Table 1 Suppl. Geographical origins of *Arabidopsis thaliana* accessions used in this study and the percentage of identity with Col-0 *ICE1* and *ICE2* sequences.

Name	Origin	Percentage of identity		Name	Origin	Percentage of identity		Name	Origin	Percentage of identity	
Northern		*ICE1*	*ICE2*	Temperate		*ICE1*	*ICE2*	Southern		*ICE1*	*ICE2*
Oy-0	Norway	97	100	Bur-0	Ireland	100	97	Sus-1	Kyrgyzstan	100	99
Ber	Denmark	99	99	Col-0	USA	100	100	Co-1	Portugal	100	99
Hau-0	Denmark	99	100	Di-G	France	100	99	Aitba-1	Morocco	100	98
St-0	Sweden	100	99	Edi-0	Scotland	97	97	Can-0	Spain	100	96
Pog-0	Canada	99	99	Gre-0	USA	100	100	Fei-0	Portugal	100	98
Est	Estonia	100	99	Hi-0	Netherlands	100	96	Ct-1	Italy	100	96
Es-1	Finland	100	100	Kn-0	Lithuania	100	96	Mt-0	Libya	100	96
Lom-1-1	Norway	100	99	Ler-1	Poland	100	96	Sf-0	Spain	97	99
Lu-1	Sweden	100	99	No-0	Germany	97	96	Had-1	Lebanon	100	99
Hel-3	Finland	100	99	Pi-0	Austria	99	99	Bik-1	Lebanon	99	99
Spr1-2	Sweden	100	99	Po-0	Germany	97	100	Hal-1	Italy	100	100
Spr1-6	Sweden	100	99	Rsch-0	Russia	100	96	Cvi-0	Cape Verde Islands	100	97
Ko-2	Denmark	100	99	Rub-1	Ukraine	100	99	Anz-0	Iran	99	99
Van-0	Canada	99	99	Stw-0	Russia	100	99	Dja-1	Kyrgyzstan	100	99
Tamm-2	Finland	100	99	Tsu-0	Japan	98	96	Shahdara	Tajikistan	100	99
Ull2-3	Sweden	100	99	Wil-2	Lithuania	100	96	Kondara	Tajikistan	100	99
Ull2-5	Sweden	99	99	Ws-0	Belarus	100	96	Bla-1	Spain	100	99
Var2-6	Sweden	99	100	Wu-0	Germany	98	96	Bl-1	Italy	99	99
Fab-2	Sweden	100	99	Yo-0	USA	100	100	Nemrut-1	Turkey	100	98
Bil-5	Sweden	100	100	Zu-0	Switzerland	100	99	Kas-1	India	100	100

Table 2 Suppl. Patterns of nucleotide variation across the *ICE1* region of *A. thaliana.* S - a number of variable sites, π - nucleotide diversity per site, n.d. - not determined.

	Total coding	Synonymous	Nonsynonymous	Total noncoding	5' Flanking	3' Flanking	Silent sites	Total
All the ecotypes (*n* = 60)								
Number of sites	1492	321.69	1145.31	938	294	263	1231.69	2419
S	37	4	32	26	3	10	31	63
π	0.00646	0.00334	0.00708	0.00524	0.00034	0.00550	0.00474	0.00678
Tajima's D	0.6843	0.55030	0.59187	-0.5655	-1.6758	-0.9030	-0.39327	0.15548
Northern accessions (*n* = 20)								
Number of sites	1485	331.53	1147.48	934	297	267	1242.52	2419
S	31	5	25	17	1	5	22	48
π	0.00675	0.00494	0.00691	0.00397	0.00034	0.00334	0.00423	0.00570
Tajima's D	0.5720	0.49391	0.48599	-0.9139	-1.1644	-1.1516	-0.58278	0.03024
Temperate accessions (*n* = 20)								
Number of sites	1482	332.73	1149.28	910	295	263	1242.72	2419
S	31	5	26	21	0	10	27	53
π	0.00781	0.00557	0.00846	0.00767	0	0.00973	0.00711	0.00776
Tajima's D	1.27468	0.96241	1.26715	0.4838	n.d.	-0.3236	0.62717	0.97705
Southern accessions (*n* = 20)								
Number of sites	1485	333.85	1151.15	934	295	263	1244.85	2419
S	30	4	26	19	2	5	23	49
π	0.00498	0.00329	0.00637	0.00389	0.00068	0.00302	0.00373	0.00457
Tajima's D	-0.4895	-0.07055	-0.54480	-1.2768	-1.5128	-1.3344	-1.08880	-0.83385

Table 3 Suppl. Patterns of nucleotide variation across the *ICE2* region of *A. thaliana.* S - a number of variable sites, π - nucleotide diversity per site, n.d. - not determined.

