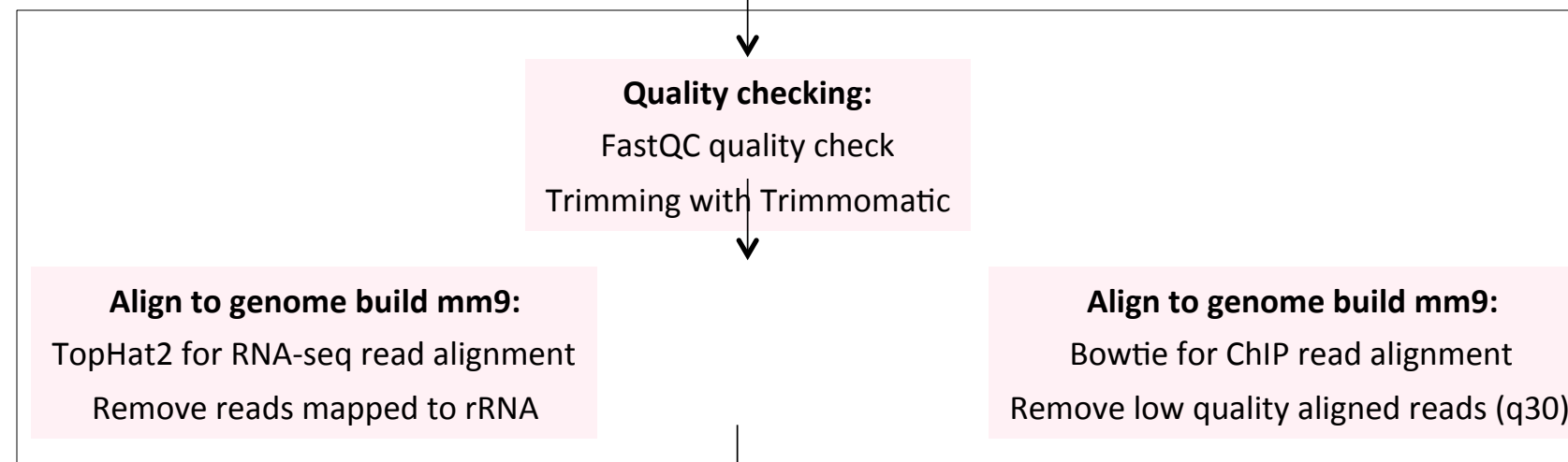


Quality control and alignment:

Input: Illumina HiSeq 2500 short reads



Output: Aligned bam files

RNA-seq:

Input: BA2 rep1, BA2 rep2, PBA rep1, PBA rep2 bam files

Splicing aware read counting:
Cufflinks

Output: FPKM

Output: Raw Read Counts

Differential expression:
edgeR

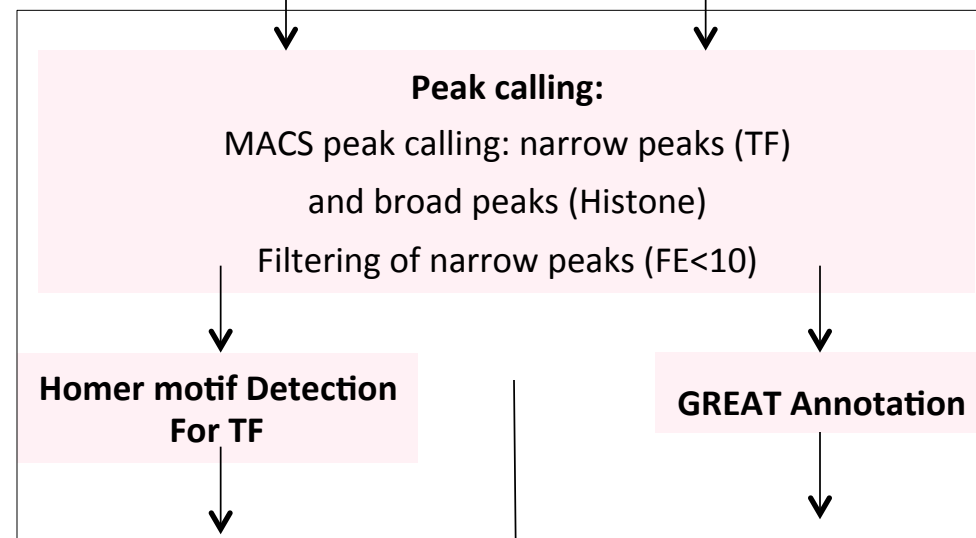
Output: Gene expression: FPKM values

Output: Differentially expressed genes

ChIP-seq peak calling:

Input: IP bam

Input: Input bam



Output: Binding site motif

Output: Peaks

Output: Annotation

Meis differential binding sites:

Input: Meis PBA IP bam files

Input: Meis BA2 IP bam files

Differential binding:
diffReps with replicates
Remove Fold change < log3

Output: Meis PBA>BA2

Intersect with Meis
Peaks FE>=10

Input: Meis PBA peaks

Output: High Confidence Meis binding higher in PBA