Supplemental Figure Legends

Supplemental Figure 1. Haplotype cluster analysis (K = 3) of *Arabidopsis thaliana* lines from North America and Euarasia conducted without geographic origin information for lines. Data generated from Structure analysis on 228 EA lines and 180 NA lines genotyped at 136 genome-wide SNP loci. See text for details.

Supplemental Figure 2. Haplotype cluster analysis (K = 5) of *Arabidopsis thaliana* lines from North America clustered into ancestral populations based on Eurasian haplotypes. Data generated from Structure analysis on 228 EA lines and 180 NA lines genotyped at 136 genome-wide SNP loci. See text for details.

Supplemental Figure 3. Changes in allele frequency between the native and introduced range for 136 SNPs. On the horizontal axis, the minor allele frequency is plotted, excluding singletons. The vertical axis depicts the corresponding allele frequencies in the introduced range. The diagonal line depicts the 1:1 relationship (no change in frequency), while the horizontal line is provided as a reference to distinguish alleles that changed from minor alleles to major alleles (above the line), or remained minor alleles (below the line). *FRI*, *FLC*, and *PHYC* are shown for reference.

Figure S1.

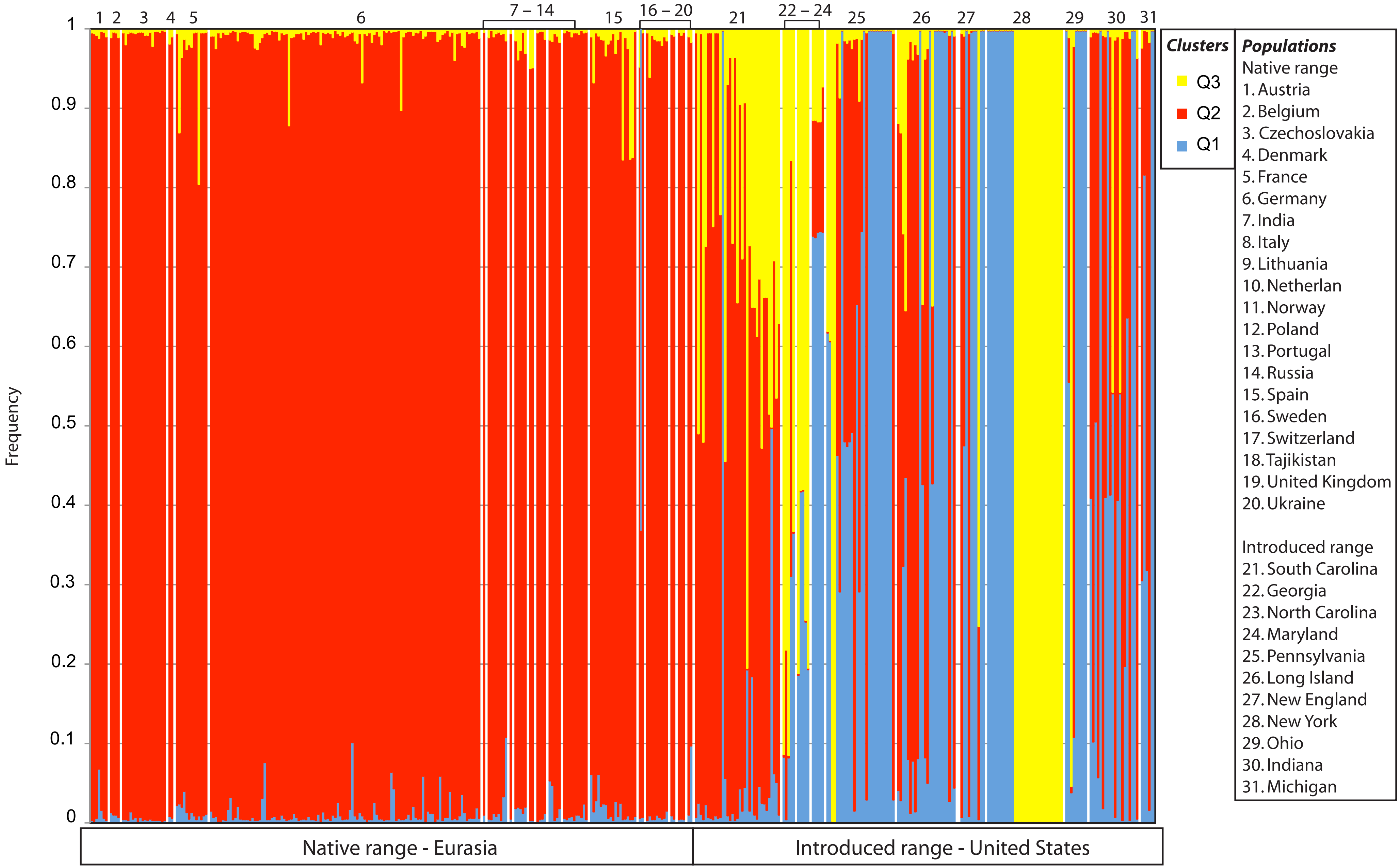
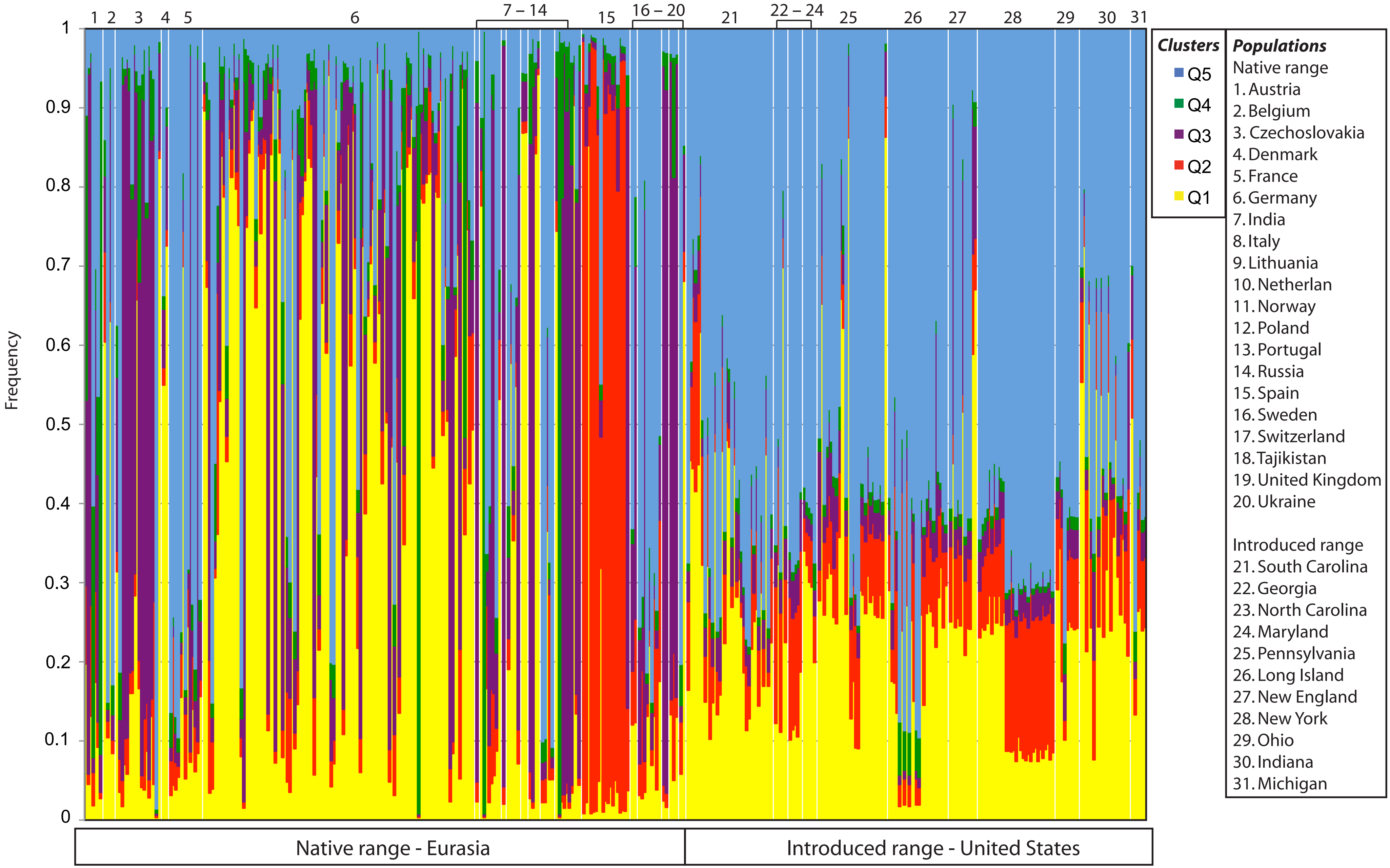
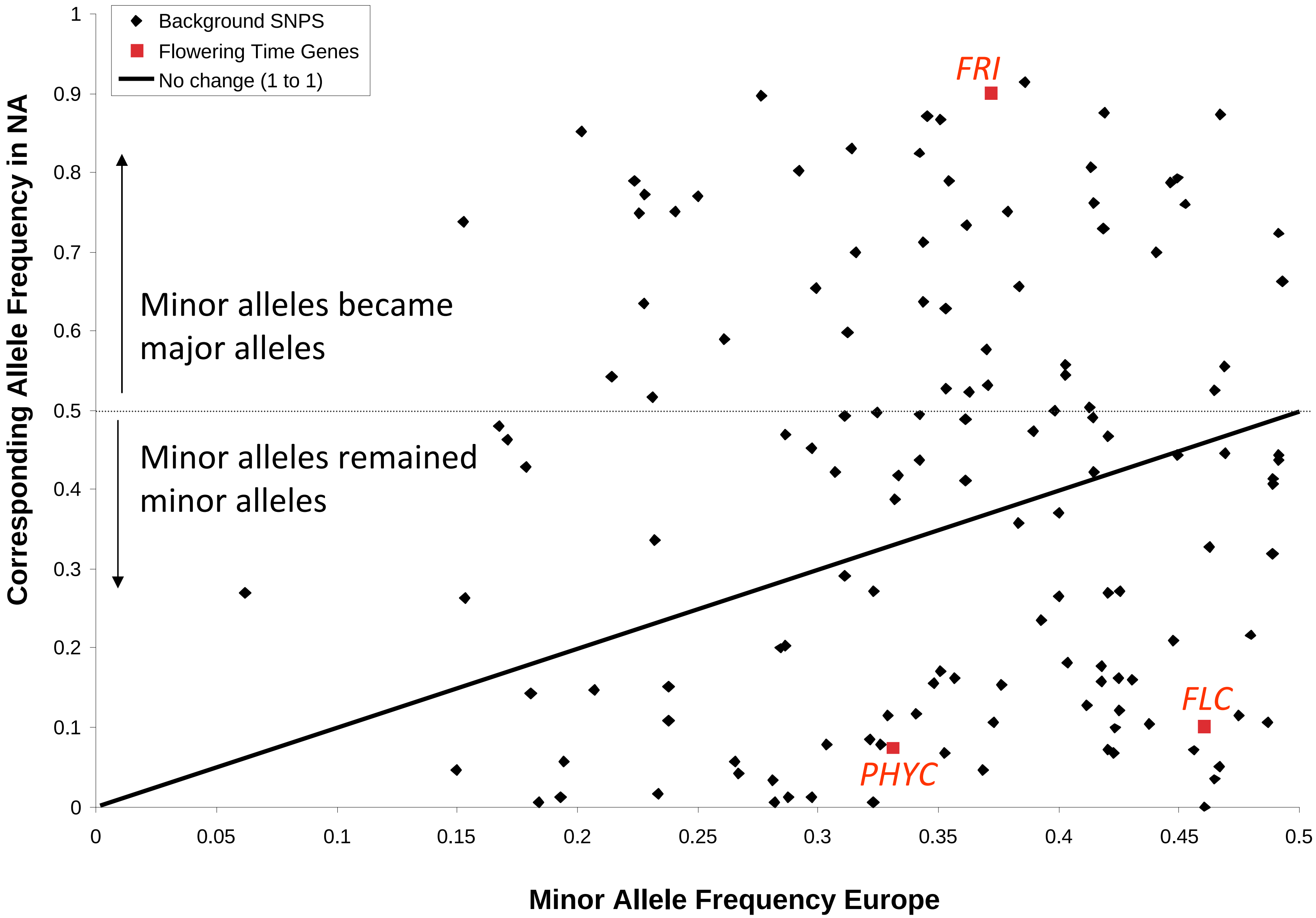

