

Supplementary Materials for:

Gram-positive bacteria-like DNA binding machineries involved in the replication initiation and termination mechanisms of Mimivirus

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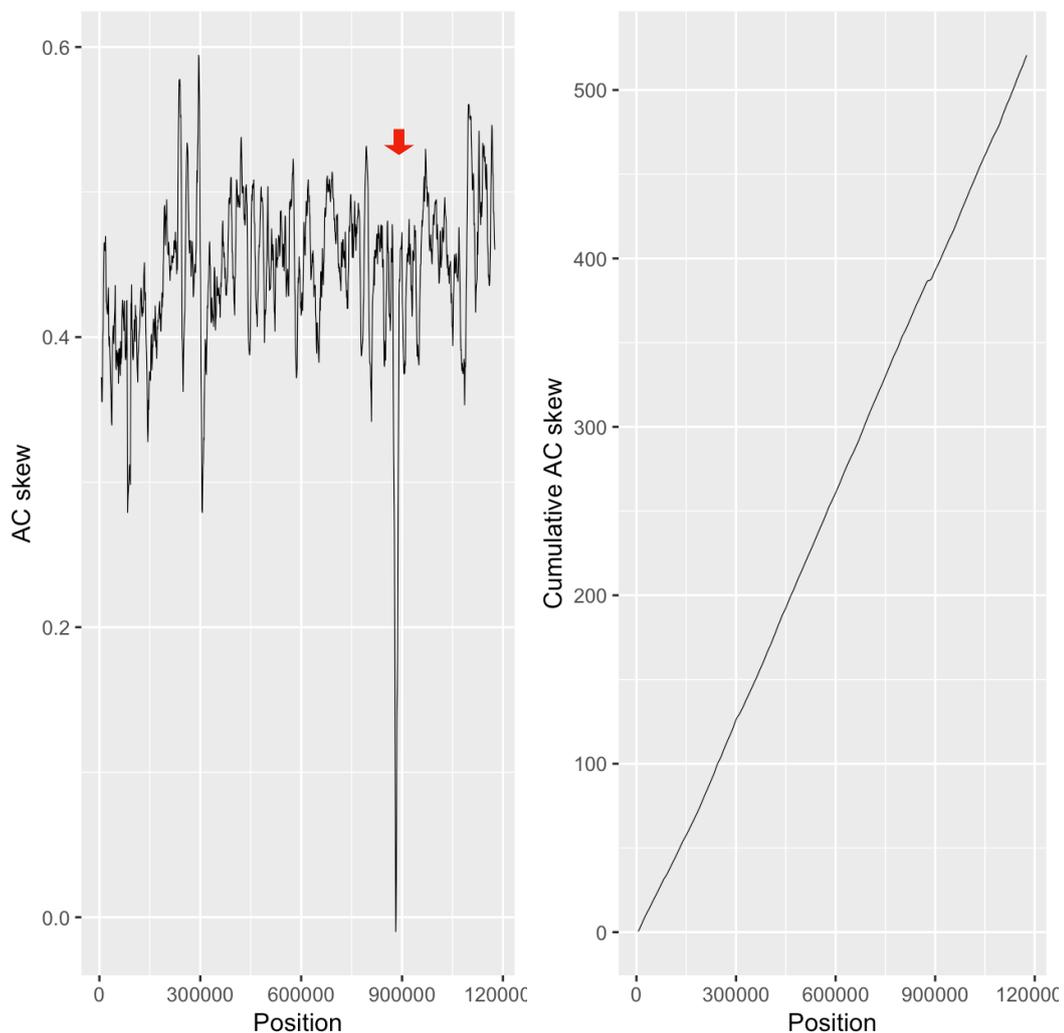


Figure S1. AC skew analyses of the *Acanthamoeba polyphaga mimivirus* (APMV) genome. AC skew plot (left) and cumulative AC skew plot (right) of APMV genome (AY653733.1). Red arrows indicate the lowest peak ($881,000 \pm 5,000$ bp), which corresponds to one of the lowest values on the GC skew plot ($882,000$ bp).

