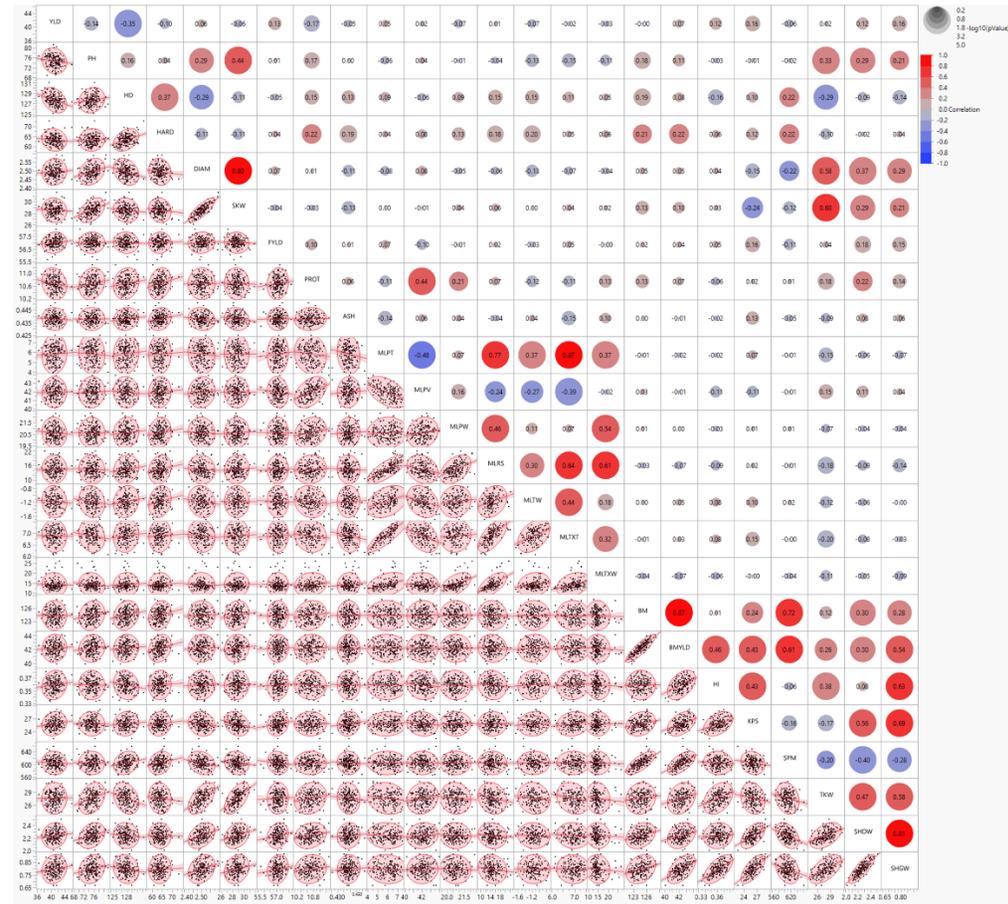
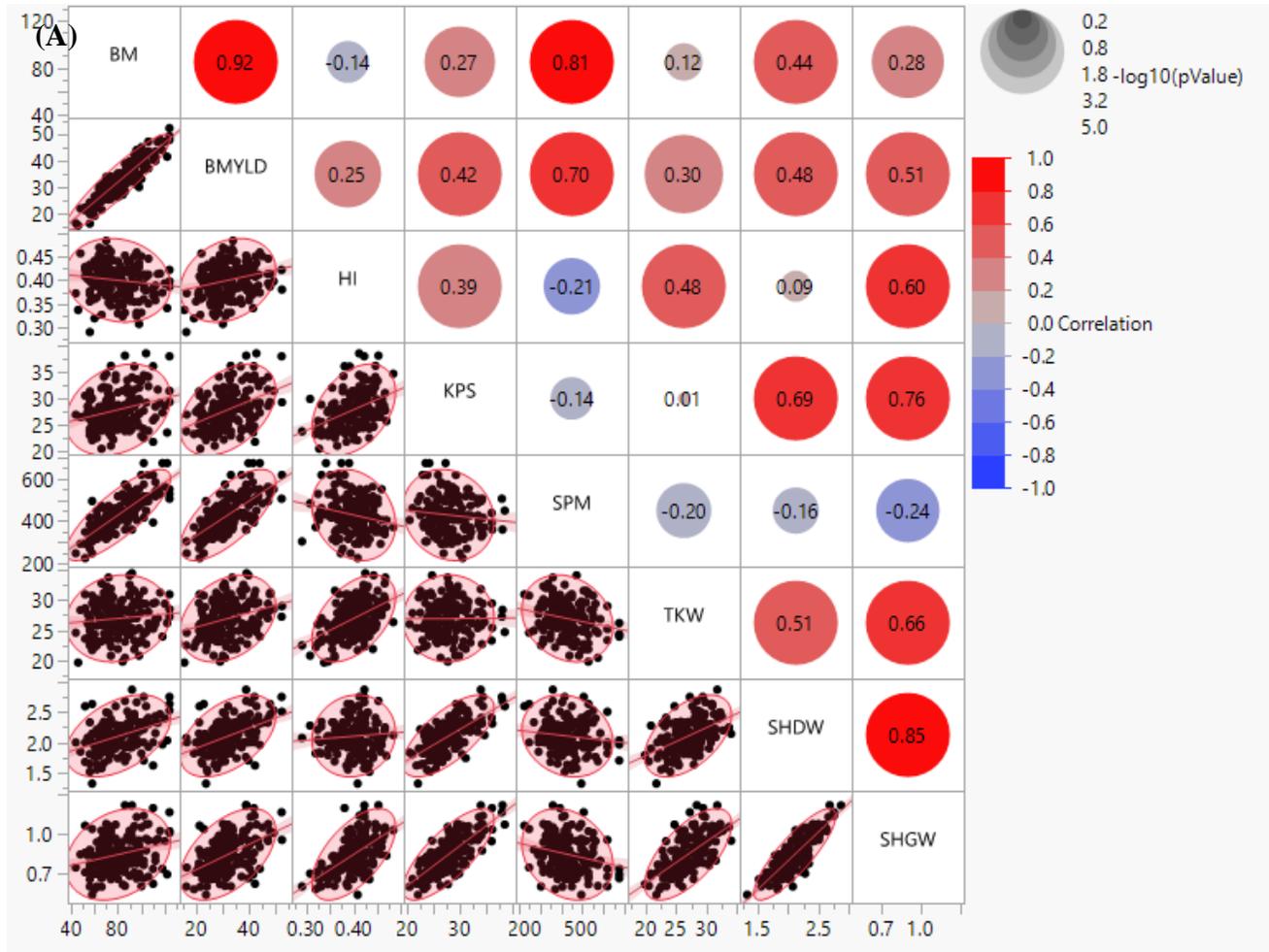
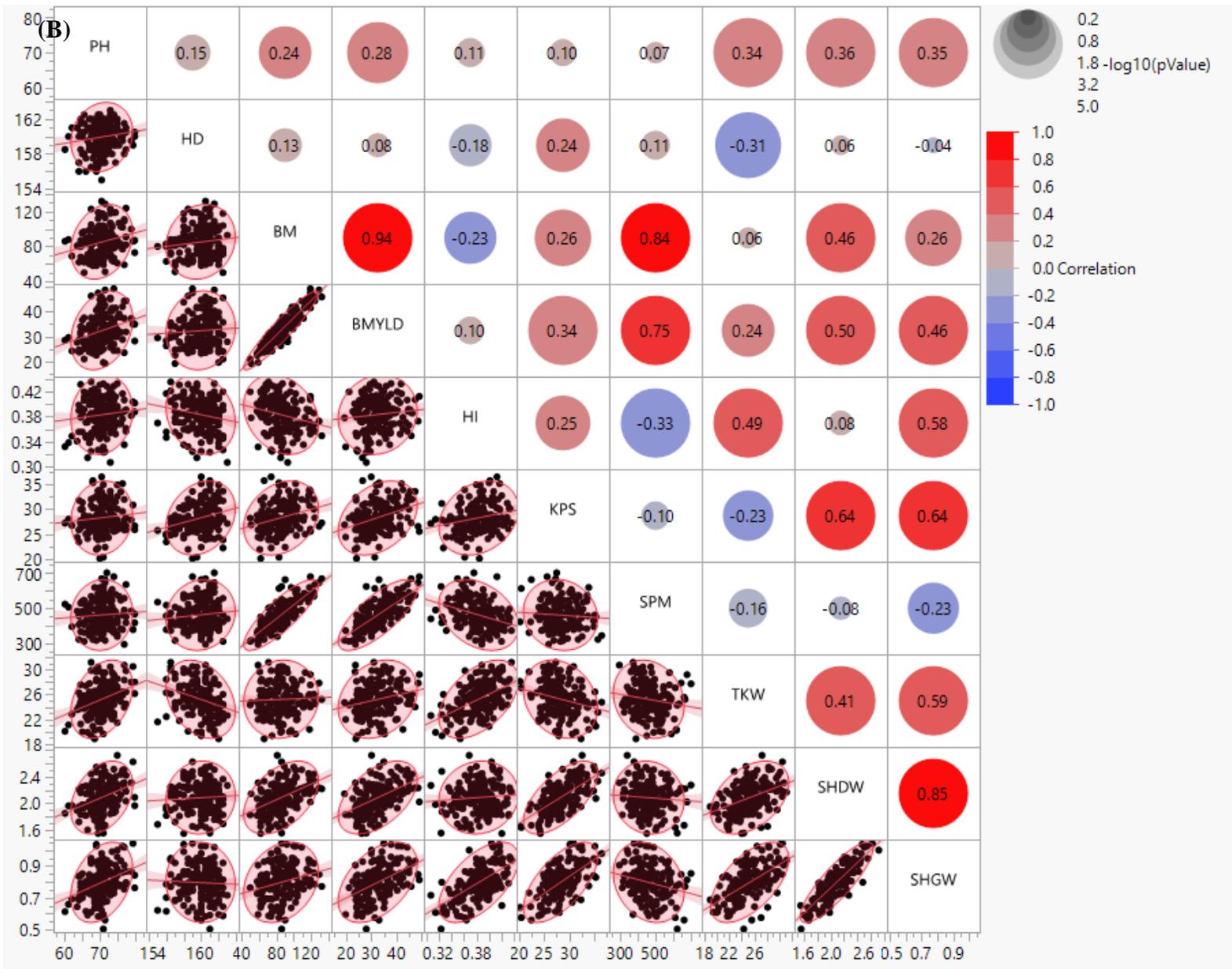


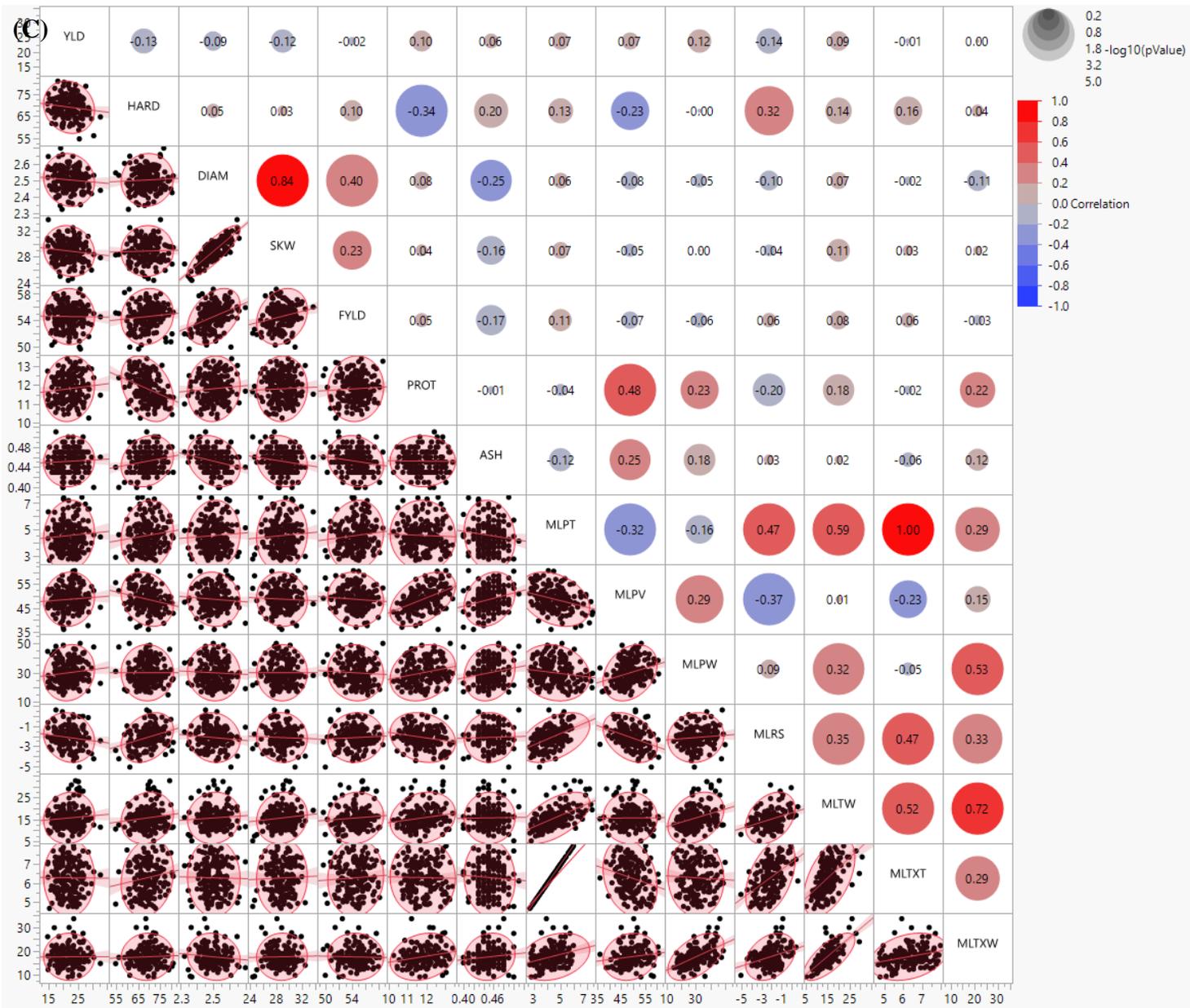
Supplemental Fig S1a: Pearson correlation coefficient matrix for end-use quality, yield-related, agronomy and kernel-related traits for best linear unbiased predictors (BLUPs) across all environments. Traits: YLD: grain yield, PH: plant height, HD: heading day, HARD: hardness, DIAM: kernel diameter, SKW: single kernel weight, FYLD: flour yield, PROT: flour protein at 14% moisture basis, ASH: flour ash content at 14% moisture, MLPT: midline peak time, MLPV: midline peak value, MLPW: midline peak width, MLRS: midline right slope, MLTW: midline tail width, MLTXT: midline time X time, MLTXW: midline time X width, BM: biomass dry weight of sample of 0.5 meter long of inner row, BMYLD: yield from biomass sample of 0.5 m long in an inner row, HI: harvest index, KPS: kernels spike-1, SPM: spikes m-2, TKW: thousand kernel weight, SHDW: single head dry weight, SHGW: single head grain weight, KAREA: kernel area, KLEN: kernel length, KWID: kernel width, KPERI: kernel perimeter.

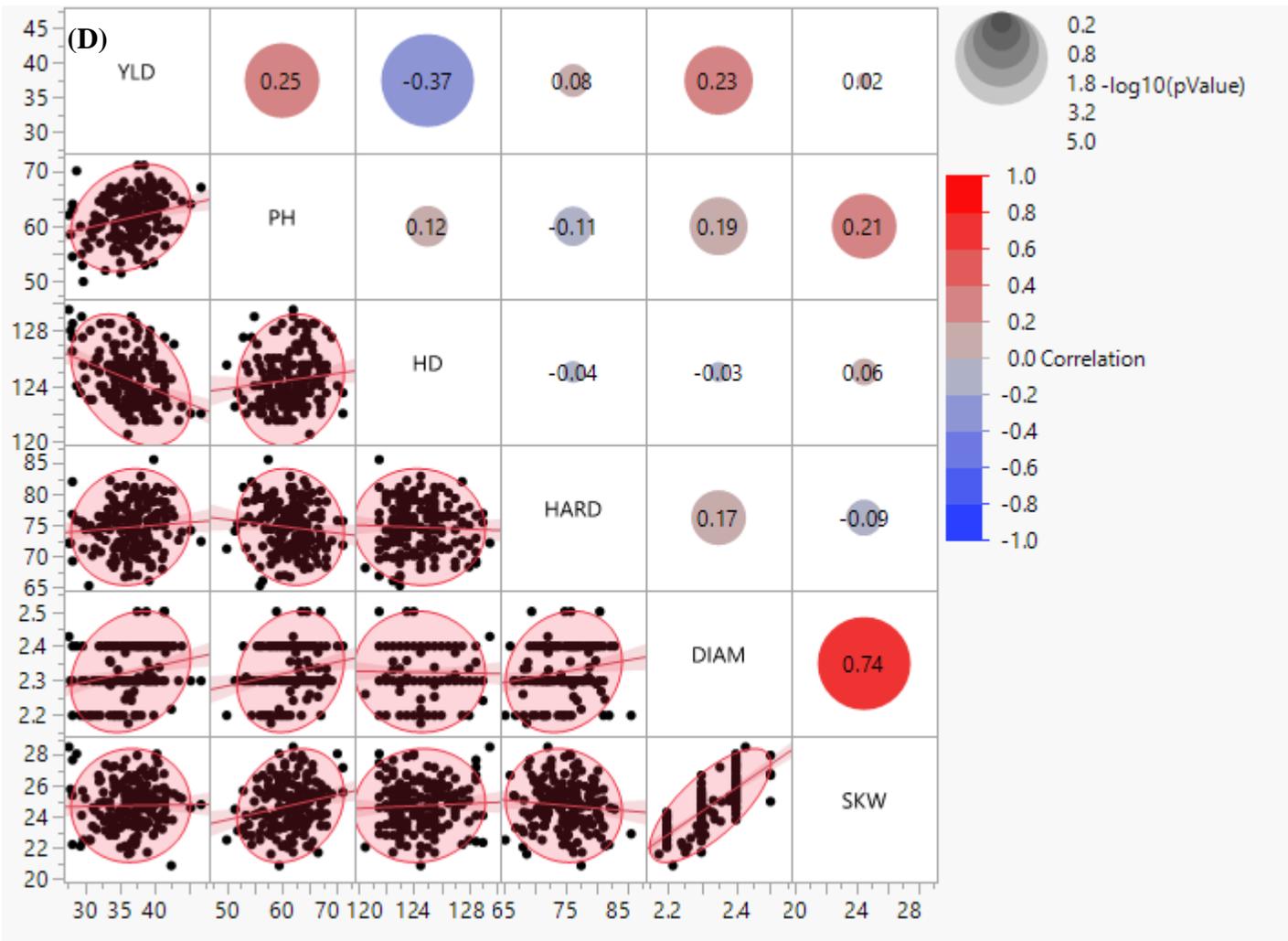


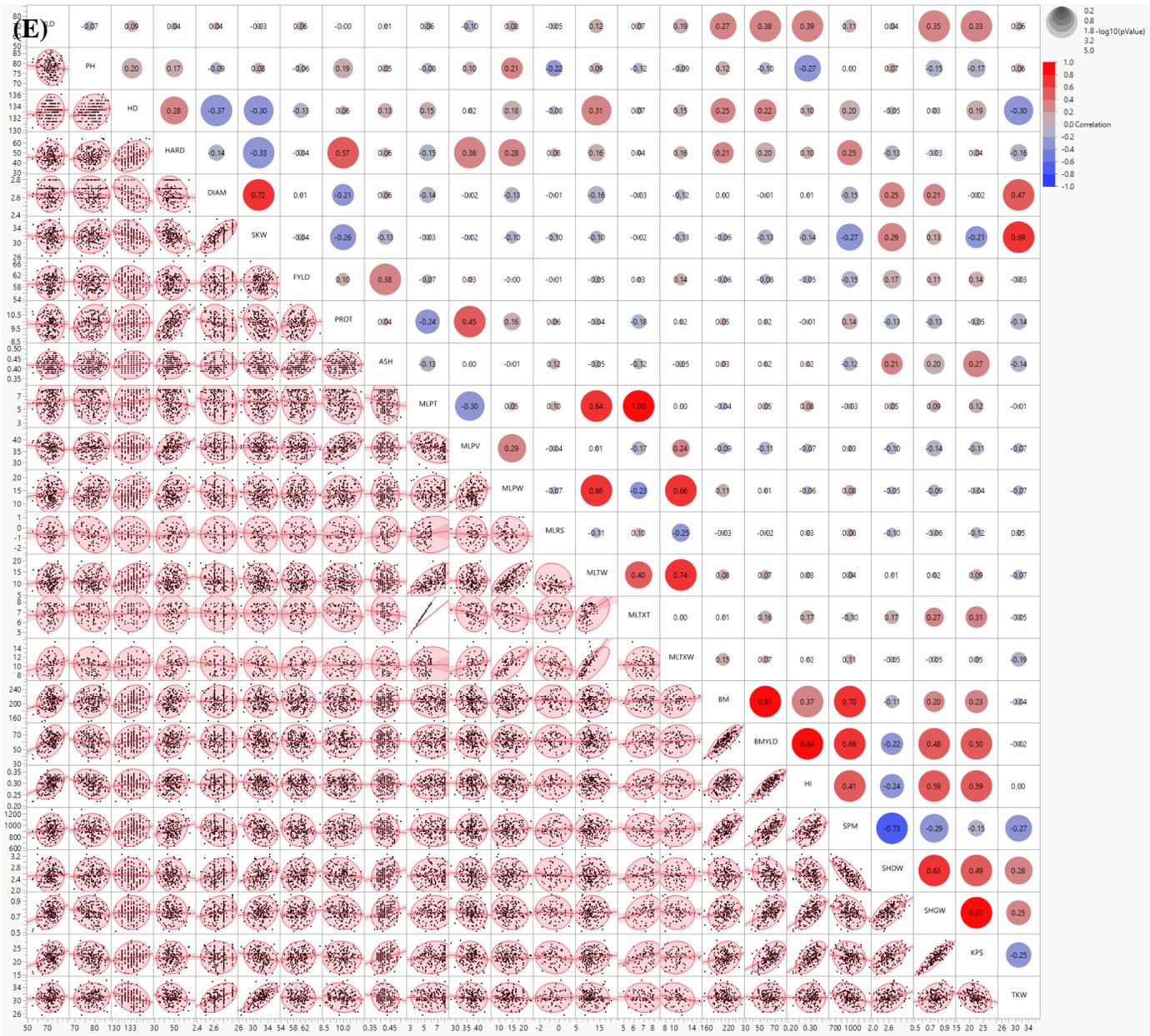
Supplemental Fig S1b: Pearson Correlation coefficient matrix for agronomical, end-use quality, yield component and seed-related traits in the individual environment. Individual environments: Chillicothe (17CH), and Bushland (17BSP67 and 17BSP100), in the 2016/17 growing season and Dumas (18DMS), McGregor (18MCG), Bushland (18BSP100), and Uvalde (18UVL) in the growing season 2017/18. DMS18, 17BSP67, 17BSP100 and 18BSP100 were irrigated, but other trials 17CH and 18MCG18 were dryland (rain-fed). A) 17BSP67, B) 17BSP100, C) 17CH, D) 18BSP100, E) 18DMS, and F) 18MCG.

