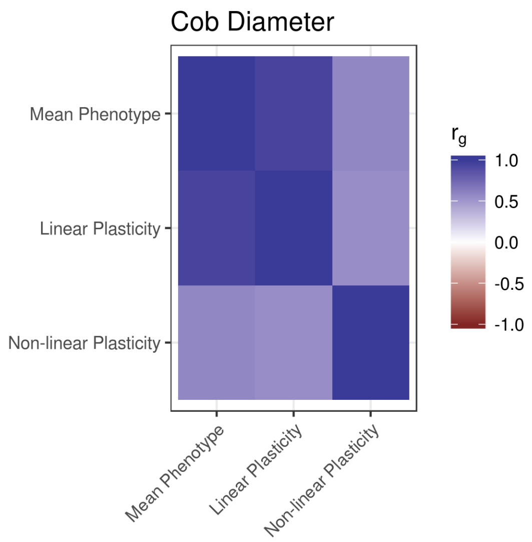
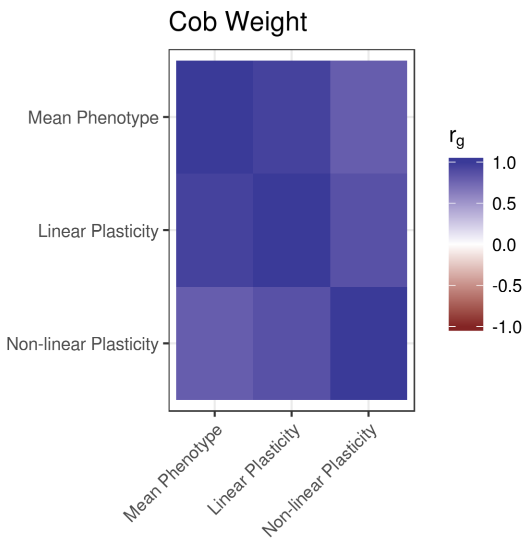
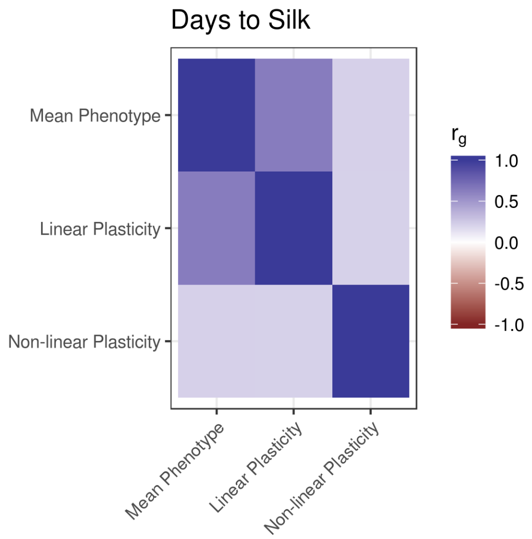
SUPPLEMENTARY FIGURES



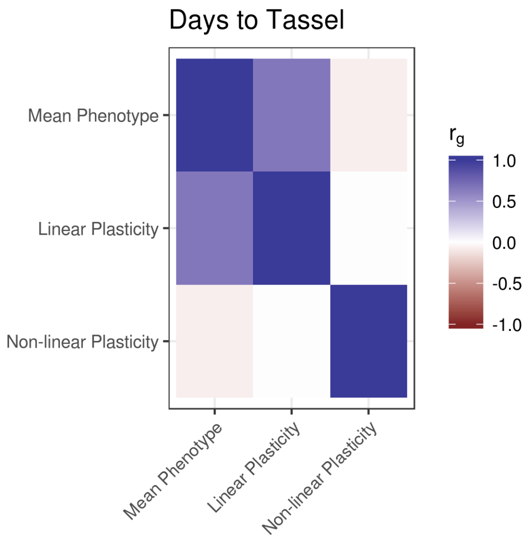
Cob Diameter



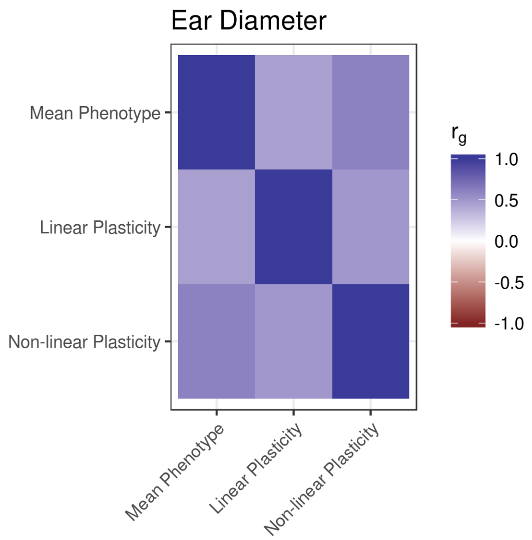
Cob Weight



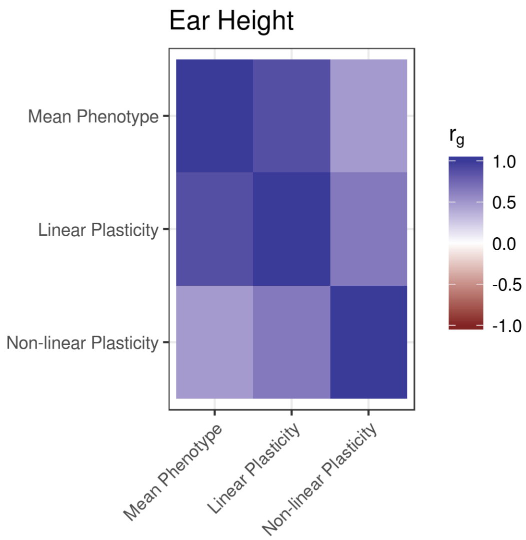
Days to Silk



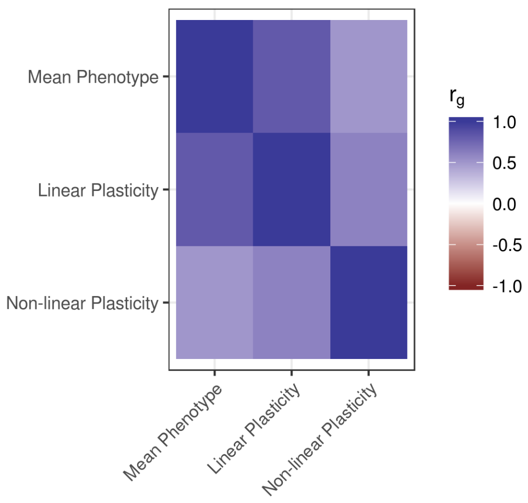
Days to Tassel

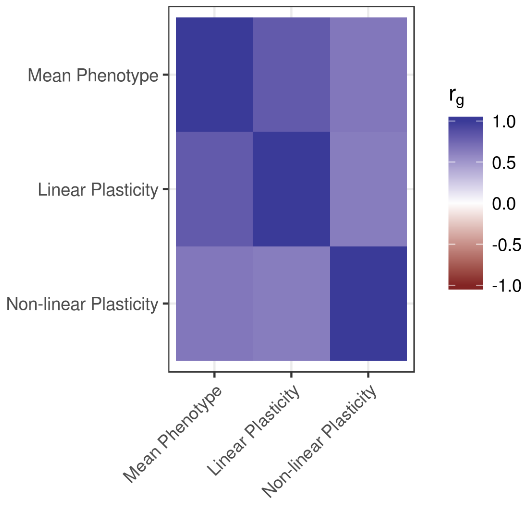


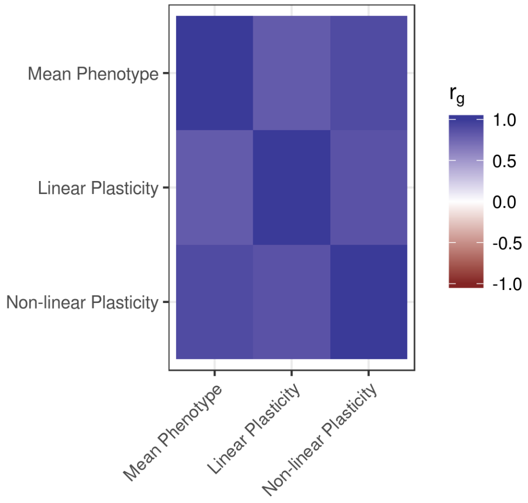
Ear Diameter

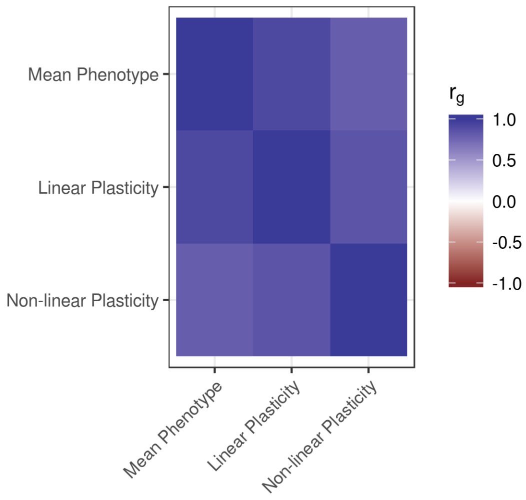


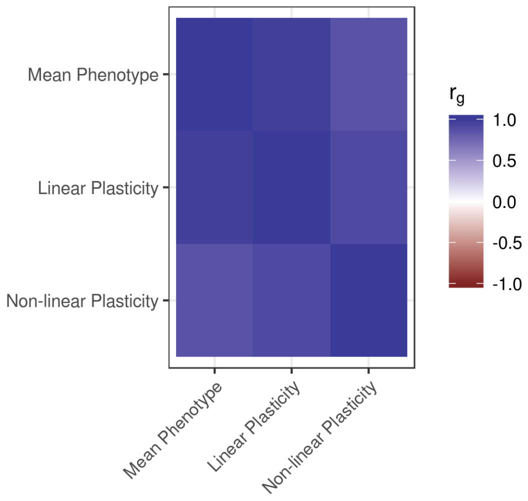
Ear Height

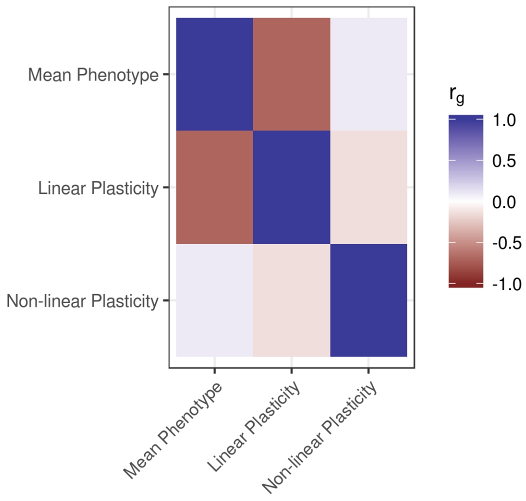

Ear Length

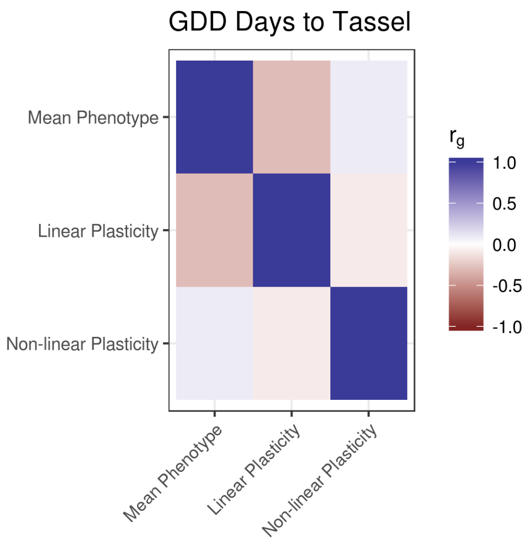

Ear Rank Number

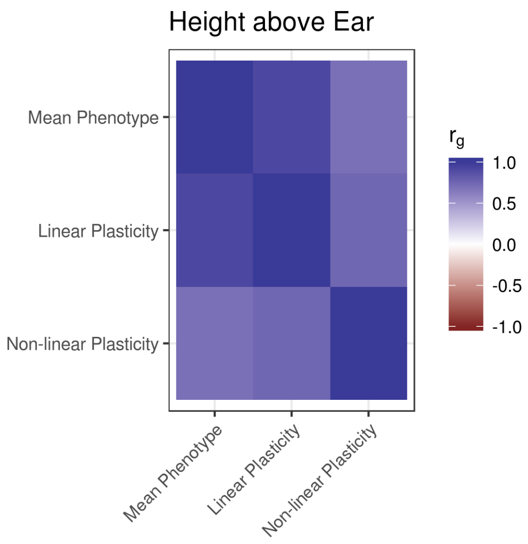

Ear Row Number

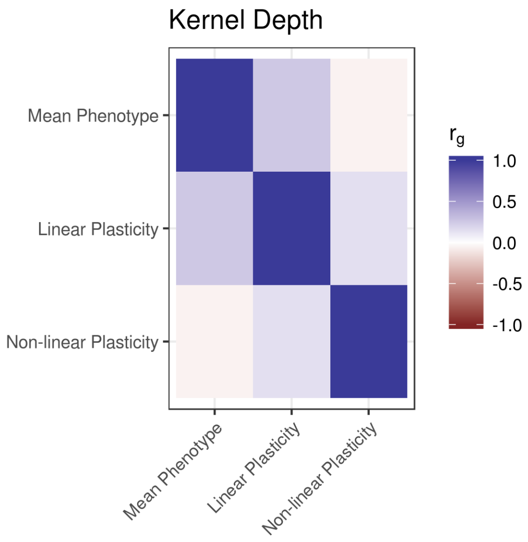

Ear Weight

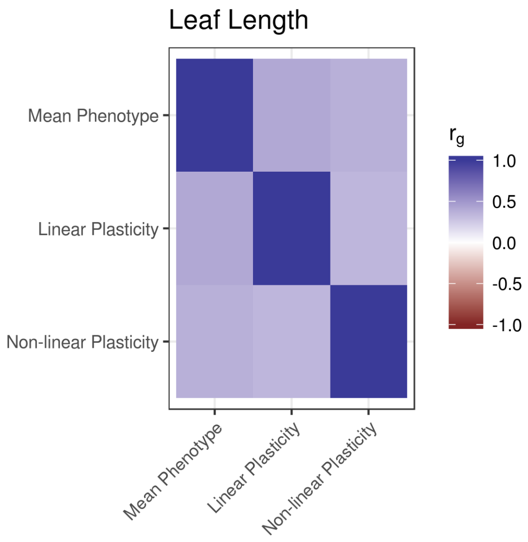

GDD Anthesis Silking Interval

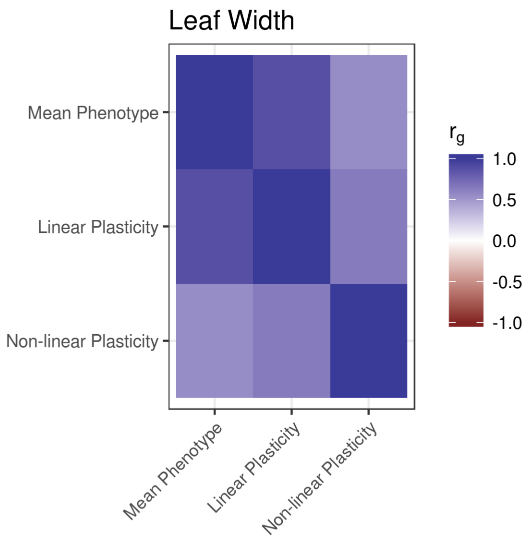

GDD Days to Silk

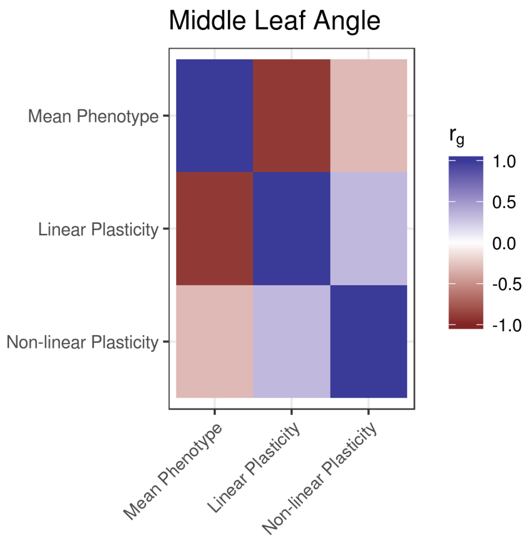

GDD Days to Tassel
Mean Phenotype
Linear Plasticity
Non-linear Plasticity
Mean Phenotype
Linear Plasticity
Non-linear Plasticity
r_g
1.0
0.5
0.0
-0.5
-1.0


