

## Supplementary Material

# Domestication Genomics of the open-pollinated Scarlet Runner Bean (*Phaseolus coccineus* L.)

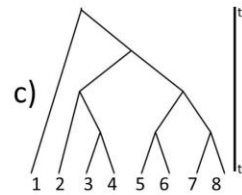
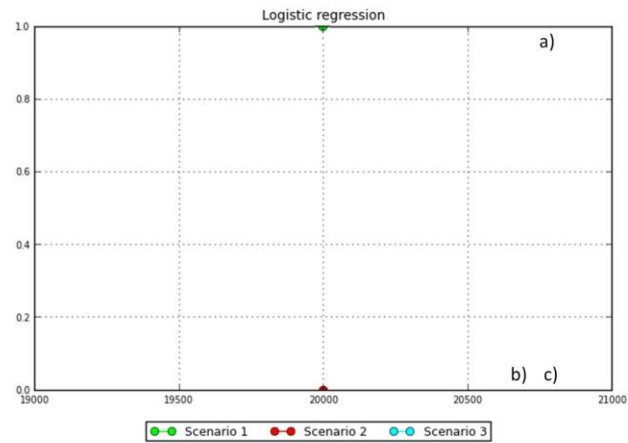
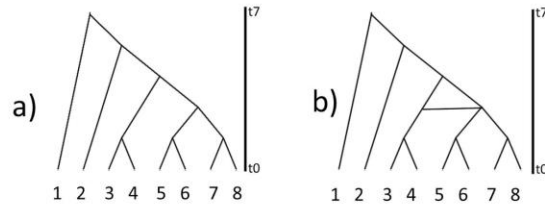
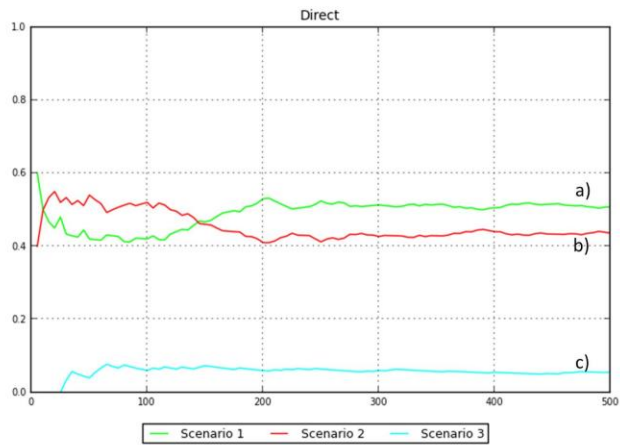
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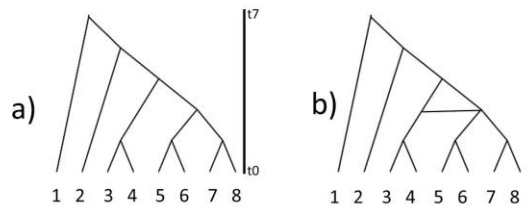
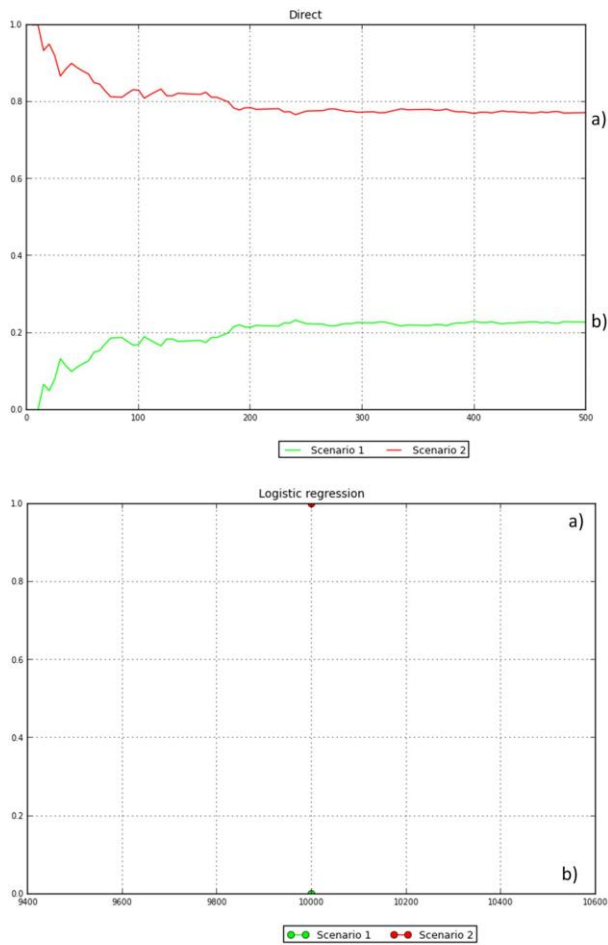
**Table S1.** Sampling information

