

Figure S1

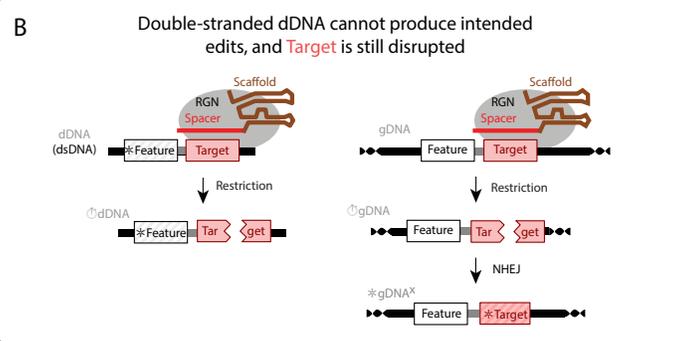
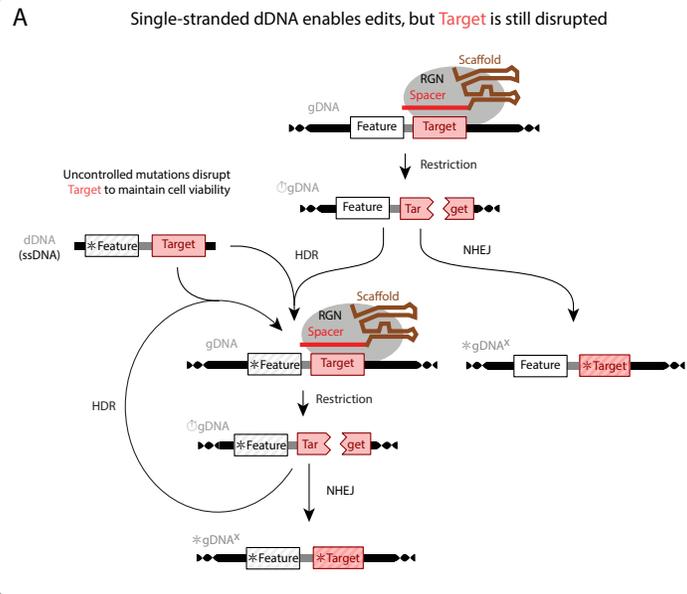


Figure S2

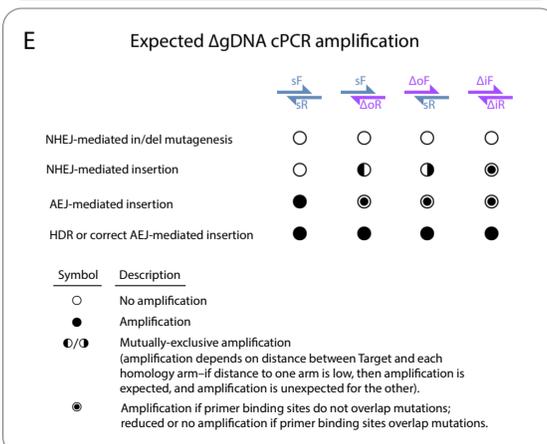
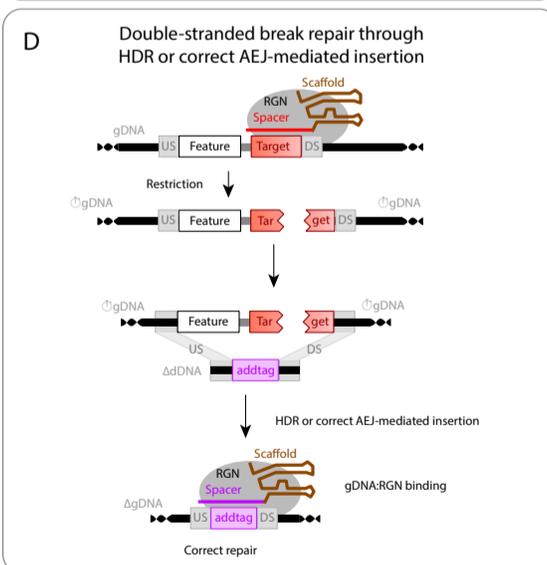
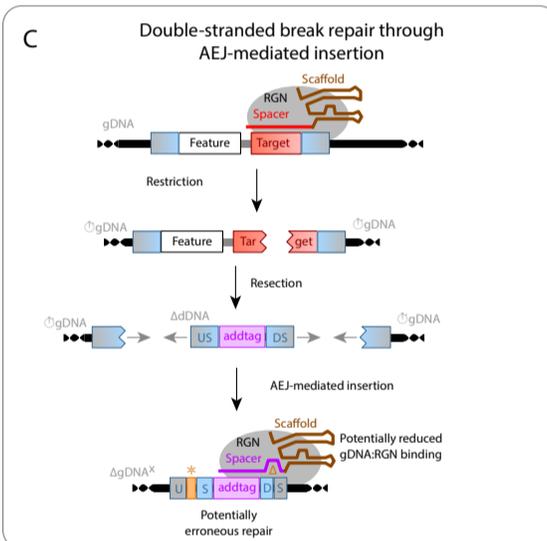
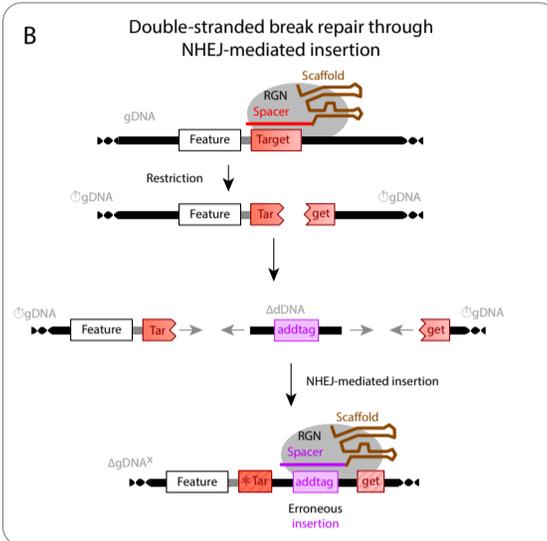
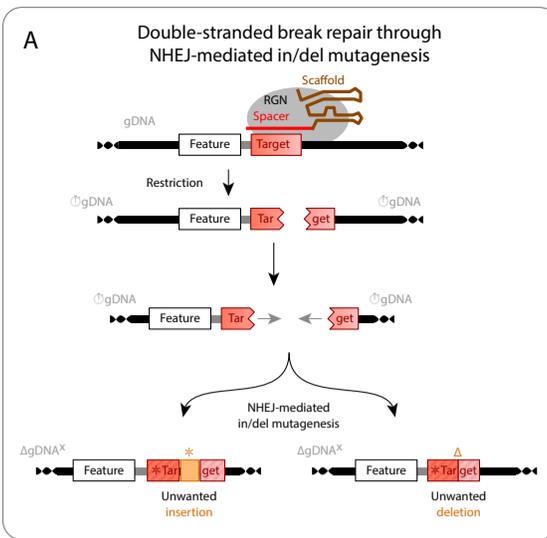


