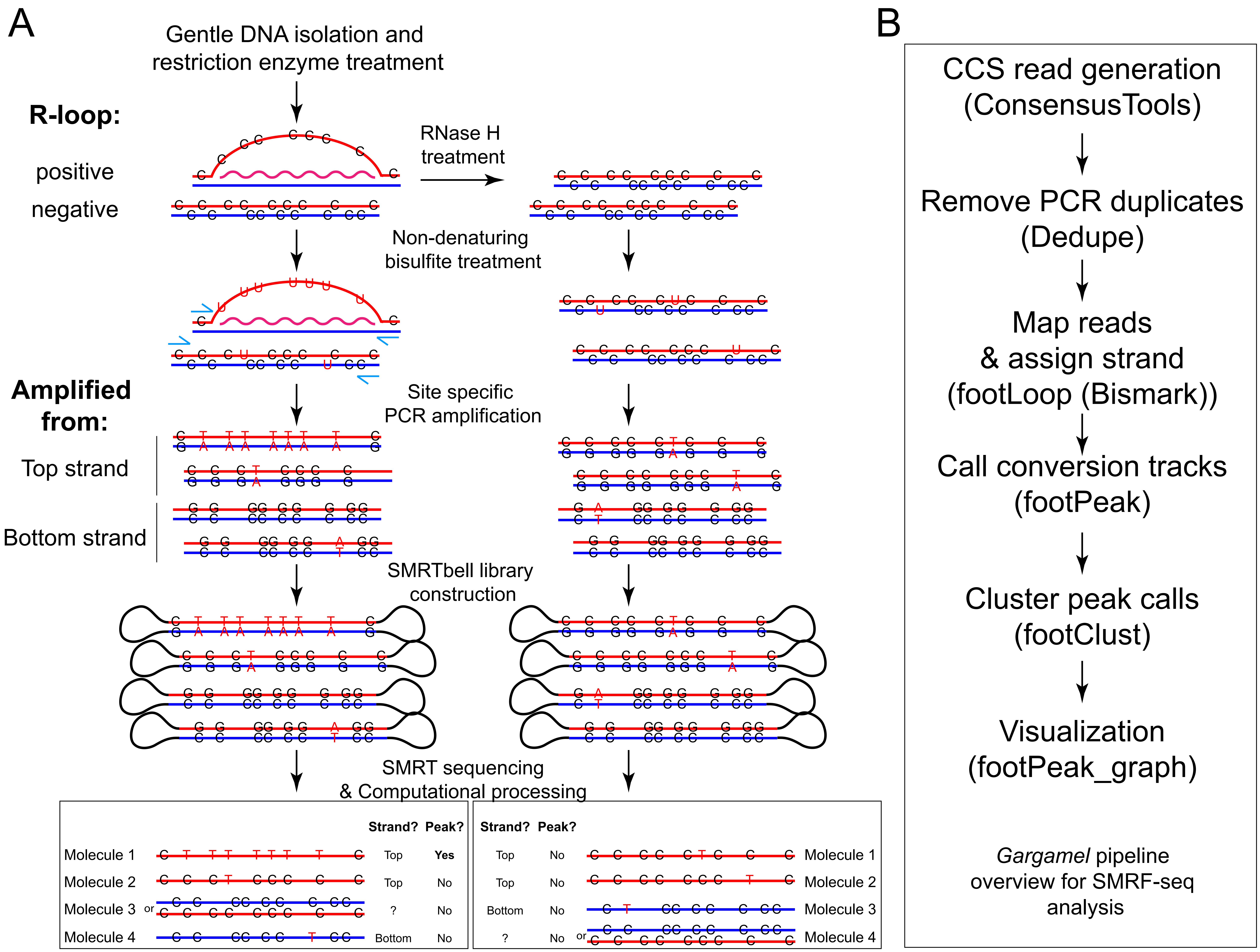
Figure S1


A
Gentle DNA isolation and restriction enzyme treatment
R-loop:
positive
negative
RNase H treatment
Non-denaturing bisulfite treatment
Amplified from:
Top strand
Bottom strand
Site specific PCR amplification
SMRTbell library construction
SMRT sequencing & Computational processing
Strand? Peak?
Molecule 1 Top Yes
Molecule 2 Top No
Molecule 3 or ? No
Molecule 4 Bottom No
Strand? Peak?
Top No Molecule 1
Top No Molecule 2
Bottom No Molecule 3
? No or Molecule 4
B
CCS read generation (ConsensusTools)
Remove PCR duplicates (Dedupe)
Map reads & assign strand (footLoop (Bismark))
Call conversion tracks (footPeak)
Cluster peak calls (footClust)
Visualization (footPeak_graph)
Gargamel pipeline overview for SMRF-seq analysis