CRISPRnano V2.0

Suite for DNA Editing Event Analysis

User guide manual for CRISPRnano V2.0 Genome Editing Analyzer (December 2024)

How CRISPRnano Works

Any sequencing data

ONT | Illumina | PacBio

→ Upload FASTQ files →

Input Data and Results

Single or multiple clones

Multiple genotypes

Off-Target

Step 1: Input Data

GENERAL ANALYZER | PRIME EDITING ANALYZER | RESULTS | BULK/SINGLE CLONE VIEWER | OFF-TARGET ANALYSIS | TEST DATA

Enter sequencing data

FASTQ Files (*): Choose files — 6 files

Upload FASTQ files

97_S97_L001_R1_001 05/02/202... FASTQ Sequence T...

98_S98_L001_R1_001 05/02/202... FASTQ Sequence T...

Data type: Illumina

Illumina

Nanopore

PacBio or Nanopore Duplex

Select data type

Maximum expected genotype (ML mode only): 10

BOOSTING mode

Use machine learning classification model, faster but less accurate

Choose BOOSTING mode for fast analysis

Provide genotype details

Gene Name: AHR

Enter Gene Name

Opportunity for custom-made reference!

gRNA (*): (? Click here!) TTTGAAGACATCAGACACATGCAG

NOTE: this is pegRNA for Prime Editing Mode

Targeting mutagenesis oligonucleotide (Knock-in), OR Base Editing:

Knockin-only mode (exclude INDEL) | Non-homology end joining KI

Enter Target or Knock-in site sequence

Custom-made reference or self-designed!

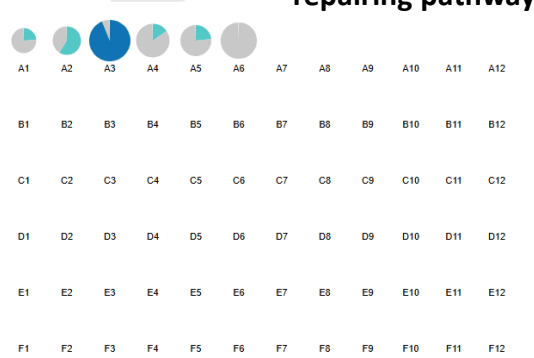
Step 2: Multiple Clone View Results

GENOTYPE | RIMA

Click on sample for detailed information

GENOTYPE | RIMA

Click on RIMA for viewing repairing pathway



Scroll down and view summary of generated genotypes in respective sample

Reference sequence on top and genotypes below! Click and scroll left/right to view total sequence!

