

Data analysis procedure for SMURF-seq reads

1 Introduction

At this point, we assume that the reads generated from a SMURF-seq experiment are base-called and are in a fastq or fasta file.

2 Mapping SMURF-seq reads

Environment variables:

2.1 Prerequisites

2.2 Mapping SMURF-seq reads with BWA-MEM

2.3 Mapping SMURF-seq reads with Minimap2

2.4 Mapping SMURF-seq reads with LAST

2.5 Test data

3 Generation of copy-number profiles

3.1 Prerequisites

3.2 Generating CNV profiles

3.3 Test data

4 Miscellaneous analysis of sequenced reads and mapped fragments

4.1 Read length distribution

4.2 Fragment length distribution

4.3 Closeness to RE sites