Supplementary Information for

Climate change is predicted to disrupt patterns of local adaptation in wild and cultivated maize

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Supplementary Methods

Genomic dataset

We combined the SNPs datasets of ref.[1] and ref.[2] to obtain a dataset of 33,454 SNPs distributed across all chromosomes of maize. Genotyping quality was set with a threshold of 0.15 for the GC_{50} score and by removing monomorphic SNPs and clusters with call rates below 0.85. See ref.[1] and [2] for more details.

Defining putative adaptive SNPs (paSNPs). The dataset including the locally adapted SNPs identified by ref.[2] was subdivided based on the power of individual SNPs to discriminate among climatically defined groups of populations. Based on the values of the first environmental principal component, associated with temperature[2], we categorized populations for each species into four groups based on the quartile distribution of temperature values across sampled populations: Group 1-cold (6 *parviglumis* and 7 *mexicana* populations); Group 2-normal cold (6 *parviglumis* and 6 *mexicana* populations); Group 3-normal warm (6 *parviglumis* and 6 *mexicana* populations); and Group 4-warm (6 *parviglumis* and 6 *mexicana* populations).

We tested the power of locally adapted SNPs to discriminate among the above-mentioned groups of populations by performing a Discriminant Analyses on Principal Components (DAPC)[3] for each teosintes species separately using ten principal components (summarizing 25% of the genetic variability across populations) and retaining the first four discriminant functions. These first four discriminant functions explained ~ 67% of the among-population environmental

variance for *parviglumis* and ~ 77% for *mexicana.* We plotted the contribution of individual SNPs to the discriminant functions using the *loadingplot* function of the *adegenet* package[3] in R[4] with the default parameters. We selected the locally adapted SNPs with the highest discrimination power (paSNPs) using the default parameters (*i.e.,* the third quartile of the distribution of loadings (fig. S1).

Predictive models using Gradient Forest

Gradient Forest uses a machine-learning algorithm to divide biological data into bins (allele frequencies) occurring at numerous split values along a given environmental gradient[5]. Moving throughout an environmental gradient, the algorithm estimates the amount of variation in the data (in this case allele frequencies) explained by the different split values (split importance). In principle, the estimation of split importance along a gradient does not depend on the initial allele frequency in any given population, but on the amount of change observed among populations located along different regions of the gradient. Gradient Forest cumulatively sums the split importance along a gradient, which then reflects the overall association of an environmental gradient with allele frequency changes, using this information to construct allele turnover functions[6] along the environmental gradient. Given the correspondence between environmental and geographic space[7], these functions can be directly projected into geographic space, allowing the visualization of differences in genetic composition throughout the species' distribution ranges, even in places were no populations have been sampled.

To estimate the genomic offset under different future scenarios of climate change, Euclidian distances between present and future models are used to identify regions with a more pronounced disruptive effect of climate change, where larger distances are indicative of higher populations vulnerability[6]. More specifically, the Euclidean distances are estimated as follows,

$$\sqrt{\sum_{i}^{n}(present_i - future_i)^2}$$

where n represents the number of bioclimatic variables used in the analyses, and i represents the contribution of a grid (coordinate) to the allelic turnover function for a given environment.

For each subspecies and each set of SNPs (putative adaptive, candidate and reference), we estimated the allelic turnover models using the *gradientforest*[5] package in R[4]. These allelic turnover models were used to predict the genomic offset across the teosintes distribution. Values of genomic offset were standardized relative to the maximum observed Euclidian distance[6] estimated across known teosintes occurrences[8], setting areas with a standardized value > 1 to NA. The genomic offset values across the distribution of teosintes were transformed into a raster grid and the estimated values of genomic offset were extracted for all known teosintes occurrences[8] and sampled populations using the *raster* package[9] in R[4].

In addition to the Gradient Forest analyses using the three sets of SNPs, we estimated allele turnover functions using the complete set of 33,454 SNPs

identified in teosintes[1,2]. Due to computational limitation, we only estimated allele

turnover and not genomic offset for the complete set of SNPs and classified them

based on their overall contribution to the model (i.e., gradient forest's R^2). Based

on the individual contribution of each SNP to the model (R^2), we assessed

whether the candidate and putative adaptive SNPs are a representative sample

of SNP-climate association across the genome. For SNPs with significant

contribution to the turnover model we used the quartile distribution to categorize

SNPs as having low, moderate, high, and very high climate-frequency

associations. We compared the contribution of different SNPs categories to the

contribution estimated by the Gradient Forest analyses on the candidate and

putative adaptive SNPs, showing that these two sets of SNPs are representative

of strong genome-wide climate-frequency associations (figs. S3, S4).

Validation of allele turnover models. Gradient Forest analyses can be sensitive to

the presence of habitat heterogeneity masking the presence of climate-frequency

associations. In order to test the predictive ability of the resulting allele turnover

models, we used simple Mantel correlations to test for significant associations

between predicted allele turnover and pairwise genetic differentiation between

populations (F_{ST}). We also tested for the correlation between allele turnover and

environmental distances among populations.

We used the *bedassle*[10] package in R[4] to estimate the pairwise genetic

differentiation (F_{ST}) between populations for putative adaptive, candidate and

reference SNPs, separately. To estimate environmental differentiation, we

extracted environmental information of the 19 bioclimatic layers[11] used in the

species distribution models for each pixel predicted by the species distribution

models. We then performed a Principal Component Analyses (PCA) on these

data to reduce environmental variation down to six principal components and

obtain values for each sampled population of teosintes. We used the data for the

six principal components to calculate Euclidian distances between populations

(environmental differentiation) using the *stats* package in R[4]. Finally, for each

Gradient Forest model (e.g., paSNPs, canSNPs, refSNPs) we modified the

original script of ref.[6] to perform a PCA and reduce the contribution of the 19

bioclimatic variables to the allelic turnover function into six principal components.

These principal components were used to estimate Euclidian distances between

populations, which reflect the predicted allelic dissimilarity between populations

(predicted genetic differentiation).

      For each SNPs set, we evaluate the correlation between: (1) predicted

genetic dissimilarity and genetic differentiation; and (2) predicted genetic

dissimilarities and environmental differentiation. For both teosintes species we

found strong associations (all *p-values* < 0.05) between predicted genetic

dissimilarity and environmental differentiation between populations (fig. S10). In

addition, we found strong significant associations between genetic differentiation

and predicted genetic dissimilarities for putative adaptive and candidate SNPs,

after controlling for environmental distances. We observed a low, yet significant

association between genetic differentiation and predicted genetic dissimilarities for reference SNPs (fig. S10).

The lower power of Gradient Forest to predict pairwise genetic differentiation using reference SNPs is expected because these SNPs have an overall low contribution to the model (fig. S3). Accordingly, we found that allele turnover functions have a stronger predictive power in *mexicana* than in *parviglumis*, the latter having a higher environmental variation and a stronger genetic structure than the former[1,2]. This indicates that habitat heterogeneity and genetic structure can have significant impacts on the results of Gradient Forest. However, in the case of teosintes the allele turnover functions for candidate and putative adaptive SNPs were robust to the effects of habitat heterogeneity. *Allele frequency differences among SNP sets.* The allelic turnover models show that putative adaptive and candidate SNPs have significantly higher contribution to model construction than reference SNPs (fig. S3). Although this is expected and reflects the stronger frequency-environment associations (i.e., local adaptation) putative adaptive and candidate SNPs, these differences can be biased by significant discrepancies in allele frequencies for reference SNPs compared to locally adapted SNPs. In the present case, putative adaptive and candidate SNPs were defined using methods that rely on identifying outlier F_{ST} values among SNPs[2]. If higher predictability of allelic turnover is affected by the stronger differences in allele frequencies and not local adaptation, then using

reference SNPs with marked differences in allelic frequencies among populations should generate models with significantly higher allelic turnover[12].

To assess the impacts of allele frequencies on allele turnover models using reference SNPs, we performed additional Gradient Forest analyses using a set of reference SNPs for which the among-population frequencies more closely matched those observed for candidate and putative adaptive SNPs. For this, we estimated the standard deviation of allele frequencies among populations for the candidate and putative adaptive SNPs. Then, we selected a new set of reference SNPs (hereafter n_SNPs) showing a standard deviation higher than the median standard deviation observed for candidate SNPs (very few SNPs had standard deviation within the range observed for putative adaptive SNPs) and showing no significant associations with environmental variables.

We performed a GF analysis using the putative adaptive, candidate, reference SNPs, and n_refSNPs to assess the contribution of each SNP to the turnover function. For both teosintes species we found that the n_refSNPs had a lower predictability than putative adaptive SNPs. However, we found that the model contribution of n_refSNPs was similar to that estimated for reference SNPs only in *mexicana*, whereas for *parviglumis* there was a greater variance in the predictive power of n_refSNPs with some overlap with candidate SNPs (fig. S3). Although this might indicate a possible bias in the signal recovered for candidate SNPs due to genetic structure in *parviglumis*, it is important to recall that candidate SNPs were selected by employing outlier tests (*e.g.*, *bayescenv*,

bayenv) that controlled for possible gene surfing[2]. The estimated allele turnover

for putative adaptive SNPs appears to be robust to differences in among-

population allele frequencies in both species.

Identification of candidate SNPs. Another important source of bias for the

modeling of allele turnover is the proper identification of genes responsible for

local adaptation[12]. In this context, modeling and interpreting the results for only a

handful of SNPs (e.g., putative adaptive SNPs) may be an over-simplification of

the genomic processes affecting local adaptation to climate[13]. Thus, we

assessed the impact of including varying number of SNPs for the construction of

allele turnover models and the estimation of genomic offset under future climate

change scenarios. For this, we performed Gradient Forest analyses to estimate

the genomic offset based on different sets of outlier SNPs identified by ref.[2]: (1)

candidate SNPs + putative adaptive SNPs (USNPs); (2) outlier SNPs detected by

bayescenv (scenvSNPs); (3) outlier SNPs detected by *bayenv* (baySNPs); and

(4) outlier SNPs detected by *bayenv* and *bayescenv* (baynscenvSNPs). For

details on the procedures for outlier detection see ref.[2].

Overall, these analyses show that many outlier SNPs can be informative

about allele turnover and thus have elevated contribution to the genomic offset of

populations (fig. S3). For instance, as expected the scenvSNPs and baySNPs

showed a lower genomic offset than that observed for putative adaptive SNPs,

yet the estimated values are greater than those estimated for reference SNPs.

These results highlight two important points. First, the method to identify outlier

SNPs is crucially important for the estimation of genomic offset[12], particularly in situation where populations have pronounced patterns of genetic and environmental differentiation, such as *parviglumis*. Second, the estimated genomic offset for populations using a handful of locally adapted SNPs appears to be robust to the number of SNPs included in the model (fig. S3, S4). Increasing the number of SNPs did not produce significantly distinct patterns of estimated genomic offset than those observed using the reduced set of candidate and putative adaptive SNPs. Although there is variation in the range of estimated genomic offset among different sets of SNPs (fig. S3), expected due to varying levels of SNP-climate associations (*i.e.*, allele effects), we found that the per-population genomic offset was highly correlated among all outlier SNP sets (fig. S3i). This suggest that unseen candidate SNPs or new candidate SNPs entering a population (either by migration, mutation or pre-adaptation) will most probably have small impact on the observed patterns of local adaptation and genomic offset estimated across populations (information on individual SNPs can be found at github.com/spiritu-santi/teosintes).

Initial allele frequencies and climate change. To gauge the influence of initial allele frequencies on the resulting levels of genomic offset, we tested the correlation between the genomic offset estimated for each population and the frequency of putative adaptive alleles at putative adaptive SNPs within populations. Since we are interested in the response of populations to increasing temperature, we used the frequencies of the warm-adapted alleles at putative

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adaptive SNPs, identified as the alleles with higher frequencies in populations growing at the warm-end of the species' climatic niche (climatic groups 3 and 4, see above). For simplicity, we estimated an adaptive score for each population by summing up adaptive allele frequencies over all putative adaptive SNPs (see below) and tested the relationship with genomic offset only under the two most extreme models: CCSM 4.5 2050 and CCSM 8.5 2070 (fig. S5).

We also tested the correlation between genomic offset and the estimated change in climatic conditions expected for each population, which were measured as the sum of the absolute differences between the present and future values for the 19 bioclimatic variables[11] used for the species distribution modeling and Gradient Forest analyses. We employed simple linear regressions using the *stats* package in R[4] (fig. S5).

Ecological niche modeling

Species distribution models. We used 254 (*mexicana*) and 329 (*parviglumis*) occurrence data points (available at: www.biodiversidad.gob.mx/genes/ proyectoMaices.html) and performed the modeling with Maxent v.3.3.3[14] using previously described settings and validation procedures[2,15,16]. We used all 19 available variables in the WorldClim database[11] following the same procedures as of refs.[2,15,16]. In addition, ref.[16] compared species distribution models for the two teosinte subspecies obtained using the 19 bioclimatic variables with models constructed after removing correlated variables, finding strong correlations

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between the predictions (> 0.9). For validation we used 10 bootstrap replicates for each model using a 30% random sample of occurrence records as test data. We used the Area Under the Curve (AUC) of the Receiver Pperating Characteristic (ROC) to assess model performance, resulting in species models with AUC values of 0.982 and 0.972 for *mexicana* and *parviglumis*, respectively, indicating good model performance.

To generate binary presence/absence maps for the present and future, we applied a minimum presence logistic threshold (*i.e.*, the minimum model value observed among species occurrences) to the models. The change in the predicted geographic distribution of the species was simply estimated as the number of grid-cells predicted in the future relative to the present (models available at https://github.com/spiritu-santi/teosintes). We also estimated overlap between present and future models using the corresponding binary maps.

Given that the sum of two binary maps (presence = 1, absence = 0) does not distinguish between present-only and future-only regions (both with values of 1 in the overlap map), we arbitrarily set a presence value of two for the present models and a value of four for the future models. These values were treated as categorical variables. We summed the values of the two models and defined three sets of regions: (1) regions uniquely predicted for the present (present-only grid-cells, value of two); (2) regions uniquely predicted for the future (future-only grid-cells, value of four); (3) regions of overlap between the two time models (overlap grid-cells, value of six).

Allele distribution models. We predicted the geographic distribution for warm-adapted alleles segregating at putative adaptive SNPs using Maxent v.3.3.3[14]. Since we were interested in modeling the distribution of the warm-adapted alleles, we used as input the populations' geographic coordinates where these alleles were present. Populations that were fixed with the non-adaptive allele did not contribute to the models. We used the same climatic variables; setting and validation procedures used for the species distribution modeling (see above). Overall, the resulting models for the warm-adapted alleles showed a good performance, with the lowest AUC values being 0.972 and 0.976 for *mexicana* and *parviglumis*, respectively.

For each warm-adapted allele distribution model (8 for *mexicana* and 9 for *parviglumis*) we created binary presence/absence maps as depicted above for the species distribution models. Then, for each grid-cell we estimated the sum across allele models constructed for the present-day and under each of the eight future climate change scenarios. We transformed the resulting *raster* grids into binary maps by setting areas with five or more alleles present to 1 and areas with fewer than five alleles to 0.

We extracted values for the bioclimatic variables for every grid-cell with a binary value of 1 and generated a data frame combining the climatic conditions for areas predicted in present and future. We used these data to perform a Principal Component Analysis (PCA) with the *prcomp* function in

R^4, retaining the first four principal components that explained more than 85% of the total variance in climatic variables.

Because we were interested in obtaining the future distribution of warm-adapted alleles, we estimated the present-day climatic range over the first principal component, for two groups of populations for each subspecies (see above): the normal-warm and warm populations. Thus, we obtained the current environmental range defining the warm-end niche of the two teosinte subspecies. Subsequently, we selected areas within the present and future predicted distributions that had climatic values within the present-day environmental range. Basically, this allowed us to define the geographic regions that presently lay within the environmental range of warm-adapted populations and those that will show the same range in future scenarios.

Based on the genomic offset of populations, we cross validated the final adaptive allele distribution models using the Gradient Forests models described above, basically inspecting the genomic offset of populations estimated with Gradient Forests for the three sets of regions (i.e., present-only, future-only, overlap). These analyses show that in general areas laying outside the predicted distribution for warm-adapted alleles have a higher mean and variance for genomic offset than areas predicted by either future or present allele models, particularly in *mexicana* (fig. S6).

Maxent's suitability and allele frequencies. For each putative adaptive and candidate SNPs, we tested for the correlation between the mean allele

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frequencies in each population and the mean suitability estimated by Maxent (*e.g.,* logistic output) across models for individual SNPs. Overall, we found that suitability values are not correlated with mean allele frequencies (fig. S11), which is consistent with previous analyses showing the inability of Maxent to predict species abundance[17]. Although some individual putative adaptive SNPs showed significant associations with suitability, particularly in *parviglumis*, these were non-significant after correcting for multiple comparisons using the Bonferroni test. All analyses were performed using the *raster*[9] and *stats* packages in R[4].

Migration analyses

We first identified areas with climatic conditions outside the present environmental range estimated for populations (see above) and treated these areas as hard barriers to migration by setting their value to NA. This assumes that teosintes populations are not capable of establishing in regions outside particular climatic conditions, namely regions with higher temperatures than currently inhabited.

We defined routes of potential migration by identifying regions predicted in the overlapped present and future distribution models for putative warm-adapted alleles, corresponding to the transition surfaces used in circuit theory[18]. These surfaces are built by assigning different resistance values to migration (i.e., environmental costs) to distinct environmental elements[19]. In the present case, different resistance values were assigned across the landscape based on the

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predicted distribution warm-adapted alleles. Then, we defined areas of potential

settlement corresponding to sites where populations could eventually establish in

the future, by identifying areas predicted only in the future allele models. These

areas correspond to the geographic locations into which potential migration

would be favored by the maintenance of current patterns of gene-environment

associations.

We used the *Gdistance* package[20] in R[4] to build transition layers around

each focal population, defining a transition function of 1/mean(x) for each pixel

(*i.e.,* grid-cell) between the eight neighboring grid-cells (*i.e.,* rooks move). Then

we used the geographic coordinates of potential settlement sites and

implemented a cost-distance function to determine the resistance values

(environmental distances) from the focal population to all sites, as a proxy of

migration limitation. To estimate the overall migration limitation of every

population, we estimated the overall distribution of environmental distances

across all potential settlement sites. We then identified settlement sites with

estimated resistance values below the 10, 20, 30, 40 and 50 percentiles of the

distribution of environmental distances. These percentiles can be interpreted as

the overall resistance to the successful migration into 10, 20, 30, 40, and 50% of

the future areas of potential settlement. We identified populations with the least

probabilities of migrating (migration unlikely) as those with undefined

environmental costs at the 10-precentile thresholds, namely those populations for

which the transition matrices become infinity due to the presence of hard barriers

to migration. All other populations with positive environmental costs were treated as having high chances of migrating (migration likely) into suitable areas in the future (results of migration analyses under all climate change models are available at github.com/spiritu-santi/teosintes).

Migration potential. Ultimately, the likelihood of successful migration of a particular population would be proportional, not only to the estimated migration costs, but also to the initial frequencies of adaptive alleles present in the population. Thus, for each population we evaluated the combined frequencies of warm-adapted alleles across putative adaptive SNPs. This score ranges between 0 and 1, with higher values indicating a higher frequency of adaptive alleles. We tested for differences in adaptive score between populations with likely and unlikely migration using an Analysis of Variance (ANOVA) as implemented in the *stats* package in R[4], but only under the two most extreme climate change models: CCSM_2050_RCP4.5 and CCSM_2070_RCP8.5. In general, populations predicted to have increased migration potential have significantly higher frequencies of adaptive alleles (measured by the adaptive score) than population predicted with low chances of migrating (fig. S8). Accordingly, the estimated genomic offset was higher for populations without migration potential than for those with migration potential, a pattern that is more pronounced in *mexicana* than in *parviglumis* (fig. S8).

Besides the possibility of tracking climate change by migrating into new locations, populations can evolve to respond to future climate conditions by

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receiving adaptive variants via gene flow from other populations. For *Zea mays* in particular, pollen is wind-dispersed[21], yet studies have shown that the viability of pollen decreases significantly over short scales[22-24]. To assess the potential contribution of adaptive introgression to the response of teosintes populations to climate change, we used the geographic distances and allele frequencies as proxies for the potential for gene flow among populations[25]. These analyses do not consider the presence of known teosintes populations that remain unsampled and with no genetic data[8,26], which may otherwise serve as sources of adaptive alleles or bridges to gene flow between sampled populations.

Basically, for each population we estimated the minimum distances to populations that could serve as sources of adaptive alleles through gene flow. In any given population, incoming gene flow can only increase the frequency of an adaptive allele if the initial frequency of that allele in the source population is greater than in the target population. Thus, we calculated the minimum distance to a population with an adaptive score greater than 0.5 and higher than the adaptive score of the focal population. All else being equal, as geographic distance between two populations increases, the probabilities for gene flow between these populations would decrease. In addition, for each population we identified the set of neighboring populations (arbitrarily set to four populations, corresponding to ~15% of populations) and then evaluated whether these had a higher adaptive score than the focal population. We used ANOVA tests as implemented in the *'stats'* package in R[4] to determine whether geographic

distances differed between populations identified as having migration potential

and those without migration potential.

We estimated the probability of population migration and gene flow under

the two more extreme climate change models (*i.e.,* CCSM-RCP4.5-2005, CCSM-

RCP8.5-2070); the results of all tests are summarized in table S7. Populations

that are predicted to have increased chances of migrating also appear to be

closer to populations that could serve as sources of adaptive alleles via gene

flow, than populations with low chances of migrating (fig. S12).

Identifying putative adaptive SNPs in maize landraces

The MaizeSNP50 BeadChip used by ref.[1] and ref.[2] to genotype teosintes, was

originally designed to detect genetic diversity among maize landraces. We

explored whether the warm adapted-alleles at putative adaptive SNPs identified

for teosintes have been documented in particular landraces of maize[27]. For this,

we downloaded the genotype data for maize[27], consisting of 36,931 SNPs across

46 landraces in Mexico.

Briefly, we obtained the adaptive score for each landrace (see above) by

adding the frequency of the warm-adapted alleles recorded in each accession,

i.e., 1.0 for the adapted homozygous genotype, 0.5 for a heterozygous genotype,

and 0.0 for the non-adapted homozygous genotype. The 'adaptive' score relates

to the frequency of alleles, where a lower score indicates that adaptive alleles

tend to be less represented in a particular landrace. A higher adaptive score

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would suggest that warm-adapted alleles are near fixation in particular landraces, probably resulting from past adaptation to warm and dry environments or the probable introgression of alleles from teosintes[28]. On the contrary, lower adaptive scores indicate that landraces have the potential to adapt to changing environmental conditions, with the maximum adaptive potential at intermediate allele frequencies. In principle, the adaptive score is not related to the genetic diversity within a population, because both homozygous states have the same genetic diversity but contrasting adaptive potential scores (i.e., genetic diversity would be greatest at intermediate adaptive potential scores), whereas the heterozygous state has the highest genetic diversity, but intermediate adaptive potential scores.

We acknowledge two limitations of our approach to identifying adaptive alleles in maize landraces. First, although gene-climate associations can be analyzed using single individuals per population[29], the direct application in maize of ecological models using allele frequency data, such as Gradient Forest, is prevented because the available SNPs dataset for maize is limited to one or a few accessions per landrace. Accordingly, we might expect a non-negligible number of unseen adaptive alleles across landraces purely due to sampling artifacts. Second, extrapolating from wild relatives to maize is not straightforward because the latter are highly dependent on humans for reproduction and usually grow under conditions that act as possible buffers against local- and regional-level climatic trends[30]. Nevertheless, ecological analyses indicate similar trends

of shrinking habitat in both teosintes and maize landraces in response to rising temperature and increasing aridity[31].

For each landrace of maize, we approximated the geographic range by estimating a spatial convex hull distribution model[32] around the reported occurrences[8] as implemented in the *dismo* package[33] in R[4]. Unlike species distribution modeling, the convex hull estimates species geographic ranges using spatial data alone and can be easily implemented for multiple species[32]. We chose to use convex hulls to estimate the geographic range of maize landraces, because these are easy to apply and are independent from environmental data. Basically, a convex hull model predicts that a species (landrace) is present inside the convex hull of a set of geographic occurrences and absent outside this area, yet the model assumes that a species is present throughout the entire hull[32].

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Supplementary Figure 1. Diffrent candidate SNPs have varying power to discriminate among climatically defined groups of sampled populations of two species of teosintes in Mexico (*Zea mays* spp. *parviglumis* and *Z. mays* spp. *mexicana*). Bars represent the loadings for the first discriminant function of the Discriminant Analysis of Principal Components (DAPC) estimated for candidate SNPs. Red bars represent the loadings for the putative adaptive SNPs selected for each species.
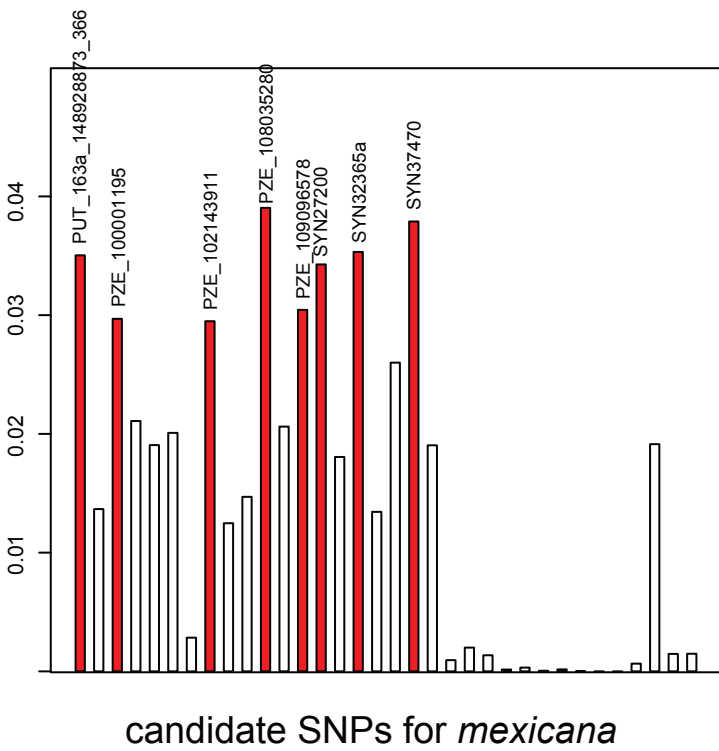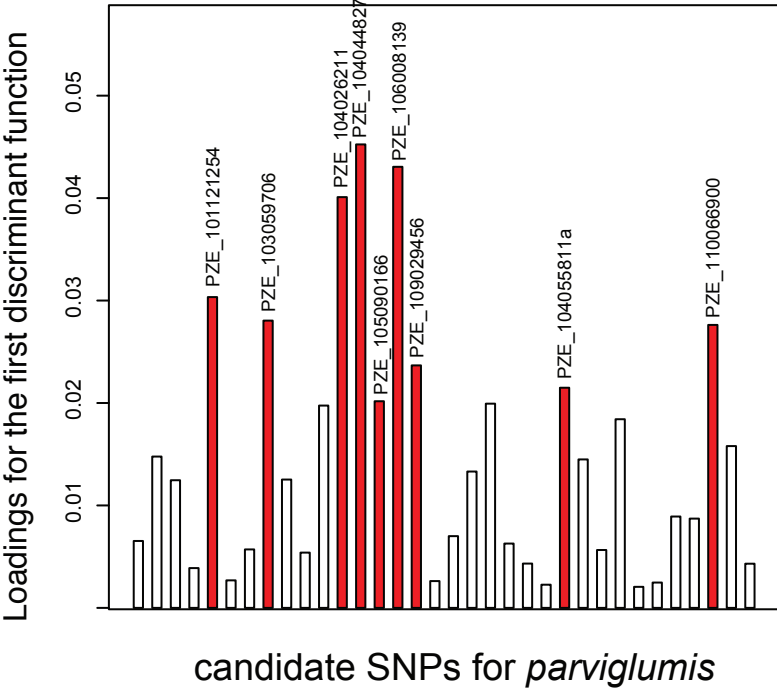
Supplementary Figure 2. Geographic distribution of two species of teosintes in Mexico: (*Zea mays* spp. *parviglumis* and *Z. mays* spp. *mexicana*) as predicted by ecological niche modeling. Overlap between the present-day and future distirbution of teosintes under the eight models of climate change. Ecological niche models were constructed using all known ocurrence records for the two teosinte species in Mexico. Distribution areas predicted only in the present-day are shown in light blue, areas predicted only in future models are shown in yellow, and areas predicted to overlap by present and future models ares shown in black (models available in ASCII format at https://github.com/spiritu-santi/teosintes).

