



GENOME-WIDE ASSOCIATION STUDY OF INFECTIOUS PANCREATIC NECROSIS IN TWO SUCCESSIVE GENERATIONS OF RAINBOW TROUT

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GENOME-WIDE ASSOCIATION STUDY OF INFECTIOUS PANCREATIC NECROSIS IN TWO SUCCESSIVE GENERATIONS OF RAINBOW TROUT

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Aims of the study

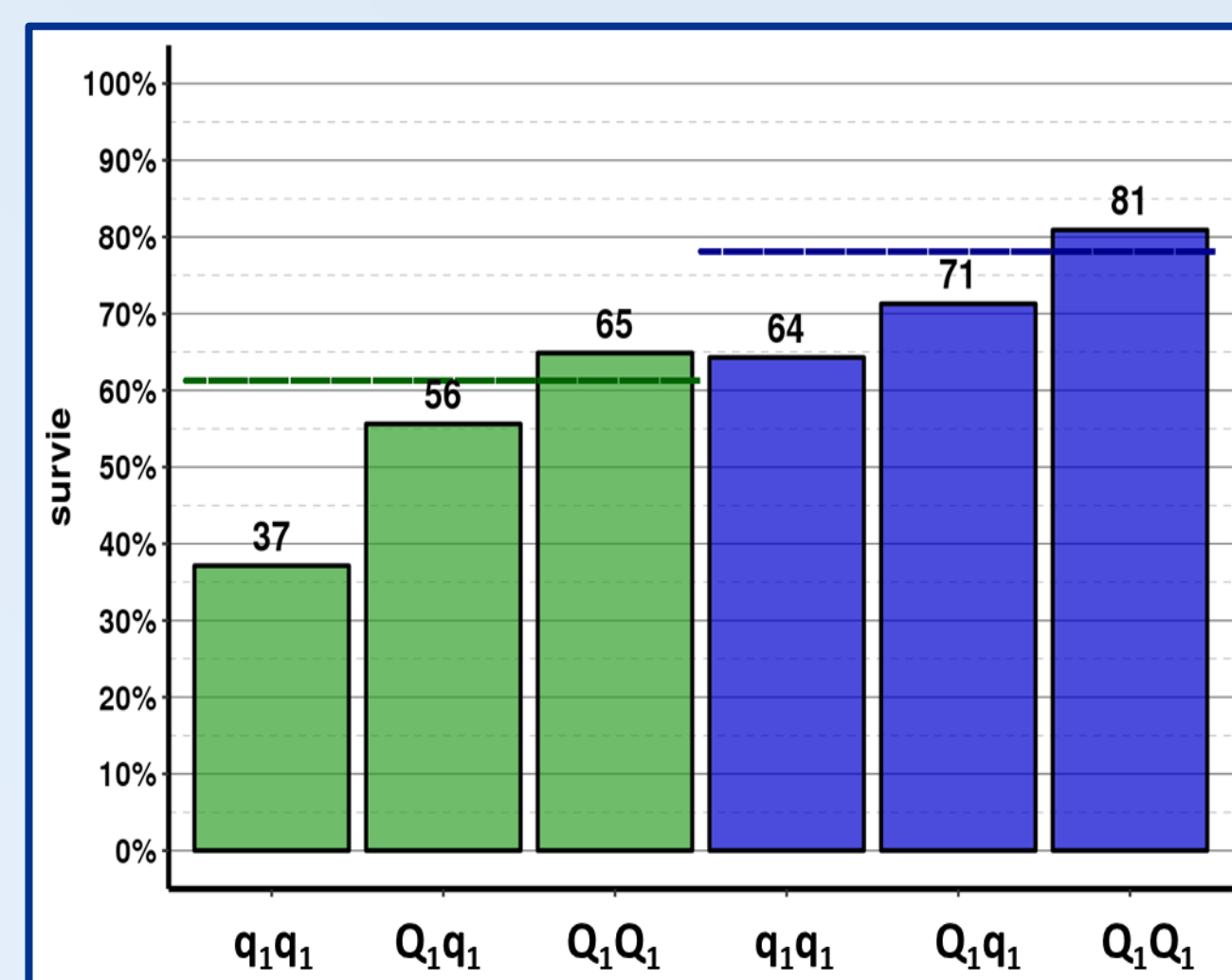
- ❖ Moderate heritability was estimated for Infectious Pancreatic Necrosis (IPN) resistance. However, there is little work to precisely characterize the architecture of IPN resistance in rainbow trout and **previous analyses only included a single cohort of phenotyped fish.**
- ❖ Therefore, the two objectives of this study were to **estimate heritability** and to **detect quantitative trait loci (QTLs)** associated with IPN resistance **in two successive generations of a commercial French rainbow trout line.**