Figure S3

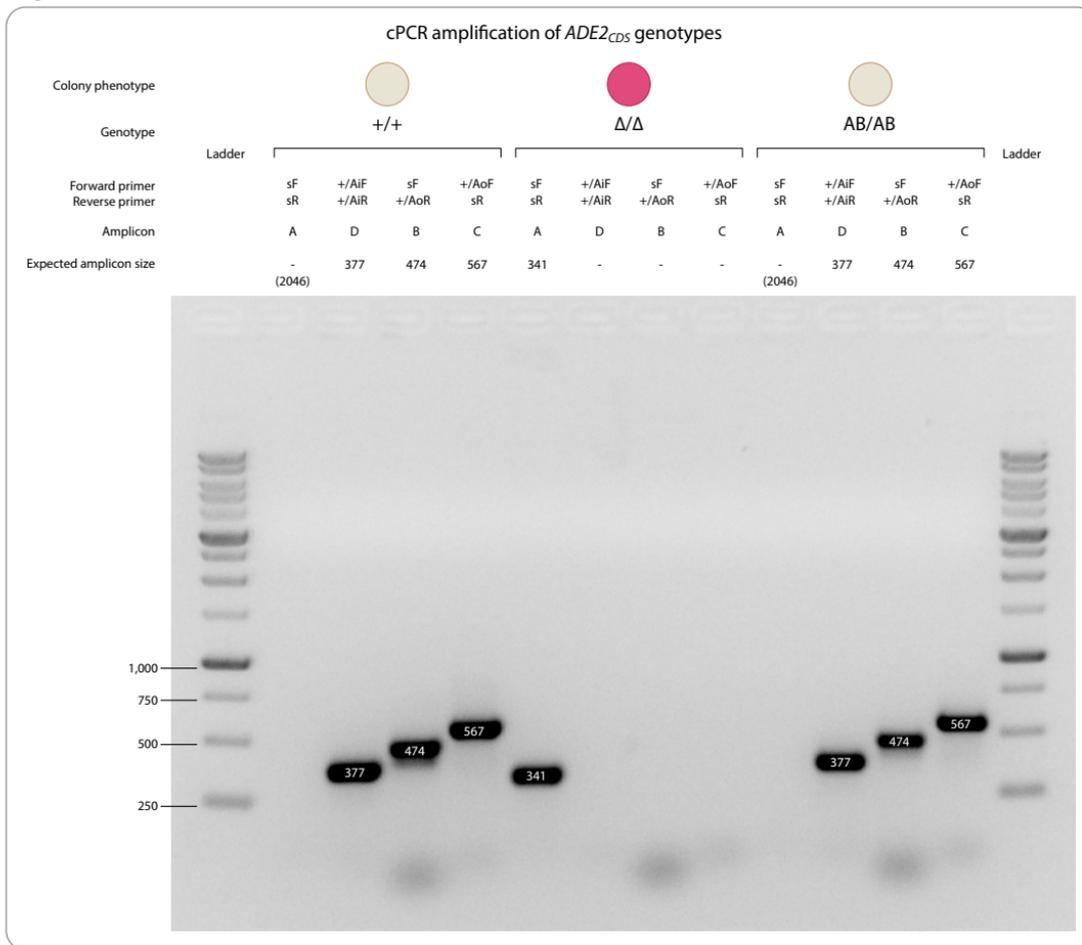
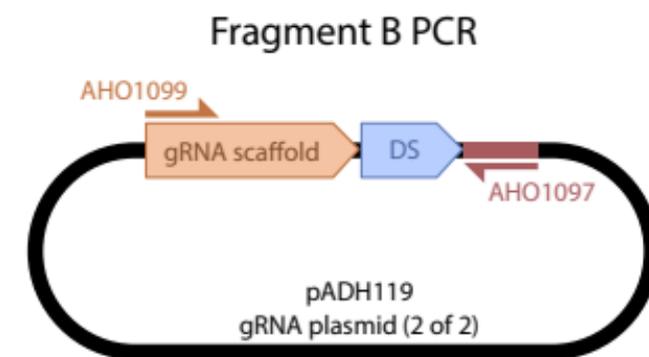
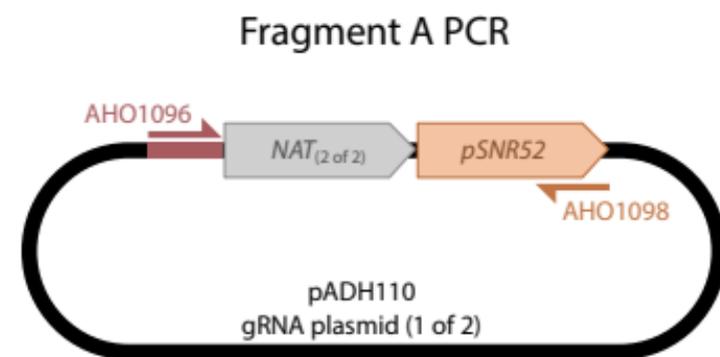


