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Climate, heat-stress, and genetics impact whole-blood gene expression levels in crossbred pigs

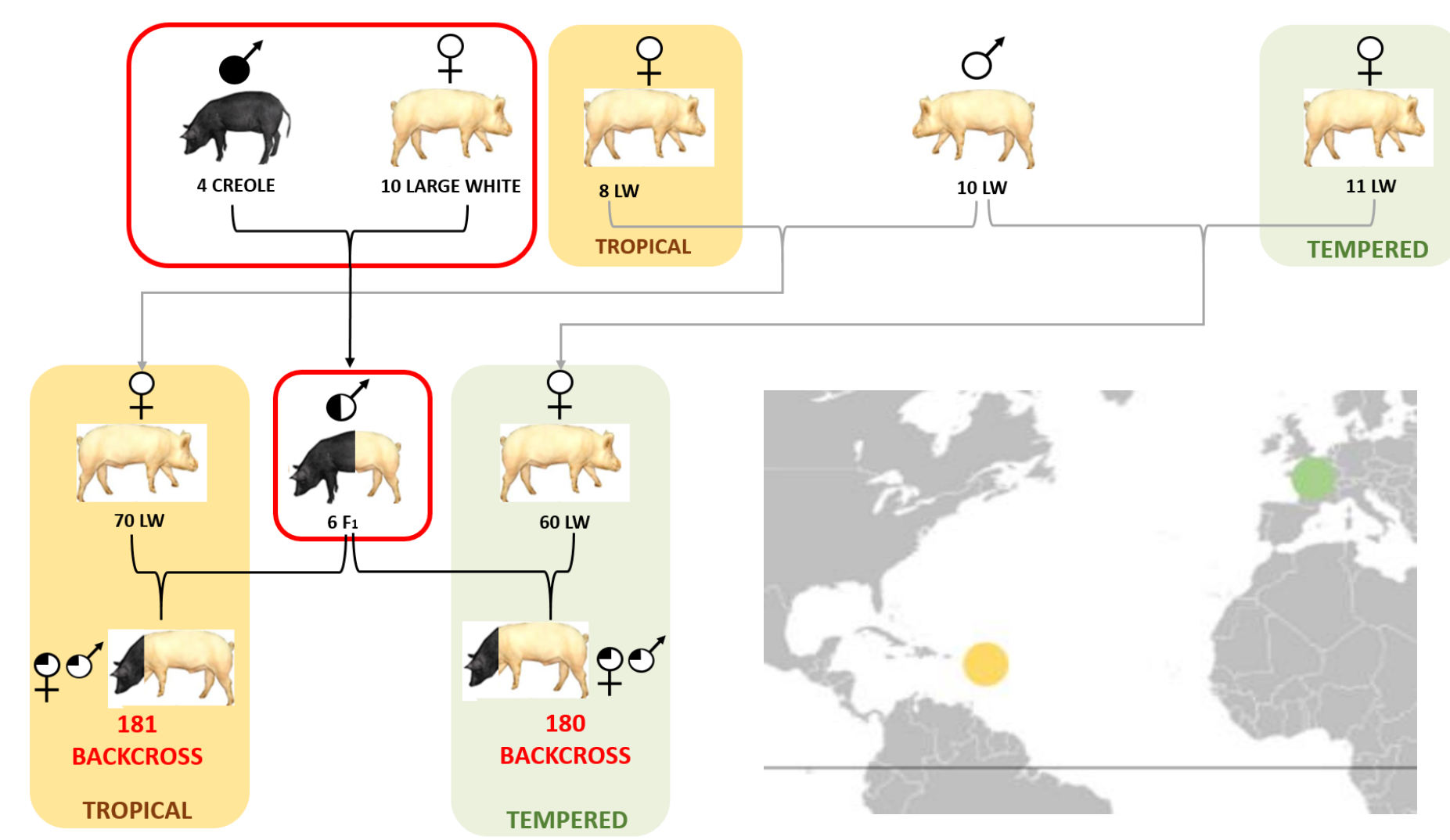
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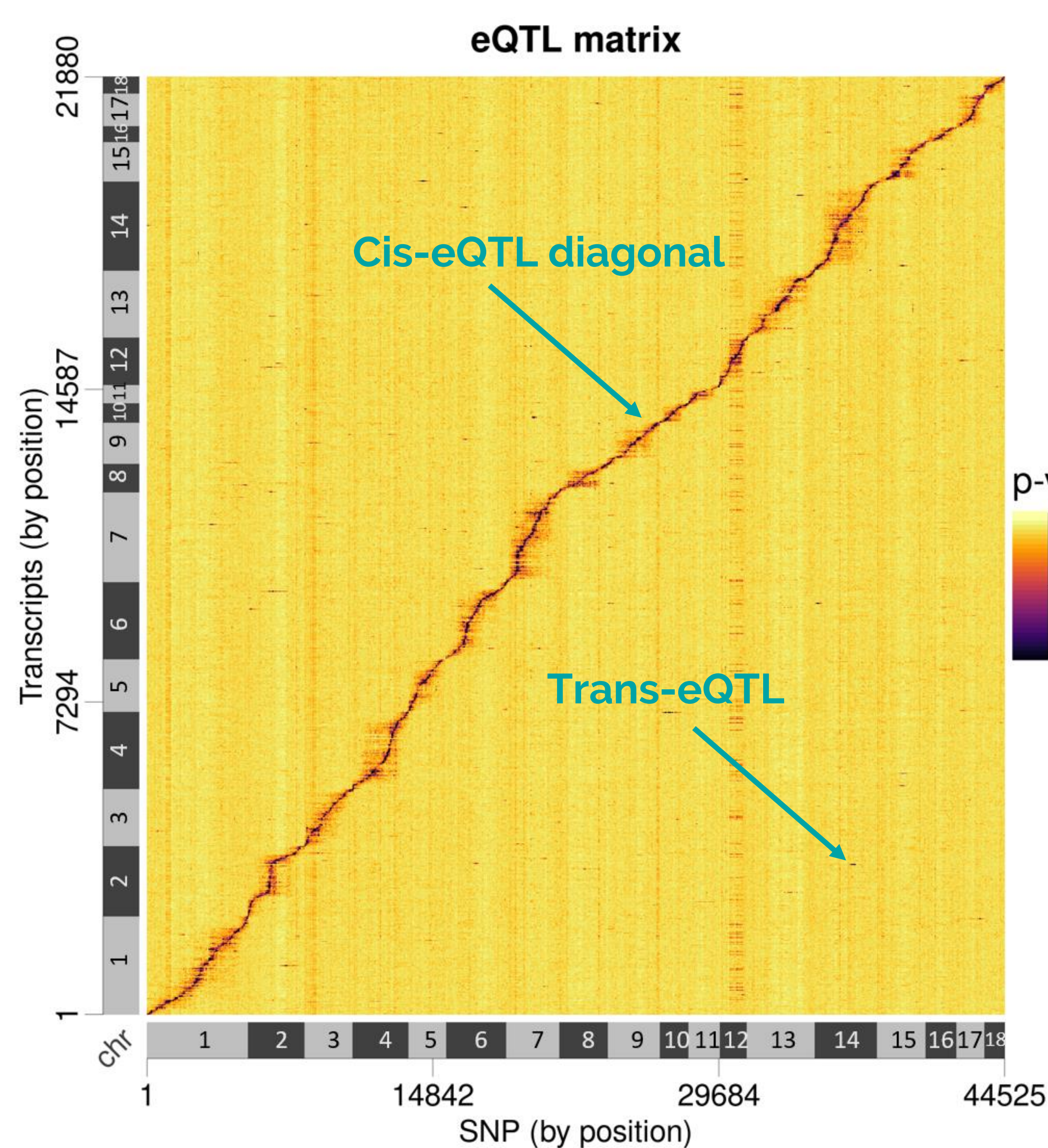
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Summary:

