

Figure S1 (related to Table 1 and Figure 1). Population genetic structure in diploid *M. annua*

Bar plots, as defined by fastStructure (see *STAR Methods*) and using the full SNP dataset (578,125 SNPs) for (A) $K=2$ and (B) $K=3$, clearly separate the core eastern Mediterranean population from the Atlantic and (western) Mediterranean range fronts. (C) Bar plots computed separately for each population show no further population structure. (D) Phylogenetic networks built using the NeighborNet method, with 1,000 bootstraps (see *STAR Methods* for details); each network is based on a random subset of 100,000 variable sites (sampled without replacement).

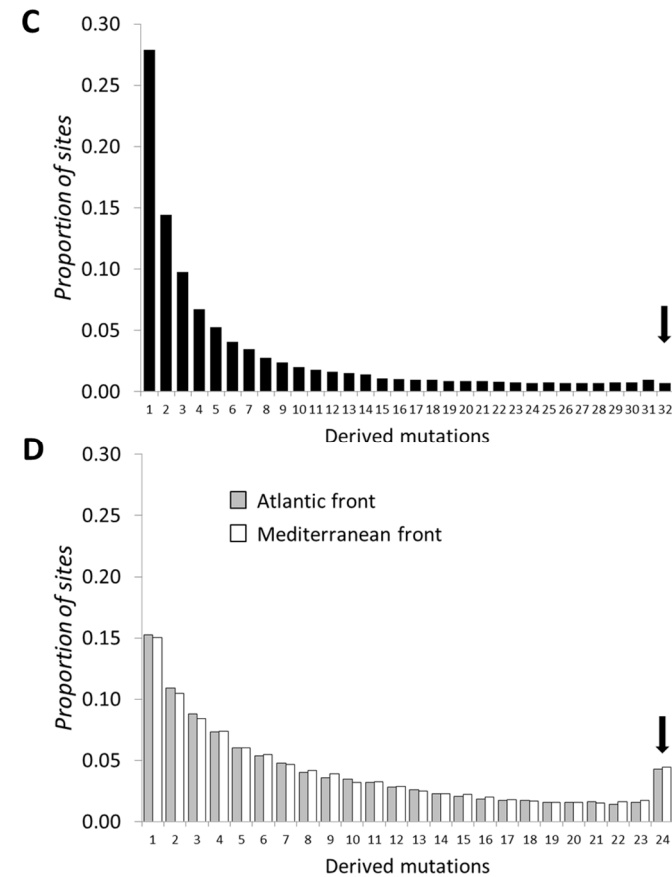
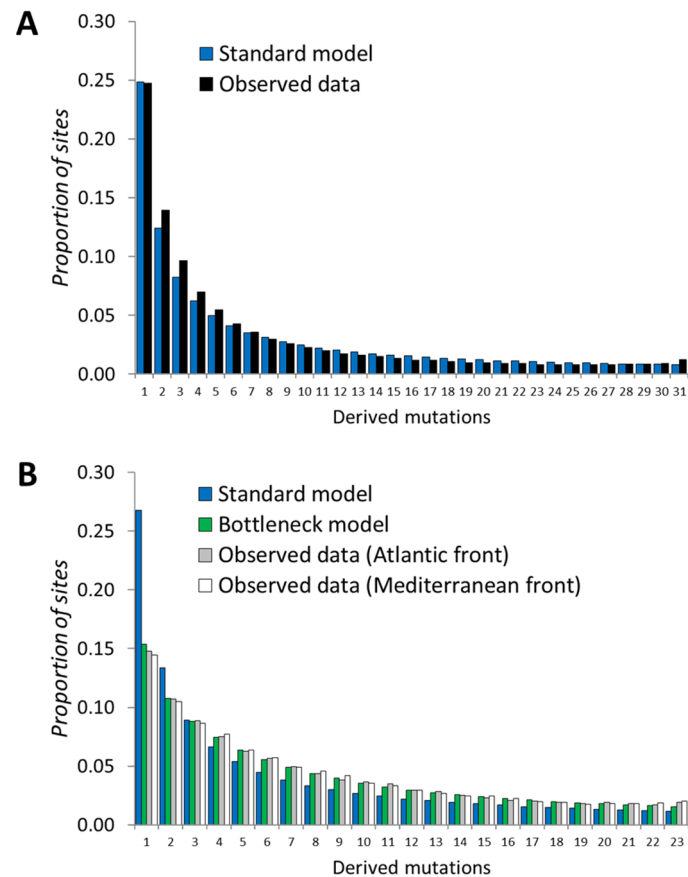


