

**Title: Prioritizing QTLs for root system architecture in tetraploid wheat
Supplementary Figure S1-S4.**

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Supplementary Figure 1. frequency distribution of root seminal architecture (RSA) traits measured in the recombinant inbred populations Colosseo×Lloyd and Meridiano×Claudio.

Distributions are reported for the most relevant RSA traits.

List of RSA acronyms:

Root seminal architecture traits

TRN, total root number

Rt6, presence of the 6th asymmetric seminal root

PRL, primary root length

TRL, total root length

ARL, average root length

LRN, lateral root number

RGA, root growth angle

SL, shoot length

SDW, shoot dry weight

RDW, root dry weight

RSR, root to shoot ratio

iTGW, thousand grain weight of seeds used in the RSA experiment

Field traits

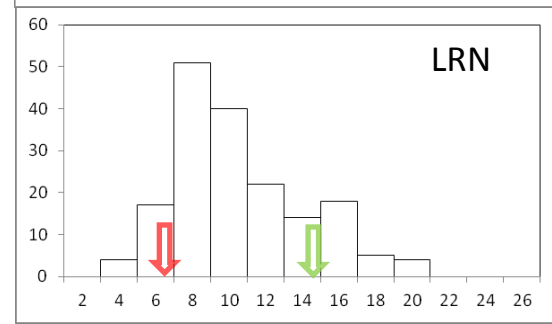
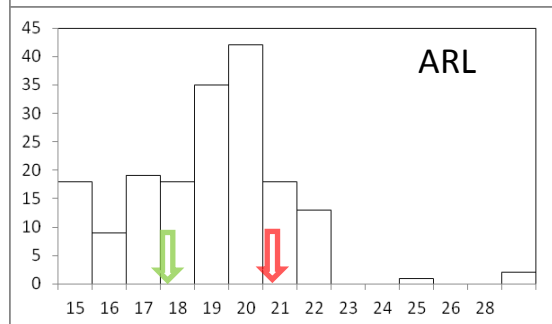
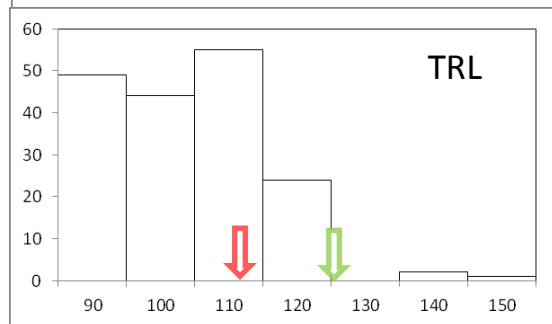
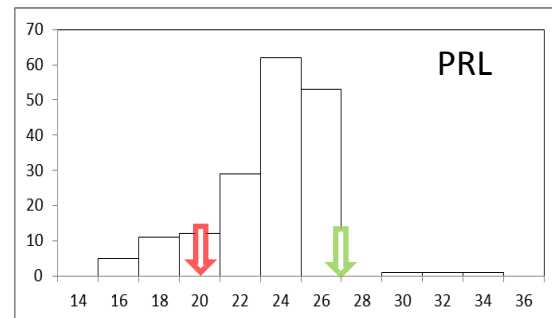
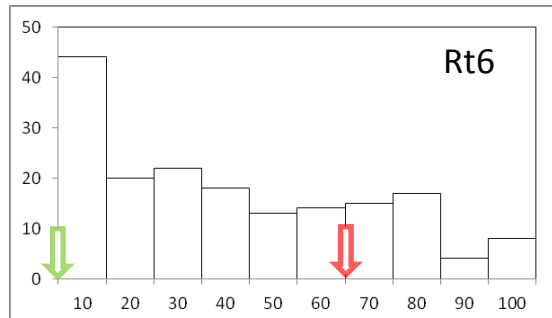
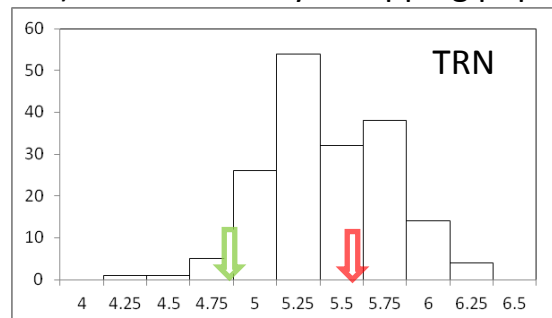
GY, grain yield

TGW, thousand grain weight in field trials

1A) Colosseo x Lloyd mapping population

↓ Colosseo

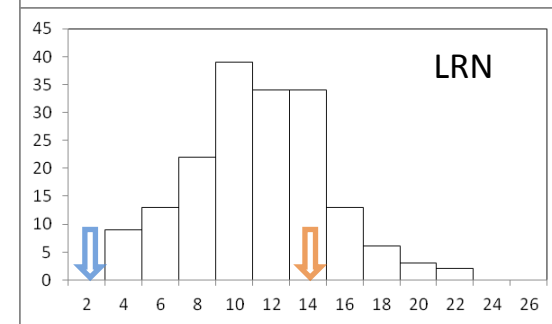
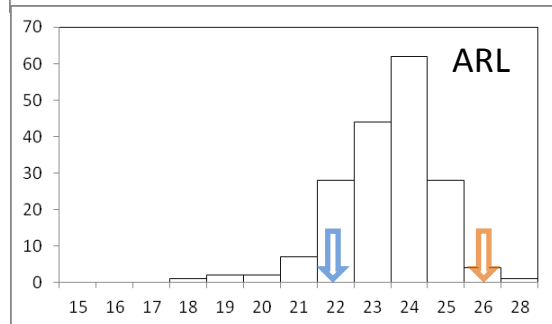
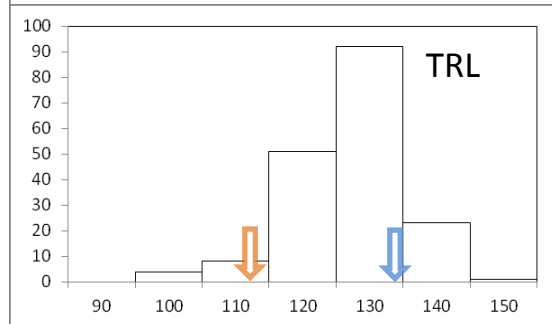
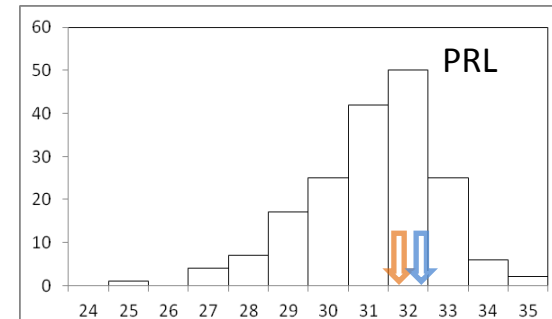
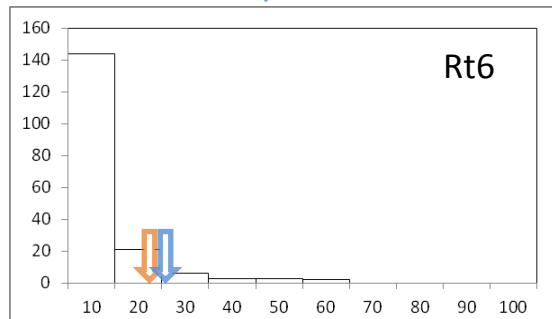
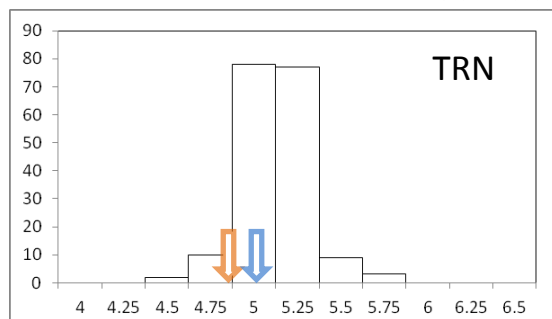
↓ Lloyd



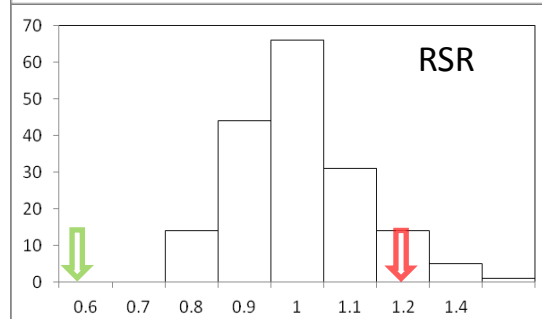
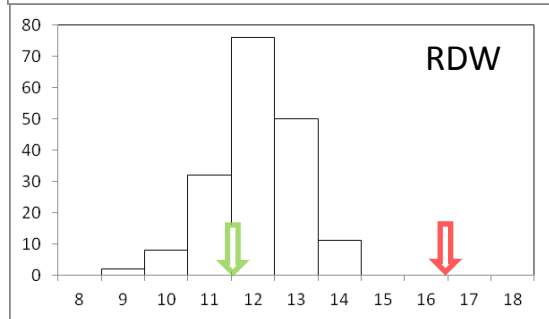
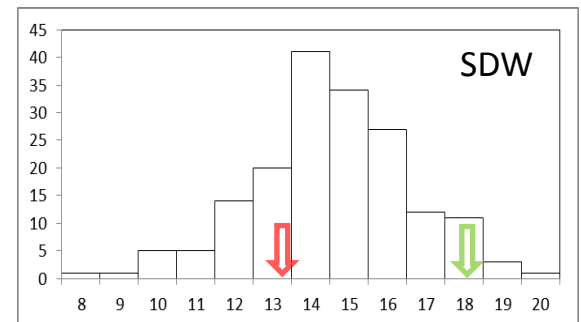
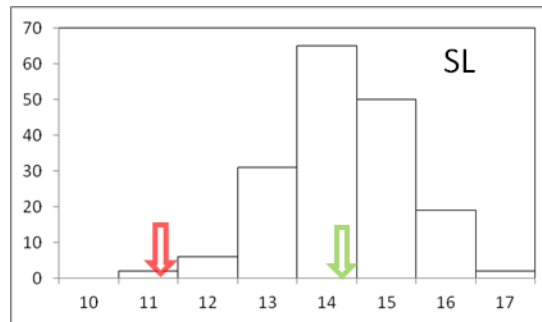
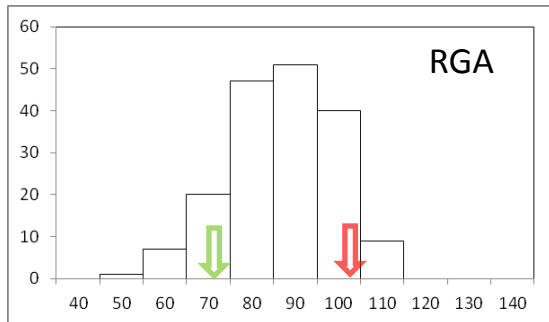
1B) Meridiano x Claudio mapping population

↓ Meridiano

↓ Claudio



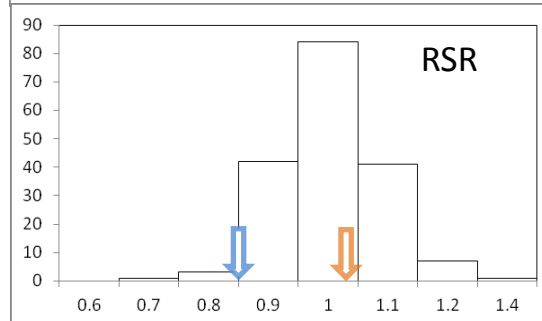
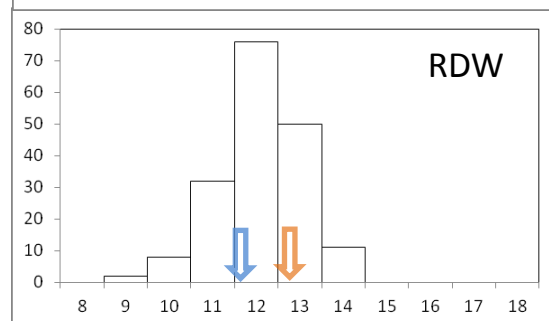
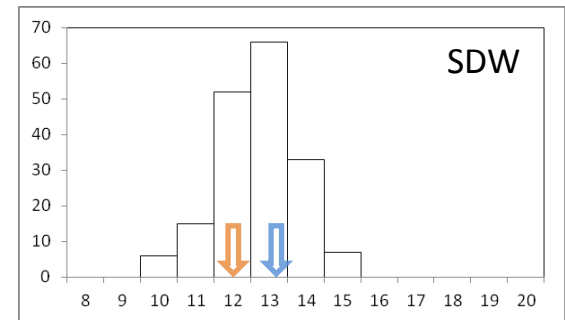
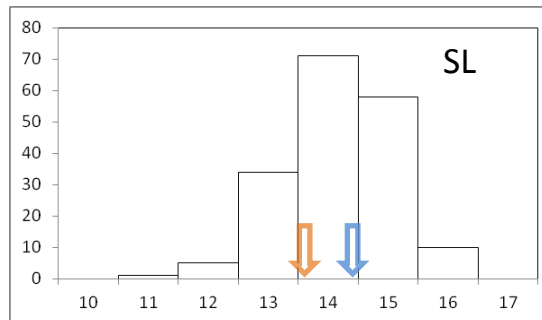
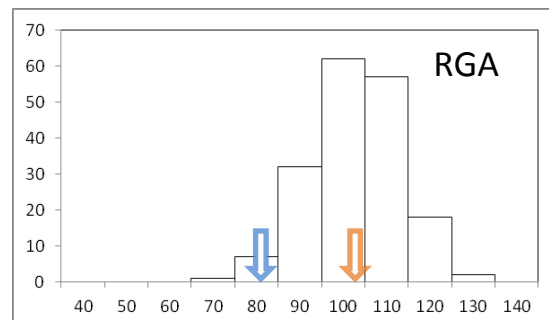
2A) Colosseo x Lloyd mapping population



↓ Colosseo

↓ Lloyd

2B) Meridiano x Claudio mapping population



↓ Meridiano

↓ Claudio

Supplementary Figure S2. Schematic representation of root system architecture (RSA) QTLs in tetraploid wheat projected onto an SNP-based tetraploid consensus map.

