

Input

Reads with 3'(A)_{≥ 5nt}

Mapping and priming
site identification

Removal of internal
priming sites

overlap with
annotations

3'UTR,exon,intron,intergenic

Extension based
on RNaseq

Counting windows
from annotations

High confidence
ends

$\Sigma \text{reads} \geq 90\%$ of total reads
per gene

Counting windows