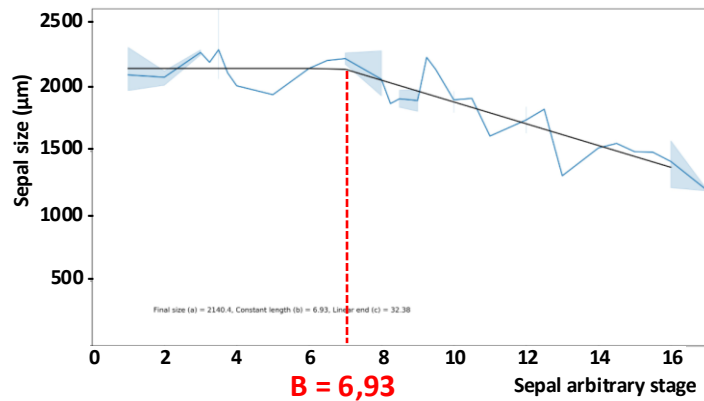
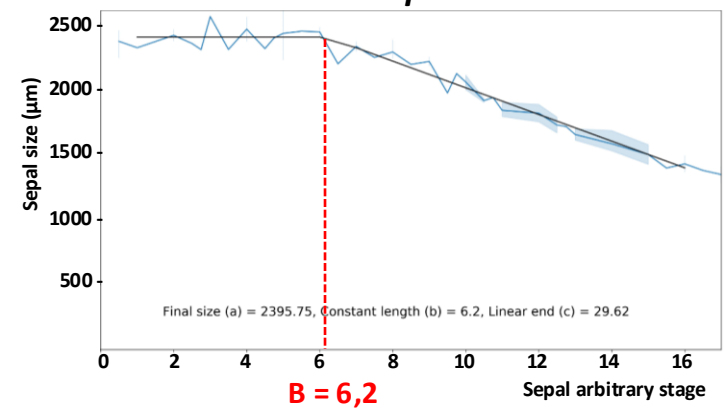
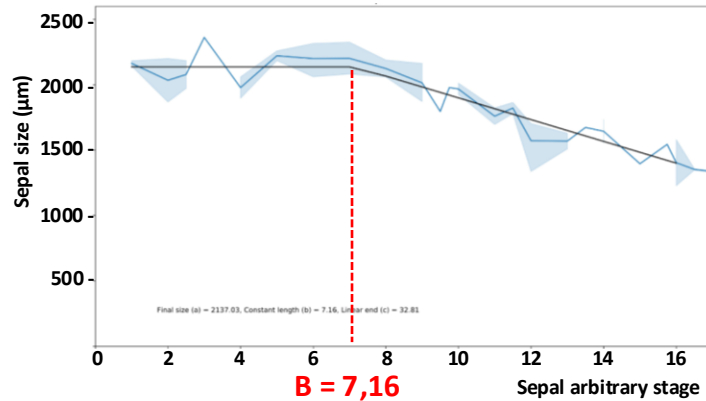
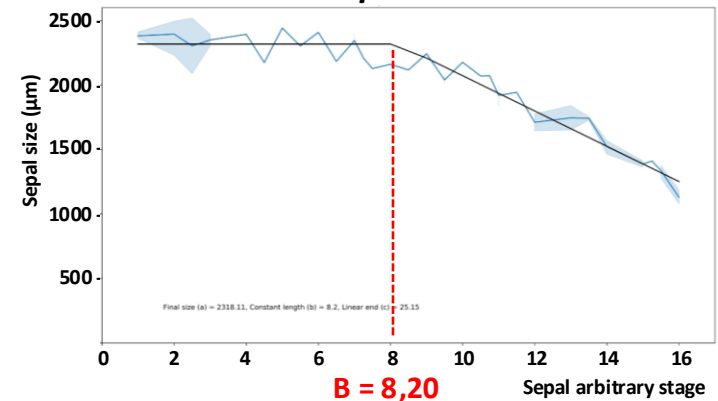
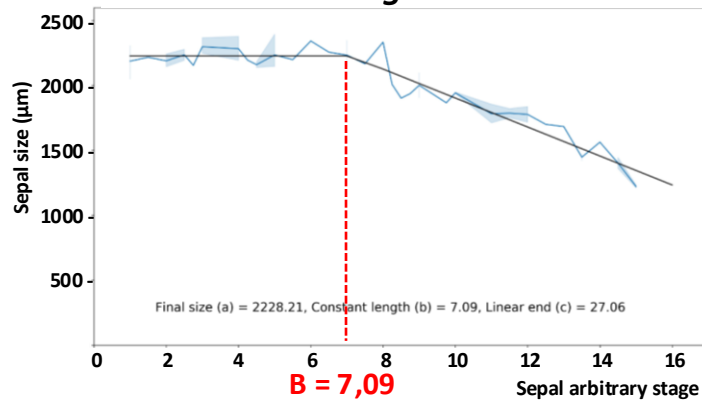
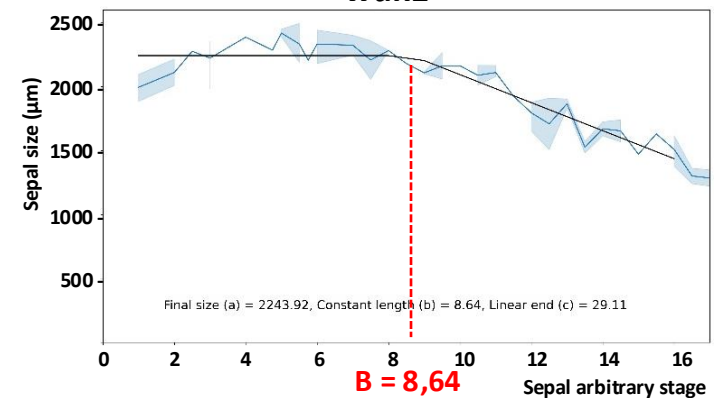
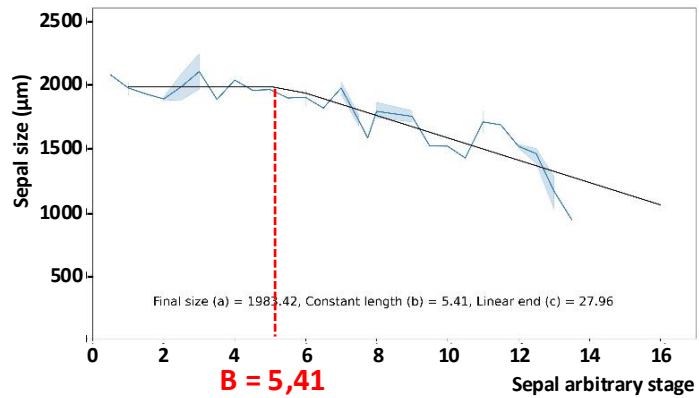
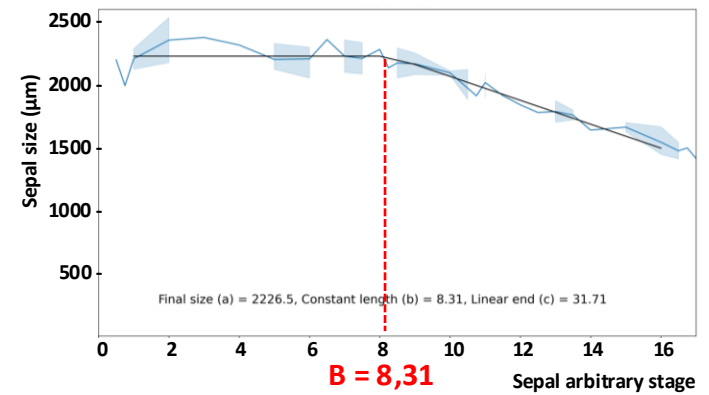
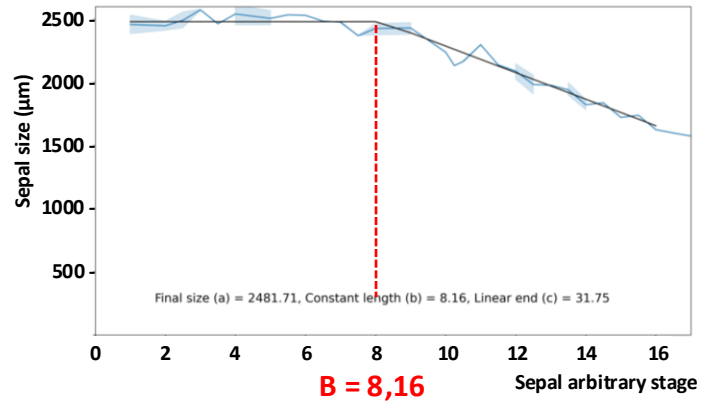
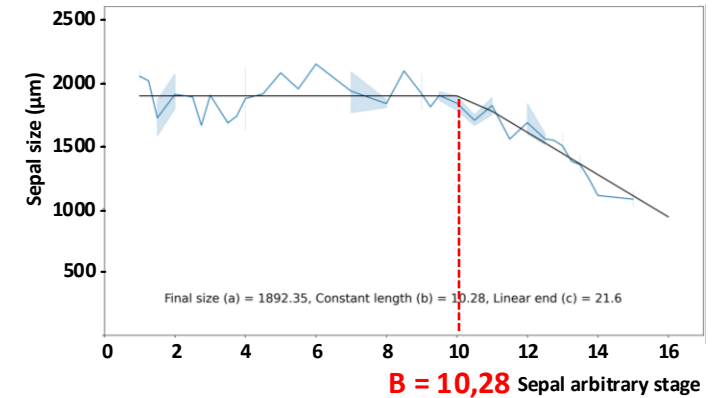
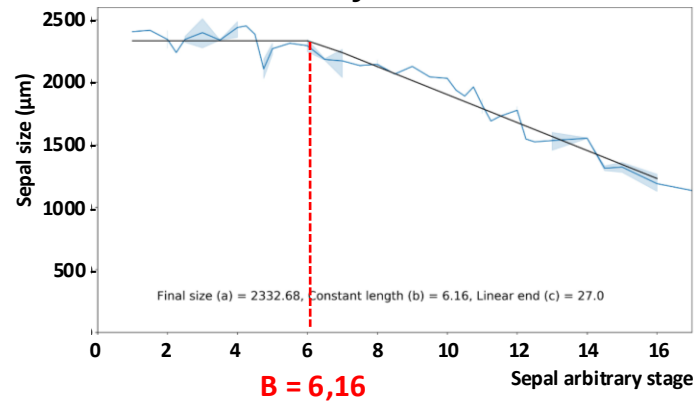
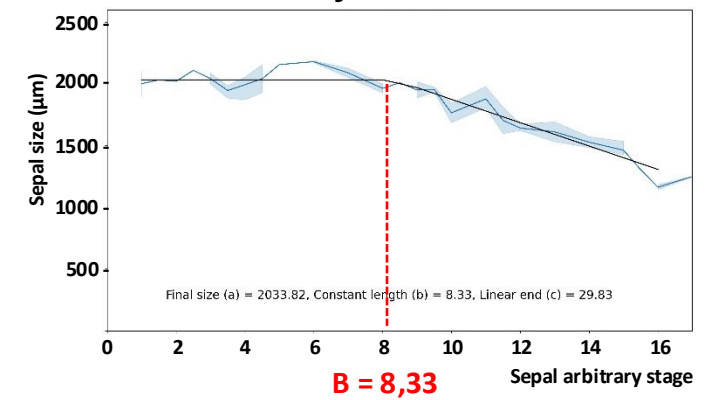
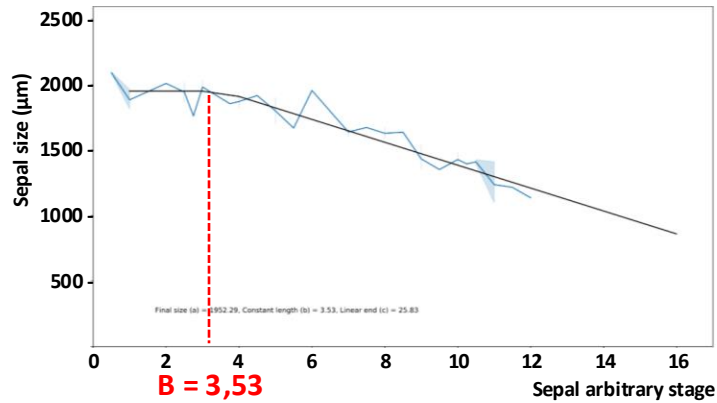


