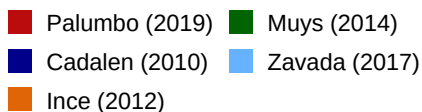
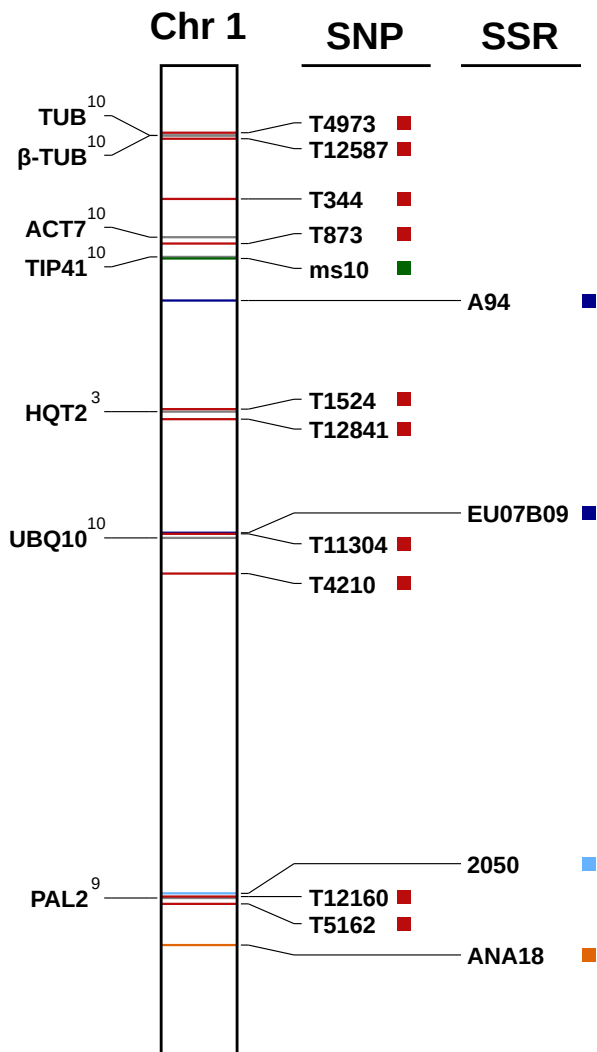
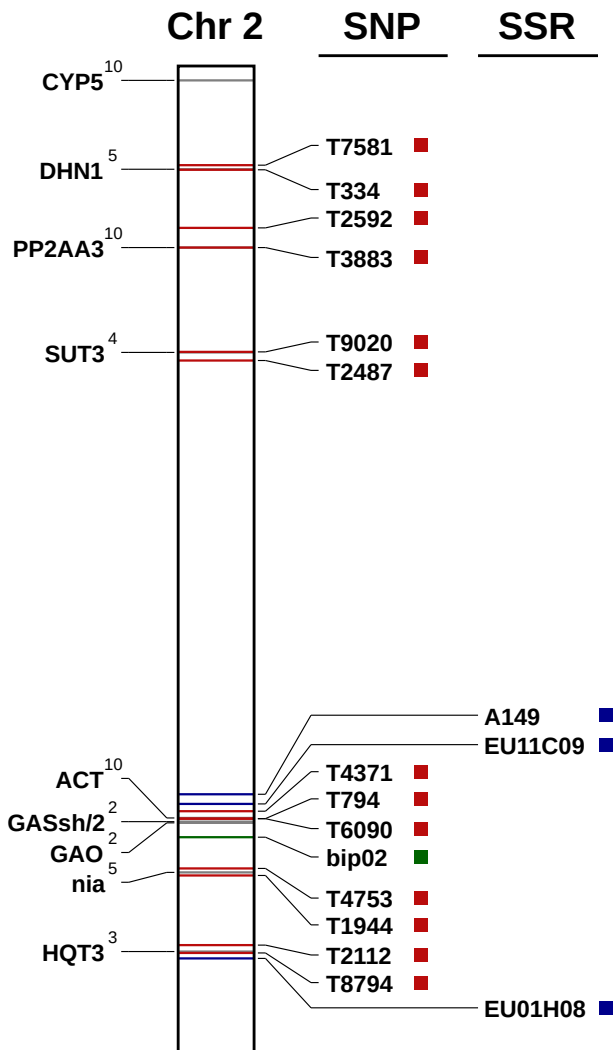
