

Supplementary Figures

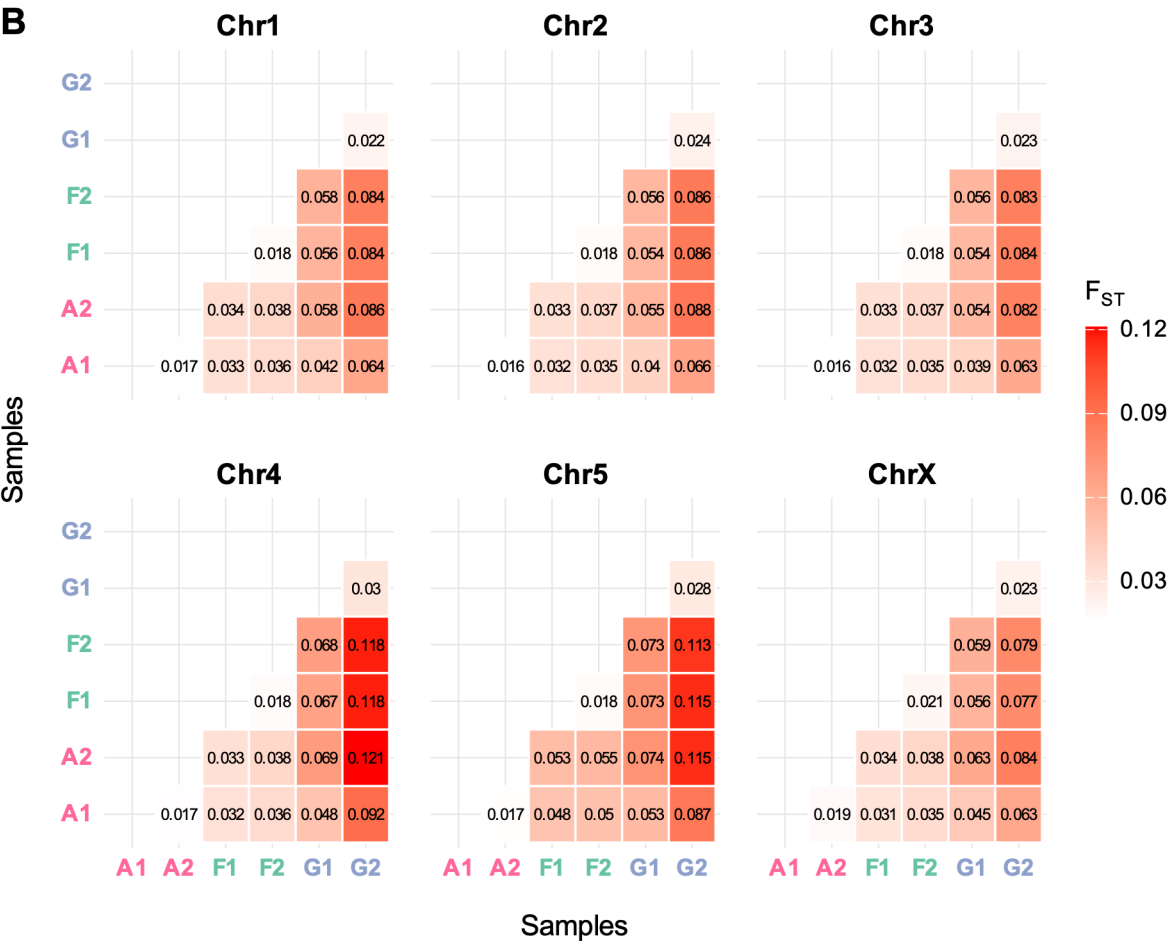
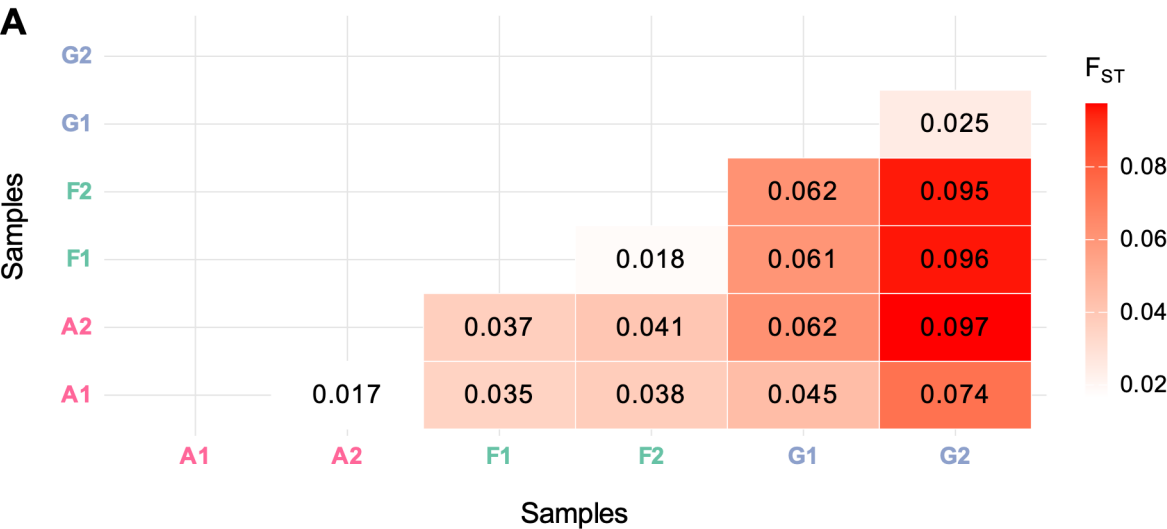