CCSM_2050_RCP4.5

Supplementary Figure 2. Continued
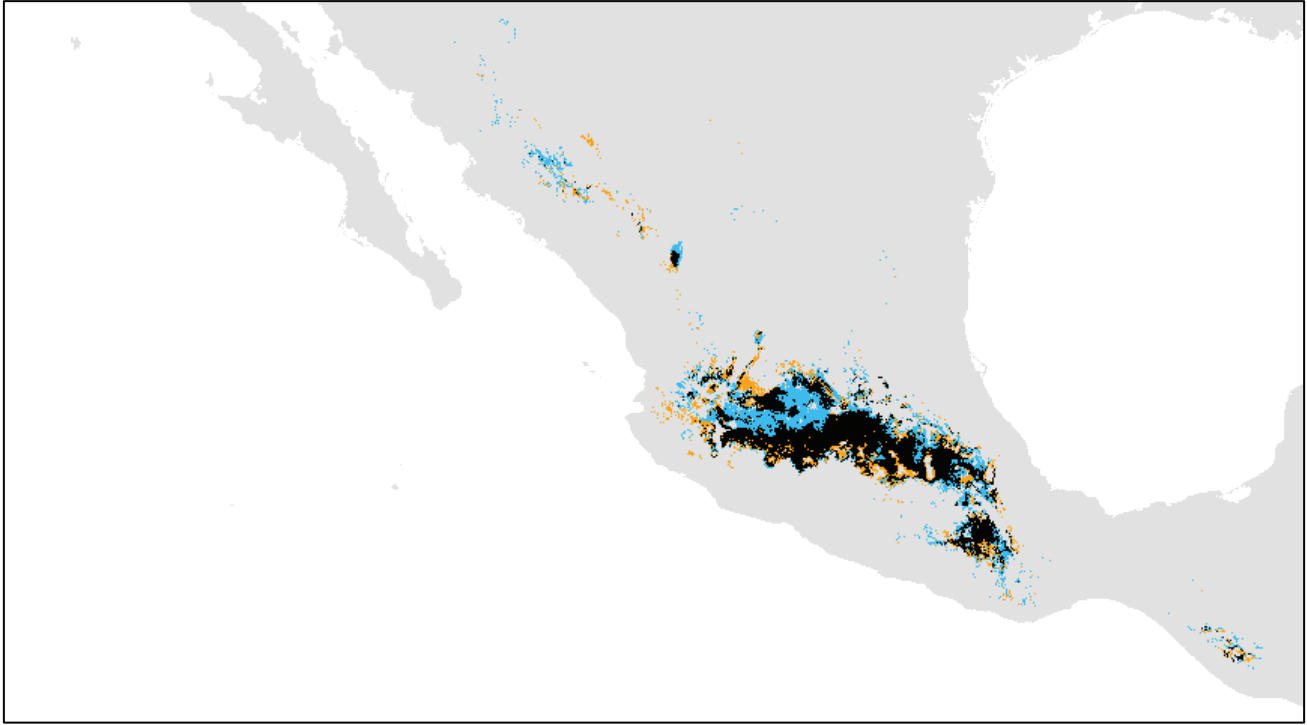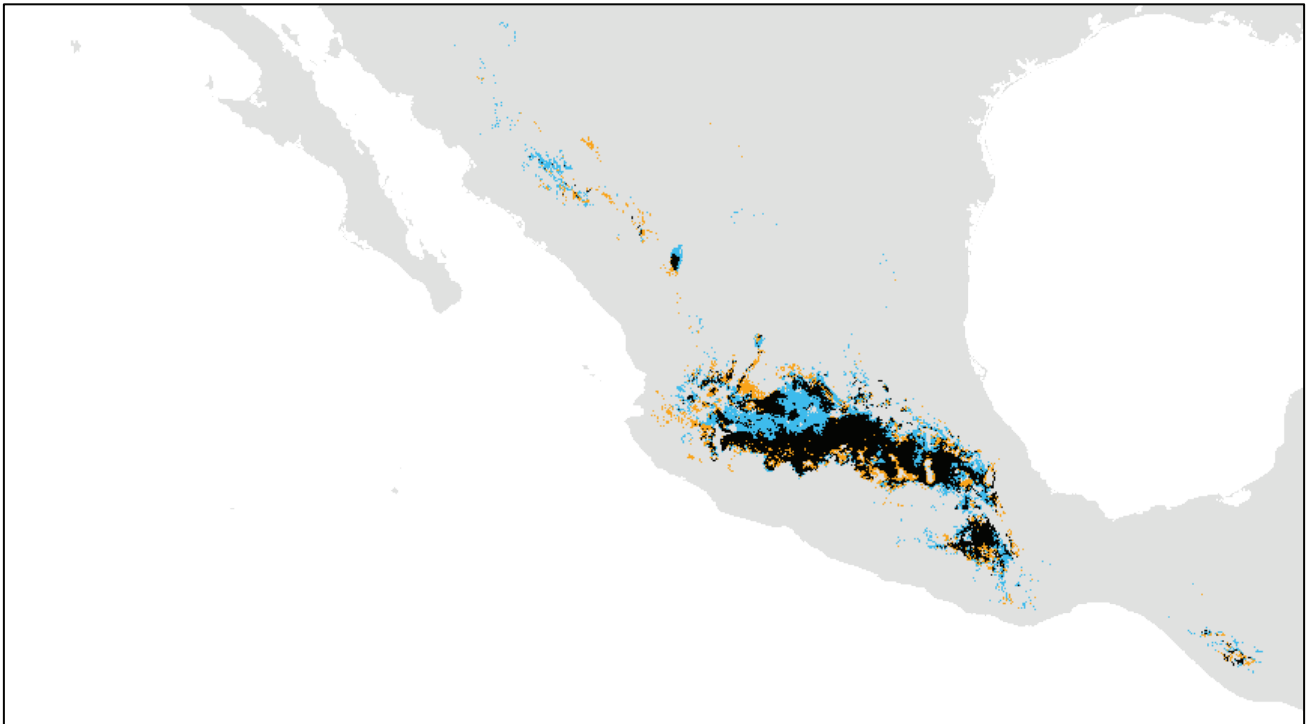
CCSM_2050_RCP8.5

Zea mays spp. *mexicana*

Zea mays spp. *parviglumis*

CCSM_2070_RCP4.5

Zea mays spp. mexicana

Zea mays spp. parviglumis

Supplementary Figure 2. Continued
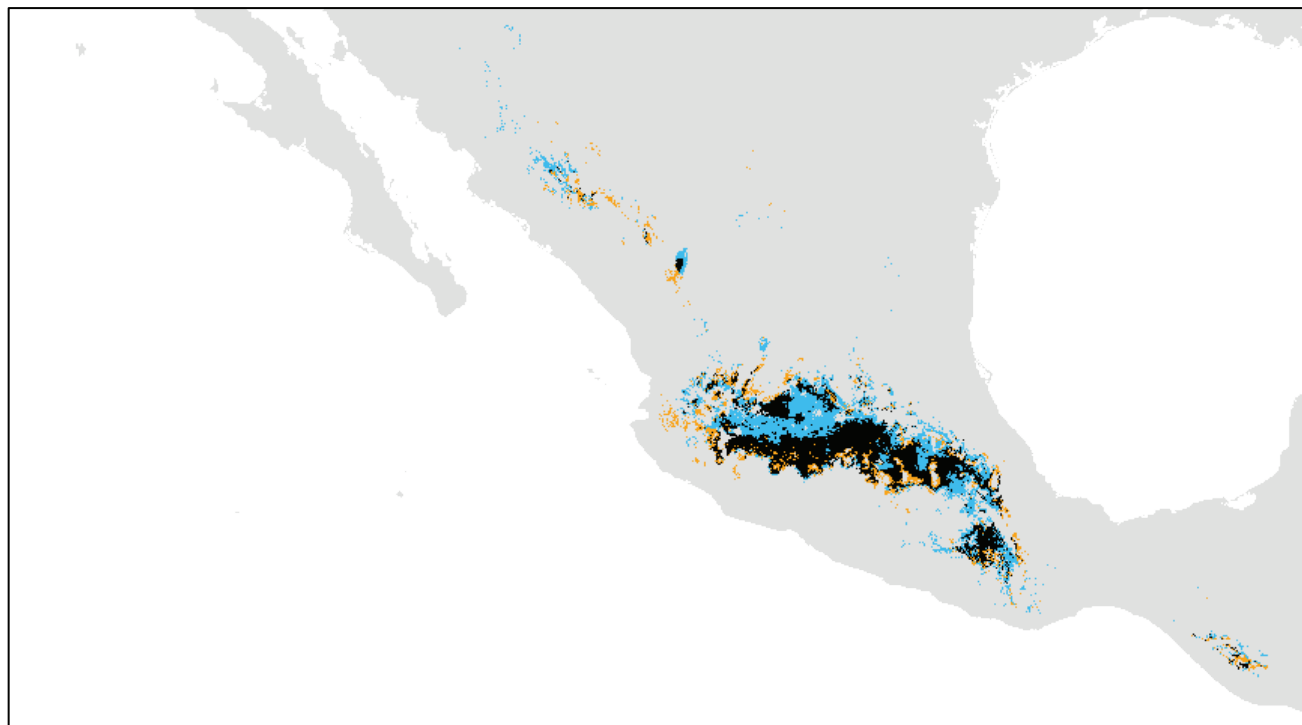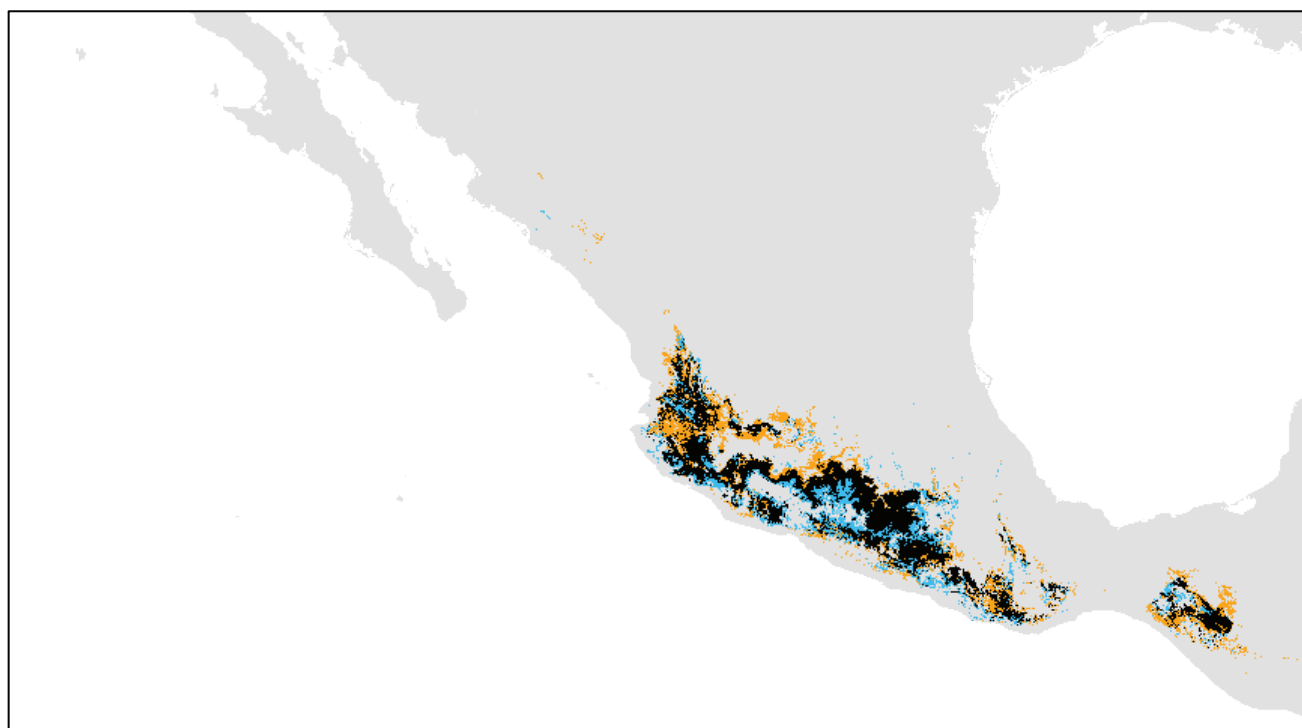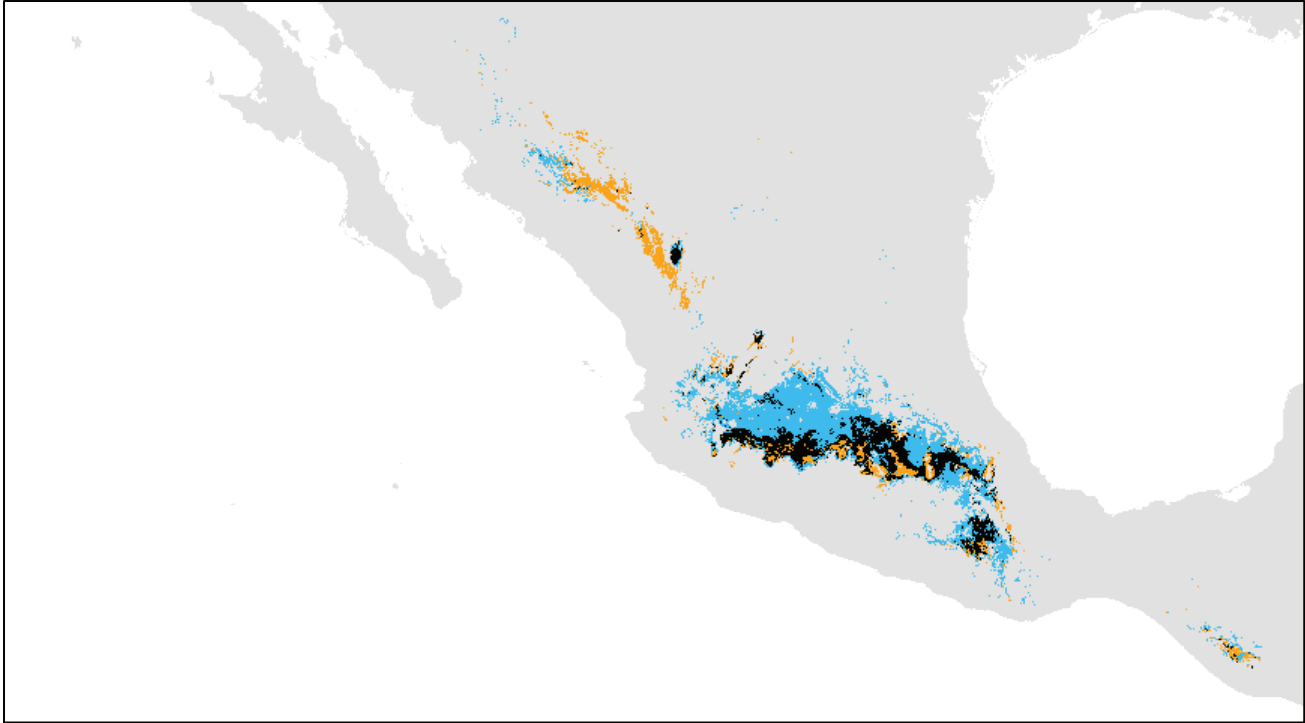
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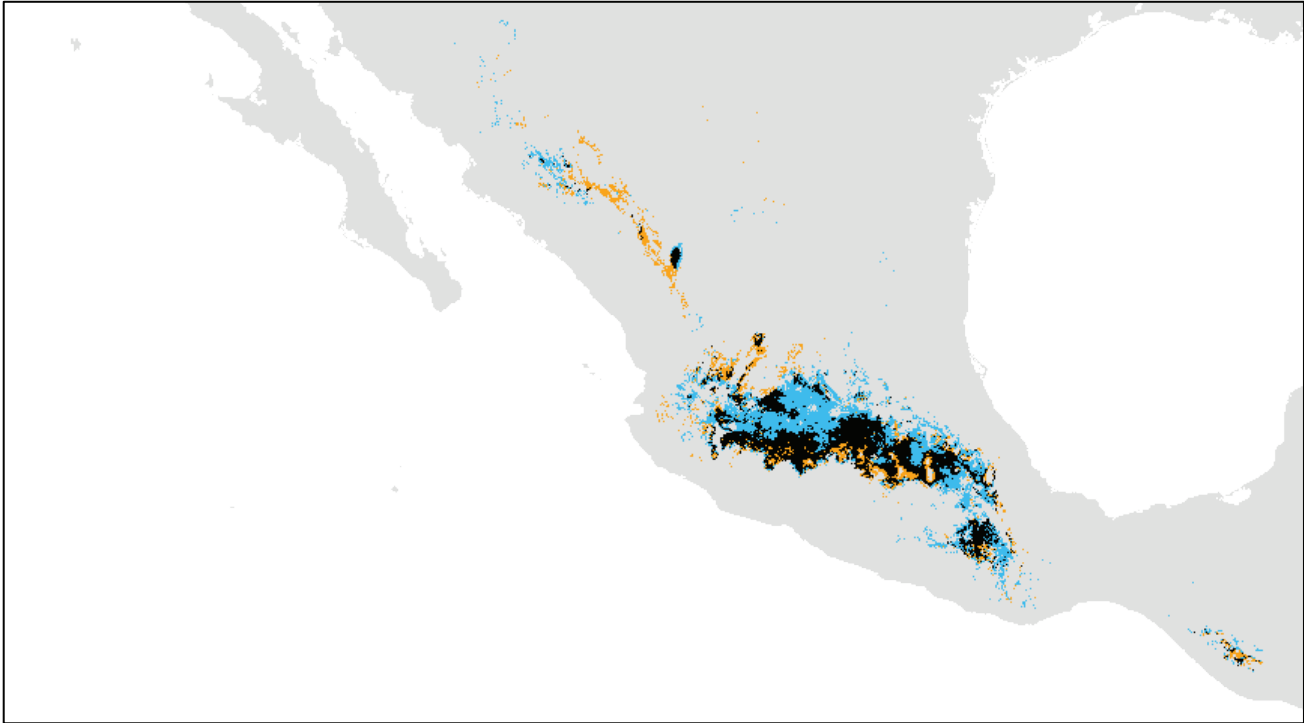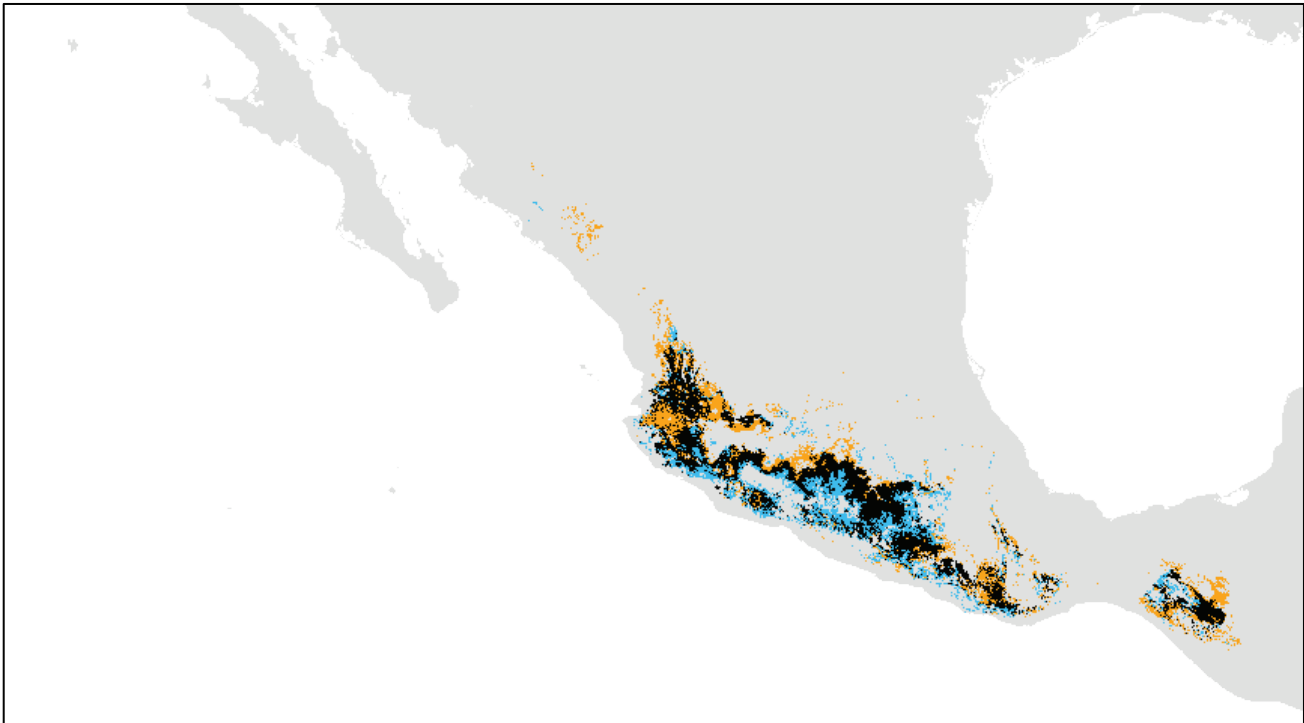

Zea mays spp. mexicana
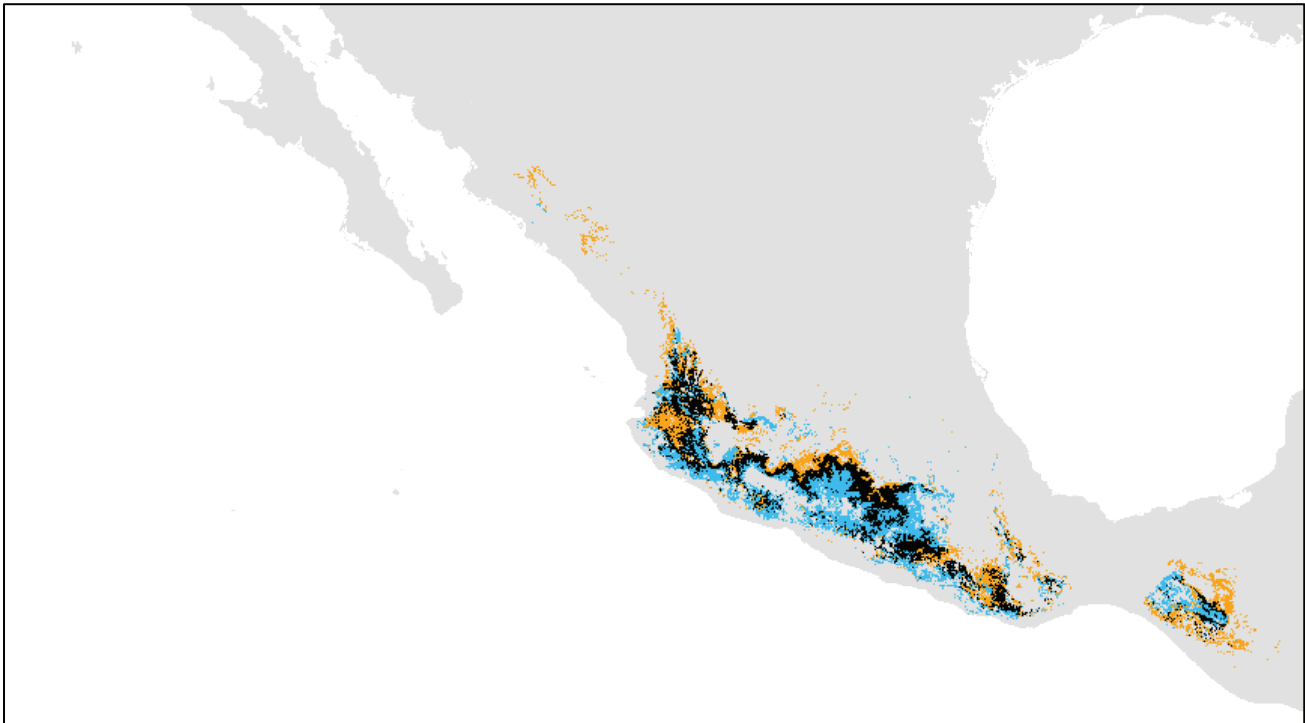
Zea mays spp. parviglumis

MIROC_2050_RCP4.5

Zea mays spp. mexicana
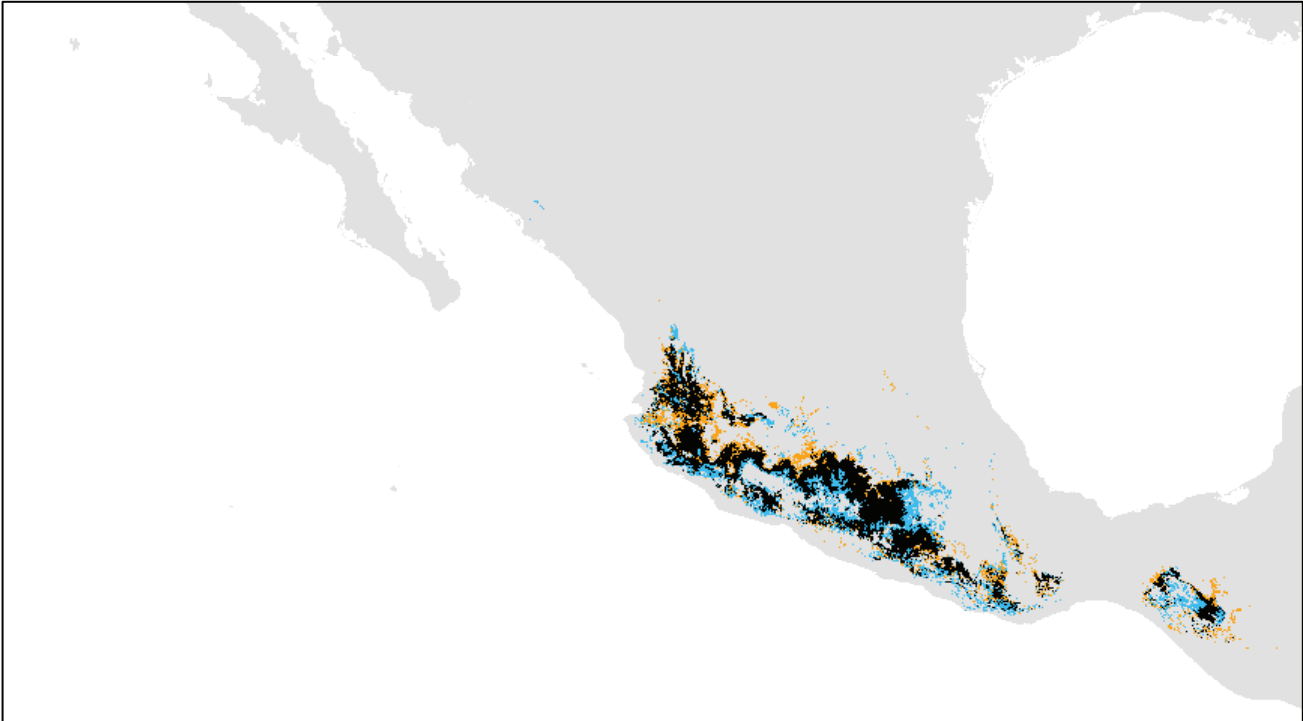
Zea mays spp. parviglumis

