Figure S1: Comparison of down-sampled DNA/RNA-seq data size and detected RDDs number between whole dataset and down-sampled subsets.

Figure S2: The distribution of RDD site type across different regions in the genome.

A: Intergenic
B: All repeat
C: Non-repeat
D: Transcript
**Figure S3:** RDD site type distribution in Alu repeat, non-Alu repeat and non-repeat regions

![RDD site type distribution](image)

**Figure S4:** The distribution of RDDs in genic regions. The ratio of intronic RDDs ranges from 8.45% to 61.09% while ncRNAs’ ranges from 13.9% to 68.55% and correlation coefficient is -0.95.

![Genic regions distribution](image)

**Figure S5:** Percentage of the genes with miRNA target RDDs that were up-regulated in primary prostate tumor in published microarray datasets.

![Gene expression distribution](image)