Species	Status	State and location	Latitude	Longitude	Altitude
<i>P. coccineus</i> subsp. <i>coccineus</i>	Cultivated	Oaxaca, Cuilapam	16.99	-96.78	1577
<i>P. coccineus</i> subsp. <i>coccineus</i>	Cultivated	Durango	NA	NA	NA
<i>P. coccineus</i> subsp. <i>coccineus</i>	Cultivated	Veracruz, Frijol Colorado	19.59	-97.35	2419
<i>P. coccineus</i> subsp. <i>coccineus</i>	Cultivated	Chiapas, González León	16.51	-92.06	1579
<i>P. coccineus</i> subsp. <i>coccineus</i>	Cultivated	España	NA	NA	NA
<i>P. coccineus</i> subsp. <i>coccineus</i>	Cultivated	Chiapas, Nahá	16.94	-91.59	917
<i>P. coccineus</i> subsp. <i>coccineus</i>	Cultivated	Veracruz, Orilla del Monte	19.66	-97.29	2402
<i>P. coccineus</i> subsp. <i>coccineus</i>	Cultivated	Chaipas, Oxchuc	16.80	-92.32	2001
<i>P. coccineus</i> subsp. <i>coccineus</i>	Cultivated	Puebla, Tlalanecaneca	19.36	-98.51	2372
<i>P. coccineus</i> subsp. <i>coccineus</i>	Cultivated	Durango, Regocijo	23.68	-105.12	2566
<i>P. coccineus</i> subsp. <i>coccineus</i>	Cultivated	Durango, Villa Unión	23.97	-104.04	1901
<i>P. coccineus</i> subsp. <i>coccineus</i>	Cultivated	Puebla	NA	NA	NA
<i>P. coccineus</i> subsp. <i>coccineus</i>	Feral	Veracruz, Altotonga	19.75	-97.25	1959

