

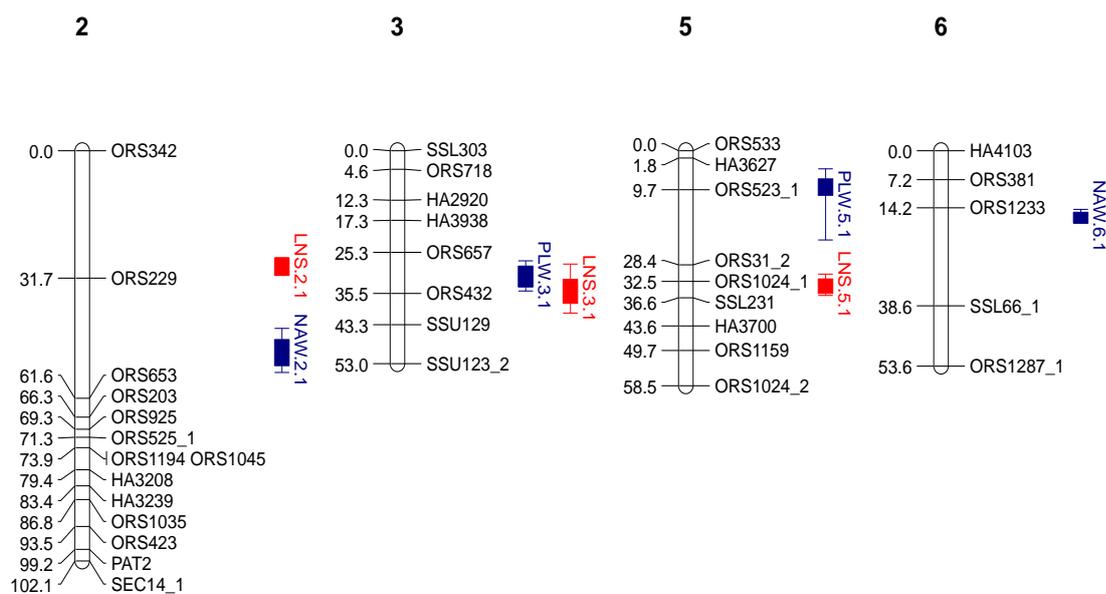
Supplementary data

Genetic analysis and QTL mapping of agro-morphological traits in sunflower (*Helianthus annuus* L.) under two contrasting water treatment conditionsN. Abdi¹, R. Darvishzadeh^{1,2}, M. Jafari¹, A. Pirzad¹ and P. Haddadi²

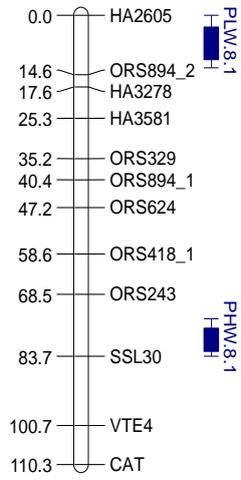
Supplementary data 1

Linkage groups of the sunflower genome presenting QTLs associated with agro-morphological traits in two water treatment conditions. The sunflower reference map was constructed by using 123 PAC2 × RHA266 recombinant inbred lines. A decrease in the LOD score of 1.0, determined the end point of support interval for each QTL. QTL names are constructed using the trait abbreviation name suffixed with numbers presenting the linkage group (LG) and order of QTL on the linkage group. The QTLs names were also followed by W or S presenting well-watered and water-stressed conditions, respectively.

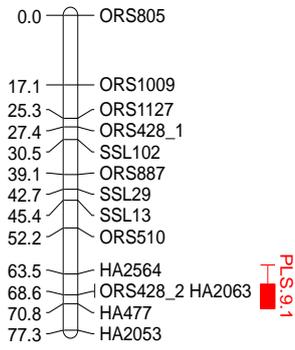
PH: plant height; HD: head diameter; SD: stem diameter; GYP: grain yield per plant; HGW: 100-grain weight; NA: number of achene; LAD: leaf area duration; BIO: total dry matter; PL: petiole length and LN: leaf number per plant.