Figure S2 (related to Figure 2). Demographic models and proportion of fixed derived mutations

Unfolded site frequency spectrum (SFS) for observed sequence variation (only silent sites) and proportion of fixed derived mutations (indicated by a black arrow) for (A and C, respectively) the core population, compared with a standard model for a demographically stable population (A); and (B and D, respectively) the Atlantic and Mediterranean range fronts, compared with the same model together with the best-fitting bottleneck model (B). Note the much lower proportion of fixed derived mutations (C and D) in the core population (0.72%) compared to the front populations (4.29% and 4.46% in the Atlantic and Mediterranean range fronts, respectively).

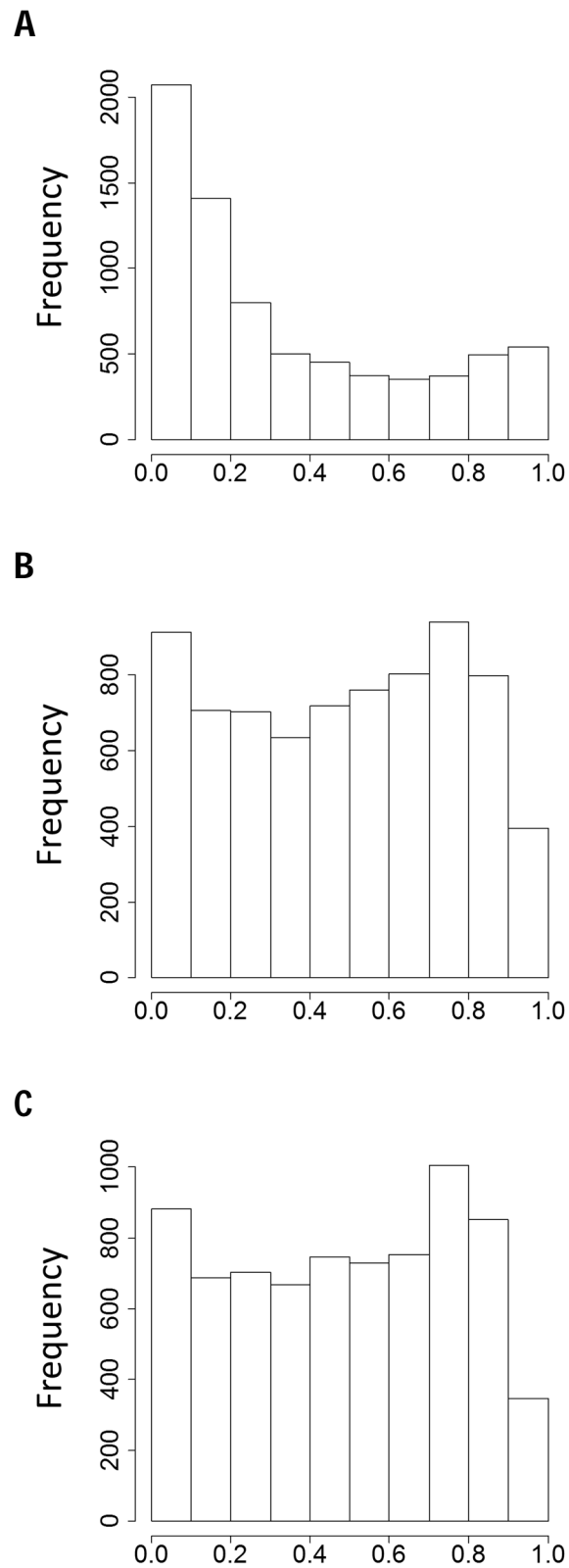


Figure S3 (related to Figure 3). Distribution of empirical p values for CLRTs

Nearly uniform distributions of P values in range-front populations (B: Atlantic front; C: Mediterranean front) suggest an overall lower number of significant tests than in the core population (A).