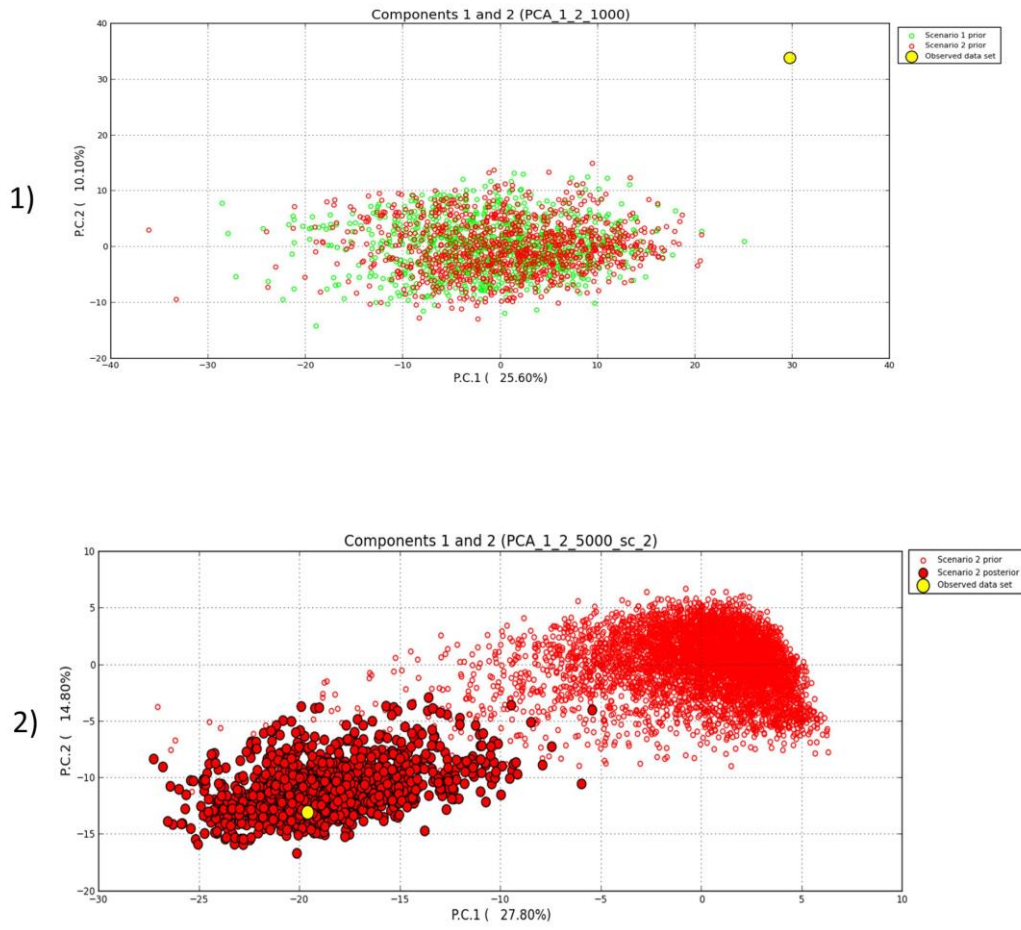
<i>P. coccineus</i> subsp. <i>coccineus</i>	Feral	Oaxaca, Huautla	18.10	-96.83	1746
<i>P. coccineus</i> subsp. <i>coccineus</i>	Feral	Chiapas, Zicanantán	16.75	-92.73	2408
<i>P. coccineus</i> subsp. <i>coccineus</i>	Breeding line	Blanco Tlaxcala	NA	NA	NA
<i>P. coccineus</i> subsp. <i>coccineus</i>	Wild	Jalisco, Ciudad Gúzman	19.58	-103.53	2100
<i>P. coccineus</i> subsp. <i>coccineus</i>	Wild	Oaxaca, Comaltepec	17.55	-96.53	2876
<i>P. coccineus</i> subsp. <i>coccineus</i>	Wild	Durango, Espinazo del Diablo	23.64	-105.82	1422
<i>P. coccineus</i> subsp. <i>coccineus</i>	Wild	Durango, Regocijo	23.68	-105.12	2566
<i>P. coccineus</i> subsp. <i>coccineus</i>	Wild	Ciudad de México, REPSA	19.32	-99.20	2328
<i>P. coccineus</i> subsp. <i>coccineus</i>	Wild	Querétaro, San Joaquín	20.93	-99.56	2381
<i>P. coccineus</i> subsp. <i>coccineus</i>	Wild	Chiapas, San Cristóbal	16.70	-92.60	2229
<i>P. coccineus</i> subsp. <i>coccineus</i>	Wild	Morelos, Tepoztlán	19.00	-99.13	1953
<i>P. coccineus</i> subsp. <i>coccineus</i>	Wild	Ciudad de México, Tlalpan	19.29	-99.19	2334
<i>P. coccineus</i> subsp. <i>striatus</i>	Wild	Morelos, Tres Marías	19.10	-99.21	3024
<i>P. dumosus</i>	Cultivated	Veracruz, Altotonga	19.75	-97.25	1959
<i>P. dumosus</i>	Cultivated	Chiapas, Chiquinivalvo	16.71	-92.86	1467
<i>P. dumosus</i>	Cultivated	Puebla, Cuetzalan	19.99	-97.54	1684
<i>P. dumosus</i>	Cultivated	Oaxaca, Huautla	18.10	-96.83	1746
<i>P. dumosus</i>	Cultivated	Chiapas, Motozintla	15.43	-92.33	2671
<i>P. dumosus</i>	Cultivated	Chiapas, Talquián	15.09	-92.08	1728
<i>P. vulgaris</i>	Cultivated	España	NA	NA	NA
<i>P. vulgaris</i>	Wild	Jalisco	NA	NA	NA
<i>P. vulgaris</i>	Wild	Ciudad de México, REPSA	19.32	-99.20	2328
<i>P. vulgaris</i>	Wild	Morelos, Yautepec	18.95	-99.08	1386