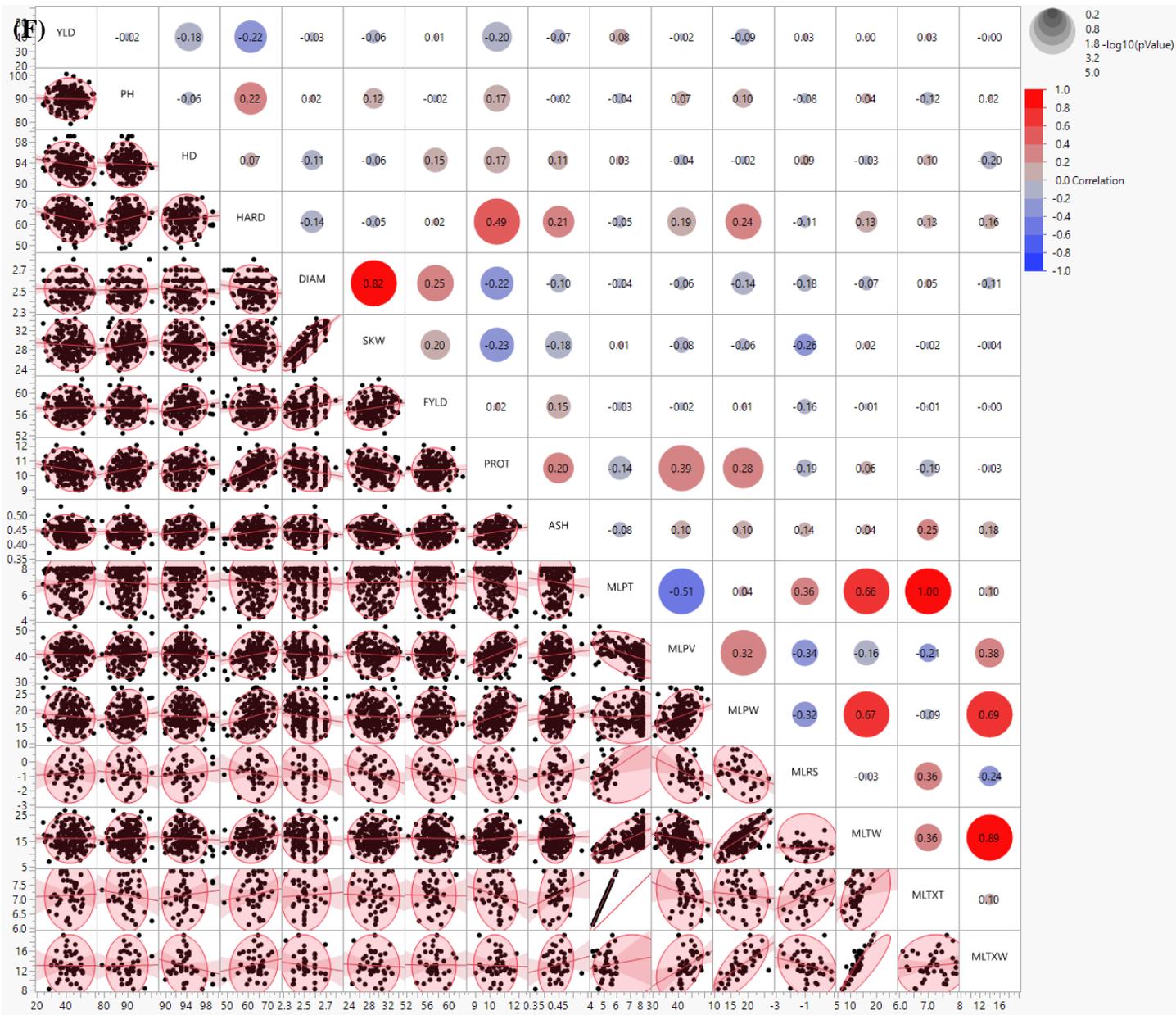




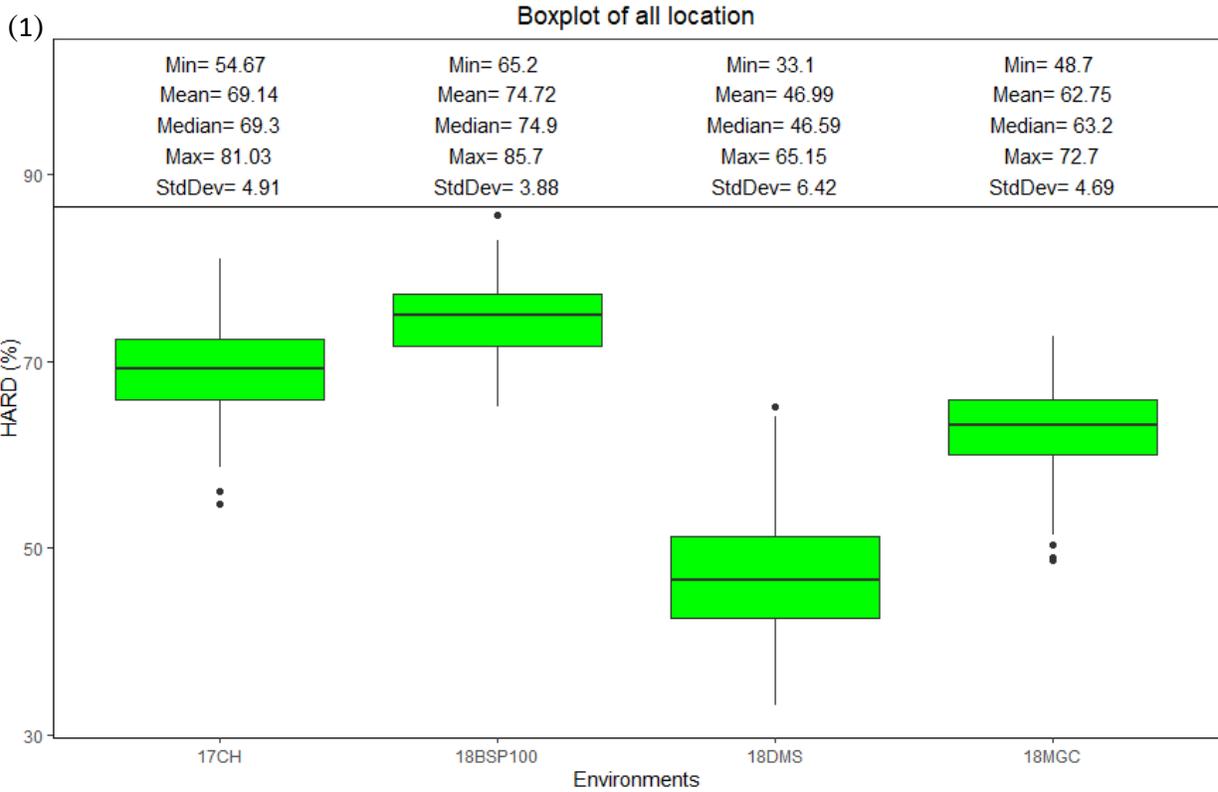






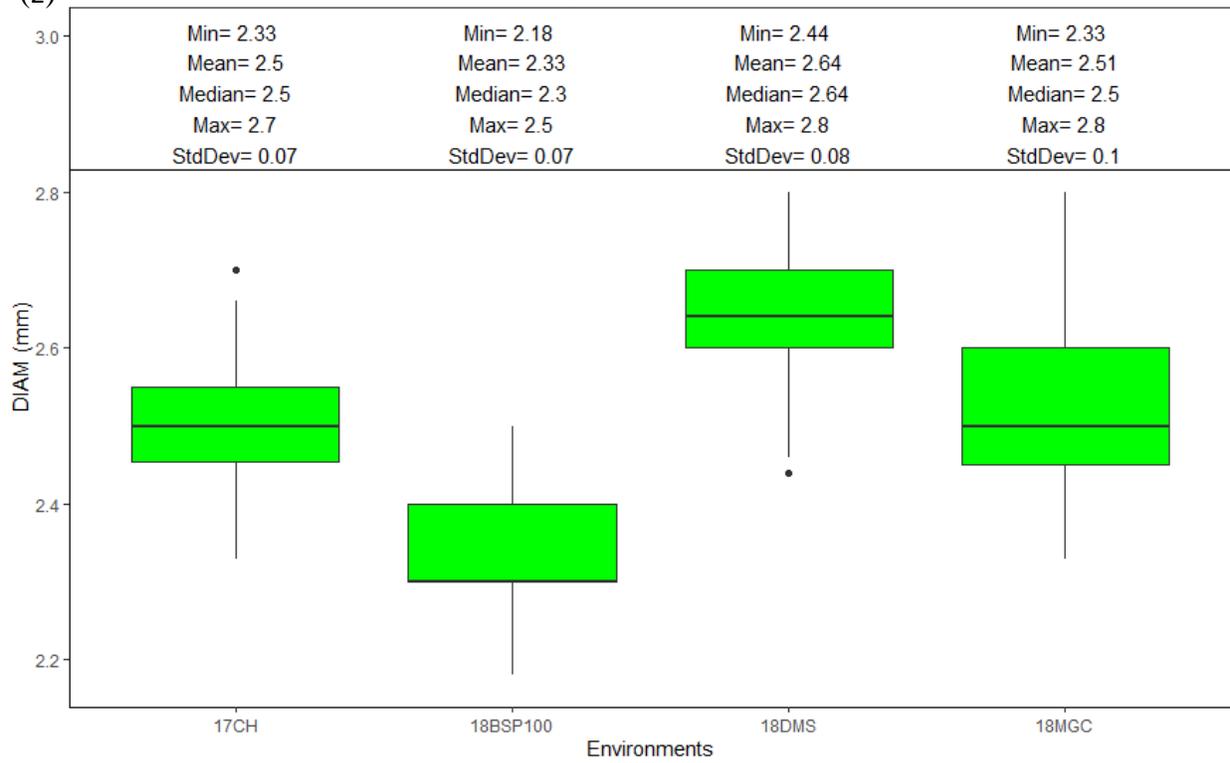


Supplemental Fig S2: Boxplot Analysis of end-use quality, agronomical, yield components and seed-related traits. Environments: Chillicothe (17CH), and Bushland (17BSP67 and 17BSP100), in the 2016/17 growing season and Dumas (18DMS), McGregor (18MCG), Bushland (18BSP100), and Uvalde (18UVL) in the growing season 2017/18. DMS18, 17BSP67, 17BSP100 and 18BSP100 were irrigated, but other trials 17CH and 18MCG18 were dryland (rain-fed). Traits: 1) hardness (HARD), 2) kernel diameter (DIAM), 3) single kernel weight (SKW), 4) flour yield (FYLD), 5) flour protein at 14% moisture (PROT), 6) flour ash at 14% moisture (ASH), 7) midline peak time (MLPT), 8) midline peak value (MLPV), 9) midline peak width (MLPW), 10) midline right slope (MLRS), 11) midline tail width MLTW, 12) midline time X time (MLTXT), 13) midline time X width (MLTXW), 14) grain yield from whole plot (YLD), 15) plant height (PH), 16) heading date in Julian Calendar from January (HD), 17) dry biomass from hand harvested 0.5 m long inner row sample from plot (BM), 18) grain weight from 17) as hand harvested dry grain weight (BMYLD), 19) harvest index (HI), 20) kernels spike⁻¹ (KPS), 21) spikes m⁻² (SPM), 22) thousand kernel weight (TKW), 23) single head dry weight (SHDW), 24) single head dry grain weight (SHGW), 25) kernel area (KAREA), 26) kernel length (KLEN), 27) kernel perimeter (KPERI), 28) kernel width (KWID).



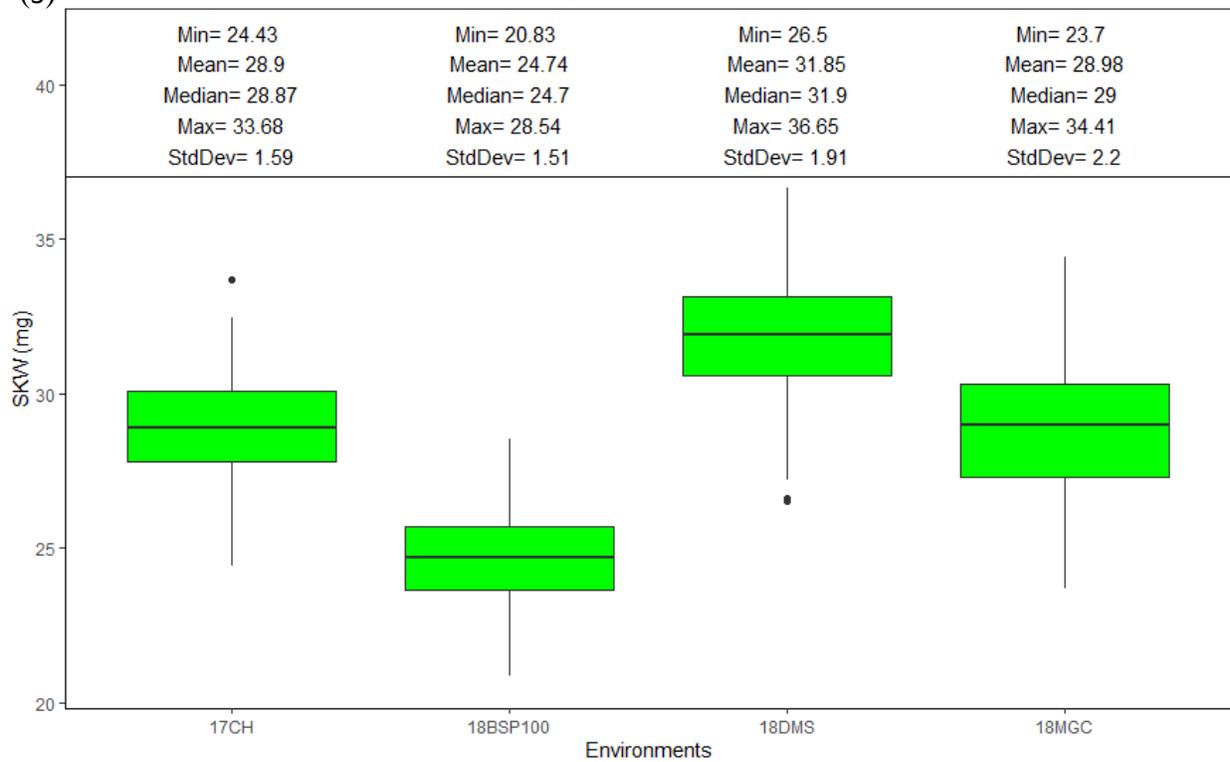
(2)

Boxplot of all location



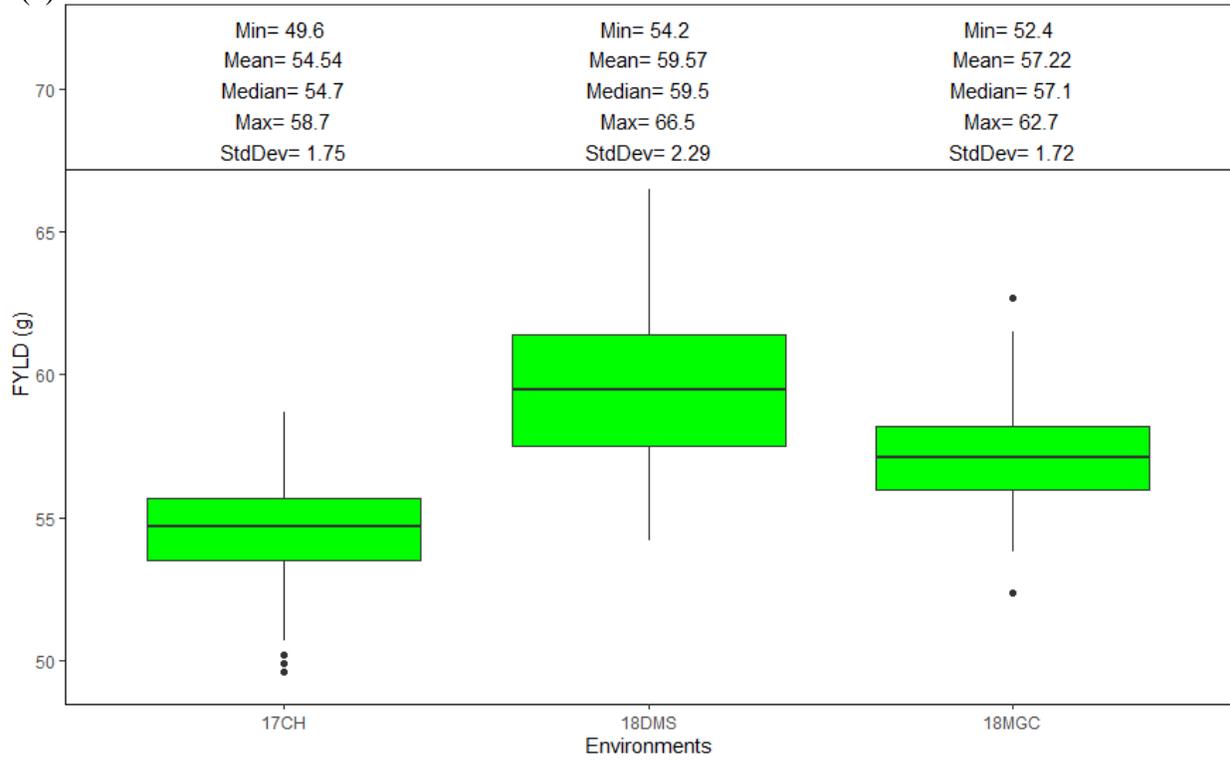
(3)

Boxplot of all location



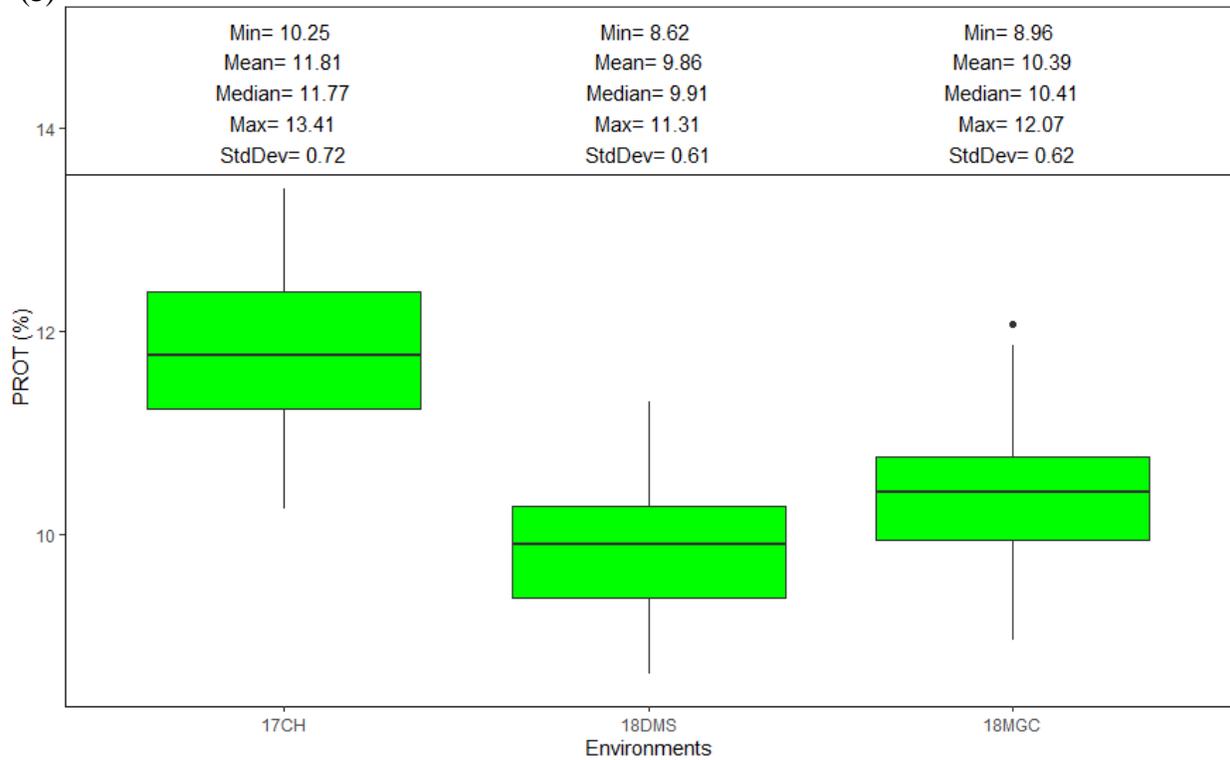
(4)

Boxplot of all location



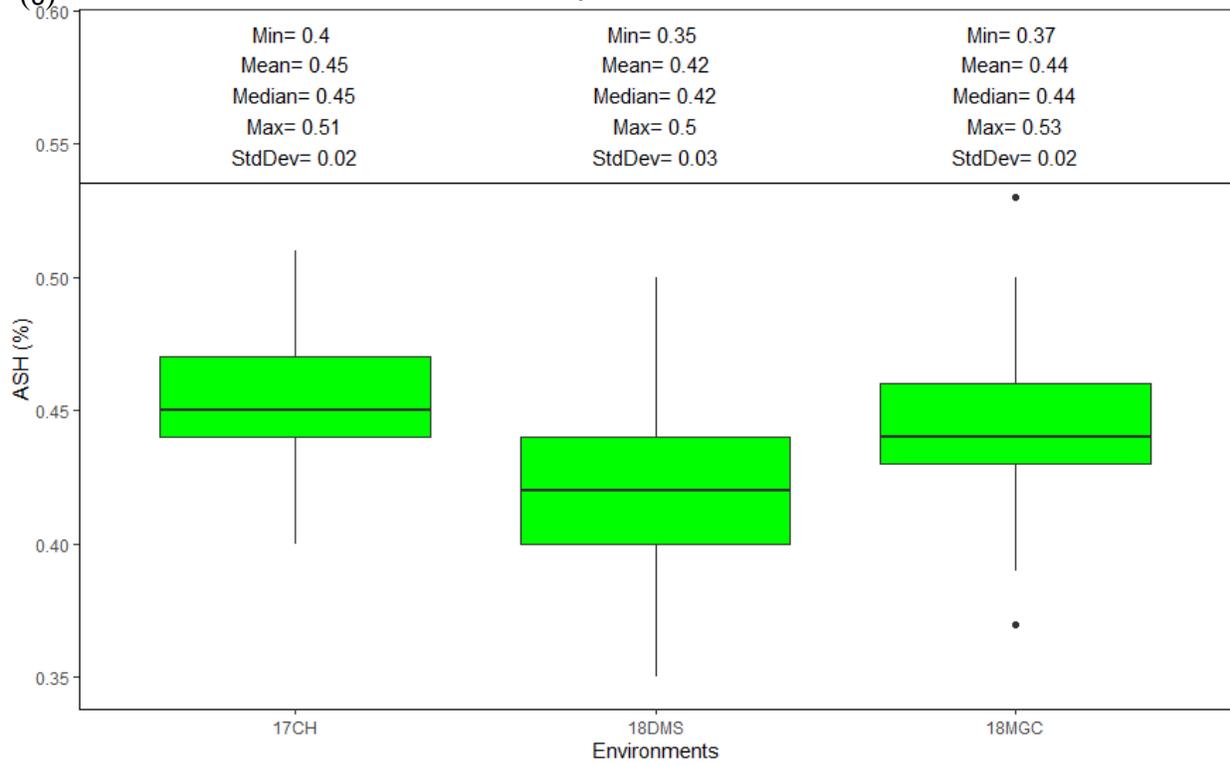
(5)

Boxplot of all location



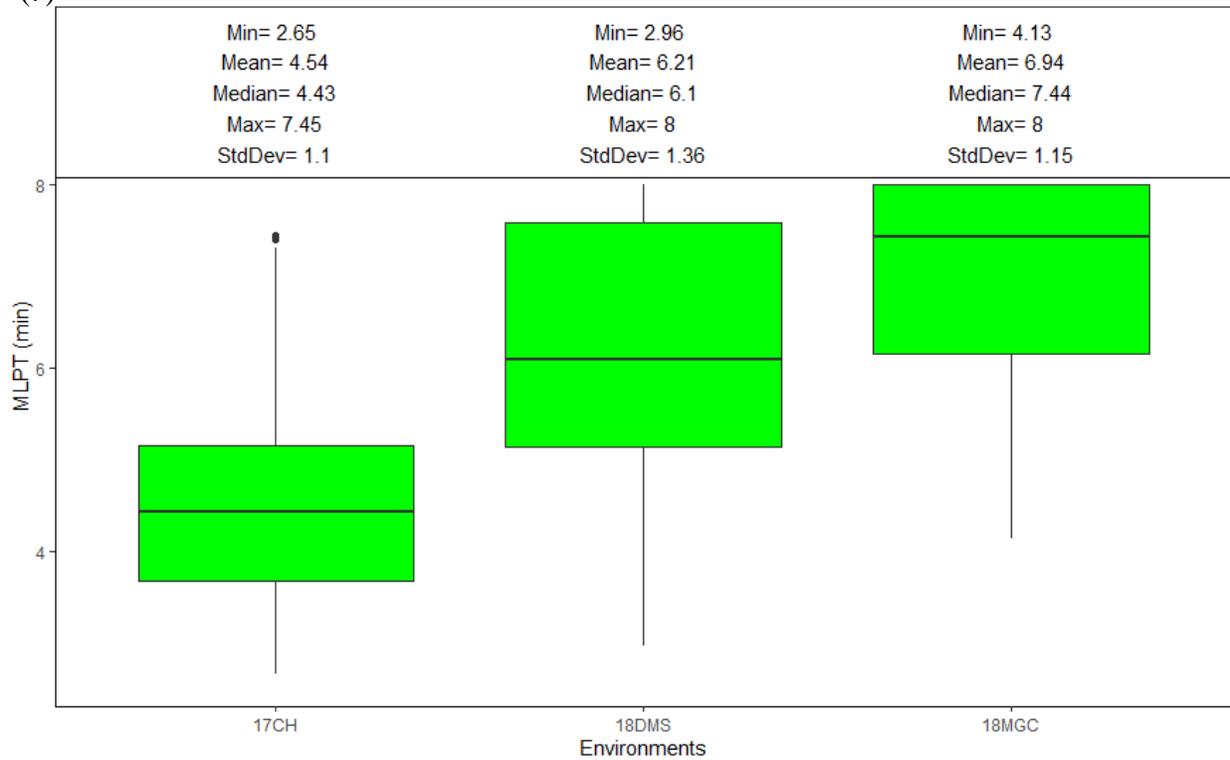
(6)

Boxplot of all location



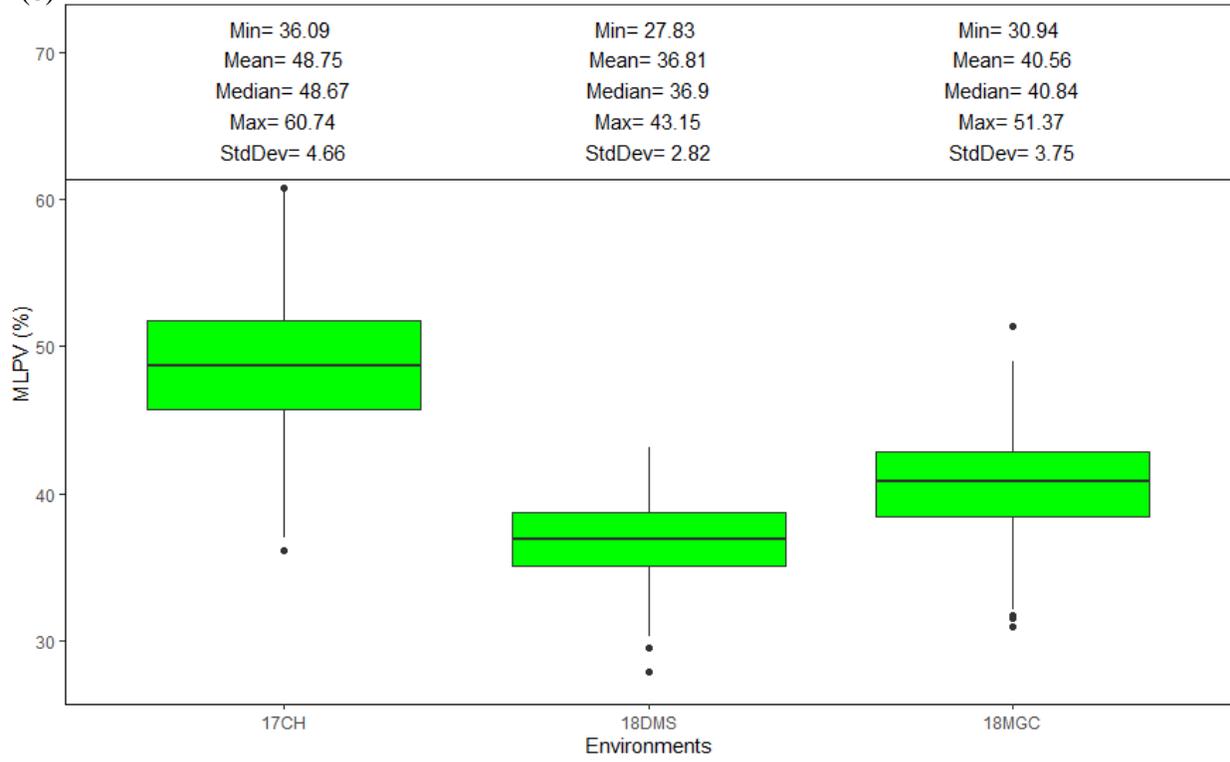
(7)

Boxplot of all location



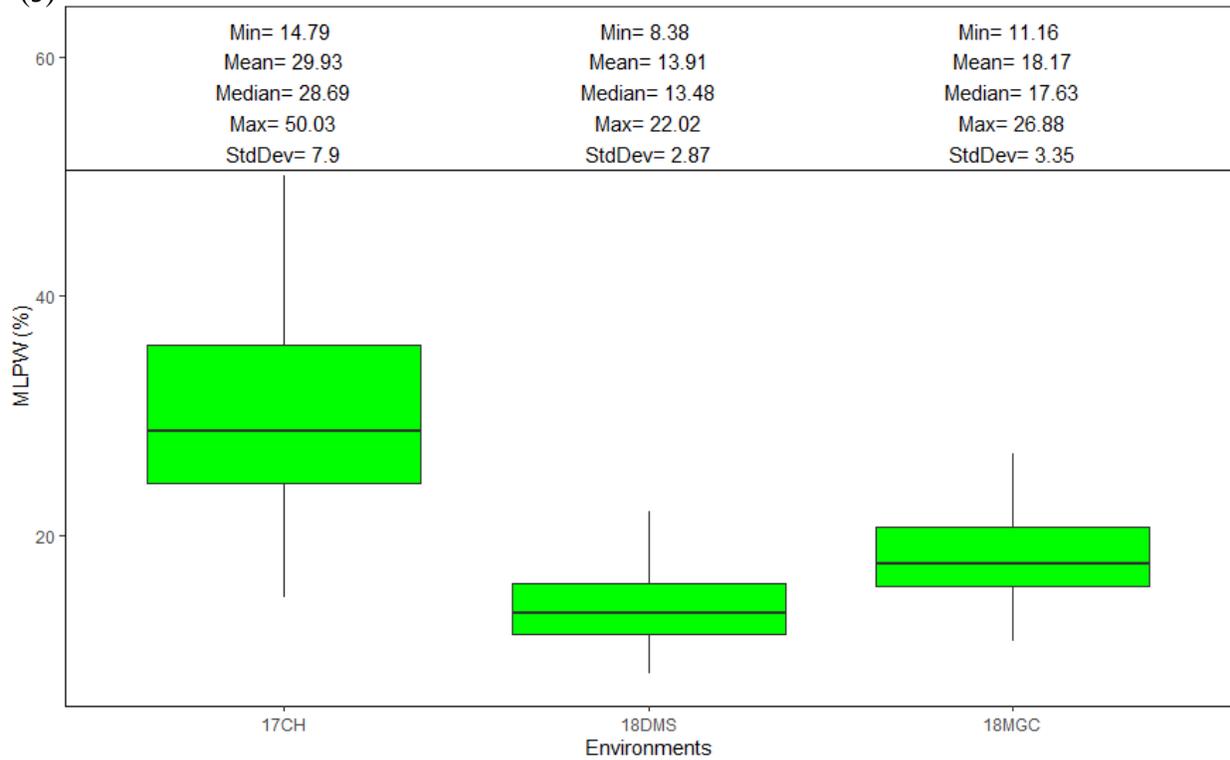
(8)

Boxplot of all location



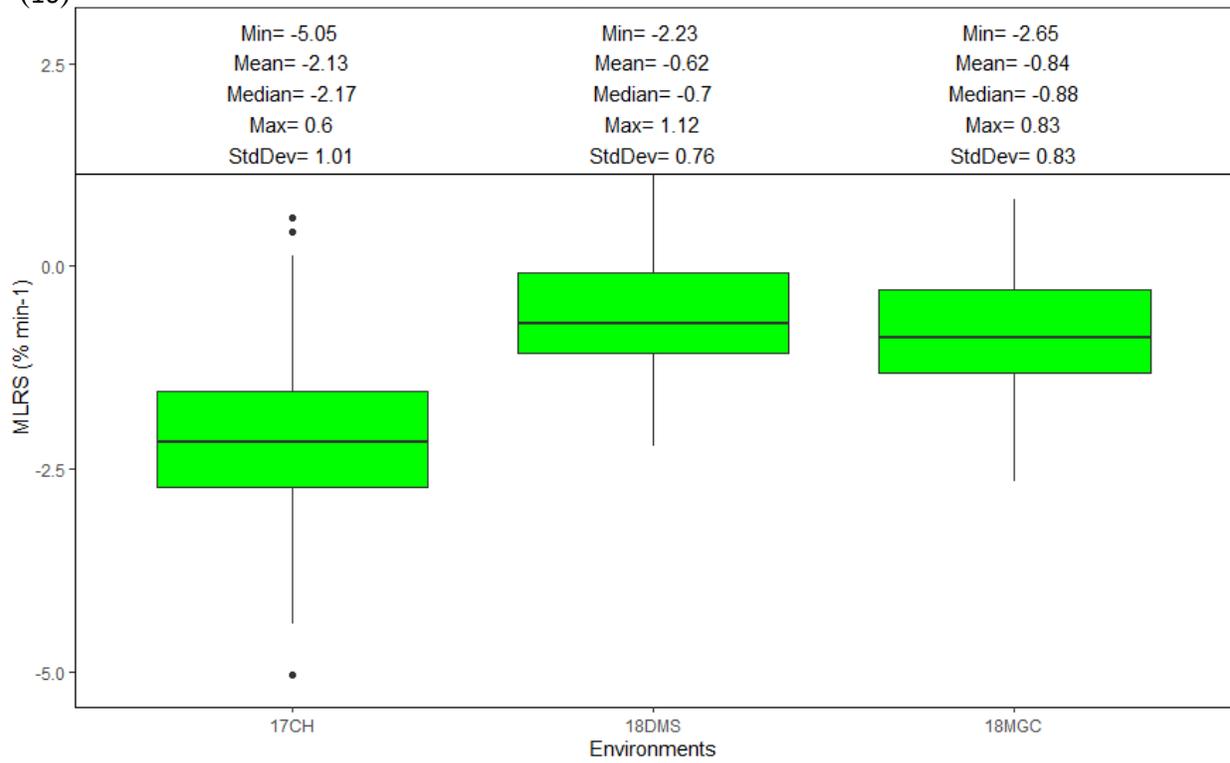
(9)

Boxplot of all location



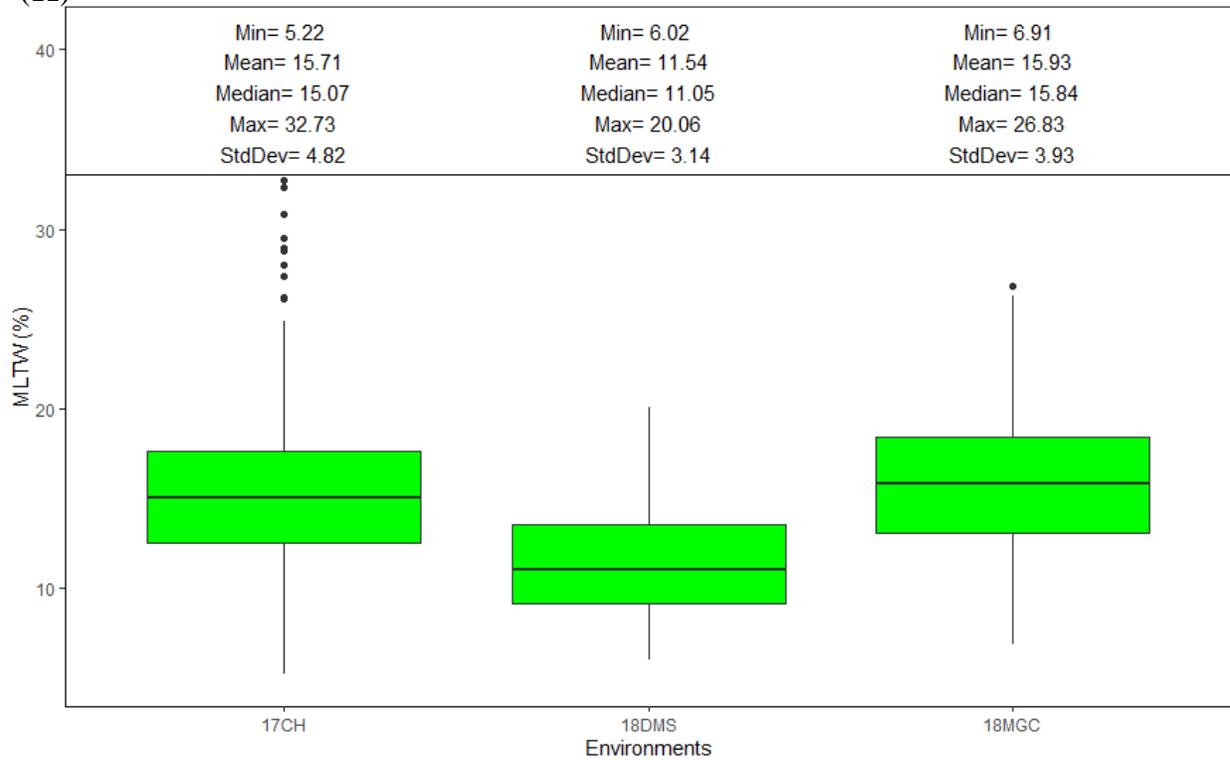
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Boxplot of all location