Figure S1. Within-farm genetic differentiation among biological *H. contortus* population replicates (sliding-window F_{ST} , 1 kb window size with 0.5 kb step size). (A) Genome-wide pairwise F_{ST} between replicates from the farms A, F and G. (B) Chromosome-wide pairwise F_{ST} between replicates from the farms A, F and G (chromosomes 1-5 and X). Biological replicates are indicated as follows: samples A1 and A2 from Farm A (pink), samples F1 and F2 from Farm F (green), and samples G1 and G2 from Farm G (purple). Each cell reports an F_{ST} value; The opacity of the red colour cell fill indicates the degree of differentiation.

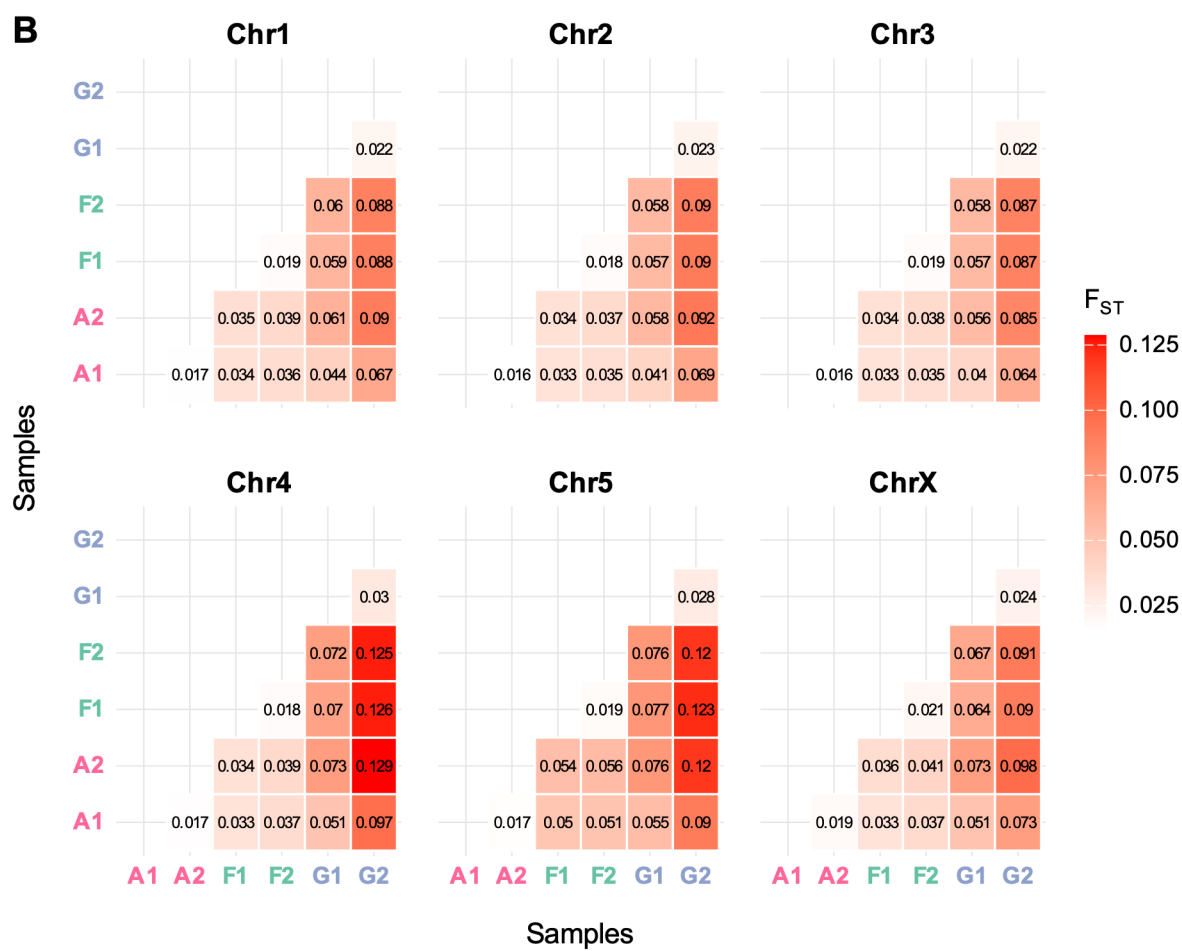
