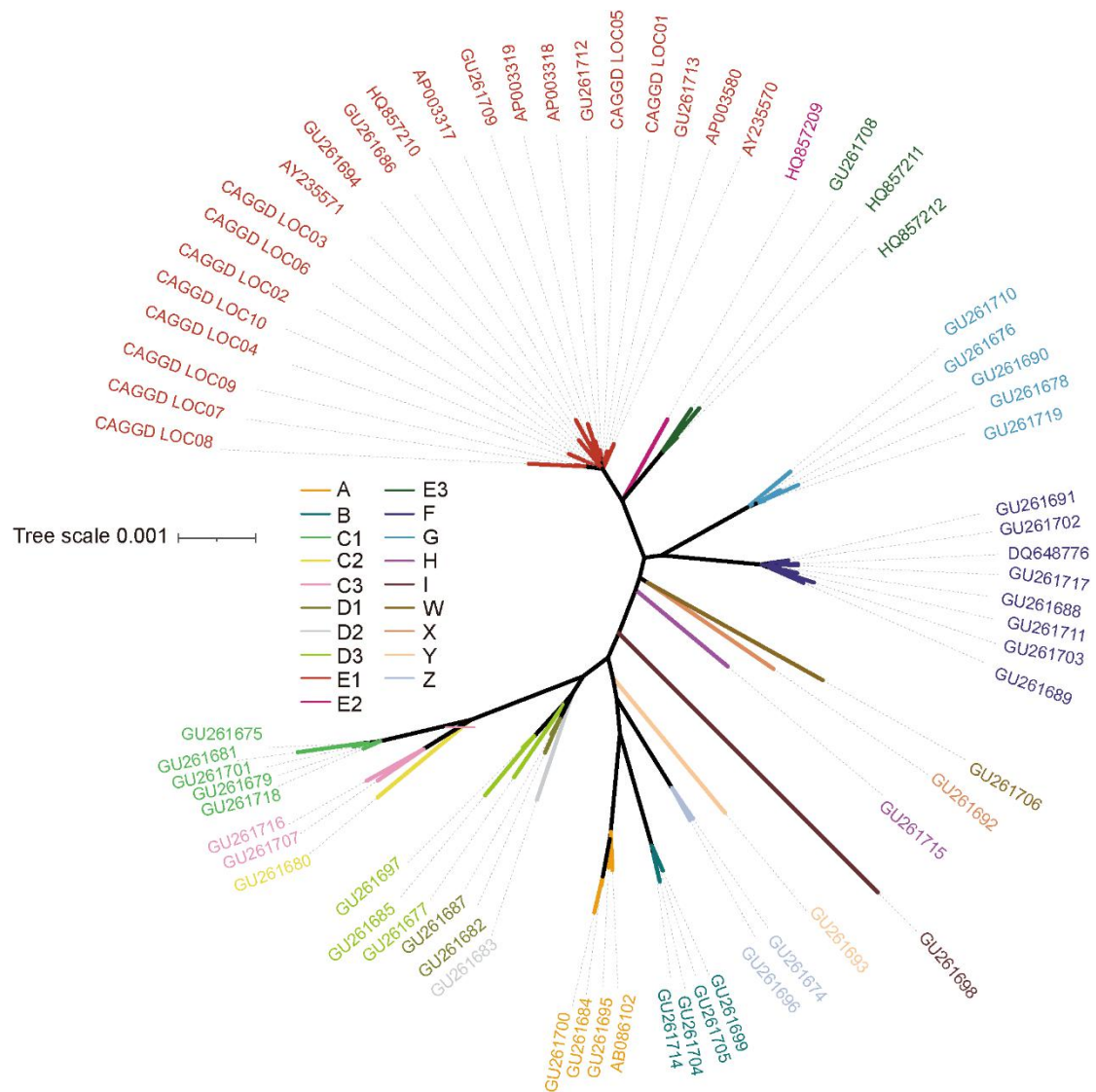


Supplementary Materials

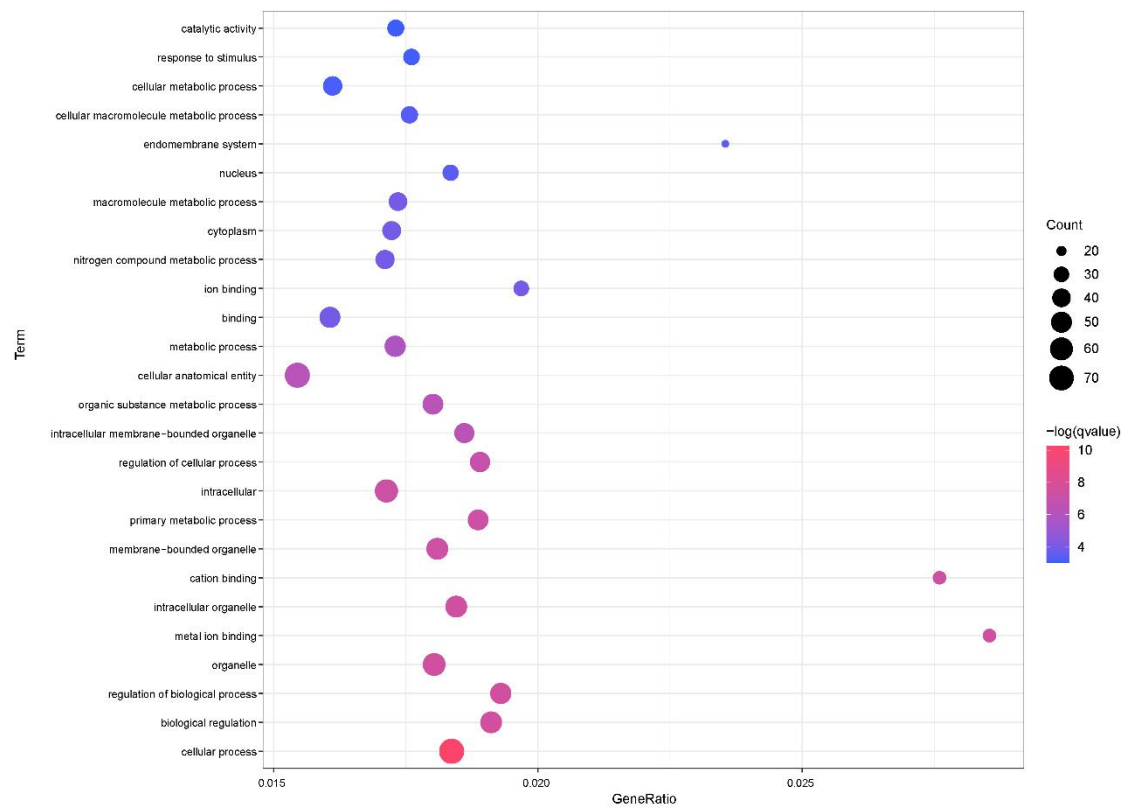
Supplementary Figures



Supplementary Figure S1. Classification tree of mtDNA haplogroups in CA chickens and 58 downloaded complete mtDNA sequences. Different mitochondrial haplotypes are represented by different colors.



Supplementary Figure S2. GO analysis of 310 PSGs detected by *Fst*_{CA-to-ME}. Bubble chart shows significant enrichment of terms. Size and color of bubble represent number of significantly enriched genes in pathway and enrichment significance, respectively.

