# Chipseq pipeline

31/05/2016

Outline

Mapping, Merge, Model

- uses the GEM mapper and tools

    1. gem-mapper with default parameters
    2. gt.filter: max edit distance (2 - absolute number of bases)
    3. gt.filter: max 10 output alignments
    4. exclude SAM flag 256: keep primary alignments only

- merge BAM files on metadata key and produce single output with read groups

- uses SPP to estimate fragment size and produce cross-correlation plot

Peak Calling

- uses MACS2 to call peaks - works with or without input

    1. pileup signal tracks - **input is not used**
    2. fold enrichment signal tracks - **input is used and required**
    3. -log10(p-value) signal tracks - **input is used and required**

    4. narrow peaks - **input is used**
    5. broad and gapped peaks - **input is used**

- narrowPeak, peak locations with peak summit, pvalue and qvalue (BED6+4)
- broadPeak, similar to narrowPeak (BED6+3)
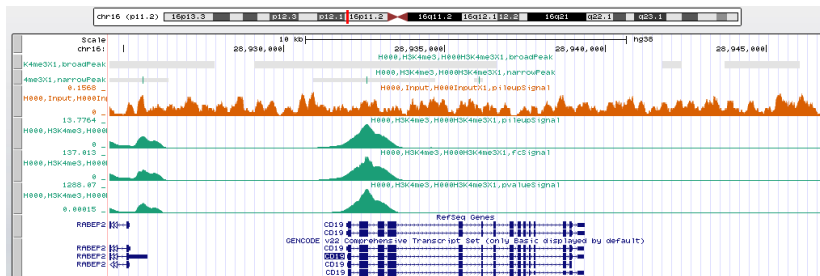- gappedPeak, both narrow and broad peaks (BED12+3)

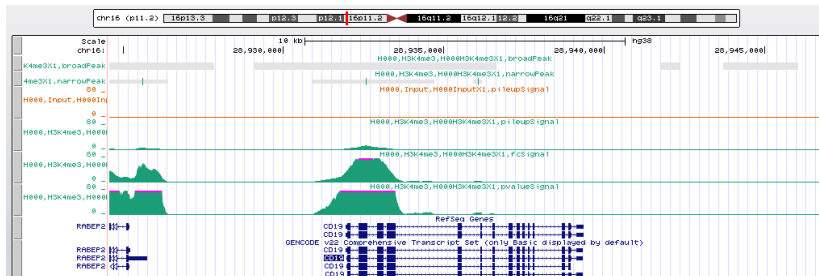# Example tracks - cebpa autoscale
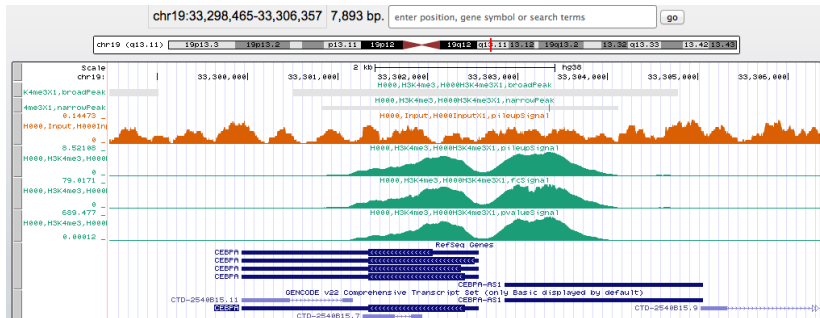
Example tracks - cebpa vertical
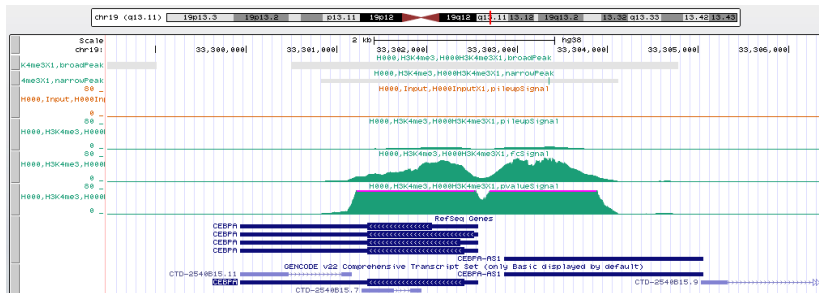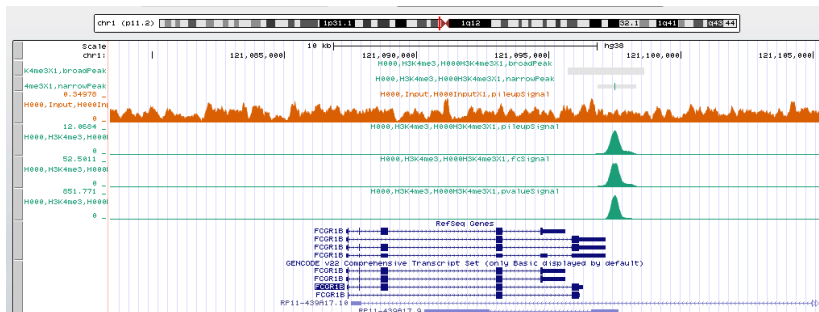
Example tracks - CD19 autoscale
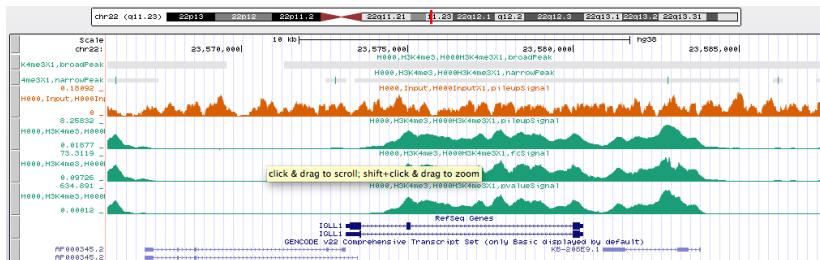
Example tracks - CD19 vertical

Example tracks - FCGR1B autoscale

Example tracks - FCGR1B vertical

Example tracks - IGLL1 autoscale

Example tracks - IGLL1 vertical