MIROC_2050_RCP8.5

Zea mays spp. *parviglumis*
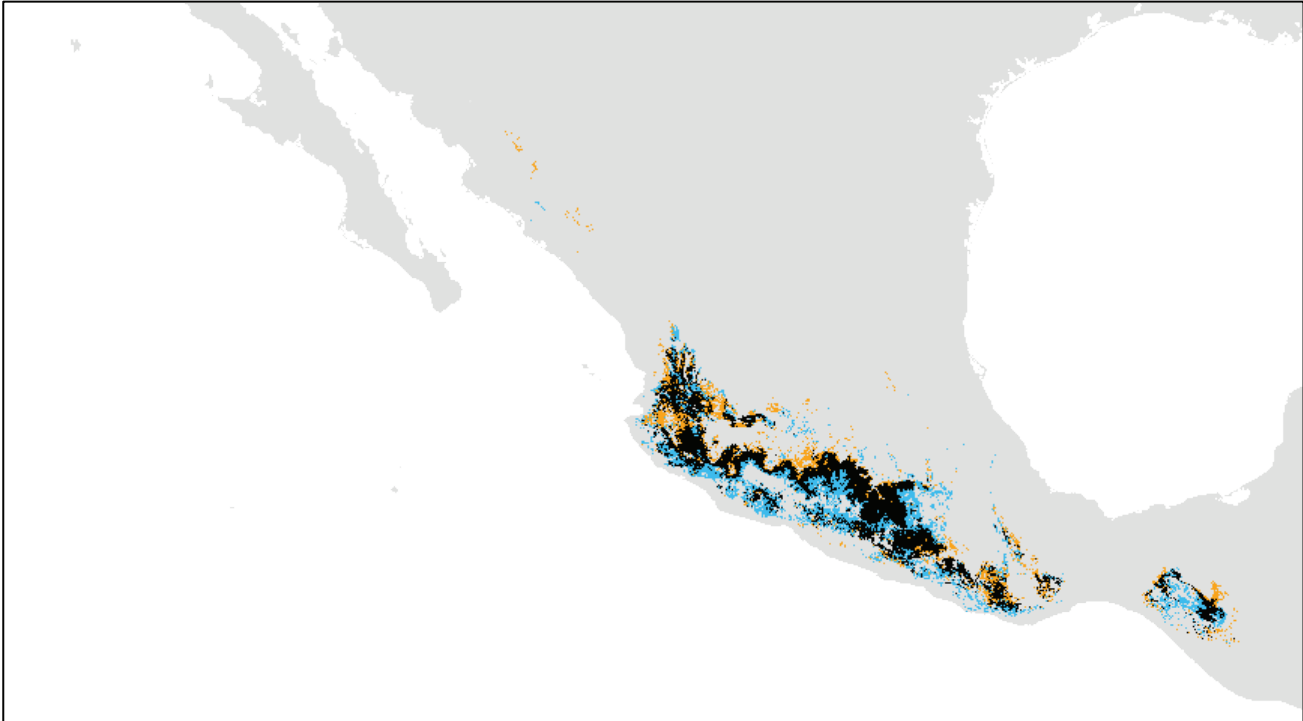
Zea mays spp. *mexicana*

MIROC_2070_RCP4.5
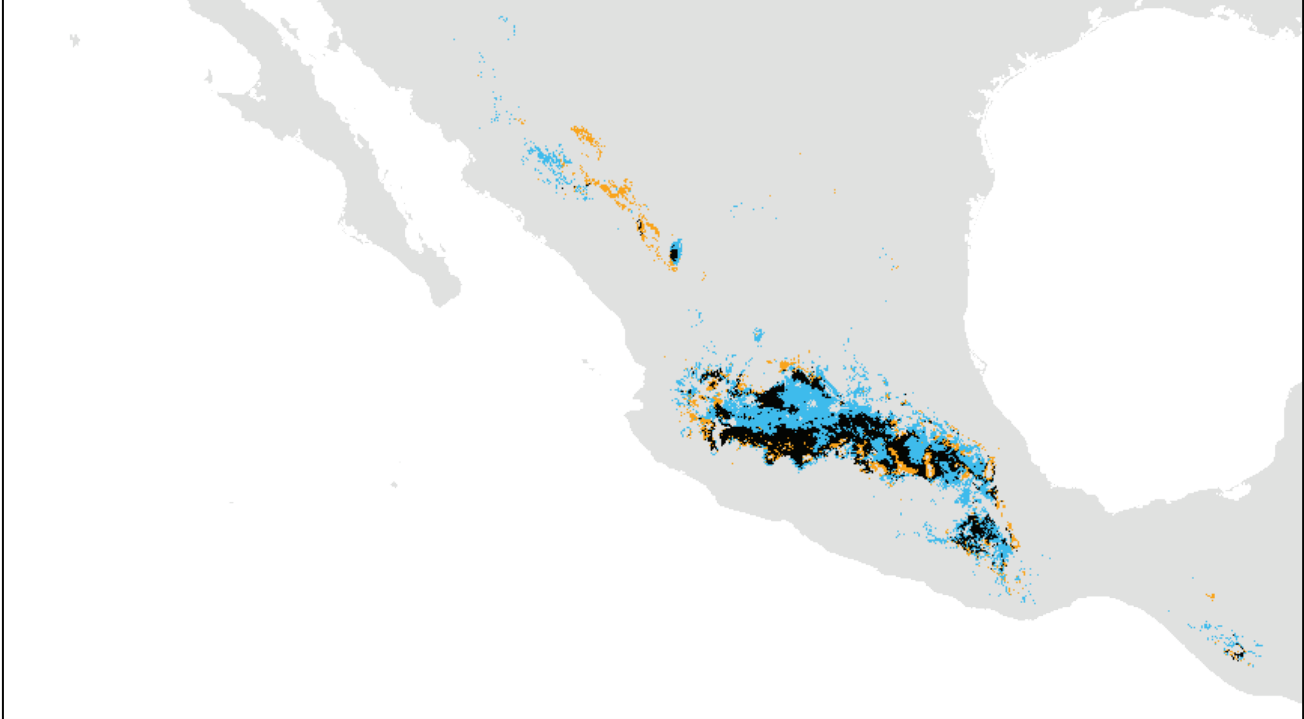
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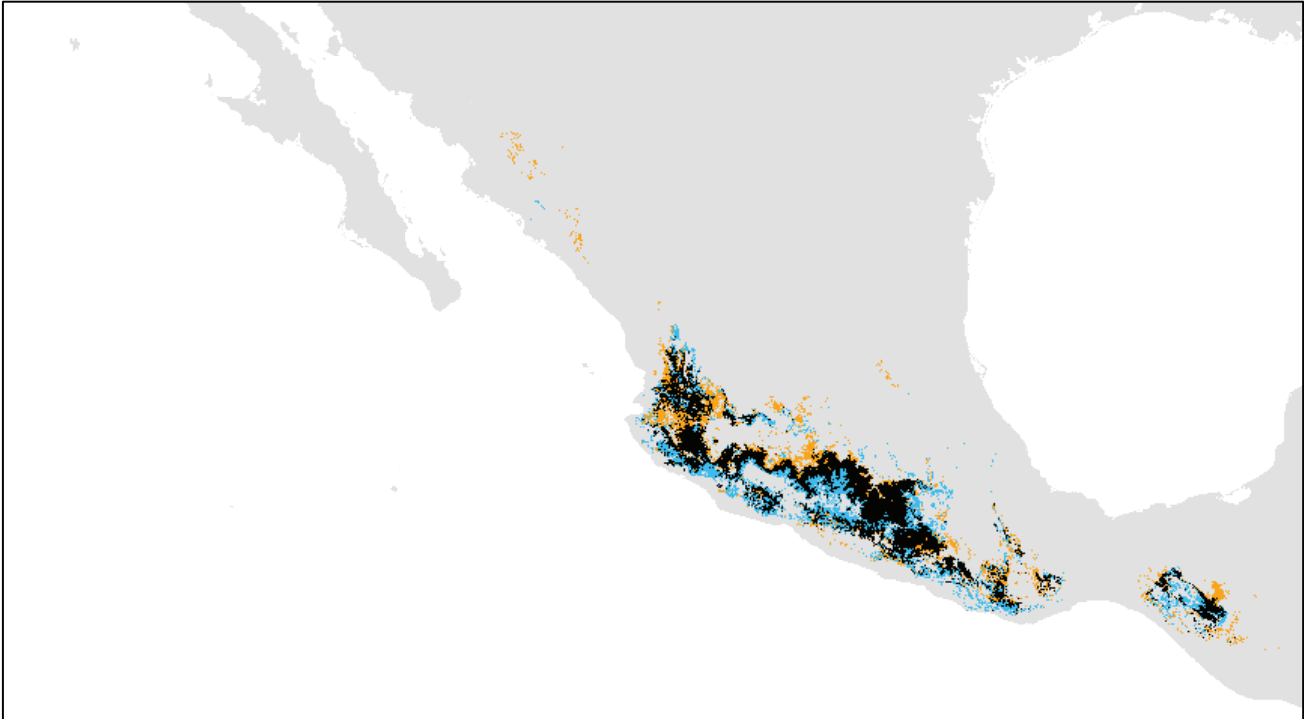
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MIROC_2070_RCP8.5
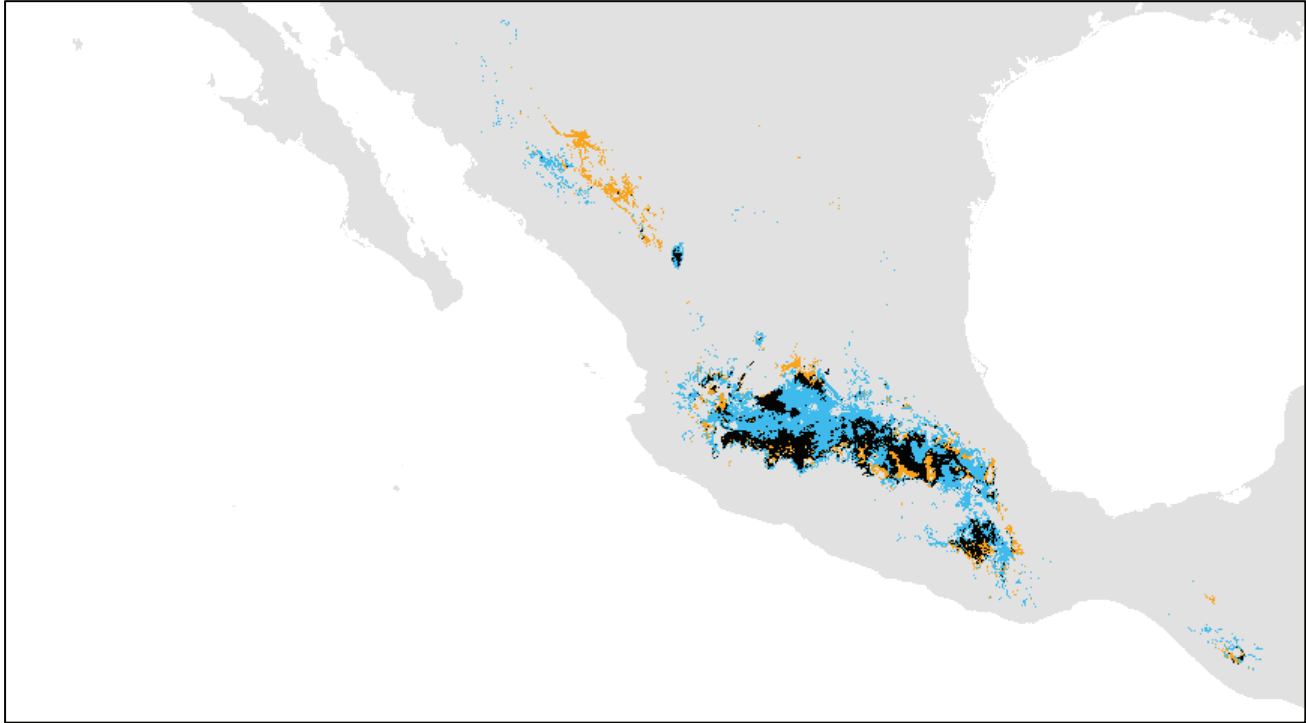
Zea mays spp. parviglumis
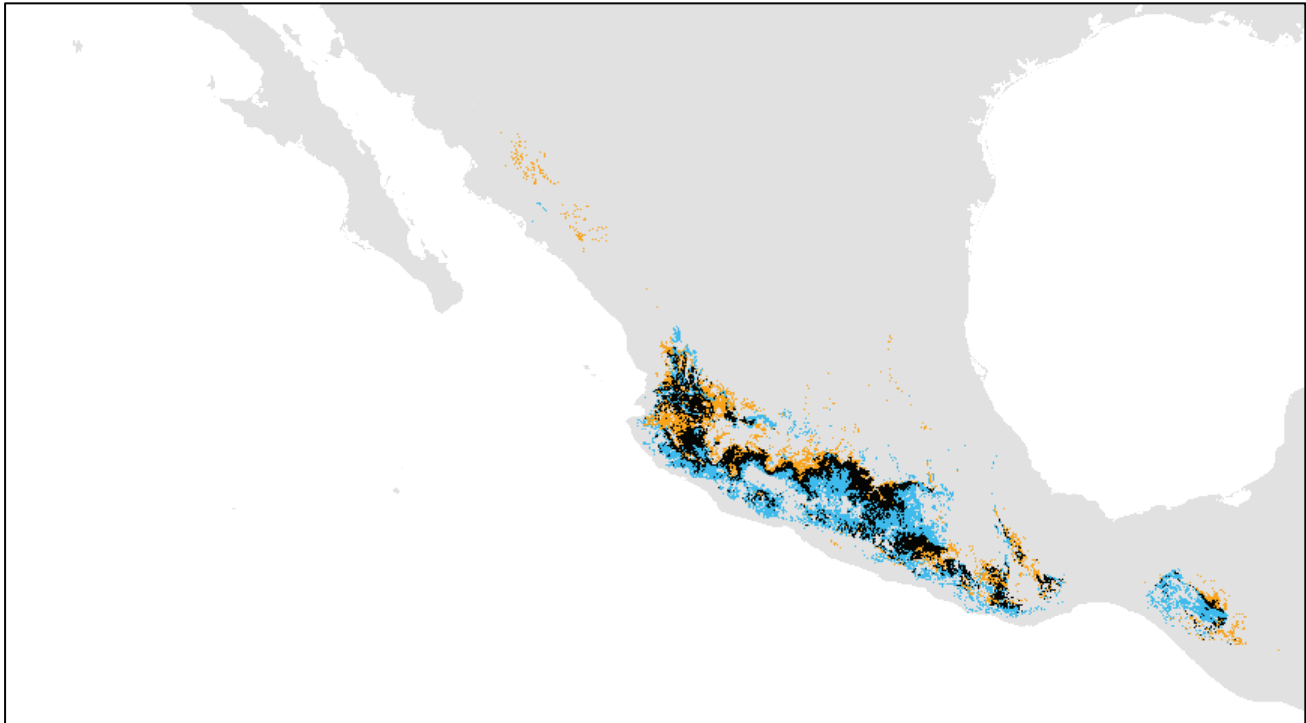
Zea mays spp. mexicana

Supplementary Figure 3. a-h, Genomic offset estimated with Gradient Forest analyses under the eight models of climate change for sampled populations of two species of teosintes in Mexico (*Zea mays* spp. *parviglumis* and *Z. mays* spp. *mexicana*). **i,** Correlation between per-population genomic offset estimated with paSNPs (red) and canSNPs (orange) versus the rest of the SNPs sets across the eight models of climate change. paSNPs: putative adaptive; canSNPs: candidate; refSNPs: reference; n_refSNPS: reference controled for allele frequencies; USNPs: putative adaptive plus candidate;baySNPs: outlier detected with bayenv; scenvSNPs: outlier detected with bayescenv; bay∩scenvzSNPs: outlier detected with bayenv and bayescenv. Total number of SNPs in each category with significant contribution to the model are given in parenthesis.

Supplementary Figure 3. continued

Supplementary Figure 3. continued

Supplementary Figure 3. continued

i
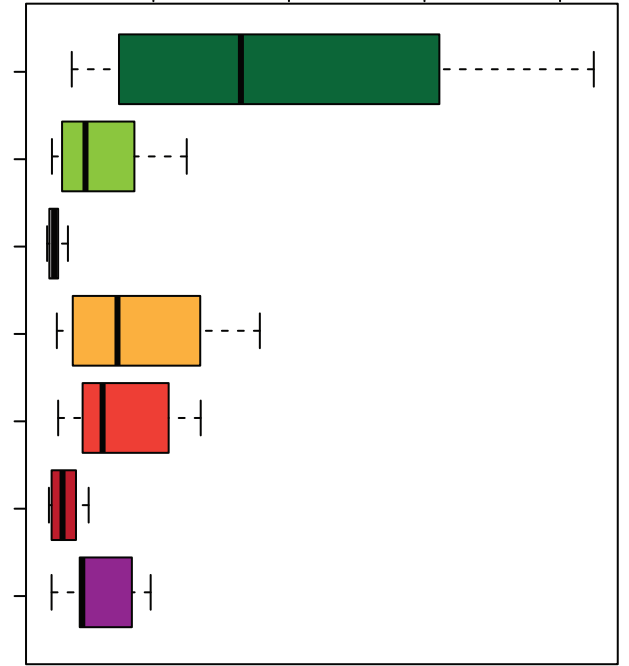
Zea mays spp. mexicana

Zea mays spp. parviglumis

Supplementary Figure 4. Contribution of different SNPs to the allele turnover function (R^2) constructed with a genome-wide Gradient Forest analyses for sampled populations of two species of teosintes in Mexico: (*Zea mays* spp. *parviglumis* and *Z. mays* spp. *mexicana*). Allele turnover functions were constructed using the complete set of 33,454 SNPs identified in teosintes. Boxplots showing the distribution of R^2 among SNPs with varying levels of climate-frequency associations. Gray boxes represent the distribution of R^2 for SNPS subsets according to their overall contribution to the allele turnover function. For the definition of SNP categories we used the quartile distribution of R^2 (1Q, median, 3Q) estimated for all SNPs. Total number of SNPs in each category are given in parenthesis. The number of refSNPs is less than the 500 sampled because only the SNPs with significant contributions are plotted.
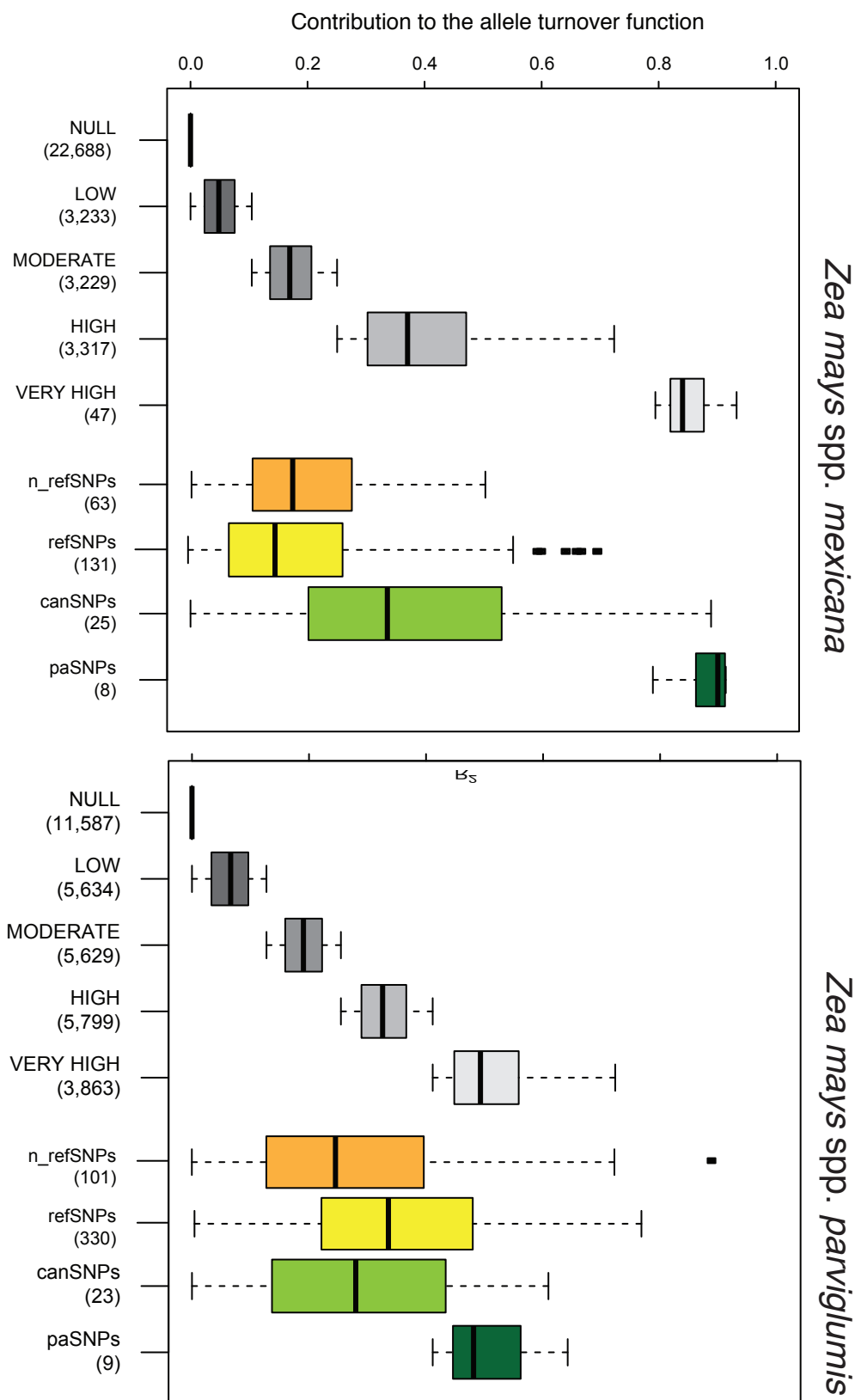
Supplementary Figure 5. Linear regressions between the estimated genomic offset under the two most extreme models of climate change (CCSM_2050_RCP4.5 and CCSM_2070_RCP8.5) versus the adaptive scores and the degree of climate change expected for sampled populations of two species of teosintes in Mexico: (*Zea mays* spp. *parviglumis* and *Z. mays* spp. *mexicana*). Open and black circles represent the genomic offset of populations under CCSM_2050_RCP4.5 and CCSM_2070_RCP8.5, respectively. Regression coefficients and statistical significance are given for each linear model.