Root system architecture (RSA) QTLs from two durum wheat mapping population, the association mapping panel (Durum Panel, DP) and RSA QTLs from previously published studies in wheat are projected.

The consensus tetraploid wheat map has been published in Maccaferri *et al.* (2015).

QTLs from Colosseo × Lloyd (CxL) and Meridiano × Claudio (MxC) are reported on the left of chromosome bars while association mapping QTLs (AM-QTLs) are reported on the right. QTLs for root length and number are reported as blue-filled bars, seminal root angle (RGA) QTLs are reported in orange, shoot-related QTLs in green, grain weight (GWT) QTLs in red.

QTLs from RIL populations with $R^2 < 10\%$ are reported as thin half-tone coloured bars, while QTLs with $R^2 > 10\%$ are reported as tick full-tone bars.

The parental allele with a positive associated effect is reported as round-bracketing using the acronyms: **Co**, Colosseo; **Ld**, Lloyd; **Me**, Meridiano; **Cl**, Claudio.

QTLs from association mapping (GWAS-QTLs, reported as DP QTLs) have been reported together with their significance level: **, marker-wise significance $P < 0.01$ ($-\text{LOG}P=2$); ***, marker-wise significance, $P < 0.001$ ($-\text{LOG}P=3$); ****, experiment-wise significance, $P < 0.05$ ($-\text{LOG}P=4$).

root system architecture (RSA) QTLs from previously published studies in wheat have been projected on the consensus map and reported as black-filled confidence interval bars. QTL references are reported as round-bracketed alpha-numeric acronyms using **Tt** for *Triticum turgidum* QTLs and **Ta** for *Triticum aestivum* QTLs.

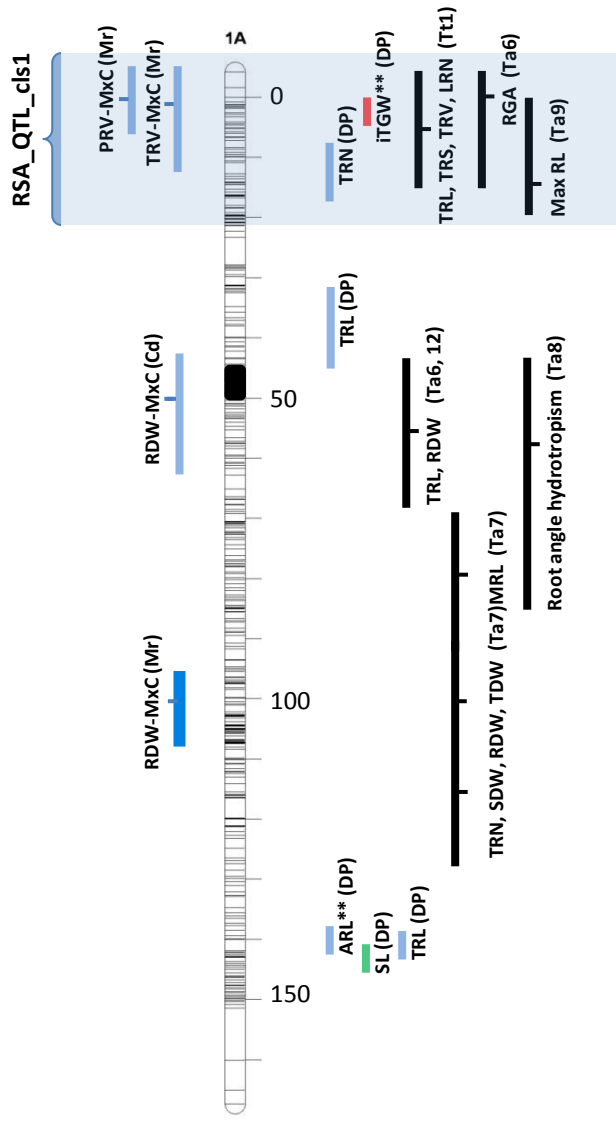
Syntenic intervals of rice deep rooting and root growth angle QTLs have been projected and reported on the extreme-right of chromosome bars as orange-filled bars using the **Os** acronym.

Major RSA QTL-clusters based on concomitant co-location of RSA QTL confidence intervals from multiple wheat mapping stocks are reported as grey-banded intervals.

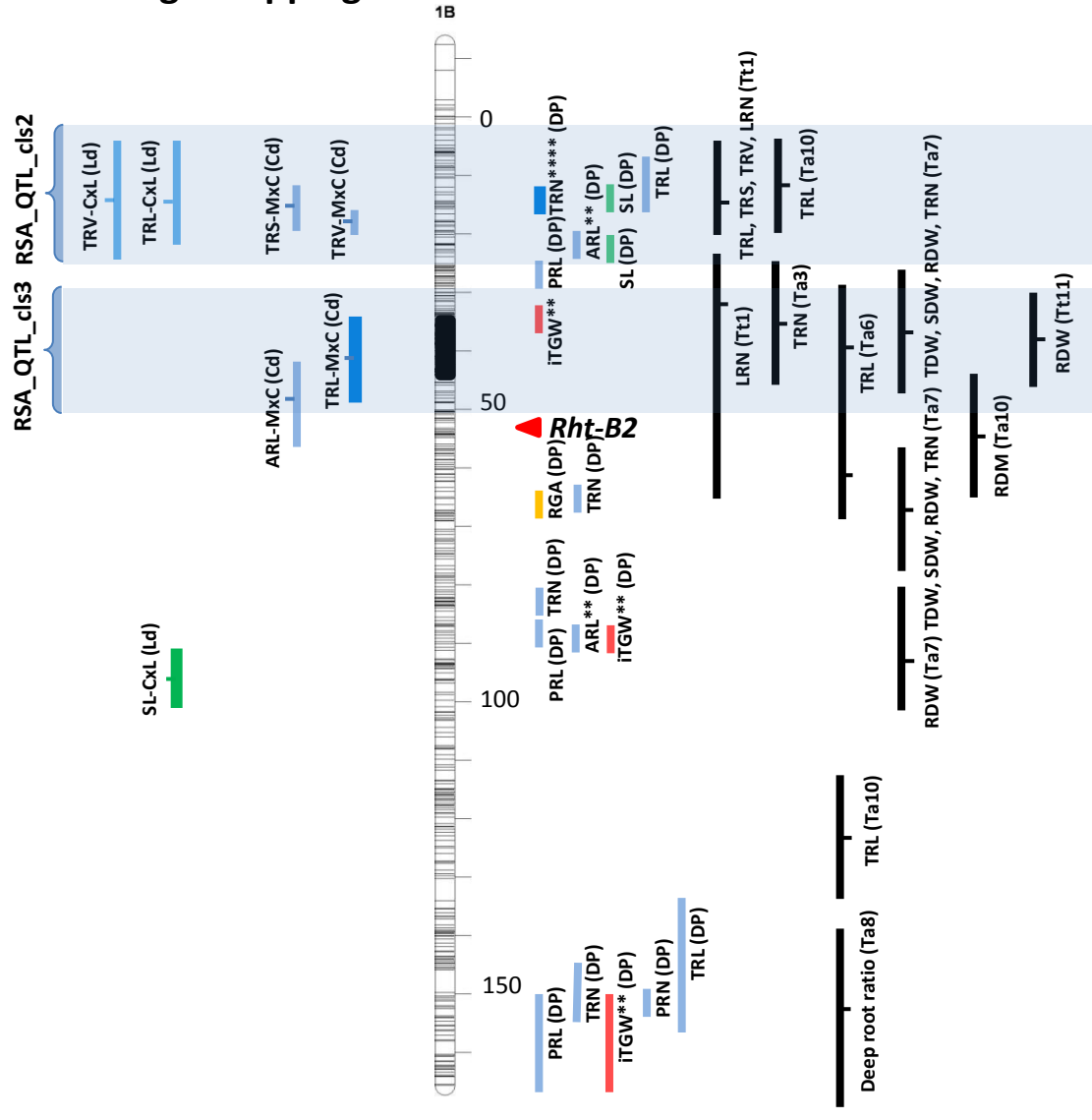
RSA trait acronyms: TRN, Total root number; R6th, Presence of the 6th asymmetric seminal root; PRL, primary root length; TRL, total root length; ARL, average root length; LRN, lateral root number; RGA, root growth angle; RDW, root dry weight; SDW, shoot dry weight; SL, shoot length; RSR, root-to-shoot ratio; RS, root surface; RD, root diameter; RV, root volume; GY, grain yield; iTGW, initial thousand grain weight of seeds used in the RSA experiment; TGW, thousand grain weight in field trials

References for projected root system architecture QTLs from previous studies in wheat

Code	Reference	Population	Species
Tt1	Petrarulo et al. (2015) Mol Genet Genomics 290:785-806.	Creso x Pedroso	Tetraploid wheat (Tt)
Ta2	Cao et al. (2014)	Xiaoyan 54 x Jing 411	Hexaploid wheat (Ta)
Ta3	Christopher et al. (2013) Theor Appl Genet 126:1563-1574.	Seri x Hartog	Hexaploid wheat (Ta)
Ta4	Atkinson et al. (2015) J Exp Bot 66:2283-2292.	Savannah x Rialto	Hexaploid wheat (Ta)
Ta5	Bai et al. (2013) J Exp Bot 64:1745-1753.	Avalon x cadenza	Hexaploid wheat (Ta)
Ta6	Liu et al. (2013) Euphytica 189:51-	Hanxuan 10 and Lumai 14	Hexaploid wheat (Ta)
Ta7	Guo et al. (2012)	Chuan 35050 x Shannong 483	Hexaploid wheat (Ta)
Ta8	Hamada et al. (2012)	U24 x AyahiKari	Hexaploid wheat (Ta)
Ta9	Ren et al. (2012)	Xiaoyan 54 x Jing 411	Hexaploid wheat (Ta)
Ta10	Laperche et al. (2006) Theor Appl Genet 113:1131-1146.	Arche x Recital	Hexaploid wheat (Ta)
Tt11	Kubo et al. (2007)	Jennah Khetifa x Cham1	Tetraploid wheat (Ta)
Ta12	An et al. (2006)	Hanxuan 10 x Lumai 14	Hexaploid wheat (Tt)