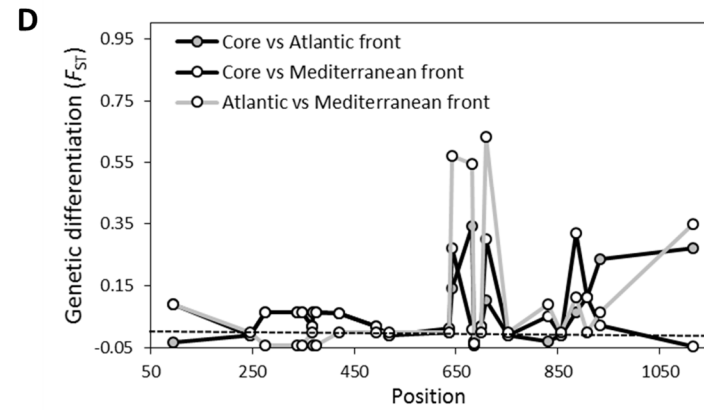
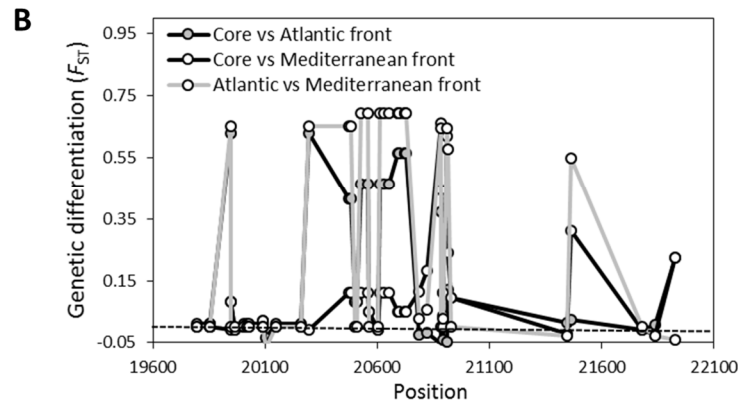
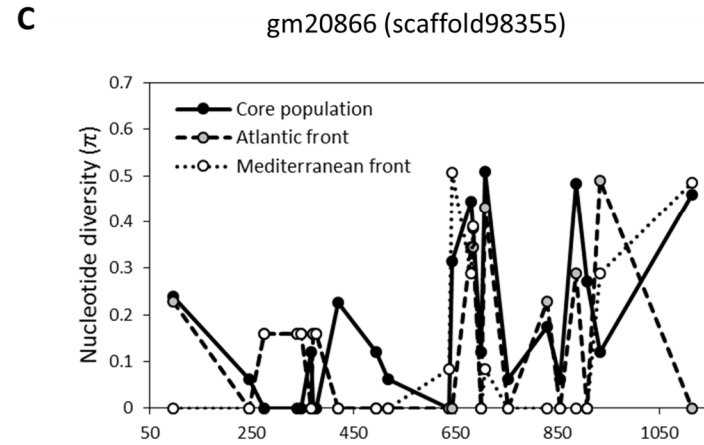
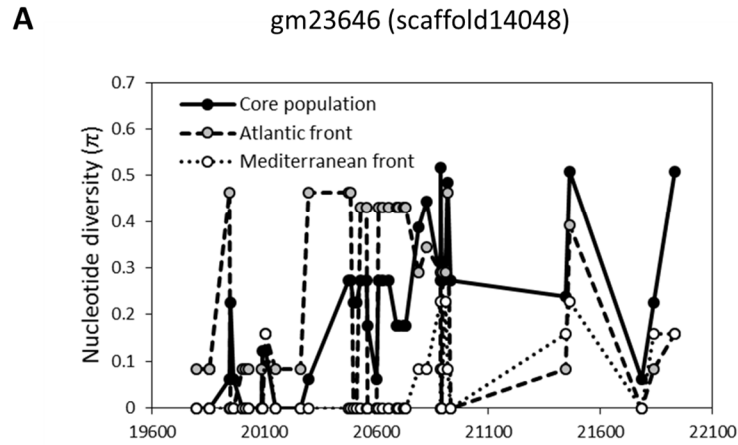


Figure S4 (related to Figure 3). Selective sweeps shared between the core and Mediterranean-front populations

Polymorphism (nucleotide diversity, π ; A and C) and divergence (pairwise F_{ST} ; B and D) by site for the selective sweeps shared between the core (eastern Mediterranean) population and the (western) Mediterranean front. Data are shown for gm23646 in scaffold14048 (A and B) and gm20866 in scaffold98355 (C and D).

