

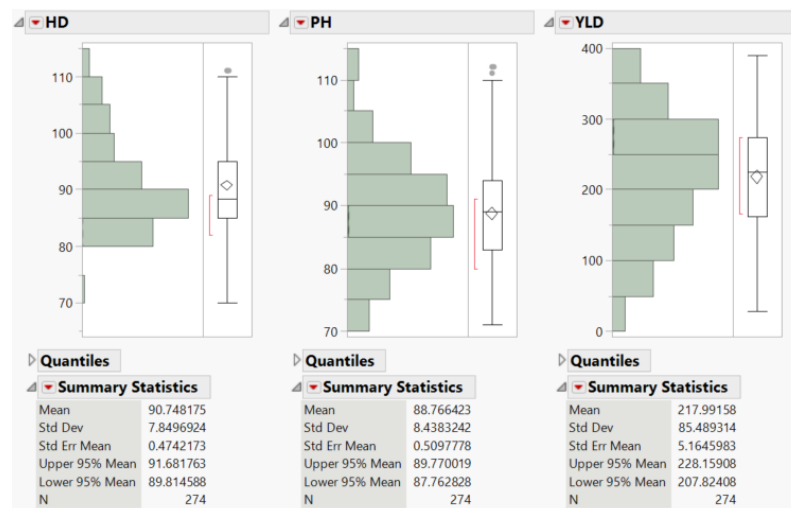
Supplemental Figure S1. Histogram and Phenotypic distributions of the predicted (BLUP) values for all traits of recombinant inbred lines (RIL) at individual environments.

Environments: Texas A&M AgriLife Research stations in Bushland, TX in 2019, 2020, and 2021, in McGregor, TX in 2019 and 2020, in College Station, TX in 2019 and 2020.

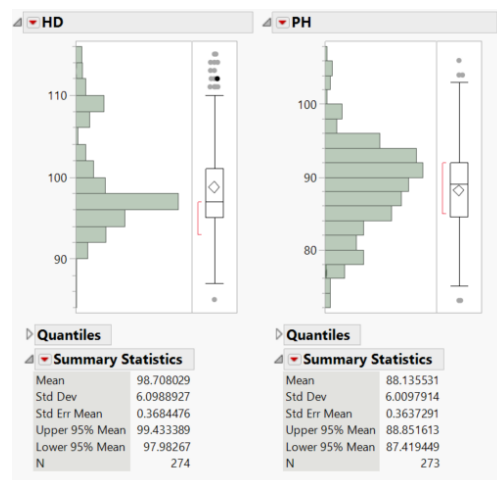
Environments A) College Station 2019 (19CS), B) McGregor 2019 (19MCG), C) College Station 2020 (20CS), D) McGregor 2020 (20MCG), E) Emny land in Bushland 2020 (20EMN), F) Bushland South Pivot in Bushland 2019 (19BSP), and G) Bushland Dryland 2021 (21BD).

Traits: Heading date (HD), Plant height (PH), Grain yield from combine harvester (YLD), Single kernel weight (SKW), Kernel diameter (DIAM), Spikes m⁻² (SPM), Biomass (BM), Biomass grain yield from 0.5-meter inner row (BMYLD), Kernel area (KAREA), Thousand kernel weight (TKW), Harvest index (HI), Kernel perimeter (KPERI), Kernel hardness index (KHI), Kernel length (KLEN), Kernel width (KWID), Kernels spike⁻¹ (KPS), Single head dry weight (SHDW), Single Stem Weight (SSW), Single head grain weight (SHGW).

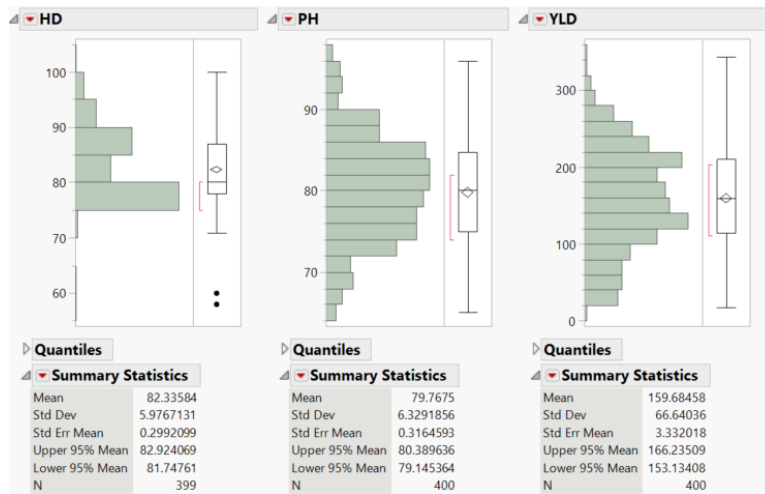
A) 19CS



B) 19MCG



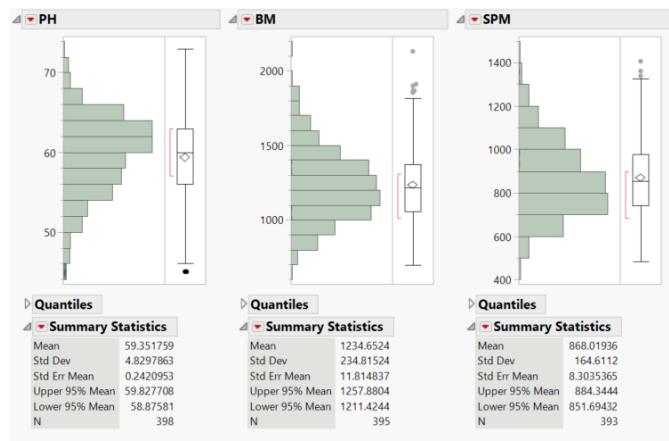
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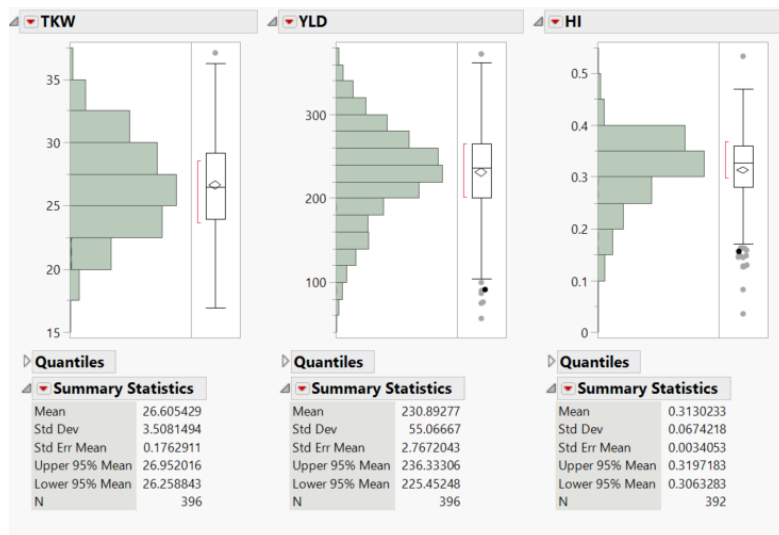
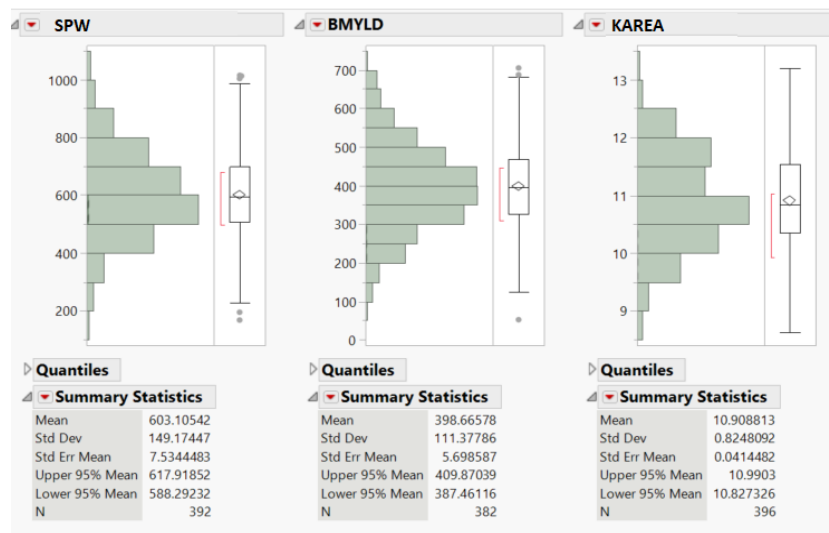


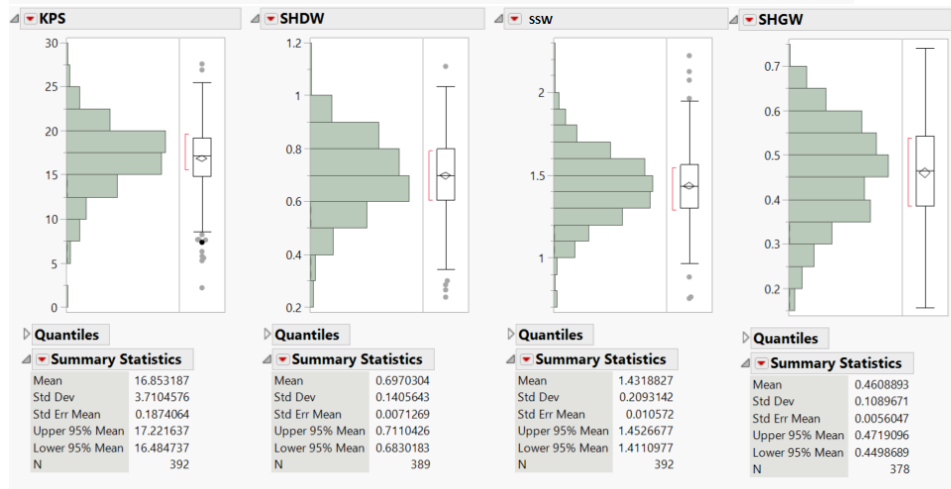
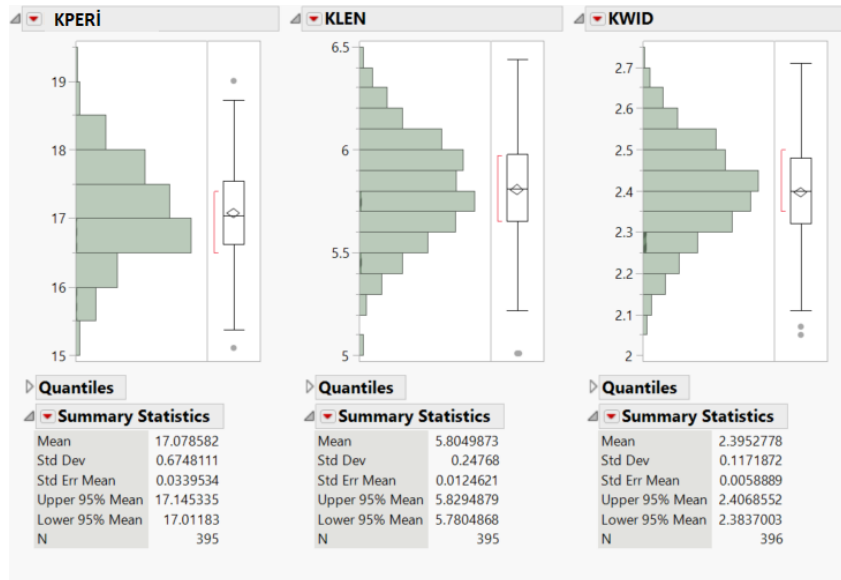
D) 20MCG