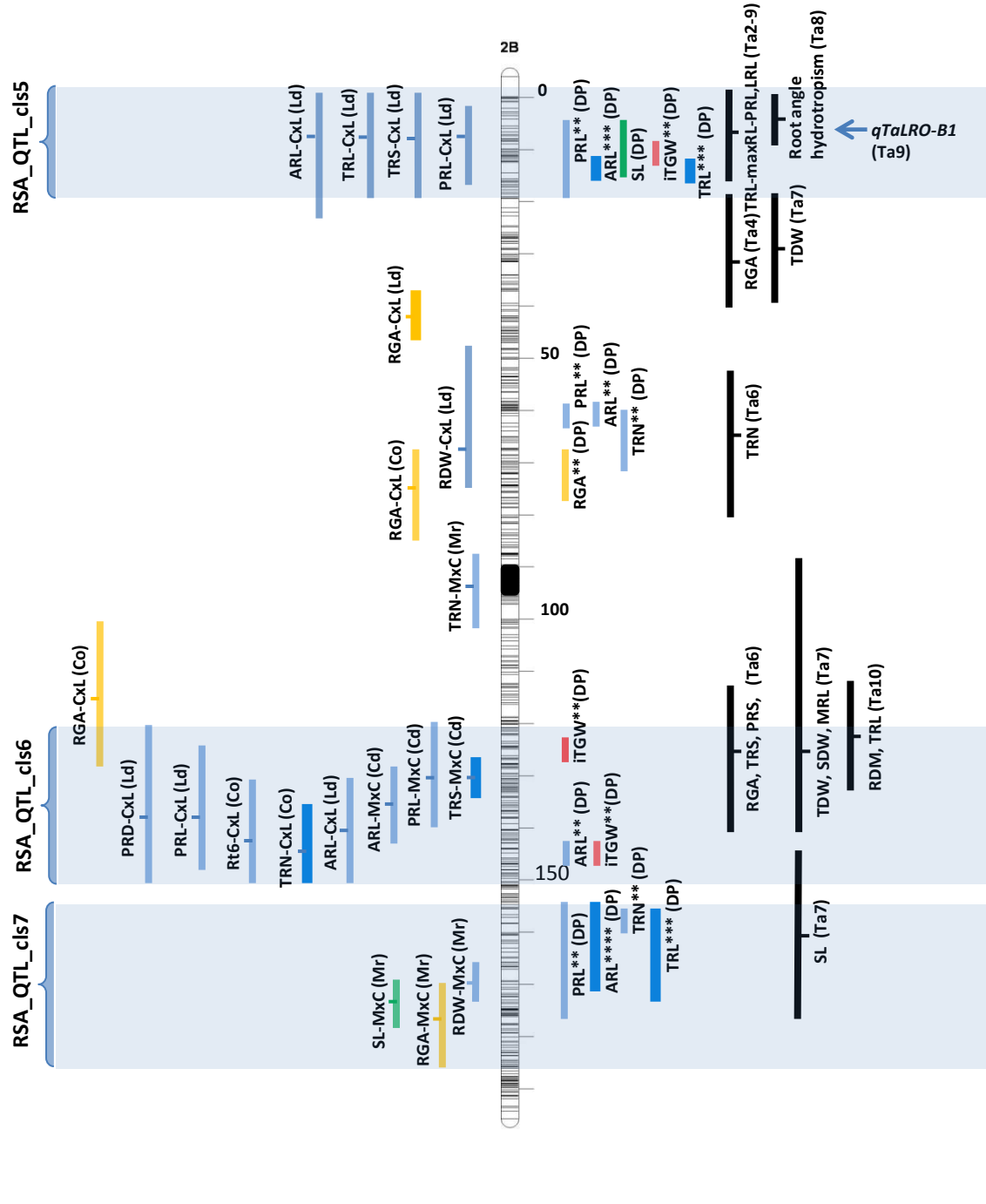
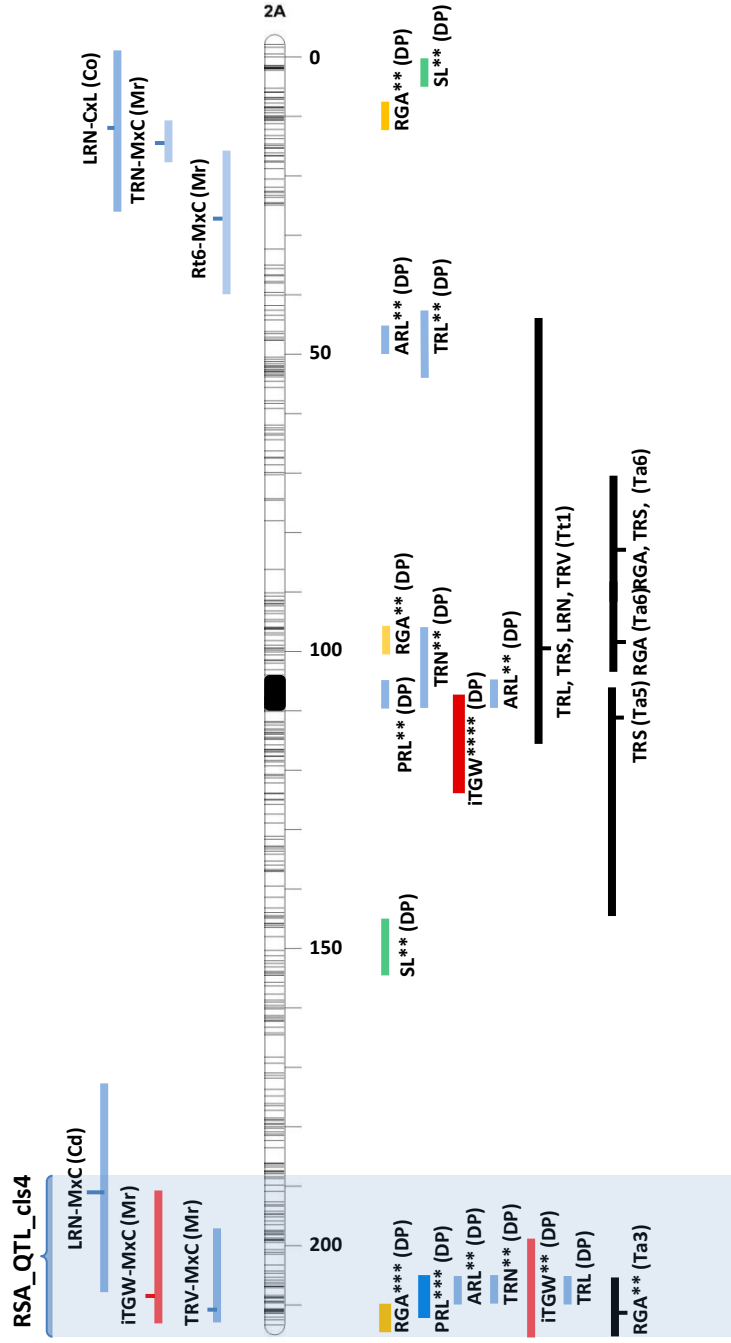


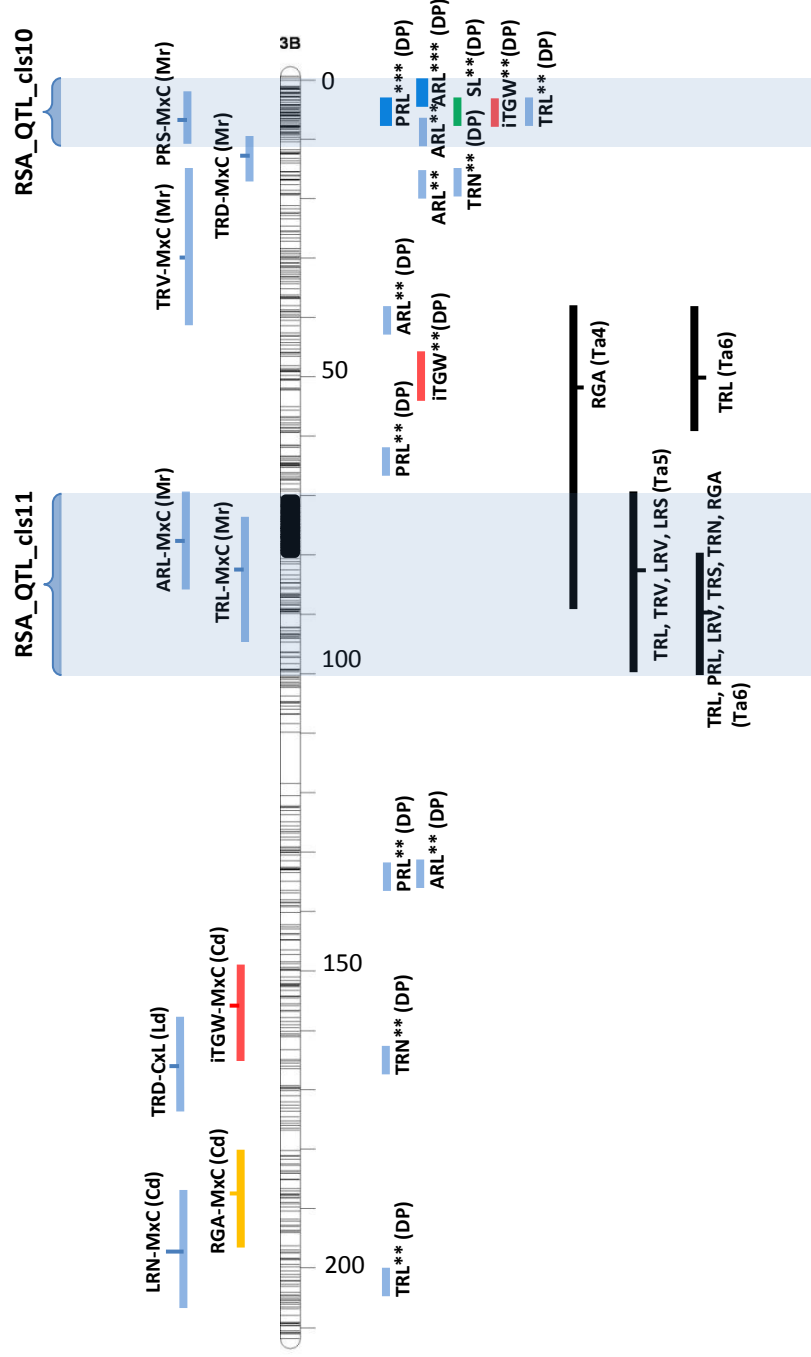
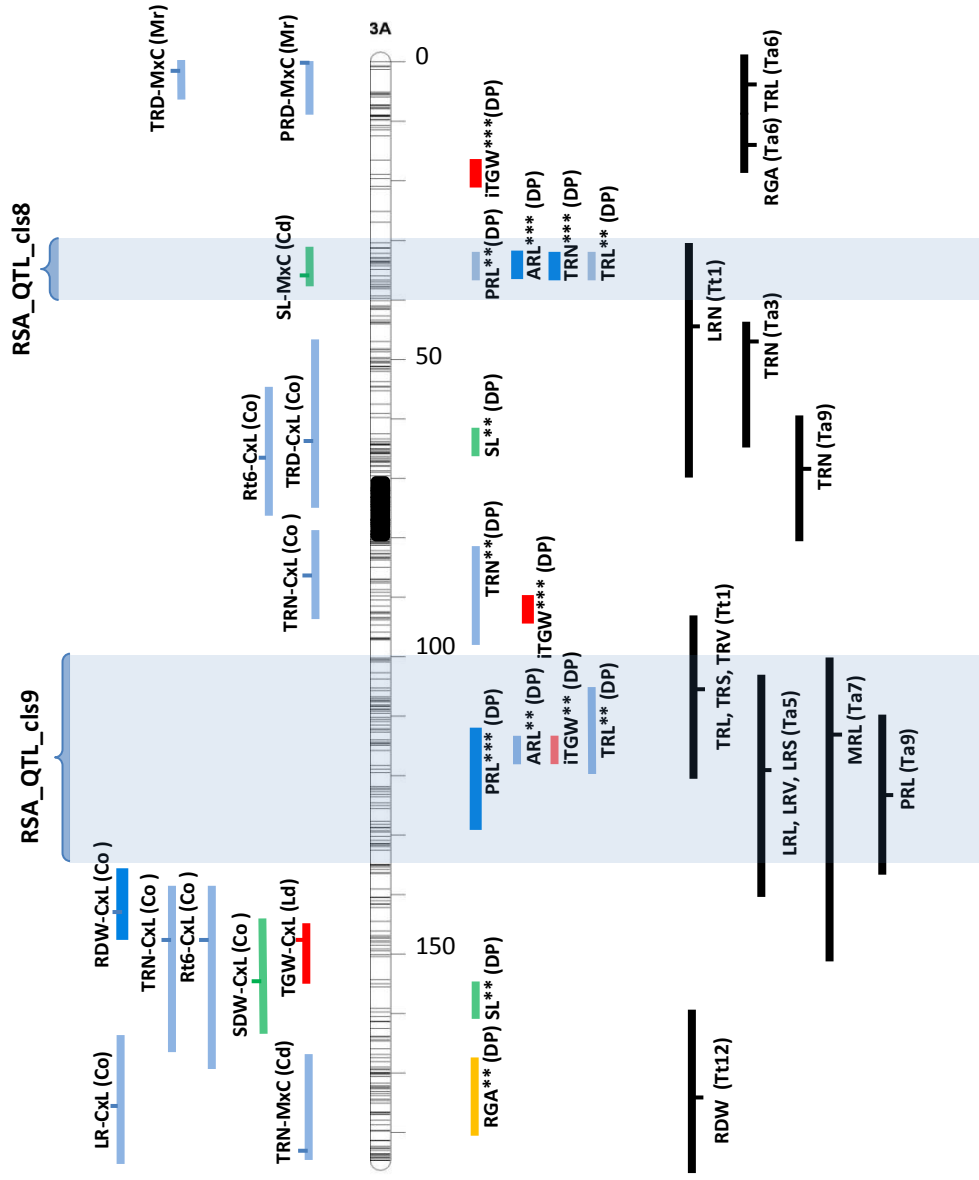
Linkage mapping

