

A) LG1

4B.1

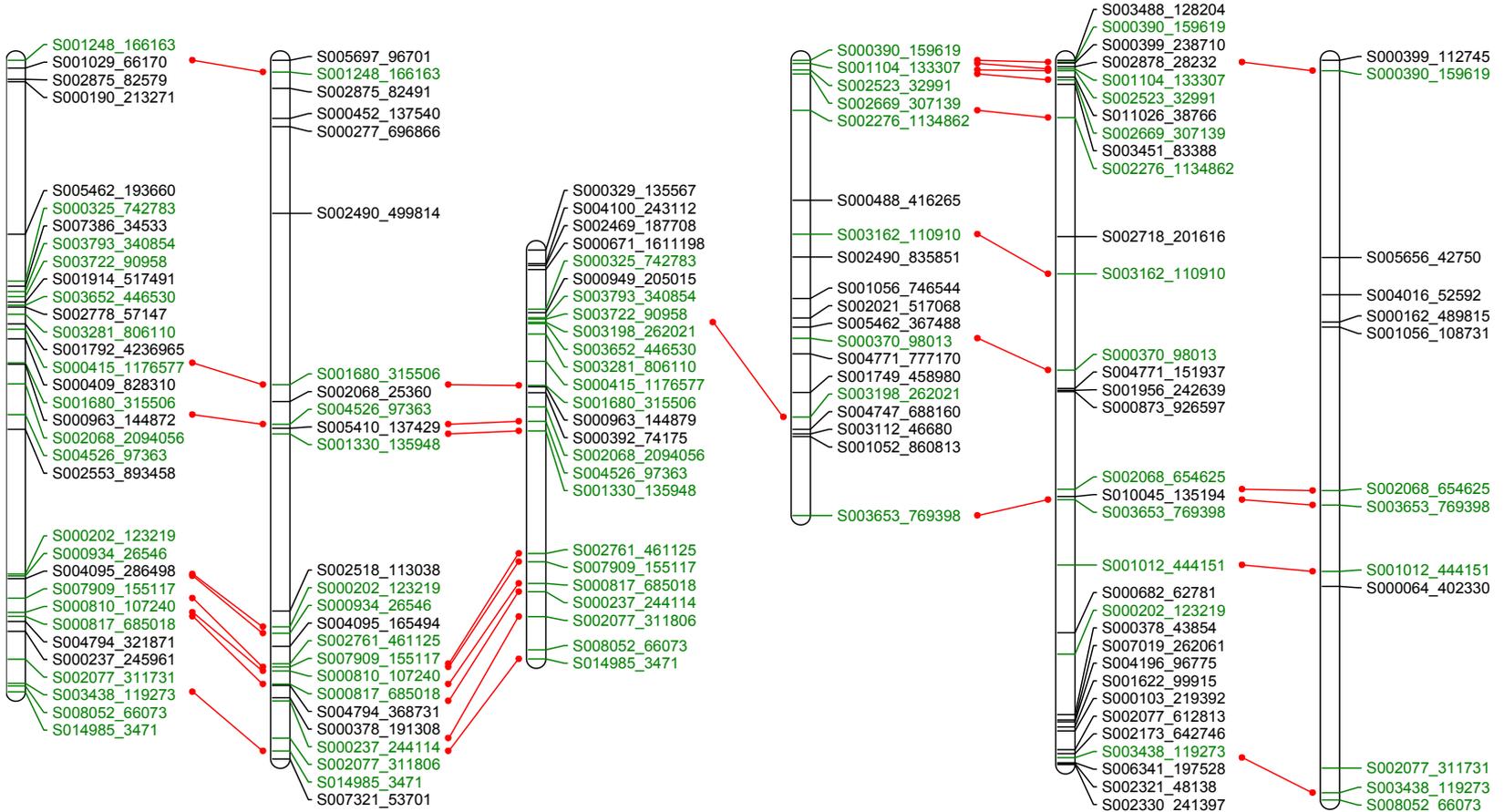
4B.2

4B.3

4C.5

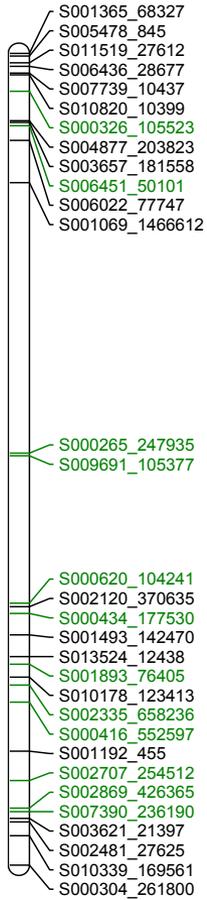
4C.9

4E.1

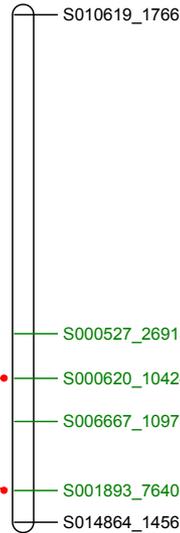


B) LG2

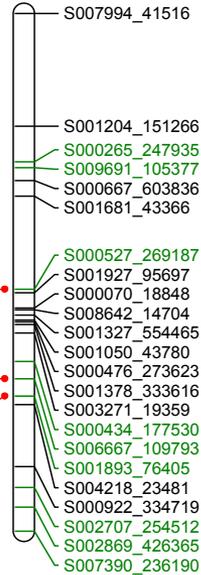
4B.1



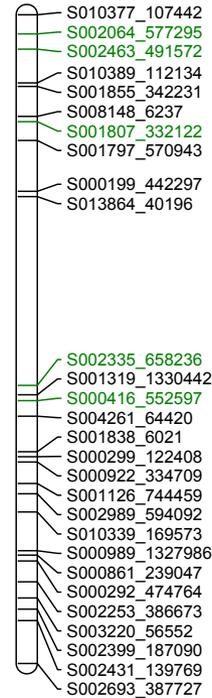