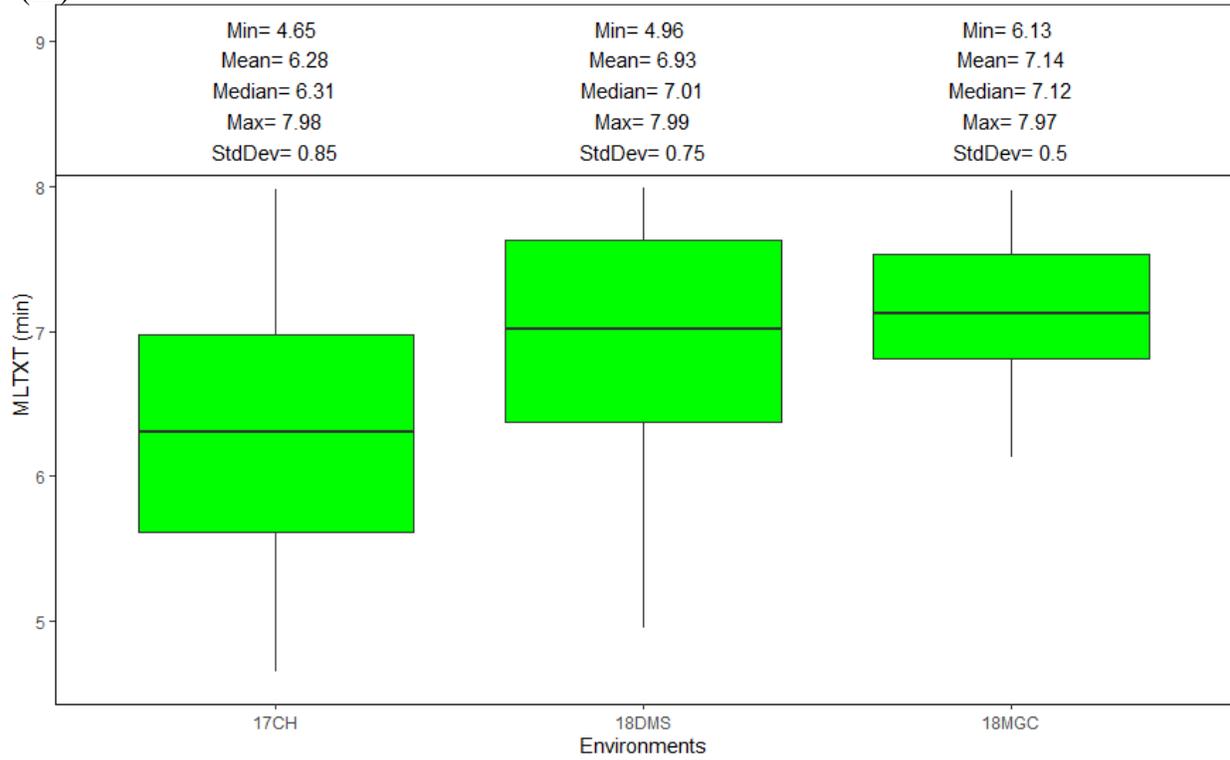
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Boxplot of all location



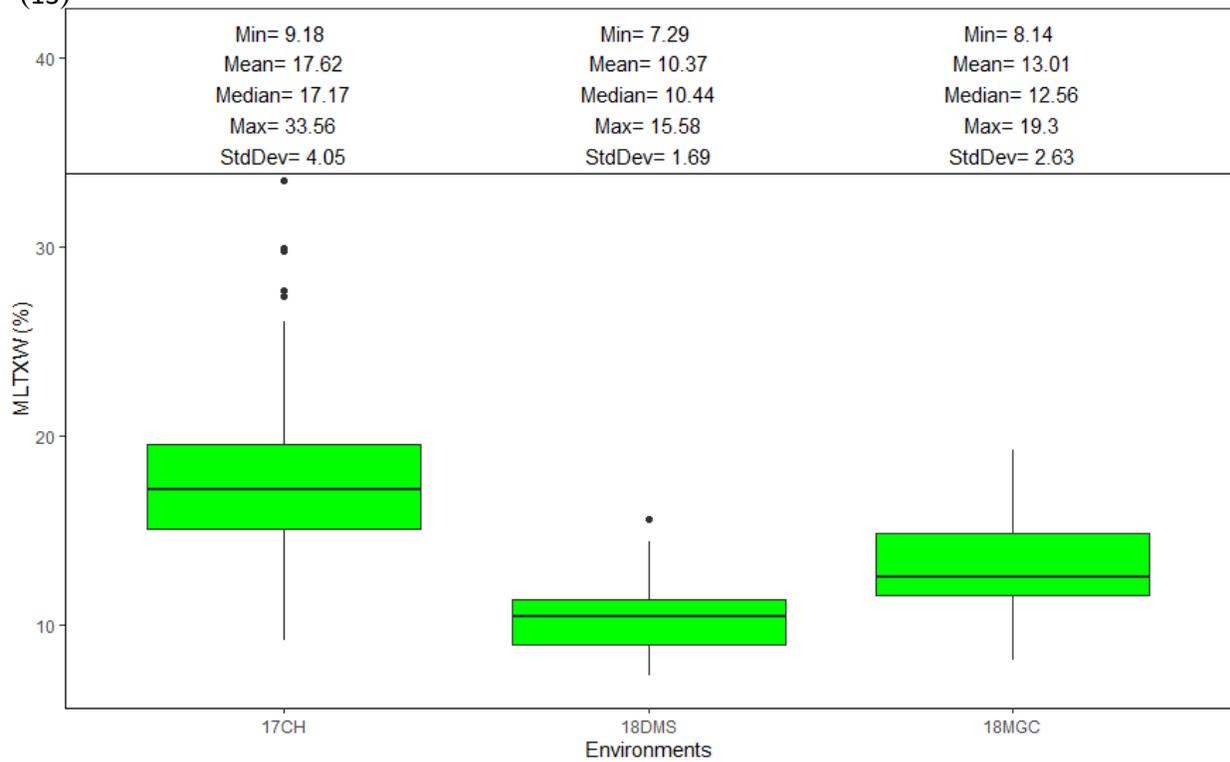
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Boxplot of all location



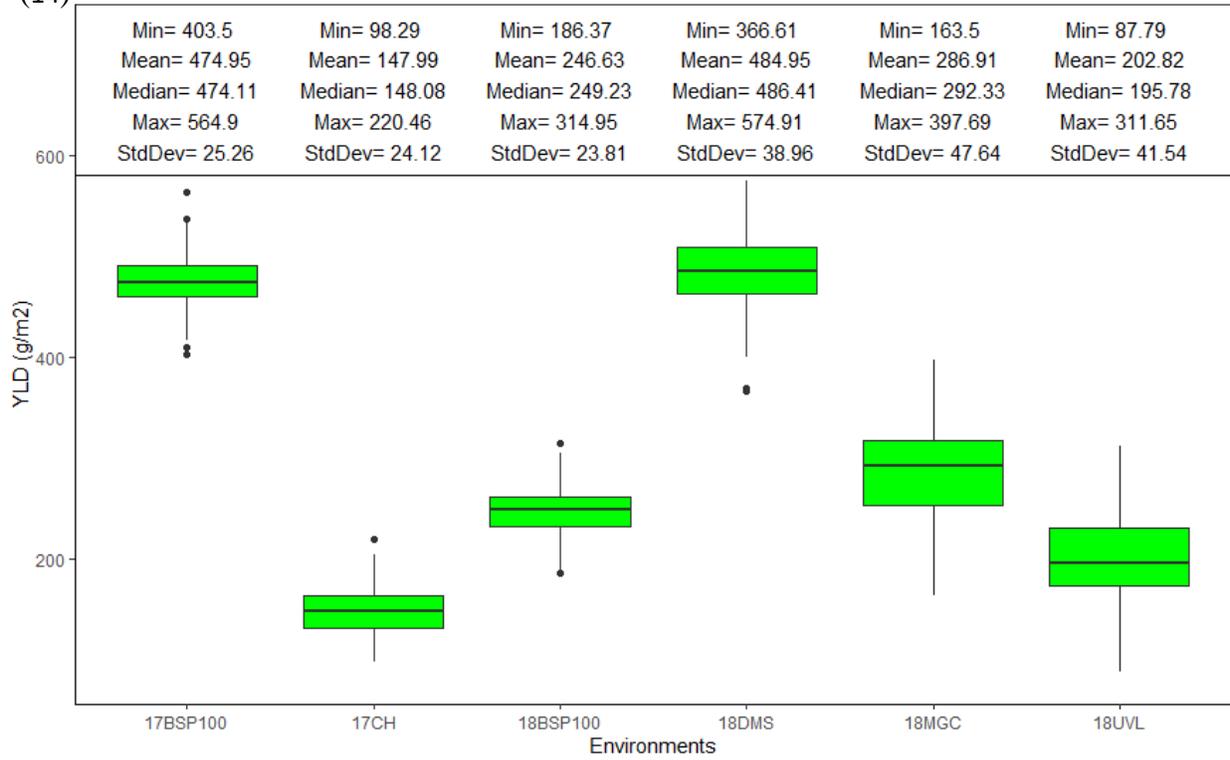
(13)

Boxplot of all location



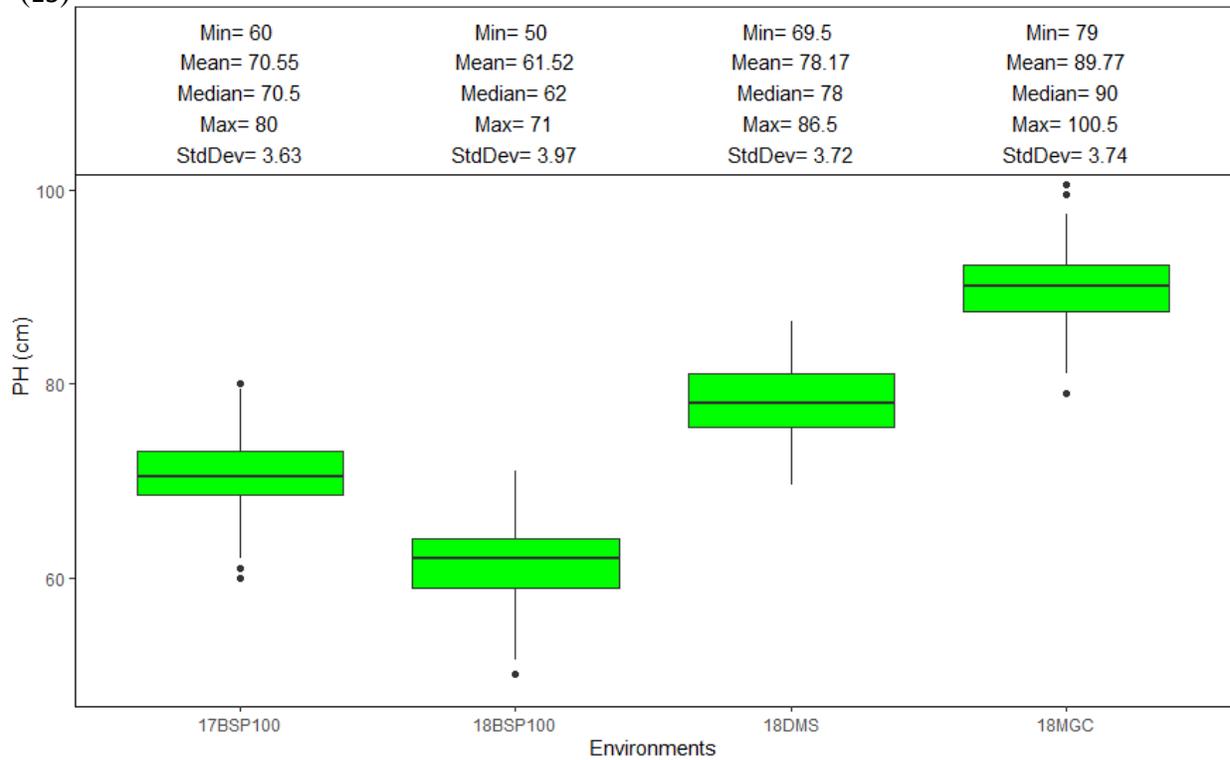
(14)

Boxplot of all location



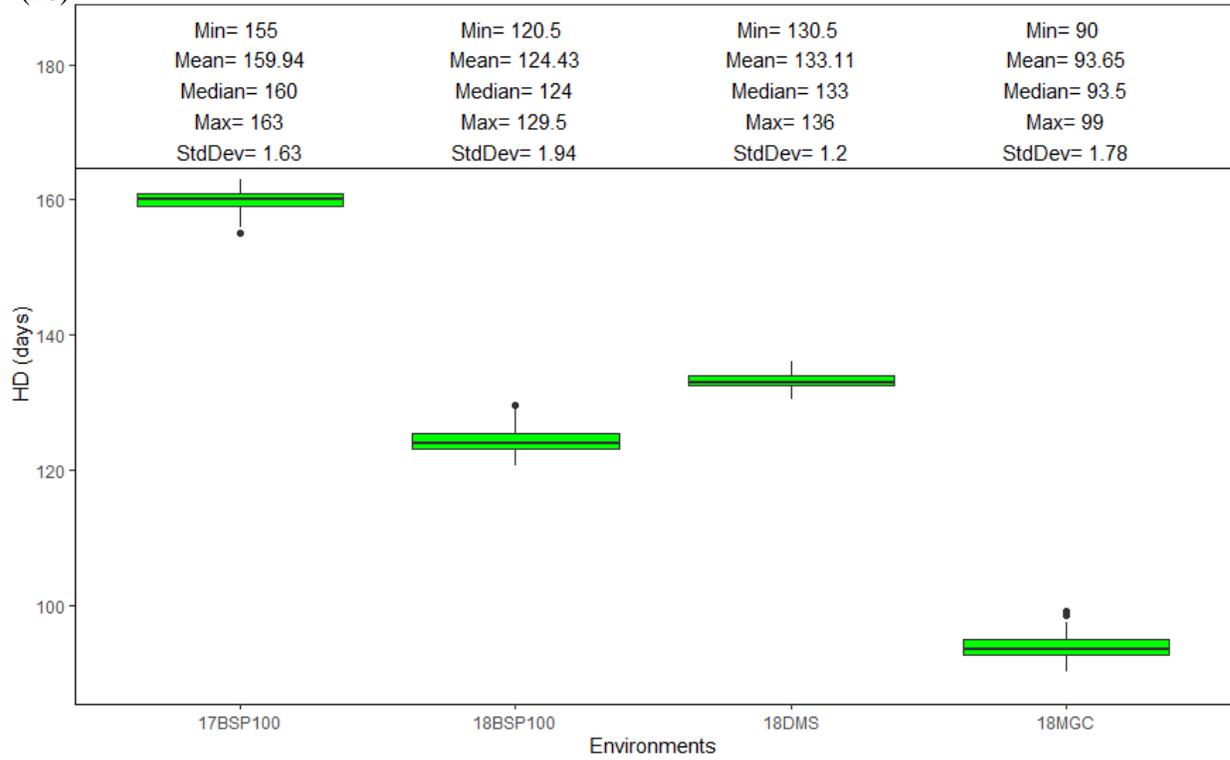
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Boxplot of all location



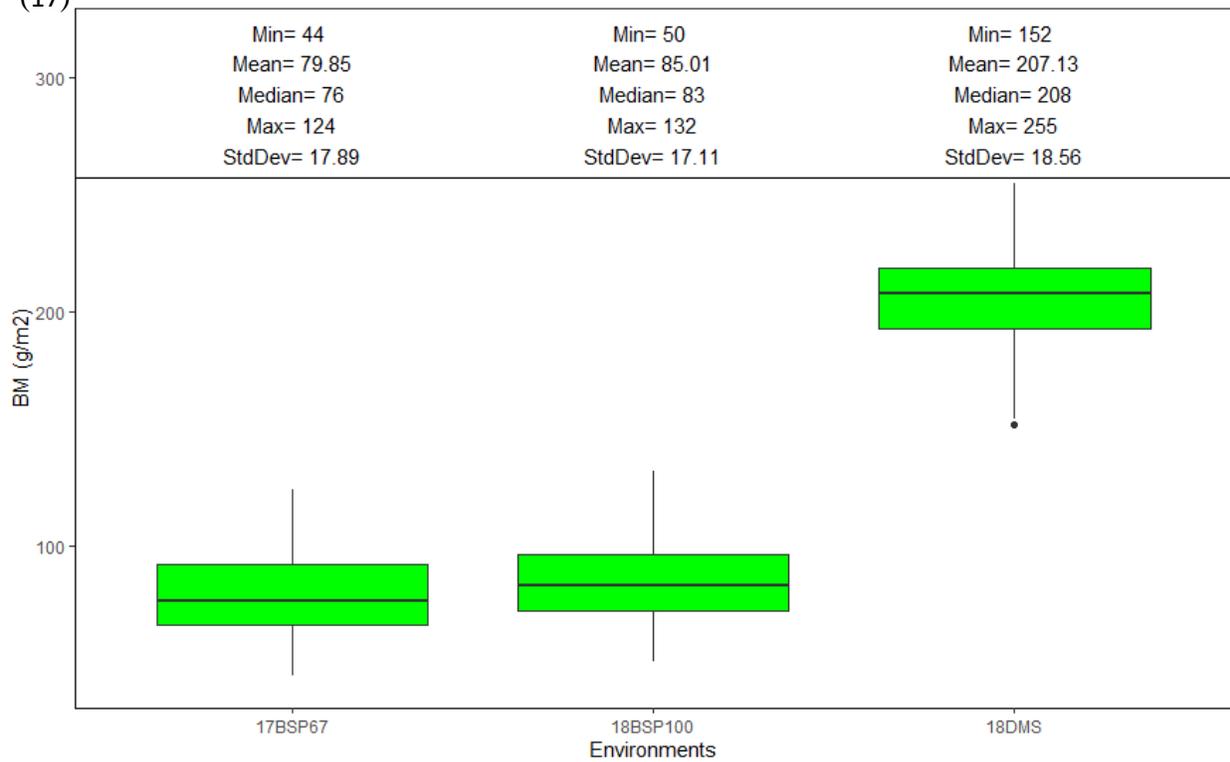
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Boxplot of all location



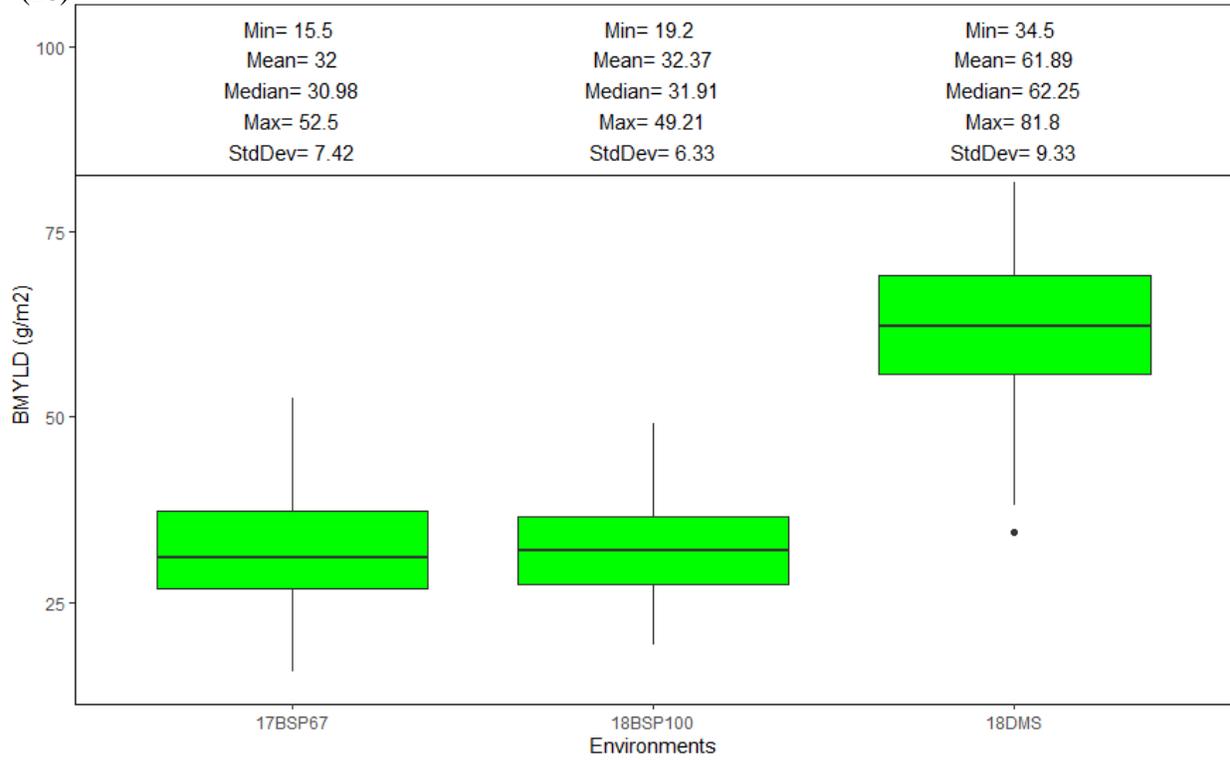
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Boxplot of all location



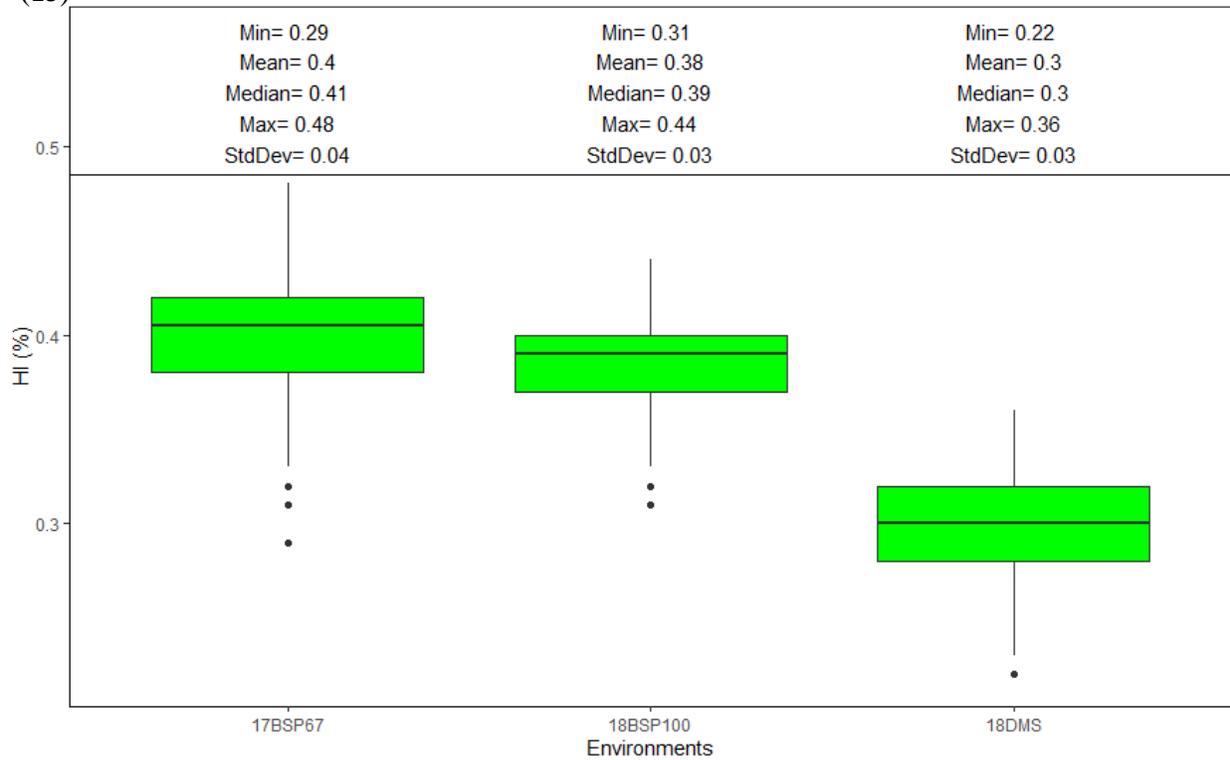
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Boxplot of all location



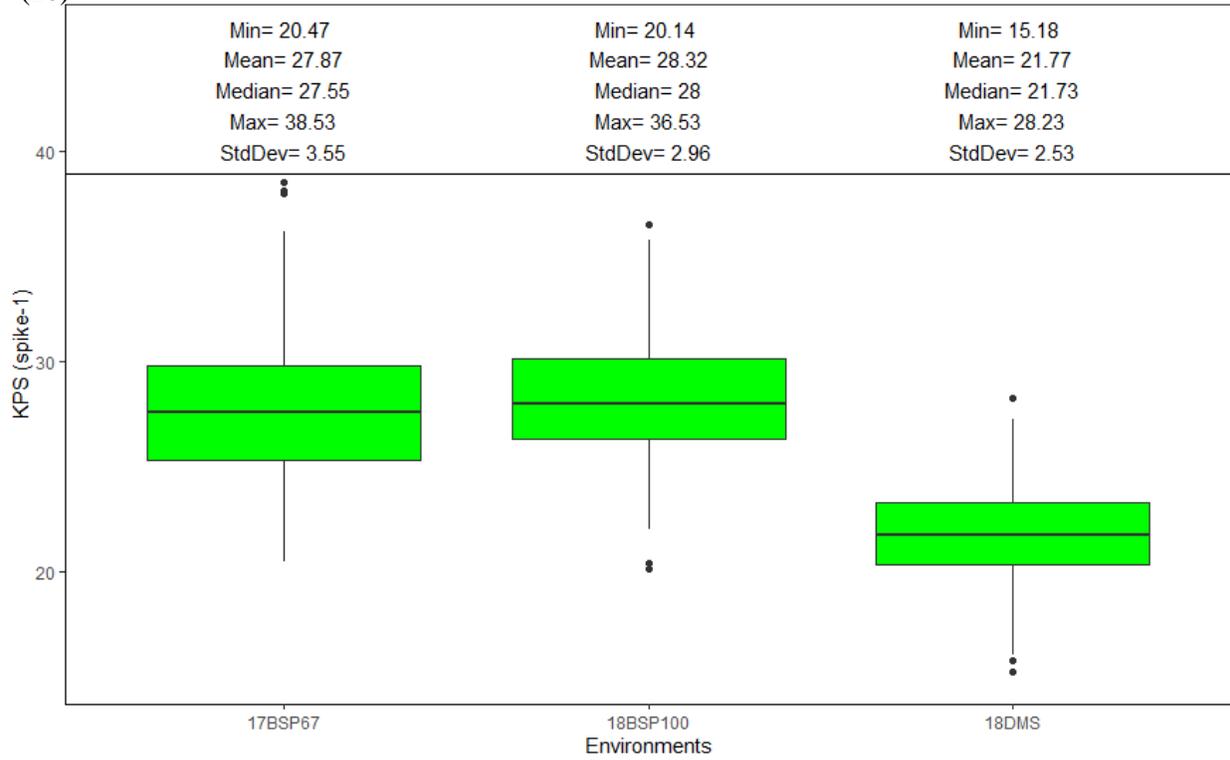
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Boxplot of all location



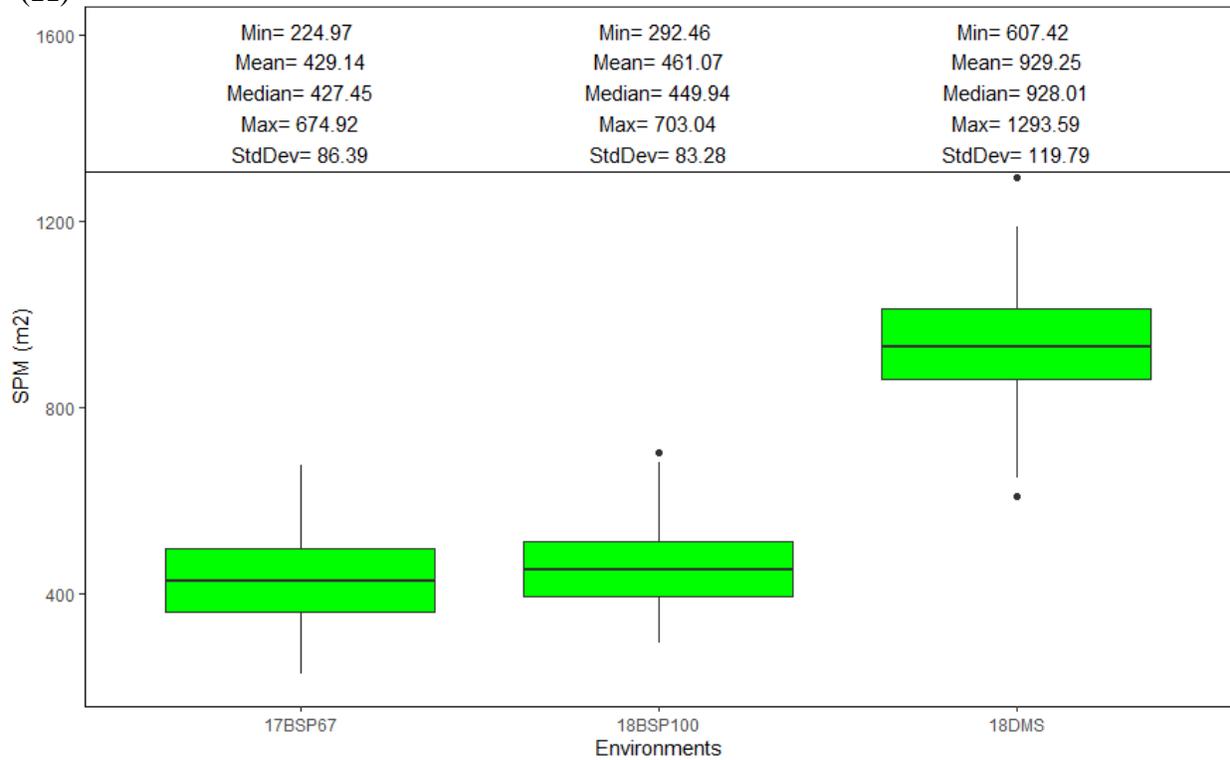
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Boxplot of all location



