

## **Supplemental Figures**

Ecological connectivity and habitat loss shape patterns of genetic diversity in a threatened salamander

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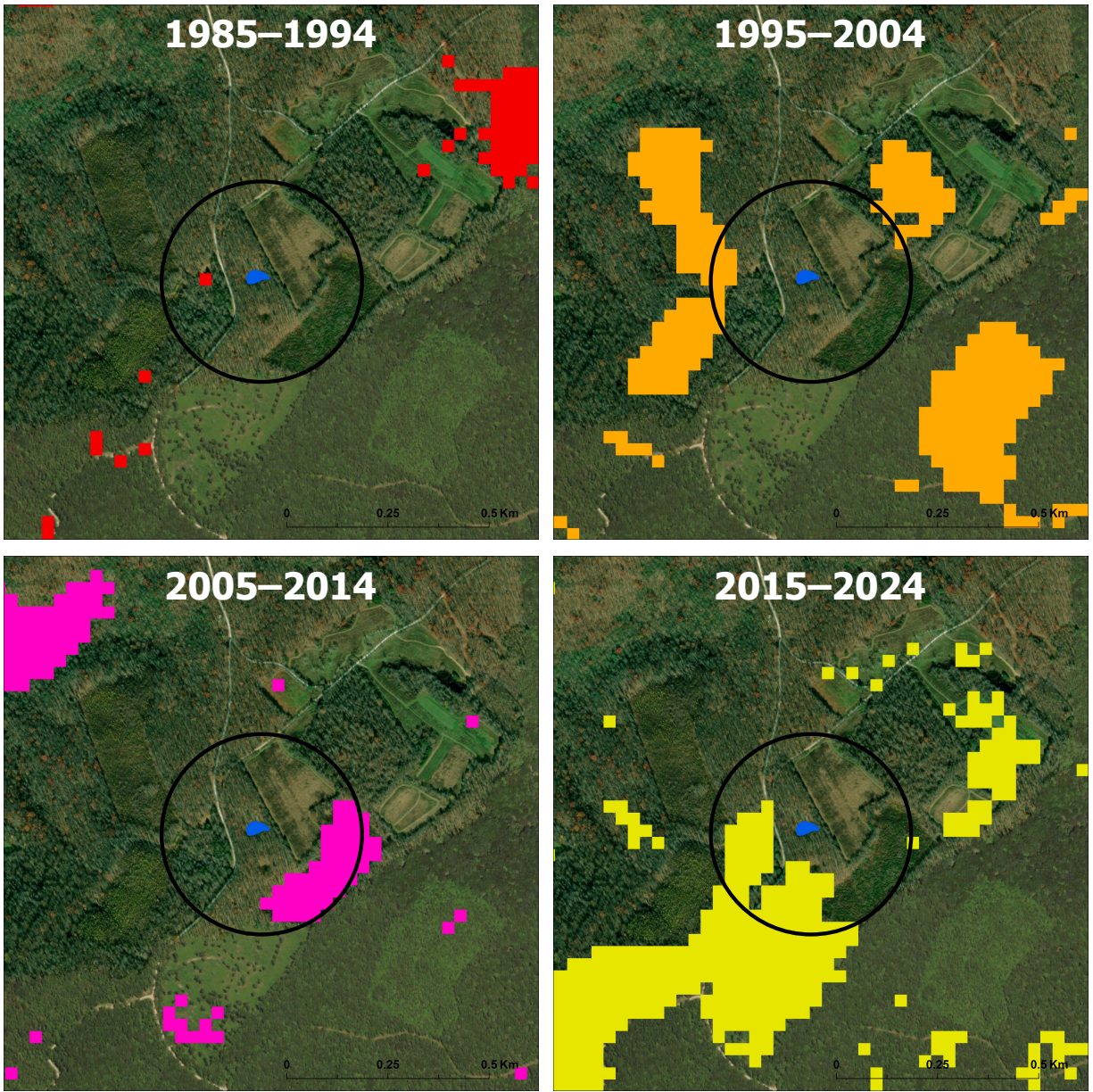
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