

Supplementary information

Whole genome re-sequencing reveals recent signatures of selection in three strains of farmed Nile tilapia (*Oreochromis niloticus*)

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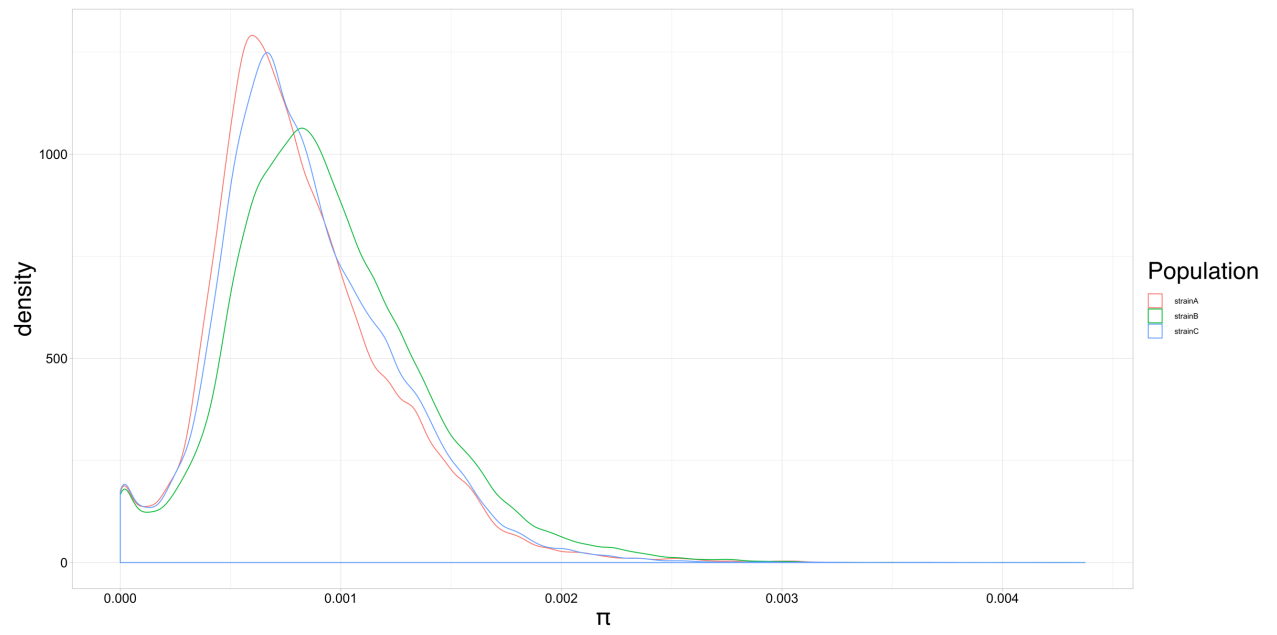
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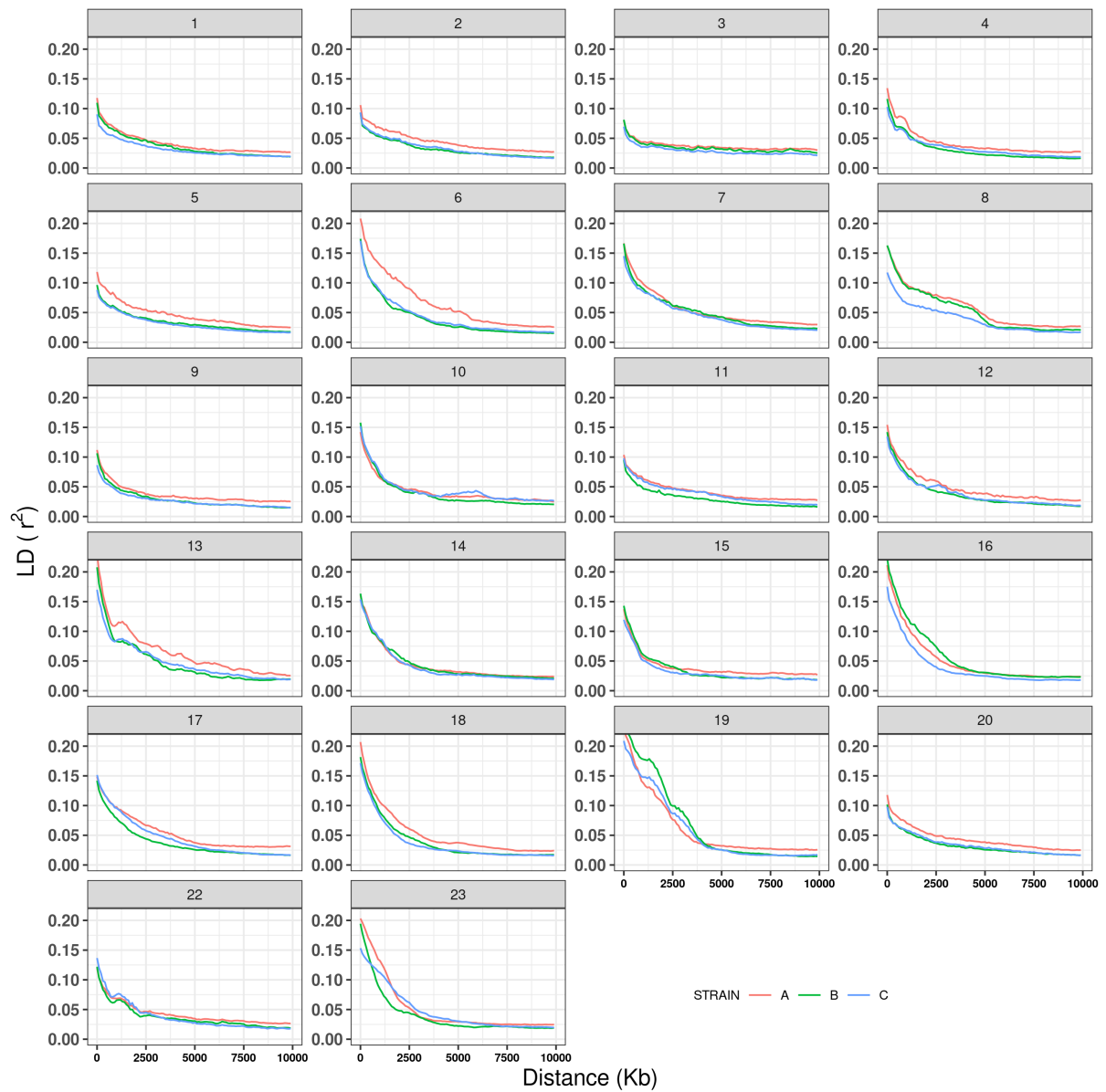
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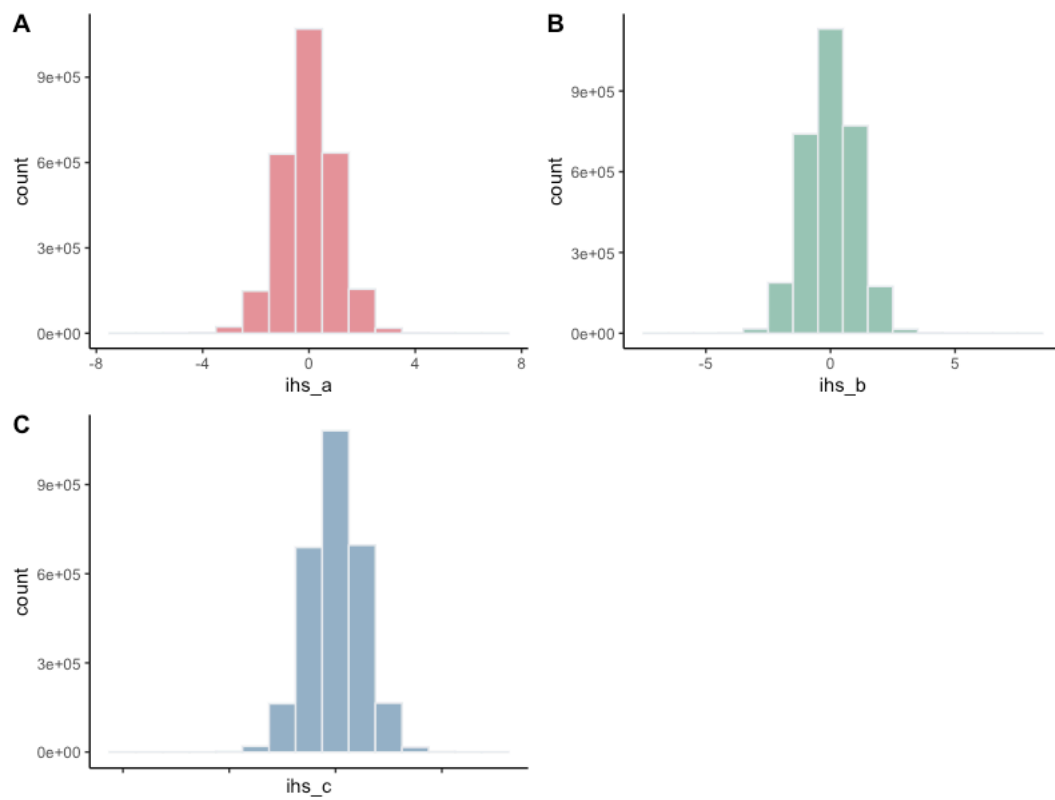