4B.2



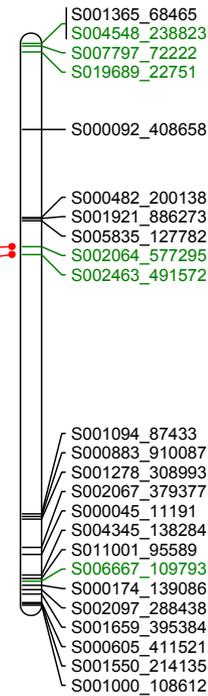
4B.3



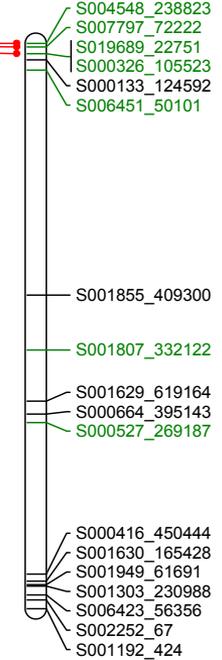
4C.5



4C.9

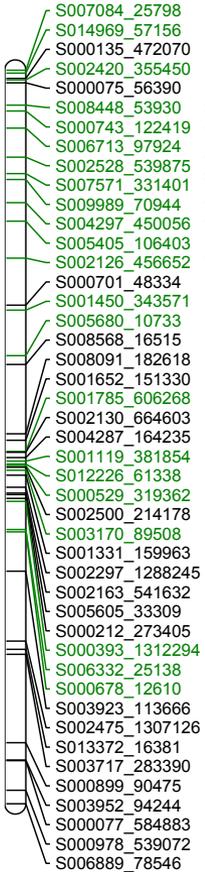


4E.1

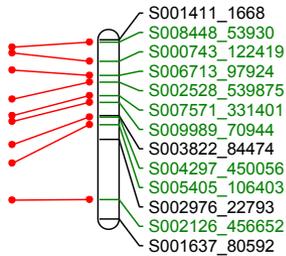


C) LG3

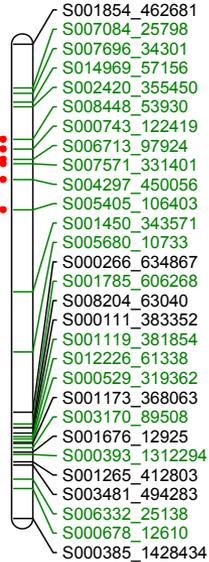
4B.1