Zea mays spp. parviglumis
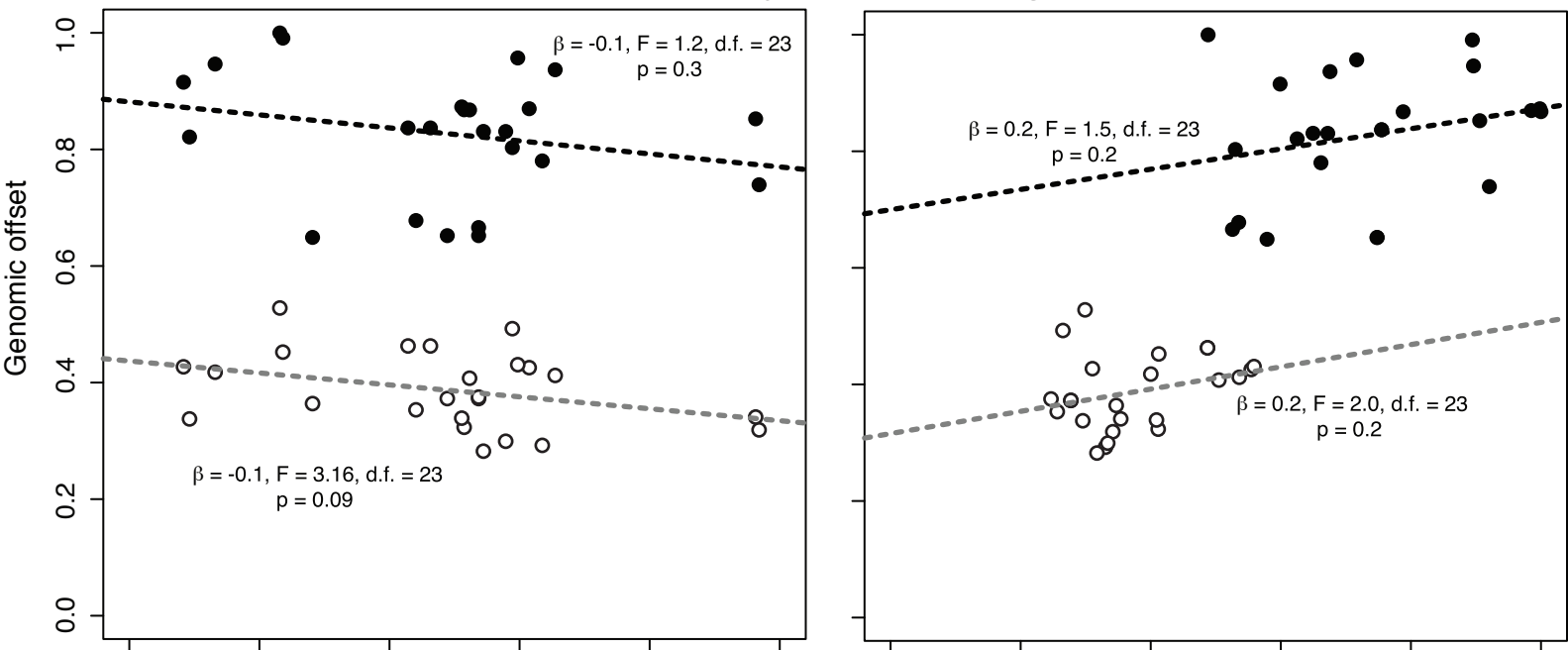
Zea mays spp. mexicana
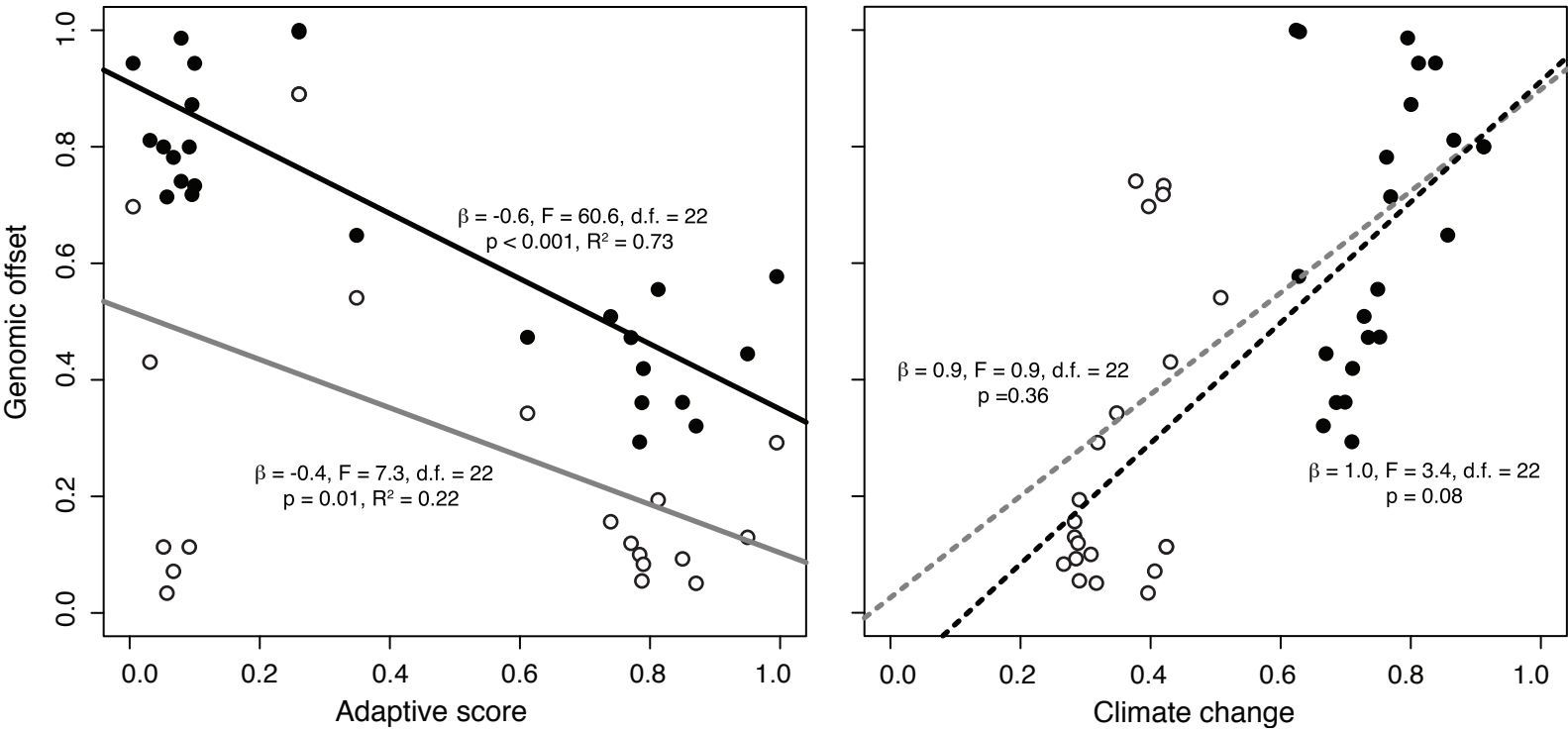
Supplementary Figure 6. Genomic offset estimated under the eight models of climate change for areas within the present-day and future allele distribution models for putative adaptive SNPs for two species of teosintes in Mexico: (*Zea mays* spp. *parviglumis* and *Z. mays* spp. *mexicana*). NP: areas outside the present-day and future distribution of paSNPs; P: areas only within the present-day distribution of paSNPs; F: areas only within the future distribution of paSNPs; P+F: areas within the overlapped present-day and future distribution of paSNPs. Missing values for F and P+F signify that predicted areas overlap with the present-day models.
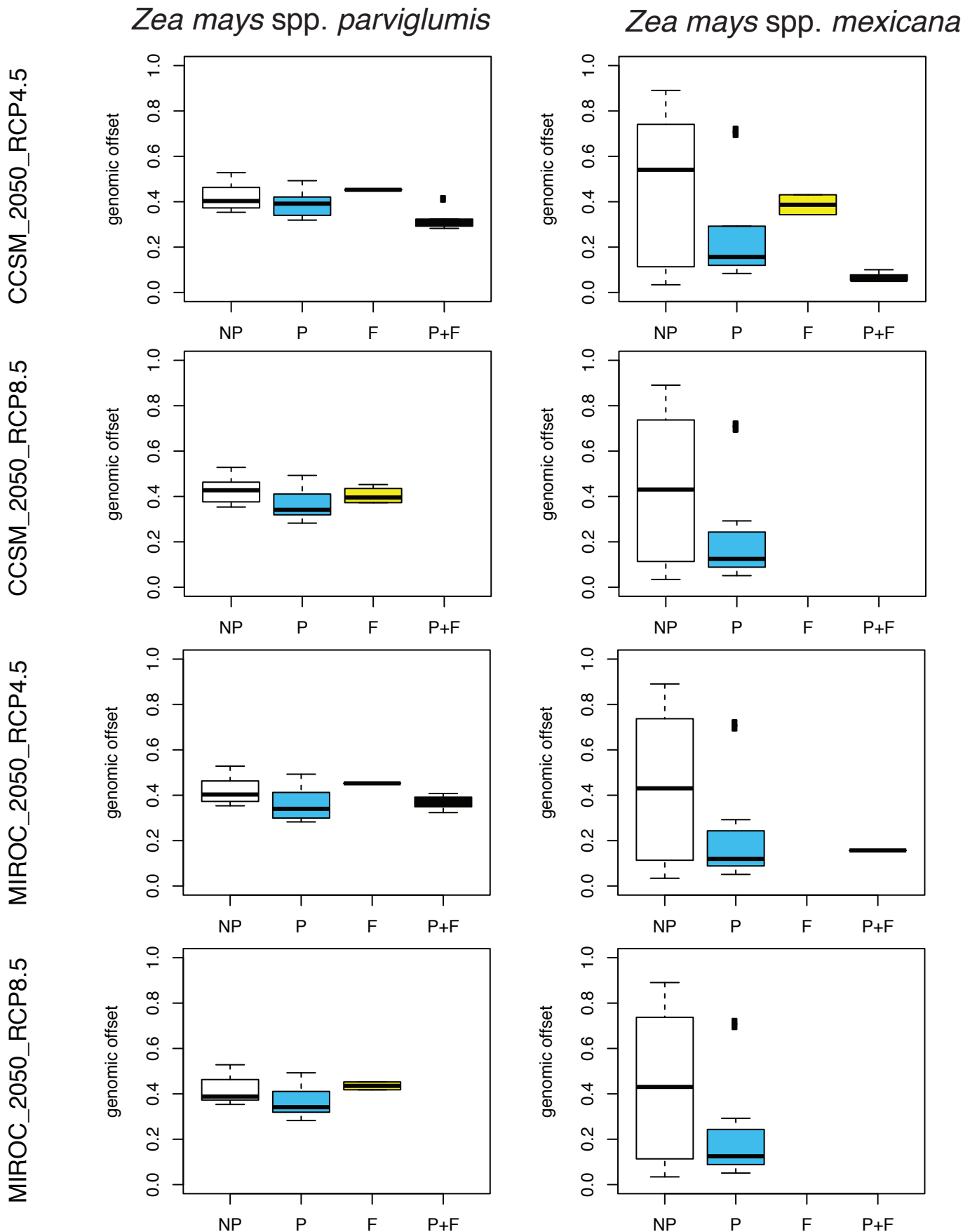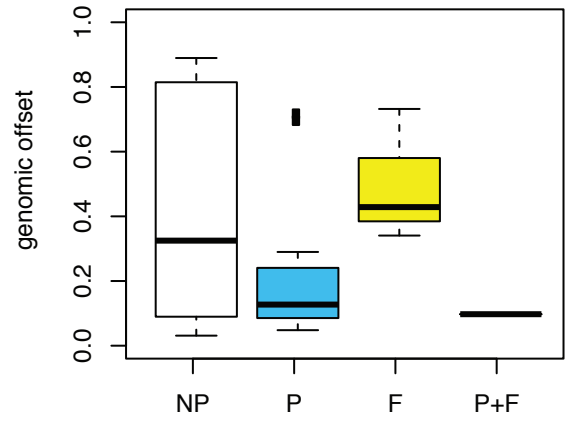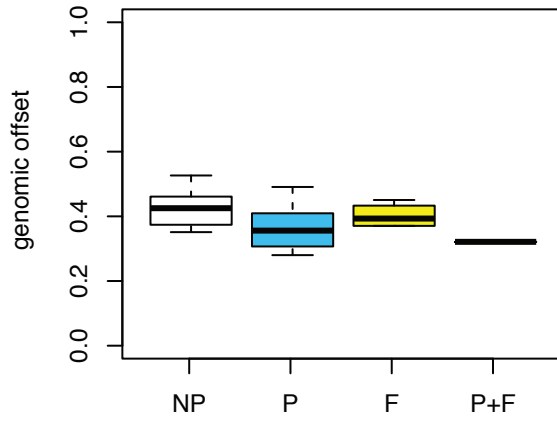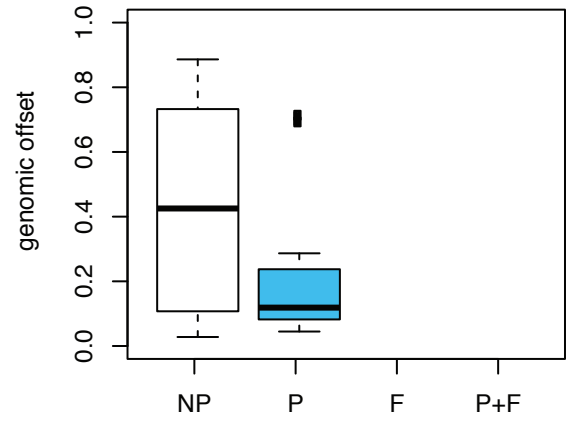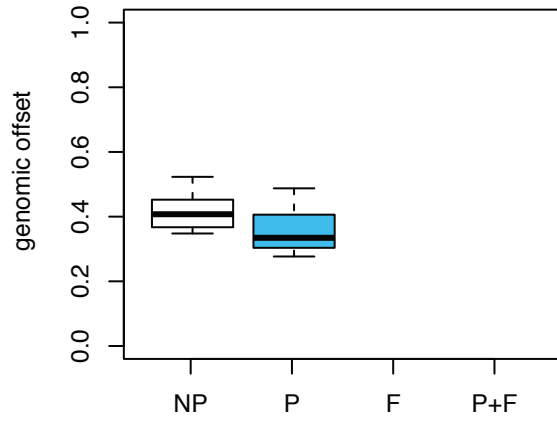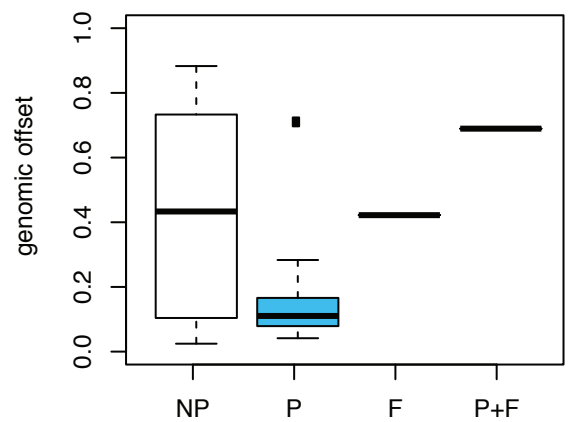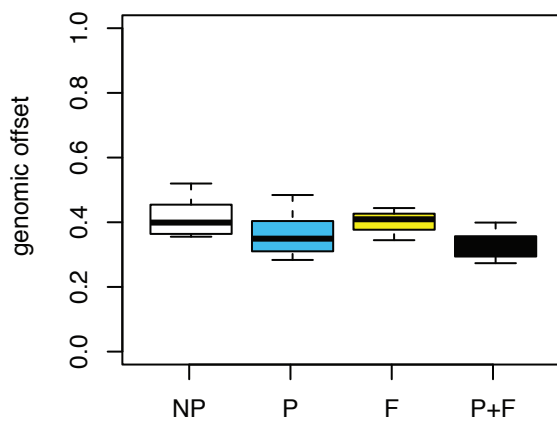
Supplementary Figure 6. Continued
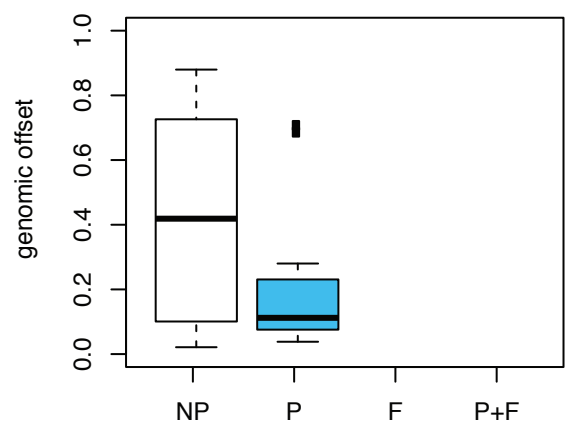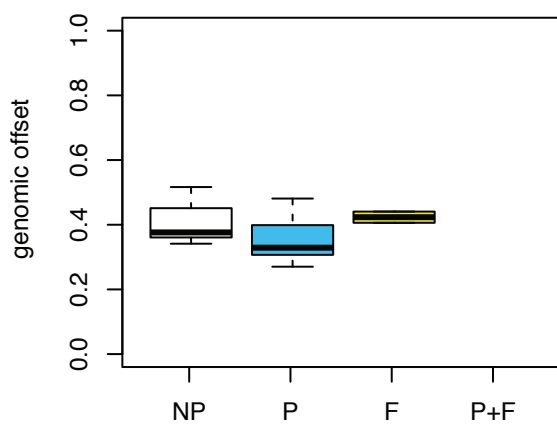
Supplementary Figure 7. Linear regressions between the estimated genomic offset under the eight models of climate change versus populations' genetic diversity (Hs) of sampled populations of two species of teosintes in Mexico: (*Zea mays* spp. *parviglumis* and *Z. mays* spp. *mexicana*). Regression coefficients and statistical significance are given for each linear model.

Zea mays spp. *parviglumis*

CCSM_2050_RCP4.5
$\beta = -0.04$, F = 7.0, d.f. = 22
p = 0.02, R^2 = 0.21

CCSM_2050_RCP8.5
$\beta = -0.05$, F = 8.79, d.f. = 22
p = 0.01, R^2 = 0.26

MIROC_2050_RCP4.5
$\beta = -0.04$, F = 7.9, d.f. = 22
p = 0.01, R^2 = 0.24

MIROC_2050_RCP8.5
$\beta = -0.04$, F = 8.7, d.f. = 22
p = 0.01, R^2 = 0.26

CCSM_2070_RCP4.5
$\beta = -0.04$, F = 6.6, d.f. = 22
p = 0.02, R^2 = 0.2

CCSM_2070_RCP8.5
$\beta = -0.06$, F = 10.7, d.f. = 22
p < 0.001, R^2 = 0.3

MIROC_2070_RCP4.5
$\beta = -0.04$, F = 6.9, d.f. = 22
p = 0.02, R^2 = 0.2

MIROC_2070_RCP8.5
$\beta = -0.05$, F = 8.3, d.f. = 22
p = 0.01, R^2 = 0.25
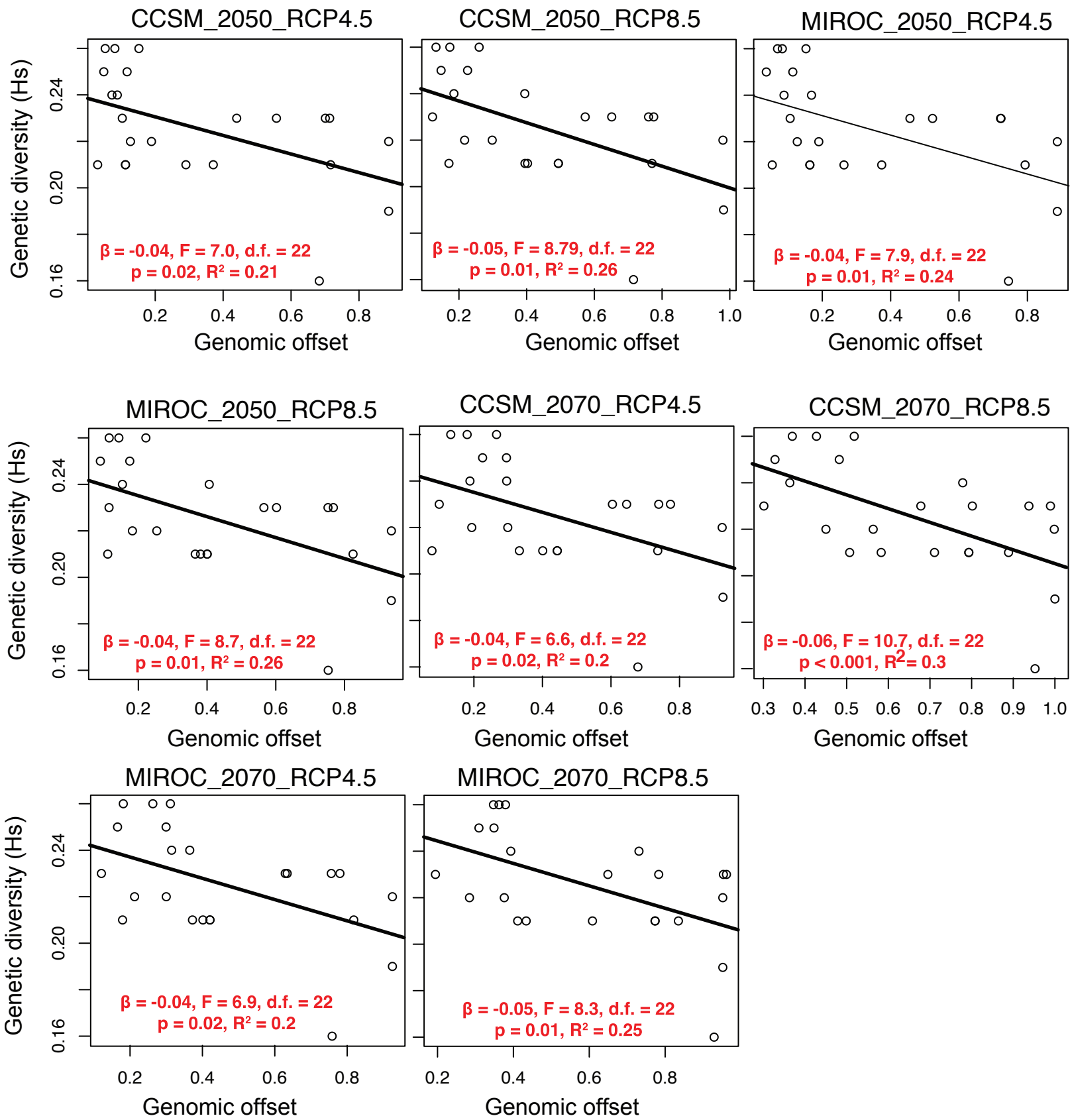
Zea mays spp. *mexicana*
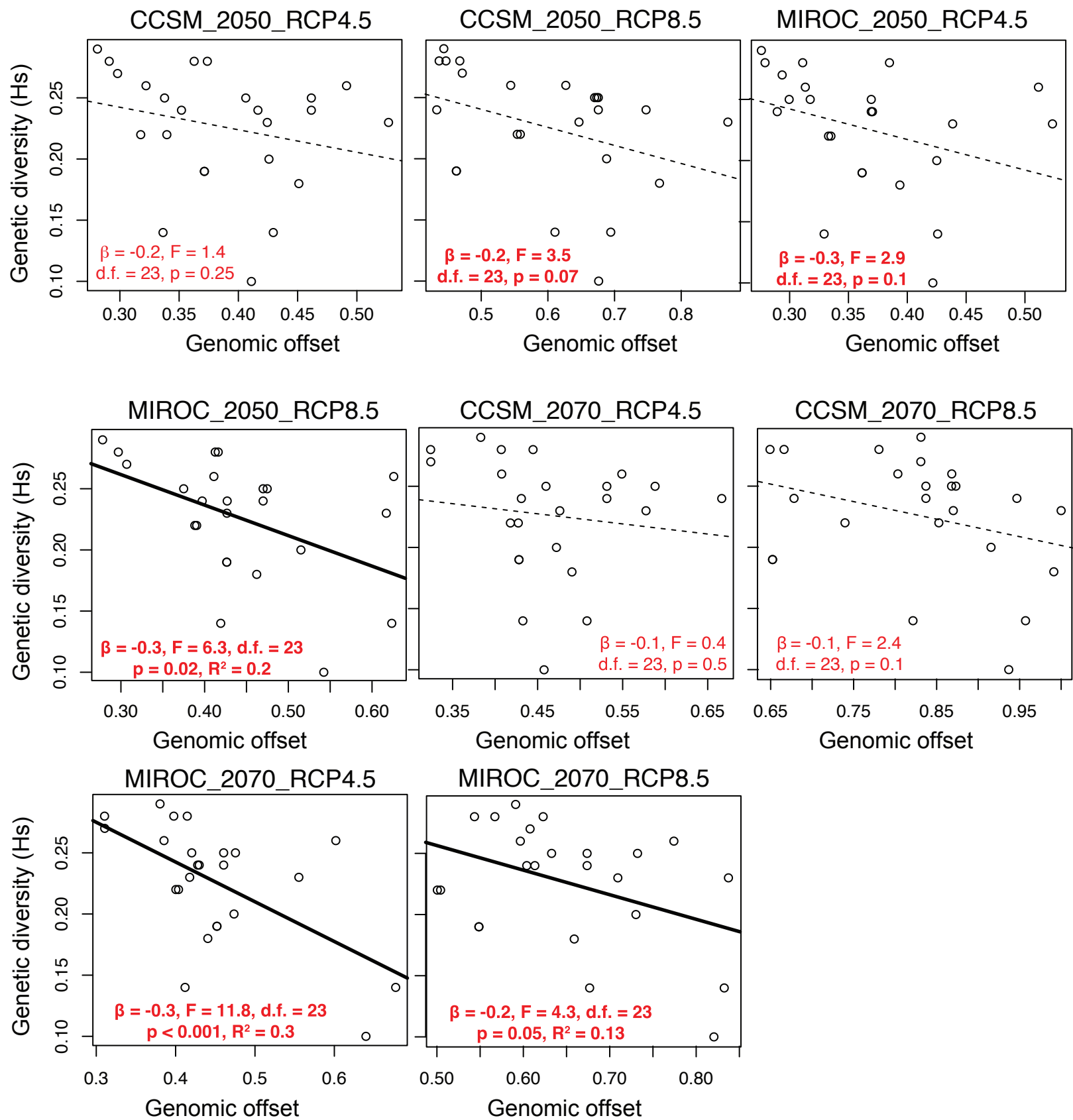
Supplementary Figure 8. Adaptive score and genomic offset as a function of migration probabilities estimated using circuit theory and allele distribution models under the two most extreme models of climate change (CCSM_2050_RCP4.5 and CCSM_2070_RCP8.5) for sampled populations of two species of teosintes in Mexico: (*Zea mays* spp. *parviglumis* and *Z. mays* spp. *mexicana*).Genomic offset was estimated using the paSNPs. Except otherwise stated, F-statistics are statistically significant with p-val < 0.01 (d.f. = 21).
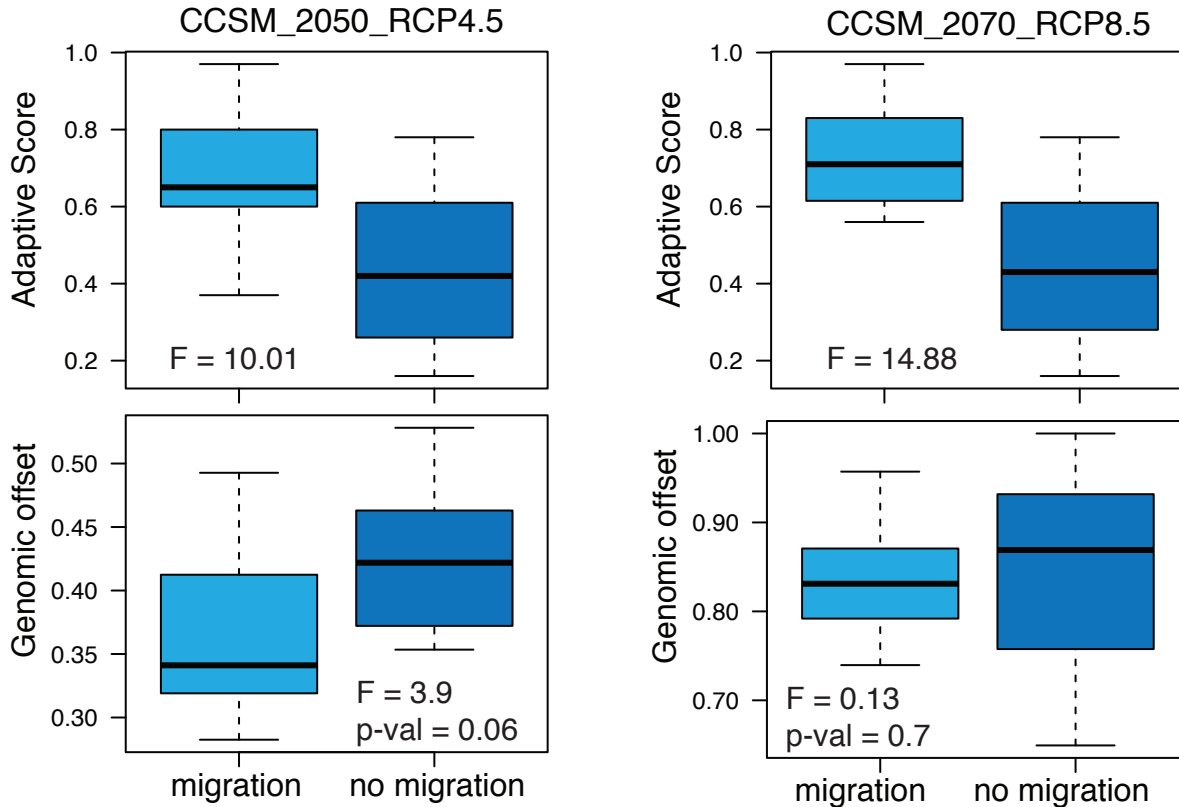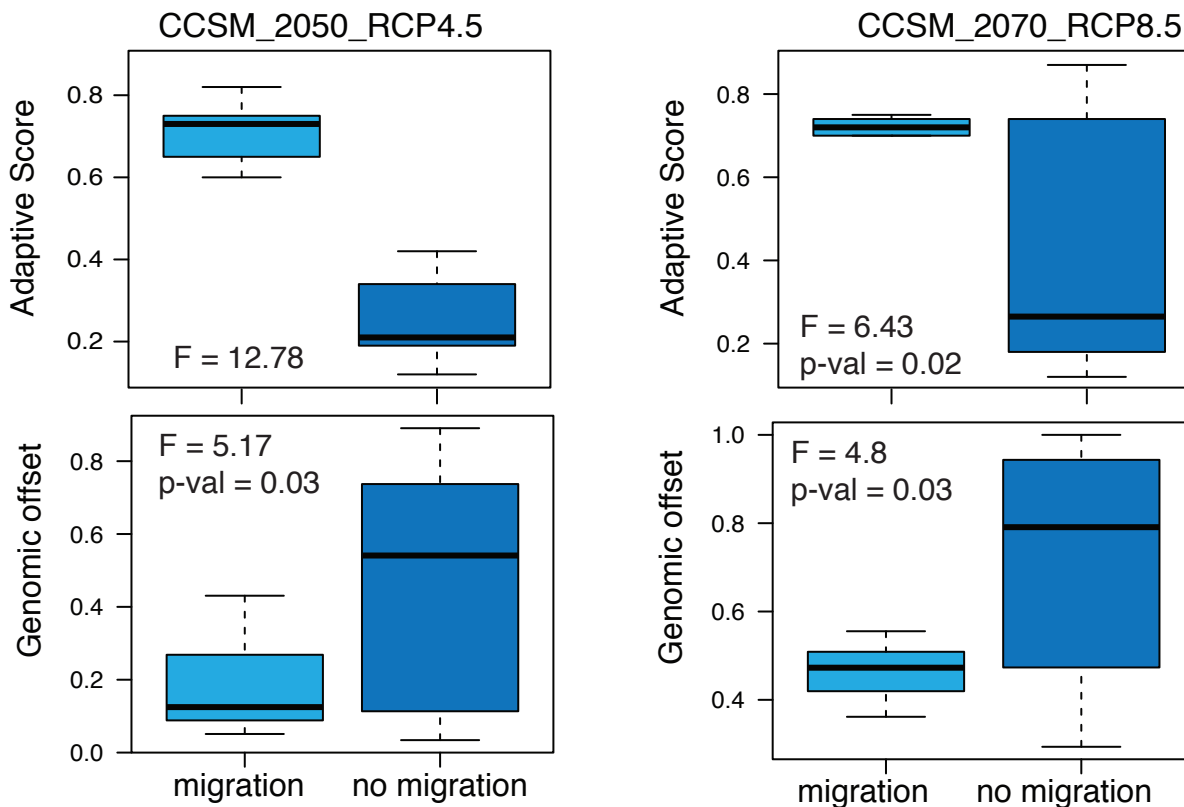
Supplementary Figure 9. Linear regressions between the estimated adaptive score versus mean annual temperature, geographic range size, and mean genomic offset for 46 maize landraces in Mexico. a, Association between adaptive scores using paSNPs and mean temperature across known occurrence of landraces (same as in Figure 2d). b, Association between adaptive scores using the paSNPs and geographic range size for landraces (same as in Figure 2c). c-d, Association between adaptive scores using paSNPs and mean genomic offset estimated from known occurrence of landraces under two most extreme models: CCSM_2050_RCP4.5 (same as in Figure 2e) and CCSM_2070_RCP8.5. Frequency histograms show the distribution of regression coefficients and adjusted R^2 estimated for 1,000 sub-samples of refSNPs and the red vertical lines represent the estimates using paSNPs.

