

Recombination rate variation and linked selection in the *Chlamydomonas reinhardtii* genome

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Recombination rate variation in the genome

RECOMBINATION RATE (RR) variation is an important driver of genome evolution. Without recombination to uncouple selected alleles from their backgrounds, selection efficacy is reduced, affecting neutral polymorphism. This process of **linked selection** manifests as a loss of linked neutral variation, the extent of which is modulated by RR. Here, we investigated recombination rate variation in the facultatively sexual unicellular alga *Chlamydomonas reinhardtii*, asking the questions:

1. What is the extent of RR variation in the genome, and where in the genome is RR highest?
2. How does RR variation relate to nucleotide diversity, and is there evidence for linked selection?

The landscape of recombination in *C. reinhardtii*

FOLLOWING whole genome resequencing of *C. reinhardtii* field isolates, we used **LDHelmet** [1] to estimate RR using population genomic data.

Recombination varies over two orders of magnitude in the hotspot-punctuated genome

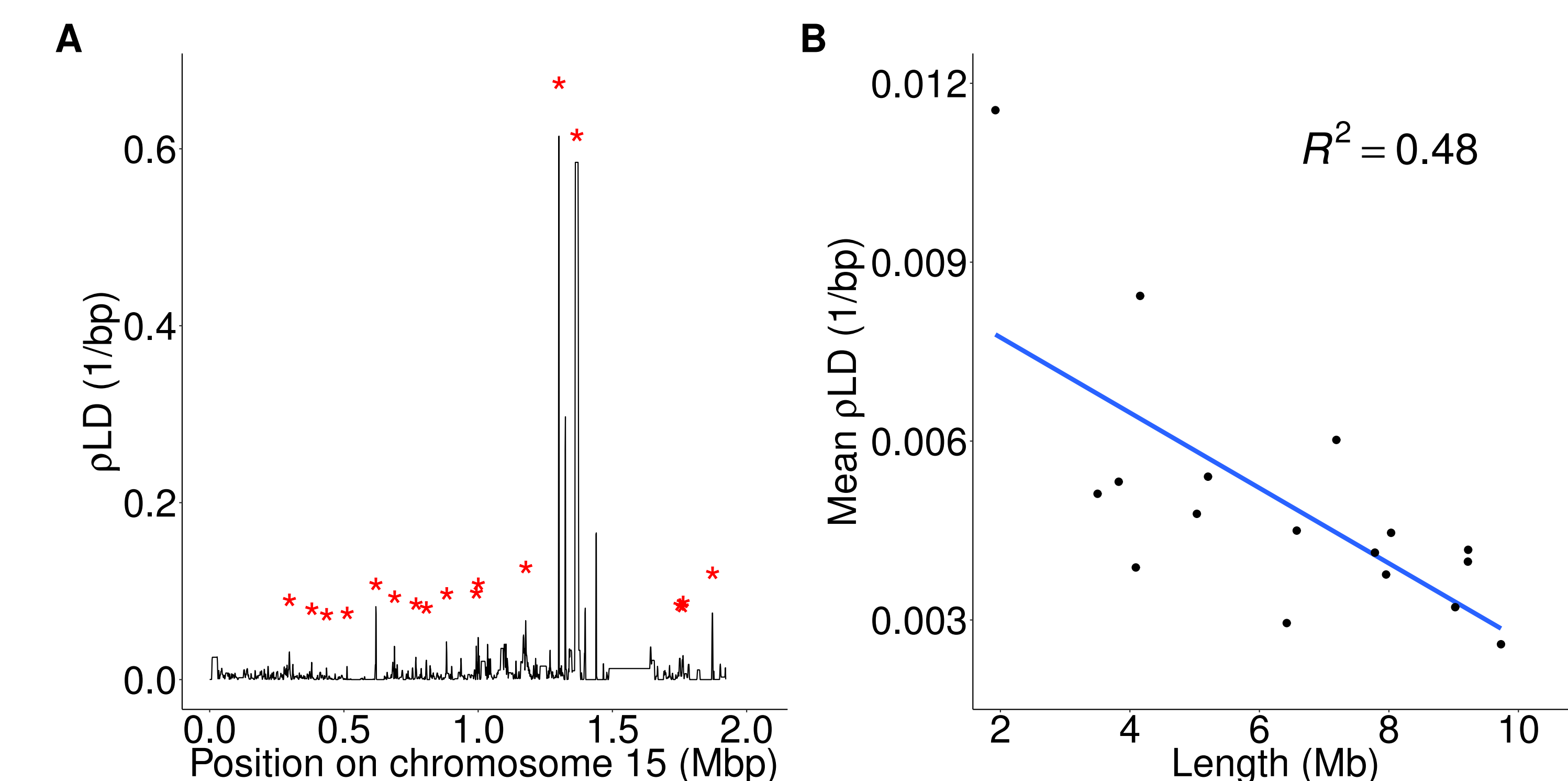


Fig. 1. **A** RR variation over chromosome 15. Hotspots are indicated in red. **B** Mean chromosomal RR inversely correlates with chromosome length.

