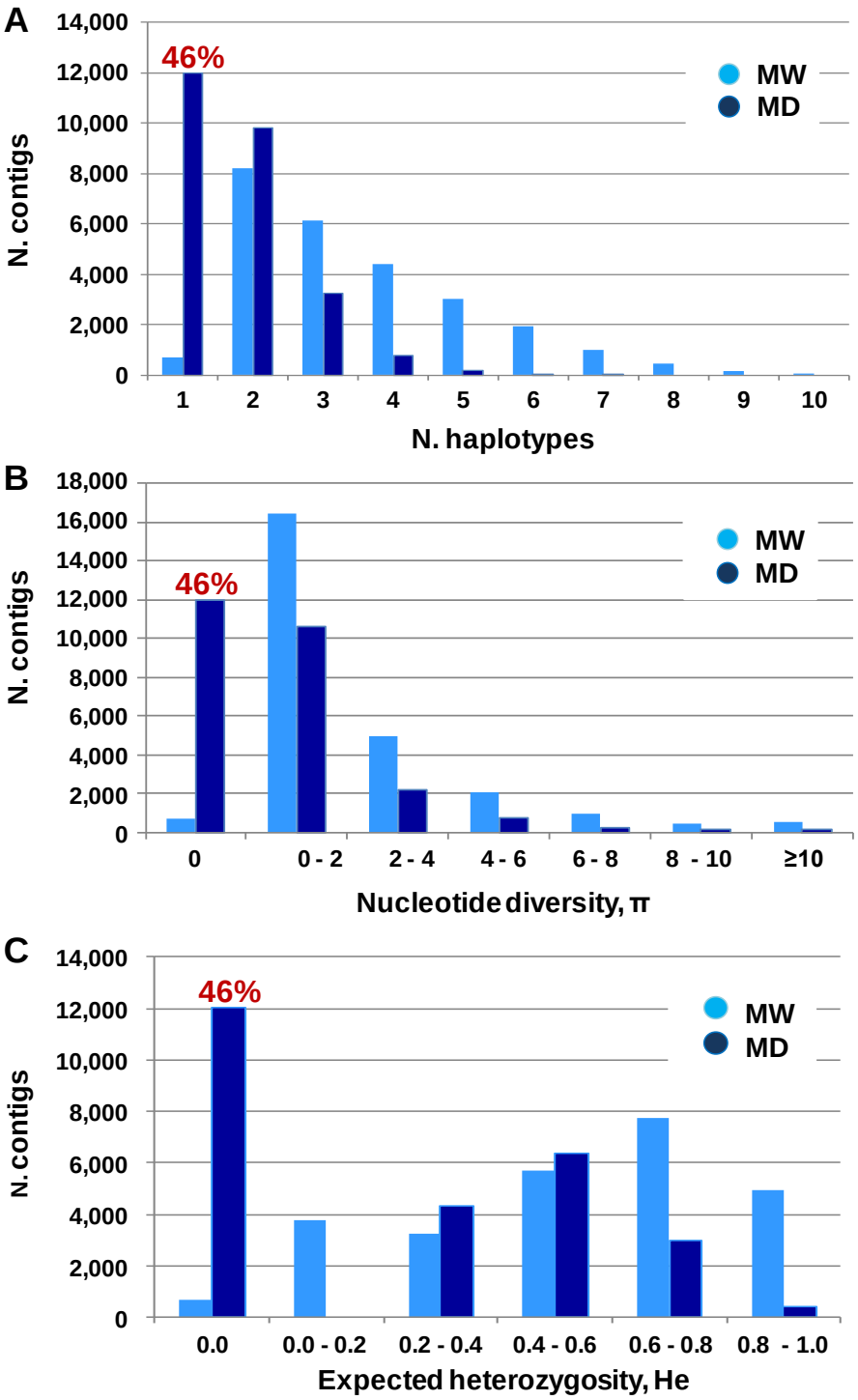


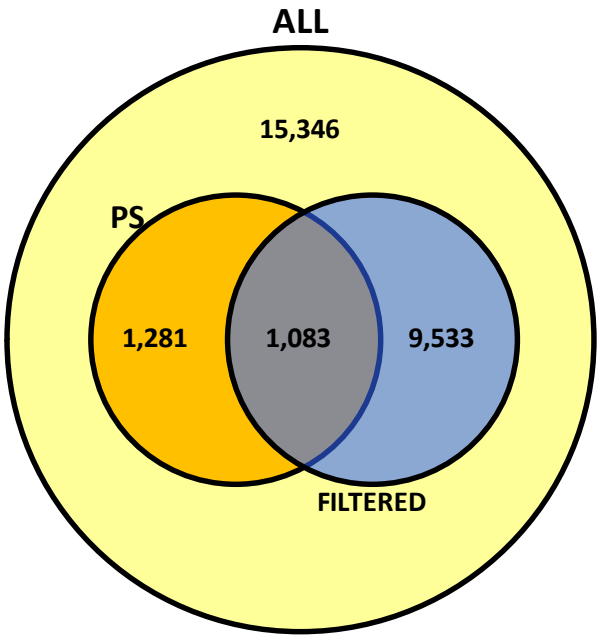
Supplemental Figure 1. Diversity estimates in MW and MD populations.

Number of contigs for the different classes.

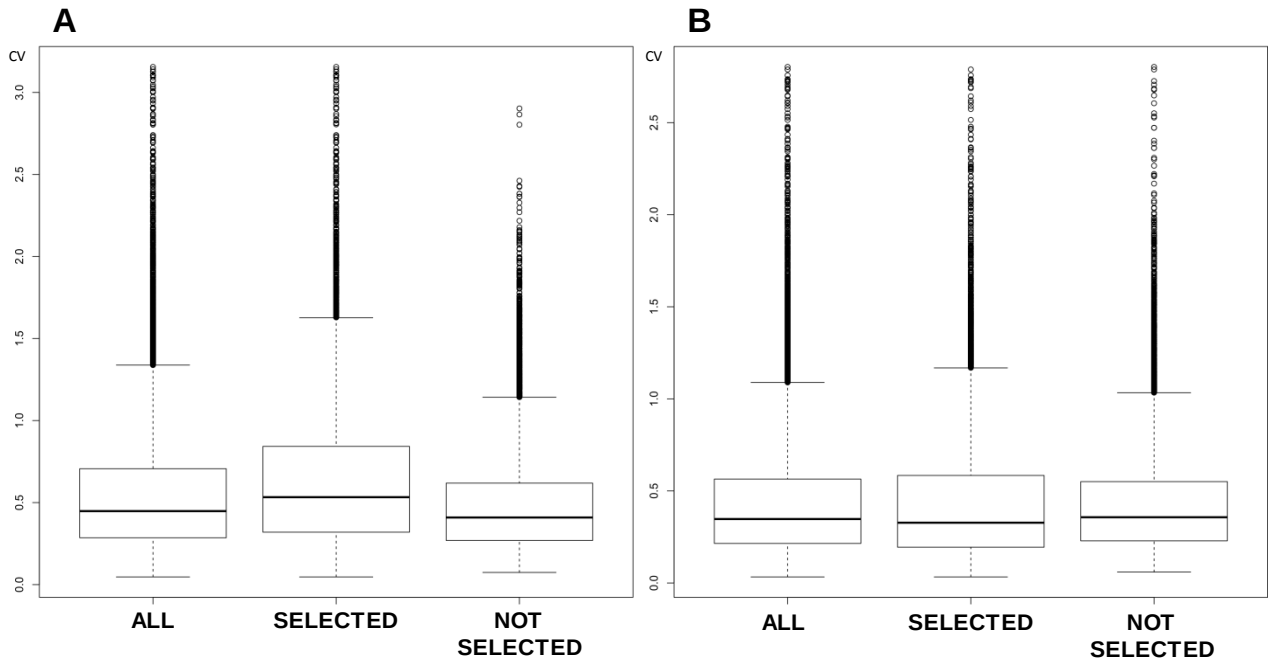
(A) Number of haplotypes (nH).

(B) Nucleotide diversity (π).

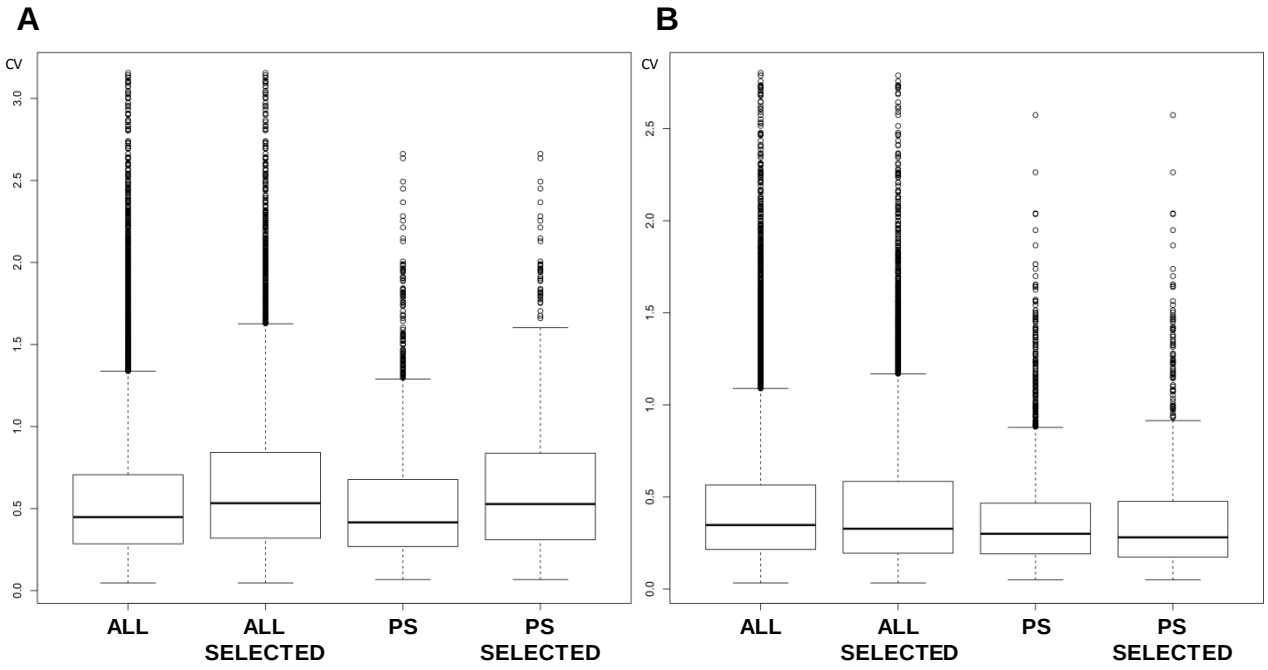
(C) Expected heterozygosity (He).