a

$\beta = 0.01$, F = 17.7, d.f. = 45
$p < 0.001$, $R^2 = 0.27$

b

$\beta = 0.02, F = 1.1, d.f. = 45$
$p = 0.31, R^2 = 0.002$

Adaptive score

Geographic range size (log)

0.002

Adjusted R²
for refSNPs

0.02

Regression coefficients (β)
for refSNPs

C

β = -3.31, F = 3.8, d.f. = 45
p = 0.06, R² = 0.06

d

$\beta = -4.34, F = 11.27, d.f. = 45$
$p = 0.001, R^2 = 0.19$
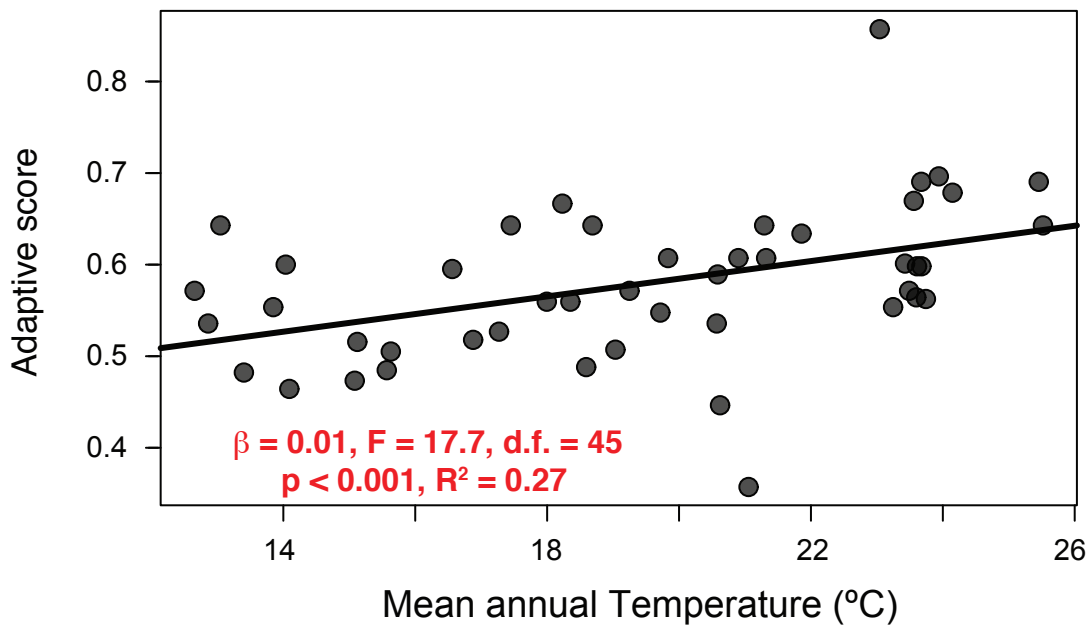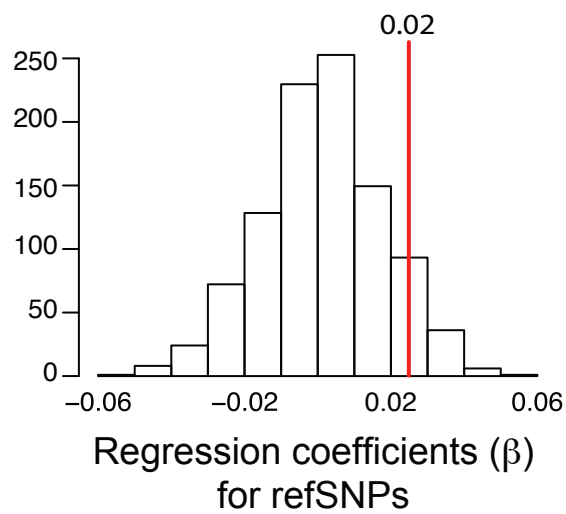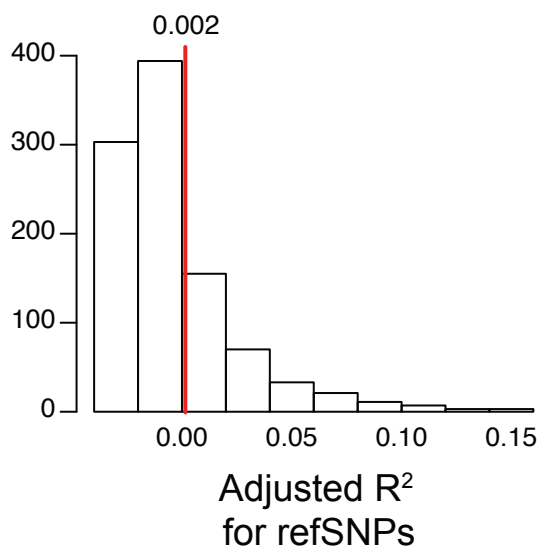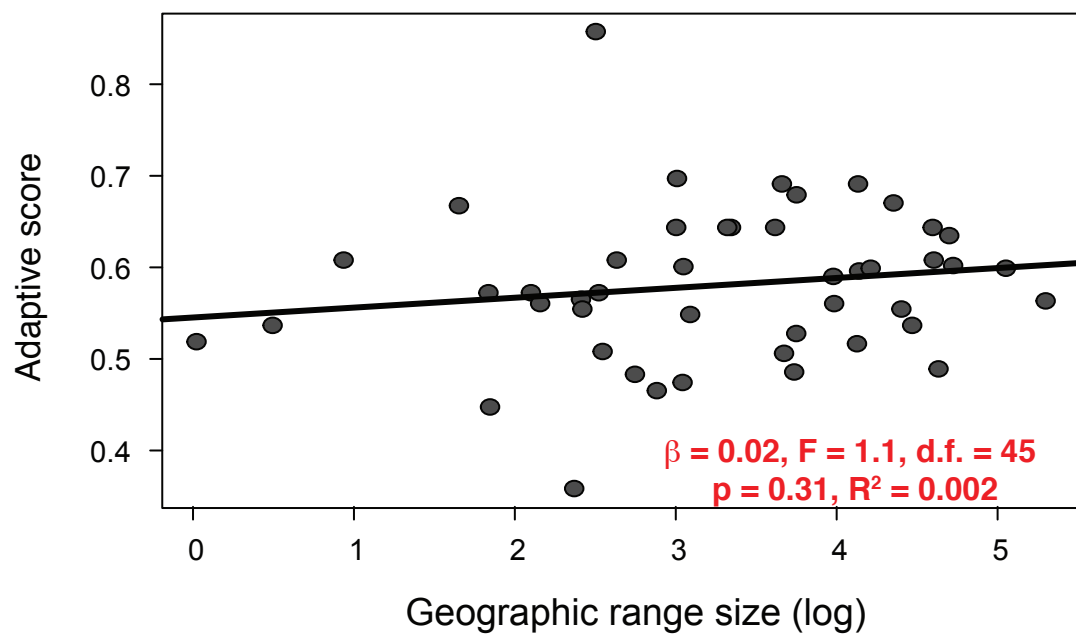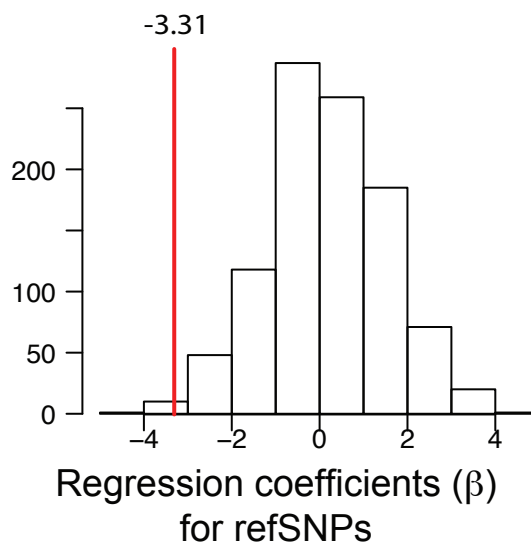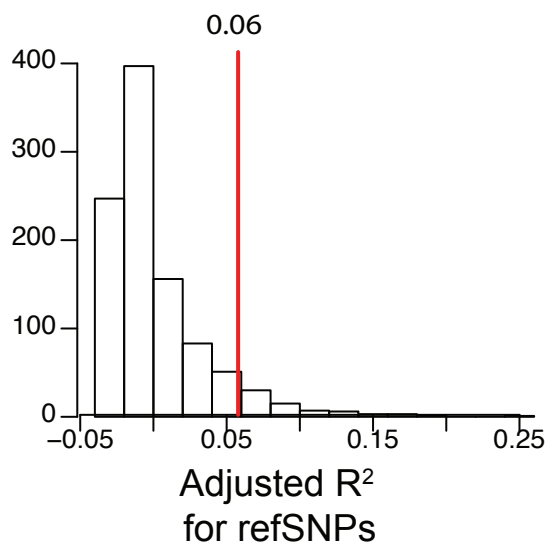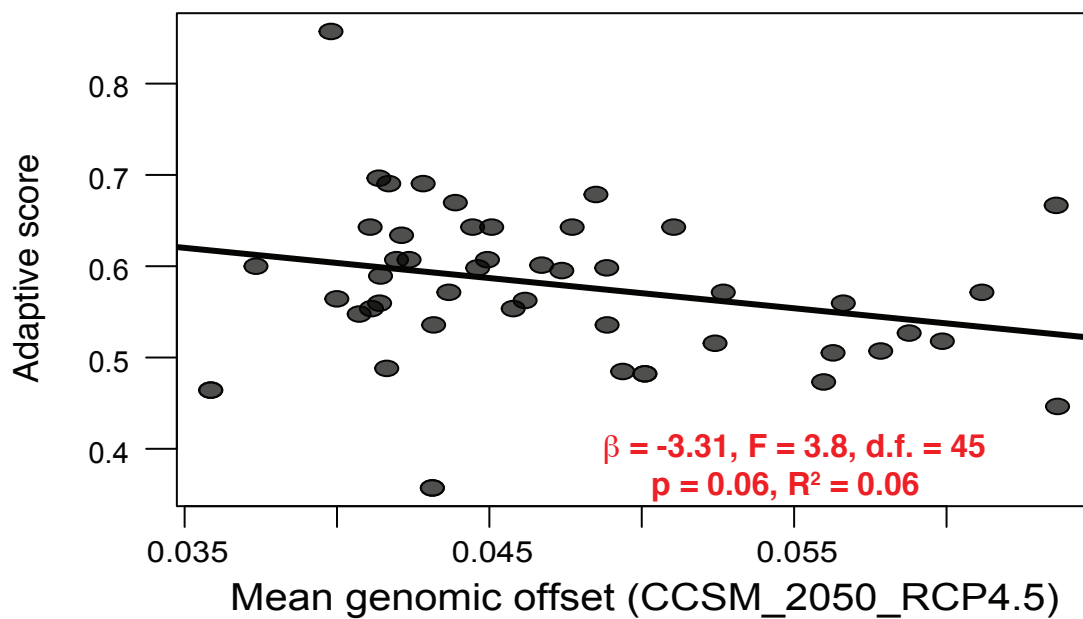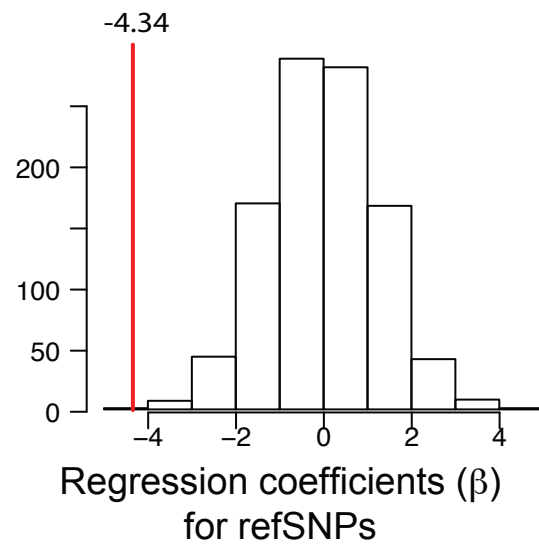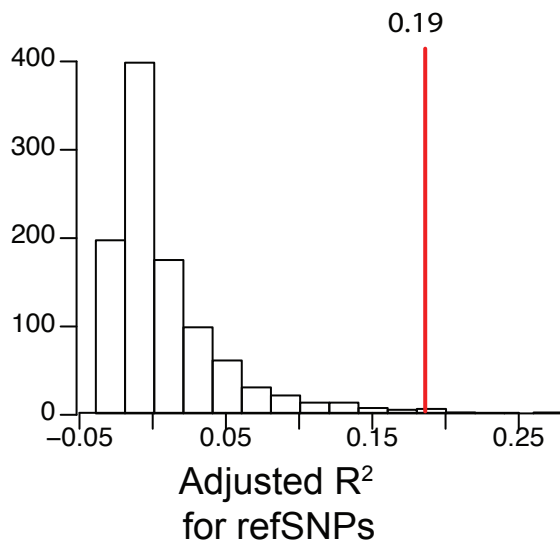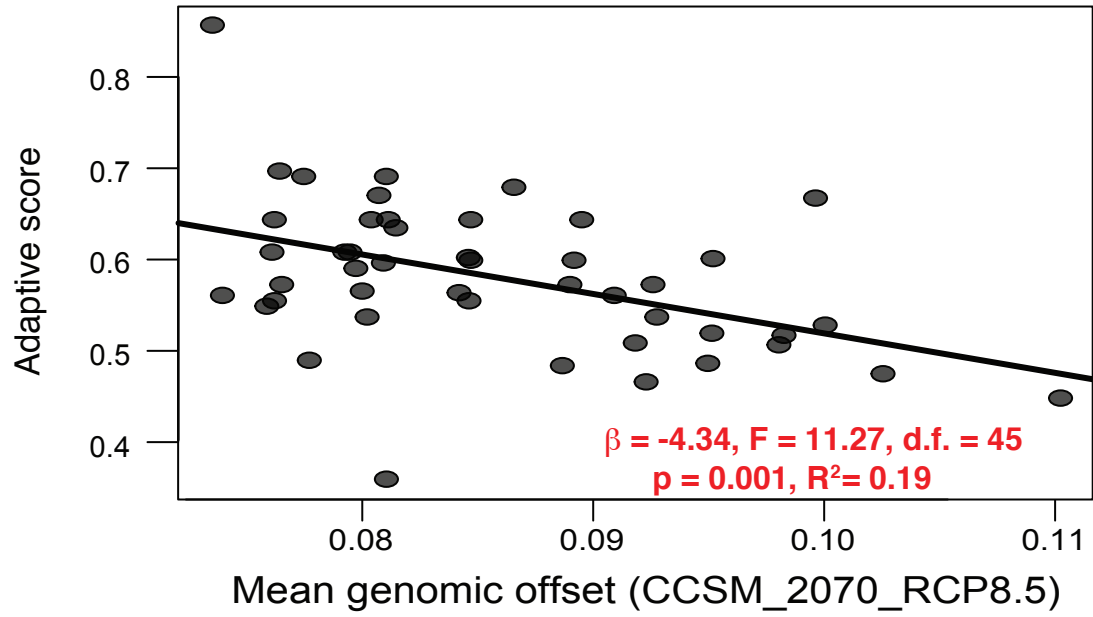
Supplementary Figure 10. Correlations between pairwise genetic differentiation (F_{ST}) and estimated allele turnover as predicted by Gradient Forest among sampled populations of two species of teosintes in Mexico: (*Zea mays* spp. *parviglumis* and *Z. mays* spp. *mexicana*). Allele turnover and F_{ST} were estimated separately for each set of SNPs. a-b, correlations for reference SNPs. c-d, correaltions for candidate SNPs. e-f, correlations for putative adaptive SNPs. Correlation statistics (r) are given for partial Mantel tests performed controlling for environmental distances among populations. All correlations were sistically significant with p-value < 0.001.

Zea mays spp. *parviglumis*

Zea mays spp. *mexicana*
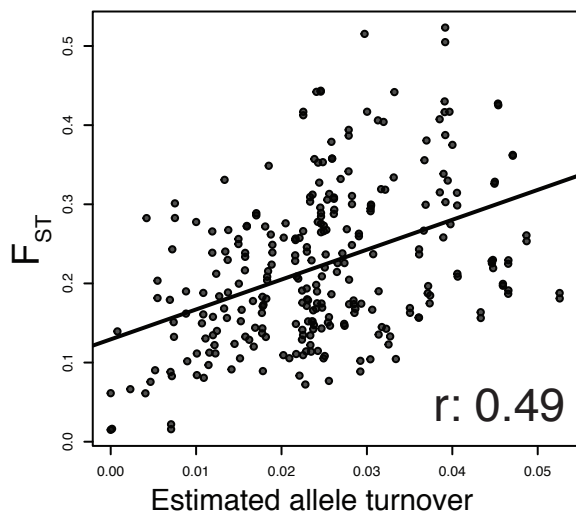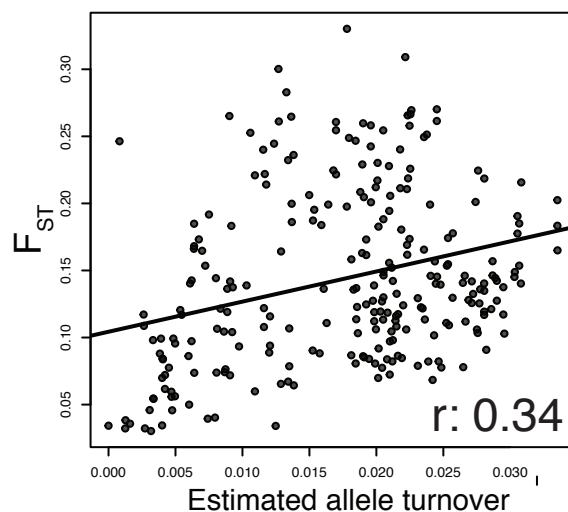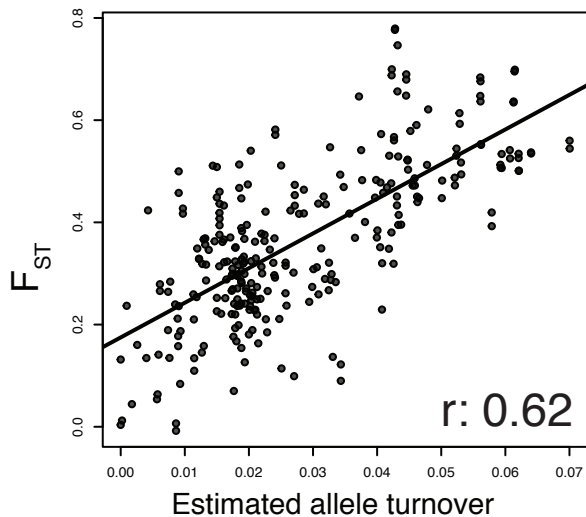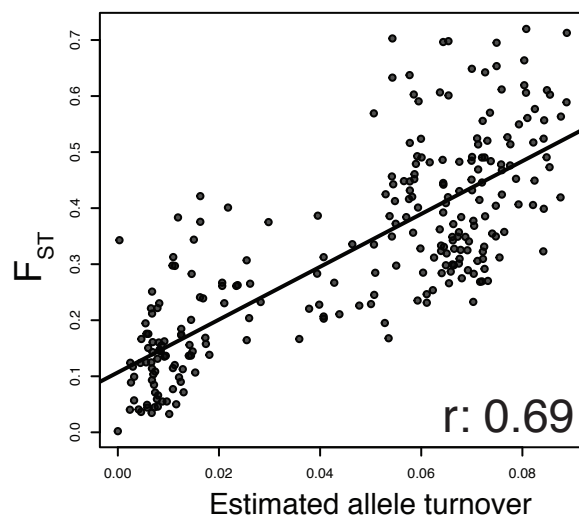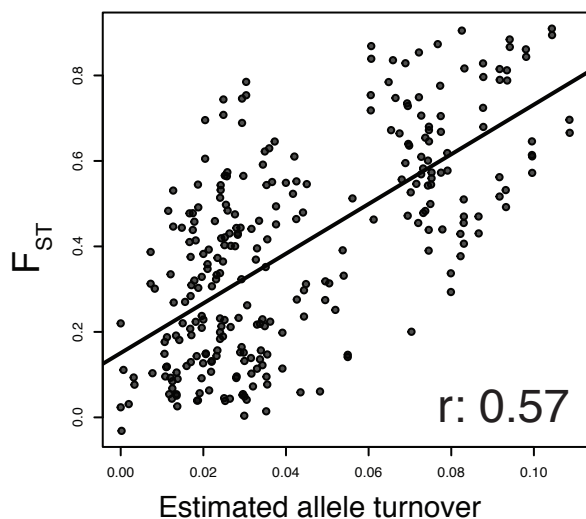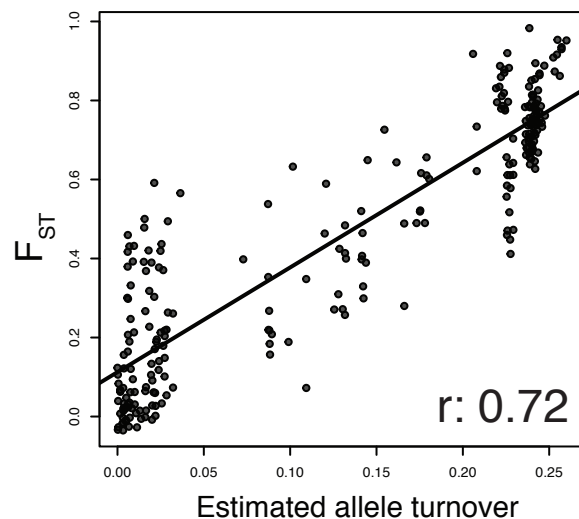
Supplementary Figure 11. Linear regressions between climatic suitability values for candidate and putative adaptive SNPs as predicted by ecological niche modeling and allele frequencies for sampled population of two species of teosintes in Mexico: (*Zea mays* spp. *parviglumis* and *Z. mays* spp. *mexicana*). Ecological niche models were constructed for each SNPs separately (models available in ASCII format at https://github.com/spiritu-santi/teosintes) and mean suitability was estimated for candidate SNPs and putative adaptive SNPs separately. All regressions were statistically non-significant with p-value > 0.05.
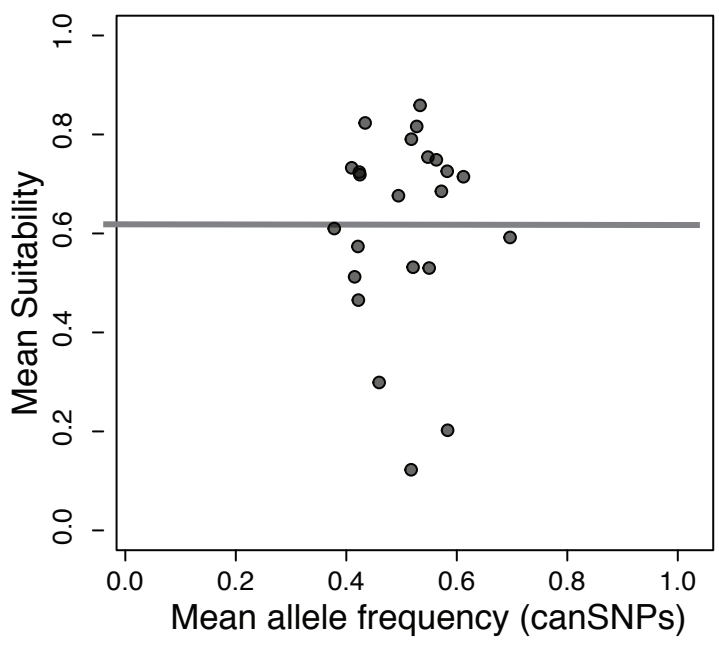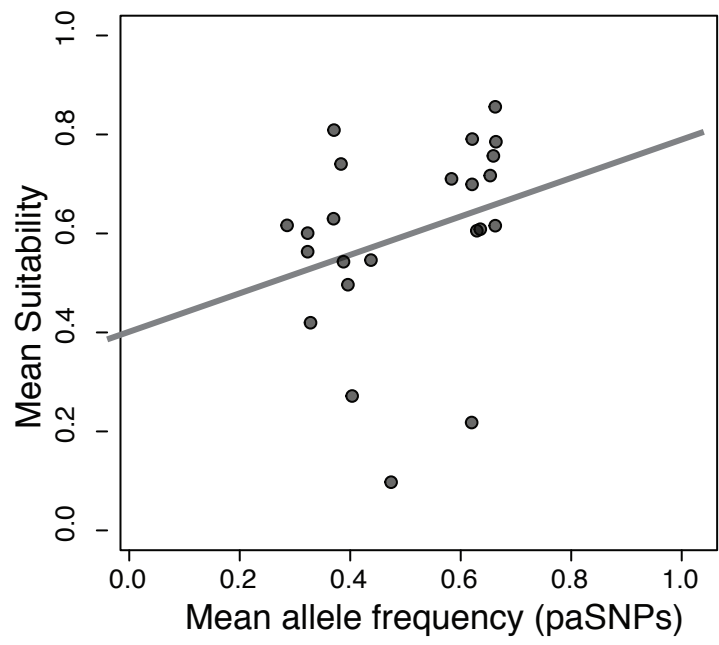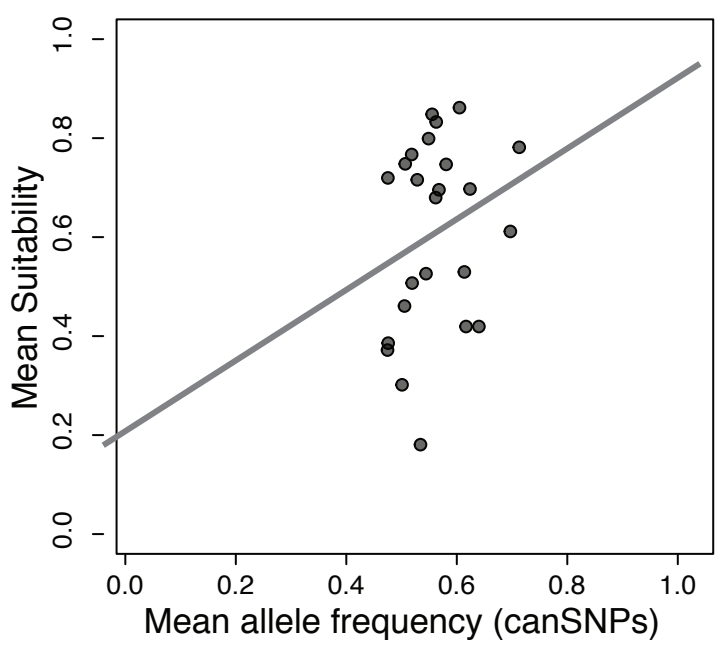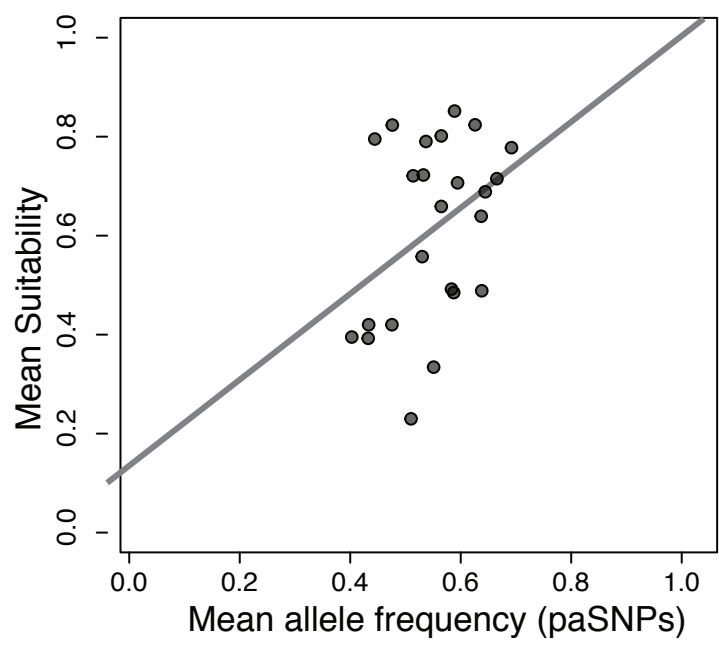
Supplementary Figure 12. Minimum geogaphic distances to population with the highest adaptive score as a function of migration probabilities estimated using circuit theory and allele distribution models under the two most extreme models of climate change (CCSM_2050_RCP4.5 and CCSM_2070_RCP8.5) for sampled populations of two species of teosintes in Mexico (*Zea mays* spp. *parviglumis* and *Z. mays* spp. *mexicana*).Geographic distances were measured in kilometers and correspond to the the minimum distances to the population with the highest adaptive score (best population) and to the neighboring population with a higher adaptive than the focal population (best neighbor). Except otherwise stated, F-statistics are statistically significant with p-val < 0.01 (d.f. = 21).
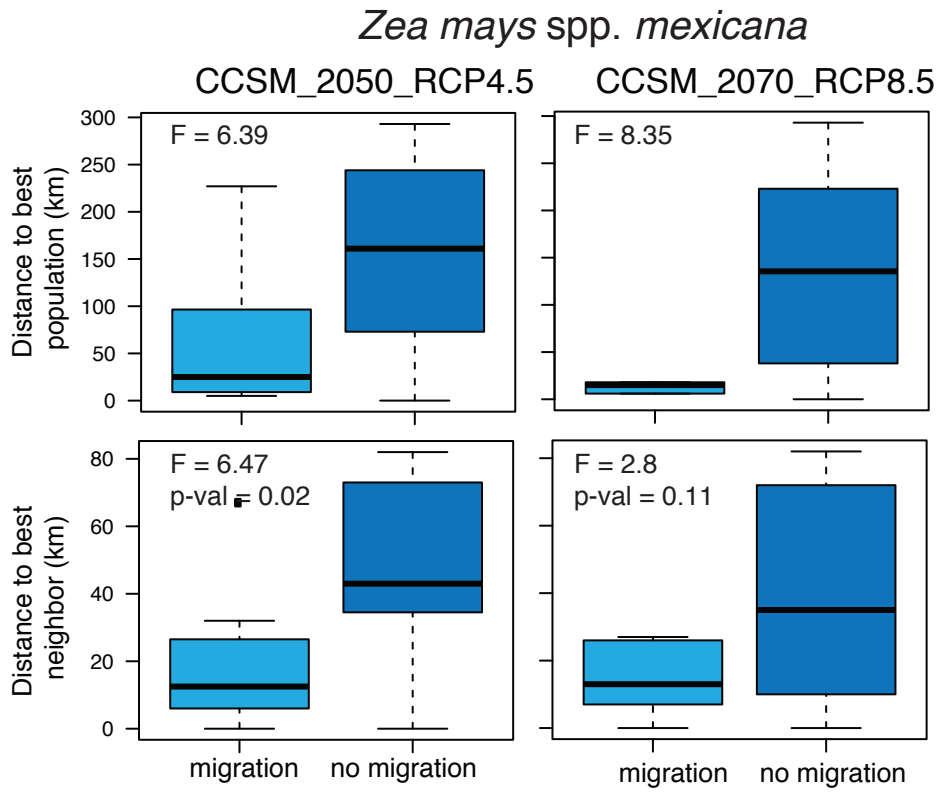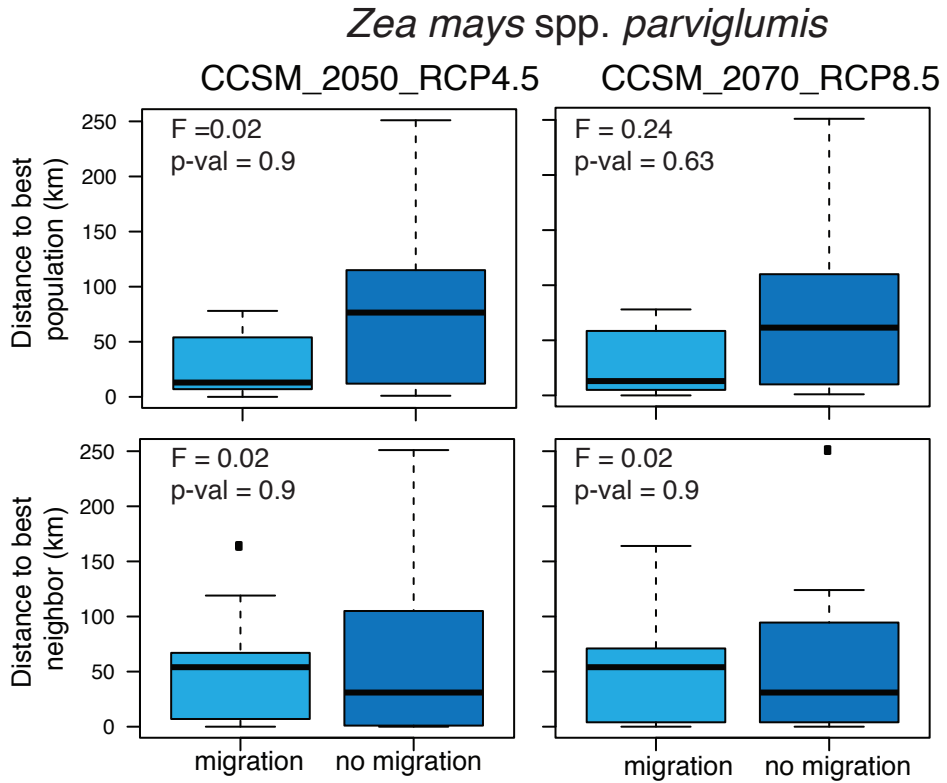
Supplementary Table 1. Reduction in the geographical distribution predicted for the two species of teosintes in Mexico under eight different models of climate change: *Zea mays* spp. *mexicana* (*mexicana*) and *Zea mays* spp. *parviglumis* (*parviglumis*). Proportion of known occurrences (ref. 14) and sampled populations within the future predicted distribution for each species. Teosintes occurrences obtained from www.biodiversidad.gob.mx/genes/proyectoMaices.html