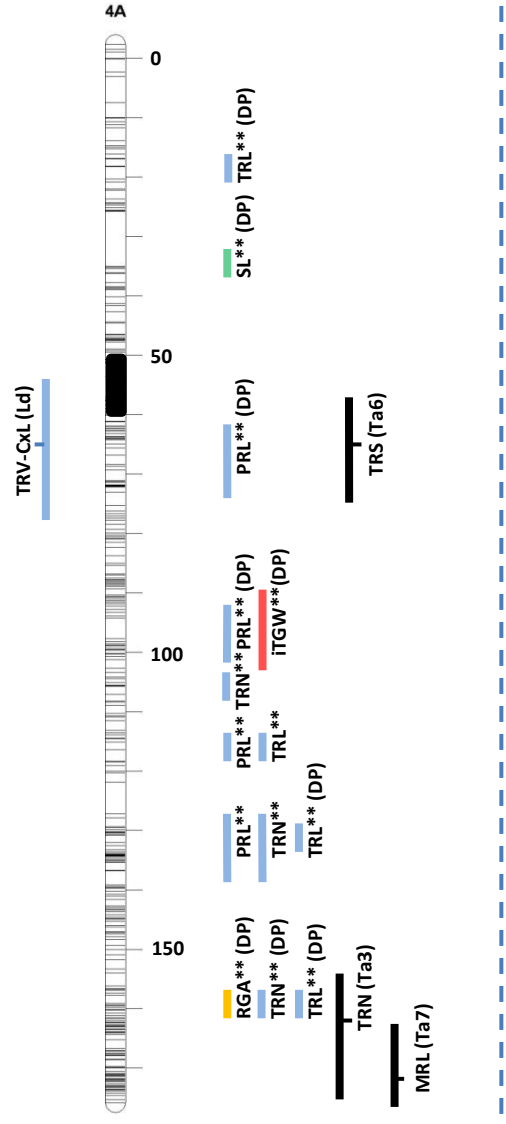


GWAS

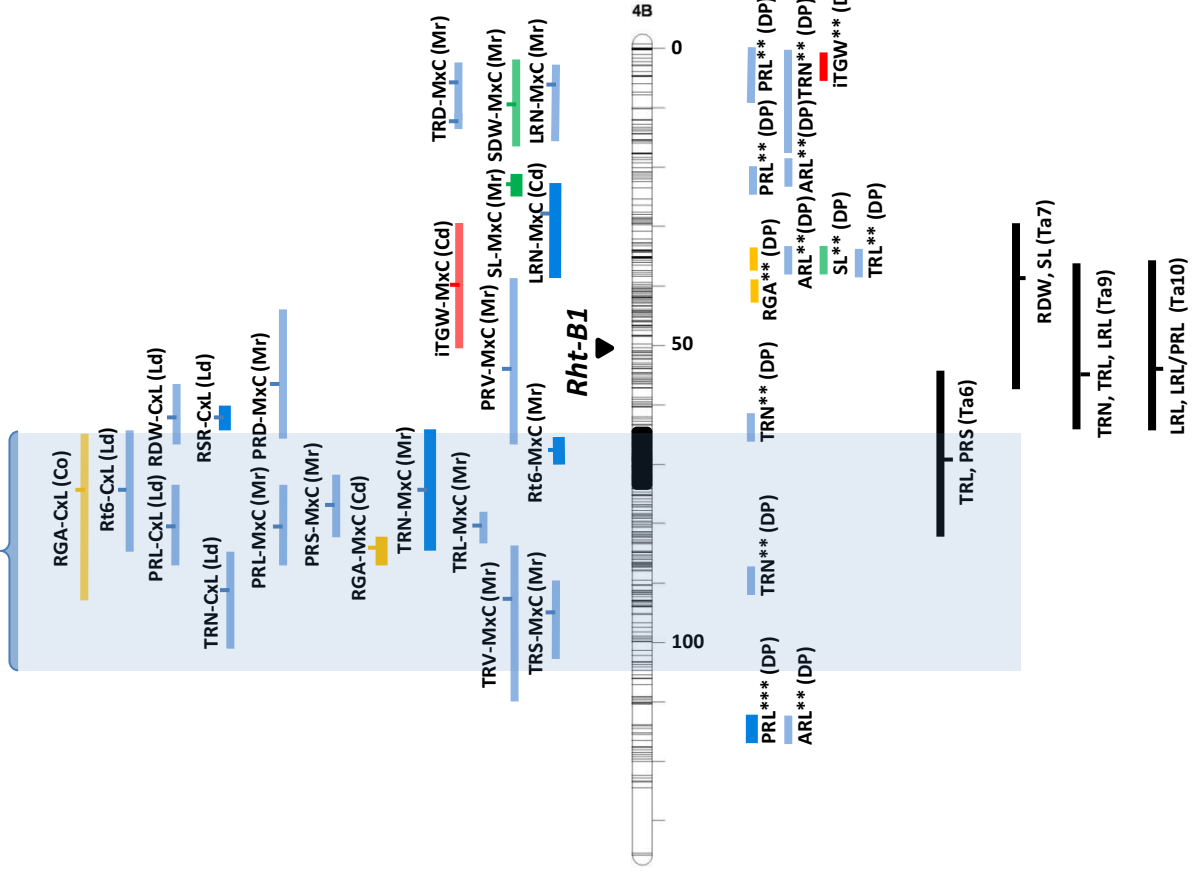
Bread wheat

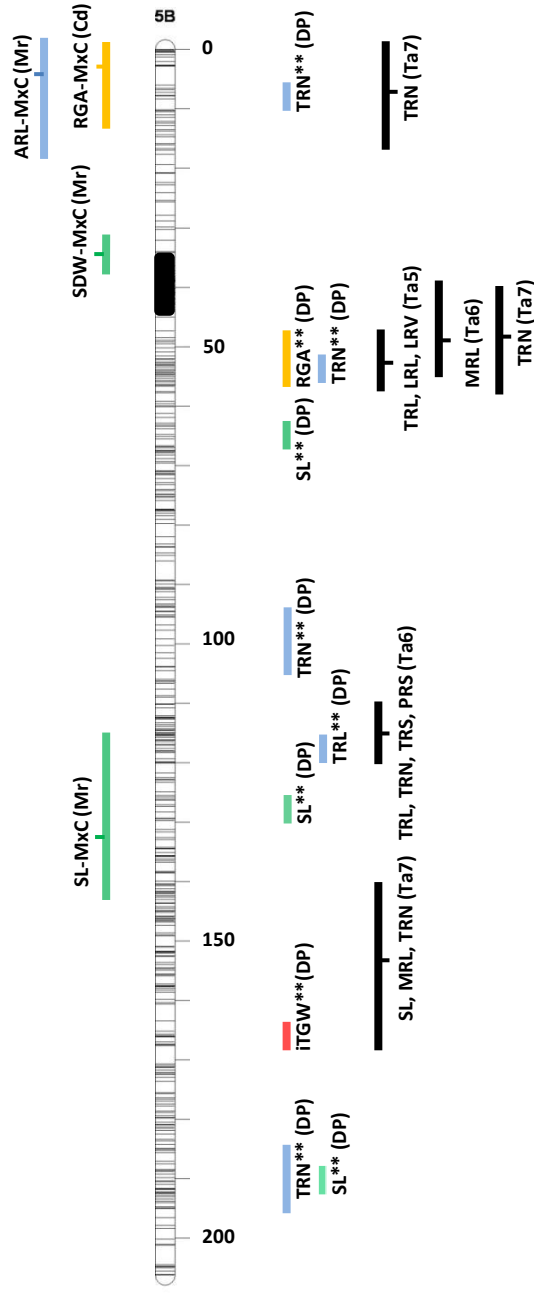
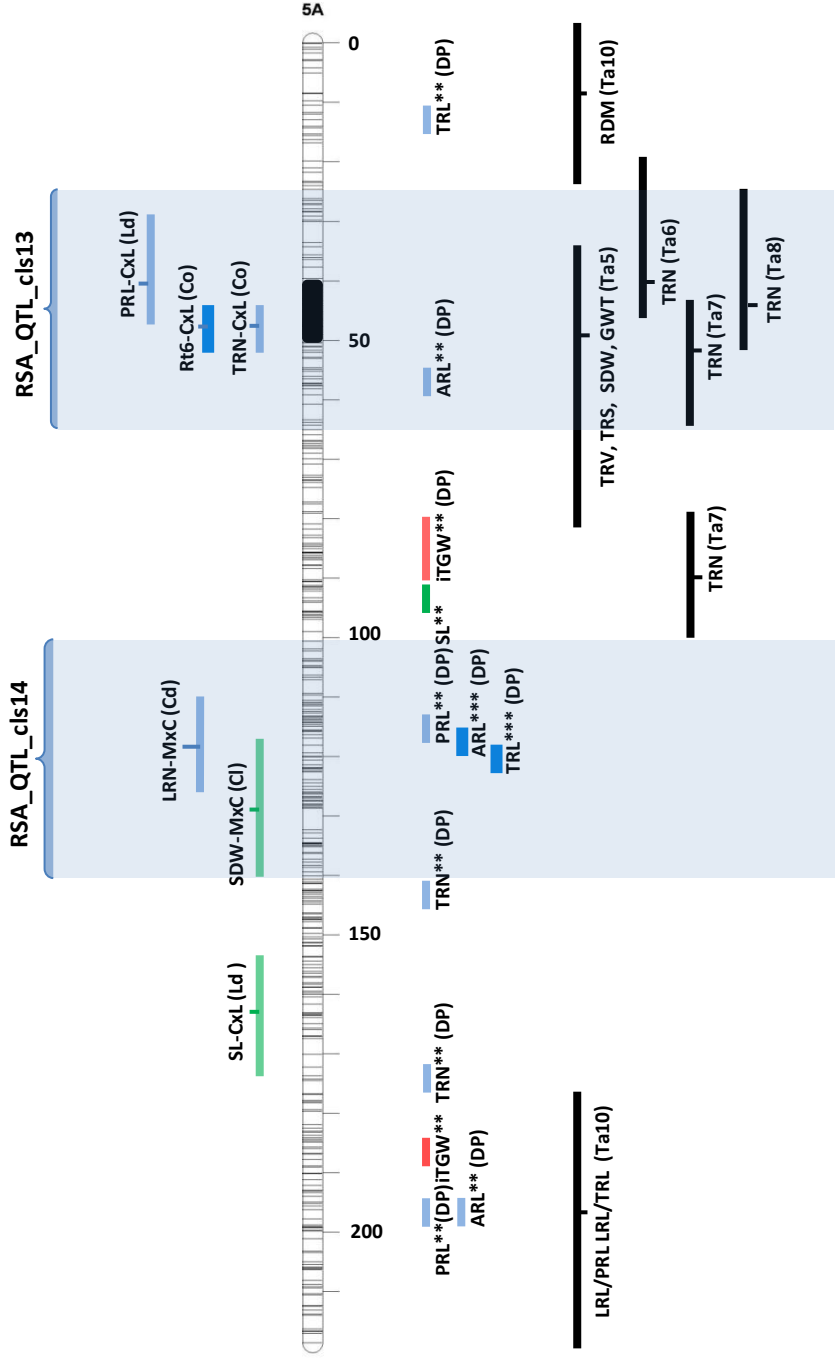