Parameter	Description	Prior distribution	Minimum values	Maximum values	Values for best-fitting demographic model		
					Core population	Atlantic front	Mediterranean front
<i>Standard model</i>							
MUTRATE	Mutation rate	uniform	1.00E-06	1.00E-09	5.10E-07		
NPOP	Effective population size	uniform	10	1.00E+06	511,504		
<i>Bottleneck model</i>							
NCUR	Current effective population size	uniform	10	1.00E+06		53,423	39,024
NANC	Ancestral effective population size	uniform	10	1.00E+06		313,932	309,067
NBOT	Effective population size during the bottleneck	uniform	10	1.00E+06		17,624	36,443
TBOT	Time of the bottleneck	uniform	10	5.00E+04		1,678	1,108
DBOT	Duration of the bottleneck	uniform	10	1.00E+04		2,171	5,450

Table S1 (related to Table 1 and Figure 2). Description of parameters included in demographical models, search ranges, and best-fitting values

Best-fitting demographic models for the core population and the two range fronts of *M. annua* were obtained by comparison with observed site frequency spectrum (SFS) for silent sites, using fastsimcoal2 v2.5.2.8 (see *STAR Methods*). Times are given in number of generations, which can be translated directly to years in annual *M. annua*, ignoring effects of a possible seedbank.

All mutations

	Recessive genetic load			Additive genetic load		
	Class B or C	Class A	BC/A	Class B or C	Class A	BC/A
	mutations	mutations		mutations	mutations	
Core population	4331.31	6229.62	0.695	17732.31	23570.87	0.752
Atlantic front	5197.25	7345.83	0.707	18442.00	24456.08	0.754
Mediterranean front	5381.42	7381.58	0.729	18494.67	24010.17	0.770

Recessive genetic load

	Shared mutations (old mutations)			Mutations private to both fronts			Only private mutations (new mutations)		
	Class B or C	Class A	BC/A	Class B or C	Class A	BC/A	Class B or C	Class A	BC/A
	mutations	mutations		mutations	mutations		mutations	mutations	
Core population	3785.31	6632.75	0.571	NA	NA	NA	237.50	303.50	0.786
Atlantic front	4678.42	8110.08	0.577	232.83	274.92	0.855	98.50	90.42	1.113
Mediterranean front	4869.25	8212.33	0.593	226.17	259.92	0.872	97.92	80.00	1.263

Additive genetic load

	Shared mutations (old mutations)			Mutations private to both fronts			Only private mutations (new mutations)		
	Class B or C	Class A	BC/A	Class B or C	Class A	BC/A	Class B or C	Class A	BC/A
	mutations	mutations		mutations	mutations		mutations	mutations	
Core population	12652.62	21581.87	0.586	NA	NA	NA	2886.69	3212.19	0.906
Atlantic front	14952.25	25010.66	0.598	1237.42	1395.08	0.887	884.33	720.75	1.229
Mediterranean front	15178.83	24987.92	0.607	1221.50	1340.50	0.911	827.50	662.33	1.251

Table S2 (related to Figure 2). Recessive and additive genetic load per individual in range-front and core populations

Estimates of genetic load for class B and class C derived mutations, as well those scaled by class A (i.e., synonymous) mutations (i.e., BC/A). The average recessive and additive genetic load per individual in each population was obtained for the full SNP dataset (396,450 SNPs with known ancestral allele), for only shared mutations between range-front and core populations (i.e., presumably older mutations), for mutations private to the two fronts, and for private mutations in each population (i.e., presumably newer mutations).