	Year	Climate model	Projected future extent of species relative to the present-day distribution	Proportion of predicted occurrences within the future distribution	Proportion of sampled populations predicted within the future distribution
mexicana					23 populations
	2050	CCSM_4.5	83%	81%	84%
		CCSM_8.5	70%	67%	52%
		MIROC_4.5	67%	75%	72%
		MIROC_8.5	60%	61%	60%
		Mean for 2050	**70%**	**70.9%**	**67%**
	2070	CCSM_4.5	72%	72%	68%
		CCSM_8.5	57%	47%	44%
		MIROC_4.5	60%	53%	44%
		MIROC_8.5	57%	46%	40%
		Mean for 2070	**61%**	**54.6%**	**49%**
parviglumis					24 populations
	2050	CCSM_4.5	106%	89%	88%
		CCSM_8.5	102%	81%	79%
		MIROC_4.5	91%	88%	79%
		MIROC_8.5	84%	84%	83%
		Mean for 2050	**96%**	**85.3%**	**82%**
	2070	CCSM_4.5	109%	85%	83%
		CCSM_8.5	88%	55%	50%
		MIROC_4.5	92%	83%	75%
		MIROC_8.5	75%	62%	67%
		Mean for 2070	**91%**	**71.3%**	**69%**

Supplementary Table 2. Gene annotation for specific putative adaptive SNPs (paSNPs) identified in the two species of teosintes in Mexico: Zea mays spp. mexicana (mexicana) and Zea mays spp. parviglumis (parviglumis). Gene positions were obtained by blasting the chip sequences to the Hapmap2 maize genome reference (Chia et al., 2012). Based on the chip primers, SNPs were identified as being within or near coding regions known for maize. All sequences that were found in a coding regions were annotated against the Phytozome database. Finally, the literature was searched for evidences of local adaptation associated to the putative identified genes (For more details of the methods see ref. 20). According to the annotations, some genes are associated to drought or heat resistance in maize or other plants, while other genes are associated to other stressed related traits. Even if not all SNPs are found to be associated to climate change related traits, we are still finding a strong discriminative power and treating these SNPs as putative adaptive. We believe it is possible that not finding the precise annotations can be explained by the fact that there is a large phylogenetic distance between some species. For instance, an homologous gene of GRMZM2G144985 has been found to be related to phosphorus-impoverished soils response in *Hakea prostrata* (Proteaceae). For a functional validation of these SNPs it will be necessary to perform experimental tests that are outside the scope of the present study.

	Gene Name	Chip Name	Chromosome	Position	Gene	Associated response	Species	Reference
mexicana	GRMZM2G141596	SYN32365	9	140,846,908	CONSTANS interacting protein 4	flowering time	*Zea mays* (Poaceae)	Fjellheim et al. (2014). *Frontiers in plant science*, 5, 431.
mexicana	GRMZM2G144985	PUT.163a.148928873.366	9	142,293,132	long-chain base1	phosphorus-impoverished soils response	*Hakea prostrata* (Proteaceae)	Kuppusamy et al. (2014). *Plant physiology*, 166, 1891-1911.
mexicana	GRMZM2G145085	PZE.109096578	9	142,298,030	transcription activators;DNA binding;RNA polymerase II transcription factors;catalytics;transcription initiation factors	ABA and drought responses	*Arabidopsis thaliana* (Brassicaceae)	Jin et al. (2011). *New Phytologist*, 190, 57-74.
mexicana	GRMZM2G166780	SYN27200	9	139,374,933	RNA recognition motif in THO complex subunit 4 (THOC4) and similar proteins	abiotic stress	*Oryza sativa* (Poaceae)	Sharma et al (2016). *Frontiers in plant science*, 7.
parviglumis	GRMZM2G063306	PZE.103059706	3	112,045,081	zinc induced facilitator-like 1	drought tolerance by regulating stomatal closure	*Arabidopsis thaliana* (Brassicaceae)	Remy et al. (2013). *The Plant Cell*, 25, 901-926.
parviglumis	GRMZM2G081928	PZE.106008139	6	23,525,249	Peroxidase superfamily protein	Arsenic stress	*Oryza sativa* (Poaceae)	Yu et al. (2012). *New Phytologist*, 195, 97-112.
parviglumis	GRMZM2G165090	PZE.101131254	1	168,430,002	phytochrome interacting factor 3	improves drought and salt stress tolerance in rice	*Oryza sativa* (Poaceae)	Gao et al. (2015). *Plant molecular biology*, 87, 413-428.

Supplementary Table 3. Summary of the genomic offset estimated for species of teosintes in Mexico using different sets of SNPs and eight different models of climate change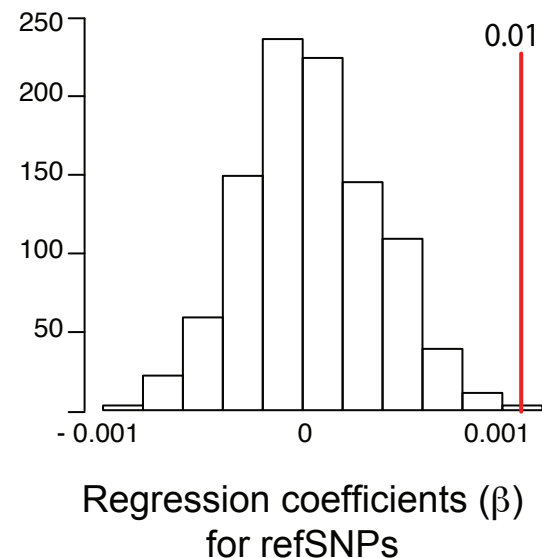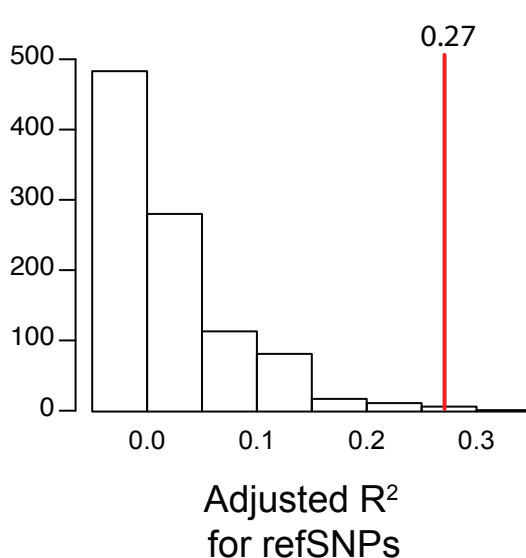: Zea mays spp. mexicana (mexicana) and Zea mays spp. parviglumis (parviglumis). For each climatic model we estimated the range and the median of the estimated genomic offset for teosintes occurrences (ref. 14) and sampled populations, separately. Teosintes occurrences obtained from www.biodiversidad.gob.mx/genes/proyectoMaices.html

SNP dataset	Projected year	Climate model	Range (median) of genomic offset for occurrences	Range (median) of genomic offset for sampled populations	SNP dataset
mexicana	refSNPs	2050	CCSM_4.5	0.04- 0.07 (0.05)	0.04-0.08 (0.05)
			CCSM_8.5	0.05- 0.09 (0.06)	0.05-0.10 (0.06)
			MIROC_4.5	0.04- 0.08 (0.05)	0.04-0.08 (0.05)
			MIROC_8.5	0.05-0.10 (0.06)	0.05-0.11 (0.06)
		2070	CCSM_4.5	0.05-0.08 (0.06)	0.05-0.09 (0.06)
			CCSM_8.5	0.08-0.13 (0.09)	0.08-0.13 (0.09)
			MIROC_4.5	0.05-0.12 (0.06)	0.04-0.12 (0.06)
			MIROC_8.5	0.07- 0.15 (0.08)	0.07-0.16 (0.09)
	canSNPs	2050	CCSM_4.5	0.04-0.24 (0.06)	0.03-0.23 (0.08)
			CCSM_8.5	0.06- 0.26 (0.13)	0.06-0.24 (0.12)
			MIROC_4.5	0.04- 0.29 (0.07)	0.04-0.25 (0.08)
			MIROC_8.5	0.06- 0.27 (0.11)	0.05-0.27 (0.11)
		2070	CCSM_4.5	0.05-0.24 (0.10)	0.04-0.24 (0.10)
			CCSM_8.5	0.11- 0.28 (0.21)	0.11-0.30 (0.21)
			MIROC_4.5	0.06- 0.29 (0.11)	0.05-0.29 (0.11)
			MIROC_8.5	0.08- 0.32 (0.18)	0.09-0.32 (0.18)
	paSNPs	2050	CCSM_4.5	0.034- 0.88 (0.19)	0.01-0.90 (0.23)
			CCSM_8.5	0.11- 0.97 (0.39)	0.10-0.92 (0.37)
			MIROC_4.5	0.035- 0.88 (0.18)	0.02-0.90 (0.24)
			MIROC_8.5	0.087- 0.93 (0.36)	0.07-0.93 (0.36)
		2070	CCSM_4.5	0.077- 0.92 (0.33)	0.07-0.92 (0.32)
			CCSM_8.5	0.29- 0.99 (0.57)	0.25-1.00 (0.66)
			MIROC_4.5	0.11- 0.92 (0.36)	0.07-0.92 (0.36)
			MIROC_8.5	0.19- 0.95 (0.50)	0.18-0.97 (0.63)

	SNP dataset	Projected year	Climate model	Range (median) of genomic offset for occurrences	Range (median) of genomic offset for sampled populations
parviglumis	refSNPs	2050	CCSM_4.5	0.097- 0.28 (0.16)	0.09-0.58 (0.14)
			CCSM_8.5	0.13- 0.32 (0.23)	0.11-0.58 (0.19)
			MIROC_4.5	0.10- 0.19 (0.14)	0.07-0.50 (0.13)
			MIROC_8.5	0.11-0.28 (0.18)	0.10-0.62 (0.16)
		2070	CCSM_4.5	0.12- 0.31 (0.21)	0.11-0.66 (0.18)
			CCSM_8.5	0.18- 0.43 (0.29)	0.16-0.59 (0.26)
			MIROC_4.5	0.11- 0.26 (0.18)	0.10-0.50 (0.17)
			MIROC_8.5	0.15- 0.44 (0.25)	0.14-0.58 (0.21)
	canSNPs	2050	CCSM_4.5	0.14- 0.27 (0.20)	0.11-0.44 (0.19)
			CCSM_8.5	0.18-0.36 (0.27)	0.15-0.57 (0.27)
			MIROC_4.5	0.12- 0.26 (0.17)	0.11-0.44 (0.18)
			MIROC_8.5	0.16- 0.33 (0.20)	0.13-0.49 (0.22)
		2070	CCSM_4.5	0.17-0.34 (0.23)	0.13-0.54 (0.24)
			CCSM_8.5	0.28- 0.49 (0.38)	0.24 -0.64 (0.38)
			MIROC_4.5	0.15- 0.36 (0.21)	0.14-0.45 (0.23)
			MIROC_8.5	0.24- 0.45 (0.29)	0.18-0.50 (0.33)
	paSNPs	2050	CCSM_4.5	0.21-0.40 (0.28)	0.16-0.72 (0.30)
			CCSM_8.5	0.33- 0.65 (0.46)	0.2-0.92 (0.44)
			MIROC_4.5	0.21-0.39 (0.27)	0.13-0.75 (0.29)
			MIROC_8.5	0.21- 0.47 (0.32)	0.20-0.69 (0.35)
		2070	CCSM_4.5	0.24- 0.50 (0.34)	0.21-0.85 (0.36)
			CCSM_8.5	0.49- 0.75 (0.63)	0.31- 1.0 (0.6)
			MIROC_4.5	0.23-0.51 (0.32)	0.19-0.75 (0.35)
			MIROC_8.5	0.38- 0.63 (0.47)	0.32- 0.77 (0.52)

Supplementary Table 4. Raw values of genomic offset for sampled populations of the two species of teosintes in Mexico using different sets of SNPs and eight different models of climate change: Zea mays spp. mexicana (mexicana) and Zea mays spp. parviglumis (parviglumis)

Population	subespecies	paSNPs CCSM_4.5_2050	paSNPs CCSM_8.5_2050	paSNPs MIROC_4.5_2050	paSNPs MIROC_8.5_2050
Teloloapan_Teloloapan	parviglumis	0.29	0.45	0.28	0.30
Alcholoa_Teloloapan	parviglumis	0.28	0.44	0.28	0.28
Teconoapan_Teconoapa	parviglumis	0.32	0.55	0.34	0.39
Chilpancingo_Chilpancingo	parviglumis	0.32	0.54	0.31	0.41
Mochitlan_Mochitlan	parviglumis	0.34	0.67	0.30	0.47
PasoMorelos_Huitzuco	parviglumis	0.43	0.65	0.44	0.43
Guachinango_Guauchinango	parviglumis	0.36	0.47	0.31	0.42
Telpitita_VillaPurificacion	parviglumis	0.43	0.69	0.43	0.62
SMH565_Ejutla	parviglumis	0.46	0.68	0.37	0.47
SMH577_VilladePurificacion	parviglumis	0.41	0.68	0.42	0.54
SMH578_Toliman	parviglumis	0.42	0.75	0.29	0.40
SMHMGCH581_Zitacuaro	parviglumis	0.35	0.43	0.37	0.43
SanCristobalHonduras_SanJeronim	parviglumis	0.37	0.46	0.36	0.43
Ahuacatitlan	parviglumis	0.30	0.47	0.29	0.31
AmatlandeCasas	parviglumis	0.53	0.87	0.52	0.62
CruceroLagunitas	parviglumis	0.34	0.56	0.33	0.39
EjutlaA	parviglumis	0.46	0.68	0.37	0.47
EjutlaB	parviglumis	0.41	0.67	0.32	0.37
ElRodeo	parviglumis	0.37	0.46	0.36	0.43
ElSauz	parviglumis	0.45	0.77	0.39	0.46
LaCadena	parviglumis	0.49	0.63	0.51	0.63
LaMesa	parviglumis	0.43	0.69	0.43	0.52
LosGuajes	parviglumis	0.38	0.44	0.38	0.41
SanLorenzo	parviglumis	0.34	0.61	0.33	0.42
VillaSeca_Otzolotepec	mexicana	0.08	0.39	0.17	0.41
Churintzio_Churintzio	mexicana	0.13	0.22	0.13	0.18
SMH571_Acambaro	mexicana	0.11	0.12	0.11	0.11
SMH572_Acambaro	mexicana	0.05	0.15	0.04	0.09
SMH573_Acambaro	mexicana	0.06	0.13	0.07	0.12
SMH575_SantaAnaMaya	mexicana	0.09	0.19	0.09	0.15
SMH576_Yuriria	mexicana	0.19	0.30	0.19	0.25
SMHMGCH579_Puruandiro	mexicana	0.12	0.23	0.11	0.18
SMHMGCH580_Huandacareo	mexicana	0.09	0.17	0.08	0.14
SMHMGCH582_JesusMaria	mexicana	0.38	0.40	0.37	0.38
Cocotitlan_Cocotitlan	mexicana	0.72	0.76	0.72	0.75
SanNicolas_SnNicolasBuenosAires	mexicana	0.71	0.78	0.72	0.77
Tenancingo_Tenancingo	mexicana	0.45	0.65	0.46	0.60
Calpan_Calpan	mexicana	0.12	0.49	0.16	0.40
Texcoco_Texcoco	mexicana	0.72	0.77	0.79	0.82
ElPorvenir	mexicana	0.56	0.57	0.52	0.57
Ixtlan	mexicana	0.30	0.40	0.26	0.37
Opopeo	mexicana	0.89	0.98	0.89	0.94
Puruandiro	mexicana	0.16	0.26	0.15	0.22
SanPedro	mexicana	0.12	0.49	0.16	0.40
SantaClara	mexicana	0.89	0.98	0.89	0.94
TenangodelAire	mexicana	0.04	0.17	0.05	0.11
Xochimilco	mexicana	0.69	0.72	0.74	0.75

Population	subspecies	canSNPs CCSM_4.5_2050	canSNPs CCSM_8.5_2050	canSNPs MIROC_4.5_2050	canSNPs MIROC_8.5_2050
Teloloapan_Teloloapan	parviglumis	0.22	0.29	0.22	0.23
Alcholoa_Teloloapan	parviglumis	0.24	0.29	0.22	0.23
Teconoapan_Teconoapa	parviglumis	0.22	0.32	0.23	0.26
Chilpancingo_Chilpancingo	parviglumis	0.21	0.34	0.19	0.28
Mochitlan_Mochitlan	parviglumis	0.32	0.48	0.26	0.38
PasoMorelos_Huitzuco	parviglumis	0.31	0.41	0.33	0.31
Guachinango_Guauchinango	parviglumis	0.26	0.35	0.26	0.30
Telpitita_VillaPurificacion	parviglumis	0.35	0.48	0.34	0.44
SMH565_Ejutla	parviglumis	0.29	0.38	0.17	0.25
SMH577_VilladePurificacion	parviglumis	0.34	0.48	0.34	0.41
SMH578_Toliman	parviglumis	0.28	0.48	0.21	0.23
SMHMGCH581_Zitacuaro	parviglumis	0.21	0.24	0.18	0.22
SanCristobalHonduras_SanJeronim	parviglumis	0.19	0.26	0.17	0.21
Ahuacatitlan	parviglumis	0.23	0.30	0.22	0.25
AmatlandeCasas	parviglumis	0.27	0.41	0.26	0.29
CruceroLagunitas	parviglumis	0.24	0.33	0.23	0.26
EjutlaA	parviglumis	0.29	0.38	0.17	0.25
EjutlaB	parviglumis	0.36	0.46	0.25	0.31
ElRodeo	parviglumis	0.19	0.26	0.17	0.21
ElSauz	parviglumis	0.21	0.41	0.16	0.22
LaCadena	parviglumis	0.28	0.35	0.28	0.37
LaMesa	parviglumis	0.22	0.36	0.20	0.27
LosGuajes	parviglumis	0.26	0.31	0.27	0.28
SanLorenzo	parviglumis	0.31	0.41	0.27	0.32
VillaSeca_Otzolotepec	mexicana	0.06	0.15	0.08	0.13
Churintzio_Churintzio	mexicana	0.06	0.08	0.07	0.07
SMH571_Acambaro	mexicana	0.05	0.06	0.04	0.06
SMH572_Acambaro	mexicana	0.05	0.07	0.04	0.06
SMH573_Acambaro	mexicana	0.04	0.06	0.04	0.06
SMH575_SantaAnaMaya	mexicana	0.05	0.08	0.05	0.07
SMH576_Yuriria	mexicana	0.06	0.09	0.06	0.08
SMHMGCH579_Puruandiro	mexicana	0.06	0.09	0.05	0.07
SMHMGCH580_Huandacareo	mexicana	0.05	0.07	0.04	0.07
SMHMGCH582_JesusMaria	mexicana	0.09	0.11	0.10	0.10
Cocotitlan_Cocotitlan	mexicana	0.19	0.21	0.20	0.21
SanNicolas_SnNicolasBuenosAires	mexicana	0.19	0.21	0.20	0.21
Tenancingo_Tenancingo	mexicana	0.13	0.19	0.14	0.18
Calpan_Calpan	mexicana	0.05	0.15	0.07	0.12
Texcoco_Texcoco	mexicana	0.20	0.21	0.21	0.22
ElPorvenir	mexicana	0.17	0.20	0.15	0.17
Ixtlan	mexicana	0.09	0.12	0.08	0.11
Opopeo	mexicana	0.24	0.26	0.29	0.27
Puruandiro	mexicana	0.06	0.09	0.06	0.08
SanPedro	mexicana	0.05	0.15	0.07	0.12
SantaClara	mexicana	0.23	0.26	0.29	0.27
TenangodelAire	mexicana	0.05	0.07	0.04	0.06
Xochimilco	mexicana	0.18	0.19	0.19	0.20

