

## Genetic variation in recombination rate in the pig

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### BACKGROUND

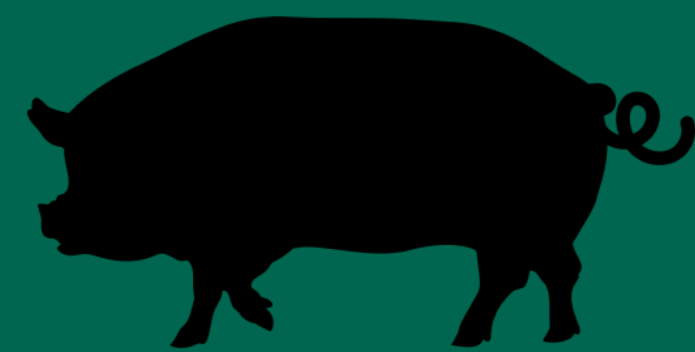
Meiotic recombination rate is genetically variable in several animals and associated with meiosis-related genes [1-2]. We want to know if this is the case in the pig.

### METHODS

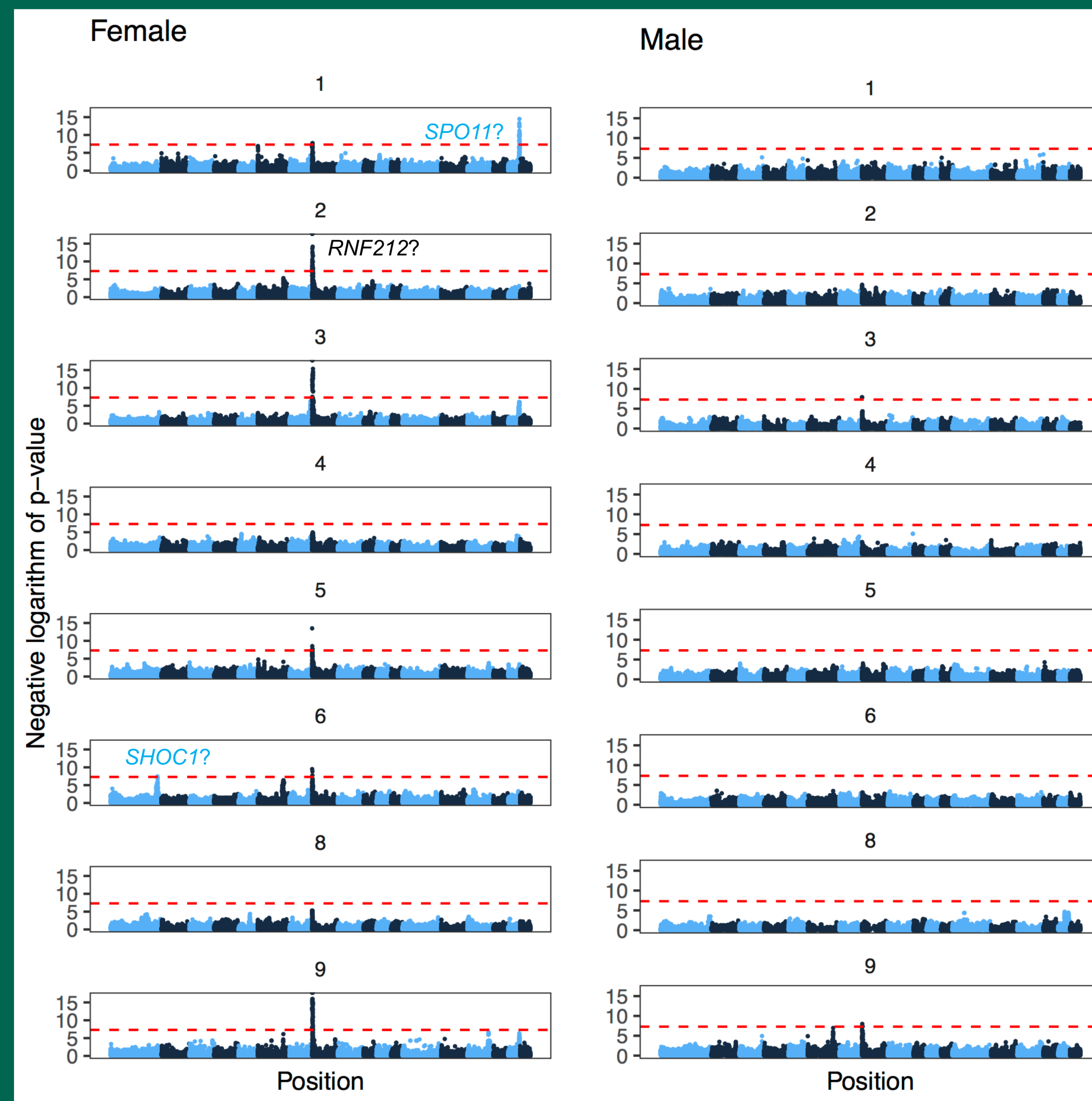
1. A new multilocus peeling method to estimate recombinations while imputing genotypes.
2. A large dataset from a pig breeding program (9 lines; estimates from 150,000 pigs).
3. Estimated heritability with animal models (MCMCglmm) and performed GWAS with a linear mixed model (RepeatAble).