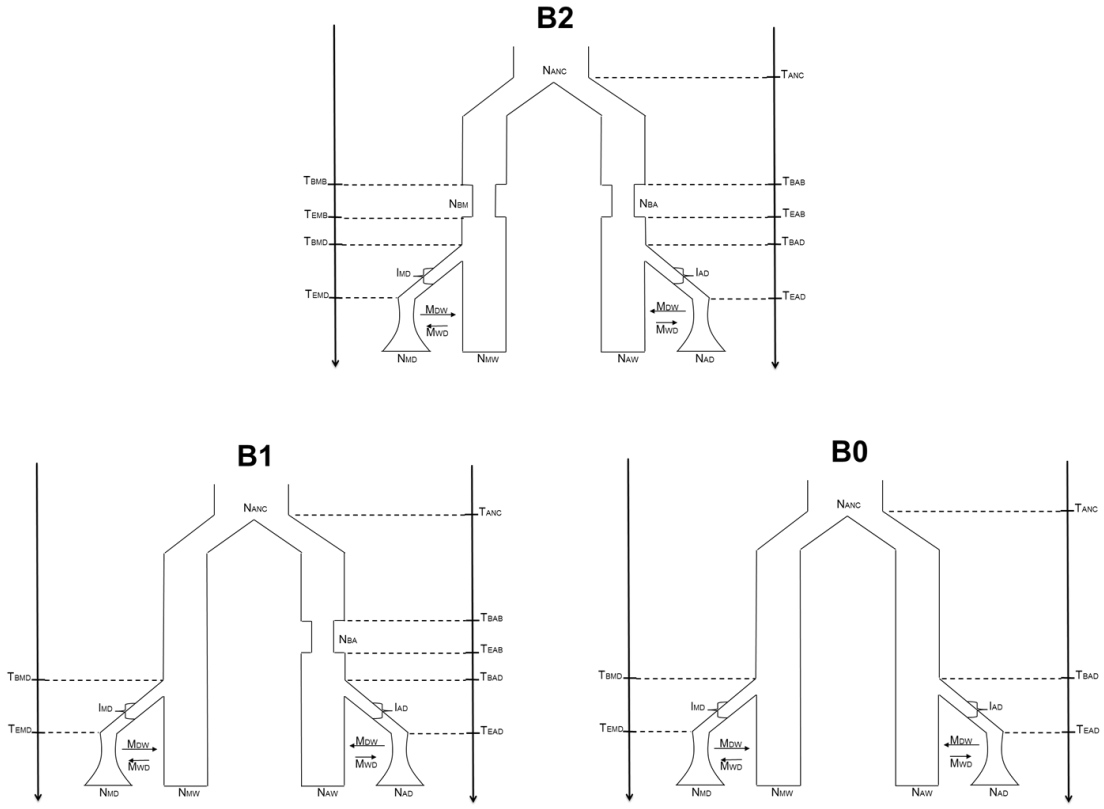
Supplemental Figure 2. Network-Based Analysis: Results of the selection strategy. The Venn diagram illustrates the overlap between the entire set of contigs (yellow), the putatively under selection (PS) contigs (orange), and the contigs selected using the outlined strategy for subsequent network-based analysis (blue). Altogether 1,083 of 2,364 PS contigs were retained for the network-based analysis.



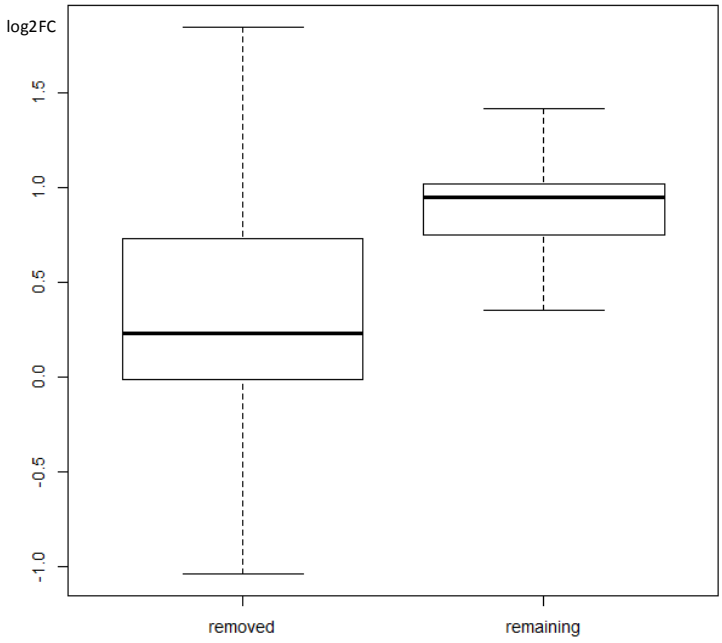
Supplemental Figure 3. Network-Based Analysis: Selection strategy and bias of the CVs. Boxplots of the CVs over all of the contigs (ALL), those selected for the subsequent network-based analysis (SELECTED), and those not selected by the strategy used (NOT SELECTED), for the MW **(A)** and MD **(B)** populations. The boxplots support the absence of systemic bias.



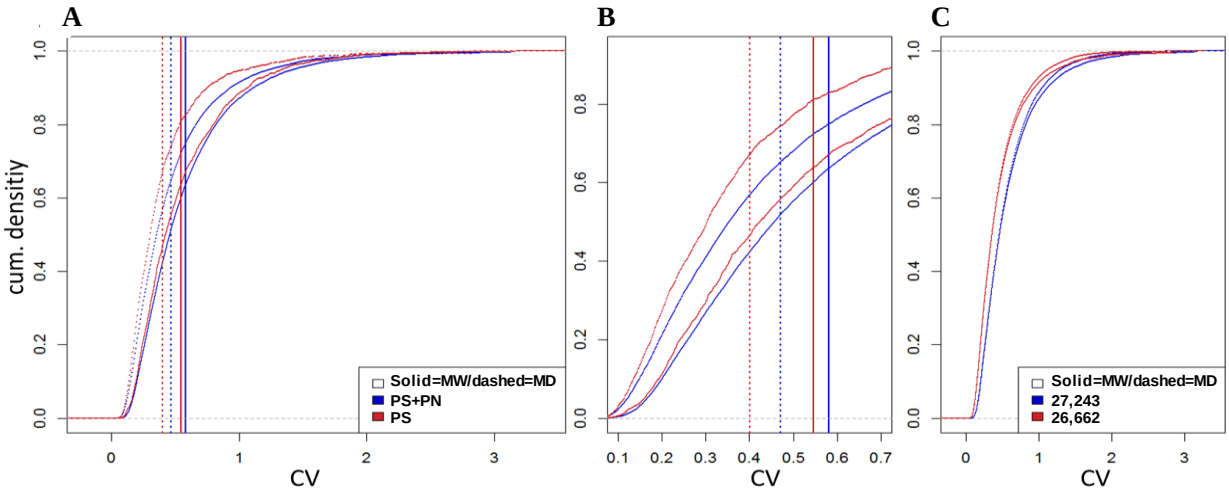
Supplemental Figure 4. Network-Based Analysis: Selection strategy and bias of CVs in the PS contigs. Boxplots of the CVs for all of the contigs (ALL), and those selected for the network-based analysis (ALL SELECTED), and of all the PS contigs (PS) and those retained (PS SELECTED) for the network-based analysis, in the MW **(A)** and MD **(B)** populations. The boxplots support the absence of systematic bias; i.e., no shifts towards higher/ lower values in the CVs for the PS contigs that were retained for further analysis.



Supplemental Figure 5. Demographic models used in this study. Demographic scenarios for the Mesoamerican and the Andean populations. See Supplemental Table 7 online for the details of the parameters.



Supplemental Figure 6. Boxplot illustrating the differences in the log2FC for the 581 removed contigs (removed) and the remaining 26,662 contigs (remaining). Note that negative values indicate higher expression levels in the MD forms.

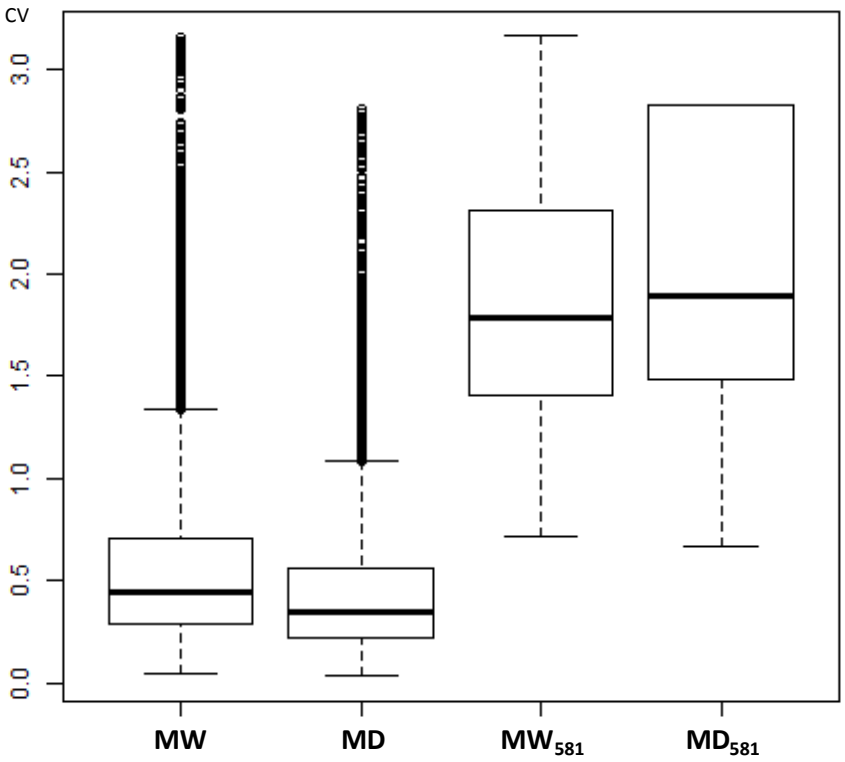


Supplemental Figure 7. Empirical cumulative density functions for the CVs considering all of the 27,243 contigs as reference.