	Total coding	Synonymous	Nonsynonymous	Total noncoding	5’ Flanking	3’ Flanking	Silent sites	Total
All the ecotypes (*n* = 60)								
Number of sites	1319	300.32	1001.68	895	399	216	1186.97	2258
S	38	24	14	49	7	17	23	88
π	0.007	0.02328	0.00248	0.01673	0.00104	0.2749	0.01829	0.0109
Tajima’s D	0.52448	1,21937	-0.50771	1.2261	-1.8488	1.6463	1.27398	0.90567
Northern accessions (*n* = 20)								
Number of sites	1344	297.58	1043.42	906	405	221	1203.52	2258
S	22	18	5	21	2	7	39	44
π	0.00595	0.02234	0.00129	0.00740	0.00108	0.00741	0.01109	0.00653
Tajima’s D	0.89668	1,24109	0.25395	0.5034	-0.5278	-0.5603	0.88841	0.73977
Temperate accessions (*n* = 20)								
Number of sites	1327	294.39	1025.61	896	399	216	1190.39	2258
S	25	13	12	43	2	16	56	68
π	0.0062	0.01550	0.00357	0.01907	0.00073	0.0317	0.01819	0.01139
Tajima’s D	0.64498	0.88980	0.29234	1.6390	-1.1407	1.9264	1.50253	1.30389
Southern accessions (*n* = 20)								
Number of sites	1321	282.16	1028.84	903	402	221	1185.16	2258
S	31	13	18	42	3	17	55	73
π	0.00727	0.01265	0.00587	0.01584	0.00075	0.02815	0.01508	0.01075
Tajima’s D	0.38986	0.00407	0.78447	0.8321	-1.7233	0.8508	0.64376	0.66054

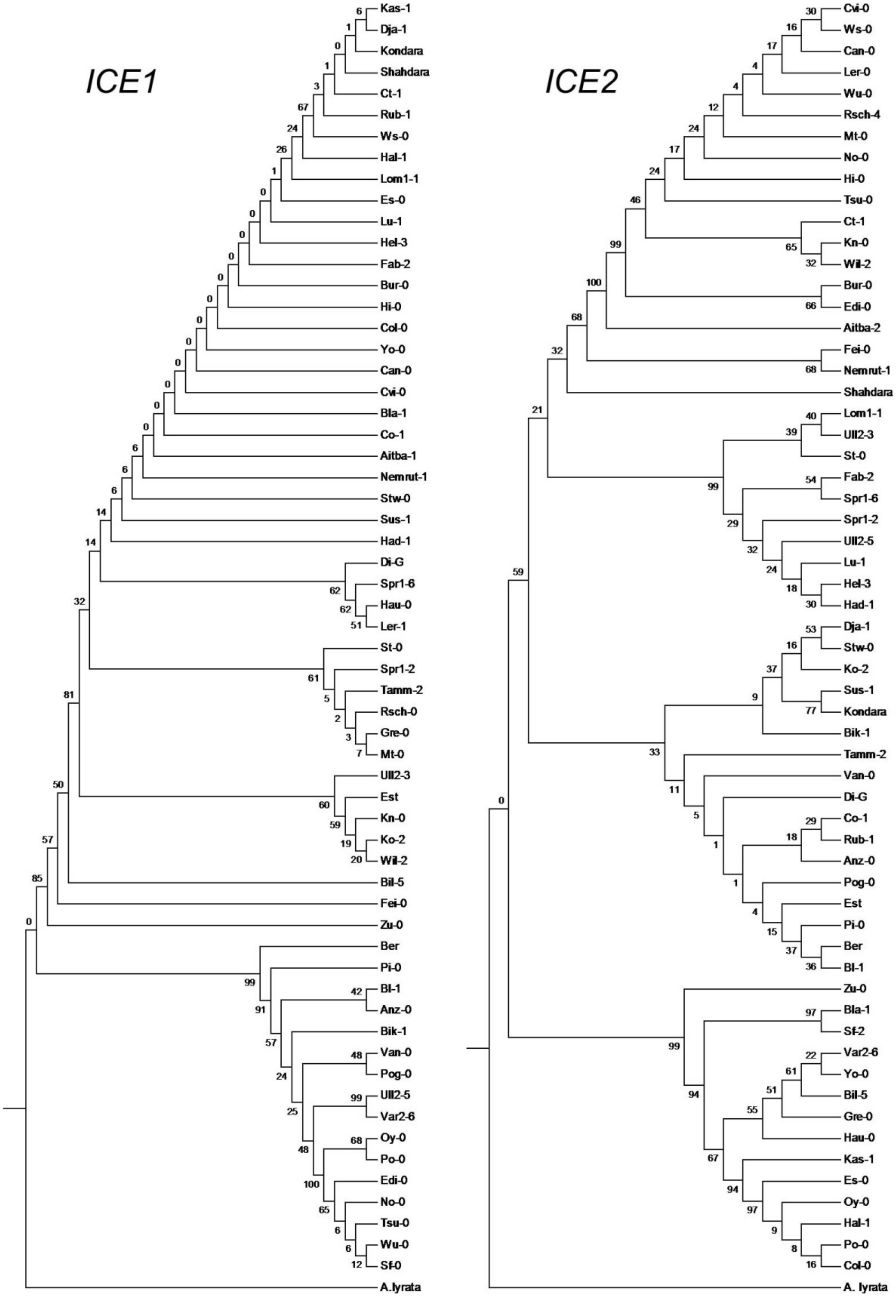

Fig. 1 Suppl. Neighbor-joining trees based on nucleotide variations in *ICE1* and *ICE2*. *A. lyrata ICE1* and *ICE2* gene sequences were used as outgroup accordingly. The number of bootstrap replications was 1 000.