### RESULTS

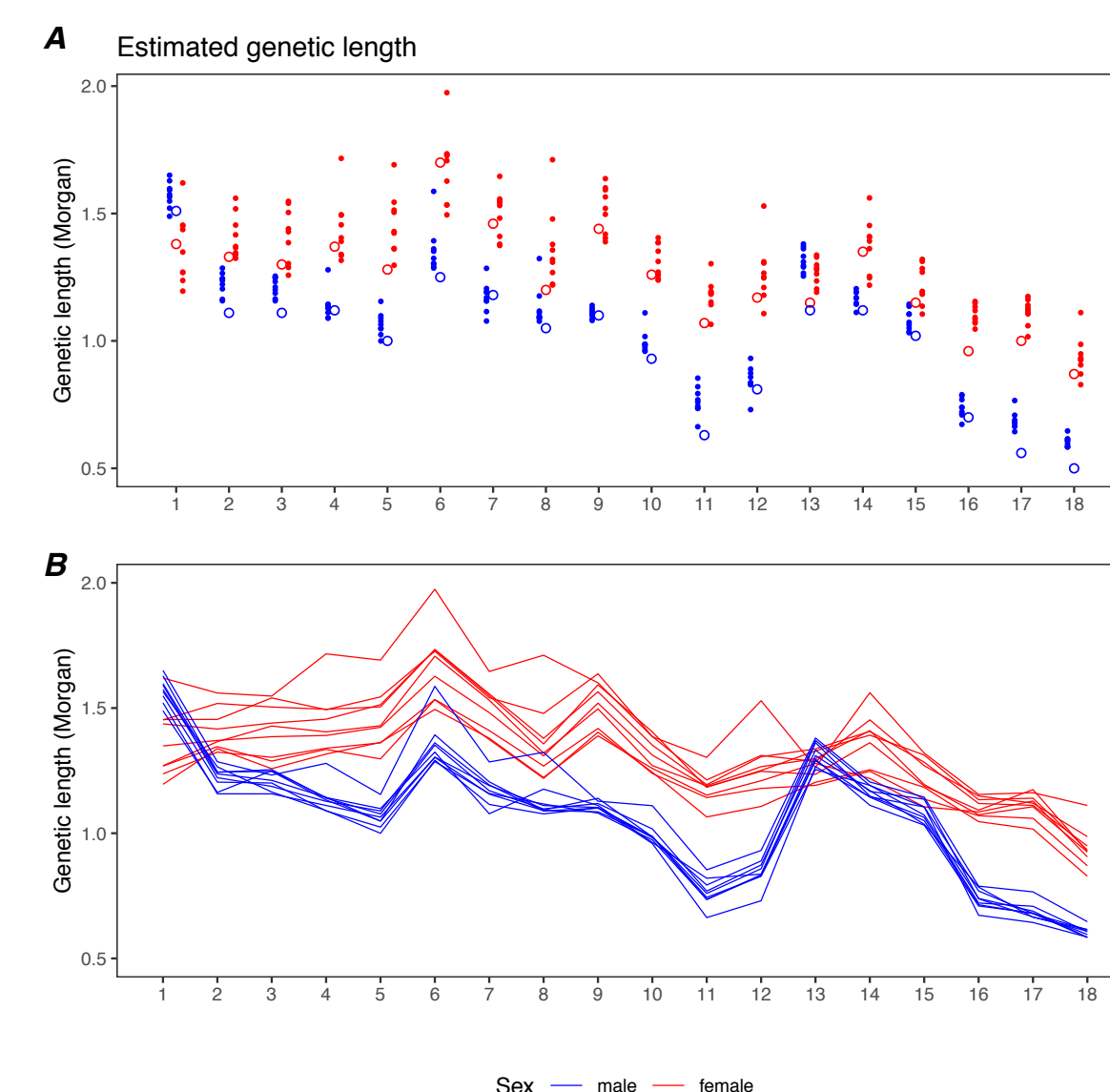
- Confirm known features of recombination in the pig, including sex difference.
- Narrow-sense heritability of 0.05 in males and 0.07 in females.
- Three associations, one of them near *RNF212*. *RNF212* is also associated with recombination in humans, cattle, sheep and chickens.