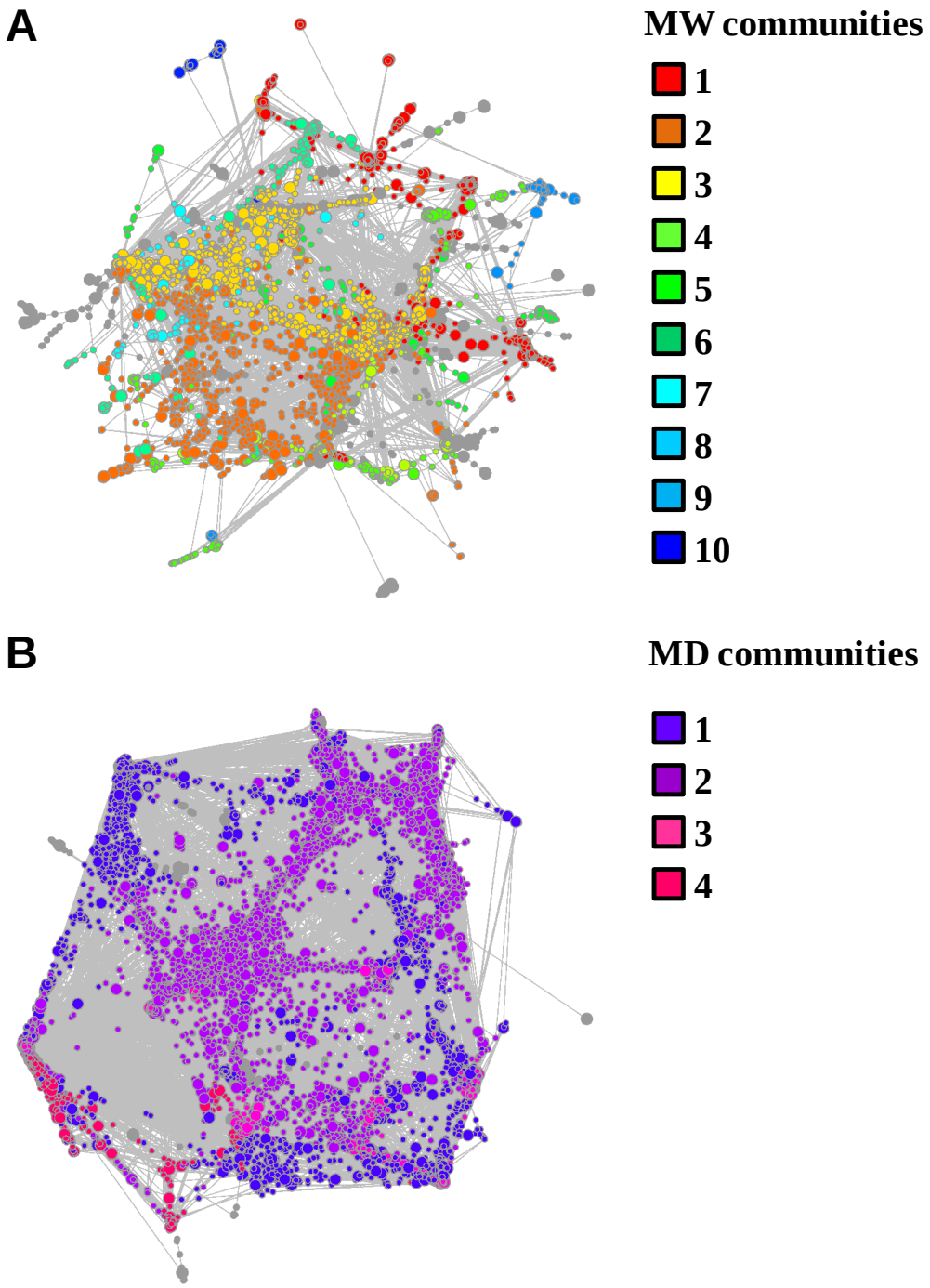
(A) Comparison of the empirical cumulative density functions of the CVs considering all of the contigs and PS.

(B) Detail of the panel in **(A)**, to show the range of the CVs between 0.1 and 0.7.

(C) Effect on the CVs with the removal of the 581 contigs containing more than nine individuals with zero expression levels.



Supplemental Figure 8. Boxplot illustrating the differences in the CVs for the 26,662 contigs (MW, MD) after the removal of the 581 contigs (MW_{581}, MD_{581}) in the MW and MD populations. Note: the majority of high CVs observed for the 581 contigs arise from the very small mean expression values.



Supplemental Figure 9. Relevance network from the MW (A) and MD (B) populations. The relevance network was extracted to match the density of the proximity networks. The different colors indicate the different communities of size ≥40 in the network; the nodes of larger sizes correspond to contigs under selective pressure; isolated nodes are not visualized.

SUPPLEMENTAL TABLES

Supplemental Table 1. Transcriptome assembly statistics. Assembly statistics for the four *P. vulgaris* reference genotypes and for the final nonredundant dataset.

	Assembly statistics			
	G24378	**W617475**	**G12873**	**G12979**
Number of sequences	55,069	65,273	70,826	61,141
Assembled bases	46,396,157	52,104,578	59,851,108	51,083,455
Average length	842.51	798.26	845.04	835.50
Median length	448	431	458	447
N50	1,515	1,393	1,486	1,491
	Nonredundant dataset statistics			
Number of sequences	124,166			
Assembled bases	104,901,858			
Maximum length	16,891			
Minimum length	201			
Average length	844.85			
Median length	428			
N50	1,595			

Supplemental Table 2. Jaccard similarity of the community structure in the MW and MD proximity networks. The Jaccard index was determined for each pair of communities for the extracted MW and MD proximity networks. The low similarity supports the comparison of the corresponding node partitions based on the adjusted Rand index.

		MD network				
		1	**2**	**3**	**4**	**5**
MW network	**1**	0.188	0.214	0.122	0.004	0.066
	2	0.202	0.245	0.133	0.003	0.042
	3	0.066	0.037	0.209	0.002	0.024
	4	0.133	0.052	0.092	0.004	0.054
	5	0.095	0.125	0.104	0.004	0.052
	6	0.001	0.001	0	0	0
	7	0.002	0	0.001	0	0

MW, Mesoamerican wild accessions; MD, Mesoamerican domesticated accessions.

Supplemental Table 3. Community gene function enrichment: List of selected enriched gene functions for each of the communities determined for the MW and MD networks (the full list of enriched terms and corresponding p-values is given in Supplemental Data Sets 1B and 1C online for MW and MD, respectively).

Network	Function
MW	
Community 1	Cell wall (hemicellulose synthesis, glucuronoxylan, cellulose synthesis)
	OPP oxidative PP.6-phosphogluconate dehydrogenase
	Amino acid metabolism (aromatic), hormone metabolism
	RNA regulation
Community 2	Protein synthesis (ribosomal proteins)
	RNA regulation and transcription (HSF, HAD, and AS2-lateral organ boundaries)
	Secondary metabolism (flavanoids and flavanols)
	N-metabolism (ammonia)
	Hormone metabolism (jasmonate and absisic acid synthesis-degradation)
	Signaling
Community 3	DNA synthesis (chromatin structure); lipid metabolism
Community 4	Hormone synthesis (jasmonate synthesis-degradation)
	PS lightreaction (photosystem II)
	Minor CHO metabolism
Community 5	Major CHO biosynthesis (starch)
	Redox (thioredoxin)
	Protein degradation (AAA type)
Community 6	Not enriched for any MapMan bins at significance level of α = 0.05
Community 7	Not enriched for any MapMan bins at significance level of α = 0.05
MD	
Community 1	PS lightreaction (photosystem II and other electron carrier)
	Cell wall (hemicellulose and cellulose synthesis, precursor synthesis (UXS), and glucuronoxylan)
	Minor CHO metabolism (raffinose family)
	RNA regulation of transcription (MYB domain and MADS box transcription factor family, Aux/IAA family, and Trihelix and Triple-Helix transcription factor family),
	N-metabolism (ammonia)
	Stress (abiotic)
	Hormone metabolism (slicylic and abscisic acid)
Community 2	Protein synthesis (ribosomal protein)
	Protein degradation (ubiquitin)
	Protein targeting (secretory pathway)
	Post-transcriptional modification (kinase)
	Signaling (receptor kinase)
	RNA regulation of transcription (bZIP and WRKY domain transcription factor family)
	Fermentation (aldehyde dehydrogenase)
Community 3	DNA synthesis (chromatin structure)
	RNA regulation of transcription (zf-HD)
	Cell wall degradation (mannan-xylose-arabinose-fucose)
Community 4	Not enriched for any MapMan bins at significance level of α = 0.05
Community 5	Not enriched for any MapMan bins at significance level of α = 0.05

MW, Mesoamerican wild accessions; MD, Mesoamerican domesticated accessions.

Supplemental Table 4. Difference in mean node centralities of contigs under selective pressure, and the rest of the nodes in the MW and MD networks. The centrality of each node was estimated for the MW and MD proximity networks. The differences in means between the contigs under selective pressure and the rest of the nodes in the networks were tested. Negligible, although statistically significant, differences were observed for closeness centrality in both the MW and MD proximity networks.

Difference factor	MW proximity network			MD proximity network		
	Mean value of contigs		p value	Mean value of contigs		p value
	Under selective pressure	Remaining		Under selective pressure	Remaining	
Betweenness	26,890	25,470	**0.0063**	28,220	27,920	0.6068
Closeness	1.632E-05	1.621E-05	**3.96E-05**	1.518E-05	1.511E-05	**0.0167**
Degree	12.69	12.88	0.1059	13.69	13.64	0.5963
Ev centr.	0.00217	0.002651	0.7984	0.001401	0.003122	0.025
Page rank	9.356E-05	9.427E-05	0.2401	9.44E-05	9.417E-05	0.6278
Eccentricity	9.208	9.258	0.0031	10.42	10.44	0.6459
Burt's constraint	0.1244	0.1245	0.9176	0.1204	0.1213	0.1221
Transitivity	0.2468	0.2533	0.033	0.2832	0.2886	0.01287

Supplemental Table 5. Difference in assortativity, both nominal and based on the 'selection index', between the MW and MD networks. Significance obtained with permutation tests (permutation of node labels) for the observed assortativity values for the MW and MD networks, and their difference.