Figure S4



Fragment C "all-in-one" stitching PCR

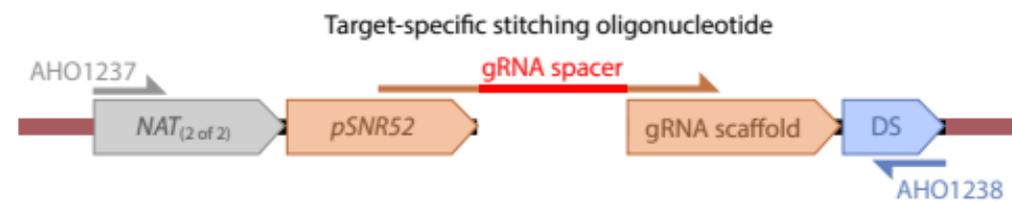
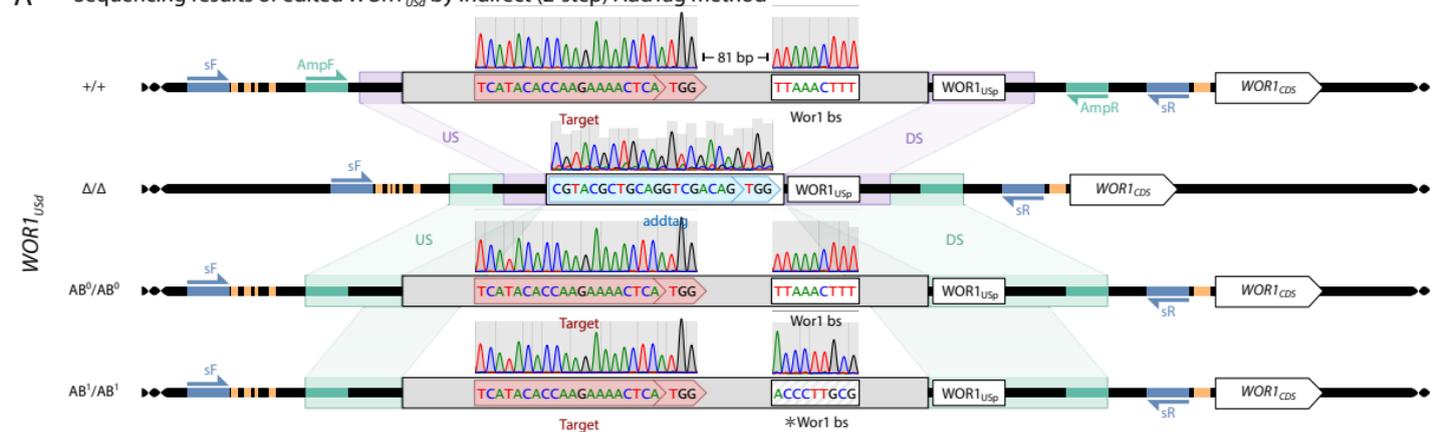


