

## **Supplemental Material**

### **The molecular basis of parallel adaptation to highland climate in domesticated maize.**

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Later we should separate all Text S1, figs and tables in this file if we submit PLoS G.

## Text S1

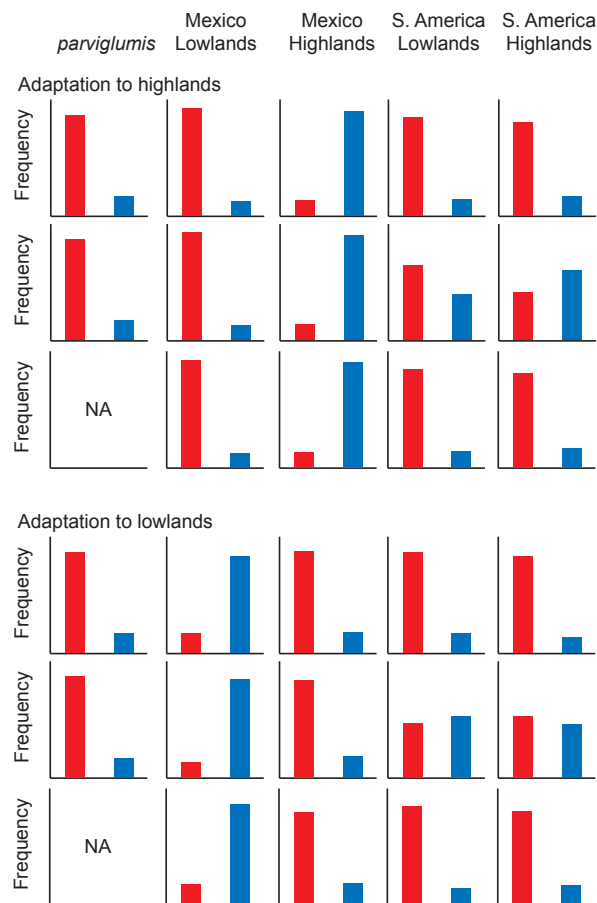
We classified the patterns of allelic differentiation among highland and lowland populations in Mexico and S. America together with the information of *parviglumis* in an *ad hoc* manner; the allelic differentiation pattern is consistent with highland or lowland adaptation scenario. In Figure I, we illustrate the frequency of putative ancestral and derived alleles in the five populations, drawn by red and blue, respectively.

First, we focus on the SNPs with the signature of adaptation only in Mexican populations (Figure IA). The first and second rows shows the typical patterns of highland adaptation with *parviglumis* data available. We simply assume that the allele in higher frequency in *parviglumis* is ancestral. Both rows show the consistent pattern to highland adaptation in Mexico because the frequency of the putative derived allele in Mexican highlands is highly differentiated from those in both *parviglumis* and Mexican lowlands. The patterns in S. America are different between the first and second rows. However, we do not take the patterns in S. American populations into account because there is no adaptive signature in S. American. On the other hand, we should consider the allelic pattern in S. America in the case of the third row; we cannot utilize the information of *parviglumis*. It is impossible to infer the ancestral allele, so we assume the pattern is consistent with highland adaptation if one allele is in higher frequency in Mexican lowlands and S. American populations and the others is in higher frequency in Mexican highlands. We classified the SNPs into lowland adaptation in the same way (from fourth to sixth rows in Figure IA).