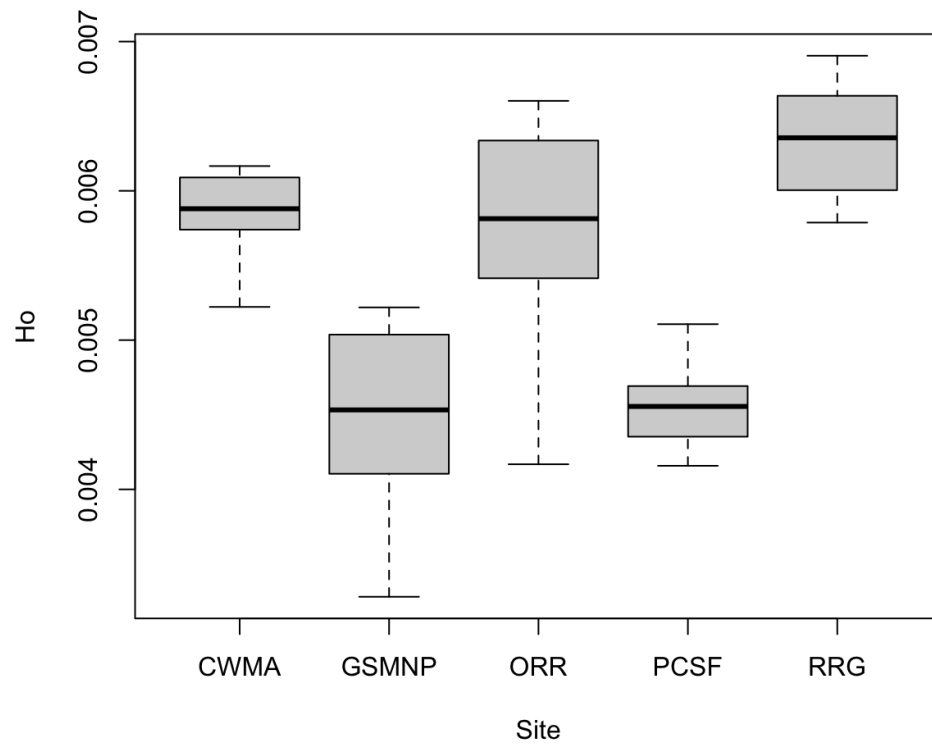
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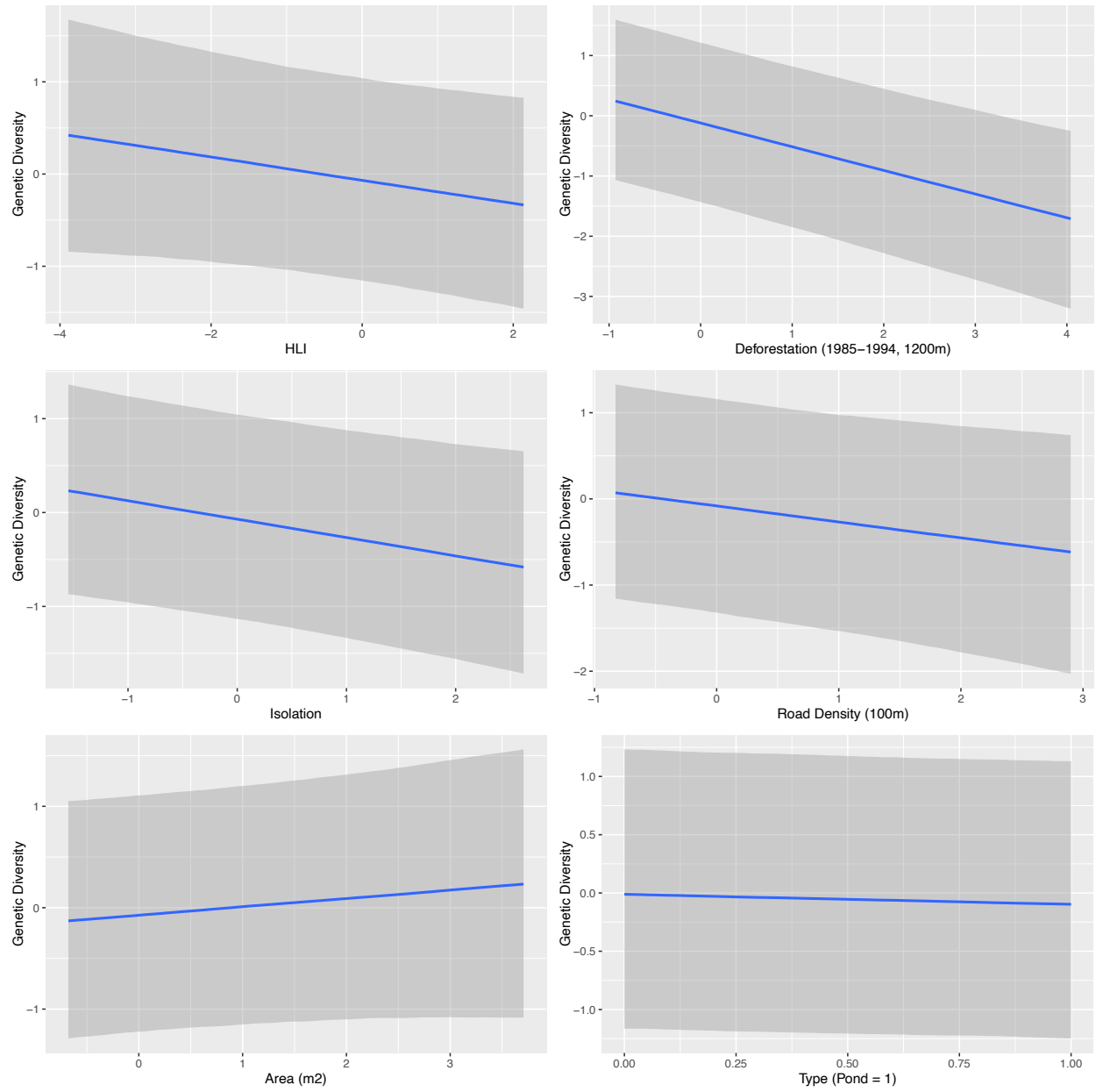
**Fig S1** A comparison of a wetlands classified as a bog/seep (A) and a true pond (B) for four-toed salamanders (*Hemidactylium scutatum*)