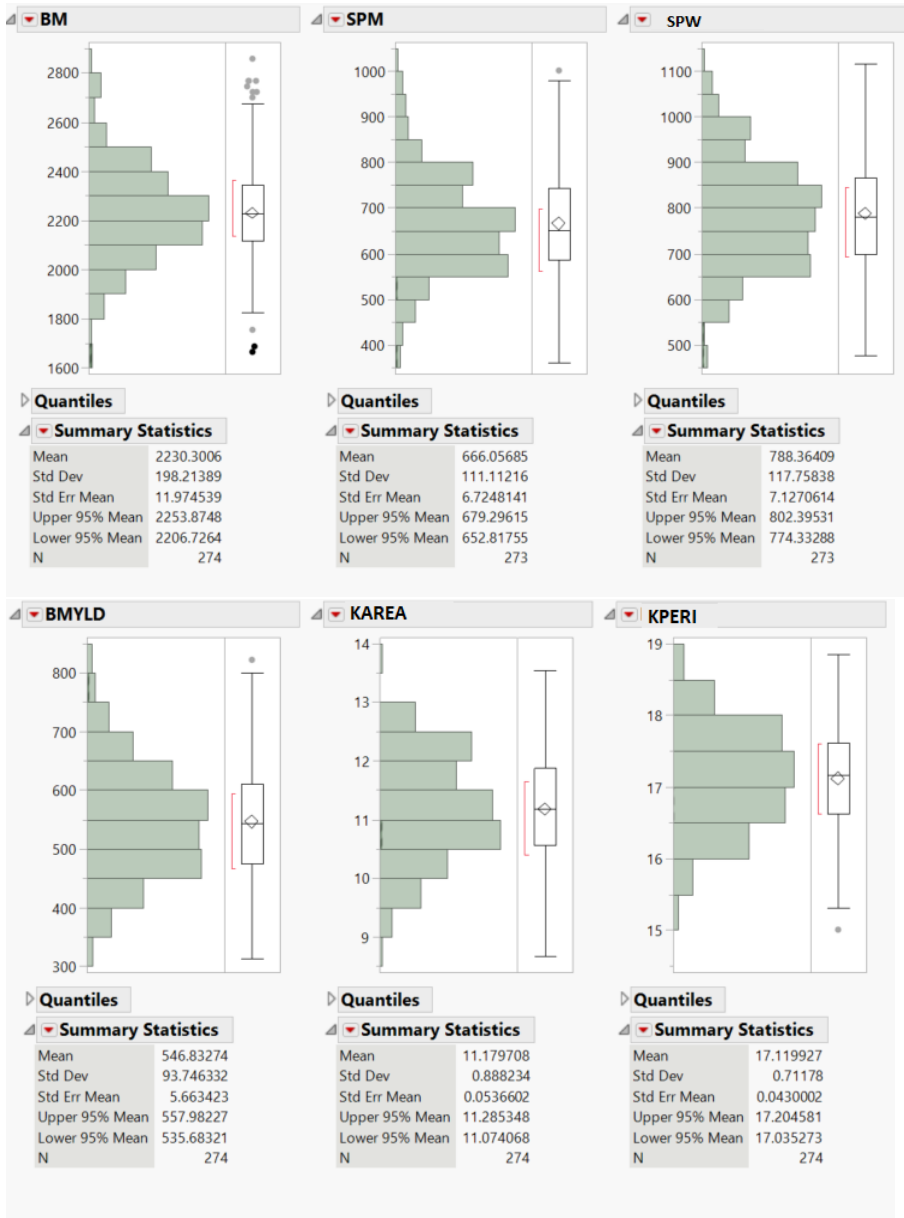
E) 20EMN

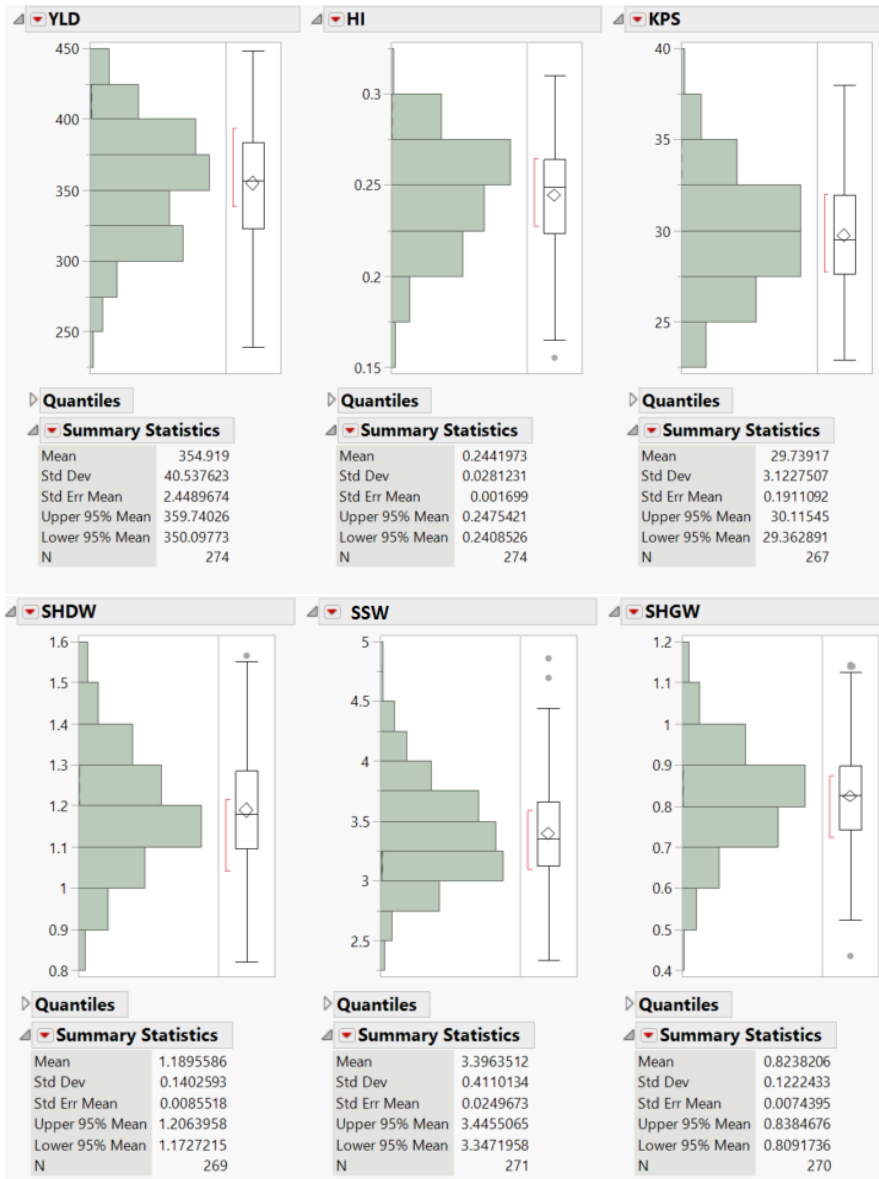




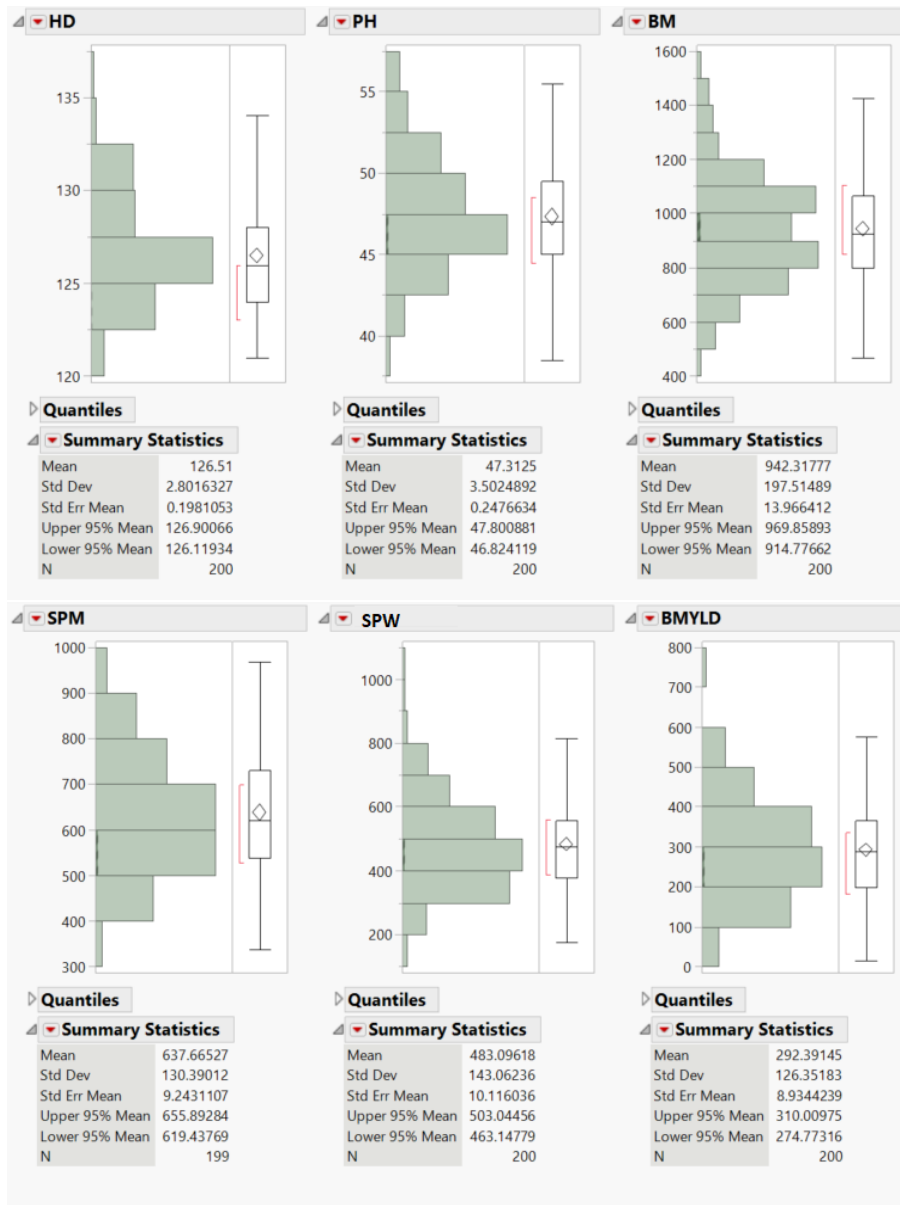


F) 19BSP





G) 21BD





KLEN

Quantiles

Summary Statistics

Mean	5.8674636
Std Dev	0.2359274
Std Err Mean	0.0167245
Upper 95% Mean	5.9004445
Lower 95% Mean	5.8344827
N	199

KWID

Quantiles

Summary Statistics

Mean	2.5048752
Std Dev	0.0934699
Std Err Mean	0.0066259
Upper 95% Mean	2.5179416
Lower 95% Mean	2.4918088
N	199

TKW

Quantiles

Summary Statistics

Mean	29.587487
Std Dev	2.7352118
Std Err Mean	0.193894
Upper 95% Mean	29.96985
Lower 95% Mean	29.205125
N	199

YLD

Quantiles

Summary Statistics

Mean	200.74629
Std Dev	41.16775
Std Err Mean	2.9109995
Upper 95% Mean	206.48666
Lower 95% Mean	195.00593
N	200

HI

Quantiles

Summary Statistics

Mean	0.2986113
Std Dev	0.0922003
Std Err Mean	0.006569
Upper 95% Mean	0.3115663
Lower 95% Mean	0.2856562
N	197

KPS

Quantiles

Summary Statistics

Mean	15.971706
Std Dev	5.2033232
Std Err Mean	0.3745434
Upper 95% Mean	16.710454
Lower 95% Mean	15.232958
N	193

SHDW

Quantiles

Summary Statistics

Mean	0.7622615
Std Dev	0.1751347
Std Err Mean	0.012415
Upper 95% Mean	0.786744
Lower 95% Mean	0.737779
N	199

SSW

Quantiles

Summary Statistics

Mean	1.497674
Std Dev	0.2435138
Std Err Mean	0.0172622
Upper 95% Mean	1.5317154
Lower 95% Mean	1.4636326
N	199