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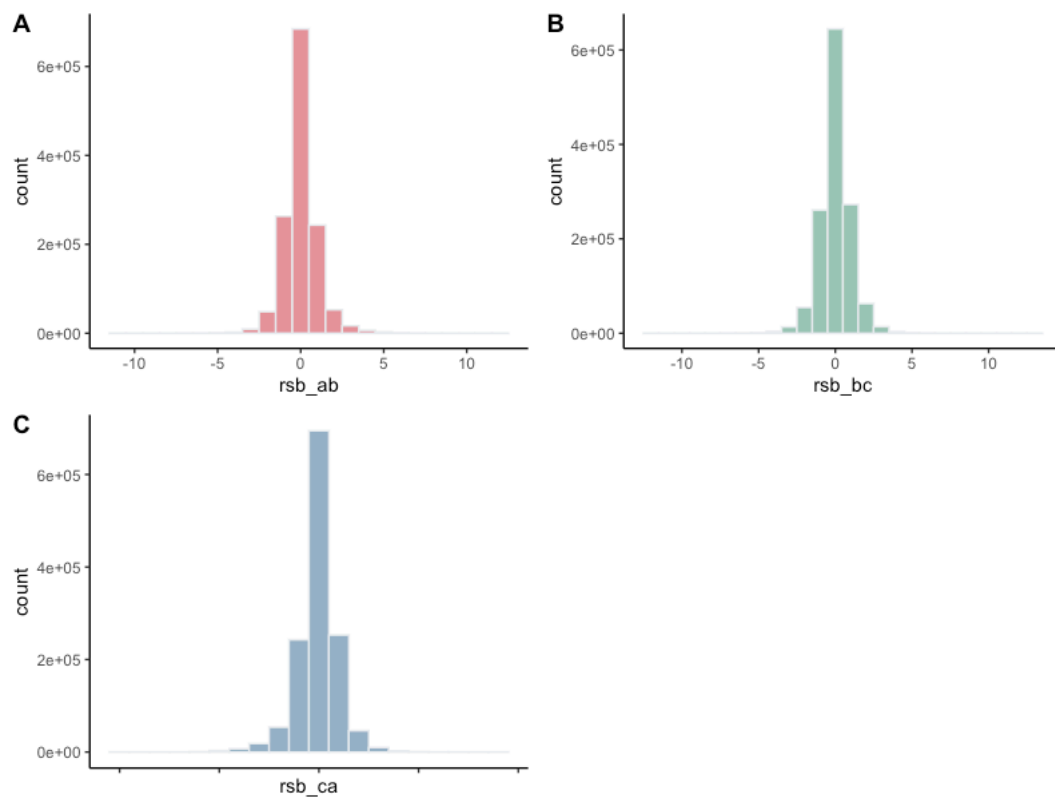
Supplementary Figure S1. Nucleotide diversity of strain A (red line), B (green line) and C (blue line) of Nile tilapia.