Population	CHR	Gene models involved	GI	Max score	Total score	E-value	Locus	Annotation
core	scaffold102146	gm23393	gi 255583454	553	567	0	XP_002532486	Glutamate-tRNA ligase [Ricinus communis]
core	scaffold10238	gm23917	gi 255542816	364	354	0	XP_002512471	Probable protein phosphatase 2C 34 [Ricinus communis]
core	scaffold106281	gm13553	gi 255571375	550	559	0	XP_002526636	BTB/POZ domain-containing protein At2g13690 [Ricinus communis]
core	scaffold1111	gm23049	gi 255586244	415	419	0	XP_002533776	U-box domain-containing protein 21 [Ricinus communis]
core	scaffold11966	gm15951	gi 255546477	432	432	0	XP_002514298	Probable chlorophyll(ide) b reductase NYC1 [Ricinus communis]
core	scaffold120	gm24097	gi 255543821	435	435	0	XP_015570701	Xylulose kinase [Ricinus communis]
core	scaffold13015	gm14331	gi 255540103	712	510	0	XP_002511116	Uncharacterized protein LOC8275517 [Ricinus communis]
core	scaffold13501	downstream gm9711	gi 255557729	478	489	0	XP_002519894	Spermidine-binding periplasmic protein SpuE [Ricinus communis]
core	scaffold13573	gm22694	gi 8843794	91	69	3E-38	NP_200682	HSP20-like chaperones superfamily protein [Arabidopsis thaliana]
core	scaffold14048	intergenic region, gm23661 and gm23646	gi 255585601	344	344	0	EEF28892	Pentatricopeptide repeat-containing protein, putative [Ricinus communis]
			gi 255585601	163	158	7E-85	EEF28892	Pentatricopeptide repeat-containing protein, putative [Ricinus communis]
core	scaffold14272	gm10129	gi 255545040	794	824	0	XP_002513581	ATP-dependent zinc metalloprotease FTSH 11 [Ricinus communis]
core	scaffold14412	gm22840	gi 255559715	360	323	3E-127	XP_002520877	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 [Ricinus communis]
core	scaffold151157	gm10475	gi 255553221	416	416	0	XP_002517653	PTI1-like tyrosine-protein kinase At3g15890 [Ricinus communis]
core	scaffold16262	gm15916	gi 255578542	1916	1938	0	XP_015581453	Putative callose synthase 8 [Ricinus communis]
core	scaffold1698	gm15738	gi 449452422	153	137	7E-89	XP_002509917	Ubiquitin-conjugating enzyme E2 28 [Ricinus communis]
core	scaffold18075	gm18992	gi 255539813	1066	957	0	XP_002510971	Structural maintenance of chromosomes protein 6B [Ricinus communis]
core	scaffold1899	upstream gm14458	gi 357480717	2554	2696	0	XP_003610644	Serine/Threonine-kinase TOR [Medicago truncatula]
core	scaffold208	upstream gm16661	gi 298155591	266	253	4E-87	XP_016739466	E3 ubiquitin-protein ligase RING1 [Gossypium hirsutum]
core	scaffold20824	gm20852	gi 255571548	1142	427	0	XP_015579391	Uncharacterized protein LOC8278946 [Ricinus communis]
core	scaffold22784	gm9739	gi 255547121	452	483	2E-140	XP_002514618	Uncharacterized protein LOC8265052 [Ricinus communis]
core	scaffold23073	gm12371	gi 8261844	114	287	2E-43	XP_002511825	Phosphomannomutase [Ricinus communis]
core	scaffold2329	upstream gm19791	gi 255570116	1062	983	0	XP_002526020	ATP-dependent DNA helicase homolog RECG [Ricinus communis]
core	scaffold26072	intergenic region, gm14914 and gm14911	NA	NA	NA	NA	NA	unknown
			gi 8266430	426	477	5E-142	XP_002534154.1	Thaumatococcus-like protein 1b [Ricinus communis]
core	scaffold29453	upstream gm17948	NA	NA	NA	NA	NA	unknown
core	scaffold29727	gm14136	gi 255579462	570	606	0	XP_015581724	Something about silencing protein 10 [Ricinus communis]