Figure S5

A Sequencing results of edited *WOR1_{USD}* by indirect (2-step) AddTag method



B Sequencing results of edited *WOR1_{USP}* by indirect (2-step) AddTag method

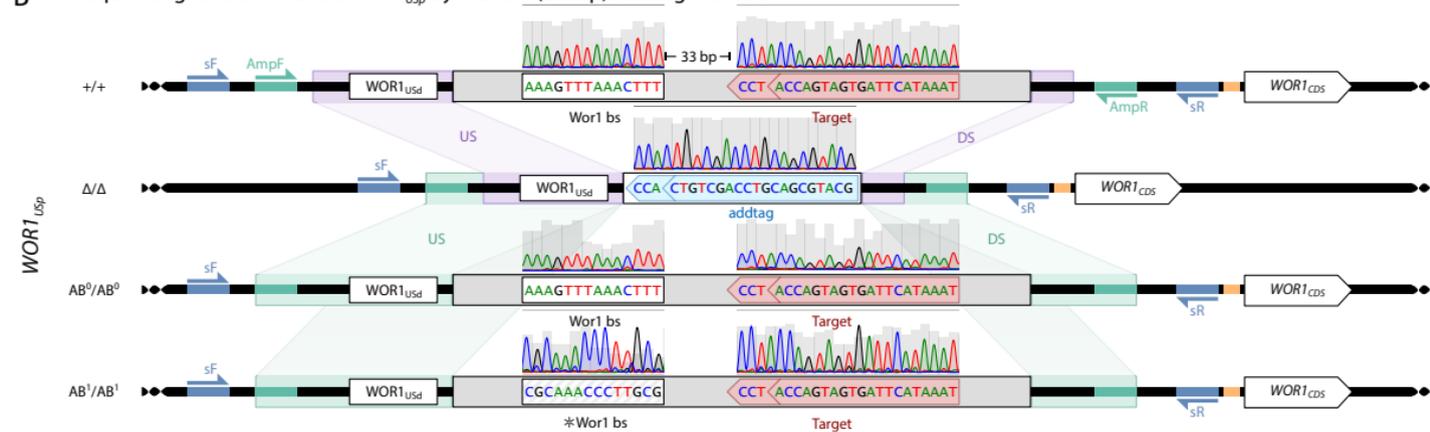


Figure S6

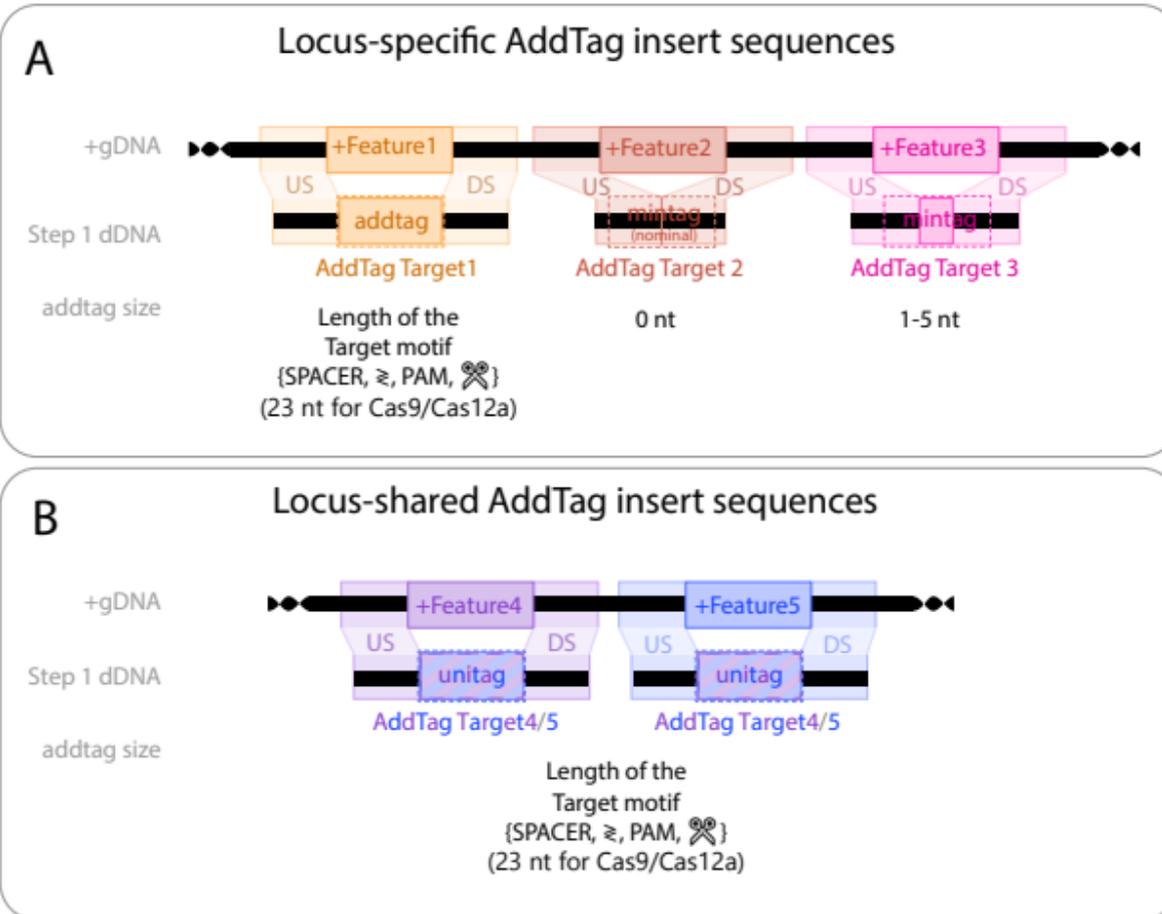


Figure S7

A priori weight functions for on-target Algorithm scores

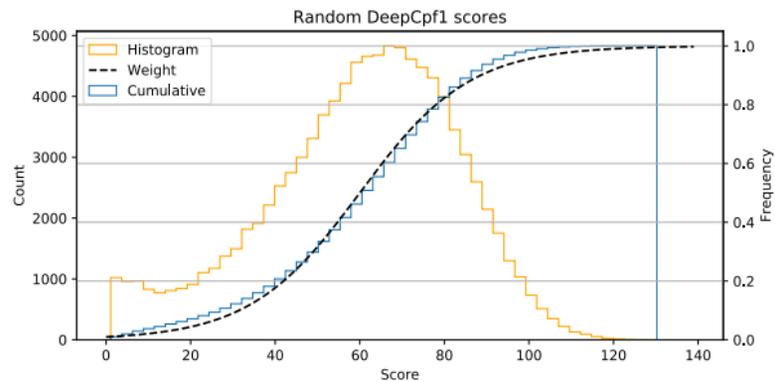
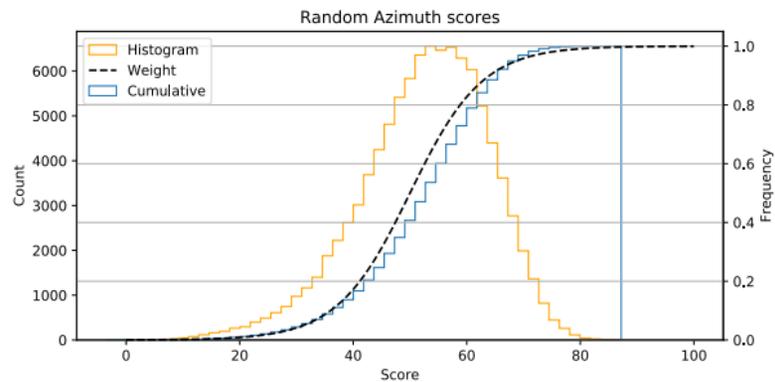