Permutation test	**Network**	**Node (n = 10,000)**	
		Observed	**p value**
Assortativity (nominal)	MW	0.005828	0.0608
	MD	0.011888	9.00E-04
	MW-MD	-0.00606	0.1246667
Assortativity (S-Index)	MW	0.008214	0.0154
	MD	0.014609	1.00E-04
	MW-MD	-0.00639	0.1135

MW, Mesoamerican wild accessions; MD, Mesoamerican domesticated accessions.

Supplemental Table 6. Accessions used in this study.

	Accession number/name	Population code[1]	Source[2]	Country	Department, State or Province	Biological status	Altitude (m s.l.m.)	Latitude (°N)	Longitude (°E)
1	G12873*	MW	CIAT	Mexico	Morelos	Wild	1981	19.000	-99.250
2	G9989	MW	CIAT	Mexico	Jalisco	Wild	1400	20.500	-104.817
3	G11050	MW	CIAT	Mexico	Michoacan	Wild	2040	19.683	-101.267
4	G12979*	MW	CIAT	Mexico	Jalisco	Wild	/	20.117	-104.367
5	G22837	MW	CIAT	Mexico	Chihuahua	Wild	1750	26.933	-106.417
6	G24378*	MW	CIAT	Mexico	Oaxaca	Wild	1250	16.040	-97.083
7	PI325677	MW	USDA	Mexico	Morelos	Wild	1828	18.967	-99.100
8	PI417770	MW	USDA	Mexico	Nayarit	Wild	2000	20.667	-102.383
9	G20515	MW	CIAT	Mexico	Puebla	Wild	/	19.800	-97.783
10	G12922	MW	CIAT	Mexico	Jalisco	Wild	1829	20.700	-102.350
11	G5191	MD	CIAT	Venezuela	Distrito Federal	Landrace	/	10.500	-66.917
12	PI151017	MD	USDA	Chile	/	Landrace	660	-33.450	-70.667
13	PI201349	MD	USDA	Mexico	Puebla	Landrace	1000	20.183	-98.050
14	PI281981	MD	USDA	Mexico	Jalisco	Landrace	/	20.417	-103.667
15	PI300668	MD	USDA	Chile	/	Landrace	/	/	/
16	PI309831	MD	USDA	Costa Rica	Cartago	Landrace	1200	9.867	-83.783
17	PI310660	MD	USDA	Guatemala	Chimaltenango	Landrace	2000	14.667	-90.817
18	PI311794	MD	USDA	El Salvador	Santa Ana	Landrace	660	13.983	-89.567
19	W617475*	AW	USDA	Argentina	Salta	Wild	1470	-25.167	-65.617
20	Midas	AD	P.Gepts	Argentina	/	Cultivar	/	/	/
21	PI298109	AD	USDA	Brazil	/	Landrace	/	/	/

[1]MW, Mesoamerican wild; MD, Mesoamerican domesticated; AW, Andean wild; AD, Andean domesticated;
[2]CIAT, International Centre for Tropical Agriculture; USDA, United States Department of Agriculture. Seeds of Midas accession were kindly provided by Prof. Paul Gepts, Department of Plant Sciences, Section of Crop and Ecosystem Sciences, UC Davis, CA, USA.
*Accessions of the hyper-core collection used for the *de novo* assembly.

Supplemental Table 7. Demographic parameters in the B0, B1 and B2 models.

Model	Parameter	Description	Units	Distribution	Mean	S.D.	Min	Max
B0,B1,B2	T_{ANC}	Divergence time between Andean and Mesoamerican gene pools	Generations	Normal	111,000	40,000	67,330	192,835
B2	T_{BMB}	Time of the beginning of the Mesoamerican founder bottleneck	Generations	Normal	99,833	750	98,375	99,833
B1,B2	T_{BAB}	Time of the beginning of the Andean founder bottleneck	Generations	Normal	98,845	3,000	94,051	104,027
B2	T_{EMB}	Time of the ending of the Mesoamerican founder bottleneck	Generations	Normal	67,341	1,400	64,568	67,341
B1,B2	T_{EAB}	Time of the ending of the Andean founder bottleneck	Generations	Normal	67,858	1,500	64,655	70,865
B0,B1,B2	T_{BMD}	Time of the beginning of the Mesoamerican domestication	Generations	Normal	8,160	133	7,922	8,426
B0,B1,B2	T_{BAD}	Time of the beginning of the Andean domestication	Generations	Normal	8,500	8	8,495	8,517
B0,B1,B2	T_{EMD}	Time of the ending of the Mesoamerican domestication	Generations	Normal	6,260	150	5,971	6,567
B0,B1,B2	T_{EAD}	Time of the ending of the Andean domestication	Generations	Normal	7,012	35	6,945	7,075
B0,B1,B2	N_{ANC}	Ancestral effective population size	Haploid individuals	Normal	418,000	105,000	266,000	628,000
B2	N_{BM}	Mesoamerican effective population size during the founder bottleneck	Haploid individuals	Normal	168,000	7,500	153,000	170,000
B1,B2	N_{BA}	Andean effective population size during the founder bottleneck	Haploid individuals	Normal	105,000	20,000	65,000	142,000
B0,B1,B2	N_{MD}	Effective population size of the domesticated Mesoamerican population	Haploid individuals	Uniform			100,000	100,000
B0,B1,B2	N_{MW}	Effective population size of the wild Mesoamerican population	Haploid individuals	Normal	292,000	240,000	125,000	773,000
B0,B1,B2	N_{AW}	Effective population size of the wild Andean population	Haploid individuals	Normal	137,000	182,000	70,000	502,000
B0,B1,B2	N_{AD}	Effective population size of the domesticated Andean population	Haploid individuals	Uniform			100,000	100,000
B0,B1,B2	I_{MD}	Intensity of the domestication bottleneck in Mesoamerica	Ratio	Normal	47.65	3	41.66	52.13
B0,B1,B2	I_{AD}	Intensity of the domestication bottleneck in the Andes	Ratio	Normal	47.26	0.5	46.25	48.59
B0,B1,B2	M_{WD}	Migration rate from wild to domesticated population	Rate	Uniform			0.000001	0.00001
B0,B1,B2	XM	Asymmetric migration factor	Rate	Uniform			2	6
B0,B1,B2	M_{DW}	Migration rate from domesticated to wild population	Rate	XM*MWD				
B0,B1,B2	μ	Mutation rate (per site per generation)	Rate	Normal	$1E^{-9}$	$5E^{-9}$	$1E^{-10}$	$1E^{-8}$
B0,B1,B2	L	Length of the simulated sequences	Base pairs	Normal	1,300	1,500	250	5,000

Supplemental Table 8. Enriched MapMan bins for 581 (140 annotated) contigs removed prior to the network analysis. These 581 contigs were removed from the set of contigs subjected to the network-based analysis due to zero expression estimates in at least nine individuals. These contigs are enriched for the MapMan bins included in the first two columns at a significance level of 0.05.

MapMan bin	Description	p value
28.1.3.2	DNA.synthesis/chromatin structure.histone.core	1.94e-08
28.1.3	DNA.synthesis/chromatin structure.histone	5.01e-08
28.1.3.2.4	DNA.synthesis/chromatin structure.histone.core.H4	0.000118
30.8	Signaling.misc	0.000153
28.1.3.2.3	DNA.synthesis/chromatin structure.histone.core.H3	0.000294
28.1	DNA.synthesis/chromatin structure	0.000978
27.3.24	RNA.regulation of transcription.MADS box transcription factor family	0.002902
30.2.8.1	Signaling.receptor kinases.leucine rich repeat VIII.VIII-1	0.00347
10.2.1	Cell wall.cellulose synthesis.cellulose synthase	0.004913
33	Development	0.005296
28.1.3.2.1	DNA.synthesis/chromatin structure.histone.core.H2A	0.00622
33.99	Development.unspecified	0.006365
30	Signaling	0.01005
10.5.1	Cell wall.cell wall proteins.AGPs	0.01069
10.5.1.1	Cell wall.cell wall proteins.AGPs.AGP	0.01069
28	DNA	0.0132
10.2	Cell wall.cellulose synthesis	0.01921
10	Cell wall	0.02384
30.2.8	Signaling.receptor kinases.leucine rich repeat VIII	0.02721
24	Biodegradation of Xenobiotics	0.03194
27.3.67	RNA.regulation of transcription.putative transcription regulator	0.04299
10.5	Cell wall.cell wall proteins	0.04417
29.7	Protein.glycosylation	0.0499

GLOSSARY

MD: Mesoamerican domesticated accessions.

MW: Mesoamerican wild accessions.

S, ***nH***, ***π***, ***Θ***, ***He***: statistics for the estimation of the levels of molecular diversity.

L_{π}, L_{Θ}, L_{He}: loss in molecular diversity (in MD compared to MW).

Lcv: loss in gene expression diversity (in MD compared to MW).

Log2FC: when significantly shifted, indicates down-regulation or up-regulation of gene expression.

CV: coefficient of variation, estimated for gene expression.

Selection indices: based on two between-groups and one within-groups genetic variation statistics that were likely to have been affected by differential selection for MD compared to MW (see Online Methods for details). Used to identify PS contigs.

PS contigs: contigs putatively under selection in MD compared to MW, identified by computing two selection indices and testing their significance with a coalescent simulation (see Online Methods for details). The opposite is PN contigs (i.e., putatively neutral contigs).

Coalescent simulations of domestication models: used to identify PS contigs by computing two selection indices and testing their significance. Coalescent simulations are used to generate neutral distributions of summary statistics, assuming three likely domestication scenarios (models) that are reconstructed and based on the population histories and demographic parameters estimated in previous studies.

PCCs: Pearson correlation coefficients among gene expression profiles; a wider distribution of PCCs supports stronger correlations.

Network analysis (proximity networks, relevance networks): concerns gene co-expression. In a network, a community is a group of genes with correlated expression (see Online Methods for details).

Rank index, Jaccard similarity: allow the comparison of networks.

Enrichment gene-function analysis and gene-set enrichment analysis: comparative degree of enrichment in gene functions in a comparison among communities and/or groups (e.g., MW *versus* MD; PS *versus* PN), and used to determine biological signals (in the communities) or to examine the functional characterization (PS contigs).