1
2
3
4
5
6
7 – 14
15
16 – 20
21
22 – 24
25
26
27
28
29
30
31
Frequency
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
Native range - Eurasia
Introduced range - United States
Clusters
Q3
Q2
Q1
Populations
Native range
1. Austria
2. Belgium
3. Czechoslovakia
4. Denmark
5. France
6. Germany
7. India
8. Italy
9. Lithuania
10. Netherlan
11. Norway
12. Poland
13. Portugal
14. Russia
15. Spain
16. Sweden
17. Switzerland
18. Tajikistan
19. United Kingdom
20. Ukraine
Introduced range
21. South Carolina
22. Georgia
23. North Carolina
24. Maryland
25. Pennsylvania
26. Long Island
27. New England
28. New York
29. Ohio
30. Indiana
31. Michigan

Figure S2.


1
2
3
4
5
6
7 – 14
15
16 – 20
21
22 – 24
25
26
27
28
29
30
31
Frequency
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
Native range - Eurasia
Introduced range - United States
Clusters
Q5
Q4
Q3
Q2
Q1
Populations
Native range
1. Austria
2. Belgium
3. Czechoslovakia
4. Denmark
5. France
6. Germany
7. India
8. Italy
9. Lithuania
10. Netherlan
11. Norway
12. Poland
13. Portugal
14. Russia
15. Spain
16. Sweden
17. Switzerland
18. Tajikistan
19. United Kingdom
20. Ukraine
Introduced range
21. South Carolina
22. Georgia
23. North Carolina
24. Maryland
25. Pennsylvania
26. Long Island
27. New England
28. New York
29. Ohio
30. Indiana
31. Michigan


◆ Background SNPS
■ Flowering Time Genes
No change (1 to 1)
FRI
PHYC
FLC
Minor alleles became major alleles
Minor alleles remained minor alleles
Corresponding Allele Frequency in NA
Minor Allele Frequency Europe
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
0
0.05
0.1
0.15
0.2
0.25
0.3
0.35
0.4
0.45
0.5