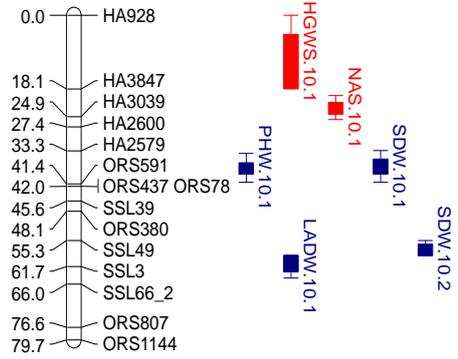
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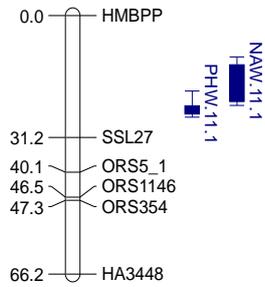
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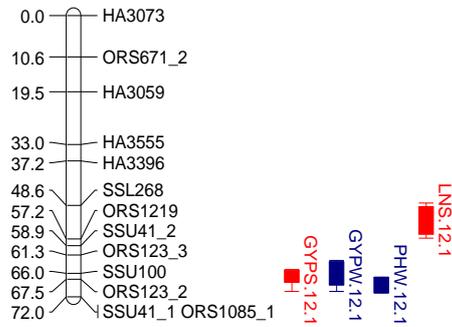
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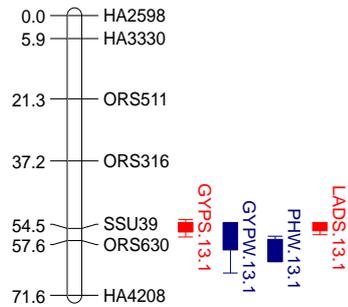
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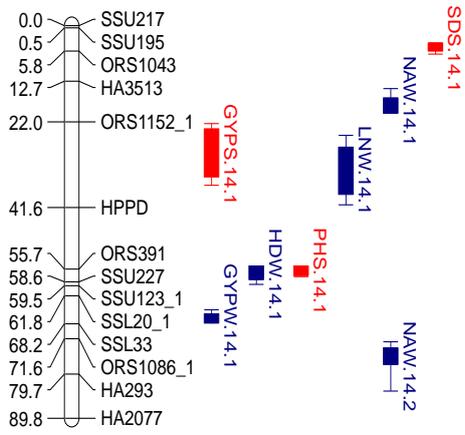
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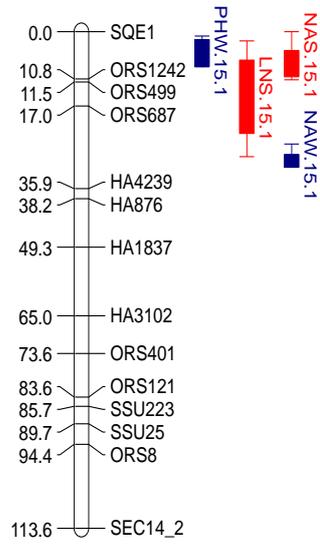
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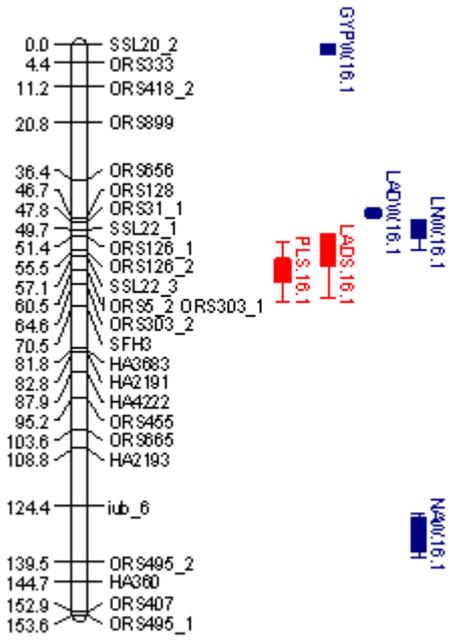
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