

Exploring natural variation in meiotic recombination rates in barley

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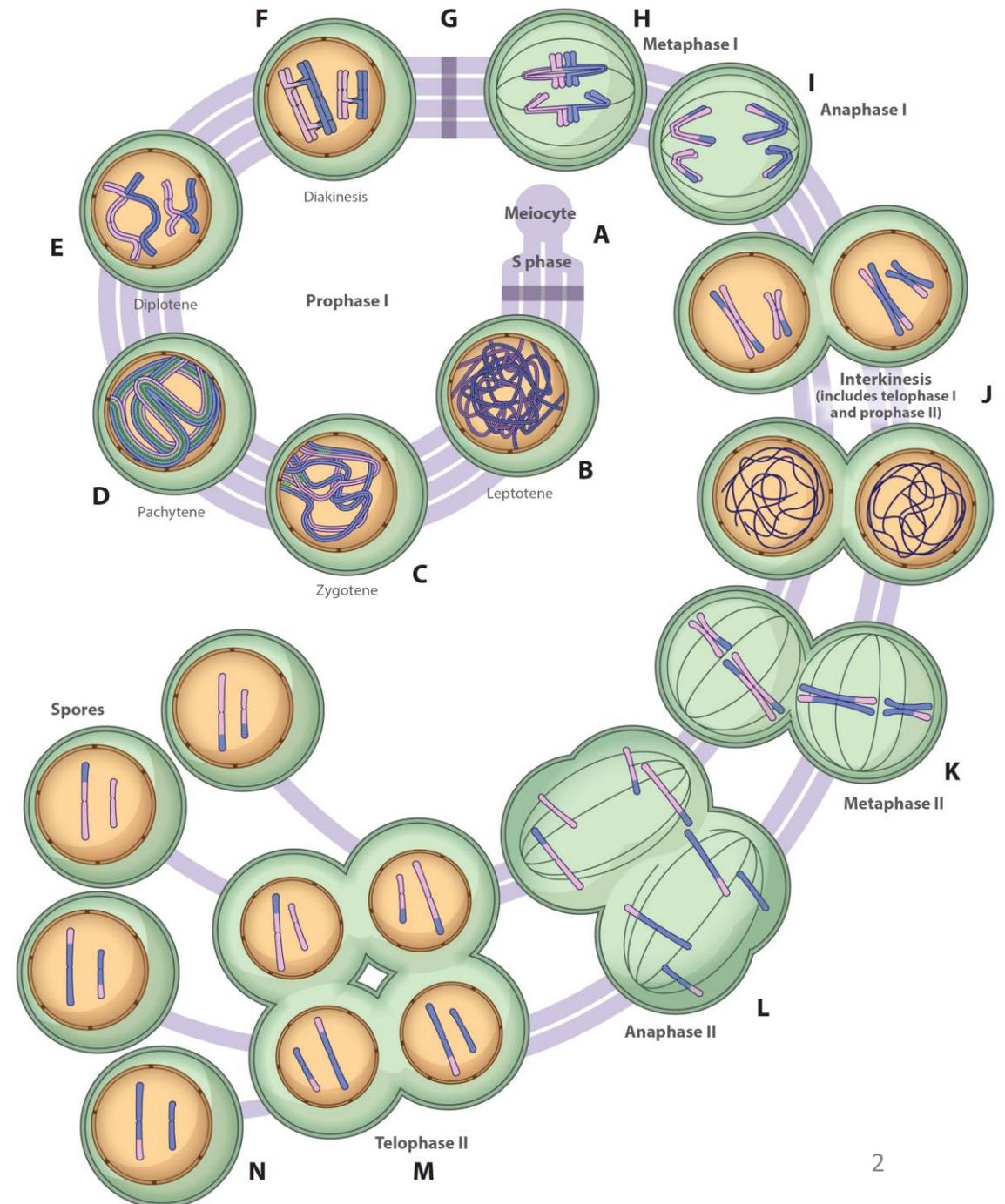
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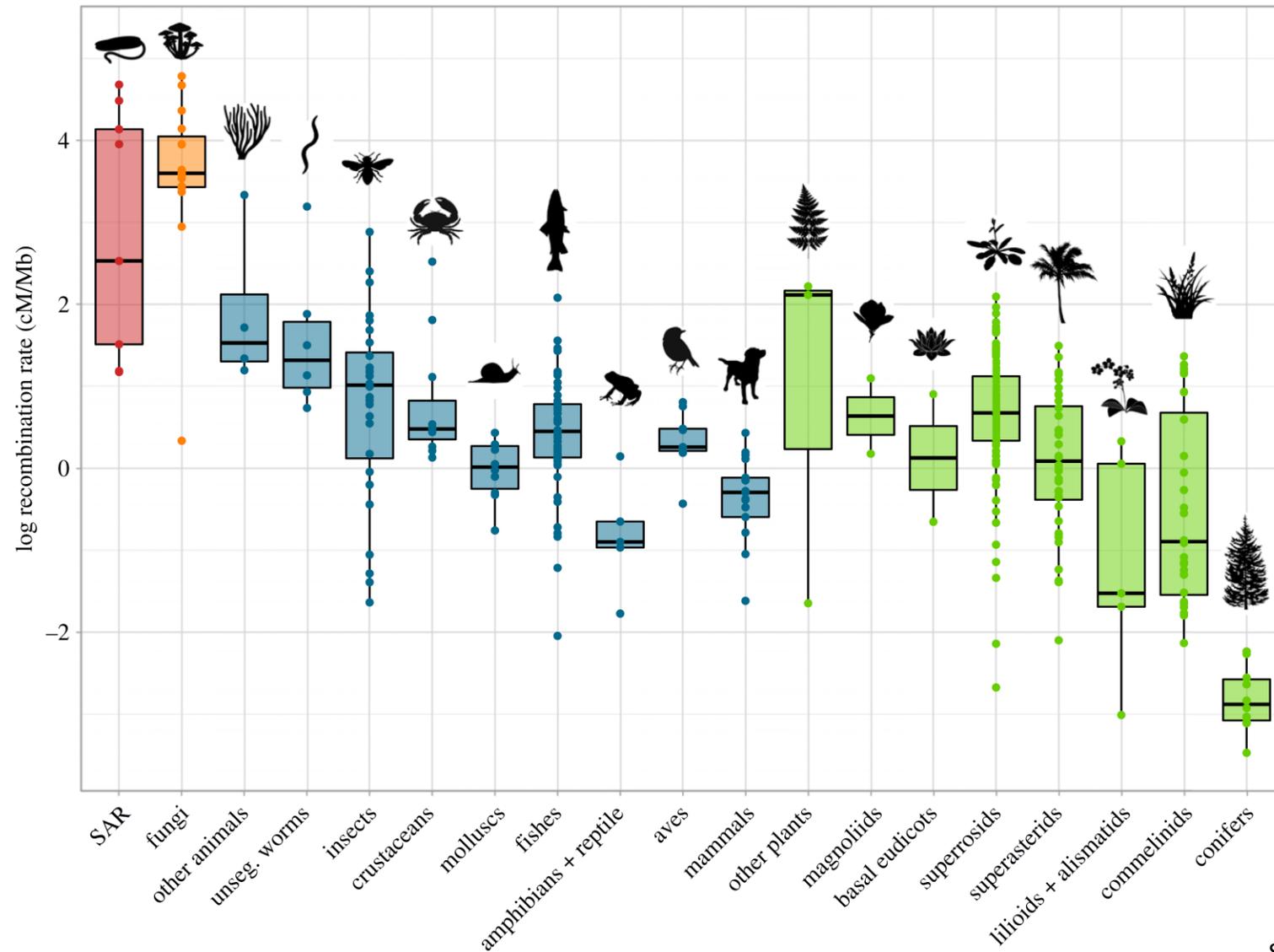


A brief introduction to meiosis

- fundamental to eukaryotic reproduction
- one round of DNA replication followed by two rounds of cell division
- > 80 genes known to be involved in plant meiosis
- genetic recombination
- reshuffling of alleles

