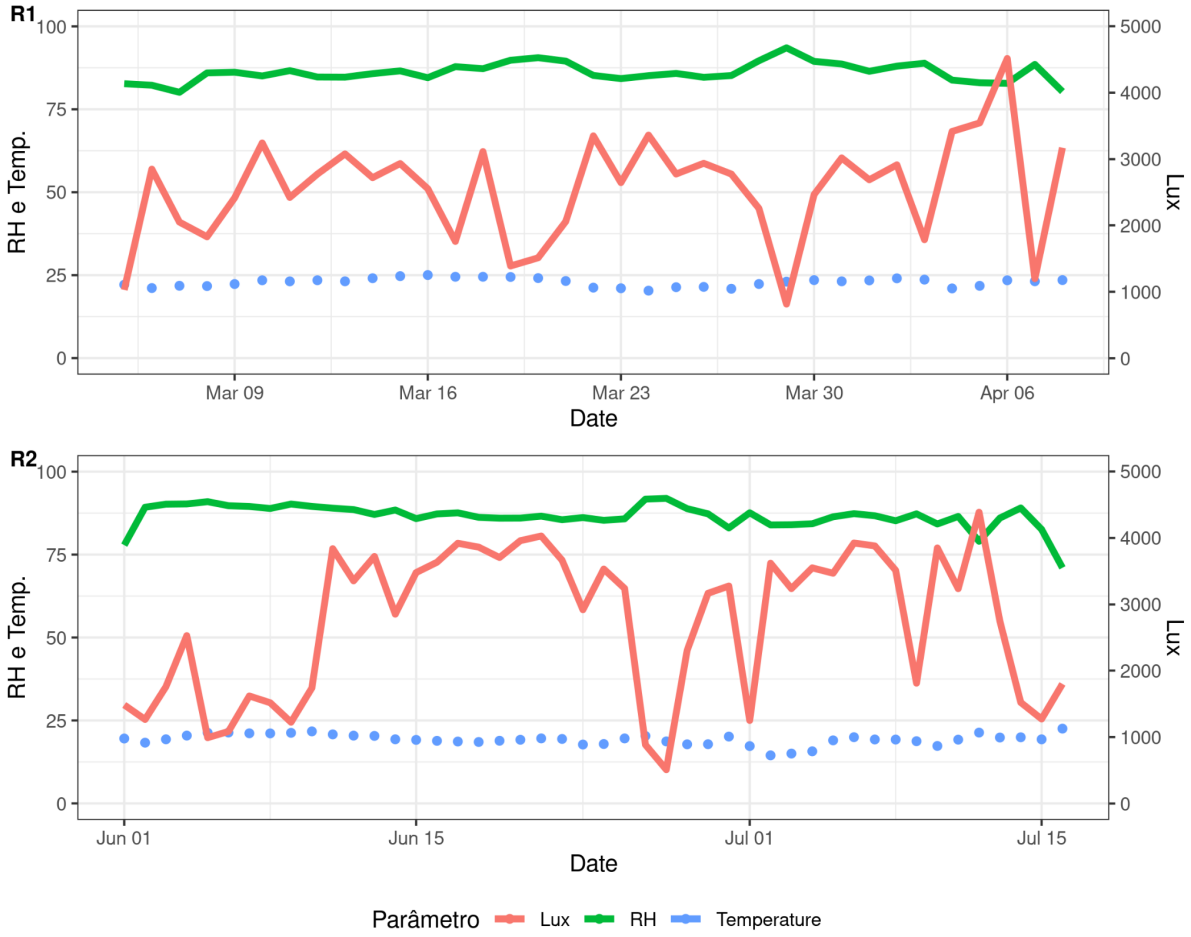
SUPPLEMENTARY MATERIAL



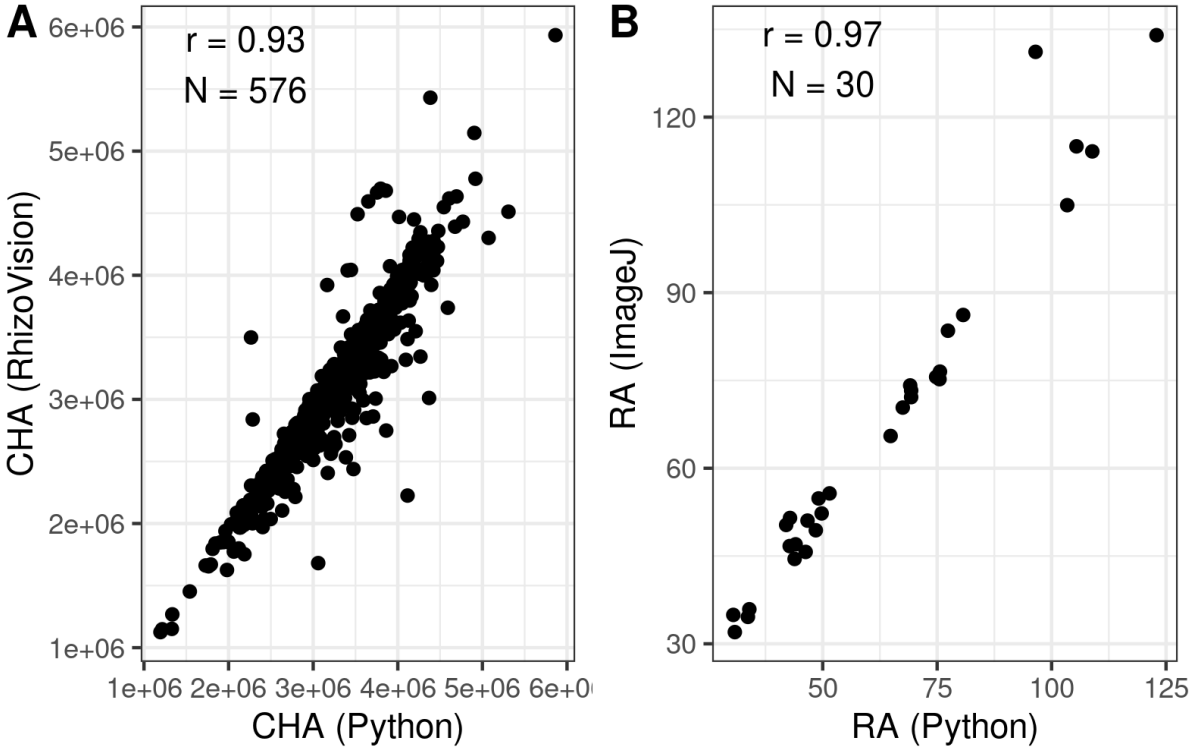
Supplemental Figure 1. Summary of environmental data (average of the day for temperature (T, Cº), relative humidity (RH, %), and lux for both replicates (R1 and R2).

Supplementary Table 1. Summary of soil analysis.