As global warming becomes more potent, heat waves and overall temperature increase causes damage to agronomical systems. Excessive heat causes animal welfare and production complications within developed and developing countries. INRAE designed an experimental cross to study the genetic basis of heat sensibility in pigs. This cross was between the cosmopolitan **Large-White** race (industrially selected for its growth capacity) and the **Creole** race, from Guadeloupe, and adapted to tropical environments. Crossbred offsprings were raised in two distinct climates (**n=180 per environment**). Here, we focus on the effects of genetics, climate and heat-stress on gene expression levels in the whole blood



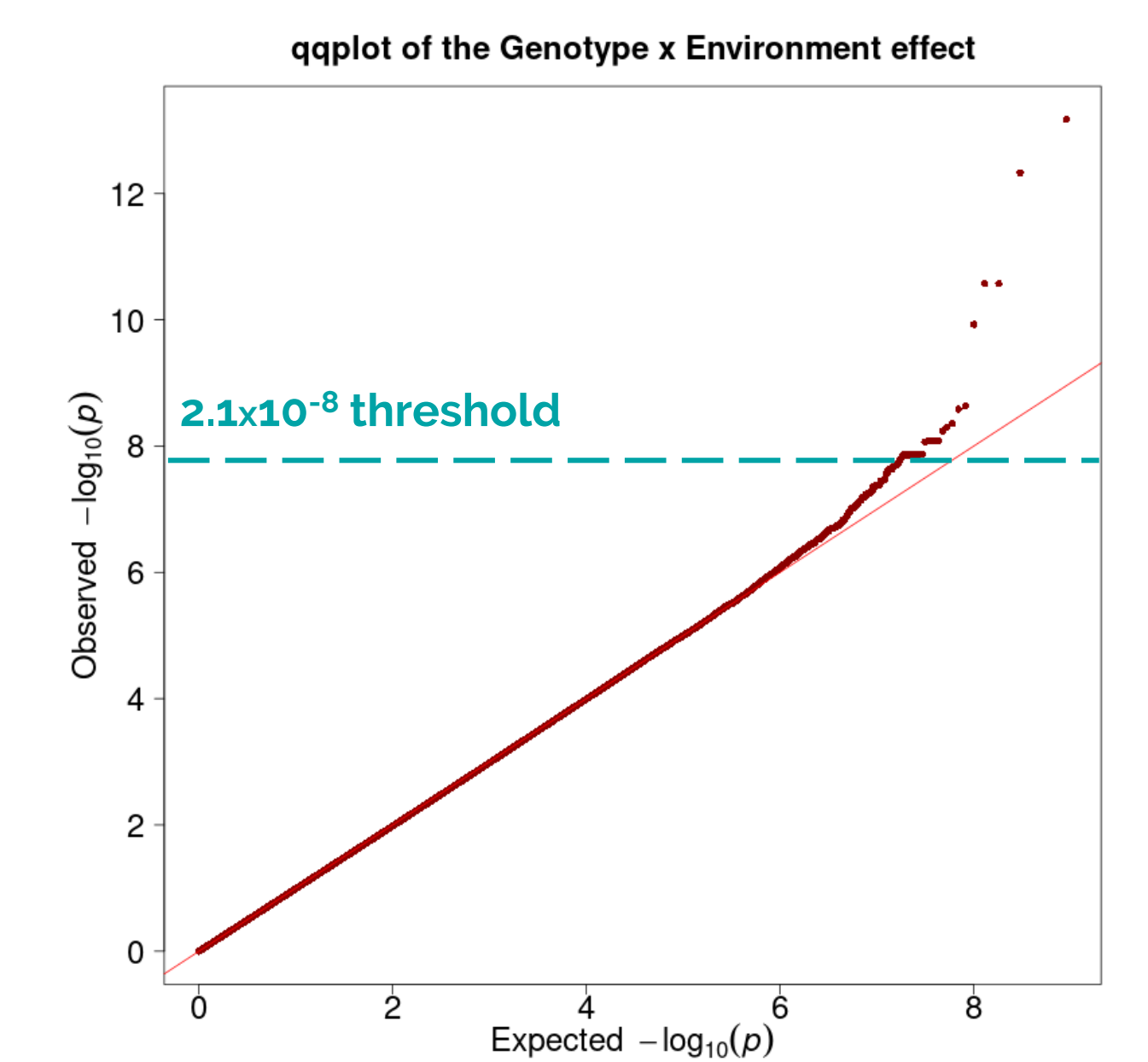
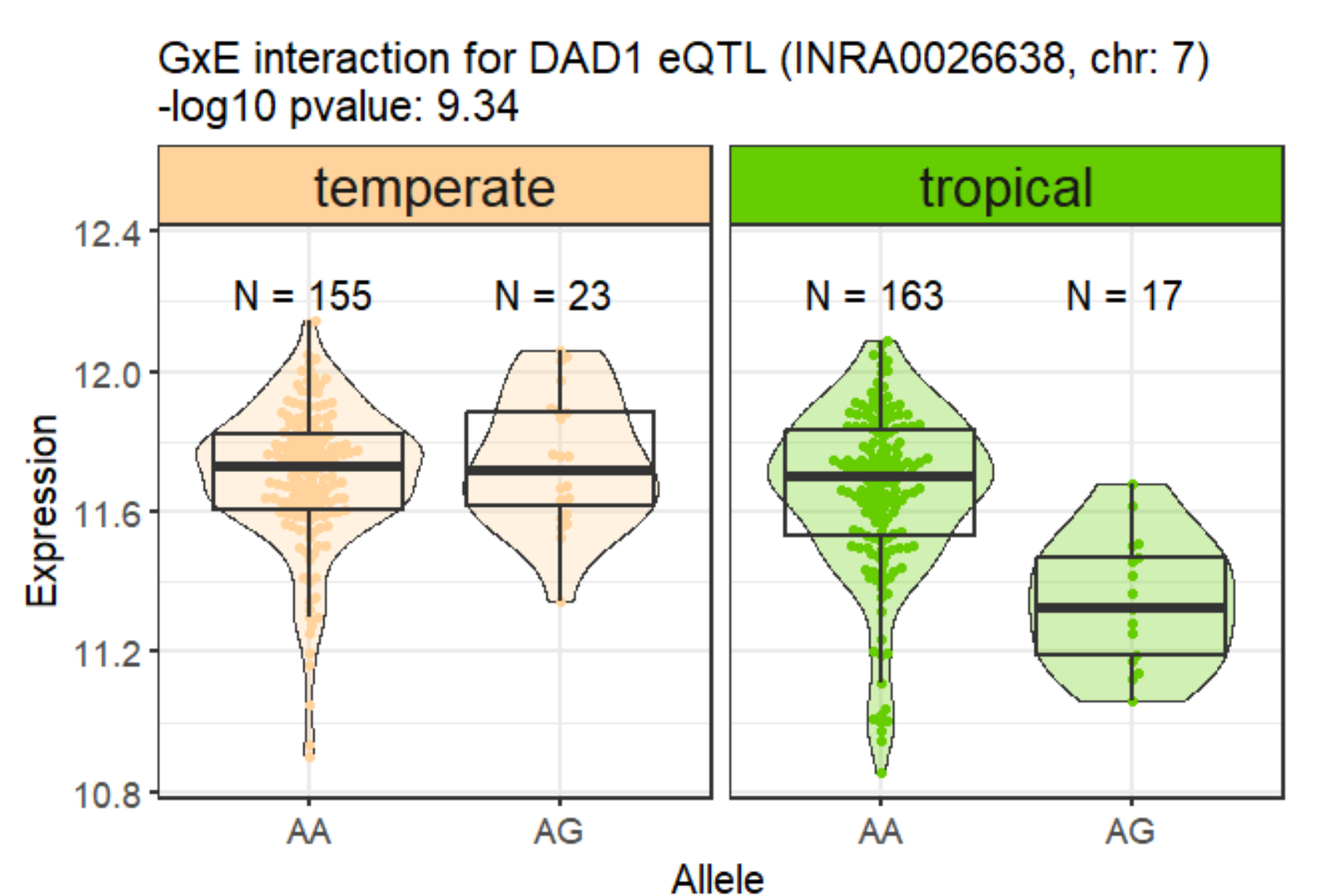
eQTL detection & GxE interactions:



