

# A) LG1

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4B.2

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4C.5

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4C.9

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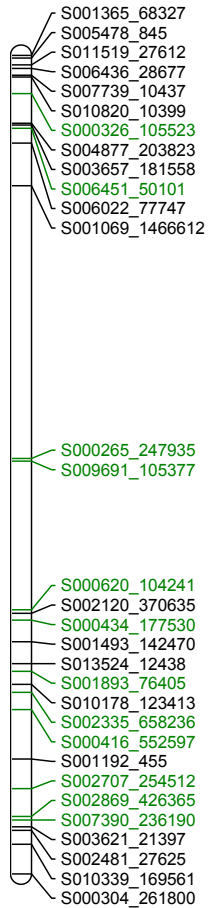
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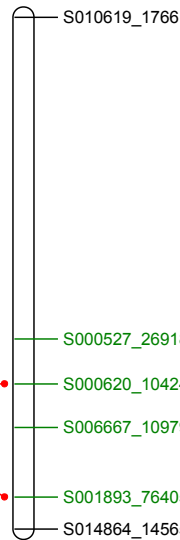
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## B) LG2

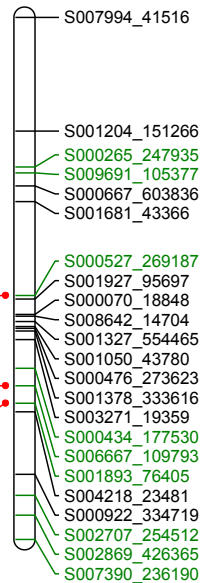
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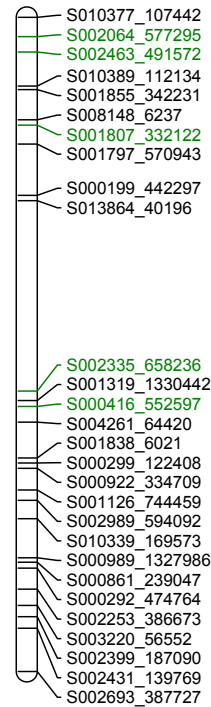
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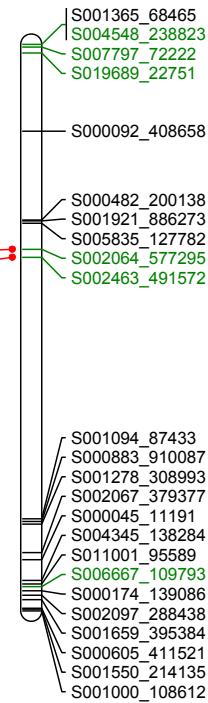
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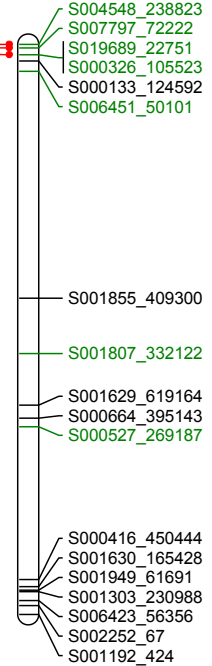
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4C.9

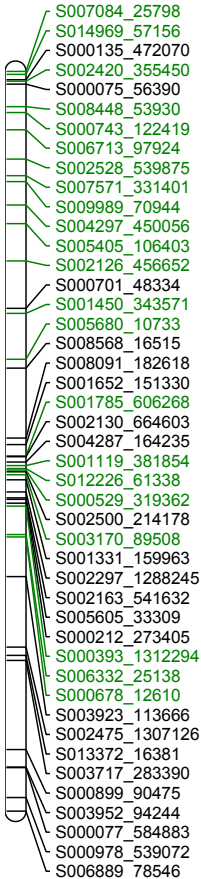


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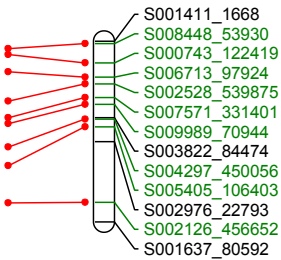