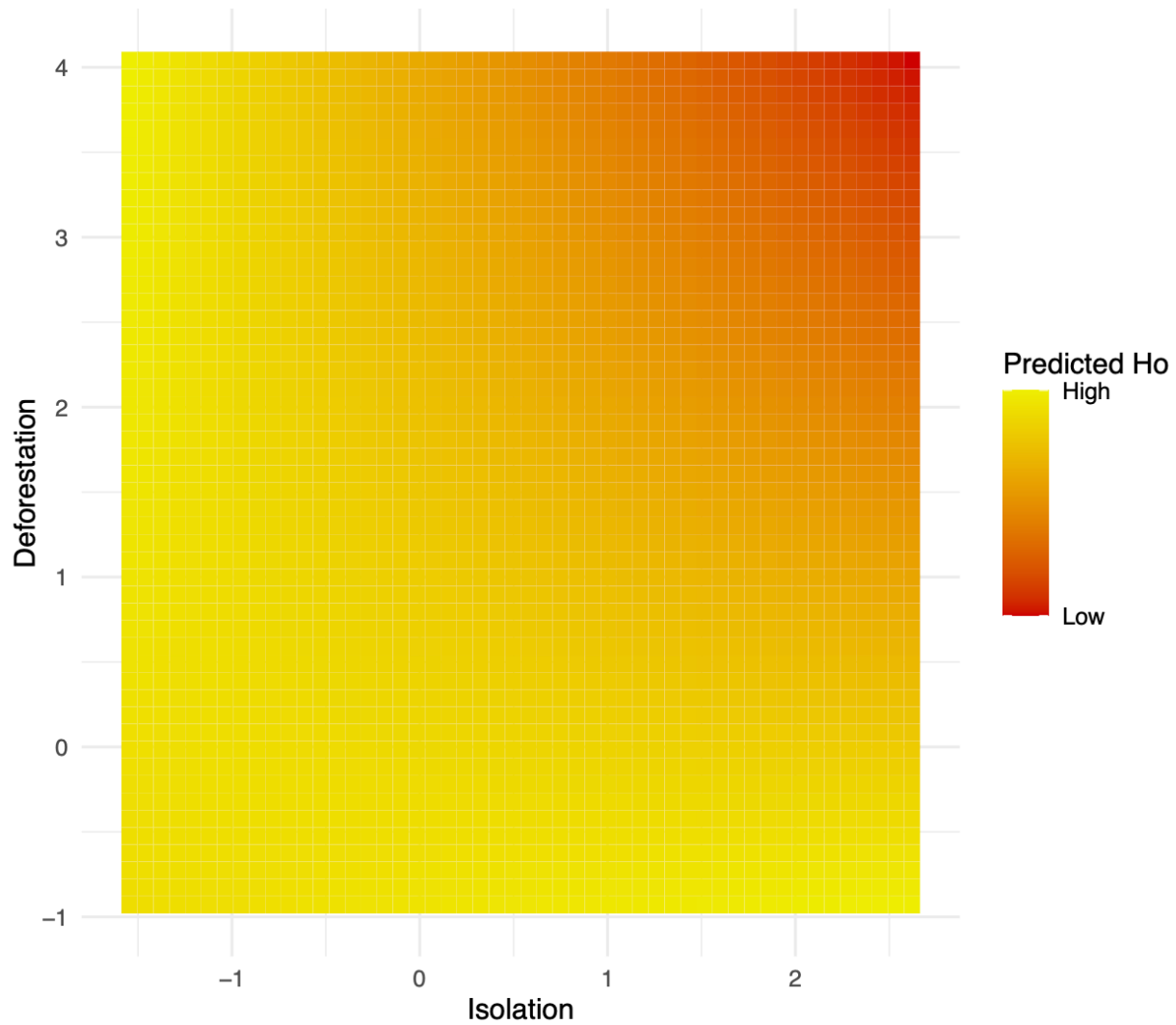
**Fig S2** Maps showing examples of forest loss data near a single pond at Catoosa Wildlife Management Area (blue polygon) between 1985 and 1994 (red), 1995 and 2004 (orange), 2005 and 2014 (pink), and 2015 and 2024 (yellow) overlaid on satellite imagery from 2025. Black circles represent potential buffers. The percent of that buffer that is deforested represents the amount of deforestation for this scale used for all analyses