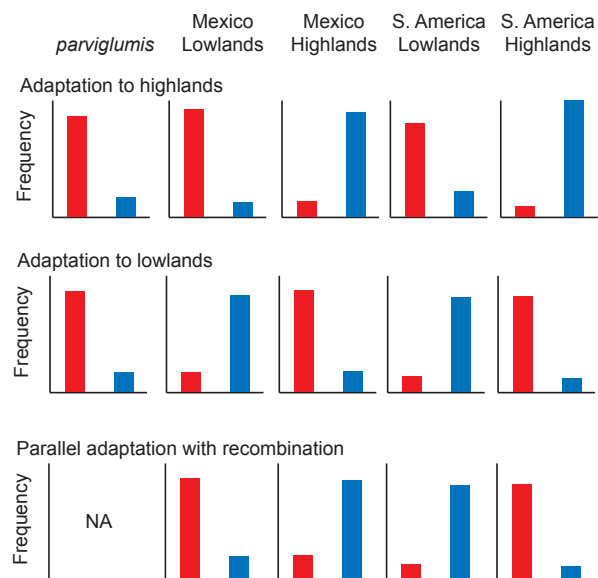
Next, we consider the SNPs with the signatures of adaptation in both Mexico and S. America (Figure IB). The pattern in the first row is consistent with parallel highland adaptation, whereas the second row shows parallel lowland adaptation. We cannot infer lowland or highland adaptation without the outgroup, so we ignore such SNPs. The pattern in the third row is the special case: the allele frequency is similar between Mexican lowlands and S. American highlands and similar between Mexican highlands and S. American lowlands. This pattern could be explained by that the SNP is linked to a read adaptive SNP and recombination breaks down the linkage between them.

Finally, we tested whether PHS test supports highland and lowland adaptation scenario. Consider the case of highland adaptation. We assumed that the putative derived allele is adaptive in highlands and checked whether the haplotype length is longer in highlands than that in lowlands. However, haplotype length cannot be compared directly because the derived allele frequency is different between highlands and lowlands. Thus, we compared the  $P$ -values of PHS test as a indicator of haplotype length given allele frequency ( $\Pr(PHS_{xA} \leq PHS_{null|p}$  in Materials and Methods). We just say that the PHS test is consistent if the  $P$ -value in highlands is smaller than the  $P$ -value in lowlands (haplotype length is longer as  $P$ -value is smaller). The result is summarized in Table S3.

### A Mexico-specific adaptation



### B Adaptation both in Mexico and South America



**Figure I** Illustration of allele frequency changes in maize and *parviglumis*. Red and blue bars represent the allele frequency of ancestral and derived, adaptive alleles, respectively. The allele frequencies in the five populations are shown: *parviglumis*, Mexican lowlands and highlands, and S. America lowlands and highlands. NA in *parviglumis* indicates that there is no SNP data in the site.