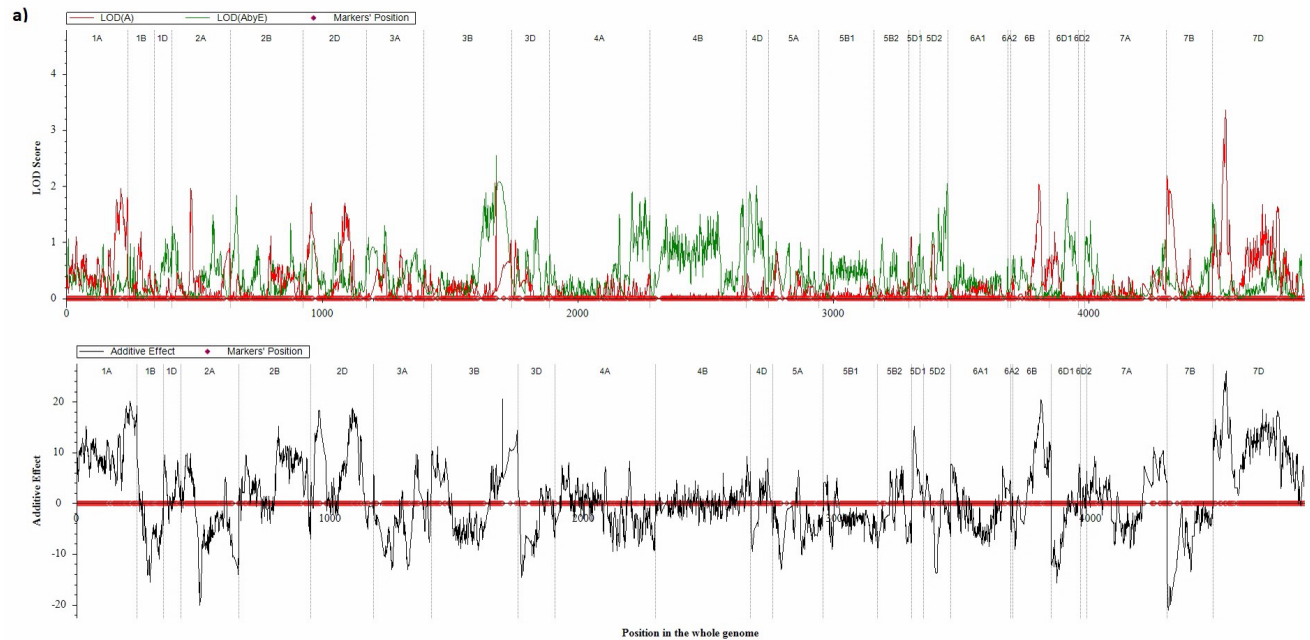
SHGW

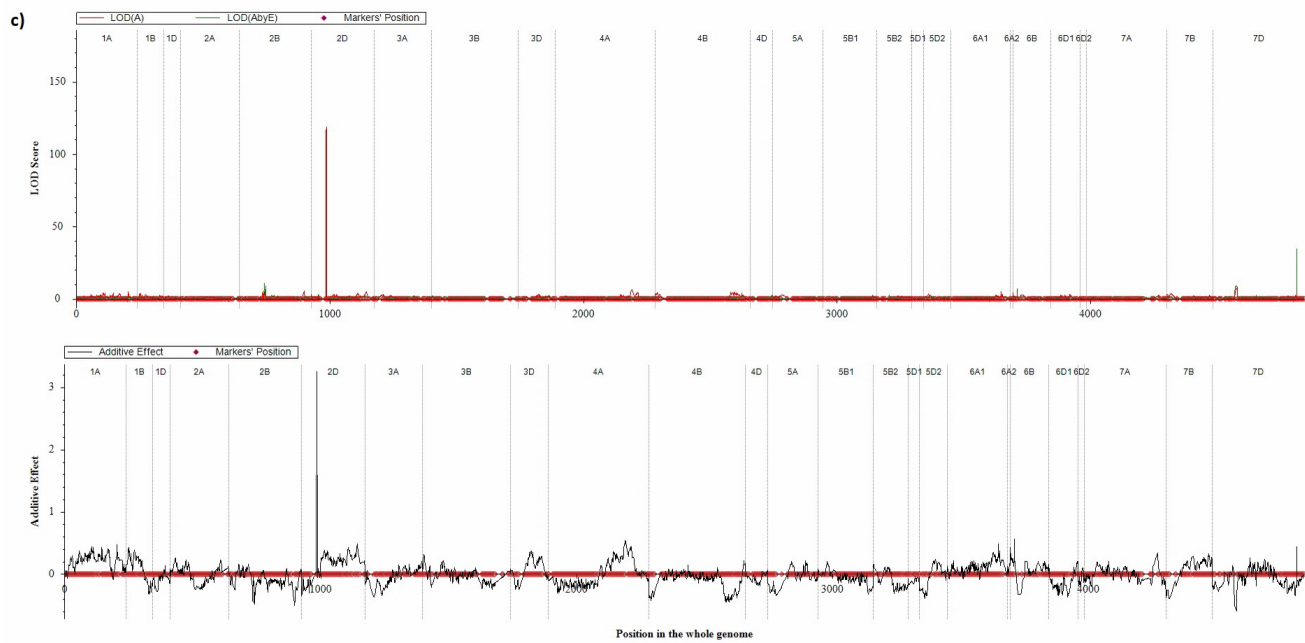
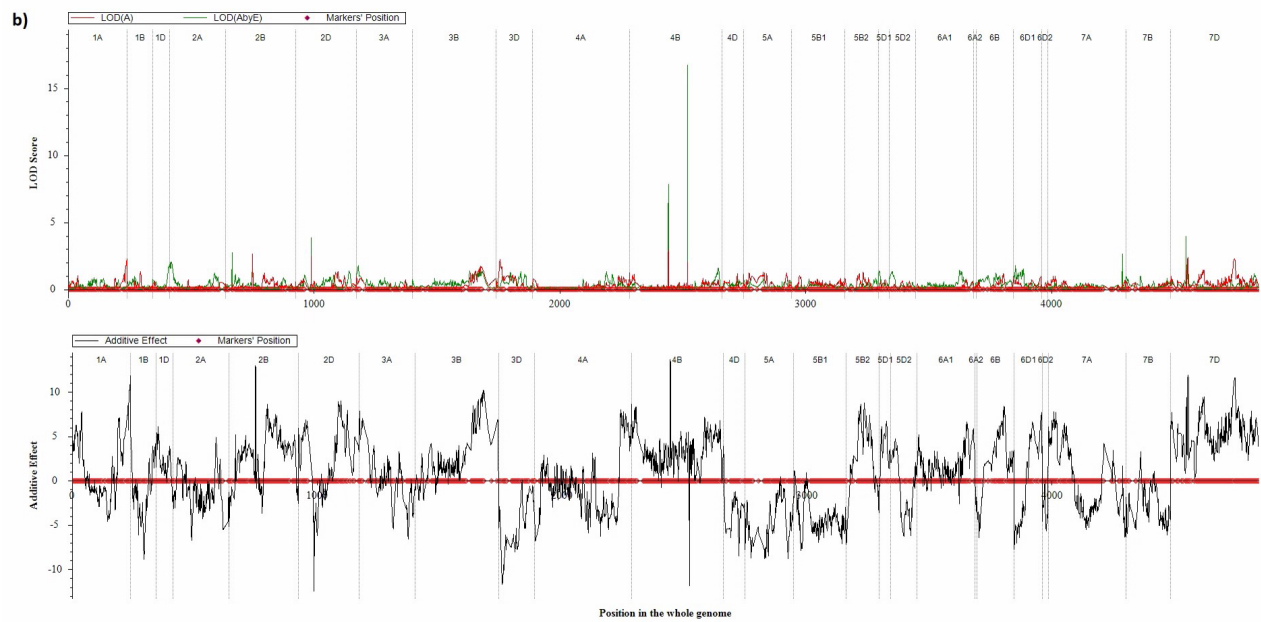
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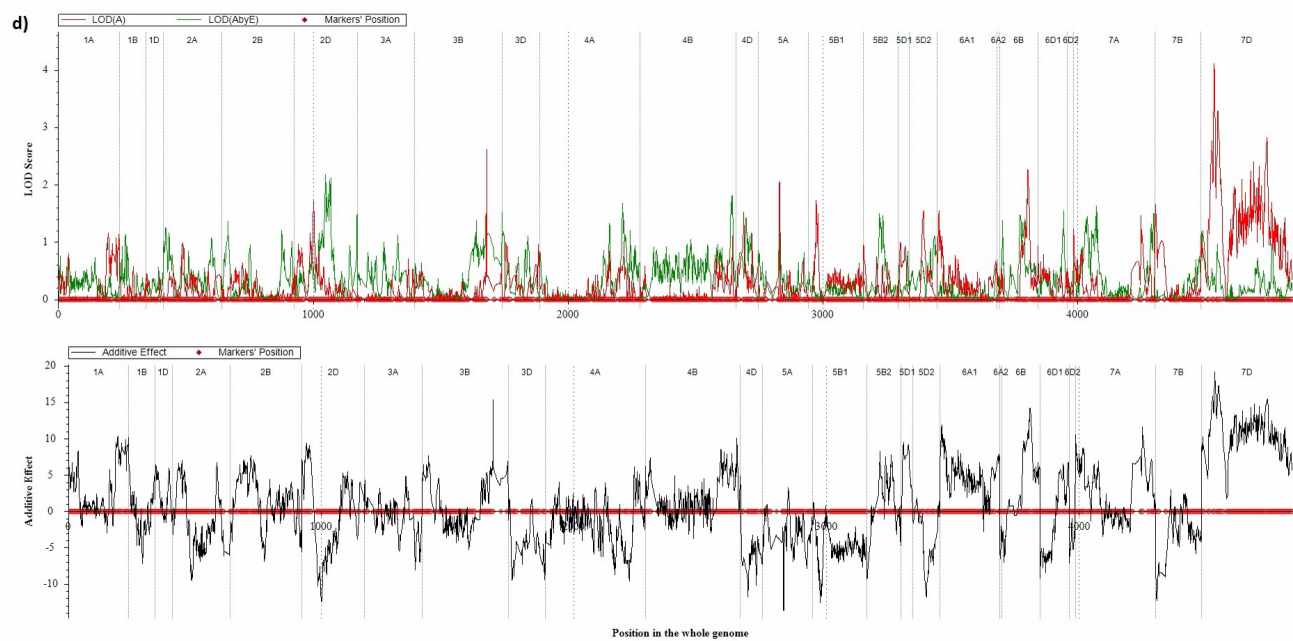
