

BEscreen: a versatile toolkit to design base editing libraries

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SUPPLEMENTARY DATA

Supplementary Figure 1

	BEscreen ¹	PnB-Designer ²	SNP-CRISPR ³	beditor ⁴	BE-Designer ⁵	base-editor-design-tool ⁶	BE-target ⁷
Availability							
Web server	✓	✓	✓	✗	✗	✓	✓
Command line interface	✓	✓	✓	✓	✗	✓	✗
No login/E-Mail required	✓	✓	✗	✓	✓	✓	✓
Guide customization							
Guide length	✓	✗	✗	✗	✓	✓	✓
Fully customizable PAM	✓	✗	✗	✗	✗	✗	✓
Editing window	✓	✗	✗	✗	✓	✓	✗
Input options							
Manual input	✓	✓	✗	✗	✓	✗	✓
File input	✓	✓	✓	✓	✓	✓	✗
Genomic location	✓	✓	✓	✓	✗	✗	✗
Amino acid change	✓	✗	✗	✗	✗	✗	✗
dbSNP rsID	✓	✗	✗	✗	✗	✗	✗
Genomic regions	✓	✗	✗	✓	✓ [†]	✓	✓ [‡]
Gene (CDS)	✓	✗	✗	✗	✗	✓	✗
Output options							
Filter by biol. consequence	✓	✗	✗	✗	✗	✗	✗
Splice site recognition	✓	✗	✗	✗	✗	✗	✗
Vis. of genomic alignment	✓	✗	✗	✗	✗	✗	✗
Results download	✓	✓	✗ [*]	✗	✓	✗	✓

^{*}not functional at time of access
[†](≤1 kbp) [‡](≤10 kbp)

Links:
¹ bescreen.charite.de
² fgcz-shiny.uzh.ch/
³ flyrnai.org/tools/snp_crispr/web/
⁴ pypi.org/project/beditor/
⁵ rgenome.net/be-designer/
⁶ github.com/mhegde/base-editor-design-tool
⁷ skl.scau.edu.cn/targetdesign/

Supplementary Figure 1: Comparison of BEscreen's features with alternative tools.