

Supplemental material for 'Local adaptation contributes to gene expression divergence in maize'

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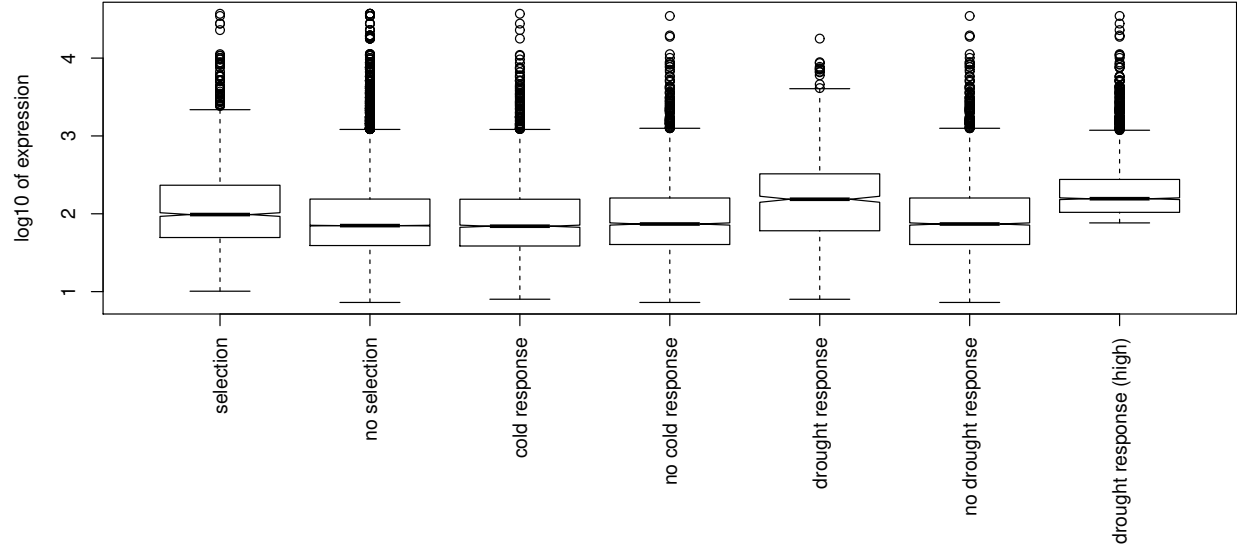


Figure S1: Expression level of genes in different environmental response categories

Tissue	Gene Number	Individual Number
Kernel	9,814	207
Germinating shoot	10,195	239
Germinating root	10,500	232
Adult leaf night	8,435	110
Adult leaf day	8,879	109
3 rd leaf tip	8,489	237
3 rd leaf base	11,555	236

Table S1: Number of genes and individuals used to test for selection in each tissue

Table S2: A list of all genes that were significant for selection at a $FDR < 0.1$ level, along with information about whether each gene is drought or cold responsive and information about gene function from a literature search. Because of its size, this table is included in supplemental material as a text file.

Tissue	PC 1	PC 2	PC 3	PC 4	PC
Kernel	507	331	376	131	116
Germinating shoot	106	191	61	123	151
Germinating root	74	153	46	77	92
Adult leaf night	345	344	511	257	432
Adult leaf day	330	551	293	222	617
3 rd leaf tip	99	306	88	68	77
3 rd leaf base	390	352	79	70	91

Table S3: The number of genes where $p < 0.05$ in each of the 7 tissues for the first 5 PCs. Equivalent to Figure 1A with a less stringent significance cutoff.