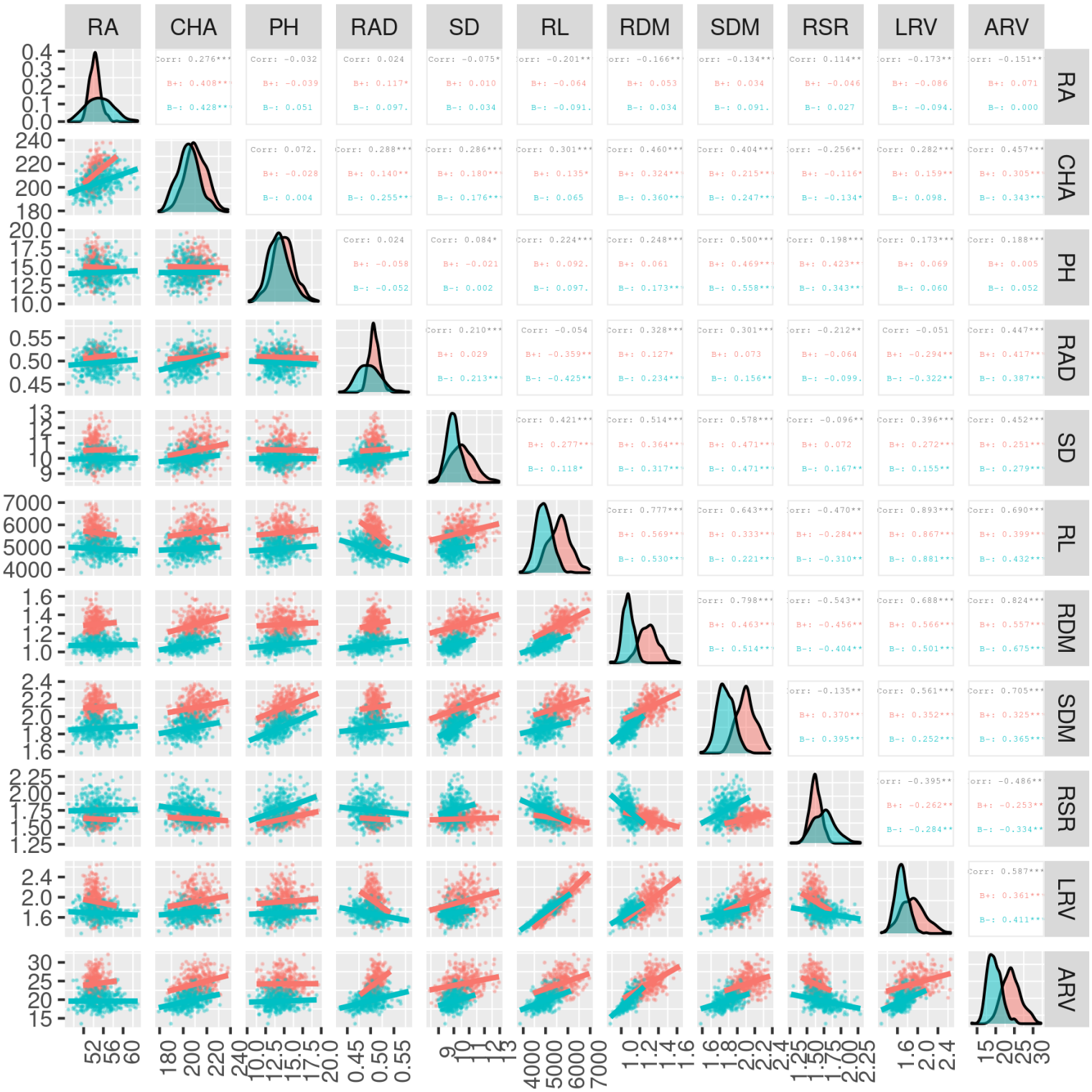
Rep	Soil physic analysis			Micronutrients				
	Sand	Silt	Clay	B	Cu	Fe	Mn	Zn
		g kg^{-3}				mg dm^{-3}		
1	191	175	635	0.04	0.2	2	0.8	0.1
2	277	21	702	0.04	0.9	3	1.3	0.6

Rep	Macronutrients								
	pH CaCl2	O.M.*	P	S	K	Ca	Mg	Al	H+AL
		g dm^{-3}	mg dm^{-3}		mmolc dm^{-3}				
1	5.1	4	<3	11	<0.9	4	3	<0.02	18
2	5.7	<1	14	110	<0.9	13	10	<0.02	13