C) LG3

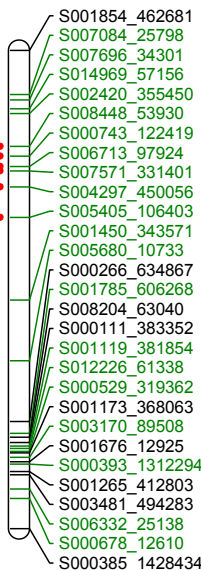
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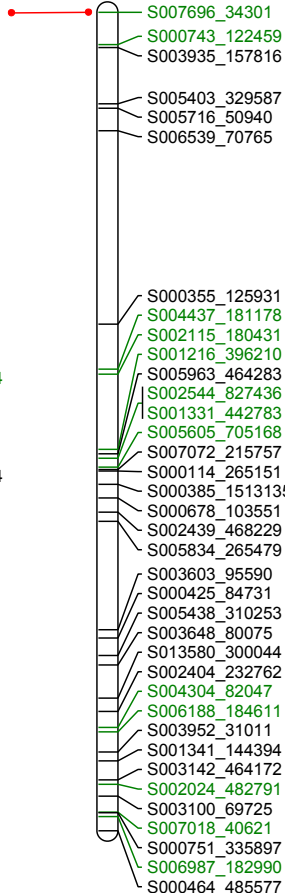
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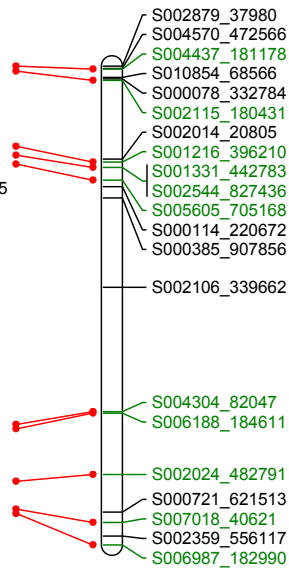
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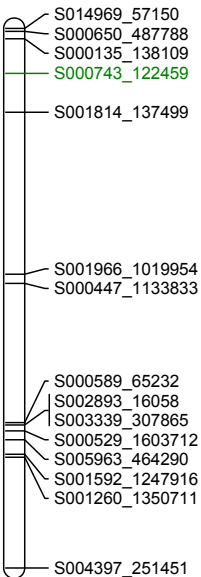
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4C.9

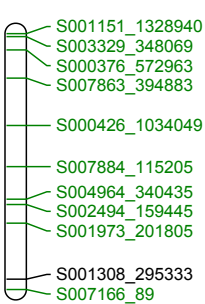


4E.1

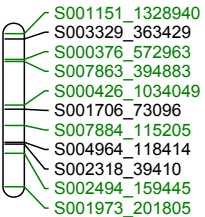


D) LG4

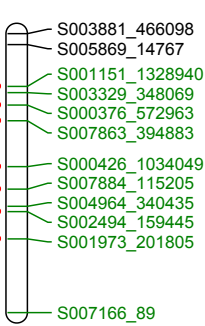
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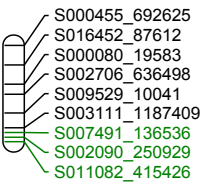
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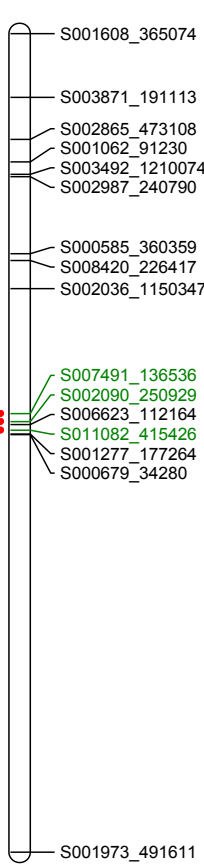
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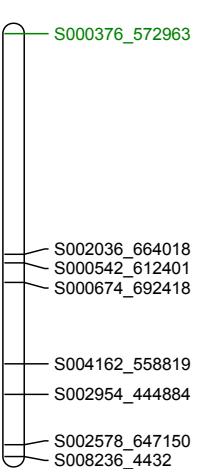
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4C.9