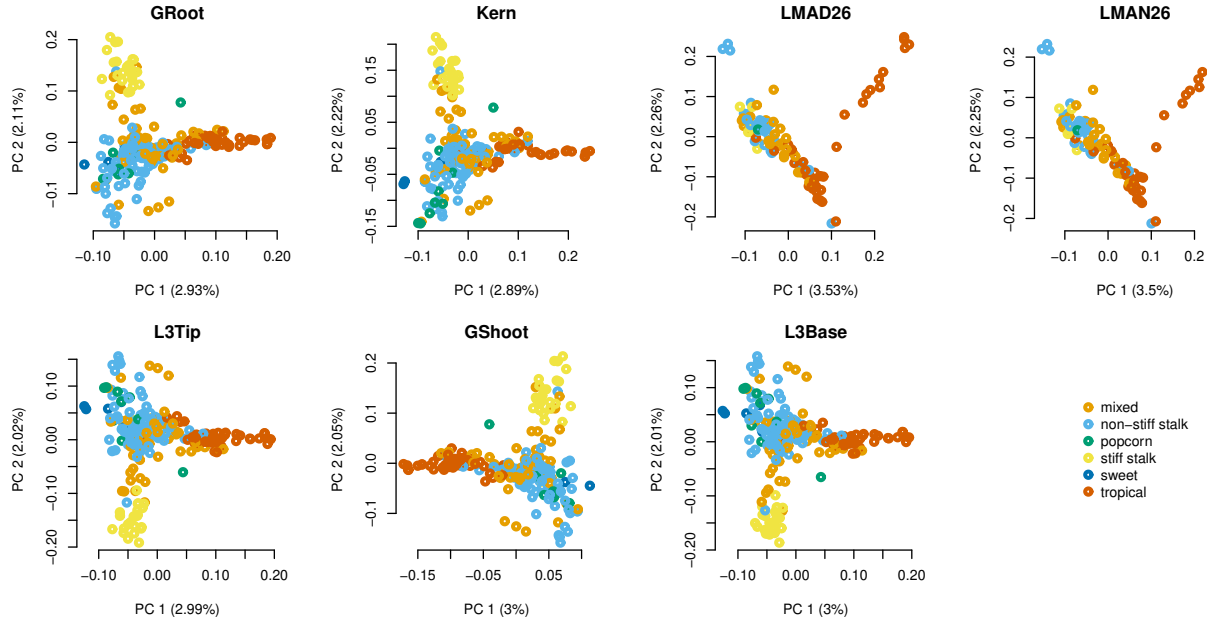


Figure S2: The first two genetic PCs of genotypes in each tissue expression dataset. Each point represents one genotype, colored by subpopulation. The x axis is PC 1 and the Y axis is PC 2, labeled by the percentage of variation that each PC explains.

Table S4: A list of all genes that were significant for selection at a $p < 0.05$ level. Because of its size, this table is included in supplemental material as a text file.

Tissue	PC 1	PC 2	PC 3	PC 4	PC 5	Number of Genes	Cold-Response Genes
Kernel	NA	0.776	0.362	1.000	NA	9426	4741
Germinating shoot	NA	0.882	NA	NA	NA	9889	5011
Germinating root	NA	NA	NA	NA	NA	10147	5215
Adult leaf night	0.699	NA	0.031	NA	0.083	8329	4251
Adult leaf day	0.778	0.756	1.00	NA	0.004	8787	4500
3 rd leaf tip	NA	0.771	NA	0.807	NA	8403	4279
3 rd leaf base	NA	0.785	0.817	NA	NA	11377	5830

Table S5: Uncorrected p-values and sample sizes for chi-squared test for enrichment of signals of selection in cold-response genes. P-values only shown for PC/tissue combinations with at least 1 significantly selected gene (FDR < 0.1).

Tissue	PC 1	PC 2	PC 3	PC 4	PC 5	Number of Genes	Down-Regulated Drought-Response Genes
Kernel	NA	0.391	0.878	0.023	NA	3031	352
Germinating shoot	NA	0.696	NA	NA	NA	3450	463
Germinating root	NA	NA	NA	NA	NA	3045	366
Adult leaf night	0.083	NA	0.344	NA	0.0000109	3605	464
Adult leaf day	0.198	0.033	0.639	NA	0.000242	4065	566
3 rd leaf tip	NA	0.720	NA	0.451	NA	3735	476
3 rd leaf base	NA	0.034	0.5723	NA	NA	3687	511

Table S6: Uncorrected p-values for chi-squared test for enrichment of signals of selection in down-regulated drought-response genes. P-values only shown for PC/tissue combinations with at least 1 significantly selected gene (FDR < 0.1).