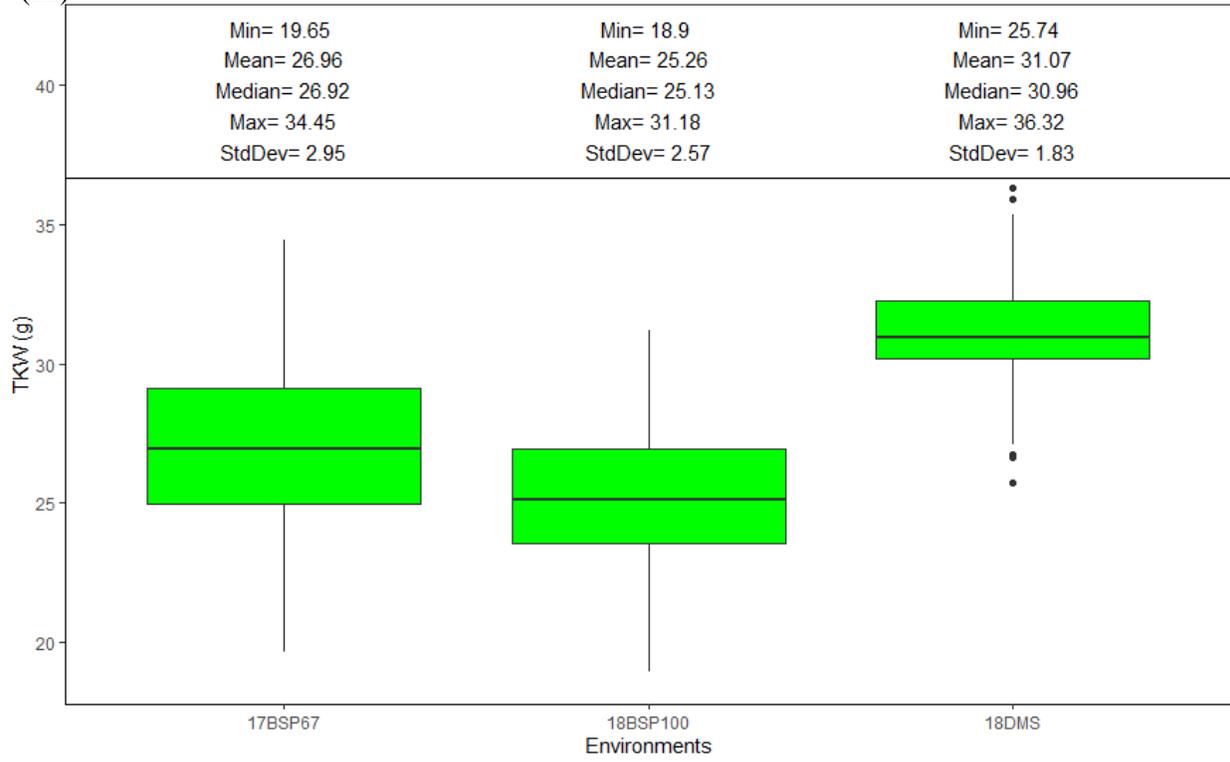
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Boxplot of all location



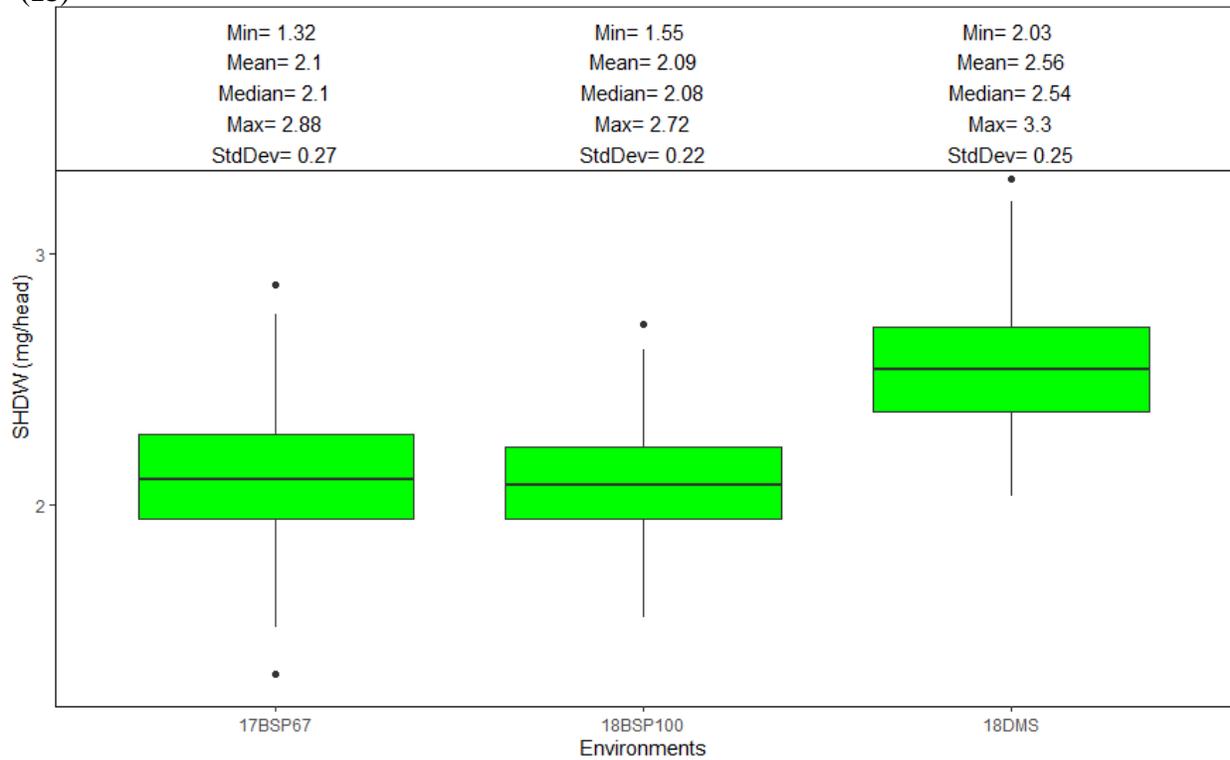
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Boxplot of all location



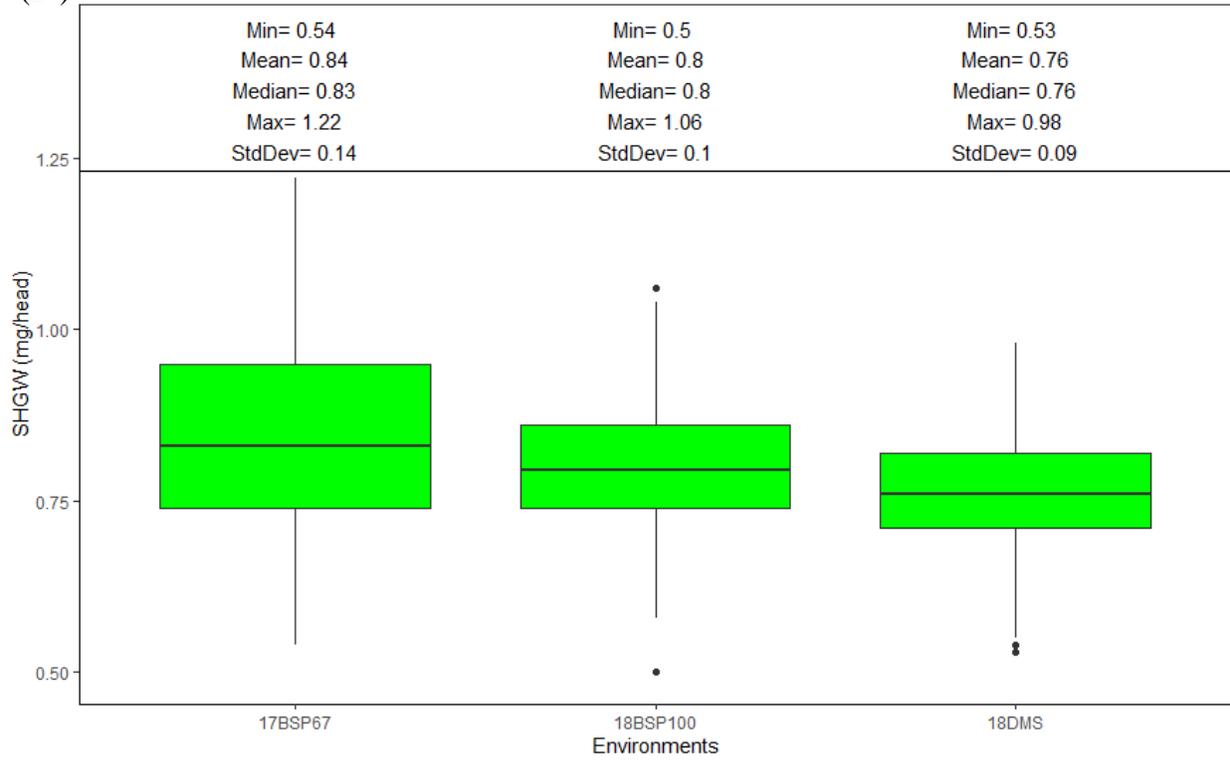
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Boxplot of all location



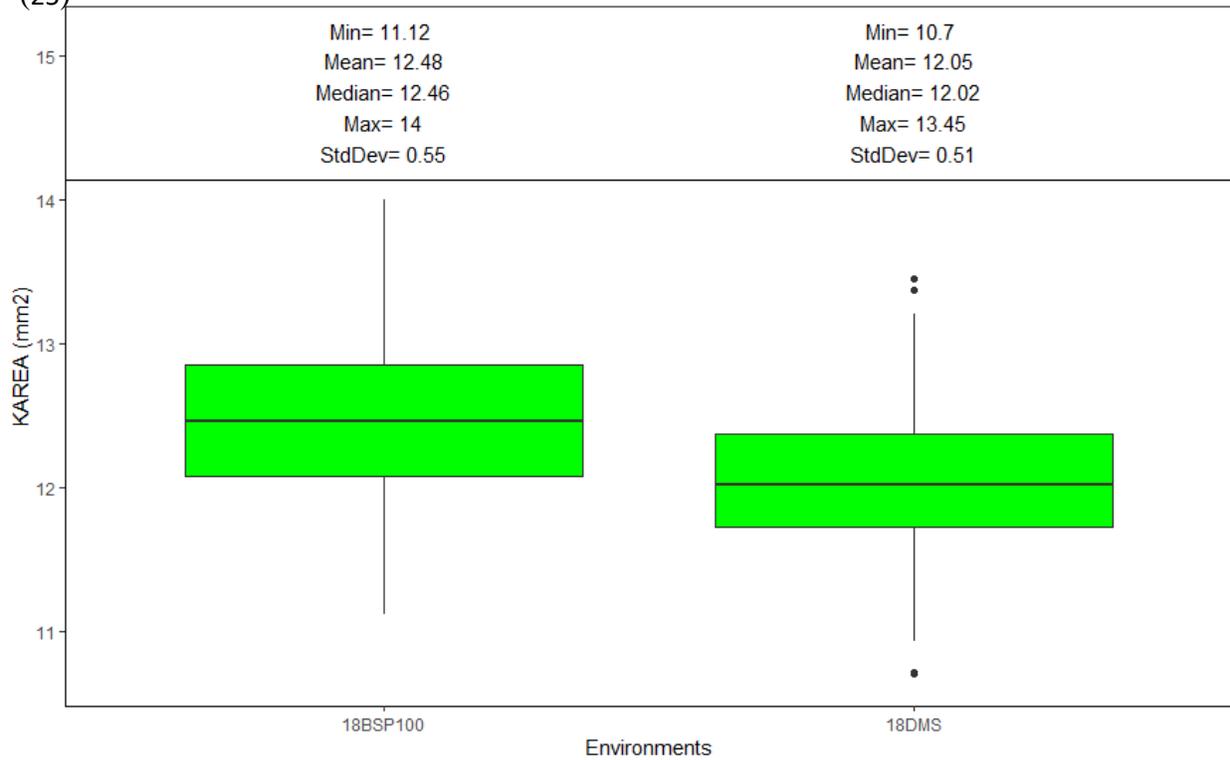
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Boxplot of all location



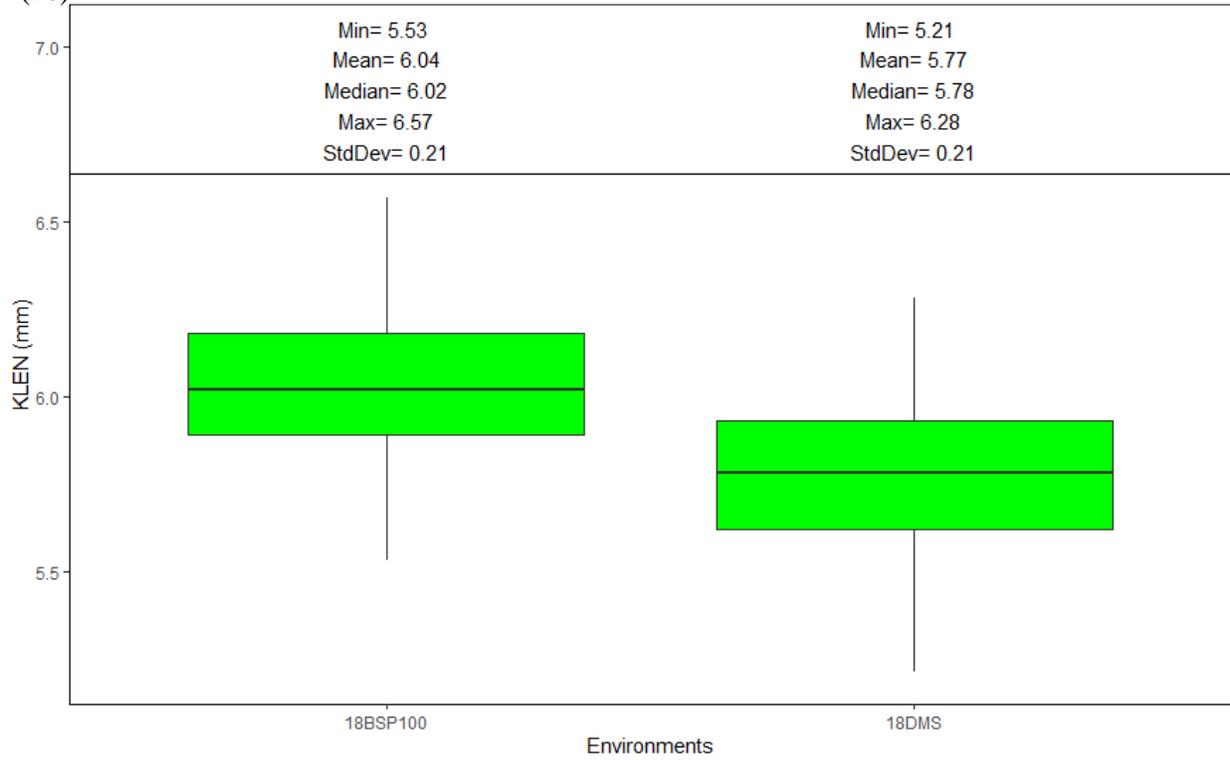
(25)

Boxplot of all location



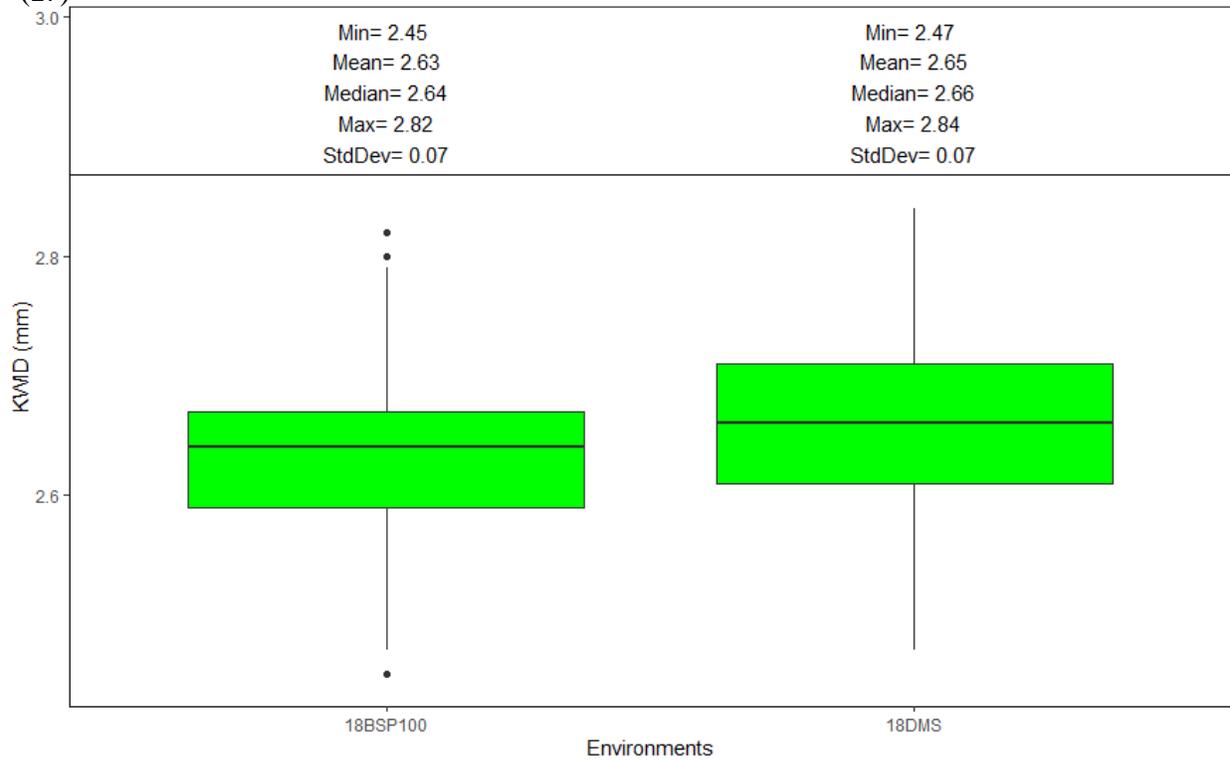
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Boxplot of all location



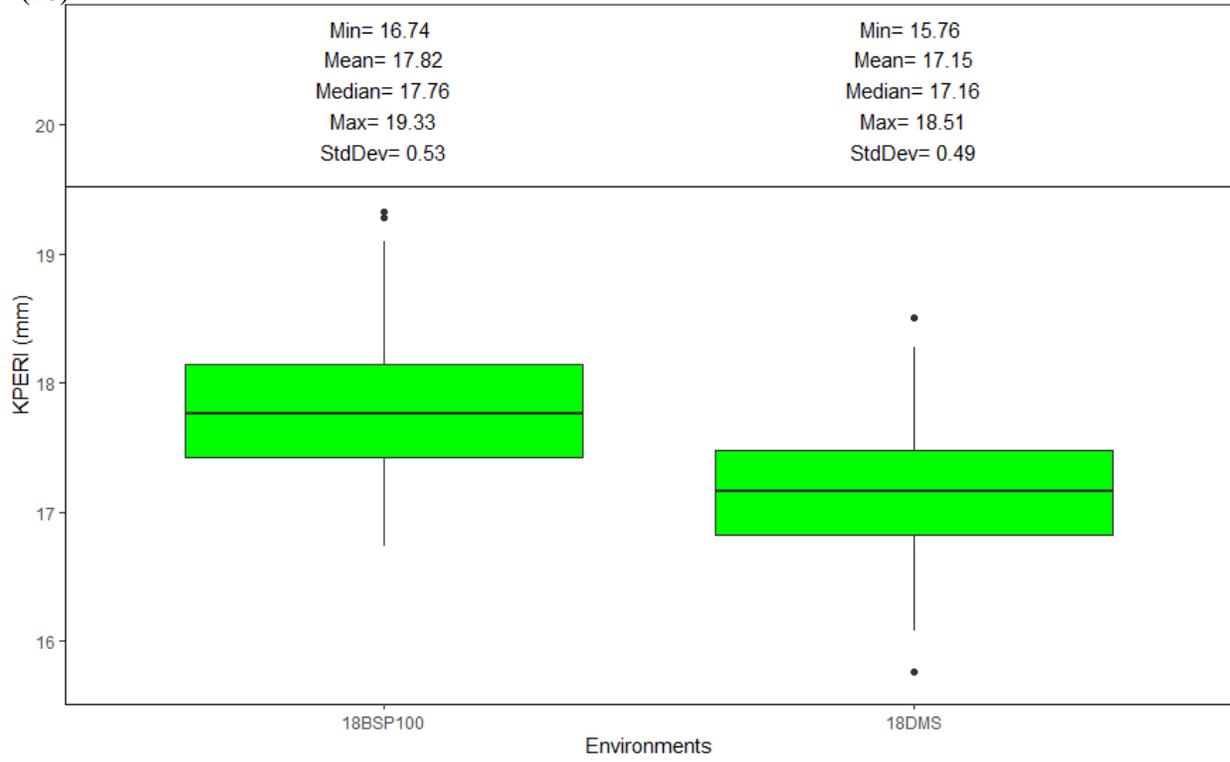
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Boxplot of all location

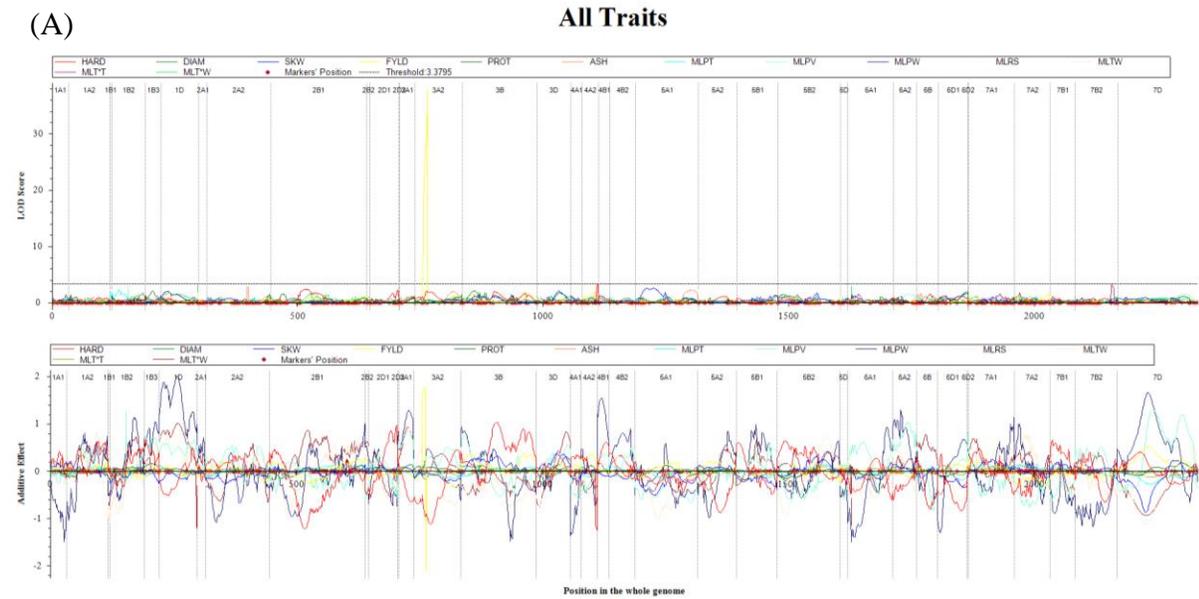


(28)

Boxplot of all location

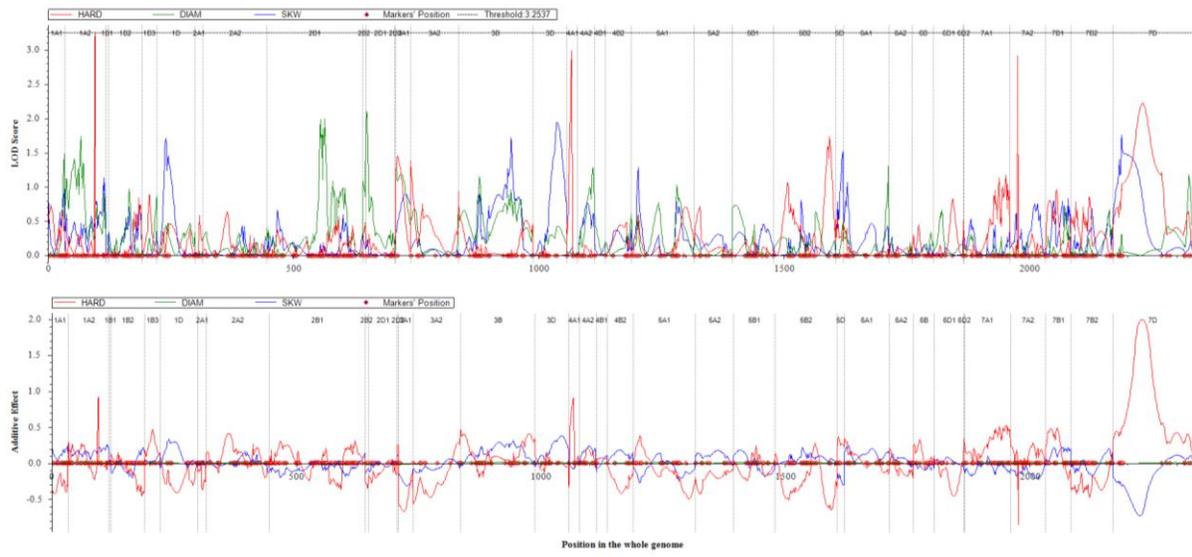


Supplemental Fig S3a: LOD profile and additive effects of detected QTL for end-use quality traits in each of the environments. Top figure shows LOD profile with chromosomal position along the x-axis (cM of 35 LGs) and LOD score on the y-axis. Bottom figure shows additive effect profile with chromosomal position along the x-axis and additive effects on the y-axis. Different end-use quality traits are color coded as shown on the top of each panel. The positive additive effect value indicates that the favorable alleles were from TAM 111 while the negative additive effect value indicates that favorable alleles were from TX05A001822. Traits include 1) hardness index, (HARD); 2) kernel diameter, (DIAM); 3) single kernel weight, (SKW); 4) flour yield, (FYLD); 5) flour protein at 14% moisture, (PROT); 6) flour ash at 14% moisture, (ASH); 7) midline peak time, (MLPT); 8) midline peak value, (MLPV); 9) midline peak width, (MLPW); 10) midline right slope, (MLRS); 11) midline tail width, MLTW; 12) midline time X time, (MLTXT); 13) midline time X width, (MLTXW). Individual environments include A) Chillicothe (17CH), B) Bushland (18BSP100), C) McGregor (18MCG), D) Dumas (18DMS). Combined environment (BLUP values of three environment includes E) COMB.