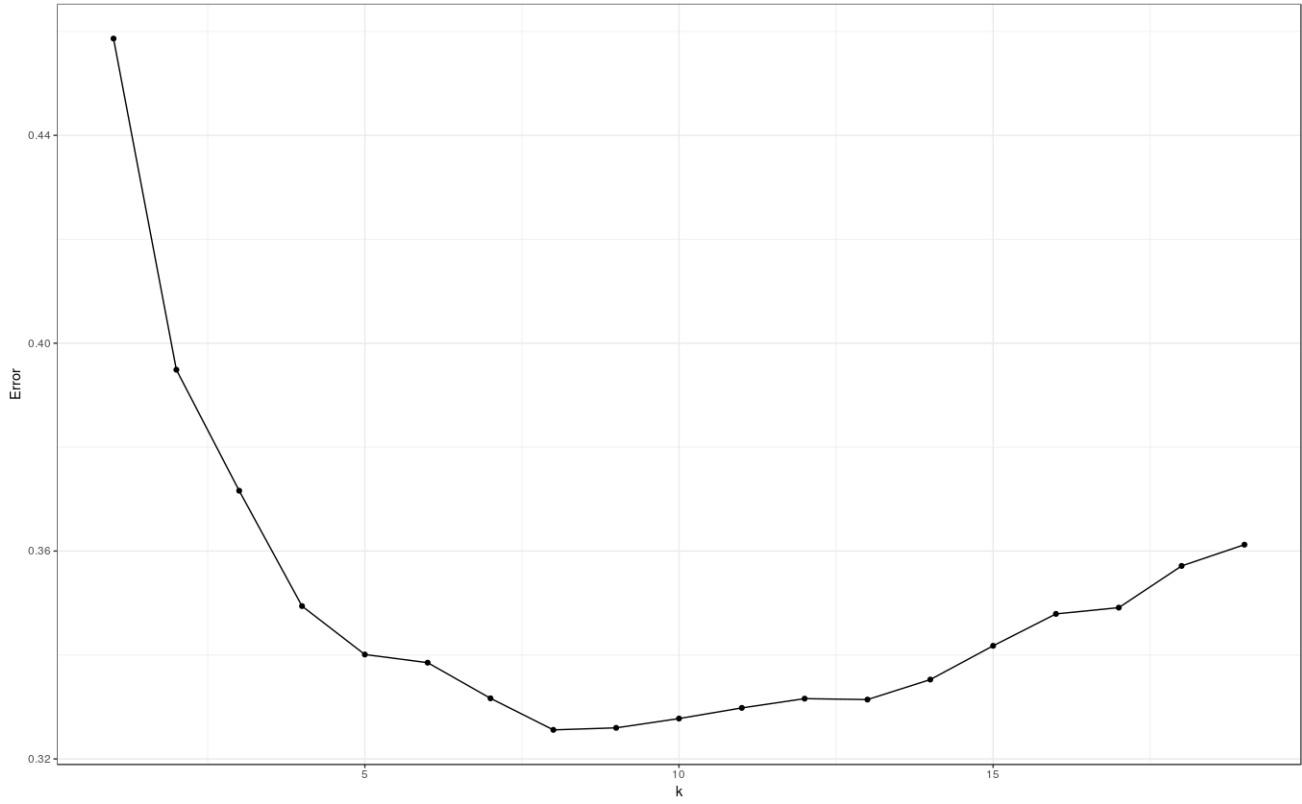
**Figure S1.** Posterior probabilities (Direct and Logistic) of the three main domestication scenarios tested with DIYABC, among eight wild and cultivated populations of *Phaseolus coccineus* in Mexico. In this preliminary evaluation: a) monophyletic origin of Wild populations b) and c) paraphyletic relationships among Wild populations.