core	scaffold30712	gm20837	gi 225462037	317	287	6E-178	XP_002274648	KH domain-containing protein At5g56140 [Vitis vinifera]
core	scaffold34061	gm14931	gi 255563719	568	567	0	XP_002522861	COBRA-like protein 10 [Ricinus communis]
core	scaffold34508	gm18298	gi 255584650	1352	198	6E-89	XP_015583217	ATPase family AAA domain-containing protein At1g05910 [Ricinus communis]
core	scaffold3691	gm21706	NA	NA	NA	NA	NA	unknown
core	scaffold40963	gm12464	gi 255546773	1135	1165	0	XP_002514445	Phospholipid-transporting ATPase 1 [Ricinus communis]
core	scaffold41980	downstream gm12564	gi 550325718	435	345	3E-132	XP_006376442	Hypothetical protein POPTR_0013s13080g [Populus trichocarpa]
core	scaffold44909	gm24588	gi 255563514	108	108	2E-35	XP_002522759	Uncharacterized protein LOC8286844 [Ricinus communis]
core	scaffold4518	gm21441	gi 255581121	188	171	5E-79	XP_002531375	THO complex subunit 4A [Ricinus communis]
core	scaffold4877	gm19015	gi 255550040	323	330	0	XP_015572785	Methyltransferase-like protein 22 [Ricinus communis]
core	scaffold54244	upstream gm23528	gi 255585152	373	373	0	XP_002533281	Pentatricopeptide repeat-containing protein At5g66631 [Ricinus communis]
core	scaffold5459	gm13405	gi 255538860	446	443	0	XP_002510495	Probable polyamine transporter At1g31830 [Ricinus communis]
core	scaffold61544	gm17107	gi 255561146	395	210	3E-111	XP_015576283	N-acetyl-D-glucosamine kinase [Ricinus communis]
core	scaffold64831	gm19740	gi 255553619	988	974	0	XP_002517850	Receptor-like protein kinase HSL1 [Ricinus communis]
core	scaffold67870	downstream gm17232	gi 410519446	306	317	3E-145	NP_001295712	Transcription factor MYB44-like [Jatropha curcas]
core	scaffold7590	gm19767	gi 255558742	1205	1214	0	XP_002520395	DExH-box ATP-dependent RNA helicase DEXH6 [Ricinus communis]
core	scaffold8416	gm11376	gi 550335346	515	161	2E-36	XP_002308857	Hypothetical protein POPTR_0006s03080g [Populus trichocarpa]
core	scaffold85182	gm19965	gi 255568832	599	609	0	XP_002525387	Uncharacterized protein LOC8276467 [Ricinus communis]
core	scaffold87330	gm9714	gi 255548471	624	520	0	EEF47276	Pentatricopeptide repeat-containing protein, putative [Ricinus communis]
core	scaffold90863	downstream gm18571	gi 356569566	1437	1453	0	XP_003552970	ATP-dependent RNA helicase SKI2 [Glycine max]
core	scaffold98355	gm20866	gi 255538518	278	276	1E-157	XP_002510324	Probable E3 ubiquitin-protein ligase ARI8 [Ricinus communis]
Atlantic front	scaffold105331	gm14172 and downstream	gi 255557182	146	143	8E-96	XP_015574934	Uncharacterized protein LOC8262254 [Ricinus communis]
Atlantic front	scaffold10546	gm20533	gi 255537357	192	162	4E-73	XP_002509745	CASP-like protein 4A4 [Ricinus communis]
Atlantic front	scaffold17977	gm9429	gi 255578656	429	405	0	XP_002530189	Peptidyl-prolyl cis-trans isomerase [Ricinus communis]
Atlantic front	scaffold29453	gm17958	gi 255583154	359	316	7E-163	XP_015582800	Squamosa promoter-binding-like protein 9 [Ricinus communis]
Atlantic front	scaffold3627	gm15432	gi 255583551	208	139	4E-69	XP_002532532	Protein At-4/1 [Ricinus communis]
		gm15433	gi 550319182	431	429	0	XP_015582938	Putative pentatricopeptide repeat-containing protein At1g09680 [Ricinus communis]
Atlantic front	scaffold4518	gm21447	NA	NA	NA	NA	NA	unknown
Atlantic front	scaffold51653	gm10628	gi 255541720	497	112	3E-25	XP_002511924	Proline iminopeptidase [Ricinus communis]
Atlantic front	scaffold59853	gm15353	gi 568848258	731	694	0	XP_015582231	Pentatricopeptide repeat-containing protein At1g53600 [Ricinus communis]