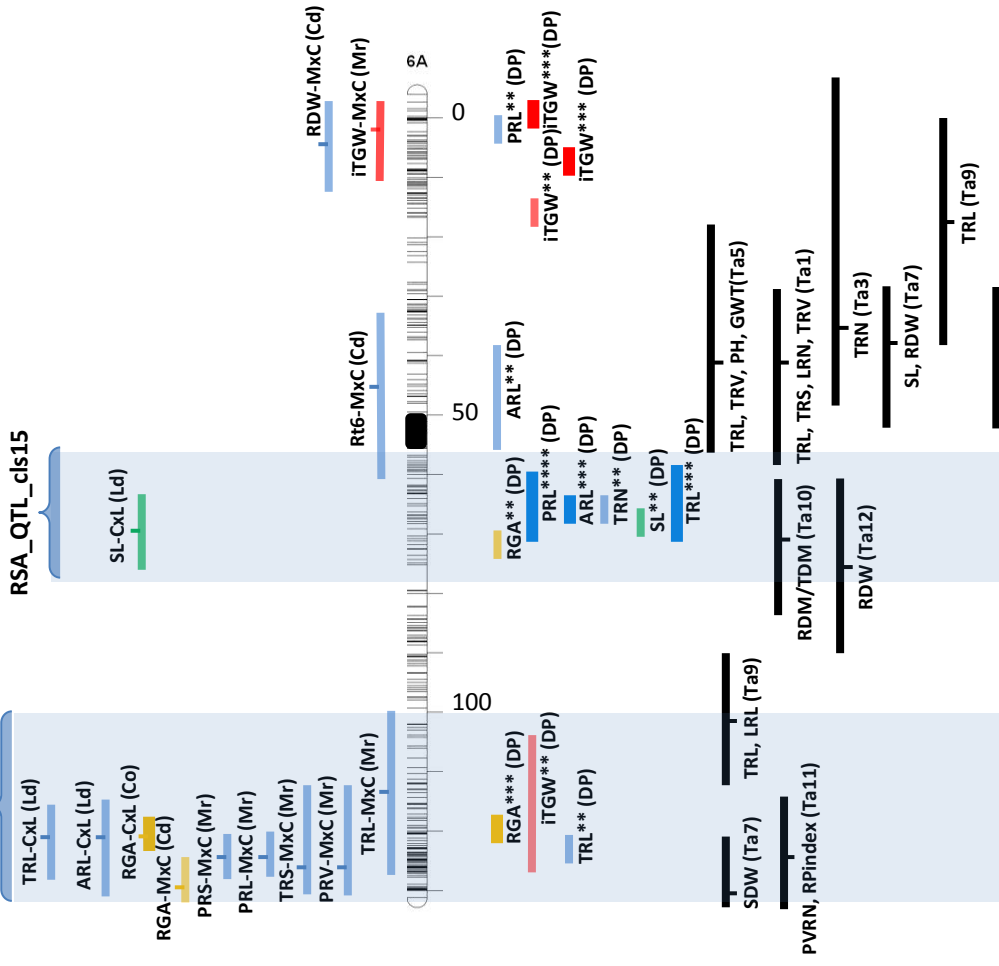


RSA_QTL_cls12

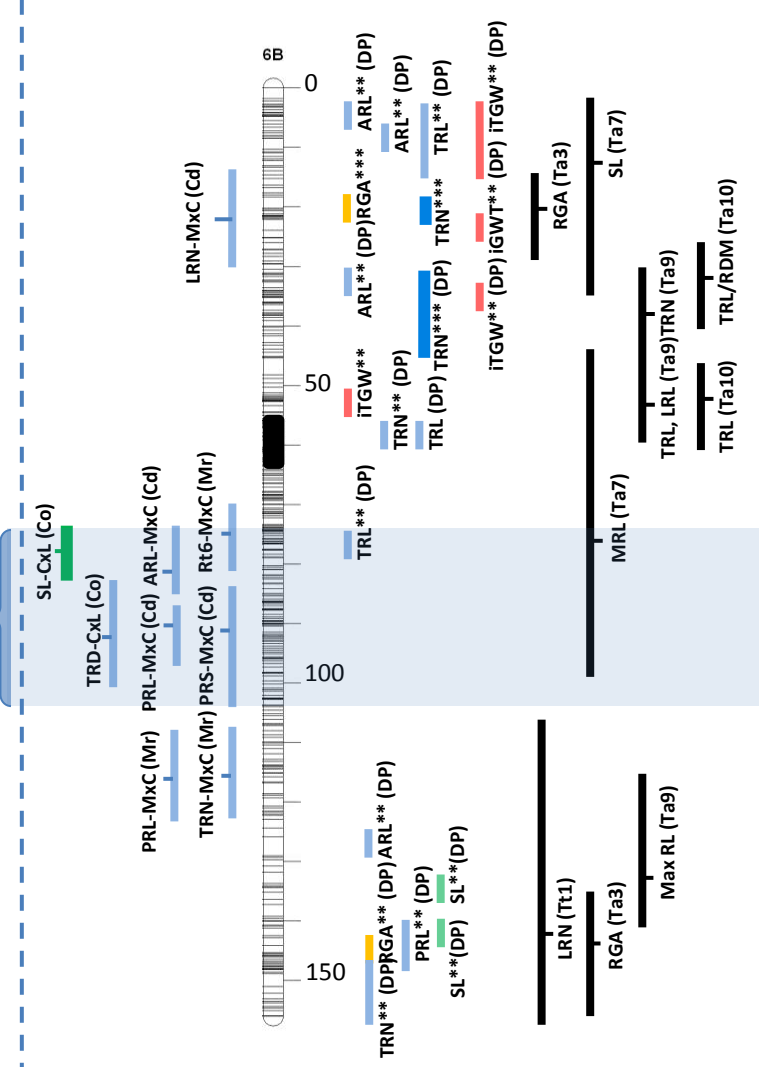




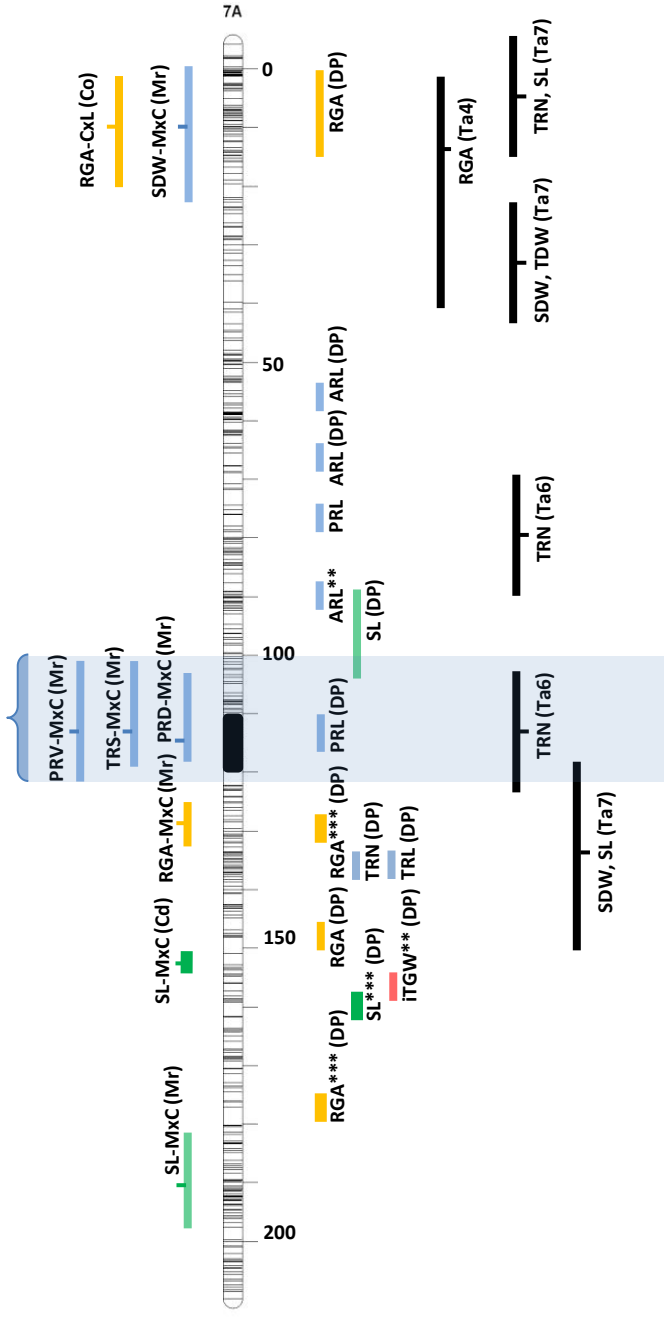
RSA_QTL_cls16



RSA_QTL_cls17



RSA_QTL_cis18



RSA_QTL_cis20

TRL-CxL (Co)
 TRS-CxL (Ld)
 ARL-CxL (Co)

RSA_QTL_cis19

PRS-MxC (Mir)
 PRL-MxC (Mir)

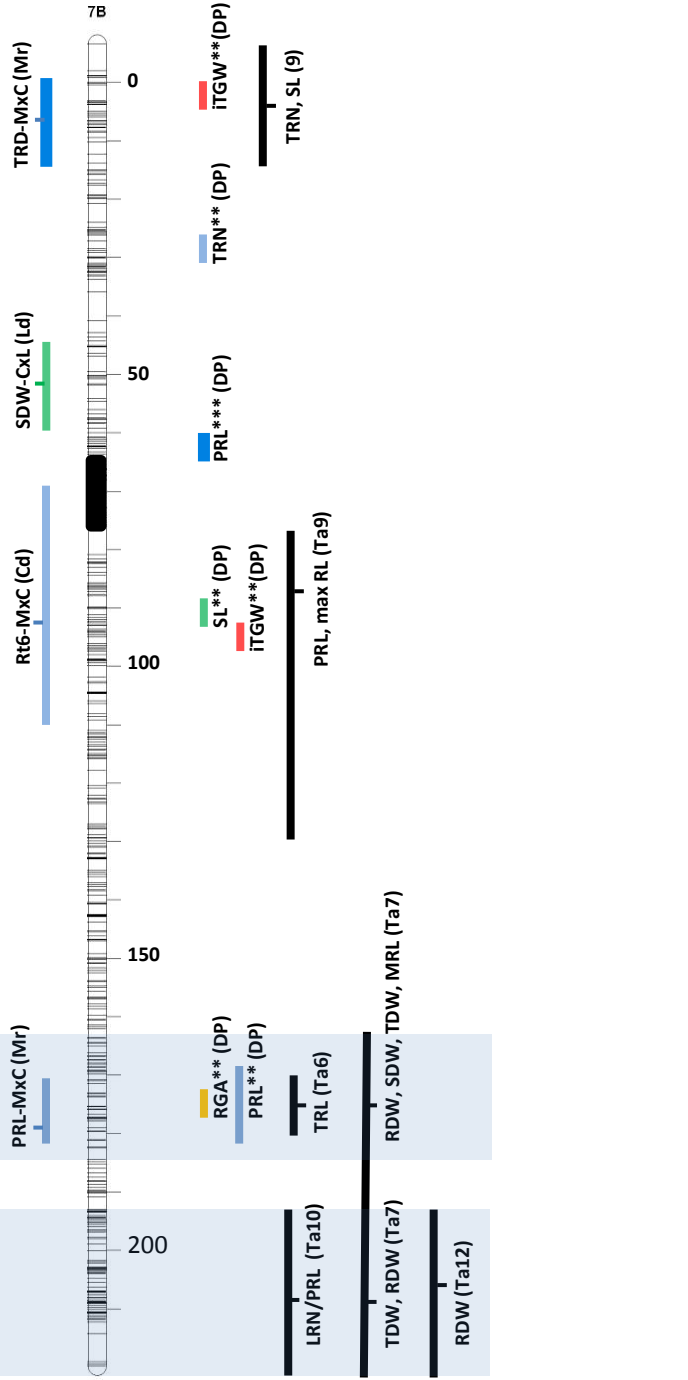
RGA** (DP)
 PRL*** (DP)
 TRL (Ta6)

RDW, SDW, TDW, MRL (Ta7)

TDW, RDW (Ta7)

RDW (Ta12)

7B



Supplementary Figure S3. Schematic representation of root system architecture (RSA) QTLs , grain yield (GY) and thousand grain weight (TKW) in tetraploid wheat projected onto an SNP-based tetraploid consensus map.

Root system architecture (RSA) QTLs were identified in two durum wheat mapping population and the association mapping panel and RSA QTLs from previously published studies in wheat are projected. The tetraploid wheat consensus map used as a reference has been published by Maccaferri et al. (2015).

QTLs from Colosseo × Lloyd and Meridiano × Claudio are reported on the left of chromosome bars while association mapping QTLs (AM-QTLs) are reported on the right. QTLs for root length and number are reported as blue-filled bars, seminal root angle (RGA) QTLs are reported in orange, shoot-related QTLs in green, grain weight (GWT) QTLs in red.

QTLs from RIL populations with $R^2 < 10\%$ are reported as thin half-tone coloured bars, while QTLs with $R^2 > 10\%$ are reported as tick full-tone bars.

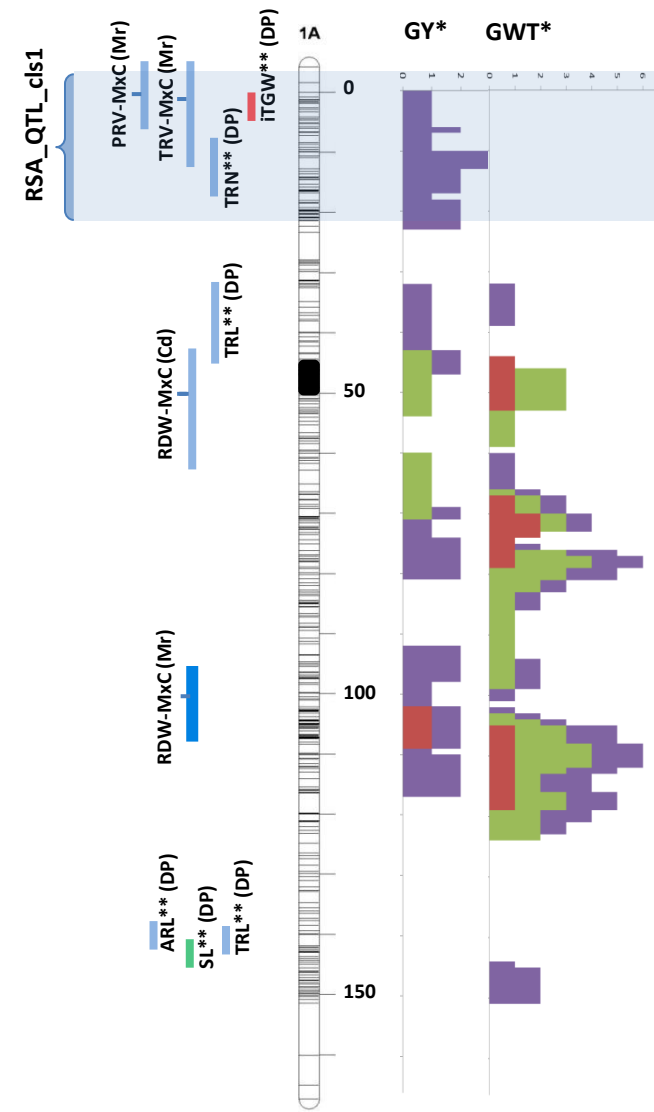
The parental allele with increasing trait effect is reported as round-bracketed using acronyms: **Co**, Colosseo; **Ld**, Lloyd; **Me**, Meridiano; **Cl**, Claudio.

RSA QTLs from association mapping (Durum Panel, DP) are reported on the left of chromosome bars together with their significance level: **, marker-wise significance P 0.01; ***, marker-wise significance, P 0.001; ****, experiment-wise significance, P 0.05

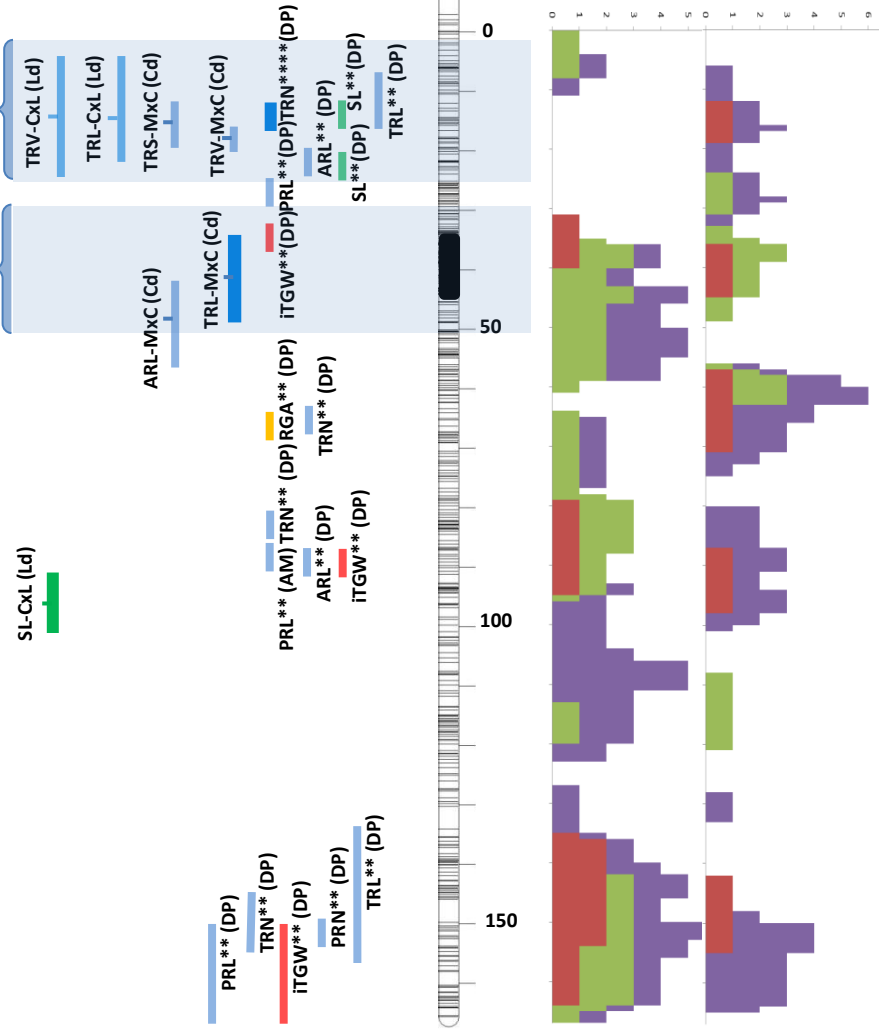
Grain yield (GY) and grain weight (TKW) QTLs from association mapping (Durum Panel, DP) are reported on the right of the chromosome bars. GY and TKW QTLs have been searched in the Durum Panel using data from 15 field trials carried out in Mediterranean environments as reported in Maccaferri et al. (2011). Association mapping QTLs have been graphically reported as a plot of QTL density on a 1 cM basis along the chromosomes, based on the QTL significance intervals. According to Maccaferri et al. (2011), QTL density has been reported as a cumulated density plot for: (i) highly stressed low-yielding environments (**red plot**, three environments), (ii) medium yielding, stressed environments (**green plot**, five envs.), (iii) high-yielding environments (**dark violet plot**, seven envs.).