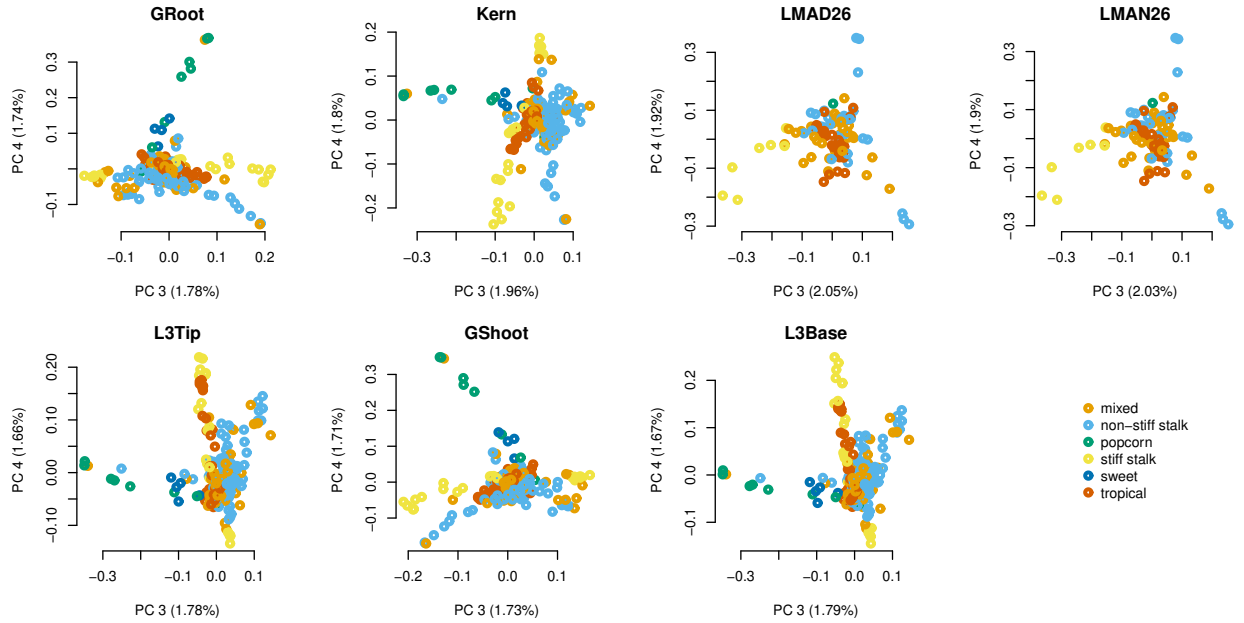


Figure S3: The third and fourth genetic PCs of genotypes in each tissue expression dataset. Each point represents one genotype, colored by subpopulation. The x axis is PC 3 and the Y axis is PC 4, labeled by the percentage of variation that each PC explains.

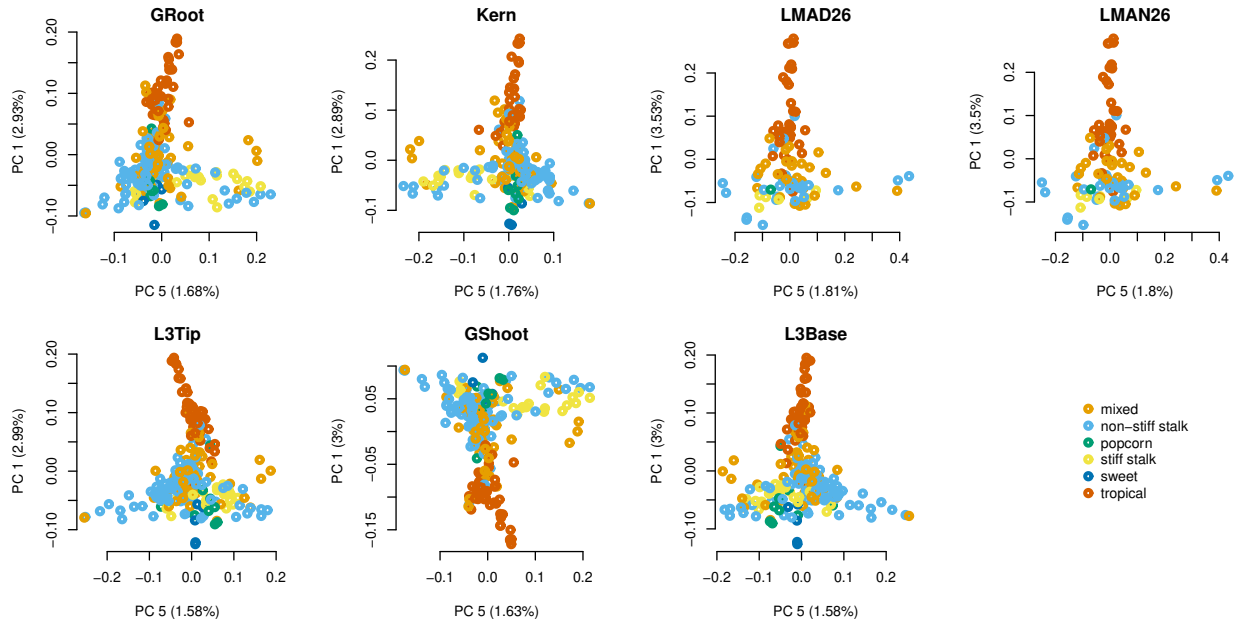


Figure S4: The first and fifth genetic PCs of genotypes in each tissue expression dataset. Each point represents one genotype, colored by subpopulation. The x axis is PC 5 and the Y axis is PC 1, labeled by the percentage of variation that each PC explains.