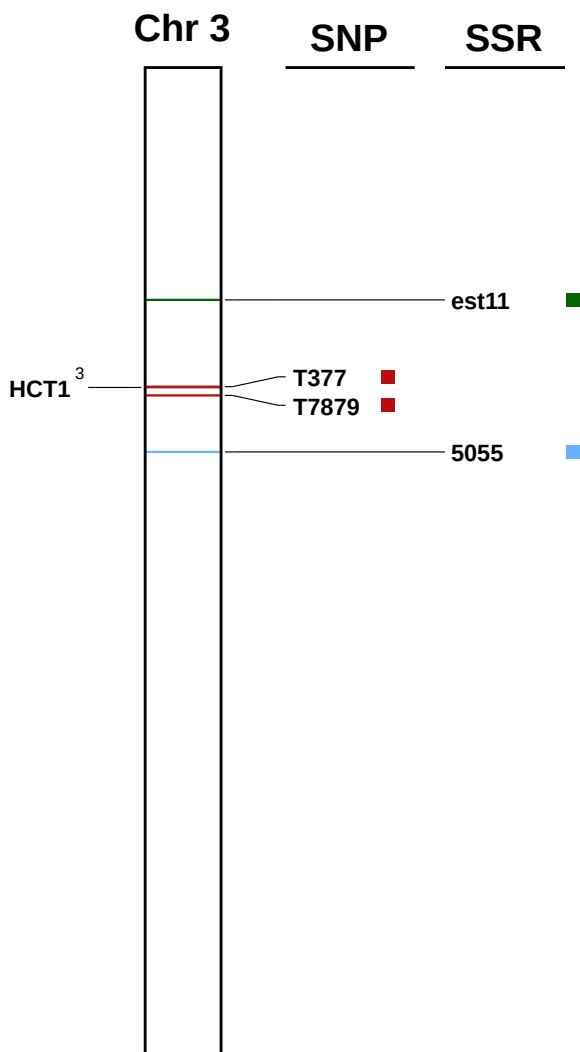
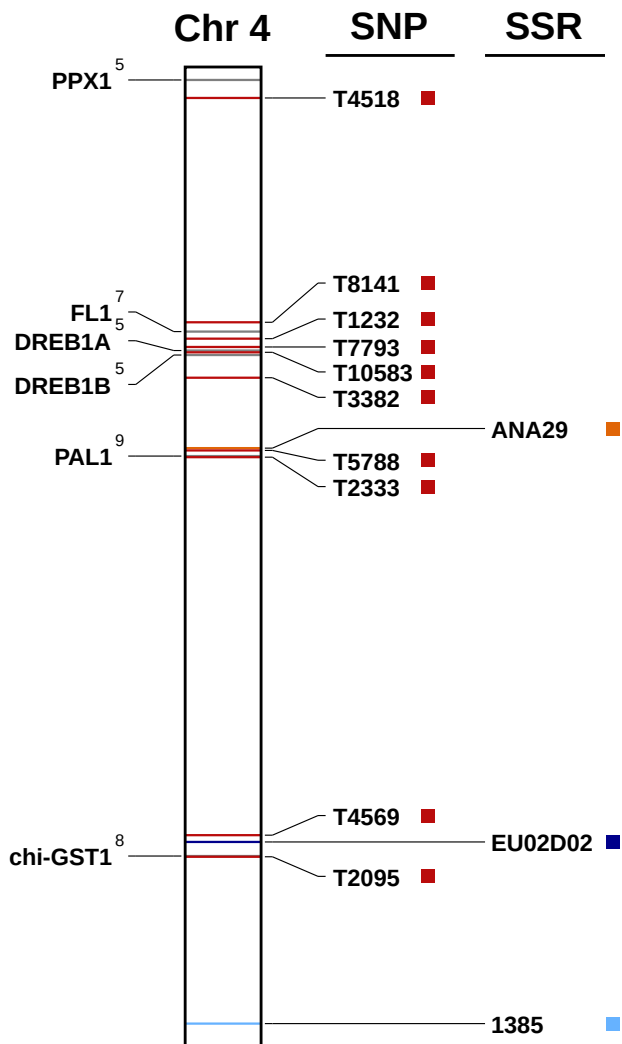