**Table S1 List of maize landraces used in this study**

ID <sup>a</sup>	USDA ID	Population	Landrace	Locality	Latitude	Longitude	Elevation	Origin
<b>RIMMA0409</b>	PI 478968	Mexico	Tepecintle	Chiapas, Mexico	15.4	-92.9	107	USDA
RIMMA0410	PI 478970	Lowland	Vandeno	Chiapas, Mexico	15.4	-92.9	107	USDA
<b>RIMMA0433</b>	PI 490825		Nal Tel ATB	Chiquimula, Guatemala	14.7	-89.5	457	USDA
<b>RIMMA0441</b>	PI 515538		Coscomatepec	Veracruz, Mexico	19.2	-97.0	1320	USDA
<b>RIMMA0615</b>	PI 628480		Tuxpeno	Puebla, Mexico	20.1	-97.2	152	USDA
<b>RIMMA0619</b>	PI 645772		Pepitilla	Guerrero, Mexico	18.4	-99.5	747	USDA
<b>RIMMA0628</b>	PI 646017		Tuxpeno Norteno	Tamaulipas, Mexico	23.3	-99.0	300	USDA
<b>RIMMA0696</b>	Ames 28568		Tuxpeno	El Progreso, Guatemala	16.5	-90.2	30	Goodman
<b>RIMMA0700</b>	NSL 291626		Olotillo	Chiapas, Mexico	16.8	-93.2	579	Goodman
<b>RIMMA0701</b>	PI 484808		Olotillo	Chiapas, Mexico	16.6	-92.7	686	Goodman
<b>RIMMA0702</b>	Ames 28534		Negro de Tierra Caliente	Sacatepequez, Guatemala	14.5	-90.8	1052	Goodman
<b>RIMMA0703</b>	NSL 283390		Nal Tel	Yucatan, Mexico	20.8	-88.5	30	Goodman
<b>RIMMA0709</b>	Ames 28452		Tehua	Chiapas, Mexico	16.5	-92.5	747	Goodman
<b>RIMMA0710</b>	PI 478988		Tepecintle	Chiapas, Mexico	15.3	-92.6	91	Goodman
<b>RIMMA0712</b>	NSL 291696 CYMT		Oloton	Baja Verapaz, Guatemala	15.3	-90.3	1220	Goodman
<b>RIMMA0716</b>	Ames 28459		Zapalote Grande	Chiapas, Mexico	15.3	-92.7	91	Goodman
<b>RIMMA0720</b>	PI 489372		Negro de Tierra Caliente	Guatemala	15.5	-88.9	39	Goodman
<b>RIMMA0721</b>	Ames 28485		Nal Tel ATB	Chiquimula, Guatemala	14.6	-90.1	915	Goodman
<b>RIMMA0722</b>	Ames 28564		Dzit Bacal	Jutiapa, Guatemala	14.3	-89.7	737	Goodman
<b>RIMMA0727</b>	Ames 28555		Comiteco	Guatemala	14.4	-90.5	1151	Goodman
<b>RIMMA0729</b>	PI 504090		Tepecintle	Guatemala	15.4	-89.7	122	Goodman
<b>RIMMA0730</b>	Ames 28517		Quicheno Late	Sacatepequez, Guatemala	14.5	-90.8	1067	Goodman
<b>RIMMA0731</b>	PI 484137		Bolita	Oaxaca, Mexico	16.8	-96.7	1520	Goodman