Height above Ear
Mean Phenotype
Linear Plasticity
Non-linear Plasticity
Mean Phenotype
Linear Plasticity
Non-linear Plasticity
r_g
1.0
0.5
0.0
-0.5
-1.0

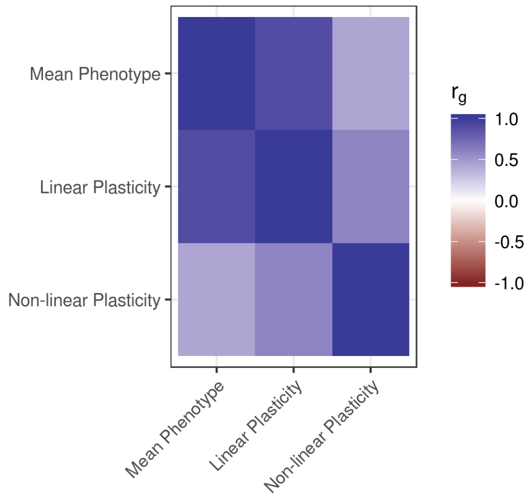

Kernel Depth
Mean Phenotype
Linear Plasticity
Non-linear Plasticity
Mean Phenotype
Linear Plasticity
Non-linear Plasticity
r_g
1.0
0.5
0.0
-0.5
-1.0


Leaf Length
Mean Phenotype
Linear Plasticity
Non-linear Plasticity
Mean Phenotype
Linear Plasticity
Non-linear Plasticity
r_g
1.0
0.5
0.0
-0.5
-1.0

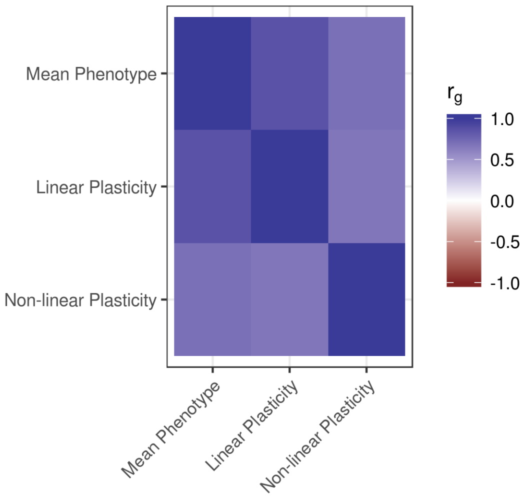

Leaf Width
Mean Phenotype
Linear Plasticity
Non-linear Plasticity
Mean Phenotype
Linear Plasticity
Non-linear Plasticity
r_g
1.0
0.5
0.0
-0.5
-1.0


Middle Leaf Angle
Mean Phenotype
Linear Plasticity
Non-linear Plasticity
Mean Phenotype
Linear Plasticity
Non-linear Plasticity
r_g
1.0
0.5
0.0
-0.5
-1.0

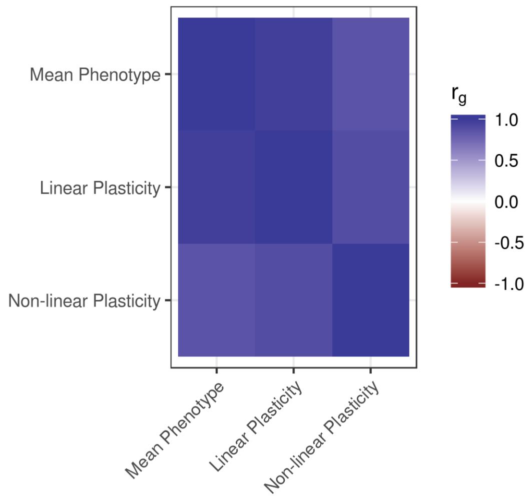
Plant Height



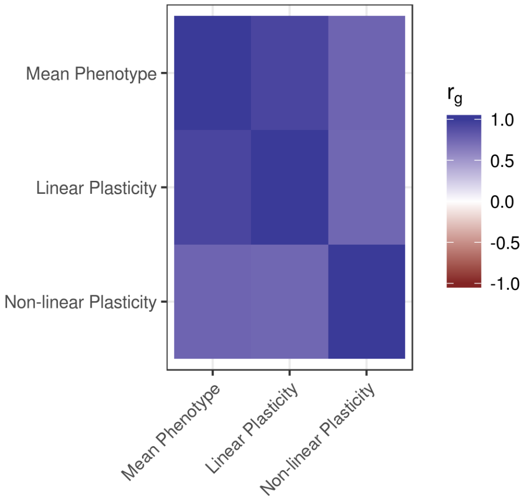
Tassel Length



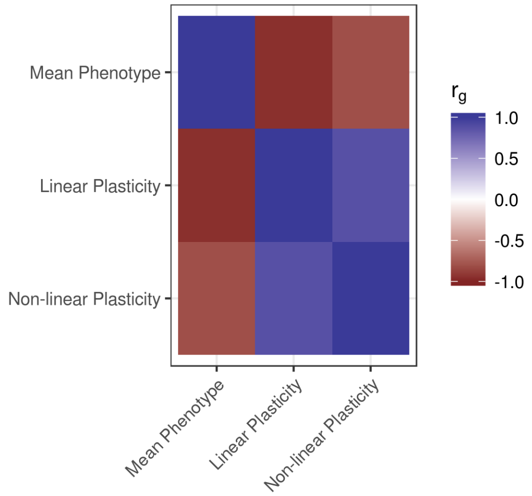
Tassel Primary Branches



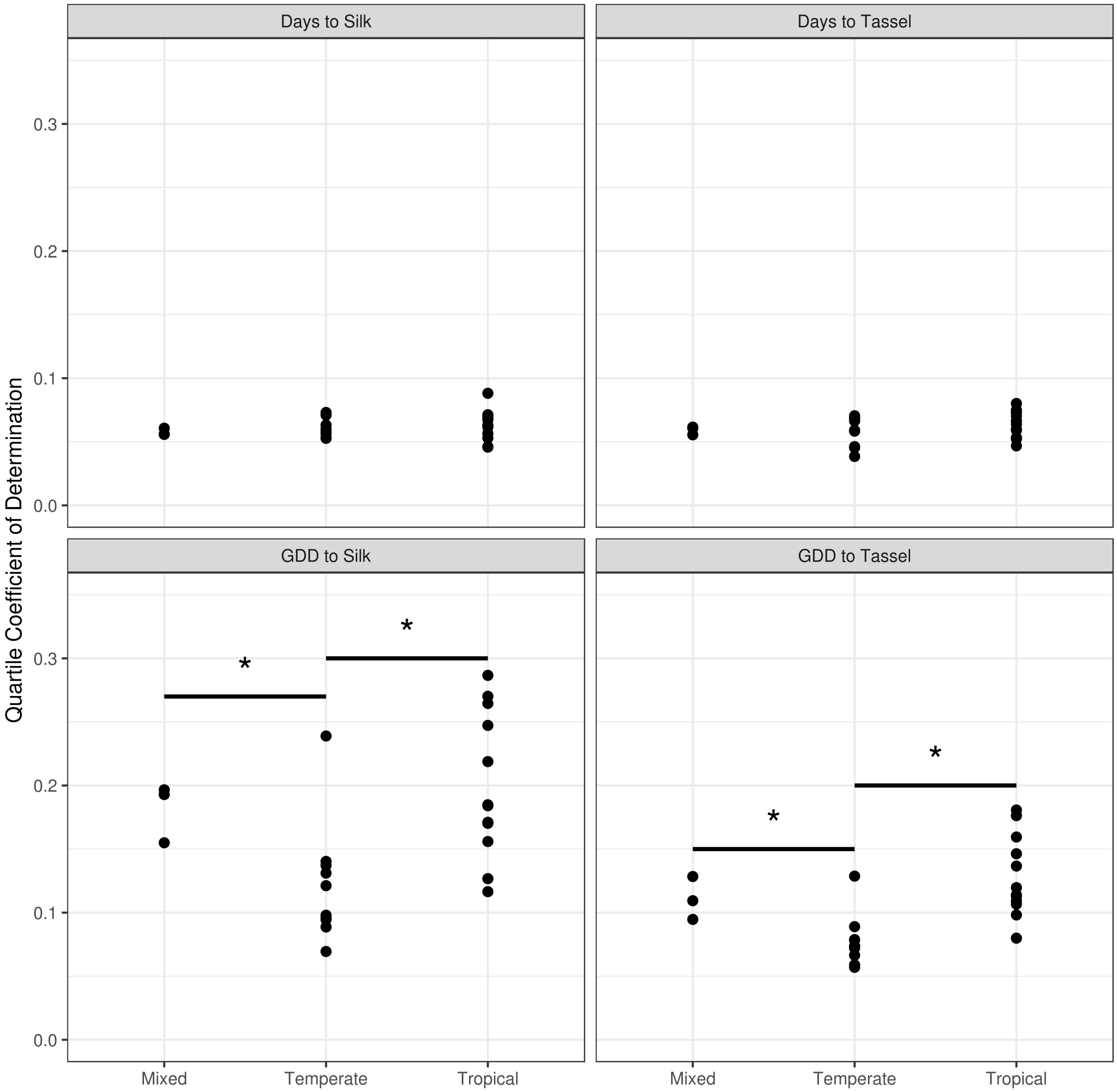
Total Kernel Volume



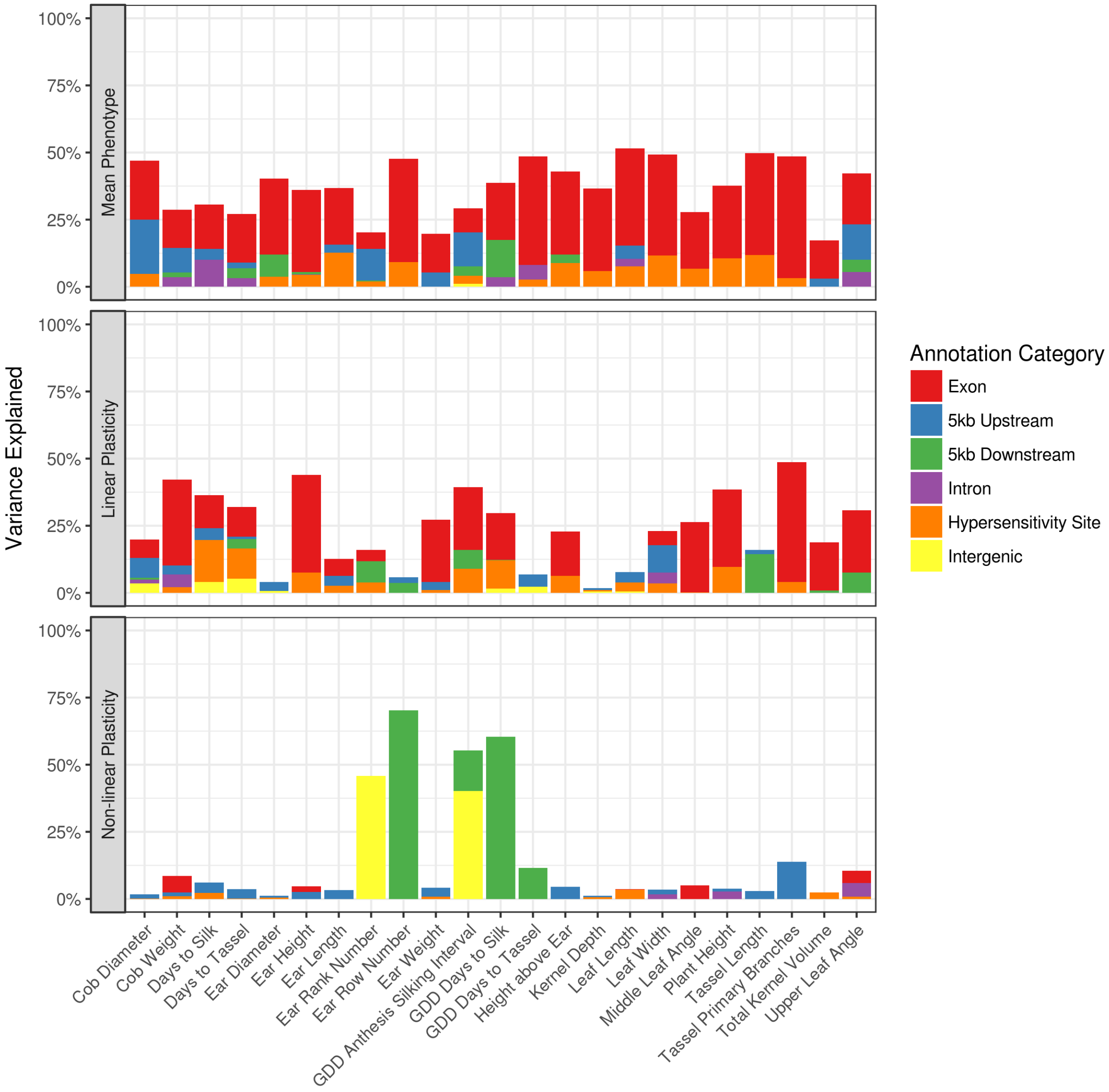
Upper Leaf Angle



Supplementary Figure 1. Genetic correlations between mean phenotype values, linear plasticity, and non-linear plasticity for each phenotype.

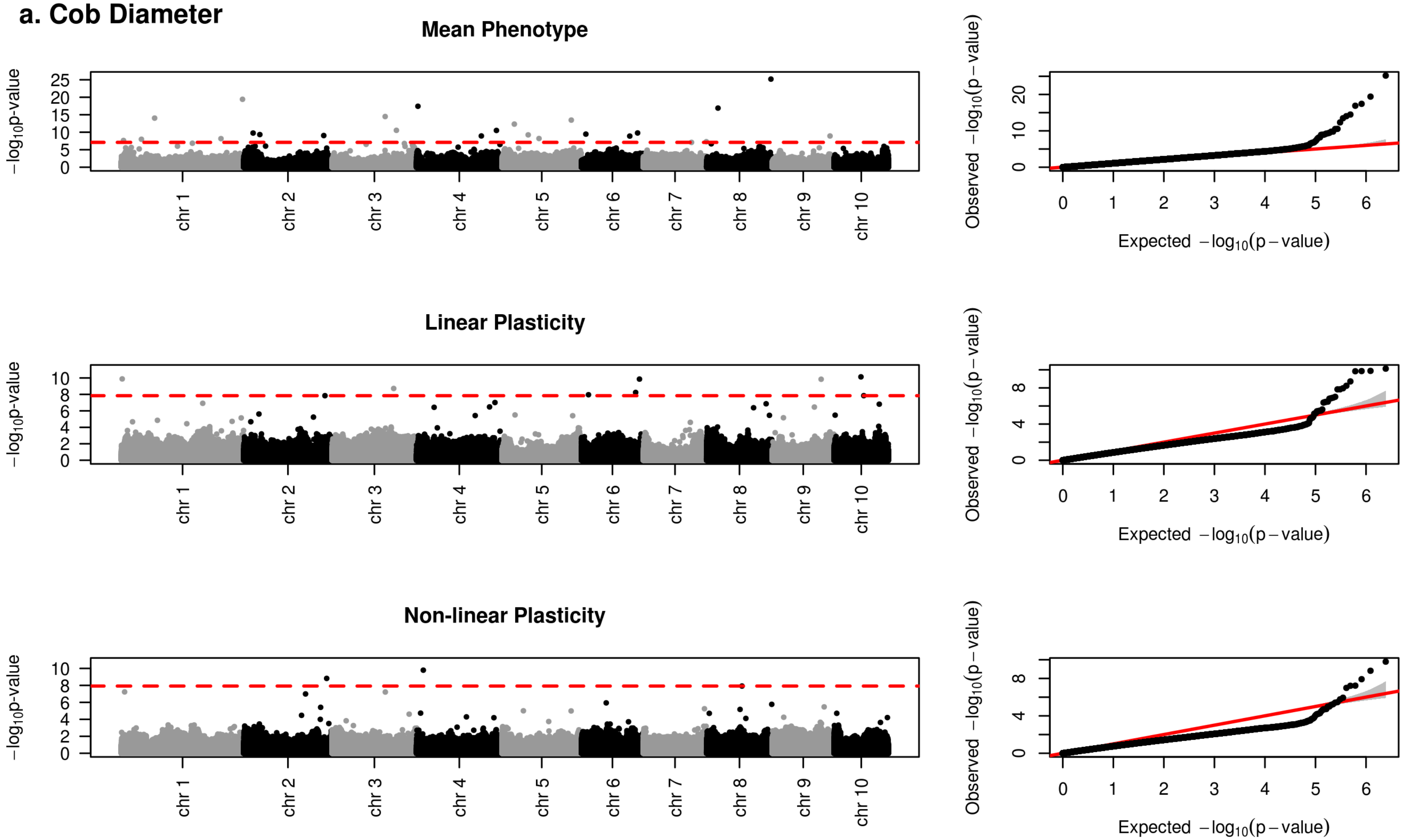


Supplementary Figure 2. Family-wise quartile coefficients of dispersion for flowering time phenotypes. Germplasm group assignments are taken from Yan *et al.*[1]. n = 3 for mixed, 10 for temperate, and 13 for tropical. Asterisks indicate that two groups have different distributions of dispersion coefficients at the $\alpha = 0.05$ level (two-sided Mann-Whitney U test).