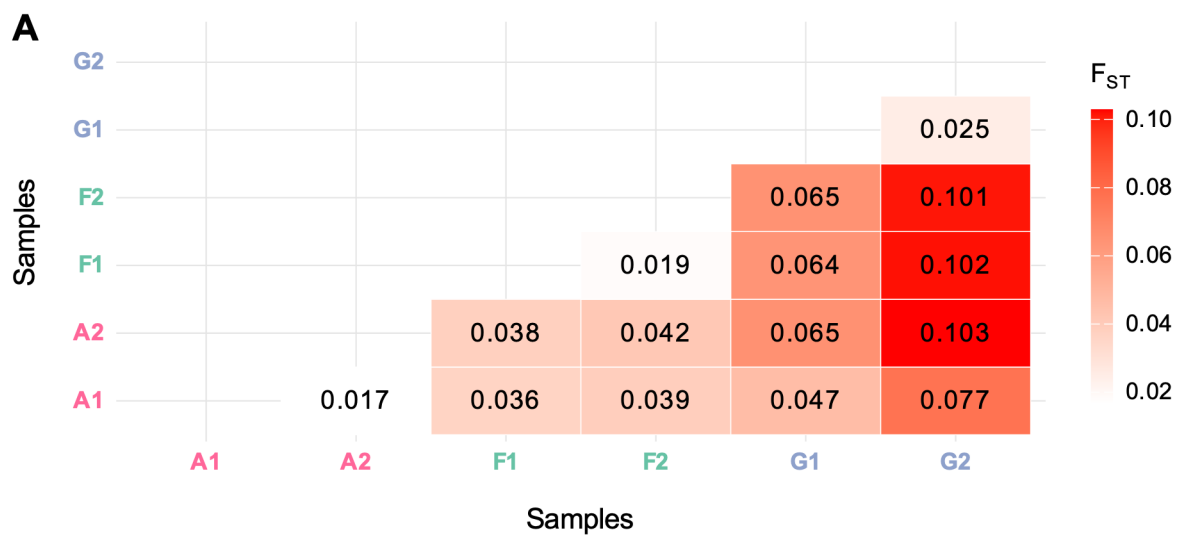


Figure S2. Within-farm genetic differentiation among biological *H. contortus* population replicates (sliding-window F_{ST} , 100 kb window size with 50 kb step size). (A) Genome-wide pairwise F_{ST} between replicates from the farms A, F and G. (B) Chromosome-wide pairwise F_{ST} between replicates from the farms A, F and G (chromosomes 1-5 and X). Biological replicates are indicated as follows: samples A1 and A2 from Farm A (pink), samples F1 and F2 from Farm F (green), and samples G1 and G2 from Farm G (purple). Each cell reports an F_{ST} value; The opacity of the red colour cell fill indicates the degree of differentiation.

