

Walk-through GEMs Shiny-B&P-Editing

An R Shiny web application for Base and Prime
editing guide design in animals and plants

GEMs Shiny-B&P-Editing

User Interface:



Please Select your editing strategy

Base editing ▼

☐ Multiplex

☐ Single Variant

Search Reset

GEMs Shiny-B&P-Editing



Please Select your editing strategy

Base editing

Base editing

Prime editing

☐ Single variant

Search

Reset

Select Editing Strategy



GEMs Base & Prime Editing App (BasePEG)



Please Select your editing strategy

Prime editing ▼

☒ Multiplex

☐ Single Variant

Choose CSV File

Browse... No file selected

☐ Show all possible Oligos

Search Reset

← Select Running Mode (only tick one of the two)

Multiplex Running Mode



Please Select your editing strategy

Prime editing ▼

☒ Multiplex

☐ Single Variant

Choose CSV File

Browse... No file selected

☐ Show all possible Oligos

Search Reset

Browse sample file from your computer

Templates for import file (.csv)

Prime editing:

Variant	Chromosome	Position_hg38	Edit	GeneOrientat	PBS	RT
HEK3_1CTTins	9	107422356	insCTT	+	13	10
HEK3_1Tdel	9	107422356	delT	+	13	10
HEK3_1Ains	9	107422356	insA	+	13	10

Base editing:

Variant	Chromosome	Position_hg38	SNP	GeneOrientation
Variant 1	2	58161573	G>A	-
Variant 2	2	58226727	G>A	-
Variant 3	3	10028690	G>A	+

GEMs Base & Prime Editing App (BasePEG)



Please Select your editing strategy

Prime editing ▼

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Choose CSV File

Browse... No file selected

☐ Show all possible Oligos

Search Reset

Browse Sample file from your computer

geml Base & Prime Editing App

Please Select your editing strategy

Prime editing ▼

☒ Multiplex

☐ Single Variant

Choose CSV File

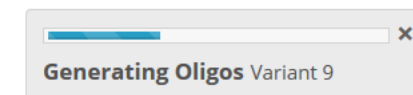
Browse... testfile_HEK3_RNF2.csv

Upload complete

☐ Show all possible Oligos

Search Reset

Loading bar shows progress of computation



geml Base & Prime Editing App

How many Variants can be targeted?

Please Select your editing strategy

Prime editing

☒ Multiplex

☐ Single Variant

Choose CSV File

Browse...

testfile_HEK3_RNF2.csv

Upload complete

☐ Show all possible Oligos

Search

Reset

15 out of 15 Variants could be targeted

Show entries

Search:

	Variant	Score	Protospacer.Sense.	Protospacer.Antisense.	TargetPos.	Extension.Sense.
10	HEK3_1CTTins	-1	caccGGCCCAGACTGAGCACGTGAgtttt	ctctaaaacTCACGTGCTCAGTCTGGGCC	1	gtgcGCCATCAAAGCGTGCTCAGTCTG
11	HEK3_1Tdel	-9	caccGGCCCAGACTGAGCACGTGAgtttt	ctctaaaacTCACGTGCTCAGTCTGGGCC	1	gtgcCTCTGCCATCCGTGCTCAGTCTG
9	HEK3_1Ains	-9	caccGGCCCAGACTGAGCACGTGAgtttt	ctctaaaacTCACGTGCTCAGTCTGGGCC	1	gtgcCTGCCATCATCGTGCTCAGTCTG
13	RNF2_4f_1Tins	-1	caccGTCATCTTAGTCATTACCTGgtttt	ctctaaaacCAGGTAATGACTAAGATGAC	1	gtgcAACGAACACCTCAGAGTAATGAC
12	RNF2_4f_1GTins	-1	caccGTCATCTTAGTCATTACCTGgtttt	ctctaaaacCAGGTAATGACTAAGATGAC	1	gtgcAACGAACACCTCAGTACGTAATG
15	RNF2_4f_4Adel	-2	caccGTGAGTTACAACGAACACCTCgtttt	ctctaaaacGAGGTGTTTCGTTGTAAC	2	gtgcAGTCATTACCTGGGTGTTTCGTTG
14	RNF2_4f_3-5GAdel	-1	caccGTGAGTTACAACGAACACCTCgtttt	ctctaaaacGAGGTGTTTCGTTGTAAC	1	gtgcAGTCATTACCTGTGTTTCGTTGTA
8	EMX1_4f_6Tins	-6	caccGAGTCCGAGCAGAAGAAGAAgtttt	ctctaaaacTTCTTCTTCTGCTCGGACTC	6	gtgcGTGATGGGAGCACCTTCTTCTCTG
5	EMX1_4f_1TGCins	-1	caccGAGTCCGAGCAGAAGAAGAAgtttt	ctctaaaacTTCTTCTTCTGCTCGGACTC	1	gtgcGTGATGGGAGCCCTTCGCATTCT
7	EMX1_4f_5Gdel	-5	caccGAGTCCGAGCAGAAGAAGAAgtttt	ctctaaaacTTCTTCTTCTGCTCGGACTC	5	gtgcGTGATGGGAGCCCTTCTTCTCTG

