

Figure S1. FASTQ quality control plots generated using the quality_plot function in TADbit. (a) Quality plots for the BR dataset. Top plot shows the PHRED score (blue line) and number of “N” positions (black line) as a function of the sequence position in the reads. Bottom plot shows the number of undigested sites (red), dangling ends (yellow) and re-ligated sites (blue) as a function of the nucleotide position in the reads. (b) TR1 dataset. (c) TR2 dataset. (d) SUM dataset. Panels b, c, and d show the same data as described in panel a