**Figure S2:** Reference Marker Assisted Selection (MAS) map in chicory. On the left are the genes with their trait-identity number (in the form of apex; 1: Reproductive barriers; 2: Sesquiterpene Lactone biosynthesis (STL); 3: Hydroxycinnamates biosynthesis (HCAs); 4: Inulin metabolism; 5: Stress response; 6: Blue-lilac color; 7: Flowering time; 8: Somatic embryogenesis; 9: Red discoloration; 10: Gene normalization). Each gene is also described in detail in Table 3 whereas Table S1 reports their respective GenBank accession numbers. On the right are reported the two markers (SSRs or SNPs) closest to each gene. The color of square near each marker refers to the source study of the marker (Cadalen *et al.* [25], Muys *et al.* [27], Palumbo *et al.* [28], Patella *et al.* [13], Ince *et al.* [29], Zavada *et al.* [30])



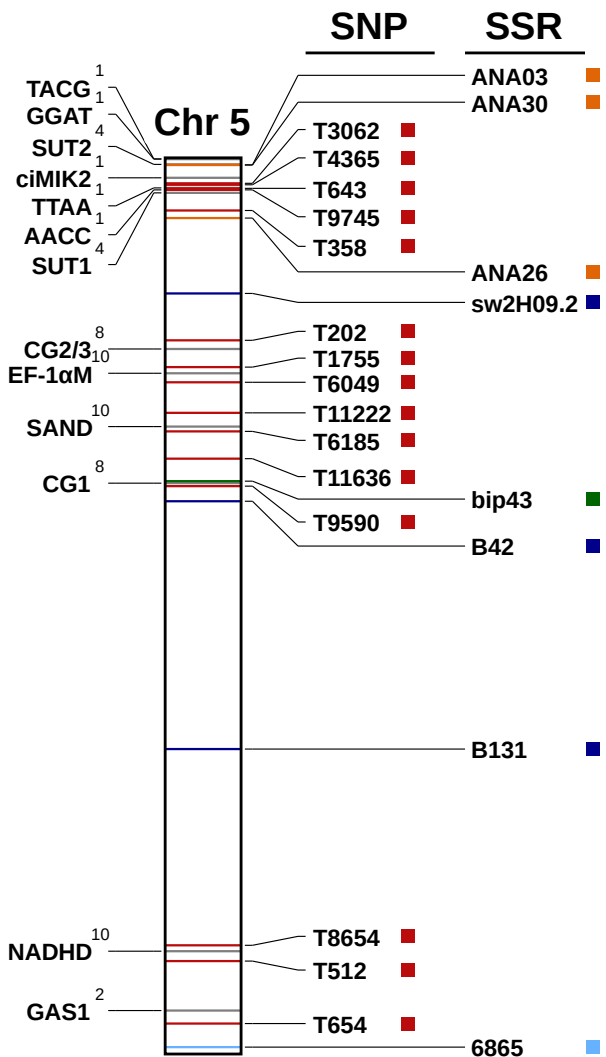


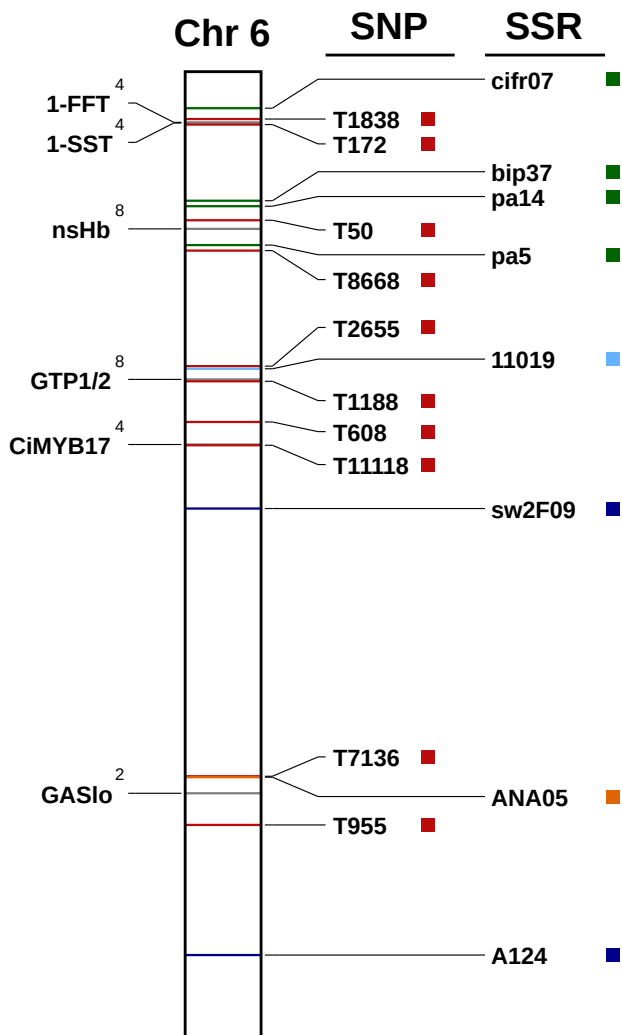




10 Mb

■ Palumbo (2019) 
 ■ Ince (2012) 
 ■ Cadalen (2010) 
 ■ Zavada (2017)