<b>RIMMA0733</b>	PI 479054		Zapalote Chico	Oaxaca, Mexico	16.6	-94.6	107	Goodman
<b>RIMMA0416</b>	PI 484428	Mexico	Cristalino de Chihuahua	Chihuahua, Mexico	29.4	-107.8	2140	NA
<b>RIMMA0417</b>	PI 484431	Highland	Azul	Chihuahua, Mexico	28.6	-107.5	2040	USDA
<b>RIMMA0418</b>	PI 484476		Gordo	Chihuahua, Mexico	28.6	-107.5	2040	USDA
<b>RIMMA0421</b>	PI 484595		Conico	Puebla, Mexico	19.9	-98.0	2250	USDA
<b>RIMMA0422</b>	PI 485071		Elotes Conicos	Puebla, Mexico	19.1	-98.3	2200	USDA
<b>RIMMA0423</b>	PI 485116		Cristalino de Chihuahua	Chihuahua, Mexico	29.2	-108.1	2095	NA
<b>RIMMA0424</b>	PI 485120		Apachito	Chihuahua, Mexico	28.0	-107.6	2400	USDA
<b>RIMMA0425</b>	PI 485128		Palomero Tipo Chihuahua	Chihuahua, Mexico	26.8	-107.1	2130	USDA
<b>RIMMA0614</b>	PI 628445		Mountain Yellow	Jalisco, Mexico	20.0	-103.8	2060	USDA
<b>RIMMA0616</b>	PI 629202		Zamorano Amarillo	Jalisco, Mexico	20.8	-102.8	1800	USDA
<b>RIMMA0620</b>	PI 645786		Celaya	Guanajuato, Mexico	20.2	-100.9	1799	USDA
<b>RIMMA0621</b>	PI 645804		Zamorano Amarillo	Guanajuato, Mexico	21.1	-101.7	1870	USDA
<b>RIMMA0623</b>	PI 645841		Palomero de Jalisco	Jalisco, Mexico	20.0	-103.7	2520	USDA
<b>RIMMA0625</b>	PI 645984		Cacahuacintle	Puebla, Mexico	19.0	-97.4	2600	USDA
RIMMA0626	PI 645993		Arrocillo Amarillo	Puebla, Mexico	19.9	-97.6	2260	USDA
<b>RIMMA0630</b>	PI 646069		Arrocillo Amarillo	Veracruz, Mexico	19.8	-97.3	2220	USDA
<b>RIMMA0670</b>	Ames 28508		San Marceno	San Marcos, Guatemala	15.0	-91.8	2378	Goodman
<b>RIMMA0671</b>	Ames 28538		Salpor Tardio	Solola, Guatemala	14.8	-91.3	2477	Goodman
<b>RIMMA0672</b>	PI 483613		Chalqueno	Mexico, Mexico	19.7	-99.1	2256	Goodman
<b>RIMMA0674</b>	PI 483617		Toluca	Mexico, Mexico	19.3	-99.7	2652	Goodman
<b>RIMMA0677</b>	Ames 28476		Conico Norteno	Zacatecas, Mexico	21.4	-102.9	1951	Goodman
<b>RIMMA0680</b>	Ames 28448		Tabloncillo	Jalisco, Mexico	20.4	-102.2	1890	Goodman
<b>RIMMA0682</b>	PI 484571		Tablilla de Ocho	Jalisco, Mexico	22.1	-103.2	1700	Goodman
<b>RIMMA0687</b>	Ames 28473		Conico Norteno	Queretaro, Mexico	20.4	-100.0	1921	Goodman