[illegible]

Figure 1 displays heatmaps of amino acid substitution rates for five chromosomes (Chr1, Chr2, Chr3, Chr4, Chr5) and the X chromosome (ChrX). The heatmaps show the relative substitution rates between 20 amino acids (A, C, D, E, F, G, H, I, K, L, N, Q, R, S, T, V, W, Y). The color scale ranges from 0 (white) to 0.2 (red). The diagonal elements are all 0.05. The off-diagonal elements represent the relative substitution rates between pairs of amino acids. The X chromosome heatmap is labeled 'ChrX'.

Figure S3. Between-farm genetic differentiation among *H. contortus* populations (sliding-window F_{ST} , 1 kb window size with 0.5 kb step size). (A) Genome-wide pairwise F_{ST} between *H. contortus* populations from all 12 farms. (B) Chromosome-wide pairwise F_{ST} between *H. contortus* populations from all 12 farms (chromosomes 1-5 and X). For farms A, F, and G, average F_{ST} values of the two biological replicates were used; each cell reports the pairwise F_{ST} value, sorted in an increasing manner, with the opacity of the red colour cell fill indicating the degree of differentiation.

[illegible]

Figure S4. Between-farm genetic differentiation among *H. contortus* populations (sliding-window F_{ST} , 100 kb window size with 50 kb step size). (A) Genome-wide pairwise F_{ST} between *H. contortus* populations from all 12 farms. (B) Chromosome-wide pairwise F_{ST} between *H. contortus* populations from all 12 farms (chromosomes 1-5 and X). For farms A, F, and G, average F_{ST} values of the two biological replicates were used; each cell reports the pairwise F_{ST} value, sorted in an increasing manner, with the opacity of the red colour cell fill indicating the degree of differentiation.

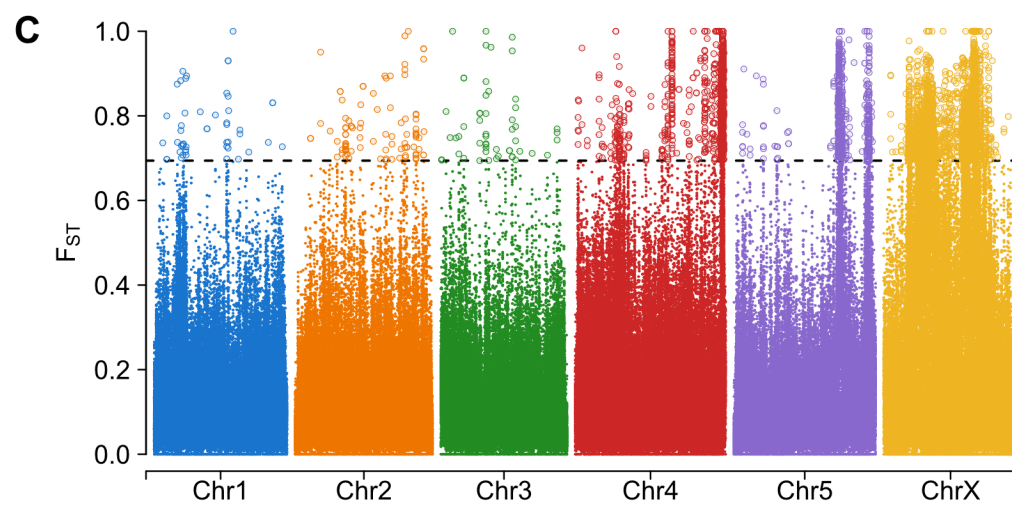
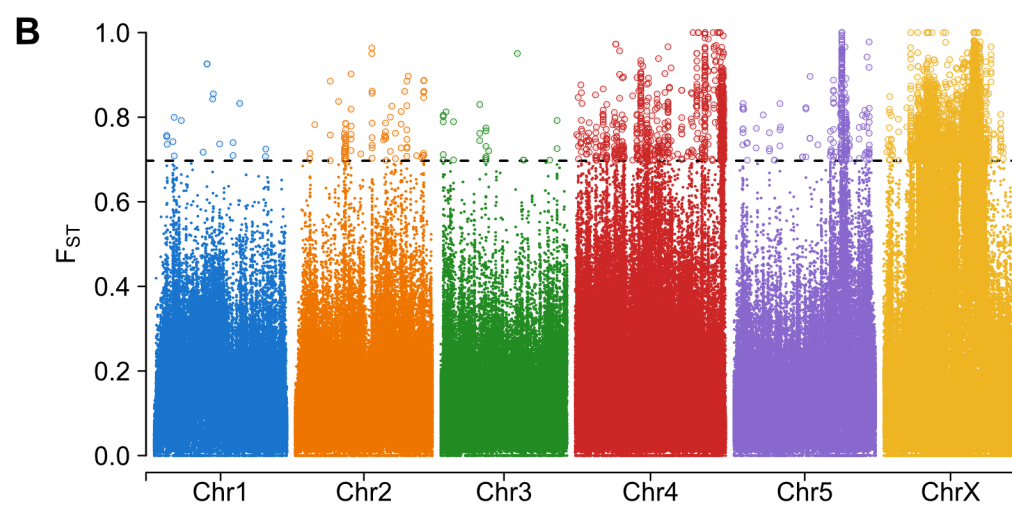
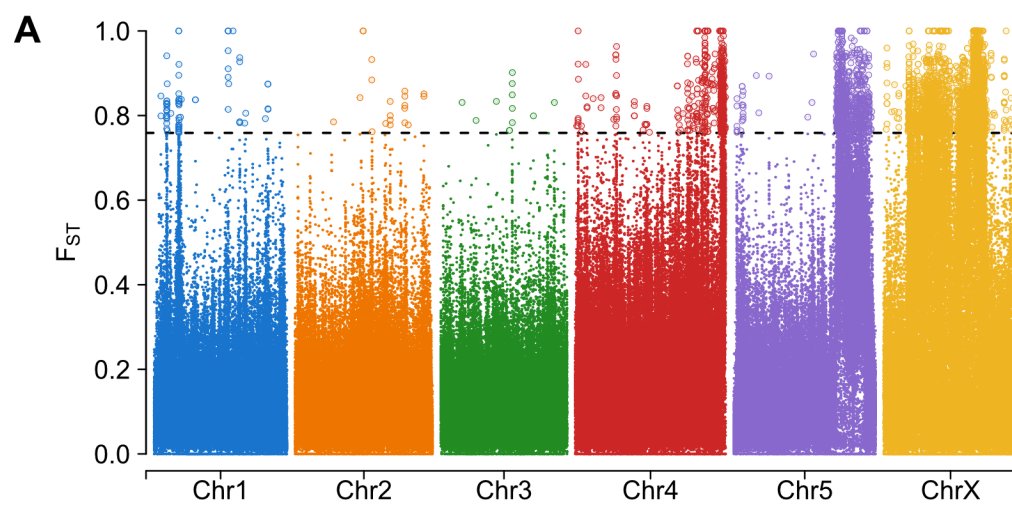


