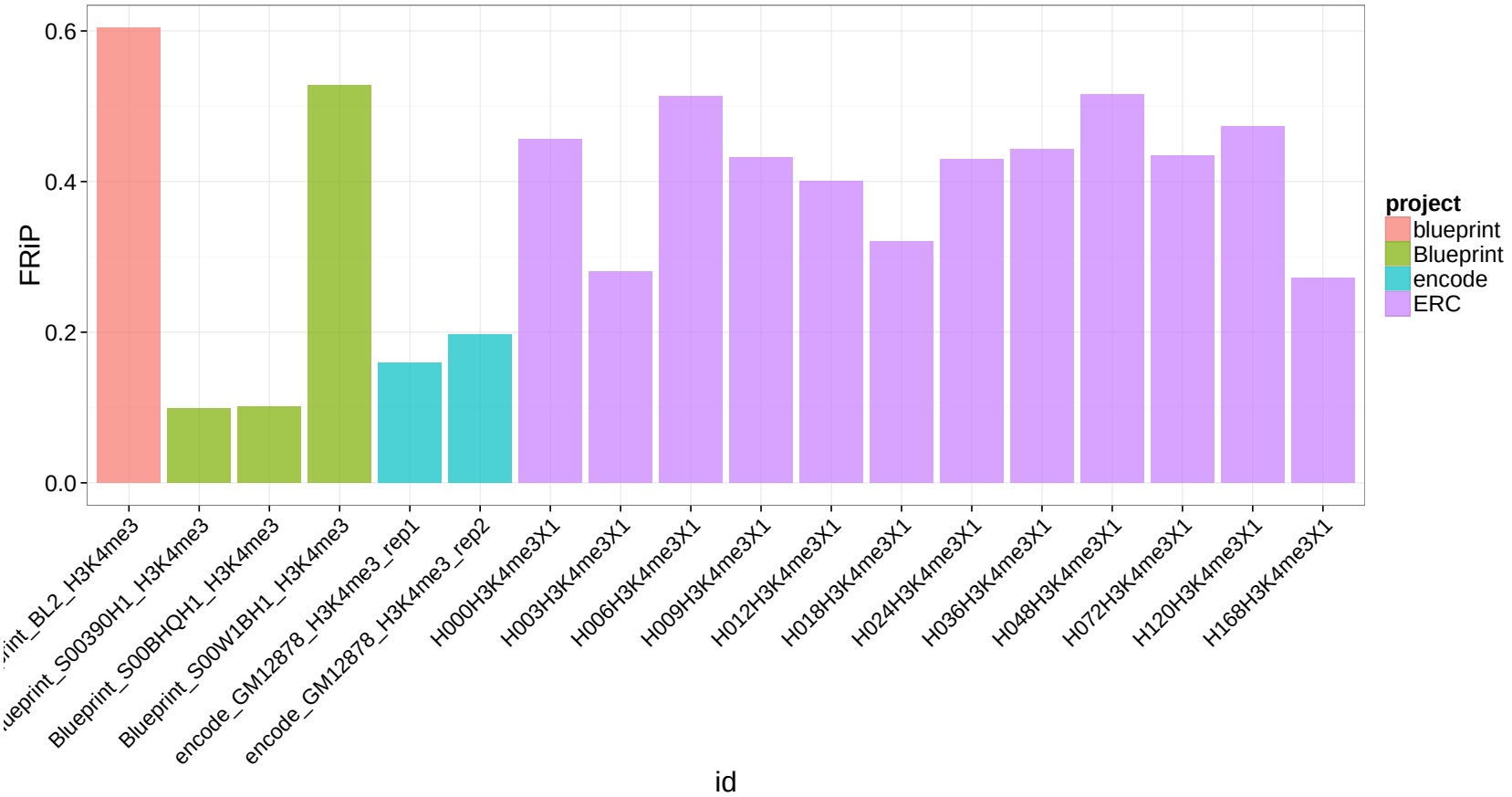
NRF: nonredundant fraction

NRF= nb unique start positions of uniquely mappable reads/nb uniquely mappable reads

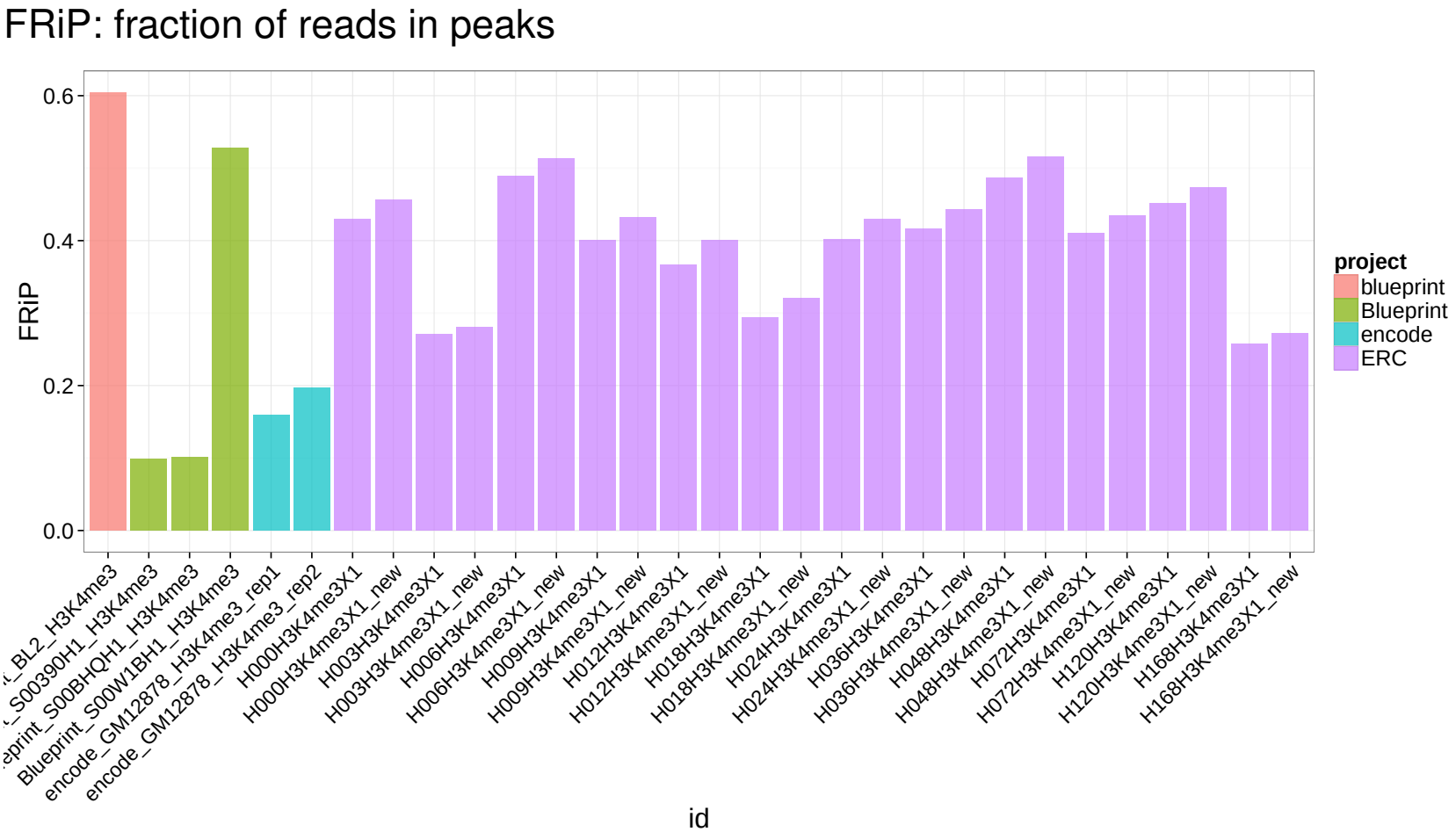


H3K4me3 - FRiP

FRiP: fraction of reads in peaks



H3K4me3 - FRiP (compare old VS new inputs)