**Fig S3** A boxplot displaying the distribution of genome-wide heterozygosity within each study area



**Fig S4** Plots of conditional effects for each single-predictor Bayesian model



**Fig S5** A plot showing the effect of deforestation, isolation, and an interaction term on predicted genome-wide heterozygosity. Yellow color represent higher genome-wide heterozygosity and red color is lower. Note that axes are in scaled and centered units.

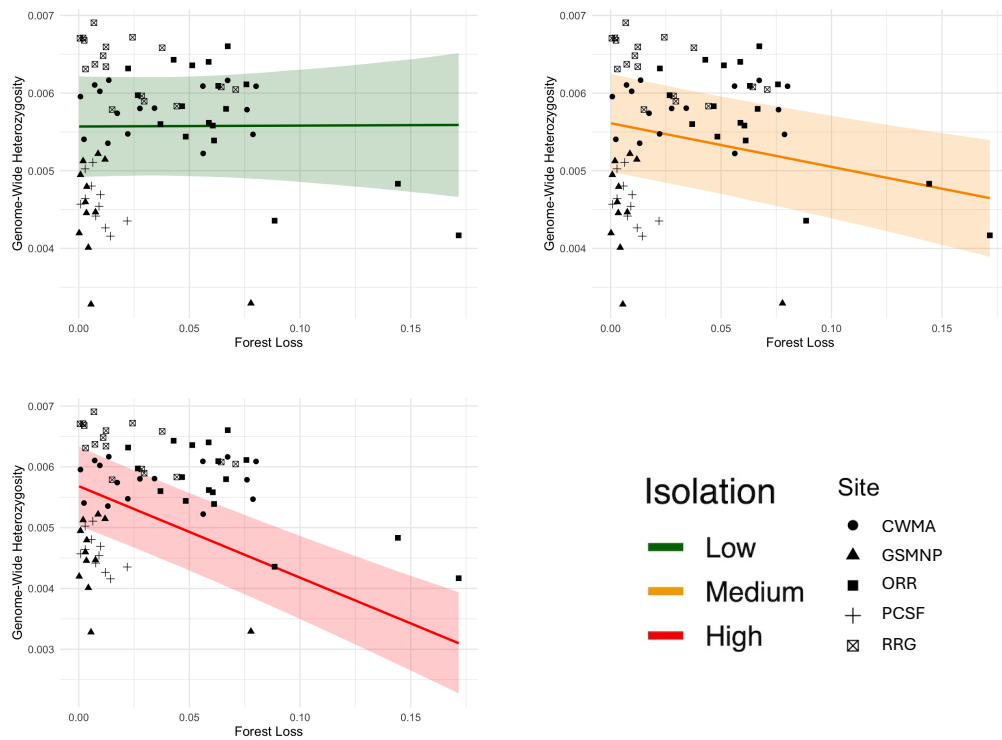
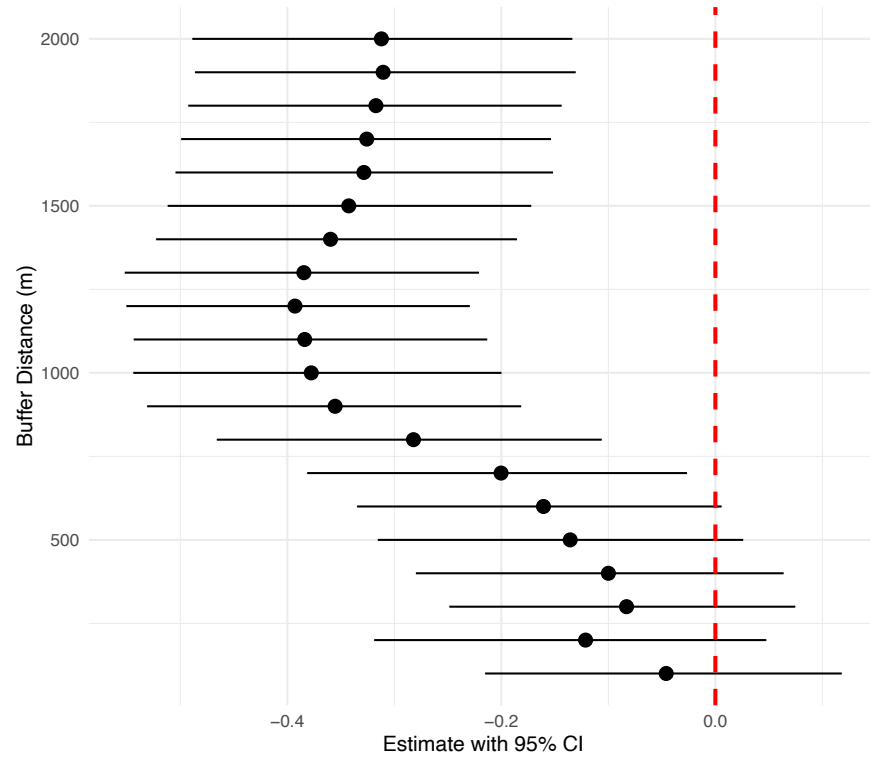
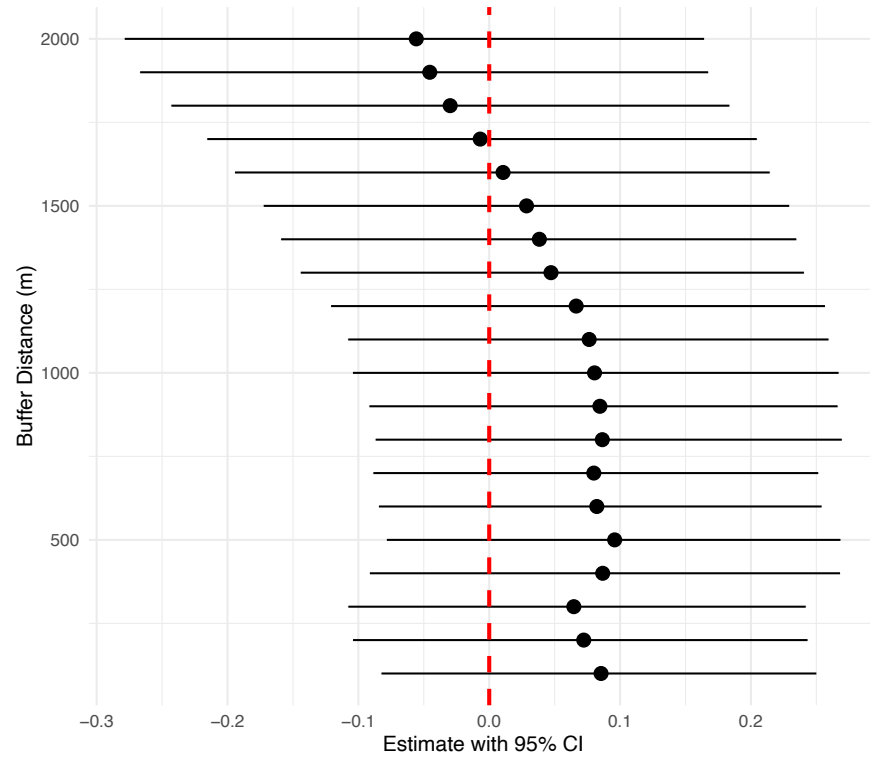


