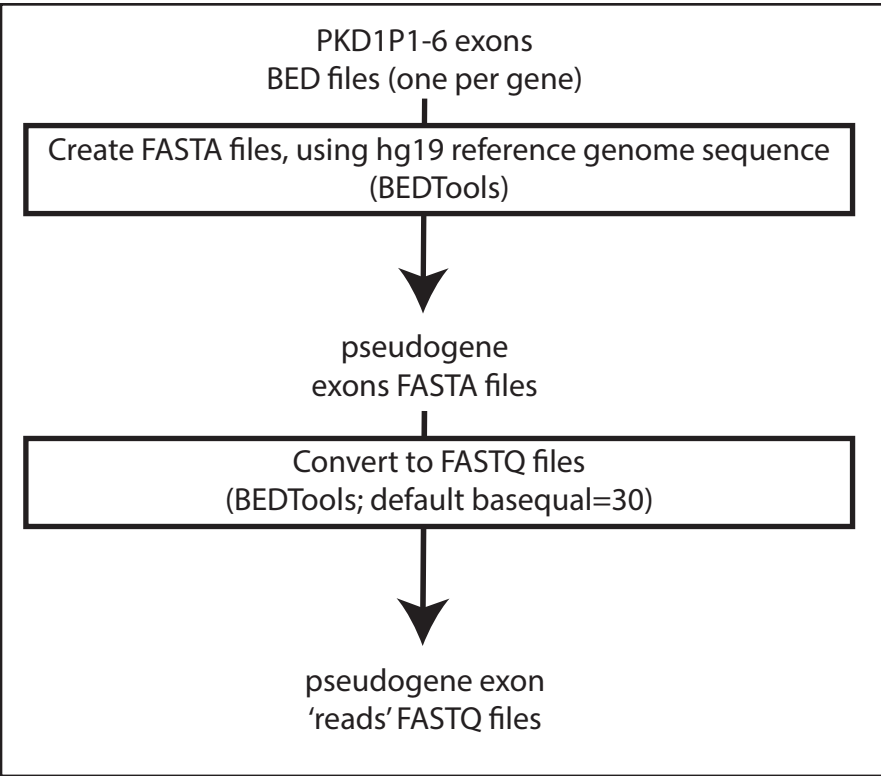
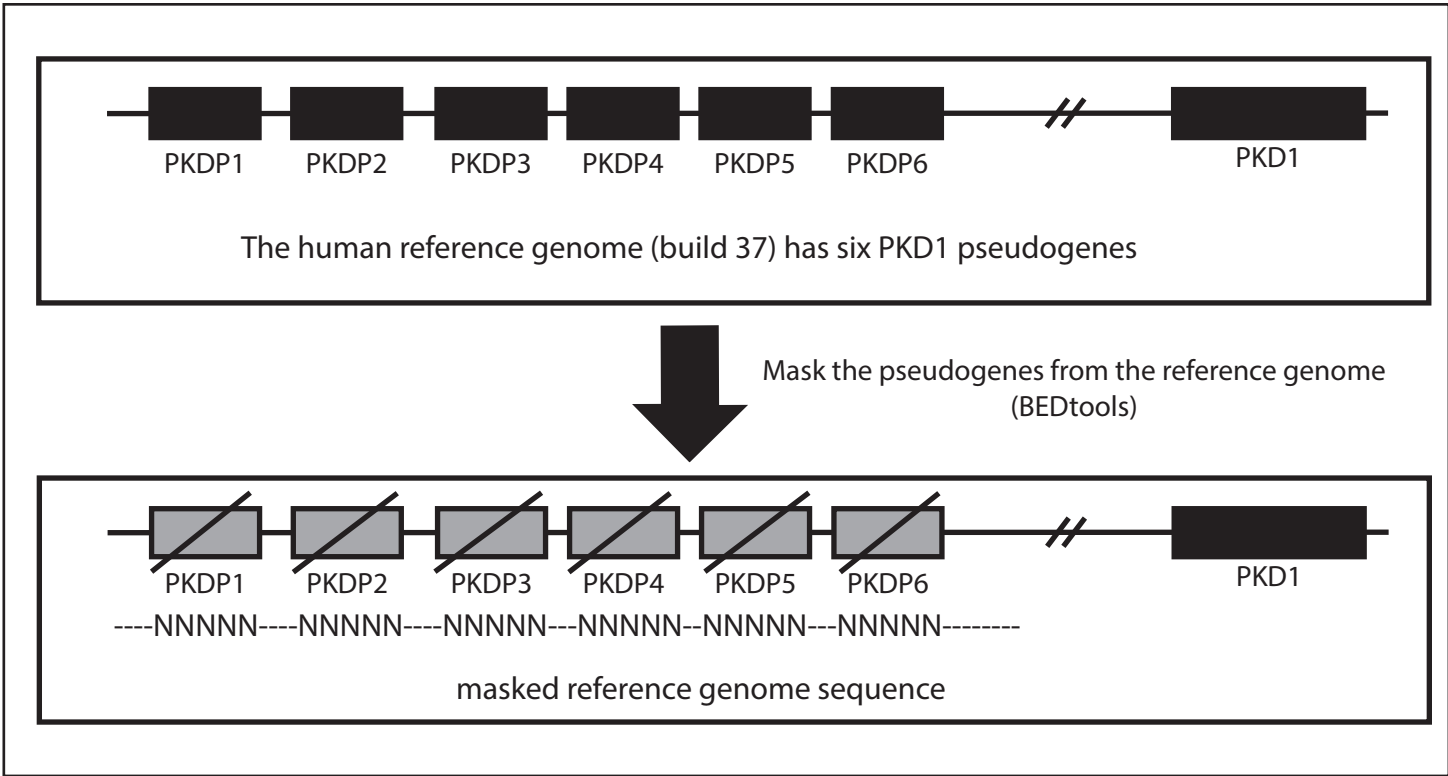