MapMan ontology and test on hypergeometric function: allows the functional characterization of contigs, and to derive which MapMan bins are statistically significantly over-represented.

SUPPLEMENTAL METHODS 1

1. Network-based analysis

1.1 Contig selection strategy and investigation of bias

The contigs for the network analyses were selected to avoid the inclusion of potentially noisy or invariant gene expression profiles, which might lead to the inclusion of spurious edges in the extracted networks.

We removed 581 contigs that showed zero expression levels in at least nine genotypes from the analysis. Of these, 40 were determined to be under selective pressure (PS), with 17 of these contigs having expression values of zero in all of the investigated samples. The removal of these contigs from the total of 27,243 did not introduce bias with respect to the contigs that were determined as PS, as their proportion was within the expected range (binomial test, p-value >0.2). In addition, 140 of these 581 contigs were annotated by MapMan bins. The results of the enrichment analysis are presented in Supplemental Table 8 online.

The log2FC between the MW and MD populations for the 581 contigs show negative values due to the larger expression values in the MD samples (see Supplemental Figure 6 online). There is a shift towards smaller CVs between MD and MW (Supplemental Figures 7A and 7B online), and this also holds when focusing on the PS contigs. The effect of removing the 581 contigs on the distribution of CVs was not pronounced (Supplemental Figure 7C online). However, there were statistically significant differences between the CVs of the 26,662 contigs and the CVs for the 581 removed contigs; these are, however, artefacts due to the high CVs for the removed contigs as a result of their small mean expression levels; this is a common drawback of the CV statistic (Supplemental Figure 8 online).

To select a subset of contigs to use for the network analysis, two statistical tests were performed for each of the remaining 26,662 contigs: the differences in the means and variance of the expression levels between the MW and MD populations, based on ANOVA and on the F-test, respectively (Ho et al., 2008). A very loose level of significance ($\alpha = 0.1$) was considered for both of these tests. The Wilcoxon rank sum test with continuity correction (Hollander and Wolf, 1973) was applied to the CVs computed for MW and MD for each chosen contig, to determine whether the strategy applied for the contig selection had introduced any systematic bias with respect to favoring contigs that vary strongly in both the MW and MD populations, in comparison to the entire set of contigs that were considered. The possibility of a shift in the CV towards higher/ lower values for the PS contigs retained and those excluded from subsequent analysis was also tested.

These tests resulted in the selection of 10,616 contigs, the profiles of which were further subjected to network-based analysis (Supplemental Figure 2 online). There was no bias associated with the contigs variation of gene expression (as shown in Supplemental Figure 3 online). From the remaining 2,324 PS contigs, about 50% were included in the network analysis (Supplemental Figure 2 online). However, we derived two much larger networks using cut-offs of 0.2 and 0.3 for ANOVA and homogeneity of variance (the F-test). We found that the results remained qualitatively unchanged.

1.2 Proximity and relevance networks

The MW and MD expression profiles for the 10,616 contigs were subjected to network-based analysis following two procedures, both of which were based on the Pearson correlation coefficients (PCCs): (i) generation of relevance networks; and (ii) extraction of proximity networks (Klie et al., 2012; Klessen et al., 2013). With the first procedure, an edge is established between two nodes (which represent genes) if the PCC between the corresponding expression profiles is higher than a threshold τ that ensures a given level of statistical significance. According to the second procedure, for a fixed k, an edge is created between two nodes, *u* and *v*, if *u* appears in the list of the k genes with the highest PCC to *v*, and if *v* is in the list of the k genes with the highest PCC to *u*. As a result, the second procedure, which generates a proximity network, takes into consideration the observation that the genes can often be activated as modules of a program to fulfill a particular function.

To compare the networks generated by these two procedures, we required that they were equally informative, as quantified by their density (i.e., the total number of edges divided by the number of edges in a complete network on the same number of nodes). This also implies that the selection of the threshold values in the procedures for network generation has to guarantee an (almost) equal density. The density is a number ranging from 0 to 1, with 0 where there are no edges between any two nodes, and 1 when any two nodes are connected by an edge.

It can be shown that the null distribution for k is almost uniform; therefore, with 10,000 genes, k = 100 will ensure a significance level of $\alpha = 0.01$. Here, we present and discuss the results for k = 15. To examine the robustness of the findings, we also repeated the analysis for $k \in \{10,20\}$ (data not shown). To specify the threshold value τ, we determined the value of the PCC that ensured that the generated network was of (almost) equal density as the proximity network (as established based on the same dataset). For instance, $\tau = 0.91$ in the procedure for extraction of the relevance network corresponds to k = 15 in the procedure for generating proximity networks. These thresholds were applied to both the MW and MD gene expression profiles, and the resulting networks were compared and contrasted based on their network properties.

1.3 Analysis based on relevance networks

The proximity network generation and properties are described in the main text (Online Methods and Results sections). As already indicated above, the relevance networks were extracted so that their densities matched those of the proximity networks. This facilitates further comparative analysis between the two procedures for network generation. With the corresponding threshold value of $\tau = 0.92$, the MW relevance network is again sparser than the MD relevance network: 1,661 isolated nodes (i.e., nodes without any edge) in MW, and 105 isolated nodes in MD. The largest connected component in the MW network included 8,257 nodes, while in the MD network, this contained 10,439 nodes. The relevance networks have a characteristic heavy-tailed degree distribution. As a result, there was a finer community structure in both of the relevance networks (Supplemental Figures 9A and 9B online), with 152 communities with at least two nodes in the MW network and 27 in the MD network. In the MW relevance network, the largest community contained 2,662 nodes, while in the MD relevance network contained 4,665 nodes. Altogether, nine and four communities included more than 100 nodes in the MW and MD networks, respectively. The enrichment analysis largely matched that for the proximity networks.

Regarding the assortativity with respect to the contigs under selection pressure, our findings were similar to those from proximity networks: 0.010 for MW and 0.008 for MD. For assortativity with respect to the CVs, as in the case of proximity networks, we found that MW showed higher clustering of similar contigs (0.44) in comparison to MD (0.35). The findings regarding the centrality of the PS contigs were in line with those obtained from the proximity networks.

2. Gene-set enrichment analysis using MapMan

To characterize the molecular functions and biological processes of the *Phaseolus* contigs under study, the latest version that was available for MapMan and *Arabidopsis* (version 1.1 from January 2010, http://mapman.gabipd.org/) was used (Thimm et al., 2004). By using the sequence homology of *Phaseolus* contigs and *Arabidopsis* genes, a total of 13,228 contigs were assigned with MapMan bins, disregarding the 35 MapMan (sub-)bins that corresponded to '*not assigned*'. The *Phaseolus* contig-to-MapMan mapping that was obtained was further processed to include the parent bins and to remove inconsistencies, as described in Klie and Nikoloski (2012).

To further assess whether a particular set of contigs (i.e., members of network communities, PS contigs, or contigs up-regulated in the wild forms) is predominantly involved in similar molecular functions or biochemical processes in MW and MD, gene-set enrichment analysis (GSEA) was performed (Subramanian et al., 2005). Briefly, for a given set of contigs, it was statistically tested whether certain MapMan bins are over-represented within this particular group of contigs; i.e., over-enriched. Classically, hypergeometric tests are used to derive which MapMan bins are statistically significantly over-represented (Rivals et al., 2007). The enrichment results presented throughout this manuscript were obtained using the previously mentioned hypergeometric test and the Benjamini-Hochberg false discovery rate correction to obtain *p* values

(Benjamini and Hochberg, 1995), as implemented in the statistical environment R. For all of the enrichment tests, the significance level was set to 5%.

SUPPLEMENTAL METHODS 2

3. Survey of enriched gene functions for the MW and MD communities

To determine whether the network communities carry biological signals, the enriched gene functions for each of the communities determined were investigated (at a significance level of $\alpha = 0.01$) using the MapMan ontology. The communities corresponded to modular structures of largely different functions (Supplemental Table 3 online; Supplemental Data Sets 1B and 1C online). We investigated whether the different classes of genes that were over-represented in either MW or MD were shown to be involved in the domestication process, either through direct experiment or by implication on the basis of function. The results of this survey are reported below.

- MADS-BOX. The MADS-BOX class of genes, which includes *APETALA1* (AP1; Mandel et al., 1992; Gustafson-Brown et al., 1994) and *CAULIFLOWER* (*CAL*; Kempin et al., 1995), have been shown to control the specification of floral meristem identity (Alvarez-Buylla et al., 2006). In maize, a domestication candidate gene, *GRMZM2G448355* (Hufford et al., 2012), is an ortholog of the Os*MADS56* gene, which delays flowering under long-day conditions in rice (Ryu et al., 2009). Interestingly, the evolution of the domesticated cauliflower (*B. oleracea* spp. *botrytis*) appears to be associated with mutations in the MADS-BOX floral meristem identity genes *CAL* and *AP1* (Kempin et al., 1995; Lowman and Purugganan, 1999).

- bZIP, WRKY. Drought responses include the induction of proteins belonging to several transcription factor and regulator families used in the reprogramming of the transcriptome to initiate adaptation strategies (Ramanjulu and Bartels, 2002), such as the bZIP, the MYB transcription factors, WRKY, and zinc-finger proteins. The bZIP transcription factor family induces transcription by binding to upstream abscisic-acid-responsive elements (Ramanjulu and Bartels, 2002), and differential expression of a member of this transcription-factor family was observed in a leaf subtractive cDNA library of a drought-sensitive genotype of wheat (*TTD-22*; Ergen and Budak, 2008). It is worth noting that several bZIP genes have been postulated to be involved in domestication. In maize, the *OPAQUE 2* (*O2*) gene, for example, was shown to encode a transcriptional activator that has a role in alterations to the grain phenotype during domestication (Henry et al., 2005). In addition, studies of natural variations in the seed dormancy in *Arabidopsis* led to the cloning of a QTL, *DELAY OF GERMINATION 1* (*DOG1*), which affects embryonic dormancy (Bentsink et al., 2006). *DOG1* encodes a member of a plant-specific protein family with a domain shared by the D class bZIP DNA-binding proteins (Sugimoto et al., 2010).

Interestingly, members of the WRKY family of proteins (Eulgem and Somssich, 2007) that are well-known for their roles in response to several abiotic stresses (Ramanjulu and Bartels, 2002) were almost exclusively induced in a drought-tolerant emmer wheat genotype (TR39477; Ergen and Budak, 2008). A number of transcription factors including many from the WRKY, AP2/EREBP, and MYB families, are also involved in leaf senescence (Eulgem et al., 2000; Chen et al., 2002).