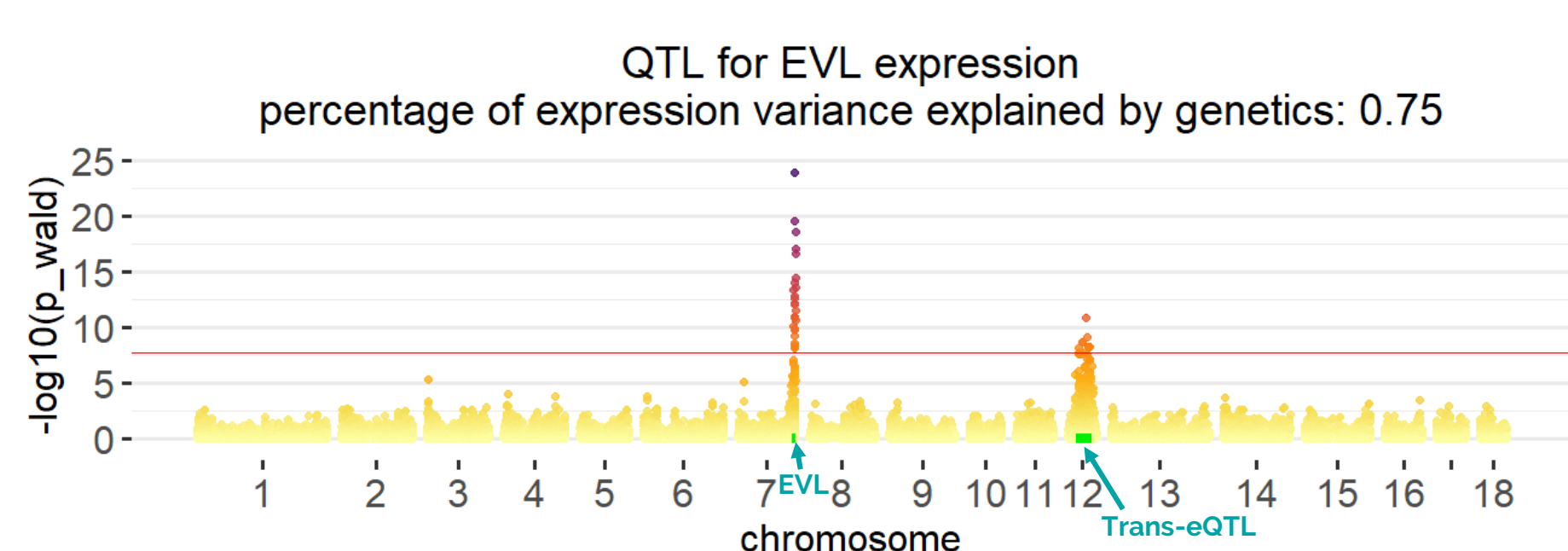
➤ We identified **7139 expression QTL** over a genome-wide significant level of **2.1×10^{-8}** . Amongst those were **4607 cis-eQTL** (eQTL within 10 Mb of the associated gene) and **1448 trans-eQTL** (distal from the associated gene).