A: Convert pseudogene exons/introns into 'reads'

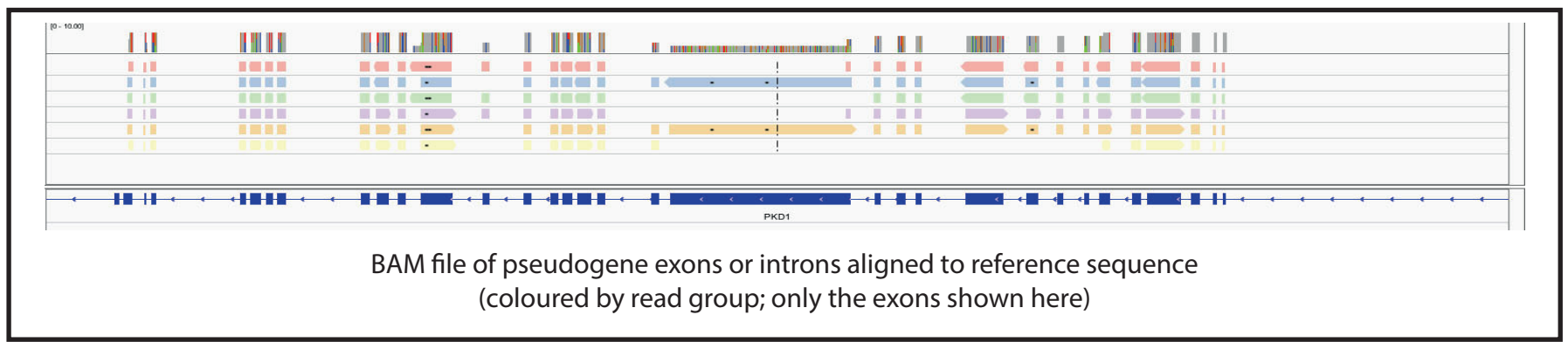


B: Mask the pseudogenes from the reference genome



C: Align reads and identify variants consistent with pseudogene misalignment

align all 'reads' from PKD1 pseudogene exons, or introns to the masked reference genome (BWA mem). Merge BAM files, and set read group to the pseudogene name



Call variants in the BAM file samtools + bcftools