The maternally expressed *Arabidopsis* WRKY transcription factor *TRANSPARENT TESTA GLABRA 2* (*TTG2*) appears to have a controlling role in seed size via the integument growth pathway; the seed length of a *ttg2* mutant is much smaller than the wild-type (Garcia et al., 2005).

Duplicated WRKY genes have been maintained in wild and cultivated plant species in the course of selection during domestication and polyploidization (Petitot et al., 2008). However, the majority of the WRKY genes analyzed respond to pathogen attack and to the endogenous signaling molecule salicylic acid (Eulgem and Somssich, 2007).

- Trihelix. The rice *Shattering 1* (*SHA1*) gene that encodes a GT-1-type factor has an important role in the activation of cell separation, and a mutation in the trihelix domain resulted in the elimination of seed shattering in cultivated rice (Lin et al., 2007). All of the the domesticated rice cultivars analysed harbor the mutant *sha1* gene, and have thus lost the ability to shed their seeds at maturity.

- Xylan. The cell wall mediates growth responses and often acts as the first barrier in interactions with a wide range of environmental factors (Stebbins, 1992; Somerville et al., 2004). Selection during the domestication process produced changes in the cell wall structure and composition; in this regard, in the study of Zhang et al. (2012), it was shown that the wild rice Yuanj has a reduced level of xylan associated with a less upright growth habit. Domestication appears to have conferred an increased level of xylan backbone to cultivated rice plants, along with an erect growth habit.

- Raffinose family. The most common of the raffinose family oligosaccharides (RFOs) are raffinose (RFO-trisaccharide) and stachyose (RFO-tetrasaccharide). The RFOs have diverse roles in plants, as they are used for transport and storage of carbon, and as solutes for the protection against abiotic stress (Bachmann et al., 1994; Haritatos et al., 1996; Taji et al., 2002). In many plant species, raffinose is also stored in high amounts in seeds, where it is thought to have an additional role in desiccation tolerance (Obendorf, 1997). The sucrose and RFO content in seeds might determine and indicate their storing capacity. Tahir et al. (2012) reported variations in relative concentrations of stachyose and raffinose between wild and domesticated lentil genotypes.

- MYB. Anthocyanin accumulation is controlled through the coordinated expression of genes encoding the anthocyanin biosynthetic pathway enzymes. From studies in a diverse array of plant species, it is apparent that this coordinated expression is controlled at the transcriptional level, usually by an R2R3 MYB and/or a basic helix-loop-helix transcription factor (Mol et al., 1996; Winkel-Shirley, 2001). More recently, advances have been achieved in apple (*Malus* × *domestica*) where the R2R3 MYB tanscriptional factors responsible for apple anthocyanin accumulation were identified (Espley et al., 2007). In a study seeking to examine the control of apple fruit skin anthocyanins (Ban et al., 2007), Md-MYBA was isolated from a pale red-skinned apple cultivar and characterized in a deep red-skinned cultivar.

A member of the MYB transcription factor family proteins that is involved in the control of several biological functions upon biotic and abiotic stresses (Lee et al., 2007) was differentially induced in a drought-sensitive genotype of wheat (TTD-22; Ergen and Budak 2008).

A gene identified in rice as producing a non-shattering phenotype (*sh4*) has a MYB3 DNA binding domain, which suggests that it is a transcription factor. A single SNP that leads to a single conserved amino-acid change has resulted in a change in function, which appears to result in either the incomplete formation of the abscission zone (Li et al., 2006) or the failure to initiate cell degradation (Lin et al., 2007). In the case of rice, two independent genetic pathways to nonshattering have occurred. The nonshattering phenotype probably came after other mutations that were associated with an increase in grain size and the waxy phenotype (Shomura et al., 2008), which supports the idea that the mutation arose in the domesticated population of rice.

- ZF-HD. Abscission is a process that is often implicated in domestication. Nakano et al. (2013) examined the transcriptomes of three tomato flower pedicel regions, the abscission zone and the flanking proximal and distal regions. They identified 89 genes that were preferentially expressed in the abscission zone compared to both the proximal and distal regions. These genes included several transcription factors that regulate apical or axillary shoot meristem activity. Nine genes belonging to seven transcription factor families were identified, among which there was a zinc-finger homeodomain (ZF-HD) family gene (*CK715116*). In particular, this gene encodes a protein with sequence similarity to the *Arabidopsis* ZF-HD family gene *HOMEOBOX PROTEIN33* product, which is involved in the abscisic acid response pathway (Wang et al., 2011).

4. Gene-function investigation

A survey of the function of a subset of PS contigs was carried out to investigate whether they are known to be associated to the domestication process in other species, using either direct experimentation or because of their function. In particular, we focused our survey on the 380 contigs that had the highest selection index (290), and considering also different patterns of polymorphism, all of the 23 PS contigs with alternative allelic states in MW and MD, and all of the 67 PS contigs that are monomorphic in MW and polymorphic in MD. Almost all of these contigs investigated had a BLASTX e-value ≤$10e^{-4}$, with few exceptions (six contigs had an e-value ≤$10e^{-2}$ and their functions were not relevant to domestication).

4.1 Contigs with the highest selection indices

The survey of the function of 221 annotated contigs among the 290 with the highest selection indices resulted in the following main points:

- Genes involved in "light" response pathway: Under directional selection, several genes were identified as involved in light perception or signaling and circadian and rhythm determination (*PHYA*, *EARLY FLOWERING4-Like 3*), photoperiod response (*GIGANTEA*), photoperiod adaptation (*DWARF IN LIGHT*), and timing of bolting and flowering (*VERNALIZATION INDEPENDENCE 5*, *AROGENATE DEHYDRATASE 1*, *AGAMOUS-LIKE8*). Another gene that was under positive selection, *KANADI2* (that together with *K1* modulates *PIN1*, a gene that, in turn, encodes an auxin transport protein), is a target (as also for *AGAMOUS* [see below] and other genes) of *LEAFY*, a master gene that has a central role in the regulation of the transition from vegetative growth to flower formation (Winter et al., 2011). *BRIZ1* is another interesting gene here, which has been shown to be comprised in the interval of Flt-2L QTL for flowering time in barley (Chen et al., 2009a). This QTL comprises Hv-*AP2*, which is highly similar to the wheat domestication gene Q (Förster et al., 2013). Finally, there is the *HIGH MOBILITY GROUP A* (*HMGA*) gene that encodes a DNA binding protein that interacts with A/T-rich stretches of DNA. Although this specific gene has an unknown function, it should be noted that other proteins, such as AHL22, that contain an AT-hook motif in *Arabidopsis* regulate flowering initiation by modifying the *FLOWERING LOCUS T* chromatin (Yun et al., 2012).

Among these genes, *GIGANTEA* (*GI*) has a pivotal role in the photoperiod response, as it controls flowering under long days in a circadian clock-controlled flowering pathway. In *Arabidopsis*, *GI* acts earlier than *CONSTANS* (*CO*) and *FLOWERING TIME* (*FT*) in the pathway, by increasing the levels of *CO* and *FT* mRNA (Mizoguchi et al., 2005). Literature surveys have shown that the genes with which *GI* interacts directly (i.e., *FT*, *CO*) were targets of selection during the domestication in crops like rice (*DTH CONSTANS*-like, Wu et al., 2013; and *Hd1 CONSTANS* homolog, Takahashi and Shimamoto, 2011) and sunflower (*HaFT1* and paralogs, Blackman et al., 2011). In pea, Hecht et al. (2007) identified *LATE BLOOMER 1* (*LATE1*) as the pea ortholog of *Arabidopsis GI*, and showed that it is necessary for promotion of flowering, production of a mobile flowering stimulus, and induction of an *FT* homolog under long-day conditions. Moreover, several other genes involved in flowering time were selected under domestication, such as in rice, wheat, barley, maize, rapeseed, sunflower, lentil, pea and sorghum (see Lenser and Theißen, 2013; Olsen and Wendel, 2013, for reviews). Interestingly, in *Arabidopsis*, it has been shown that *GIGANTEA* and *EARLY FLOWERING 4* (*ELF4*) show differential phase-specific genetic influences over a diurnal cycle (Kim et al., 2012), and that *GI* is epistatic to *ELF4* in flowering time determination, while *ELF4* is epistatic to *GI* in hypocotyl growth regulation. Moreover, *GI* and *ELF4* have a synergistic or additive effect on endogenous clock regulation. Kim et al. (2012), which suggests that this might allow diversity in the regulation of circadian physiological outputs to be achieved, including flowering time and hypocotyl growth. However, the present study is the first that reports that *GI* was selected during the process of domestication, while a putative transcriptional regulator that potentially functions in the Phytochrome A light signaling pathway was shown to be under selection during domestication of soybean (*E1* gene; Xia et al., 2012). This congruence is relevant, as the recent divergence of flowering-related genes in three legume species has been documented (*Glycine soya, Lotus japonicus*, *Medicago truncatula*; Kim et al., 2013).

AGL8 is another gene of outstanding interest. In *Arabidopsis*, it is negatively regulated by *APETALA 1*. The homolog of *APETALA 1* in wheat has been found to be selected under domestication (Yan et al., 2003; Golovnina et al., 2010). Moreover, *AGAMOUS* occupies a nodal position between the "floral induction" pathway and the "floral identity genes and meristem maintenance" pathway that control the formation of stamens, carpels, ovule and fruit development, and that determine the flowers across all angiosperms (Lenser and Theißen, 2013). Mutations in this "input-output" gene might alter a trait (or a series of traits) in a way that might otherwise only be achieved by concerted mutations within several upstream or downstream genes simultaneously, and it is for this reason that it is regarded as a good example to explain the molecular basis of convergent evolution during domestication (Lenser and Theißen, 2013).

Furthermore, the homolog of *AGL8* in soybean is considered as one of the three candidates for a major QTL for flowering time on chromosome 6 (Zhang et al., 2013).