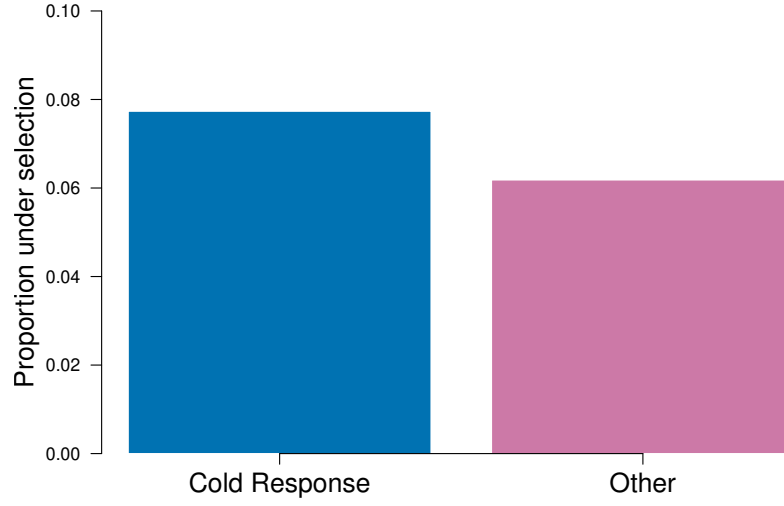


Figure S5: Enrichment for signals of selection in genes with differential response to cold treatment. The percentage of genes that show evidence of selection along PC 5 ($p < 0.05$) in adult leaf expression during the day for genes that have expression change in cold and no change in response to cold. While there is a slight enrichment of signals of selection in cold-response genes, this enrichment is not significant after a Bonferroni correction for multiple testing ($p = 0.09$)

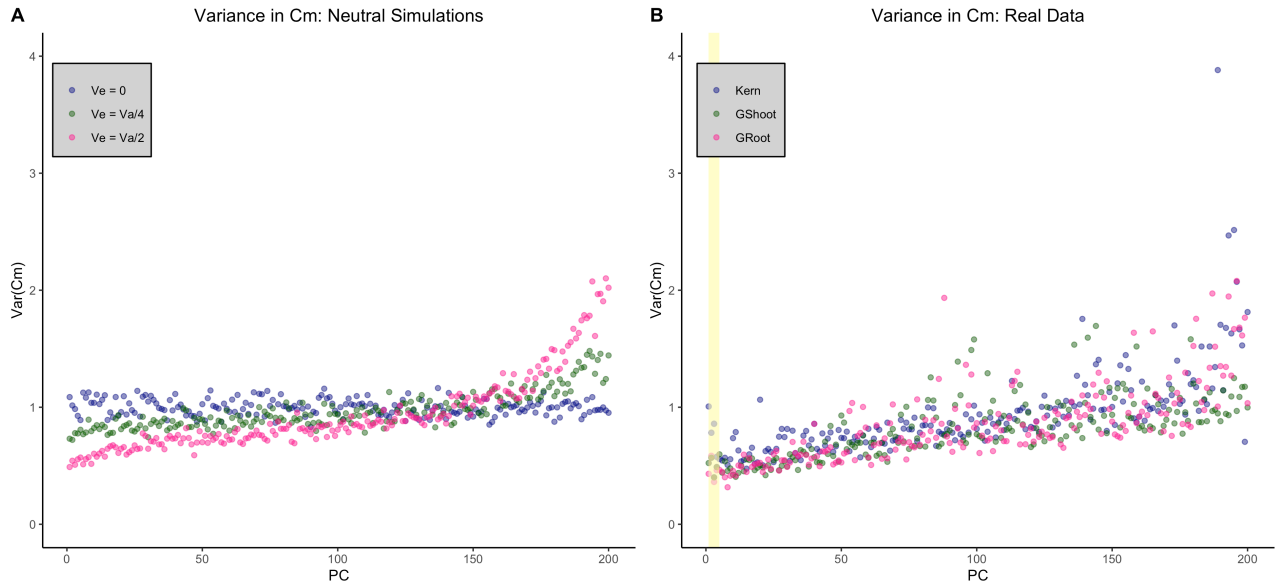


Figure S6: (A) Variance in C_m values for neutral simulations with different levels of environmental variance using the kinship matrix generated from the 207 Kernel lines. (B) Variance in C_m values for actual expression values for 3 different tissue types. The yellow box highlights the five 5 PCs along which expression divergence was tested.

Tissue	PC 1	PC 2	PC 3	PC 4	PC 5	Number of Genes	Up-Regulated Drought-Response Genes
Kernel	NA	0.689	0.051	0.124	NA	2844	165
Germinating shoot	NA	0.181	NA	NA	NA	3142	155
Germinating root	NA	NA	NA	NA	NA	2679	161
Adult leaf night	0.379	NA	1.000	NA	0.077	3394	253
Adult leaf day	0.337	0.915	0.104	NA	0.319	3827	328
3 rd leaf tip	NA	0.434	NA	0.305	NA	3513	254
3 rd leaf base	NA	0.485	1.000	NA	NA	3337	161

Table S7: Uncorrected p-values and sample sizes for chi-squared test for enrichment of signals of selection in up-regulated drought-response genes. P-values only shown for PC/tissue combinations with at least 1 significantly selected gene (FDR < 0.1).