Supplementary Material for

# Smash++: finding rearrangements

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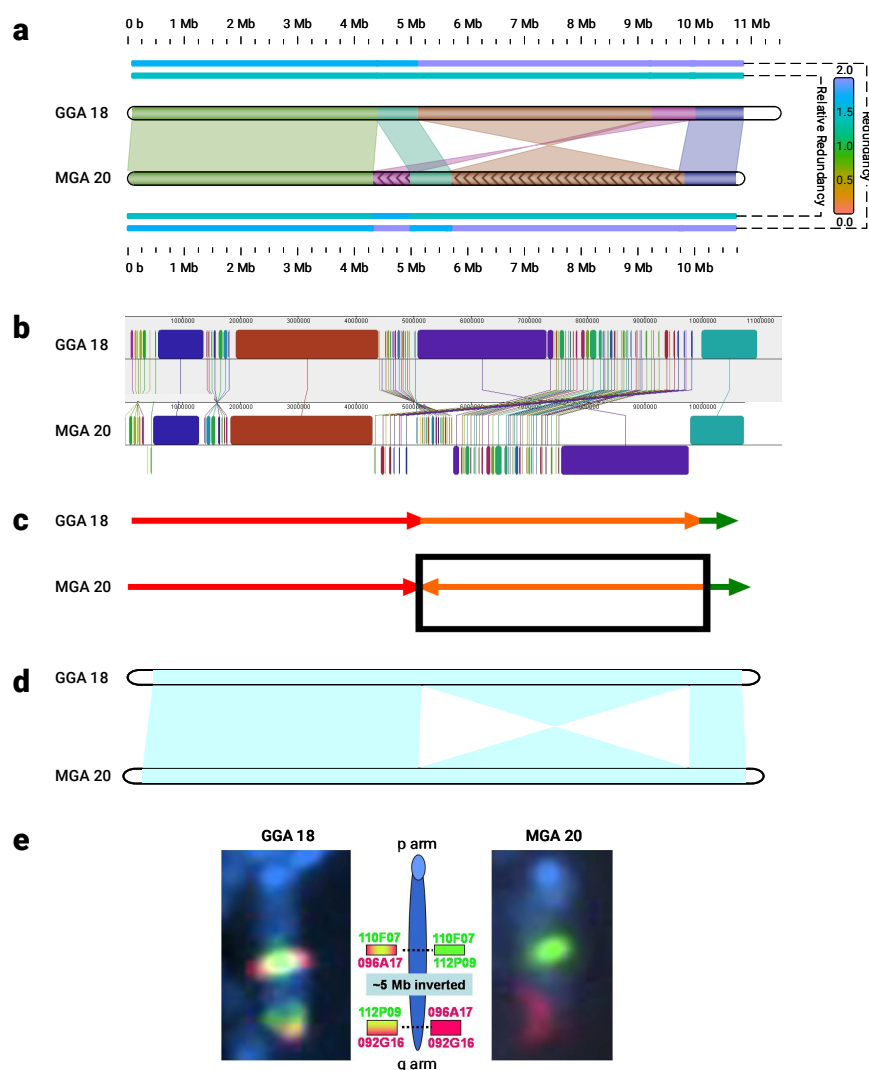
## Note S1   GGA 18 compared to MGA 20



**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 of 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 –minimum size of a reference block– of 150 Kb; (e) adopted from [4], which confirms an inversion rearrangement of size ∼5 Mb by FISH analysis.

## References

[1] A. E. Darling, B. Mau, and N. T. Perna, "progressivemauve: multiple genome alignment with gene gain, loss and rearrangement," *PloS one*, vol. 5, no. 6, p. e11147, 2010.

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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.

[4] R. A. Dalloul, J. A. Long, A. V. Zimin, L. Aslam, K. Beal, L. A. Blomberg, P. Bouffard, D. W. Burt, O. Crasta, R. P. Crooijmans *et al.*, "Multi-platform next-generation sequencing of the domestic turkey (*Meleagris gallopavo*): genome assembly and analysis," *PLoS biology*, vol. 8, no. 9, p. e1000475, 2010.