ELAND (1-36 bp alignment)

Scan for EcoP15I tag

- No: Discard the reads
- Yes: Mask tag sequence as "n"

ELAND (2-28 bp alignment)

Unique/multiple aligned

- Quality failed/not aligned: Discard the reads
- Distance from neighboring HpaII site:
  - ≤27 bp: Discard the reads
  - ≥27 bp:
    - Unique hit:
      - Weighted based on aligned number
    - Multiple aligned hits:
      - aligned >10: Discard the reads
      - aligned ≤10

Map to annotated HpaII site?

- No: Putative polymorphic HpaII sites → dbSNP check
- Yes: Count hit number
  - MspI=0: Putative polymorphic HpaII sites → dbSNP check
  - Unique/multiple aligned:
    - aligned >10: Discard the reads
    - aligned ≤10

Normalize HpaII with MspI by angle calculation

Generate bedGraph files

UCSC genome browser