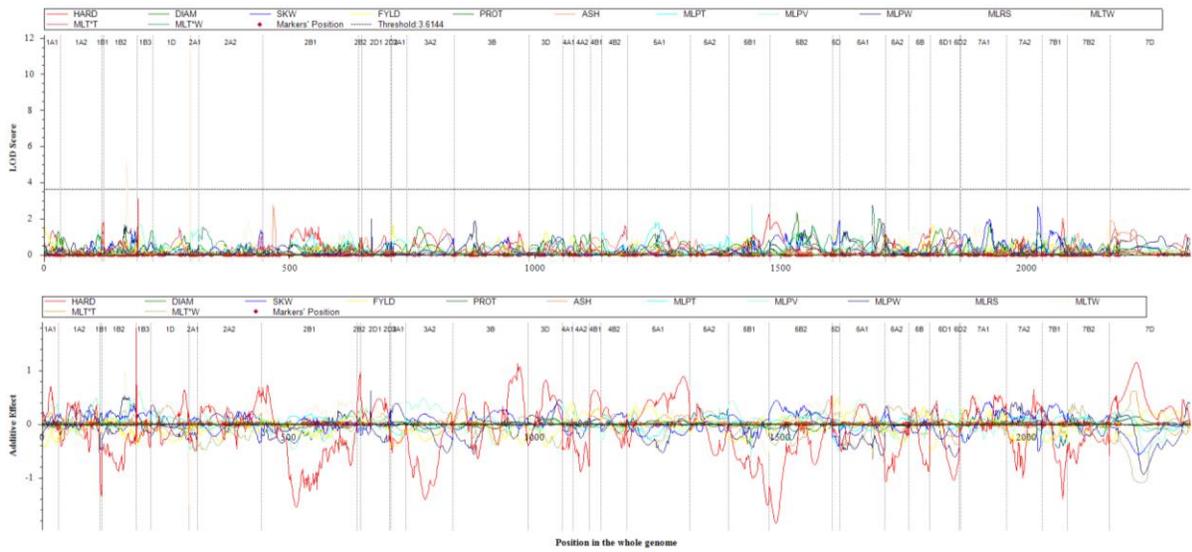
(B)

All Traits



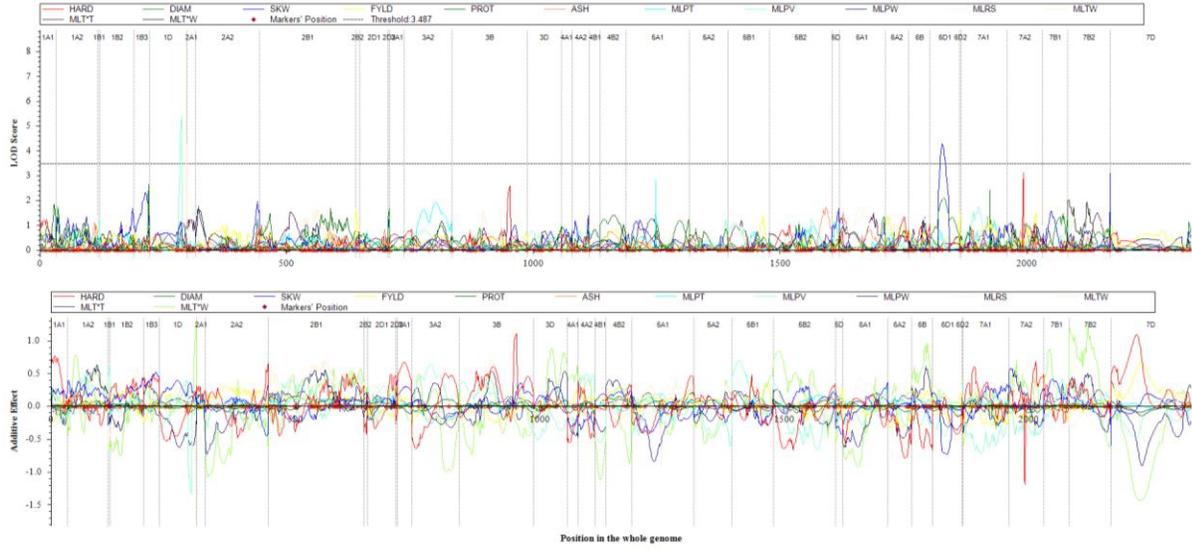
(C)

All Traits



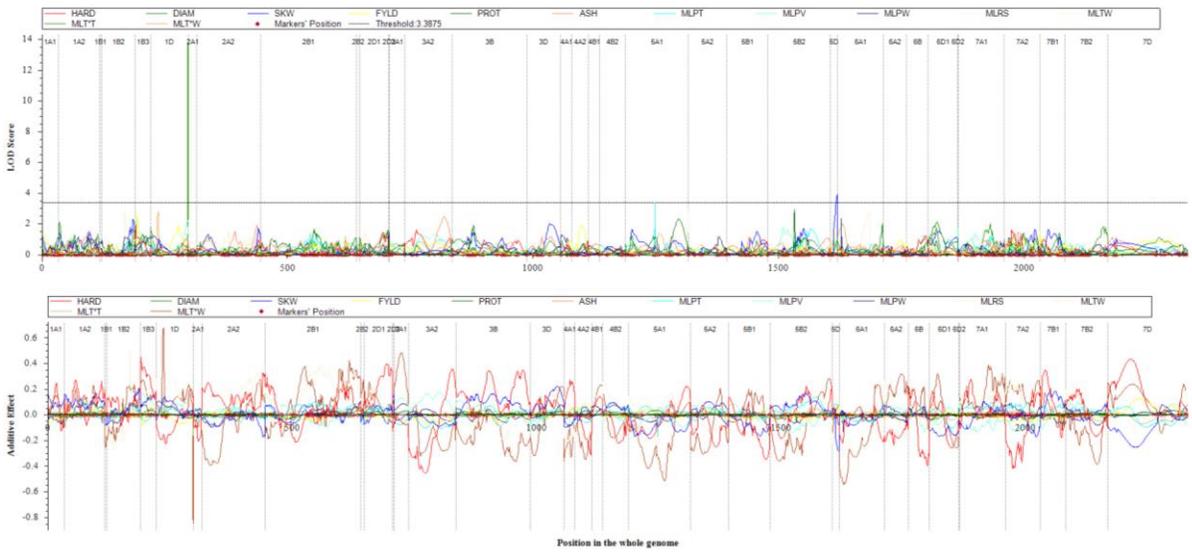
(D)

All Traits



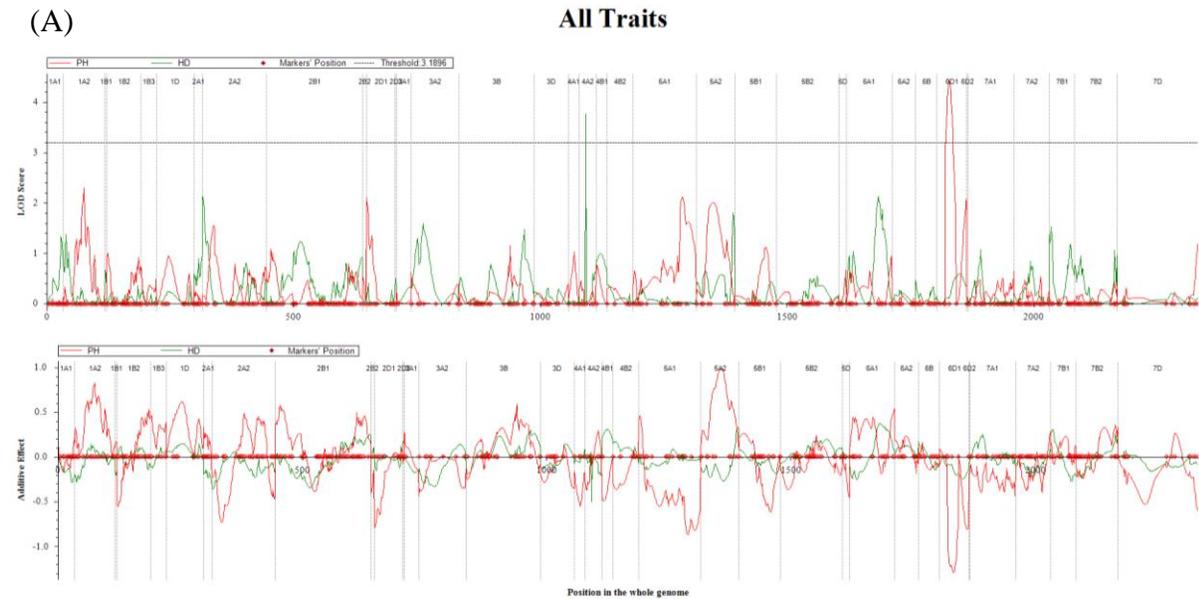
(D)

All Traits



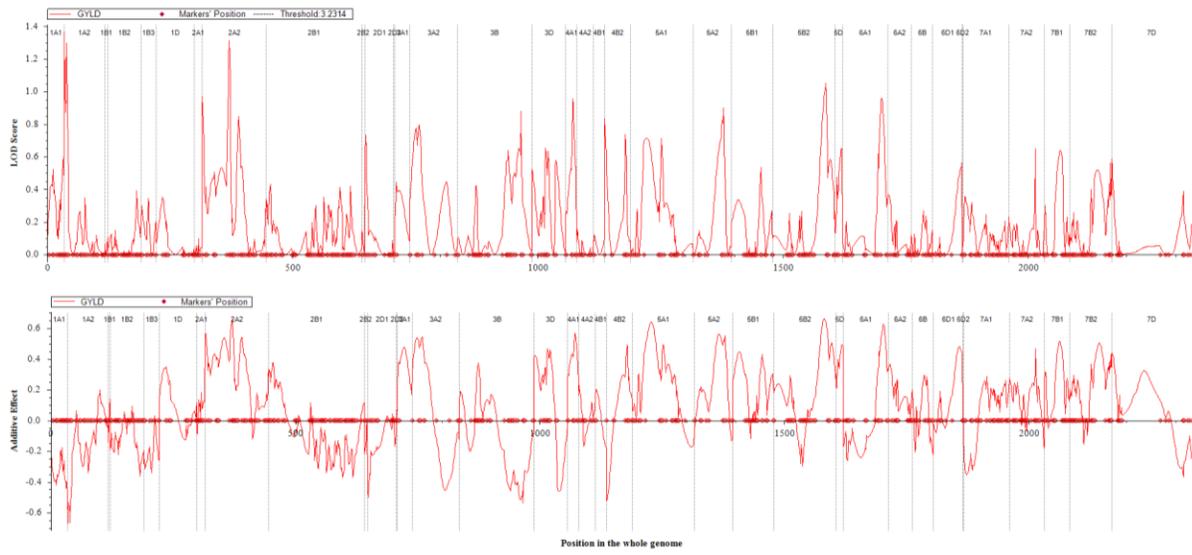
Supplemental Fig S3b: LOD profile and additive effects of detected QTL for agronomical traits in each of the environments. Top figure shows LOD profile with chromosomal position along the x-axis (cM of 35 LGs) and LOD score on the y-axis. Bottom figure shows additive effect profile with chromosomal position along the x-axis and additive effects on the y-axis. Yield and the agronomical traits are color coded as shown on the top of each panel. The positive additive effect means that the favorable alleles increasing the traits were from TAM 111 while those QTL with negative additive effects had favorable alleles from TX05A001822. Traits include 1) grain yield (YLD); 2) plant height (PH); 3) heading date in Julian Calendar from January (HD). Individual environments include A) Bushland (17BSP100) B) Chillicothe (17CH), C) Bushland (18BSP100), D) Dumas (18DMS), E) McGregor (18MCG). Combined environment (BLUP values of the environment includes G) COMB.

NOTE: Data for YLD was collected from 5 environments (17CH, 18BSP100, 18DMS, 18MCG, UVL18) while data for PH and HD was collected from 4 environments (17BSP100, 18BSP100, 18DMS, 18MCG).



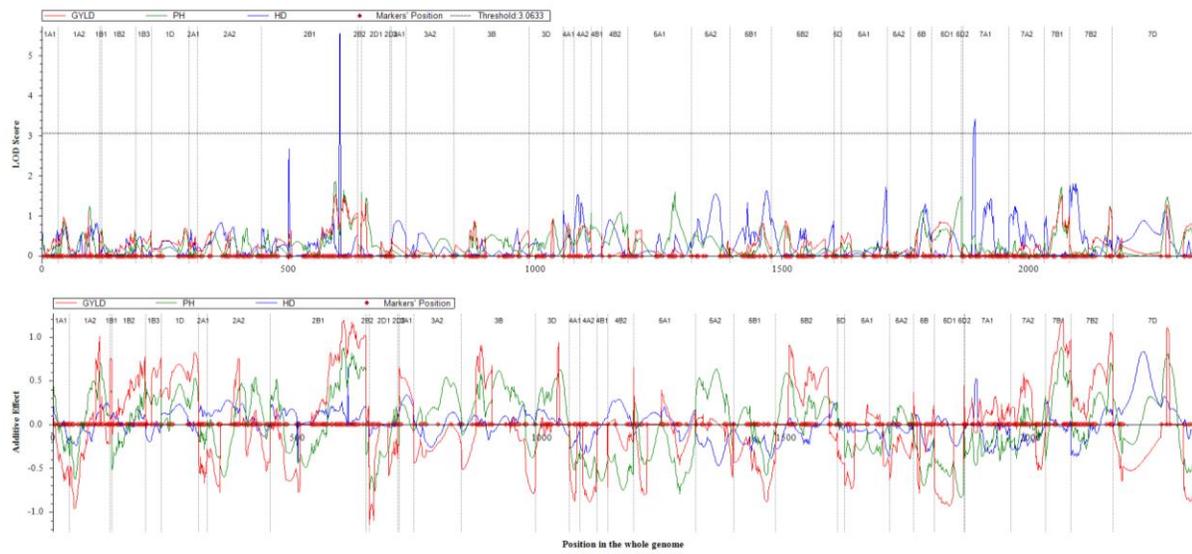
(B)

All Traits



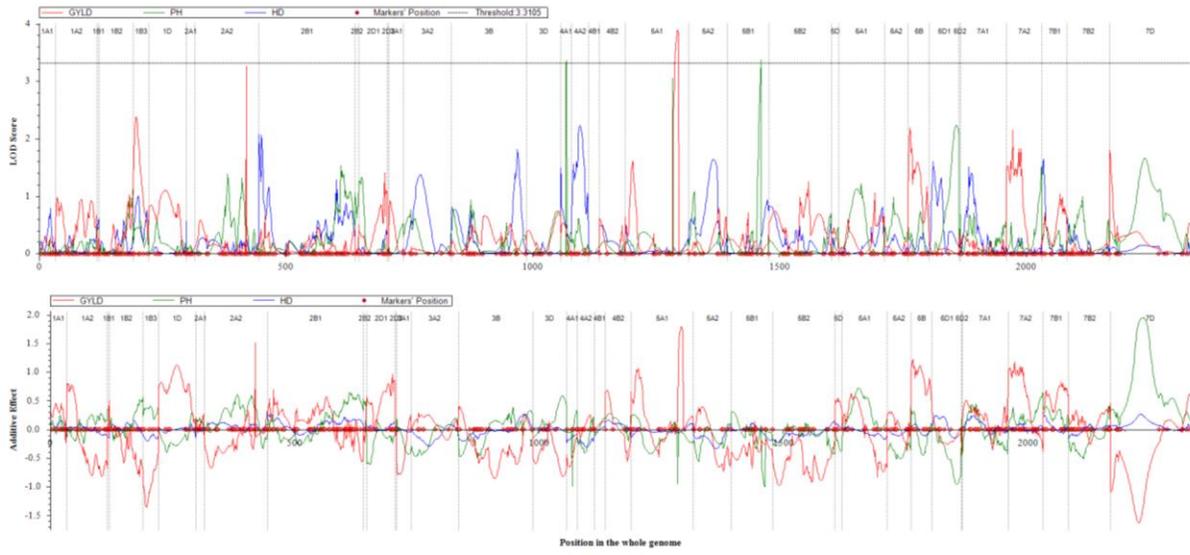
(C)

All Traits



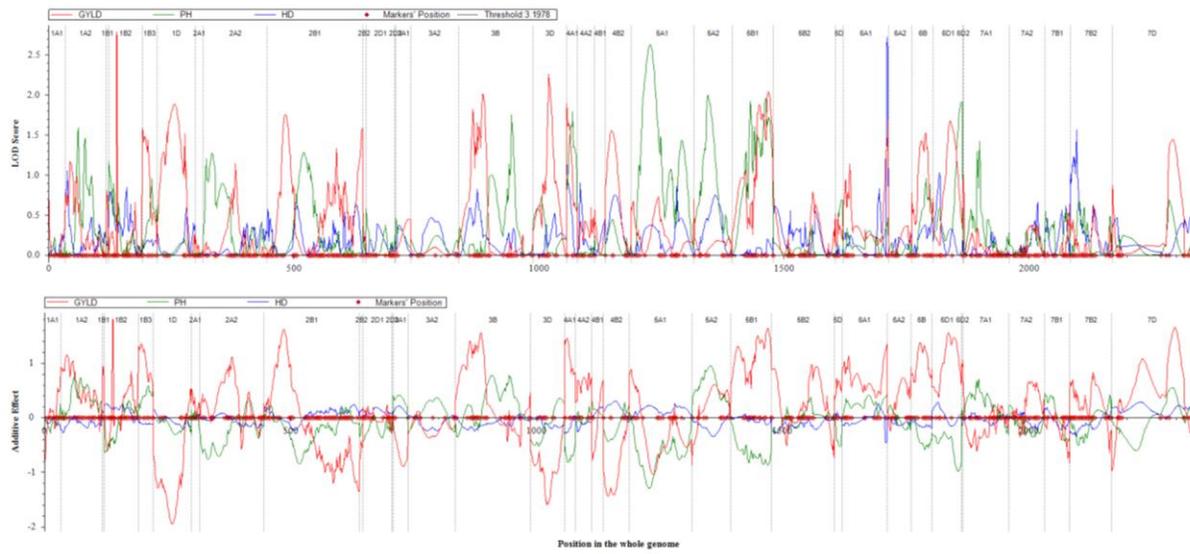
(D)

All Traits



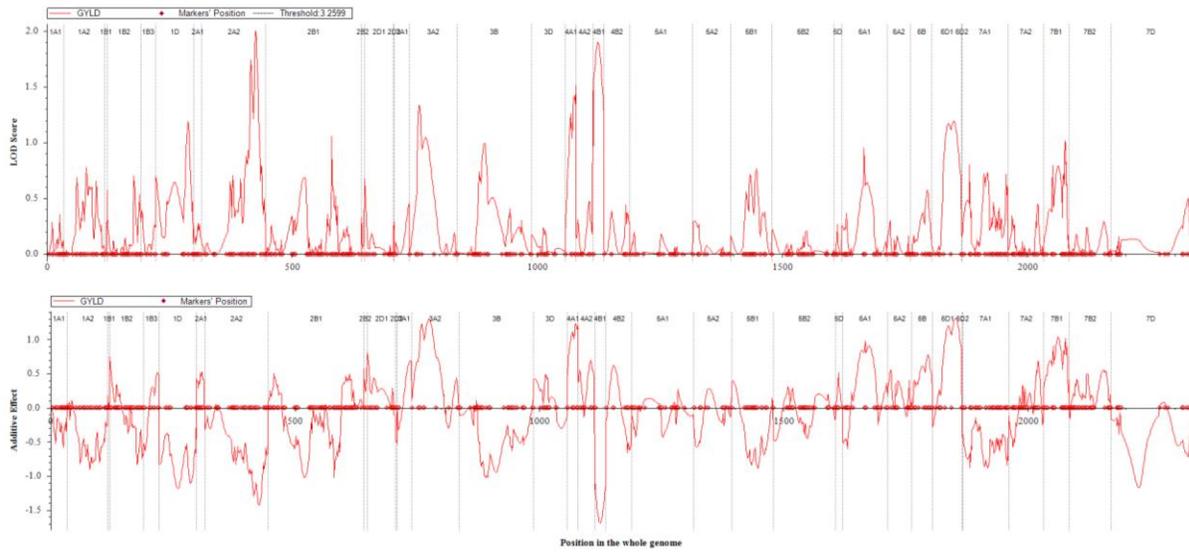
(E)

All Traits



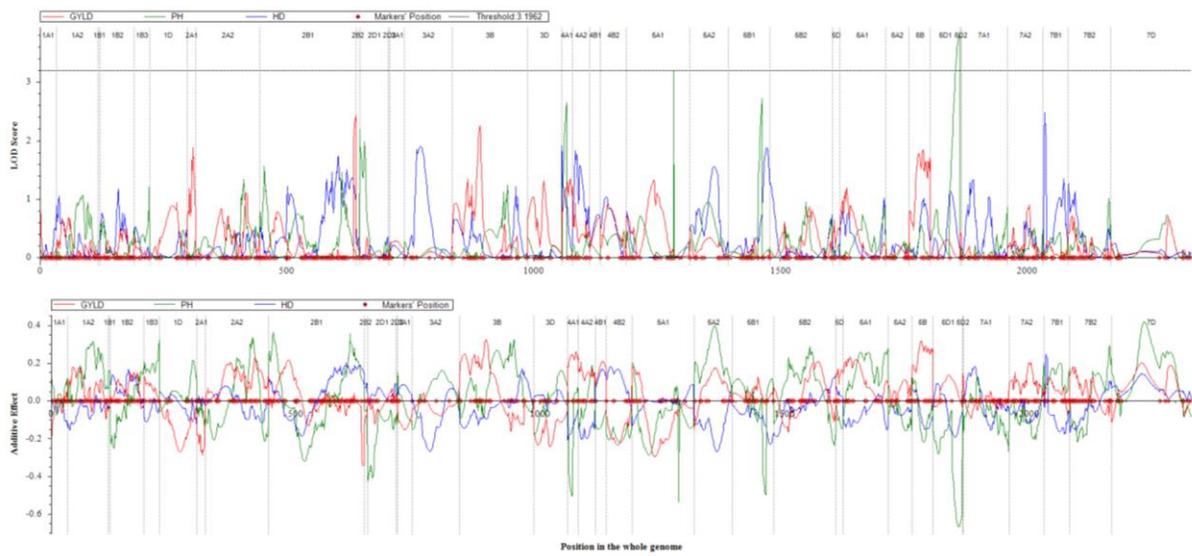
(F)

All Traits

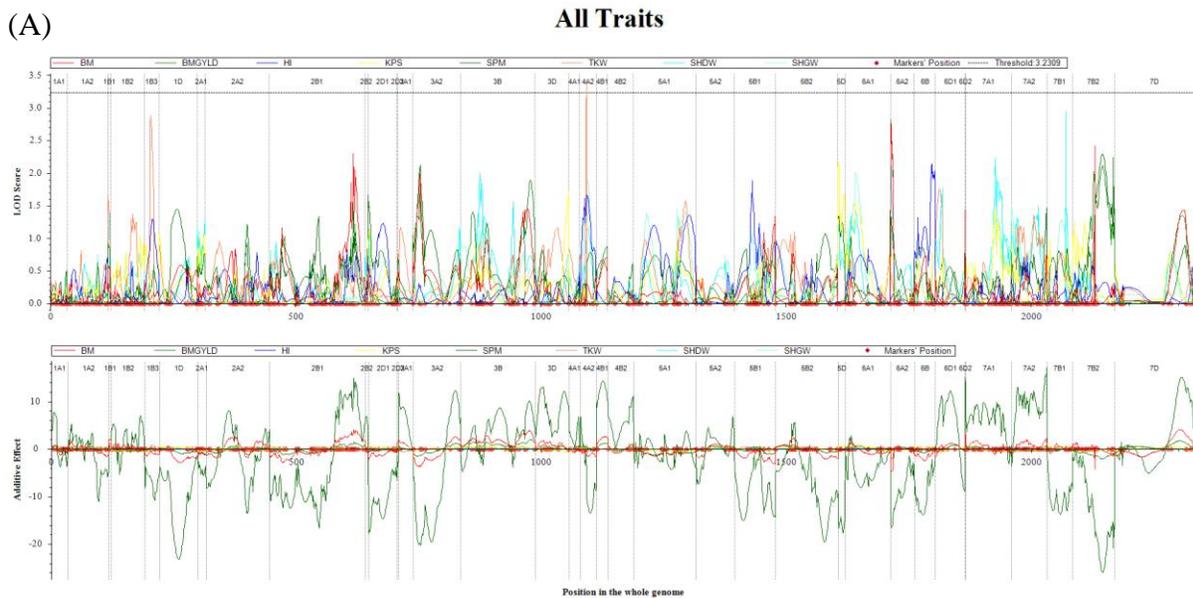


(G)

All Traits

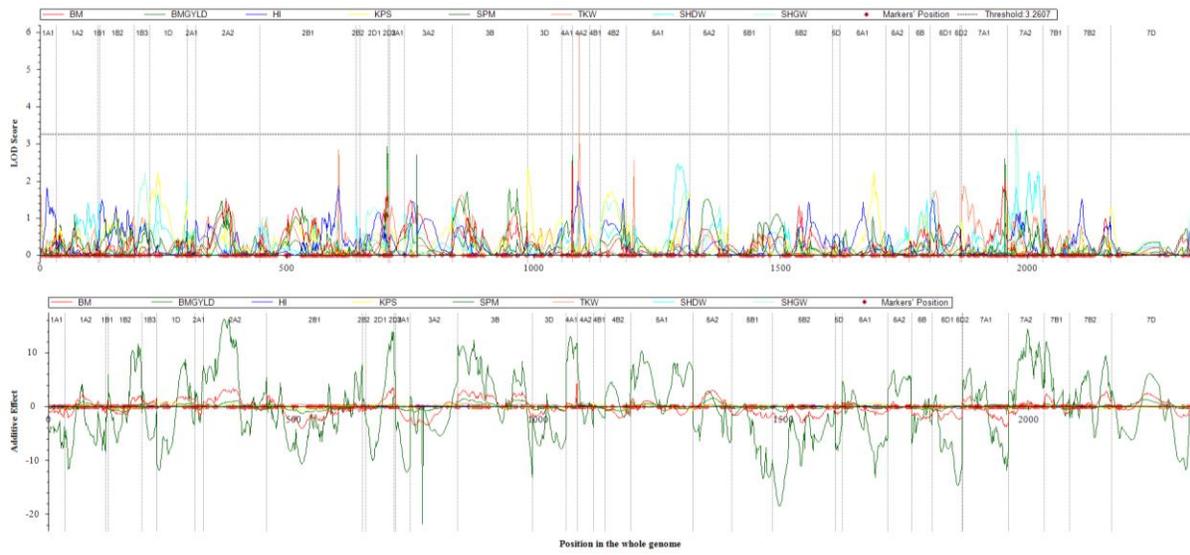


Supplemental Fig S3c: LOD profile and additive effects of detected QTL for yield-related traits in each of the environments. Top figure shows LOD profile with chromosomal position along the x-axis (cM of 35 LGs) and LOD score on the y-axis. Bottom figure shows additive effect profile with chromosomal position along the x-axis and additive effects on the y-axis. Different yield and yield components traits are color coded as shown on the top of each panel. The positive additive effect means that the favorable alleles increasing the traits were from TAM 111 while those QTL with negative additive effects had favorable alleles from TX05A001822. Traits include 1) dry biomass from hand harvested 0.5 m long inner row sample from crown (BM); 2) grain weight from 1) as hand harvested dry grain weight (BMYLD); 3) harvest index (HI); 4) kernels spike⁻¹ (KPS); 5) spikes m⁻² (SPM); 6) thousand kernel weight (TKW); 7) single head dry weight (SHDW); 8) single head dry grain weight (SHGW). Individual environments include A) Bushland (17BSP67), B) Bushland (18BSP100), C) Dumas (18DMS). Combined environment (BLUP values of three environment includes D) COMB.



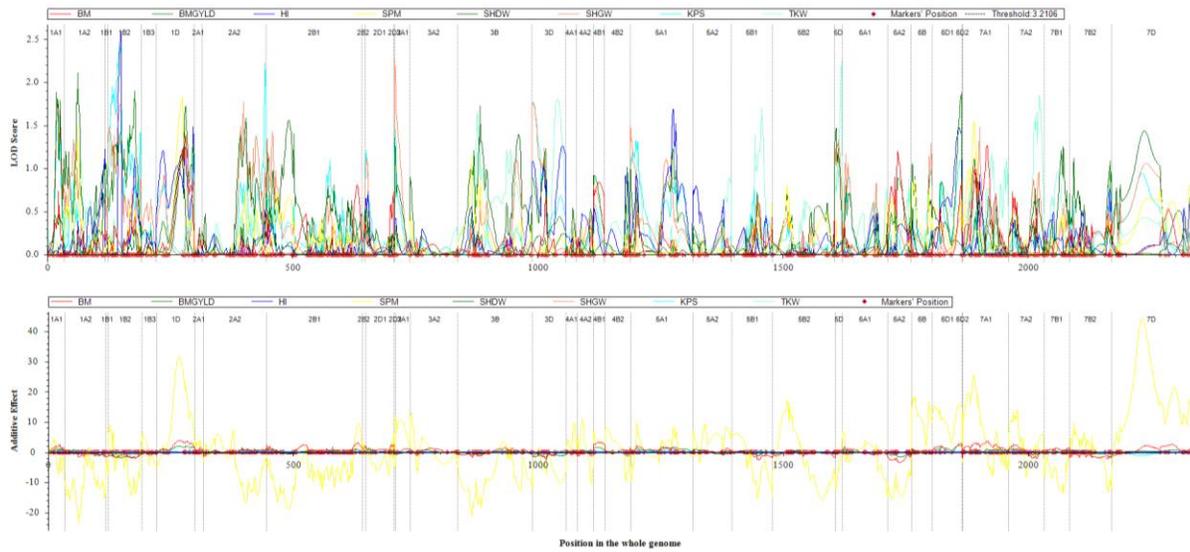
(B)

All Traits



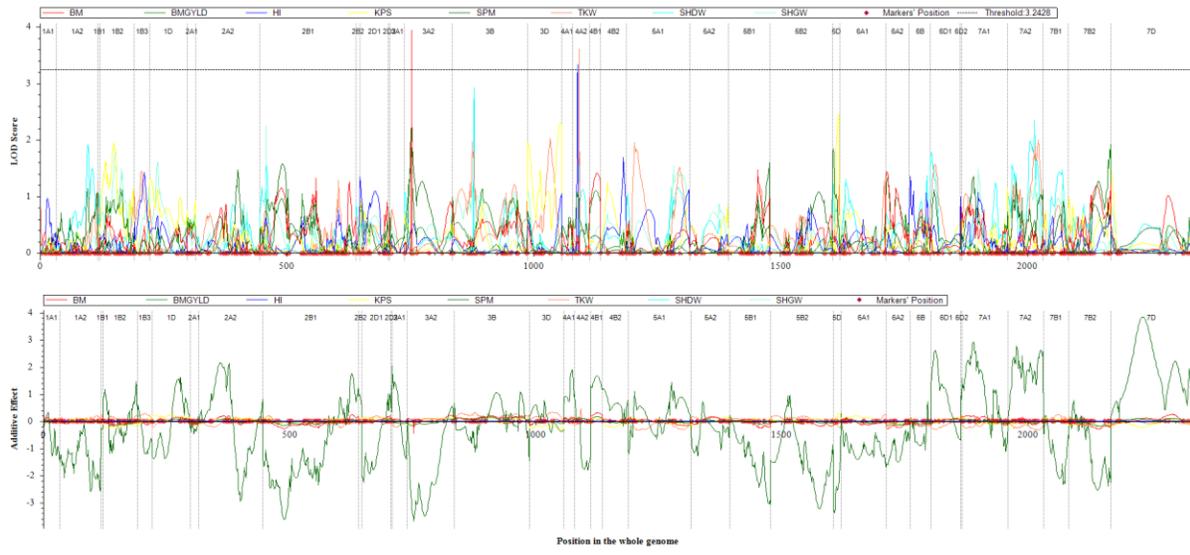
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All Traits