Showing 1 to 10 of 15 entries

Previous

1

2

Next

Output Table (One entry with the highest score for each Variant):

15 out of 15 Variants could be targeted

Show 10 entries

Oligos with cloning sites

Search:

	Variant	Score	Protospacer.Sense.	Protospacer.Antisense.	TargetPos.	Extension.Sense.	Extension.Antisense.	PAM	PAM.Strand	id
10	HEK3_1CTTins	-1	caccGGCCCAGACTGAGCACGTGAgtttt	ctctaaaacTCACGTGCTCAGTCTGGGCC	1	gtgcGCCATCAAAGCGTGCTCAGTCTG	aaaaCAGACTGAGCACGCTTTGATGGC	NGG	Sense	1
11	HEK3_1Tdel	-9	caccGGCCCAGACTGAGCACGTGAgtttt	ctctaaaacTCACGTGCTCAGTCTGGGCC	1	gtgcCTCTGCCATCCGTGCTCAGTCTG	aaaaCAGACTGAGCACGGATGGCAGAG	NGG	Sense	2
9	HEK3_1Ains	-9	caccGGCCCAGACTGAGCACGTGAgtttt	ctctaaaacTCACGTGCTCAGTCTGGGCC	1	gtgcCTGCCATCATCGTGCTCAGTCTG	aaaaCAGACTGAGCACGATGATGGCAG	NGG	Sense	3
13	RNF2_4f_1Tins	-1	caccGTCATCTTAGTCATTACCTGgtttt	ctctaaaacCAGGTAATGACTAAGATGAC	1	gtgcAACGAACACCTCAGAGTAATGACTAAGATG	aaaaCATCTTAGTCATTACTCTGAGGTGTTCTGTT	NGG	Antisense	5
12	RNF2_4f_1GTins	-1	caccGTCATCTTAGTCATTACCTGgtttt	ctctaaaacCAGGTAATGACTAAGATGAC	1	gtgcAACGAACACCTCAGTACGTAATGACTAAGATG	aaaaCATCTTAGTCATTACGTAAGGTGTTCTGTT	NGG	Antisense	7
15	RNF2_4f_4Adel	-2	caccGTGAGTTACAACGAACACCTCgtttt	ctctaaaacGAGGTGTTCTGTTGTAACCTAC	2	gtgcAGTCATTACCTGGGTGTTCTGTTGTAAC	aaaaAGTTACAACGAACACCCAGGTAATGACT	NGG	Sense	8
14	RNF2_4f_3-5GAGdel	-1	caccGTGAGTTACAACGAACACCTCgtttt	ctctaaaacGAGGTGTTCTGTTGTAACCTAC	1	gtgcAGTCATTACCTGTGTTCTGTTGTAAC	aaaaAGTTACAACGAACACAGGTAATGACT	NGG	Sense	10
8	EMX1_4f_6Tins	-6	caccGAGTCCGAGCAGAAGAAGAgtttt	ctctaaaacTTCTTCTTCTGCTCGGACTC	6	gtgcGTGATGGGAGCACCTTCTTCTGCTCGGA	aaaaTCCGAGCAGAAGAAGAAGGTGCTCCCATCAC	NGG	Sense	13
5	EMX1_4f_1TGCins	-1	caccGAGTCCGAGCAGAAGAAGAgtttt	ctctaaaacTTCTTCTTCTGCTCGGACTC	1	gtgcGTGATGGGAGCCCTTCGATTCTTCTGCTCGGA	aaaaTCCGAGCAGAAGAATGCGAAGGGTCCCATCAC	NGG	Sense	17
7	EMX1_4f_5Gdel	-5	caccGAGTCCGAGCAGAAGAAGAgtttt	ctctaaaacTTCTTCTTCTGCTCGGACTC	5	gtgcGTGATGGGAGCCTTCTTCTGCTCGGA	aaaaTCCGAGCAGAAGAAGAAGGTGCTCCCATCAC	NGG	Sense	21

Showing 1 to 10 of 15 entries

Previous 1 2 Next

Variant name

The pegRNA Score
(See next page)

Target position
(See Anzalone et. al., 2019)

The pegRNA Score

The higher the better!