➤ Genotype x Environment (GxE) Interactions are defined by **dissimilar genetic effects between environments**.

➤ **43 genes** were detected to be affected by GxE interactions.

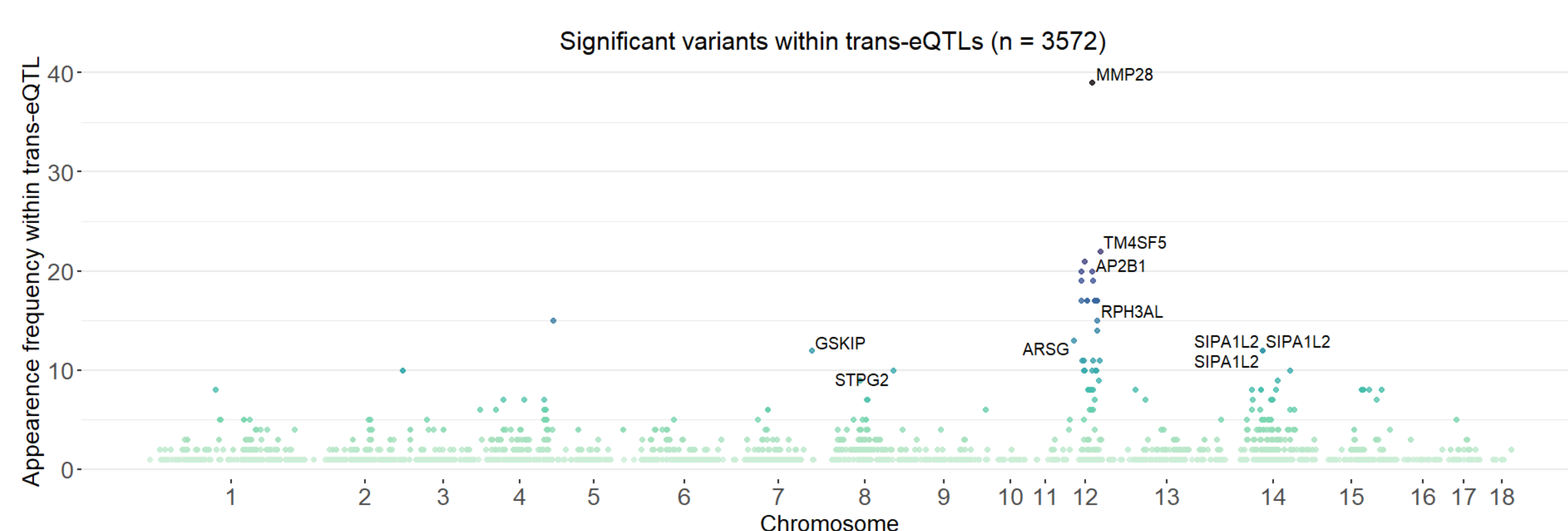


Trans-eQTL:

