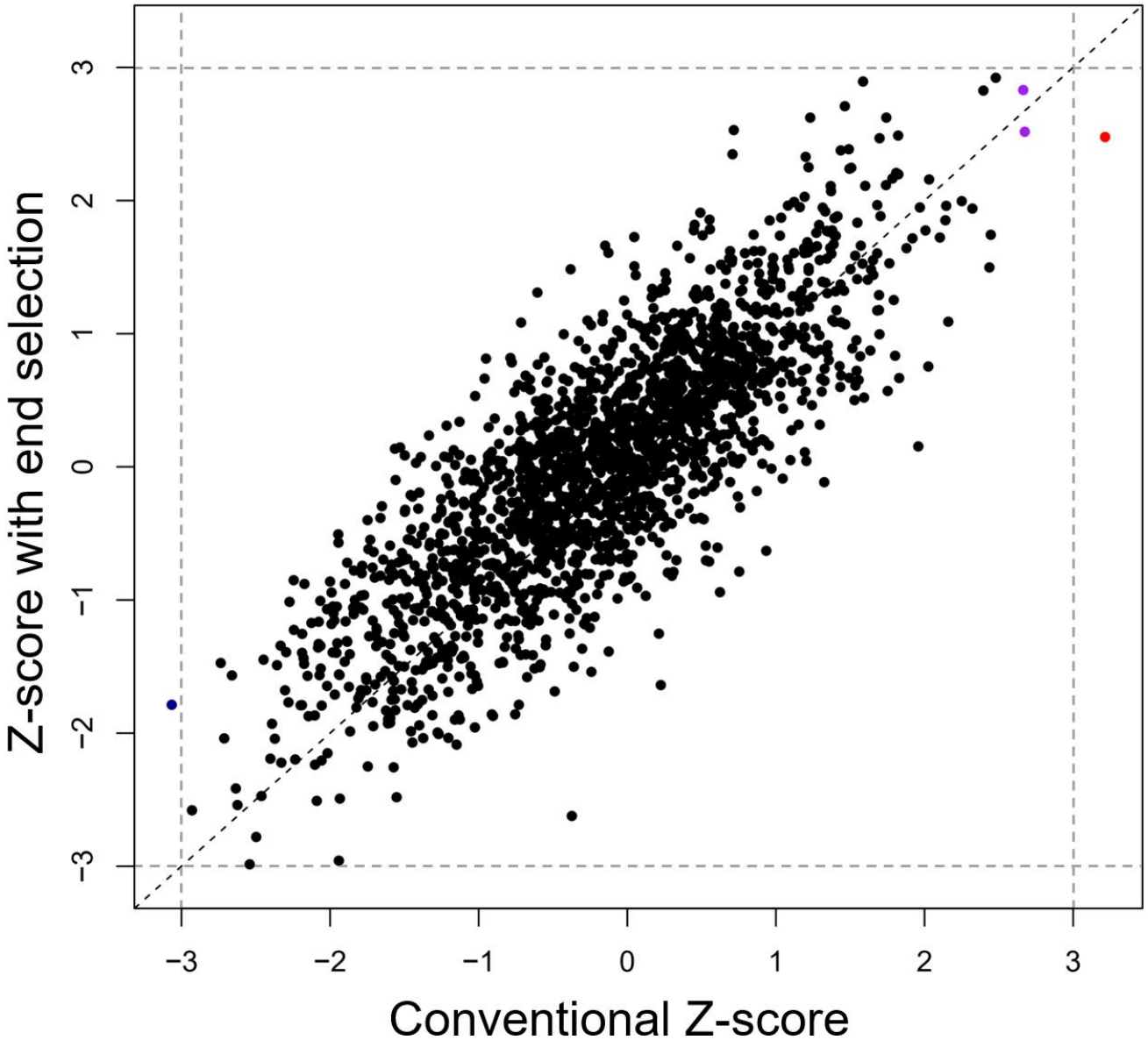

Fig. S1. Comparison of Z-scores in euploid samples. Each dot represents one sample. Blue and red dots represent samples that would be falsely called as monosomy (i.e., Z-score < -3) or T21 (i.e., Z-score > 3) in the conventional approach while corrected by our approach; purple dots (N=2) represent samples that would be falsely called as T21 when a lower Z-score threshold (i.e., 2.6433) was used to rescue the false negative results in the conventional approach.

