

Extended GUIDE-Seq Analysis

Cleavage, Repair, and Translocation Information

Postcede every gene edit experience with KBioBox's secondary analysis to gain vital information to the exact results of the edit. Identify **actual cleavage sites, correct and incorrect repairs, observed and potential translocations** and the changes to peptide/protein sequences.

Better GUIDE-Seq Analysis

KBioBox's secondary analysis is used to **extend standard GUIDE-Seq** analysis or any analogous gene edit pipeline. Obtain easier to read reports with additional analyses on nuclease fidelity and other off target activity. Our extended GUIDE-Seq analysis can be adapted to unique edits or situations outside of the standard GUIDE-Seq protocol such as other exogenous genomes and reservoirs.

Cleavages

Where did the nuclease cleave in intended and unintended targets, and how frequently. Ensure the accuracy of the nuclease and guide.



Repairs

Correct Repairs (red indicates GUIDE-seq dsODN)

```
GAGCGAAGGGATCGAAACCCGGG - WT
TATGACAACCTCAATTAAACACCCGGGAGCG - 37
CATATGTTAATAACGGTATACCCGGGAGCG - 32
TATGACAACCTCAATTAAACCCCGGGAGCG - 207
CATATGTTAATAACGGTATACCCGGGAGCG - 549
TATGACAACCTCAATTAAACCCCGGGAGCG - 197
CATATGTTAATAACGGTATACCCGGGAGCG - 45
```

Did the DNA/RNA repair as intended or did undesired indels, SNPs, or translocations occur

For more information please visit www.kbiobox.com or email info@kbiobox.com

Translocations

Potential Translocation Products

Key: Upstream Sequence + Downstream Sequence

SEQUENCE HUMAN SEQUENCE
Potential protein product up to stop codon

Primer Sets

HIV Upstream + Chr 15 Downstream

ATGATGTTTCAGGACCCGGTCTCTGAAACATAAGCAACCCAGACAGGAAGTCCGGAG
Met Met P Q D P V L K H K Q P R Q E V G S H Q K R T A L :

Forward Primers	GC	Tm	Reverse Primers	GC
GGCTGTCTCCAAACCGTT	58.80	55.56	TGATGAGAGGCAAGAGAGACAGCC	58
ATGGCTGTCTCCAAACCG	58.56	55.56	CCCACCTGTATGCCCGAATCAG	59.