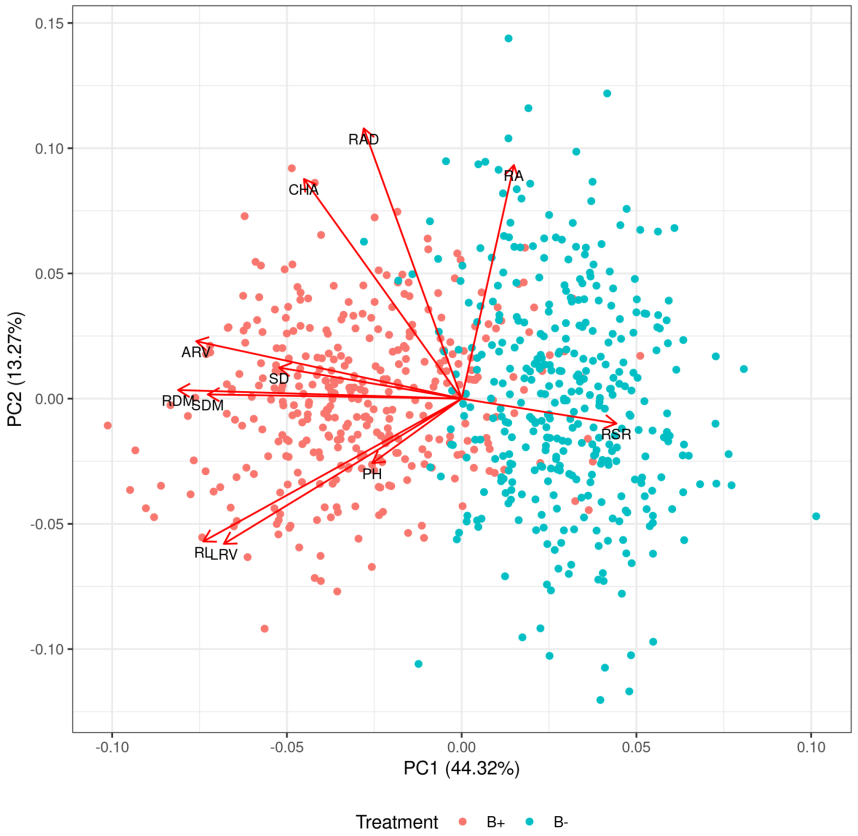
* Organic matter



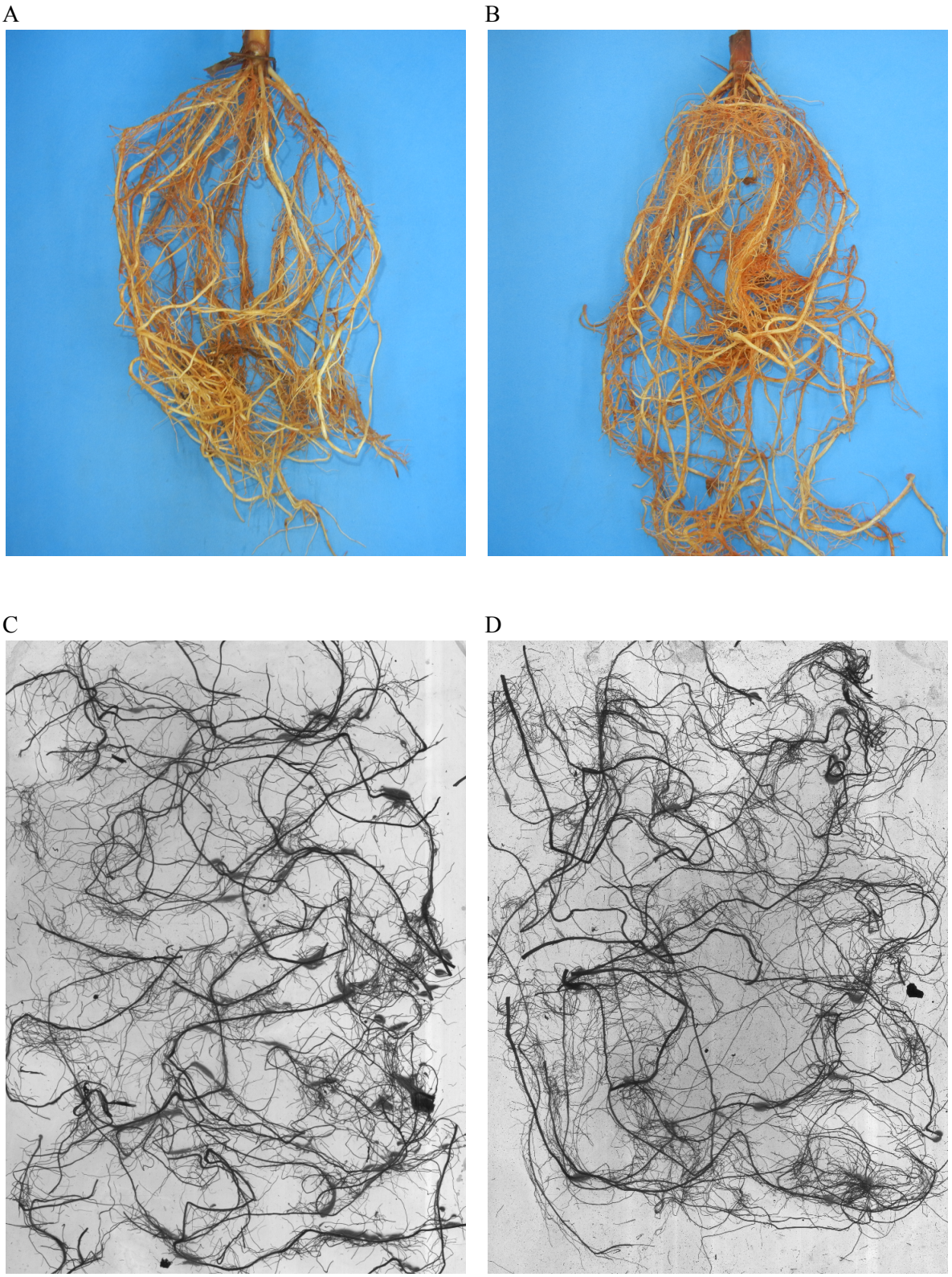
Supplemental Figure 2. Validation of the trait extraction pipeline. A. Correlation between Convex Hull Area (CHA) calculated using the software RhizoVision Explorer and the Python pipeline. B. Correlation between root angle obtained by ImageJ and the Python pipeline.



Supplementary figure 3. A. Correlation and exploratory analysis for phenotypic data considering 360 genotypes inoculate (B+) and no inoculate (B-) with PGPB in red and blue, respectively.



Supplementary figure 4. Principal components analysis using 11 phenotypic traits and 360 genotypes with (B+) and without (B-) inoculation with PGPB.



Supplementary figure 5. Representative images of root phenotypes for B+ (B, D) and B- (A,C) treatments for Convex Hull Area and Root angle (A,B) and WinRHIZO related traits (C,D).

Supplementary table 2. Wald test of fixed effects, likelihood ratio test (LRT) of random effects, and heritability for several traits in tropical maize

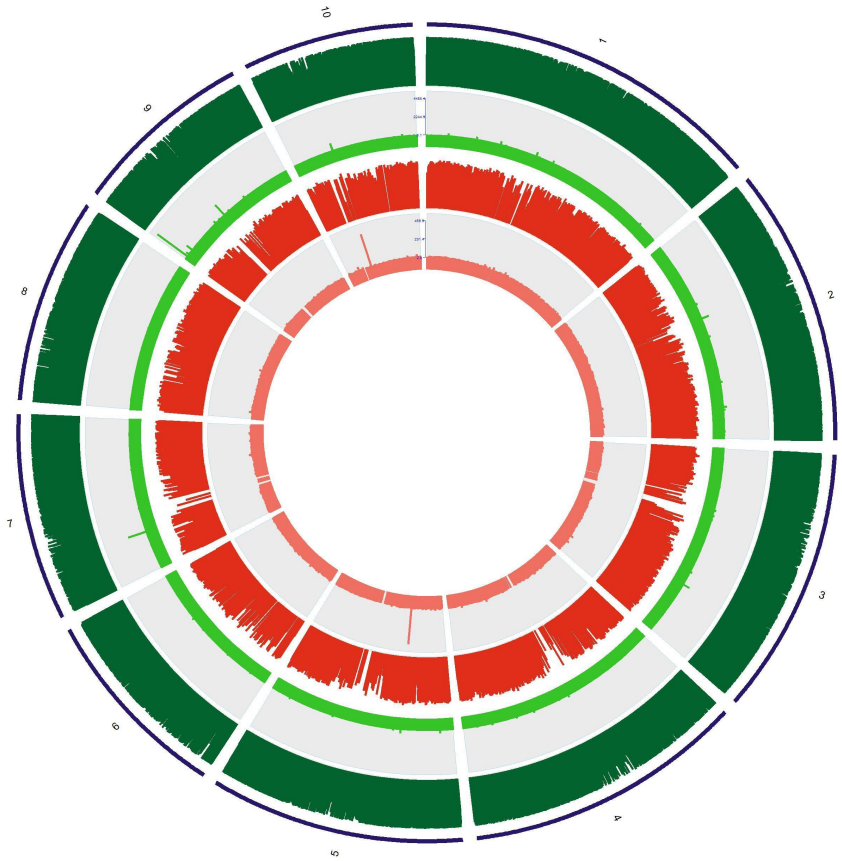
Variation factor	PH		SD		RDM		SDM		RSR	
Fixed effect					Wald statistic					
Treatment	51.52	***	75.29	***	140.82	***	60.76	***	26.94	***
Random effects					LRT					
Gen	154.33	***	104.30	***	41.25	***	28.51	***	38.9	***
Gen*Treat	0.42	ns	0	ns	0	ns	0	ns	0.38	ns
Rep	11.53	***	9.76	***	14.79	***	23.76	***	1.63	ns
Block	59.37	***	63.54	***	24.94	***	5.77	***	25.75	***