<sup>a</sup> GBS data are available for the accessions in bold font.

Table S1 (continued)

ID	USDA ID	Population	Landrace	Locality	Latitude	Longitude	Elevation	Origin
<b>RIMMA0388</b>	PI 443820	South America	Amagaceno	Antioquia, Colombia	6.9	-75.3	1500	USDA
<b>RIMMA0389</b>	PI 444005	Lowland	Costeno	Atlantico, Colombia	10.4	-74.9	7	USDA
<b>RIMMA0390</b>	PI 444254		Comun	Caldas, Colombia	4.5	-75.6	353	USDA
<b>RIMMA0391</b>	PI 444296		Andaqui	Caqueta, Colombia	1.4	-75.8	700	USDA
<b>RIMMA0392</b>	PI 444309		Andaqui	Caqueta, Colombia	1.8	-75.6	555	USDA
<b>RIMMA0393</b>	PI 444473		Costeno	Cordoba, Colombia	8.3	-75.2	100	USDA
<b>RIMMA0394</b>	PI 444621		Pira	Cundinamarca, Colombia	4.8	-74.7	1000	USDA
<b>RIMMA0395</b>	PI 444731		Negrito	Choco, Colombia	8.5	-77.3	30	USDA
<b>RIMMA0396</b>	PI 444834		Caqueteno	Huila, Colombia	2.6	-75.3	1100	USDA
<b>RIMMA0397</b>	PI 444897		Negrito	Magdalena, Colombia	11.6	-72.9	50	USDA
<b>RIMMA0398</b>	PI 444923		Puya	Magdalena, Colombia	9.4	-75.7	27	USDA
<b>RIMMA0399</b>	PI 444954		Cariaco	Magdalena, Colombia	10.2	-74.1	250	USDA
<b>RIMMA0403</b>	PI 445163		Pira Naranja	Narino, Colombia	1.3	-77.5	1000	USDA
<b>RIMMA0404</b>	PI 445322		Puya Grande	Norte de Santander, Colombia	7.3	-72.5	1500	USDA
<b>RIMMA0405</b>	PI 445355		Puya	Norte de Santander, Colombia	8.4	-73.3	1100	USDA
<b>RIMMA0406</b>	PI 445514		Yucatan	Tolima, Colombia	5.0	-74.9	450	USDA
<b>RIMMA0407</b>	PI 445528		Pira	Tolima, Colombia	4.2	-74.9	450	USDA
<b>RIMMA0428</b>	PI 485354		Aleman	Huanuco, Peru	-9.3	-76.0	700	NA
<b>RIMMA0462</b>	PI 445073		Amagaceno	Narino, Colombia	1.6	-77.2	1700	USDA
<b>RIMMA0690</b>	PI 444946		Puya	Magdalena, Colombia	8.3	-73.6	250	Goodman
<b>RIMMA0691</b>	PI 445391		Cacao	Santander, Colombia	6.6	-73.1	1098	NA
<b>RIMMA0707</b>	PI 487930		Tuxpeno	Ecuador	-1.1	-80.5	30	Goodman
<b>RIMMA0708</b>	PI 488376		Yunquillano F Andaqui	Ecuador	-3.5	-78.6	1098	Goodman
<b>RIMMA0426</b>	PI 485151	South America	Rabo de Zorro	Ancash, Peru	-9.1	-77.8	2500	NA
<b>RIMMA0430</b>	PI 485362	Highland	Sarco	Ancash, Peru	-9.2	-77.7	2585	NA
<b>RIMMA0431</b>	PI 485363	(Andean)	Perlilla	Huanuco, Peru	-8.7	-77.1	2900	NA
<b>RIMMA0436</b>	PI 514723		Morocho Cajabambino	Amazonas, Peru	-6.2	-77.9	2200	NA
<b>RIMMA0437</b>	PI 514752		Ancashino	Ancash, Peru	-9.3	-77.6	2688	NA
<b>RIMMA0438</b>	PI 514809		Maranon	Ancash, Peru	-8.7	-77.4	2820	NA
<b>RIMMA0439</b>	PI 514969		Maranon	La Libertad, Peru	-8.5	-77.2	2900	NA
<b>RIMMA0464</b>	PI 571438		Chullpi	Huancavelica, Peru	-12.3	-74.7	1800	USDA
<b>RIMMA0465</b>	PI 571457		Huarmaca	Piura, Peru	-5.6	-79.5	2300	USDA
<b>RIMMA0466</b>	PI 571577		Confite Puneno	Apurimac, Peru	-14.3	-72.9	3600	USDA
<b>RIMMA0467</b>	PI 571871		Paro	Apurimac, Peru	-13.6	-72.9	2800	USDA
<b>RIMMA0468</b>	PI 571960		Sarco	Ancash, Peru	-9.4	-77.2	3150	USDA
<b>RIMMA0473</b>	PI 445114		Sabanero	Narino, Colombia	1.1	-77.6	3104	USDA
<b>RIMMA0656</b>	Ames 28799		Culli	Jujuy, Argentina	-23.2	-65.4	2287	Goodman
<b>RIMMA0657</b>	NSL 286594		Chake Sara	Bolivia	-17.5	-65.7	2201	Goodman
<b>RIMMA0658</b>	NSL 286812		Uchuquilla	Bolivia	-21.8	-64.1	1948	Goodman
<b>RIMMA0661</b>	PI 488066		Chillo	Ecuador	-2.9	-78.7	2195	Goodman
<b>RIMMA0662</b>	NSL 287008		Cuzco	Ecuador	0.0	-78.0	2195	Goodman
<b>RIMMA0663</b>	PI 488102		Mishca	Ecuador	0.4	-78.2	2067	Goodman
<b>RIMMA0664</b>	PI 488113		Blanco Blandito	Ecuador	0.4	-78.4	2122	Goodman
<b>RIMMA0665</b>	PI 489324		Racimo de Uva	Ecuador	-0.9	-78.9	2931	Goodman
<b>RIMMA0667</b>	Ames 28737		Patillo	Chuquisaca, Bolivia	-21.8	-64.1	2201	NA
<b>RIMMA0668</b>	Ames 28668		Granada	Puno, Peru	-14.9	-70.6	3925	Goodman