Figure S5. Sliding-window F_{ST} analysis for the three most divergent *H. contortus* farm population pairs: (A) farms D and K, (B) farms D and G, (C) farms D and C (1 kb window size with 0.5 kb step size). Each dot represents an F_{ST} value calculated for a genomic window along the six *H. contortus* chromosomes. The horizontal dashed lines indicate the top 1% F_{ST} thresholds (A: 0.758, B: 0.697, C: 0.694), and windows exceeding these thresholds are highlighted with larger open circles.

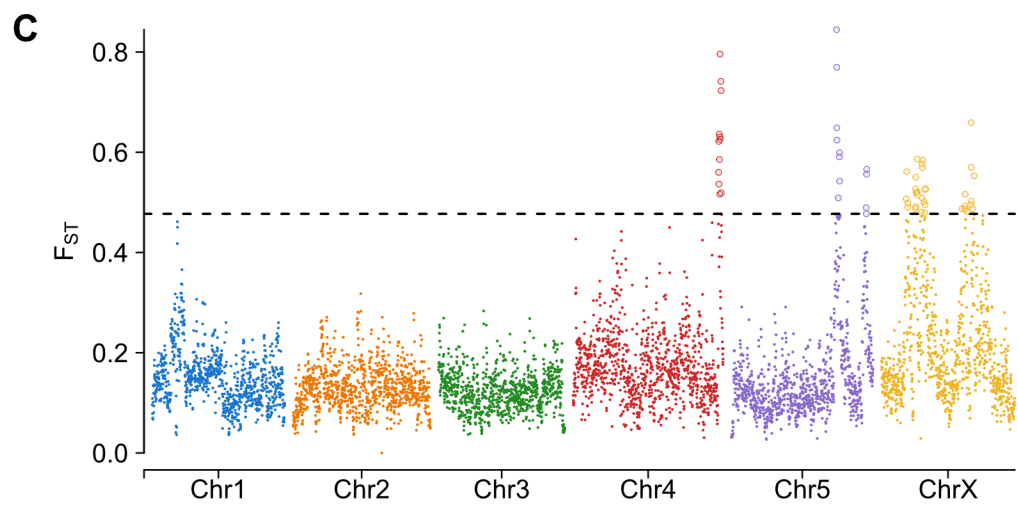
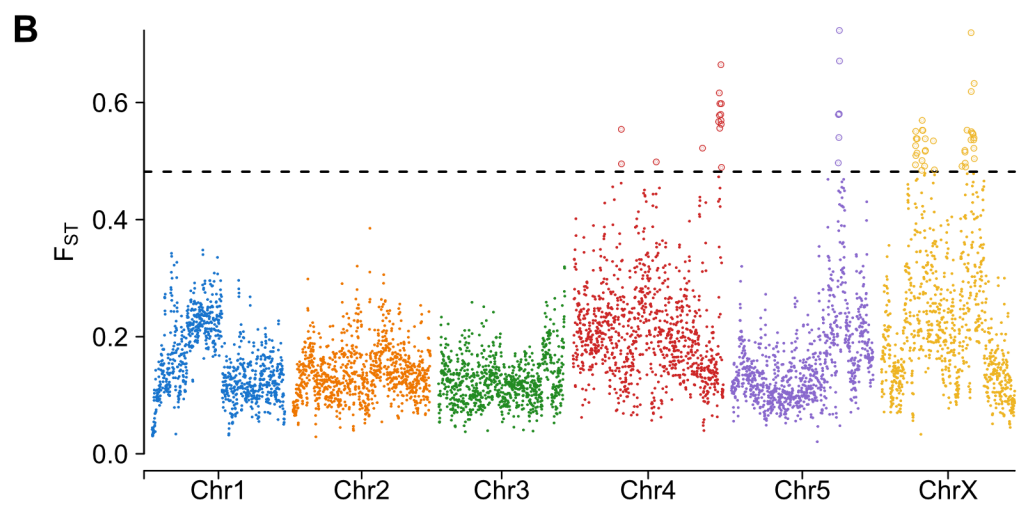
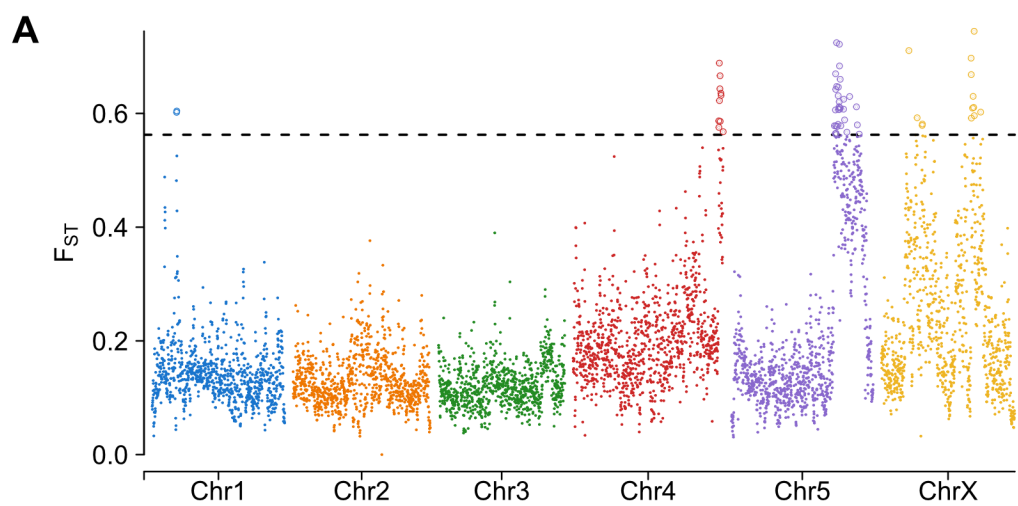


Figure S6. Sliding-window F_{ST} analysis for the three most divergent *H. contortus* farm population pairs: (A) farms D and K, (B) farms D and G, (C) farms D and C (100 kb window size with 50 kb step size). Each dot represents an F_{ST} value calculated for a genomic window along the six *H. contortus* chromosomes. The horizontal dashed lines indicate the top 1% F_{ST} thresholds (A: 0.562, B: 0.481, C: 0.477), and windows exceeding these thresholds are highlighted with larger open circles.

