Note S1   GGA 18 compared to MGA 20
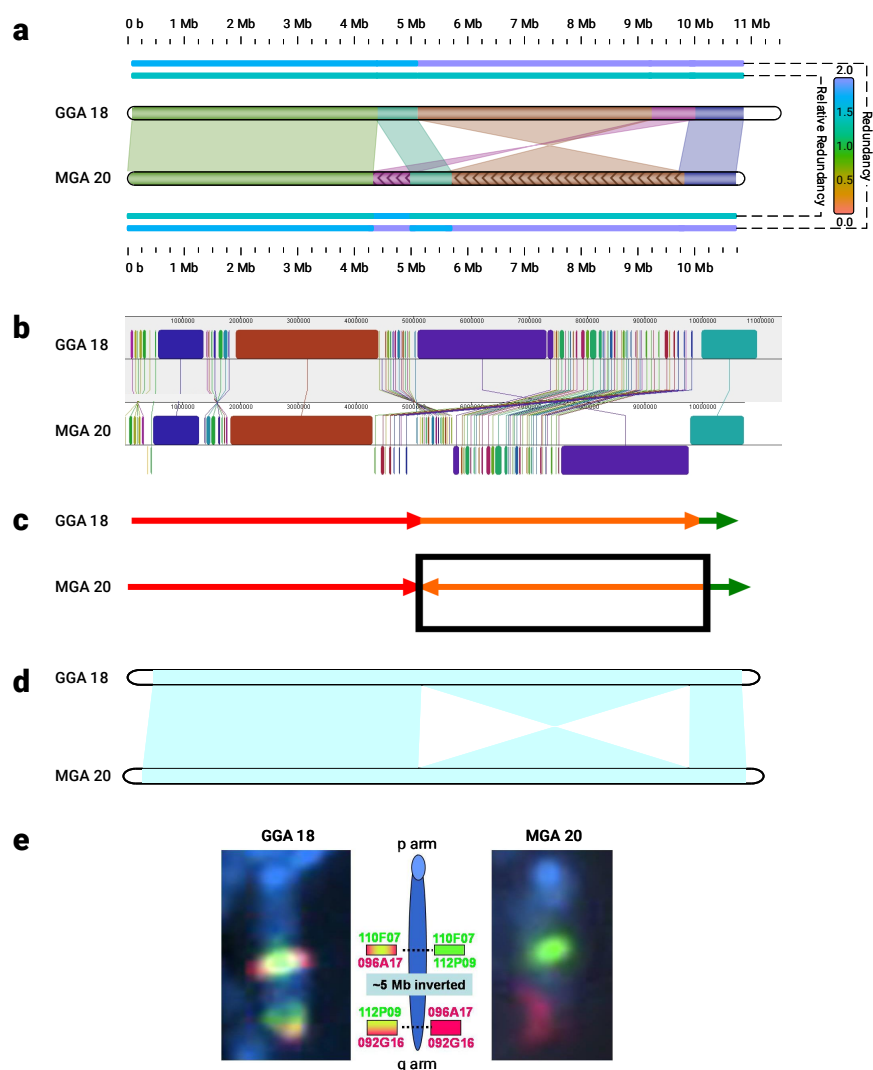

Fig. S1. Pair-wise comparison of *G. gallus* chromosome 18 and *M. gallopavo* chromosome 20. (a) Smash++, with $k = 14$ and 5 used by an FCM and an STMM, respectively. The blocks smaller than 500 Kb are discarded; (b) progressiveMauve [1], with LCB (locally collinear block) weight of 18692. Reverse complements 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 of 150 Kb (minimum size of a reference block); (e) adopted from [4], which confirms an inversion rearrangement of size ∼5 Mb by FISH analysis.
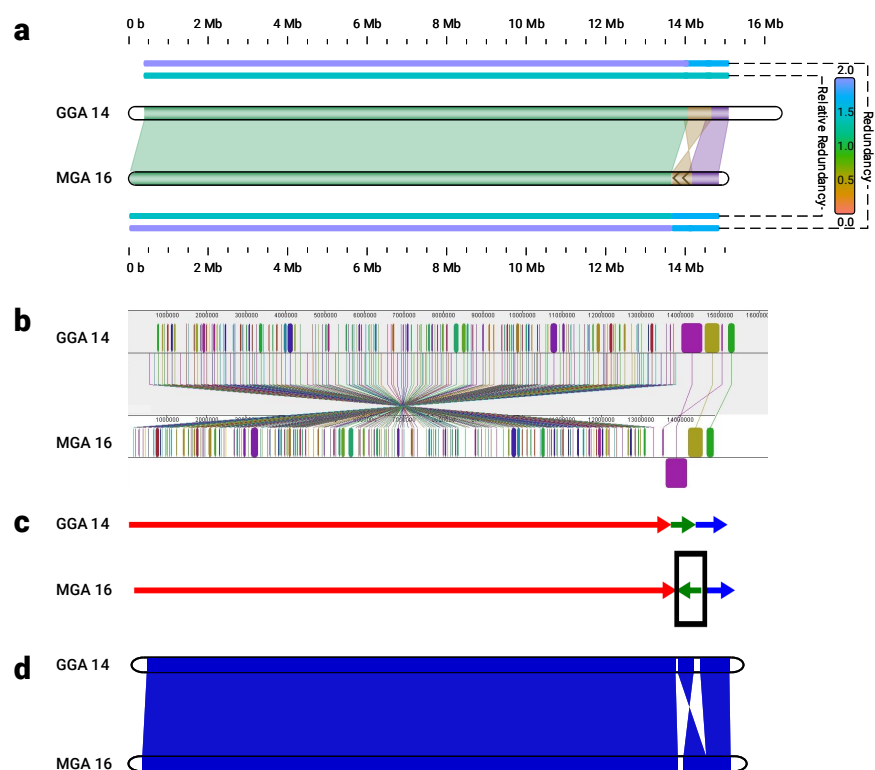
Note S2   GGA 14 compared to MGA 16