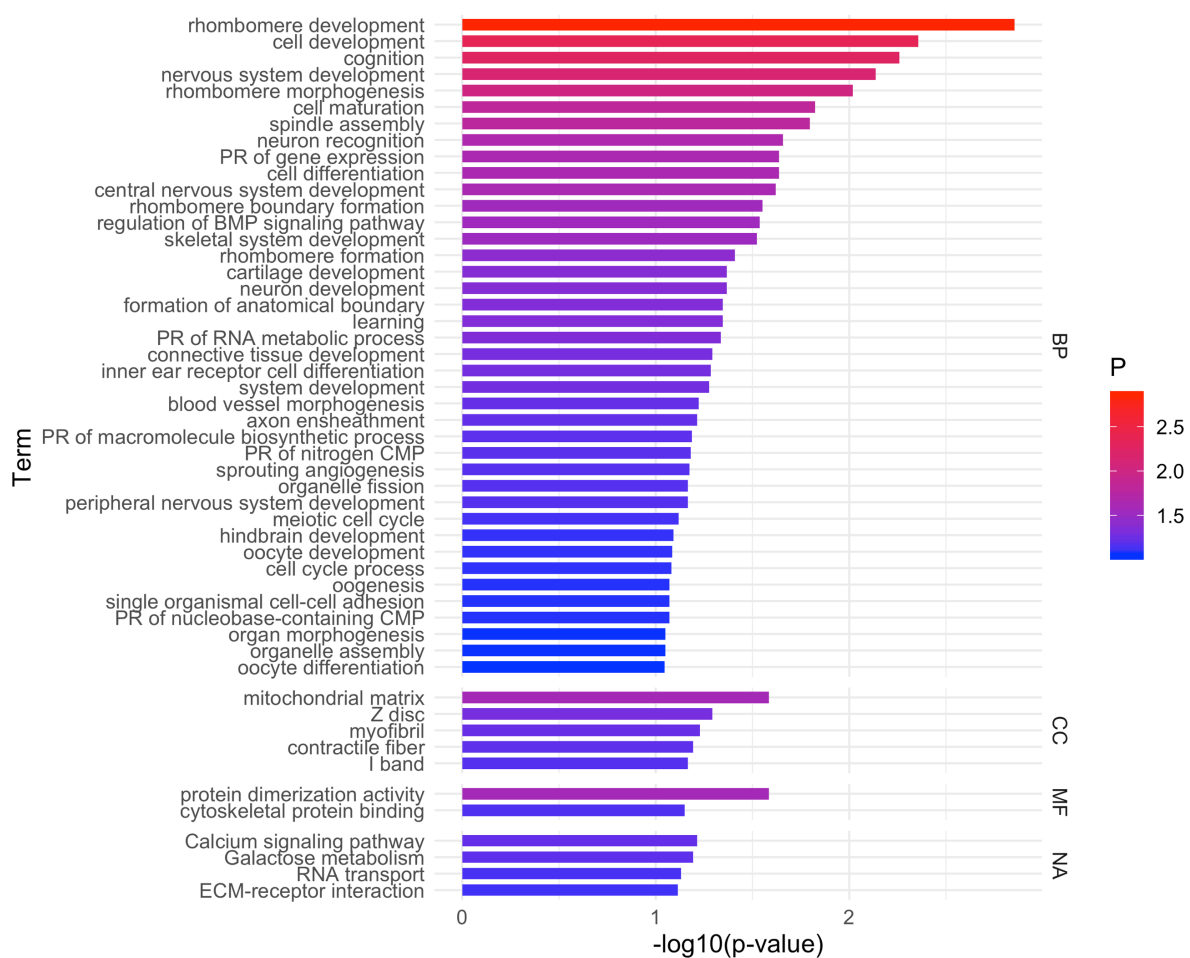
Supplementary Figure S2. Decay of average linkage disequilibrium (r^2) over distance across in each chromosome of three strain of Nile tilapia.