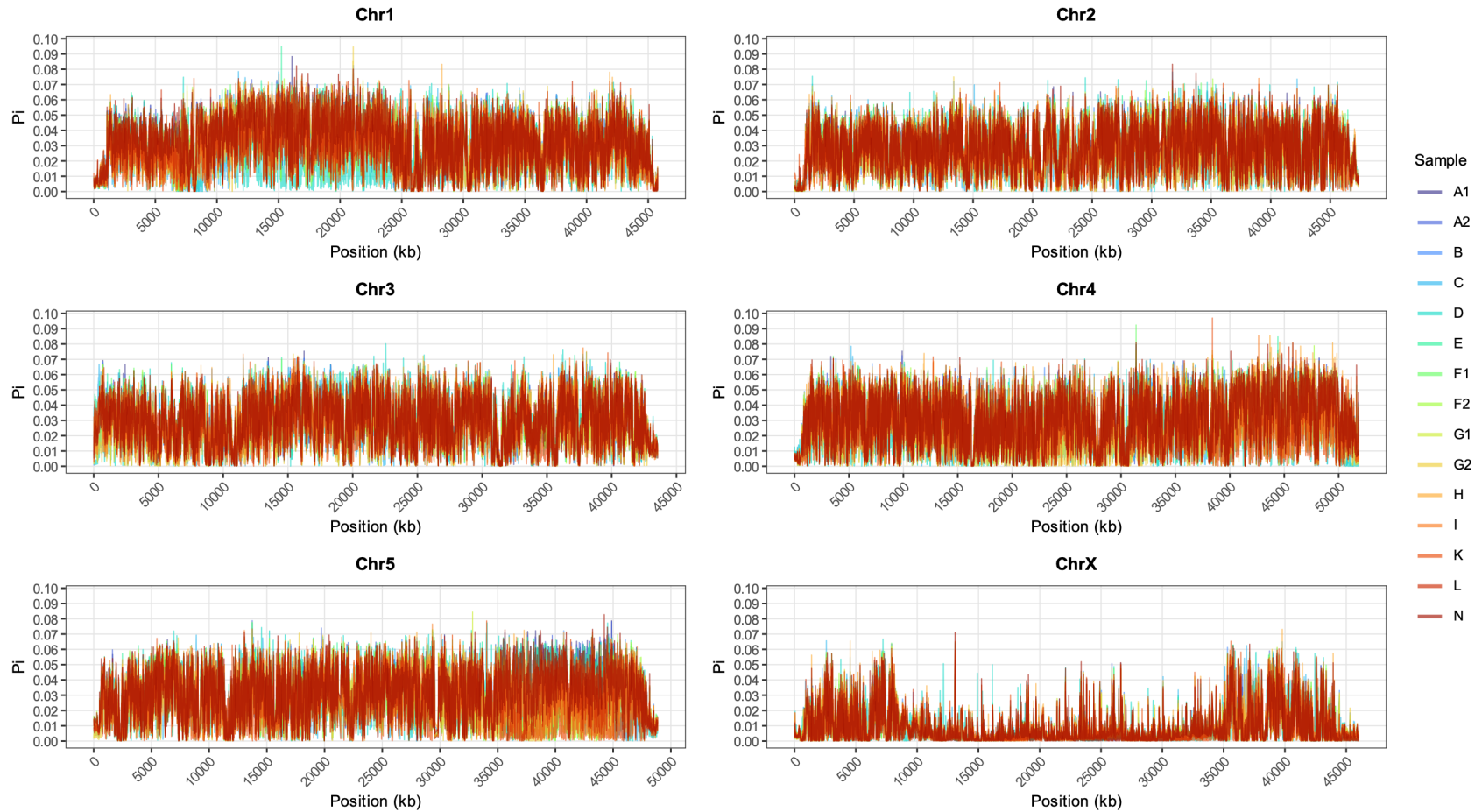


Figure S7. Chromosome-wide landscapes of window-based nucleotide diversity (P_i) estimates within the 15 *H. contortus* population samples from the 12 farms (Farms A, F, and G, each contributed two biological replicates). Window-based P_i estimates are shown in 10 kb windows along chromosomes 1–5 and X, with the x-axis indicating chromosomal position (kb).