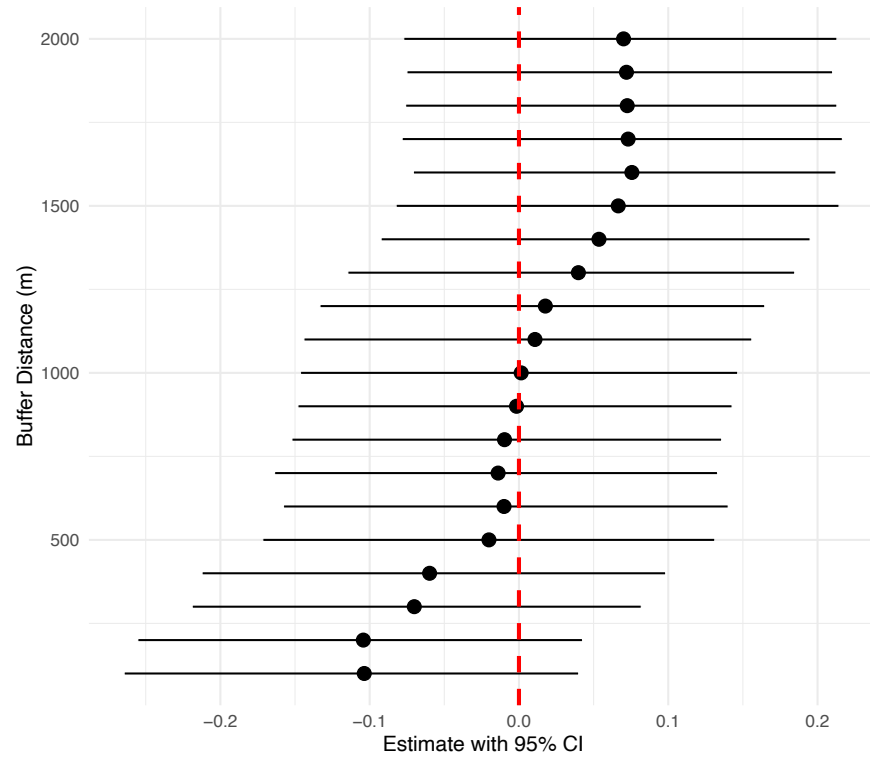
Fig S6 Predicted genome-wide heterozygosity as a function of historic forest loss (1985–1994) at 3 levels (the 10<sup>th</sup>, 50<sup>th</sup>, and 90<sup>th</sup> percentiles) of isolation. Lines represent predictions from the top performing candidate model (Deforestation\*Isolation), with colors indicating low (green), medium (orange), and high (red) isolation. Shaded areas represent 95% credible intervals for the lines of best fit. Different shapes represent different sampling sites



