

Figure S1. Mapping of selected concatemer reads with 2 or more monomers obtained from Nanopore sequencing eccDNA-enriched ddm1 DNA (red) as well as whole-genome sequencing of Col-0 (green) and ddm1 (blue) plants.

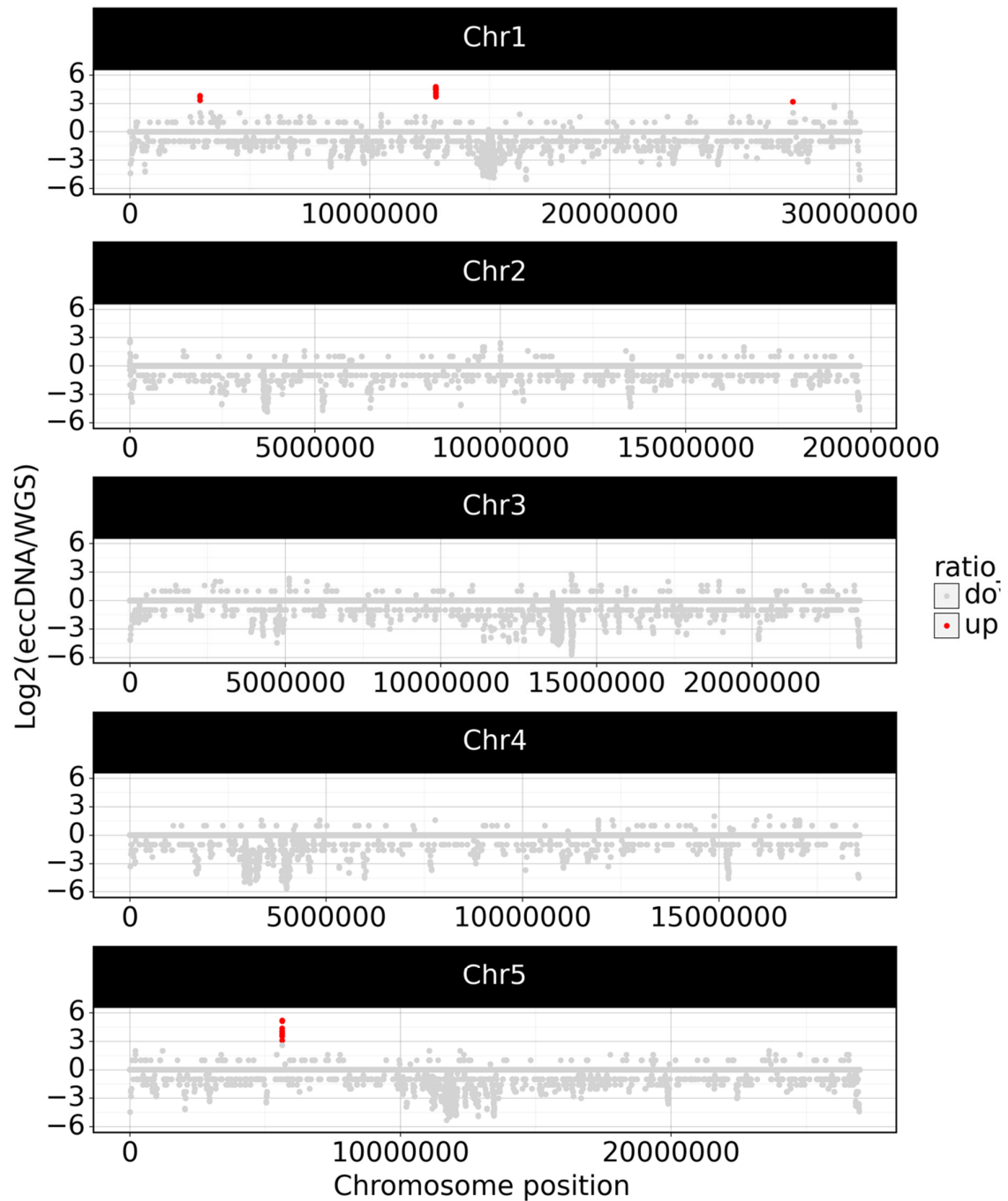
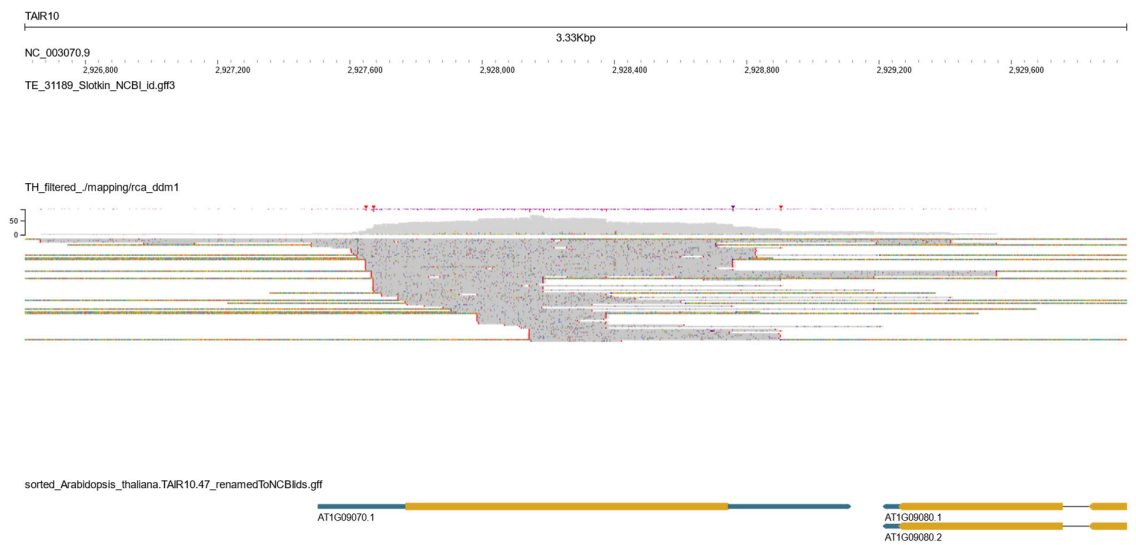