Material & methods

- ❖ Challenge : 4,000 fish were derived sibs from the Bretagne Truite multitraits breeding program challenged by immersion with IPN virus at the ANSES-SYSAAF Fortior Genetics platform.
- ❖ 3,885 fish and their 372 parents were genotyped with Axiom™ Trout Genotyping array (57K SNP).
- ❖ After quality control : 1,799 and 1,978 phenotyped and genotyped (for 25,512 SNPs) fish of two successive cohorts were retained.
- ❖ IPN resistance was calculated as a survival trait (dead/alive at 37 days).
- ❖ BLUPf90 package was used for the analysis.
- ❖ **First cohort (C1)** is represented in **green color** and **second cohort (C2)** in **blue color** in following figures.

Survival of fish according to status in QTLs

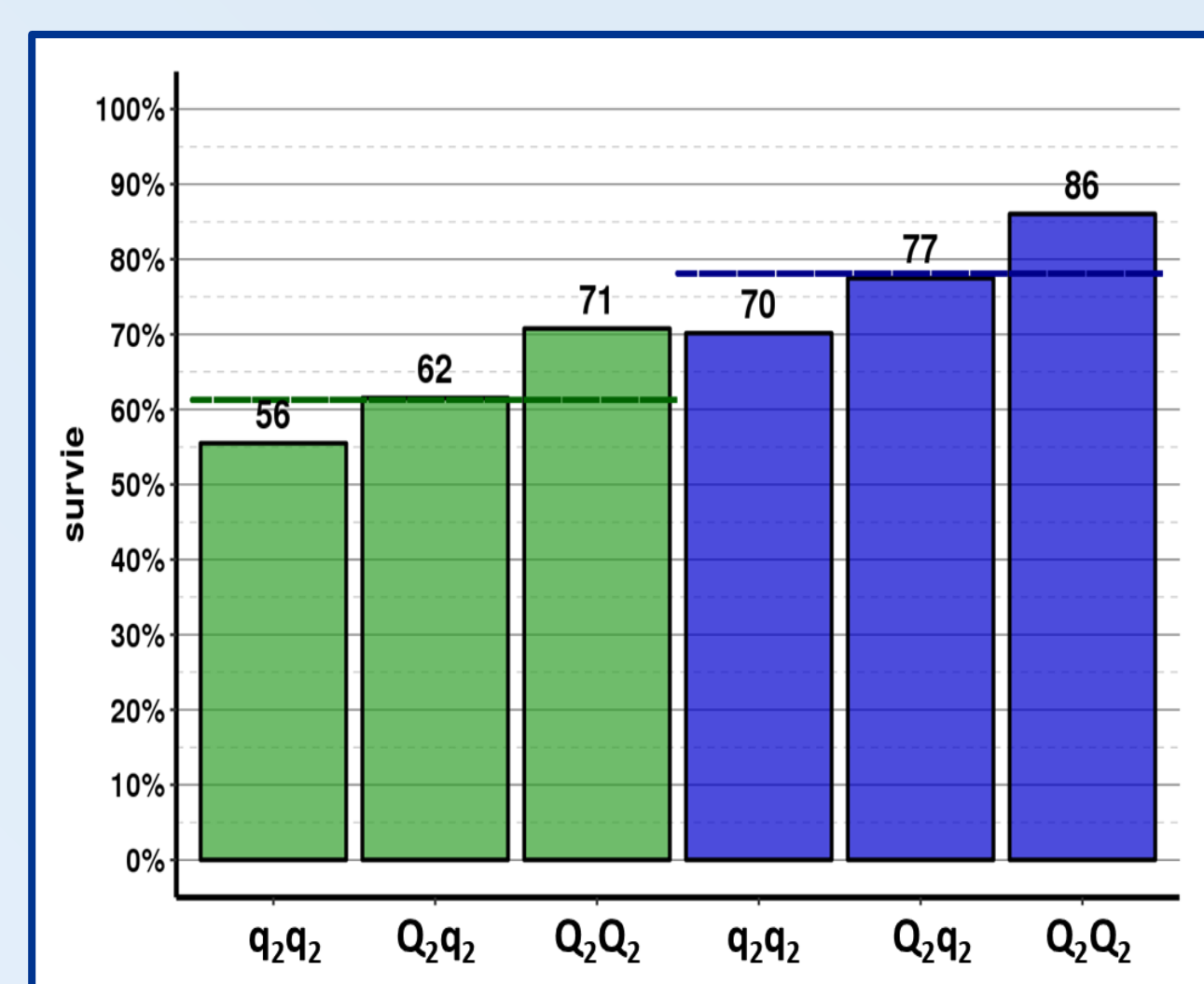
❖ Chromosome 1



➤ For C2, survivals of Q₁Q₁ and Q₁q₁ fish are respectively +27% and +11% greater than q₁q₁ trout survival.

