

How Edit-o-Matic 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

Data type:

Illumina

Illumina

Nanopore

PacBio or Nanopore Duplex

Maximum expected genotype (ML mode only):

10

☒ BOOSTING mode

Use machine learning classification model, faster but less accurate

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...

Select data type

Choose BOOSTING mode for fast analysis

Provide genotype details

Gene Name:

AHR

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 Gene Name

Opportunity for
custom-made reference!

Enter Target or Knock-in site sequence

Custom-made reference or self-designed!

Step 2: Multiple Clone View Results

GENERAL ANALYZER

PRIME EDITING ANALYZER

RESULTS

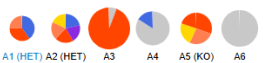
BULK/SINGLE CLONE VIEWER

OFF-TARGET ANALYSIS

TEST DATA

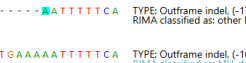
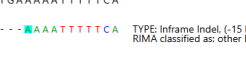
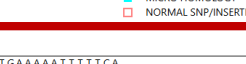
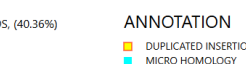
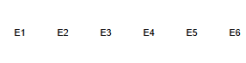
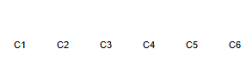
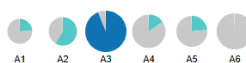
GENOTYPE

RIMA



GENOTYPE

RIMA



Click on RIMA for viewing repairing pathway

Click on sample for detailed information

SUMMARY: Gene: AHR | File A1: 97_S97_L001_R1_001.fastq

Total aligned reads: 1281 | Outframe indel: 764 READS, (59.64%) | Inframe indel: 517 READS, (40.36%)

targetingOligo reads: 0 READS, (0.00%) | No indel: 0 READS, (0.00%) | Read ambiguous: 0

MH-del: 24.04 | NHEJ: 0.00 | NHEJ-KI: 0.00 | HDR-KI: 0.00 | Other EJ: 75.96

ANNOTATION

DUPLICATED INSERTION
MICRO HOMOMOLOGY
NORMAL SNP/INSERTION

REFERENCE 5'→3' TGAACAACTAGGCATTGATTTTGAAGACATCAGACATGCAGTGAATGAAAAATTTTTC

GROUP 1 TGAACAACTAGGCATTGATTTTGAAGACATCAG-----AAATTTTTC TYPE: Inframe Indel, (-15 bp) | 517 Reads, 40.36 %

GROUP 2 TGAACAACTAGGCATTGATTTTGAAGACATCAG-----AAATTTTTC TYPE: Outframe indel, (-17 bp) | 456 Reads, 35.60 %

GROUP 3 TGAACAACTAGGCATTGATTTTGAAGACATCAG-----AAATTTTTC TYPE: Outframe indel, (-10 bp) | 308 Reads, 24.04 %

GROUP 4 TGAACAACTAGGCATTGATTTTGAAGACATCAG-----AAATTTTTC TYPE: Outframe indel, (-10 bp) | 308 Reads, 24.04 %

GROUP 5 TGAACAACTAGGCATTGATTTTGAAGACATCAG-----AAATTTTTC TYPE: Outframe indel, (-10 bp) | 308 Reads, 24.04 %

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!