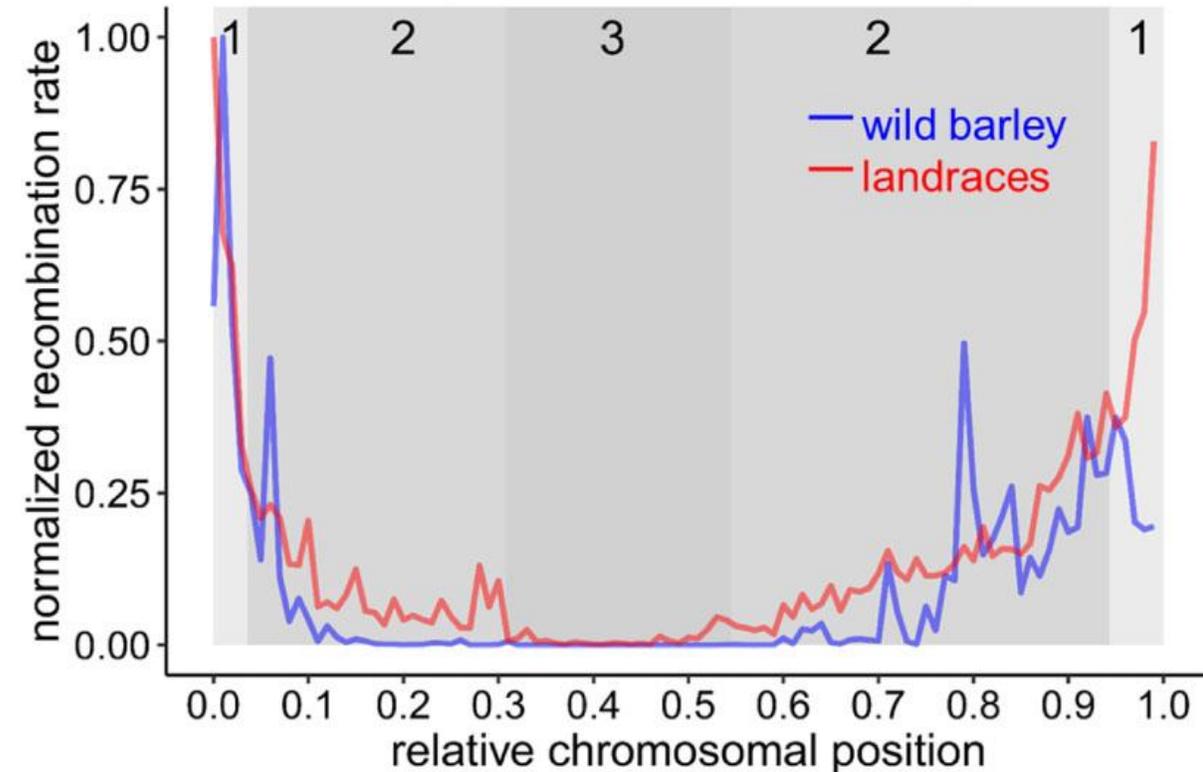


Diversity of genome-wide recombination rates across eukaryotes

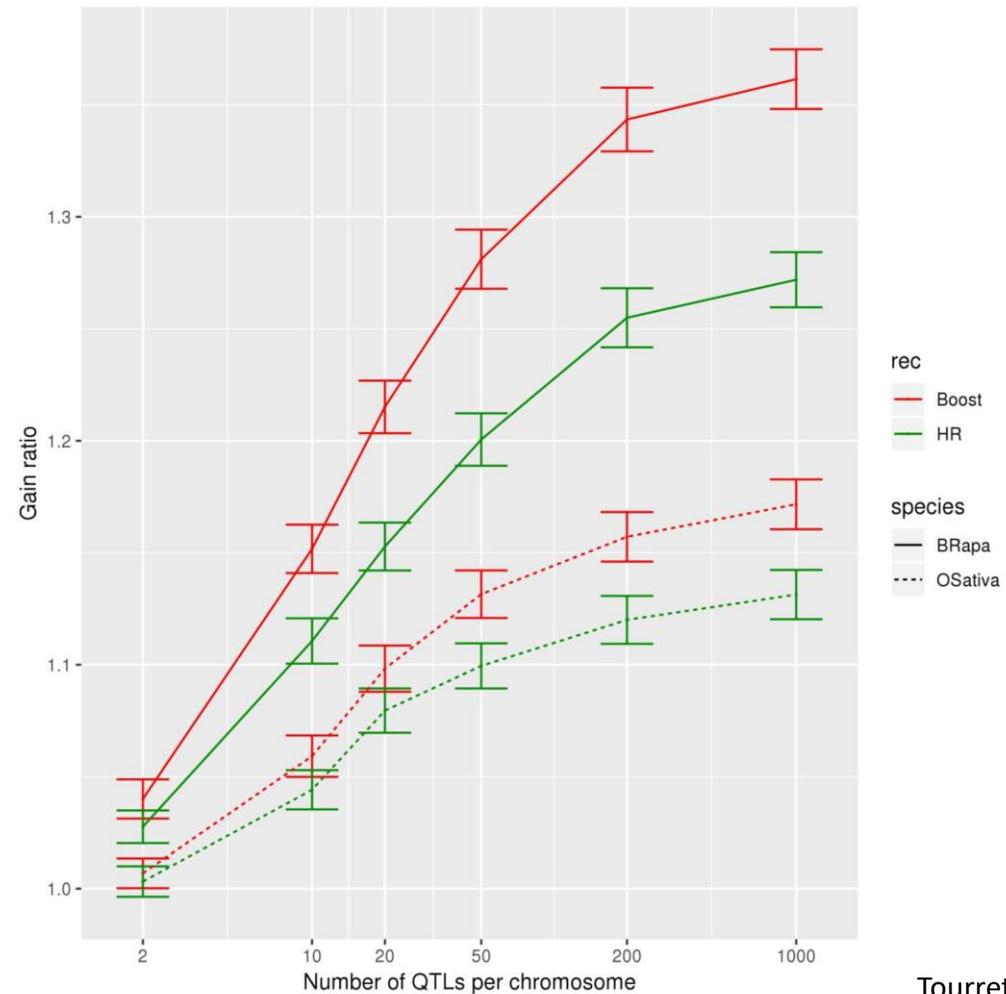


Meiotic recombination rates are drastically reduced across pericentromeric regions

- strong distal bias of recombination rates in large, heterochromatin genomes
- similar recombination landscapes in wild and domesticated barley
- up to 30% of all genes are located in low-recombining regions



Would plant breeding benefit from increased recombination rates?