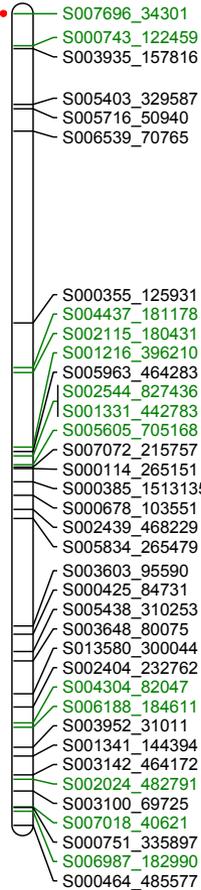
4B.2



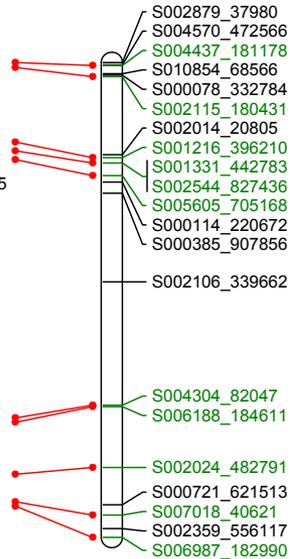
4B.3



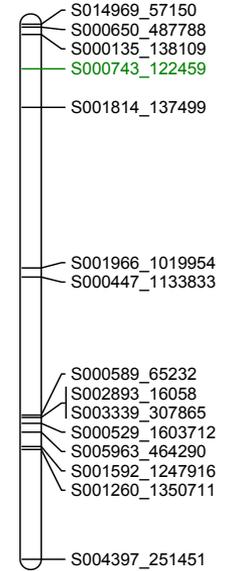
4C.5



4C.9



4E.1



D) LG4

4B.1

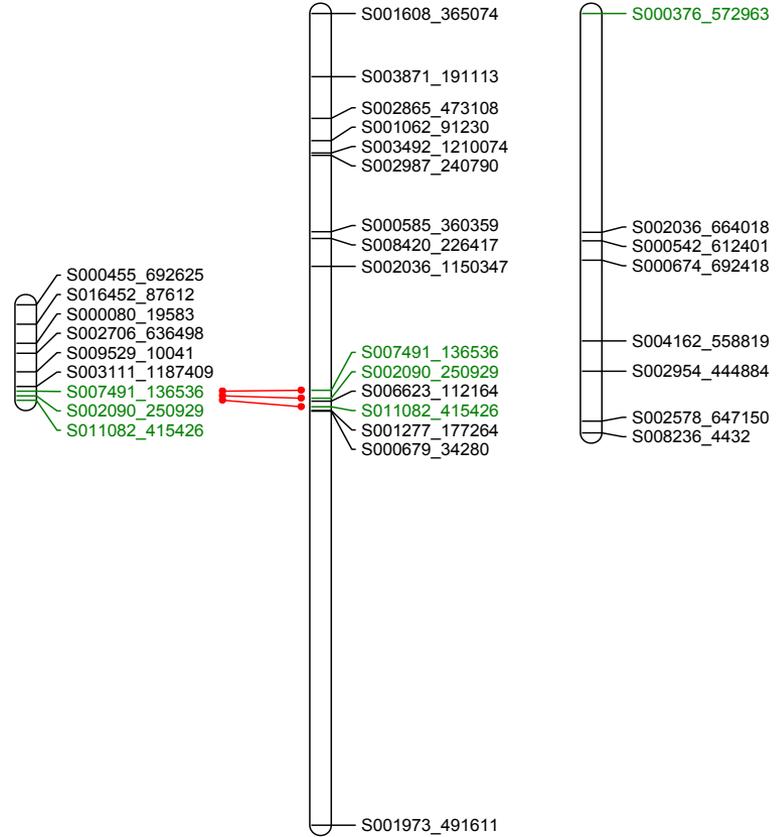
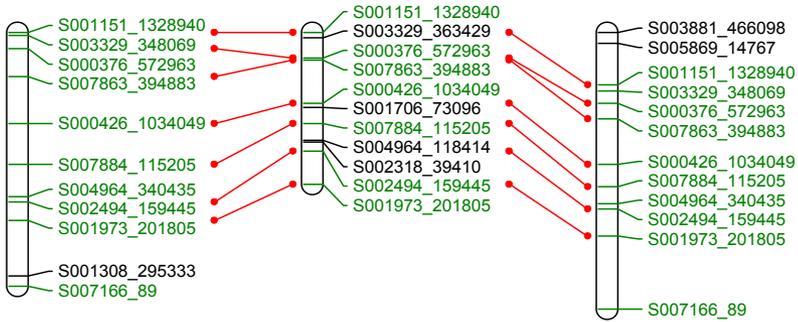
4B.2

