Type	Microhomology	Single-nucleotide microhomology	Base repeat (> 6n)
Deletions	1/12 [8.3%] p = 1	3/12 [25%] p = 1	0/12 [0%] p = 1
Deletion disagreements > 3 bp	15/47 [31.9%] p < 2.1E-3**	14/47 [29.8%] p > 0.26	3/47 [6.4%] p > 0.26
Deletion disagreements < 3 bp	8/50 [16%] p > 0.22	20/50 [40%] p > 0.13	13/50 [26%] p < 7.9E-5***
Insertion disagreements < 3 bp	17/30 [56.7%] p < 8.4E-8***	25/30 [83.3%] p < 1.9E-8***	22/30 [73.3%] p < 3.3E-14***
Random location	3/60 [5%]	12/60 [20%]	0/60 [0%]

Supplemental Table S9. Microhomology and homopolymers around deletions and duplex indel disagreements.
Data derived from Supplemental Tables S5-8. Stars indicate significance of p-values for comparison with "random location" row, computed with Fisher's exact test and corrected with Hochberg's step-up procedure (5% false discovery rate); *: p < 0.05; **: p < 0.01; ***: p < 0.001.