Summary Statistics

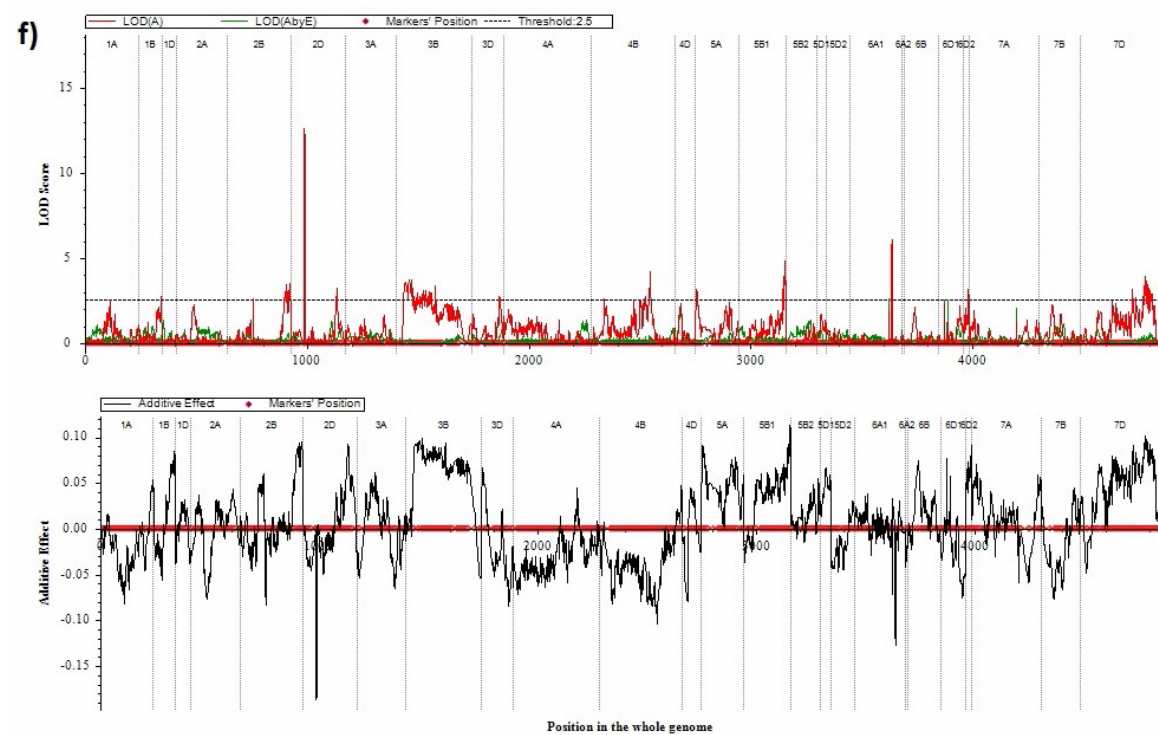
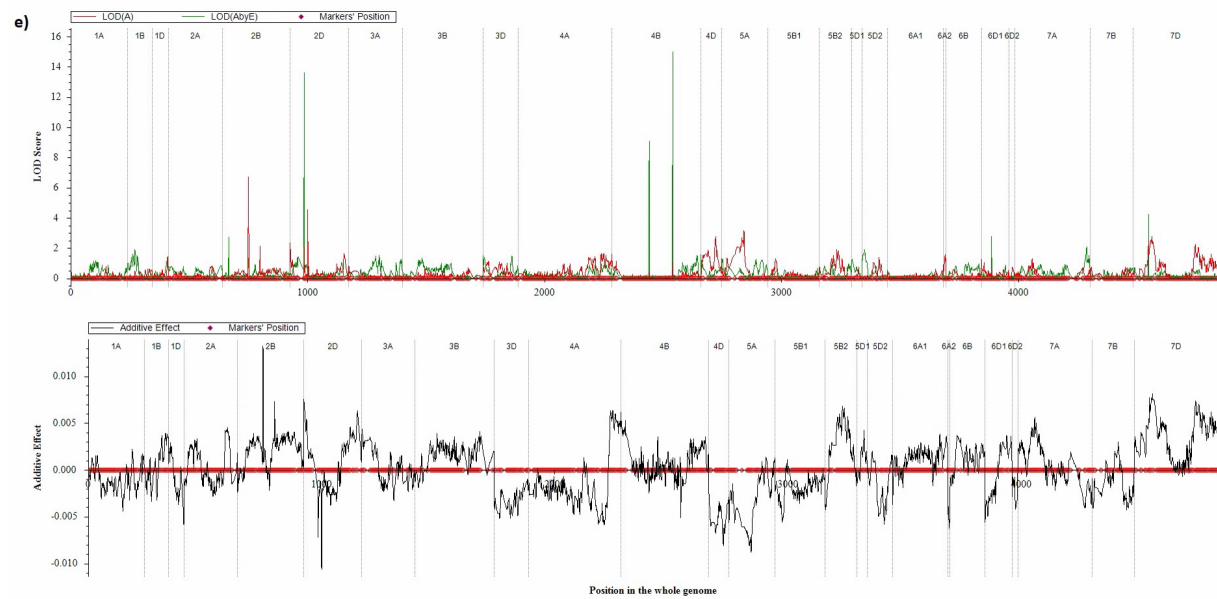
Mean	0.4572791
Std Dev	0.1672796
Std Err Mean	0.011888
Upper 95% Mean	0.4807233
Lower 95% Mean	0.433835
N	198