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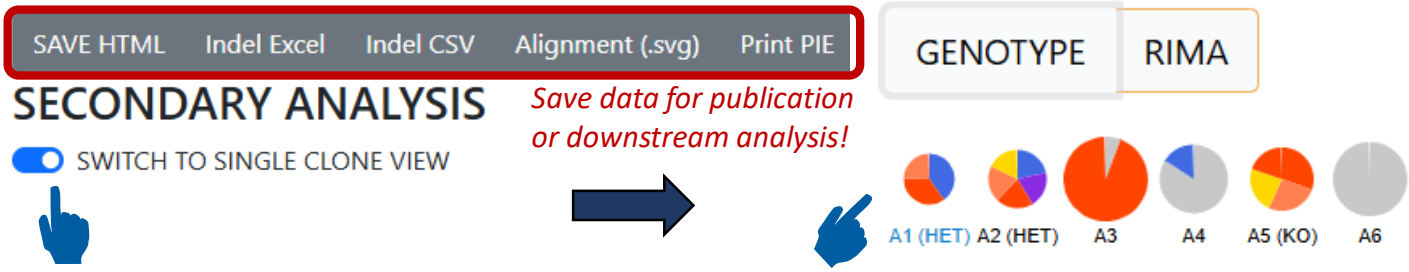
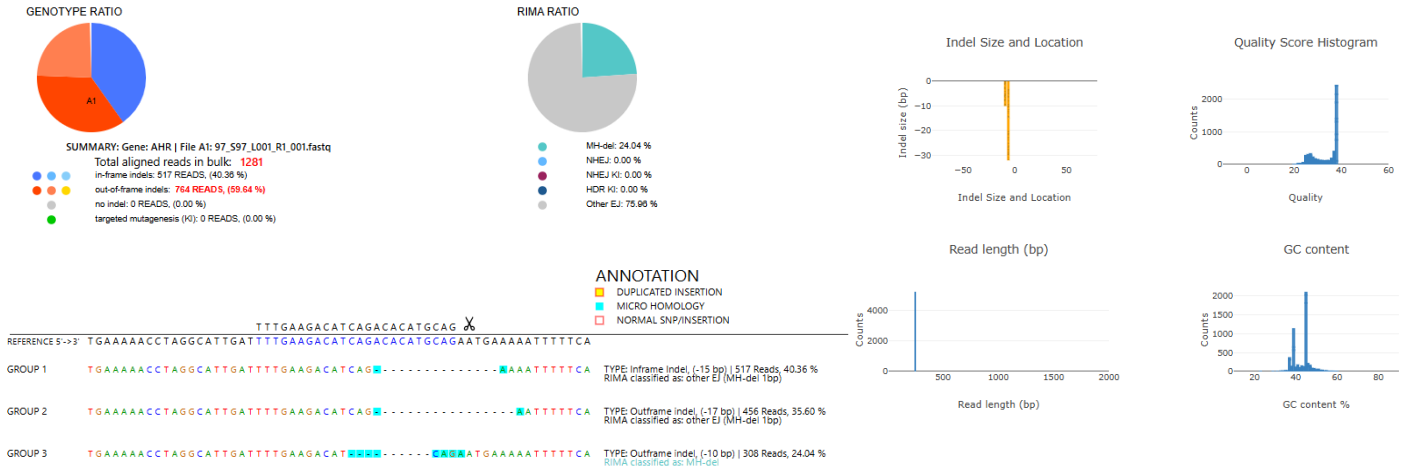
Step 3: Single Clone View Results



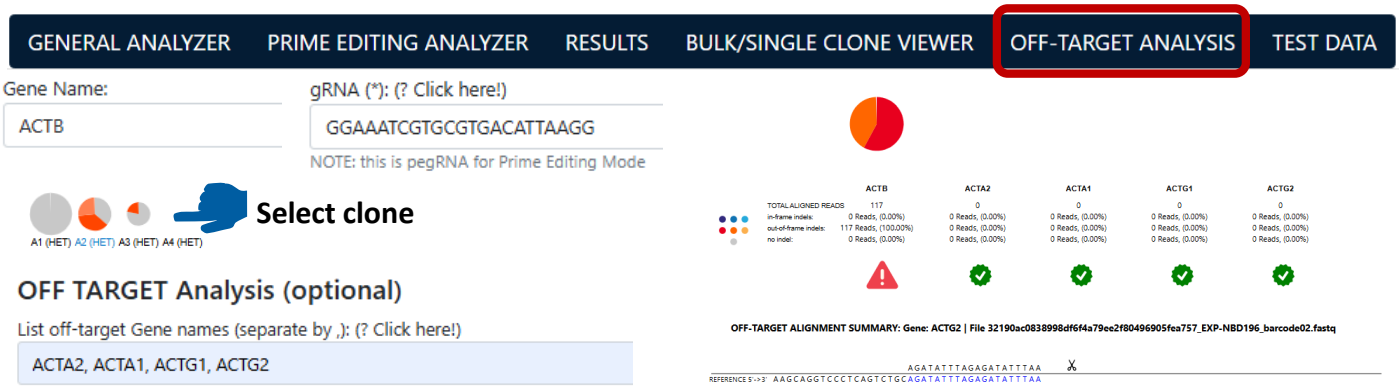
Click here to go to single clone view

Select sample of interest for detailed single clone information

You receive detailed information on detected genotypes and quality control



Step 4: Off-Target



General considerations for off-target analysis

Off-target identification tools:

- *https://ccsm.uth.edu/CRISPRoffT/*
- *NCBI Blast*
- *gRNA design pages like Chopchop*

For sample preparation it is recommended to prepare gene amplicons separately and include a wildtype control!