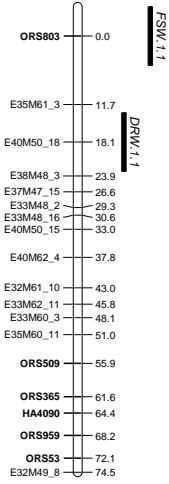


**Supplementary****Mapping quantitative trait loci for seedling vigour and development in sunflower (*Helianthus annuus* L.) using recombinant inbred line population****Supplementary data 1**

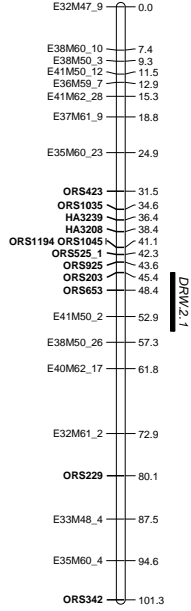
Linkage groups of the sunflower genome presenting QTLs associated with seed germination and seedling vigor, growth and developmental traits. The sunflower reference map constructed by Poormohammad Kiani et al. (2007) using 123 PAC2 × RHA266 recombinant inbred lines, was used for detection of QTLs. The map contains 304 AFLP and 191 SSR markers, with a mean density of one locus every 3.7 cM. A decrease in the LOD score of 1.0, determined the end point of support interval for each QTL. The QTLs were designated as the abbreviation of the trait followed by the corresponding number of linkage group (LG) and the corresponding number of QTLs on the group.

Sger: speed of germination, DSE: days to seedling emergence, HD: hypocotyle diameter, ShootL: shoot length, RootL: root length, DRW: dry root weight, DSW: dry shoot weight, FRW: fresh root weight, FSW: fresh shoot weight, V4: V4 stage.

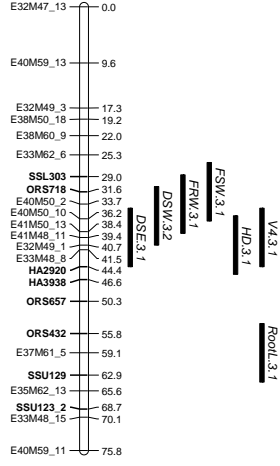
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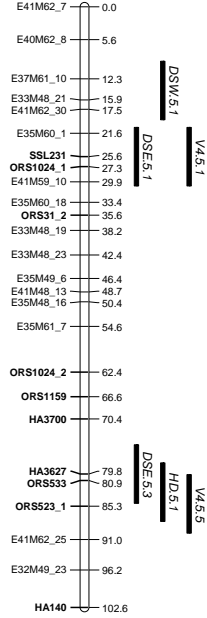
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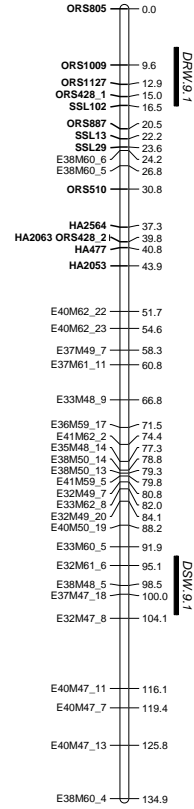
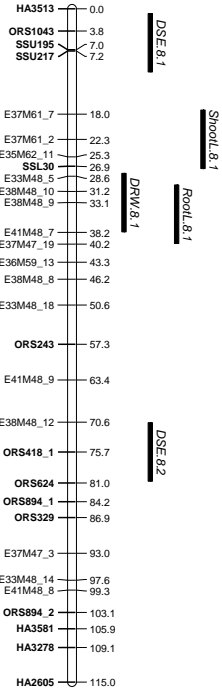
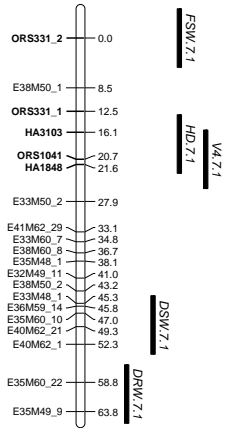
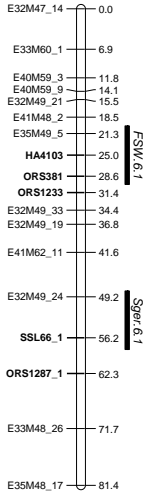