**Figure S2.** Posterior probabilities (Direct and Logistic) of the two previously selected domestication scenarios tested with DIYABC among eight wild and cultivated populations of *Phaseolus coccineus* in Mexico. Both scenarios reflect a paraphyletic relationship among Wild populations and a) with one contribution in time of Wild Populations into Cultivated ancestral genetic pool and b) with several contributions events in time of Wild Populations into Cultivated ancestral genetic pool



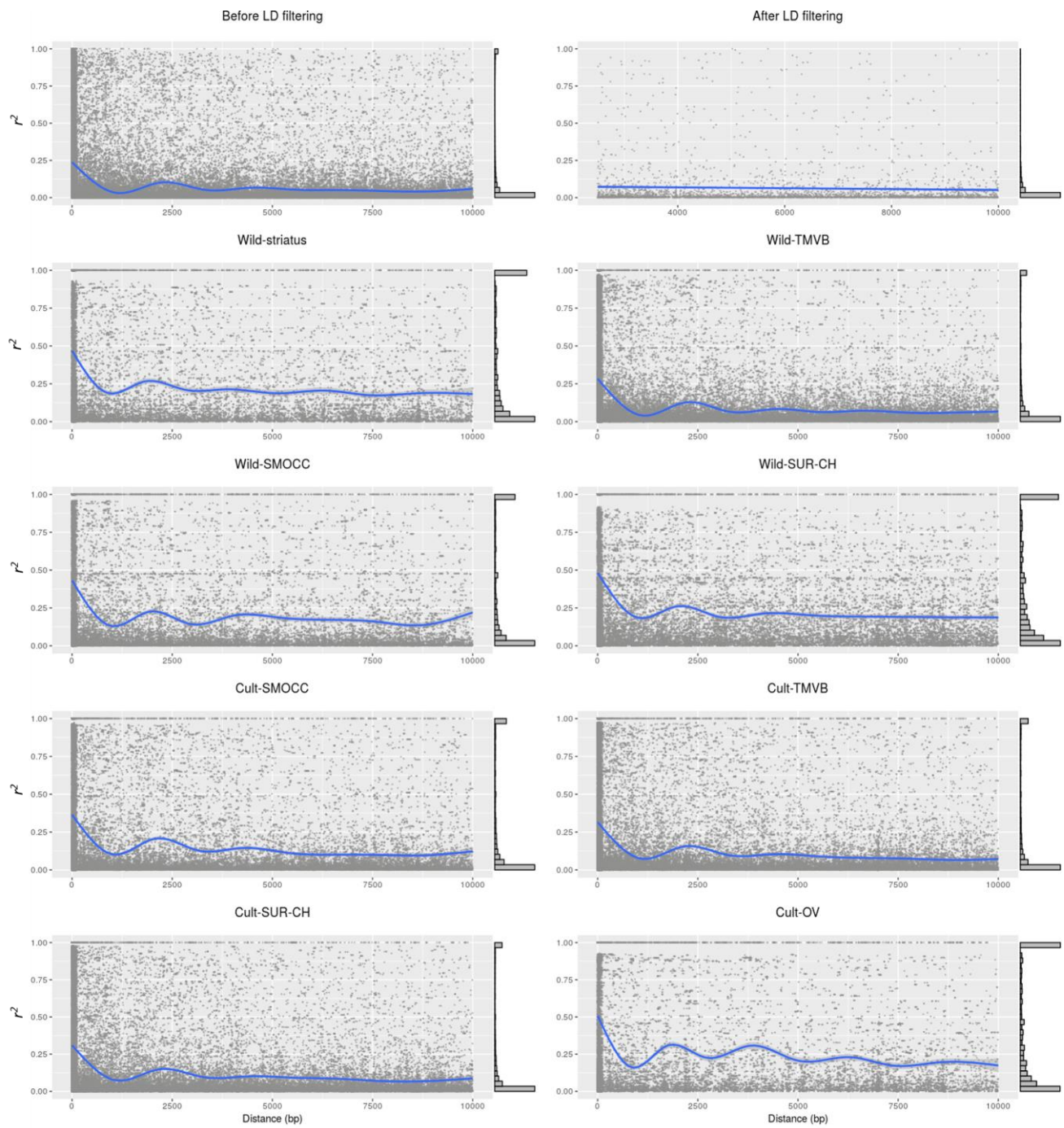
**Figure S3.** Principal component analyses of the a) Pre-evaluate scenario prior combinations of two selected scenarios in which paraphyletic relationship among Wild populations are represented and b) Model checking of the selected scenario indicating a single contribution in time of Wild Populations into Cultivated ancestral genetic pool



