



**Supplemental Figure S14.** Verification of human X-palindrome spacer deletions. PCR primers were designed based on deletion breakpoints from split reads or, in cases where reads spanning the breakpoint could not be found, based on the estimated deletion breakpoints from visualization of coverage depth. Positive control: Sequence expected to be present in both reference samples and deletion samples. Negative control: Sequence expected to be present in reference samples, and absent in deletion samples. Breakpoint: Sequence expected to be present in deletion samples, and absent in reference samples. D = deletion sample, R = reference sample.