Recombination rate is highest immediately flanking genes

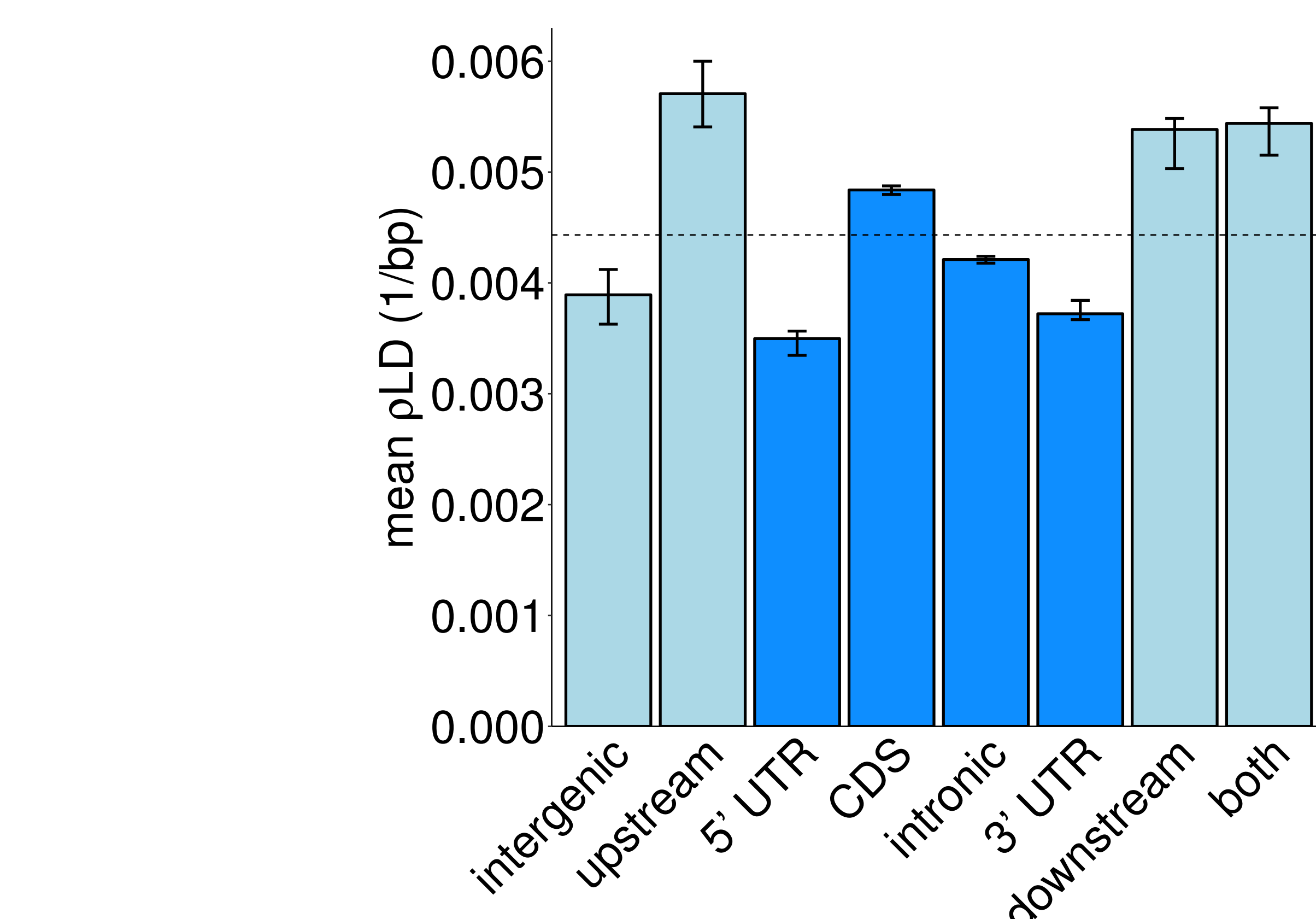


Fig. 2. RR across genome annotations. RR is highest flanking genes; within genes, RR is highest in coding regions. This is consistent with patterns observed in plant recombination [2].

References

[1] Chan et al. *PLoS Genet.*, 8(12), 2012. [2] Choi & Henderson. *Plant. J.* 83(1), 2015. [3] Begun & Aquadro. *Nature* 356, 1992. [4] Wright et al. *Genetics* 174(3), 2006. [5] Flowers et al. *Mol. Biol. Evol.* 29(2), 2012.