Outline

Status samples

H3K4me1

H3K4me2

H3K4me3

H3K9ac

- Mapping stats
- Aggregation plots
- NRF and FRiP

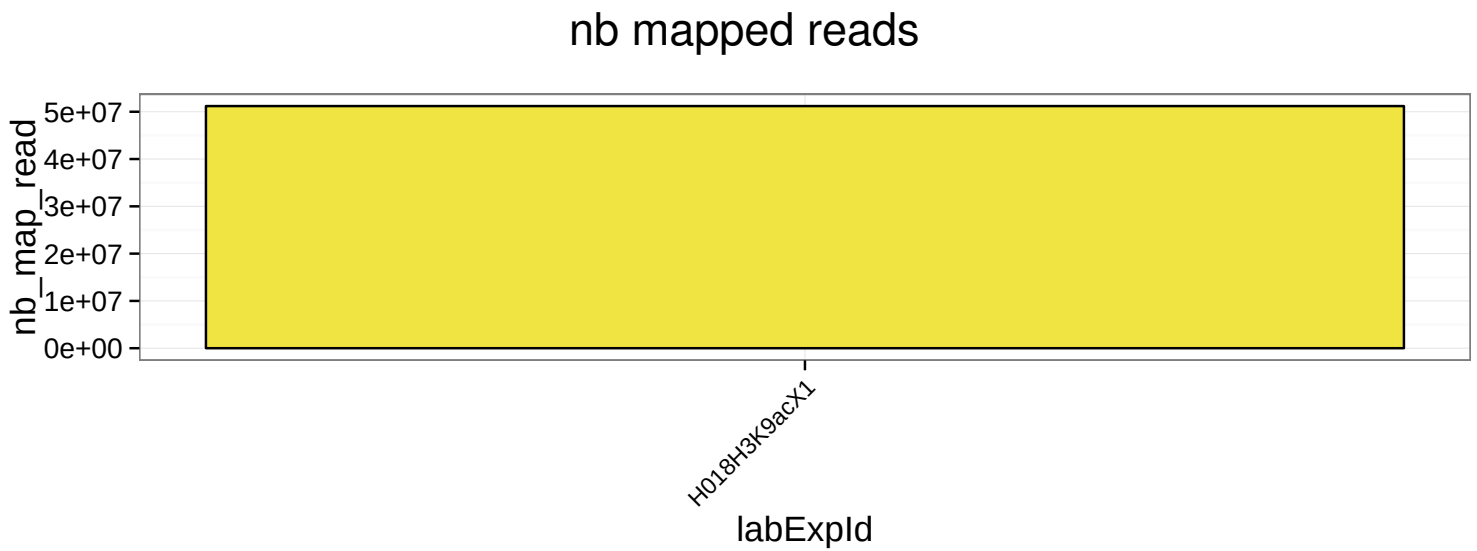
H3K9me3

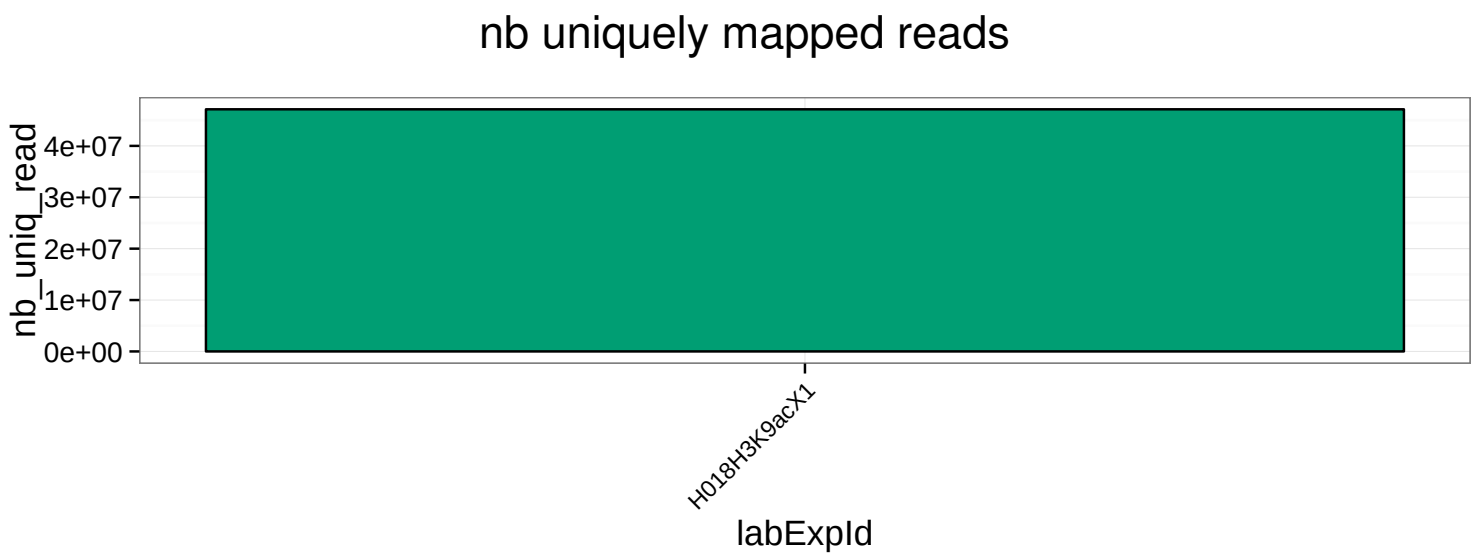
H3K27ac

H3K27me3

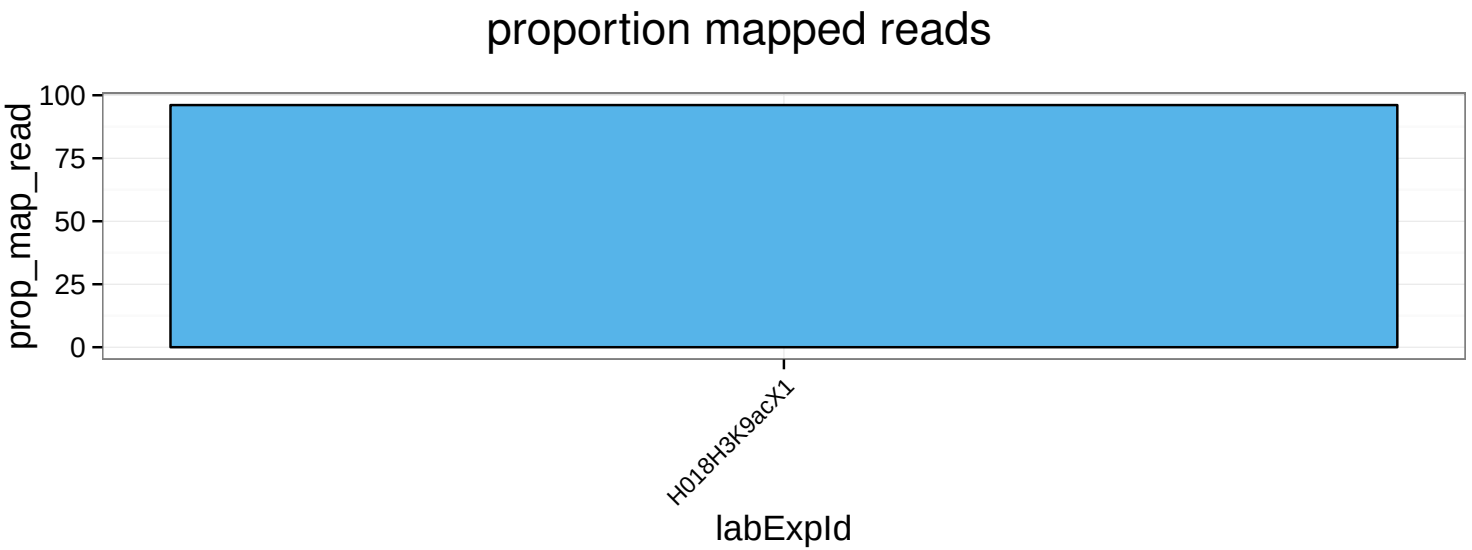
H3K36me3

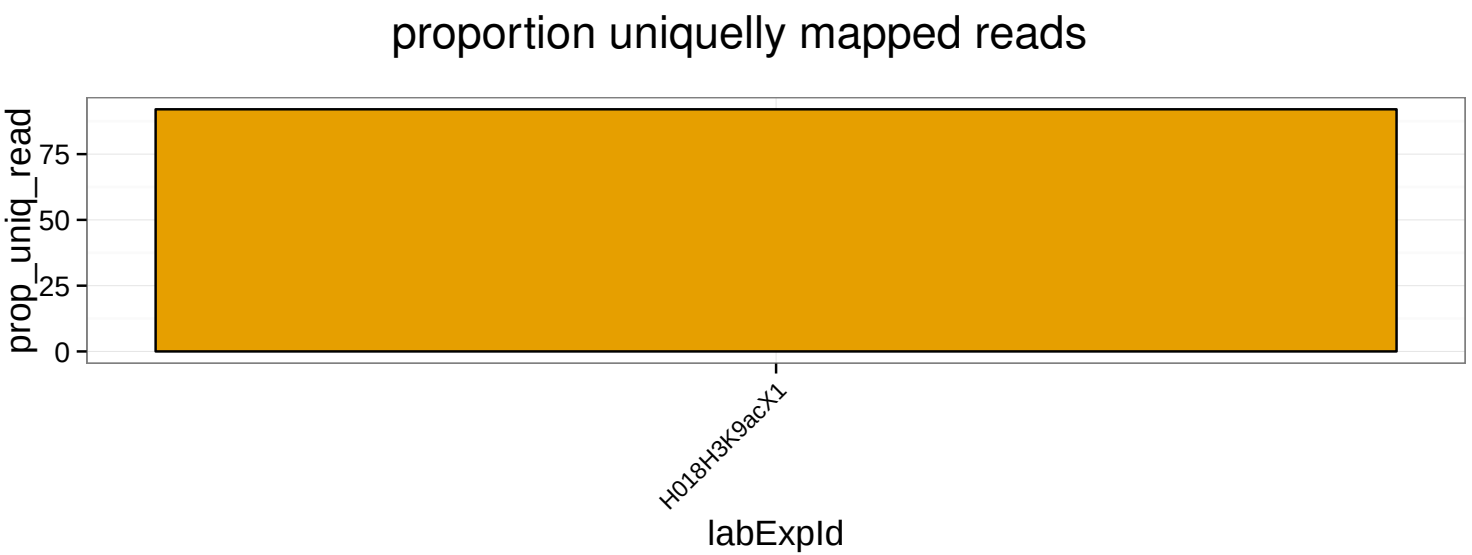
H3K9ac - mapping stats





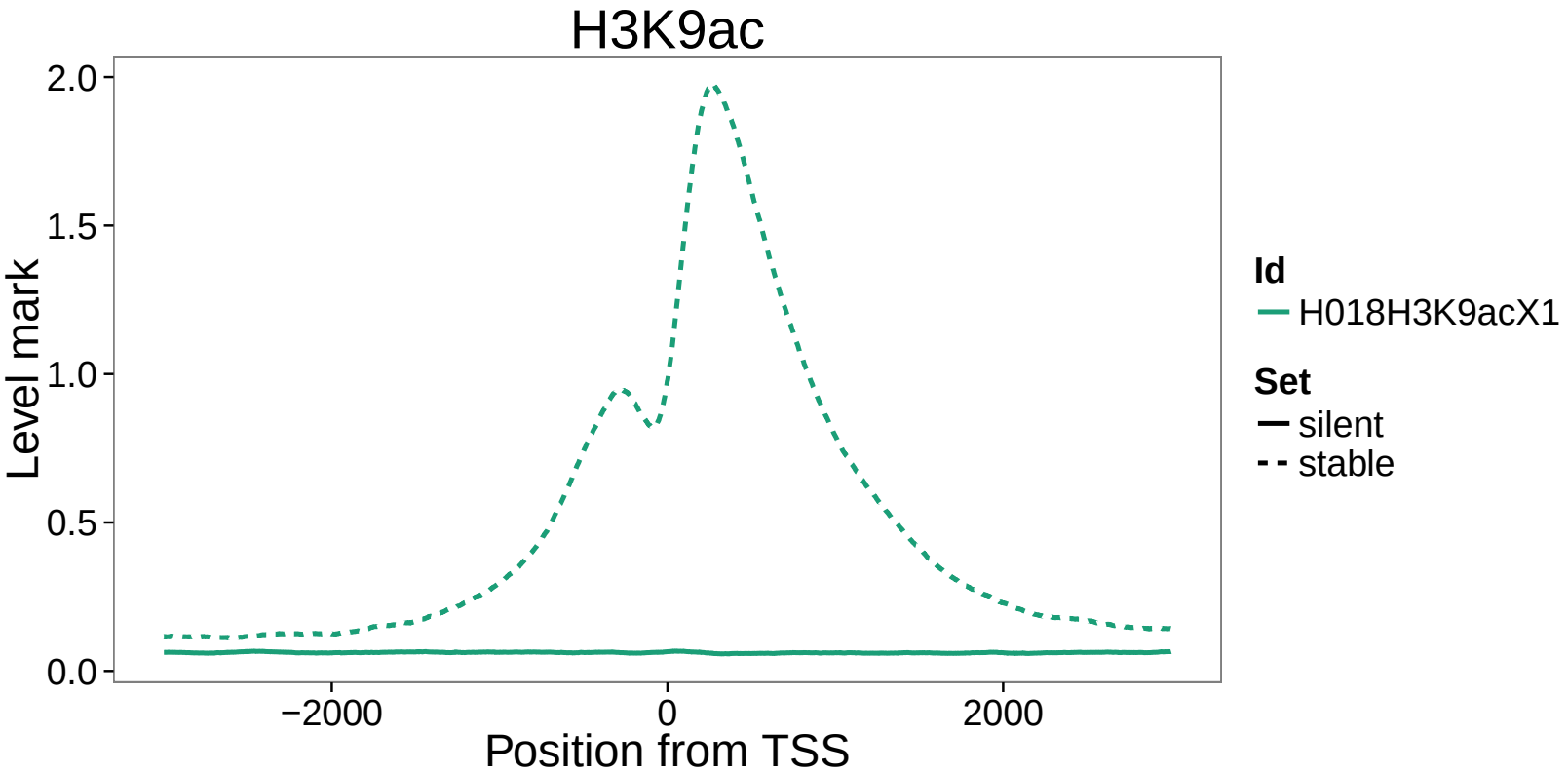
H3K9ac - mapping stats





H3K9ac

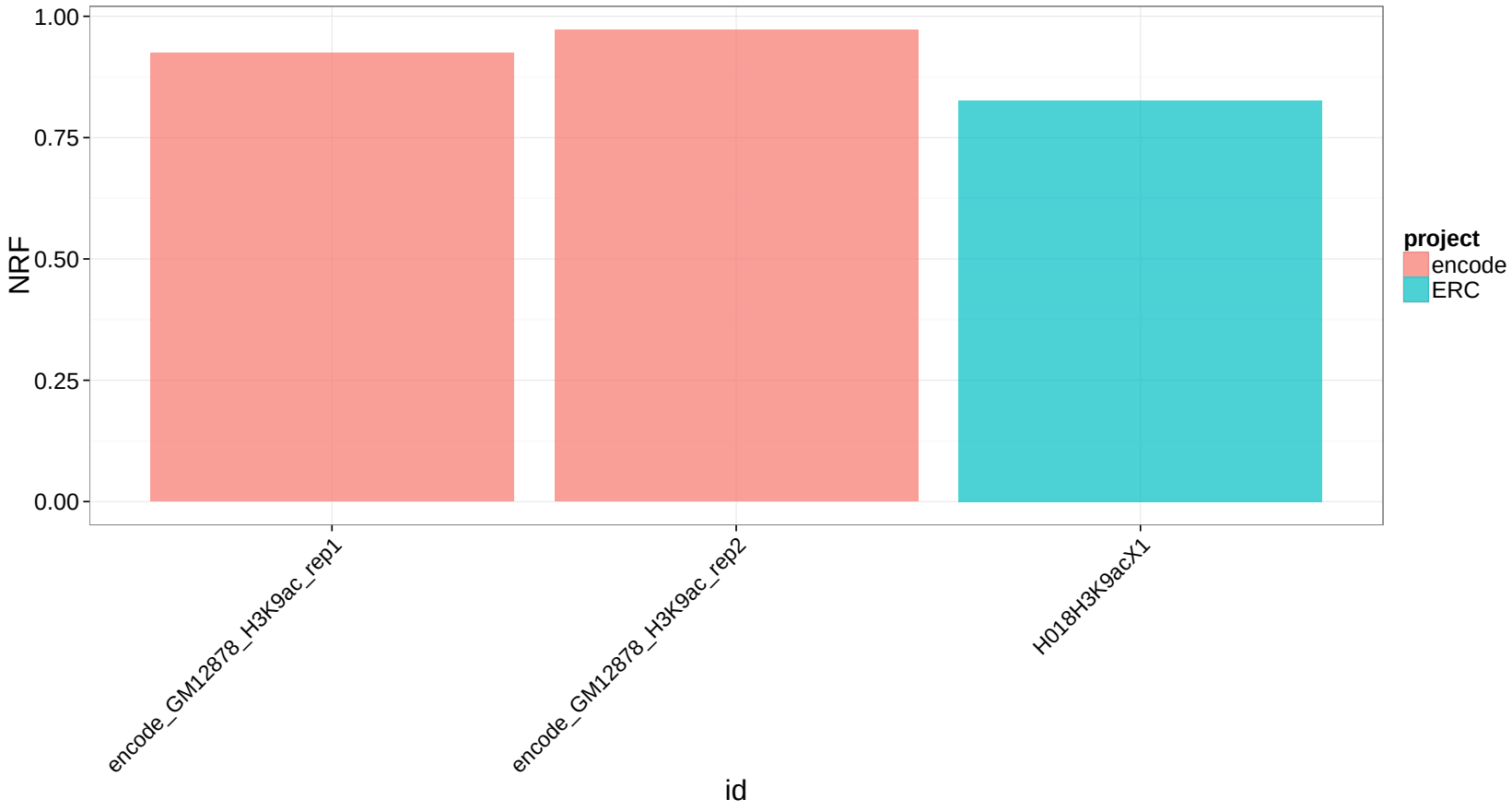
- 1000 silent genes
- 1000 stable genes (lowest CV)
- gencode v24



H3K9ac - NRF

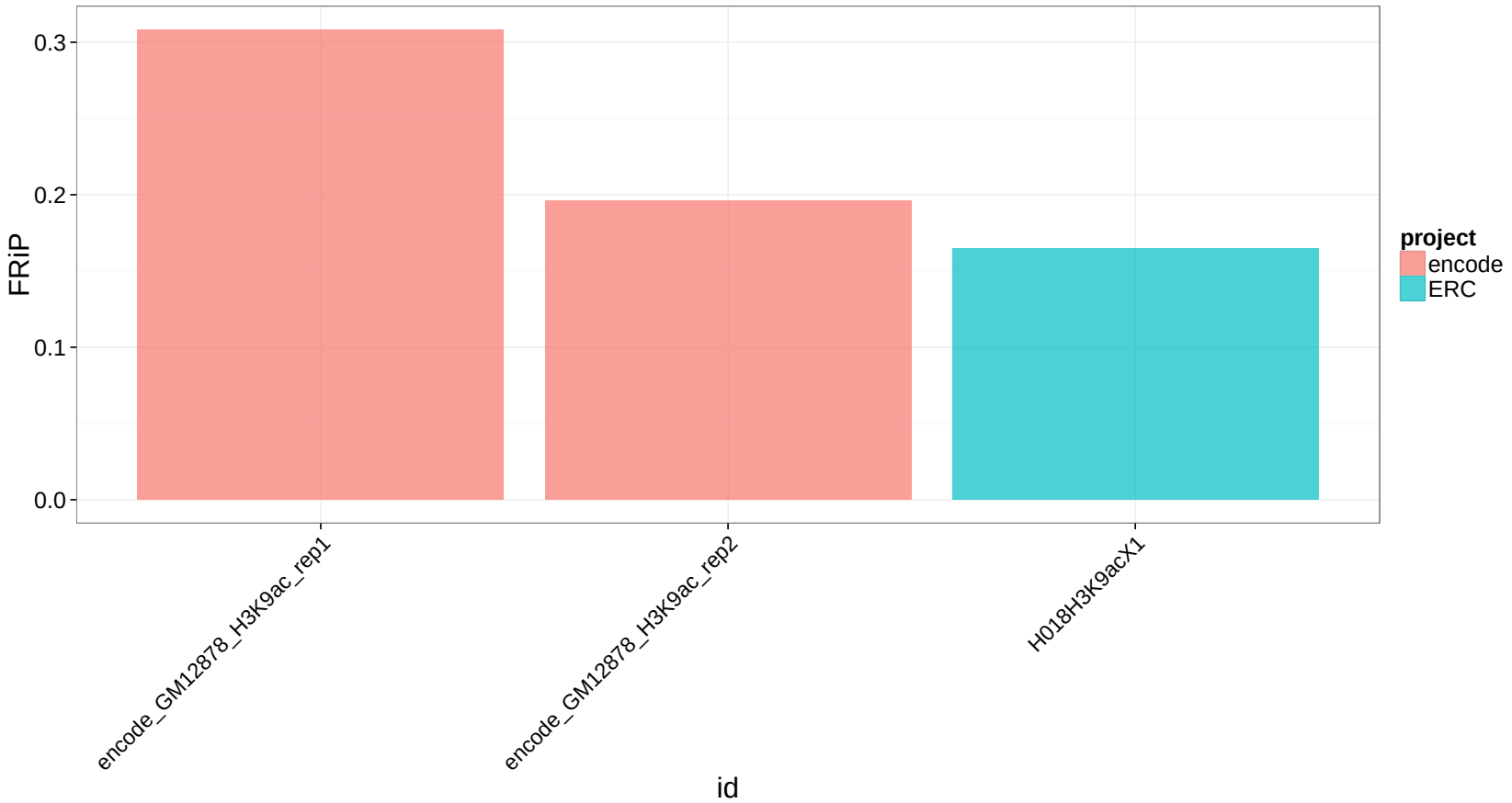
NRF: nonredundant fraction

NRF= nb unique start positions of uniquely mappable reads/nb uniquely mappable reads

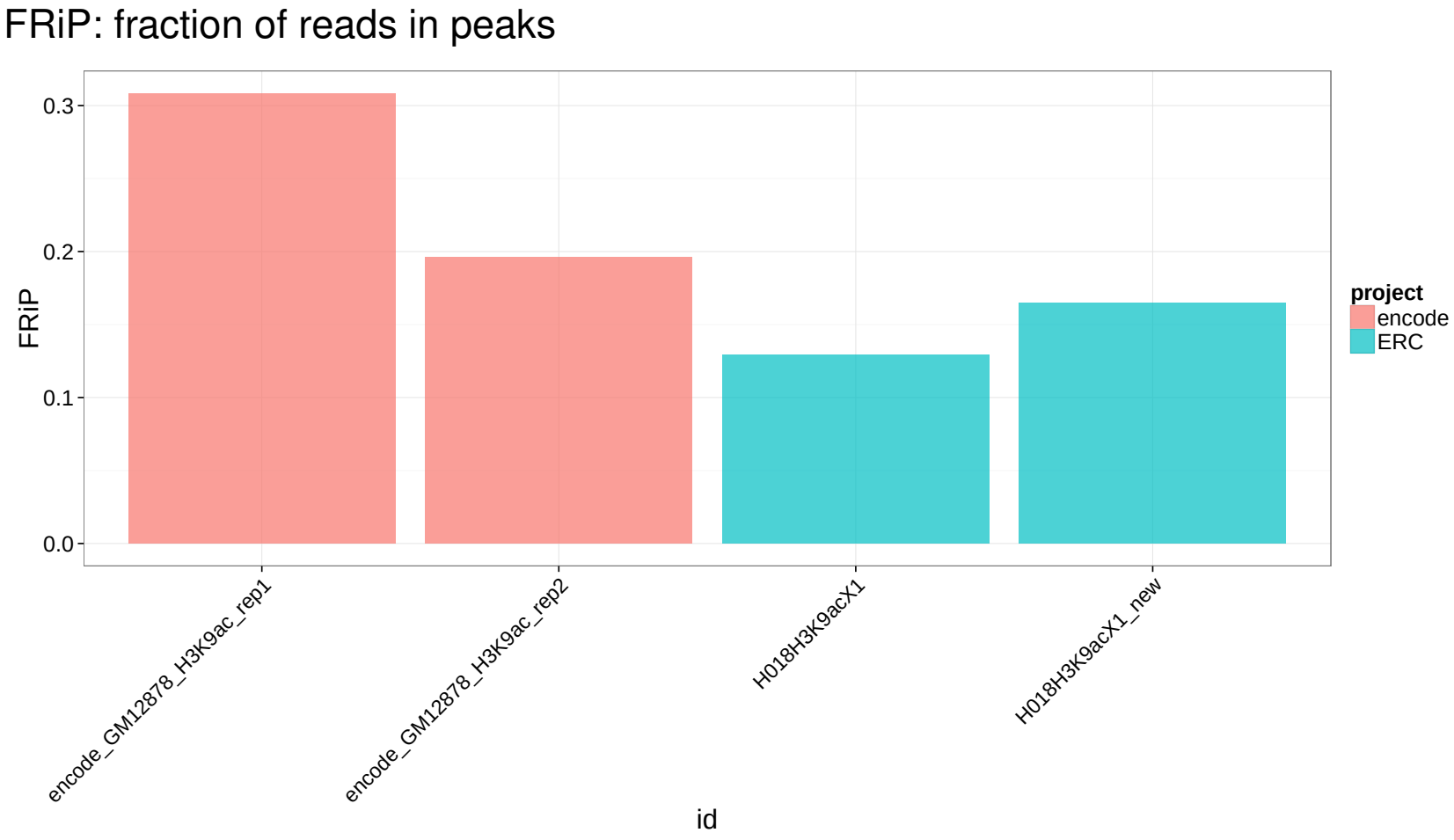


H3K9ac - FRiP

FRiP: fraction of reads in peaks



H3K9ac - FRiP (compare old VS new inputs)



Outline

Status samples

H3K4me1

H3K4me2

H3K4me3

H3K9ac

H3K9me3

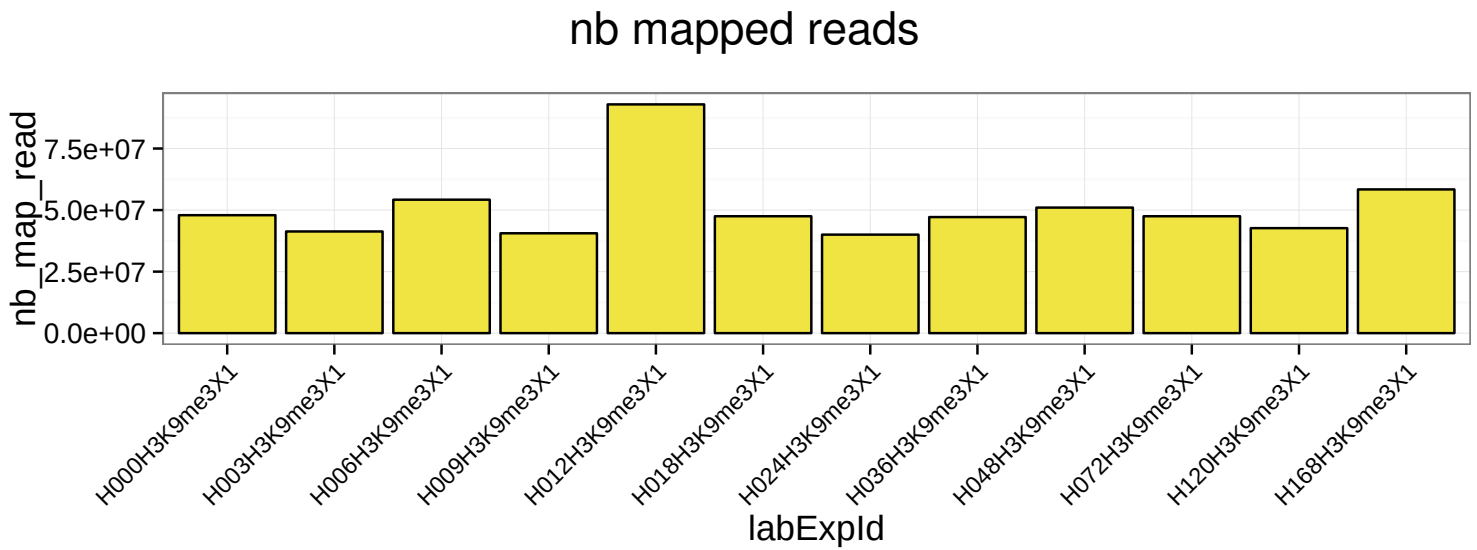
- Mapping stats
- Aggregation plots
- NRF and FRiP