Percentage of survival of fish according to their genotyping. Horizontal lines represent the average survival rates for each challenge.

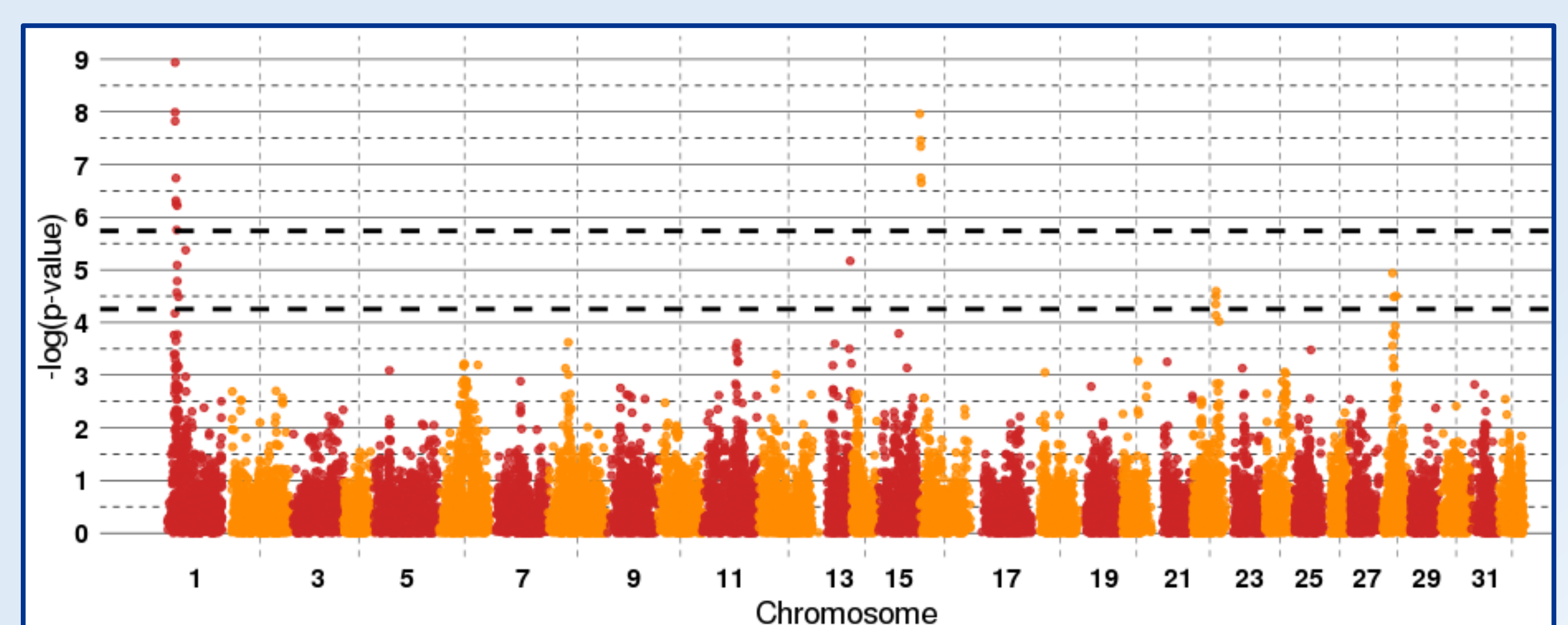
❖ Chromosome 16



➤ For C2, survivals of Q₁Q₁ and Q₁q₁ fish are respectively +23% and +10% greater than q₁q₁ trout survival.

