**Description about INPUT files**

**Name of the file:** position\_of\_the\_site.csv

Description of the output file’s columns are as follows:

Column 1: Chromosome number.

Column 2: Starting position of the target/binding site.

Column 3: End position of the target/binding site.

**Description about OUTPUT files**

**Name of the file:** sequences\_of\_plus\_strand.csv/ sequences\_of\_reverse\_strand.csv

Description of the output file’s columns are as follows:

Column 1: Name of the transcript.

Column 2: Sequences of interest.