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# TEs as a major driver of genomic variation in trees? Jumping MITEs in common beech revealed by TIPs and eccDNA

Abirami Soundiramourtty, Lauren Clement, Christel Llauro, Olivier Panaud,  
Christophe Plomion, Jean-Marc Aury, Marie Mirouze

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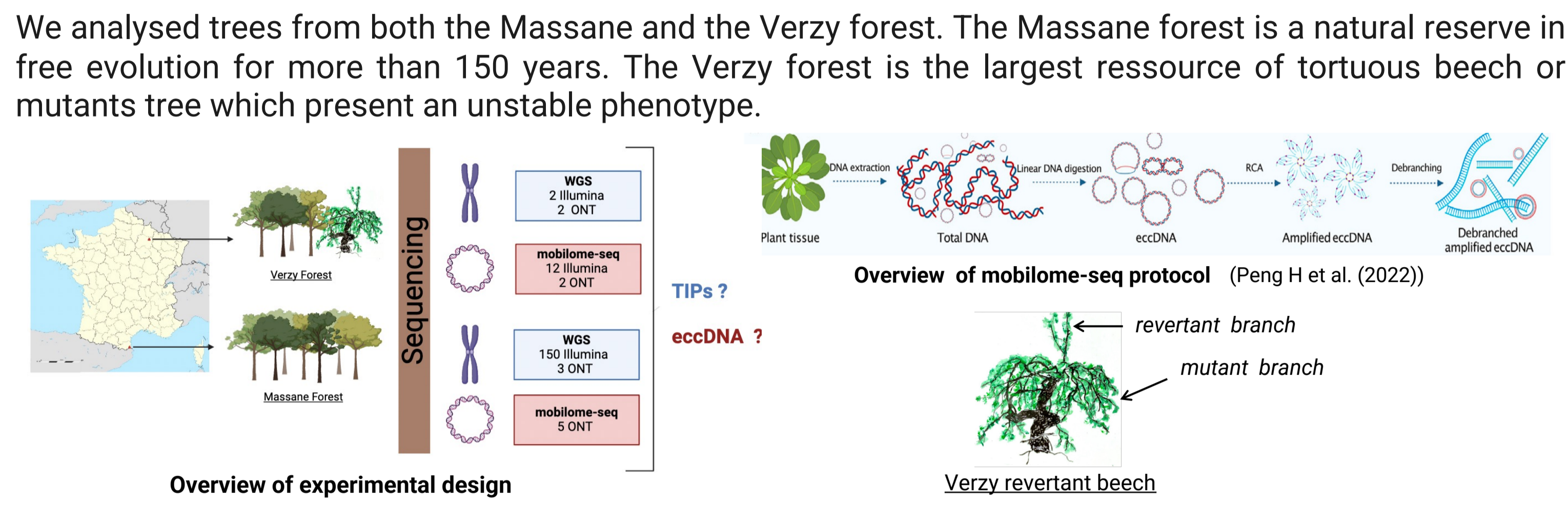


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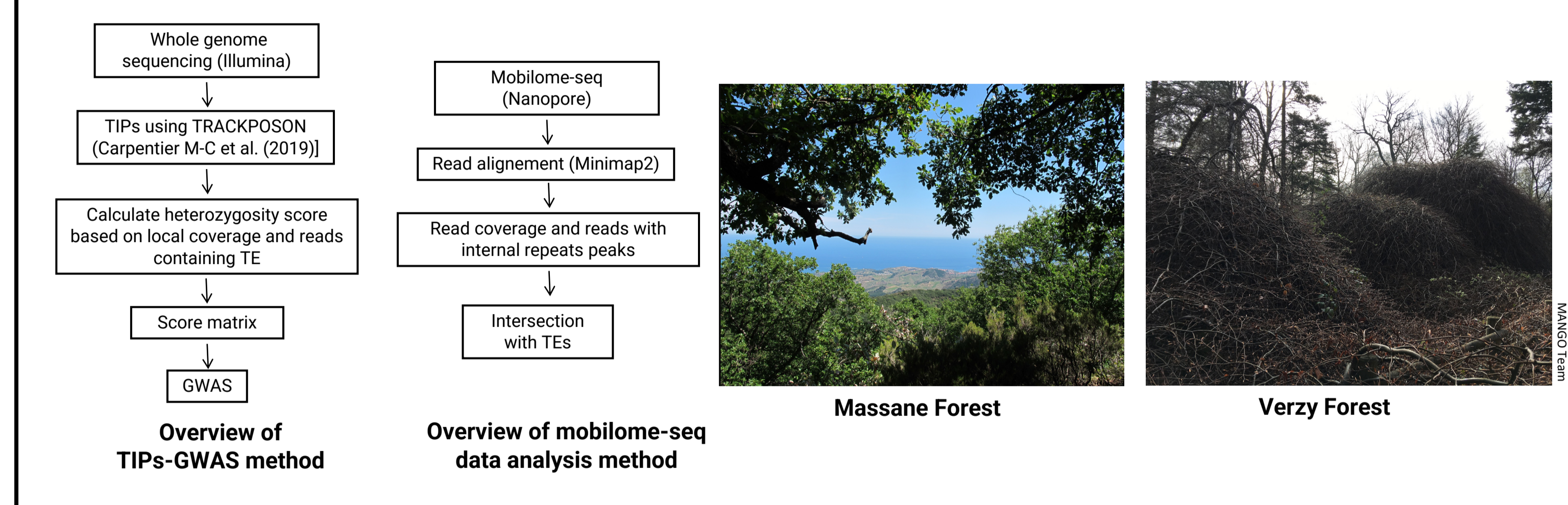