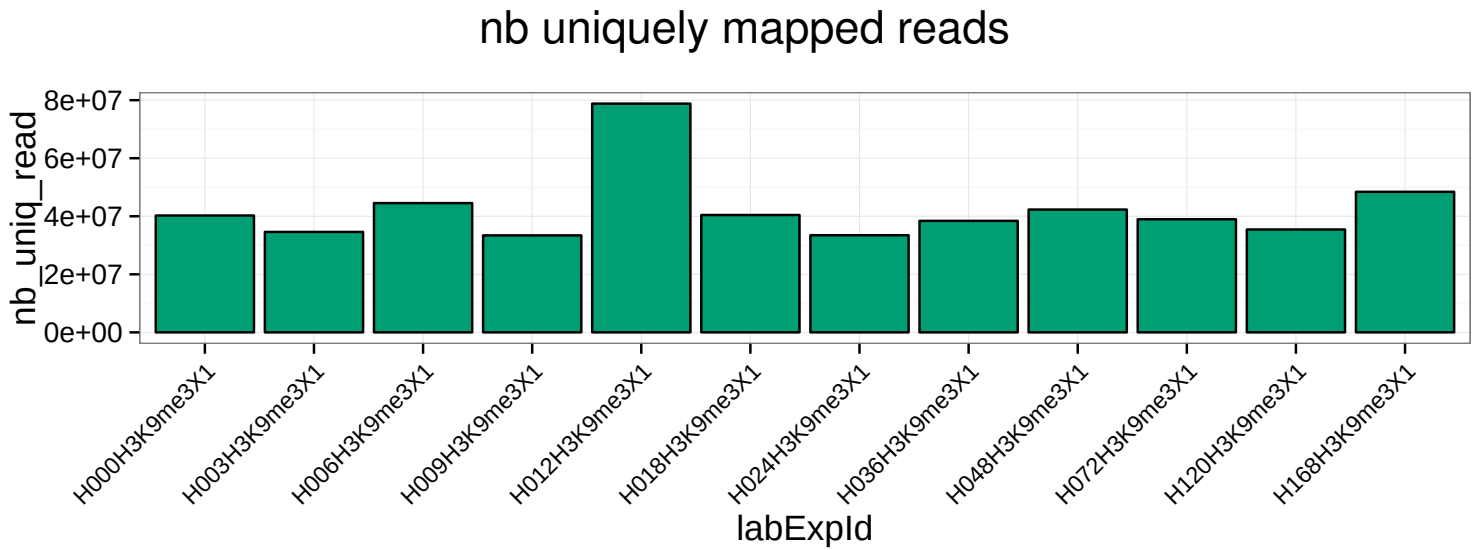
H3K27ac

H3K27me3

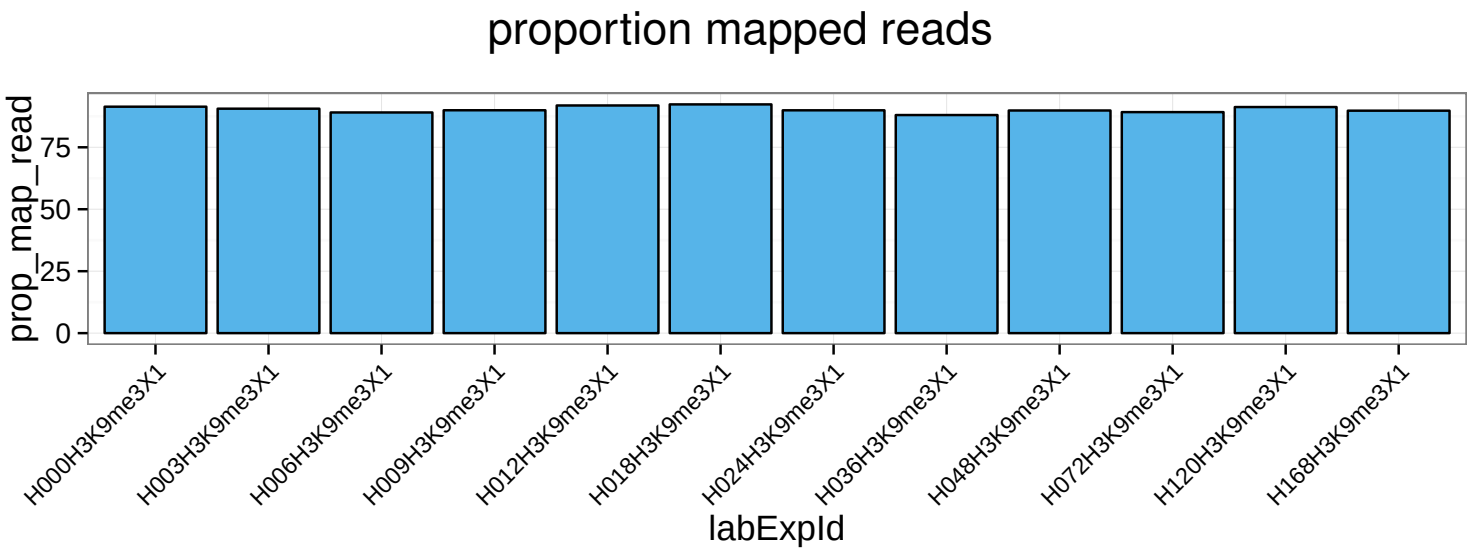
H3K36me3

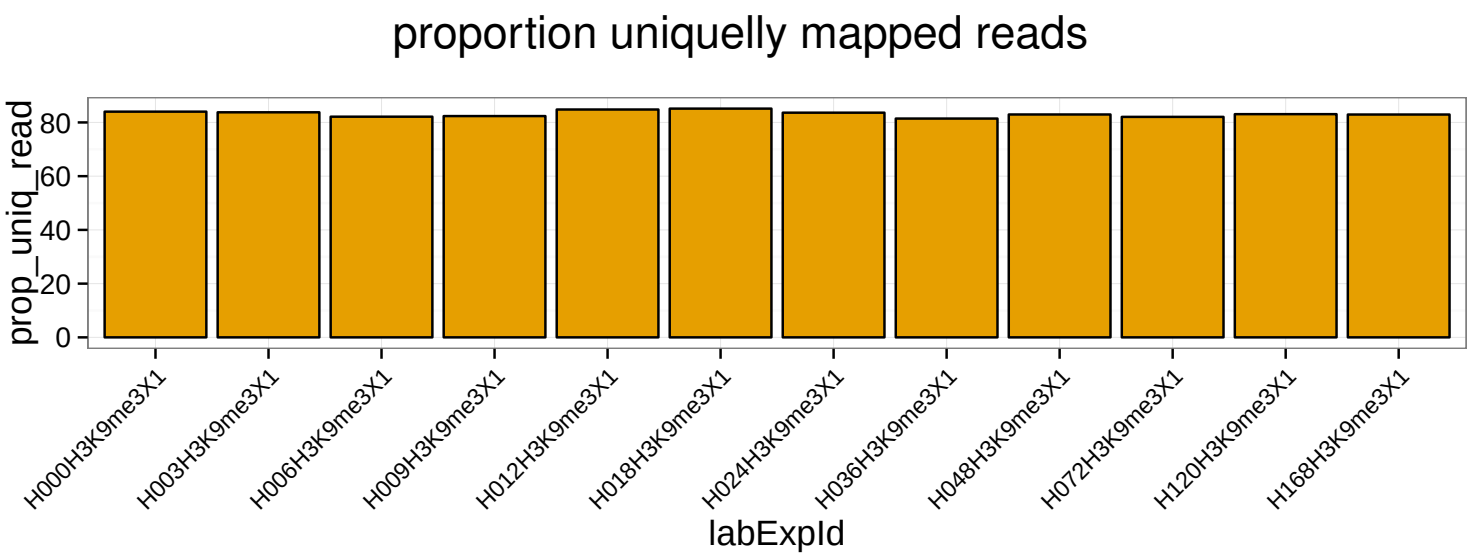
H3K9me3 - mapping stats





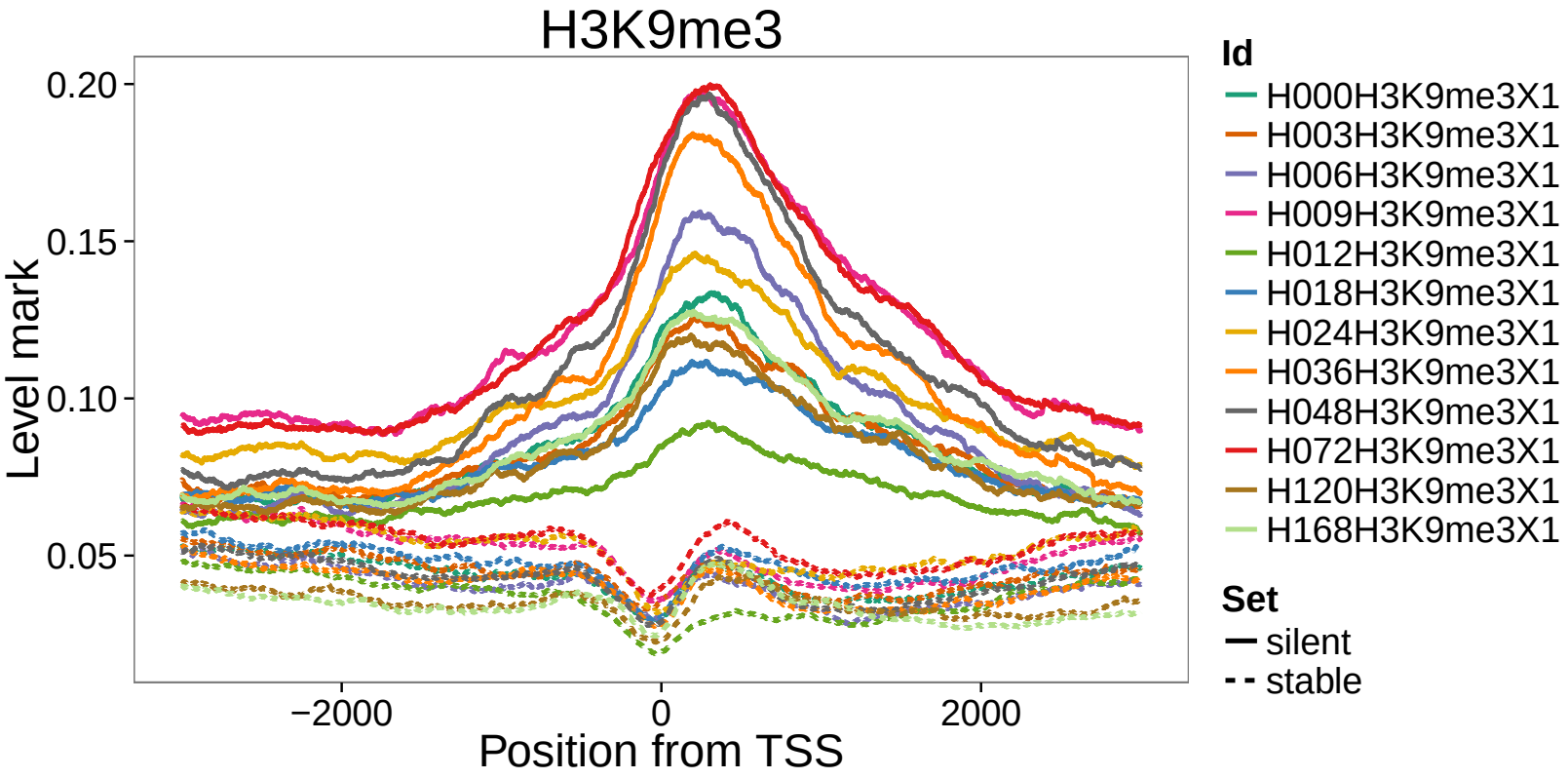
H3K9me3 - mapping stats





H3K9me3

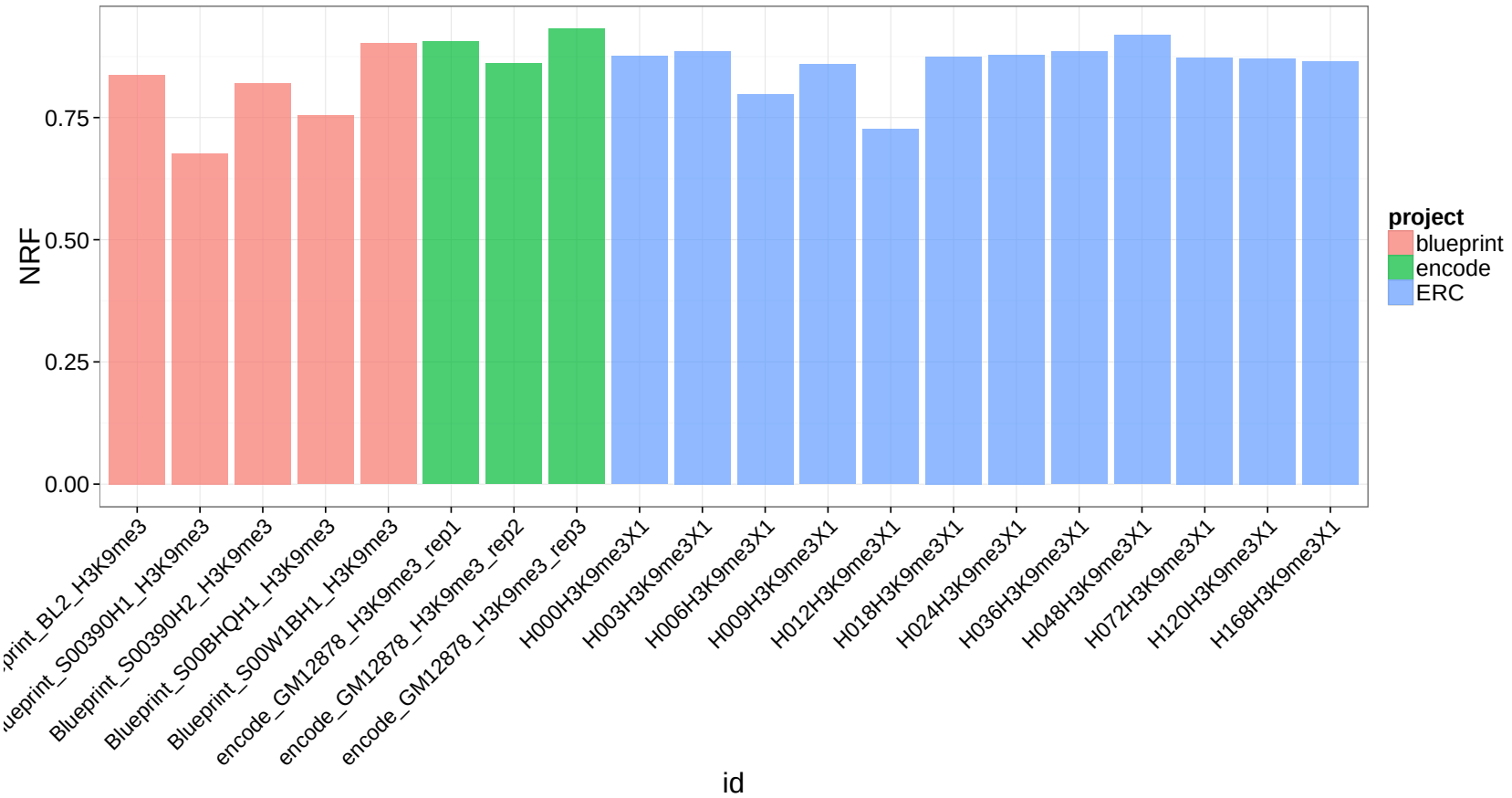
- 1000 silent genes
- 1000 stable genes (lowest CV)
- gencode v24



H3K9me3 - NRF

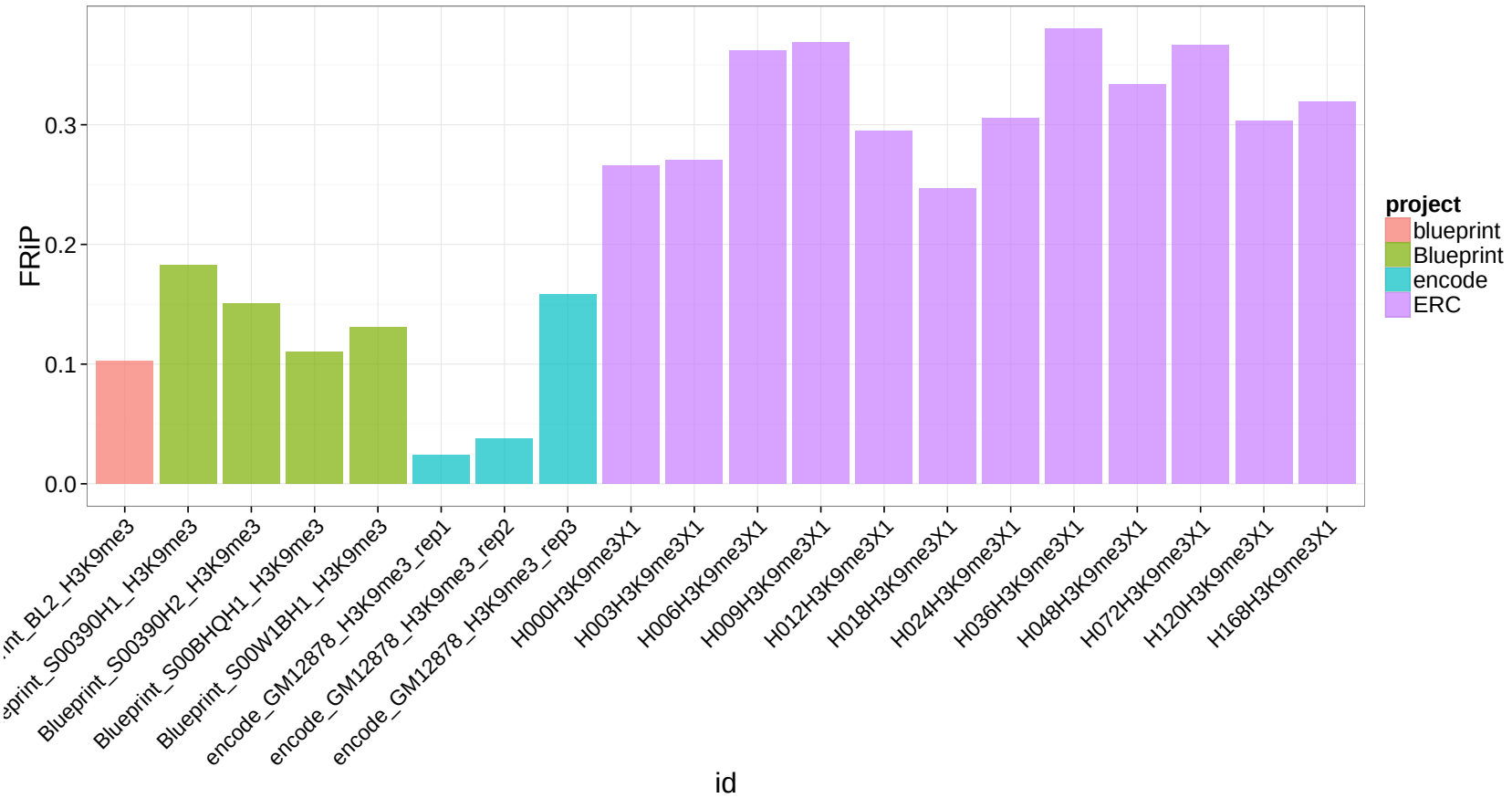
NRF: nonredundant fraction

NRF= nb unique start positions of uniquely mappable reads/nb uniquely mappable reads