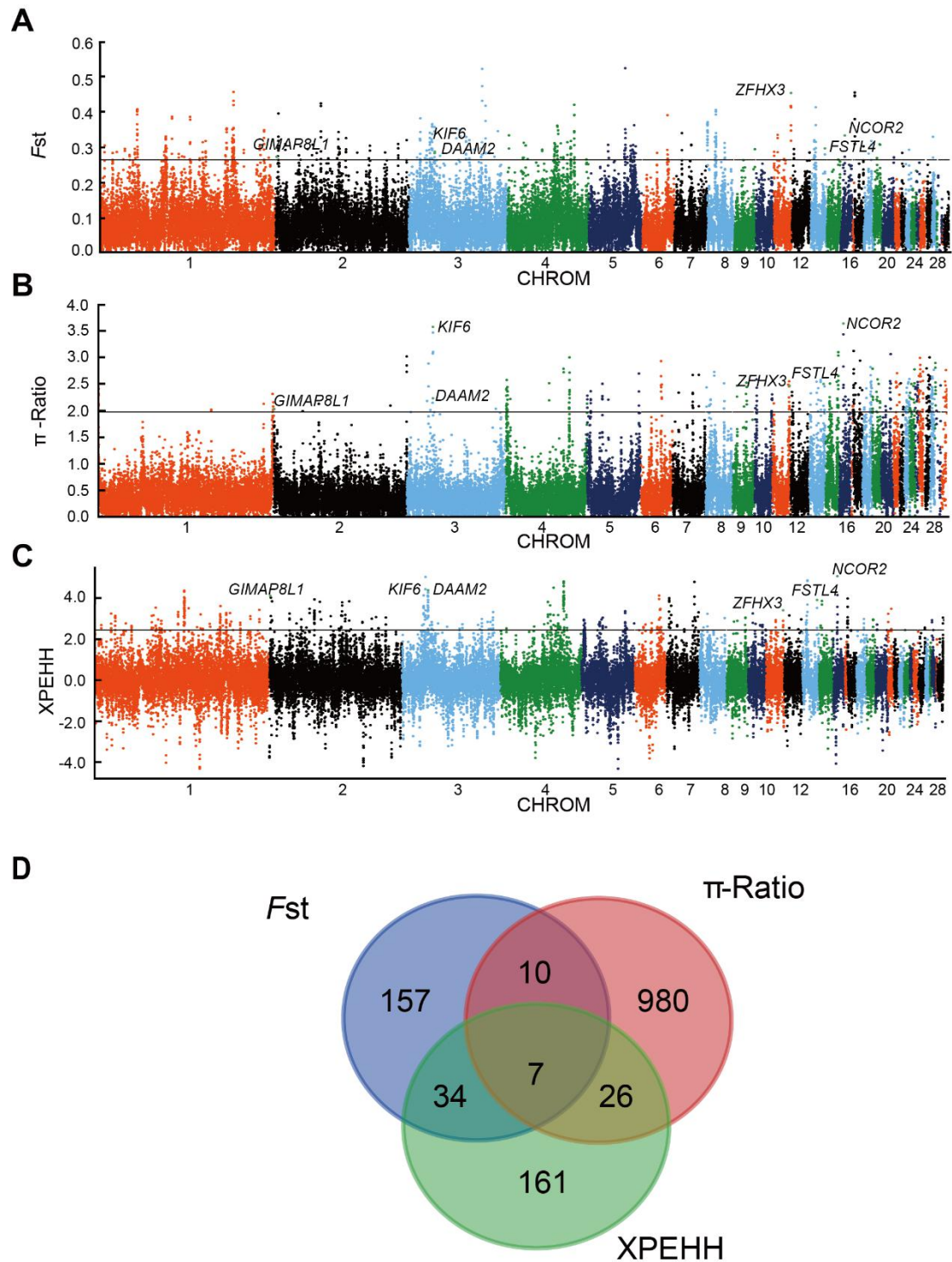


Supplementary Figure S3. GO analysis of 247 PSGs detected by π -Ratio_{ME/CA}. Bubble chart shows significant enrichment of terms. Size and color of bubble represent number of significantly enriched genes in pathway and enrichment significance, respectively.