Population	subspecies	refSNPs CCSM_4.5_2050	refSNPs CCSM_8.5_2050	refSNPs MIROC_4.5_2050	refSNPs MIROC_8.5_2050
Teloloapan_Teloloapan	parviglumis	0.23	0.23	0.23	0.21
Alcholoa_Teloloapan	parviglumis	0.16	0.18	0.16	0.15
Teconoapan_Teconoapa	parviglumis	0.20	0.26	0.18	0.24
Chilpancingo_Chilpancingo	parviglumis	0.13	0.32	0.18	0.36
Mochitlan_Mochitlan	parviglumis	0.37	0.35	0.25	0.38
PasoMorelos_Huitzuco	parviglumis	0.21	0.26	0.23	0.16
Guachinango_Guauchinango	parviglumis	0.20	0.33	0.21	0.28
Telpitita_VillaPurificacion	parviglumis	0.34	0.42	0.25	0.32
SMH565_Ejutla	parviglumis	0.24	0.39	0.18	0.25
SMH577_VilladePurificacion	parviglumis	0.34	0.43	0.25	0.31
SMH578_Toliman	parviglumis	0.24	0.41	0.17	0.20
SMHMGCH581_Zitacuaro	parviglumis	0.20	0.23	0.18	0.22
SanCristobalHonduras_SanJeronim	parviglumis	0.16	0.18	0.15	0.18
Ahuacatitlan	parviglumis	0.24	0.23	0.23	0.23
AmatlandeCasas	parviglumis	0.19	0.30	0.17	0.22
CruceroLagunitas	parviglumis	0.24	0.27	0.17	0.24
EjutlaA	parviglumis	0.24	0.39	0.18	0.25
EjutlaB	parviglumis	0.24	0.38	0.17	0.21
ElRodeo	parviglumis	0.16	0.18	0.15	0.18
ElSauz	parviglumis	0.23	0.42	0.19	0.25
LaCadena	parviglumis	0.14	0.19	0.14	0.37
LaMesa	parviglumis	0.20	0.34	0.19	0.27
LosGuajes	parviglumis	0.14	0.17	0.13	0.15
SanLorenzo	parviglumis	0.21	0.33	0.18	0.23
VillaSeca_Otzolotepec	mexicana	0.05	0.06	0.05	0.06
Churintzio_Churintzio	mexicana	0.03	0.05	0.04	0.04
SMH571_Acambaro	mexicana	0.03	0.04	0.03	0.03
SMH572_Acambaro	mexicana	0.03	0.04	0.03	0.04
SMH573_Acambaro	mexicana	0.03	0.04	0.03	0.04
SMH575_SantaAnaMaya	mexicana	0.03	0.04	0.03	0.04
SMH576_Yuriria	mexicana	0.04	0.05	0.04	0.04
SMHMGCH579_Puruandiro	mexicana	0.03	0.04	0.03	0.04
SMHMGCH580_Huandacareo	mexicana	0.03	0.04	0.03	0.04
SMHMGCH582_JesusMaria	mexicana	0.03	0.04	0.04	0.04
Cocotitlan_Cocotitlan	mexicana	0.05	0.06	0.05	0.06
SanNicolas_SnNicolasBuenosAires	mexicana	0.05	0.06	0.06	0.06
Tenancingo_Tenancingo	mexicana	0.06	0.07	0.07	0.07
Calpan_Calpan	mexicana	0.06	0.08	0.07	0.08
Texcoco_Texcoco	mexicana	0.05	0.06	0.05	0.06
ElPorvenir	mexicana	0.07	0.08	0.04	0.05
Ixtlan	mexicana	0.04	0.06	0.04	0.05
Opopeo	mexicana	0.05	0.05	0.06	0.06
Puruandiro	mexicana	0.03	0.05	0.03	0.04
SanPedro	mexicana	0.06	0.08	0.07	0.08
SantaClara	mexicana	0.04	0.05	0.06	0.06
TenangodelAire	mexicana	0.06	0.07	0.07	0.07
Xochimilco	mexicana	0.04	0.05	0.04	0.05

Population	subspecies	paSNPs CCSM_4.5_2070	paSNPs CCSM_8.5_2070	paSNPs MIROC_4.5_2070	paSNPs MIROC_8.5_2070
Teloloapan_Teloloapan	parviglumis	0.32	0.78	0.31	0.54
Alcholoa_Teloloapan	parviglumis	0.38	0.83	0.38	0.59
Teconoapan_Teconoapa	parviglumis	0.42	0.74	0.40	0.50
Chilpancingo_Chilpancingo	parviglumis	0.41	0.87	0.39	0.60
Mochitlan_Mochitlan	parviglumis	0.59	0.87	0.42	0.73
PasoMorelos_Huitzuco	parviglumis	0.48	0.87	0.42	0.71
Guachinango_Guauchinango	parviglumis	0.44	0.65	0.41	0.57
Telpitita_VillaPurificacion	parviglumis	0.51	0.96	0.68	0.83
SMH565_Ejutla	parviglumis	0.53	0.84	0.46	0.67
SMH577_VilladePurificacion	parviglumis	0.46	0.94	0.64	0.82
SMH578_Toliman	parviglumis	0.67	0.95	0.43	0.60
SMHMGCH581_Zitacuaro	parviglumis	0.43	0.68	0.43	0.61
SanCristobalHonduras_SanJeronim	parviglumis	0.43	0.65	0.45	0.55
Ahuacatitlan	parviglumis	0.32	0.83	0.31	0.61
AmatlandeCasas	parviglumis	0.58	1.00	0.56	0.84
CruceroLagunitas	parviglumis	0.43	0.85	0.40	0.50
EjutlaA	parviglumis	0.53	0.84	0.46	0.67
EjutlaB	parviglumis	0.46	0.87	0.48	0.63
ElRodeo	parviglumis	0.43	0.65	0.45	0.55
ElSauz	parviglumis	0.49	0.99	0.44	0.66
LaCadena	parviglumis	0.55	0.80	0.60	0.77
LaMesa	parviglumis	0.47	0.92	0.47	0.73
LosGuajes	parviglumis	0.41	0.67	0.40	0.62
SanLorenzo	parviglumis	0.43	0.82	0.41	0.68
VillaSeca_Otzolotepec	mexicana	0.30	0.78	0.36	0.73
Churintzio_Churintzio	mexicana	0.19	0.45	0.21	0.28
SMH571_Acambaro	mexicana	0.10	0.30	0.12	0.19
SMH572_Acambaro	mexicana	0.30	0.33	0.30	0.35
SMH573_Acambaro	mexicana	0.13	0.37	0.31	0.36
SMH575_SantaAnaMaya	mexicana	0.19	0.36	0.31	0.39
SMH576_Yuriria	mexicana	0.30	0.56	0.30	0.38
SMHMGCH579_Puruandiro	mexicana	0.23	0.48	0.17	0.31
SMHMGCH580_Huandacareo	mexicana	0.18	0.43	0.18	0.38
SMHMGCH582_JesusMaria	mexicana	0.40	0.51	0.40	0.41
Cocotitlan_Cocotitlan	mexicana	0.74	0.94	0.76	0.95
SanNicolas_SnNicolasBuenosAires	mexicana	0.77	0.99	0.78	0.96
Tenancingo_Tenancingo	mexicana	0.60	0.80	0.63	0.78
Calpan_Calpan	mexicana	0.44	0.79	0.42	0.77
Texcoco_Texcoco	mexicana	0.74	0.89	0.82	0.83
ElPorvenir	mexicana	0.65	0.68	0.63	0.65
Ixtlan	mexicana	0.33	0.58	0.37	0.43
Opopeo	mexicana	0.92	1.00	0.93	0.95
Puruandiro	mexicana	0.27	0.52	0.26	0.35
SanPedro	mexicana	0.44	0.79	0.42	0.77
SantaClara	mexicana	0.93	1.00	0.92	0.95
TenangodelAire	mexicana	0.08	0.71	0.18	0.61
Xochimilco	mexicana	0.68	0.95	0.76	0.93

Population	subspecies	canSNPs CCSM_4.5_2070	canSNPs CCSM_8.5_2070	canSNPs MIROC_4.5_2070	canSNPs MIROC_8.5_2070
Teloloapan_Teloloapan	parviglumis	0.26	0.48	0.24	0.35
Alcholoa_Teloloapan	parviglumis	0.30	0.53	0.29	0.38
Teconoapan_Teconoapa	parviglumis	0.29	0.46	0.27	0.33
Chilpancingo_Chilpancingo	parviglumis	0.28	0.57	0.26	0.40
Mochitlan_Mochitlan	parviglumis	0.44	0.61	0.35	0.50
PasoMorelos_Huitzuco	parviglumis	0.36	0.56	0.30	0.45
Guachinango_Guauchinango	parviglumis	0.32	0.46	0.30	0.42
Telpitita_VillaPurificacion	parviglumis	0.40	0.64	0.48	0.59
SMH565_Ejutla	parviglumis	0.35	0.50	0.28	0.37
SMH577_VilladePurificacion	parviglumis	0.38	0.65	0.47	0.60
SMH578_Toliman	parviglumis	0.45	0.58	0.24	0.36
SMHMGCH581_Zitacuaro	parviglumis	0.24	0.39	0.23	0.33
SanCristobalHonduras_SanJeronim	parviglumis	0.23	0.38	0.21	0.33
Ahuacatitlan	parviglumis	0.25	0.51	0.25	0.37
AmatlandeCasas	parviglumis	0.30	0.53	0.29	0.46
CruceroLagunitas	parviglumis	0.29	0.49	0.27	0.33
EjutlaA	parviglumis	0.35	0.50	0.28	0.37
EjutlaB	parviglumis	0.40	0.61	0.37	0.45
ElRodeo	parviglumis	0.23	0.38	0.21	0.33
ElSauz	parviglumis	0.27	0.54	0.22	0.32
LaCadena	parviglumis	0.33	0.46	0.34	0.45
LaMesa	parviglumis	0.28	0.51	0.25	0.40
LosGuajes	parviglumis	0.29	0.49	0.28	0.45
SanLorenzo	parviglumis	0.35	0.57	0.32	0.48
VillaSeca_Otzolotepec	mexicana	0.09	0.24	0.10	0.21
Churintzio_Churintzio	mexicana	0.07	0.15	0.09	0.11
SMH571_Acambaro	mexicana	0.06	0.11	0.06	0.08
SMH572_Acambaro	mexicana	0.08	0.13	0.09	0.11
SMH573_Acambaro	mexicana	0.06	0.13	0.09	0.11
SMH575_SantaAnaMaya	mexicana	0.07	0.14	0.09	0.12
SMH576_Yuriria	mexicana	0.09	0.17	0.09	0.12
SMHMGCH579_Puruandiro	mexicana	0.08	0.16	0.07	0.11
SMHMGCH580_Huandacareo	mexicana	0.07	0.15	0.07	0.11
SMHMGCH582_JesusMaria	mexicana	0.10	0.15	0.12	0.13
Cocotitlan_Cocotitlan	mexicana	0.21	0.26	0.21	0.26
SanNicolas_SnNicolasBuenosAires	mexicana	0.21	0.27	0.21	0.27
Tenancingo_Tenancingo	mexicana	0.17	0.23	0.19	0.22
Calpan_Calpan	mexicana	0.14	0.23	0.13	0.22
Texcoco_Texcoco	mexicana	0.20	0.26	0.22	0.25
ElPorvenir	mexicana	0.20	0.24	0.18	0.22
Ixtlan	mexicana	0.10	0.18	0.11	0.14
Opopeo	mexicana	0.24	0.28	0.29	0.32
Puruandiro	mexicana	0.08	0.16	0.08	0.11
SanPedro	mexicana	0.14	0.23	0.13	0.22
SantaClara	mexicana	0.24	0.29	0.29	0.33
TenangodelAire	mexicana	0.06	0.21	0.08	0.19
Xochimilco	mexicana	0.18	0.26	0.20	0.25

Population	subspecies	refSNPs CCSM_4.5_2070	refSNPs CCSM_8.5_2070	refSNPs MIROC_4.5_2070	refSNPs MIROC_8.5_2070
Teloloapan_Teloloapan	parviglumis	0.26	0.32	0.22	0.28
Alcholoa_Teloloapan	parviglumis	0.20	0.29	0.19	0.25
Teconoapan_Teconoapa	parviglumis	0.31	0.36	0.21	0.22
Chilpancingo_Chilpancingo	parviglumis	0.20	0.32	0.30	0.29
Mochitlan_Mochitlan	parviglumis	0.42	0.46	0.31	0.30
PasoMorelos_Huitzuco	parviglumis	0.25	0.33	0.16	0.25
Guachinango_Guauchinango	parviglumis	0.28	0.45	0.29	0.44
Telpitita_VillaPurificacion	parviglumis	0.38	0.55	0.32	0.55
SMH565_Ejutla	parviglumis	0.33	0.48	0.24	0.39
SMH577_VilladePurificacion	parviglumis	0.37	0.57	0.33	0.58
SMH578_Toliman	parviglumis	0.35	0.55	0.21	0.41
SMHMGCH581_Zitacuaro	parviglumis	0.25	0.32	0.22	0.26
SanCristobalHonduras_SanJeronim	parviglumis	0.17	0.24	0.16	0.22
Ahuacatitlan	parviglumis	0.24	0.32	0.22	0.29
AmatlandeCasas	parviglumis	0.23	0.38	0.24	0.37
CruceroLagunitas	parviglumis	0.32	0.39	0.22	0.22
EjutlaA	parviglumis	0.33	0.48	0.24	0.39
EjutlaB	parviglumis	0.30	0.49	0.26	0.38
ElRodeo	parviglumis	0.17	0.24	0.16	0.22
ElSauz	parviglumis	0.31	0.49	0.26	0.38
LaCadena	parviglumis	0.17	0.26	0.35	0.39
LaMesa	parviglumis	0.27	0.45	0.24	0.39
LosGuajes	parviglumis	0.17	0.26	0.15	0.20
SanLorenzo	parviglumis	0.29	0.45	0.25	0.40
VillaSeca_Otzolotepec	mexicana	0.06	0.09	0.06	0.09
Churintzio_Churintzio	mexicana	0.04	0.08	0.05	0.06
SMH571_Acambaro	mexicana	0.03	0.06	0.04	0.05
SMH572_Acambaro	mexicana	0.04	0.07	0.04	0.05
SMH573_Acambaro	mexicana	0.04	0.07	0.04	0.06
SMH575_SantaAnaMaya	mexicana	0.04	0.07	0.04	0.06
SMH576_Yuriria	mexicana	0.05	0.08	0.05	0.06
SMHMGCH579_Puruandiro	mexicana	0.04	0.08	0.04	0.06
SMHMGCH580_Huandacareo	mexicana	0.04	0.07	0.04	0.05
SMHMGCH582_JesusMaria	mexicana	0.04	0.07	0.05	0.06
Cocotitlan_Cocotitlan	mexicana	0.06	0.08	0.06	0.08
SanNicolas_SnNicolasBuenosAires	mexicana	0.06	0.08	0.06	0.08
Tenancingo_Tenancingo	mexicana	0.07	0.09	0.08	0.09
Calpan_Calpan	mexicana	0.07	0.10	0.08	0.10
Texcoco_Texcoco	mexicana	0.06	0.08	0.06	0.08
ElPorvenir	mexicana	0.08	0.10	0.05	0.07
Ixtlan	mexicana	0.05	0.08	0.05	0.07
Opopeo	mexicana	0.05	0.07	0.06	0.08
Puruandiro	mexicana	0.04	0.08	0.04	0.06
SanPedro	mexicana	0.07	0.10	0.08	0.10
SantaClara	mexicana	0.05	0.07	0.06	0.08
TenangodelAire	mexicana	0.07	0.10	0.07	0.09
Xochimilco	mexicana	0.05	0.07	0.05	0.07

Supplementary Table 5. Climatic variables associated with the allele frequencies of different sets of SNPs identified in the two species of teosintes in Mexico: Zea mays spp. mexicana (mexicana) and Zea mays spp. parviglumis (parviglumis). Variables with the highest weighted importance for model construction and proportion of SNPs with significant predictive power (range and median of R2 values). refSNPs: references SNPs, canSNPs: candidate SNPs; paSNPs: putative adaptive SNPs. Blioclimatic layer were obtained from www.worldclim.org

	SNP dataset	Bioclimatic variables*	Proportion of SNPs with significant predictive power	Range (median) of R^2
mexicana	refSNPs	4, 5, 8, 10, 16	28%	0.002-0.6 (0.17)
	canSNPs	9, 10, 13, 12, 16	100%	0.10-0.88 (0.36)
	paSNPs	1, 4, 5, 9, 10	100%	0.07-0.92 (0.87)
mexicana	refSNPs	2, 3, 17, 18, 19	63%	0.001-0.87 (0.26)
	canSNPs	4, 12, 16, 18, 19	96%	0.01-0.61 (0.32)
	paSNPs	6, 11, 12, 16, 18	100%	0.12-0.6 (0.46)

Variable names after ref. 53.

BIO1 Annual Mean Temperature; BIO2 Mean Diurnal Range (Mean of monthly (max temp - min temp)); BIO3 Isothermality (BIO2/BIO7) (* 100); BIO4 Temperature Seasonality (standard deviation *100); BIO5   Max Temperature of Warmest Month; BIO6   Min Temperature of Coldest Month; BIO7   Temperature Annual Range (BIO5-BIO6); BIO8 Mean Temperature of Wettest Quarter; BIO9   Mean Temperature of Driest Quarter; BIO10 Mean Temperature of Warmest Quarter; BIO11 Mean Temperature of Coldest Quarter; BIO12   Annual Precipitation; BIO13 Precipitation of Wettest Month; BIO14   Precipitation of Driest Month; BIO15   Precipitation Seasonality (Coefficient of Variation); BIO16   Precipitation of Wettest Quarter; BIO17   Precipitation of Driest Quarter; BIO18 Precipitation of Warmest Quarter; BIO19 Precipitation of Coldest Quarter

Supplementary Table 6. Reduction in the geographical distribution predicted for putative adaptive SNPs (paSNPs) in the two species of teosintes in Mexico under eight different models of climate change: Zea mays spp. mexicana (mexicana) and Zea mays spp. parviglumis (parviglumis). Proportion of known occurrences (ref. 14) and sampled populations within the predicted future distribution for paSNPs. Teosintes occurrences obtained from www.biodiversidad.gob.mx/genes/proyectoMaices.html

Subspecies	Year	Climate model	Projected future extent of species relative to the present-day	Proportion of predicted occurrences within the future distribution	Proportion of sampled populations predicted within the future distribution
mexicana	2050	CCSM_4.5	108%	14%	22%
		CCSM_8.5	44%	2%	0%
		MIROC_4.5	35%	2%	0%
		MIROC_8.5	33%	6%	0%
		Mean for 2050	**54.9%**	**6%**	**5%**
	2070	CCSM_4.5	91%	14%	17%
		CCSM_8.5	15%	1%	0%
		MIROC_4.5	46%	6%	9%
		MIROC_8.5	3%	0%	0%
		Mean for 2070	**38.8%**	**5%**	**6%**
parviglumis	2050	CCSM_4.5	73%	26%	25%
		CCSM_8.5	59%	14%	17%
		MIROC_4.5	73%	31%	17%
		MIROC_8.5	52%	14%	8%
		Mean for 2050	**64.4%**	**21%**	**17%**
	2070	CCSM_4.5	66%	24%	21%
		CCSM_8.5	36%	5%	0%
		MIROC_4.5	66%	26%	25%
		MIROC_8.5	47%	10%	8%
		Mean for 2070	**53.8%**	**16%**	**14%**

Supplementary Table 7. Migration potential for sampled populations of two species of teosintes in Mexico: *Zea mays* spp. *mexicana* (*mexicana*) and *Zea mays* spp. *parviglumis* (*parviglumis*) under the two most extreme models of climate change: CCSM_2050_RCP4.5 and CCSM_2070_RCP8.5. Minimum geographic distances to the populations with highest frequency of putative adaptive SNPs. Teosintes occurrences obtained from www.biodiversidad.gob.mx/genes/proyectoMaices.html

Species	Population	Adaptive score	Migration potential CCSM_2050_RCP4.5	Migration potential CCSM_2070_RCP8.5	Minimum distance to best population (km)	Adaptive score for best population	Minimum distance to best neighbor (km)	Adaptive score for best neighbor
mexicana	Calpan_Calpan	0.21	no migration	no migration	266	0.79	43	0.22
mexicana	Churintzio_Churintzio	0.82	migration	no migration	32	0.87	32	0.87
mexicana	Cocotitlan_Cocotitlan	0.22	no migration	no migration	223	0.79	—	Highest adaptive score locally
mexicana	ElPorvenir	0.42	no migration	no migration	38	0.79	38	0.79
mexicana	Ixtlan	0.87	no migration	no migration	—	Highest adaptive score in species	—	Highest adaptive score locally
mexicana	Opopeo	0.37	no migration	no migration	72	0.72	72	0.72
mexicana	Puruandiro	0.7	migration	migration	6	0.7	13	0.75
mexicana	SanNicolas_SnNicolasBuenosAires	0.2	no migration	no migration	293	0.79	72	0.22
mexicana	SanPedro	0.18	no migration	no migration	265	0.79	42	0.22
mexicana	SantaClara	0.31	no migration	no migration	74	0.72	74	0.72
mexicana	SMH571_Acambaro	0.74	migration	no migration	5	0.79	5	0.79
mexicana	SMH572_Acambaro	0.79	migration	no migration	129	0.82	—	Highest adaptive score locally
mexicana	SMH573_Acambaro	0.75	migration	no migration	12	0.79	12	0.79
mexicana	SMH575_SantaAnaMaya	0.74	migration	migration	15	0.75	27	0.79
mexicana	SMH576_Yuriria	0.75	migration	migration	47	0.75	—	Highest adaptive score locally
mexicana	SMHMGCH579_Puruandiro	0.7	migration	migration	6	0.7	7	0.75
mexicana	SMHMGCH580_Huandacareo	0.72	migration	migration	18	0.74	25	0.75
mexicana	SMHMGCH582_JesusMaria	0.6	migration	no migration	64	0.82	67	0.87
mexicana	Tenancingo_Tenancingo	0.15	migration	no migration	227	0.79	10	0.22
mexicana	TenangodelAire	0.12	no migration	no migration	161	0.79	77	0.22

mexicana	Texcoco_Texcoco	0.2	no migration	no migration	209	0.79	31	0.22
mexicana	VillaSeca_Otzolotepec	0.18	no migration	no migration	142	0.79	82	0.22
mexicana	Xochimilco	0.13	migration	no migration	200	0.79	24	0.22
parviglumis	Ahuacatitlan	0.71	migration	migration	3	0.72	64	0.78
parviglumis	Alcholoa_Teloloapan	0.63	migration	migration	10	0.72	75	0.78
parviglumis	AmatlandeCasas	0.3	no migration	no migration	105	0.61	105	0.61
parviglumis	Chilpancingo_Chilpancingo	0.65	migration	migration	50	0.97	50	0.97
parviglumis	CruceroLagunitas	0.96	migration	migration	1	0.97	1	0.97
parviglumis	EjutlaA	0.61	no migration	no migration	69	0.8	—	0.97 Highest adaptive score locally
parviglumis	EjutlaB	0.6	migration	no migration	7	0.61	7	0.61
parviglumis	ElSauz	0.37	migration	no migration	54	0.6	55	0.61
parviglumis	Guachinango_Guauchinango	0.35	no migration	no migration	84	0.61	84	0.61
parviglumis	LaCadena	0.6	migration	migration	78	0.6	164	0.72
parviglumis	LaMesa	0.16	no migration	no migration	8	0.6	15	0.61
parviglumis	LosGuajes	0.6	migration	migration	13	0.61	119	0.72
parviglumis	Mochitlan_Mochitlan	0.56	migration	migration	14	0.65	54	0.97
parviglumis	PasoMorelos_Huitzuco	0.78	no migration	no migration	139	0.97	—	0.97 Highest adaptive score locally
parviglumis	SanCristobalHonduras_SanJeronim oCoatlan	0.65	no migration	no migration	251	0.96	251	0.97
parviglumis	SanLorenzo	0.23	no migration	no migration	12	0.6	20	0.61
parviglumis	SMH565_Ejutla	0.49	no migration	no migration	1	0.61	1	0.61
parviglumis	SMH577_VilladePurificacion	0.86	migration	migration	664	0.97	—	0.97 Highest adaptive score locally
parviglumis	SMH578_Toliman	0.26	no migration	no migration	42	0.6	42	0.61
parviglumis	SMHMGCH581_Zitacuaro	0.61	no migration	no migration	115	0.63	124	0.72

parviglumis	Teconoapan_Teconoapa	0.97	migration	migration	—	Highest adaptive score in species	—	Highest adaptive score locally
parviglumis	Teloloapan_Teloloapan	0.72	migration	migration	67	0.78	67	0.78
parviglumis	Telpitita_VillaPurificacion	0.8	migration	migration	7	0.86	7	0.86

Supplementary Table 8. Geographical coordinates, genotype for putative adaptive SNPs, and estimated adaptive scores for maize landraces accessions in Mexico. Detailed information on landrace and known occurrences can be obtained at www.biodiversidad.gob.mx/usos/maices/maiz.html