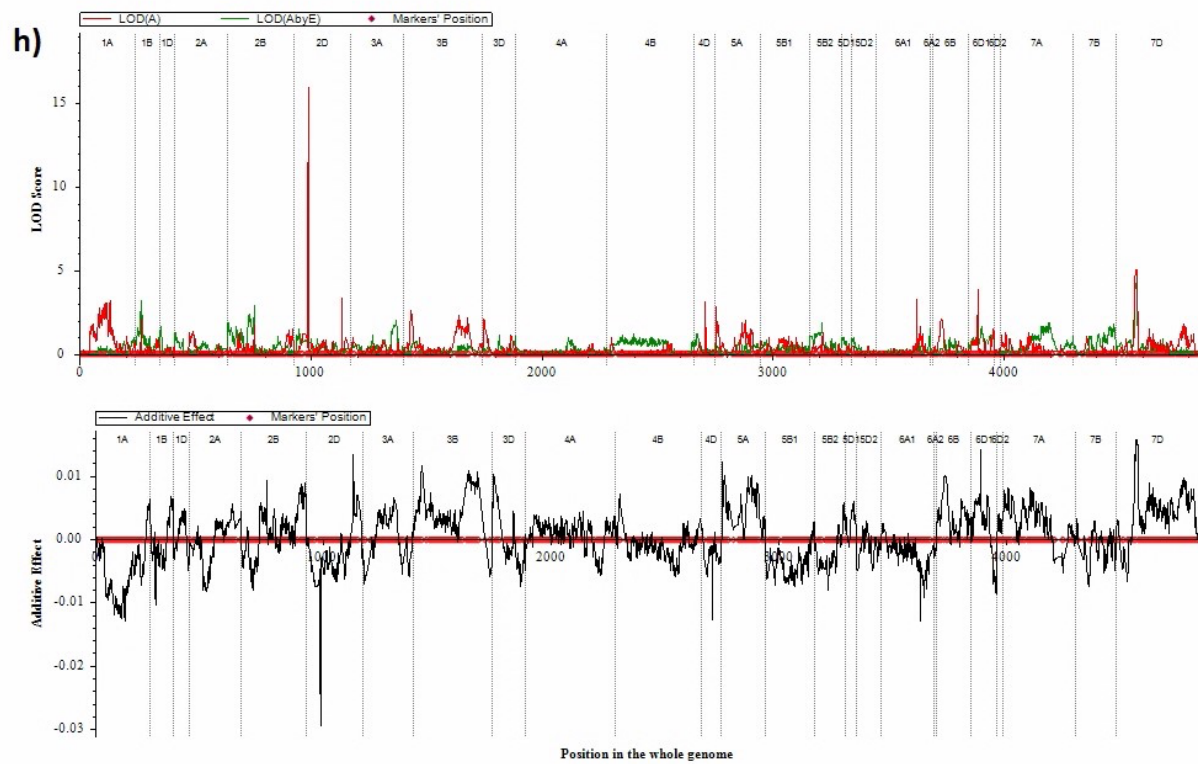
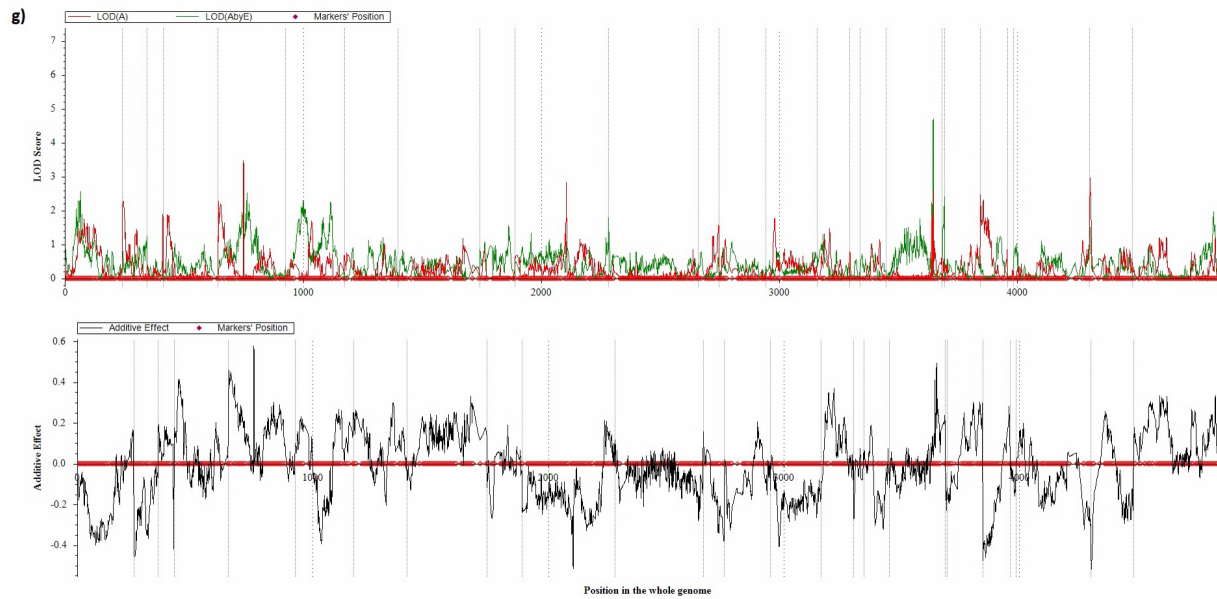
Supplemental Figures S2. Whole genome significance LOD(A) and LOD(AbyE) profiles of quantitative trait loci for yield and yield-related traits based on across all the environments for each trait. LOD for additive effect LOD(A) is in red, LOD scores of additive by environment LOD(AbyE) is in green; the dotted line paralleled the y-axis separated the 25 linkage groups (Table S2). The additive effect above the zero line in the bottom figure means that the favorable alleles increasing the traits were from TAM 113, the additive effect below the zero line means QTLs inherited by Gallagher. Abbreviation of traits; **a)** Biomass (BM); **b)** Biomass Grain Yield from 0.5-meter inner row (BMYLD); **c)** Heading Date (HD); **d)** Spikes weight (SPW); **e)** Harvest index (HI); **f)** Kernel Area (KAREA); **g)** Kernels Spike⁻¹ (KPS); **h)** Kernel Width (KWID); **i)** Kernel Length (KLEN); **j)** Perimeter (PERI); **k)** Plant Height (PH); **l)** Single Head Dry Weight (SHDW); **m)** Single Head Grain Weight (SHGW); **n)** Spikes m⁻² (SPM); **o)** Single Stem Weight (SSW); **p)** Thousand Kernel Weight (TKW); **q)** Grain Yield from combine harvester (YLD).

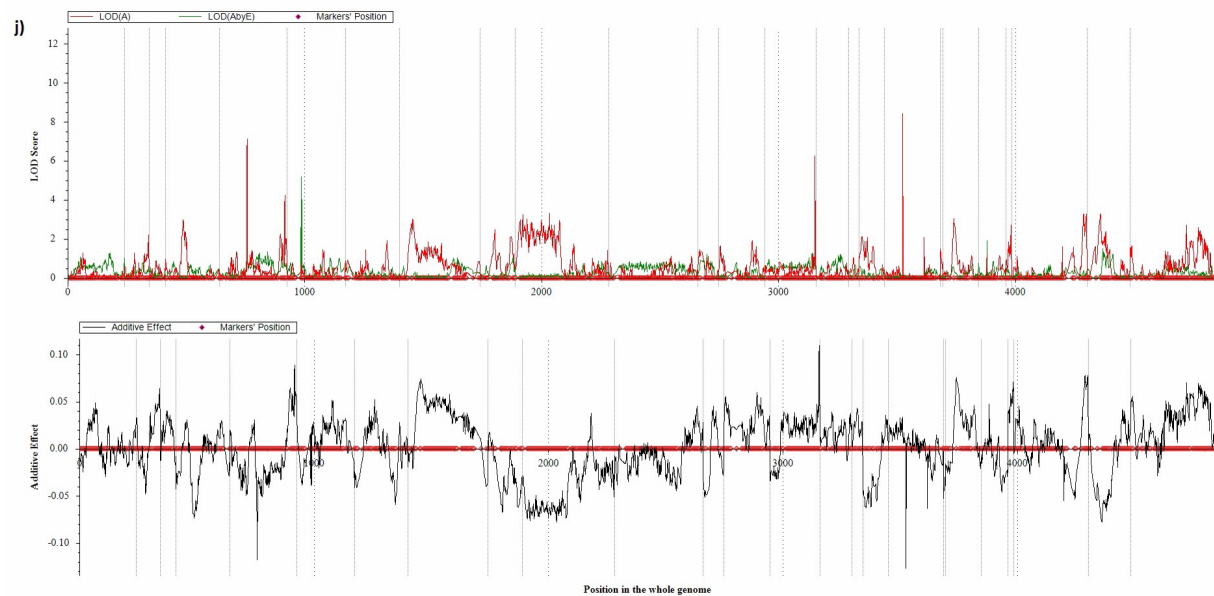
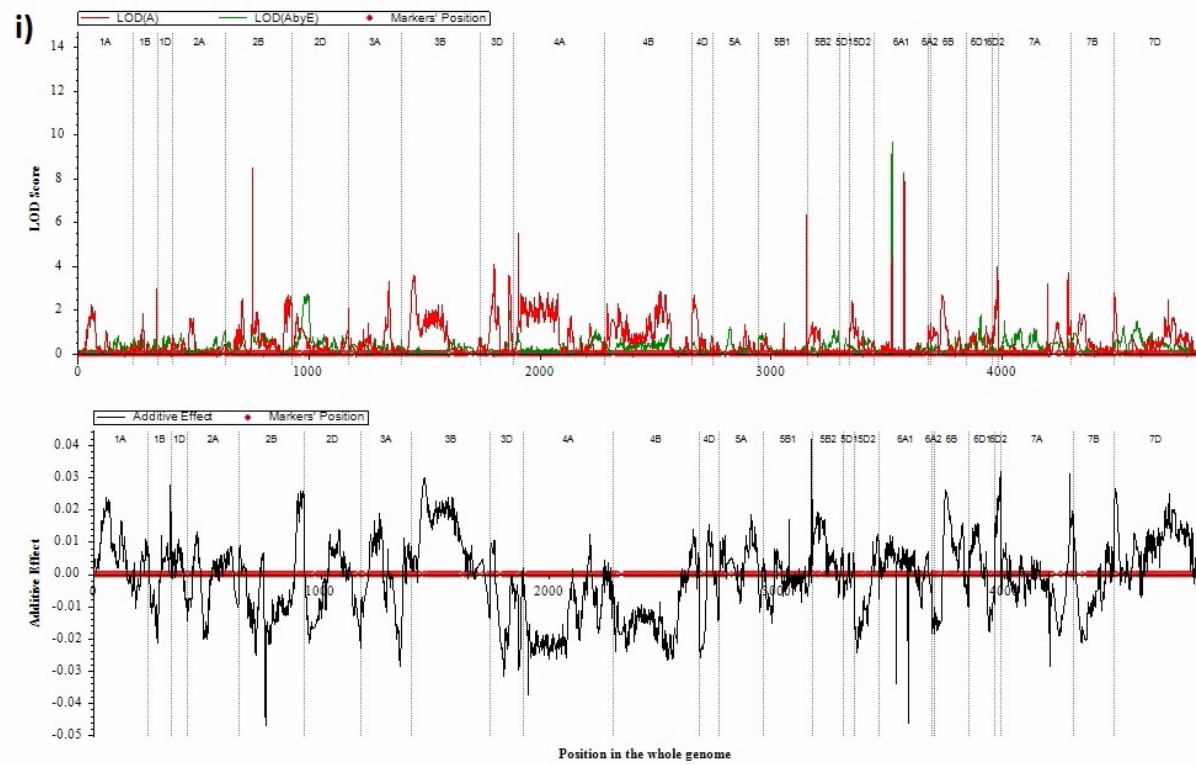