Transposable elements (TEs) are predominant in most plant genomes but their impact and activity has been mostly studied in annual species. Beech trees (*Fagus sylvatica*) make up most of European forests and are highly threatened by drought and climate change. We sought the investigation of the genomic diversity caused by TEs and their adaptive potential in this long-living species. We aimed at characterizing **Transposable Element Insertion Polymorphisms (TIPs)** playing key roles in genome evolution by analysing TIPs in a single population of 147 common beech trees, using 672 Long Terminal Repeats Retrotransposons (LTR) and 558 Miniature Inverted Transposable Elements (MITEs) families. We further analysed somatic structural variants (SV) generated by TEs. Given the high level of very recent TE activity in common beech, we investigated ongoing TE mobility using **extrachromosomal circular DNA (eccDNA)** sequencing or mobilome-seq, eccDNA being a useful proxy for identifying active TEs.

## Experimental design

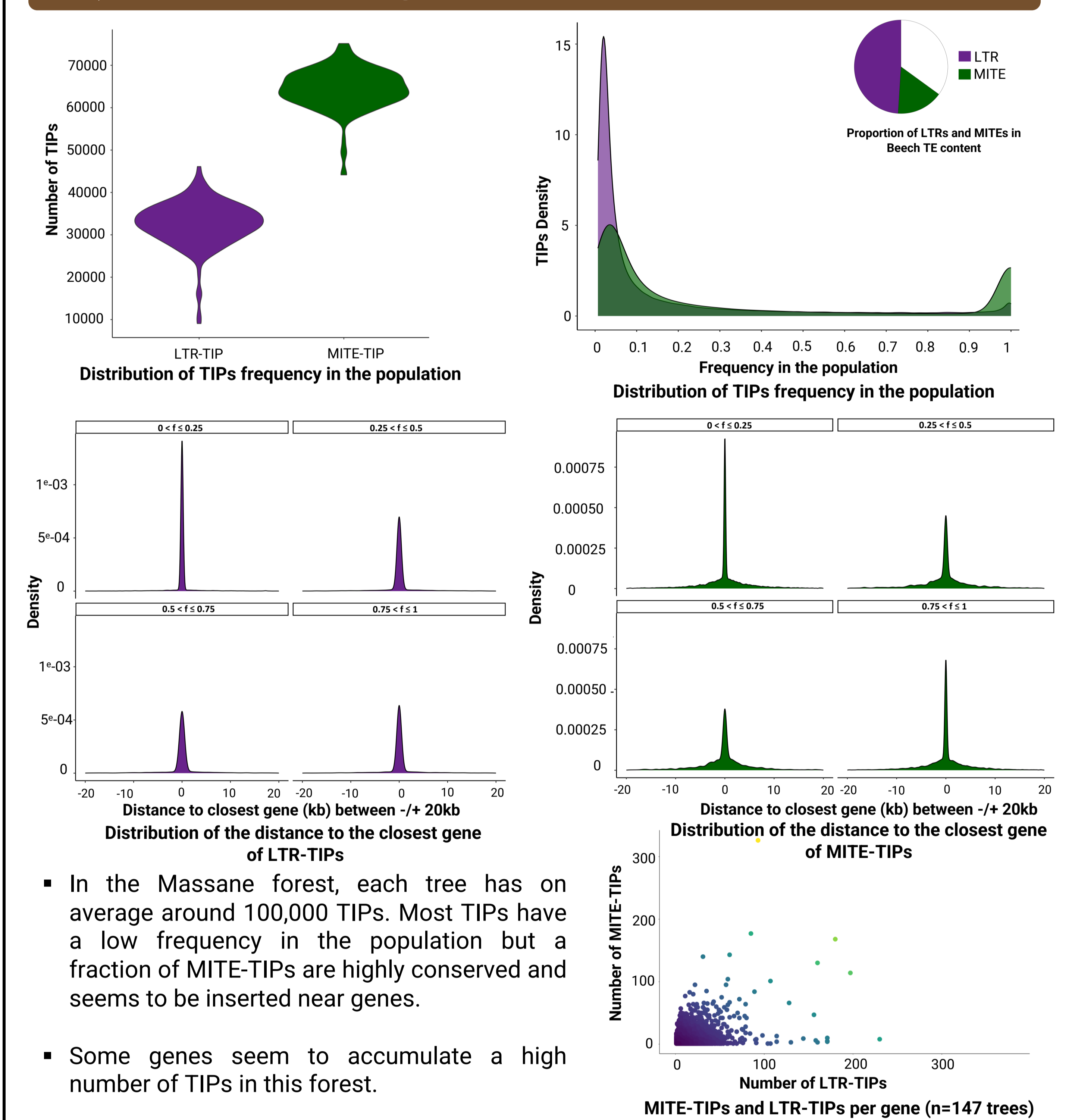


## Methods

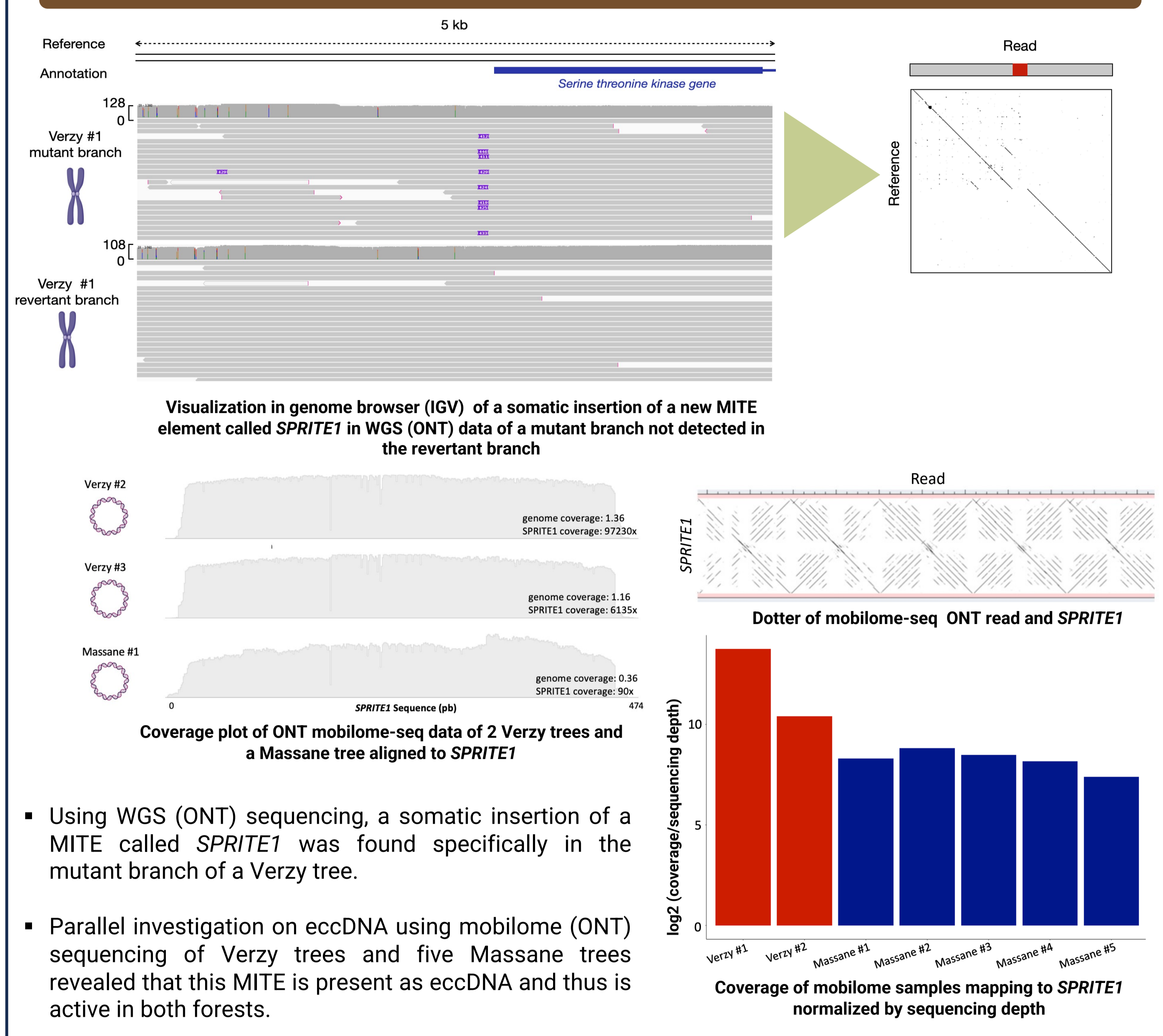


## RESULTS

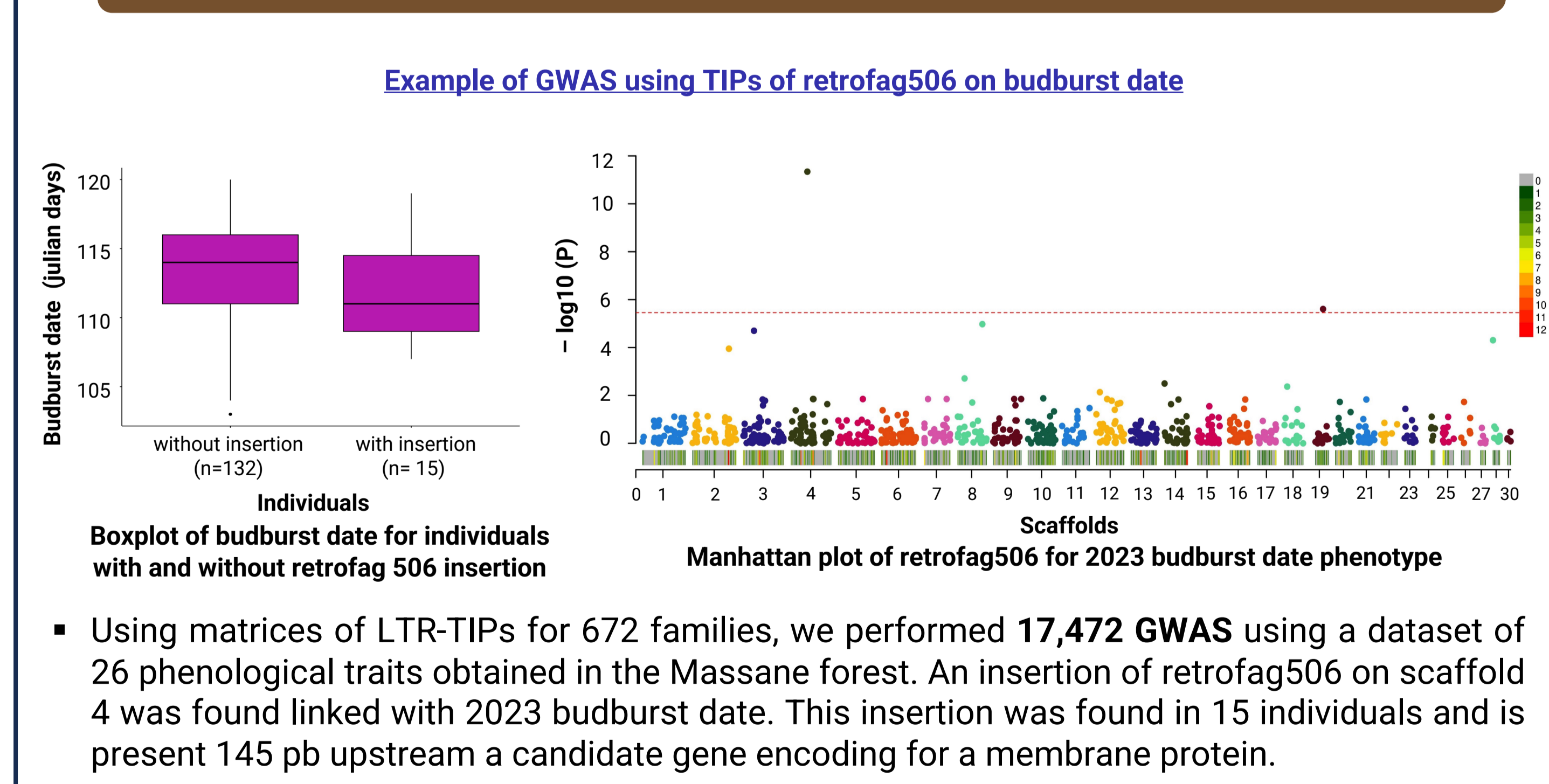
### 1) TIPs as a motor of genomic variation in the Massane forest