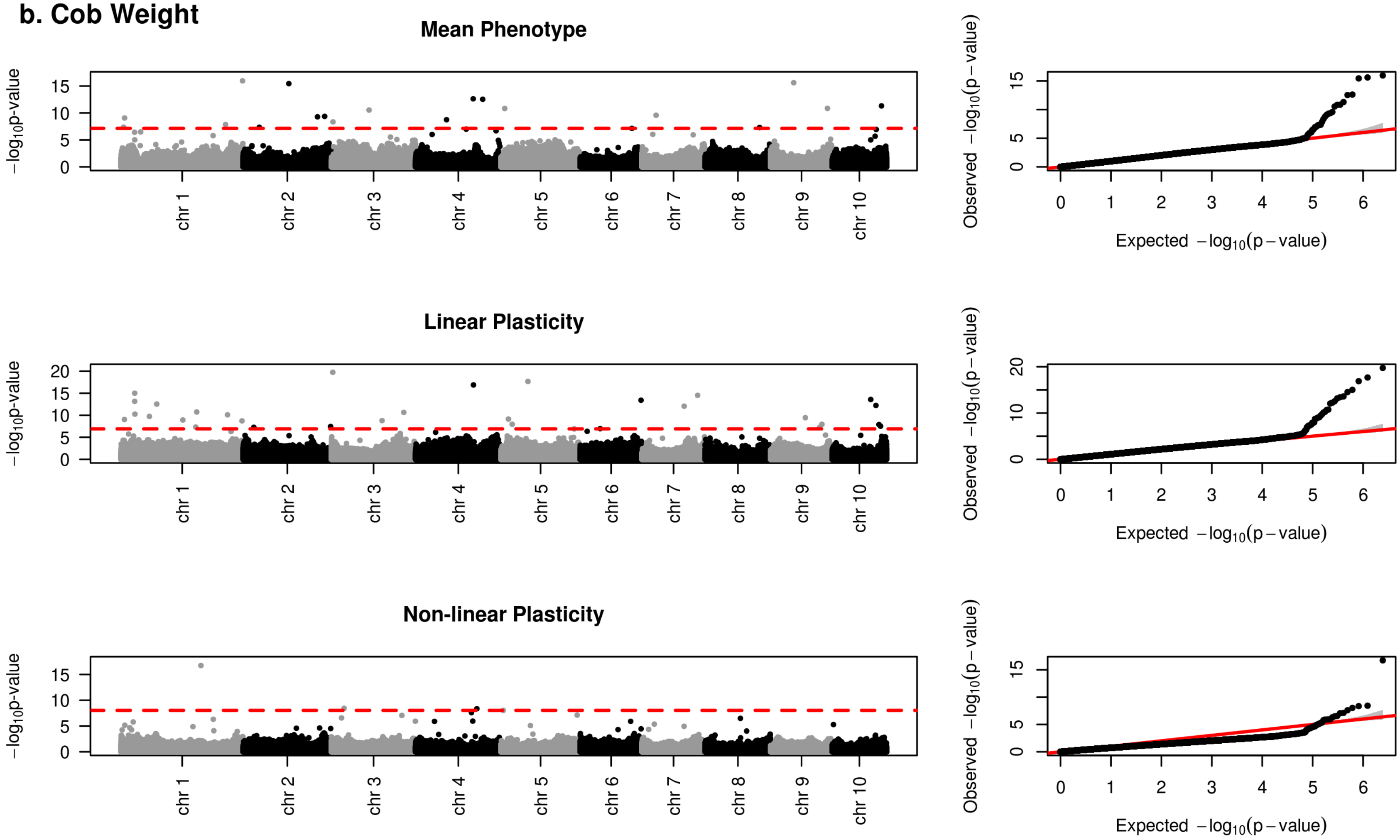


Supplementary Figure 3. Percent variance explained by genome-wide SNPs hierarchically assigned to annotation categories

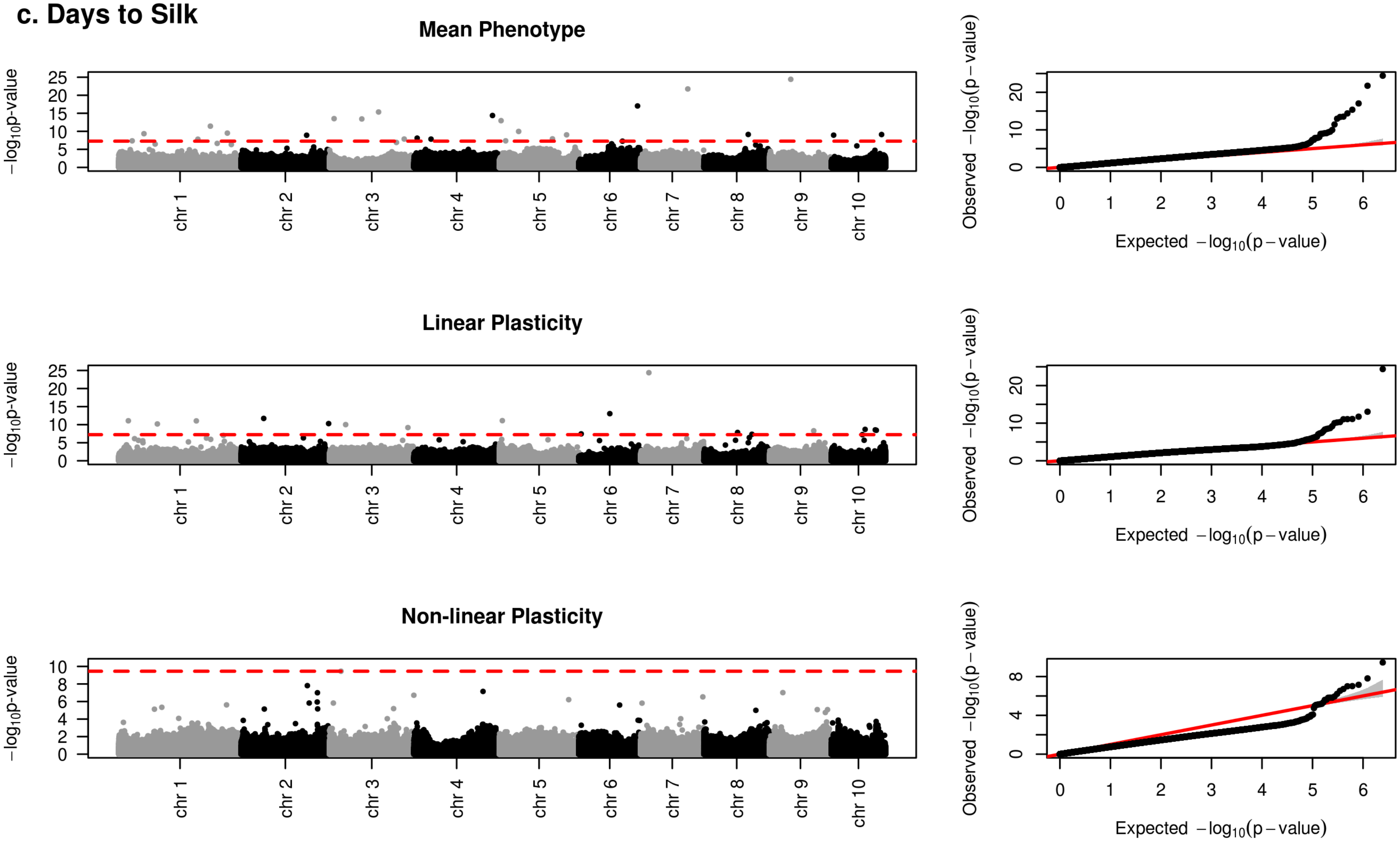
a. Cob Diameter



b. Cob Weight

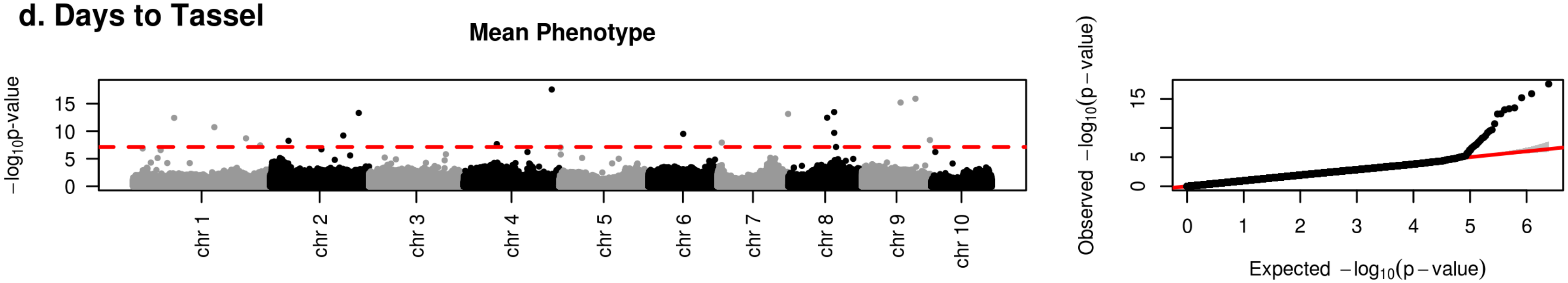

Mean Phenotype
Linear Plasticity
Non-linear Plasticity
$-\log_{10}$p-value
0
5
10
15
20
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
Observed $-\log_{10}(p-value)$
Expected $-\log_{10}(p-value)$
0
1
2
3
4
5
6