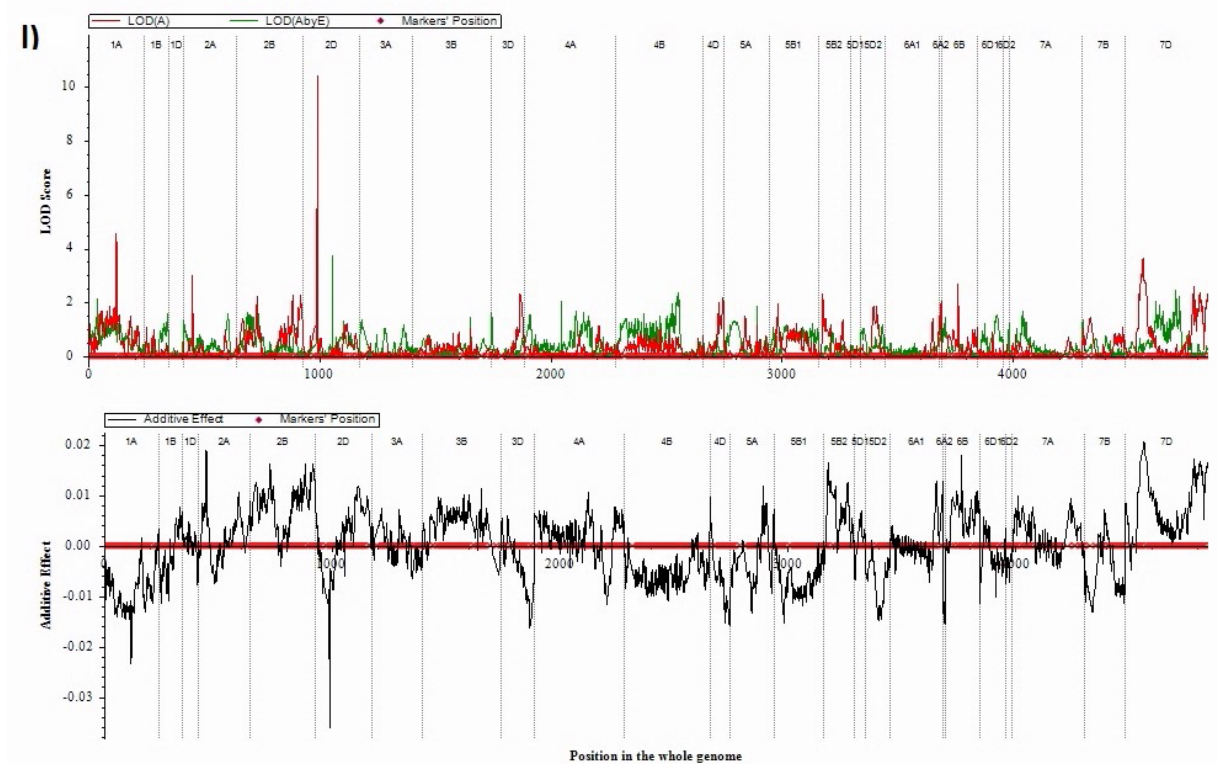
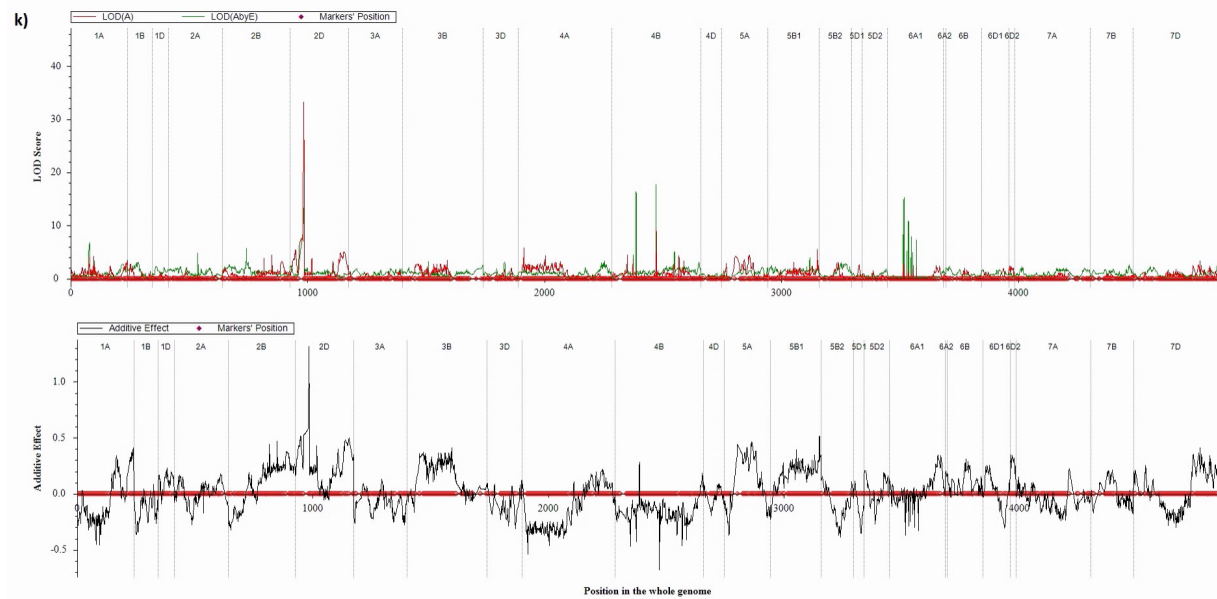


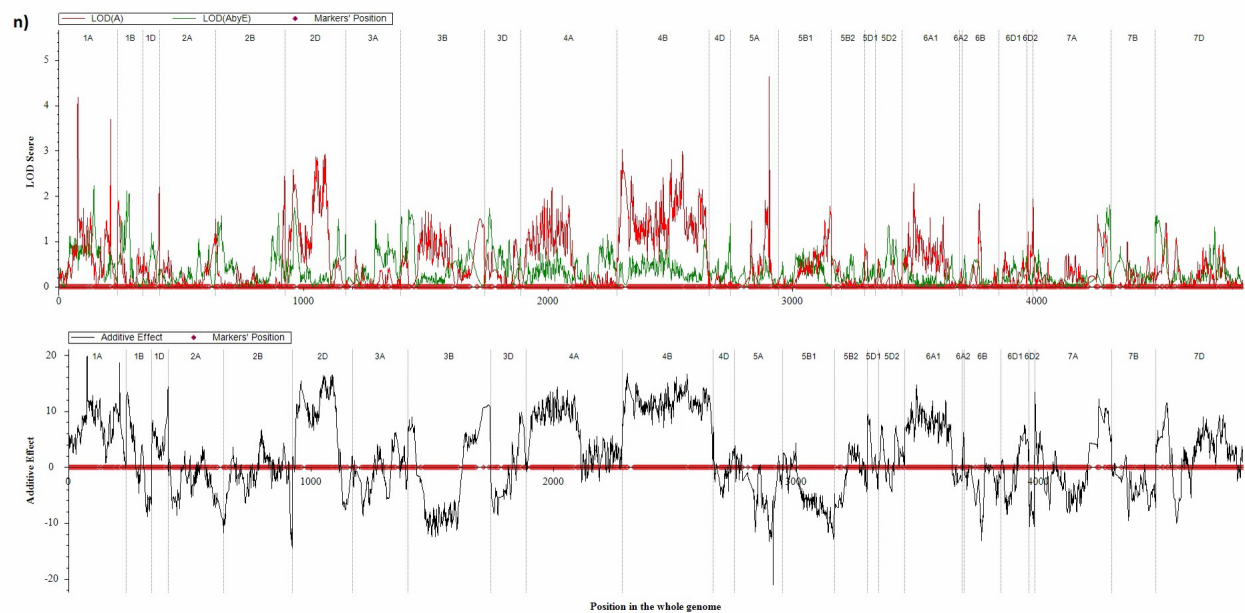
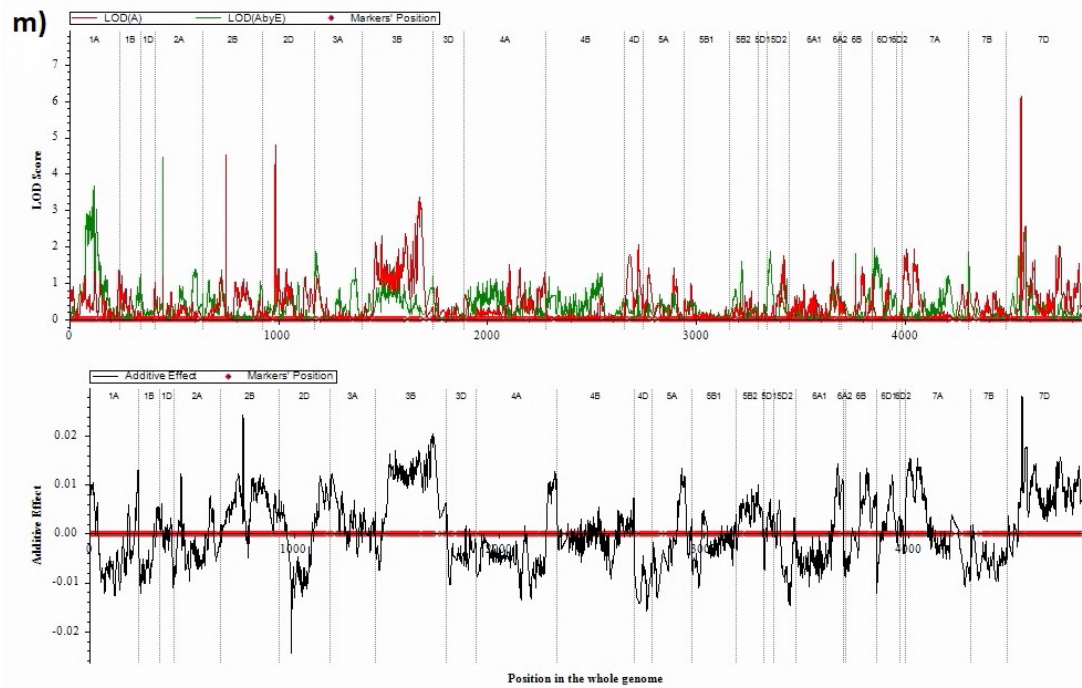