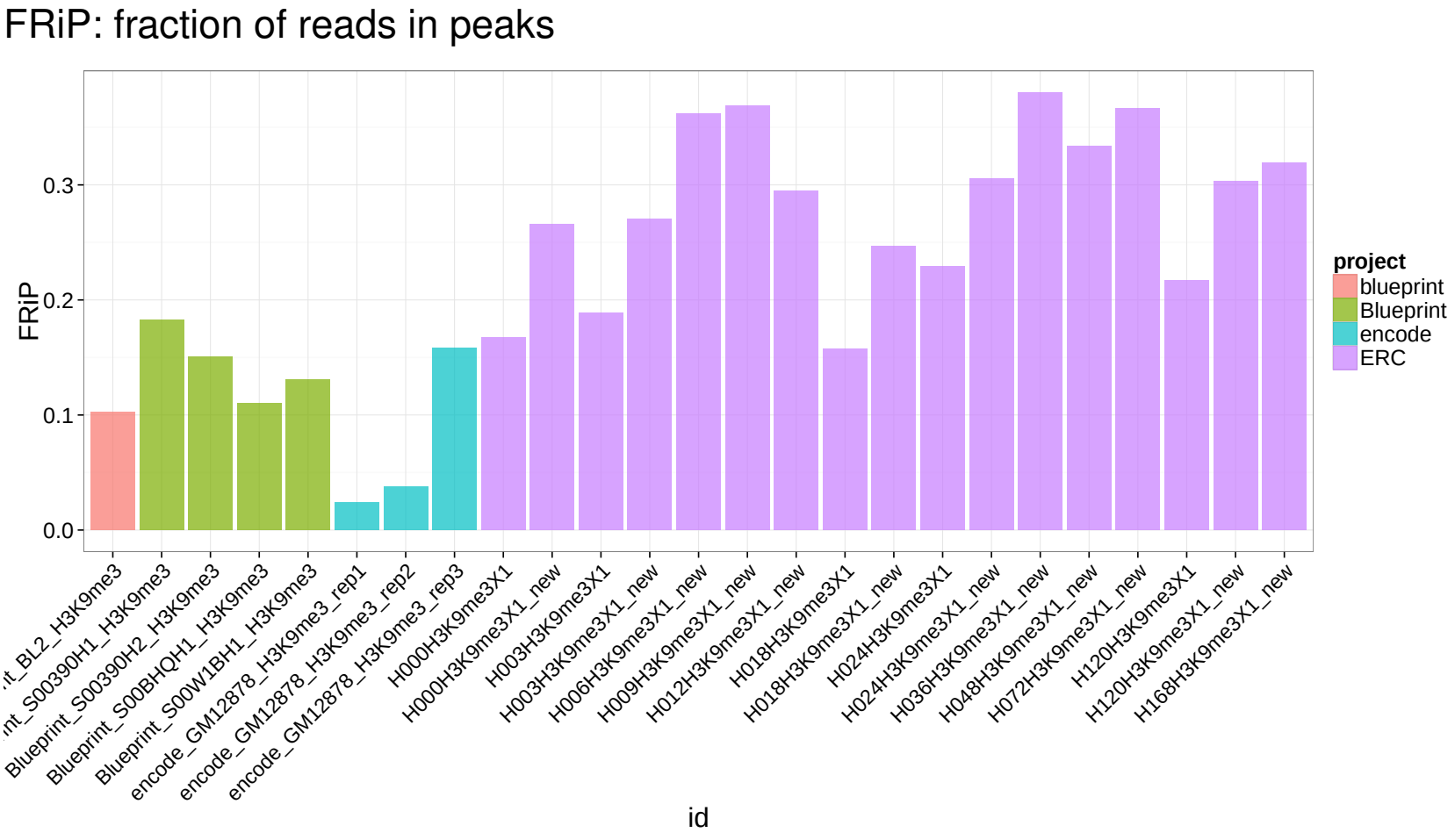


H3K9me3 - FRiP

FRiP: fraction of reads in peaks



H3K9me3 - FRiP (compare old VS new inputs)



Outline

Status samples

H3K4me1

H3K4me2

H3K4me3

H3K9ac

H3K9me3

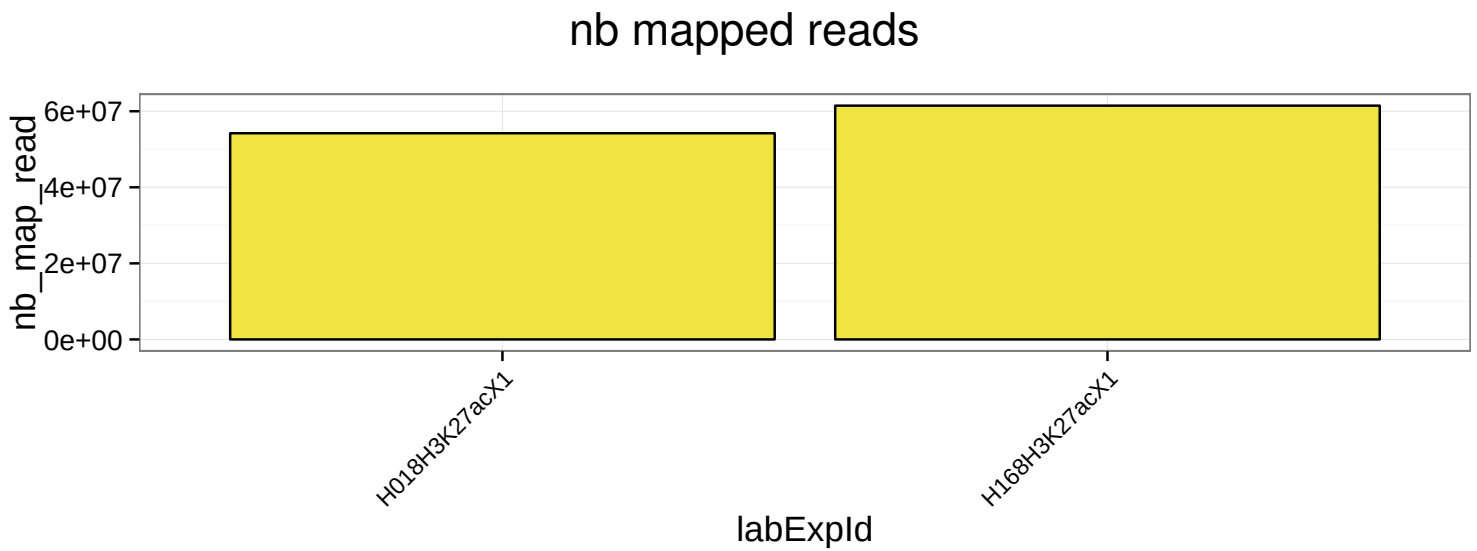
H3K27ac

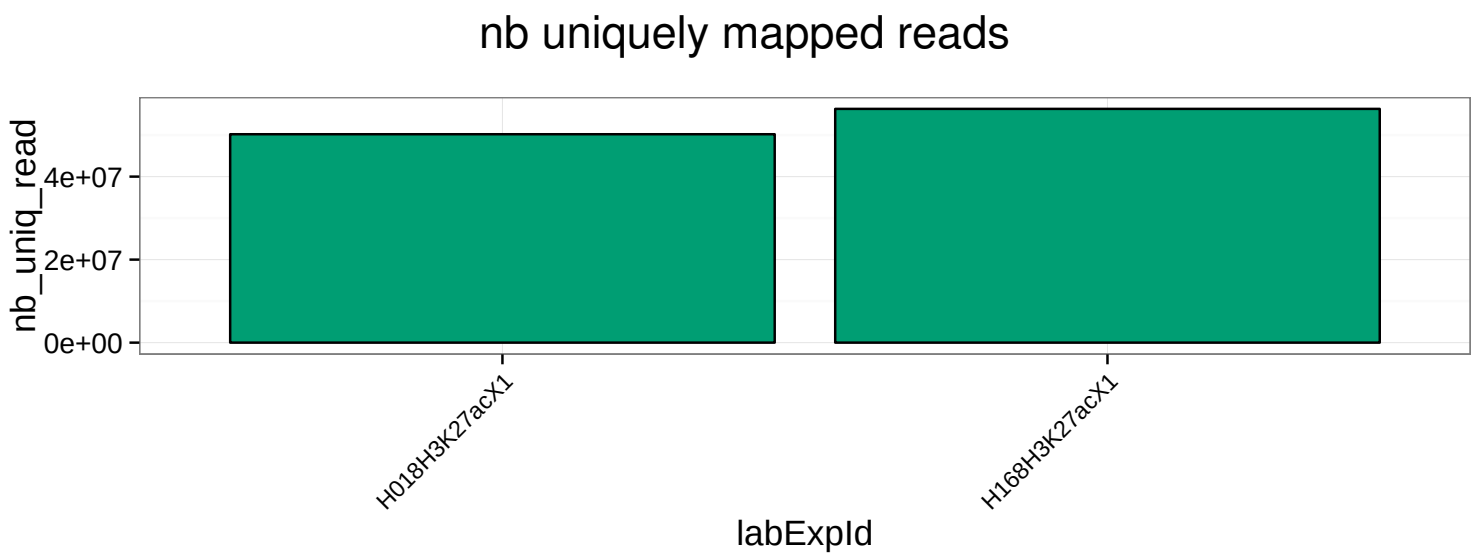
- Mapping stats
- Aggregation plots
- NRF and FRiP

H3K27me3

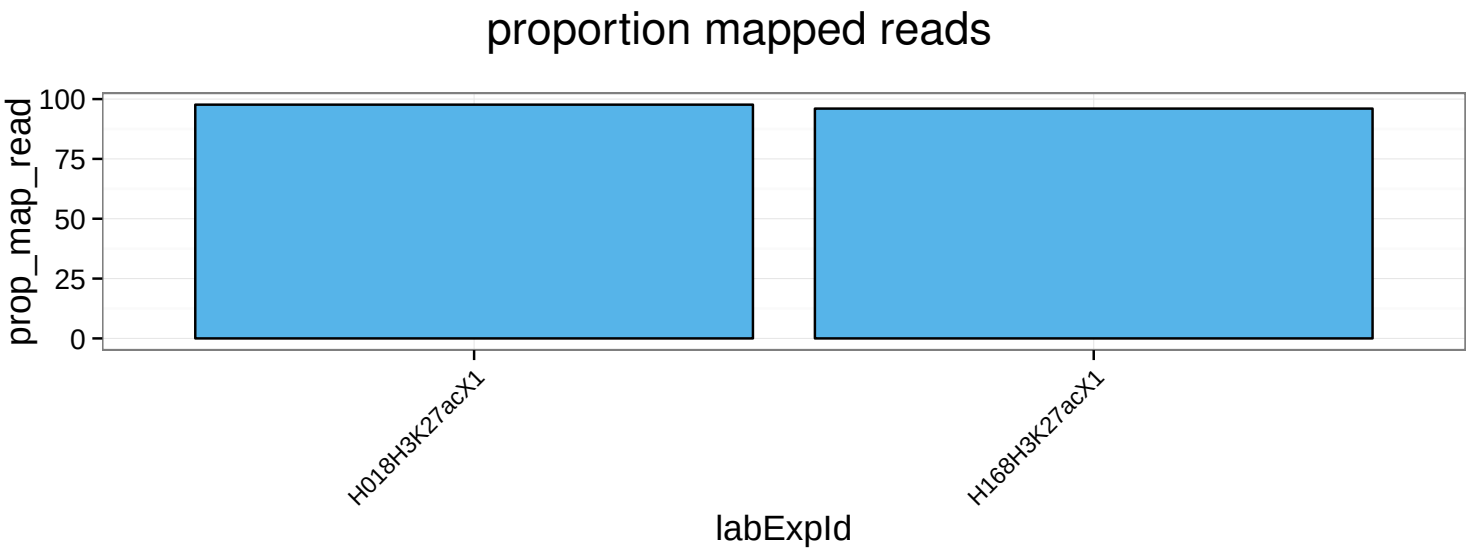
H3K36me3

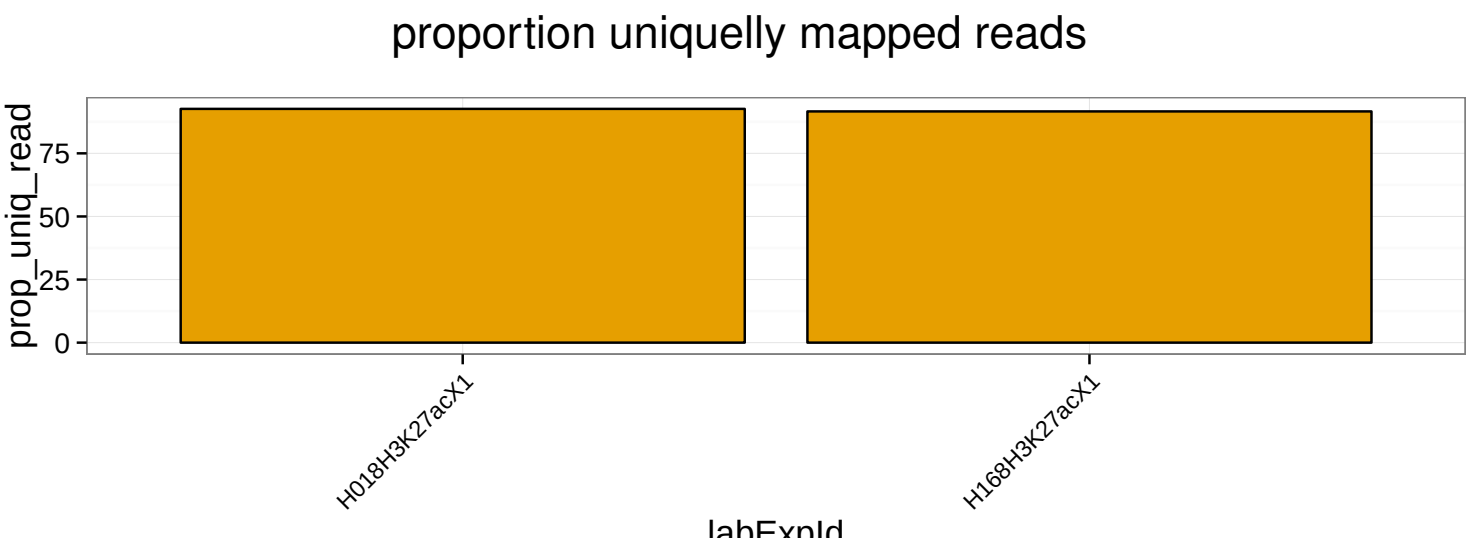
H3K27ac - mapping stats





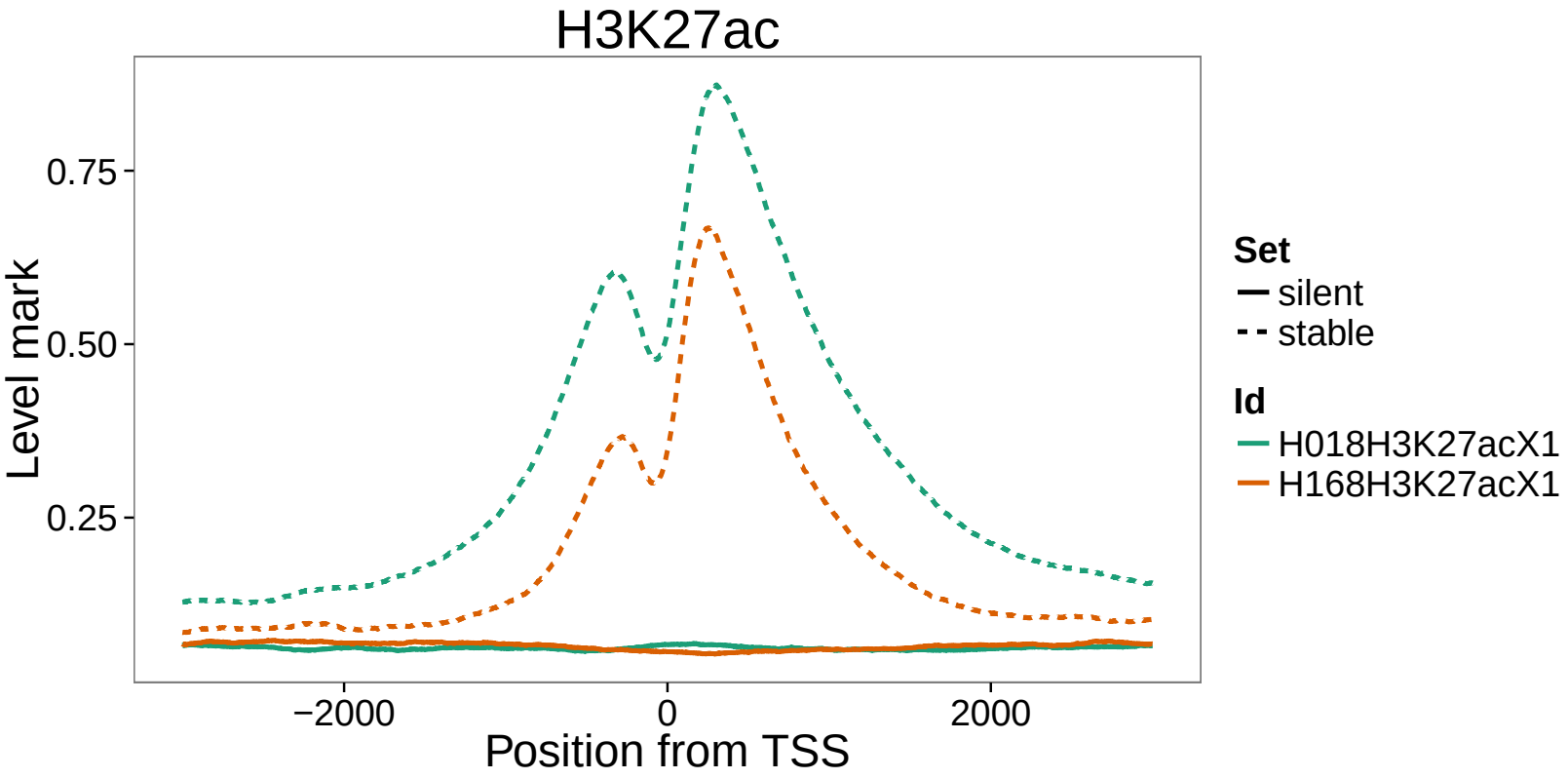
H3K27ac - mapping stats





H3K27ac

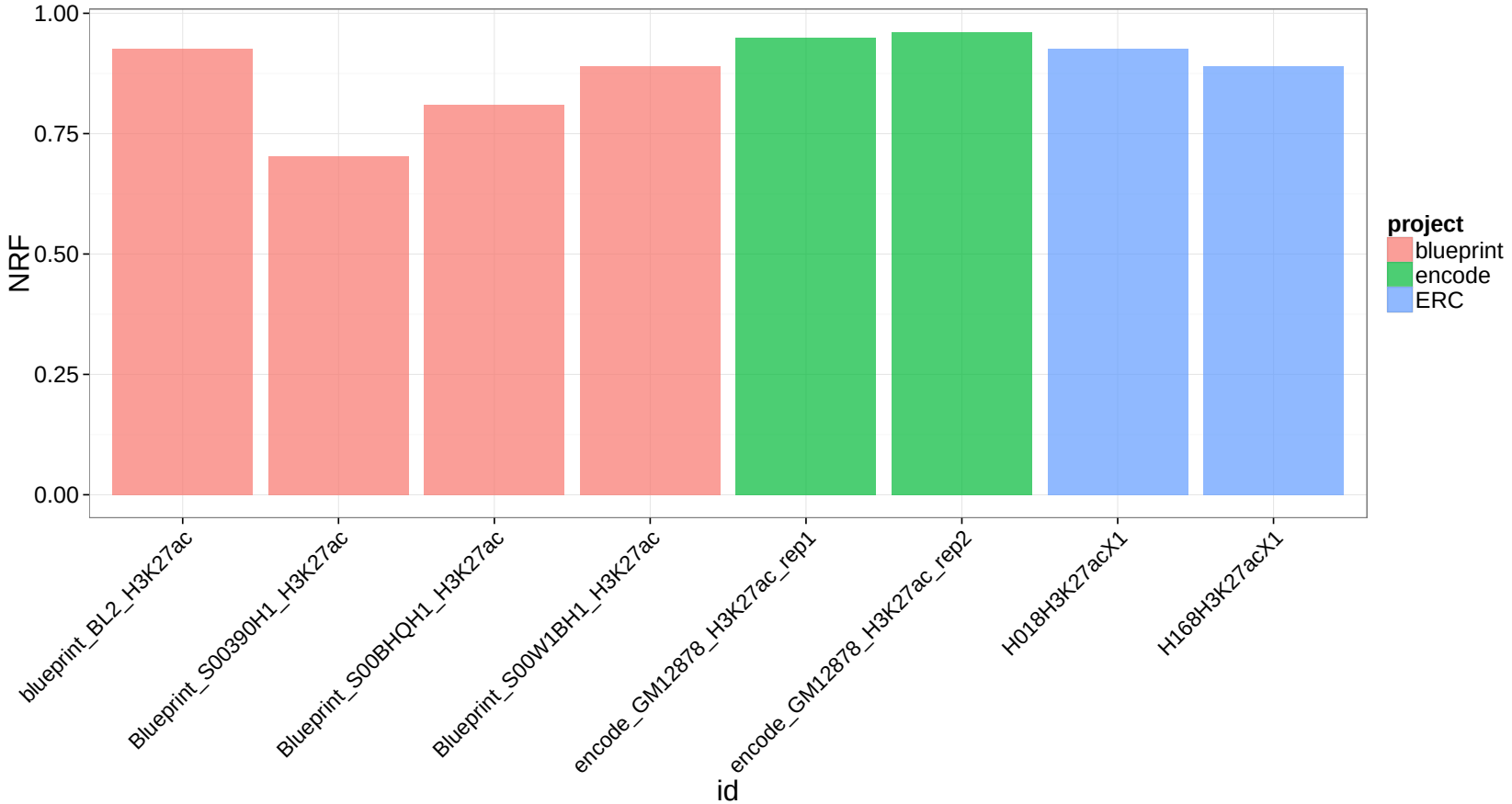
- 1000 silent genes
- 1000 stable genes (lowest CV)
- gencode v24



