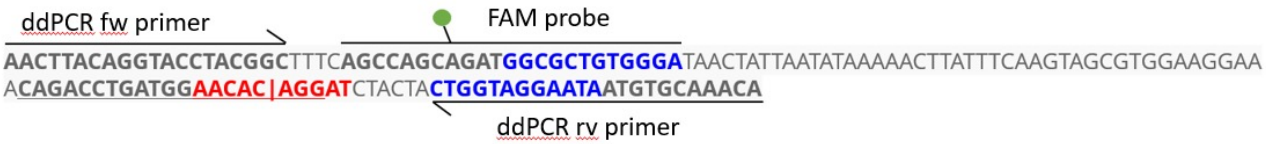
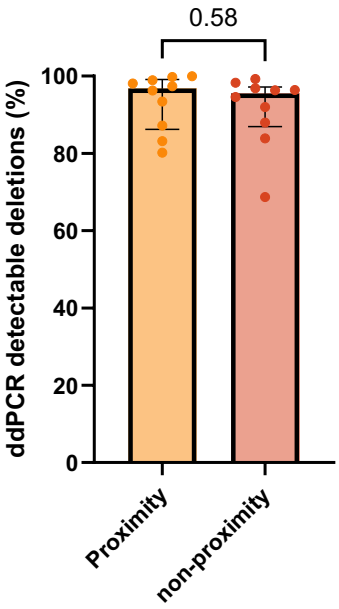
A

B



C



sgRNA pair	% ddPCR detectable
Chr2 CD	99.78
Chr2 EF	87.97
Chr2 GH	94.60
Chr6 AB	87.20
Chr6 CD	99.98
Chr6 EF	96.32
Chr10 AB	98.90
Chr10 GH	91.97
Chr17 AB	83.16
Chr17 CD	93.39
Chr17 EF	96.39
Chr17 GH	68.69
Chr21 AB	98.12
Chr21 CD	97.34
Chr21 EF	96.84
Chr21 GH	99.24
ChrX AB	80.16
ChrX CD	96.26
ChrX EF	83.86
ChrX GH	98.25

Supplemental Fig S10. Estimating the sensitivity of ddPCR to detect deletions. **(A)** The ligation product of the ChrX AB deletion is shown here as an example. The underscored and bolded sequence is the mock sgRNA sequence, containing 17 bp from guide A, and 3 bp from B. The vertical line indicates the cut/ligation site. Only reads containing both blue 15 nucleotide (nt) linker sequences were analyzed, corresponding to a comparison range (R) in Cas-analyzer of 113 bp, as Cas-analyzer allows 2 nt mismatches. If a read contained the 10 nt wild-type marker (r in Cas-analyzer) in red, Cas-analyzer would always count the read as precise repair. **(B)** The linker sequences are moved to encompass only resections that would allow undisrupted ddPCR primer and ddPCR probe sequences. **(C)** All resections detected with the settings in (B) were normalized to resections detected using the settings in (A) as a reflection of ddPCR sensibility to detect deletions.