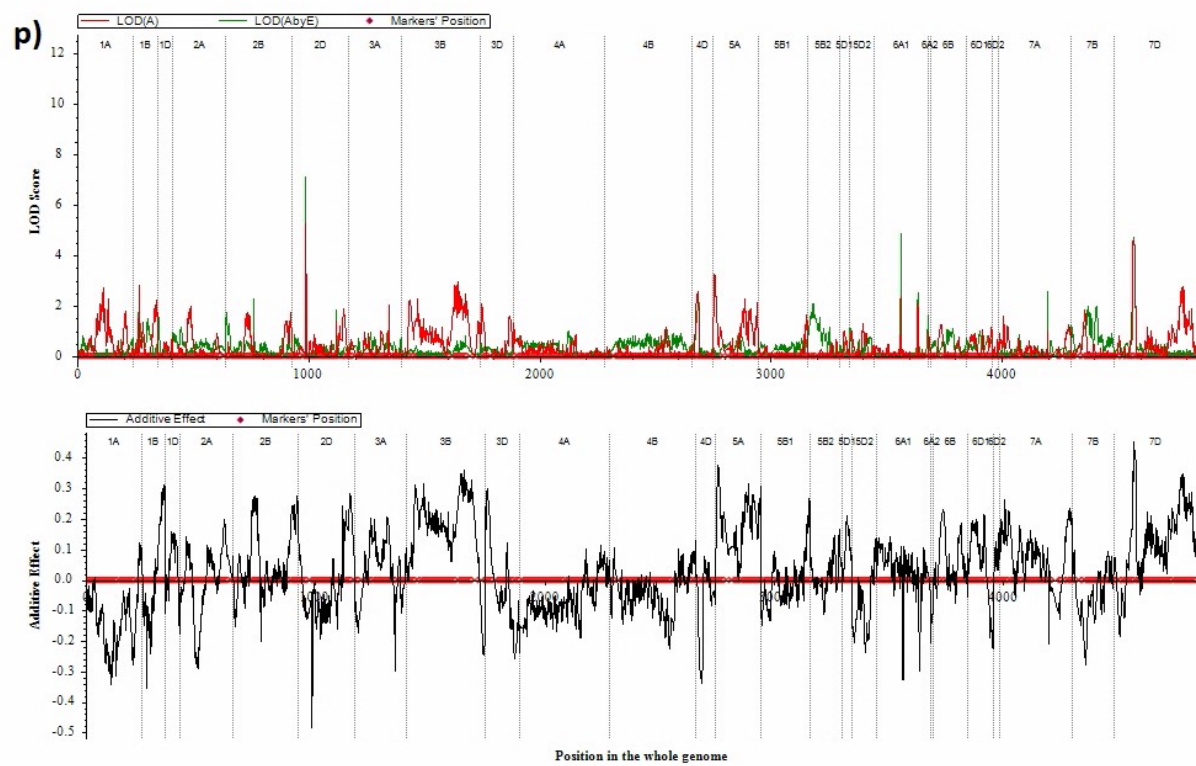
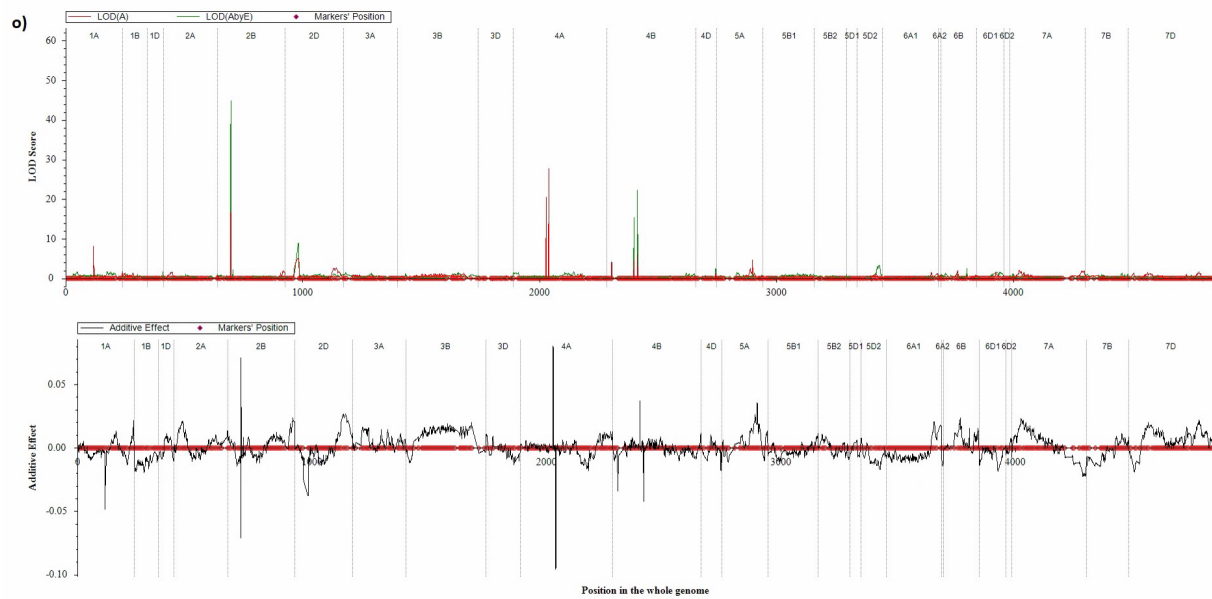


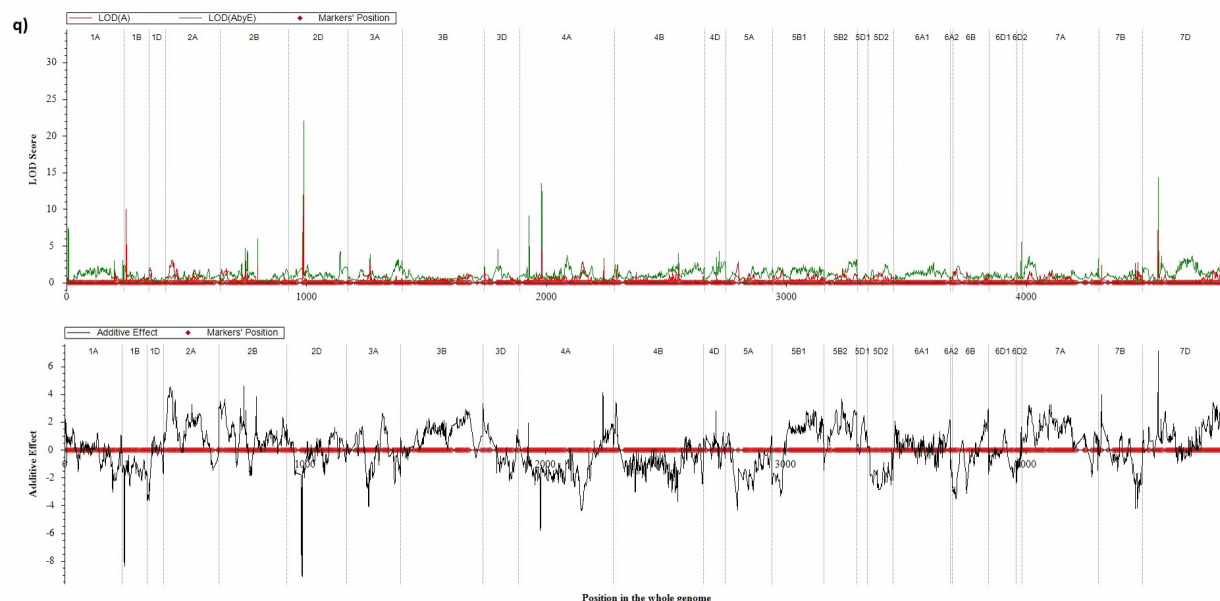






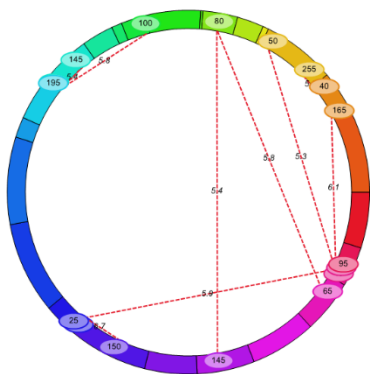






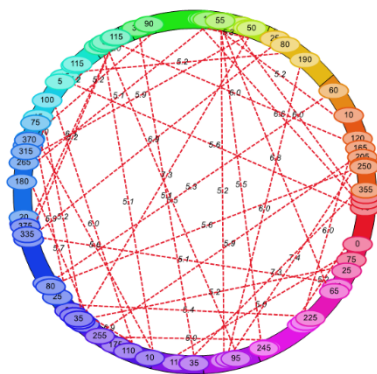
Supplemental Figures S3. Whole genome significance profiles of epistasis at LOD > 5 for yield and yield-related traits. The numbers on the rings show the peak cM position of the target SNPs on that chromosome. The numbers on each line show the total LOD score of that epistasis. Detailed information of SNP and its corresponding chromosome and cM locations, LOD scores and percentage of variations explained for total, additive, and additive by environments, additive effects for 1st and 2nd QTL linked SNPs, their corresponding additive by environment, epistasis by environment were list in Table S6, Abbreviation of traits; **a)** Biomass (BM); **b)** Biomass Grain Yield from the 0.5-meter inner row (BMYLD); **c)** Heading date (HD); **d)** Spikes weight (SPW); **e)** Harvest index (HI); **f)** Kernel Area (KAREA); **g)** Kernels Spike⁻¹ (KPS); **h)** Kernel Width (KWID); **i)** Kernel Length (KLEN); **j)** Perimeter (KPERI); **k)** Plant Height (PH); **l)** Single Head Dry Weight (SHDW); **m)** Single Head Grain Weight (SHGW); **n)** Spikes m⁻² (SPM); **o)** Single Stem Weight (SSW); **p)** Thousand Kernel Weight (TKW); **q)** Grain Yield from combine harvester (YLD).