Major RSA QTL-clusters based on concomitant co-location of RSA QTL confidence intervals from multiple wheat mapping stocks are reported as grey-banded intervals.

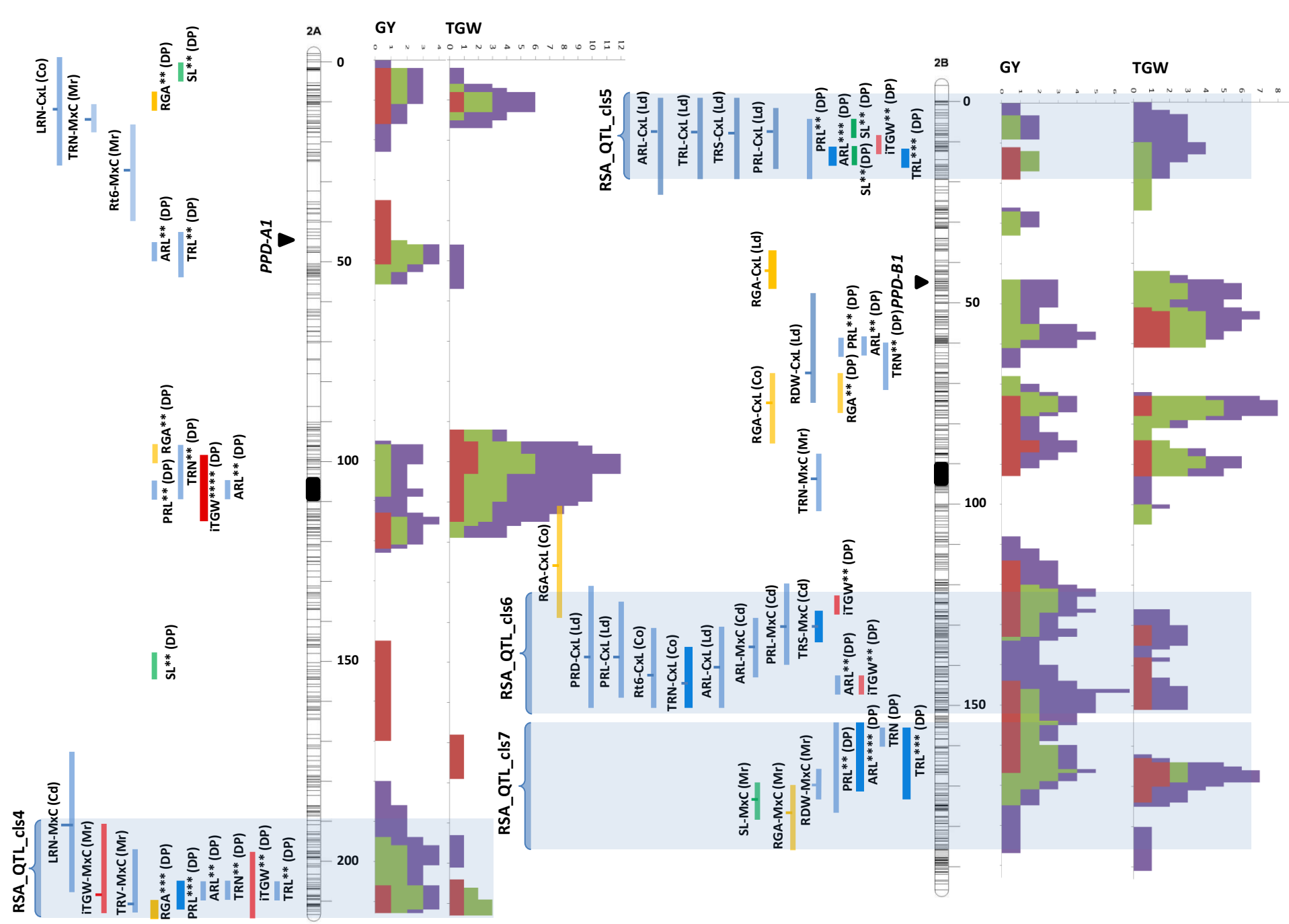
RSA and field trait acronyms: TRN, Total root number; R6th, Presence of the 6th asymmetric seminal root; PRL, primary root length; TRL, total root length; ARL, average root length; LRN, lateral root number; RGA, seminal root angle; RDW, root dry weight; SDW, shoot dry weight; SL, shoot length; RSR, root-to-shoot ratio; RS, root surface; RD, root diameter; RV, root volume; GY, grain yield; iGWT, grain weight of seeds used in the RSA experiment; fGWT, grain weight in field trials



RSA_QTL_cis3 RSA_QTL_cis2

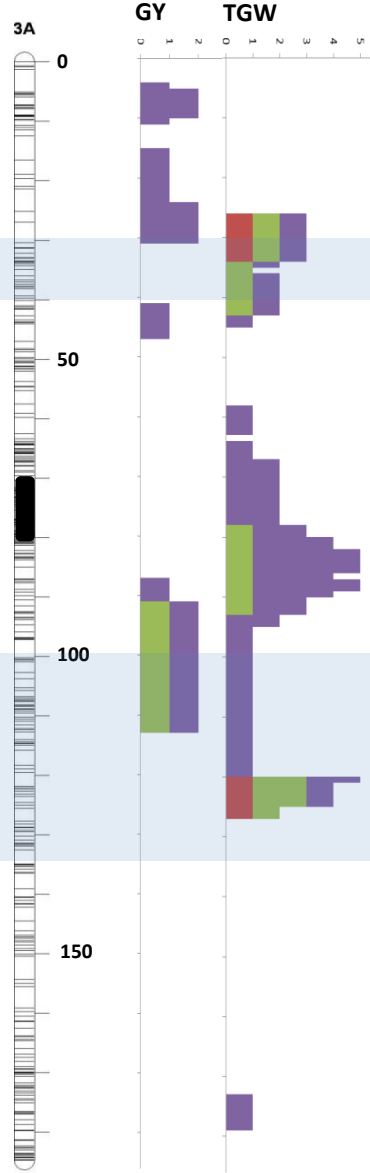
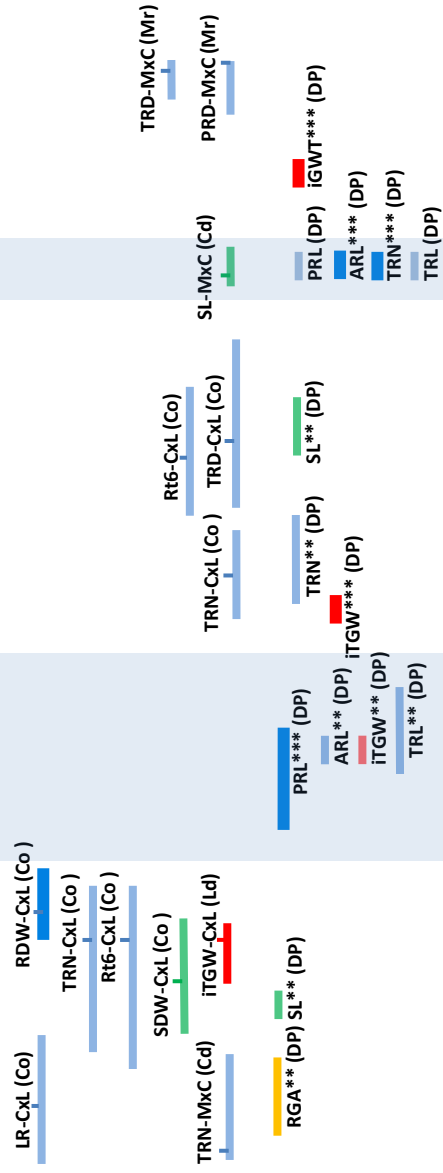


*: QTL density plot (QTL number over 15 environments in total, plotted on a 1cM basis)



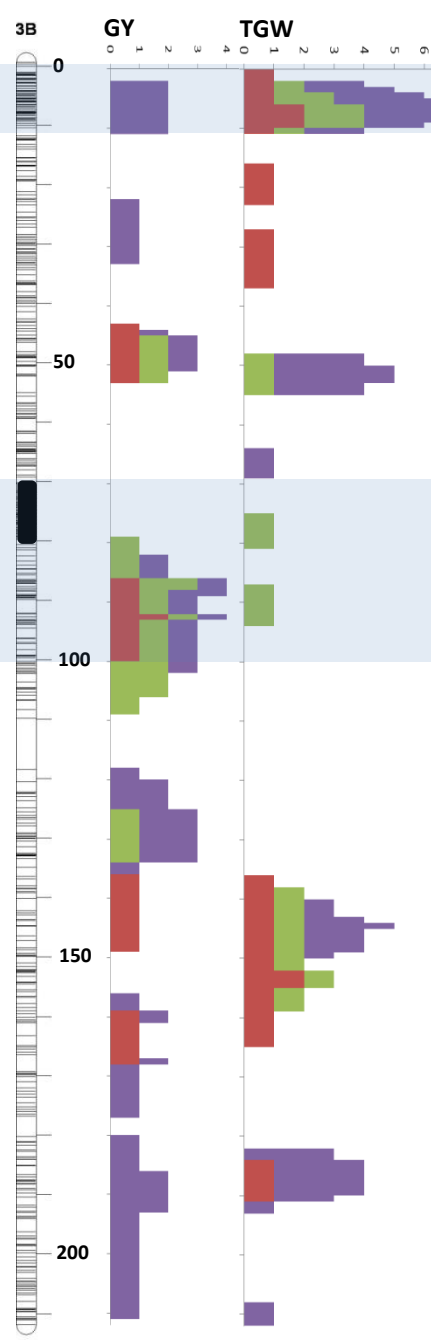
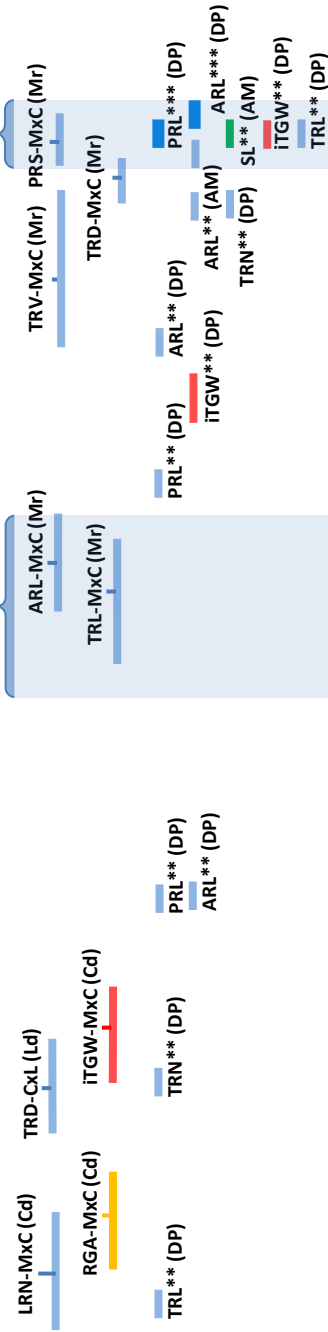
RSA_QTL_cis8

