

Select WT seq file:

Checked!

Experiment 0:  
(input)

Assay name:

AuF\_28\_Pool3

confirmed!

Sequence file1:

Checked!

Sequence file2:

Checked!

Experiment 1:

Assay name:

AuF\_40\_Pool3

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

779-1191

confirmed!

Amplicon2 range:  
format: XXX-XXX

confirm

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)

(928 964 1000 1006)

confirmed!

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

999-G

confirmed!

Mode (single or double, default is single):

single

confirmed!

Scale (Enrich2 range, default is max):

max

confirmed!

Submit