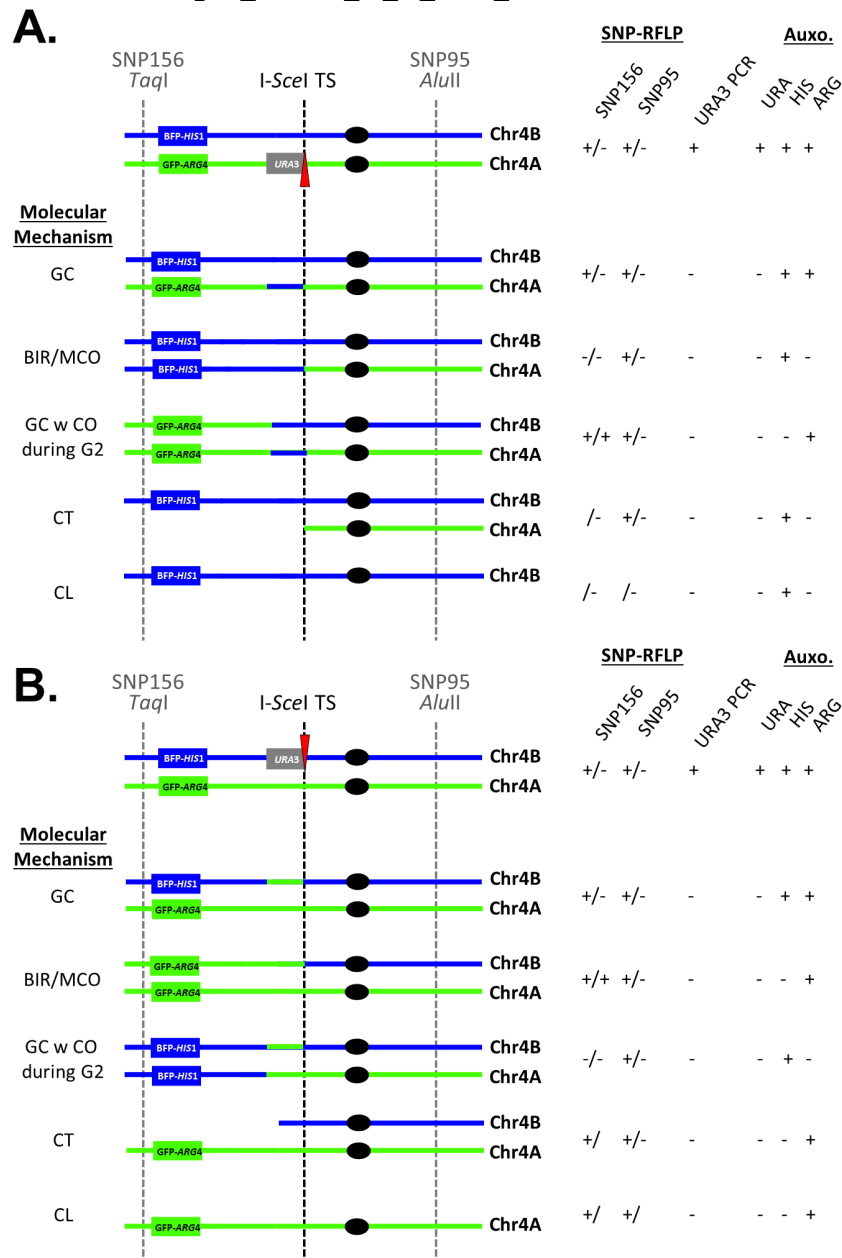


FigS2\_Marton\_et\_al\_2020\_G3-GENETICS



**Figure S2: Characterization of monofluorescent-sorted individuals leading to the identification of a molecular mechanism.**

Monofluorescence-sorted individuals underwent: (i) flow cytometry analysis to determine the fluorescence status (BFP<sup>+</sup>/GFP<sup>-</sup>, BFP<sup>-</sup>/GFP<sup>+</sup> or BFP<sup>+</sup>/GFP<sup>+</sup>), (ii) SNP typing on both arms of Chr4 using the SNP-RFLP technique (SNP number from Forche *et al.* (Forche *et al.* 2009) and restriction enzyme used), (iii) *URA3* internal PCR to determine if I-SceI- target sequence was cleaved leading to loss of *URA3* auxotrophic marker and (iv) auxotrophy spot tests to evaluate the presence or absence of *URA3* (associated to the I-SceI-target sequence), *HIS1* (associated to the BFP) and *ARG4* (associated to the GFP). These results were interpreted as illustrated in panels **A.** (analysis for strains possessing the I-SceI- target sequence on haplotype A or Chr4L) and **B.** (analysis for strains possessing the I-SceI- target sequence on haplotype B or Chr4L) in order to identify the length of the LOH tract and the appropriate molecular mechanism. Abbreviations of molecular mechanisms are as follows; gene conversion (GC), break-induced replication (BIR), mitotic crossover (MCO), gene conversion with crossover (GC with CO), chromosome truncation (CT), chromosome loss (CL).