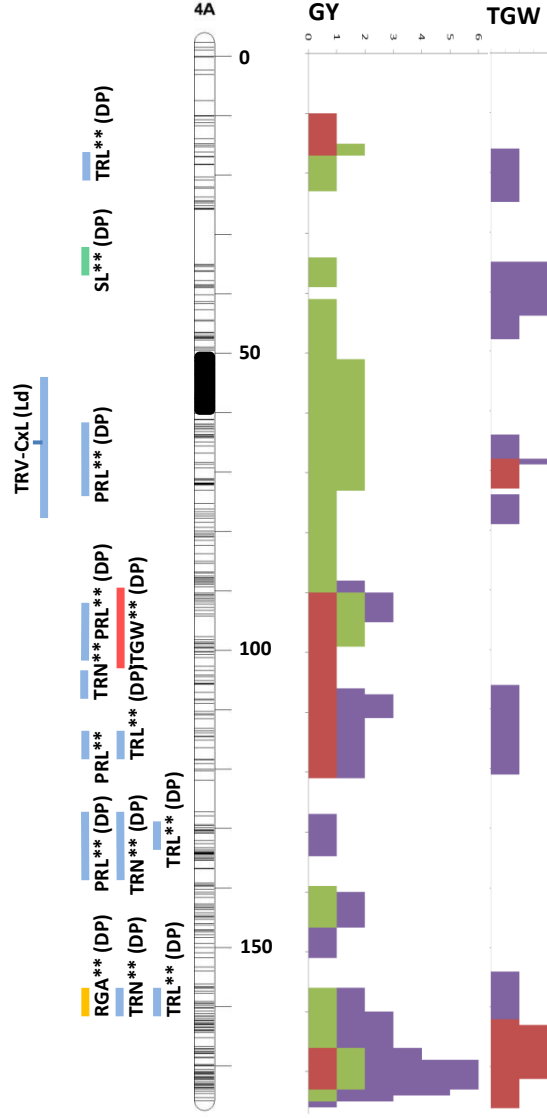
RSA_QTL_cis9



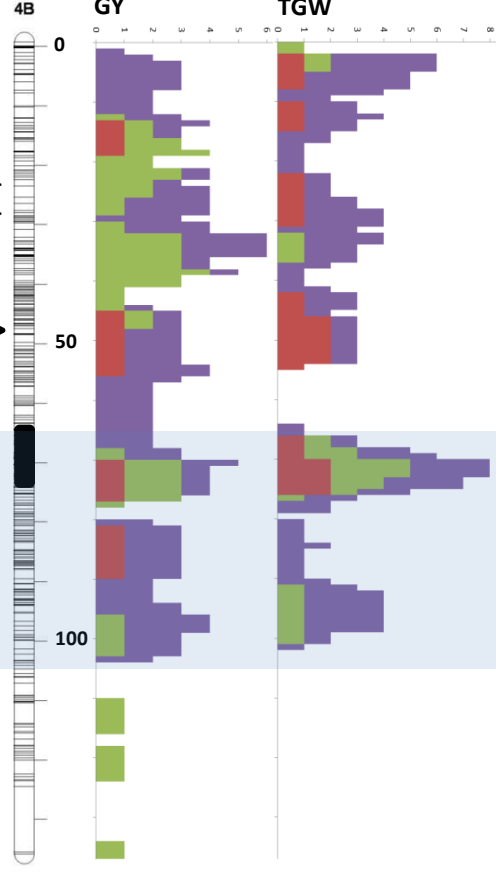
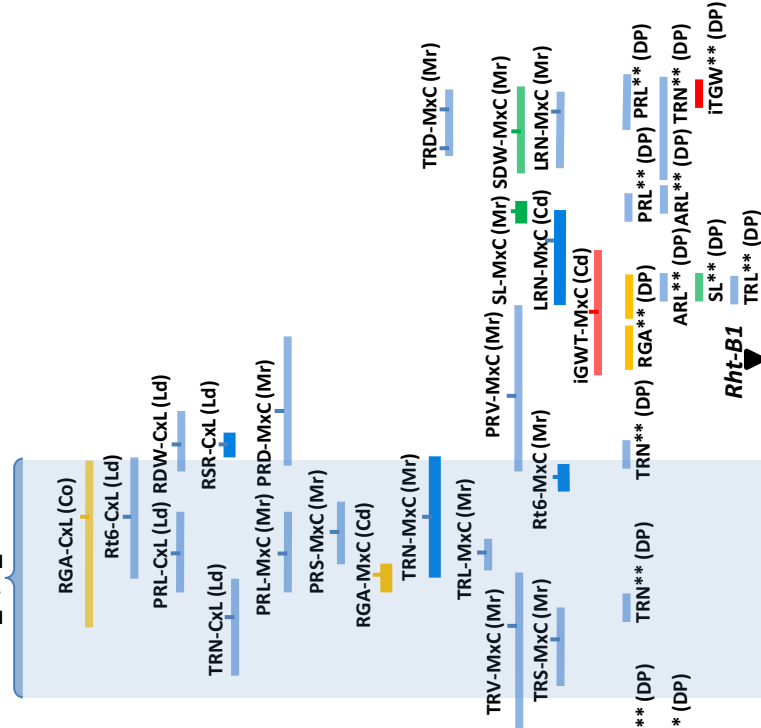
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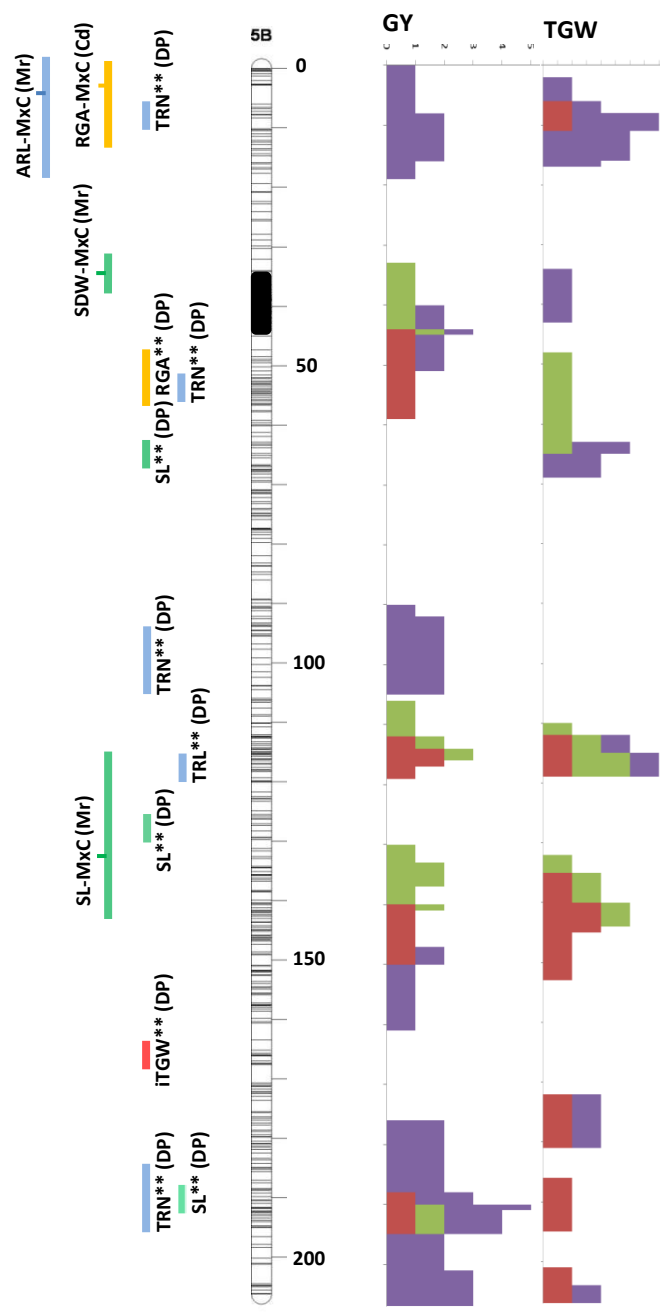
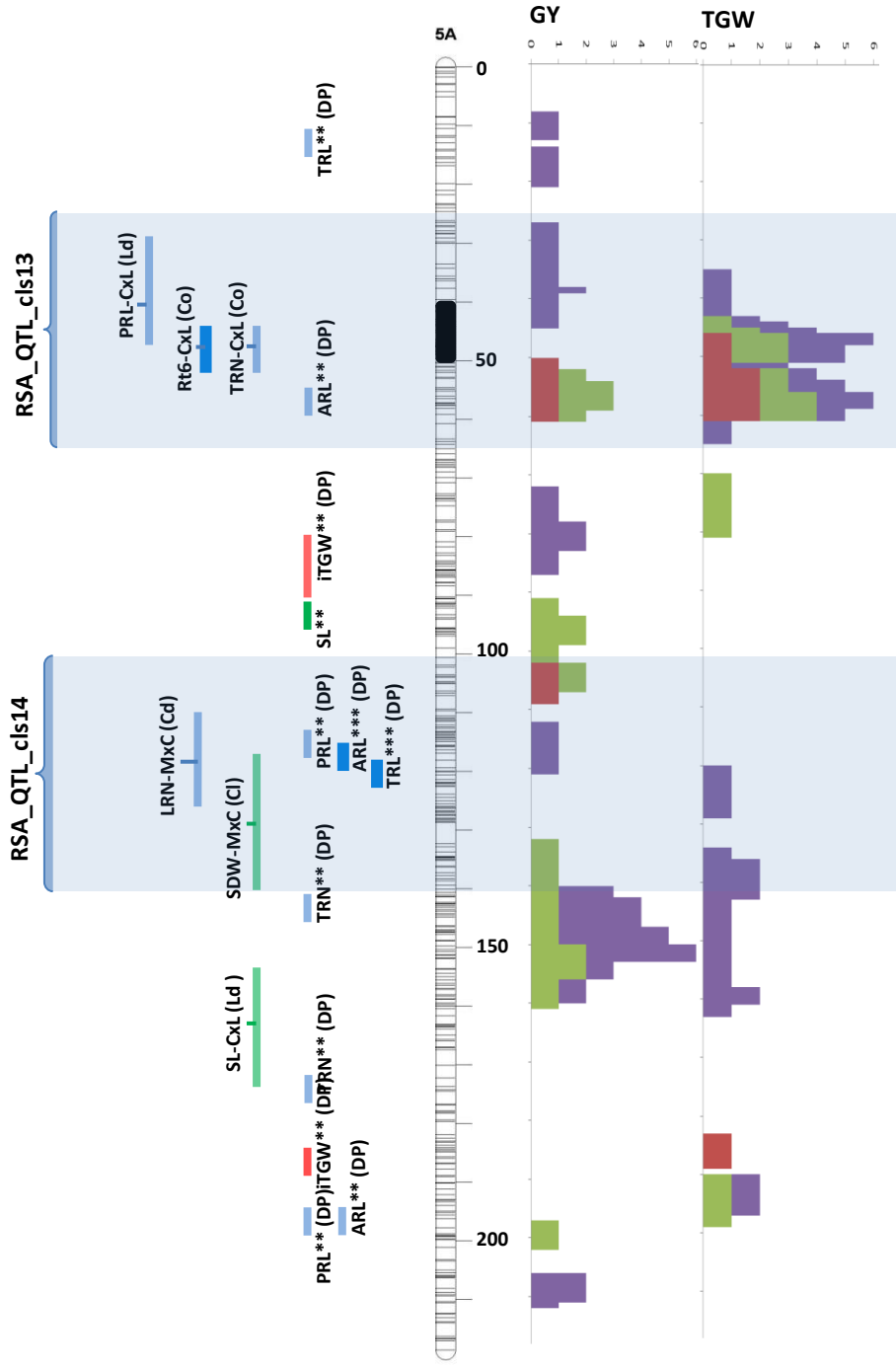
RSA_QTL_cis10





RSA_QTL_cls12





RSA_QTL_cls16

- TRL-CxL (Ld)
- ARL-CxL (Ld)
- RGA-CxL (Co)
- RGA-MxC (Cd)
- PRS-MxC (Mir)
- PRL-MxC (Mir)
- TRS-MxC (Mir)
- PRV-MxC (Mir)
- TRL-MxC (Mir)

- RGA*** (DP)
- iTGW** (DP)
- TRL** (DP)

RSA_QTL_cls15

- SL-CxL (Ld)
- Rt6-MxC (Cd)

- RGA** (DP)
- PRL**** (DP)
- ARL*** (DP)
- TRN (DP)
- SL (DP)
- TRL*** (DP)

- ARL** (DP)
- iTGW** (DP)
- iTGW**** (DP)
- iTGW*** (DP)

- RDW-MxC (Cd)
- iGWT-MxC (Mir)



GY



TGW



RSA_QTL_cls17

- SL-CxL (Co)

- TRD-CxL (Co)
- PRL-MxC (Mir)
- TRN-MxC (Mir)
- PRL-MxC (Cd)
- PRV-MxC (Cd)
- PRS-MxC (Cd)
- Rt6-MxC (Mir)
- ARL-MxC (Cd)
- LRN-MxC (Cd)

- TRN** (DP)
- RGA** (DP)
- ARL** (DP)
- PRL** (DP)
- SL** (DP)

- ARL** (DP)
- TRN** (DP)
- TRL** (DP)
- TRN**** (DP)
- TRL*** (DP)
- TRL** (DP)
- iTGW** (DP)
- iTGW**** (DP)



