

Table S6a Haplotype effects of three ZmVTE4 SNPs identified with an optimal multi-locus mixed model (MLMM) for α T/ γ T.

Haplotype	ss196416269	S5_200369481	S5_200369534	Frequency	Mean Value	S.D. ^a
A,C,G	A	C	G	50	0.10	0.09
G,C,G	G	C	G	151	0.41	0.27
A,G,G	A	G	G	1	0.06	-
G,G,G	G	G	G	28	0.95	0.46
G,C,T	G	C	T	22	0.16	0.33
R²_{LR}^b	51.30%					
Partial R²_{LR}^c	40.47%					
P-value^d	5.55E-31					
Maximum Fold Change^e	5.94					

^aS.D., Standard deviation of the BLUPs for each haplotype.

^bR²_{LR}, likelihood-ratio based R² statistic, percentage of total phenotypic variation explained by the unified mixed model.

^cPartial R²_{LR}, likelihood-ratio based partial R² statistic, percentage of total phenotypic variation explained by the haplotypes.

^dThe P-value was from a unified mixed linear model that tested for an association between haplotypes and α T levels.

^eFold change was calculated as the ratio between the most favorable (G, G, G) and least favorable (G, C, T) haplotypes for α T levels.

Table S6b Haplotype effects of three ZmVTE4 SNPs identified with an optimal multi-locus mixed model (MLMM) for $\delta T/\alpha T$.

Haplotype	ss196416269	S5_200369481	S5_200369534	Frequency	Mean Value	S.D. ^a
A,C,G	A	C	G	50	0.55	0.40
G,C,G	G	C	G	151	0.17	0.15
A,G,G	A	G	G	1	0.76	-
G,G,G	G	G	G	28	0.04	0.04
G,C,T	G	C	T	22	0.69	0.38
R²_{LR}^b	49.57%					
Partial R²_{LR}^c	39.96%					
P-value^d	2.16E-27					
Maximum Fold Change^e	0.06					

^aS.D., Standard deviation of the BLUPs for each haplotype.

^bR²_{LR}, likelihood-ratio based R² statistic, percentage of total phenotypic variation explained by the unified mixed model.

^cPartial R²_{LR}, likelihood-ratio based partial R² statistic, percentage of total phenotypic variation explained by the haplotypes.

^dThe P-value was from a unified mixed linear model that tested for an association between haplotypes and αT levels.

^eFold change was calculated as the ratio between the most favorable (G, G, G) and least favorable (G, C, T) haplotypes for αT levels.

Table S6c Haplotype effects of three ZmVTE4 SNPs identified with an optimal multi-locus mixed model (MLMM) for $\gamma T/(\gamma T + \alpha T)$.

Haplotype	ss196416269	S5_200369481	S5_200369534	Frequency	Mean Value	S.D. ^a
A,C,G	A	C	G	50	0.91	0.06
G,C,G	G	C	G	151	0.72	0.13
A,G,G	A	G	G	1	0.93	-
G,G,G	G	G	G	28	0.48	0.14
G,C,T	G	C	T	22	0.89	0.15
R²_{LR}^b	52.4%					
Partial R²_{LR}^c	41.3%					
P-value^d	2.16E-31					
Maximum Fold Change^e	0.54					

^aS.D., Standard deviation of the BLUPs for each haplotype.

^bR²_{LR}, likelihood-ratio based R² statistic, percentage of total phenotypic variation explained by the unified mixed model.

^cPartial R²_{LR}, likelihood-ratio based partial R² statistic, percentage of total phenotypic variation explained by the haplotypes.

^dThe P-value was from a unified mixed linear model that tested for an association between haplotypes and αT levels.

^eFold change was calculated as the ratio between the most favorable (G, G, G) and least favorable (G, C, T) haplotypes for αT levels.