**Figure S4.** Cross-validation errors among  $K$  values using Admixture software for the *P. coccineus* data set.

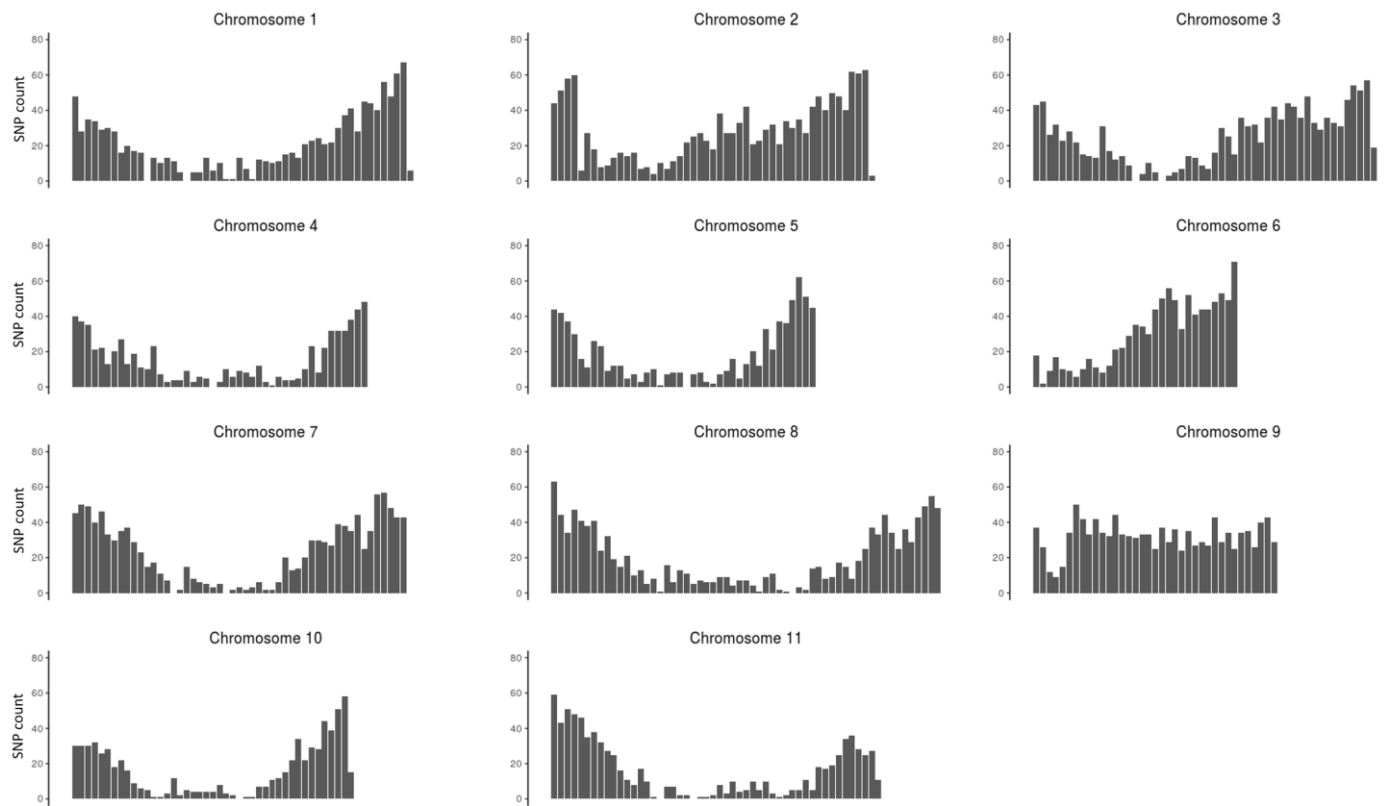
**Table S2.** Heterozygosity and inbreeding coefficient statistics of *P. coccineus* samples grouped by population.