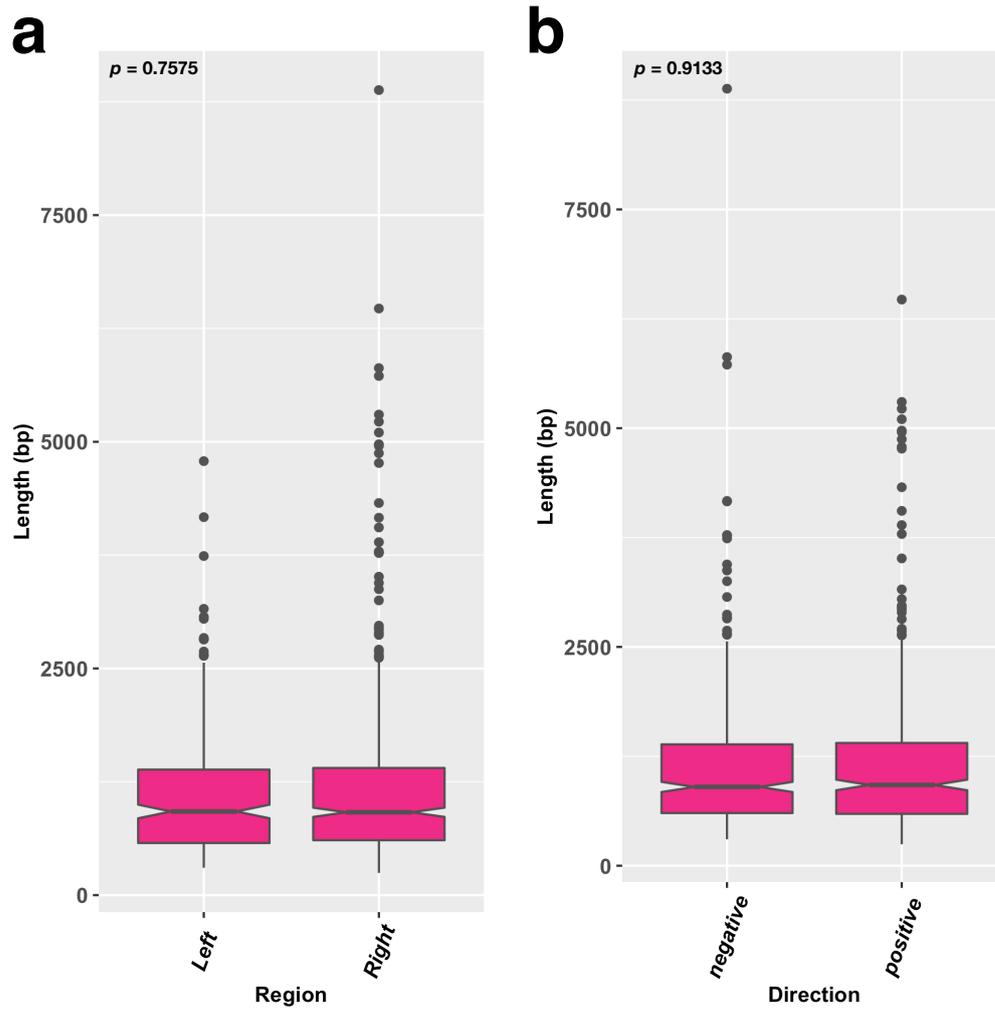


Figure S2. Correlation of the coding sequence (CDS) lengths of the left and right sides from the estimated *ori*-region. (a) CDS lengths of the left and right sides from the estimated origin (380,698 bp). (b) CDS lengths of the positive and negative direction in the APMV genome (AY653733.1). The *p*-values on the top left of each graph indicate the statistical differences between each of the two group-based results of a KS test.

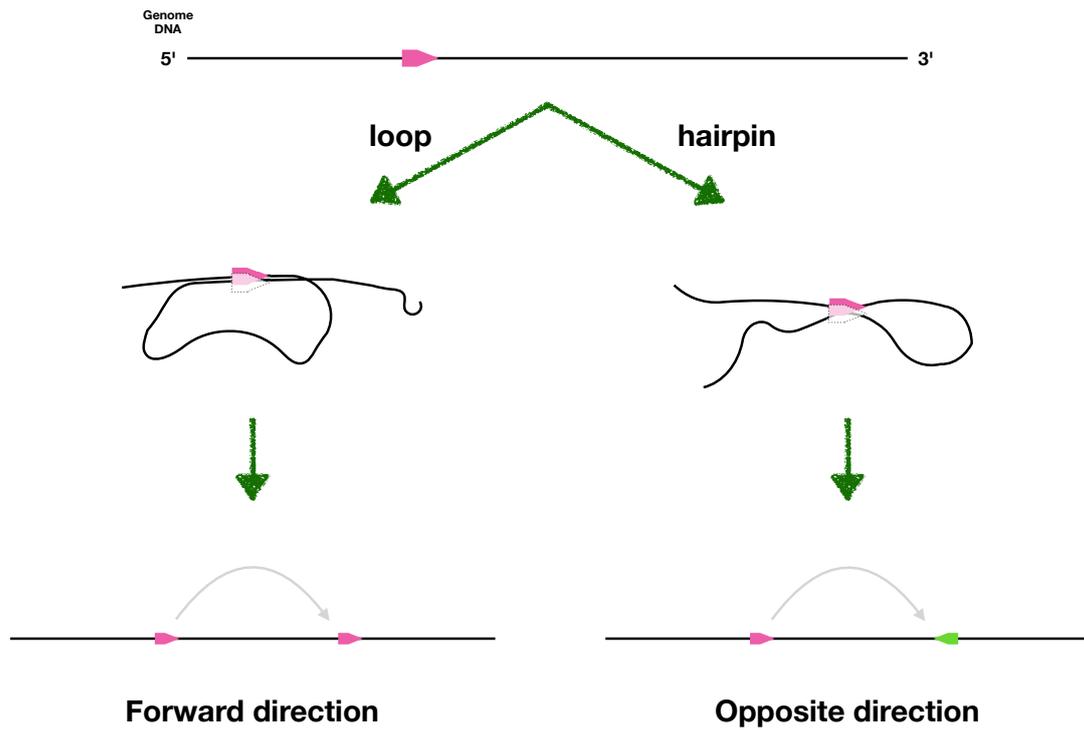


Figure S3. Models of the generation of paralogous genes far from each other and their directions on the linear genome. Pink/green arrow indicate paralogous genes with forward/opposite direction. A loop (left) or hairpin (right) structure would cause the generation of paralogous genes with forward or opposite directions via homologous recombination.



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