A role for linked selection?

If linked selection is acting in the genome, we would expect a **positive correlation between RR and neutral nucleotide diversity (θ)** [3].

Nucleotide diversity (θ_π) correlates with LD recombination rate, but not map recombination rate

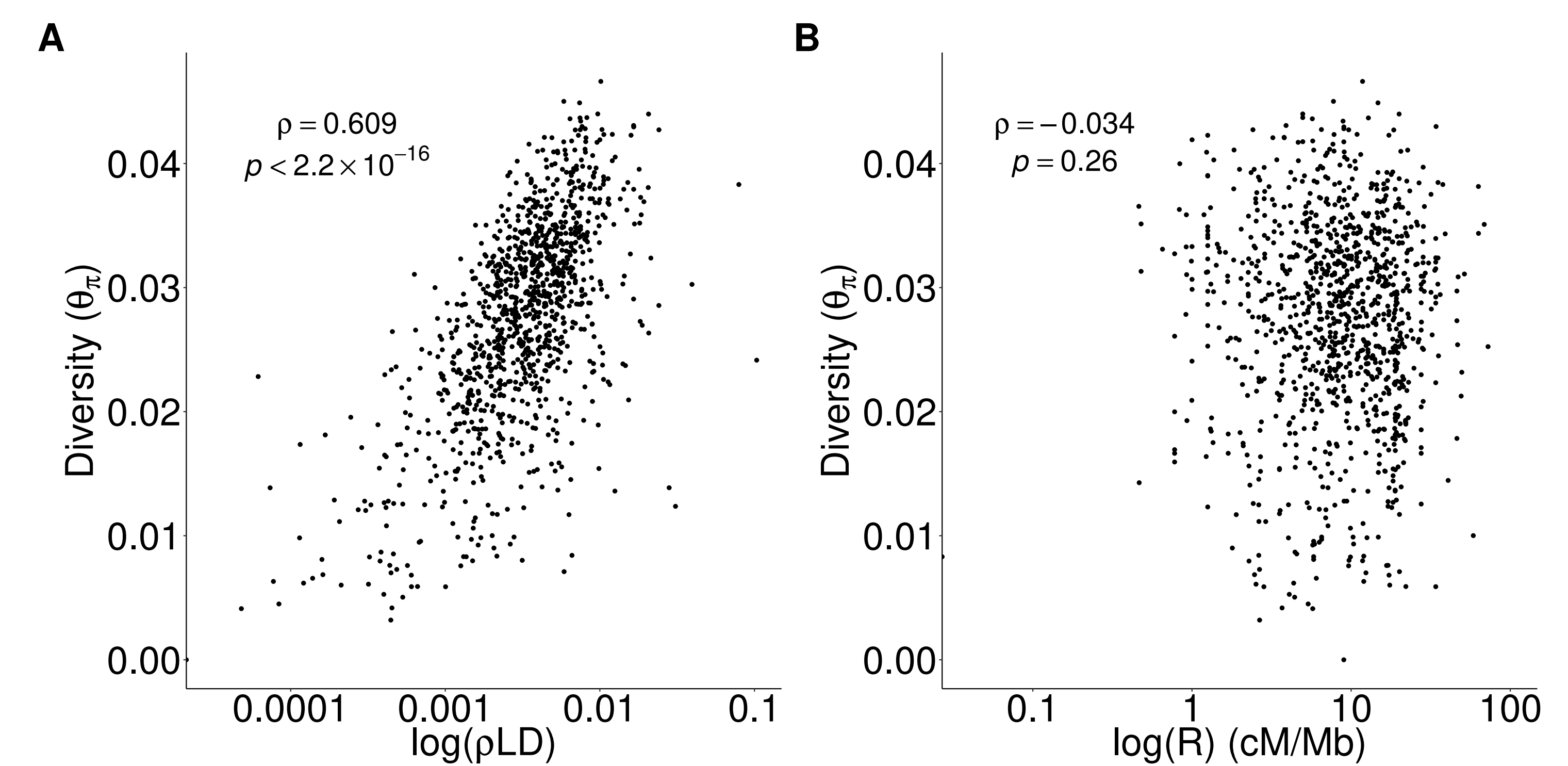


Fig. 3. **A** LD recombination rate ($\rho = 4N_e r$) correlates with $\theta_\pi (= 4N_e \mu)$. **B** Physical recombination rate estimates from the genetic map of *C. reinhardtii* do not correlate with θ_π . Correlations performed with Spearman's coefficient (ρ); values shown inline.