4B.3

4C.5

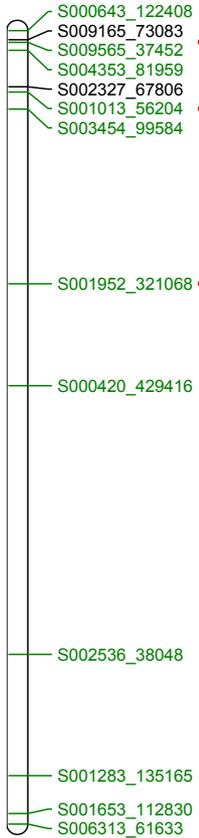
4C.9

4E.1

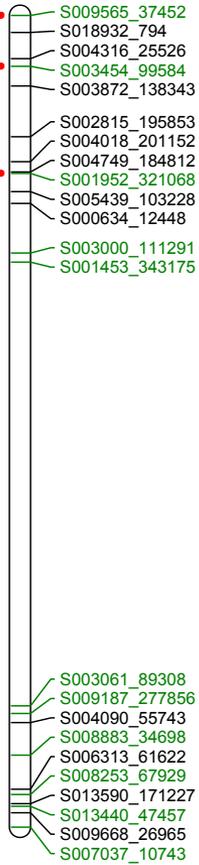


E) LG6

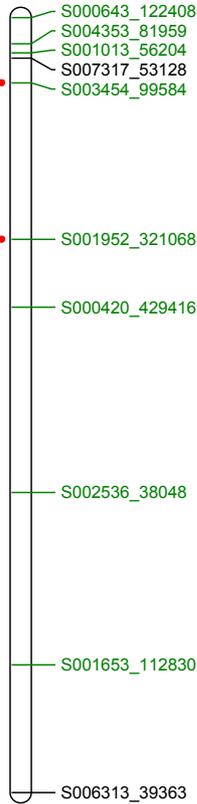
4B.1



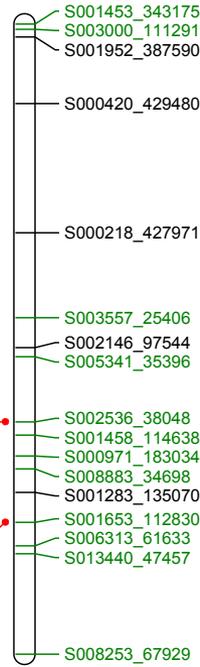
4B.2



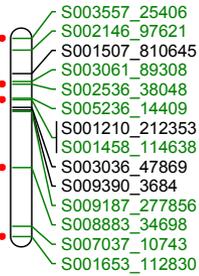
4B.3



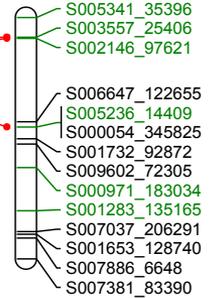
4C.5



4C.9



4E.1



F) LG7

4B.1

4B.2

4B.3