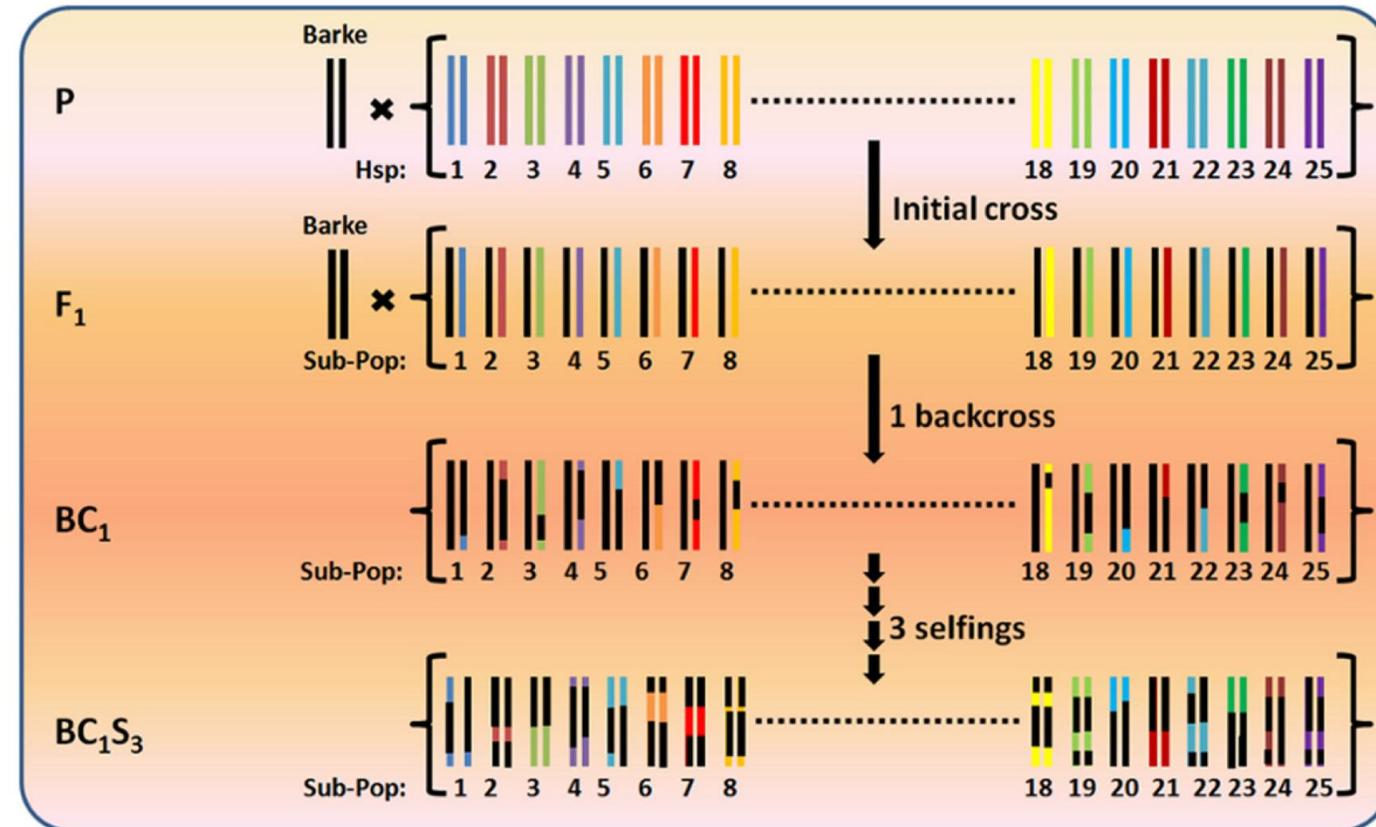


- What is the extent of natural variation in meiotic recombination rates in barley?
- Can we identify genome-wide recombination rate modifiers?
- Are patterns of introgression influenced by local and genome-wide recombination rate variation?

Exploring natural variation in meiotic recombination rates in intraspecific hybrid populations

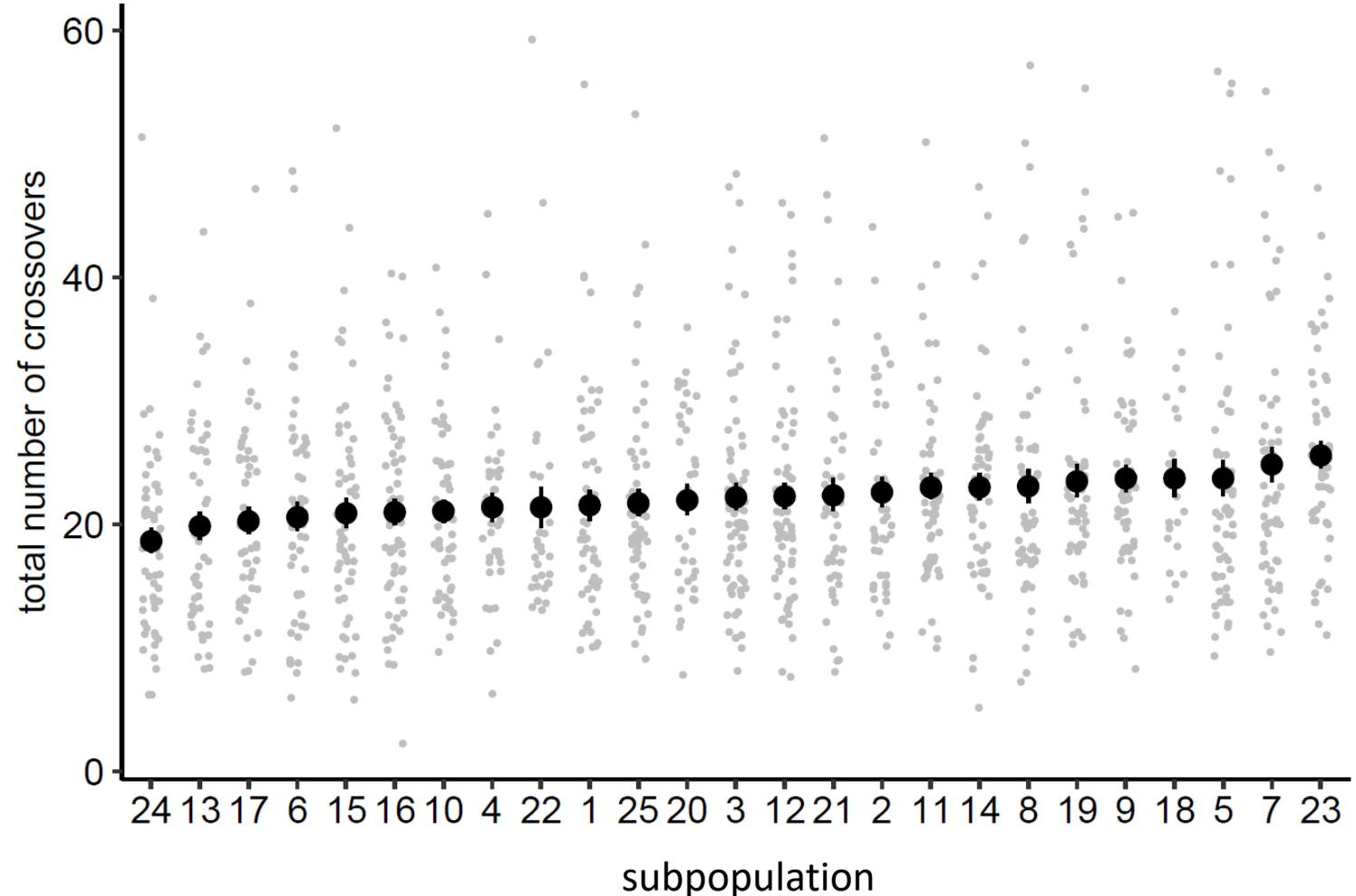
- cross between domesticated barley (*H. vulgare* cv. „Barke“) and 25 wild barleys (*H. vulgare* ssp. *spontaneum*)
- 25 sub-populations
- 1367 lines (24 – 75 per population)
- BC₁S_{3:8} -> 9 rounds of meiosis
- 50K iSelect genotype data
- 32,120 physically mapped SNPs (barley reference sequence v2.0)

HEB-25



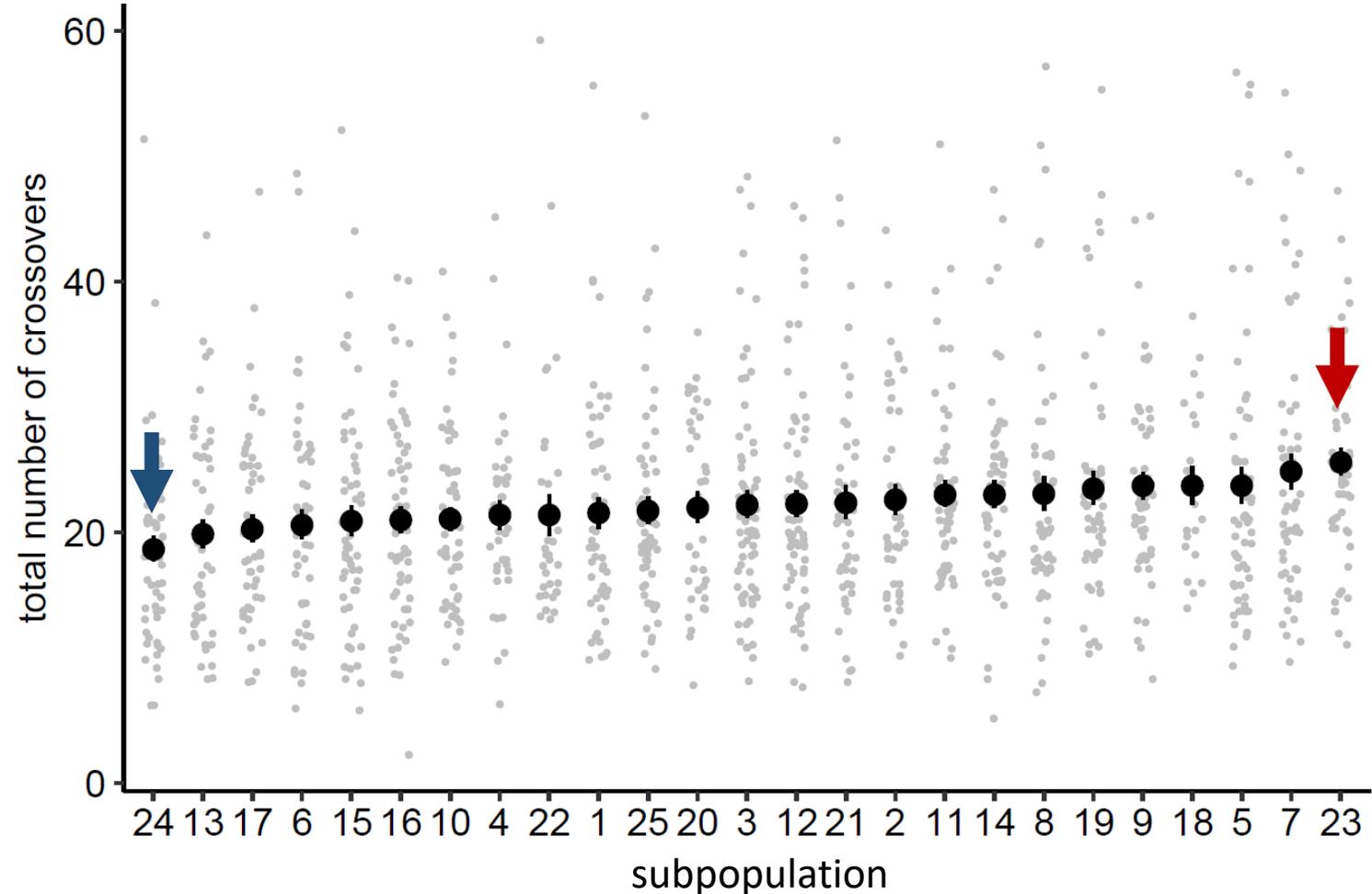
Crossover quantification at megabase resolution reveals natural variation between populations