c. Days to Silk

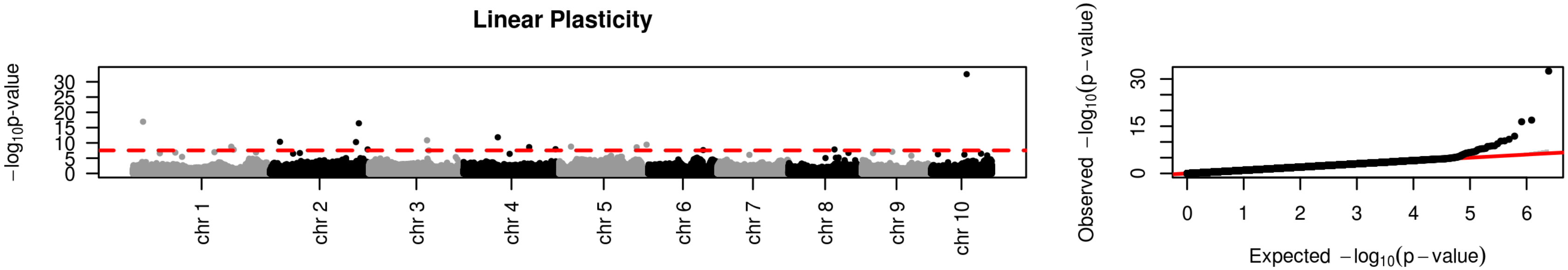


d. Days to Tassel

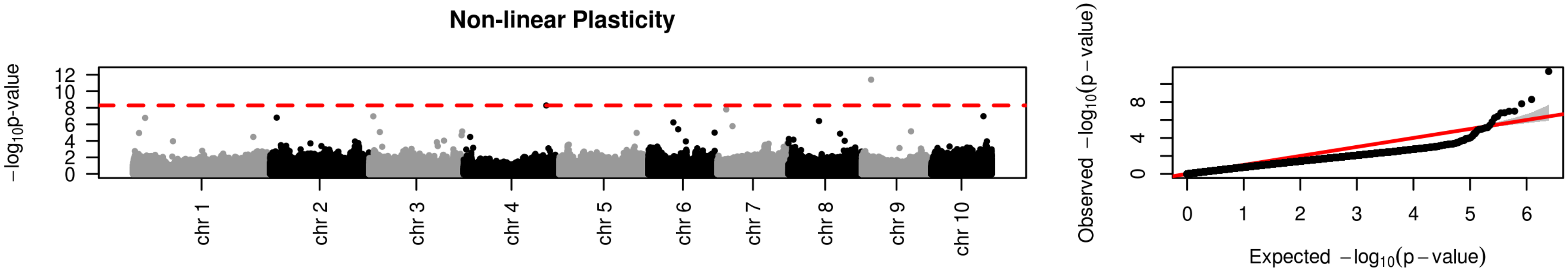
Mean Phenotype



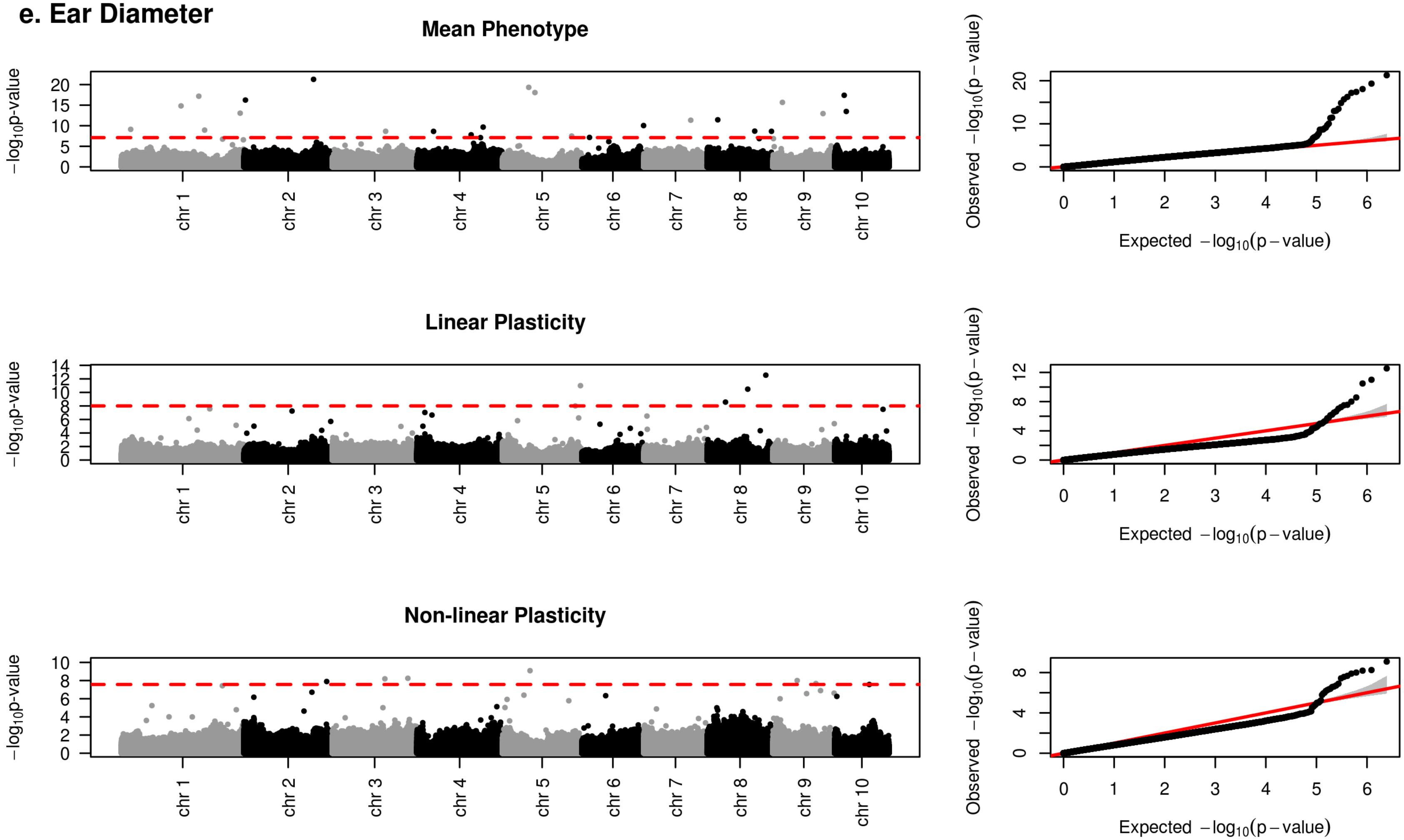
Linear Plasticity



Non-linear Plasticity



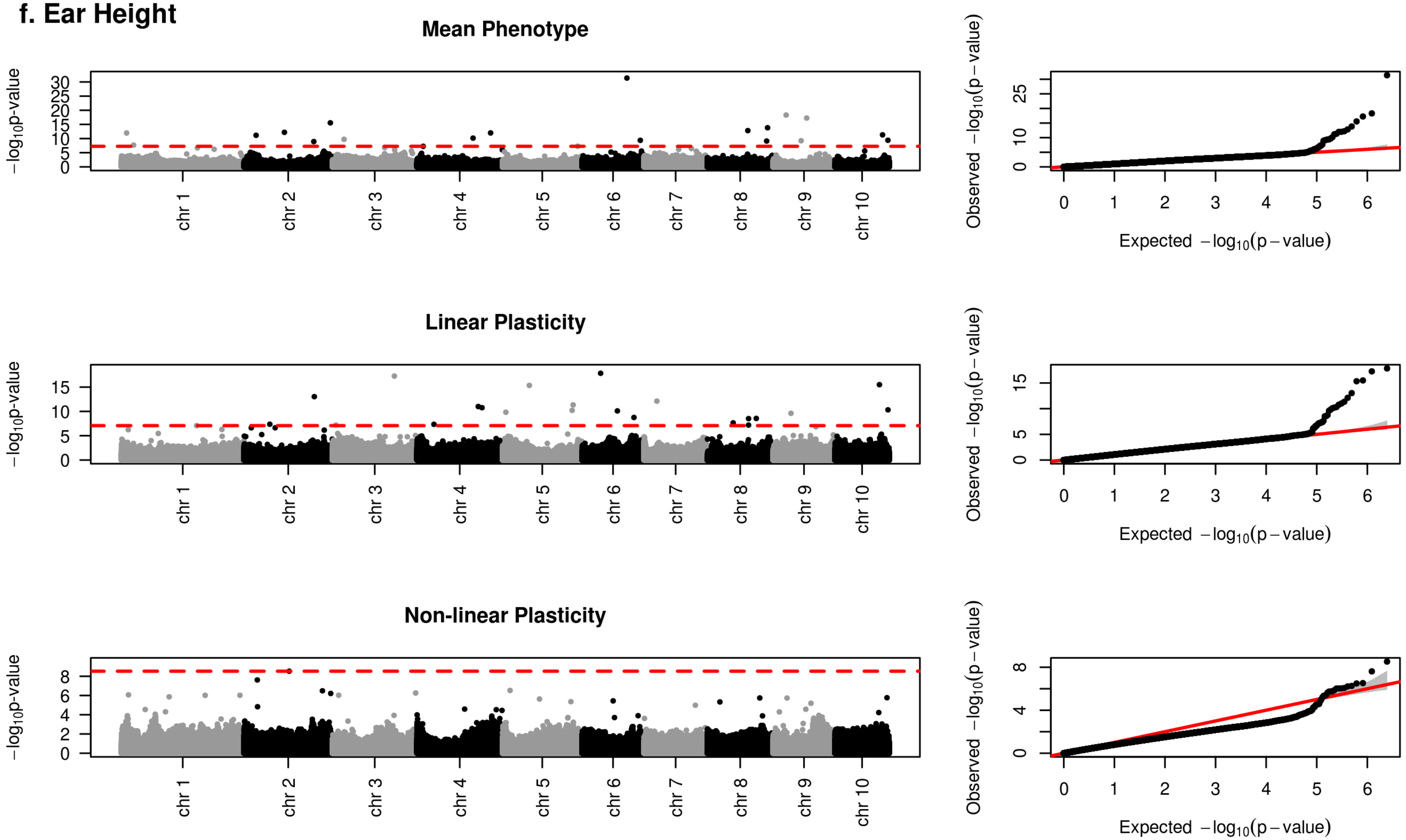
e. Ear Diameter


Mean Phenotype

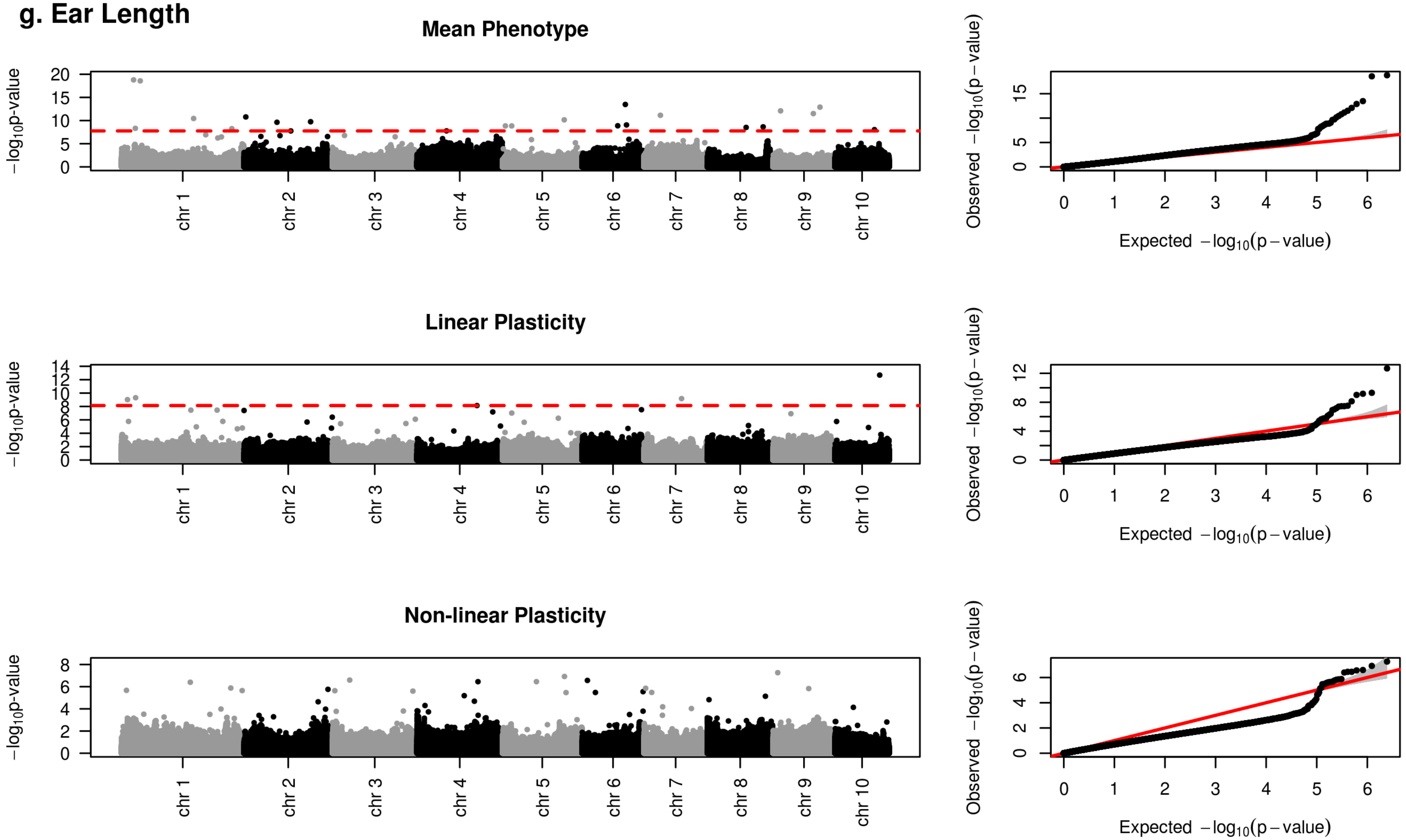
Linear Plasticity

Non-linear Plasticity

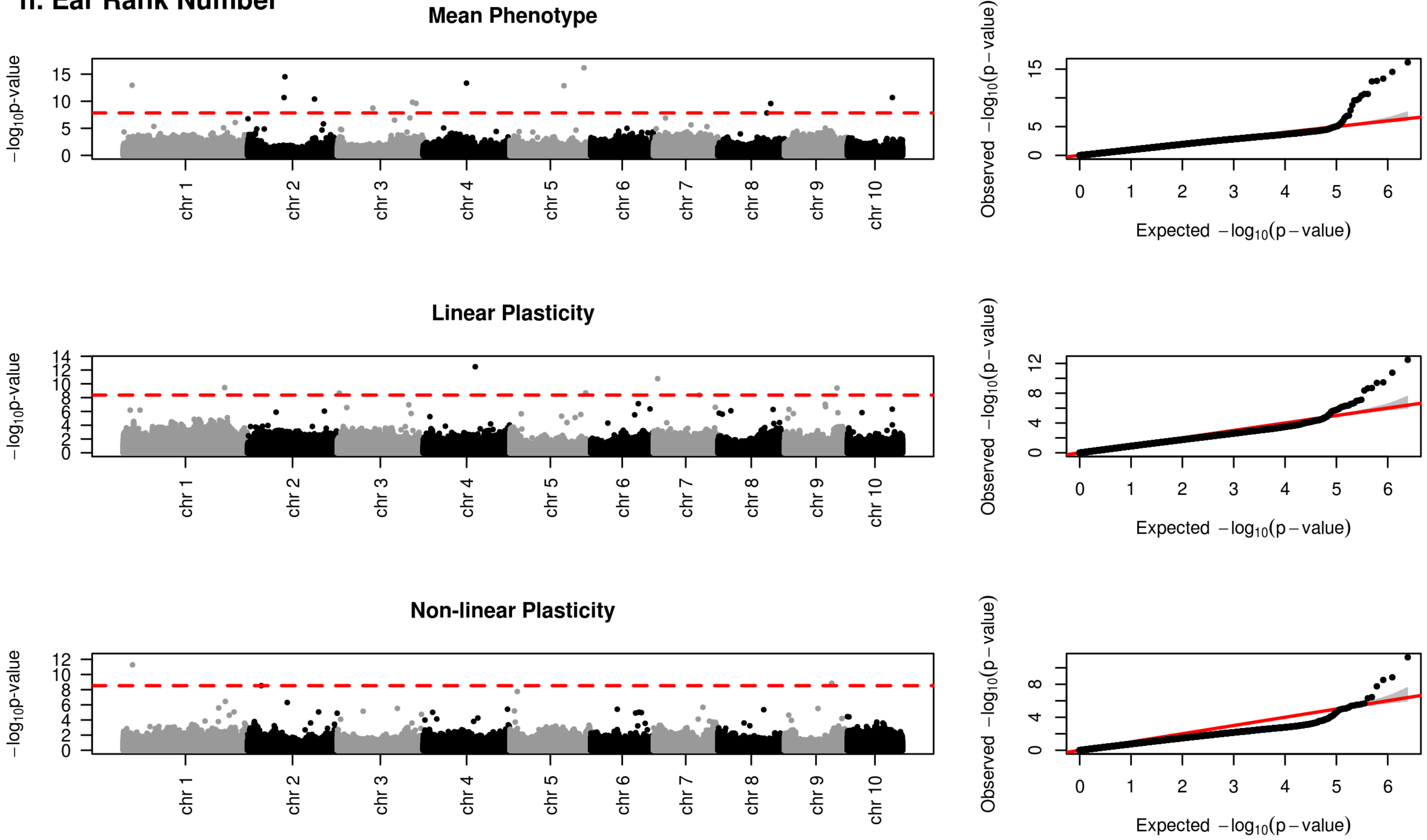
f. Ear Height


Mean Phenotype
−log10p-value
30
25
20
15
10
5
0
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
Observed −log10(p − value)
Expected −log10(p − value)
0
10
25
0
1
2
3
4
5
6
Linear Plasticity
−log10p-value
15
10
5
0
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
Observed −log10(p − value)
Expected −log10(p − value)
0
5
15
0
1
2
3
4
5
6
Non-linear Plasticity
−log10p-value
8
6
4
2
0
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
Observed −log10(p − value)
Expected −log10(p − value)
0
4
8
0
1
2
3
4
5
6

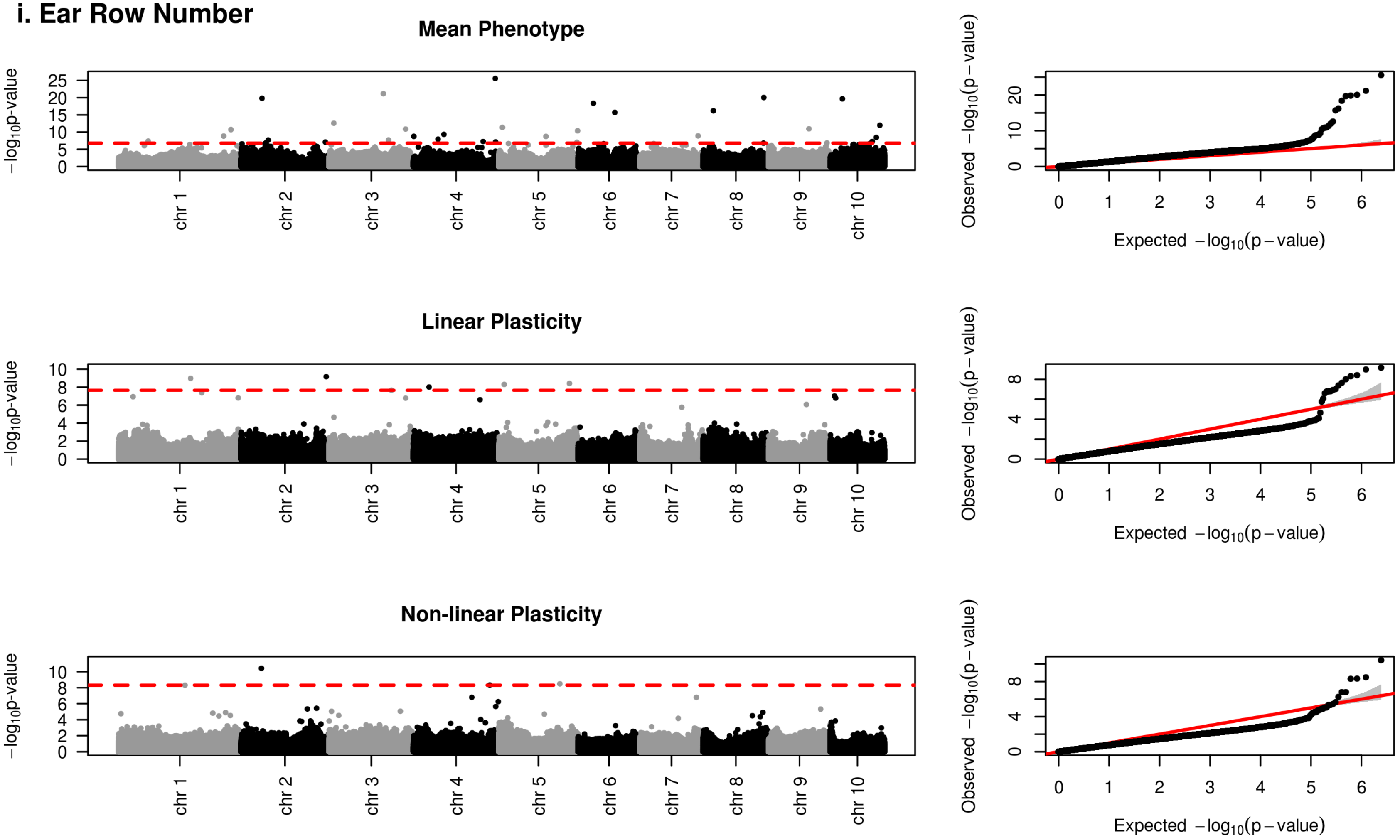
g. Ear Length


Mean Phenotype
−log10p-value
20
15
10
5
0
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
Observed −log10(p − value)
15
5
0
Expected −log10(p − value)
0 1 2 3 4 5 6
Linear Plasticity
−log10p-value
14
12
10
8
6
4
2
0
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
Observed −log10(p − value)
12
8
4
0
Expected −log10(p − value)
0 1 2 3 4 5 6
Non-linear Plasticity
−log10p-value
8
6
4
2
0
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
Observed −log10(p − value)
6
4
2
0
Expected −log10(p − value)
0 1 2 3 4 5 6