*** P < 0.001 by LRT or Wald test.
** P < 0.05 by LRT or Wald test.

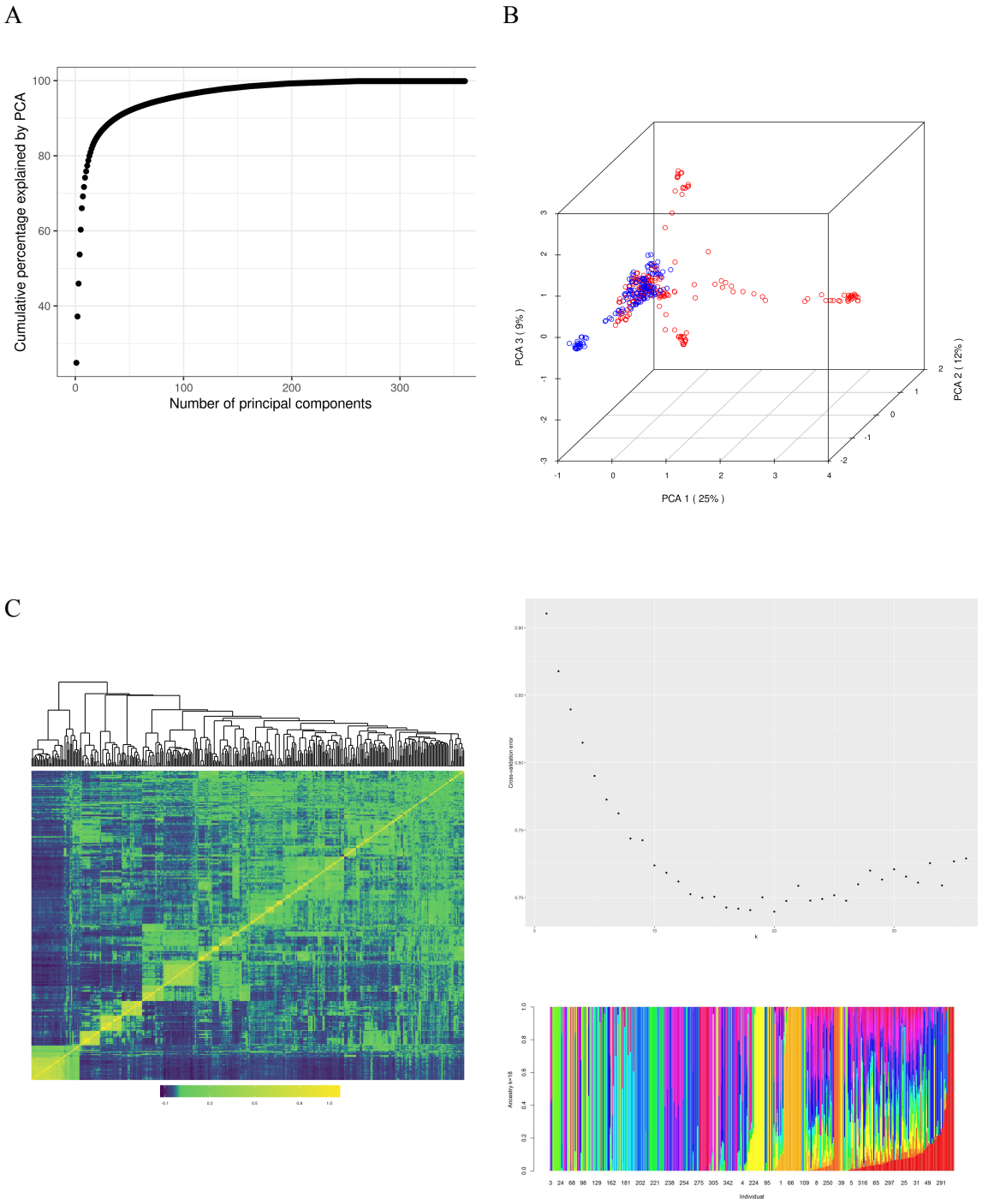
Supplementary table 2. (continued) Wald test of fixed effects, and likelihood ratio test (LRT) of random effects for several traits in tropical maize

Variation factor	RL		RAD		LRV		ARL		RA		CHA	
Fixed effect						Wald statistic						
Treatment	86.06	***	4.11	***	83.17	***	109.86	***	0.76	ns	10.6	***
Random effects						LRT						
Gen	25.91	***	24.97	***	75.13	***	24.1	***	13.54	***	28.96	***
Gen*Treat	0.13	ns	0.22	ns	0	ns	0.42	ns	0.05	ns	0	ns
Rep	1.71	ns	0.7	ns	2.52	ns	7.58	***	7.26	***	26.41	***
Block	61.52	***	16.13	***	32.18	***	27.28	***	5.15	***	0	***

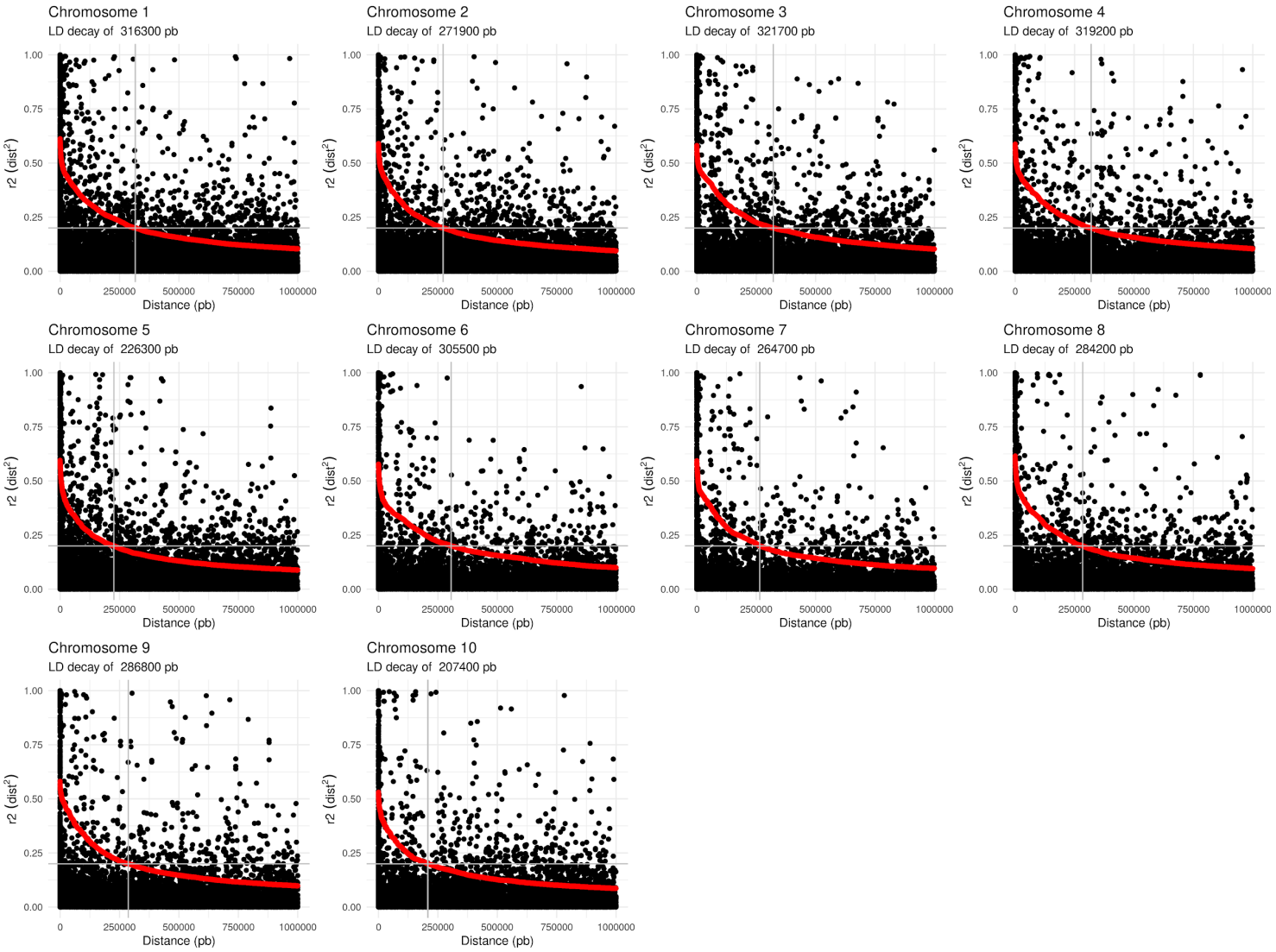
*** P < 0.01 by LRT or Wald test.
ns Non significant



