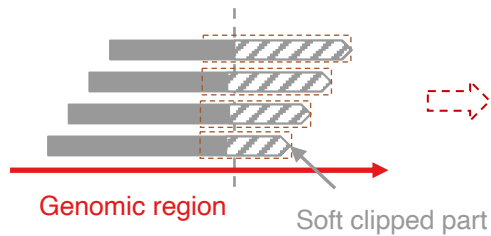


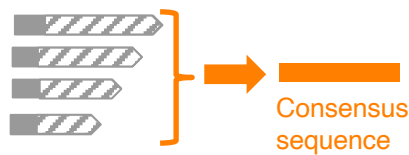
## Single breakend SV module

### (1, 2) Parsing & Clustering

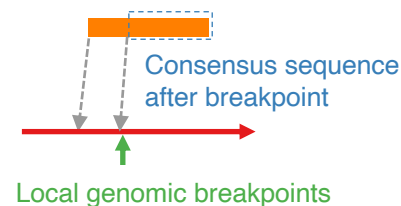


Gather soft clipping reads and cluster them by distinct putative breakends

### (3) Refinement

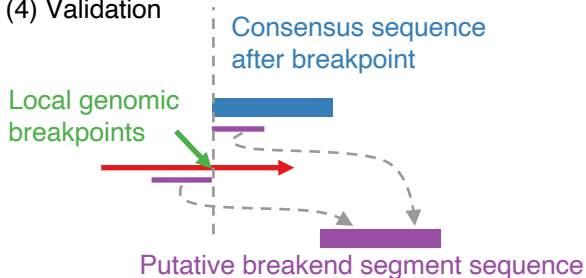


Gather soft-clipped parts of the sequences with margins and make an error-corrected consensus sequence

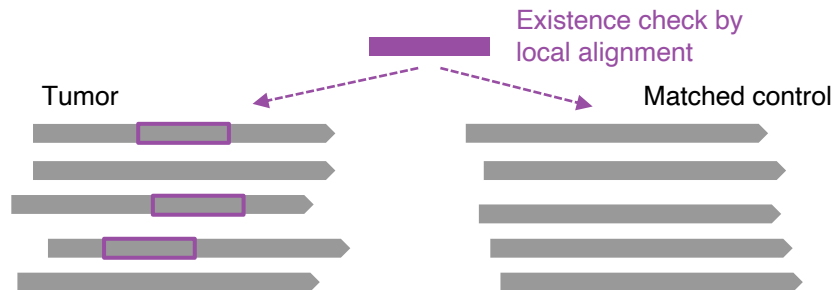


Breakpoint identification by Smith-Waterman algorithm

### (4) Validation



Generate the putative breakend segment sequence by extracting reference sequence before the breakpoint and the part of consensus sequence



Confirm that the putative breakend segment sequence is observed specifically in sequence reads in tumors.