<sup>a</sup> GBS data are available for the accessions in bold font.

**Table S2 Inference of demographic parameters**

Mexico	Model I	
	Likelihood	−3050.84
	$\alpha$	0.99
	$\beta$	0.42
	$\gamma$	1
	$\sigma$	1
South America	Model I	
	Likelihood	−2737.80
	$\alpha$	0.6
	$\beta$	0.97
	$\gamma$	$\geq 55$
	$\sigma$	1

The description of  $\alpha$ ,  $\beta$  and  $\gamma$  is in Figure 3.

$\sigma$  is a relative size of  $N_B$  to  $N_C$  ( $N_B = \sigma N_C$ ).

**Table S3 Summary of PHS test**

Population	Pattern of adaptation	No. SNPs	No. SNPs supported by PHS test
Mexico	Highland adaptation	414	278 (67.1%)
	Lowland adaptation	199	113 (56.8%)
S. America	Highland adaptation	453	307 (67.7%)
	Lowland adaptation	144	78 (54.2%)

**Table S4 ms command**

Model I for Mexico populations

Population 1: Mexico lowland population

Population 2: Mexico highland population

-l 2  $n_{m1}$   $n_{m2}$  -n 1 0.3496 -n 2 0.5704 -ej 0.01 2 1 -en 0.01 1 0.92 -en 0.0133 1 0.0163 -en 0.015 1 1.0

Model II for Mexico populations

Population 1: Mexico lowland population

Population 2: Mexico highland population

Population 3: *mexicana* population

-l 2  $n_{m1}$   $n_{m2}$  -n 1 1.125 -n 2 0.375 -es 0.01 2 0.8 -en 0.01 3 1.0667 -ej 0.01 2 1 -en 0.01 1 1.5 -en 0.0133 1 0.0163 -en 0.015 1 1.0 -ej 0.1 3 1

Model I for SA populations

Population 1: SA lowland population

Population 2: SA highland population

-l 2  $n_{s1}$   $n_{s2}$  -n 1 0.5335 -n 2 0.99 -g 2 614.1517 -ej 0.006667 2 1 -eg 0.006667 2 0.0 -en 0.006667 1 0.55 -en 0.01333 1 0.0163 -en 0.015 1 1.0

Model III for SA populations

Population 1: Mexico lowland population

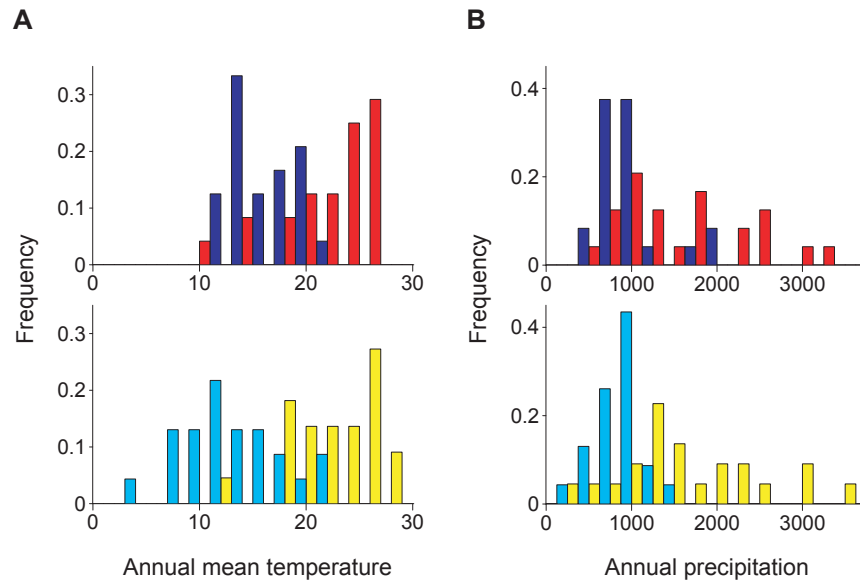
Population 2: SA lowland population

Population 3: SA highland population

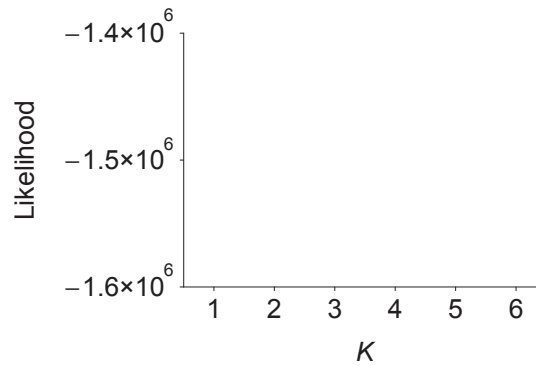
-l 3  $n_{m1}$   $n_{s1}$   $n_{s2}$  -n 1 0.64 -n 2 0.342 -n 3 0.99 -g 3 601.1000 -ej 0.006667 3 2 -eg 0.006667 3 0.0 -en 0.006667 2 0.36 -ej 0.01 2 1