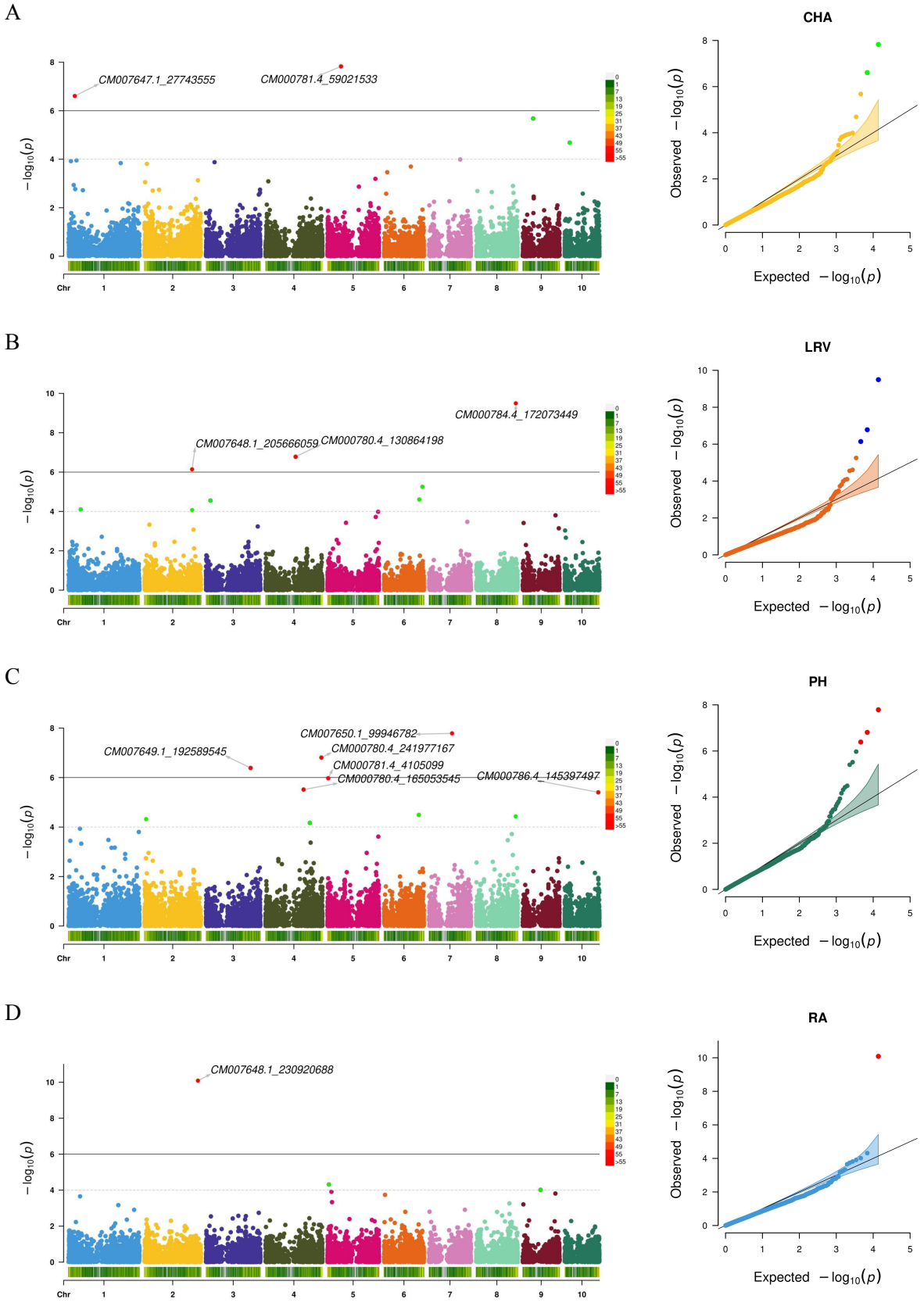
Supplementary figure 6. Genomic circle representing the covered and depth of the genotyping data. Each segmentation represents a chromosome. From outside to inside layers, the plot is divided in five layers: *i)* Chromosomes, *ii)* Number of alleles in the raw data of the SNPs distributed in the genome, *iii)* Mean depth per SNP in the raw data, *iv)* Number of alleles in the filtered data of the SNPs distributed in the genome, *v)* Mean depth per SNP in the filtered data.



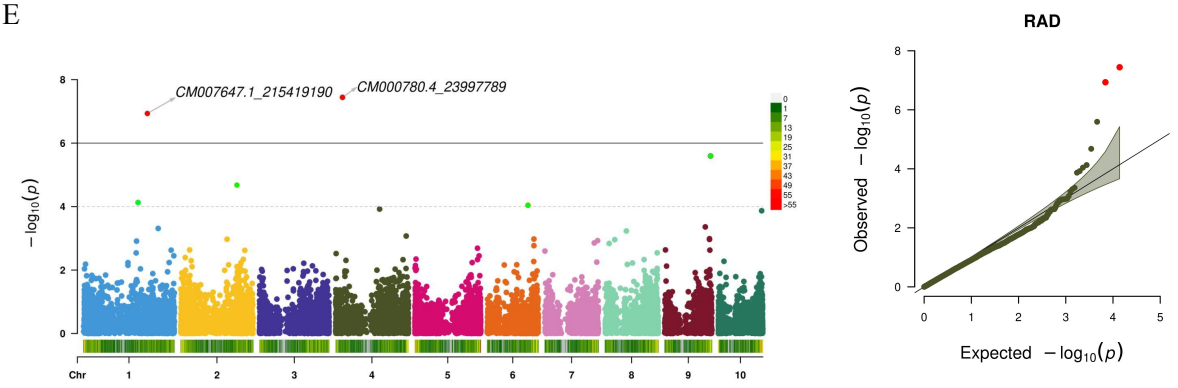
Supplementary figure 7. Population structure of 360 endogamic lines from tropical maize germplasm. A. Cumulative percentage explained by PCA. B. The plot from the first three principal components from Esalq and IAPAR, in blue and red, respectively. C. VanRaden genomic matrix heatmap, clustered by k-means. D. The optimal number of K based on cross-validation is 18, and bar plots indicate assignment probabilities from ADMIXTURE analysis for 360 inbred lines.



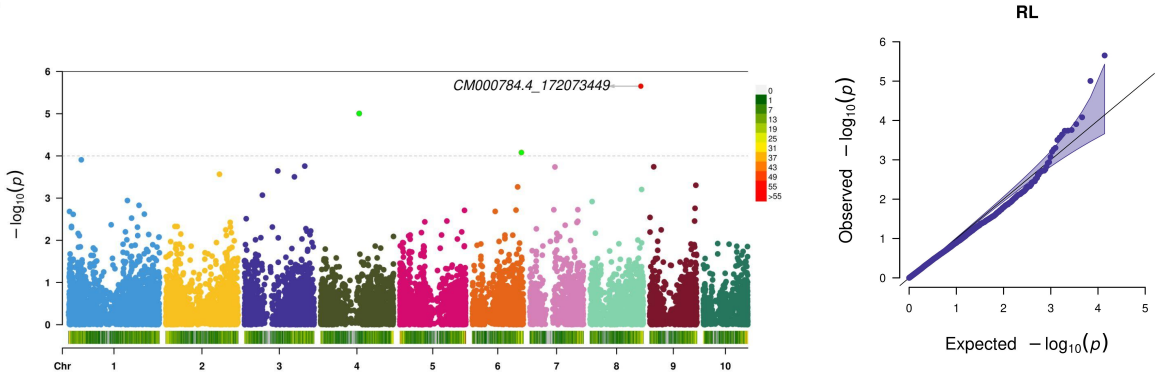
Supplementary figure 8. LD decay by chromosome. The red line shows the mean LD in each 100 bp sliding window, and the intersection between the two black lines represents the decline of LD decay considering $r^2 = 0.2$.