h. Ear Rank Number



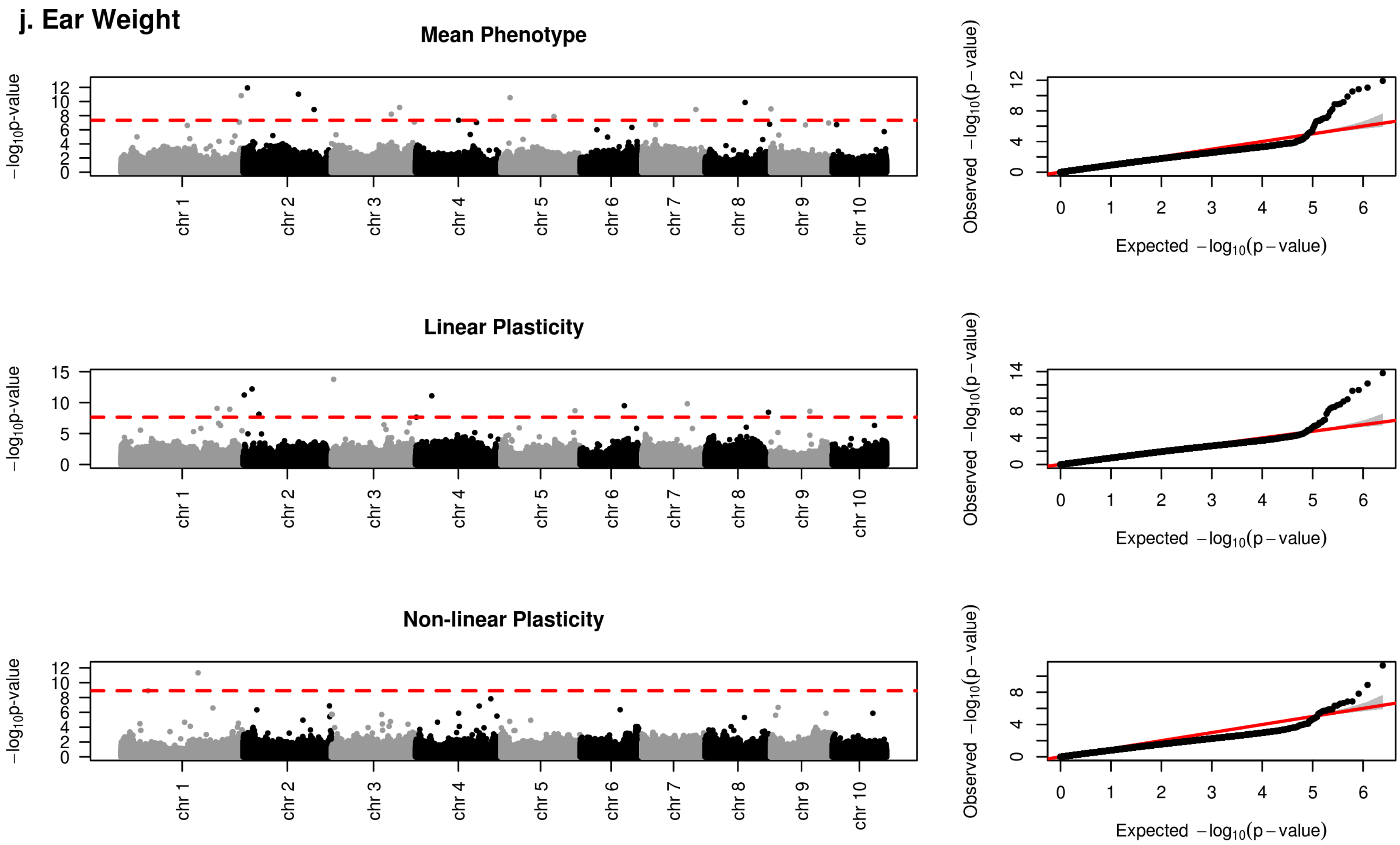
i. Ear Row Number



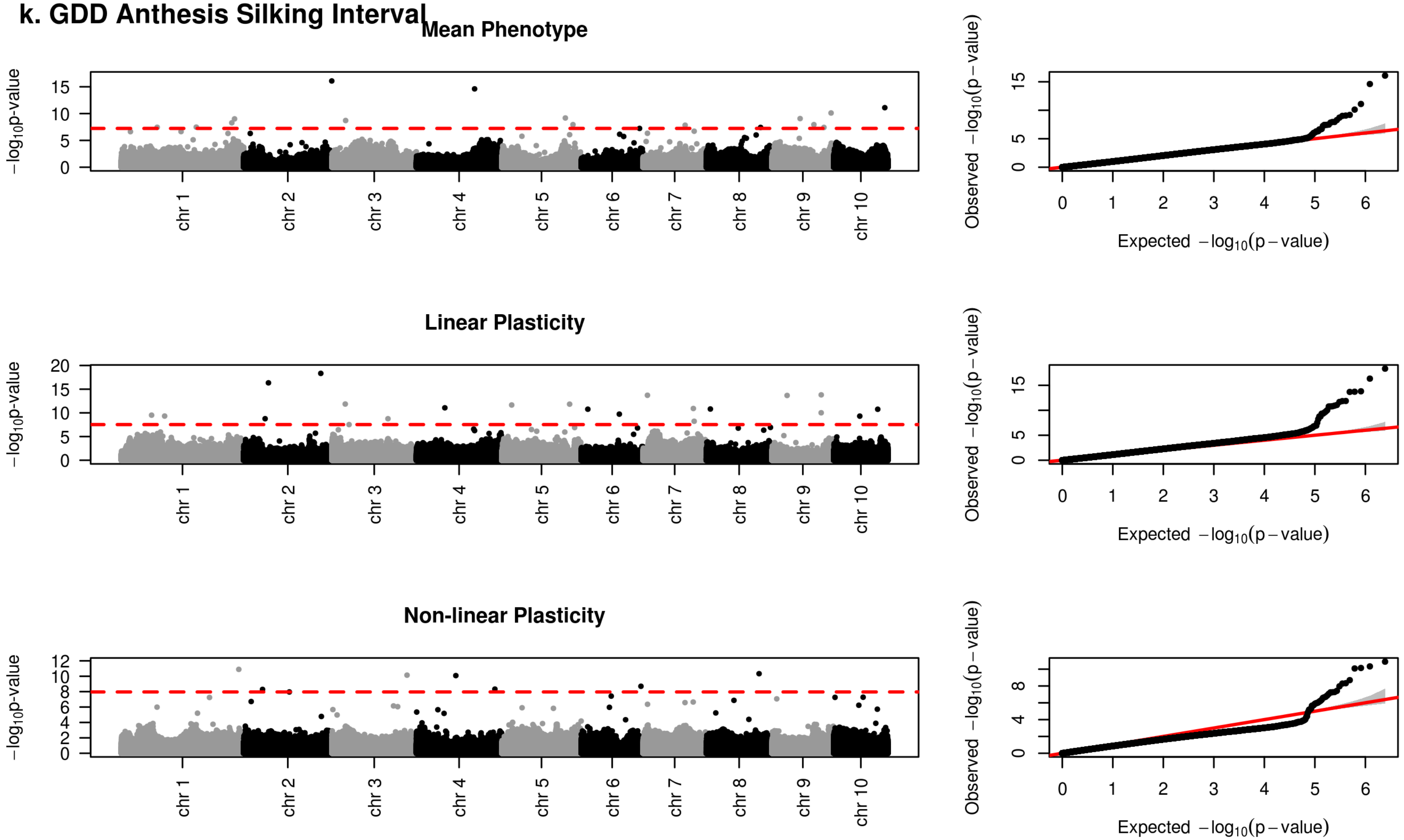
Mean Phenotype

Linear Plasticity

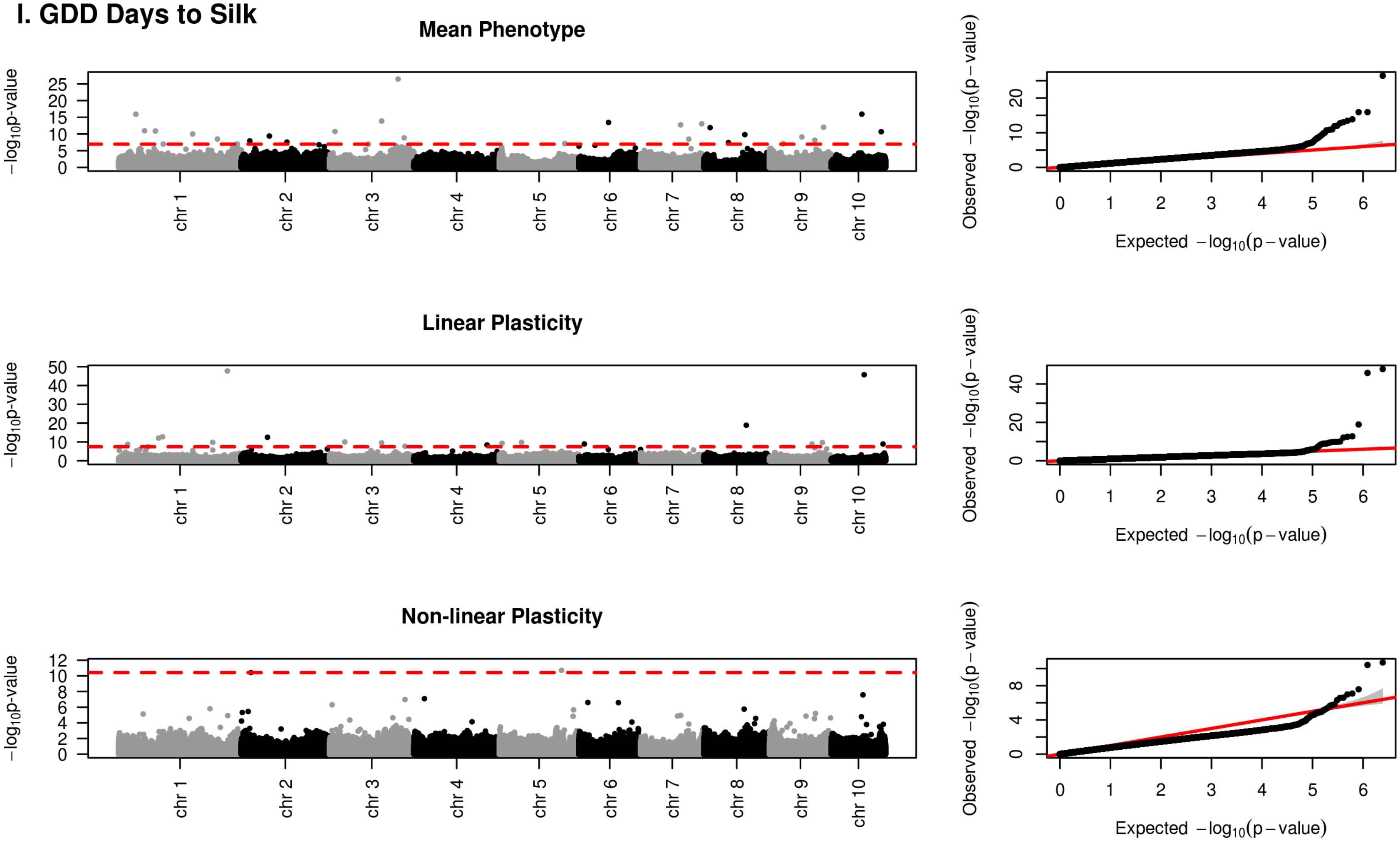
Non-linear Plasticity

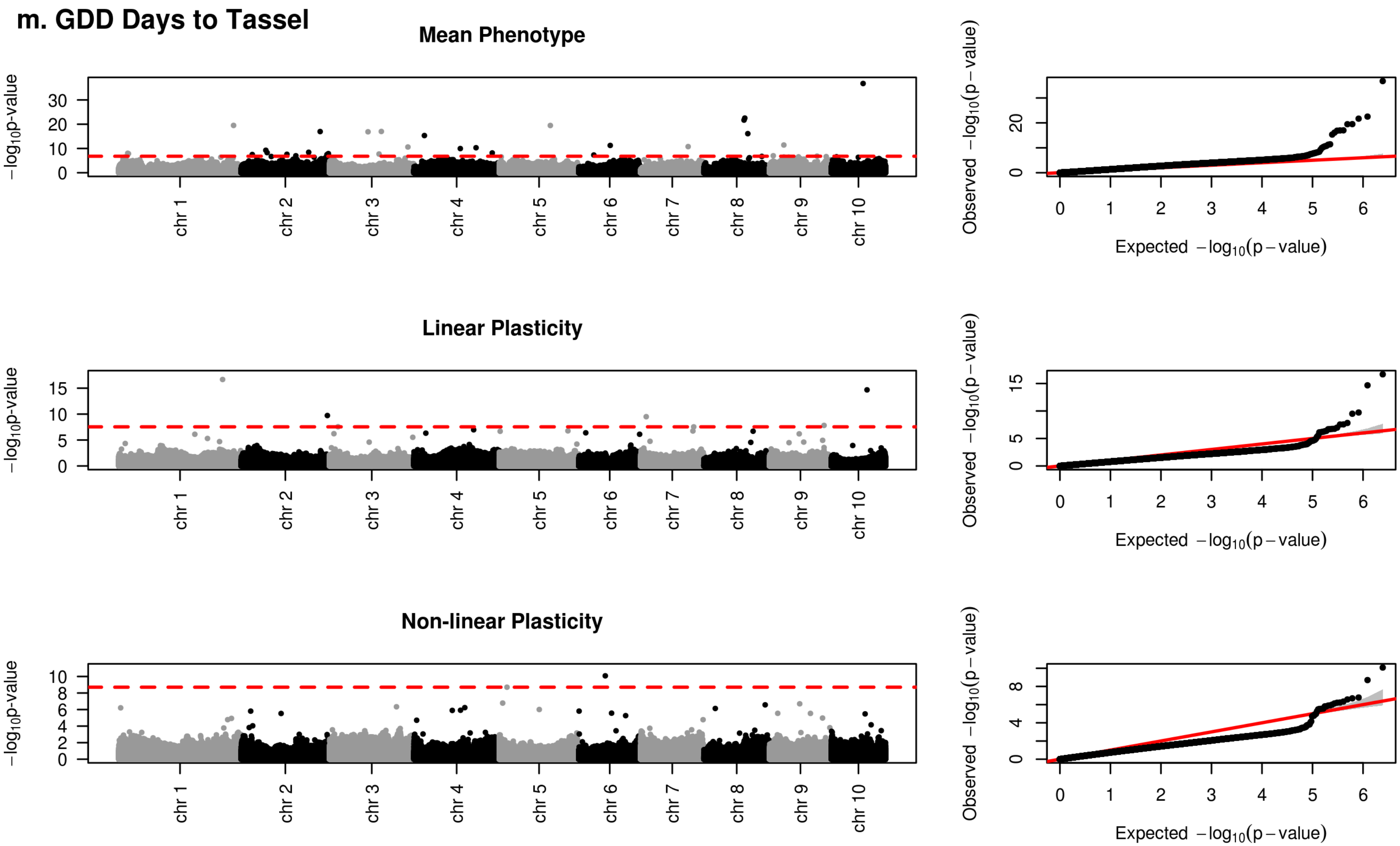

j. Ear Weight
Mean Phenotype
Linear Plasticity
Non-linear Plasticity
$-\log_{10}$p-value
0 2 4 6 8 10 12
0 5 10 15
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
Observed $-\log_{10}(p-value)$
Expected $-\log_{10}(p-value)$
0 1 2 3 4 5 6
0 4 8 12
0 4 8 14
0 4 8