Atlantic front	scaffold69926	gm8714	gi 449445411	221	207	4E-99	XP_015578963	Phytanoyl-CoA dioxygenase [Ricinus communis]
Atlantic front	scaffold72879	upstream gm8766	gi 255587360	698	705	0	XP_002534244	WD repeat-containing protein 44 [Ricinus communis]
Atlantic front	scaffold96626	gm16840	gi 255562960	1001	1006	0	XP_002522485	ARF guanine-nucleotide exchange factor GNOM [Ricinus communis]
Mediterranean front	scaffold105331	gm14172 and downstream	gi 255557182	146	143	8E-96	XP_015574934	Uncharacterized protein LOC8262254 [Ricinus communis]
Mediterranean front	scaffold10781	gm10792	gi 255560600	416	432	0	XP_002521314	Uncharacterized calcium-binding protein At1g02270-like [Gossypium hirsutum]
Mediterranean front	scaffold11254	gm10375	gi 255587521	290	259	1E-159	XP_002534300	General transcription factor IIF subunit 2 [Ricinus communis]
Mediterranean front	scaffold14048	gm23646	gi 255585601	163	158	7E-85	XP_015583453	Pentatricopeptide repeat-containing protein At3g02330 isoform X2 [Ricinus communis]
Mediterranean front	scaffold26177	upstream gm13335	gi 255581480	1327	1352	0	XP_015582328	Centromere-associated protein E [Ricinus communis]
Mediterranean front	scaffold27955	gm22658	gi 255588437	941	953	0	XP_002534605	Vacuolar protein-sorting-associated protein 11 homolog [Ricinus communis]
Mediterranean front	scaffold43203	gm19459	NA	NA	NA	NA	NA	unknown
Mediterranean front	scaffold47530	gm9405	gi 255563993	170	176	8E-92	XP_002522996	Protein LHCP TRANSLOCATION DEFECT [Ricinus communis]
Mediterranean front	scaffold7543	intergenic region, gm22288	gi 8286584	335	1469	1E-176	XP_002515852.1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase [Ricinus communis]
		and gm22289	gi 255549603	650	630	0	XP_015572771	Importin subunit beta-1 [Ricinus communis]
Mediterranean front	scaffold8169	gm15646	gi 255543445	704	721	0	XP_002512785	Acetyl-coenzyme A synthetase [Ricinus communis]
		gm15651	gi 255543447	382	362	0	EEF49289	Conserved hypothetical protein [Ricinus communis]
Mediterranean front	scaffold98355	gm20866	gi 255538518	278	276	1E-157	XP_002510324	Probable E3 ubiquitin-protein ligase ARI8 [Ricinus communis]

Table S3 (related to Figure 3). Annotation of selective sweeps detected by CLTRs

Only selective sweeps with CLRT values higher than the maximum obtained in the coalescent simulations without selection are reported. The table includes the best BLAST hit from NCBI's GenBank, maximum and total scores, and E-values. Only BLAST hits with E-value lower than E-20 are reported.