- Genes that are pivotal to ensure correct hormonal perception, transport or biosynthesis: *TINY2* is an AP2/ERF (APETALA/Ethylene-responsive factor). In *Glycine max*, this gene regulates the Gm-*GA2ox4* gene, causing dwarfism (Suo et al., 2012). Another gene, At-*GRXS17*, has a critical role in redox homeostasis and hormone perception, to mediate temperature-dependent post-embryonic growth (Cheng et al., 2011); its mutants are altered in their perception of the phytohormone auxin and its polar transport. The *PIN3* gene encodes an auxin transport protein that is crucial for correct cellular coordination, and has a direct involvement in gravitropism and phototropism. It is implicated in the shade avoidance response regulated by phyA (here also found under selection) and phyB (Devlin et al., 2003). Moreover, *PIN* interacts with *INDEHISCENT* (*IND*) in regulation of the separation layer cells. The gene *WALL ARE THIN 1* is involved in numerous processes, such as auxin polar transport, positive regulation of auxins, regulation of meristem growth, anthocyanin accumulation in tissues in response to UV light, cell-wall organization and secondary cell-wall biogenesis in fibers, cell growth, regulation of cell size, root hair elongation, root morphogenesis, water transport, response to salt stress, and stem elongation (Ranocha et al., 2010). The gene *FRAGILE FIBER 1* (*FRA1*) is also an interesting candidate, as its mutants show altered orientation of cellulose microfibrils and reduced mechanical strength of fibers. Moreover, phylogenetic studies have shown that the rice gene *GIBBERELLIN INSENSITIVE DWARF1* (*GDD1*) is most similar to *At5g47820* (*FRA1*) of *Arabidopsis*. Mutation of rice *GDD1*, which encodes a kinesin-like protein that binds to a gibberellic acid biosynthesis gene promoter, leads to dwarfism with impaired cell elongation (Li et al., 2011). *FRA1* appears to be located 0.4 cM downstream of the *DINAGZ* QTL (a QTL for fiber digestibility) of chromosome 5 (Barriere et al., 2005). Finally, we found that apyrase 2 (*APY2*) is under selection. At-*APY1* and At-*APY2* have key roles in pollen germination and vegetative growth (Wu et al., 2007; Wolf et al., 2007). In *Arabidopsis*, the *apy1* and *apy2* double knock-out showed failed pollen germination. Moreover, lines silenced under RNA interference showed a dwarf phenotype in overall vegetative growth, and had dramatically reduced growth of the primary root and etiolated hypocotyls (Wu et al., 2007), and abnormal cotyledons (Wolf et al., 2007). Recent studies have indicated that a critical step connecting apyrase suppression to growth suppression is the inhibition of polar auxin transport (Liu et al., 2012). *AHP1* has a role in cytokinin signaling and affects multiple aspects of plant development. Cytokinins have diverse functions that include control of meristem activity, hormonal cross-talk, nutrient acquisition, responses to light (interactions with *PHYB*) and various stress responses (Jones et al., 2010; Brenner et al., 2012). Together with four other *AHP* genes and a histidine kinase, *CYTOKININ-INDEPENDENT1* (*CKI1*) gene, *AHP1* is implicated in the regulation of female gametophyte development and vegetative growth (Deng et al., 2010). Furthermore, a quintuple *ahp* mutant showed various abnormalities in growth and development, including reduced fertility, increased seed size, reduced vascular development, and a shortened primary root (Deng et al., 2010).

As indicated by Lenser and Theißen (2013), despite this seeming plurality of the domestication targets, two strategies have been repeatedly applied to promote the dwarfing habit in different species: alteration of the meristem identity to cause determinate growth (Salamini, 2003), or as the above-mentioned genes also suggest for *P. vulgaris*, interference with hormone metabolism or signaling (McGarry et al., 2012). In addition to the modulation of gibberellic acid signaling that is mainly seen in rice (Itoh et al., 2004; Asano et al., 2007, 2011), barley (Jia et al., 2009) and wheat (Doebley et al., 2006), interference with brassinosteroid signal transduction and with polar auxin transport has been shown to cause a semi-dwarfing growth habit in agronomically important varieties of barley (Chono et al., 2003) sorghum (Multani et al., 2003), and pearl millet (Parvathaeni et al., 2013). However, although in soybean and the common bean, *TERMINAL FLOWER* determines the growth habit and has been shown to be under selection during domestication (Tian et al., 2010; Kwak et al., 2012), it was not on our list of candidates.

- Genes involved in seed development and traits: Some of these genes are important for correct embryo development (*YODA*, Lukowitz et al., 2004; *POR*, Mathur, 2004; *AKRP*, Tzafrir et al., 2004; *BRIZ1*, Hsia and Callis, 2010; *EMB1211*, Liang et al., 2010; *IAA12*, Bureau et al., 2010), and others can affect the seed chemical composition, like for seed protein (*IAA12*, Yonekura et al., 2010), oil (*IAA12*, Kondo et al., 2010; and *LRR-RLK*) and fat (*FATB*, Molina et al., 2008) content,

and for seed maturation (*SEC14p*, Huang et al., 2013) and germination (*DOF6,* Rueda-Romero et al., 2012; *TKL,* Arc et al., 2012; *BGAL3*, Bui et al., 2011*; RBOHB*, Müller et al., 2009). Effects of domestication on these traits are inconceivable, as human selection might have led to seeds with development, maturation and germination that are more adapted to cultivation and field conditions. Moreover, during domestication, variations in seed chemical characteristics were also observed in several cases, such as, for example, the case of the *WAXY* gene in rice, maize, barley, sorghum, millet, and amaranth (Olsen and Wendel, 2013).

- Three genes have roles in the carbon/nitrogen (C/N) balance response: The first of these is a *trans*-membrane gamma-aminobutyrate (GABA) transporter. There is growing evidence that in plants the GABA shunt has a major role in primary C/N metabolism (Fait et al., 2008; Masclaux-Daubresse et al., 2008). The second is *TSD2* (*TUMOROUS SHOOT DEVELOPMENT2*), which encodes a putative methyltransferase with an essential role in cell adhesion that coordinates plant development (Krupková et al., 2007) and appears to be a critical modulator of the C/N nutrient balance response in *Arabidopsis* (Gao et al., 2008). Finally, a transketolase (AT3G60750) is among 16 genes involved in N nutrition and C metabolism up-regulated by NO_3^- (Girin et al., 2007). It has been shown that the transcribed segments of undomesticated plant genomes are the most N poor, with genomes and proteomes with signatures of N limitation (Acquisti et al., 2009). In this context, adaptation to N availability at the whole-plant level is highly conceivable, which would justify a role also for these genes during domestication.

- Genes involved in responses to environmental stresses: Several genes have homologs that encode proteins that are involved in biotic stresses (Ribosomal protein S14p/S29e family protein, Mitsuya et al., 2009; a tautomerase/MIF superfamily protein, Bricchi et al., 2012; HSF A4A, Kuśnierczyk et al., 2007; SIZ1, Lee et al., 2007; G6PDH1, Asai et al., 2011; Siddappaji et al., 2013). In this case, there are genes that control programmed cell death and are involved in innate immunity responses (*MKS1*, Andreasson et al., 2005; *WRKY4*, Lai et al., 2008; *ERD2*, Xu et al., 2012), and also in systemic acquired resistance (*ROF2*, Lin et al., 2012a; Copper transport protein family [*AT5G52740*], Ascencio-Ibáñez et al., 2008). Among the genes that are involved in biotic stress responses, *MKS1* and *WRKY4* are involved in the mitogen-activated protein kinase (MAPK) pathway. This is one of the main phosphorylation pathways that plants use in biotic and abiotic stress resistance. Specifically, the MAPK cascade and WRKY transcription factor functions act in response to both fungal and bacterial pathogens (Asai et al., 2002). In the case of abiotic stress, there are common genes involved in: drought tolerance or osmotic stress (RING E3 Ub ligase, Ryu et al., 2010; Cho et al., 2011; *CYCLIN H*, Zhou et al., 2013; *ERD2*, Taji et al., 1999; *SIZ1*, Catala et al., 2007), in stomata aperture/ closure (*SPHK1*, Worral et al., 2008; Guo et al., 2012), and in the control of abscissic acid synthesis (*AT5G04250*, encoding a cysteine proteinase superfamily protein, Jensen et al., 2013), response to heat (*Hsp70b*, Sung et al., 2001; *CPN10*, Kant et al., 2008; *HSFA4A*, Riechmann et al., 2000), cold (*STA1*, Lee et al., 2006), and salt (*ERD2*, Taji et al., 1999; *CYCLIN H*, Zhou et al., 2013) Stresses. Some other genes are also involved in the response to nutrient starvation (*SIZ1*, Miura et al., 2005, 2011) and in the tolerance to toxic metals in the soil, in particular to aluminum (*BCB*, Ezaki et al., 2000, 2001). The involvement of fast-evolving genes implicated in biotic and abiotic stress has recently been documented in tomato (Koenig et al., 2013). Moreover, metal tolerance is a trait found under domestication in different crops like wheat, rye, sorghum and corn, and constitutes an evident convergent selection during crop domestication (Lenser and Theißen, 2013).

Other genes that do not fall into these categories:

- *RKF1*; This RECEPTOR-LIKE KINASE IN FLOWERS gene showed the highest signal for directional selection. Twenty-five percent of the selectively expressed genes in pollen are included in the signal-transduction category. Most of these genes (26 of 37) encode putative protein kinases. *RKF1* is an example of the pollen-specific receptor kinases that are possibly involved in signaling events (Takahashi et al., 1998).

- *RPF1*; this gene encodes for RNA PROCESSING FACTOR 1 (RPF1), which is implicated in the restoration of cytoplasmic male sterility. This nuclear gene goes through mitochondrial RNA processing that leads to a protein that prevents pollen abortion. This trait is mitochondrially inherited, and it has been observed in various plant species (Holzle et al., 2011). Another gene that

is essential for pollen development and that has a crucial role in male gametophyte development and male fertility is *ATMGT9* (Chen et al., 2009b), which encodes a magnesium transporter that has been shown to have a role in local adaptation to serpentine soils (high heavy-metal content, low calcium-to-magnesium ratios) in *Arabidopsis lyrata* (Turner et al., 2010).

- The homolog of *YABBY5* (*YAB5*); *YAB5* is involved in the molecular determination of abscission in tomato fruit, a trait that is also under domestication (Nakano et al., 2013). Moreover, recently, a *YAB* homologue gene, *SH1*, and its homologs, was identified in the regulation of seed shattering in cereal species, including sorghum, rice and maize (Lin et al., 2012b). In sorghum, the shattering is determined by a single gene (*SH1*) that encodes a YABBY transcription factor. In maize and rice, these encode YABBY-LIKE transcription factors (Lin et al., 2012b).

