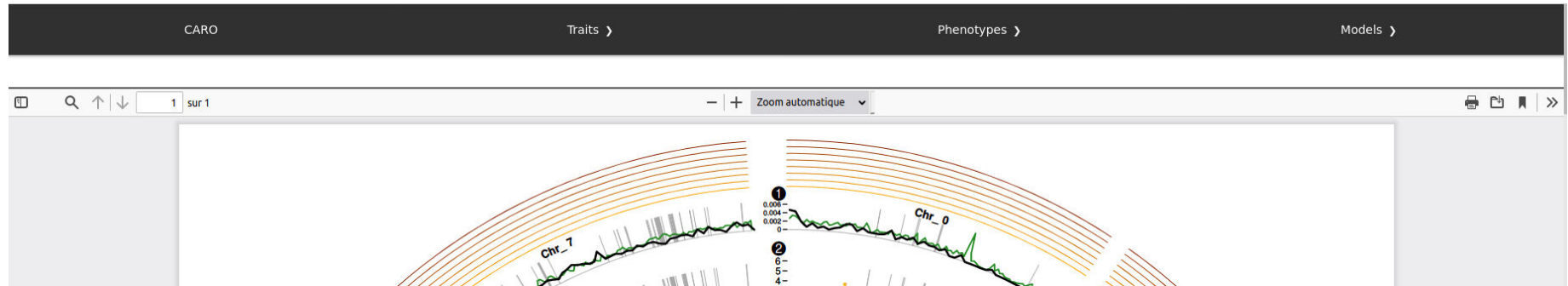


How to browse on this website

1/ First select a trait on the drop-down menu « Traits », e.g. « Black Spot »

2/ Then you will have access to a new drop-down menu « Phenotypes », « Parameters » or similar to more precisely select a phenotype of interest e.g. « Blackspot - 3 years »



3/ Then a pdf is expected to be open just below. By default, the results shown are those from the general model of GWASpoly. To know more about the GWAS poly model, see next slide.

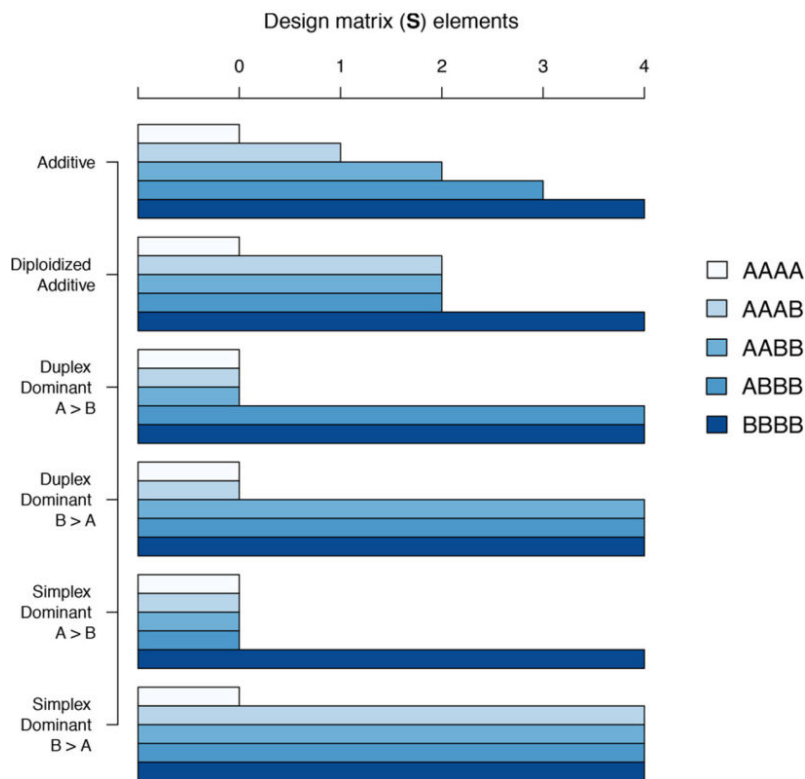
4/ To select any other model than the general model, you now have access to a new drop-down menu (« Models »), you can for instance select « additive »

Why should I select between different models ?

It is important to note that a GWAS on polyploids creates an additional degree of complexity regarding the genetic dominance of the trait.

Note that here all our 204 rose genotypes were genotyped as tetraploid (most genotypes are indeed truly tetraploids). At each SNP, each individual has 5 possible classes of alleles B {0, 1, 2, 3, 4} depending on the observed dosage levels of allele B.

i.e. AAAA, AAAB, AABB, ABBB or BBBB



The general model is a simple model where the SNP effect can be on any of the classes. This model generally show a lot of associated SNPs (and is therefore quite noisy)

The other models are more specific regarding the dominance (see opposite and the GWASpoly paper for details)

How to read the results?