Population	CHR	Gene models involved	GI	Max score	Total score	E-value	Locus	Annotation
core	scaffold57063	gm20243	gi 1000982469	976	976	0	XP_015584477	Protein DENND6A [Ricinus communis]
core	scaffold43200	gm16875	gi 223550648	123	442	6E-59	EEF52135	Ribonuclease z, putative [Ricinus communis]
core	scaffold33227	gm11333	gi 223532702	193	1178	4E-68	EEF34484	Abc transporter, putative [Ricinus communis]
core	scaffold86939	gm24196	gi 1000956321	1634	3237	0	XP_015577536	Protein CHROMATIN REMODELING 4 [Ricinus communis]
core	scaffold42462	gm13954	gi 255543315	251	707	6E-87	XP_002512720	Photosynthetic NDH subunit of subcomplex B 1 [Ricinus communis]
core	C18064493	gm16540	gi 1000942096	834	1530	0	XP_015582405	Nuclear pore complex protein NUP133 [Ricinus communis]
core	scaffold53536	gm11599	gi 1000956140	384	2133	5E-107	XP_015577619	Myosin-1 [Ricinus communis]
core	scaffold87546	gm23900	gi 1109193637	159	1052	2E-89	XP_019179930	Peroxisomal fatty acid beta-oxidation multifunctional protein AIM1-like [Ipomoea nil]
core	scaffold25849	gm13125	gi 1000945251	134	982	1E-28	XP_015581368	THO complex subunit 1 [Ricinus communis]
core	scaffold4931	gm19229	gi 848878625	242	1171	9E-143	XP_012839732	Kinesin-related protein [Erythranthe guttata]
Atlantic front	scaffold13589	downstream gm13612	gi 1000982083	1267	3523	0	XP_015584288	ATP-dependent helicase BRM [Ricinus communis]
Atlantic front	scaffold4367	gm24580	gi 1035904090	149	850	8E-34	OAY33689	Hypothetical protein MANES_13G116500 [Manihot esculenta]
Atlantic front	scaffold32307	downstream gm20800	gi 255562318	354	1379	1E-100	XP_002522166	Alpha-glucosidase YihQ [Ricinus communis]
Atlantic front	scaffold87024	gm11327	NA	NA	NA	NA	NA	unknown
Atlantic front	scaffold22117	downstream gm602	gi 1035905003	114	165	1E-26	OAY34601	Hypothetical protein MANES_12G032900 [Manihot esculenta]
Atlantic front	scaffold42716	gm9166	gi 1000966607	974	974	0	XP_015574569	Uncharacterized protein LOC8275537 [Ricinus communis]
Atlantic front	scaffold25042	gm9755	gi 1029080387	157	724	2E-84	XP_016700389	Heat shock 70 kDa protein 17-like [Gossypium hirsutum]
Atlantic front	scaffold67681	gm24129	gi 1000950561	309	1245	5E-84	XP_015579549	Vacuolar protein sorting-associated protein 54 [Ricinus communis]
Atlantic front	scaffold38772	gm19609	NA	NA	NA	NA	NA	unknown
Atlantic front	scaffold35687	gm10292	gi 1000957757	197	395	8E-54	XP_002522784	SEC14 cytosolic factor [Ricinus communis]
Mediterranean front	C18060393	downstream gm2037	gi 1000968221	118	485	2E-23	XP_015574069	Beta-galactosidase 9 [Ricinus communis]
Mediterranean front	scaffold68	gm15284	gi 255541042	519	1045	8E-163	XP_002511585	Uncharacterized protein LOC8265780 [Ricinus communis]
Mediterranean front	scaffold8416	gm11376	NA	NA	NA	NA	NA	unknown
Mediterranean front	scaffold14412	gm22840	gi 1000962574	92	479	2E-21	XP_015575797	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 [Ricinus communis]
Mediterranean front	scaffold14412	gm22837	gi 1072931374	102	1175	1E-53	XP_018476350	N-terminal kinase-like protein [Raphanus sativus]
Mediterranean front	scaffold8708	gm16765	gi 1000963086	107	641	2E-41	XP_015575553	Carnosine N-methyltransferase [Ricinus communis]
Mediterranean front	scaffold97053	gm19278	gi 1025376251	466	843	0	XP_016516023	Chromatin remodeling 8-like [Nicotiana tabacum]

		gm19275	gi 1035905016	176	466	8E-47	OAY34614	Hypothetical protein MANES_12G033800 [Manihot esculenta]
Mediterranean front	scaffold6314	gm19877	gi 255577568	431	1088	2E-164	XP_002529662	T-complex protein 1 subunit gamma [Ricinus communis]
Mediterranean front	scaffold95502	gm14806	gi 1000951193	216	1618	7E-53	XP_015579317	Rab3 GTPase-activating protein catalytic subunit [Ricinus communis]
	scaffold62280	upstream gm24515	NA	NA	NA	NA	NA	unknown
Mediterranean front	scaffold57063	gm20243	gi 1000982469	976	976	0	XP_015584477	Protein DENND6A [Ricinus communis]

Table S4 (related to Figure 3). Annotation of selective sweeps detected by nS_L

Only the top ten outliers in each population are reported. The table includes the best BLAST hit from NCBI's GenBank, maximum and total scores, and E-values. Only BLAST hits with E-value lower than E-20 are reported.