

Figure S1. Scattergraph of normalized chimera numbers and gene lengths. The chimera numbers were normalized based on the sequencing depth of genes, to 30-fold of all genes. The genes which gotten at least five chimeras were drawn on this scattergraph.

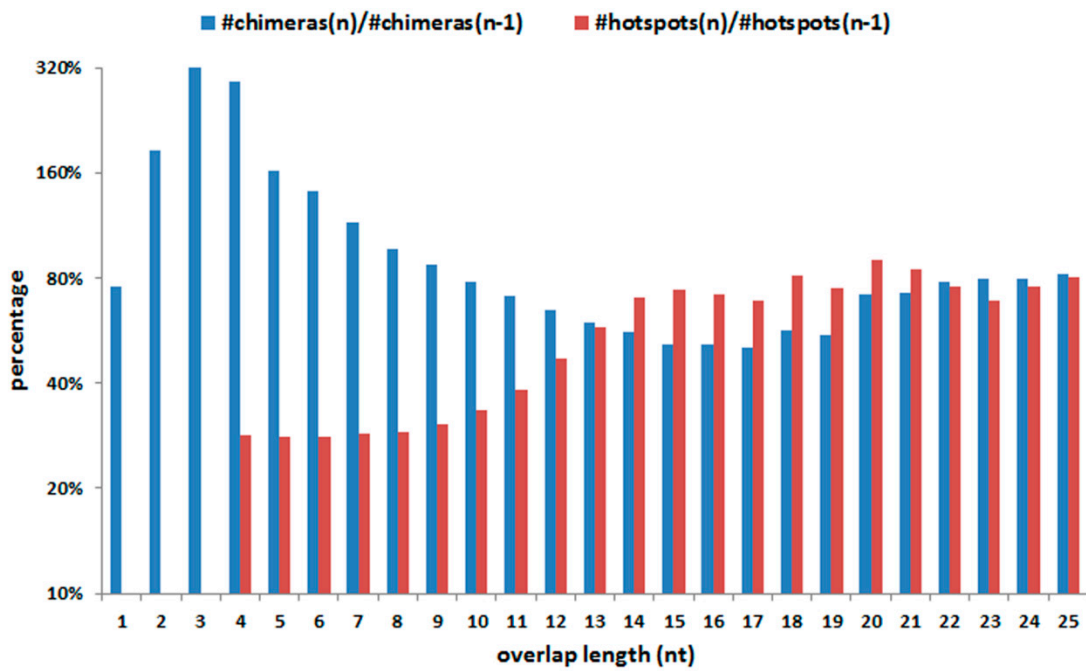


Figure S2. Ratio of the chimera or chimeric hotspots amounts between a given length overlap and 1 nt shorter overlap.

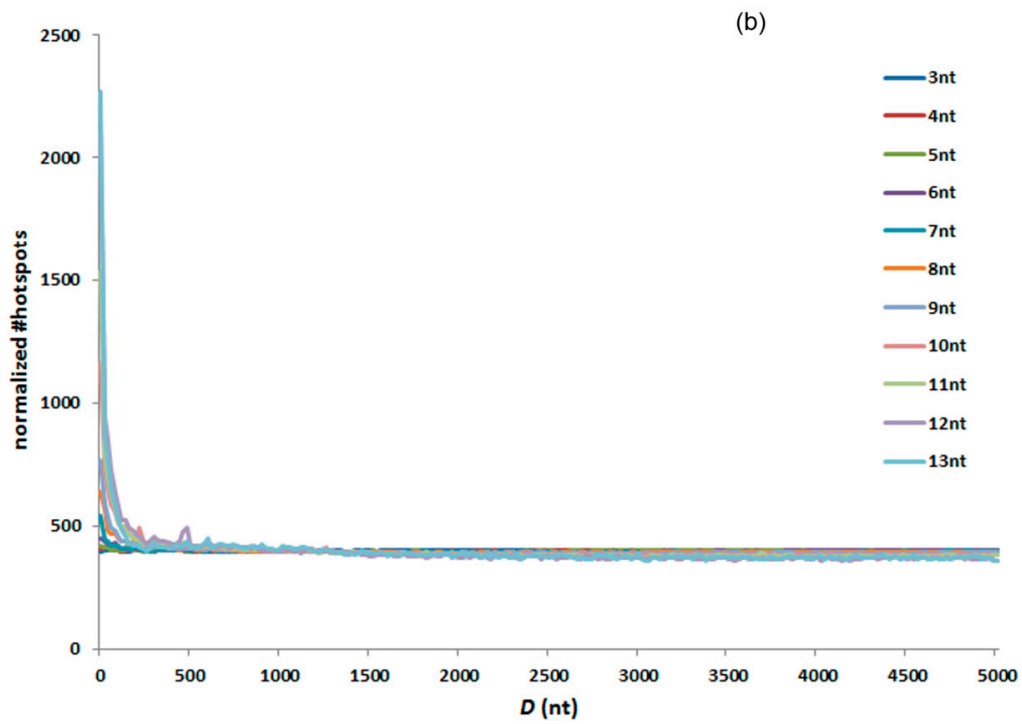
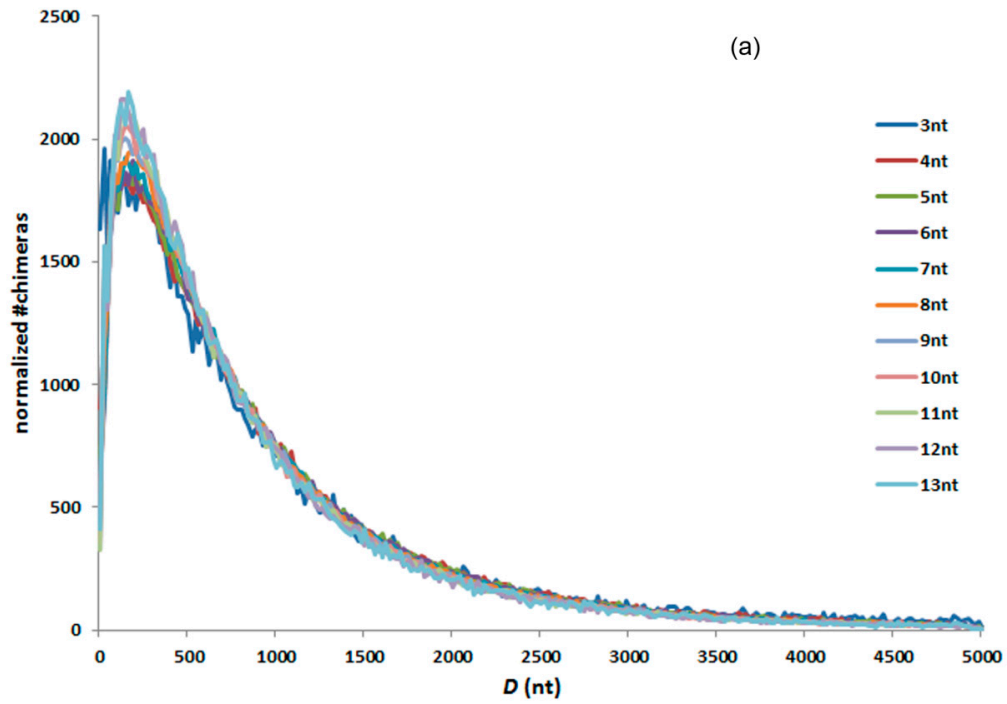


Figure S3. Distance distribution in different overlap lengths. (a) Distance distribution of chimeras in different overlap lengths. (b) Distance distribution of chimeric hotspots in different overlap lengths.