- 7174 – 11246 SNPs per population
- mean inter-SNP distance = 493 kb
- SNPs were aggregated by counting most common allele in sliding windows of 20 consecutive SNPs
- crossovers counted as changes in allelic state along the chromosome (e.g. 0 → 2, 0 → 1, 1 → 2)

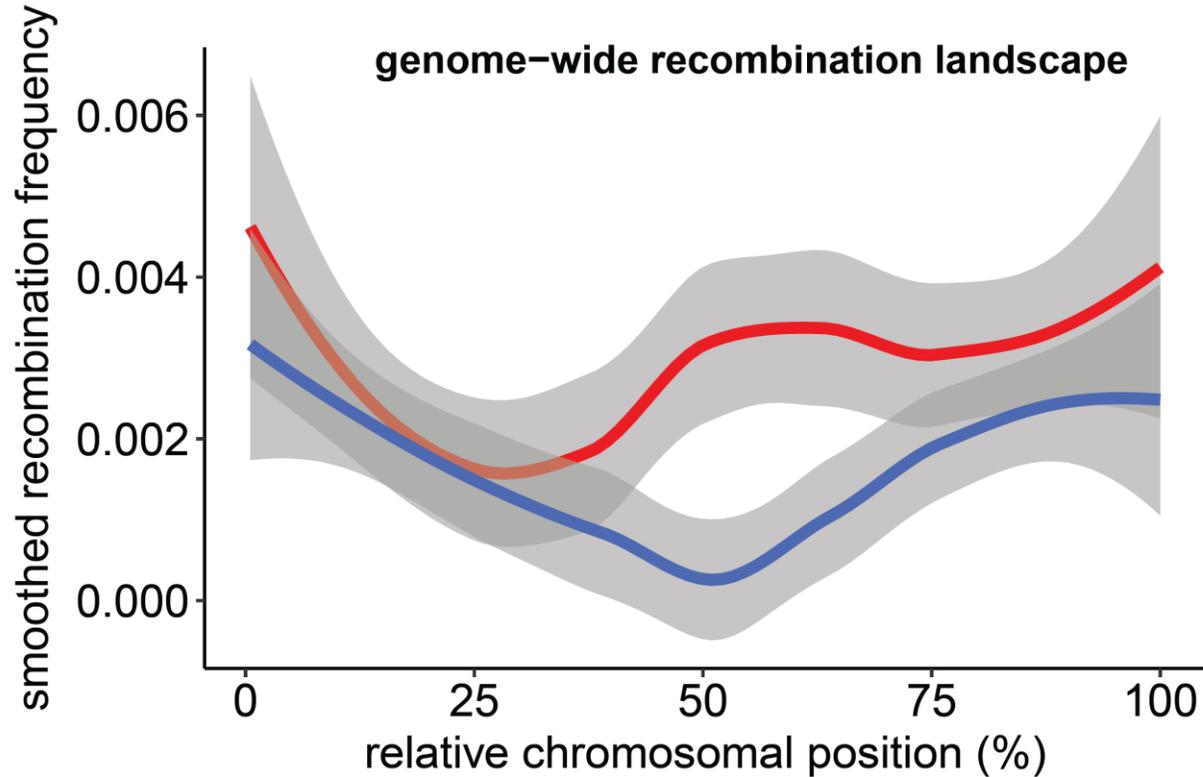


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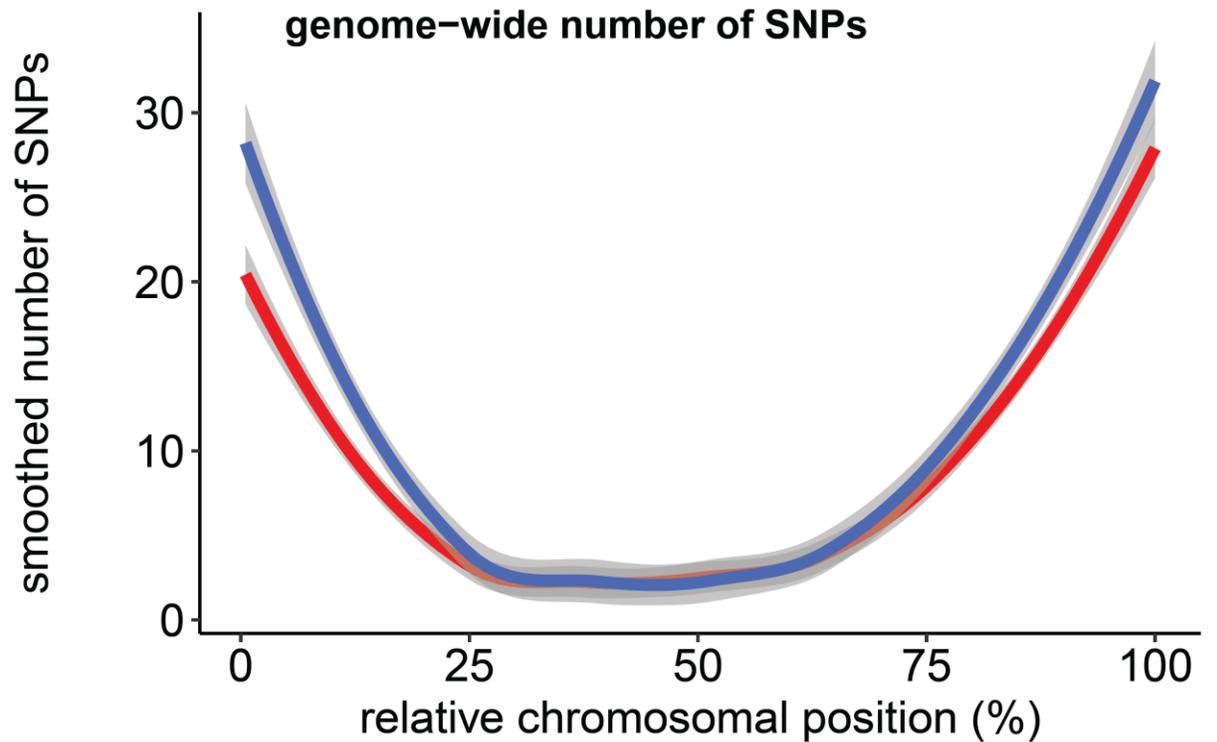
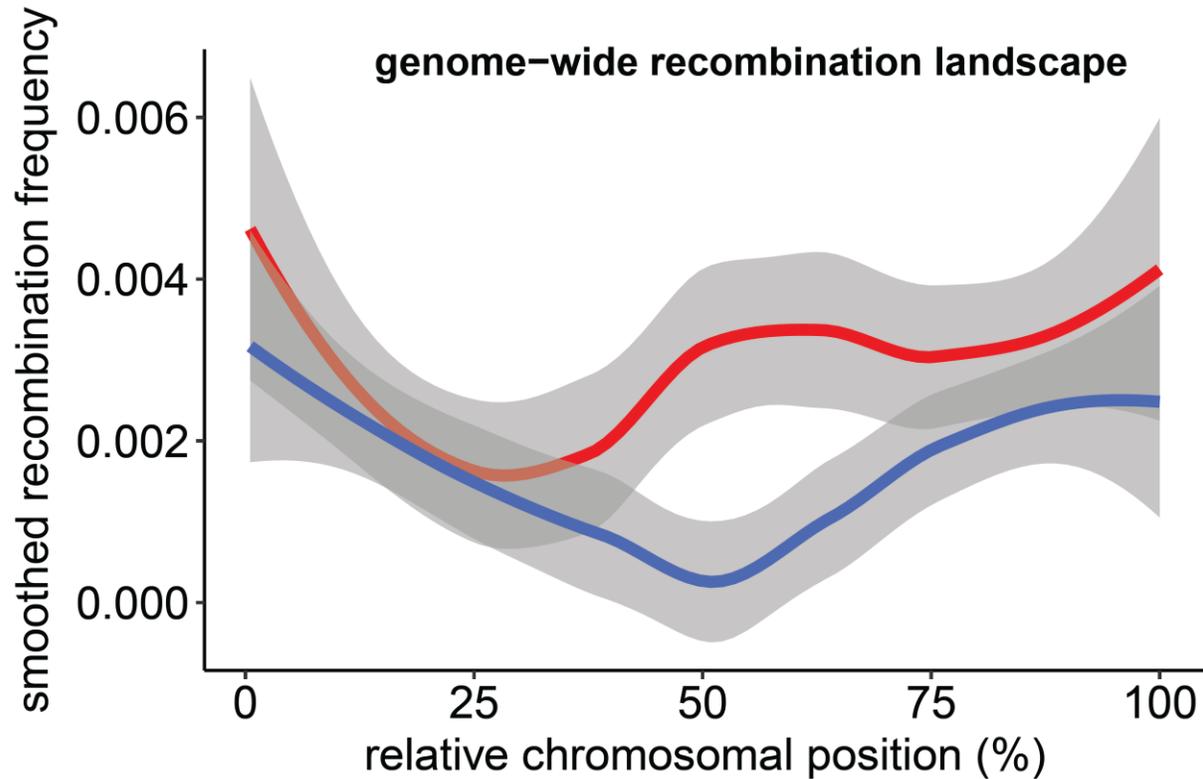