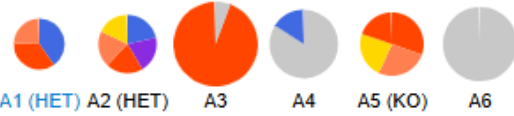
Step 3: Single Clone View Results

SAVE HTML Indel Excel Indel CSV Alignment (.svg) Print PIE

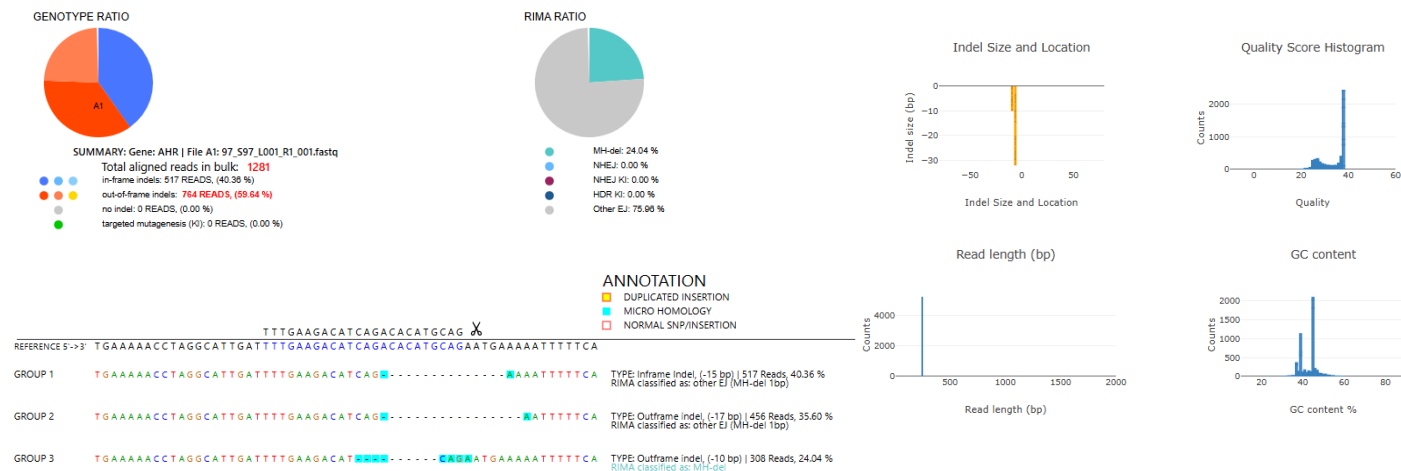
GENOTYPE

RIMA

SECONDARY ANALYSIS

Save data for publication
or downstream analysis!☒ SWITCH TO SINGLE CLONE VIEWClick here to go to single
clone viewSelect sample of interest for
detailed single clone information

You receive detailed information on detected genotypes and quality control



Step 4: Off-Target

GENERAL ANALYZER

PRIME EDITING ANALYZER

RESULTS

BULK/SINGLE CLONE VIEWER

OFF-TARGET ANALYSIS

TEST DATA

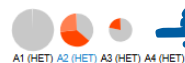
Gene Name:

gRNA (*): (? Click here!)

ACTB

GGAAATCGTGCCTGACATTAAGG

NOTE: this is pegRNA for Prime Editing Mode



Select clone

OFF TARGET Analysis (optional)

List off-target Gene names (separate by ,): (? Click here!)

ACTA2, ACTA1, ACTG1, ACTG2

Off-target analysis will check up to 4 other genes in a single run

List of offset sgRNA:

Enter off target gRNA sequences

If off-target sgRNA empty, system will take the previous sgRNA to find region of interest
sgRNA gene 1

TGAGATTGTCGGGACATCAAGG

sgRNA gene 2

CGAGATCGTGCCTGACATCAAGG

sgRNA gene 3

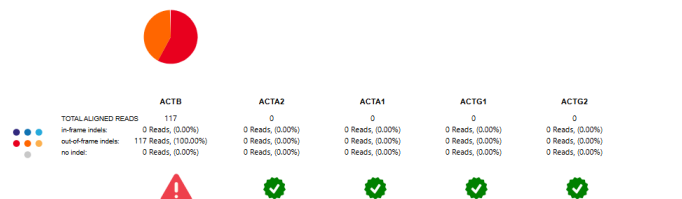
GGAAATCGTGCCTGACATCAAGG

sgRNA gene 4

AGAAATTGTGCGAGACATCAAGG

START OFFTARGET ANALYZER

Click here for off-target analysis



OFF-TARGET ALIGNMENT SUMMARY: Gene: ACTG2 | File 32190ac0838998df64a79ec2f80496905fea757_EXP-NBD196_barcode02.fastq

AGATATTAGAGATTTTAA X
REFERENCE 5'→3' AAGCAGTCCCTCAGTCTGCAGATATTAGAGATTTTAA

No off-target effect



Off-target effect

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!