k. GDD Anthesis Silking Interval

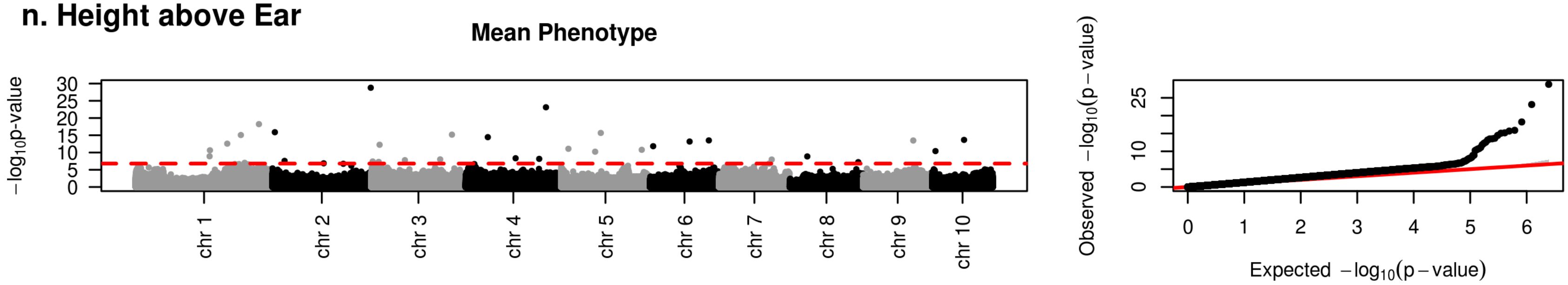


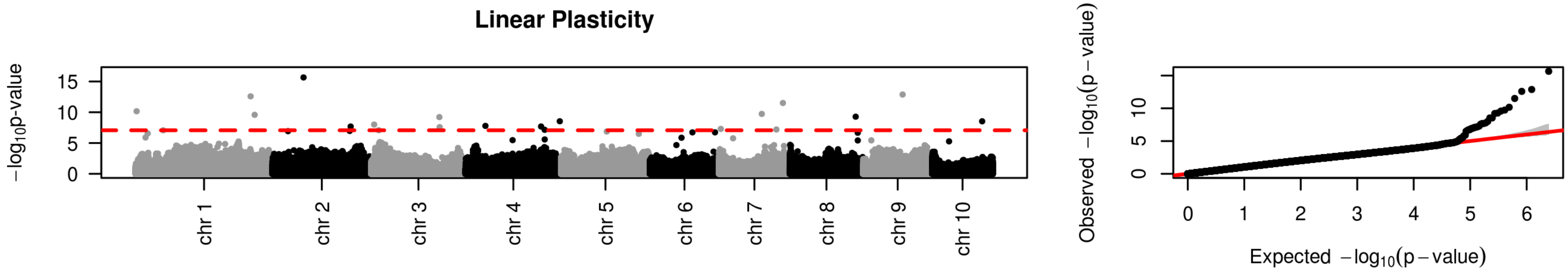
I. GDD Days to Silk

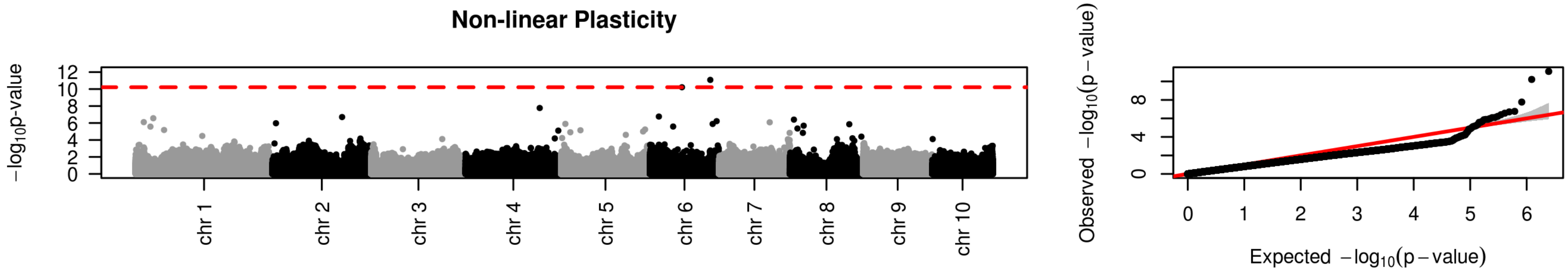



m. GDD Days to Tassel

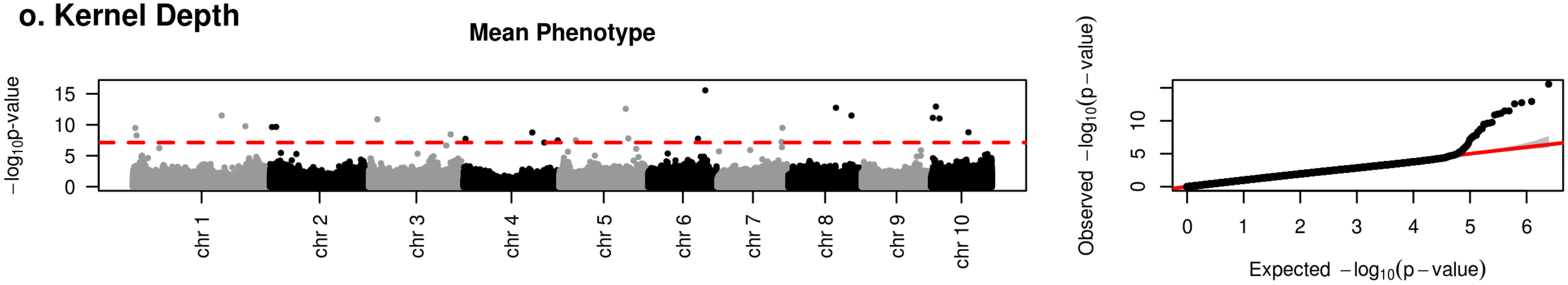
n. Height above Ear


Mean Phenotype

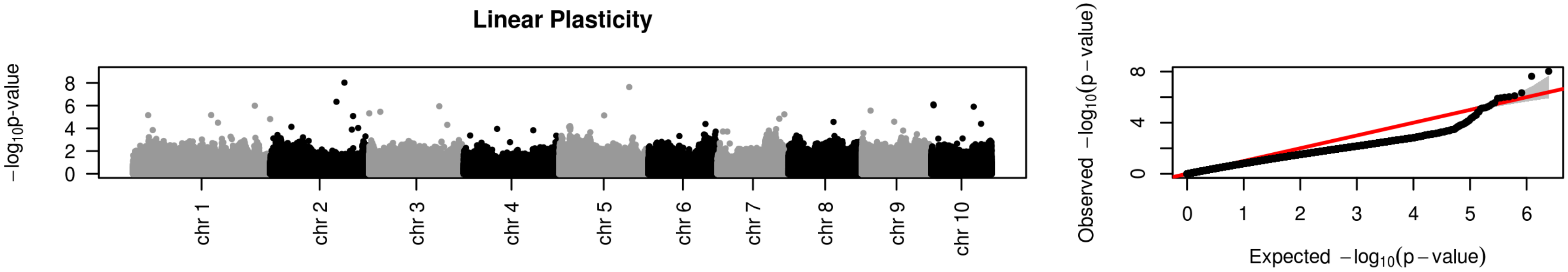

Linear Plasticity


Non-linear Plasticity

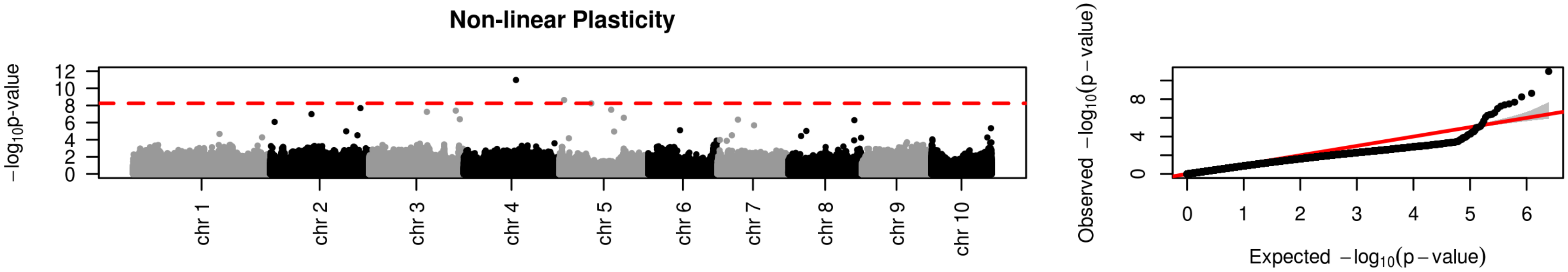
o. Kernel Depth



Mean Phenotype

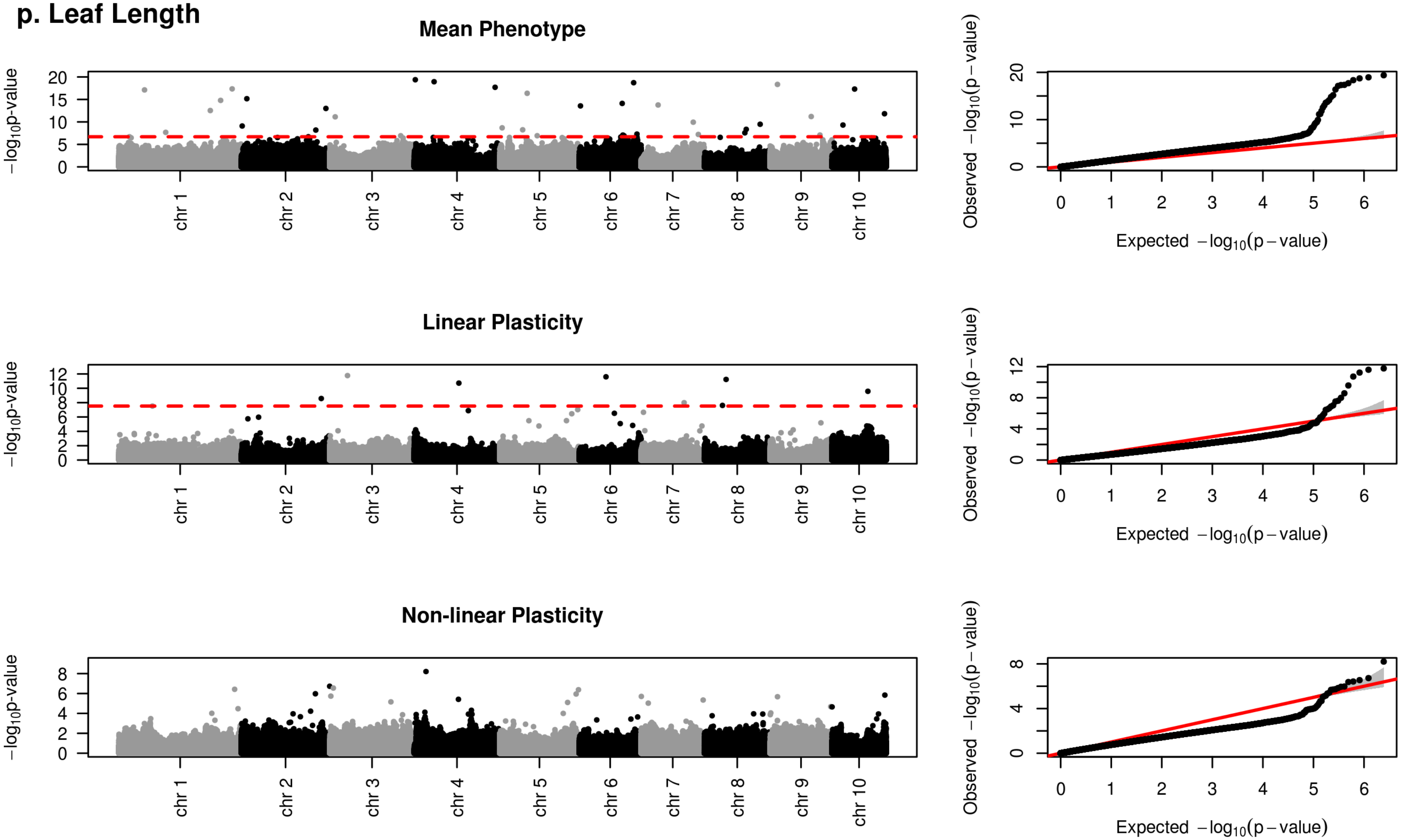


Linear Plasticity

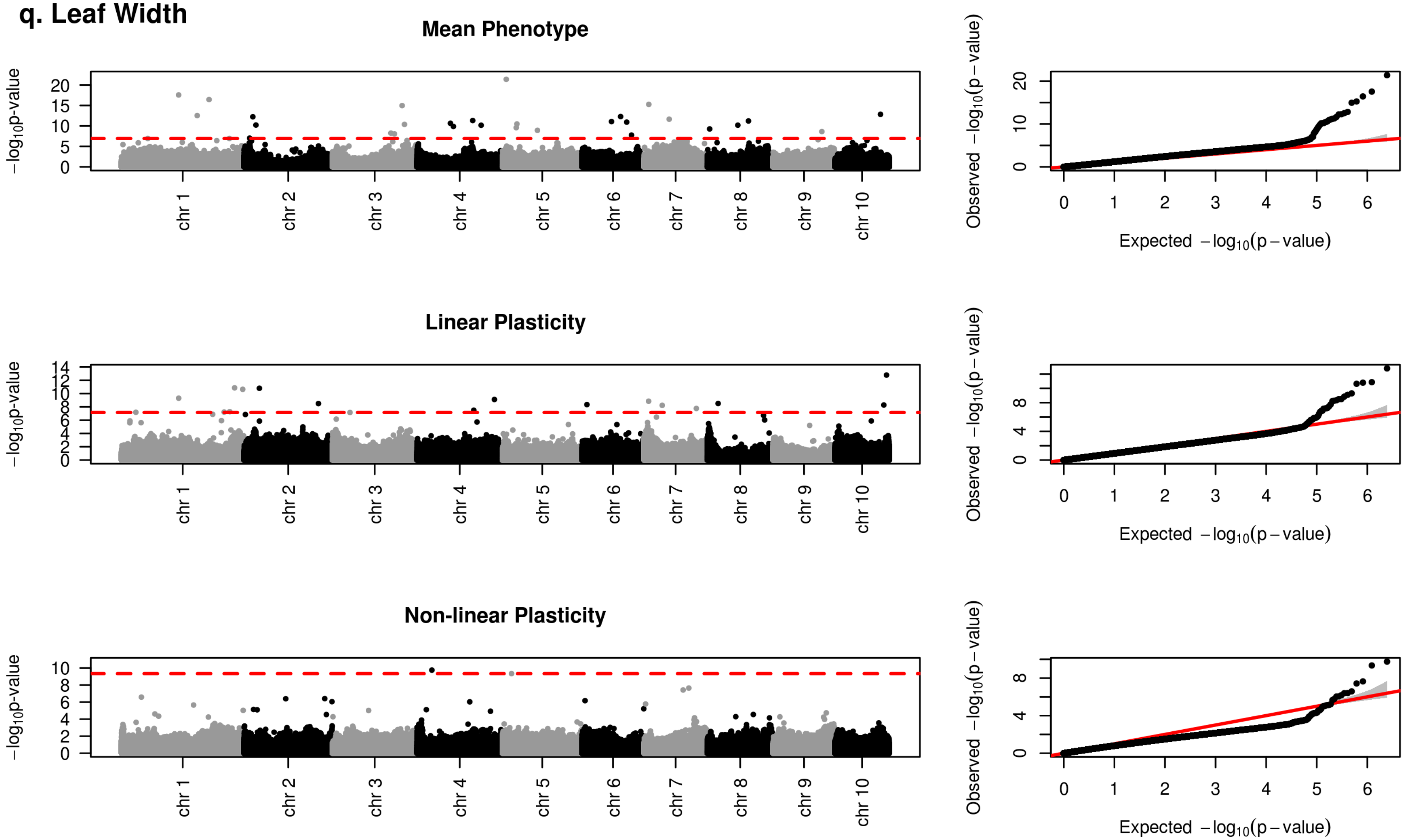


Non-linear Plasticity

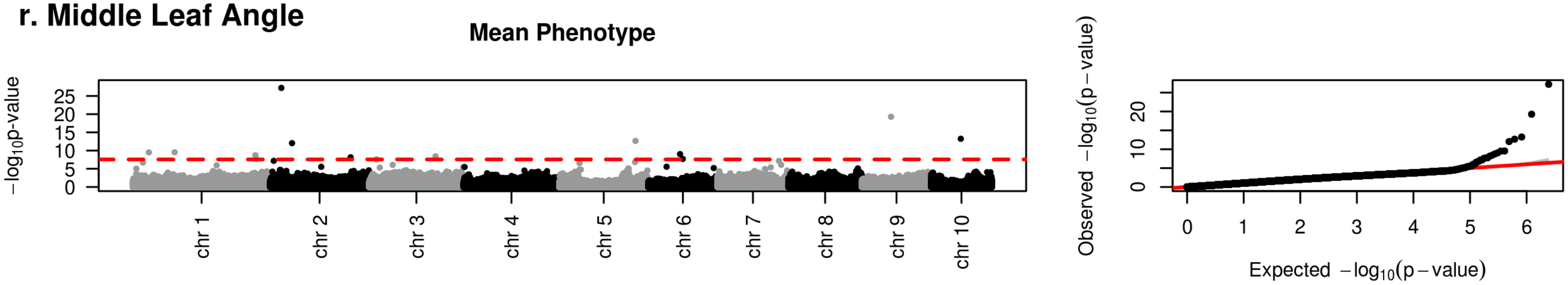
p. Leaf Length

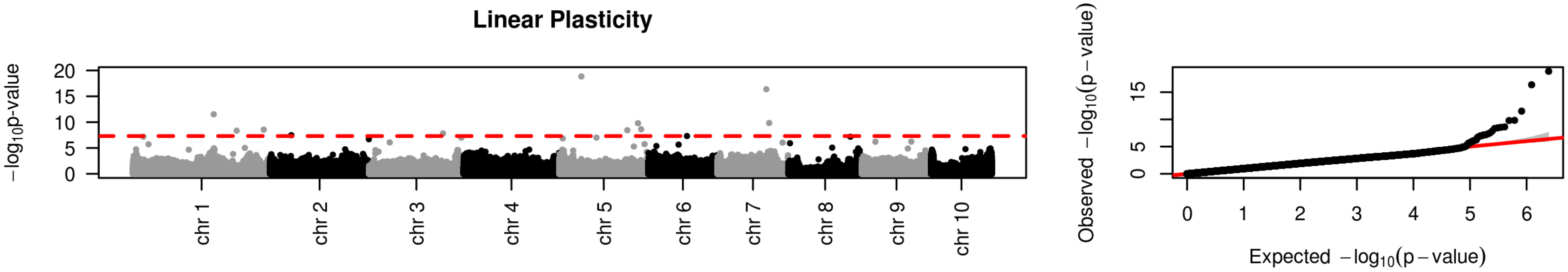


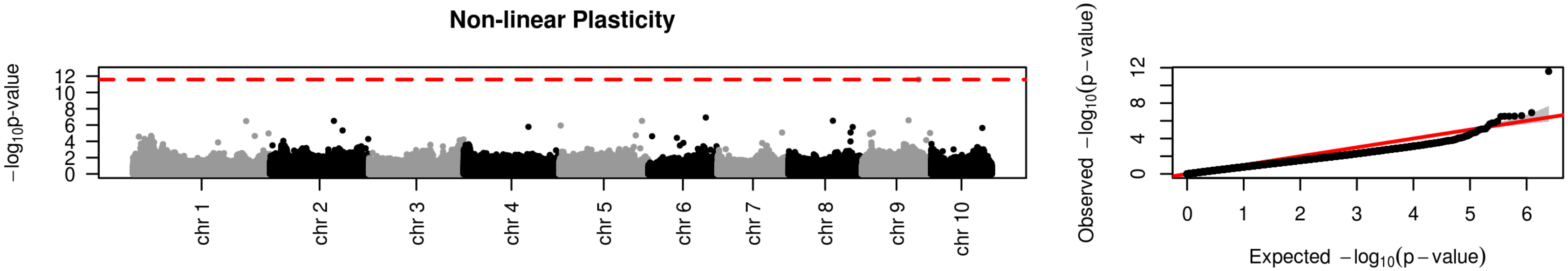
q. Leaf Width


Mean Phenotype
Linear Plasticity
Non-linear Plasticity
$-\log_{10}$p-value
0
5
10
15
20
0
2
4
6
8
10
12
14
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
Observed $-\log_{10}(p-value)$
Expected $-\log_{10}(p-value)$
0
1
2
3
4
5
6