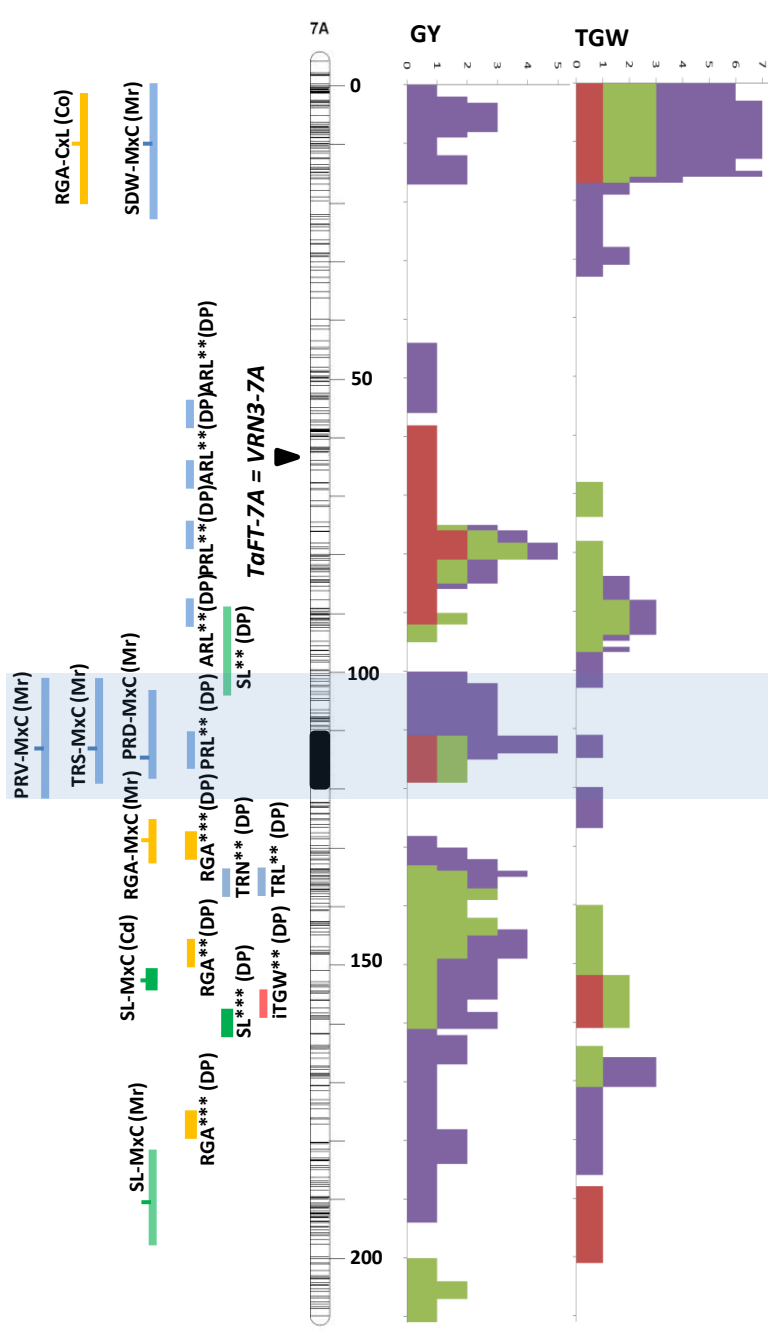
GY



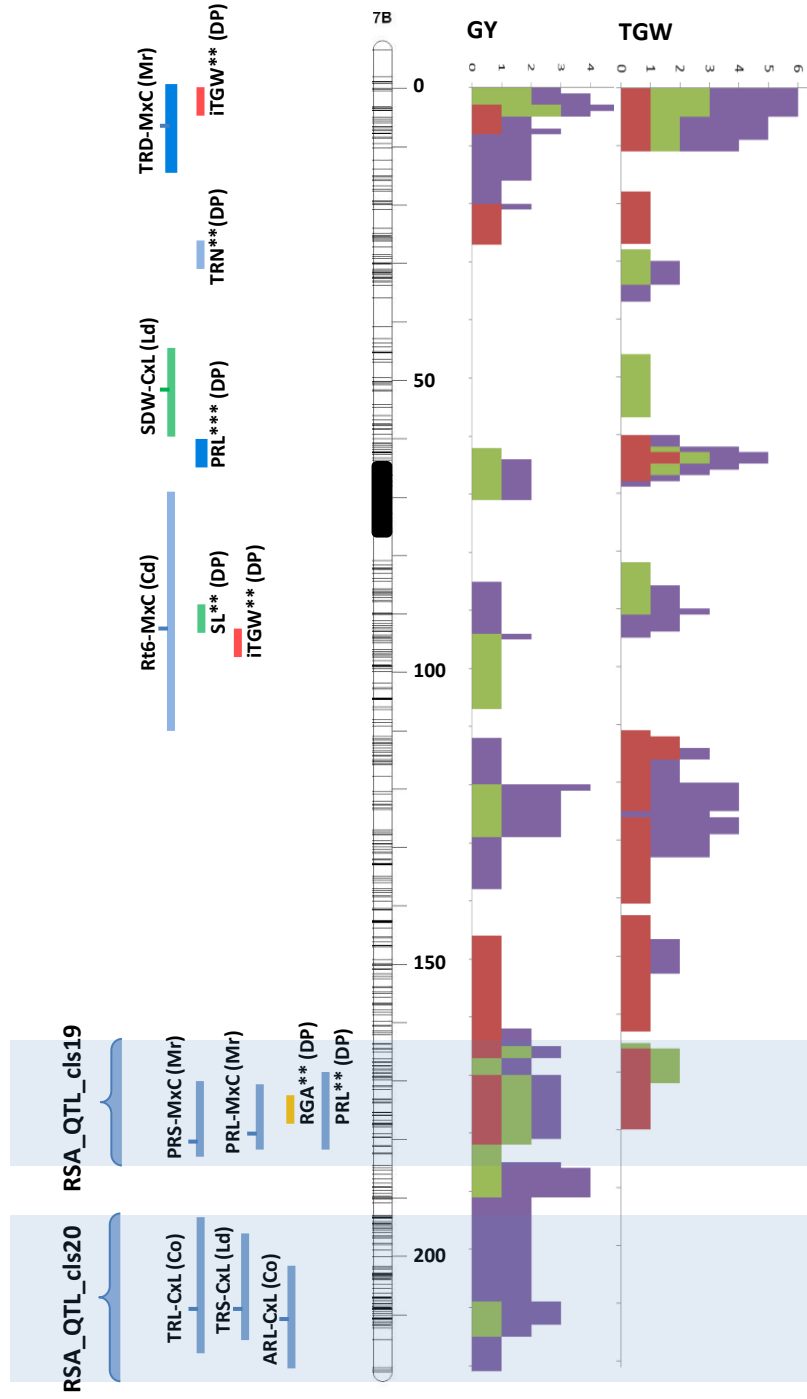
TGW



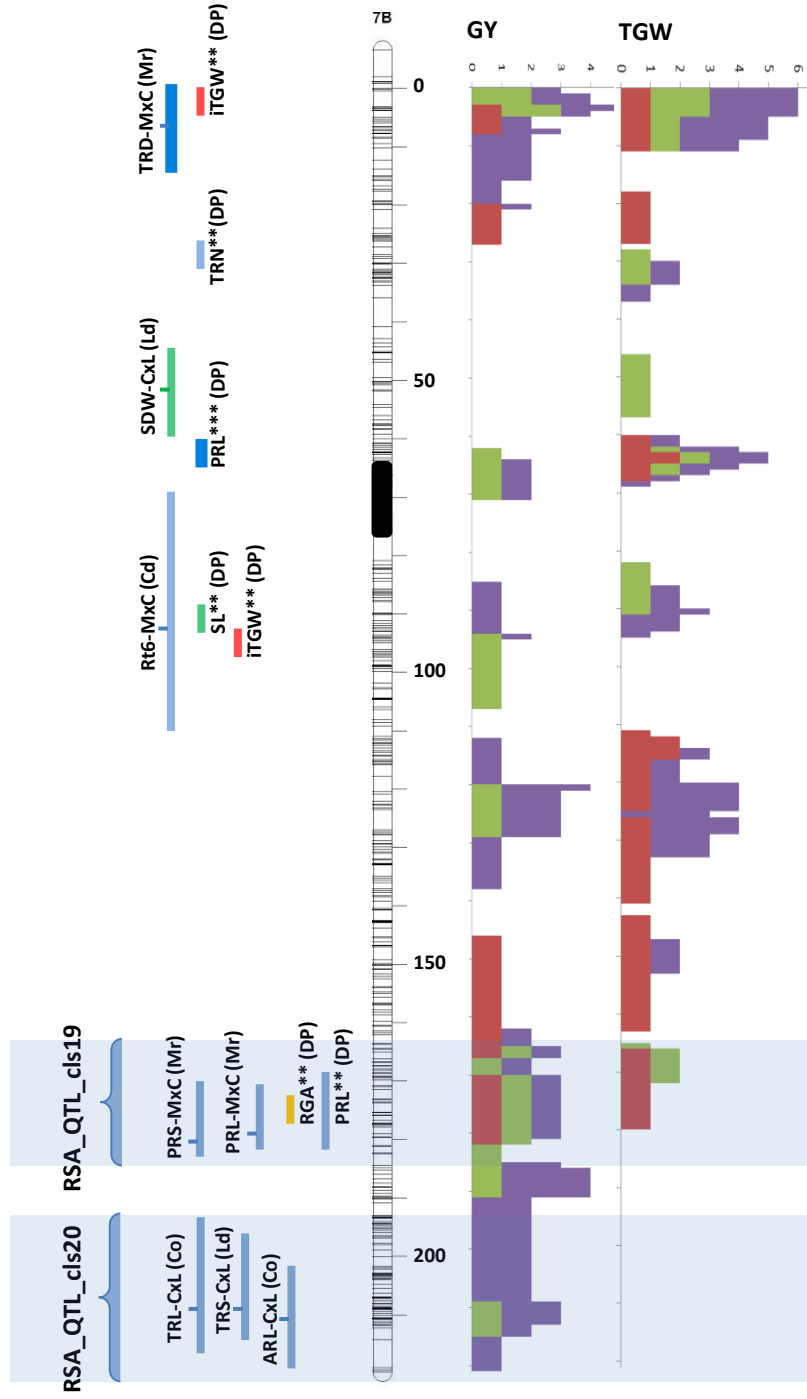
RSA_QTL_cls18



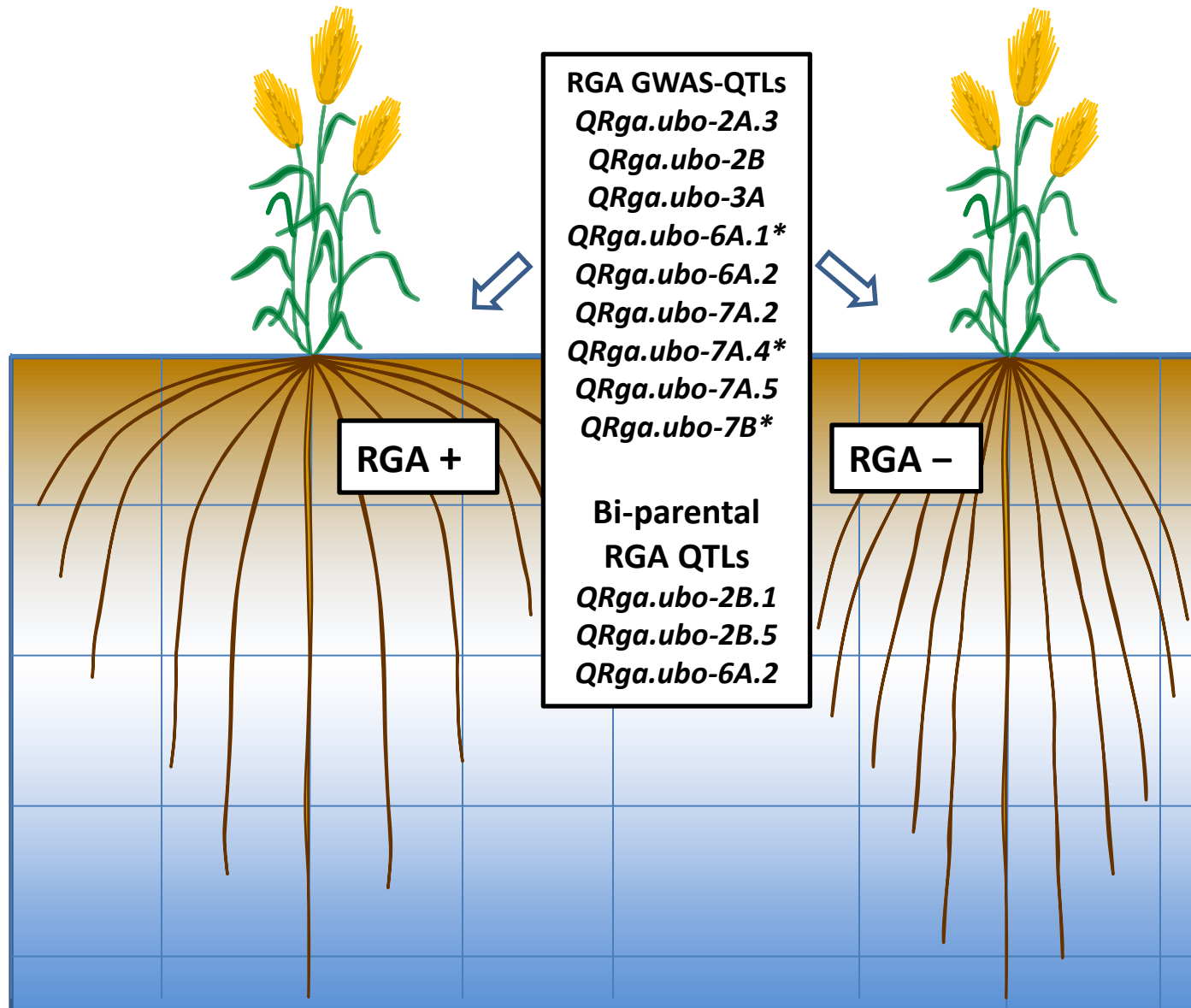
RSA_QTL_cls19



RSA_QTL_cls20



Supplementary Figure S4. Schematic ideotypes of wheat plants with shallow and deep root system architecture consequent to different seminal root growth angle (RGA) QTLs which can potentially contribute towards these ideotypes through marker-assisted selection.



* QTL effect consistently associated to GY across the majority of 15 Mediterranean environments (see Suppl. Table 7)