Different recombination landscapes in high- vs. low-recombining populations



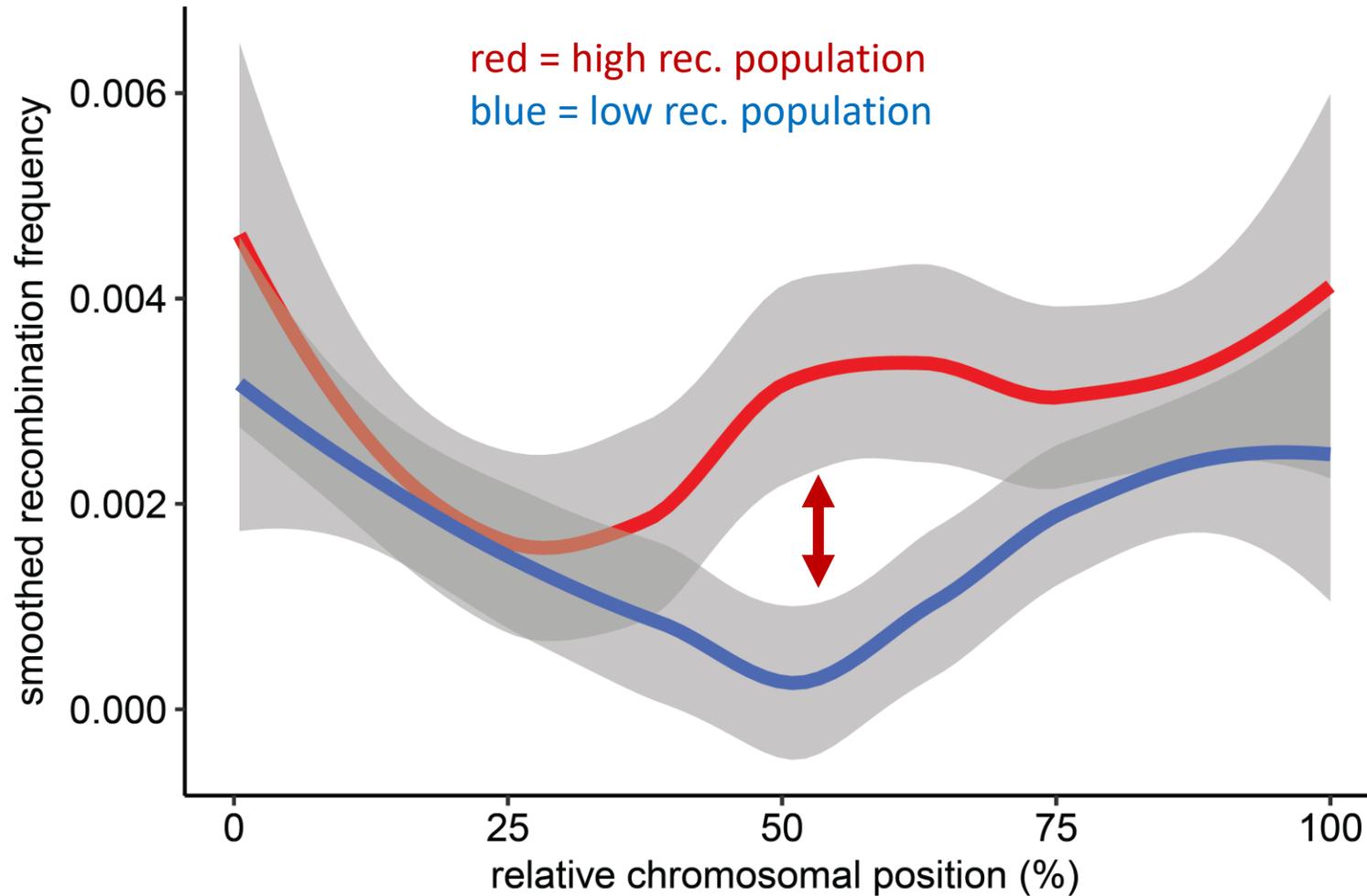
red = high recombining population
blue = low recombining population
grey = 95 % confidence interval

Different recombination landscapes in high- vs. low-recombining populations



red = high recombining population
blue = low recombining population
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Increase in recombination frequency across pericentromeric regions