<b>Genetic cluster</b>	<b>Population</b>	<b><math>H_O</math></b>	<b><math>H_E</math></b>	<b><math>F_{IS}</math> (95% CI)</b>
Cult-OV	Cuicuilapam	0.171	0.148	-0.152 (-0.164--0.142)
Cult-SMOCC	Blanco Tlaxcala	0.194	0.167	-0.159 (-0.168--0.150)
	Durango	0.218	0.173	-0.262 (-0.270--0.253)
	Regocijo	0.205	0.160	-0.280 (-0.293--0.273)
	Villa Unión	0.179	0.167	-0.072 (-0.083--0.063)
Cult-SUR-CH	Altotonga	0.215	0.177	-0.216 (-0.225--0.208)
	González de León	0.200	0.176	-0.135 (-0.144--0.126)
	Huautla	0.219	0.199	-0.103 (-0.112--0.095)
	Nahá	0.196	0.167	-0.171 (-0.182--0.162)
	Oxchuc	0.200	0.178	-0.124 (-0.133--0.114)
	Zicanantán	0.196	0.191	-0.029 (-0.091--0.064)
Cult-TMVB	España	0.166	0.134	-0.237 (-0.253--0.230)
	Frijol Colorado	0.193	0.191	-0.009 (-0.018-0.000)
	Orilla del Monte	0.221	0.195	-0.133 (-0.142--0.125)
	Tlalcananeca	0.199	0.190	-0.044 (-0.053--0.036)
	Puebla	0.206	0.191	-0.079 (-0.089--0.070)
Wild-SMOCC	Espinazo del Diablo	0.150	0.118	-0.274 (-0.293--0.268)
	Regocijo-S	0.165	0.141	-0.173 (-0.189--0.166)
Wild-striatus	Tres Marías	0.203	0.160	-0.267 (-0.277--0.261)
Wild-SUR-CH	Comaltepec	0.189	0.157	-0.200 (-0.231--0.207)
	San Cristobal	0.182	0.164	-0.105 (-0.125--0.102)
Wild-TMVB	Ciudad Guzman	0.169	0.176	-0.072 (-0.088--0.056)
	REPSA	0.237	0.202	-0.175 (-0.183--0.168)
	San Joaquín	0.195	0.160	-0.221 (-0.235--0.216)
	Tepoztlán	0.229	0.188	-0.217 (-0.225--0.210)
	Tlalpan	0.247	0.208	-0.184 (-0.192--0.177)

