Read Sam

↓

Sort by Chromosome, Position

↓

Store lines in the sam files into a list

↓

Iterate through two lines at a time

↓

Check each line (read) for strand orientation through the bit wise flag (Function)

Not PCR Duplicates

↓

Both reads opposite strands

↓

Write to deduper.sam file

Both reads are the same

Function

↓

Run soft clip reverse function for reverse read strand orientation

UMI

Function

↓

Run soft clip forward function for forward strand orientation

UMI

If either UMI in record list write to deduper.sam

Else: write to duplicates.sam