A
CHA
CM007647.1_27743555
CM000781.4_59021533
B
LRV
CM000784.4_172073449
CM007648.1_205666059
CM000780.4_130864198
C
PH
CM007650.1_99946782
CM007649.1_192589545
CM000780.4_241977167
CM000781.4_4105099
CM000780.4_165053545
CM000786.4_145397497
D
RA
CM007648.1_230920688
Chr
$-\log_{10}(p)$
Observed $-\log_{10}(p)$
Expected $-\log_{10}(p)$

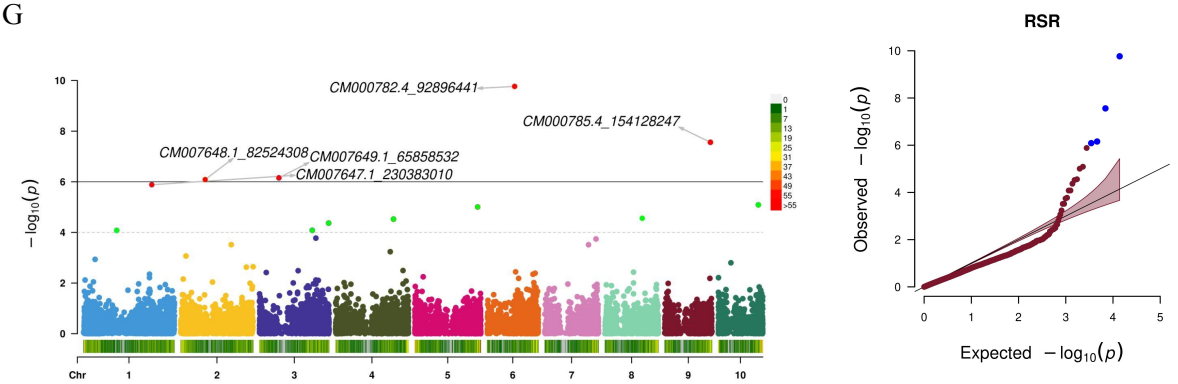
E


CM007647.1_215419190
CM000780.4_23997789
−log10(p)
Chr
RAD
Observed −log10(p)
Expected −log10(p)

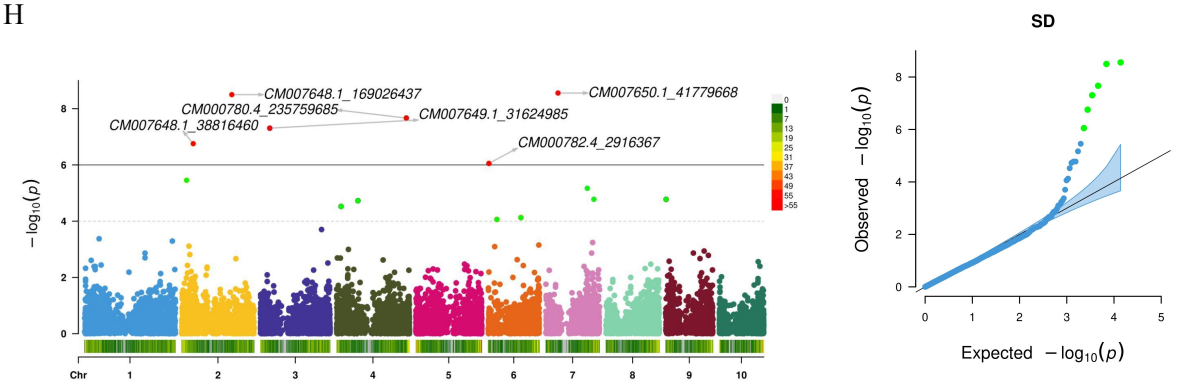
F


CM000784.4_172073449
−log10(p)
Chr
RL
Observed −log10(p)
Expected −log10(p)

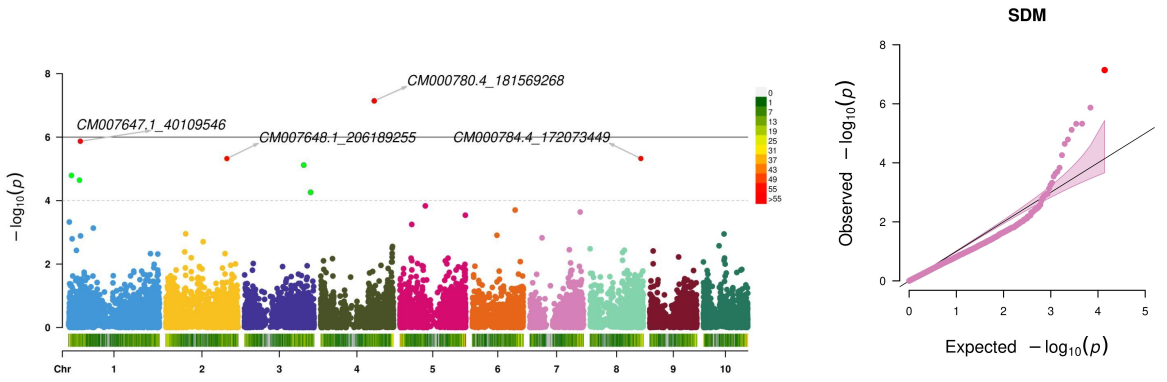
G


CM000782.4_92896441
CM000785.4_154128247
CM007648.1_82524308
CM007649.1_65858532
CM007647.1_230383010
−log10(p)
Chr
RSR
Observed −log10(p)
Expected −log10(p)

H

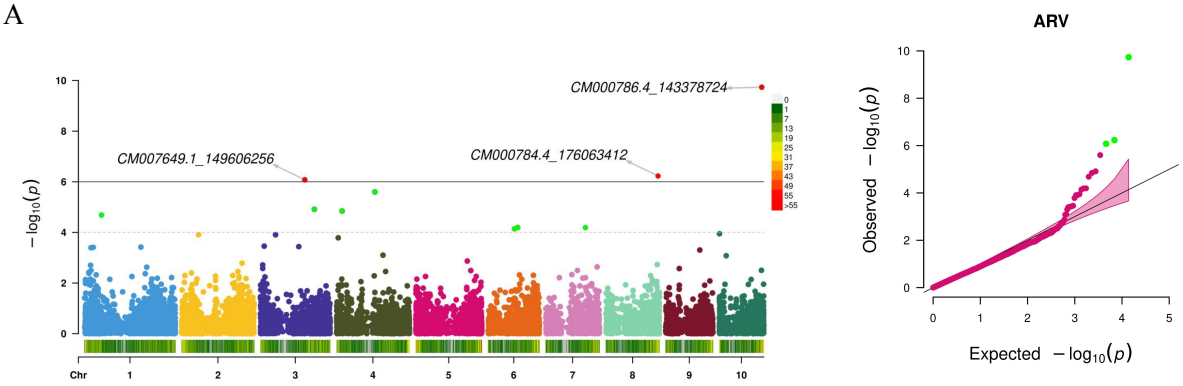

CM007648.1_169026437
CM007650.1_41779668
CM000780.4_235759685
CM007649.1_31624985
CM007648.1_38816460
CM000782.4_2916367
−log10(p)
Chr
SD
Observed −log10(p)
Expected −log10(p)

I

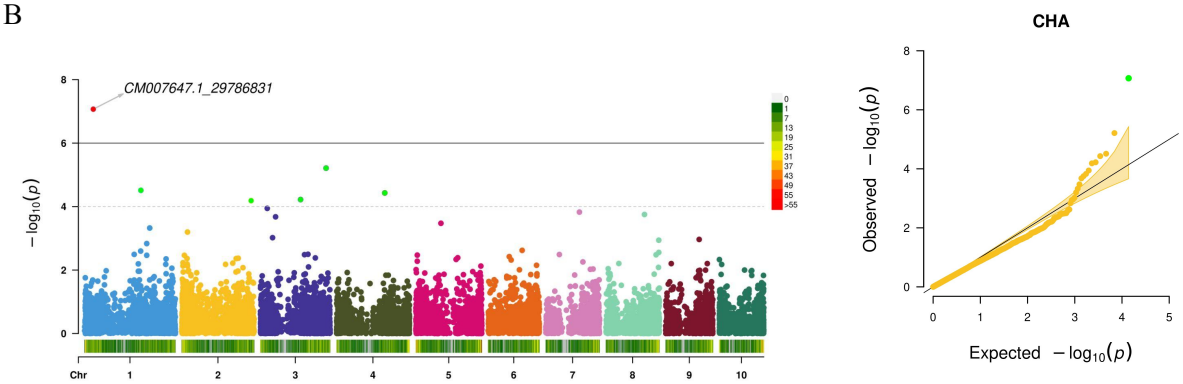


Supplementary figure 9. Manhattan and QQplot plot for the treatment B+ for the triats (A) CHA, (B) LRV, (C) PH, (D) RA, (E) RAD, (F) RL, (G) RSR, (H) SD, and (I) SDM.