Landrace	Longitude	Latitude	PZE.100001195	PZE.108035280	PZE.109096578	SYN27200	SYN32365	SYN37470	PZE.101131254	PZE.103059706	PZE.104026211	PZE.104044827	PZE.105090166	PZE.106008139	PZE.109029456	PZE.104055811	Adaptive score
Ancho	-98.77861111	18.9975	GG	AA	AA	CA	GA	GG	AA	AC	CC	GA	GG	GG	AG	GG	0.4545454545
Ancho	-98.80944444	18.96805556	AA	GG	AA	AA	AA	GG	CA	CC	AC	GA	GA	GG	GG	GA	0.5909090909
Ancho	-98.77861111	18.9975	AA	GG	AA	CA	GG	AA	CC	AC	CC	GA	GG	GG	AA	GA	0.6363636364
Apachito	-107.583	28.68577778	GG	AA	AA	AA	AA	AG	AA	AC	CC	AA	GA	GG	AA	AA	0.6818181818
Apachito	-108.0796111	29.11311111	GG	GA	AA	AA	AA	AA	AA	AC	CC	GA	AG	AG	AG	GA	0.6363636364
Arrocillo	-97.98080556	19.93408333	GG	AA	AA	CA	GA	AG	AA	AC	CC	AA	GG	AA	AA	GG	0.3636363636
Arrocillo	-97.97941667	19.95577778	AG	AA	AA	AA	GA	AA	AA	CC	AC	AA	AA	GG	GG	GG	0.5454545455
Arrocillo	-97.98033333	19.94305556	AG	GA	AA	CA	AA	AG	CA	AC	AC	AA	AA	AG	AG	GA	0.5909090909
Arrocillo	-97.97941667	19.95577778	AG	AA	AA	CA	GA	AG	AA	CC	AC	GA	AA	AG	AG	GG	0.4545454545
Azul	-108.0152222	28.45538889	GG	GA	AA	AA	AA	AA	AA	CC	CC	AA	GG	GG	GG	AA	0.6363636364
Azul	-108.0157778	28.45730556	AG	AA	AA	CC	AA	AA	AA	CC	CC	GA	GA	GG	GG	AA	0.6363636364
Blando de Sonora	-108.3833333	26.39472222	GG	GG	AA	AA	AA	AA	AA	AA	CC	GG	AA	AG	AG	AA	0.8636363636
Bofo	-108.0082222	27.43477778	AA	GA	AA	AA	GA	GG	AA	CC	AC	AA	AA	AA	AA	GA	0.4090909091
Cacahuacintle	-99.50888889	19.19638889	AG	GA	AA	AA	GA	GG	AA	AC	CC	GA	GA	AG	AG	AA	0.5909090909
Cacahuacintle	-99.61805556	19.1675	GG		0 AA	AA	GA	GG	AA	AC	CC	GG	GA	GG	AG	AA	0.6818181818
Cacahuacintle	-98.05666667	19.59972222	GG	GA	AA	AA	AA	GG	CA	AC	CC	AA	GA	GG	AA	GG	0.5909090909
Cacahuacintle	-98.43111111	20.33916667	GG	GA	AA	AA	AA	AA	CA	CC	CC	GA	AA	AA	GG	AA	0.7272727273
Cacahuacintle	-97.90083333	19.22194444	GG	AA	AA	CC	GA	AG	AA	CC	CC	GA	GA	AG	GG	GG	0.4090909091
Celaya	-101.1188889	20.09111111	GG	AA	AA	CA	AA	AG	AA	AC	CC	GA	GA	AA	AA	AA	0.5909090909
Celaya	-101.4052778	21.00861111	AG	AA	AA	CC	AA	AG	AA	CC	AC	AA	AA	AA	GG	GA	0.4090909091
Celaya	-101.1611111	20.37416667	AG	AA	AA	CA	GA	GG	AA	AC	CC	GA	AA	AG	GG	GG	0.5
Chalqueño	-97.92944444	19.29083333	AA	AA	AA	CC	GG	AG	AA	CC	CC	AA	GG	AG	AA	AA	0.3636363636
Chalqueño	-100.2275	18.66027778	GG	AA	AA	CC	AA	AG	CA	AC	CC	GA	GA	AG	AG	GG	0.5454545455
Chalqueño	-97.98805556	19.35916667	GG	AA	AA	CA	GA	AA	AA	CC	CC	GA	AA	GG	AA	GA	0.6363636364
Chalqueño	-99.59527778	19.41808889	AG	GG	AA	CA	AA	GG	AA	AA	AC	GG	AA	AG	AG	GA	0.6363636364
Chalqueño	-98.33722222	20.22138889	AG	GA	GA	CA	GA	AG	AA	CC	CC	AA	GA	GG	AG	AA	0.5
Chalqueño	-98.28055556	20.02972222	AG	GG	AA	CA	AA	GG	CA	CC	CC	GA	GG	AG	GG	GA	0.5
Chalqueño	-98.80388889	19.10361111	GG	AA	AA	CC	GA	AG	AA	AC	CC	AA	GG	GG	AG	GG	0.4090909091
Chapalote	-109.2996667	29.90441667	GG	AA	AA	AA	GG	AG	AA	AC	CC	AA	AA	AG	AG	GG	0.5
Chapalote	-109.6742778	29.80538889	GG	GG	AA	AA	AA	AG	AA	AC	CC	GA	GG	AG	GG	GG	0.5454545455
Cónico	-98.04833333	19.51888889	GG	AA	AA	AA	AA	AG	AA	CC	CC	AA	GA	GG	AG	AA	0.6363636364
Cónico	-99.50972222	19.18472222	GG	AA	AA	AA	AA	AG	AA	CC	CC	GA	GG	GG	AA	GA	0.5909090909
Cónico	-98.37861111	20.33166667	AG	AA	AA	CC	AA	AG	AA	CC	AC	AA	AA	AA	GG	GA	0.4090909091
Cónico	-97.65222222	19.31916667	GG	GA	AA	AA	AA	AG	AA	AA	CC	AA	GG	AG	AG	GA	0.5909090909
Cónico	-100.0627778	19.46055556	AG	GG	AA	AA	GA	GG	AA	CC	CC	AA	GA	GG	AA	GA	0.5
Cónico	-98.29111111	20.24333333	AA	GA	AA	AA	GA	GG	CA	AC	CC	GA	AA	GG	AG	AA	0.7272727273
Cónico	-98.405	20.28666667	AA	AA	AA	CA	GG	AG	AA	CC	CC	GA	AA	AG	GG	GA	0.5
Cónico	-98.37388889	20.35888889	AA	AA	AA	CA	GA	AA	AA	CC	CC	AA	GA	GG	AG	AA	0.5909090909
Cónico	-98.78166667	19.09055556	GG	AA	AA	AA	GA	AG	AA	CC	CC	AA	GA	GG	AG	GG	0.5
Cónico	-98.64722222	19.75944444	AG	AA	AA	CA	GA	GG	AA	AC	CC	AA	AA	AA	GG	GG	0.4090909091
Cónico	-99.95611111	19.65111111	AG	AA	AA	CC	GA	AG	AA	CC	CC	AA	AA	AG	AG	GA	0.4545454545
Cónico	-98.27472222	19.99861111	GG	AA	AA	AA	AA	GG	AA	CC	CC	GG	AA	AG	AA	AA	0.6818181818
Cónico	-99.79111111	19.56944444	GG	AA	AA	CC	AA	AG	AA	CC	CC	GA	AA	AA	AG	AA	0.5454545455
Cónico	-98.06944444	19.39388889	AG	AA	AA	CA	GA	AG	AA	CC	AC	AA	GA	GG	AA	AA	0.5
Cónico	-100.1675028	19.35202222	GG	GA	AA	CA	GG	AG	AA	AA	CC	GA	GA	AG	AA	GA	0.5454545455
Cónico	-100.0255556	19.49083333	AG	AA	AA	CA	GG	GG	AA	AC	CC	GA	AA	AG	AG	GA	0.5
Comiteco	-91.97702778	16.19611111	AA	GG	AA	AA	AA	AG	CA	AC	CC	GA	GG	AG	AG	GA	0.6363636364
Comiteco	-93.09966667	16.62313889	AG	GA	AA	CC	AA	AG	CC	CC	CC	AA	AA	GG	AG	GG	0.5909090909
Comiteco	-92.02008333	16.24877778	AG	GA	AA	CA	GA	AA	AA	AC	CC	GA	GA	GG	AA	AA	0.6818181818

Supplementary Table 8. Geographical coordinates, genotype for putative adaptive SNPs, and estimated adaptive scores for maize landraces accessions in Mexico. Detailed information on landrace and known occurrences can be obtained at www.biodiversidad.gob.mx/usos/maices/maiz.html

Landrace	Longitude	Latitude	PZE.100001195	PZE.108035280	PZE.109096578	SYN27200	SYN32365	SYN37470	PZE.101131254	PZE.103059706	PZE.104026211	PZE.104044827	PZE.105090166	PZE.106008139	PZE.109029456	PZE.104055811	Adaptive score
Comiteco	-91.97488889	16.23313889	AG	GA	AA	CA	AA	GG	AA	CC	CC	GA	AA	GG	AA	GA	0.5909090909
Comiteco	-91.93747222	16.19525	AG	GA	AA	AA	AA	GG	AA	CC	CC	AA	AA	AG	AA	AA	0.5909090909
Complejo Serrano de Jalisco	-103.6666667	19.93333333	AA	GG	AA	AA	GA	GG	CA	AC	CC	GG	GA	GG	AG	GG	0.6363636364
Complejo Serrano de Jalisco	-103.43833	19.92833	GG	GA	AA	CA	GA	AG	CA	CC	AC	AA	AA	AA	AA	GG	0.4090909091
Conejo	-98.74311111	17.78013889	AG	GA	AA	AA	AA	AG	CA	AC	CC	GA	GA	GG	AG	AA	0.7727272727
Conejo	-98.74188889	17.77797222	AG	GA	AA	AA	GA	GG	CA	AC	CC	GA	AA	AG	GG	GA	0.6363636364
Conejo	-98.68102778	17.88563889	AA	GA	AA	AA	GG	GG	CC	AC	CC	GA	GA	AG	AG	AA	0.6363636364
Conejo	-98.65641667	17.74525	GG	GG	AA	AA	AA	GG	CA	AA	CC	AA	GA	GG	AA	AA	0.7272727273
Conico_Norteno	-106.63225	28.49672222	AG	GA	AA	CC	AA	GG	AA	AA	CC	GA	GA	AG	GG	AA	0.5909090909
Conico_Norteno	-106.6291111	28.49488889	AA	GG	AA	CC	GA	AG	CA	AC	CC	GA	GA	AG	GG	AA	0.5909090909
Conico_Norteno	-106.6555	28.51872222	GG	AA	AA	CA	AA	AA	AA	AC	AC	AA	AA	AG	AA	AA	0.6363636364
Coscomatepec	-97.56488889	19.96466667	GG	GG	AA	AA	AA	GG	AA	AC	AC	AA	AA	GG	AG	GA	0.5909090909
Coscomatepec	-96.78333333	18.5	AG	GG	AA	AA	AA	AG	AA	CC	CC	GA	AA	GG	AG	GA	0.6818181818
Coscomatepec	-97.45566667	20.12658333	GG	GA	AA	CA	AA	GG	AA	CC	CC	GG	GA	GG	GG	AA	0.6363636364
Cristalino_de_Chihuahua	-106.8788889	28.19322222	AG	GA	AA	CA	AA	AG	AA	CC	CC	AA	AA	AA	AA	AA	0.5454545455
Cristalino_de_Chihuahua	-107.4748056	28.50283333	AG	GG	AA	CC	GA	AG	AA	AC	AC	AA	AA	AG	AA	GA	0.4545454545
Dulce	-108.5333333	28.13333333	AG	GA	AA	CA	GA	GG	CC	CC	AC	GA	AA	GG	GG	AA	0.6363636364
Dulcillo del Noroeste	-108.9246667	28.53702778	AG	AA	AA	AA	GA	GG	AA	AC	CC	AA	GA	GG	GG	AA	0.5909090909
Dulcillo del Noroeste	-109.106	28.613	AA	GG	AA	AA	GA	AG	AA	CC	CC	AA	AA	GG	GG	AA	0.6363636364
Dzit-Bacal	-92.97972222	16.03225	GG	GG	AA	CA	AA	GG	CC	AC	AC	GG	GG	GG	GG	GA	0.6363636364
Dzit-Bacal	-93.00194444	16.36402778	AG	GG	AA	CA	AA	AG	AA	AC	CC	AA	AA	GG	GG	AA	0.6818181818
Dzit-Bacal	-93.45688889	16.75177778	AA	GG	AA	CA	AA	AG	AA	AC	AC	GG	AA	AG	GG	GA	0.6363636364
Elotero de Sinaloa	-105.5463889	22.88972222	GG	AA	AA	CA	GA	AG	AA	CC	CC	AA	AA	AA	AG	GA	0.4545454545
Elotero de Sinaloa	-105.8916667	23.40611111	AG	GA	AA	AA	GA	GG	AA	CC	CC	GA	GA	GG	AA	AA	0.5909090909
Elotero de Sinaloa	-106.0816667	23.43083333	AA	GG	AA	CA	GA	GG	AA	AC	AC	GA	AA	GG	AA	GG	0.5
Elotero de Sinaloa	-106.4261111	23.84611111	AG	GG	AA	CA	GG	GG	CA	AA	CC	GG	GA	AG	AG	GA	0.5909090909
Elotero de Sinaloa	-105.8308333	23.4575	AG	GG	AA	AA	GG	AG	CA	AC	CC	GG	GA	GG	GG	AA	0.7272727273
Elotes Conicos	-99.79111111	19.56944444	AG	AA	AA	CC	GG	GG	AA	CC	AA	AA	AA	GG	AG	GA	0.3181818182
Elotes Conicos	-97.9725	19.32166667	AG	AA	AA	CC	GA	AG	AA	CC	AC	AA	AA	AG	AG	GG	0.3636363636
Elotes Conicos	-97.92472222	19.19055556	AG	AA	AA	CA	GA	GG	AA	AC	CC	GA	AA	AG	AA	GA	0.5454545455
Elotes Conicos	-100.0255556	19.49083333	AG	GG	AA	AA	AA	AG	CA	AA	AC	GG	GG	GG	GG	GA	0.7272727273
Elotes Conicos	-98.37388889	20.35888889	GG	GG	AA	AA	AA	AG	AA	CC	CC	GG	GA	GG	AG	GA	0.6818181818
Elotes Conicos	-98.37555556	20.35472222	AG	GG	AA	AA	GA	AG	CA	CC	AC	GA	GG	GG	AG	GG	0.5
Elotes Conicos	-98.38333333	20.3975	AG	AA	AA	CA	GA	GG	AA	AC	AA	GG	GG	AG	GG	AA	0.4545454545
Elotes Conicos	-99.05027778	19.19166667	GG	AA	AA	CA	AA	GG	AA	CC	CC	GA	GA	AG	AA	GA	0.5
Elotes Conicos	-98.31555556	19.4875	AG	GA	AA	CA	GA	GG	AA	CC	CC	GA	GA	AG	AG	GA	0.4545454545
Elotes Conicos	-98.37555556	20.35472222	AG	AA	AA	CA	AA	GG	AA	CC	CC	GA	GA	AA	AG	AA	0.5
Elotes Conicos	-98.77233333	19.05555556	GG	GA	AA	CA	GA	GG	AA	CC	AA	AA	GA	GG	AA	GA	0.3636363636
Elotes Conicos	-98.04722222	19.33861111	AG	AA	AA	AA	GG	AG	AA	AC	AC	GA	AA	AA	AG	GG	0.4545454545
Elotes Conicos	-99.92944444	19.70611111	GG	AA	AA	AA	GG	GG	AA	AC	AC	AA	GA	GG	AA	GA	0.4545454545
Elotes Conicos	-98.80666667	19.10861111	AG	AA	AA	CA	AA	AA	AA	CC	CC	AA	GA	GG	AG	GA	0.5909090909
Elotes Occidentales	-100.7658333	20.74416667	GG	AA	AA	CA	AA	AG	AA	AC	CC	AA	GA	GG	AG	AA	0.6363636364
Elotes Occidentales	-100.1083333	19.04388889	AG	GA	AA	AA	AA	AG	CA	CC	CC	GA	GG	GG	AG	AA	0.6818181818
Elotes Occidentales	-100.8147222	20.78444444	GG	GG	AA	AA	GA	AG	CC	AC	AC	AA	GA	GG	GG	GA	0.6363636364
Elotes Occidentales	-100.9355556	20.78722222	AG	GA	AA	AA	GG	AG	AA	CC	CC	GA	GG	AA	AA	GA	0.4090909091
Gordo	-108.7097222	29.84027778	AG	GG	AA	AA	GA	AG	AA	AA	CC	AA	GA	GG	AA	GG	0.5909090909
Gordo	-108.7097222	29.84027778	AG	GA	AA	AA	AA	GG	AA	CC	AC	GA	AA	GG	AA	GA	0.5909090909
Jala	-104.4286944	21.10166667	AG	GG	AA	CA	GA	AA	AA	CC	AC	GA	AA	GG	AG	AA	0.6363636364
Jala	-104.4405556	21.1	AA	GA	AA	AA	AA	GG	AA	CC	CC	GA	AA	GG	AA	GA	0.6363636364

Landrace	Longitude	Latitude	PZE.100001195	PZE.108035280	PZE.109096578	SYN27200	SYN32365	SYN37470	PZE.101131254	PZE.103059706	PZE.104026211	PZE.104044827	PZE.105090166	PZE.106008139	PZE.109029456	PZE.104055811	Adaptive score
Jala	-104.4286944	21.10166667	GG	GG	AA	AA	GA	AG	AA	AA	AC	GA	GA	AG	AG	GA	0.5909090909
Jala	-104.4399794	21.07805	GG	GA	AA	CA	GA	AG	AA	AC	AC	AA	AA	GG	AG	AA	0.5909090909
Mushito	-99.805	21.2775	AA	AA	AA	CC	AA	AG	AA	AC	CC	GA	AA	AG	GG	GA	0.5909090909
Mushito	-111.9864167	26.89047222	AG	0	GA	AA	AA	GG	AA	CC	CC	GA	GG	GG	GG	AA	0.5454545455
Mushito	-100.13722	21.3575	AG	AA	AA	CA	GA	AA	CA	AC	CC	AA	AA	GG	AG	GA	0.6818181818
Nal-tel de Altura	-98.21666667	16.3	GG	GG	AA	AA	AA	GG	CA	AA	CC	GG	0	GG	AA	AA	0.7727272727
Nal-tel de Altura	-96.73333333	18.01666667	AG	GA	AA	CA	GA	GG	CA	AC	CC	AA	GG	AA	AA	AA	0.4545454545
Nal-tel de Altura	-91.97688889	16.23319444	GG	AA	AA	CA	GA	GG	CA	AC	AC	GA	GA	AA	AA	GA	0.4545454545
Nal-tel de Altura	-91.91638944	16.21563917	GG	AA	AA	CC	GG	GG	AA	CC	CC	AA	AA	AG	AG	GA	0.3636363636
Nal-tel de Altura	-97.06666667	18.85	AG	GA	AA	AA	GA	GG	AA	CC	CC	AA	AA	GG	AG	GA	0.5454545455
Oloton	-92.3145	15.36608333	GG	GA	GA	CA	GA	AG	AA	AC	CC	AA	AA	GG	AA	AA	0.5909090909
Oloton	-92.29358333	15.36011111	AG	AA	AA	CA	AA	AG	AA	CC	AC	AA	GA	GG	AG	GA	0.5
Oloton	-92.54222222	16.63975	AG	AA	AA	CA	GA	AG	AA	CC	CC	GG	GG	AG	AA	AA	0.5454545455
Oloton	-92.18767778	15.29614444	AG	AA	AA	CC	AA	AA	AA	CC	CC	GA	AA	AG	GG	AA	0.6363636364
Olotillo	-98.43611111	21.13333333	GG	AA	AA	AA	AA	GG	AA	AC	CC	AA	AA	GG	GG	AA	0.6818181818
Olotillo	-98.34638889	21.06388889	GG	GA	AA	AA	GA	AA	AA	AC	CC	AA	GG	GG	AG	GA	0.5909090909
Olotillo	-92.97972222	16.03225	GG	AA	GA	CA	AA	AA	CA	AC	CC	GA	AA	AG	AG	AA	0.7272727273
Olotillo	-93.00194444	16.36402778	AA	AA	AA	CA	AA	AG	CA	CC	CC	GA	GA	GG	AA	GA	0.6363636364
Olotillo	-92.216925	14.90176111	AG	GG	AA	CA	AA	AG	CA	AC	CC	GA	AA	AG	GG	GG	0.6363636364
Olotillo	-92.2045	14.87376389	AA	AA	AA	CC	AA	GG	AA	AC	CC	GA	GA	GG	AG	GA	0.5454545455
Onaveño	-109.68	29.80894444	AA	GA	AA	AA	AA	GG	CA	AA	CC	GG	GG	GG	AG	GG	0.6818181818
Onaveño	-108.8240833	27.17294444	GG	GA	AA	AA	AA	GG	AA	CC	CC	AA	GG	AG	AA	AA	0.5
Palomero de Chihuahua	-106.4436667	26.35983333	AA	GG	AA	CA	GA	AA	AA	CC	CC	GA	GA	AG	GG	GG	0.5
Palomero_Toluqueno	-99.71715556	19.79833333	AA	AA	AA	CC	AA	GG	AA	AC	AC	AA	AA	GG	AG	GA	0.5
Pepitilla	-100.1686111	19.0525	GG	GA	AA	AA	GA	GG	AA	CC	CC	GG	AA	AG	AG	AA	0.6363636364
Pepitilla	-100.1686111	19.0525	GG	GA	AA	AA	GG	GG	AA	CC	CC	GG	GA	GG	AG	AA	0.5909090909
Pepitilla	-100.1083333	19.04388889	GG	GA	AA	CC	GA	AG	AA	AC	CC	AA	GA	AG	AA	GA	0.4545454545
Pepitilla	-100.1083333	19.04388889	AG	GA	AA	CA	AA	GG	CA	CC	CC	AA	GG	AG	AA	GA	0.4545454545
Raton	-100.7042778	25.68125	GG	GG	AA	AA	AA	GG	CA	CC	CC	GA	GA	GG	GG	GG	0.5909090909
Raton	-99.25505556	24.12780556	AG	GG	AA	CA	AA	GG	AA	AC	CC	AA	GA	AG	GG	GG	0.4545454545
Raton	-99.02108333	24.29011111	GG	AA	AA	AA	AA	GG	AA	AA	CC	GA	AA	AG	GG	AA	0.7272727273
Reventador	-108.9119444	26.84361111	AG	GG	AA	AA	GA	GG	AA	AC	CC	GG	AA	GG	AG	GA	0.6818181818
Reventador	-110.2101111	29.79355556	GG	GA	AA	CA	AA	AG	CA	AC	AC	GA	AA	GG	AG	AA	0.7272727273
Tablilla de Ocho	-106.6324722	28.32019444	AG	GG	AA	AA	GA	AG	CC	AA	AC	AA	AA	AA	GG	GA	0.6363636364
Tablilla de Ocho	-106.0163611	26.94213889	AG	GA	AA	CA	AA	AA	AA	AC	AC	AA	AA	0	GG	AA	0.5909090909
Tabloncillo	-105.6068056	22.94927778	GG	GG	AA	AA	GA	AG	AA	AC	CC	GA	GA	AG	AG	GA	0.5909090909
Tabloncillo	-109.2448056	27.82702778	GG	GG	AA	AA	GA	AG	AA	AC	CC	AA	AA	AG	AA	GA	0.6363636364
Tabloncillo	-107.5618889	25.40125	GG	GA	AA	AA	GG	AA	AA	AC	AC	GA	GA	AG	AG	GA	0.5454545455
Tabloncillo	-108.9255278	28.41063889	AG	GA	AA	AA	AA	AG	AA	AC	CC	AA	AA	GG	AG	AA	0.7272727273
Tabloncillo_Perla	-105.39025	21.99097222	AA	GG	AA	AA	GA	GG	AA	CC	CC	GG	AA	GG	GG	GA	0.6363636364
Tabloncillo_Perla	-105.2216111	21.94602778	AA	GG	AA	AA	GG	AA	CA	AC	CC	GA	AA	GG	AG	GA	0.7272727273
Tabloncillo_Perla	-105.1493611	20.87416667	AG	GG	AA	AA	AA	GG	AA	AC	CC	GG	AA	AG	GG	AA	0.7272727273
Tehua	-93.206	17.19680556	AA	AA	AA	CA	GA	AG	AA	AC	CC	AA	GA	GG	AA	GG	0.5
Tehua	-93.17527778	17.21630556	AA	GA	AA	CC	GA	AG	AA	CC	CC	AA	AA	GG	AG	AA	0.5454545455
Tepecintle	-92.08888889	17.32222222	GG	AA	AA	CC	AA	GG	AA	AC	CC	GA	GA	AG	AG	GG	0.4545454545
Tepecintle	-92.31925	15.36652778	AA	AA	AA	CA	GA	AG	AA	AC	CC	GA	AA	GG	AA	AA	0.6818181818
Tepecintle	-92.19657222	14.82029722	GG	GG	AA	AA	AA	AG	AA	AC	CC	GG	GG	0	GG	GG	0.5454545455
Tepecintle	-92.46687222	17.25071111	AA	GA	AA	AA	AA	AG	CA	AA	CC	GG	AA	GG	GG	GG	0.8181818182
Tuxpeno	-92.81925	16.04422222	GG	GG	AA	CA	AA	GG	AA	AC	AC	GG	AA	AG	GG	GG	0.5454545455

Supplementary Table 8. Geographical coordinates, genotype for putative adaptive SNPs, and estimated adaptive scores for maize landraces accessions in Mexico. Detailed information on landrace and known occurrences can be obtained at www.biodiversidad.gob.mx/usos/maices/maiz.html

Landrace	Longitude	Latitude	PZE.100001195	PZE.108035280	PZE.109096578	SYN27200	SYN32365	SYN37470	PZE.101131254	PZE.103059706	PZE.104026211	PZE.104044827	PZE.105090166	PZE.106008139	PZE.109029456	PZE.104055811	Adaptive score
Tuxpeno	-106.1319444	23.25388889	GG	GG	AA	AA	GA	AG	AA	CC	CC	GA	GG	AG	GG	GA	0.5
Tuxpeno	-99.72272222	24.75586111	AG	GG	AA	AA	GA	AG	AA	CC	CC	GA	GA	AA	GG	GG	0.4545454545
Tuxpeno	-92.68894972	16.1194325	AA	GA	AA	CC	AA	AG	AA	AC	AC	AA	GG	GG	AG	AA	0.5
Tuxpeno_Norteno	-99.53447222	24.85894444	AG	AA	AA	AA	AA	AG	AA	AC	CC	GA	GA	GG	GG	GA	0.6818181818
Tuxpeno_Norteno	-100.2275	18.66027778	GG	GA	AA	AA	AA	GG	AA	CC	CC	GA	AA	AG	AG	GG	0.5454545455
Vandeno	-110.2121667	29.79602778	GG	AA	AA	AA	GA	GG	AA	CC	CC	GA	AA	GG	AG	GG	0.5454545455
Vandeno	-92.97783333	16.04222222	AA	GG	AA	CA	GA	AG	CA	AC	CC	GA	AA	GG	GG	GA	0.6818181818
Vandeno	-92.69643389	16.12061694	AG	GG	AA	CC	GG	GG	AA	CC	CC	GA	AA	AG	AG	GA	0.4090909091
Vandeno	-92.46687222	17.25071111	GG	GG	AA	AA	GA	GG	AA	AC	CC	GG	GA	GG	GG	GA	0.6363636364
Zamorano Amarillo	-104.45	19.6	AA	GG	AA	AA	GA	GG	CA	AA	AC	GA	GA	GG	GG	GG	0.5909090909
Zamorano Amarillo	-102.7166667	19.96666667	AG	GA	AA	AA	GG	AG	CA	AC	AC	AA	GA	AG	AG	GA	0.5
Zamorano Amarillo	-104.6333333	19.71666667	GG	GG	AA	CC	AA	AA	AA	CC	AC	GG	GA	AG	AG	GG	0.5
Zapalote Grande	-93.00194444	16.36402778	AG	GG	AA	AA	GA	GG	CC	AC	CC	AA	AA	AG	AG	AA	0.6818181818
Zapalote_Chico	-93.00194444	16.36402778	AG	GA	AA	AA	GA	GG	CC	AC	CC	AA	AA	AG	AG	AA	0.6818181818

Supplementary Table 9. Geographic distribution, environmental information and most common use of different maize landraces in Mexico with the potential for crop improvement (ref. 14). Detailed information on landraces can be obtained at www.biodiversidad.gob.mx/usos/maices/maiz.html

Landrace	Distribution	Enviroment	Use
Azul	Chihuahua	Not reported in ref. 14	Food source
Conejo	Oaxaca, Guerrero and Michoacan	tempered and dry	Not reported in ref. 14
Cónico Norteño	Guanajuato, Chihuahua, Zacatecas, Durango, Aguascalientes, San Luis Potosi, Coahuila and Nuevo Leon	low precipitation and extreme temperatures	Improvement for drought resistance
Elotes Occidentales	Nayarit, Jalisco, Michoacan, Guanajuato, Zacatecas, San Luis Potosi, Morelos, Puebla, Guerrero and Oaxaca	Not reported in ref. 14	Food source
Olotillo	Chiapas, Oaxaca y Guerrero, Veracruz, Puebla, Hidalgo and San Luis Potosi	Humid and dry tropics, poor soils	Food source
Raton	Tamaulipas, Nuevo León, Coahuila, Chihuahua, Durango, Zacatecas, San Luis Potosí, Veracruz, Guerrero and Morelos	subtropics y deserts, needs low humidity,	Improvement for highland races
Tabloncillo	Michoacán, Jalisco, Nayarit y Sinaloa, Sonora, Chihuahua and Baja California Sur	Not reported in ref. 14	Improvement, food source
Tabloncillo perlas	Sinaloa, Nayarit, Jalisco, Colima, Michoacan, Sonora and Baja California Sur	Low lands and dry, thin soils	Food source
Tepecintle	Oxaca y Chiapas	Laderas	Food source
Tuxpeño Norteño	North, Center of Mexico	Subtropics, season,	Improvement
Vandeño	Pacific coast	Seasonaility and low precipitation	Improvement