-en 0.01 1 1 -en 0.0133 1 0.0163 -en 0.015 1 1.0

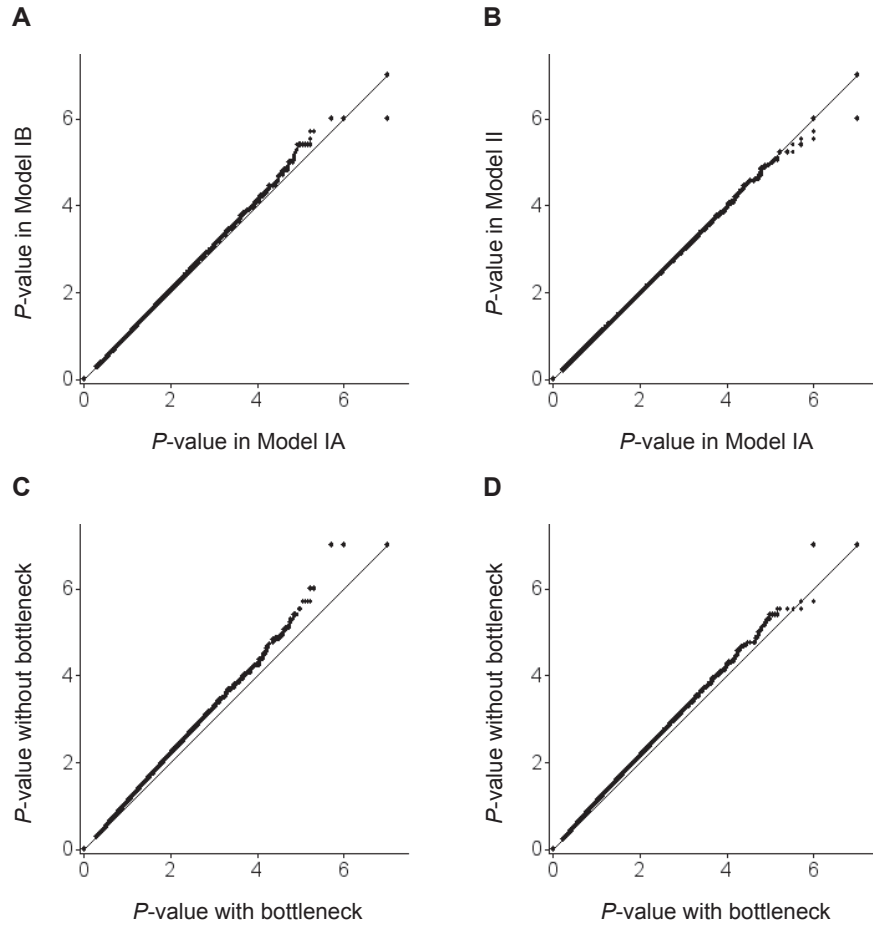
Sample size of Mexico lowland, Mexico highland, SA lowland and SA highland populations are denoted by  $n_{m1}$ ,  $n_{m2}$ ,  $n_{s1}$  and  $n_{s2}$ , respectively.



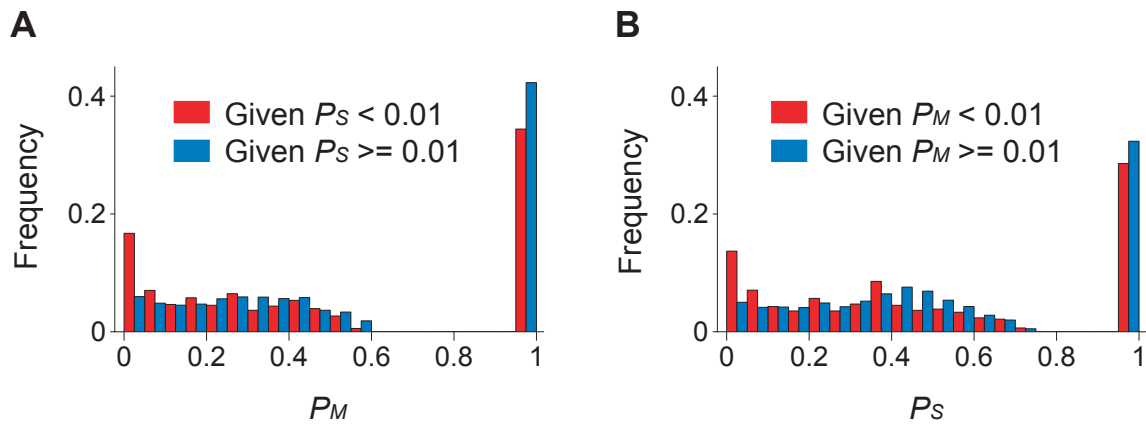
**Figure S1** Correlation of allele frequencies between GBS ( $x$ -axes) and MaizeSNP50 ( $y$ -axes) data. We used overlapped SNPs with  $n \geq 40$  for both data sets. Correlation coefficient is 0.890 ( $P < 10^{-5}$  by permutation test with  $10^5$  replications).



