

Pre-computed
in silico
digestions

Annotation for
sites of
interest

Annotation for
restriction
enzymes

Restriction
enzymes to
check

INPUT

Obtain the fragment size distribution
and the location of the sites of interest
in the digested fragments

Calculate the *Score*, $NF/1000$ and
EV variables for different size ranges

Filtering:

$Score > C_Score \cdot max_Score$

$NF/1000 \leq C_NF/1000 \cdot ref_NF/1000$

Find the **optimal size range** which
minimizes the *EV*

For each enzyme or
enzyme combination

cuRRBS

Rank the enzymes or enzyme
combinations by *EV* and
calculate their *CRF* and *robustness*

CSV file containing information about the optimal enzymes and size
ranges to use in the new cuRRBS protocol

OUTPUT