Figure S2. EccDNA read coverage of genome loci. Dots indicate log2 ratio between number of concatemer reads of eccDNA and WGS samples for *ddm1* plants. Red and grey colors show regions with the log2 ratio >3 or ≤ 3 , respectively.



Supplementary Figure S3. Coverage of AT1G09070 gene (Chr1:2,927,502..2,929,107) by Nanopore concatemer reads from eccDNA-enriched DNA of ddm1.

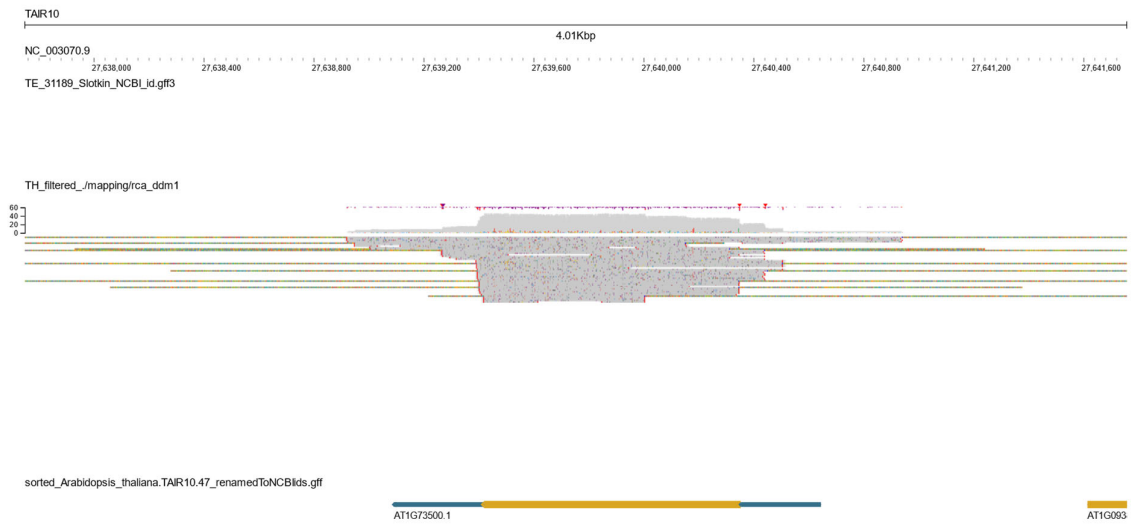


Figure S4. Coverage of AT1G73500 gene (Chr1: 27,637,748..27,641,755) by Nanopore concatemer reads from eccDNA-enriched DNA of ddm1.



Figure S5. Inhibition of *A.thaliana* Col-0 growth and development under toxin treatment (zebularine and α -amanitin). a, b, c – control plants grown *in vitro*; d, e, f – plants grown on $\frac{1}{2}$ MS supplemented with zebularine and α -amanitin.

