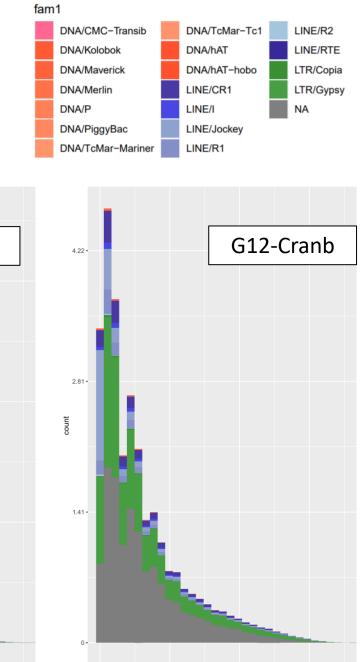
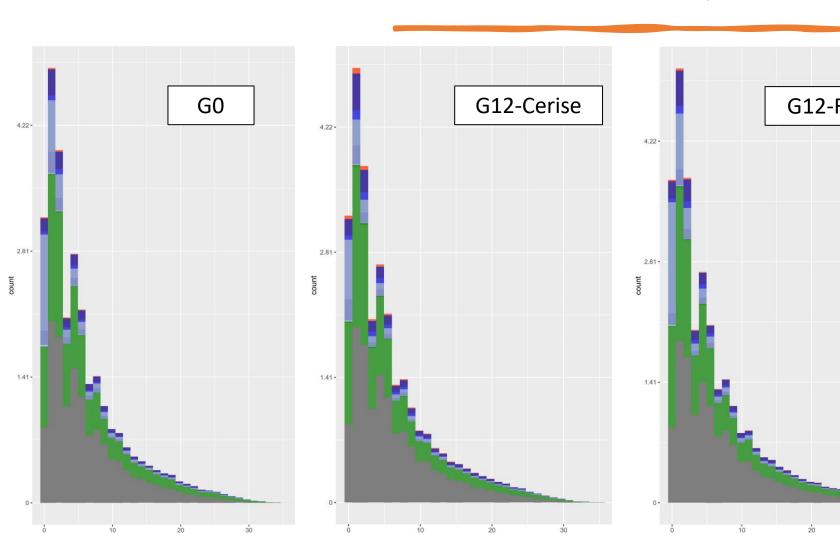
DnaPipeTE

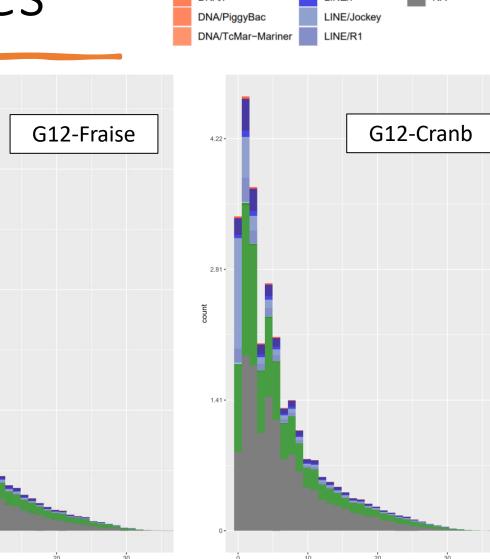
raw genomic reads (fastq) sampling blast sample 2 sample 1 sample N sample (< 1x)(<1x)reads in contig reads in contig_ Trinity assembly assembly assembly 2 dnaPipeTE Blastn 1 Contigs Estimation of TE copy number TE landscapes Annotated Repeat Masker Blastn 2 repeats Unannotated repeats Blastn 3 Estimation of the repeated content ·····> unnanoted / unmapping Quantification of the main repeat class sequences / contigs programs facultative steps