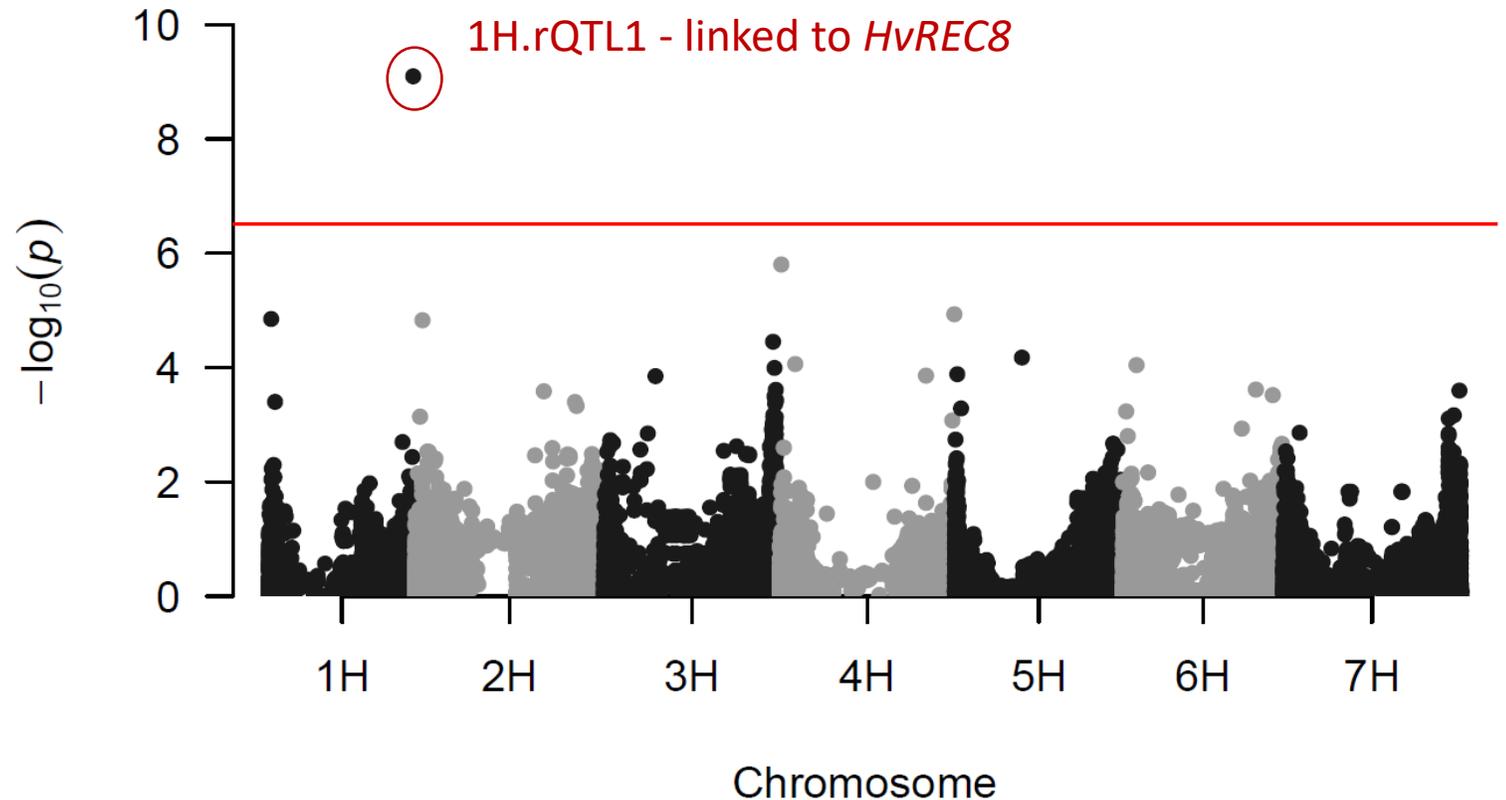
Can we identify genome-wide recombination rate modifiers?

Genome-wide association study (GWAS) hints at presence of recombination rate modifiers

- phenotype = total crossover number at $BC_1S_{3:8}$
- association with genotype of final generation
- not possible to determine whether rQTL was present/absent or homozygous/heterozygous throughout previous generations
- reduced power to detect rQTL
- additional cross-validation by removing CO counts of chromosome showing significant marker (Jordan et al. 2018)

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- additional cross-validation by removing CO counts of chromosome showing significant marker (Jordan et al. 2018)
- effect size of wild barley allele = + 42% (+ 7.84 COs)
- 1H rQTL linked (0.3 cM) to meiotic gene *REC8*



SNPs identified in *REC8* via exome capture sequencing reveal different *REC8* haplotypes in wild barley

- exome capture sequencing performed in all 1367 lines (4x) and 22 donors (20x)

- 5 SNPs identified in *REC8*

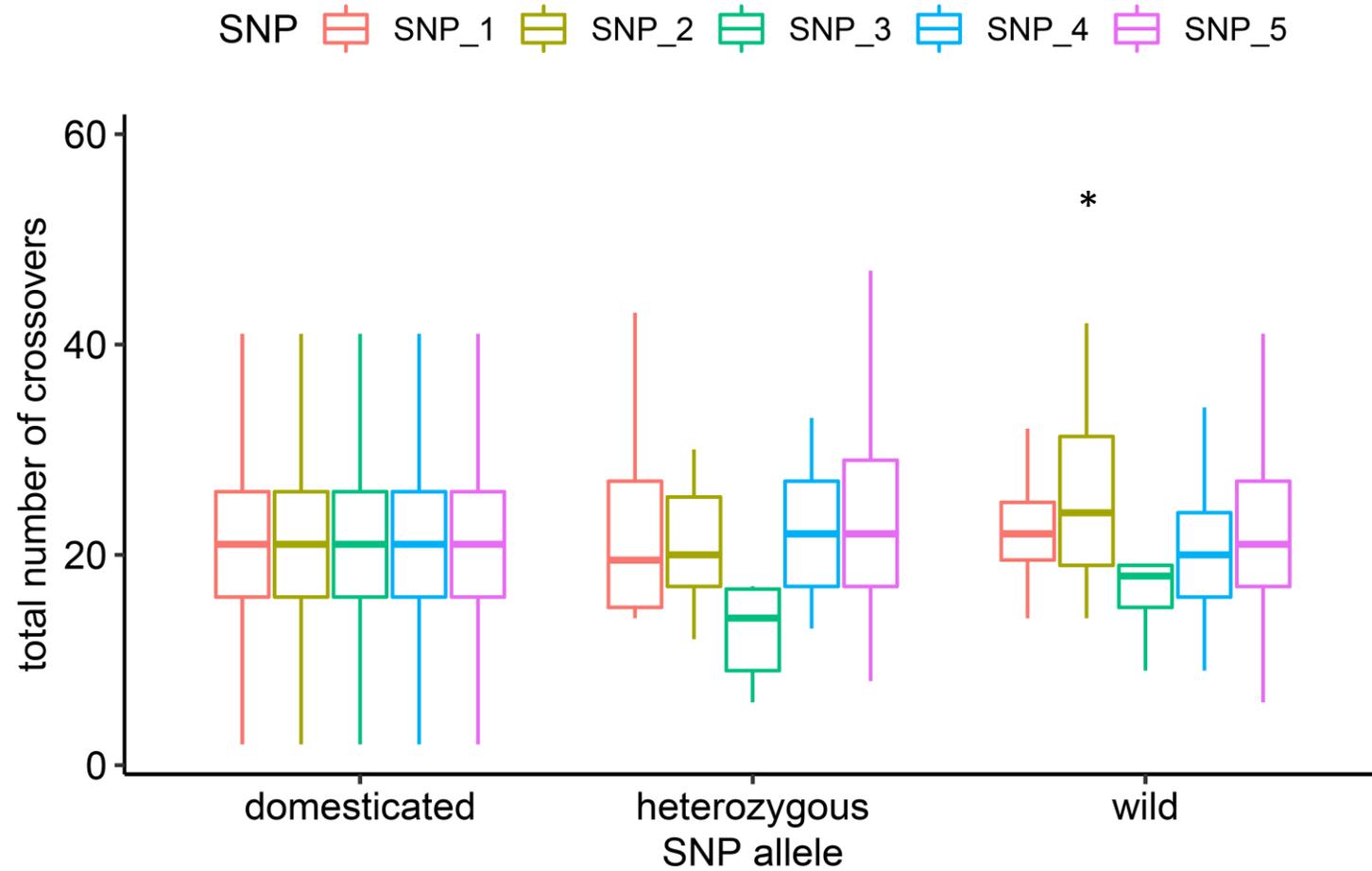
SNP_1 SNP_2 SNP_3 SNP_4 SNP_5

SNP position (bp)					Donor	sub-population
548,886,748	548,886,818	548,888,666	548,888,680	548,889,374		
TT	GG	TT	AA	AA	Barke	
TC	GA	TT	AA	AA	HID004	2
TT	GG	TT	AA	TT	HID055	3
TT	GA	TT	AA	AA	HID062	4
TT	GG	TT	AG	AT	HID069	6
TT	GA	TT	AA	AA	HID080	7
TT	GG	TT	AA	AA	HID099	8
TT	GG	TT	AA	AA	HID101	9
TT	GG	TT	AA	TT	HID102	10
TT	GG	TT	AA	AA	HID109	11
TT	GG	TT	AA	AA	HID114	12
TT	GG	TT	AA	AA	HID138	13
TT	GG	TT	AA	AA	HID140	14
TT	GG	TC	AA	TT	HID144	15
TT	AA	TT	AA	AA	HID219	16
TT	GG	TT	AA	TT	HID249	17
TT	GG	TT	AA	TT	HID270	18
CC	AA	TT	AA	AA	HID294	19
TT	AA	TT	AA	AA	HID357	21
TT	GG	TT	GG	AA	HID358	22
TT	GG	TT	AA	TT	HID359	23
TT	GG	TT	AA	AA	HID380	24

