

## Diversity and transcriptome analysis of the maize B chromosome

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B chromosomes are enigmatic elements in thousands of plant and animal genomes that persist in populations despite being nonessential. Maize (*Zea mays* L.) is one of the most important crops and serves as well established model for biological research and the maize B chromosome has been studied for many decades. However, the diversity of the maize B chromosome and its distribution within maize landraces are still not thoroughly described as well as its gene expression. Reference sequence of the maize B chromosome revealed 758 protein coding genes (Blavet et al., 2021). Here we present the first results of a gene expression atlas of 12 maize tissues using RNA-seq and gene expression pipeline based on mapping reads to the reference genome of *Z. mays* (B73 RefGen\_v4) supplemented with the reference of the maize B chromosome (Zm-B73\_B\_CHROMOSOME\_MBSC-1.0, Blavet et al., 2021) and subsequent differential-expression (DE) and gene ontology (GO) enrichment analyses.

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### **References:**

Blavet *et al.* (2021) Sequence of the supernumerary B chromosome of maize provides insight into its drive mechanism and evolution. *PNAS* 118 (23): e2104254118