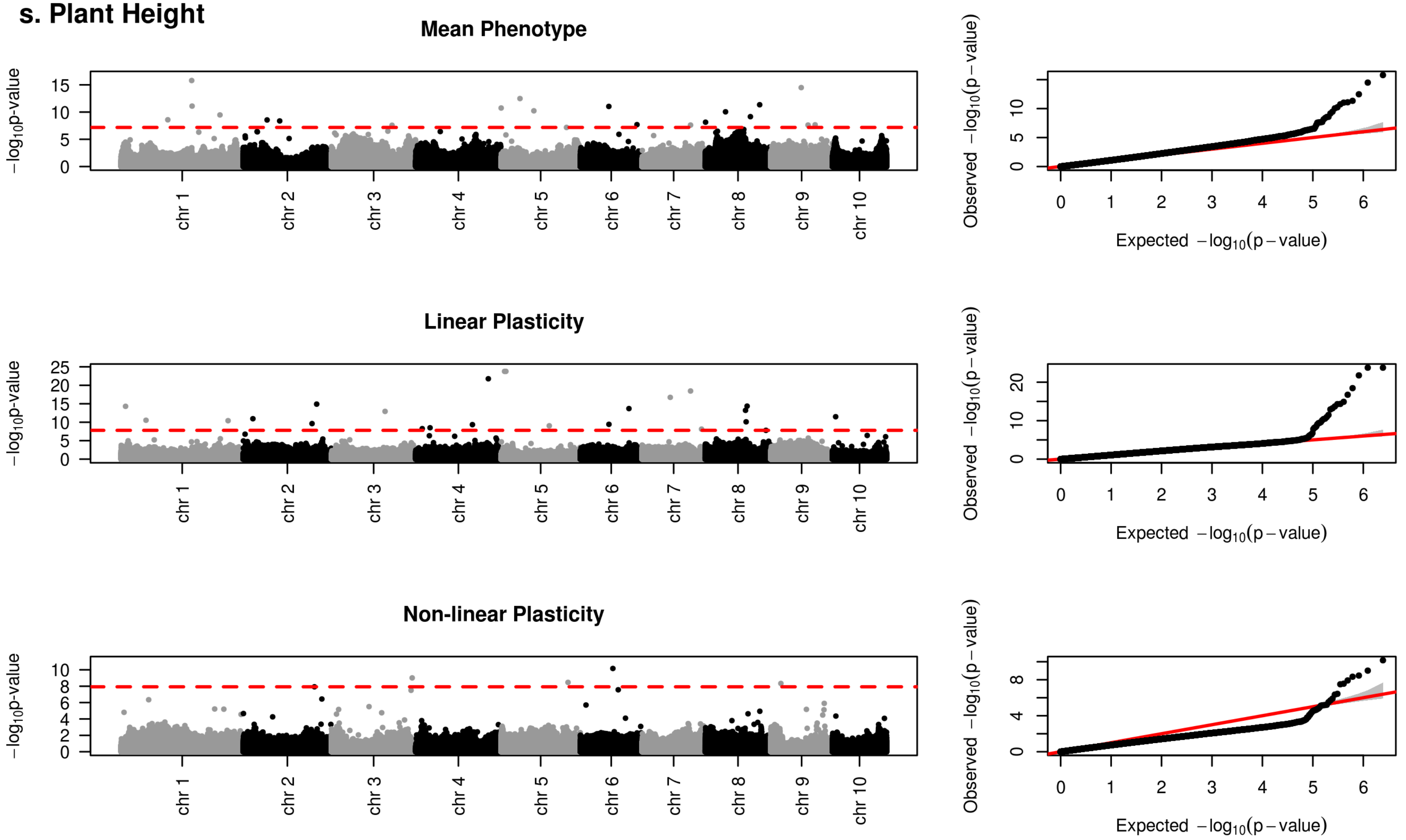
r. Middle Leaf Angle


Mean Phenotype


Linear Plasticity

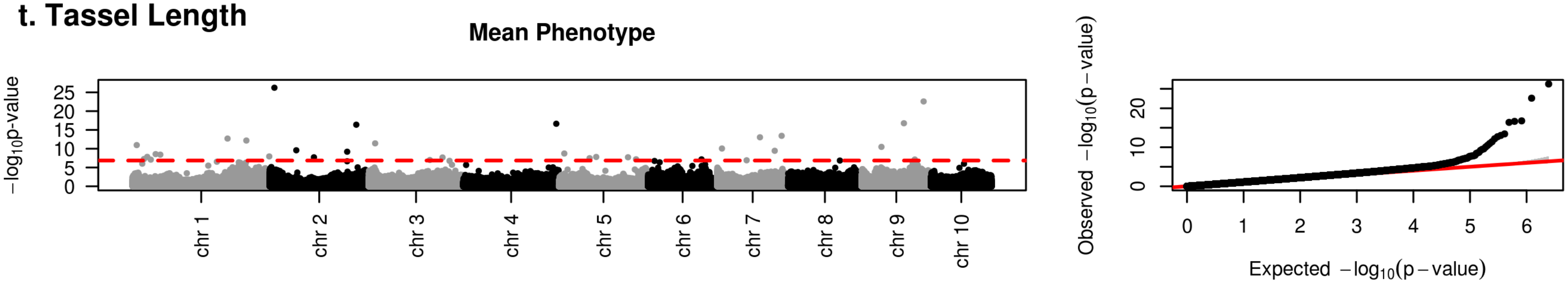

Non-linear Plasticity

s. Plant Height

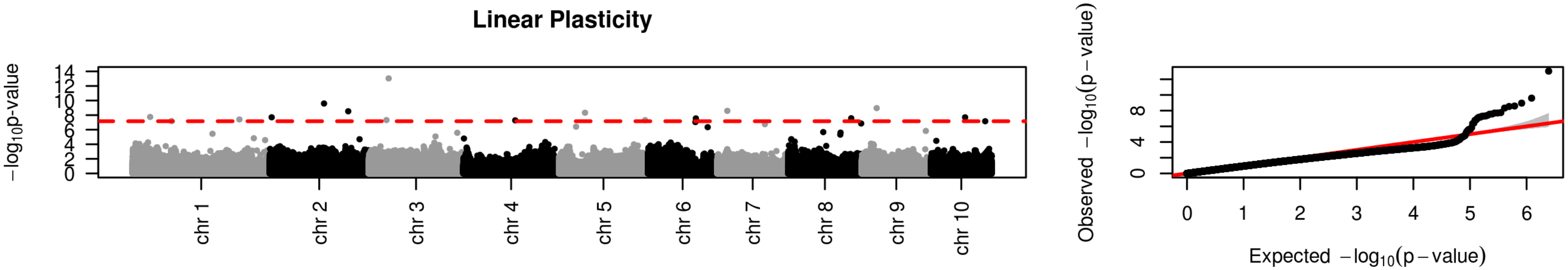


t. Tassel Length

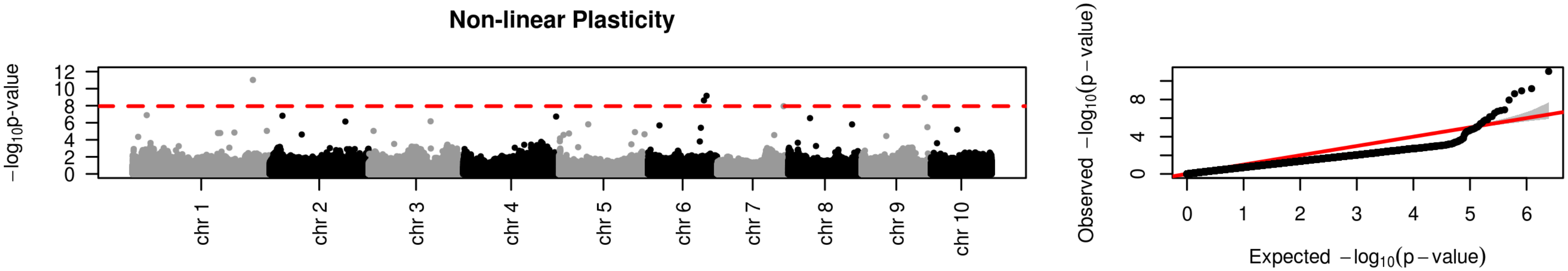
Mean Phenotype



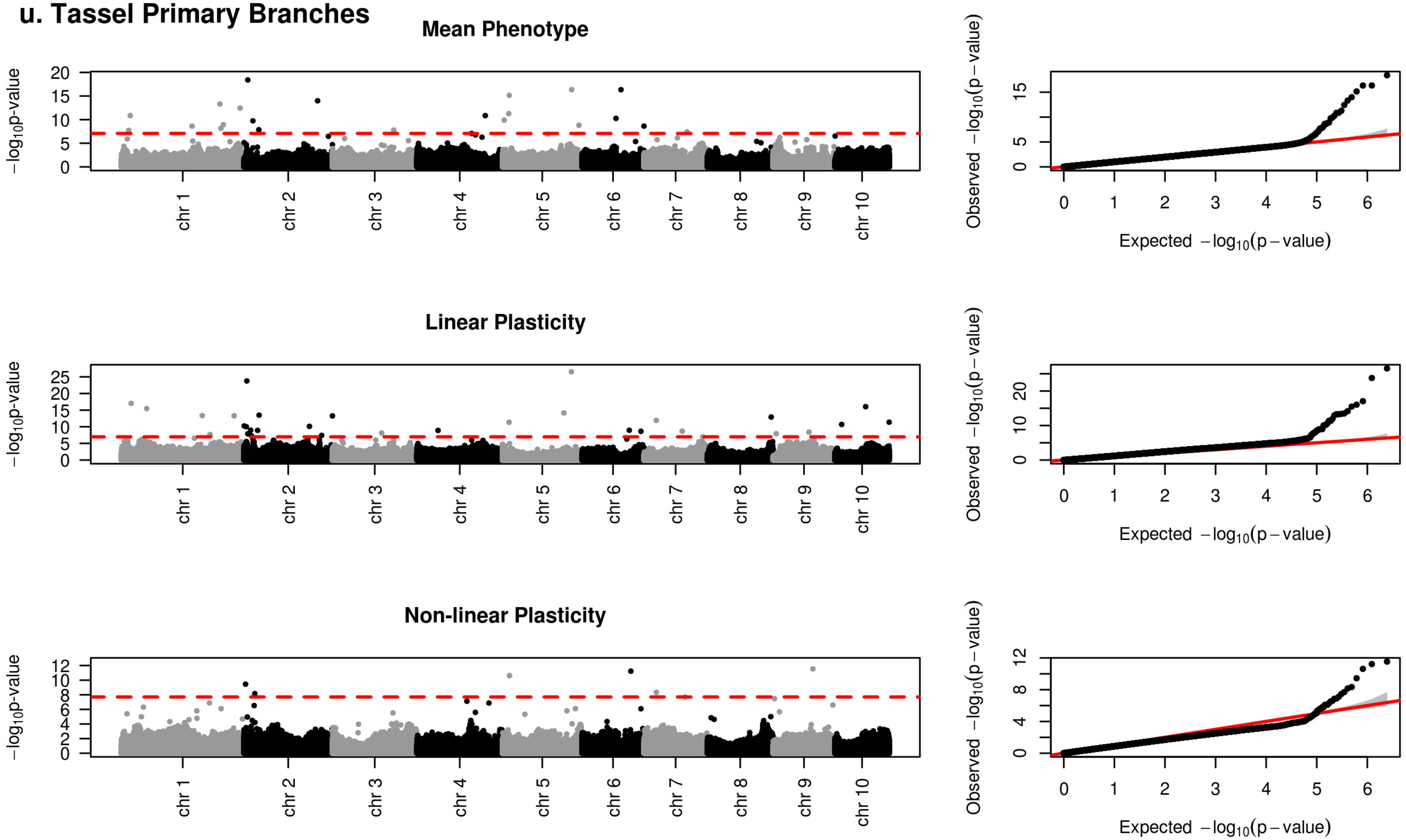
Linear Plasticity



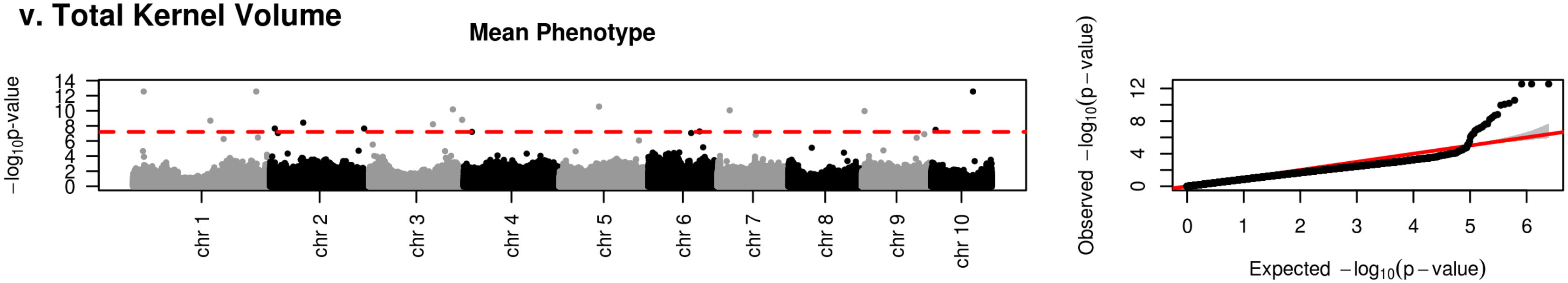
Non-linear Plasticity

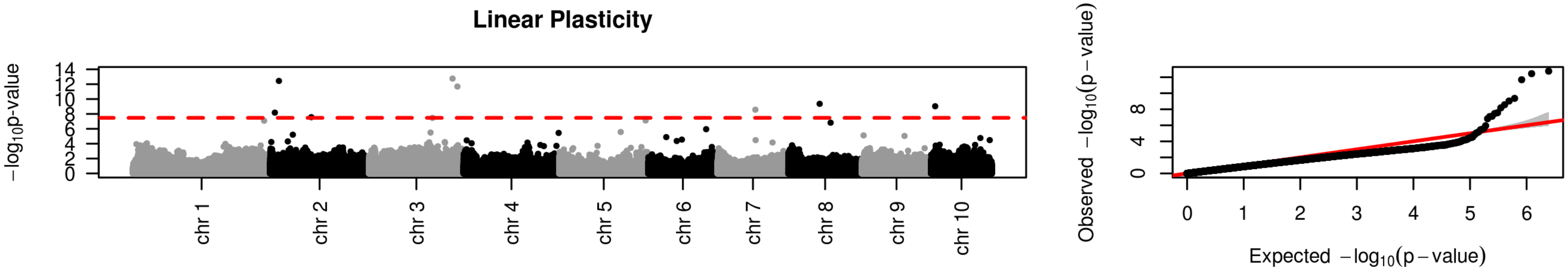


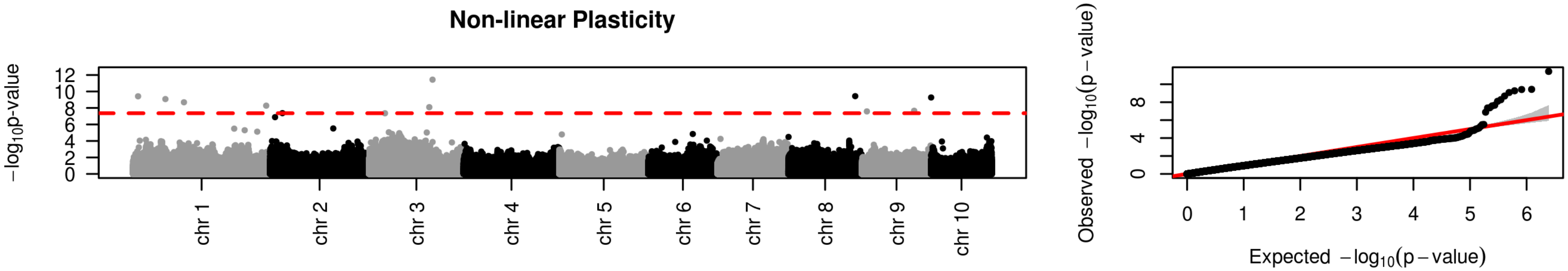
u. Tassel Primary Branches

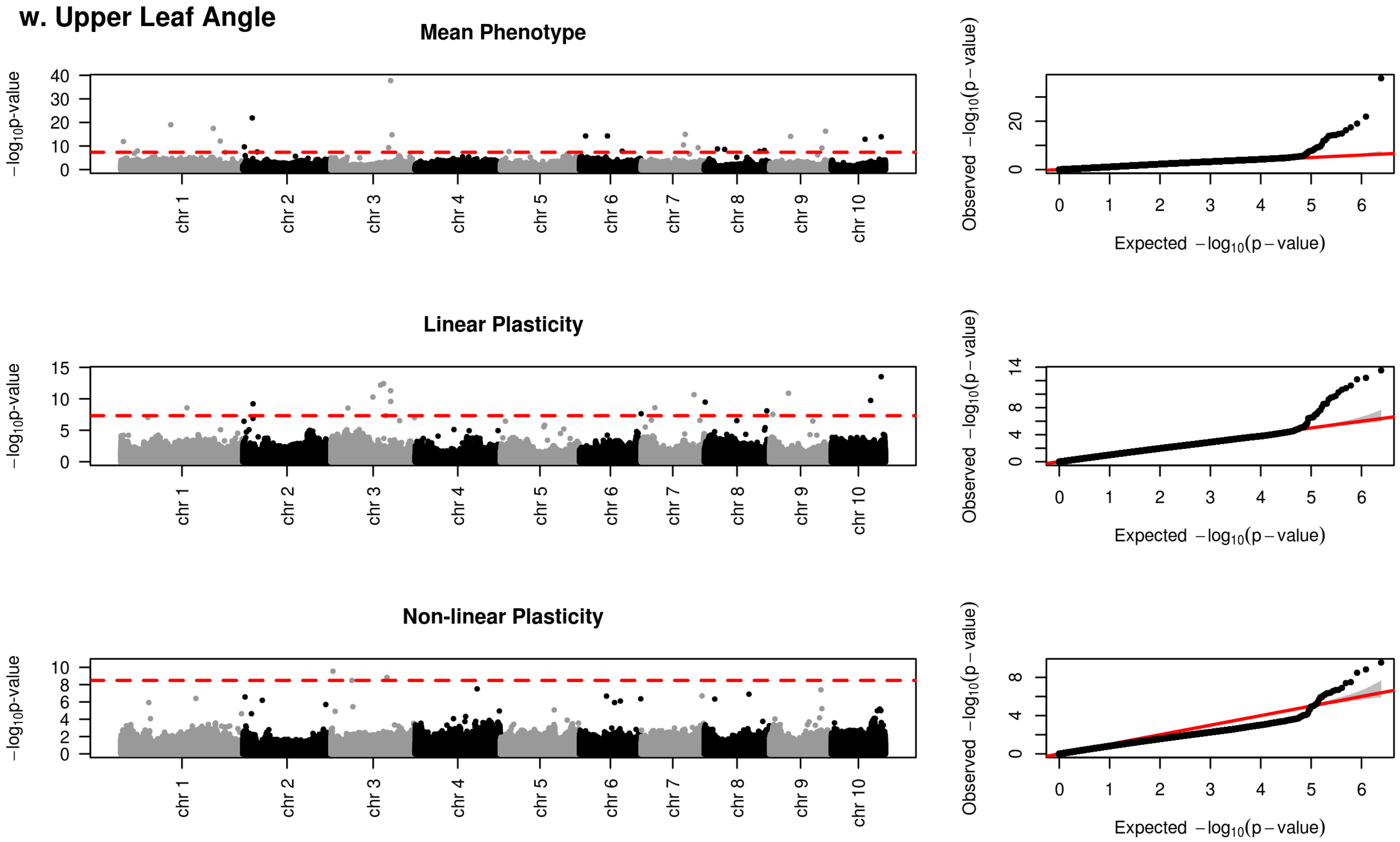


v. Total Kernel Volume

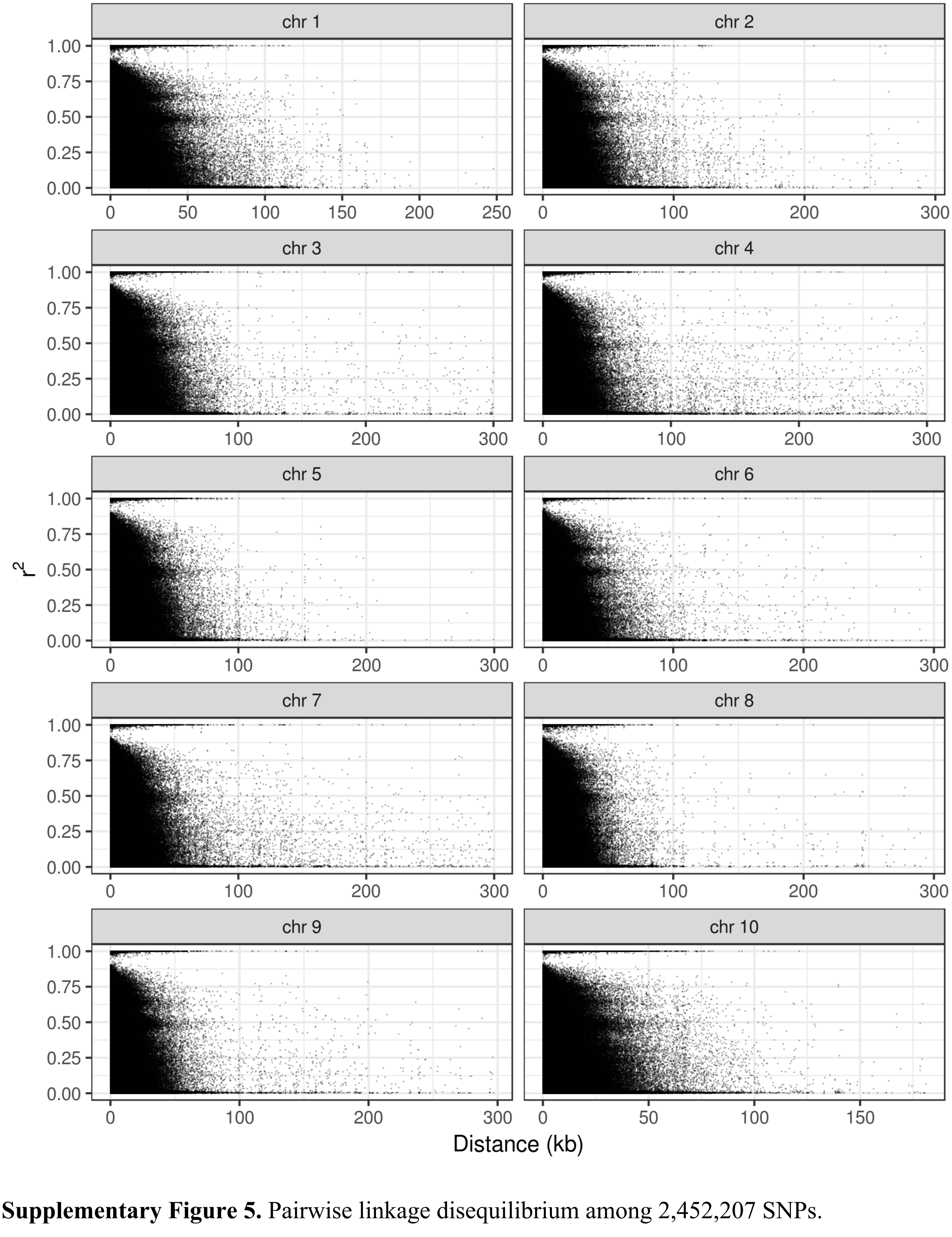




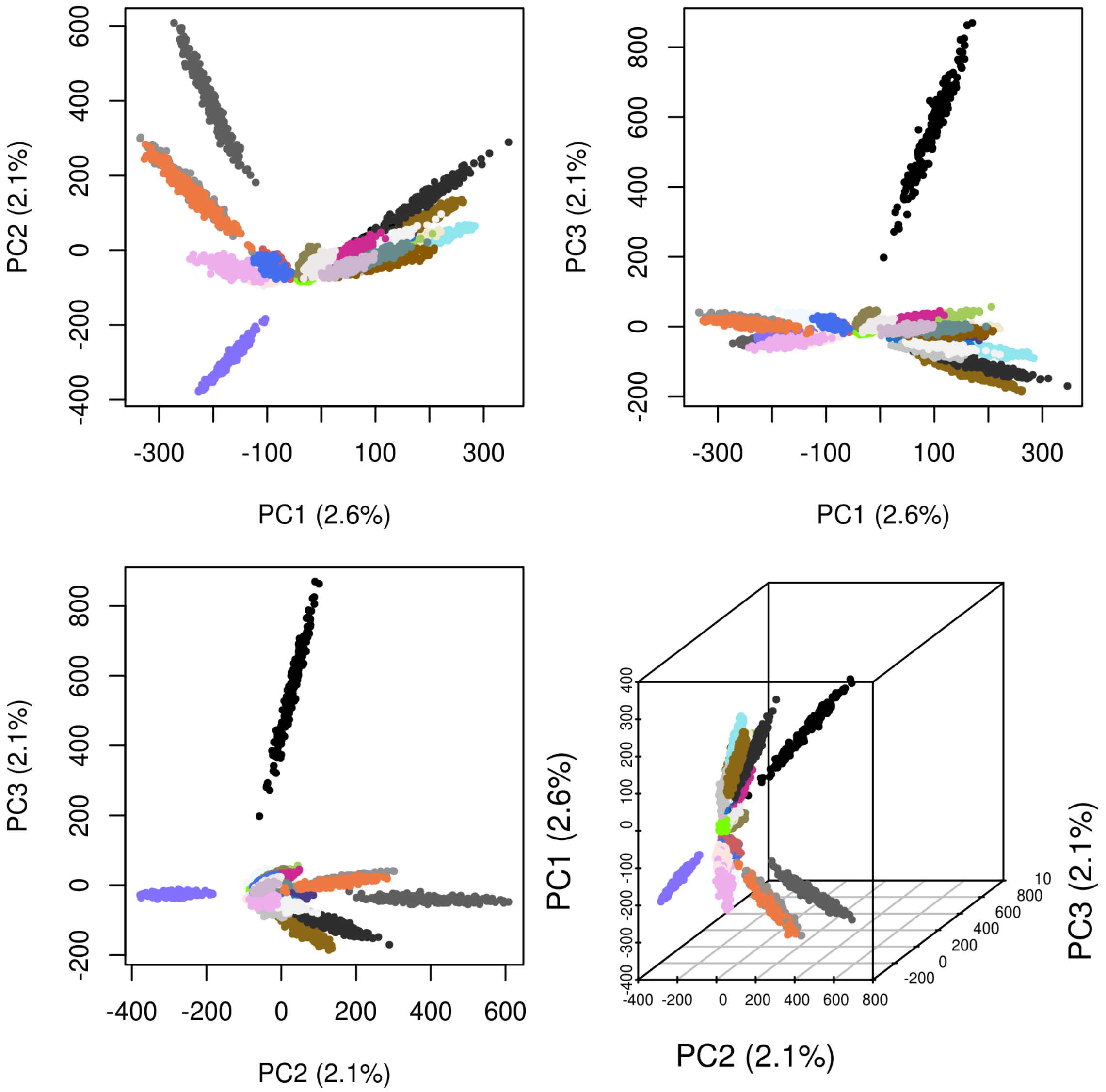




Supplementary Figure 4. Manhattan and QQ plots for the mean phenotype value, linear plasticity, and non-linear plasticity of 23 phenotypes. The red dashed line marks the 1% FDR cutoff. **a.** Cob diameter. **b.** Cob weight. **c.** Days to silk. **d.** Days to tassel. **e.** Ear diameter. **f.** Ear height. **g.** Ear length. **h.** Ear rank number. **i.** Ear row number. **j.** Ear weight. **k.** GDD anthesis silking interval. **l.** GDD to silk. **m.** GDD to tassel. **n.** Height above ear. **o.** Kernel depth. **p.** Leaf length. **q.** Leaf width. **r.** Middle leaf angle. **s.** Plant height. **t.** Tassel length. **u.** Tassel primary branches. **v.** Total kernel volume. **w.** Upper leaf angle.



Supplementary Figure 5. Pairwise linkage disequilibrium among 2,452,207 SNPs.



Supplementary Figure 6. First three principal components of the genotype matrix. Scatterplots of the first three principal components separate RILs into the 25 NAM subpopulations. The first three principal components explain 6.7% of the variation.

SUPPLEMENTARY TABLES

Supplementary Table 1. Phenotypes included in this study from Panzea. N_E is the maximum number of environments in which the phenotype was measured. N_G is the number of RILs for which the phenotype was measured in at least three environments. Papers in the reference column have previously published GWAS results on these mean phenotype values.

