

Select WT seq file:

Checked!

Experiment 0:
(input)

Assay name:

AuF_28_Pool4

confirmed!

Sequence file1:

Checked!

Sequence file2:

Checked!

Experiment 1:

Assay name:

AuF_40_Pool4

confirmed!

Sequence file1:

Checked!

Sequence file2:

Checked!

Experiment 2:

Assay name:

confirm

Sequence file1:

Click to choose

Sequence file2:

Click to choose

Amplicon1 range:
format: 1-XXX

452-696

confirmed!

Amplicon2 range:
format: XXX-XXX

779-1153

confirmed!

Amplicon3 range:
format: XXX-XXX

confirm

Amplicon4 range:
format: XXX-XXX

confirm

Amplicon5 range:
format: XXX-XXX

confirm

Target sites in WT
from each amplicon:
format: (1) (61 XXX)

(550) (934 1003)

confirmed!

Masked sites in WT
(treat as WT)
format: 1-C XXX-G

933-C

confirmed!

Mode (single or double, default is single):

single

confirmed!

Scale (Enrich2 range, default is max):

max

confirmed!

Submit