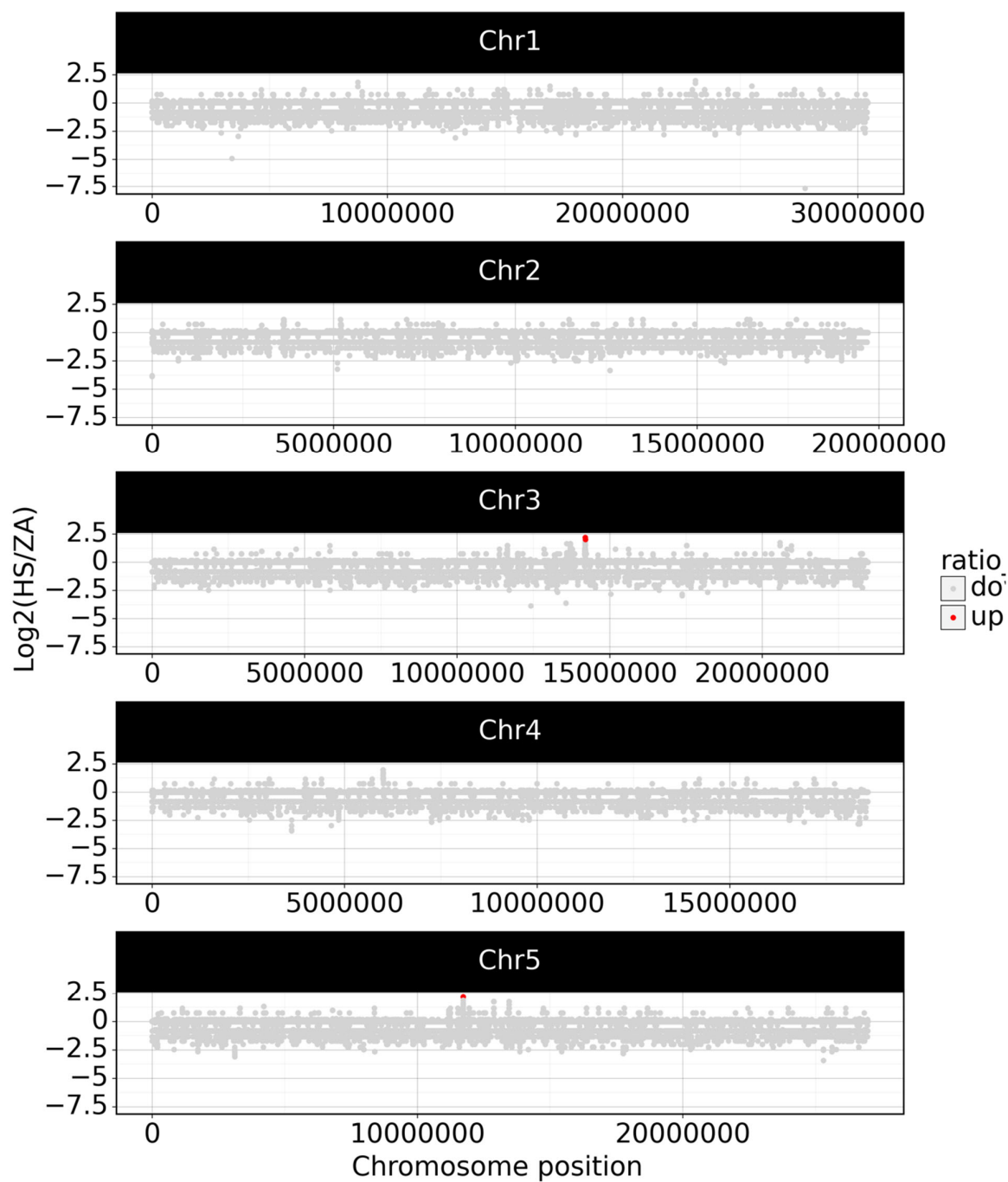


Figure S6. EccDNA read coverage of genomic loci in ZA vs K sample. Dots indicate log_2 ratio between number of concatemer reads of eccDNA for ZA vs K sample. Red and grey colors show regions with the log_2 ratio ≥ 2 or < 2 , respectively.

