Pipeline 2 - Inversion analysis and refinement of putative inversions

01. R-script that takes bed files generated from previous BAIT analysis (on selected libraries) and locates putative inversions using **InvertR** R package. List of regions to be analysed needs to be included (regions.txt)

02. Bash-script that catenates chromosome specific ROI files outputted by InvertR into a single ROI list, including all chromosomes

03. R-script that subset data in ROI file into two seperate files (AWC and NAWC ROI) depending on Watson/Crick ratio. using **Dplyr** package in R

04. Bash-script that uses intersect function of **Bedtools** package to filter out all variants in NAWC that are overlapping with events in the AWC file.

05. Bash-script that uses the filter function in **Bedtools** to filters out variants larger than 15MB.

06. Bash-script that sorts refined events on the leftmost coordinate. Outputs final list of refined inversions in .bed format. **Bedtools**

07. Bash-script that removes temporary files and files that are no longer necessary.