Phenotype	N_E	N_G	Total Observations	Reference
Cob diameter	8	4,859	29,413	Brown *et al.*[2]
Cob weight	8	4,858	29,515	-
Days to silk	10	4,881	41,091	Buckler *et al.*[3]
Days to tassel	10	4,884	40,677	Buckler *et al.*[3]; Peiffer *et al.*[4]
Ear diameter	8	4,826	28,750	-
Ear height	11	4,887	43,459	Peiffer *et al.*[4]
Ear length	8	4,859	29,707	Brown *et al.*[2]
Ear rank number	7	4,672	21,914	-
Ear row number	8	4,824	28,059	Brown *et al.*[2]
Ear weight	8	4,803	28,336	-
GDD anthesis-silking interval	11	4,888	41,735	Hung *et al.*[5]
GDD days to silk	10	4,890	38,221	Hung *et al.*[5]
GDD days to tassel	11	4,889	41,629	Hung *et al.*[5]
Height above ear	11	4,887	40,907	Peiffer *et al.*[4]
Kernel depth	8	4,819	26,655	-
Leaf length	9	4,888	39,002	Tian *et al.*[6]
Leaf width	9	4,890	39,039	Tian *et al.*[6]
Middle leaf angle	7	4,365	16,204	-
Plant height	11	4,890	42,608	Peiffer *et al.*[4]
Tassel length	8	4,880	33,149	Brown *et al.*[2]
Tassel primary branches	8	4,865	33,851	Brown *et al.*[2]
Total kernel volume	5	4,307	16,789	-
Upper leaf angle	9	4,870	35,590	Tian *et al.*[6]

SUPPLEMENTARY REFERENCES

1. Yan, J. *et al.* Genetic characterization and linkage disequilibrium estimation of a global maize collection using SNP markers. *PLoS One* **4,** e8451 (2009).
2. Brown, P. J. *et al.* Distinct genetic architectures for male and female inflorescence traits of maize. *PLoS Genet.* **7,** e1002383 (2011).
3. Buckler, E. S. *et al.* The genetic architecture of maize flowering time. *Science (80-.).* **325,** 714–718 (2009).
4. Peiffer, J. A. *et al.* The genetic architecture of maize height. *Genetics* **196,** 1337–56 (2014).
5. Hung, H.-Y. *et al.* The relationship between parental genetic or phenotypic divergence and progeny variation in the maize nested association mapping population. *Heredity (Edinb).* **108,** 490–9 (2012).
6. Tian, F. *et al.* Genome-wide association study of leaf architecture in the maize nested association mapping population. *Nat. Genet.* **43,** 159–162 (2011).