

Note S1 GGA 18 compared to MGA 20

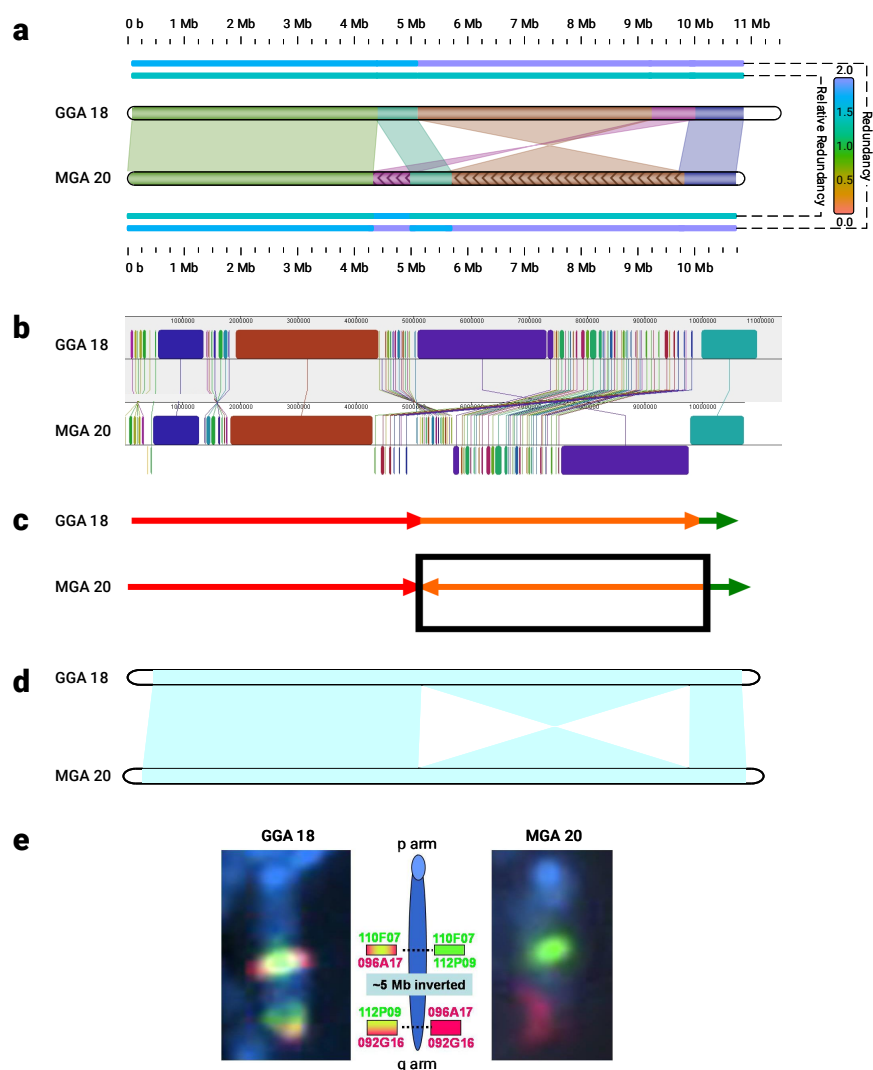


Fig. S1. Pair-wise comparison of *G. gallus* chromosome 18 and *M. gallopavo* chromosome 20. (a) Smash++, with $k = 14$ and 5 used by an FCM and an STMM, respectively. The blocks smaller than 500 Kb are discarded; (b) progressiveMauve [1], with LCB (locally collinear block) weight = 18692. Reverse complements are shown in lower level; (c) adopted from [2], which is confirmed by fluorescence *in situ* hybridization (FISH) analysis. The box shows a local rearrangement; (d) SynBrowser [3], with the resolution = 150 Kb (minimum size of a reference block); (e) adopted from [4], which confirms an inversion rearrangement of size ~5 Mb by FISH analysis.

References

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- [3] J. Lee, W.-y. Hong, M. Cho, M. Sim, D. Lee, Y. Ko, and J. Kim, “Synteny portal: a web-based application portal for synteny block analysis,” *Nucleic acids research*, vol. 44, no. W1, pp. W35–W40, 2016.
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