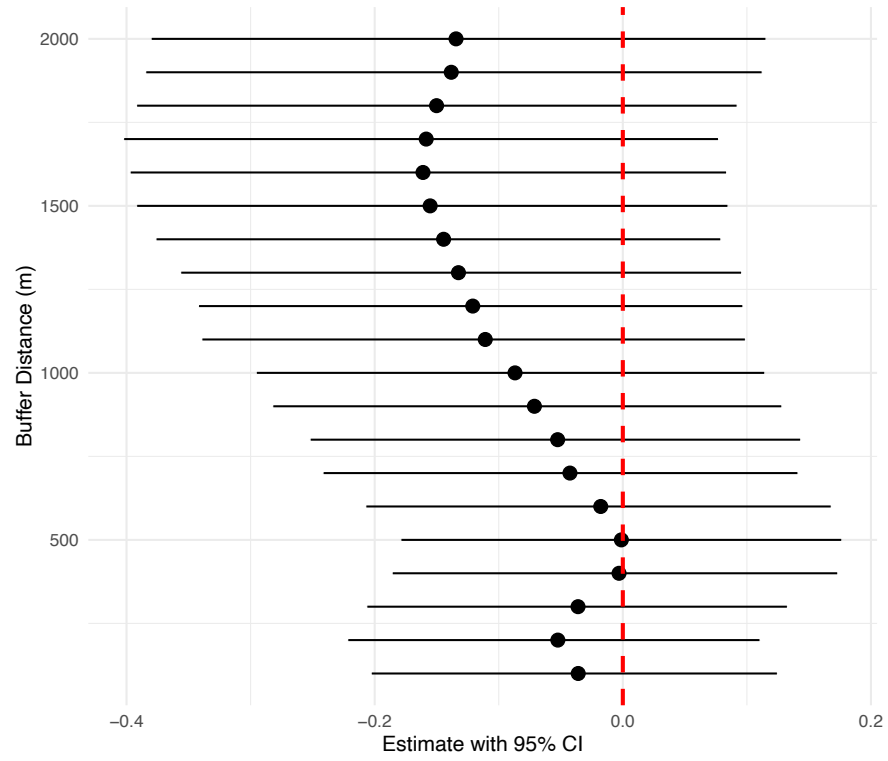
**Fig S7** Coefficient estimates (black dots) and 95% credible intervals (black lines) for each deforestation (1985–1994) buffer distance



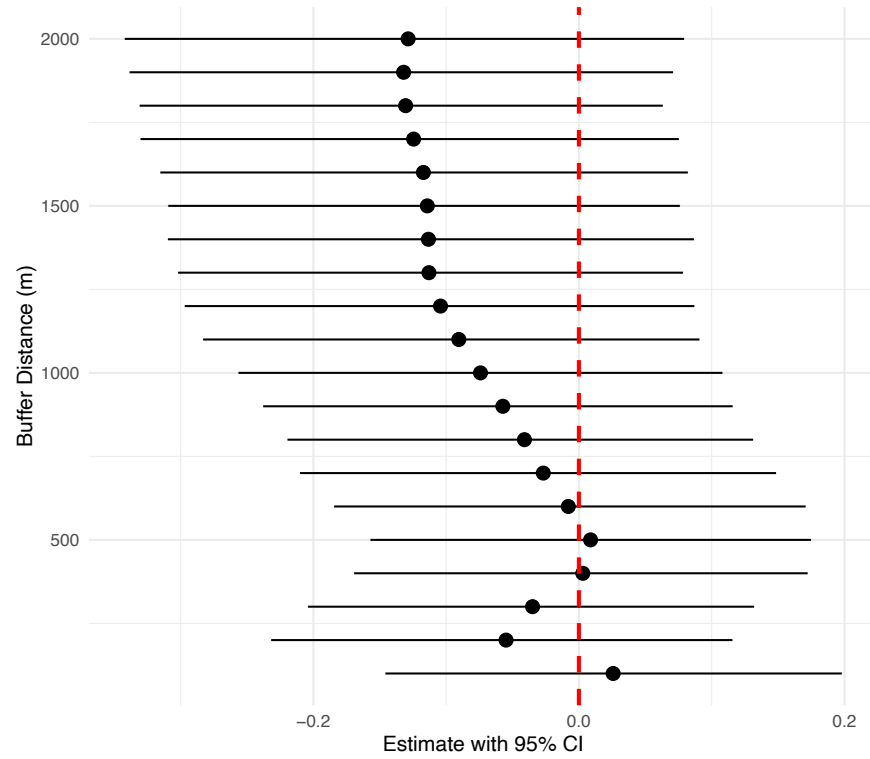
**Fig S8** Coefficient estimates (black dots) and 95% credible intervals (black lines) for each deforestation (1995–2004) buffer distance