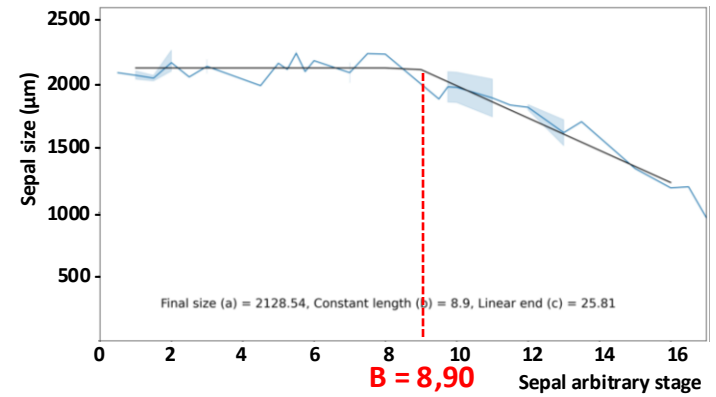
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**wak2****knat7****vnd4****ett****fer3****fer1-3-4**

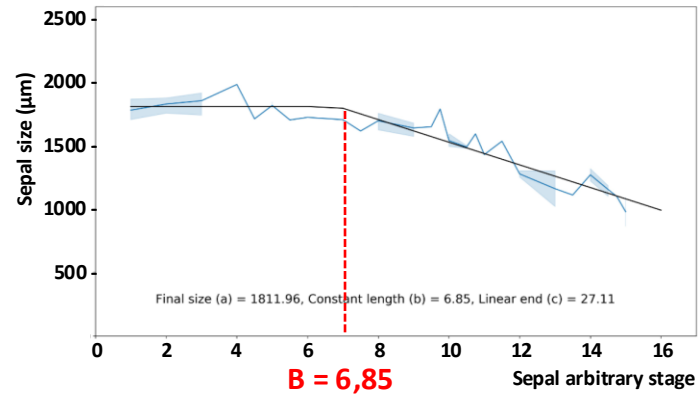
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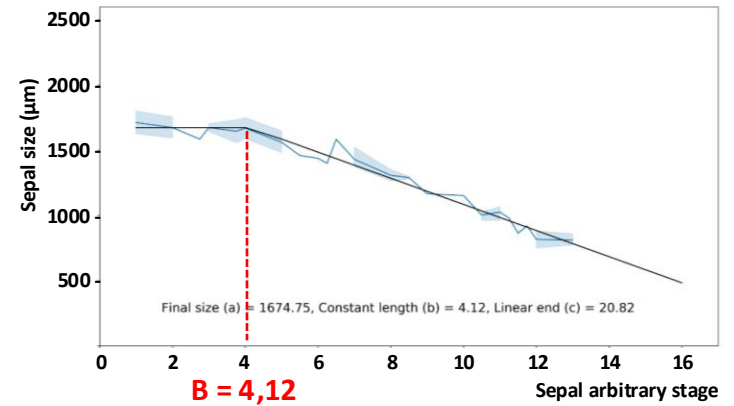
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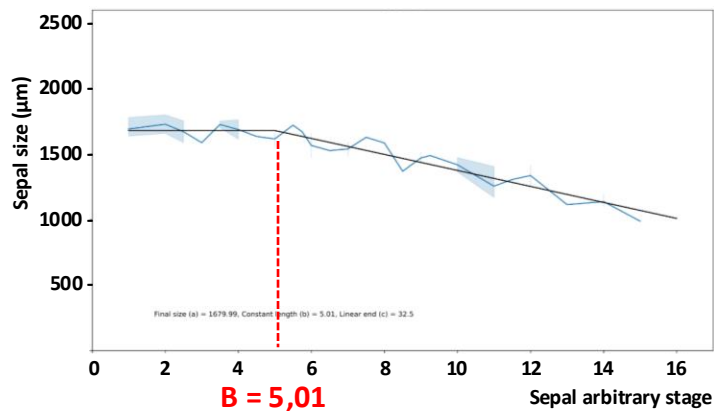
**lgo**



**pATML1:KRP1**



**crc**



**Figure S2: Sepals growth curves.**

For each genotype, we measured abaxial sepal length from all the flowers of an inflorescence, from the oldest fully open flower (arbitrary defined as stage 0) to the youngest flower buds until around 1mm long. We then opened these flowers to visualize internal organs and evaluate the developmental stage. Sepal growth curves were drawn with flowers ordered according to their developmental stage. For each genotype, growth curves were produced by pooling the flowers from four inflorescences. We used the following equation  $f(x)=A$  if  $x<B$ ,  $f(x)=A(1-(x-B)/(C-B))$  where  $f$  represents the sepal curvilinear length,  $x$  the flower stage number along the inflorescence (0 being the oldest open flower),  $A$  the final curvilinear length of the sepal,  $B$  the stage number of the last mature sepal, and  $C$  the projected sepal of length 0 following a linear projection. Fits were performed using the "curve\_fit" function of the python package "scipy.optimize" (Virtanen 2020). We determined that for all the genotypes analyzed, abaxial sepals from arbitrary stages 1 to 3 (corresponding to open flowers) have reached their final size.