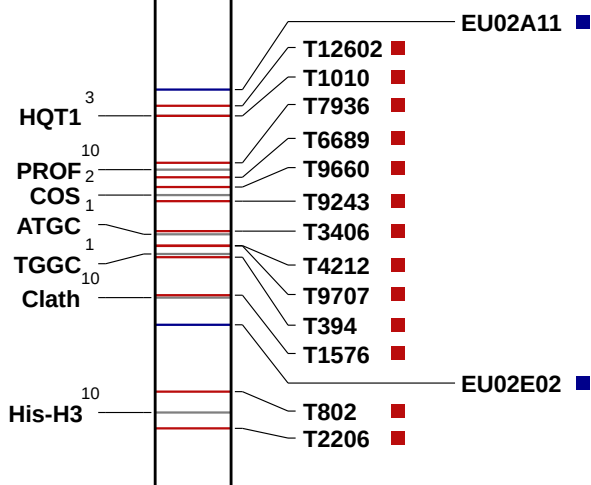




**Chr 7**

**SNP**

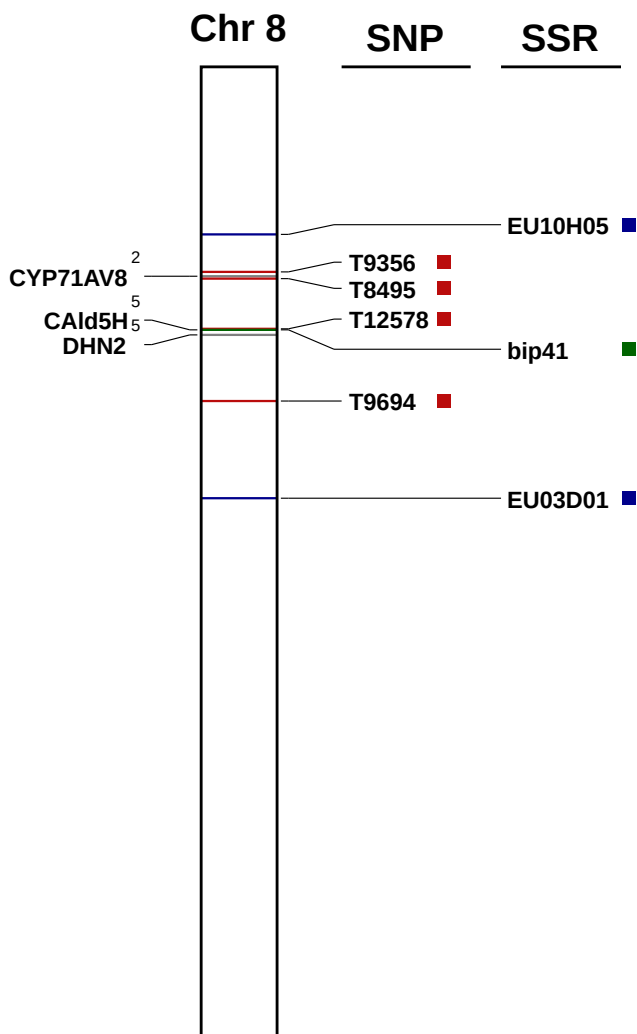
**SSR**



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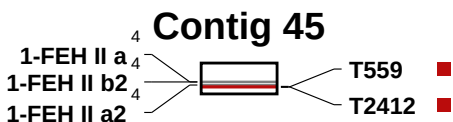