Figure S8

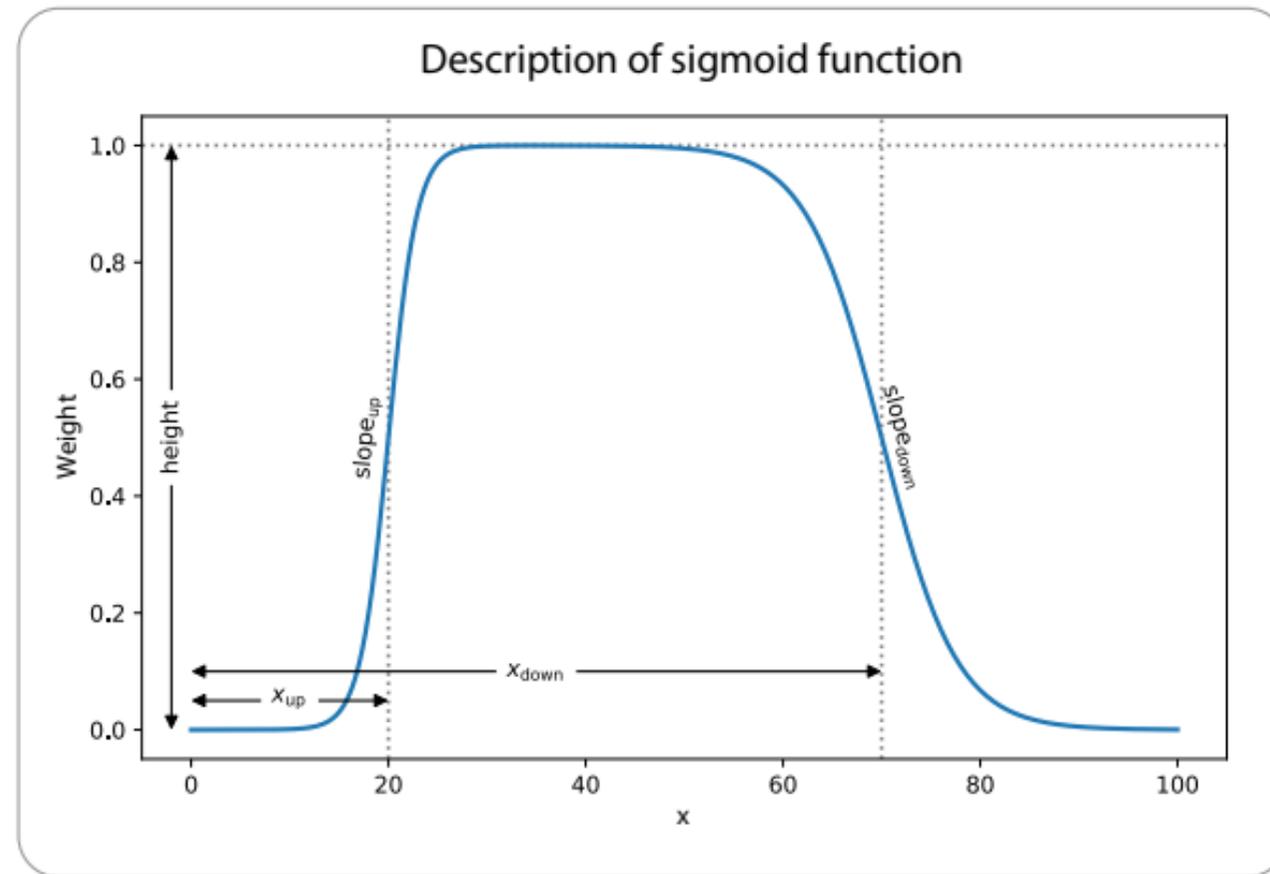


Figure S9

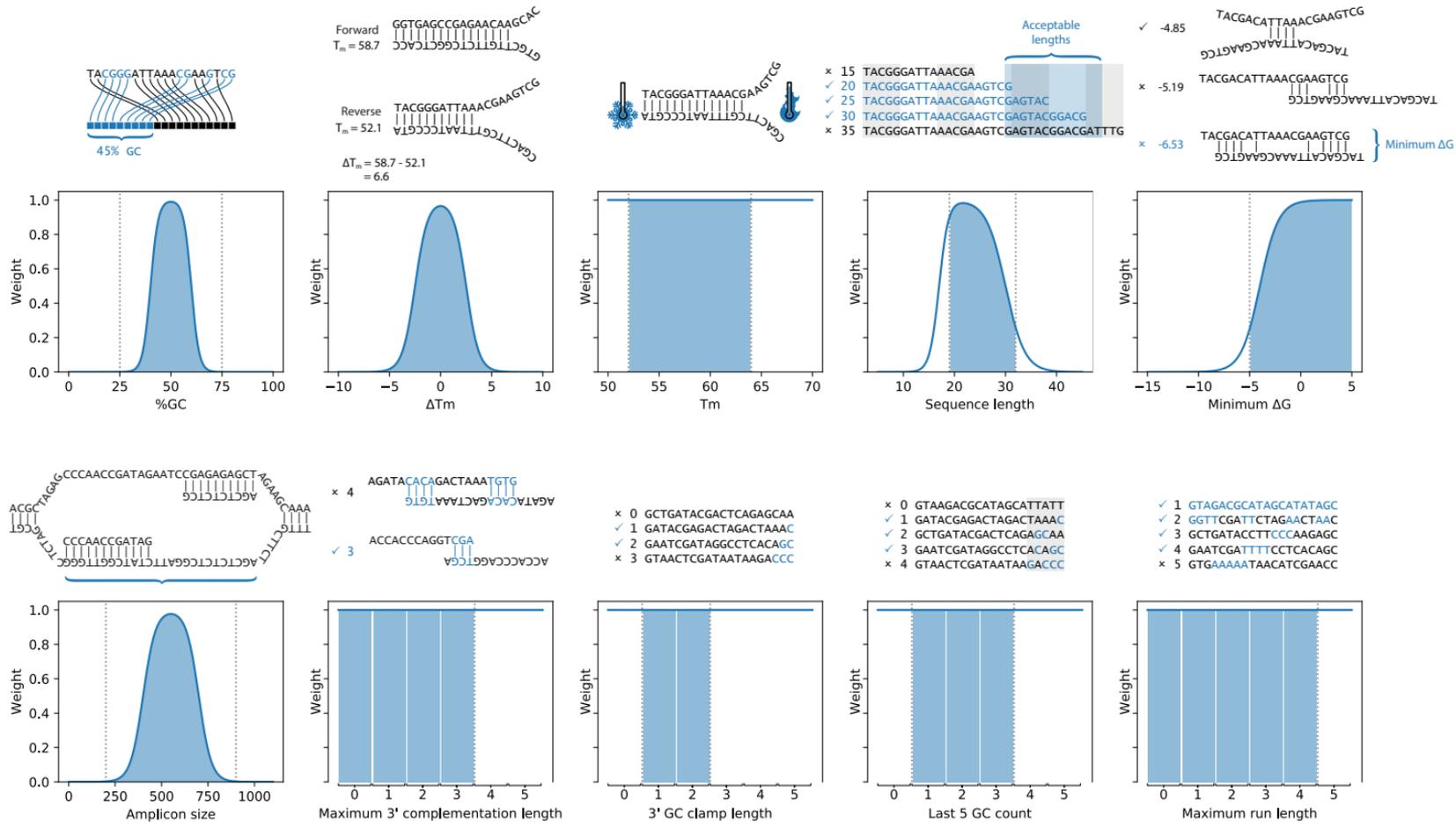