a)



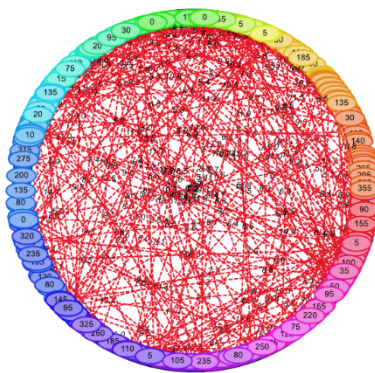
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2B 7A
2D 7B
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3B
3D
4A
4B
4D
5A
5B1
5B2
5D1
5D2
6A1

b)



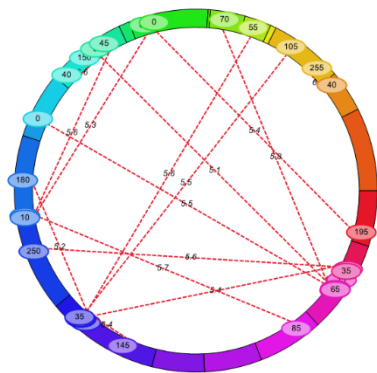
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1B 6B
1D 6D1
2A 6D2
2B 7A
2D 7B
3A 7D
3B
3D
4A
4B
4D
5A
5B1
5B2
5D1
5D2
6A1

c)



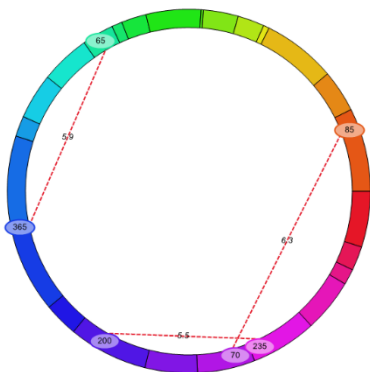
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1D 6D1
2A 6D2
2B 7A
2D 7B
3A 7D
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3D
4A
4B
4D
5A
5B1
5B2
5D1
5D2
6A1

d)



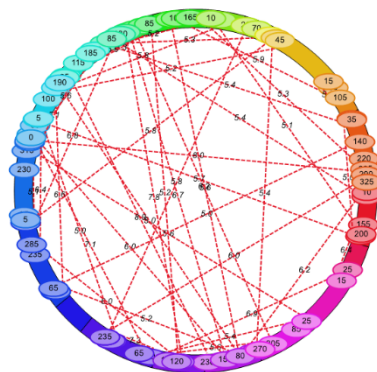
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2A 6D2
2B 7A
2D 7B
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3D
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4D
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5B2
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6A1

e)



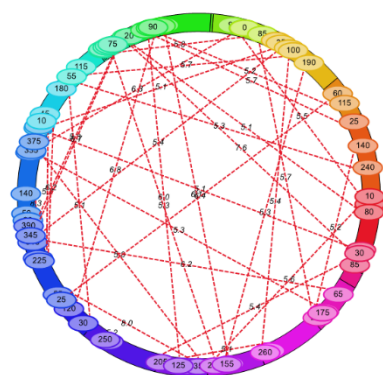
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1D 6D1
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2D 7B
3A 7D
3B
3D
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4D
5A
5B1
5B2
5D1
5D2
6A1

f)



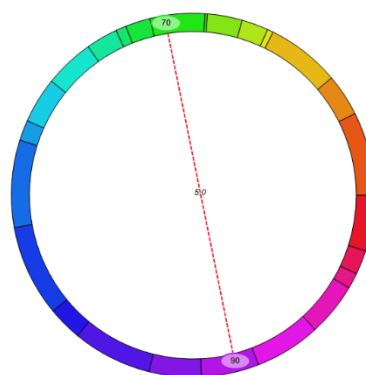
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4D
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6A1

g)



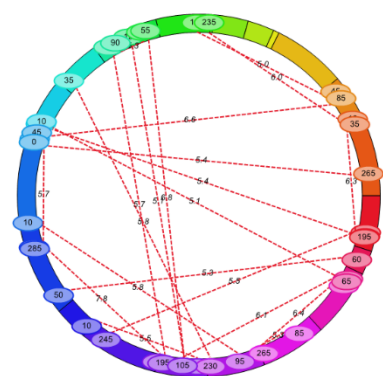
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h)



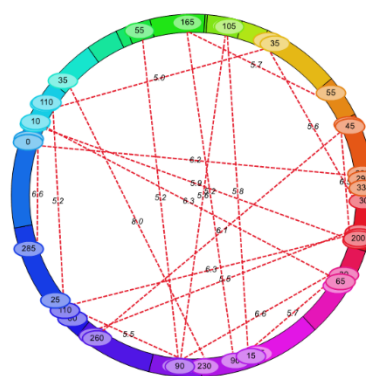
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5D1
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i)



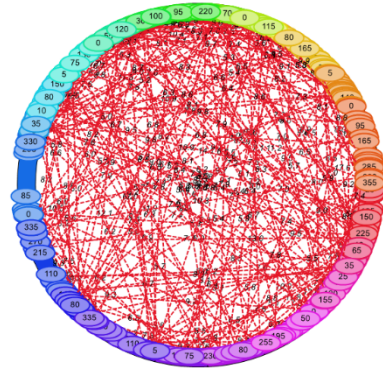
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j)



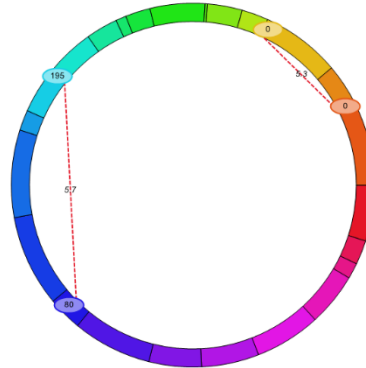
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k)



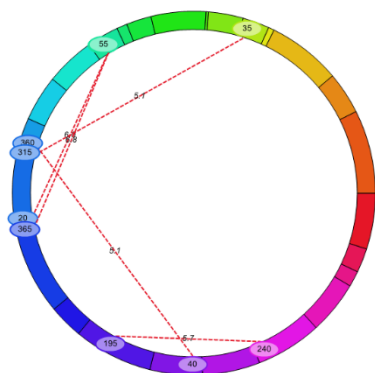
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5B2
5D1
5D2
6A1

l)



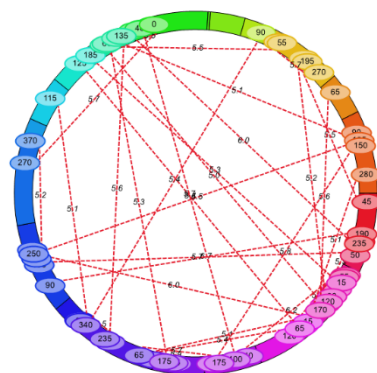
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5B2
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6A1

m)



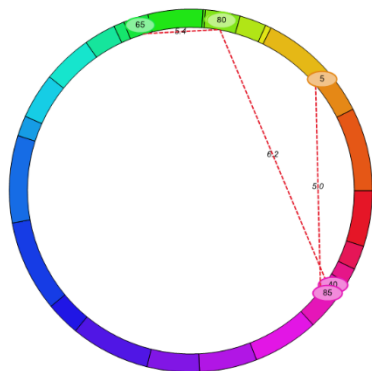
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4D
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6A1

n)



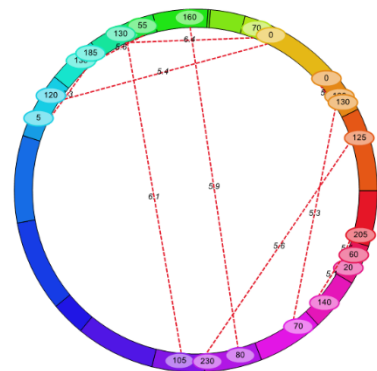
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1D 6D1
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2D 7B
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5B2
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5D2
6A1

o)



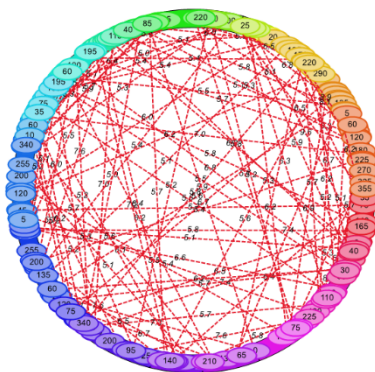
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3A 7D
3B
3D
4A
4B
4D
5A
5B1
5B2
5D1
5D2
6A1

p)



1A 6A2
1B 6B
1D 6D1
2A 6D2
2B 7A
2D 7B
3A 7D
3B
3D
4A
4B
4D
5A
5B1
5B2
5D1
5D2
6A1

q)



1A 6A2
1B 6B
1D 6D1
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2D 7B
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