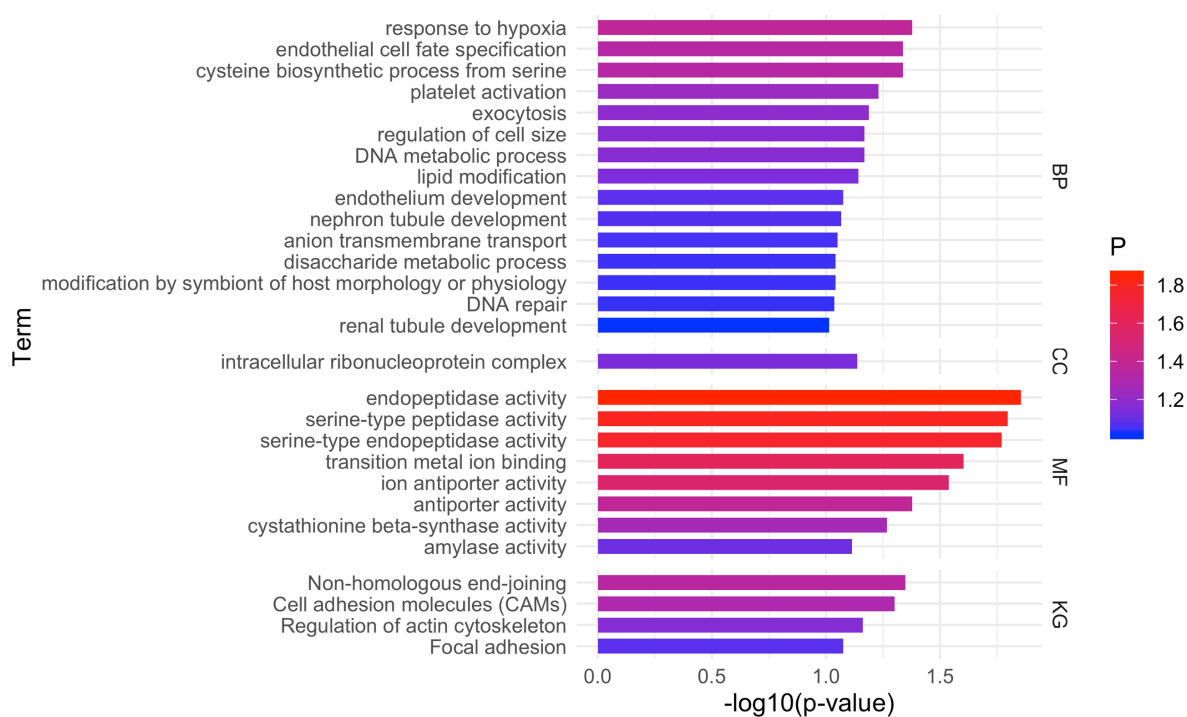
Supplementary Figure S3. Histograms showing the distribution of the iHS values in the three strain of Nile tilapia (A, B and C).