H3K27ac - NRF

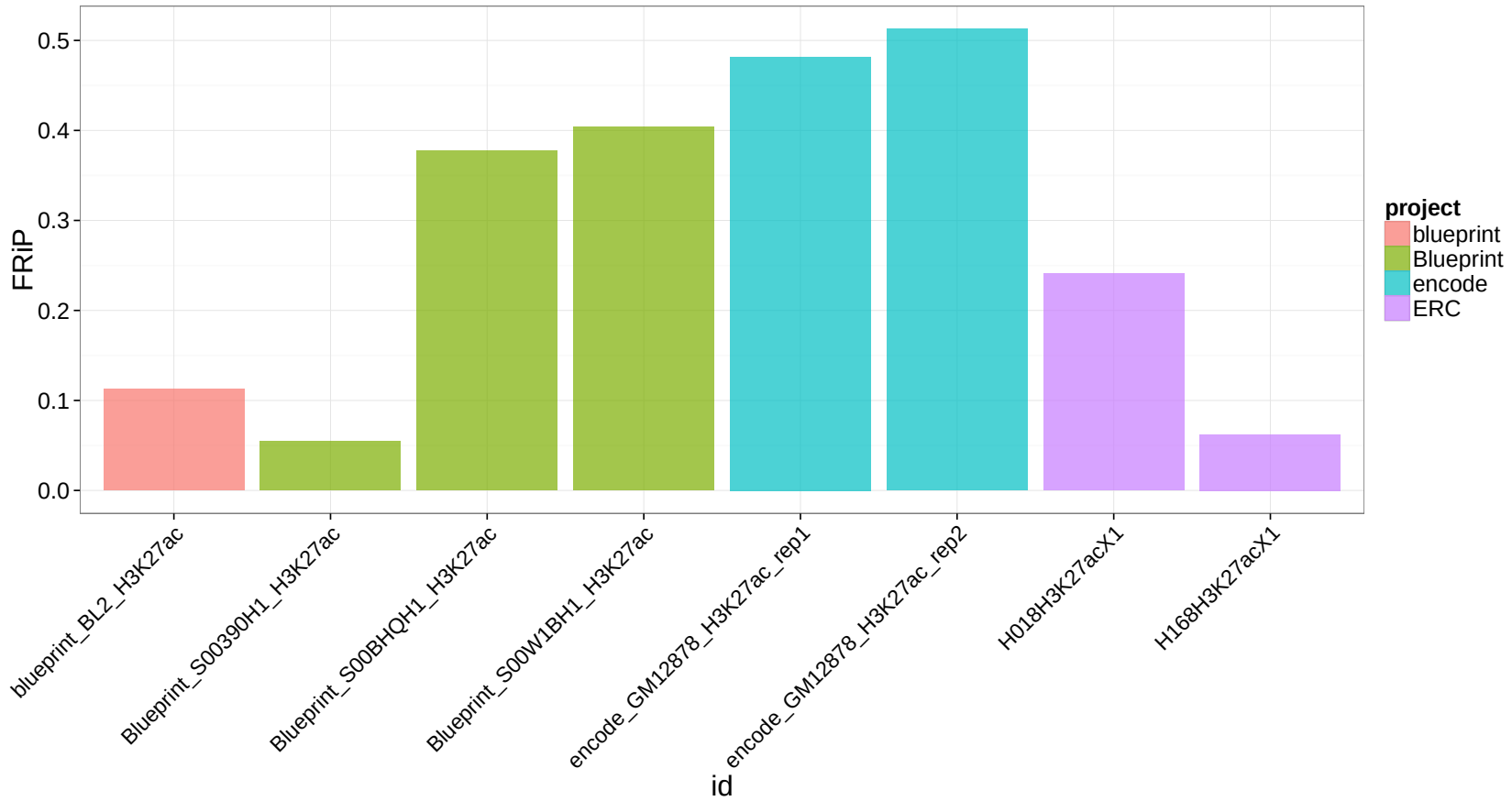
NRF: nonredundant fraction

NRF= nb unique start positions of uniquely mappable reads/nb uniquely mappable reads

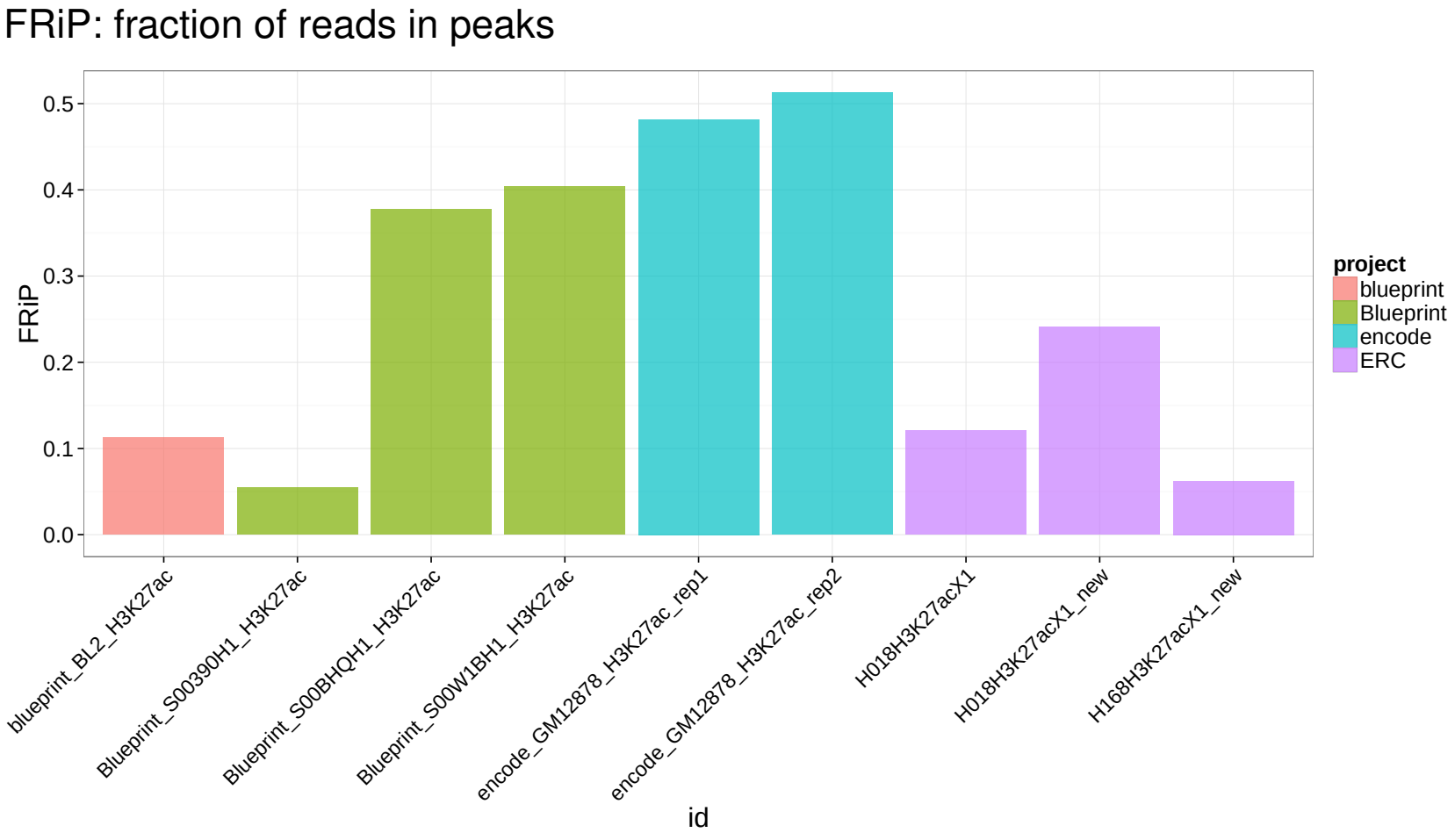


H3K27ac - FRiP

FRiP: fraction of reads in peaks



H3K27ac - FRiP (compare old VS new inputs)



Outline

Status samples

H3K4me1

H3K4me2

H3K4me3

H3K9ac

H3K9me3

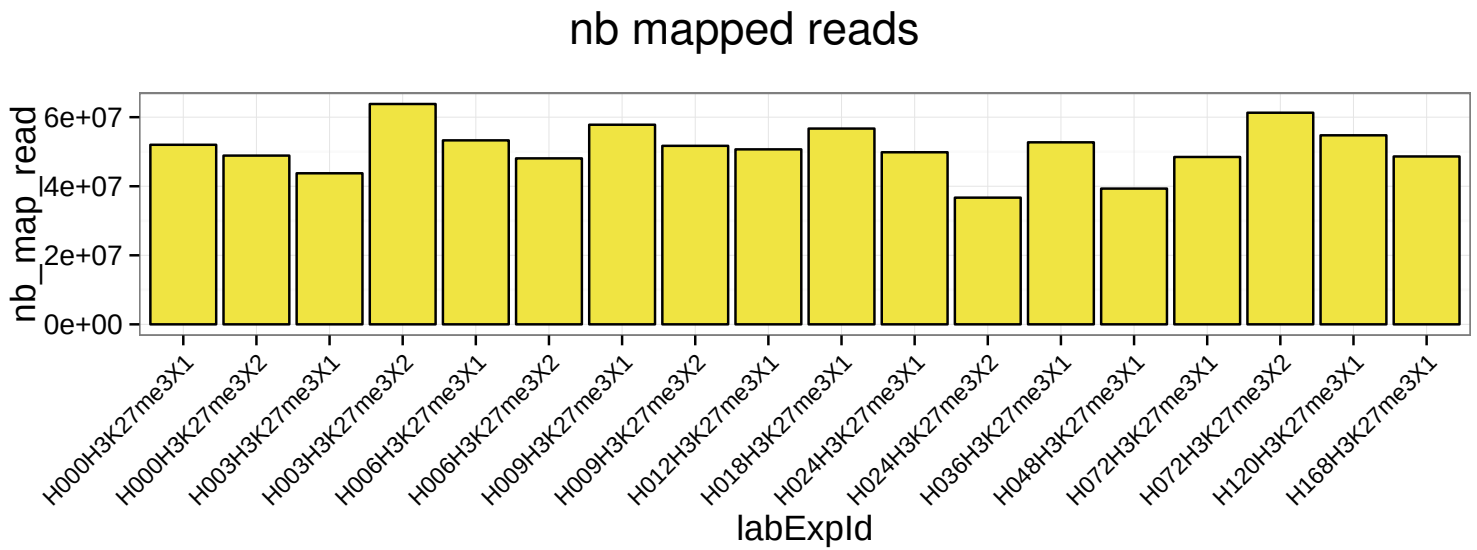
H3K27ac

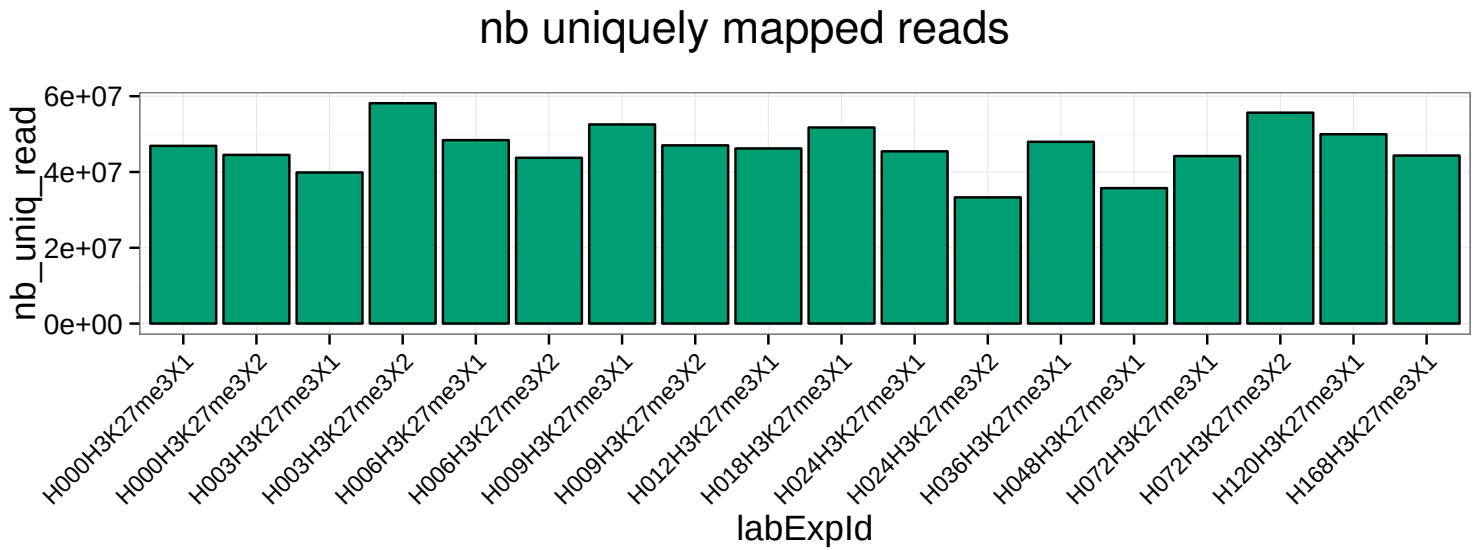
H3K27me3

- Mapping stats
- Aggregation plots
- Correlation between replicates
- NRF and FRiP