SNPs in *REC8* partially mirror QTL effects

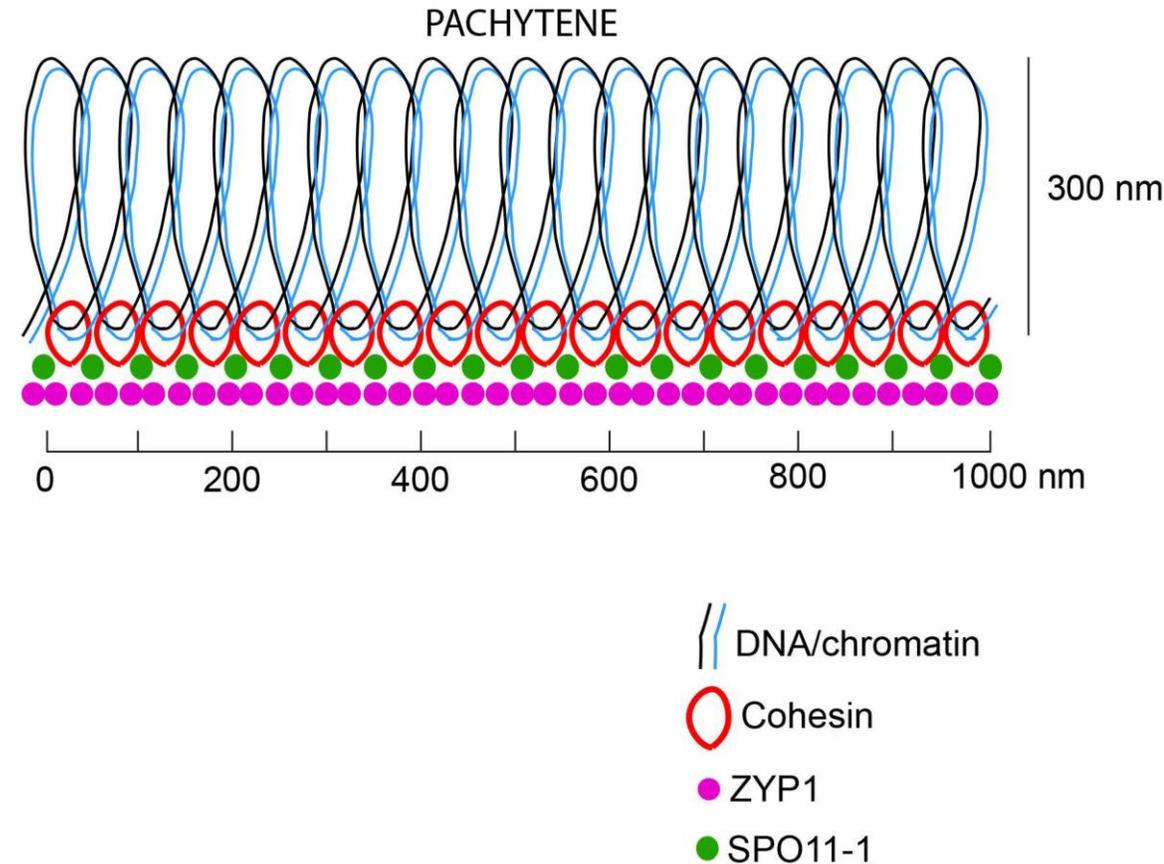
- SNP_2 in *REC8* shows effect similar to QTL
- + 17% (+ 3.8 COs)

	difference	adjusted <i>P</i> value
heterozygous-domesticated	0.346	0.974
wild-domesticated	3.792	0.020 *
wild-heterozygous	3.445	0.229



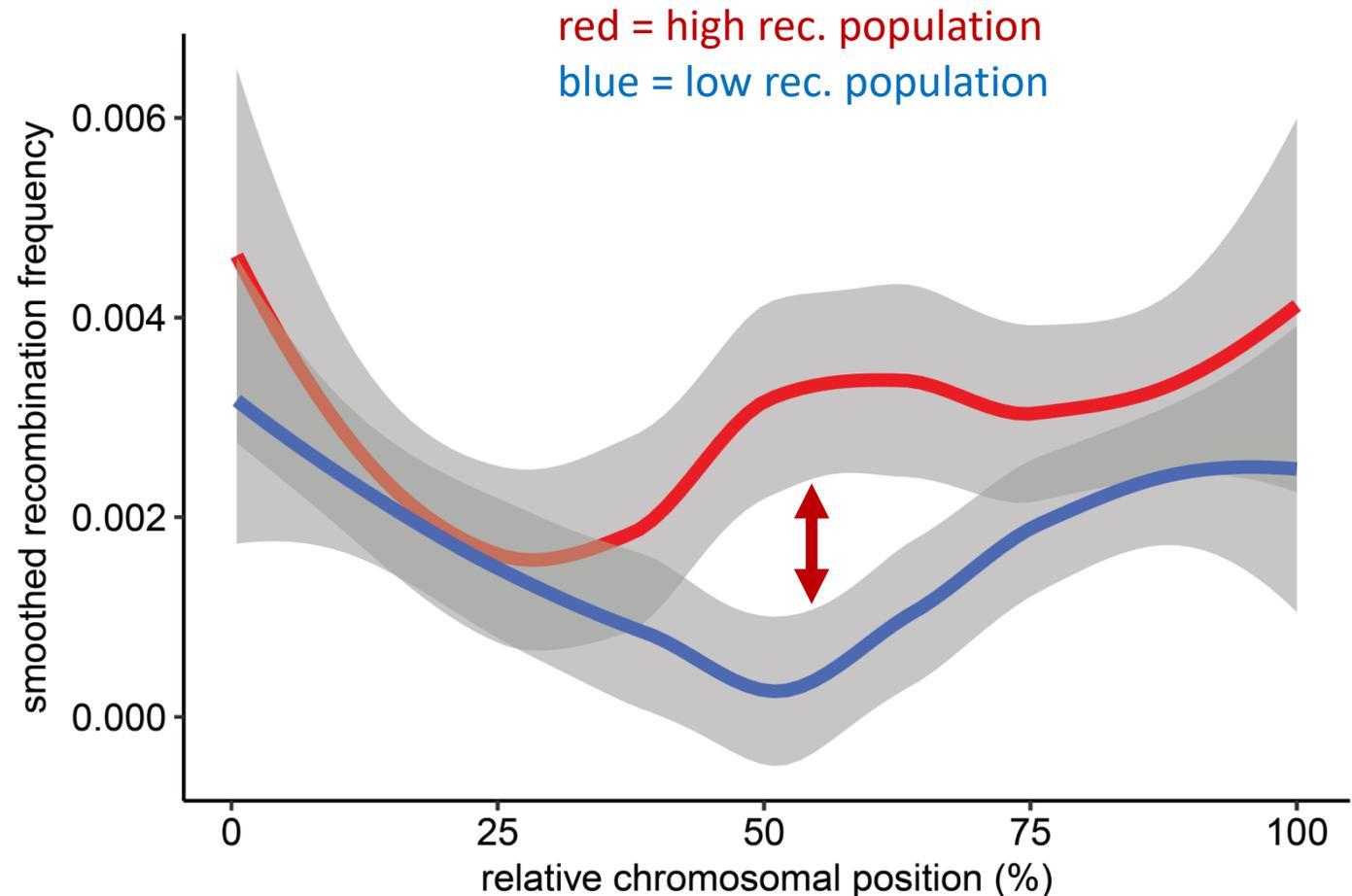
What is known about *REC8*'s role in meiosis?

- REC8-cohesin is required to connect chromosomes to the axis
- high REC8 occupancy in heterochromatin
- REC8 abundance correlates with crossover suppressions



Reduced REC8 abundance in pericentromeric regions of high-recombining populations?