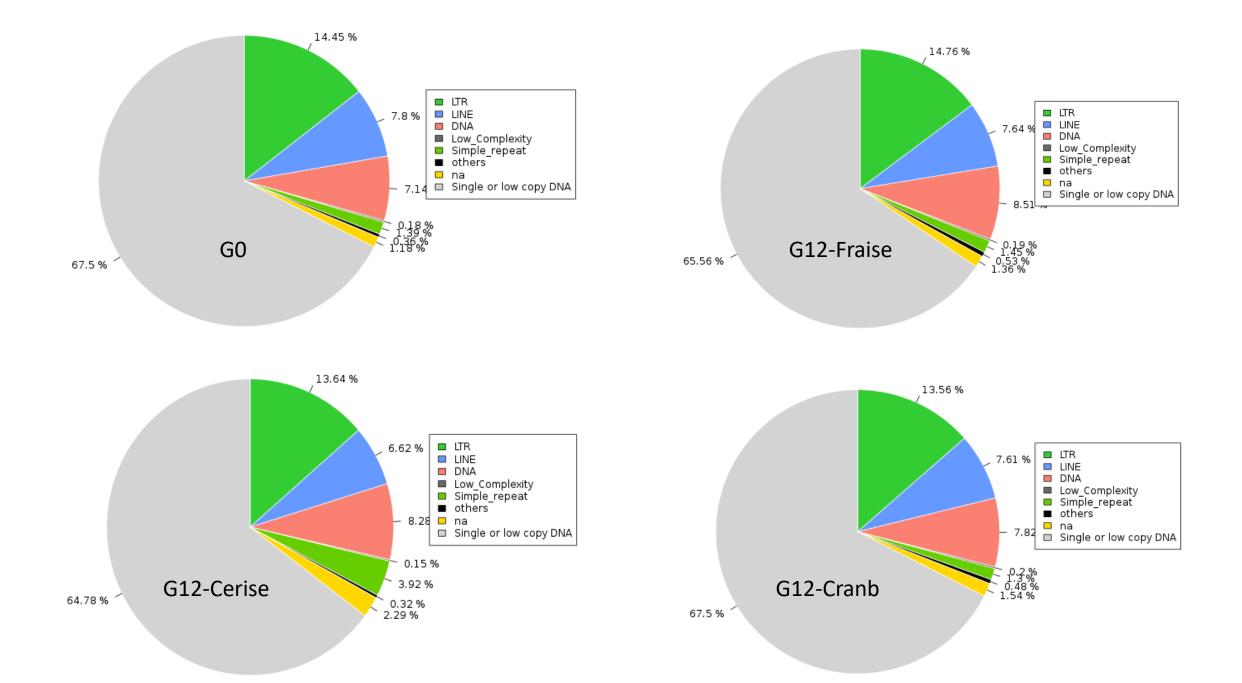
Goubert C, Modolo L, Vieira C, ValienteMoro C, Mavingui P, Boulesteix M. doi:10.1093/gbe/evv050