- A gene encoding proteins that belong to the transducin/WD40 repeat-like superfamily. This gene is involved in the responses to the auxin stimulus and has also been implicated in defense responses (Rodrigues et al., 2013). In *Arabidopsis*, it is involved in several processes, including cell-chromatin silencing by RNA interference, glucuronoxylan metabolic processes, gravitropism, hydrogen peroxide biosynthetic processes, meiotic DNA double-strand break formation, meiotic chromosome segregation, organ morphogenesis, positive regulation of organelle organization, protein desumoylation, reciprocal meiotic recombination, regulation of anion channel activity, regulation of chromosome organization, sister chromatid cohesion, tissue development, vegetative-to-reproductive phase transition of the meristem, and xylan biosynthetic processes.

Interestingly, a WD40 protein in *G. max* is involved in seed development (Joshi et al., 2013). Moreover, a *WD40* (or *WUSCHEL*, as this has not been definitely identified) gene acts to determine the number of locules (fruit size) in tomato, a trait that was under selection in this crop during domestication (Muños et al., 2011; Ranc et al., 2012). Moreover, a WD40 protein is involved in pigmentation in *Sorghum bicolor* (Wu et al., 2012).

- Two genes are homologous of genes that control the color of the “edible part”, a trait that has often been affected by domestication in several herbaceous (potato, rice) and tree crops (orange and grapevine). Again, it is also considered an example of molecular convergence underlying domestication-related phenotypic changes (Lenser and Theißen, 2013; Olsen and Wendel, 2013). The first is *BCH1* that is involved in hydroxylation of beta-carotene (Tian et al., 2003), and is implicated in the pathway that confers color to tomato and pepper (Paran and van der Knaap, 2007). A major QTL for carrot color has been found for the pigment content that is mainly determined by two genes (*Y* and *Y2*) that are associated with domestication in carrot (wild, white; domesticated, orange). The other gene, *ATCDC5*, has been shown to have a key role in plant development, secondary metabolism, hormone signal transduction, disease resistance, and abiotic stress tolerance. However, it has also been observed that the CDC5 transcription factor binds a deleted region of the *DFR-A* onion gene. Interestingly, mutations in this gene were associated with the changed colors of onion after the domestication process (Song et al., 2014).

- A gene related to yield. This encodes a leucine-rich repeat protein kinase family protein (*AT2G26730*). Wild rice (*Oryza rufipogon*) has an important role by contributing to modern rice breeding. Song et al. (2009) sequenced and analyzed a 172-kb genomic DNA region of wild rice around the RM5 locus, which is associated with the yield QTL *yld1.1*. As suggested previously, two putative receptor-like protein kinase genes (one of which is *AT2G26730*) were key suspects for *yld1.1* (Song et al., 2009).

4.2 Contigs monomorphic in MW and polymorphic in MD

We also investigated the 47 annotated contigs among the 67 PS contigs that were polymorphic in MD and monomorphic in MW:

- *ELF4-L2* (*EARLY FLOWERING4-Like 2*); This gene is involved in the control of the circadian rhythm, and also functions as part of the light-input pathway. In *Pisum sativum*, Liew et al. (2009) isolated an ortholog of the *Arabidopsis ELF4-L2* (*DIE NEUTRALIS*, *DNE*) locus, and confirmed that this gene inhibits flowering under noninductive short-day conditions. *DNE* has a role in diurnal and/or circadian regulation of several clock genes, including the pea *GI* ortholog *LATE BLOOMER 1(LATE1)*.

- *KAN1* (*KANADI1*) (that together with *K2* modulates, in turn, the *PIN1* gene, which encodes an auxin transport protein); This gene is a target of *LEAFY*, a master gene that has a central role in the regulation of the transition from vegetative growth to flower formation. Interestingly, while *ELF4-L3* and *KAN2* are under selection toward a reduction in diversity in the domesticated form, for *ELF4-L2* and *KAN1* the opposite is true; i.e., they have evolved toward an increase in diversity in the domesticated forms.

- *MYB102*; De Vos et al. (2006) showed that At-*MYB102* has a role in defense against caterpillars. This genes is also involved in wounding and osmotic stress responses; interestingly, herbivore-damaged plants also suffer from water loss (De Vos et al., 2006).

- *KUP6* (*K^+ uptake transporter 6*); Osakabe et al. (2013) demonstrated that the KUP potassium transporter family has important roles in water-stress responses and growth in plants; moreover, KUP-type K^+ transporters are induced by different stresses with an osmotic component, and specifically inhibit cell expansion while enhancing drought tolerance.

- *APC*; In rice, *APC* controls *RSS1*, which is important for maintenance of the shoot meristem under abiotic stress conditions, and is also thought to control tolerance responses to salt, drought, and cold (Ogawa et al., 2011).

- *ETT* (*ETTIN MUTATIONS*); other names *AUXIN RESPONSE TRANSCRIPTION FACTOR3* (*ARF3*); This gene positively regulates *FIL* (required for the “super-replum” phenotype) activity during leaf development (Garcia et al., 2006; Sorefan et al., 2009). Moreover, in *Arabidopsis*, González-Reig et al. (2012) hypothesized that subtle changes in the expression of the antagonistic factors involved in auxin efflux can produce drastic changes in the size of the different tissue types, including the variability of fruit shape in Brassicaceae and other related species. Another example is in rice, where at least two *ARF*s have been detected as selected genes, and where it has been suggested that these genes can be targeted by domestication selection for enhanced growth responses and productivity (Wang et al., 2010).

- Transducin/WD40 repeat-like superfamily protein; This is involved in the response to the auxin stimulus and it is also implicated in defense responses (Rodrigues et al., 2013). A WD40 protein in *G. max* is involved in seed development (Joshi et al., 2013). Moreover, a WD40 protein probably acts together with the *WUSCHEL* gene to determine the number of locules (lc) in tomato, a trait that was under selection in this crop during domestication (Muños et al., 2011; Ranc et al., 2012). Also in this case, it must be noted that members of this family protein have also been selected in the opposite direction; i.e., towards a reduction of diversity in the domesticated form (see above).

- Squamosa BP-like (*SPL*); So far, *SPL* has also been functionally linked to diverse developmental processes, such as seed germination and seedling development (Martin et al., 2010), leaf and plastocron development (Moreno et al., 1997), juvenile-to-adult and floral phase transitions (Cardon et al., 1997; Wu and Poethig, 2006; Gandikota et al., 2007; Wang et al., 2009), fruit ripening (Manning et al., 2006), copper homeostasis (Kropat et al., 2005; Yamasaki et al., 2009), programmed cell death (Stone et al., 2005), domestication (Wang et al., 2005; Preston and Hileman, 2013), and grain yield (Jiao et al., 2010; Miura et al., 2010).

- GRAS transcription factor family; This family includes monoculm1 (*moc1*), which was characterized from a rice mutant that had almost no branching (Li et al., 2003). In rice, *moc1* affects all branching meristems, so that both vegetative and inflorescence branching are severely curtailed (Doust, 2007). This gene is necessary for axillary meristem initiation. It is related to the *LATERAL SUPPRESSOR* gene (*LAve S* and *ls* in the model dicot plant systems of *Arabidopsis* and tomato, respectively), which controls aspects of branching.

- Other genes *ALEURAIN-LIKE PROTEASE* (*AALP*) and *SENESCENCE ASSOCIATED GENE2* (*SAG2*); In *Arabidopsis*, these are involved in senescence (Grbić, 2003).

4.3 Contigs fixed for alternative alleles in MW and MD

Finally, we specifically focused on the 19 annotated contigs among the 23 PS contigs that were fixed for alternative alleles in MW and MD. Some of these genes are involved in responses to biotic stress, such as insect responses (*JAZ*, also known as *TIFY*, Kazan and Manners, 2012; Schweizer et al., 2013) and responses to bacteria (*LOL2*, Epple et al., 2003). Another gene, which encodes a

GDSL-like lipase, is mainly involved in the response to water deprivation (Boyce et al., 2003). Two other genes are also interesting: the ribosomal protein L36 in *Lycopersicon pimpillinelifolium* co-maps with a QTL for wall thickness, and in *L. esculentum* for flavonoid content (Okmen et al., 2011). Finally, *CHC1* is predicted to encode a protein that belongs to the chromodomain remodeling complex. In *Arabidopsis*, two RNA-interference knock-down lines have a dwarf phenotype and reduced rates of *Agrobacterium*-mediated transformation. The low rate of root-mediated transformation might result from altered root morphology or reduced root growth rates (Crane and Gelvin, 2007; Campi et al., 2012). This genes has been suggested to enhance plant growth (De et al., 2012). Other details of these genes are reported below:

- *JAZ12* (also known as *TIFY3B*); In *Arabidospis*, this gene is involved in the jasmonic-acid-mediated signaling pathway, positive regulation of the flavonoid biosynthetic process, regulation of the plant-type hypersensitive response and the response to wounding. The JAZ/TIFY protein has MYC2, MYC3, MYC4 and NINJA as its interacting co-repressors and transcription factors (Kazan and Manners, 2012). Recently, it was shown that *Arabidopsis* basic helix-loop-helix transcription factors MYC2, MYC3, and MYC4 regulate glucosinolate biosynthesis, and insect performance and feeding behavior (Schweizer et al., 2013).

- Ribosomal protein L36; This is involved in DNA-dependent transcription and elongation, and ribosome biogenesis and translation. In *Arabidopsis*, it is ethylene regulated (De Paepe et al., 2004). This gene co-maps with a QTL for wall thickness in *L. pimpillinelifolium* and flavonoid content in *L. esculentum* (Okmen et al., 2011).

- *CHC1* (*CLATHRIN HEAVY CHAIN1*); In *Arabidopsis*, *CHC1* is predicted to encode a protein that belongs to the chromodomain remodeling complex (Crane and Gelvin, 2007; Campi et al., 2012). Two RNA-interference knock-down lines have a dwarf phenotype and reduced rates of *Agrobacterium*-mediated transformation. The low rate of root-mediated transformation might result from altered root morphology or reduced root growth rates. This gene is among those for complexes of AN3-interacting proteins. *AN3* is an “intrinsic yield gene” in *Arabidopsis*. Their use has been suggested for plant growth (De et al., 2012).

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