Fig. S2. *G. gallus* chromosome 14 compared to *M. gallopavo* chromosome 16. (a) Smash++, employing an FCM and an STMM with $k = 14$ and 5, respectively. The blocks smaller than 400 Kb are discarded; (b) progressiveMauve, with LCB weight of 27424; (c) adopted from [2]. The box shows an inversion rearrangement; (d) SynBrowser, with the resolution of 150 Kb.
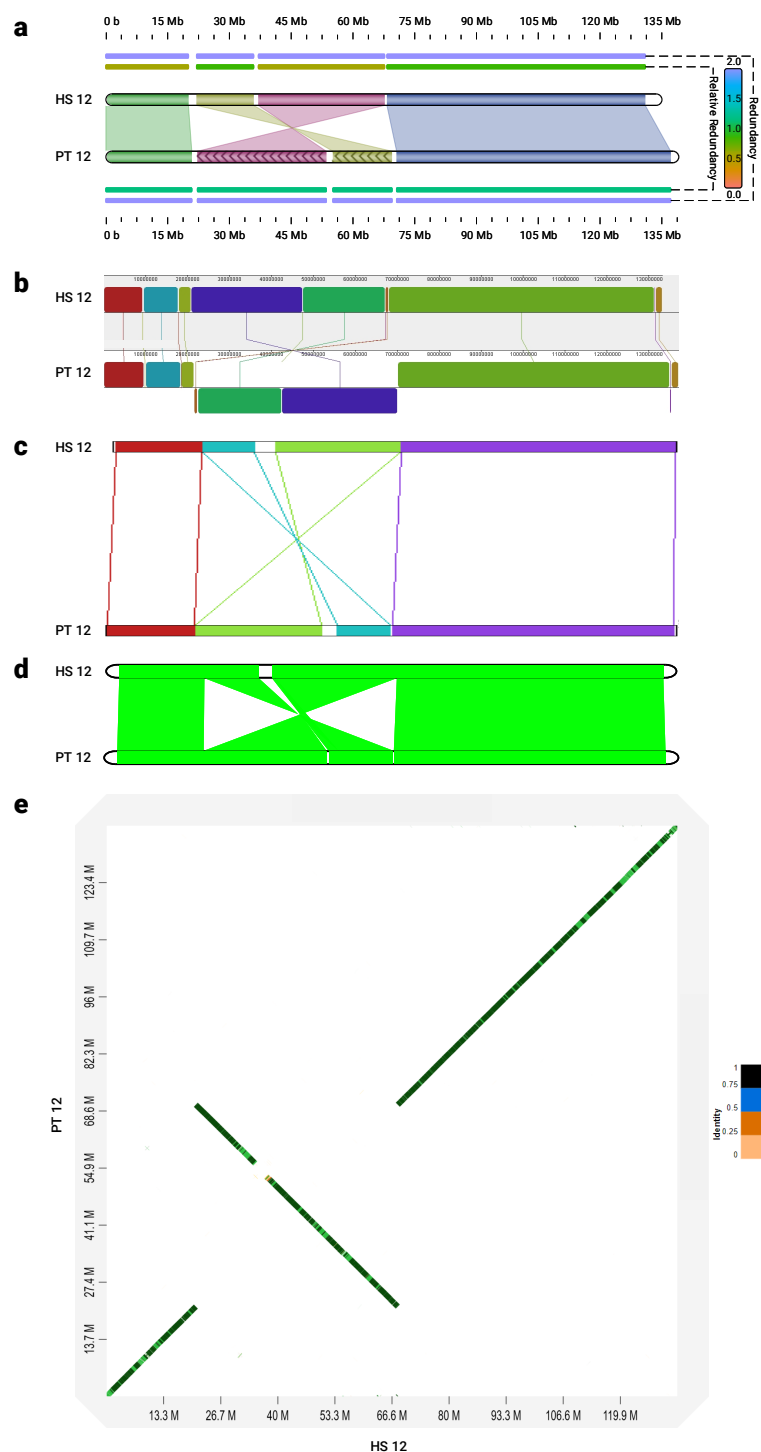
Note S3   HS 12 compared to PT 12