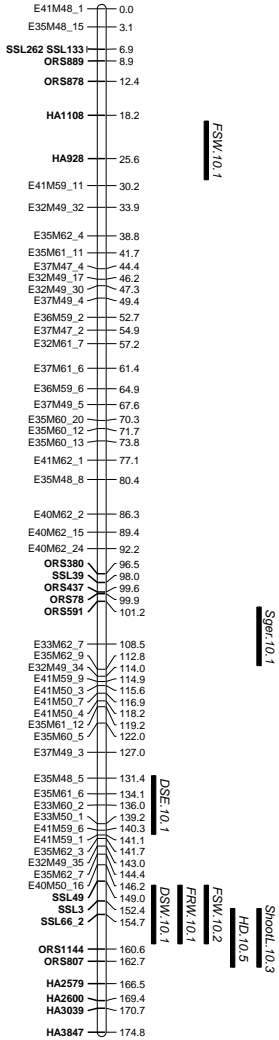
3



5







FSW/10.1

Slope/10.1

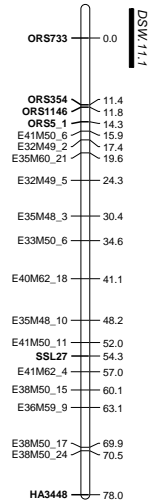
DSE/10.1

FSW/10.2

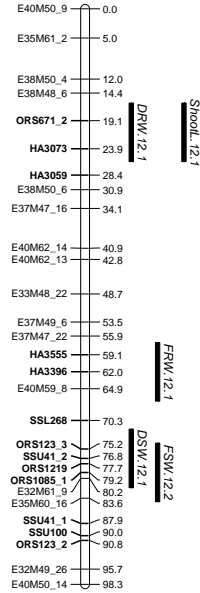
FRW/10.1

HD/10.5

Slope/10.3



DSW/11.1



FRW/12.1

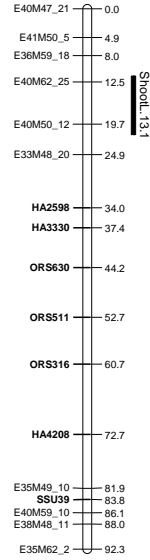
DSW/12.1

FRW/12.1

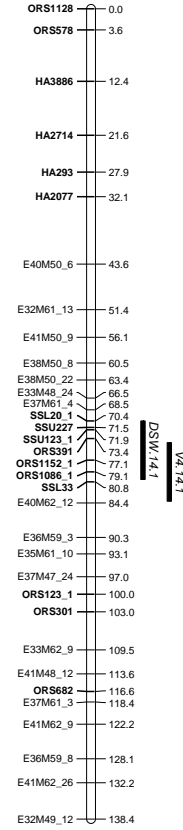
DSW/12.1

FSW/12.2

DSW/12.2

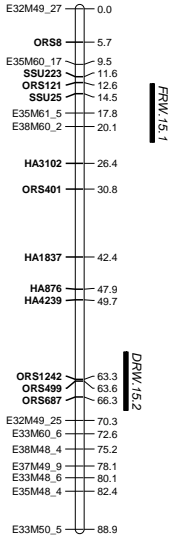


Shoal/13.1



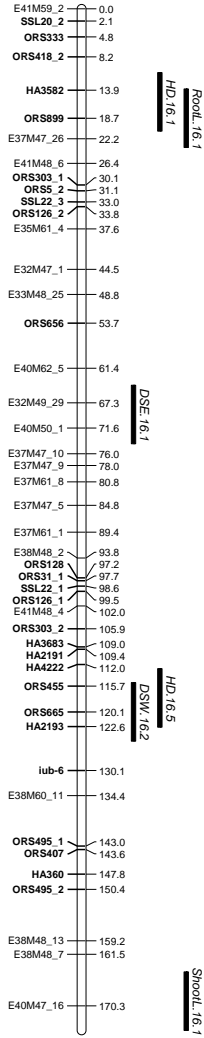
DSW/14.1

VA/14.1



FRW 15.1

DRW 15.2

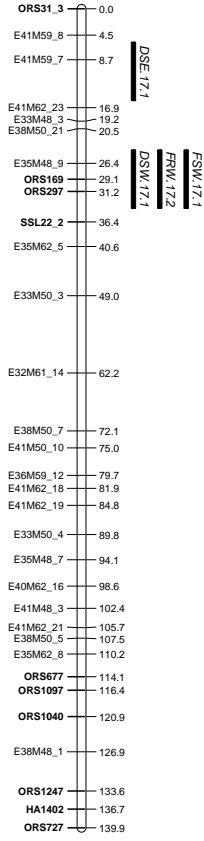


FRW 16.1

DRW 16.1

DRW 16.2

FRW 16.1



FRW 17.1

FRW 17.2

DRW 17.1