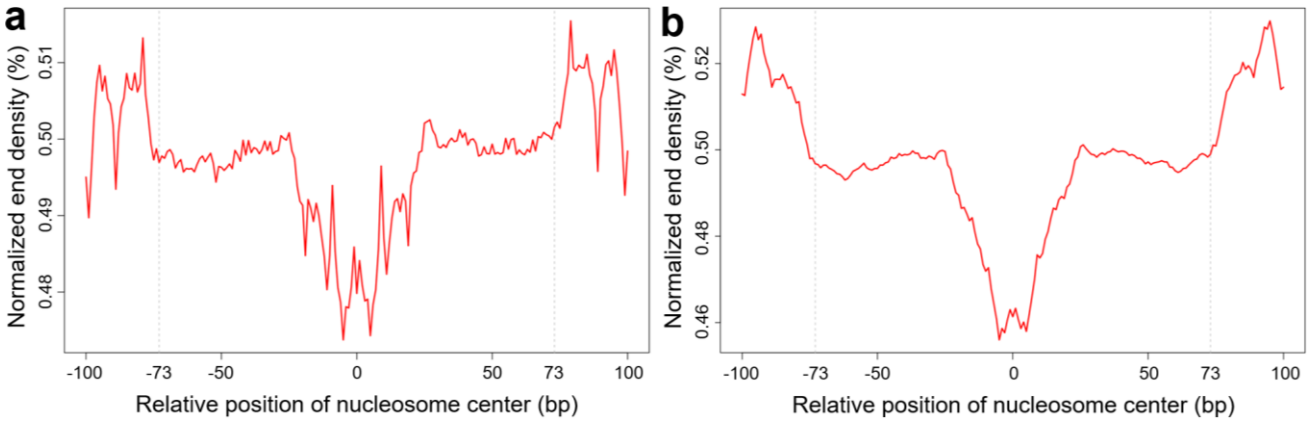

Fig. S2. Distribution of cfDNA ends within the nucleosome context in (a) Karlsson, and (b) Chandrananda datasets. Samples in each dataset are pooled together.