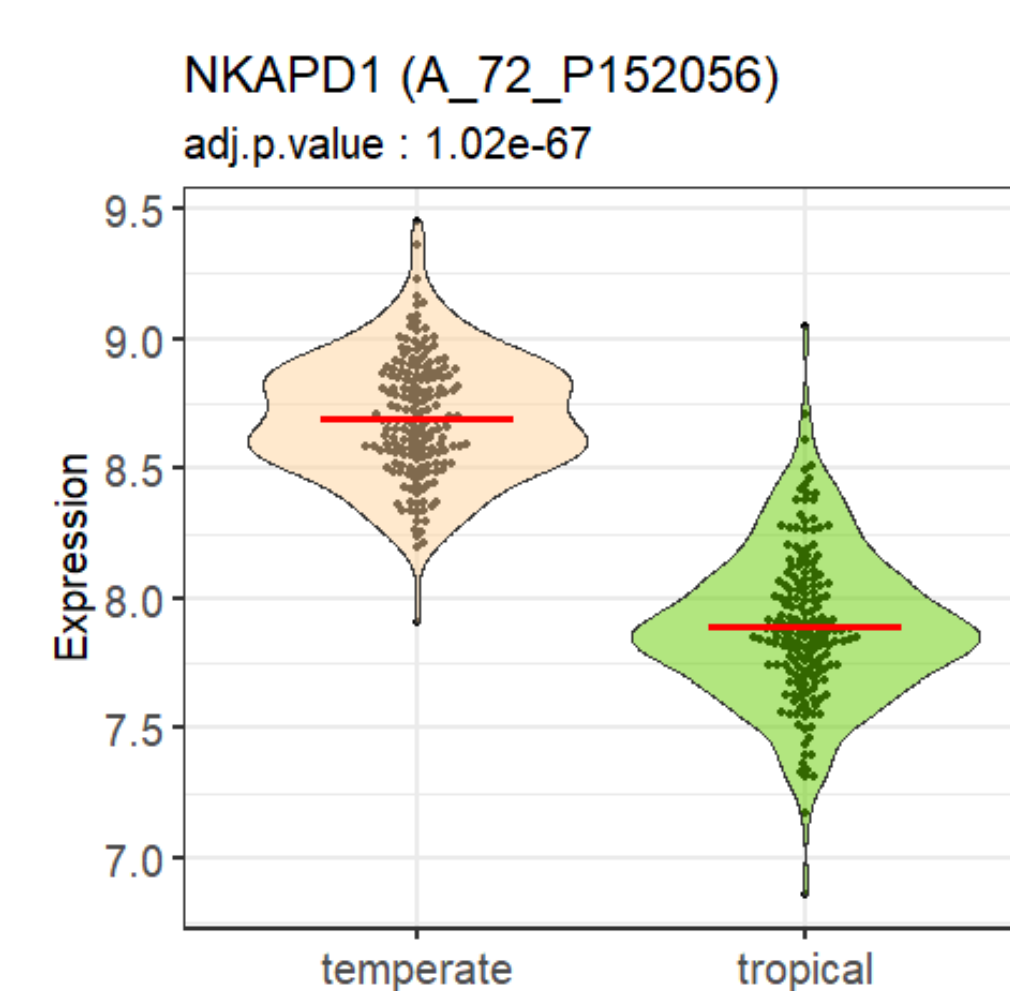


➤ **EVL** is an example of genes with a cis-eQTL and a trans-eQTL located on the chromosome 12.

➤ We identified **89 genes associated with trans-eQTLs on chromosome 12**. **39 of them shared a statistically significant SNP** located within the MMP28 gene. MMP28 was previously identified as a QTL for cell proliferation during epithelial repair (Saarialho-Kere *et al.*, 2002).



Difference in gene expression:



➤ Differential expression analysis reveals **3531 genes** whose **expression vary based on the environment**.

➤ Similar analysis were performed over an experimental heat-stress of pigs living in tempered environment.

➤ Experimental heat stress led to a transcriptomic signature distinct from the transcriptomic signature of pigs living in tropical climate