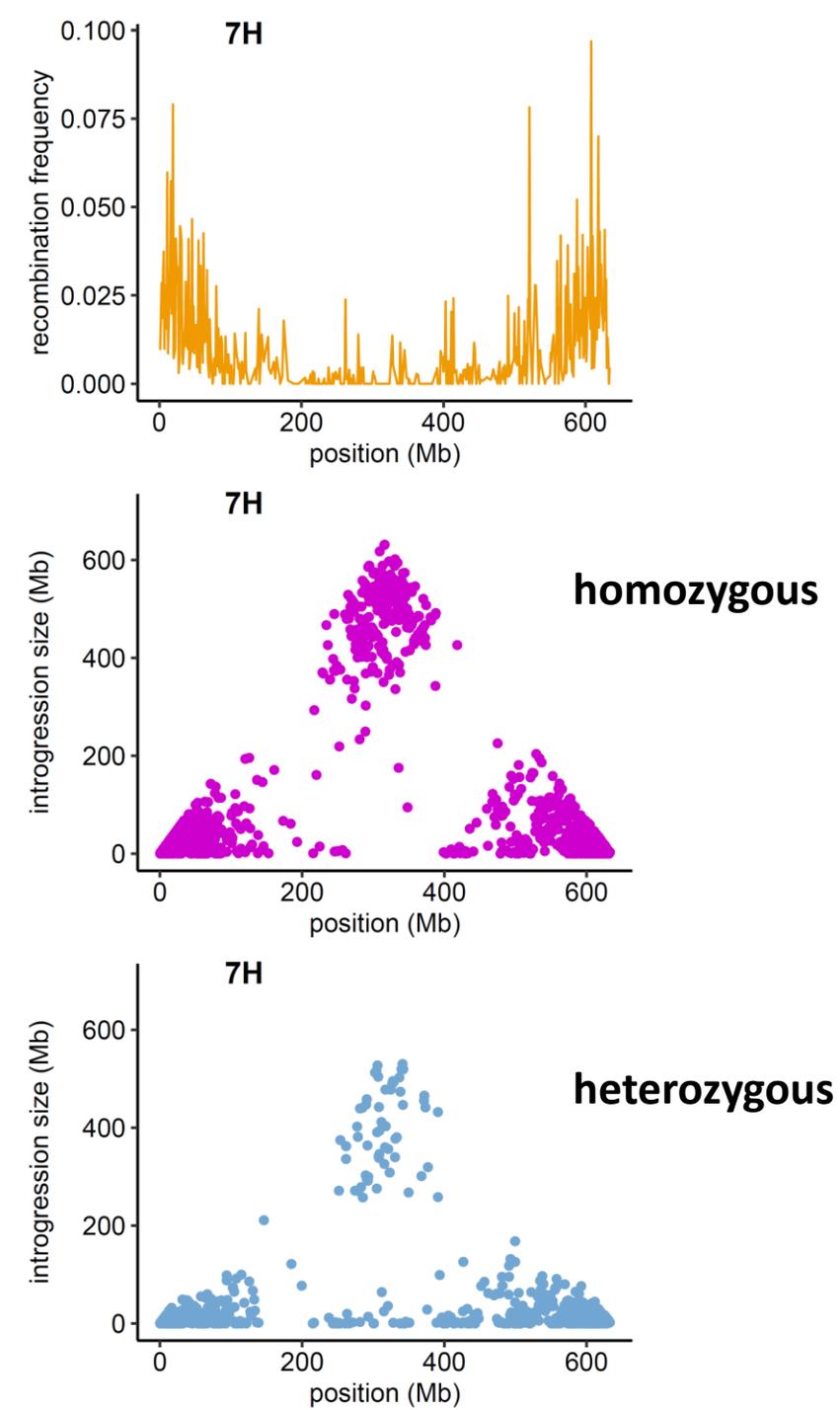
- increased recombination frequency across heterochromatic pericentromeric regions may be caused by reduced REC8 abundance
- REC8 ChIP-seq in selected populations?
- *REC8* gene expression analysis?
- re-sequencing of *REC8*?



Does variation in local and genome-wide recombination rate affect the size and distribution of introgressions?

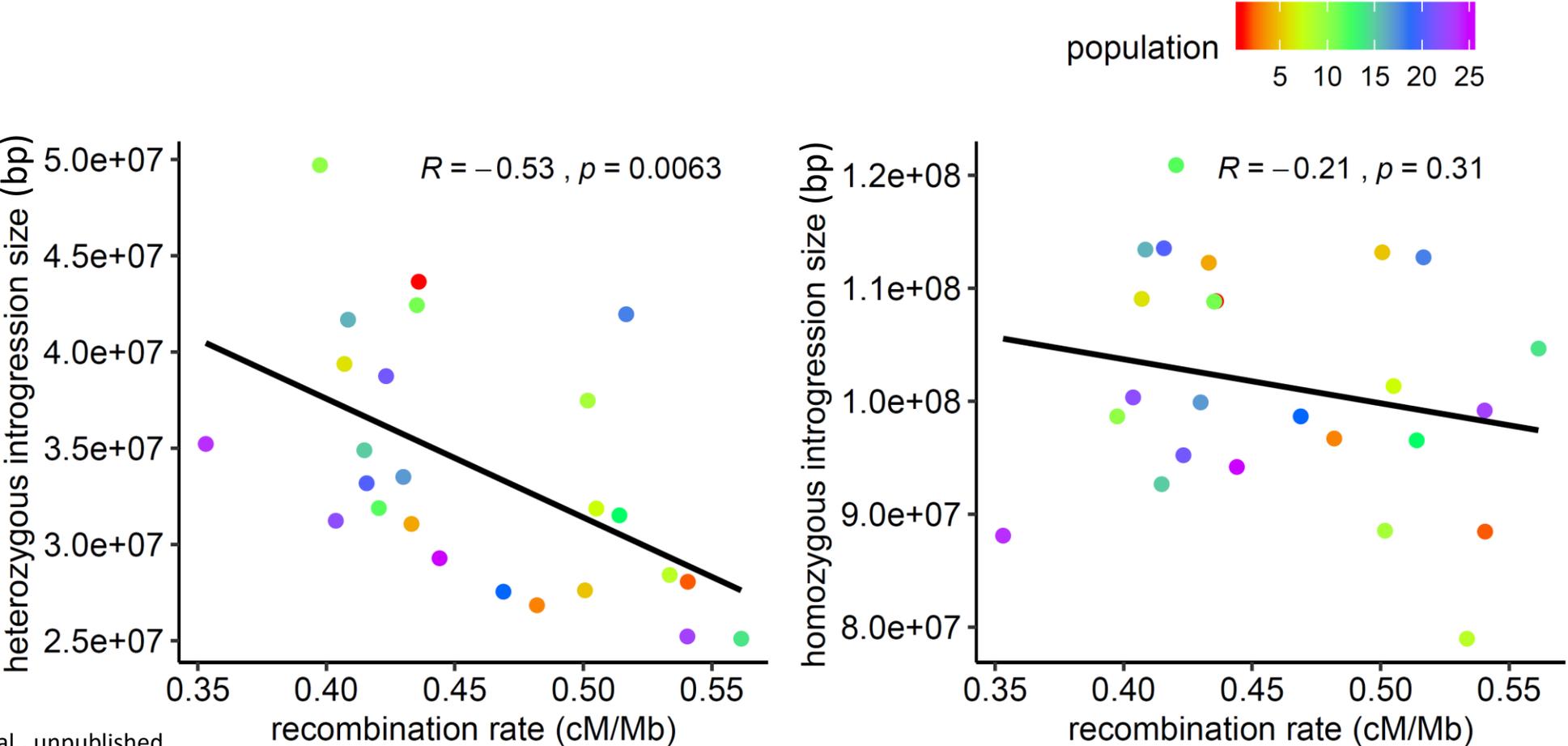
Local recombination rate variation shapes introgression patterns in intraspecific barley hybrids

- characterization of contiguous homozygous or heterozygous wild barley introgressions after 8 generations in > 1300 lines
- introgressions are smaller in high-recombining regions / larger in low-recombining regions
- local recombination rate variation has a direct effect on linkage drag



Genome-wide recombination rate variation shapes introgression patterns in intraspecific hybrids

correlation between genome-wide recombination rate and average introgression size



Summary

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Natural variation in meiotic recombination rate shapes introgression patterns in intraspecific hybrids between wild and domesticated barley.

1. recombination landscapes differ across pericentromeric regions in intraspecific hybrid populations
2. GWAS suggests *REC8* as putative candidate gene for genome-wide recombination rate modifier
3. wild barley introgressions size is shaped by local and genome-wide recombination rate variation

Acknowledgements

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