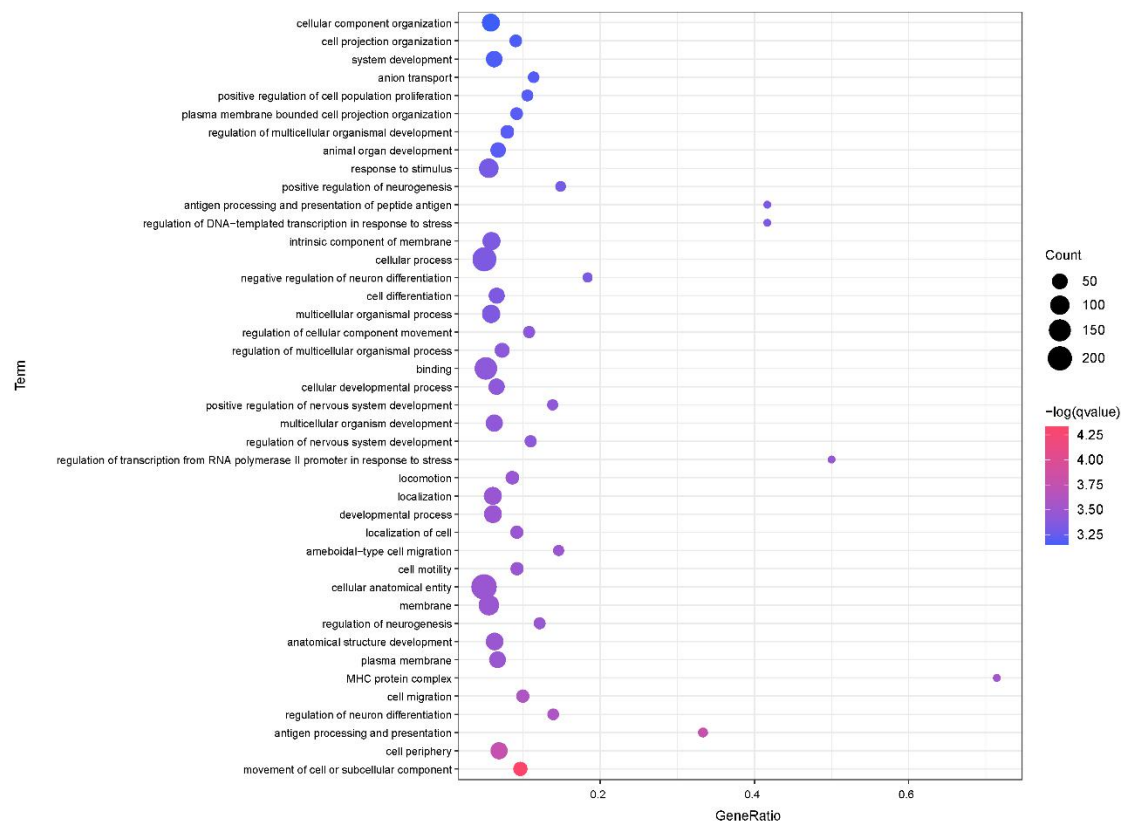
A1229T
↓

CA Chicken	NKESSEGGDNIQSAVTSQPAQGLVSPLPQ↓SEKQWHSQNLLSSHETAQGVMPKEQVQGPQVLEKQMNML
Japanese quail	NKESSEGGDNIQSAVTSQPAQGLVSPLPQASEKQWHNQSLSSHETAQGVMPKEQVQGPQVLEKQMNML
Ring-necked pheasant	NKESSEGGDNIQSAVTSQPAQGLVSPLPQASEKQWHSQNLLSSHETAQGVMPKEQVQGPQVLEKQMNML
helmeted guineafowl	NKESSEGGDNIQSAVTSQPAQGLVSPLPQASEKQWHSQNLLSSHETAQGVMPKEQVQGPQVLEKQMNML
mallard	NKESSEGGDNIQSMVTSQPAQGLVSPLPQAPEKQWHSQNLLSSHETAQGVMPKEQVQGPQVLEKQMNML
black swan	NKESSEGGDNIQNVVTSQPAQGLVSPLPQASEKQWHSQNLLSSHETAQGVMPKEQVQGPQVLEKQMNML
Corvus	NKESSEGGDNIQSAVTSQPTQGLVSPLPQASEKQWHSQNLLSSHETAQGVMPKEQVQGPQVLEKQMNML
Chrysaetos	NKESSEGGDNIQSAVTSQPTQGLVSPLPQASEKQWHSQNLLSSHETAQGVMPKEQVQGPQVLEKQMNML
Lesser kestrel	NKESSEGGDNIQSTVTSQPAQGLVSPLPQASEKQWHSQNLLSSHETAQGVMPKEQVQGPQVLEKQMNML