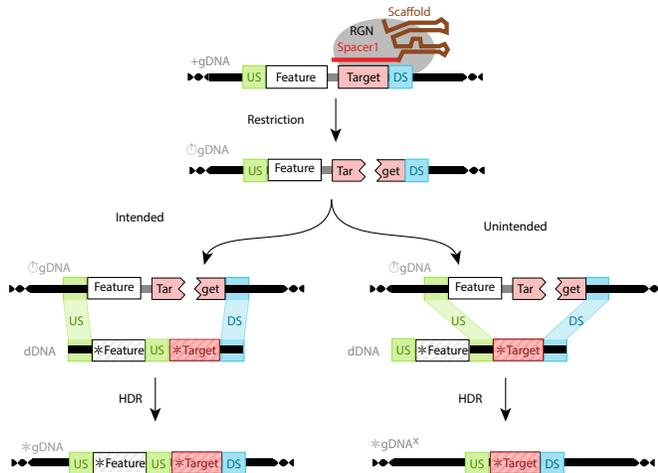
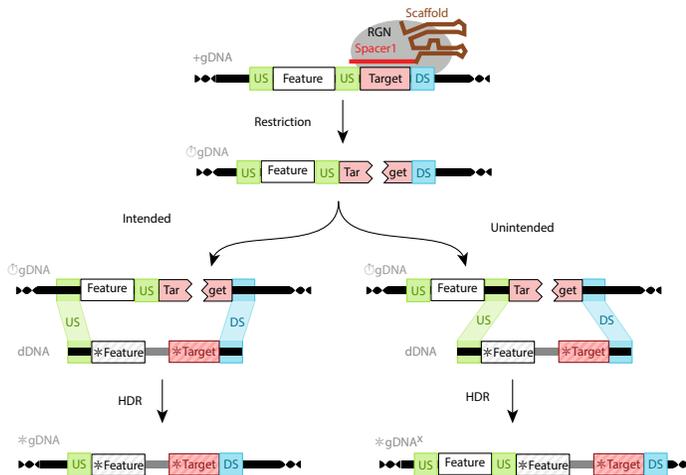