**Figure S2** Likelihood of STRUCTURE analysis given  $K$ . The  $x$ -axes represents  $K$  and the  $y$ -axes represents likelihood.

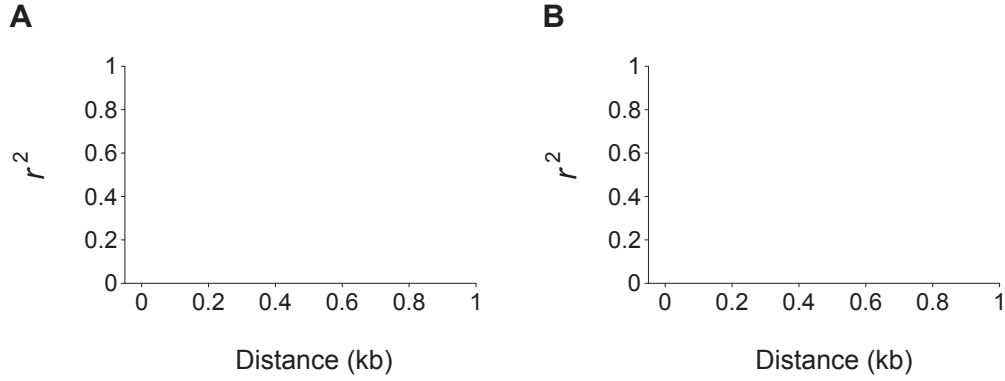


**Figure S3** Q-Q plot for  $-\log_{10}$ -scaled  $P$ -values of population differentiation between lowland and highland populations. (A) Model IA v.s. Model IB in Mexico, (B) Model IA v.s. Model II in S. America, (C) Model with v.s. without bottleneck in Mexico and (D) Model with v.s. without bottleneck in S. America.

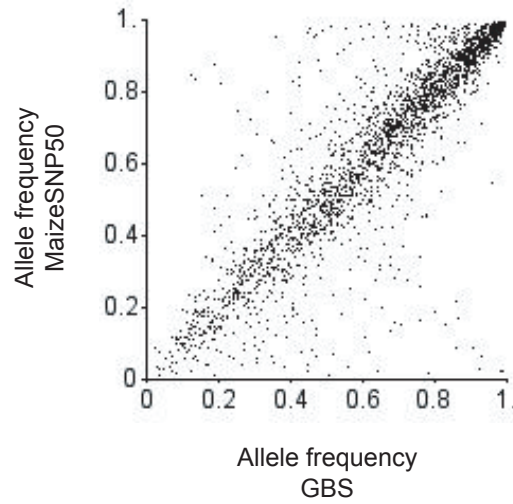


**Figure S4** (A) Frequency distribution of  $P_M$  given  $P_S < 0.01$  and  $P_S \geq 0.01$ . (B) Frequency distribution of  $P_S$  given  $P_M < 0.01$  and  $P_M \geq 0.01$ .





**Figure S5** Pattern of decay of linkage equilibrium in Mexico (A) and South America (B). Red and blue dots represent low- and highland population, respectively.  $r^2$  values were calculated as a statistics and averaged within 10-bp bins of distance between SNPs. The x- and y-axes represent distance between SNPs (kb) and average  $r^2$  values.



**Figure S6** Correlation of allele frequencies between GBS (x-axes) and MaizeSNP50 (y-axes) data. We used overlapped SNPs with  $n \geq 40$  for both data sets. Correlation coefficient is 0.890 ( $P < 10^{-5}$  by permutation test with  $10^5$  replications).