

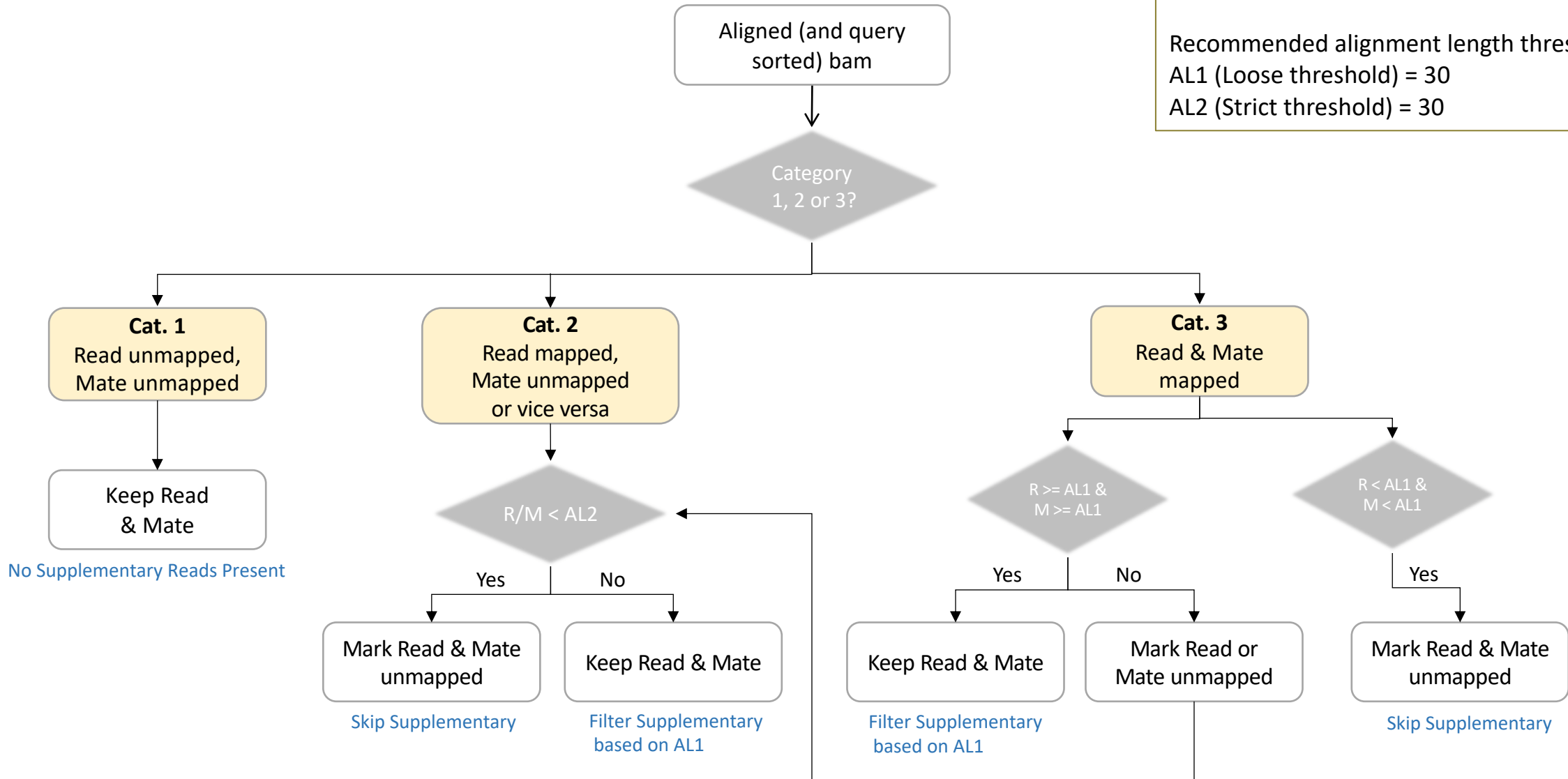
Short alignment marking workflow

R = Alignment length of read in consideration
M = Alignment length of mate of read in consideration
Alignment length = Match + Mismatch + Insertion

Recommended alignment length thresholds:

AL1 (Loose threshold) = 30

AL2 (Strict threshold) = 30



Primary alignments: can be marked as unmapped but will always remain in the output bam

Supplementary alignments: can be skipped or filtered and will be removed from the output bam