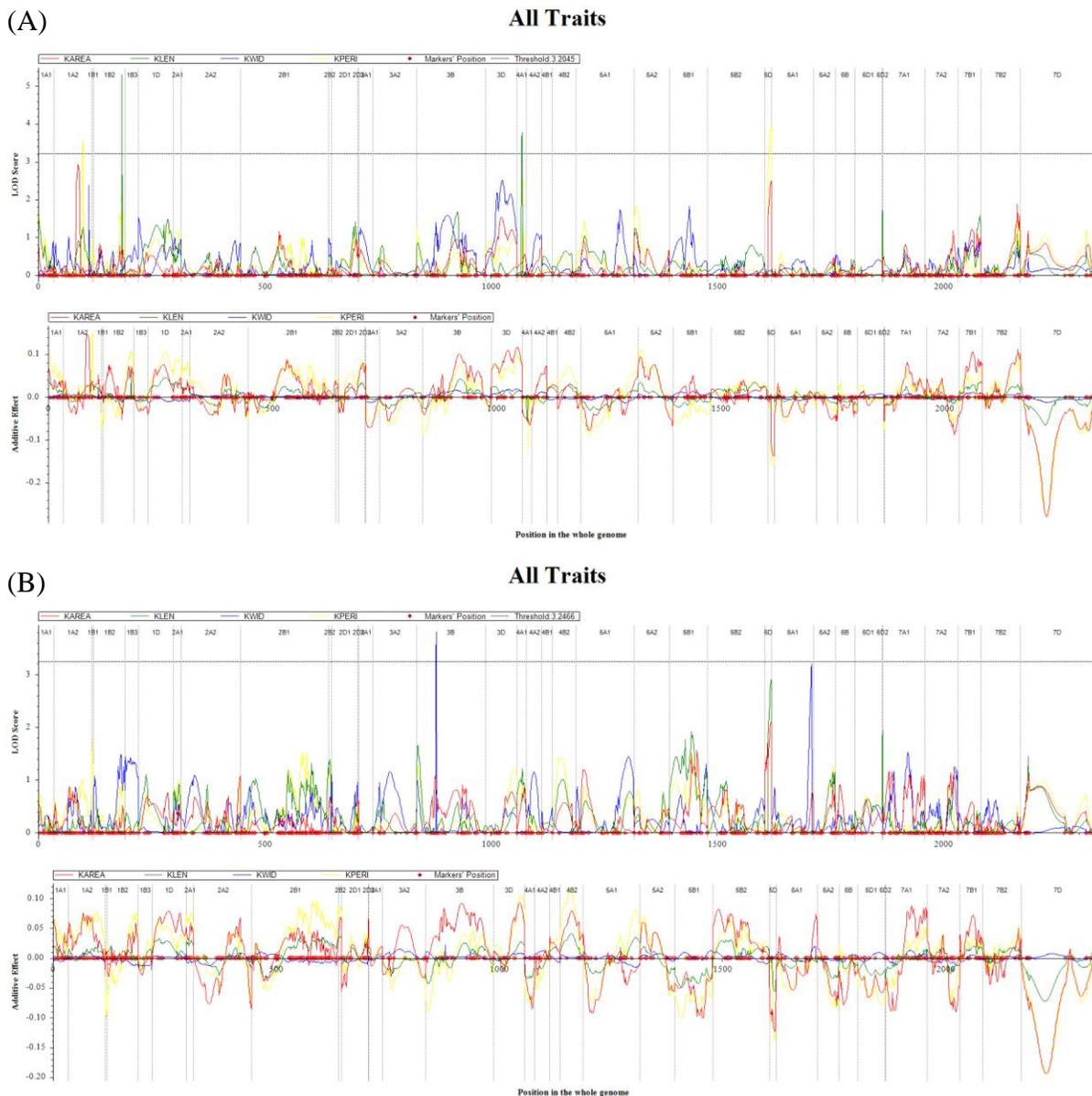
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All Traits



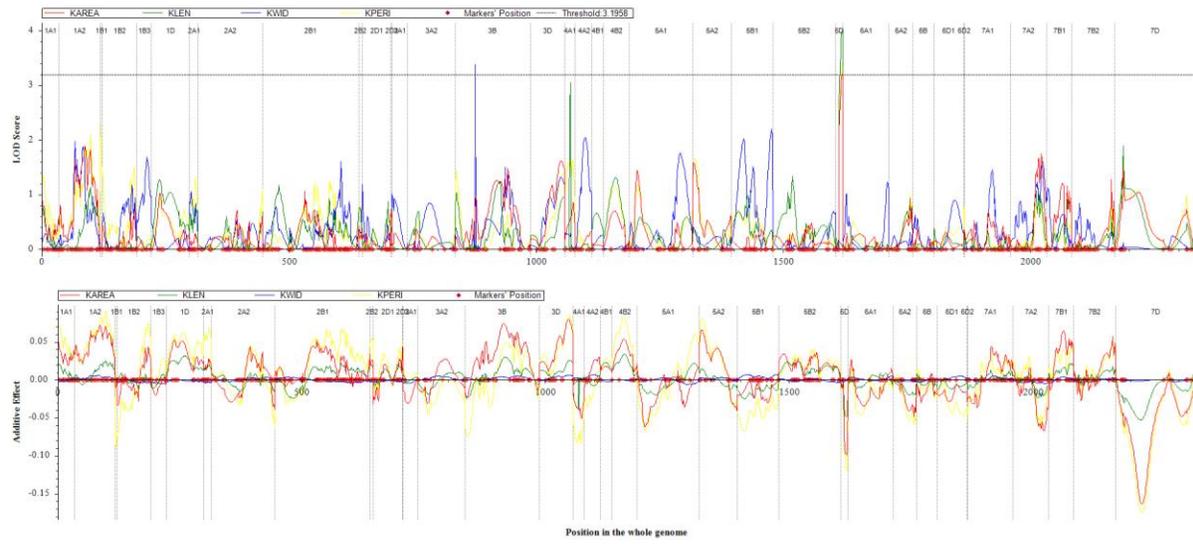
Supplemental Fig S3d: LOD profile and additive effects of detected QTL for kernel traits in each of the environments. Top figure shows LOD profile with chromosomal position along the x-axis (cM of 35 LGs) and LOD score on the y-axis. Bottom figure shows additive effect profile with chromosomal position along the x-axis and additive effects on the y-axis. Yield and the agronomical traits are color coded as shown on the top of each panel. The positive additive effect means that the favorable alleles increasing the traits were from TAM 111 while those QTL with negative additive effects had favorable alleles from TX05A001822. Traits include 1) kernel area (KAREA); 2) kernel length (KLEN); 3) kernel perimeter (KPERI); 4) kernel width (KWID). Individual environments include A) Bushland (18BSP100) B) Dumas (18DMS), and Combined environment (BLUP values of the environments) includes C) COMB.

NOTE: Data for traits was collected from 2 environments (18BSP100, 18DMS).

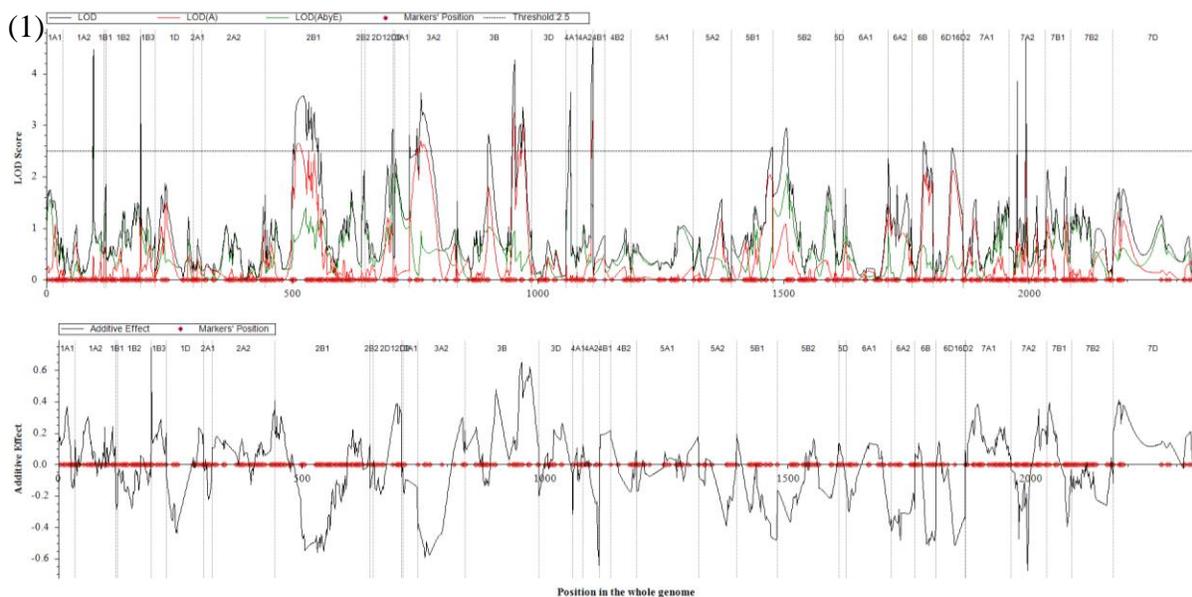


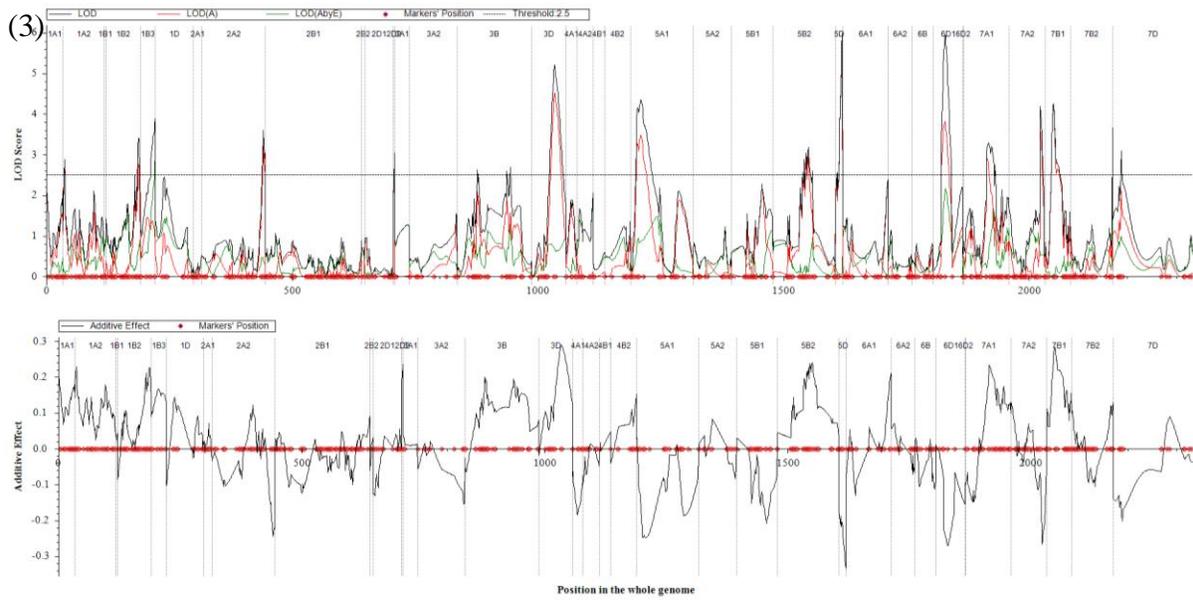
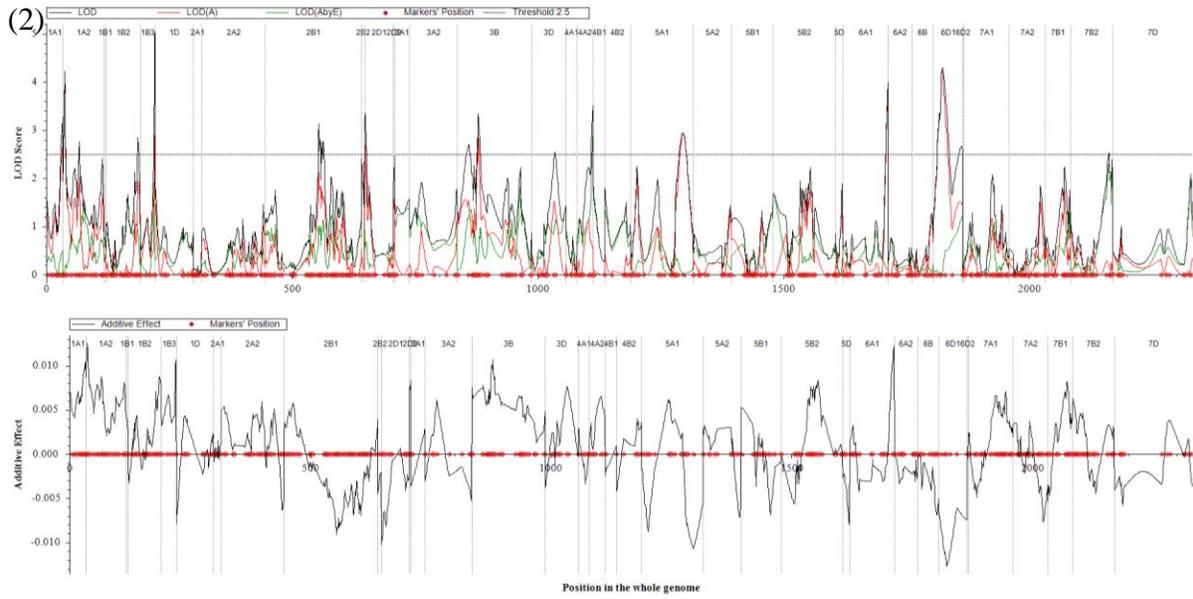
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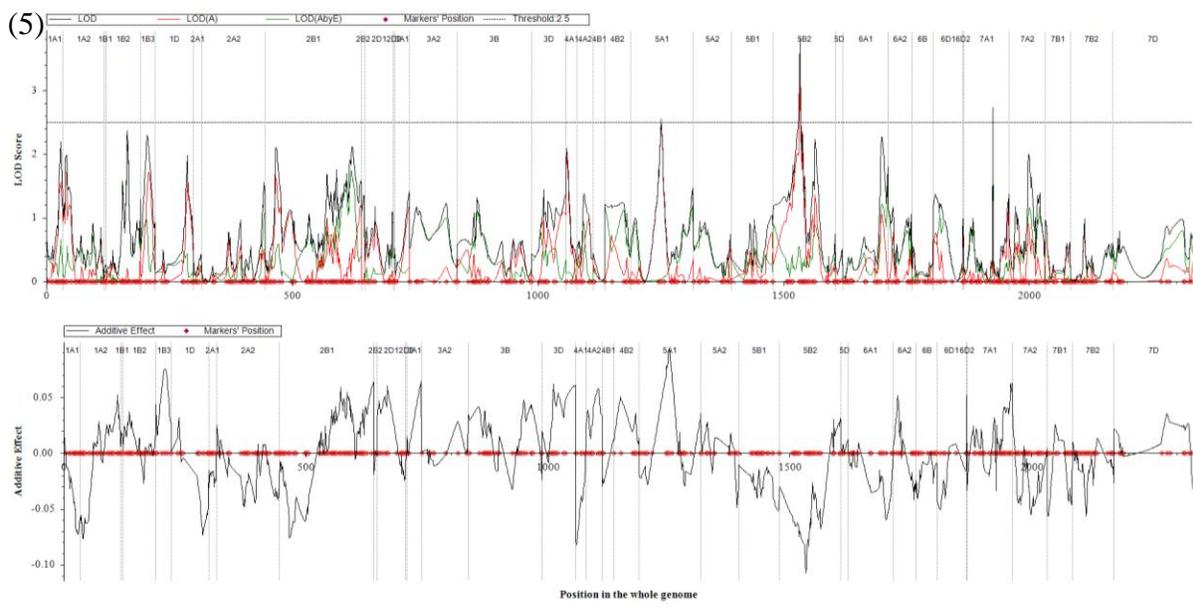
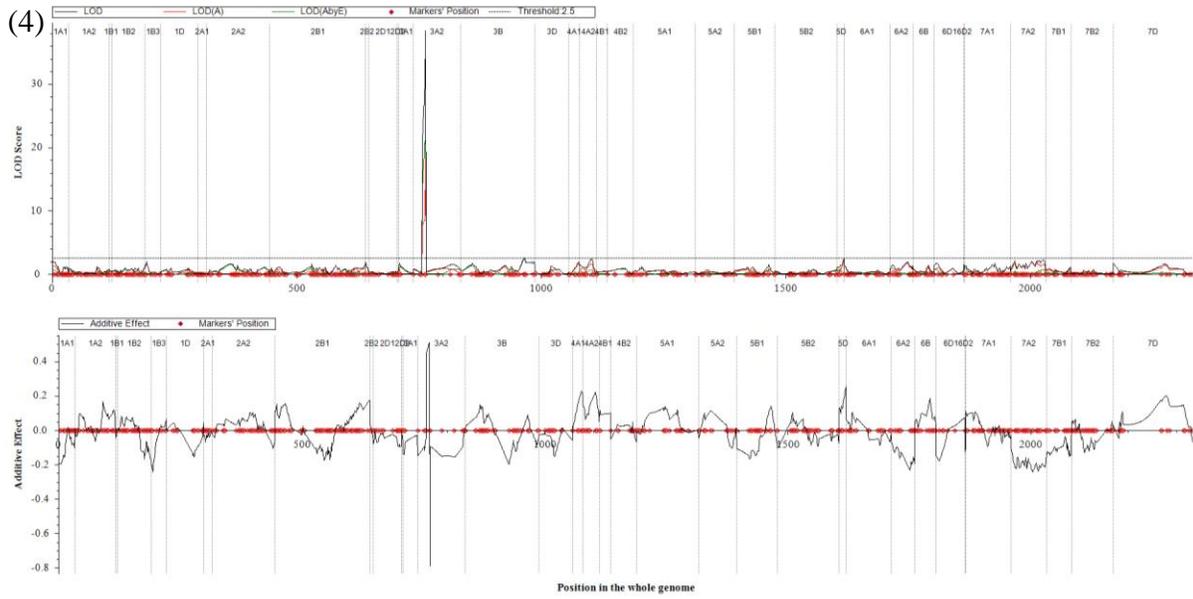
All Traits

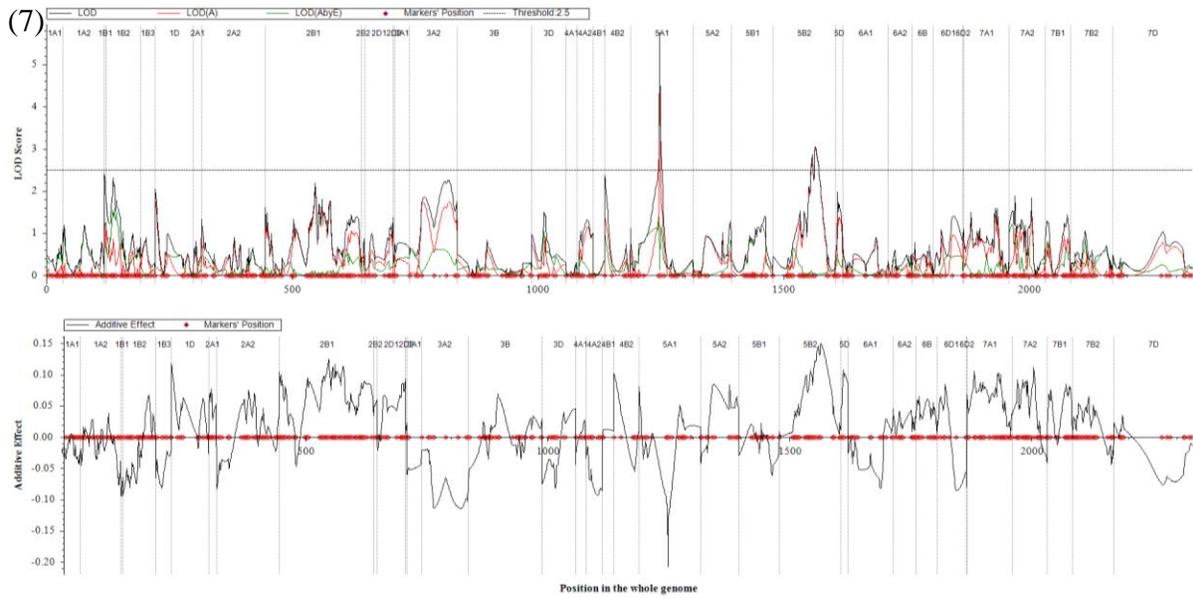
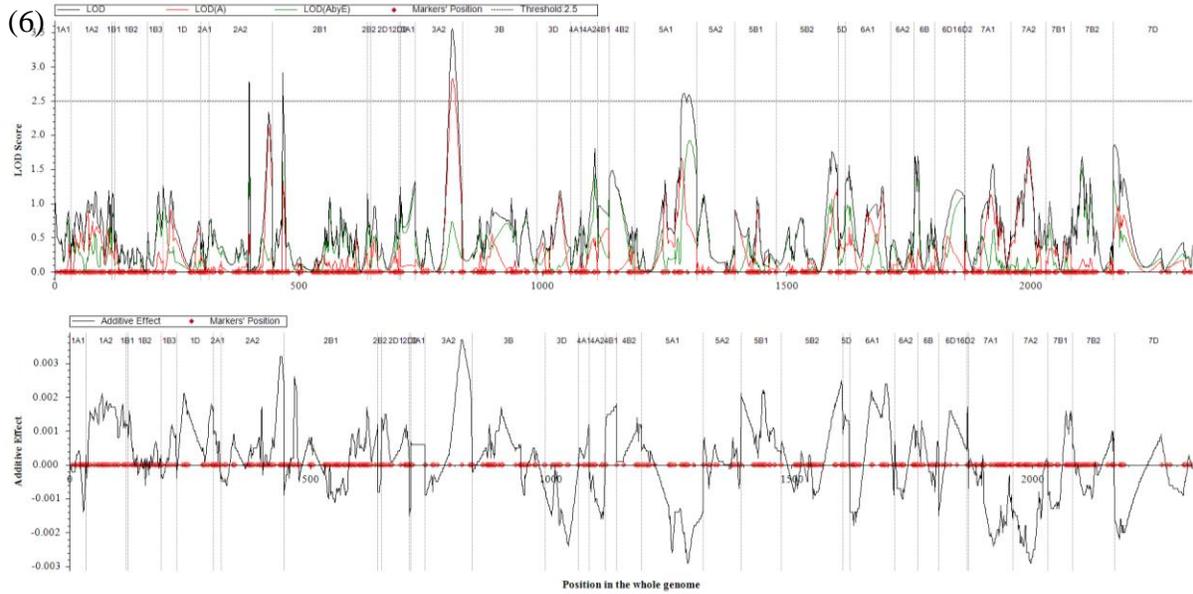


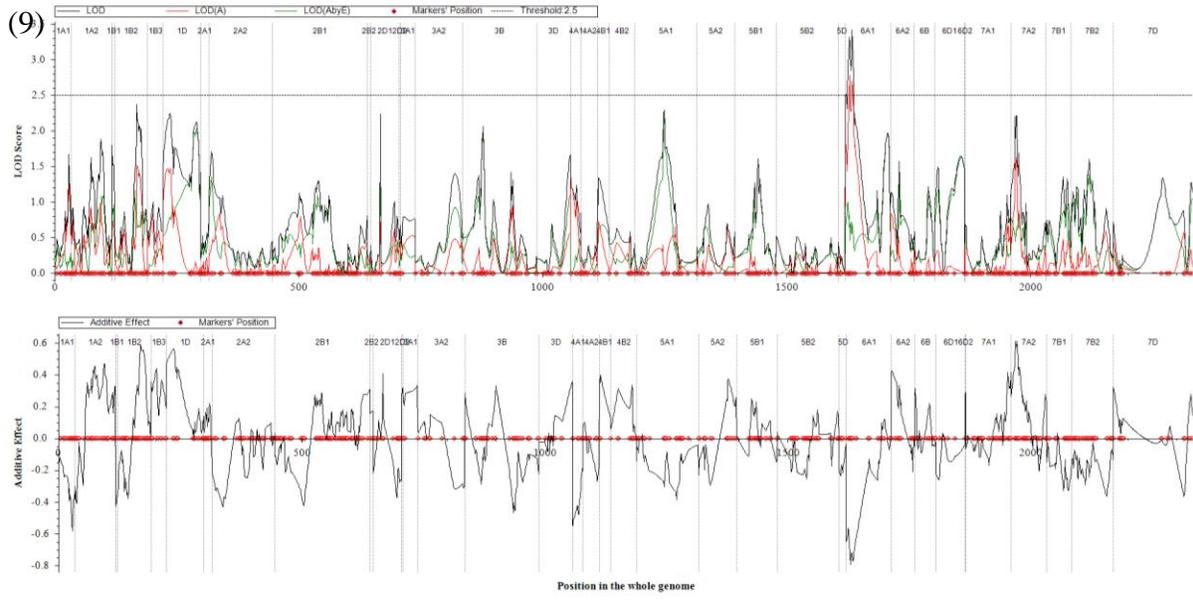
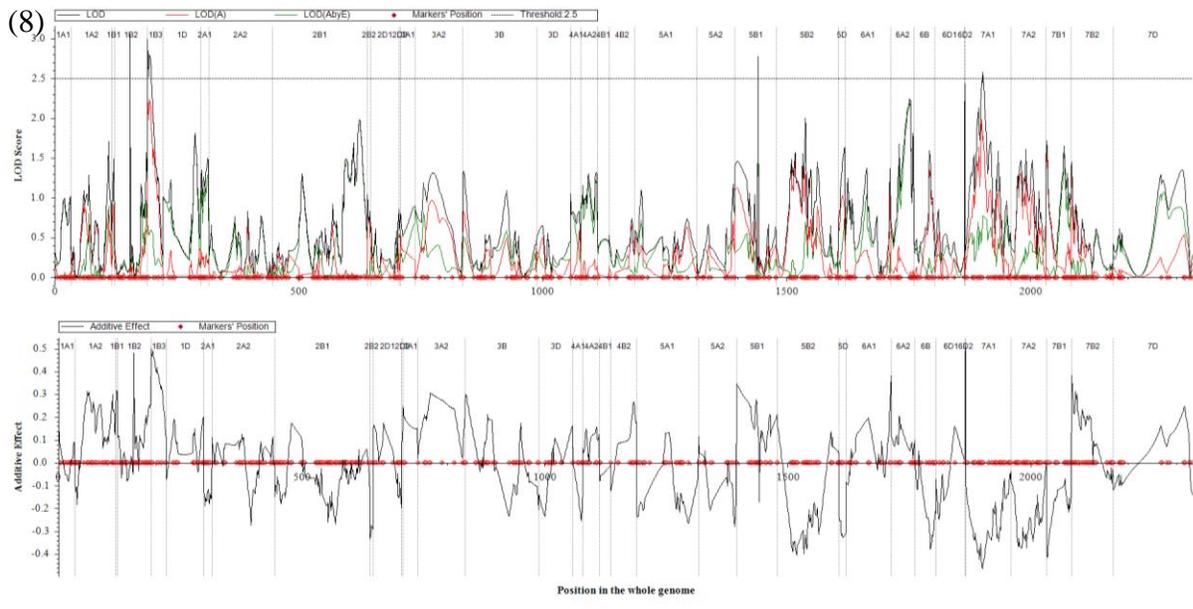
Supplemental Fig S4. Whole genome significant LOD(A) and LOD(AbyE) profiles of quantitative trait loci for end-use quality, agronomical, yield and kernel related traits based on across all the environments analyses. LOD for additive effect LOD(A) is in red color, LOD scores of additive by environment LOD(AbyE) is in green color; the dot line paralleled with the y-axis separated the 35 linkage groups while the x-axis from left to right are the total length of cM from chromosome 1A to 7D matching the 35 linkage groups (Table S3). The additive effect above and below the zero line in the bottom figure indicates that the favorable alleles were from TAM 111/TX05A001822. Traits include: 1) hardness index, (HARD); 2) kernel diameter, (DIAM); 3) single kernel weight, (SKW); 4) flour yield, (FYLD); 5) flour protein at 14% moisture, (PROT); 6) flour ash at 14% moisture, (ASH); 7) midline peak time, (MLPT); 8) midline peak value, (MLPV); 9) midline peak width, (MLPW); 10) midline right slope, (MLRS); 11) midline tail width, MLTW; 12) midline time X time, (MLTXT); 13) midline time X width, (MLTXW); 14) grain yield, (YLD); 15) plant height, (PH); 16) heading date in Julian Calendar from January, (HD); 17) dry biomass from hand harvested 0.5 m long inner row sample from crown, (BM); 18) grain weight from 17) as hand harvested dry grain weight, (BMYLD); 19) harvest index, (HI); 20) kernels spike⁻¹, (KPS); 21) spikes m⁻², (SPM); 22) thousand kernel weight, (TKW); 23) single head dry weight, (SHDW); 24) single head dry grain weight, (SHGW); 25) kernel area, (KAREA); 26) kernel length, (KLEN); 27) kernel perimeter, (KPERI); 28) kernel width, (KWID).