Computed based on recommendations from David Liu's Lab:

- (-8) 5' C in 3' extension
- (-15) Poly-T tracts (TTTTT or more) in the 3' extension
- (-27) 4 or less bp homology in the RT after the edit
- (-1) per 1 bp increase of Target Position

Σ = pegRNAs Score

Base & Prime Editing App

Please Select your editing strategy

Prime editing

☒ Multiplex

☐ Single Variant

Choose CSV File

Browse...

testfile_HEK3_RNF2.csv

Upload complete

☒ Show all possible Oligos

Search

Reset

To show all possible pegRNAs, tick this box

15 out of 15 Variants could be targeted

Show 10 entries

Search:

	Variant	Protospacer.Sense.	Protospacer.Antisense.	TargetPos.	Extension.Sense.	Extension.Antisense.
1	HEK3_1CTTins	caccGGCCCAGACTGAGCACGTGAgtttt	ctctaaaacTCACGTGCTCAGTCTGGGCC	1	gtgcGCCATCAAAGCGTGCTCAGTCTG	aaaaCAGACTGA
2	HEK3_1Tdel	caccGGCCCAGACTGAGCACGTGAgtttt	ctctaaaacTCACGTGCTCAGTCTGGGCC	1	gtgcCTCTGCCATCCGTGCTCAGTCTG	aaaaCAGACTGA
3	HEK3_1Ains	caccGGCCCAGACTGAGCACGTGAgtttt	ctctaaaacTCACGTGCTCAGTCTGGGCC	1	gtgcCTGCCATCATCGTGCTCAGTCTG	aaaaCAGACTGA
4	RNF2_4f_1Tins	caccGTGAGTTACAACGAACACCTCgtttt	ctctaaaacGAGGTGTTTCGTTGTAAC	5	gtgcAGTCATTACCTTGAGGTGTTTCGTTGTAAC	aaaaAGTTACAA
5	RNF2_4f_1Tins	caccGTCATCTTAGTCATTACCTGgtttt	ctctaaaacCAGGTAATGACTAAGATGAC	1	gtgcAACGAACACCTCAGAGTAATGACTAAGATG	aaaaCATCTTAG
6	RNF2_4f_1GTains	caccGTGAGTTACAACGAACACCTCgtttt	ctctaaaacGAGGTGTTTCGTTGTAAC	5	gtgcAGTCATTACCGTATGAGGTGTTTCGTTGTAAC	aaaaAGTTACAA
7	RNF2_4f_1GTains	caccGTCATCTTAGTCATTACCTGgtttt	ctctaaaacCAGGTAATGACTAAGATGAC	1	gtgcAACGAACACCTCAGTACGTAATGACTAAGATG	aaaaCATCTTAG
8	RNF2_4f_4Adel	caccGTGAGTTACAACGAACACCTCgtttt	ctctaaaacGAGGTGTTTCGTTGTAAC	2	gtgcAGTCATTACCTGGGTGTTTCGTTGTAAC	aaaaAGTTACAA
9	RNF2_4f_4Adel	caccGTCATCTTAGTCATTACCTGgtttt	ctctaaaacCAGGTAATGACTAAGATGAC	4	gtgcAACGAACACCCAGGTAATGACTAAGATG	aaaaCATCTTAG
10	RNF2_4f_3-5GAGdel	caccGTGAGTTACAACGAACACCTCgtttt	ctctaaaacGAGGTGTTTCGTTGTAAC	1	gtgcAGTCATTACCTGTTCGTTGTAAC	aaaaAGTTACAA

Showing 1 to 10 of 54 entries

Previous 1 2 3 4 5 6 Next

54 instead of 15 entries (also pegRNAs with lower pegRNAs Score are shown)

Single Variant Running Mode

Please Select your editing strategy

Base editing

☐ Multiplex

☒ Single Variant

Please name your variant

FANCA c.2639 G>A

Please select the Chromosome

chr16

Please select the position in hg38

89765029

Please Select the orientation of your target gene

-

Please Select your single nucleotide change you want to revert

G>A

Search Reset

Tick Single Variant Box
(Untick Multiplex if ticked)

Insert Edit on the
!selected Strand!
(here minus "-")

Please Select your editing strategy

Prime editing

☐ Multiplex

☒ Single Variant

Please name your variant

FANCA c.2639 G>A

Please select the Chromosome

chr16

Please select the position in hg38

89765029

Please Select the orientation of your target gene

-

Please Select the Edit (e.g G>A, insA, delT)

Please select the PBS length

10

Please select the RT length

13

Search Reset

Positions of tested Prime editing sites

- HEK3 +1 : chr9 107422356 (+)
- RNF2 +1 : chr1 185087640 (+)
- DNMT1 +1 : chr19 10133644 (-)
 - In Anzalone et. al., edit is on (+) Strand
 - -> Here use reverse complement Sequence and change direction for deletions
- EMX1 +1: chr2 72933870 (+)