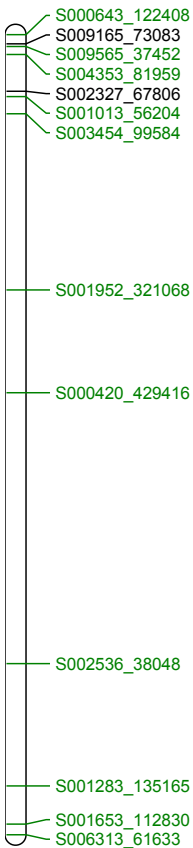


4E.1

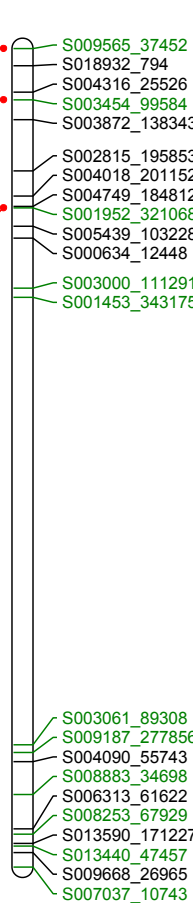


E) LG6

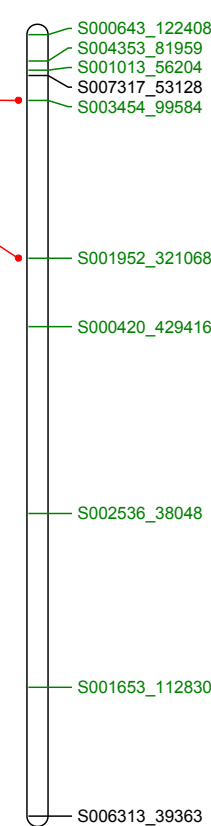
4B.1



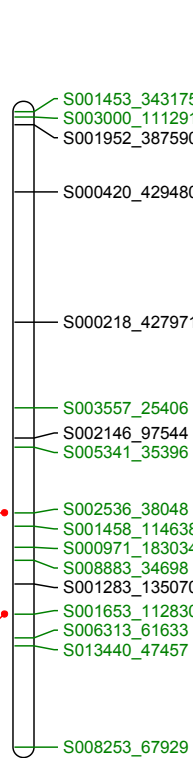
4B.2



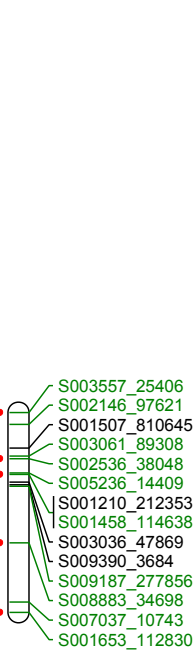
4B.3



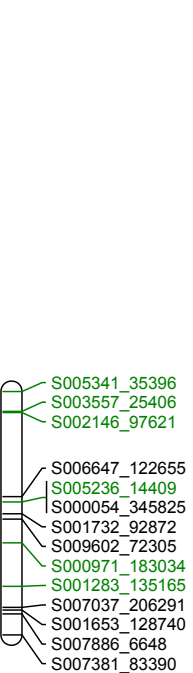
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4C.9