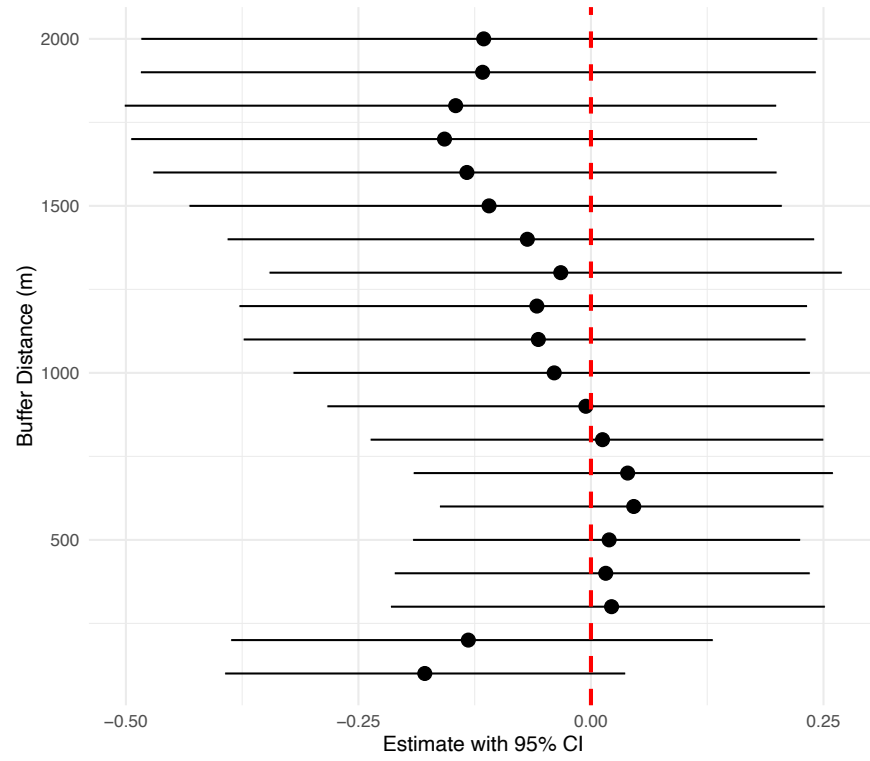
**Fig S9** Coefficient estimates (black dots) and 95% credible intervals (black lines) for each deforestation (2005–2014) buffer distance