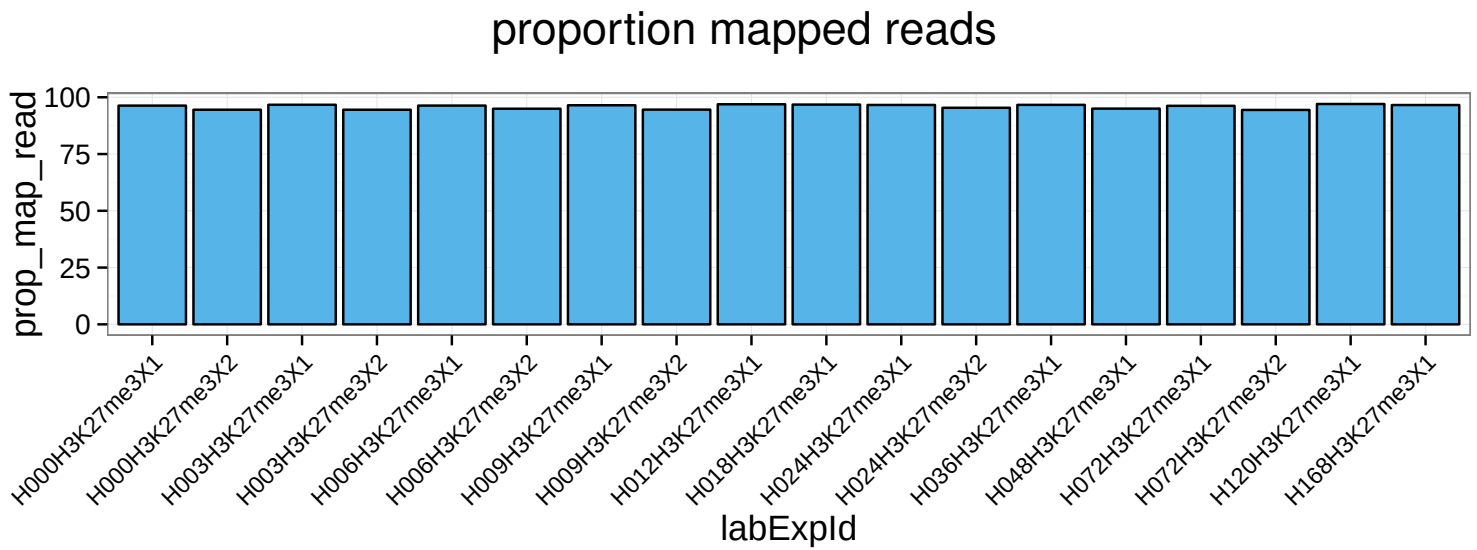
H3K36me3

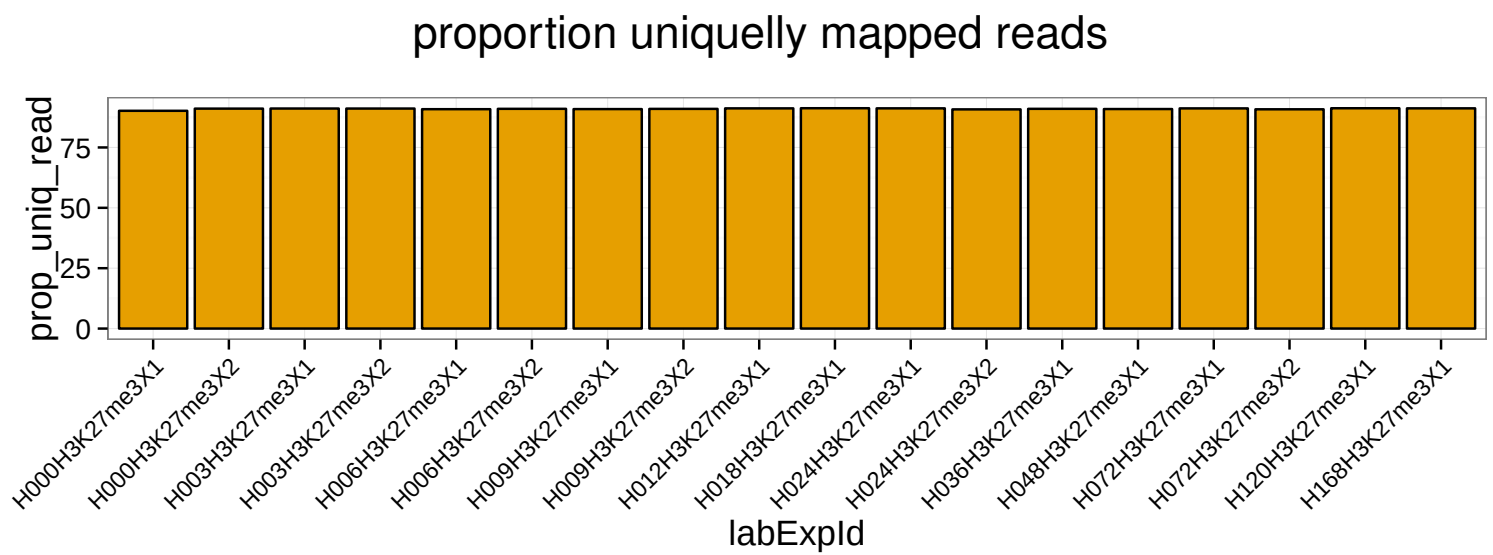
H3K27me3 - mapping stats





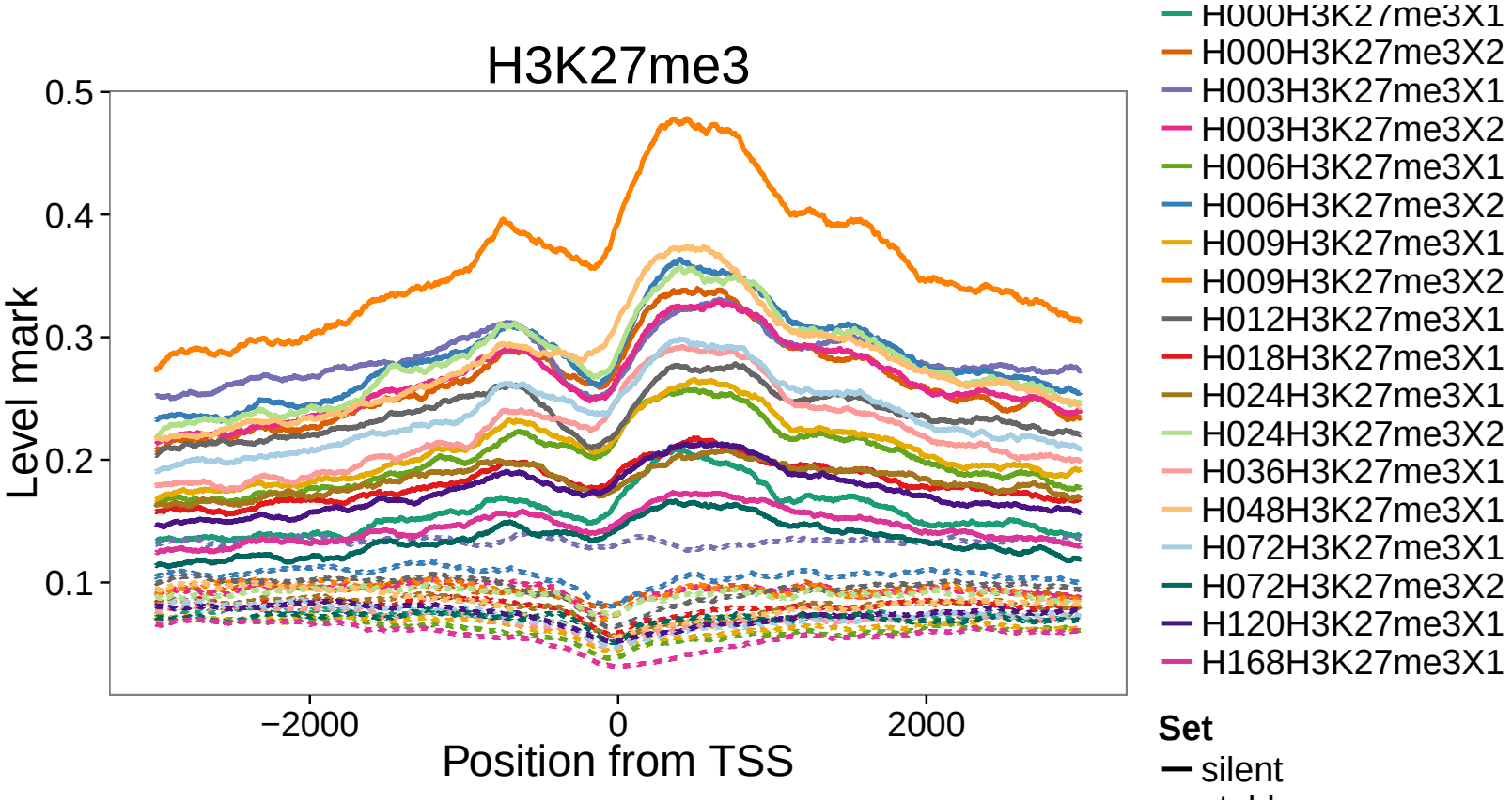
H3K27me3 - mapping stats





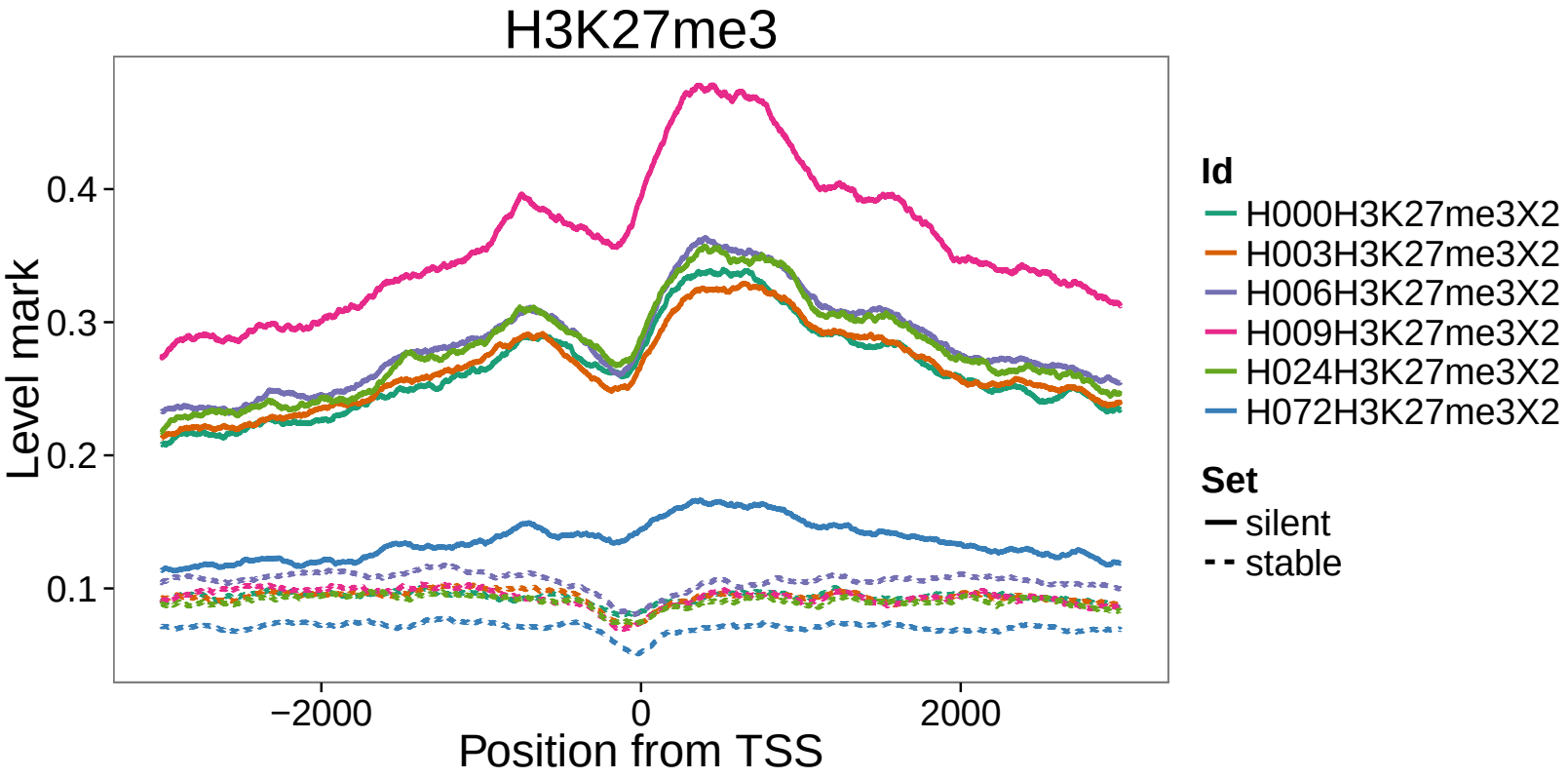
H3K27me3 - all sequenced samples

- 1000 silent genes
- 1000 stable genes (lowest CV)
- gencode v24

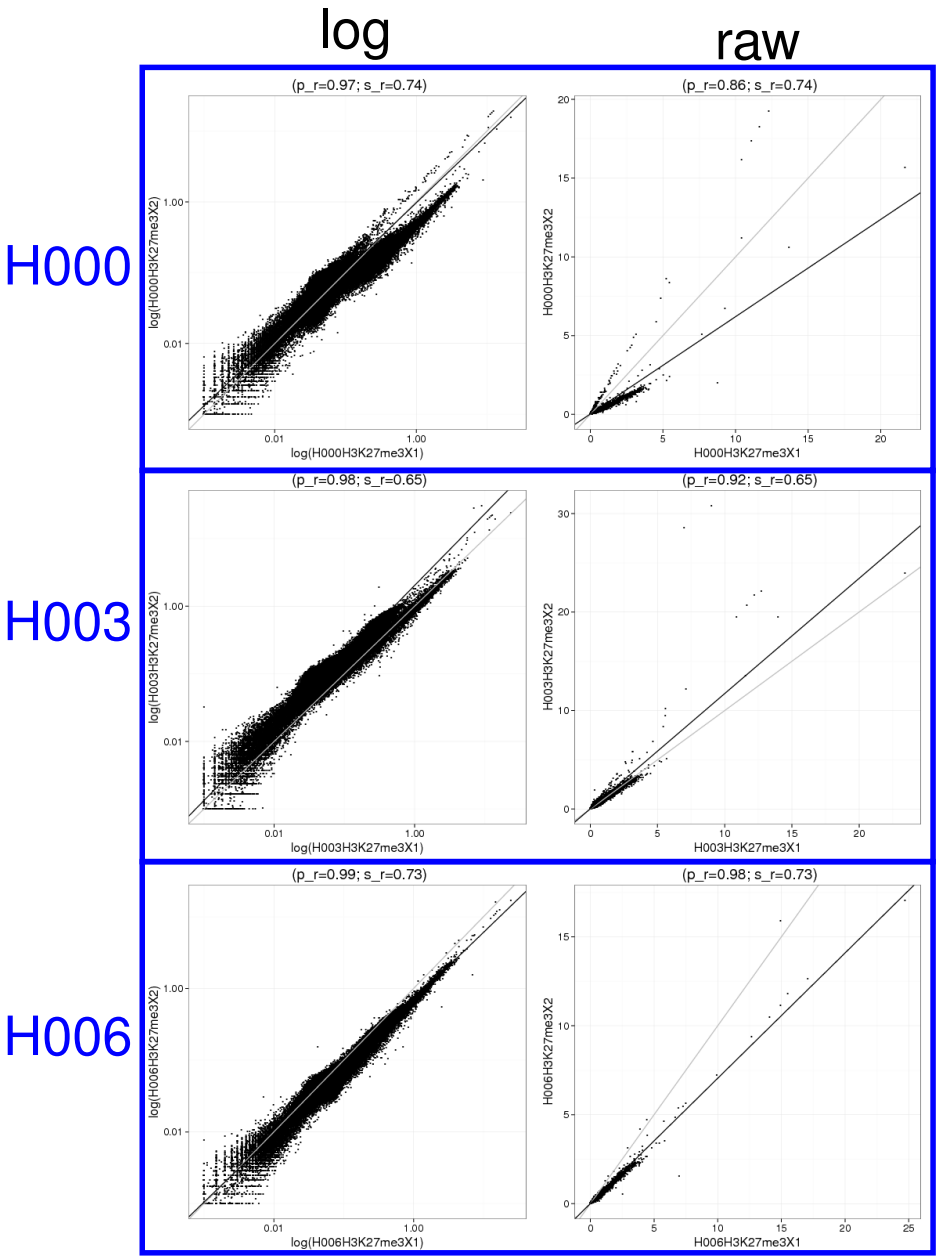


H3K27me3 - second replicate

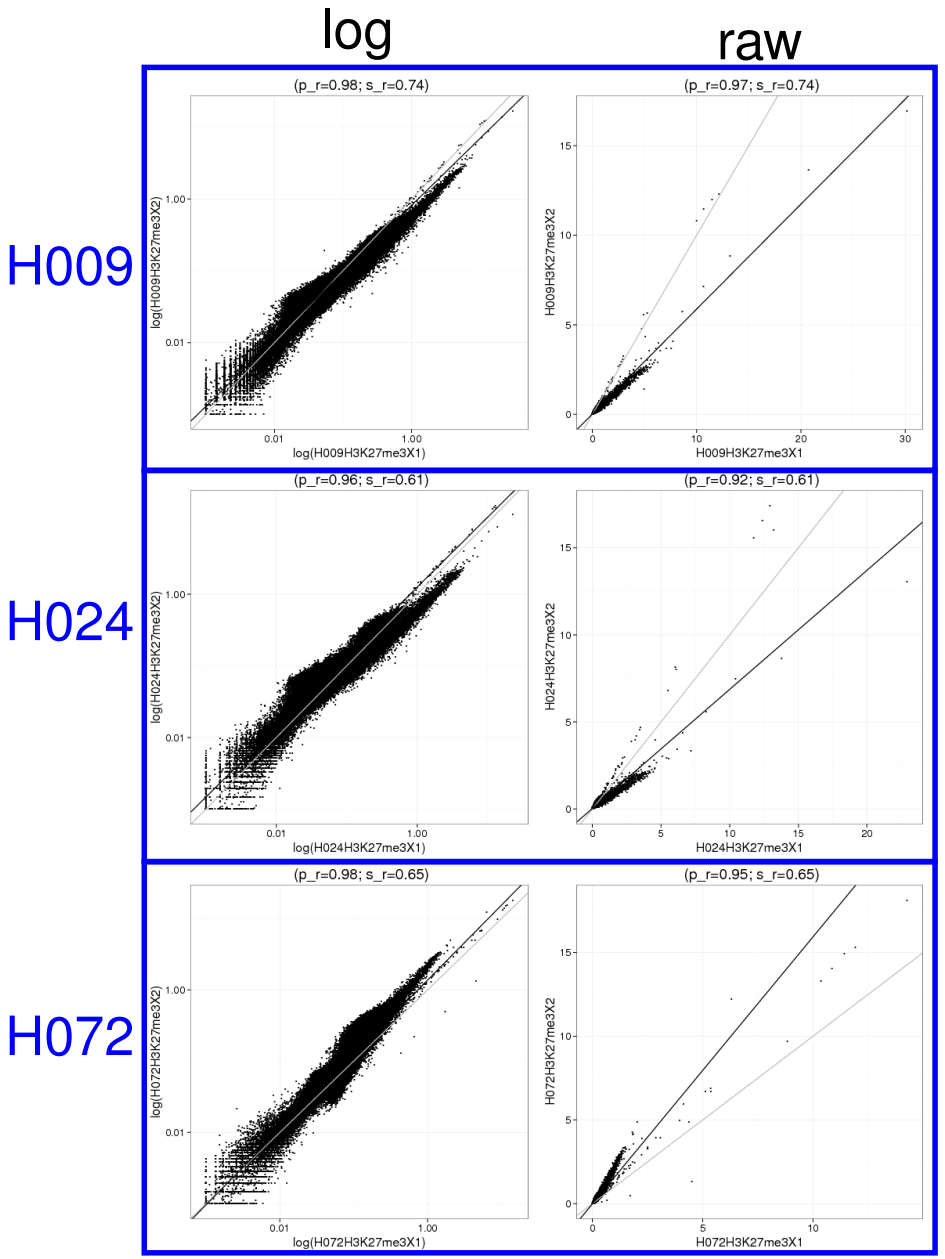
- 1000 silent genes
- 1000 stable genes (lowest CV)
- gencode v24



H3K27me3 - Correlation between replicates mean of 10kb windows



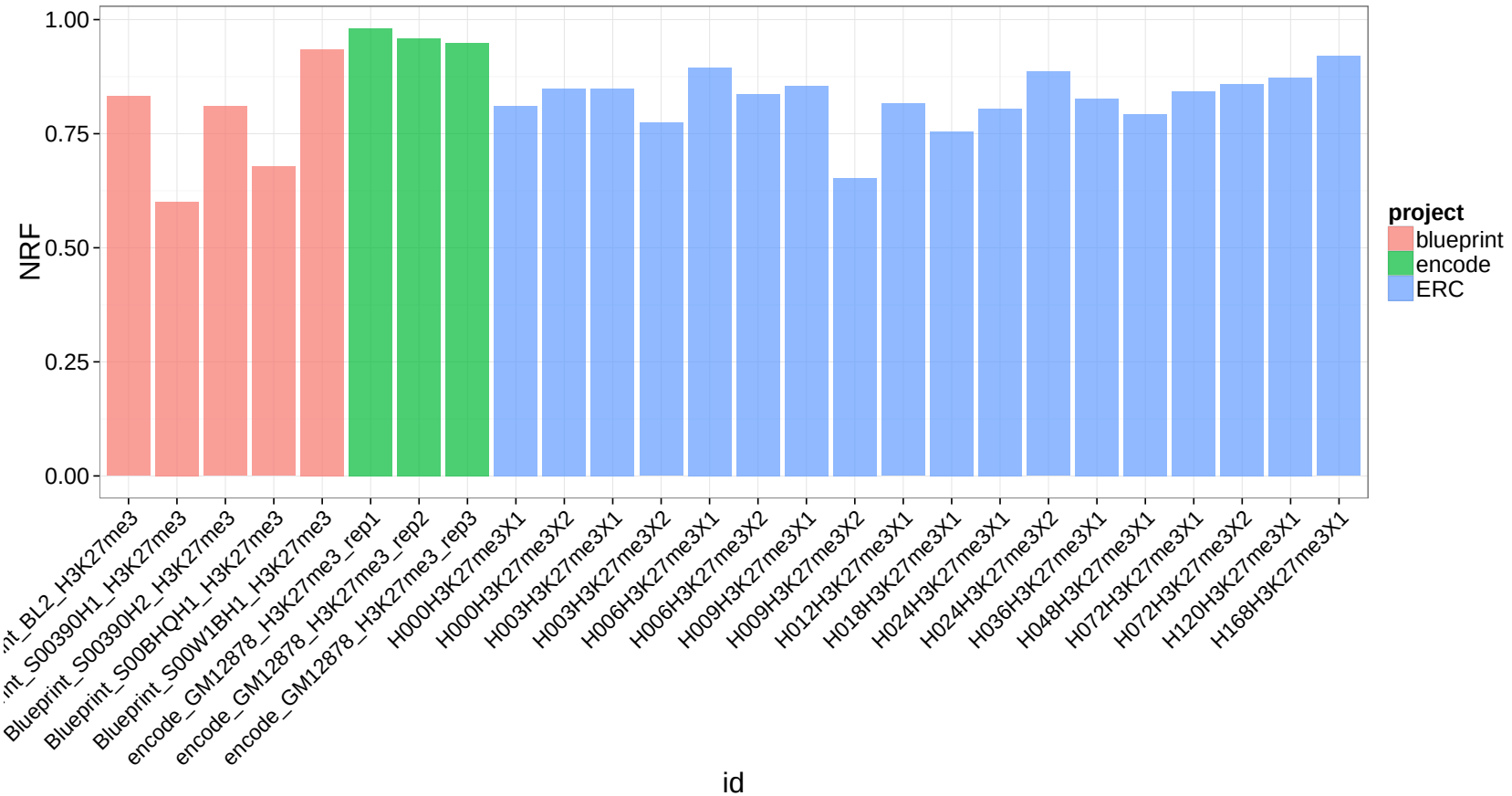
H3K27me3 - Correlation between replicates mean of 10kb windows