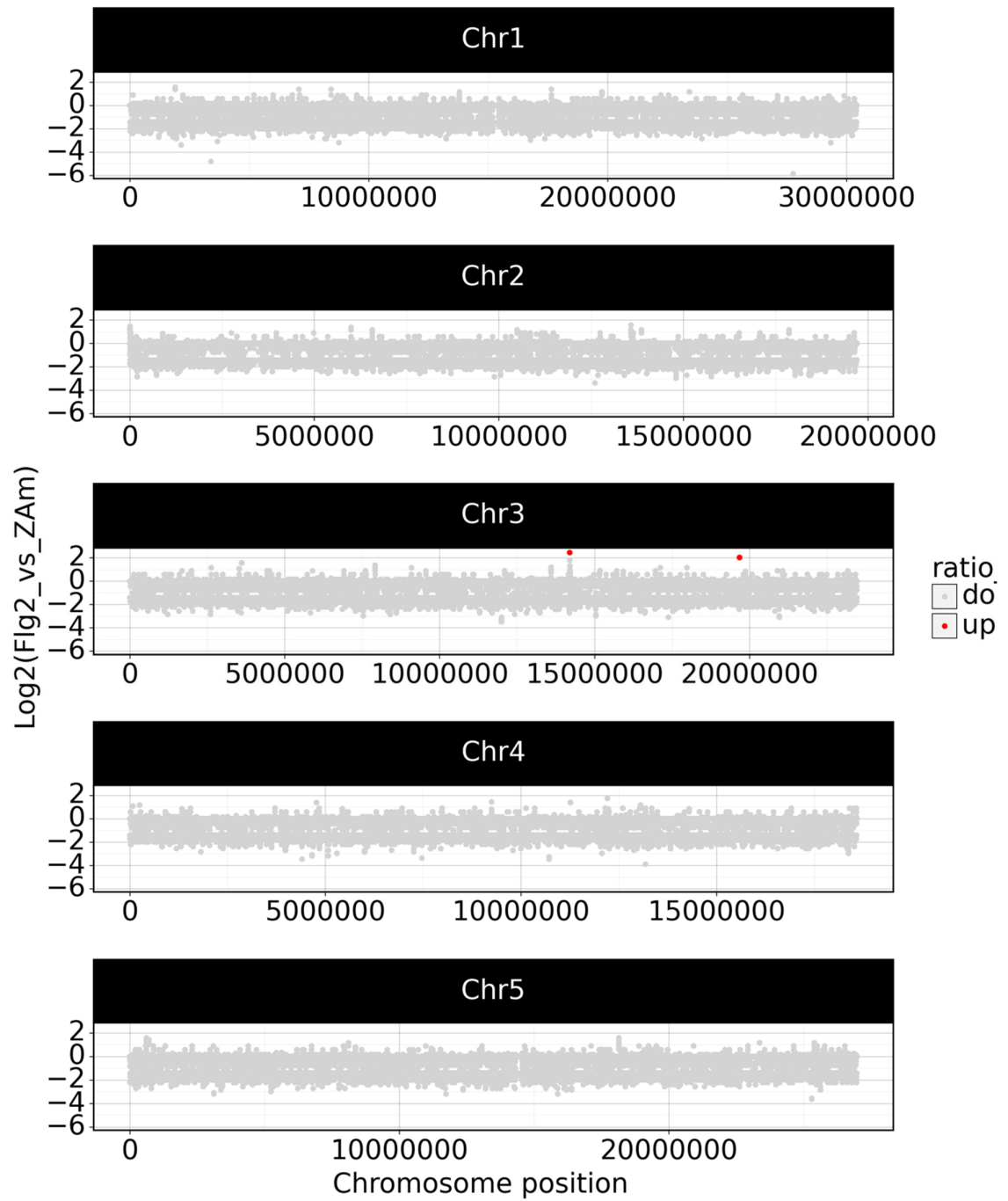


Figure S7. EccDNA read coverage of genomic loci from Flg samples (replicate 1). Dots indicate \log_2 ratio between number of concatemer reads of eccDNA for Flg vs ZA sample. Red and grey colors show regions with the \log_2 ratio ≥ 2 or < 2 , respectively.