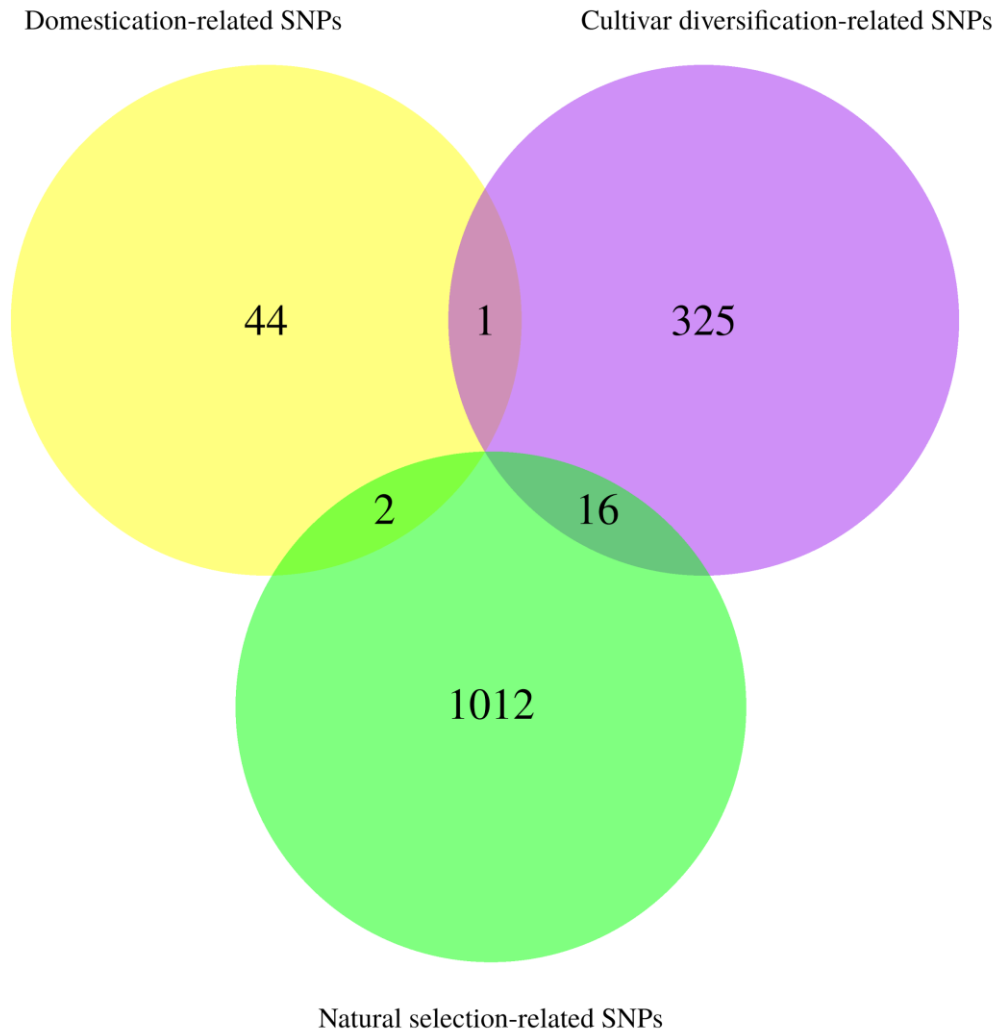


**Figure S5.** Pair  $r^2$  value among SNPs located in the same chromosome separated by a maximum distance of 10 000 bp. At the right side of each plot there is a histogram showing the frequency of  $r^2$  values.





**Figure S6.** Distribution of 11 693 SNPs detected in *P. coccineus* (after LD filtering) present in each chromosome. Each bar represents a region of one Mb. The differences in plots sizes show the discrepancies in chromosomes lengths.



**Figure S7.** Venn diagram showing share candidate SNPs detected in the three PCAdapt analysis to detect natural and artificial selective pressures.

**Table S3.** Candidate loci identified by the pcadapt and BayeScan methods.

Chr	SNP ID	Position	<i>P. vulgaris</i> transcript name	Annotation	High expression tissue	Protein homologs in <i>G. max</i>
Domestication-related candidate						
1S1_15176129	15176129					
1S1_48602792	48602792	Phvul.001G232200	Phosphomethylpyrimidine kinase		Flower, buds	Glyma.11G218700
2S1_56416681	4211050					
2S1_79642304	27436673					
2S1_81673246	29467615	Phvul.002G145600	TIR domain		Green and mature pods	Glyma.12G135600
2S1_85681762	33476131					
2S1_86298230	34092599					
3S1_128138350	26891681					
3S1_145377297	44130628					
6S1_248268696	7958113					
6S1_250412008	10101425					
6S1_252913073	12602490					
6S1_259648113	19337530					
6S1_262918075	22607492					
7S1_310062177	37774238	Phvul.007G256000	DnaJ domain		Flowers, young pods	Glyma.02G179900
7S1_313970760	41682821					
8S1_329571814	5525253					
8S1_350061425	26014864					
8S1_350157505	26110944					
8S1_375823077	51776516					
9S1_406871596	23162403	Phvul.009G156400	Dehydrogenase E1 component		Flower buds, flowers	Glyma.04G212100

11S1\_467512979 3058827

11S1\_470314329 5860177

11S1\_472148556 7694404

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Natural selection-related candidate windows

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3S1\_103319613 2072944

3S1\_108854438 7607769

3S1\_126647289 25400620

3S1\_138412433 37165764

3S1\_141480201 40233532

3S1\_143433256 42186587Phvul.003G197500 Calmodulin binding protein-like Root, stem Glyma.17G092700

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Cultivar diversification-related candidate loci

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1S1\_45827637 45827637

3S1\_146749207 45502538

4S1\_178058430 24527352

4S1\_178200752 24669674

4S1\_178417950 24886872

4S1\_181150184 27619106

4S1\_183310744 29779666

5S1\_219843009 20351812

5S1\_220112744 20621547

5S1\_225806704 26315507

6S1\_271294756 30984173

7S1\_301822240 29534301

9S1\_388863253 5154060

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