# Recombination rate in the pig is lowly heritable and associated with alleles at the *RNF212* gene.



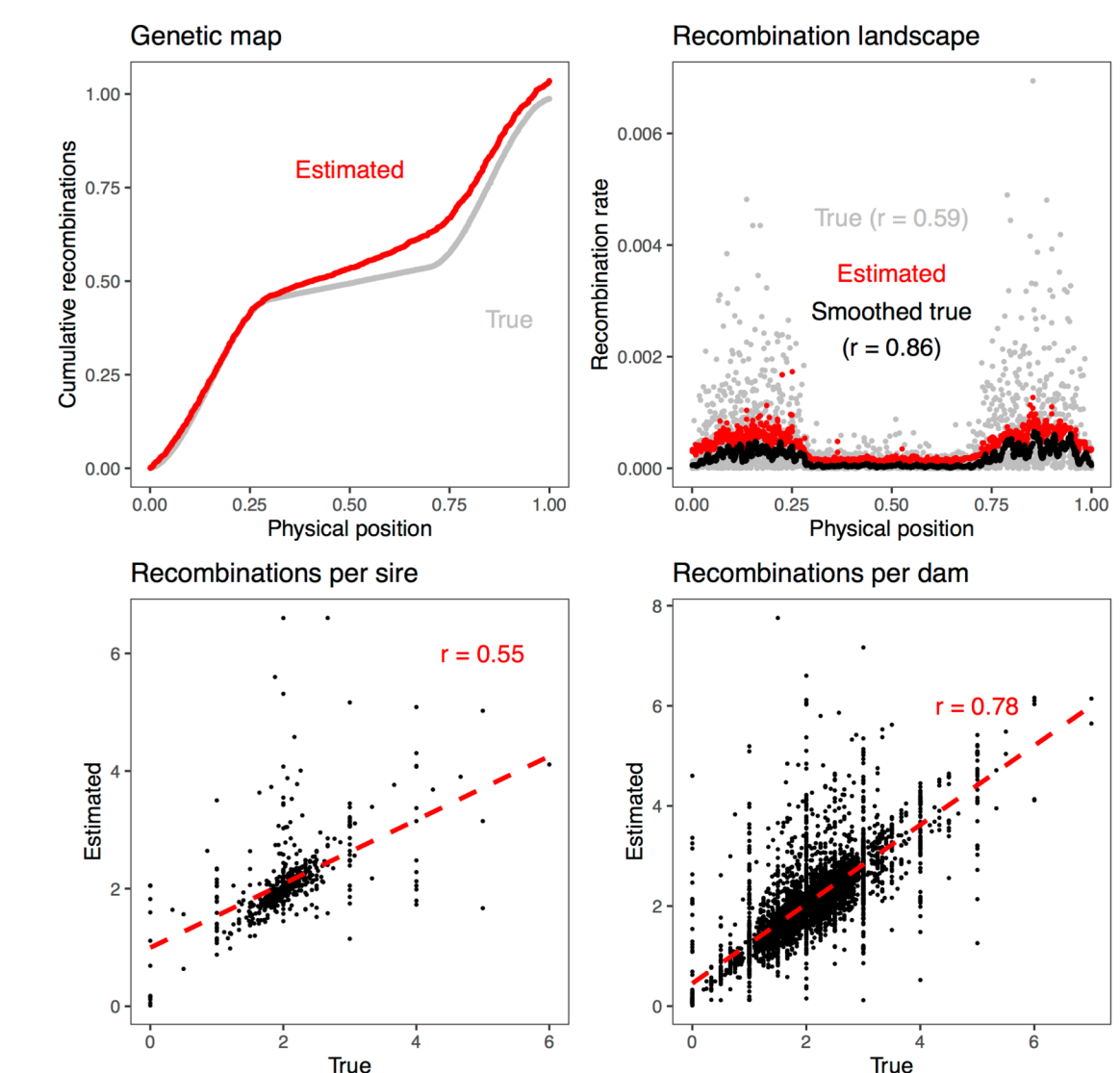
Genetic length of chromosomes in different sexes and lines. Open circles show previous estimates from [3].



We modelled recombinations at the level of dam or sire with repeated records. Resulting sample sizes:

Line	Dams	Sires
1	2651	437
2	2255	368
3	2169	215
4	1239	163
5	4349	293
6	1971	162
7	76	20
8	727	78
9	5171	492

**SIMULATION:** We tested the estimation method on synthetic data with structure similar to the largest line.



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Pig icon by Freepik from flaticon.com

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