H3K27me3 - NRF

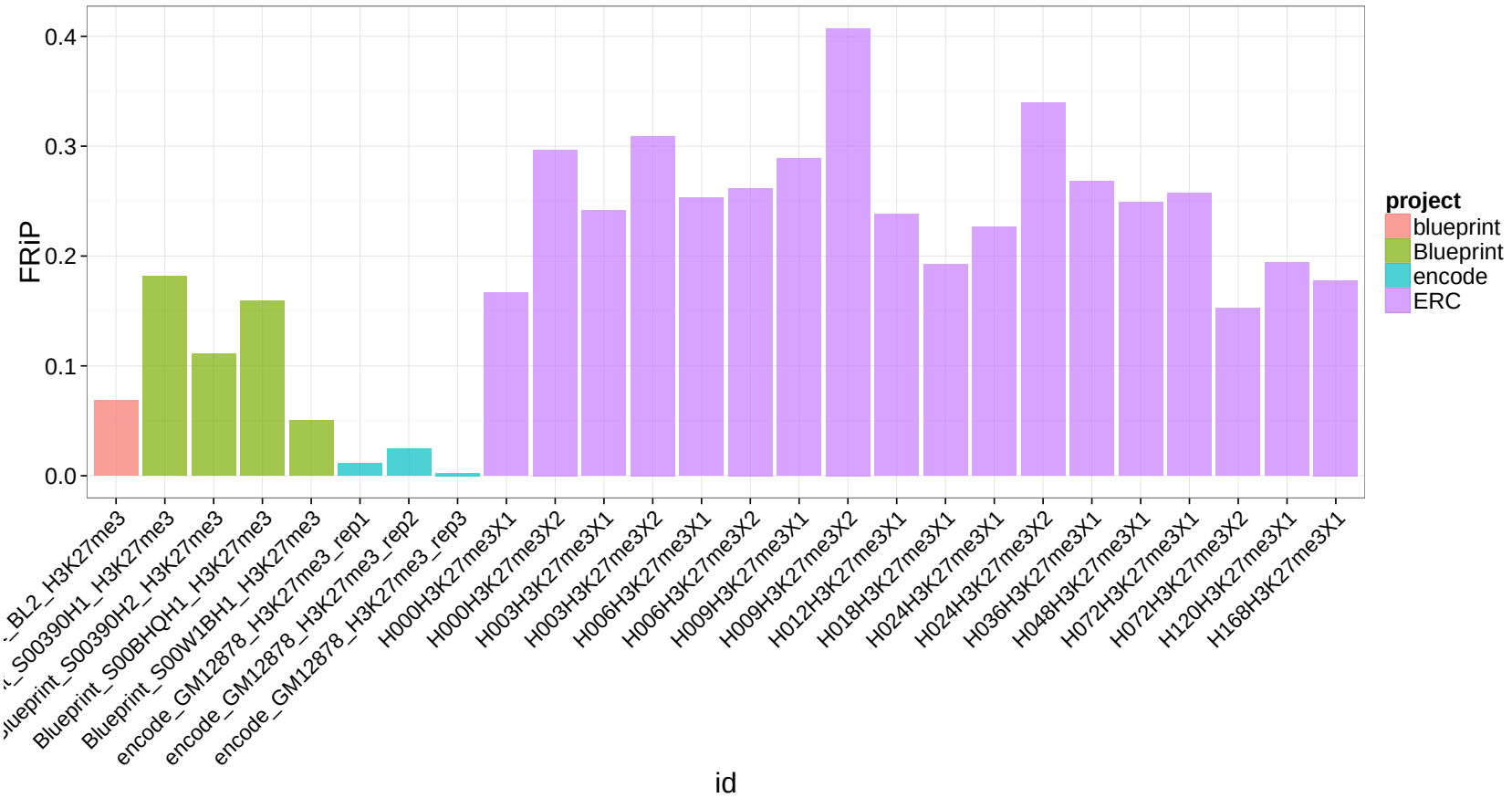
NRF: nonredundant fraction

NRF= nb unique start positions of uniquely mappable reads/nb uniquely mappable reads



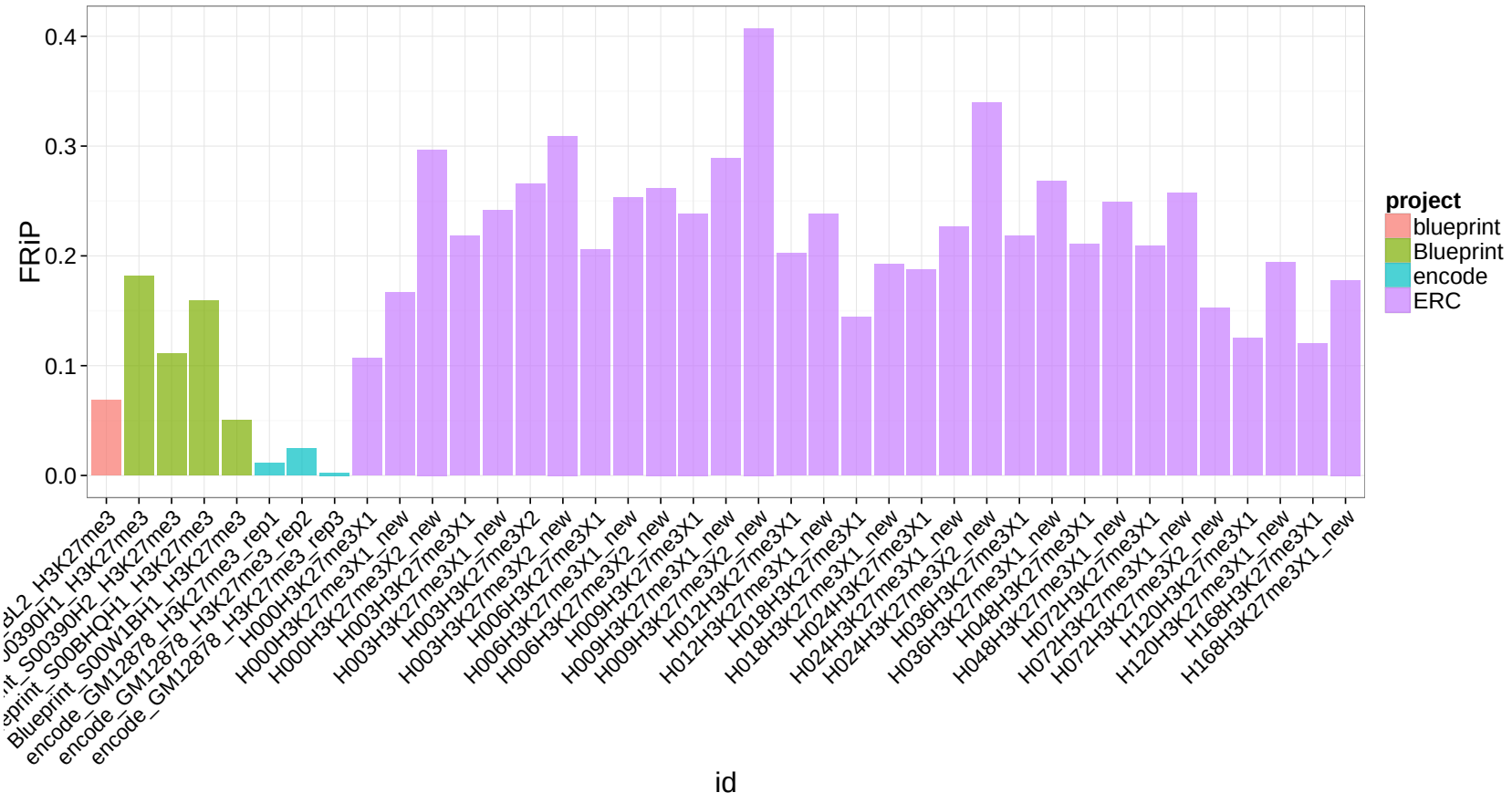
H3K27me3 - FRiP

FRiP: fraction of reads in peaks



H3K27me3 - FRiP compare old VS new inputs

FRiP: fraction of reads in peaks



Outline

Status samples

H3K4me1

H3K4me2

H3K4me3

H3K9ac

H3K9me3

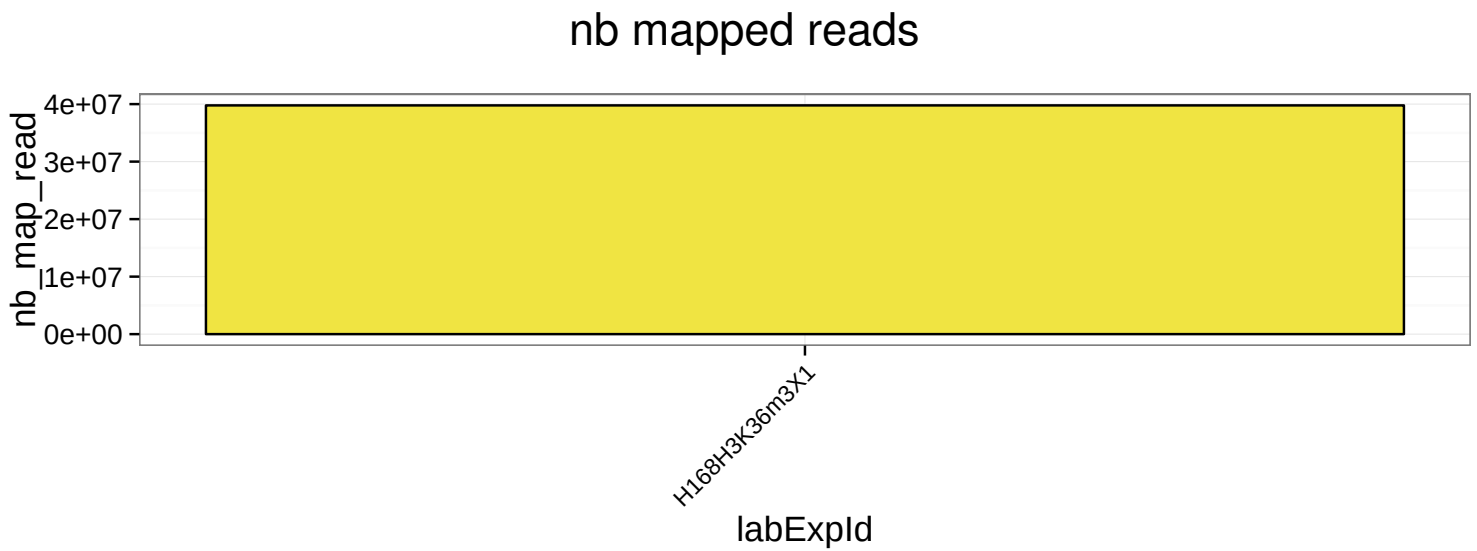
H3K27ac

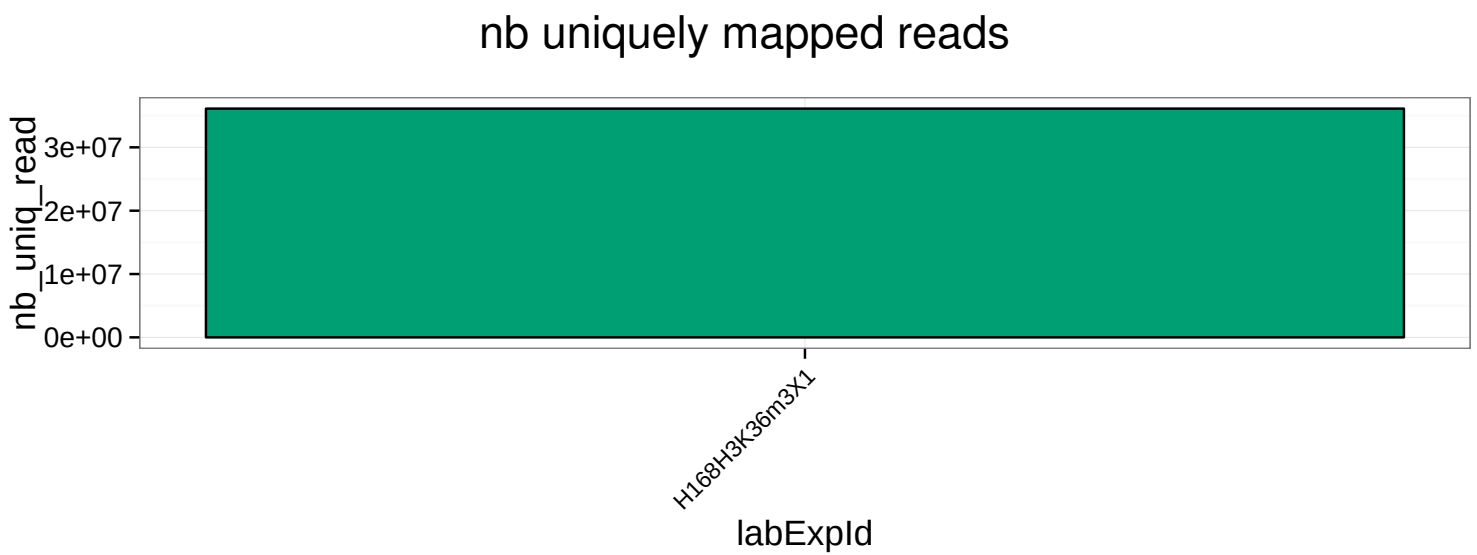
H3K27me3

H3K36me3

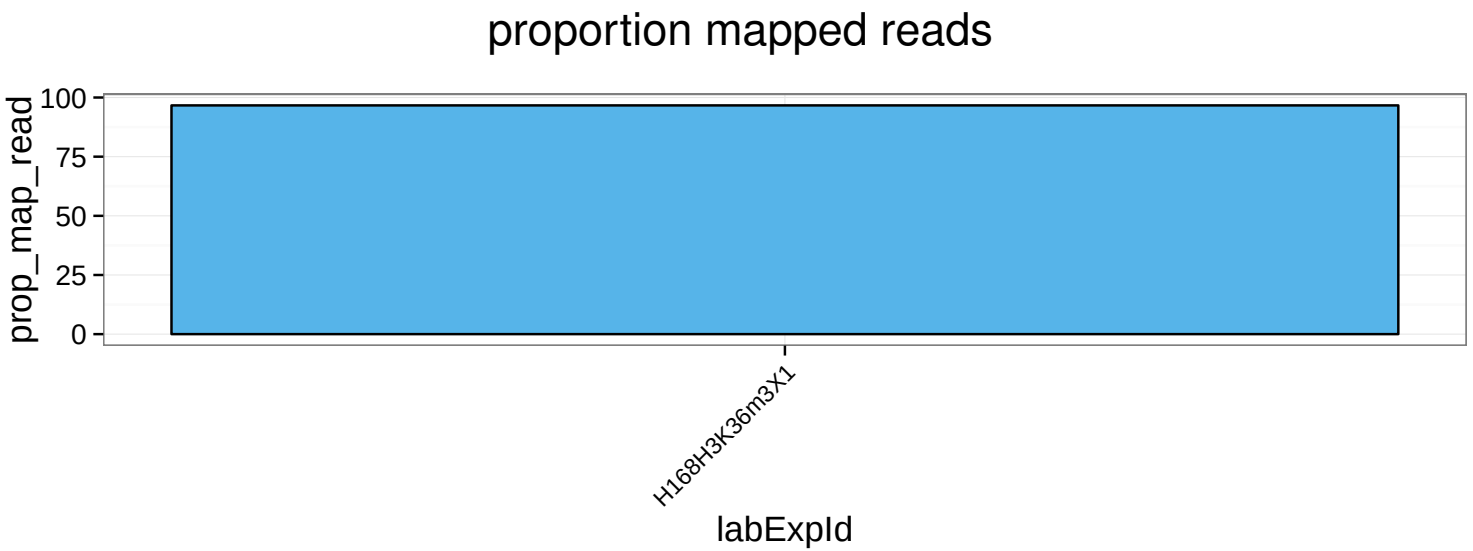
- Mapping stats
- Aggregation plots
- NRF and FRiP