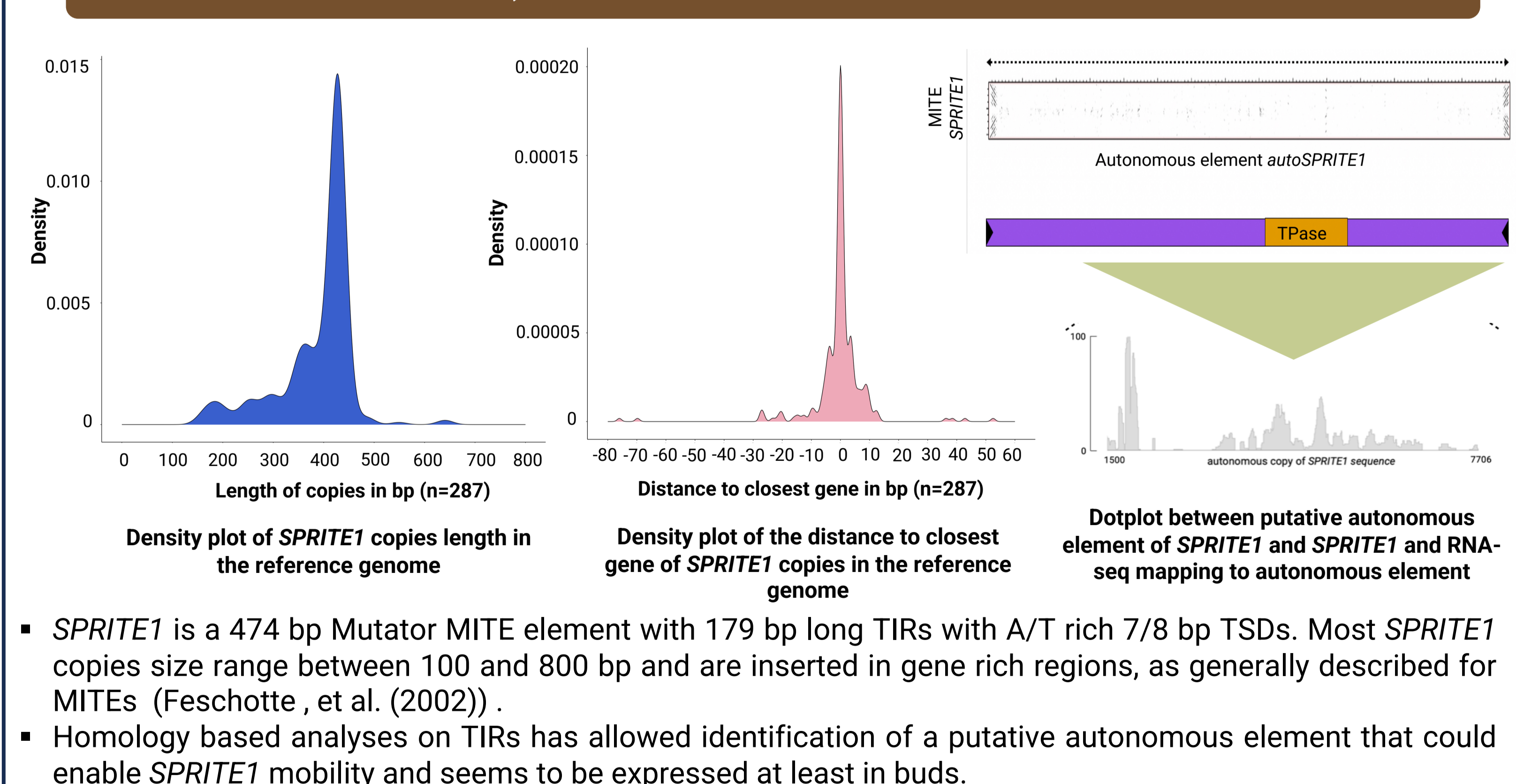
### 3) An active TE generates a somatic insertion in the Verzy forest



### 2) TIPs involved in adaptative phenotypic variation



### 4) Characterisation of SPRITE1



## CONCLUSION

- In our study, using a population of 147 beech trees, we identified around 100,000 TIPs on average in each tree generated by 1230 LTRs retrotransposons and MITEs families. We showed that most of the **TIPs are low frequency** possibly representing recent insertions. We also identified an potentially adaptive insertion in Massane.
- Using trees with somatic phenotypic variation from Verzy, we identified an active MITE called *SPRITE1* causing **somatic mutation**. Using eccDNA as a proxy, we found that this **MITE is still active** in 2 very distinct forests. This study sheds light on how TEs could impact genome evolution and adaptation in perennials non model species such as woody trees.

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