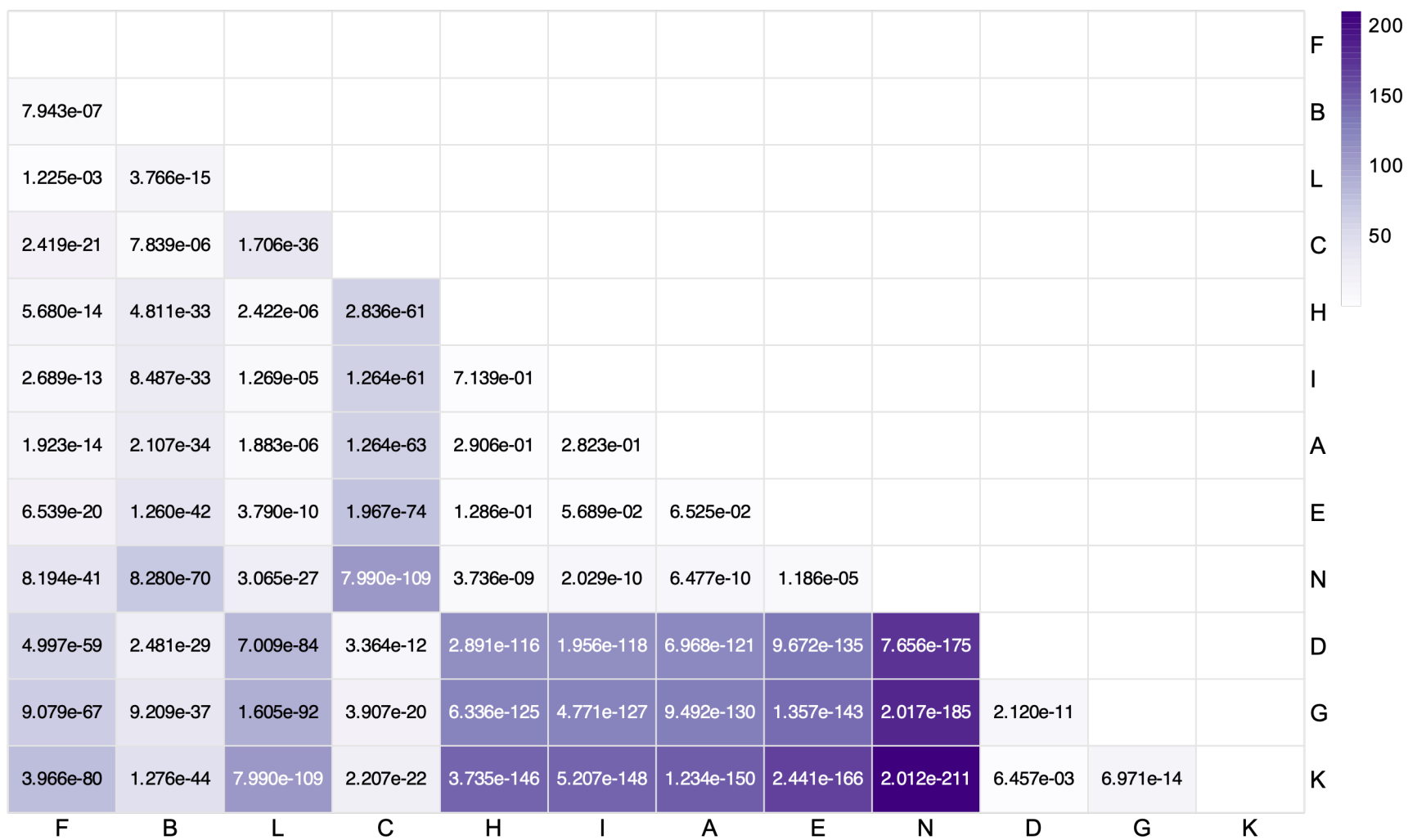


Figure S8. Pairwise comparisons of genome-wide, window-based nucleotide diversity (π) distributions between the 12 *H. contortus* farm populations. Each cell reports the Benjamini-Hochberg-adjusted P-value from a pairwise Wilcoxon Rank Sum test. Darker purple shading indicates smaller adjusted P-values and stronger statistical significance. The colour scale on the right is based on the absolute value of the exponent in scientific notation. For farms A, F and G, P-values from two replicates were combined using the geometric mean.