Diversity is positively correlated with functional density

THE lack of a correlation between R and θ has been observed in other plant species [4,5]. In these species, diversity inversely correlates with functional density, indicating that linked selection is still acting in the genome. However, we observe the opposite pattern:

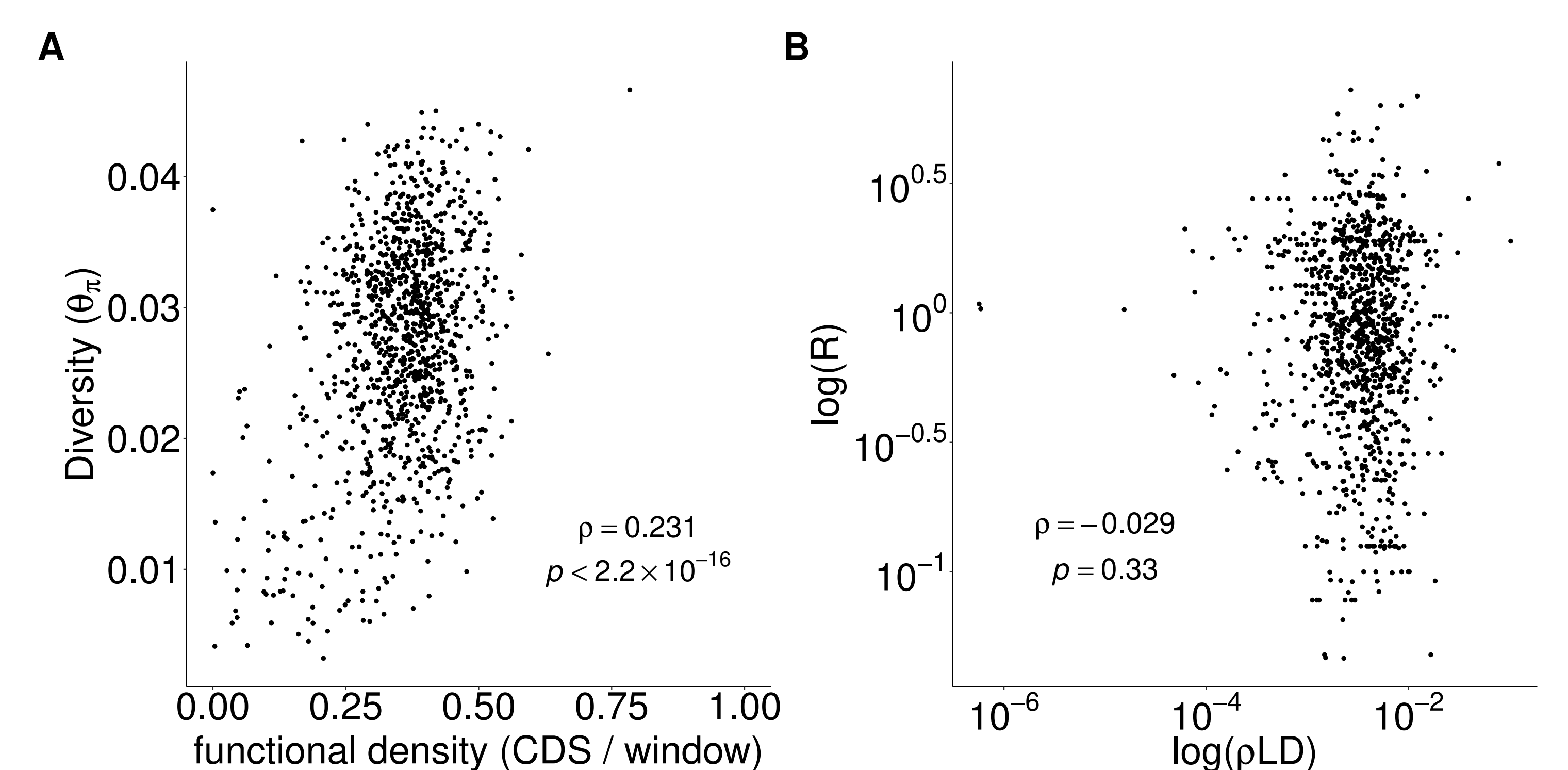


Fig. 4. **A** Functional density, measured as CDS sites per 100 kb window, positively correlates with diversity. **B** LD recombination rate does not correlate with physical recombination rate. Spearman's coefficients (ρ) shown inline.

What could be driving these patterns?

Why does R not correlate with θ while ρLD does?

- Perhaps R does not have enough resolution to tease apart fine-scale effects of diversity, due to insufficient marker density. We also see that R does not correlate with ρLD either (Fig. 4D).
- ρLD and θ_π are both scaled by N_e , which may cause autocorrelation of the two variables.

Why does diversity correlate with functional density?

- Not sure yet! This result is quite unexpected; population genetic theory predicts the opposite trend.
- A better understanding of variation in the strength of selection (s) across the *C. reinhardtii* genome may help tease apart what factors besides recombination are playing a role.