Genetic architecture

➤ Moderate heritability for survival : $h^2 = 0,20$

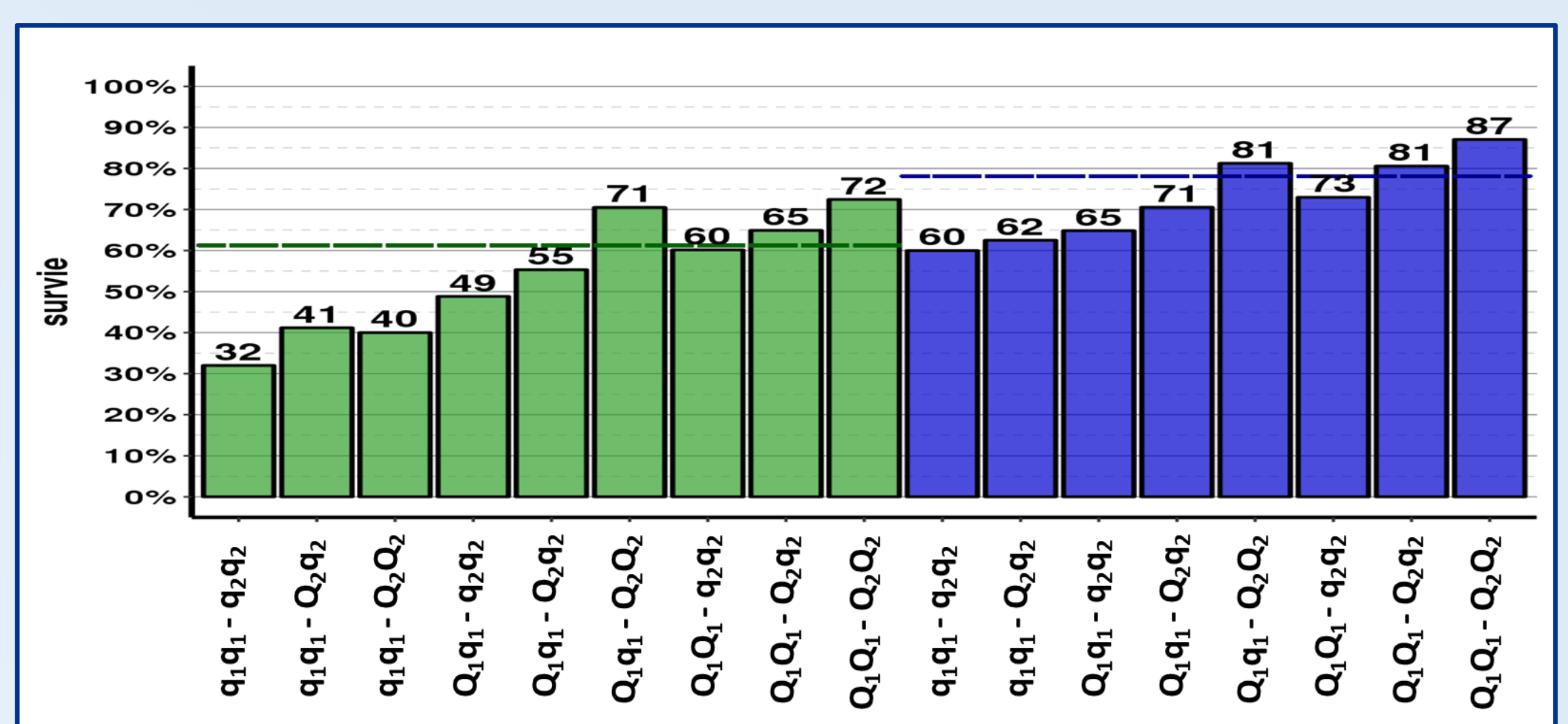


Manhattan plot showing associations between SNPs and IPN resistance. Lines correspond respectively to 1% chromosome-wide and 1% genome-wide significance thresholds (after Bonferroni correction).

- Two main QTLs for survival on chromosomes 1 and 16
- These QTLs were also observed in the two analyses of each fish cohort

Survival of fish with combination of QTLs

➤ Chromosome 1 & chromosome 16



Percentage of survival of fish according to their genotyping. Horizontal lines represent the average survival rates for each challenge.

- The association of favorable alleles across QTLs allows a small additional increase in survival.

Conclusion

- We confirm two significant and additive QTLs located on chromosomes 1 and 16. They were already identified in the literature as playing a role on IPN resistance (Santi et al. 2019; Ozaki et al. 2007).
- The two QTLs are observed in each of the two studied cohorts and are therefore consistently segregating QTLs in the population.
- These QTLs offer the possibility of marker-assisted selection for rapid dissemination of genetic improvement for IPN resistance of rainbow trout.