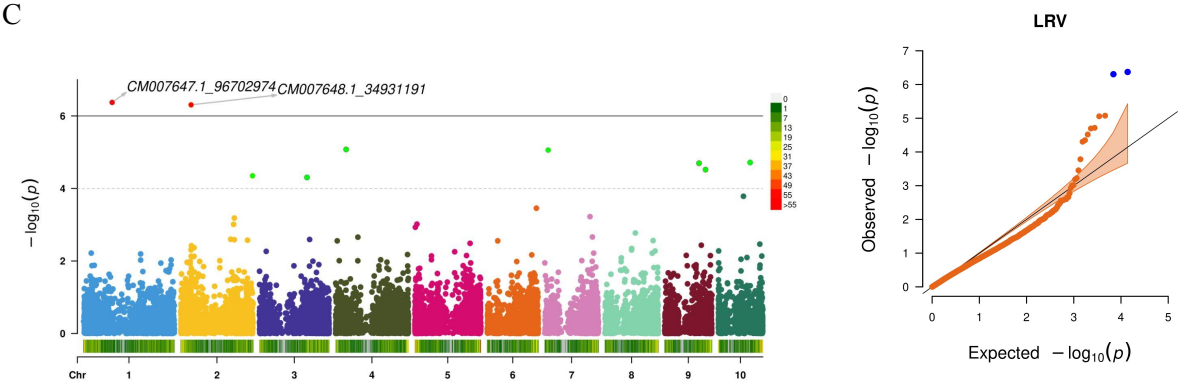
A



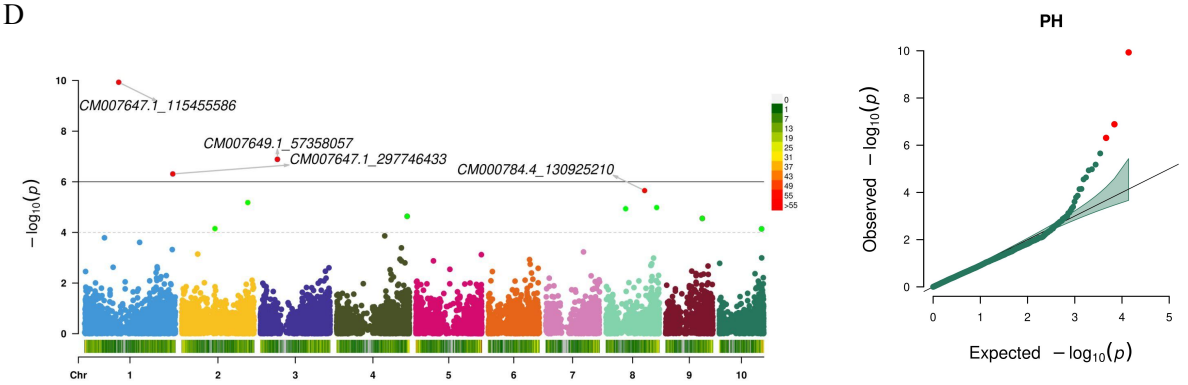
B



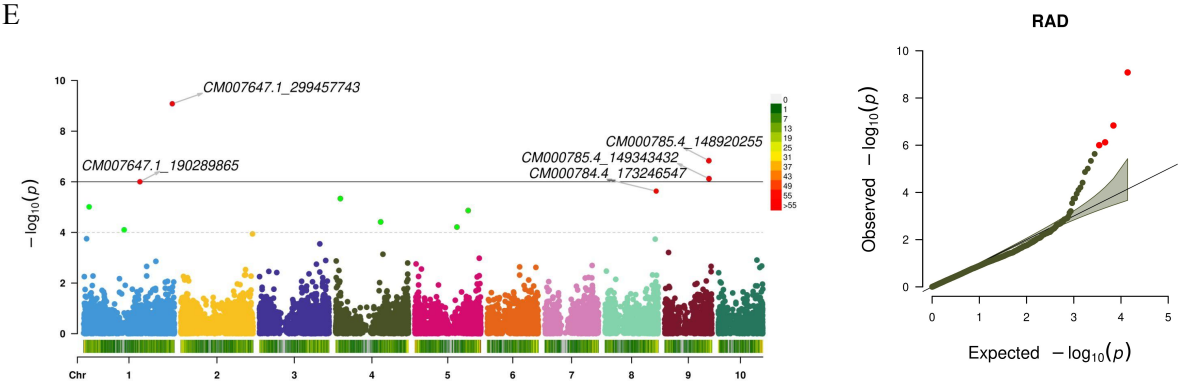
C


CM007647.1_96702974
CM007648.1_34931191
LRV
Observed −log10(p)
Expected −log10(p)
−log10(p)
Chr