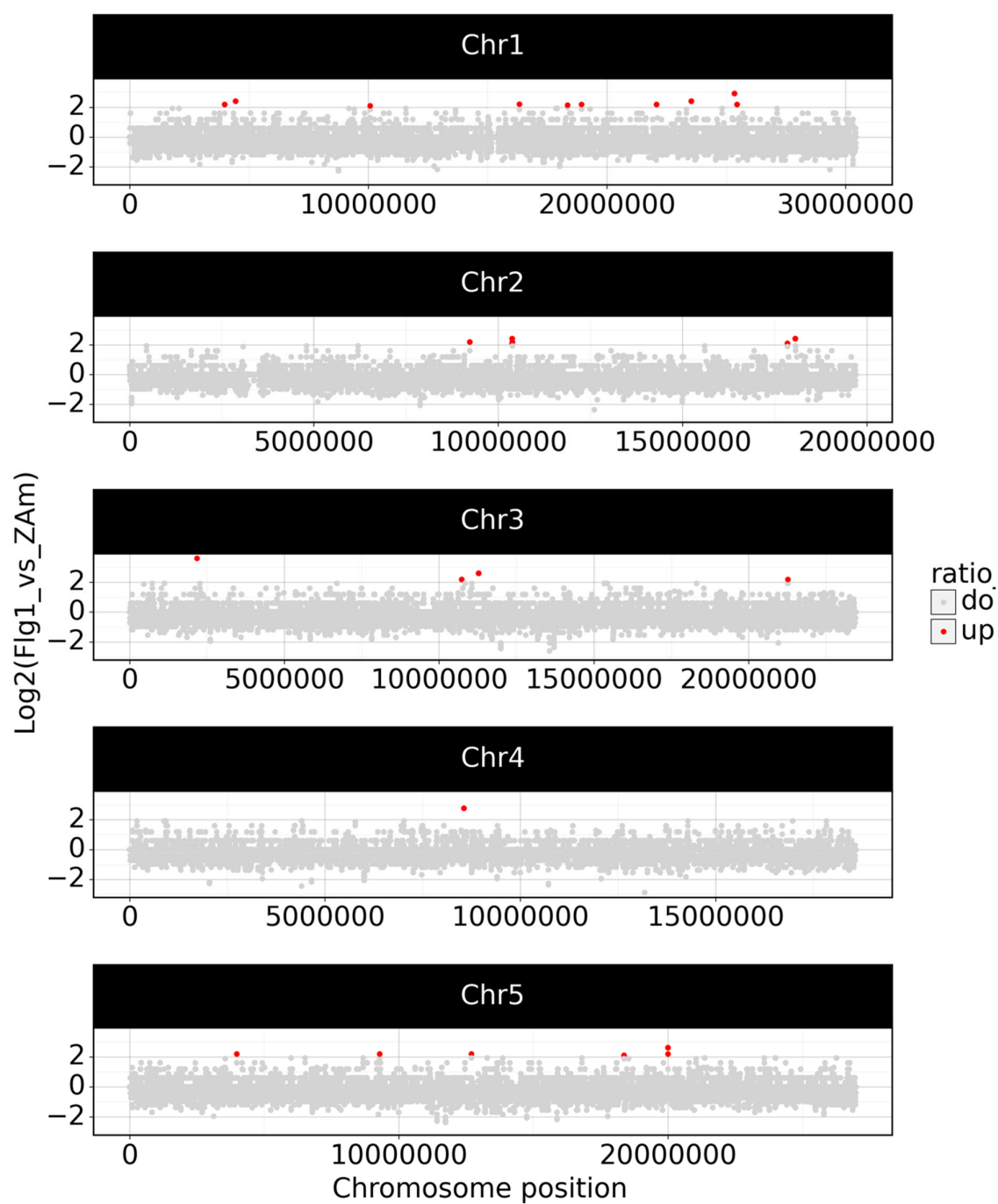


Figure S8. EccDNA read coverage of genomic loci from Flg samples (replicate 2). Dots indicate log_2 ratio between number of concatemer reads of eccDNA for Flg vs ZA sample. Red and grey colors show regions with the log_2 ratio ≥ 2 or < 2 , respectively.

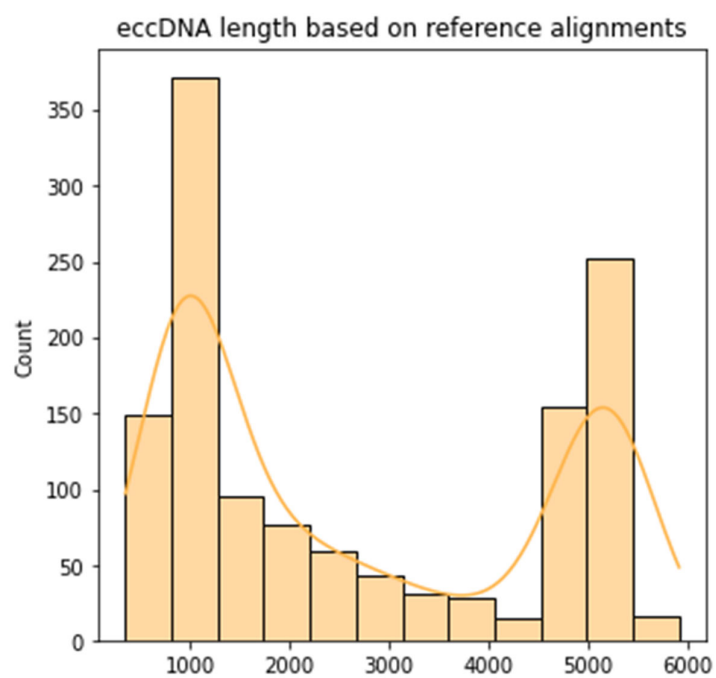


Figure S9. The histogram showing number of EVD eccDNAs of different length.