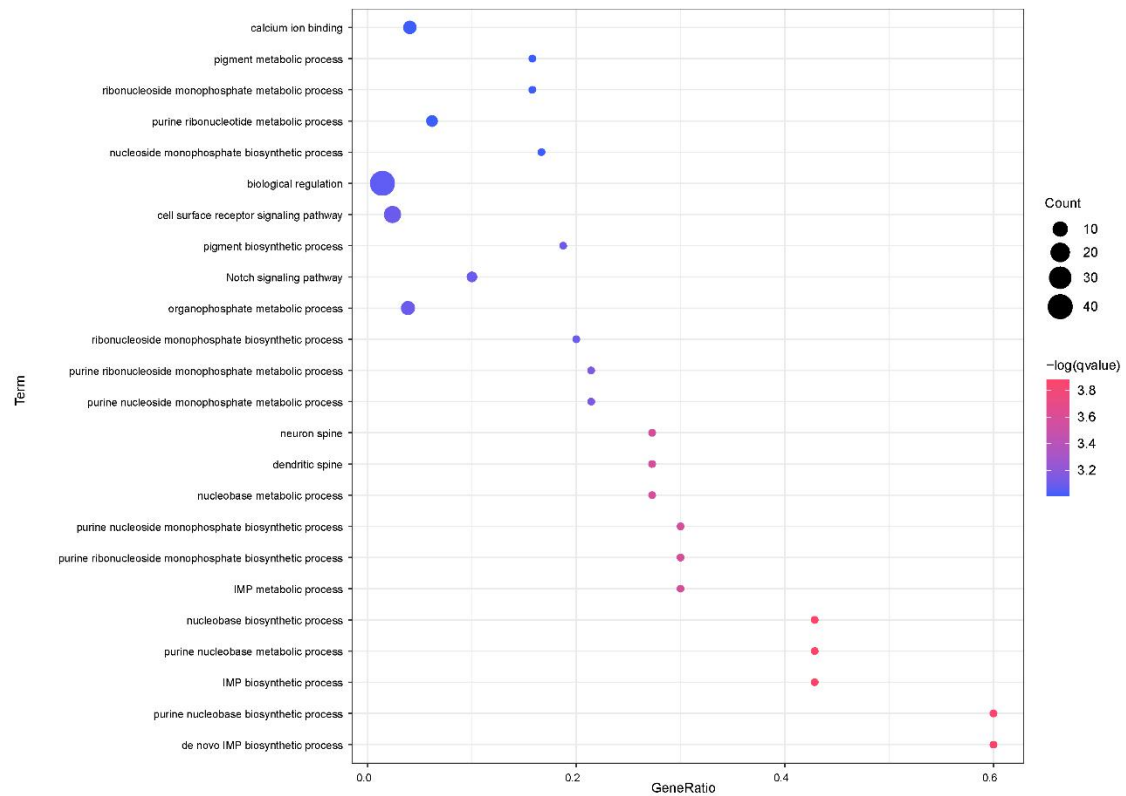
Supplementary Figure S4. Multiple protein sequence alignment of *ZNF536*. Results show one missense mutation, p.A1229T, in CA chickens, which is highly conserved in diverse birds.