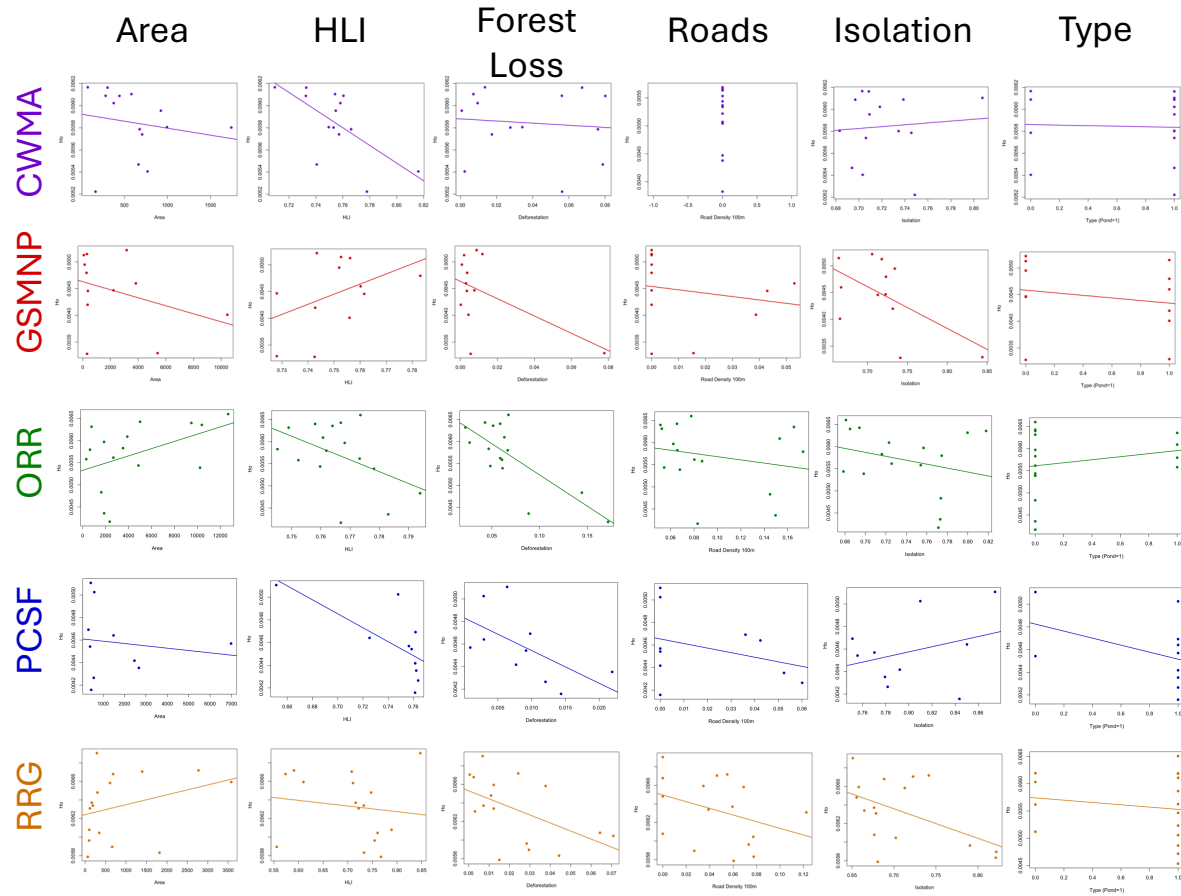
**Fig S10** Coefficient estimates (black dots) and 95% credible intervals (black lines) for each deforestation (2015–2024) buffer distance



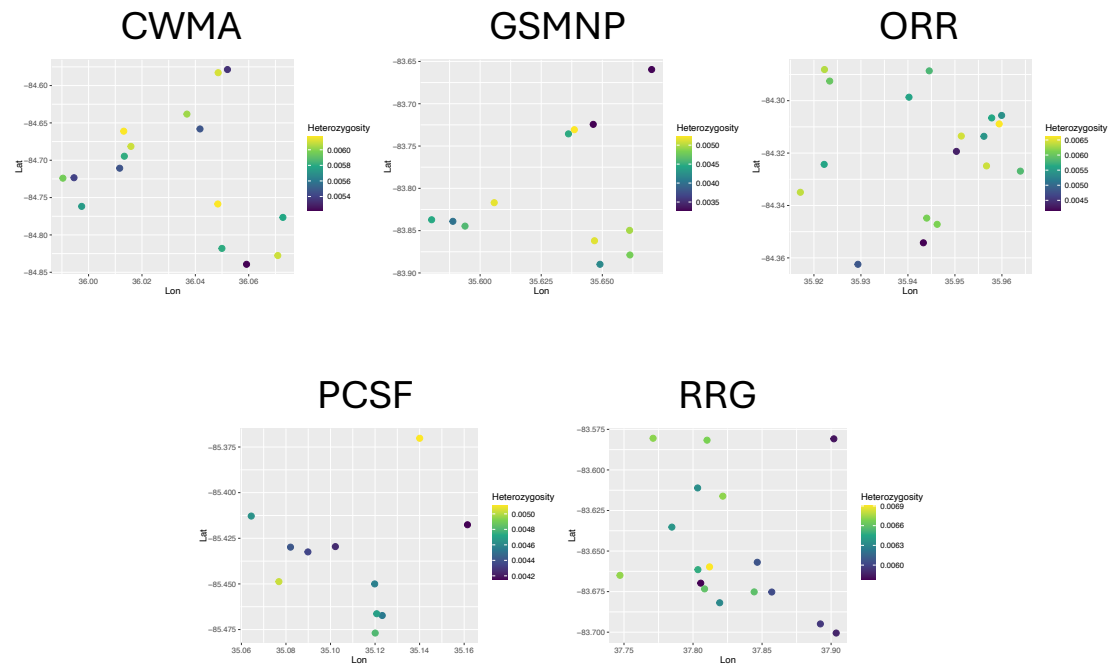
**Fig S11** Coefficient estimates (black dots) and 95% credible intervals (black lines) for each deforestation (all years combined) buffer distance



**Fig S12** Coefficient estimates (black dots) and 95% credible intervals (black lines) for each road density buffer distance



**Fig S13** Plots displaying the relationship between heterozygosity and each predictor within each study area



**Fig S14** Maps displaying the spatial distribution of genome-wide heterozygosity at each sampled wetland within each study area