4E.1



## F) LG7

4B.1

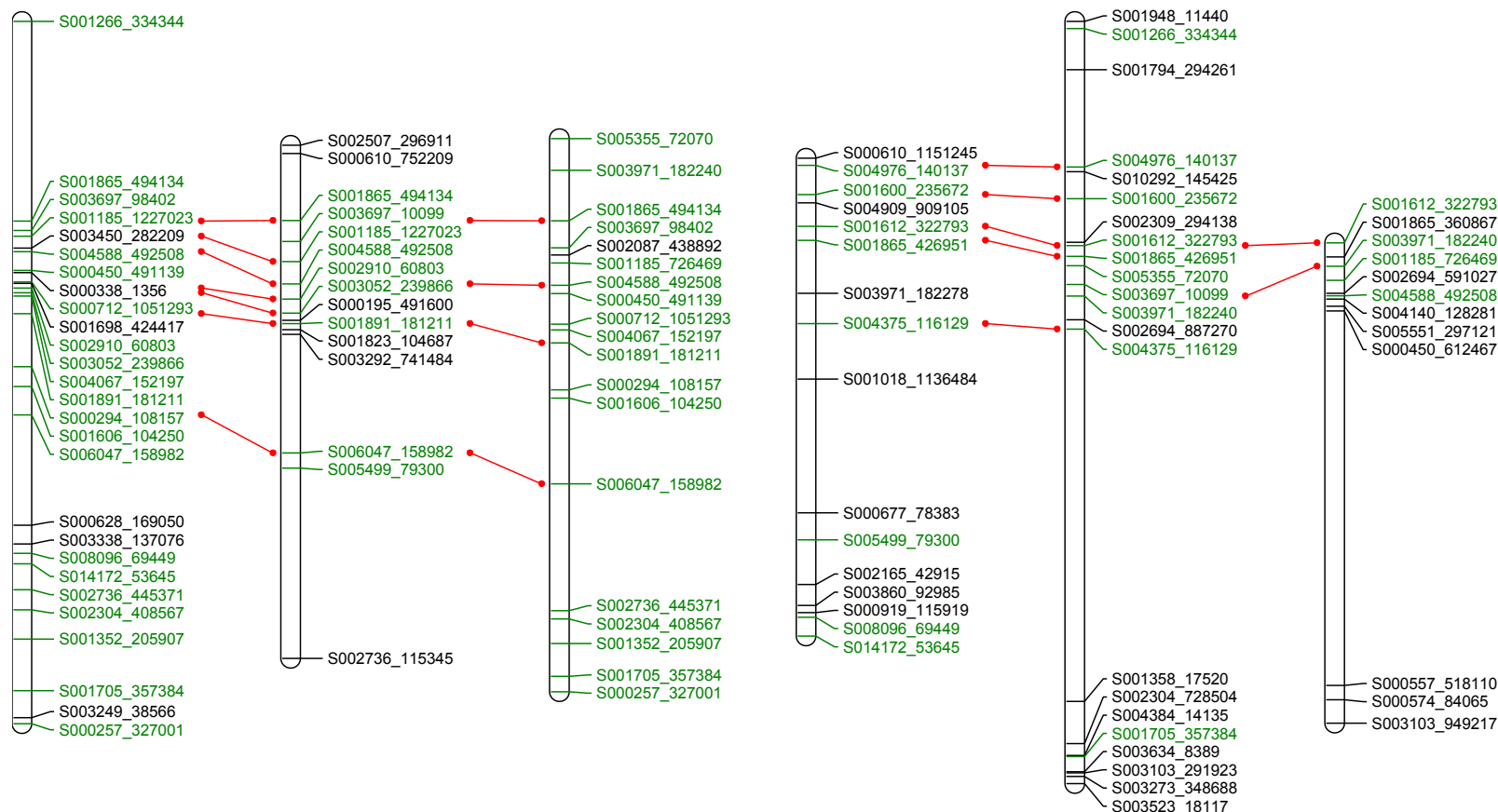
4B.2

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