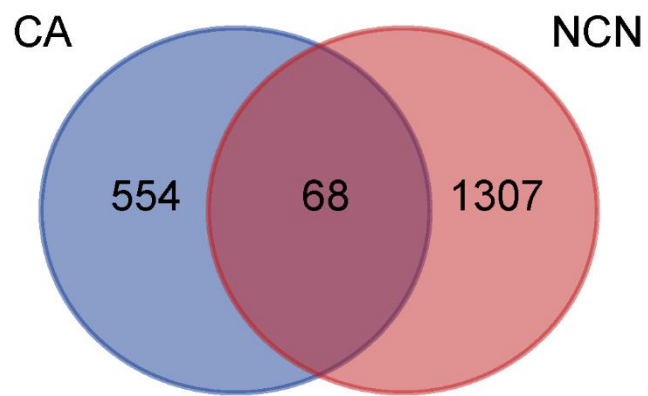
Supplementary Figure S5. Genome-wide selection scan of PSGs in cold-tolerant NCN chickens using sliding window analysis (40 kb window size, 20 kb step size, 99th percentile cutoff). A: Selective signatures of cold-tolerant NCN chickens with $F_{st_{NCN-to-ME}}$. B: Selective signatures of cold-tolerant NCN chickens with $\pi\text{-Ratio}_{ME/NCN}$. C: Selective signatures of cold-tolerant NCN chickens with $XPEHH_{NCN-to-ME}$. Top 1% of $F_{st_{NCN-to-ME}}$, $\pi\text{-Ratio}_{ME/NCN}$, and $XPEHH_{NCN-to-ME}$ values are marked with a horizontal black line. D: Number of PSGs identified in cold-tolerant NCN chickens by each method listed in each Venn diagram component.



Supplementary Figure S6. GO analysis of 1 023 PSGs detected by π -Ratio_{ME/NCN}. Bubble chart shows significant enrichment of terms. Size and color of bubble represent number of significantly enriched genes in pathway and enrichment significance, respectively.



Supplementary Figure S7. GO analysis of 228 PSGs detected by XPEHH_{NCN-to-ME}. Bubble chart shows significant enrichment of terms. Size and color of bubble represent number of significantly enriched genes in pathway and enrichment significance, respectively.



Supplementary Figure S8. Number of PSGs identified in cold-tolerant Canadian (CA) and Chinese (NCN) chickens, respectively.

Supplementary Tables

Supplementary Table S1. Sampling information on Chantecler and other downloaded chickens.

Supplementary Table S2. Summary information of downloaded mitochondrial data.

Supplementary Table S3. The 310 annotated PSGs of top 1% $F_{st_{CA-to-ME}}$.

Supplementary Table S4. The 247 annotated PSGs of top 1% $\pi\text{-Ratio}_{ME/CA}$.

Supplementary Table S5. The 212 annotated PSGs of top 1% $XPEHH_{CA-to-ME}$.

Supplementary Table S6. Summary information of 36 PSGs shared by three methods and other focused PSGs.

Supplementary Table S7. Go enrichment analysis on the 310 PSGs identified by $F_{st_{CA-to-ME}}$.

Supplementary Table S8. Go enrichment analysis on the 247 PSGs identified by $\pi\text{-Ratio}_{ME/CA}$.

Supplementary Table S9. The 208 annotated PSGs of top 1% $F_{st_{NCN-to-ME}}$.

Supplementary Table S10. The 1023 annotated PSGs of top 1% $\pi\text{-Ratio}_{ME/NCN}$.

Supplementary Table S11. The 228 annotated PSGs of top 1% $XPEHH_{NCN-to-ME}$.

Supplementary Table S12. Go enrichment analysis on the 1023 PSGs identified by $\pi\text{-Ratio}_{ME/NCN}$.

Supplementary Table S13. Go enrichment analysis on the 228 PSGs identified by $XPEHH_{NCN-to-ME}$.

Supplementary Tables S1–S13 are listed as a separate excel file due to their large size.