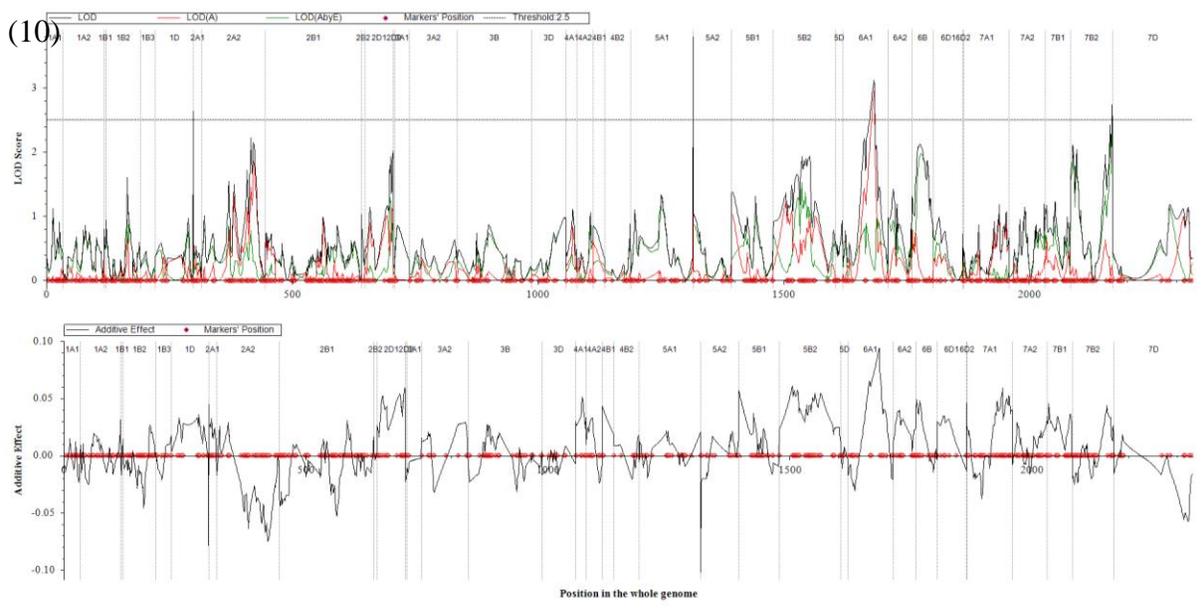




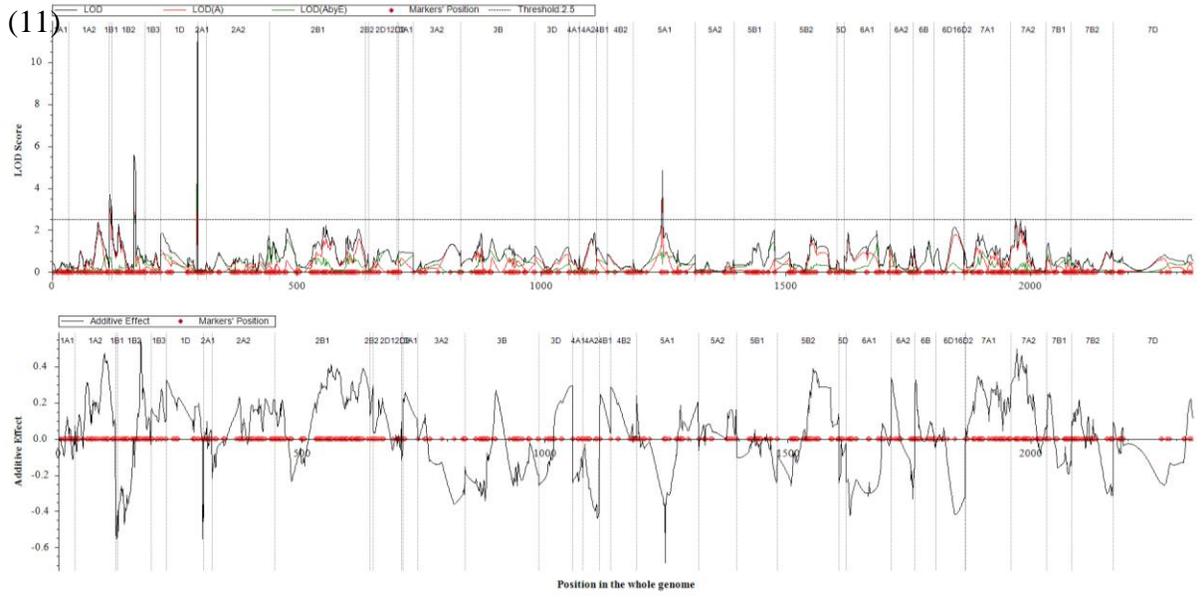




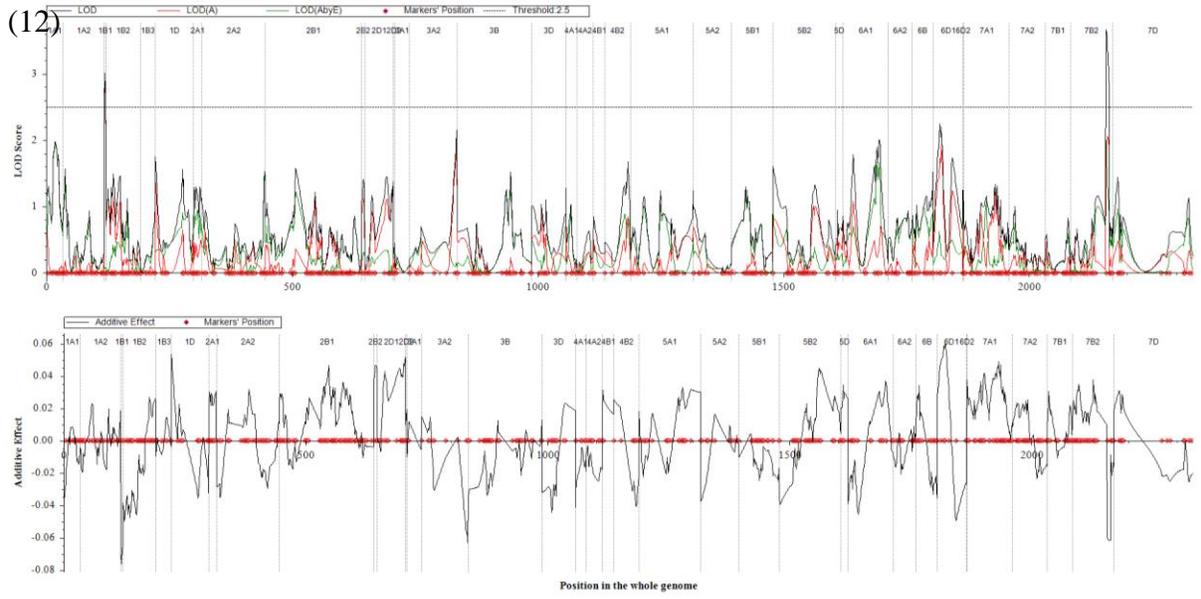
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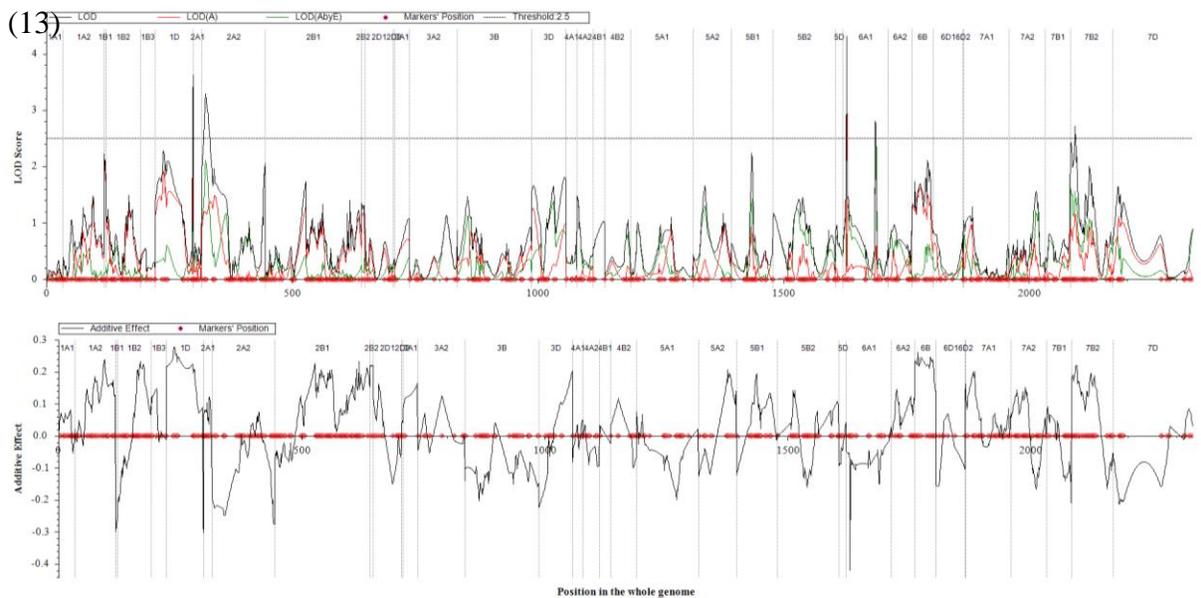
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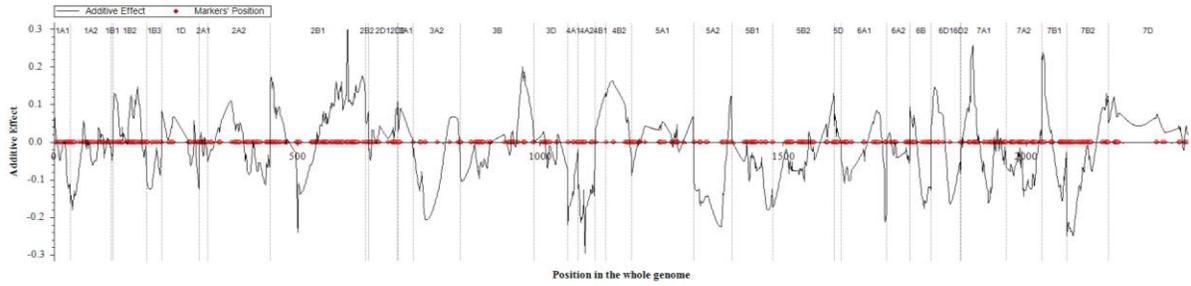
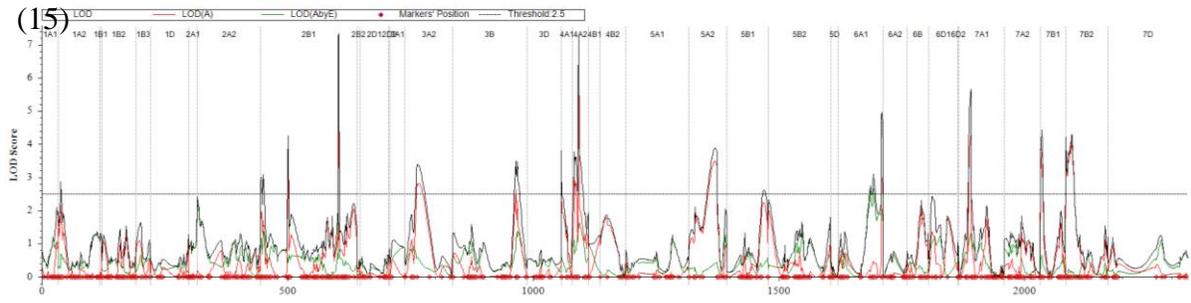
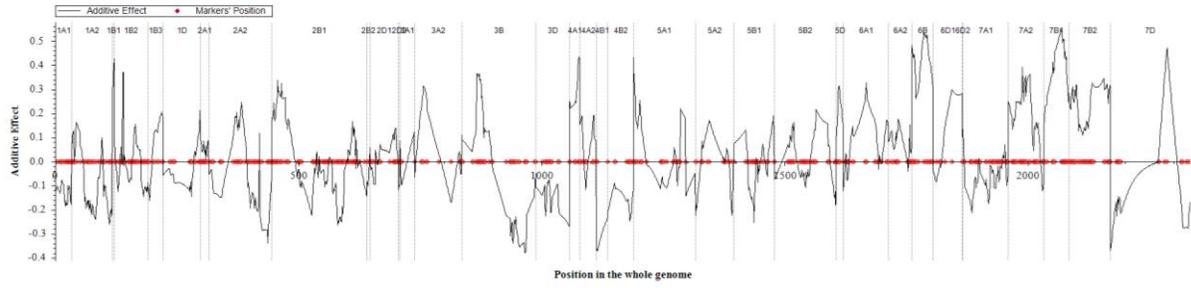
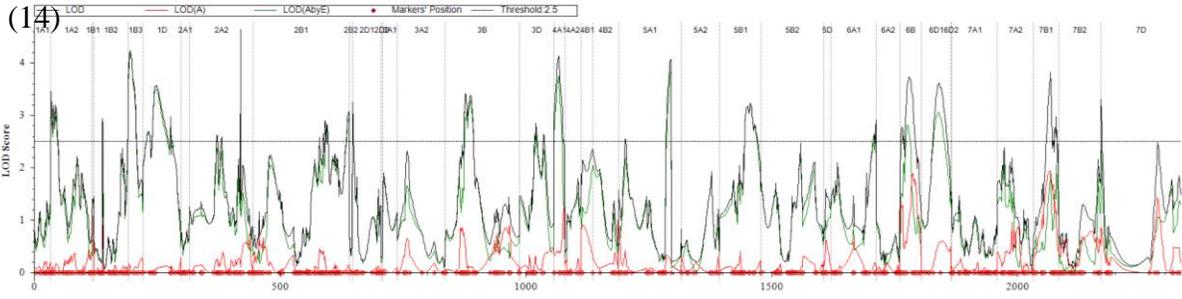


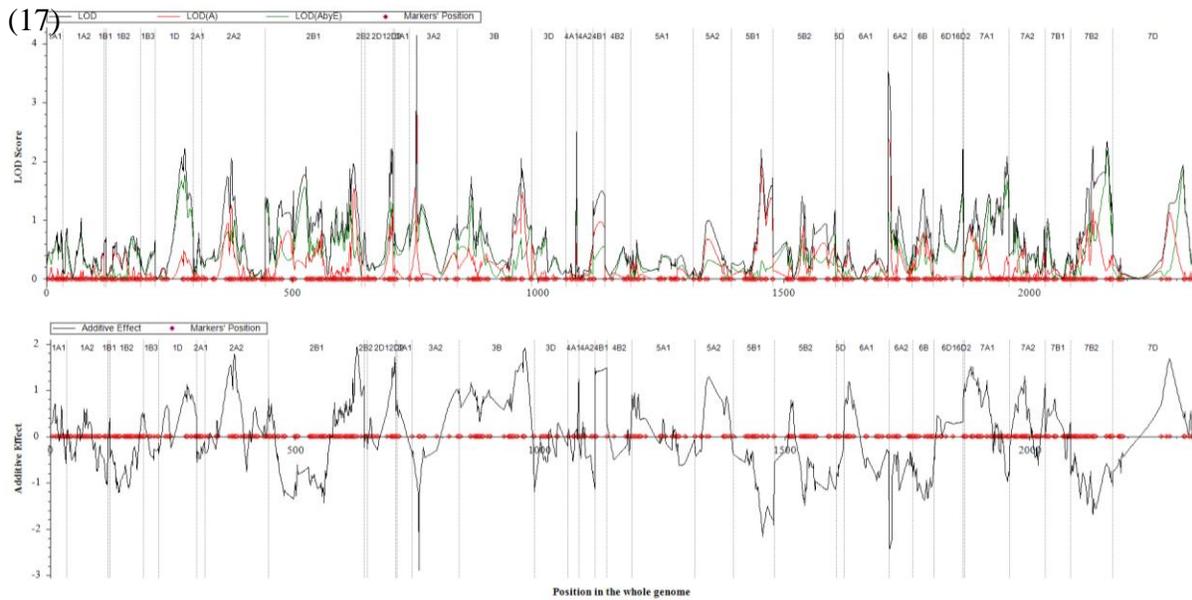
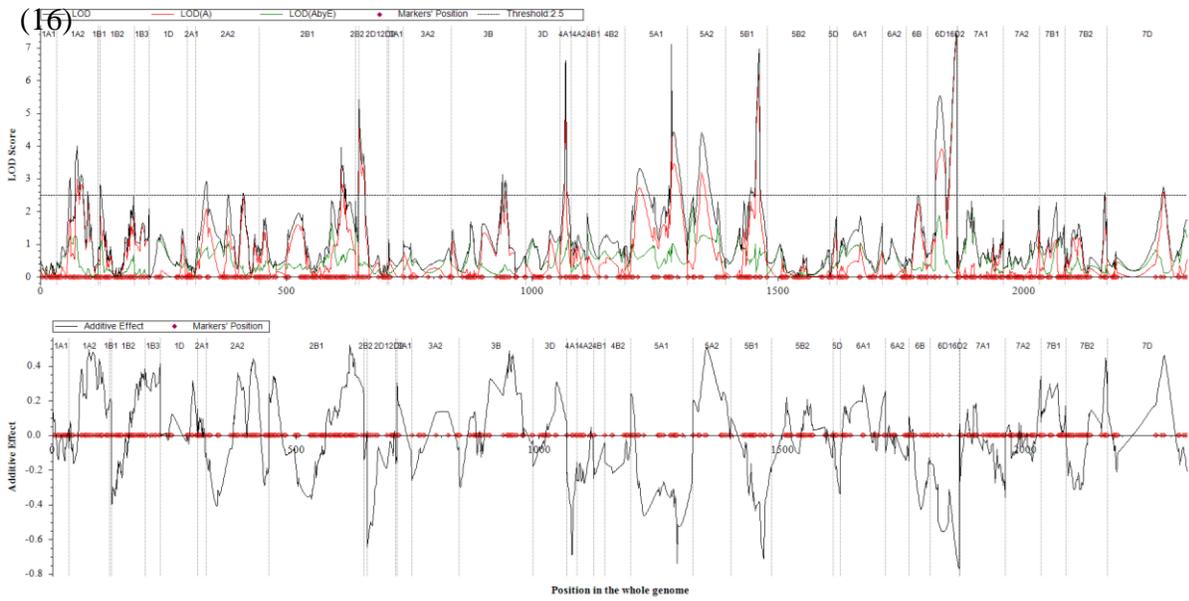
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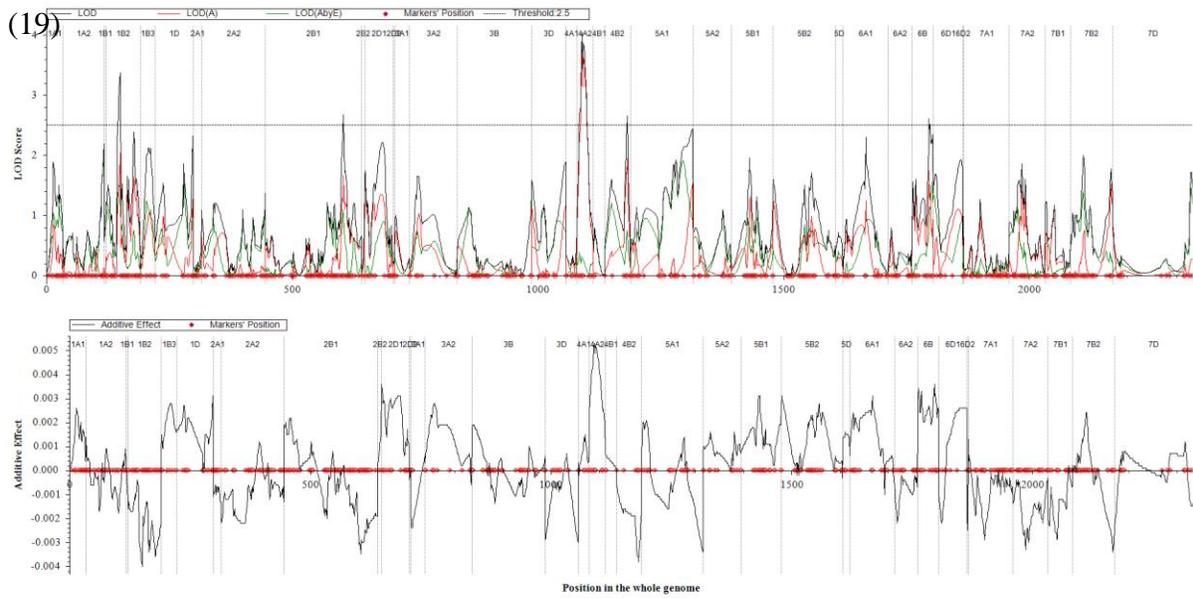
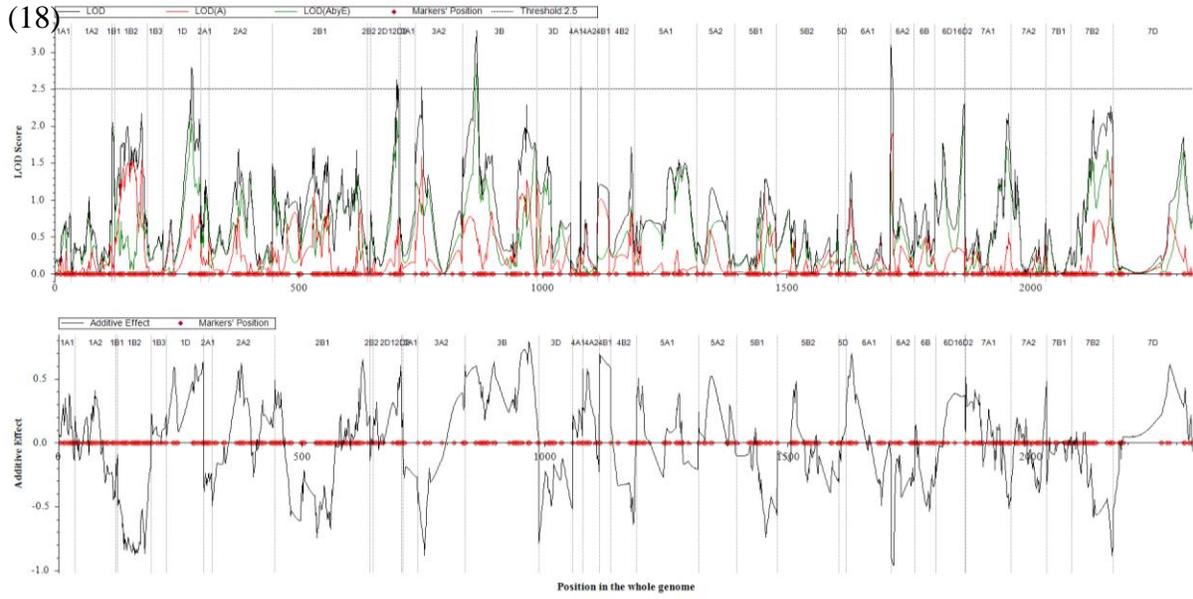


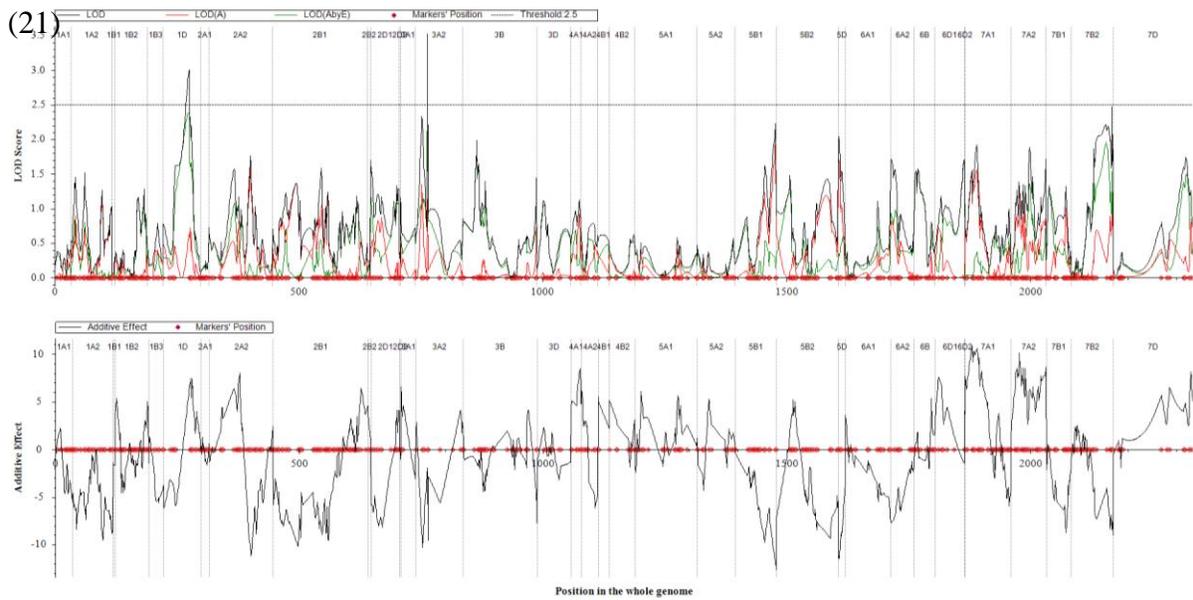
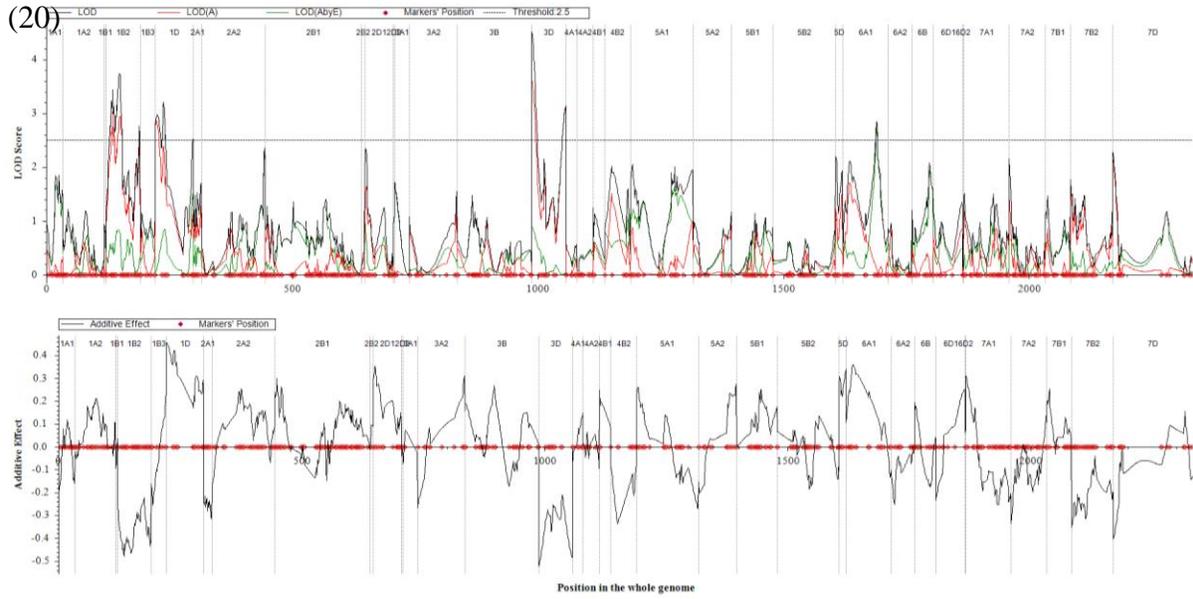
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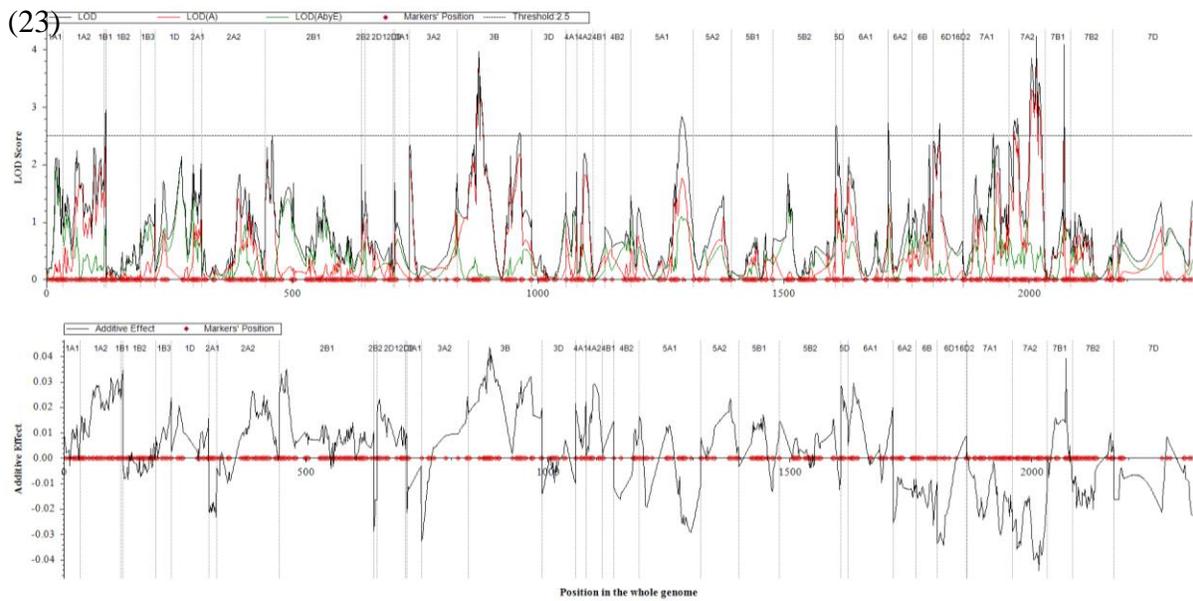
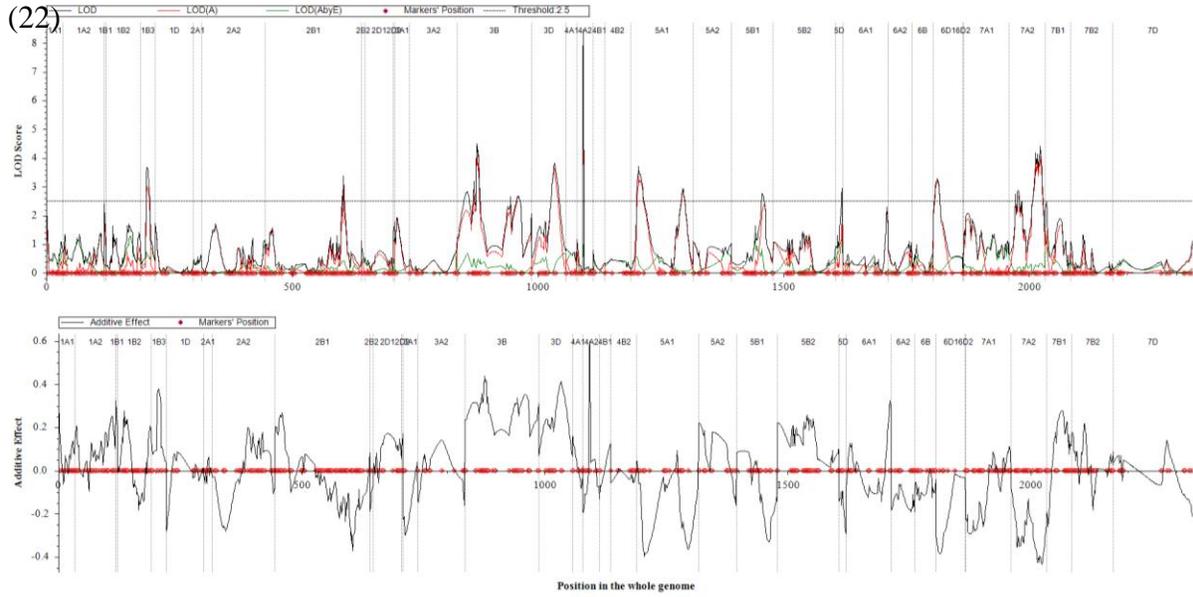