Landscapes

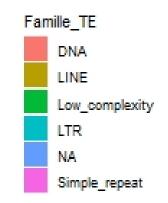


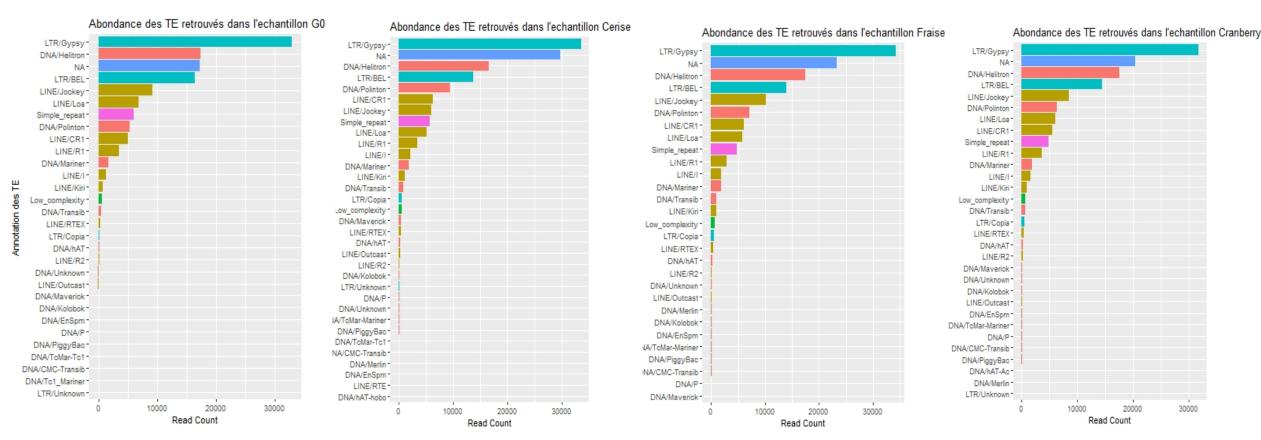




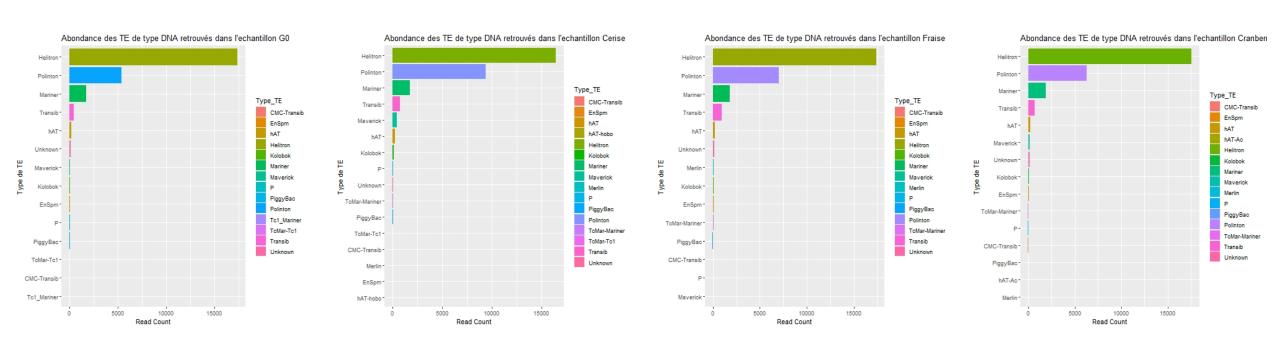


Families

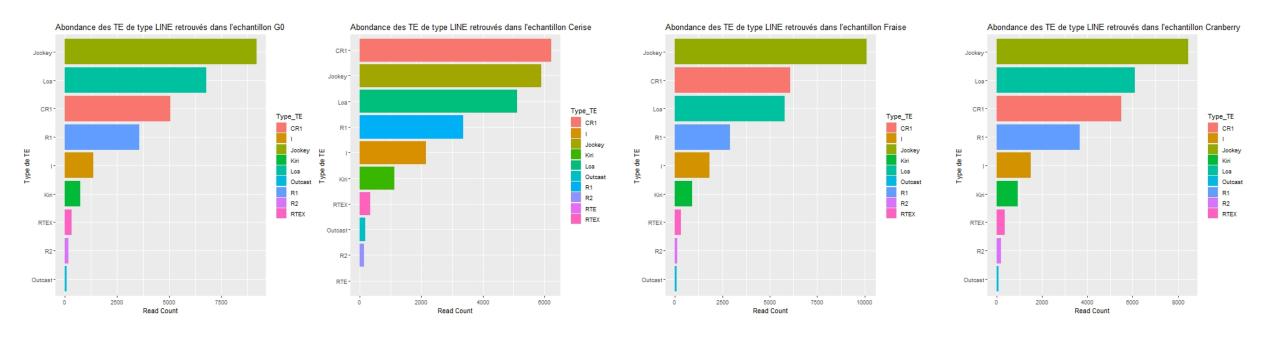




DNA TE family



LINE TE family



LTR TE family