Figure S10

A Excessive homology within dDNA reduces efficiency of intended dDNA incorporation



B Excessive homology within gDNA reduces efficiency of intended dDNA incorporation



C Excessive homology in long dDNA reduces efficiency of combinatorial direct (1-step) traditional editing

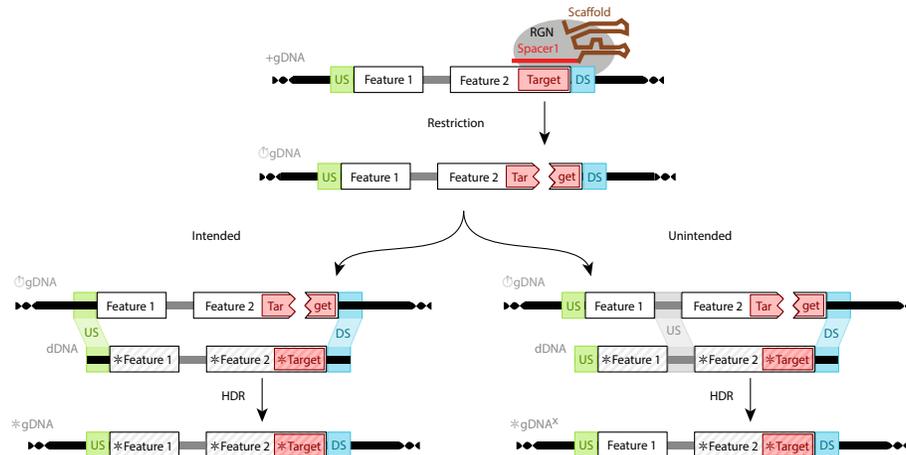


Figure S11

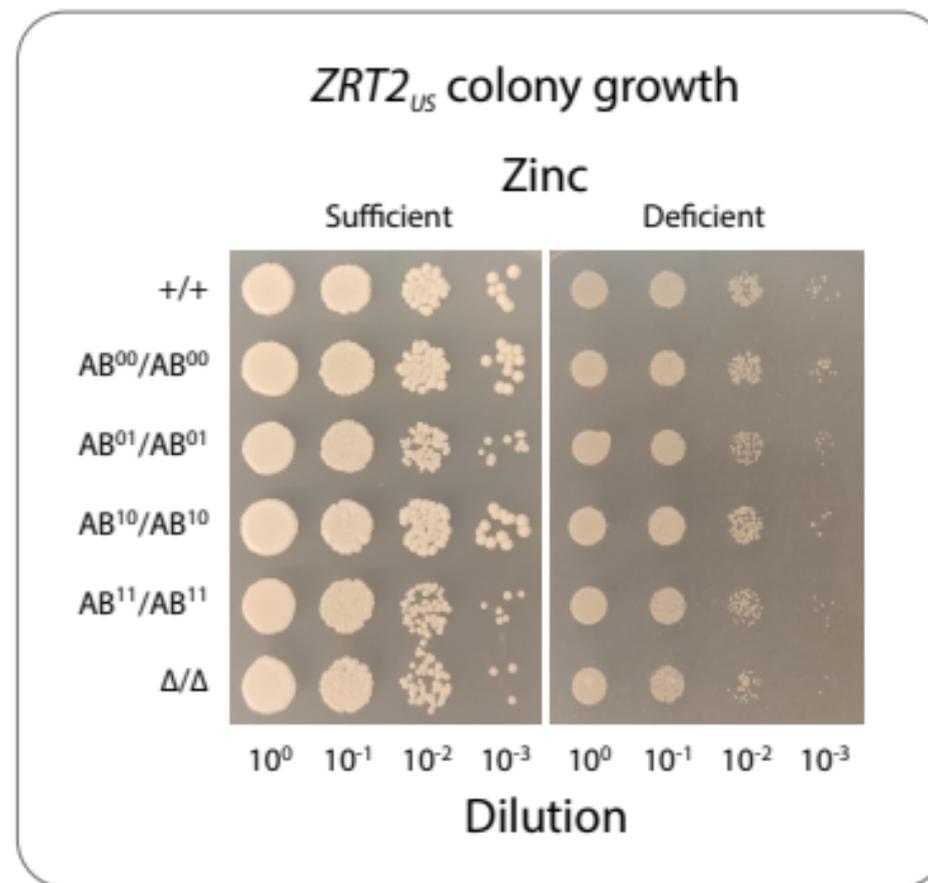
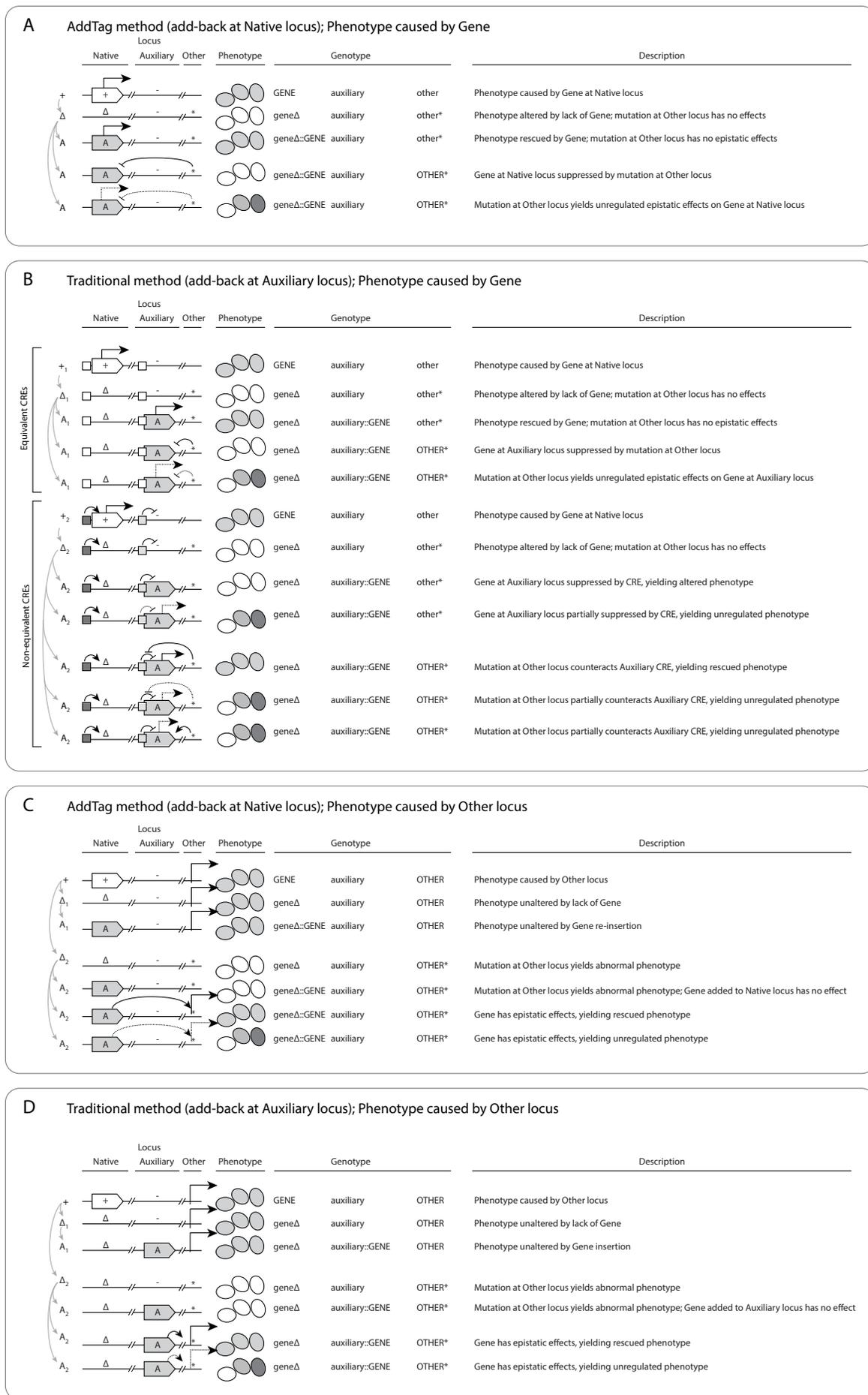


Figure S12



Symbol	Description	Symbol	Description	Symbol	Description	Symbol	Description
+	Gene naturally present		Full, positive regulation		Wild type or rescued phenotype		Locus conferring wild type or rescued phenotype
-	Gene naturally absent		Partial, positive regulation		Regulated, abnormal phenotype		Locus conferring unregulated phenotype
A	Gene artificially present		Full, negative regulation		Unregulated phenotype		
Δ	Gene artificially absent		Partital, negative regulation				
*	Uncharacterized mutation						