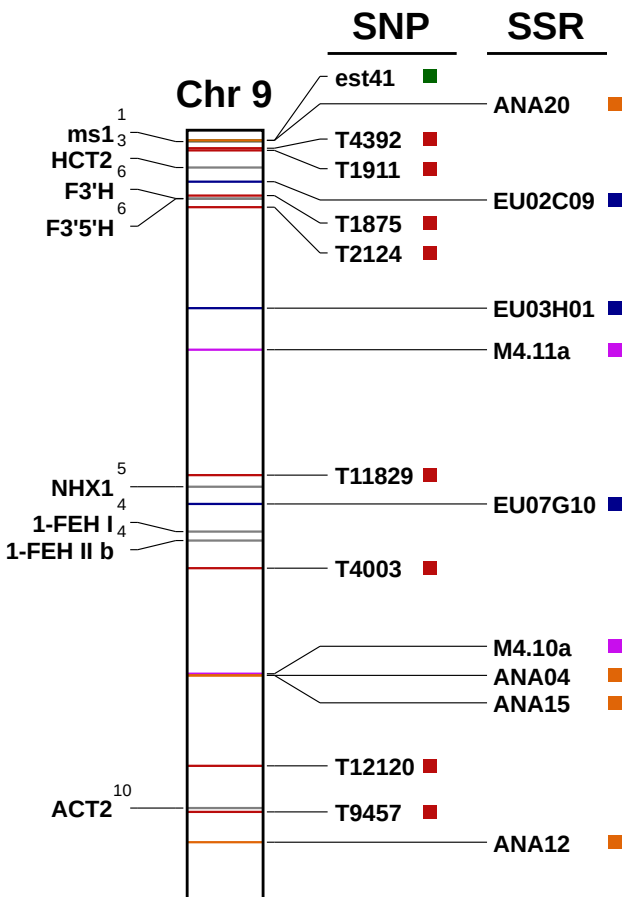
■ Cadalen (2010)  
■ Palumbo (2019)





10 Mb

- Cadalen (2010)
- Palumbo (2019)
- Muys (2014)



10 Mb

■ Muys (2014)
 ■ Ince (2012)
 ■ Palumbo (2019)
 ■ Cadalen (2010)
 ■ Patella (2019)