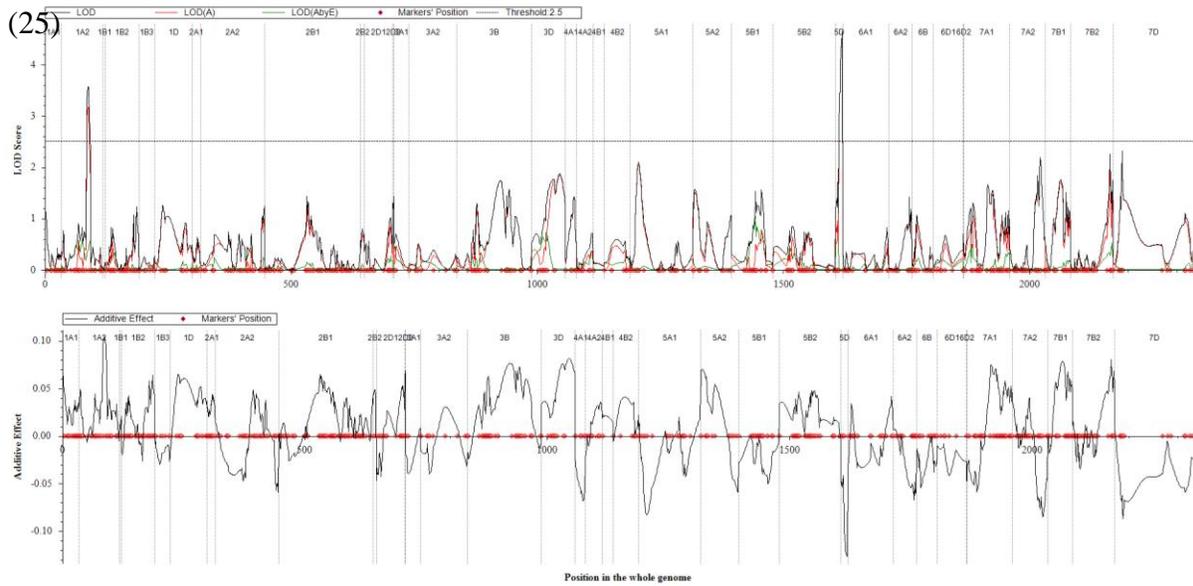
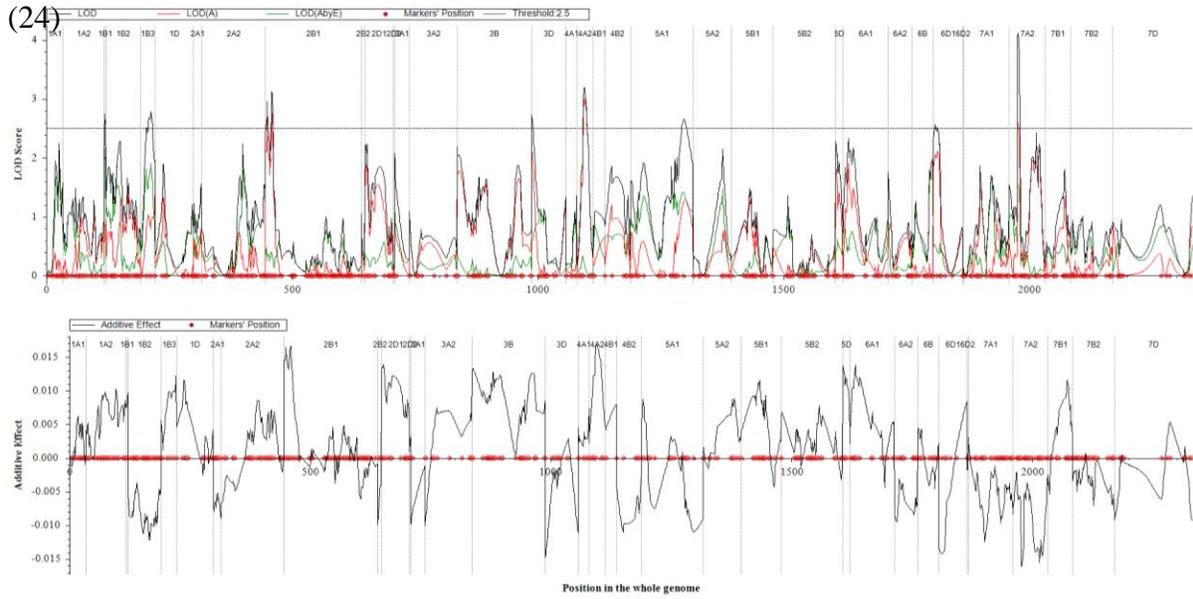




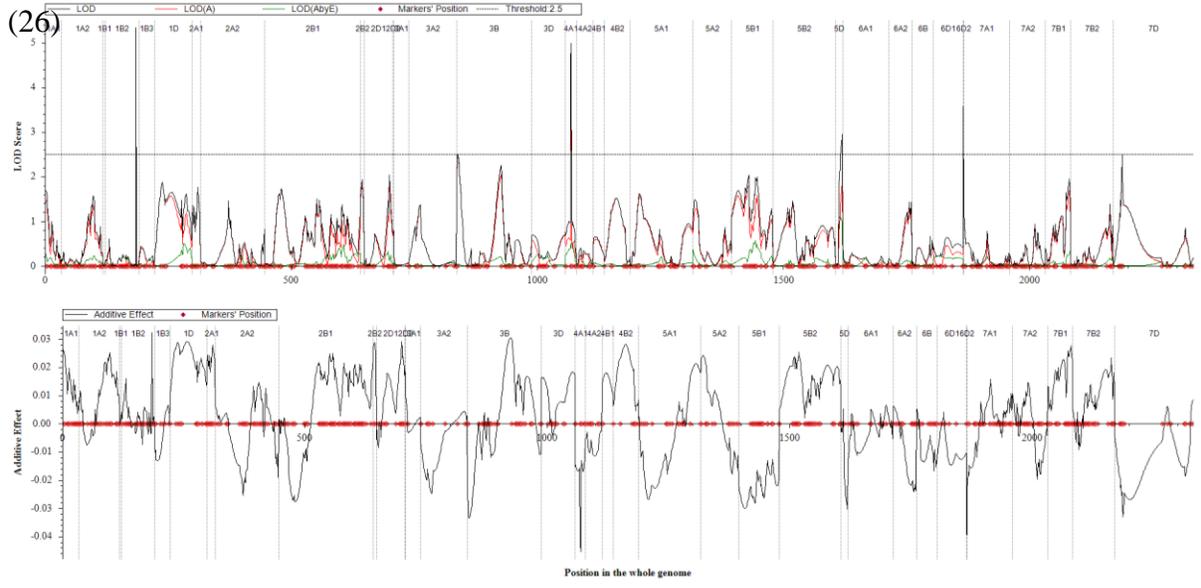




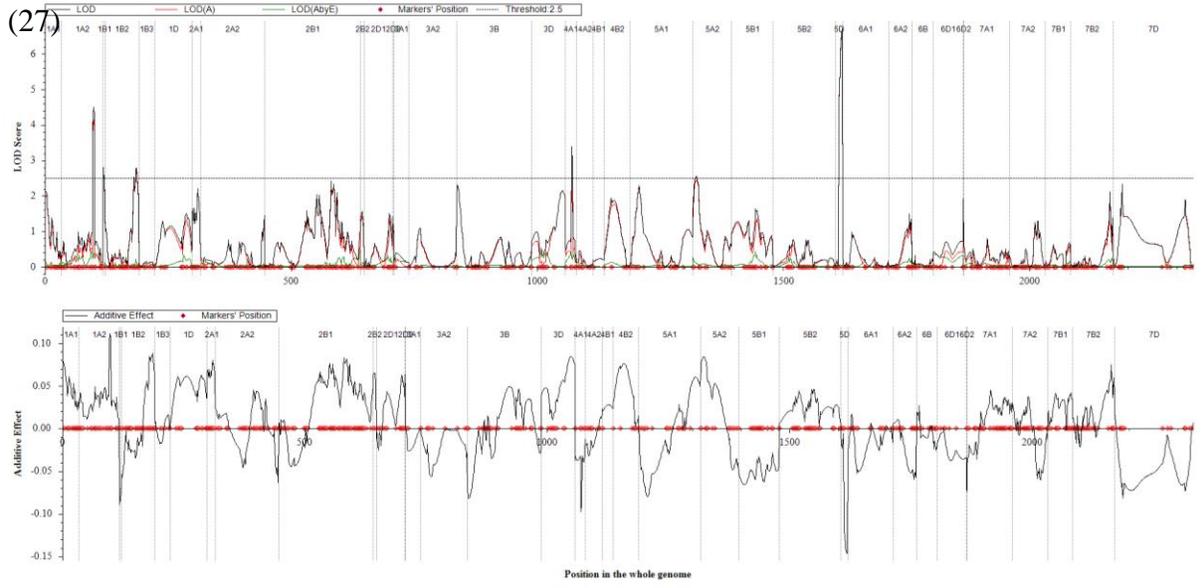




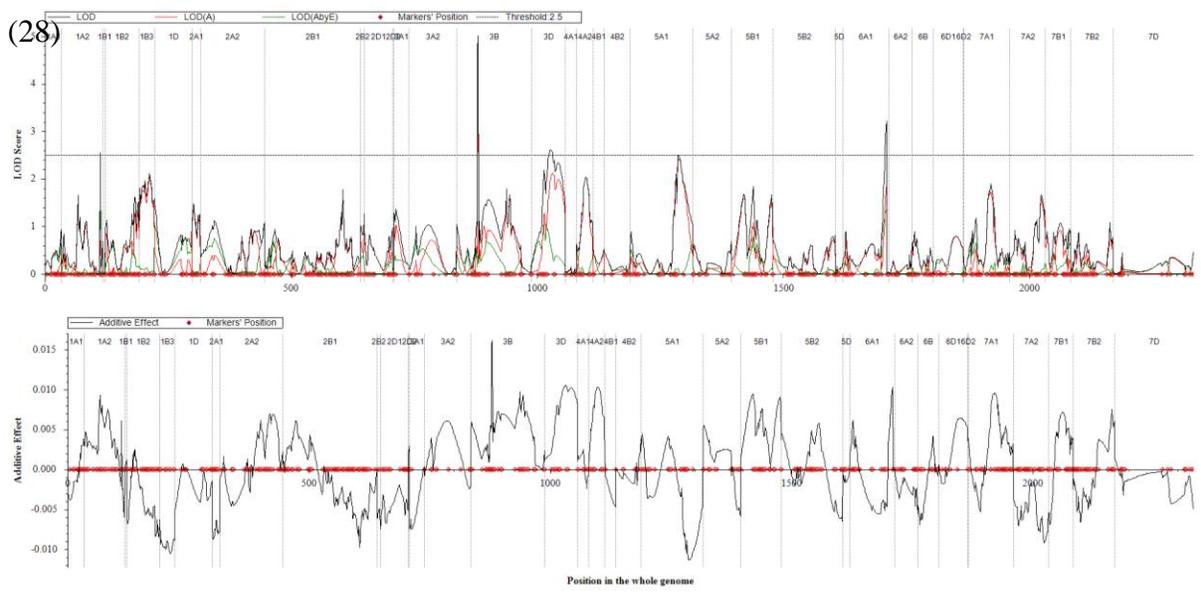
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(27)

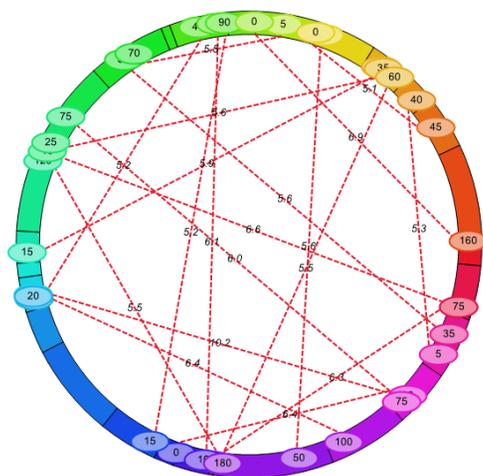


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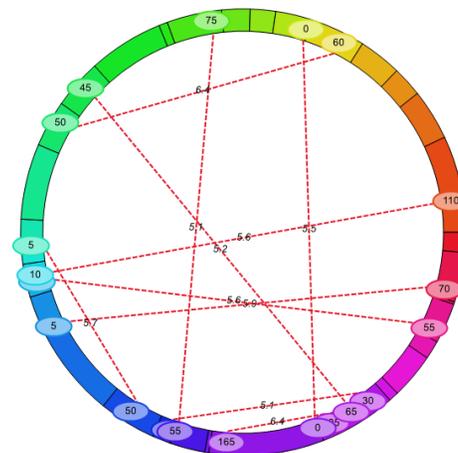


Supplemental Figure S5a: Epistatic interaction between QTL for quality traits. a) hardness index, (HARD); b) kernel diameter, (DIAM); c) single kernel weight, (SKW); d) flour yield, (FYLD); e) flour protein at 14% moisture, (PROT); f) flour ash at 14% moisture, (ASH); g) midline peak time, (MLPT); h) midline peak value, (MLPV); i) midline peak width, (MLPW); j) midline right slope, (MLRS); k) midline tail width, MLTW; l) midline time X time, (MLTXT); m) midline time X width, (MLTXW). LOD threshold was set as 5.0. QTL interaction LOD values are shown along the dashed line connecting two linkage groups. Linkage groups are color coded as shown on the right side of the figure.

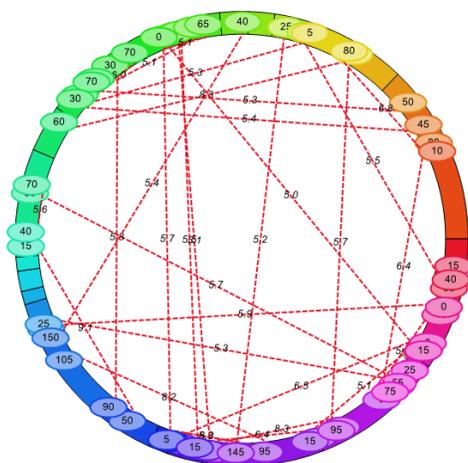
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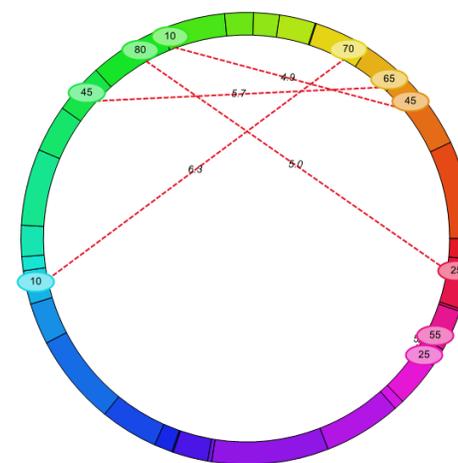
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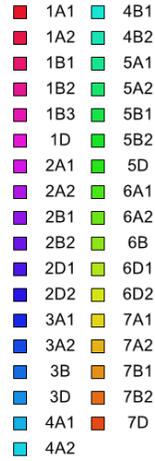
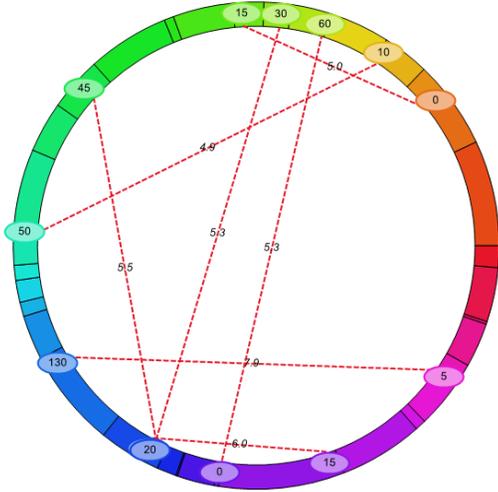
c)



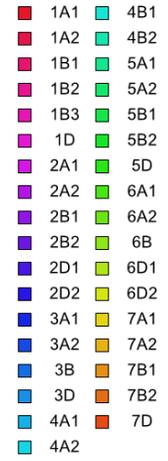
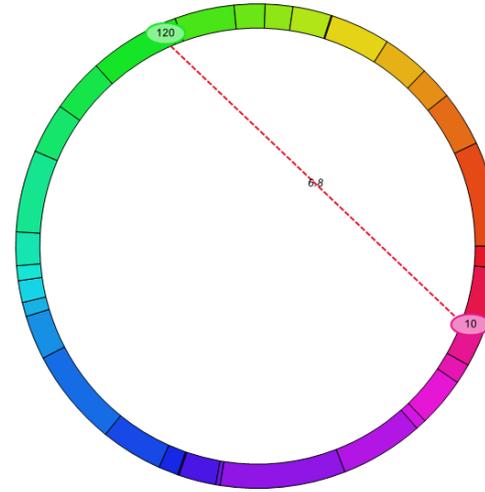
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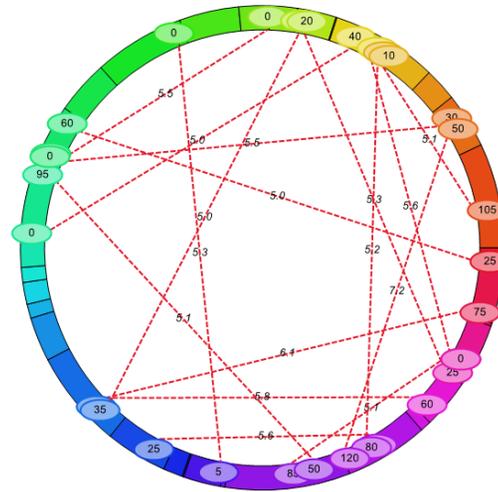
e)



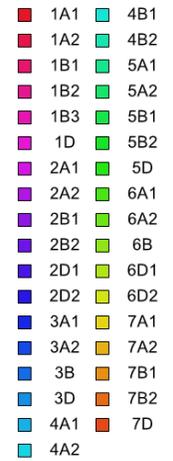
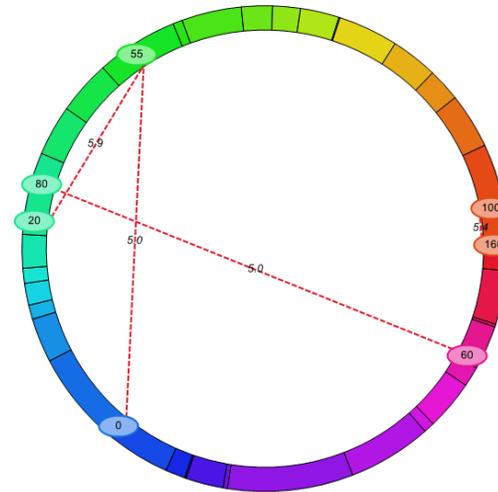
f)



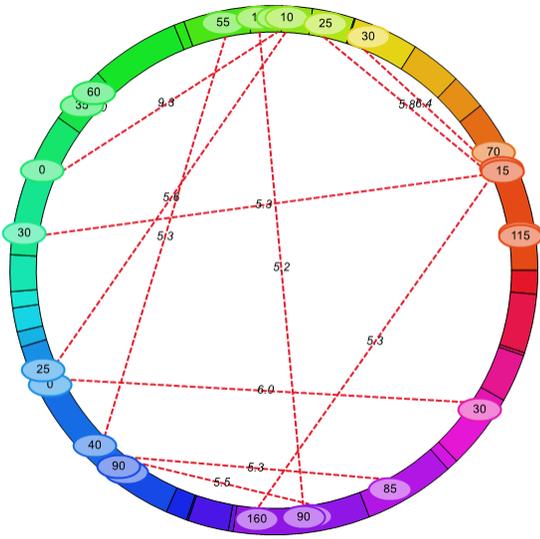
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h)



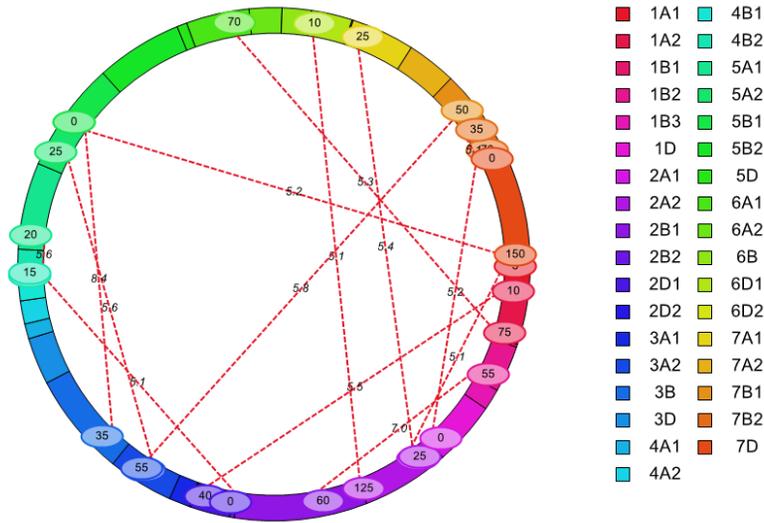
m)



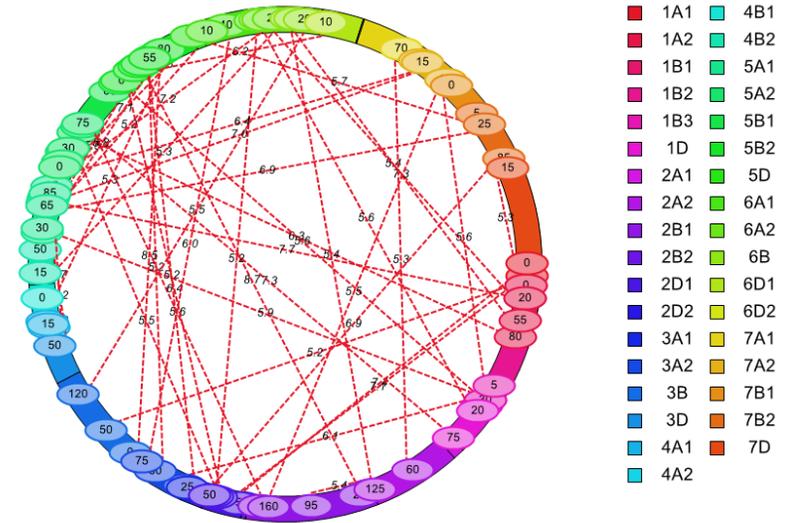
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- 1A2 ■ 4B2
- 1B1 ■ 5A1
- 1B2 ■ 5A2
- 1B3 ■ 5B1
- 1D ■ 5B2
- 2A1 ■ 5D
- 2A2 ■ 6A1
- 2B1 ■ 6A2
- 2B2 ■ 6B
- 2D1 ■ 6D1
- 2D2 ■ 6D2
- 3A1 ■ 7A1
- 3A2 ■ 7A2
- 3B ■ 7B1
- 3D ■ 7B2
- 4A1 ■ 7D
- 4A2

Supplemental Figure S5b: Epistatic interaction between QTL for agronomical traits. a) Grain Yield (YLD), b) Heading Date (HD), c) Plant Height (PH). LOD threshold was set at 5.0. QTL interaction LOD values are shown along the dashed line connecting two linkage groups. Linkage groups are color coded as shown on the right side of the figure.

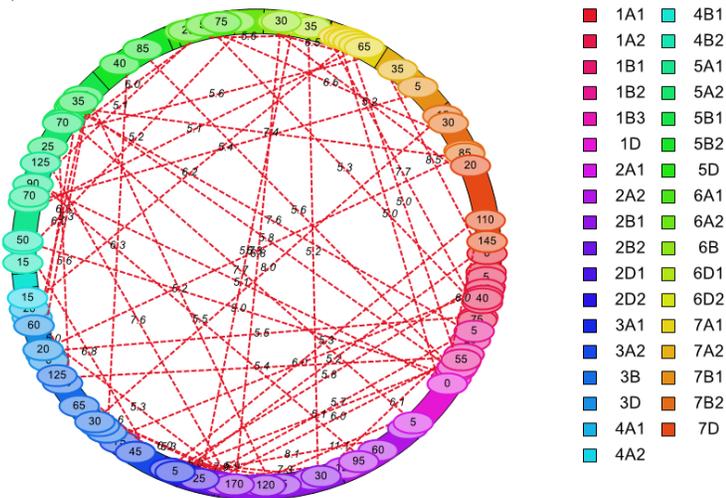
a)



b)

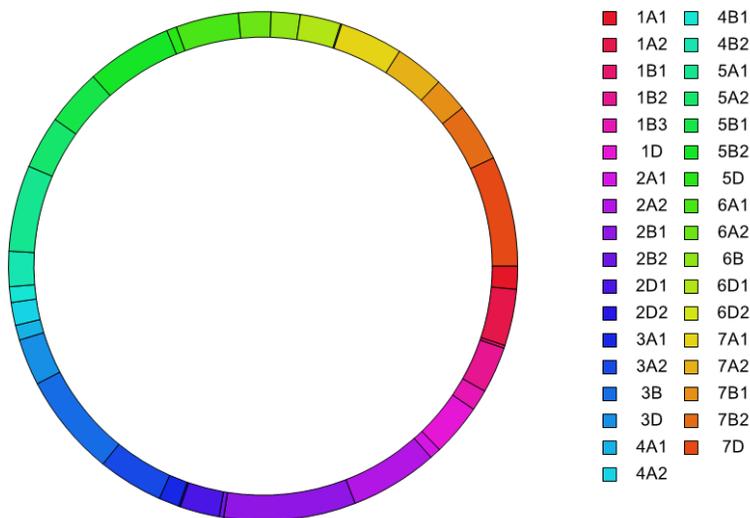


c)

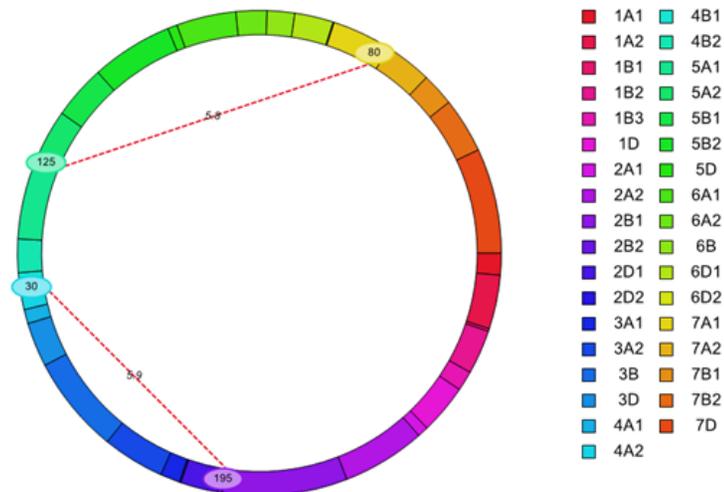


Supplemental Figure S5c: Epistatic interaction between QTL for yield-component traits. a) dry biomass from hand harvested 0.5 m long inner row sample from crown (BM); b) grain weight from as hand harvested dry grain (BMYLD); c) harvest index (HI); d) kernels spike-1 (KPS); e) spikes m⁻² (SPM); f) thousand kernel weight (TKW); g) single head dry weight (SHDW); h) single head dry grain weight (SHGW). LOD threshold was set at 5.0. QTL interaction LOD values are shown along the dashed line connecting two linkage groups. Linkage groups are color coded as shown on the right side of the figure.

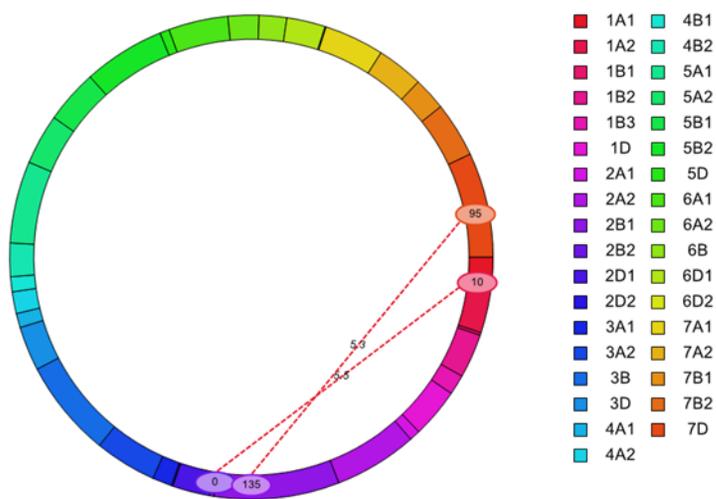
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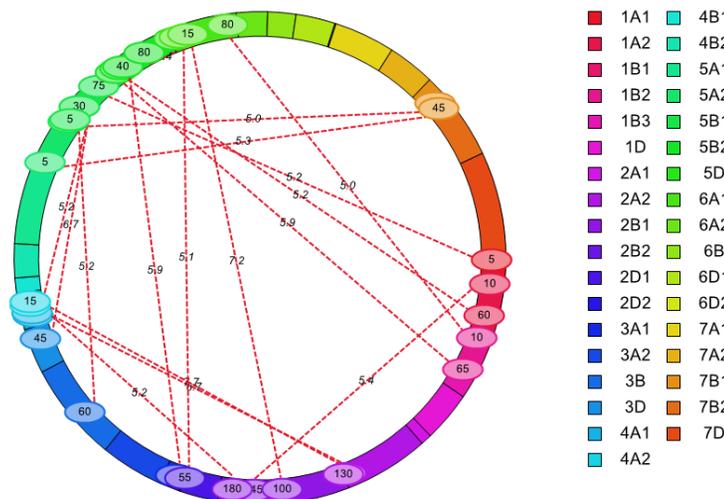
b)



c)



d)



e)

f)

Supplemental Figure S5d: Epistatic interaction between QTL for seed-related traits. a) kernel area (KAREA), b) kernel length (KLEN), c) kernel perimeter (KPERI), d) kernel width (KWID). LOD threshold was set at 5.0. QTL interaction LOD values are shown along the dashed line connecting two linkage groups. Linkage groups are color coded as shown on the right side of the figure.

