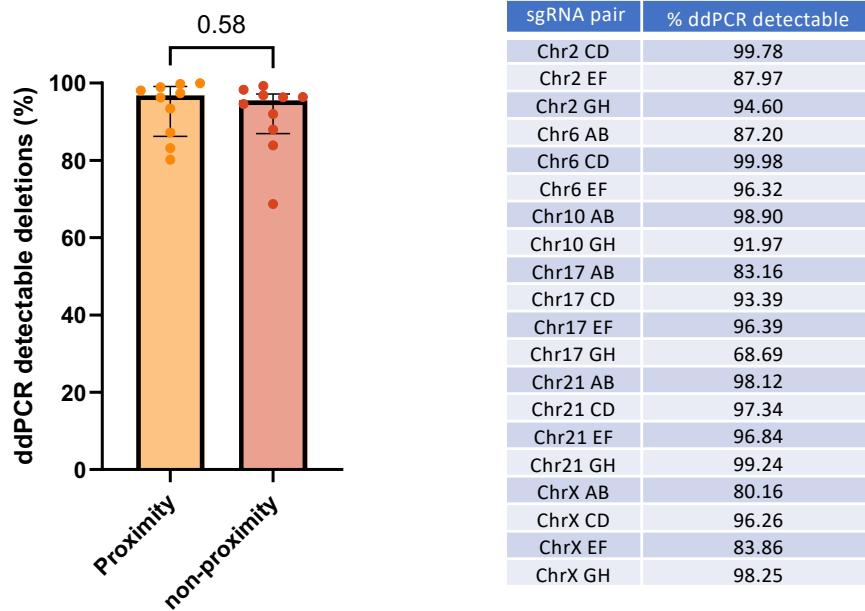


A

NGS fw primer → AACCTAACTCGACCTATTCCAACCAAGGAAACAAATCTCTTCTTTAAGAAAAAAAACCAGAAACAAACAACAACAAACAAACA
AAAAAAACCCCCGCTTGTAAATAACTACAGGTACCTACGGCTTCAGCCAGATGGCGCTGTGGGATAACTTTAAATATAAAAAC
TTATTCAGTAGCGTGGAAAGGAAACAGACCTGATGGACAC|AGGATCTACTACTGGTAGGAATAATGTGCAAACAAGTCATTAAATG
CAAAGAATAAGCCCTATATTAAAGATATTCAAATCATATGACTAAATTAACTTACATTTAATTTCAAGTAAATAATTCTATAAGTTA
TCACCATGTATTAATATGGTTCTTGACTAAATTCCAAGAGAACAGTGACAAATTCTCATTA
NGS rv primer ←

B

ddPCR fw primer → FAM probe ← AACTTACAGGTACCTACGGCTTCAGCCAGCAGATGGCCTGTGGGATAACTTTAAATATAAAAAC
ACAGACCTGATGGACAC|AGGATCTACTACTGGTAGGAATAATGTGCAAACA
ddPCR rv primer

C

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.