

**Figure S1.** Summary of genomic variant landscape per chromosome of all 12 chicken genomes sequenced in this study. Circos plot of genome variants. Different loops from outside to inside summarize the length of each chromosome (unit: Mb), gene density, SNP density (SNP density > 0.0015 is marked by a red square, 0.0005 < SNP density ≤ 0.0015 by a gray circle, and SNP density ≤ 0.0005 by a green triangle), positions of INS (structural variation of the insertion type), positions of INV (structural variation of the inverted type) on the chromosome, and the positions of ITX (structural variation of the intrachromosomal translocation type). The lines of the inner circle indicate positions of CTX (structural variation of the interchromosomal translocation type) on chromosomes.



**Figure S2.** Distribution of Wuhua yellow chicken’s SNPs and InDels. (**a**) The number of SNPs and InDels on each chromosome; (**b**) The SNPs map to SNP database; **(c**) The InDels map to InDel database.



**Figure S3.** Annotation and Transition-transversion analysis of the clean genomic SNPs of all 12 chickens sequenced in this study. Proportions of SNPs are classified according to: (**a**) the genomic locations in which they occur, (**b**) The genetic coding attributes, and (**c**) bars represent the total number of transitional SNPs (red) followed by the individual base transitions types, and the total number of transversion SNPs (green) followed by the individual base transversion types. Numbers and proportions of the two groups of variants are their constituent variants are shown.



**Figure S4.** Annotation of the clean InDels of the 12 chicken genomes generated in this study. The proportion of InDels classified according to: (**a**) the genomic locations in which they occur, and (**b**) genetic coding attributes.



**Figure S5.** Summary of the structural variations (SVs) and copy number variations (CNVs) in the 12 chicken genome generated in this study.(**a**) Proportion of different SV types. CTX (interchromosomal translocation), DEL (deletions), INV (inversion), ITX (intrachromosomal translocation); (**b**) Number of CNVs of deletion and duplication types identified in the WHYC genomic dataset; (**c**) The length distribution of CNVRs; (**d**) The frequency distribution of CNVRs.