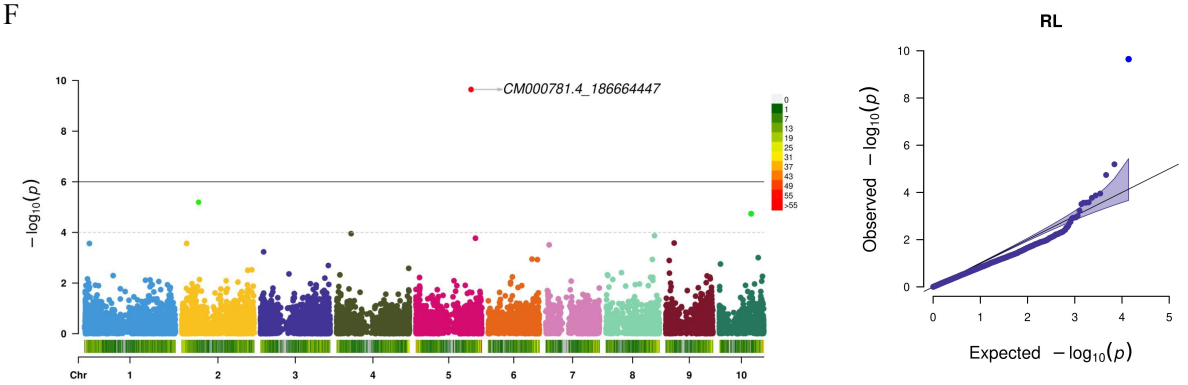
D

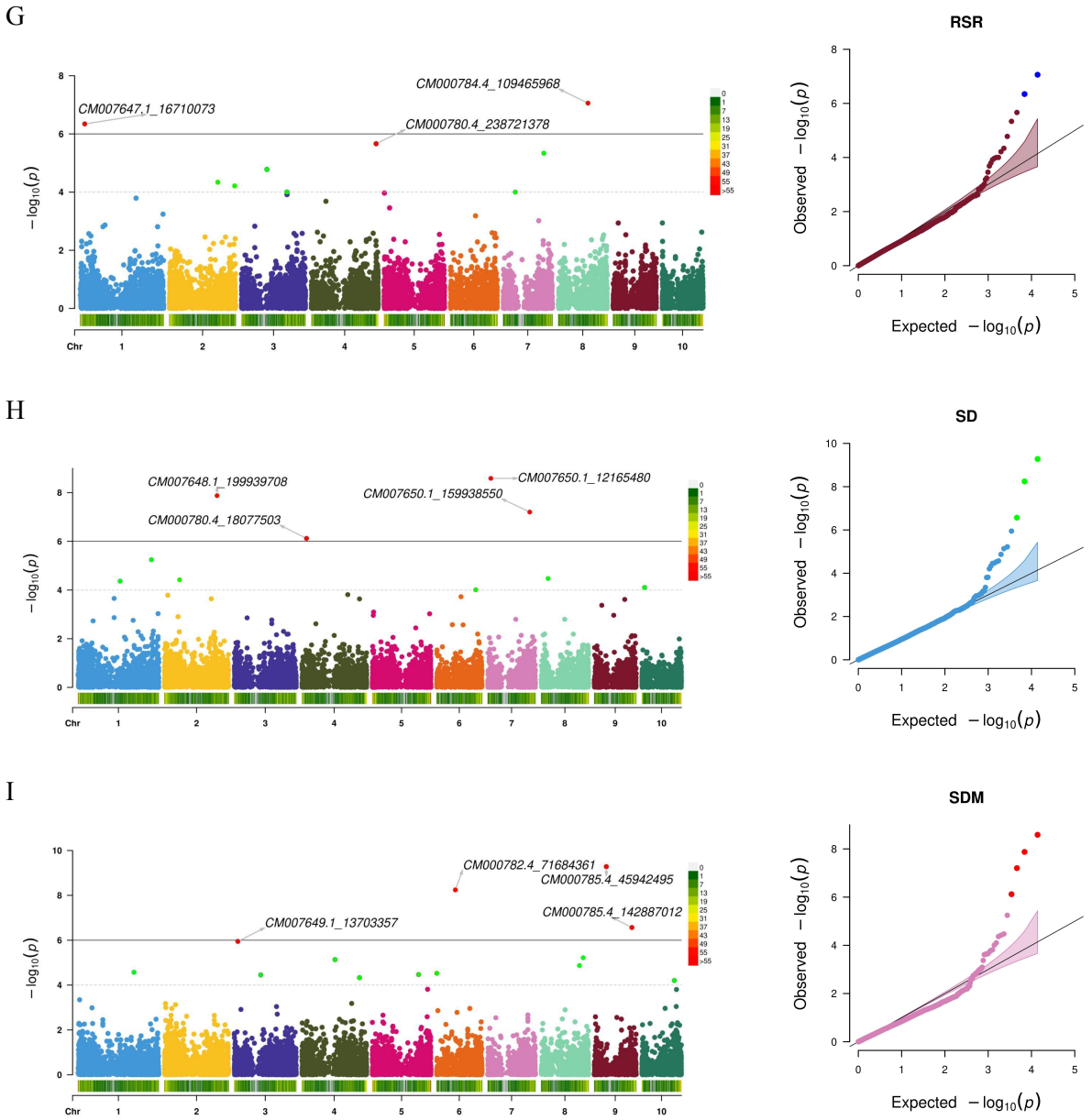

CM007647.1_115455586
CM007649.1_57358057
CM007647.1_297746433
CM000784.4_130925210
PH
Observed −log10(p)
Expected −log10(p)
−log10(p)
Chr

E

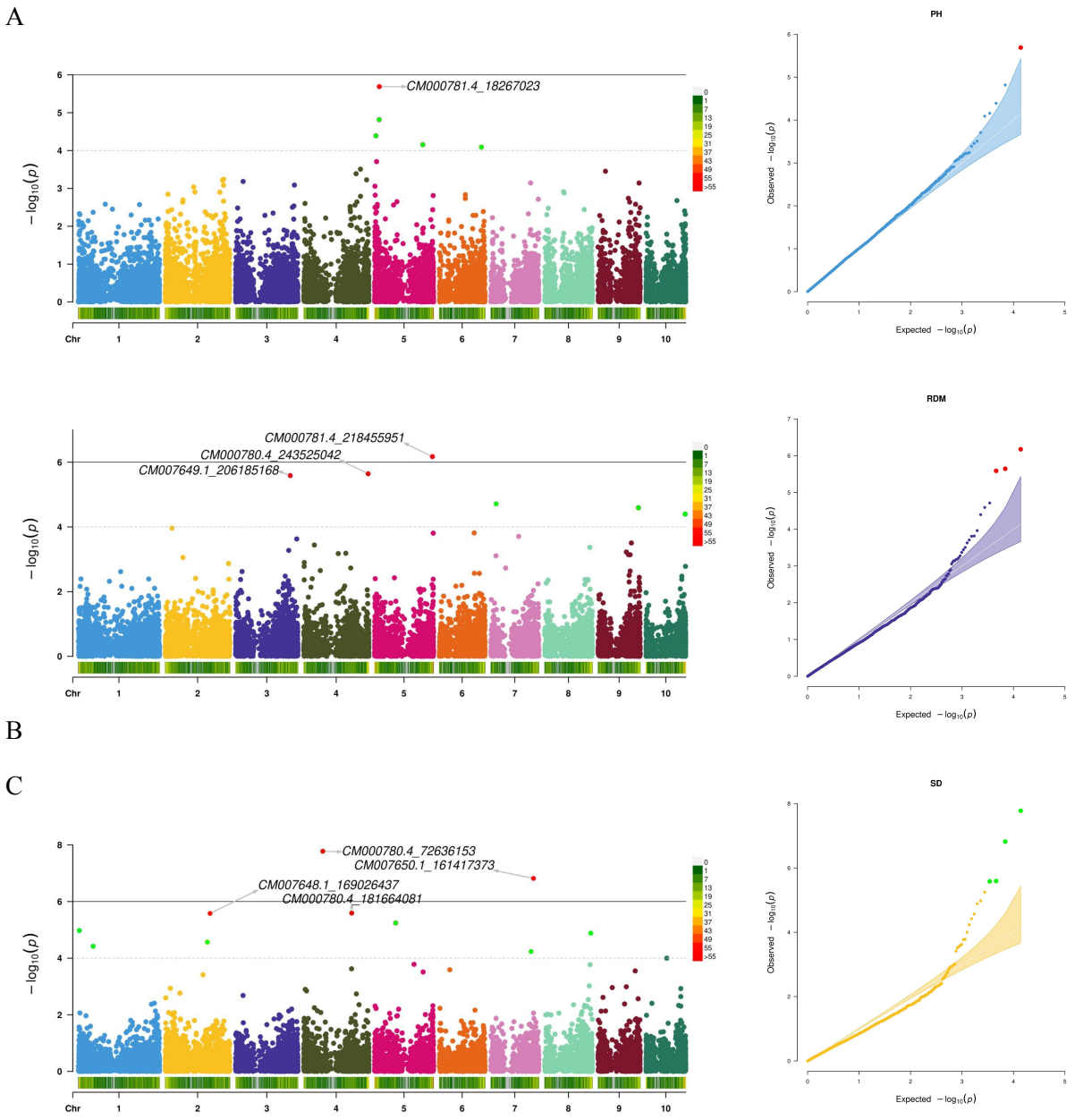

CM007647.1_299457743
CM007647.1_190289865
CM000785.4_148920255
CM000785.4_149343432
CM000784.4_173246547
RAD
Observed −log10(p)
Expected −log10(p)
−log10(p)
Chr

F


CM000781.4_186664447
RL
Observed −log10(p)
Expected −log10(p)
−log10(p)
Chr



Supplementary figure 10. Manhattan and QQplot plot for the treatment B- for the traits (A) ARV, (B) CHA, (C) LRV, (D) PH, (E) RAD, (F) RL, (G) RSR, (H) SD, and (I) SDM



Supplementary figure 11. Manhattan and QQplot plot for the treatment Delta for the triats (A) PH, (B) RDM, (C) SD.