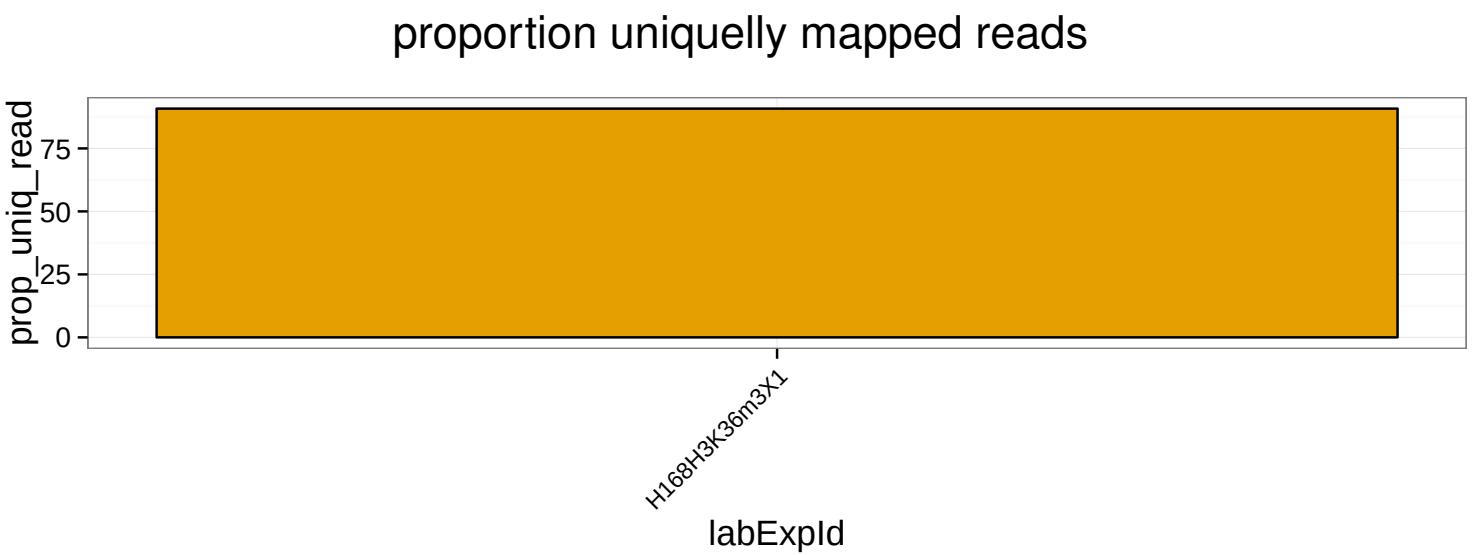
H3K36me3 - mapping stats





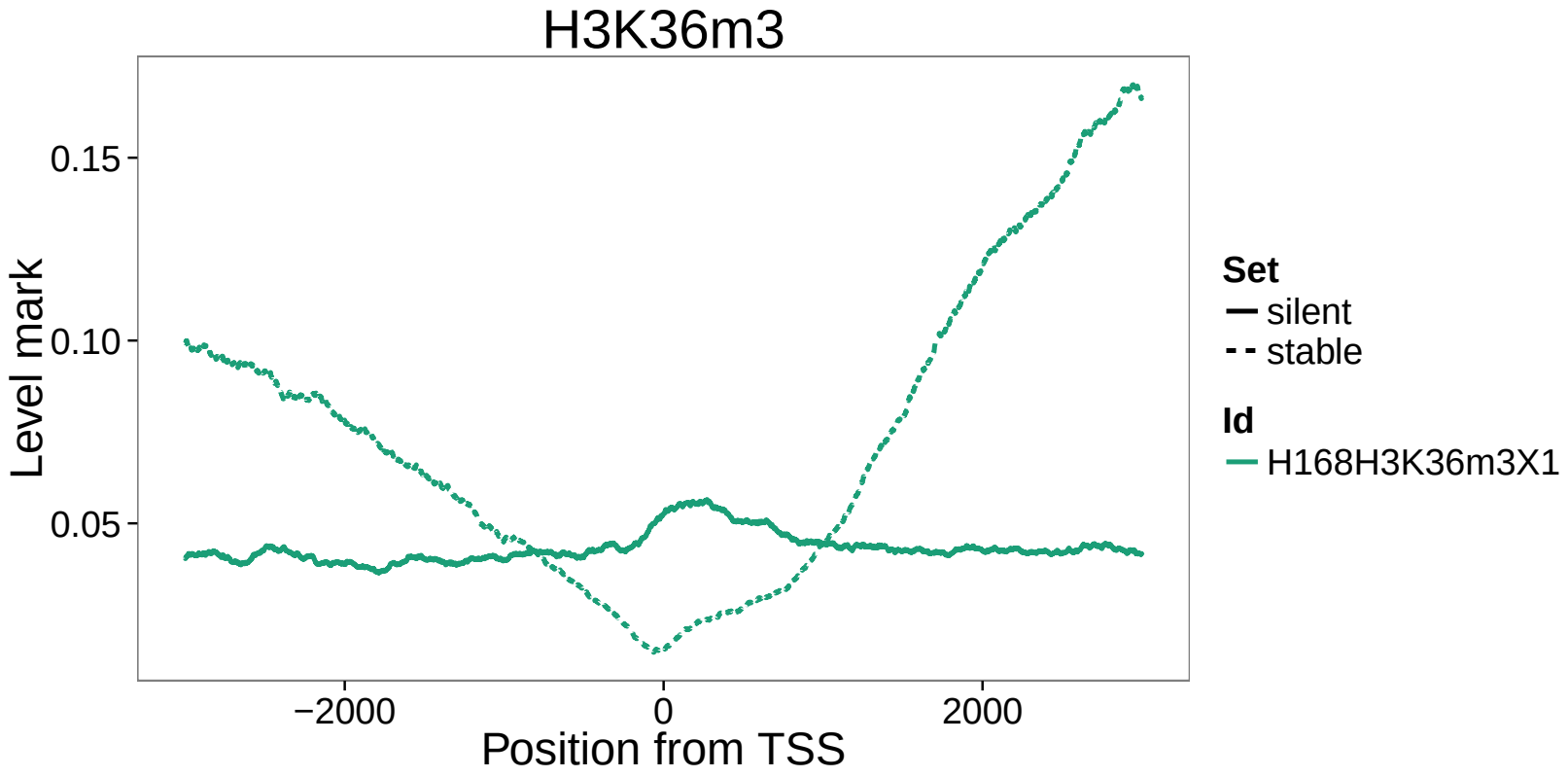
H3K36me3 - mapping stats





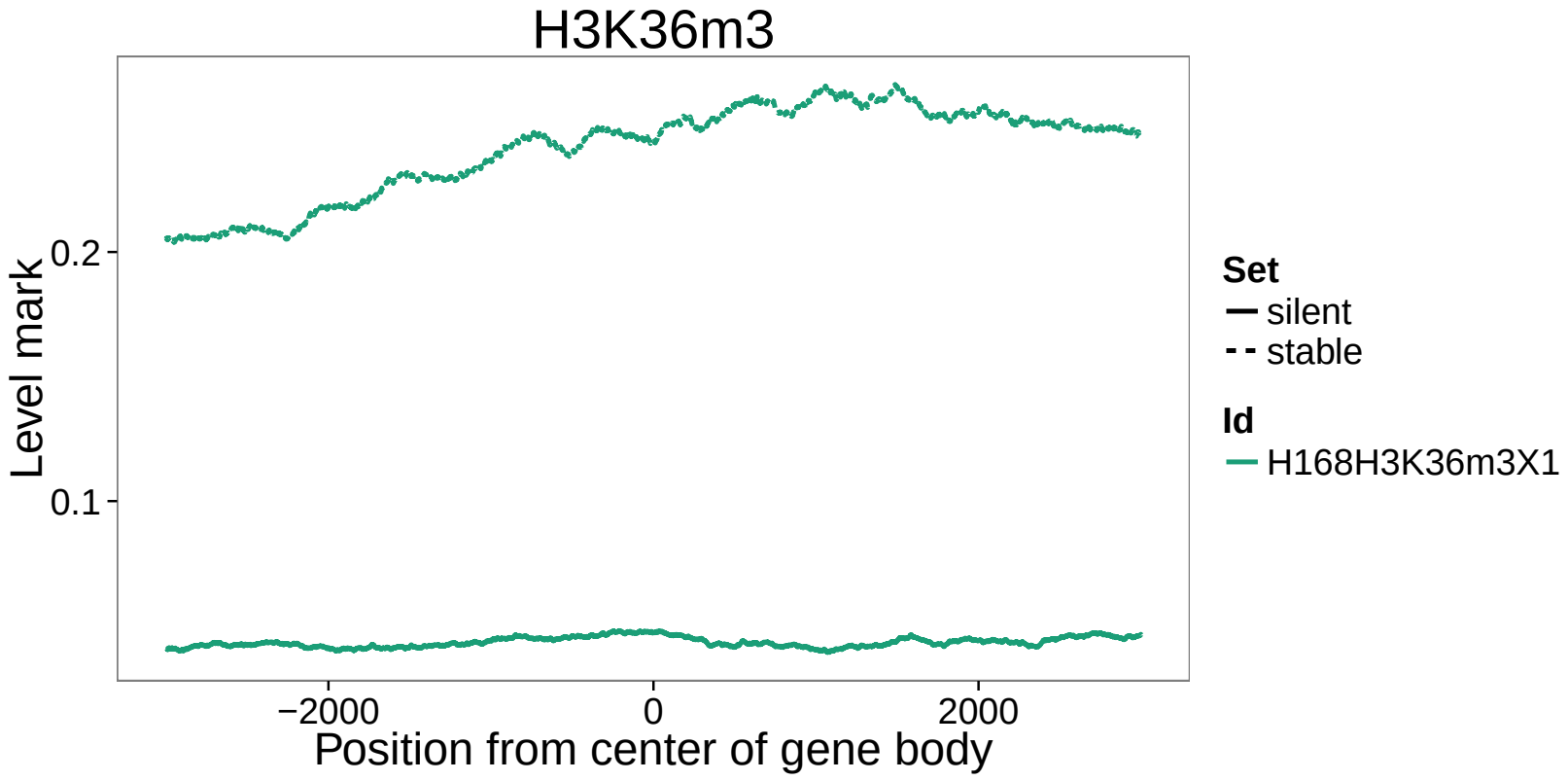
H3K36me3

- 1000 silent genes
- 1000 stable genes (lowest CV)
- gencode v24



H3K36me3 - gene body

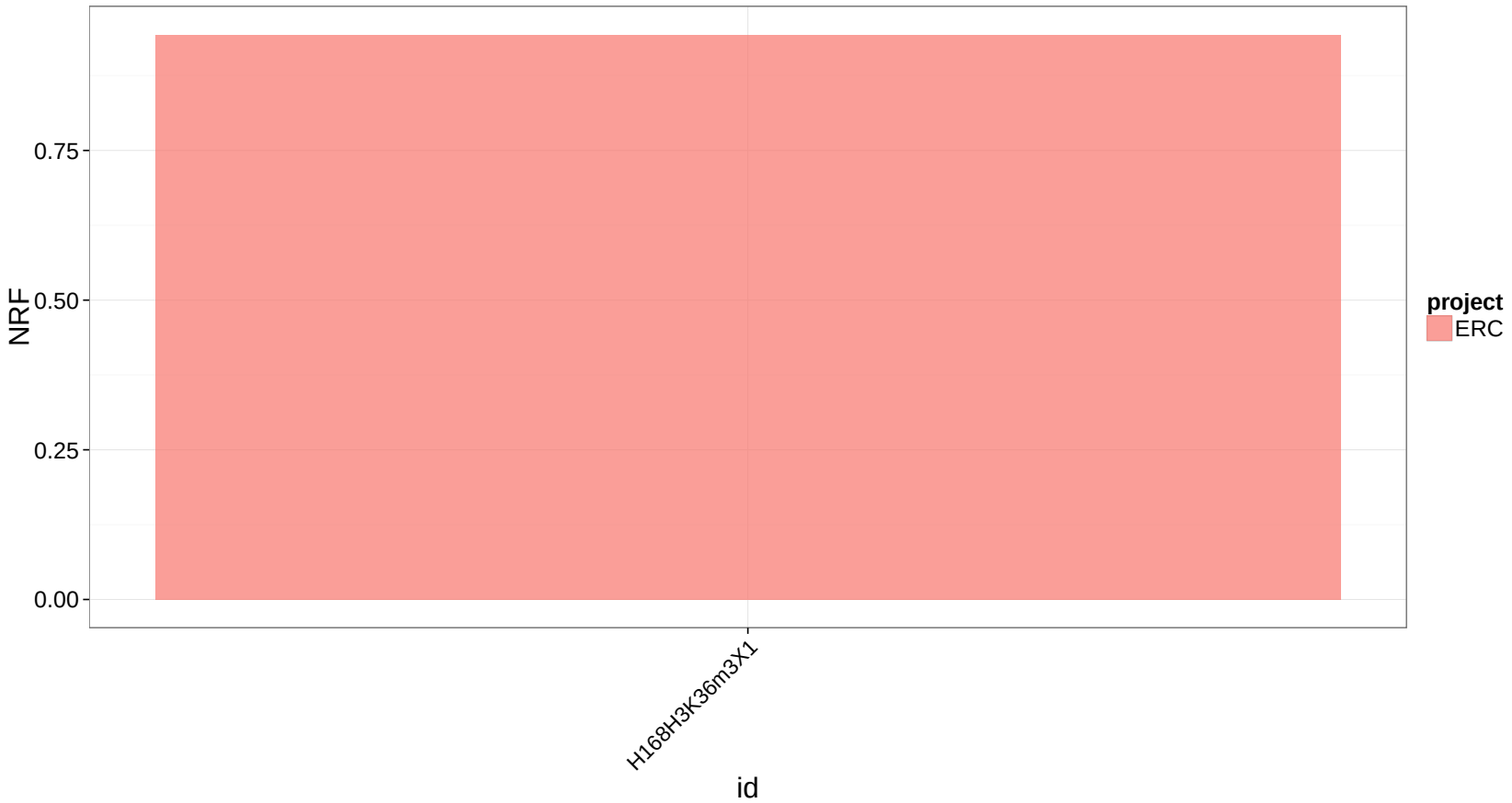
- 1000 silent genes
- 1000 stable genes (lowest CV)
- gencode v24



H3K36me3 - NRF

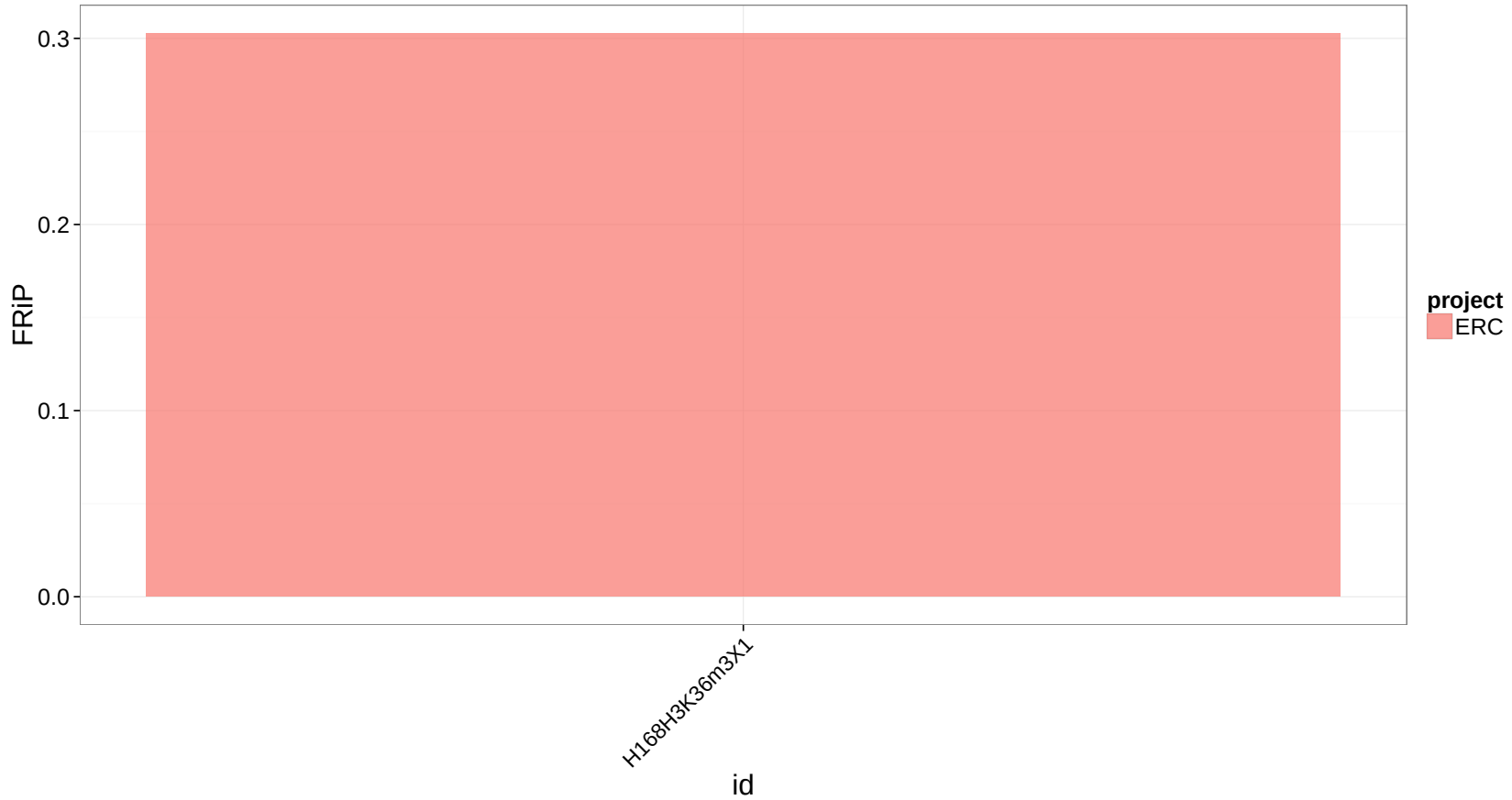
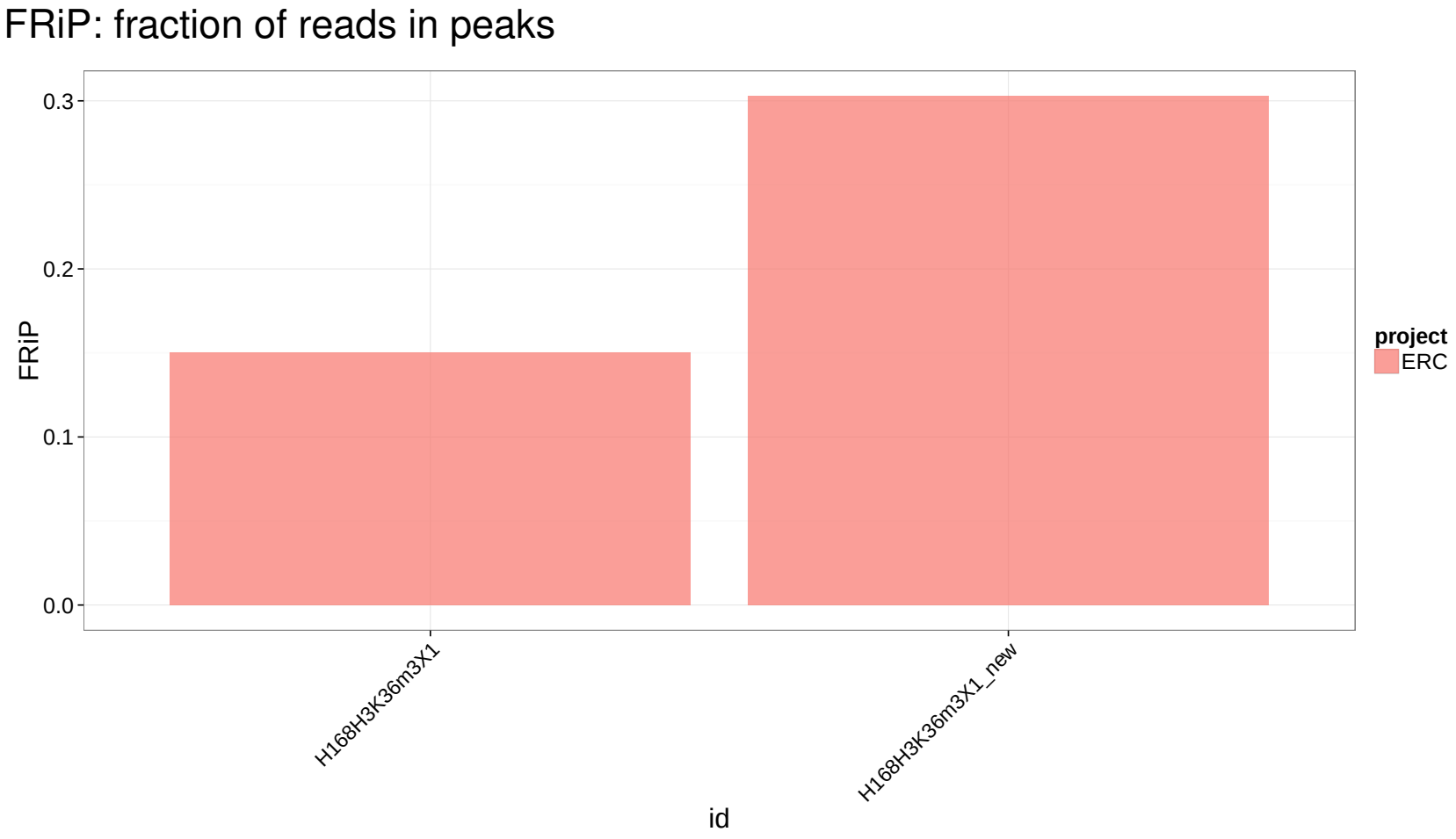
NRF: nonredundant fraction

NRF= nb unique start positions of uniquely mappable reads/nb uniquely mappable reads



H3K36me3 - FRiP

FRiP: fraction of reads in peaks



H3K36me3 - FRiP (compare old VS new inputs