Figure S13

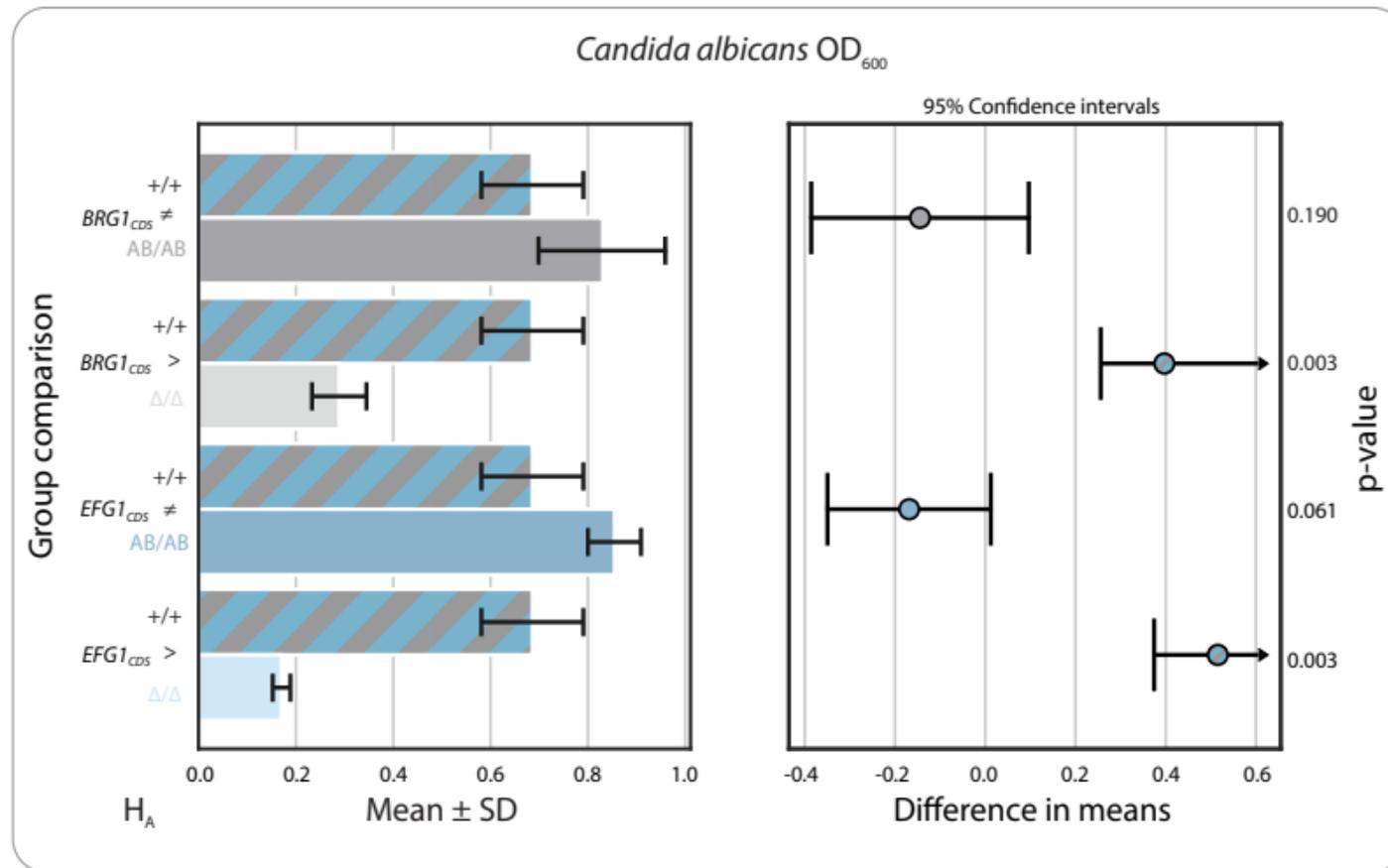


Figure S14

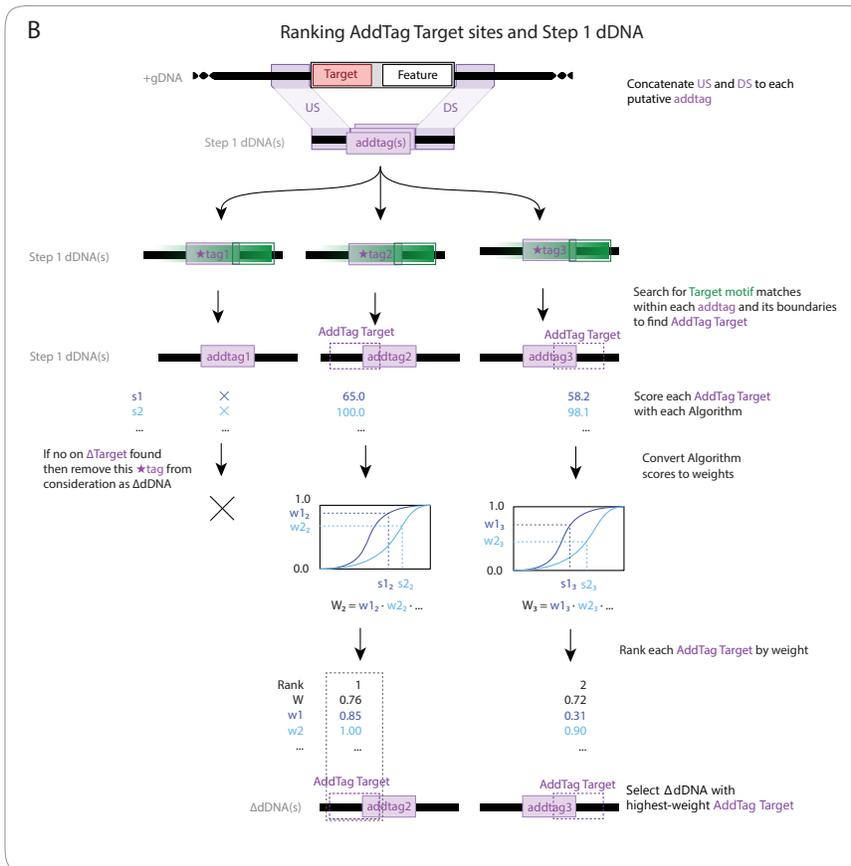
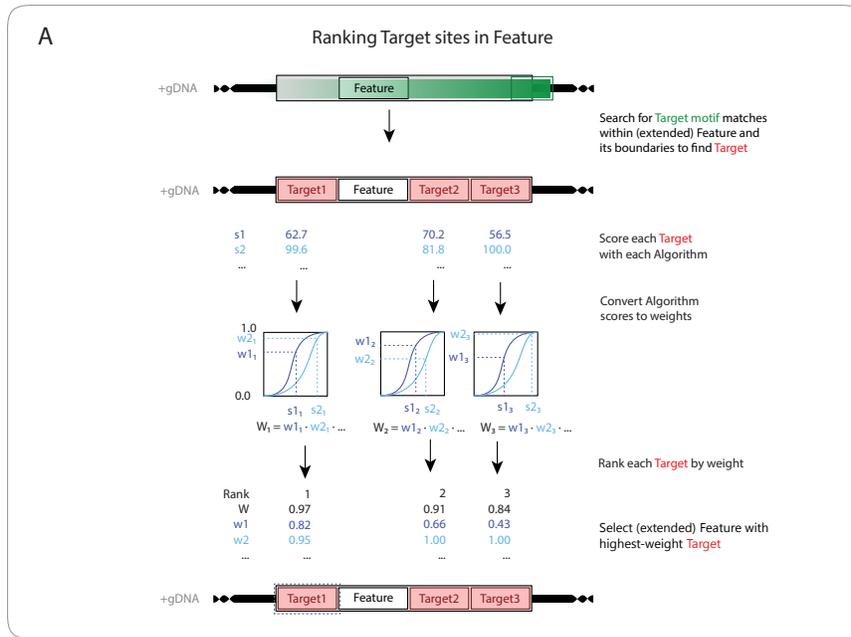


Figure S15