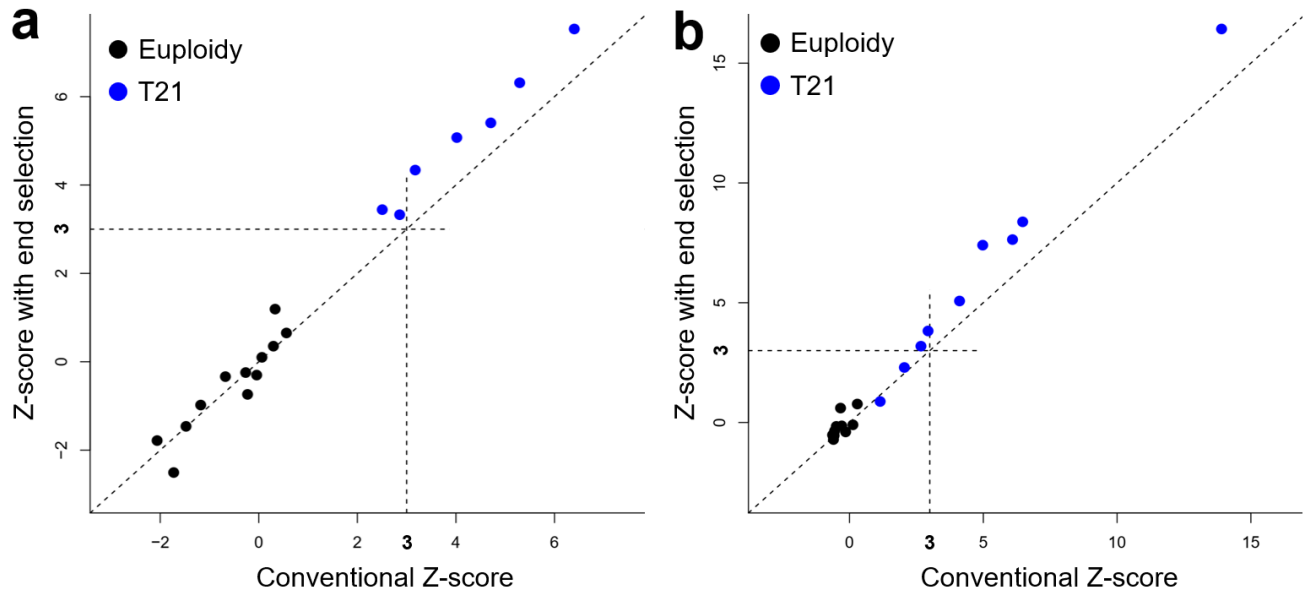

Fig. S3. Comparison of conventional Z-scores and those after end selection when keeping chr13 and chr18 into the analysis in (a) Karlsson, and (b) Chandrananda datasets.

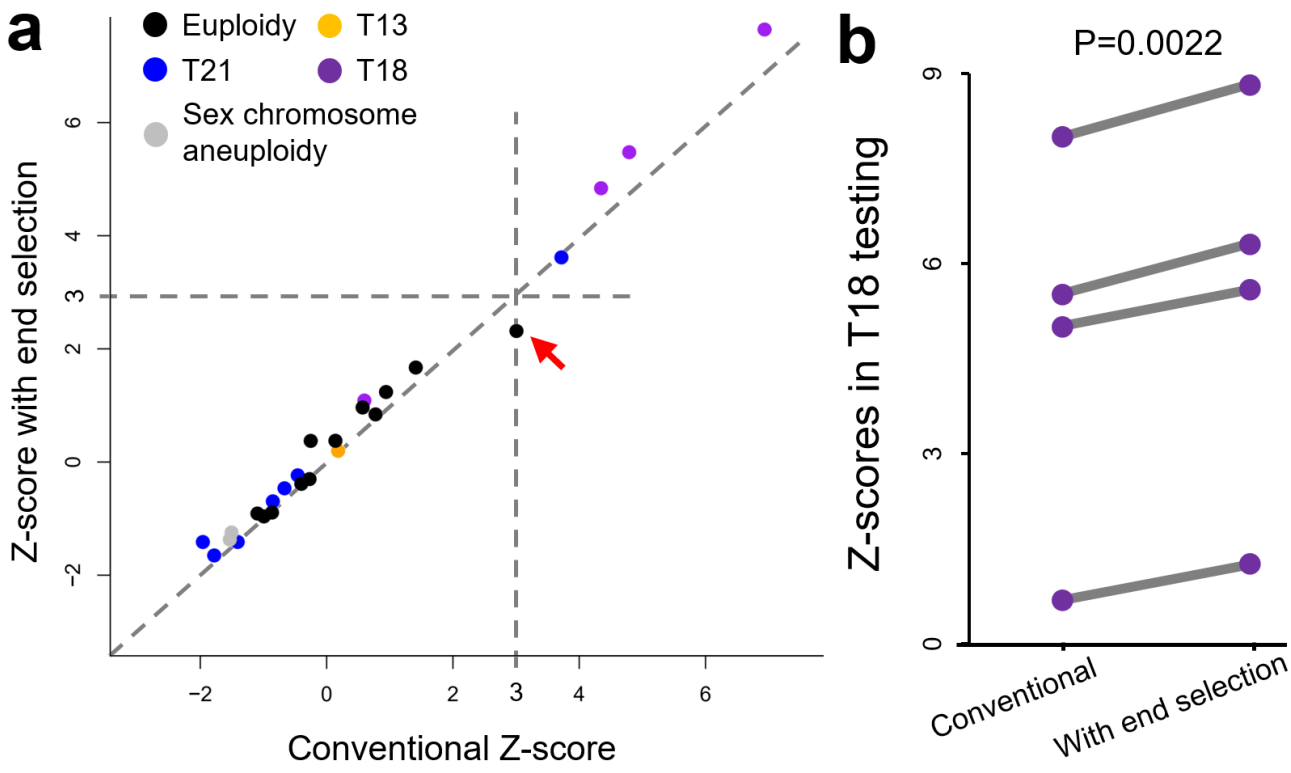

Fig. S4. Comparison of Z-scores in (a) T18 and (b) T21 testing for the 4 T18 cases in Karlsson dataset. In (a), the red arrow highlights a sample with conventional Z-score > 3 while get corrected in our end selection approach; in (b), P-value was calculated using paired t-tests.