



Supplementary Fig. 11: Microhomology around breakpoints of internal deletions (dashed line). We extracted 10nt up- and downstream of the breakpoints of internal deletions and aligned the sequences from the two breakpoints. The graph shows the average fraction of homologous bases for all internal deletions (data; hot and cold evolved populations) and a set of 10,000 random deletions (random). Note that microhomology extends 2nt up and downstream of deletion breakpoints.