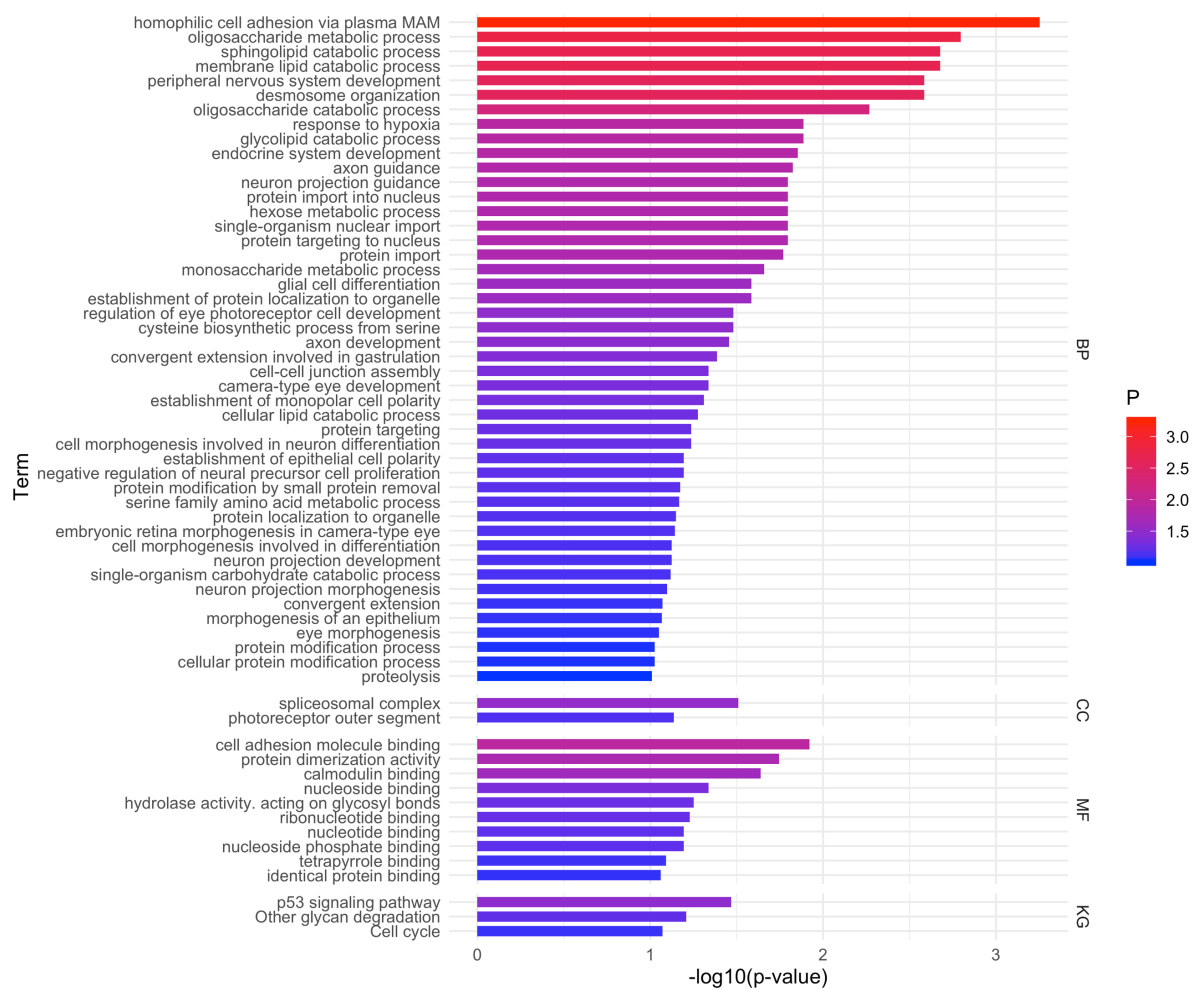
Supplementary Figure S4. Histograms showing the distribution of the Rsb values in the three strain of Nile tilapia (A, B and C).



Supplementary Figure S5. Enrichment analysis for GO and KEGG pathways term for strain A by DAVID. Each bar represents the $-\log_{10}(\text{p-value})$ for term.



Supplementary Figure S6. Enrichment analysis for GO and KEGG pathways term for strain B by DAVID. Each bar represents the $-\log_{10}(\text{p-value})$ for term.



Supplementary Figure S7. Enrichment analysis for GO and KEGG pathways term for strain C by DAVID. Each bar represents the $-\log_{10}(\text{p-value})$ for term.