Fig. S3. Comparison of *H. sapiens* chromosome 12 and *P. troglodytes* chromosome 12. (a) Smash++, with $k = 14$ used by an FCM. The blocks smaller than 100 Kb are discarded; (b) progressiveMauve, with LCB weight of 55186; (c) Cinteny [5], with minimum length of synteny block = 1 Kb, maximum gap between adjacent markers = 5 Mb and minimum number of markers = 1; (d) SynBrowser, with the resolution of 150 Kb; (e) D-Genies [6], in "strong precision" mode.
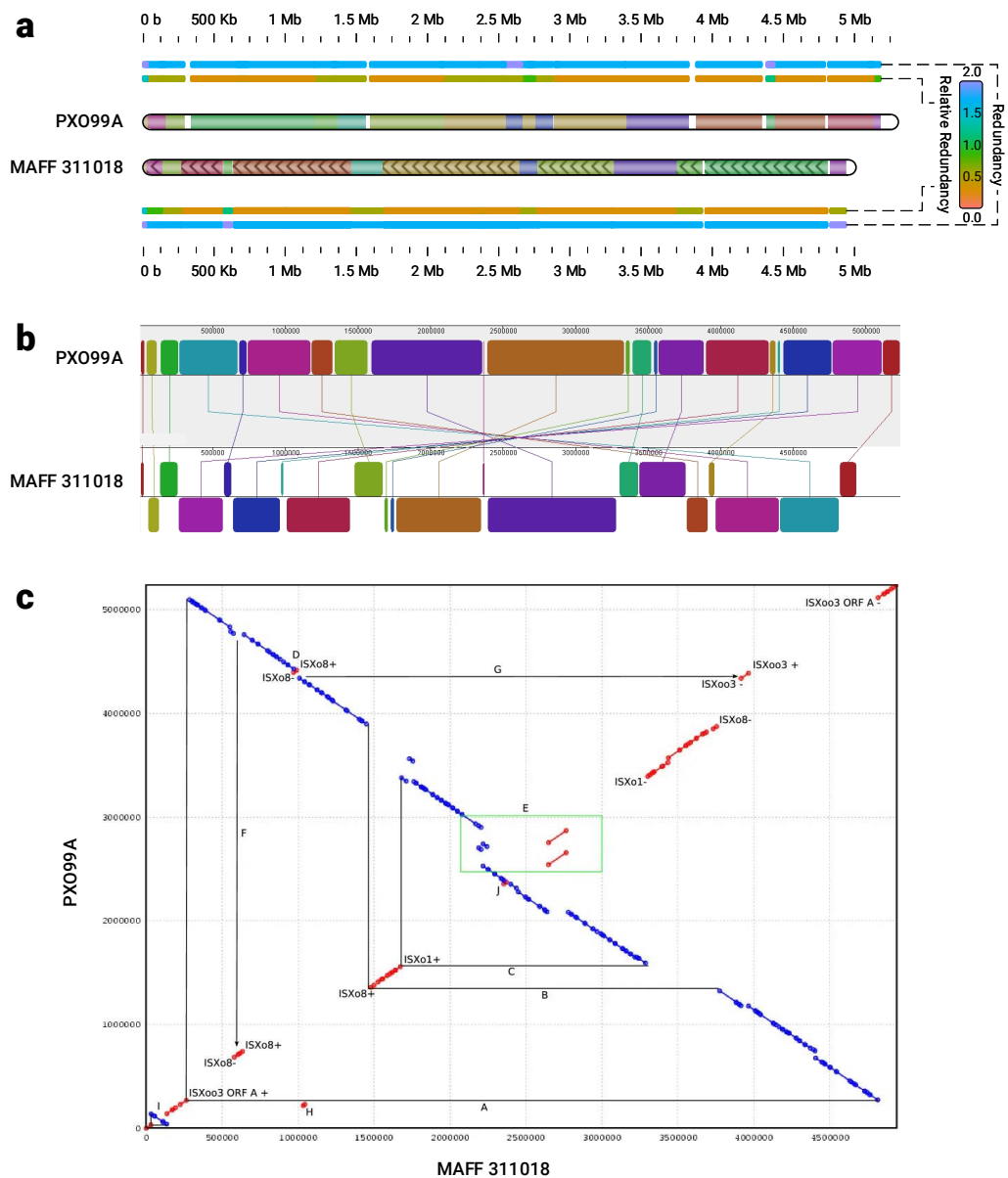
Note S4   PXO99A compared to MAFF 311018

Fig. S4. Pair-wise comparison of PXO99A and MAFF 311018. (a) Smash++, with k=13 used by an FCM. The blocks smaller than 10 Kb are discarded. In order to make the figure clearer, the shaded paths for connecting corresponding regions are not drawn; (b) progressiveMauve, with LCB weight of 3926; (c) adopted from [7], which employs an alignment-based method to obtain this dot plot. The blue and red colors shows regions of PXO99A that align to the same or opposite strand of MAFF 311018, respectively.

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