4C.5

4C.9

4E.1

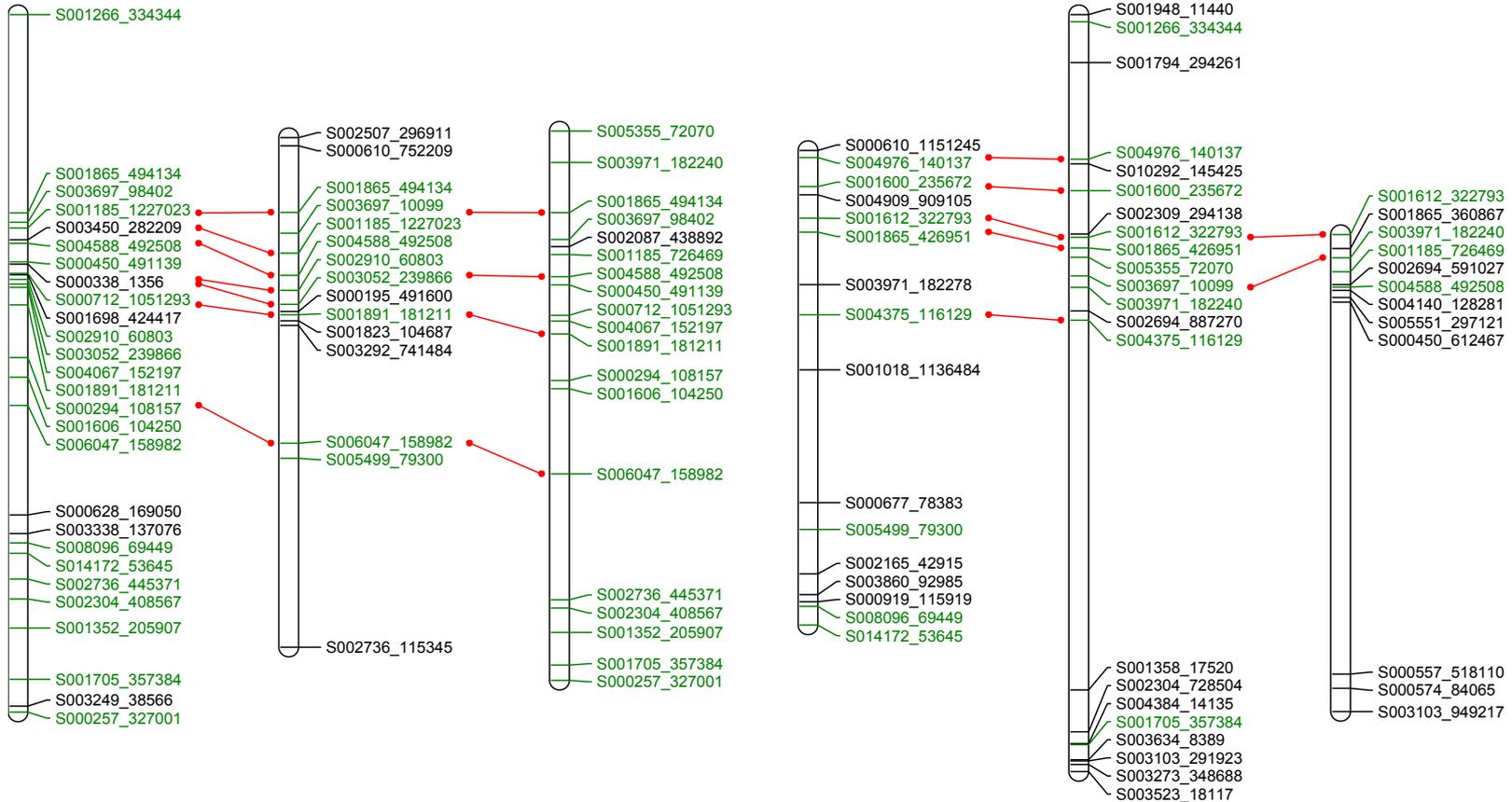


Figure S2. Homology and synteny of A) LG1, B) LG2, C) LG3, D) LG4, E) LG6, and F) LG7 among 6 F_2 families. Markers in green are shared between at least two families (including both adjacent and non-adjacent families in the figure), and red lines join the same marker in adjacent linkage maps