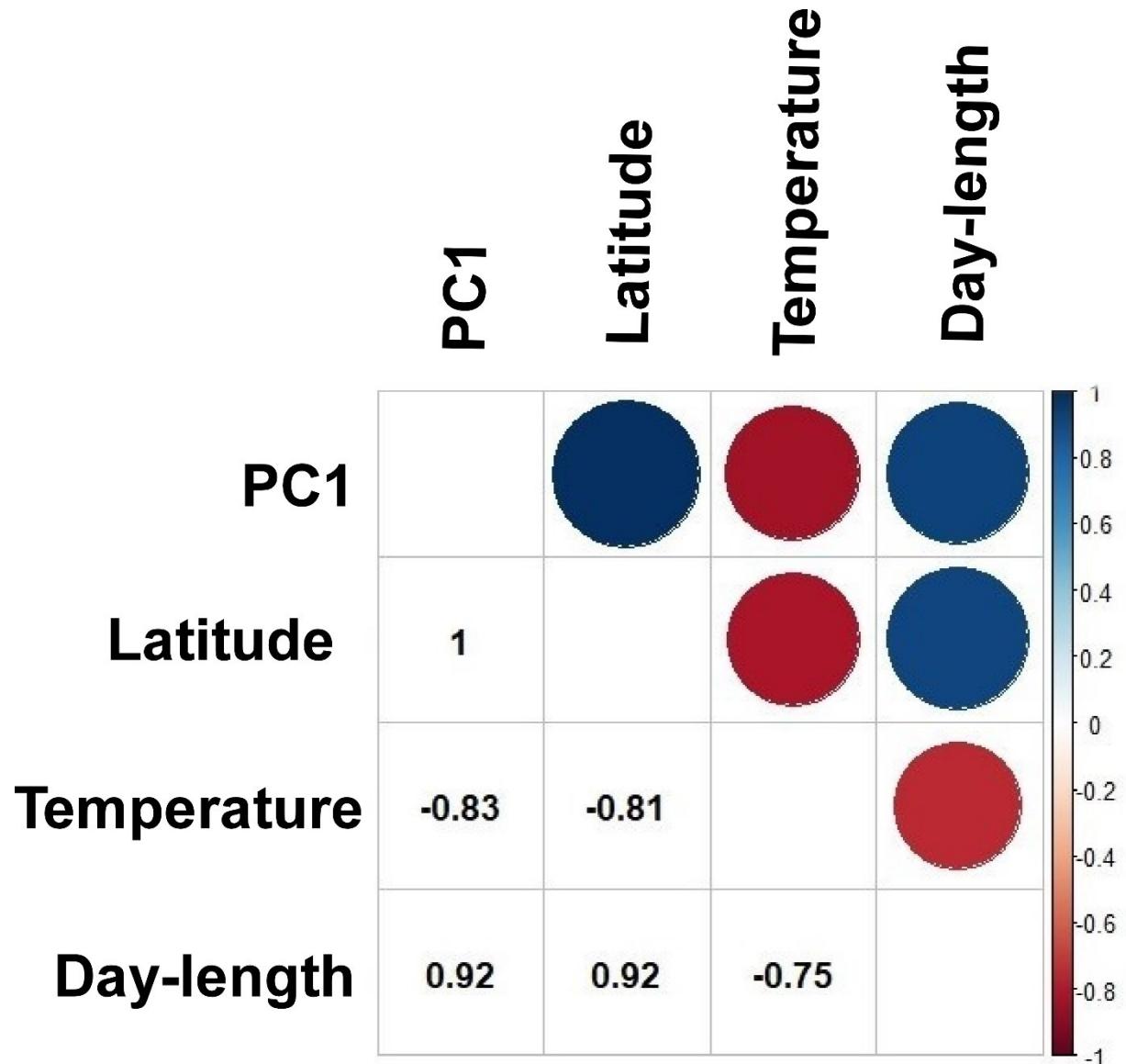
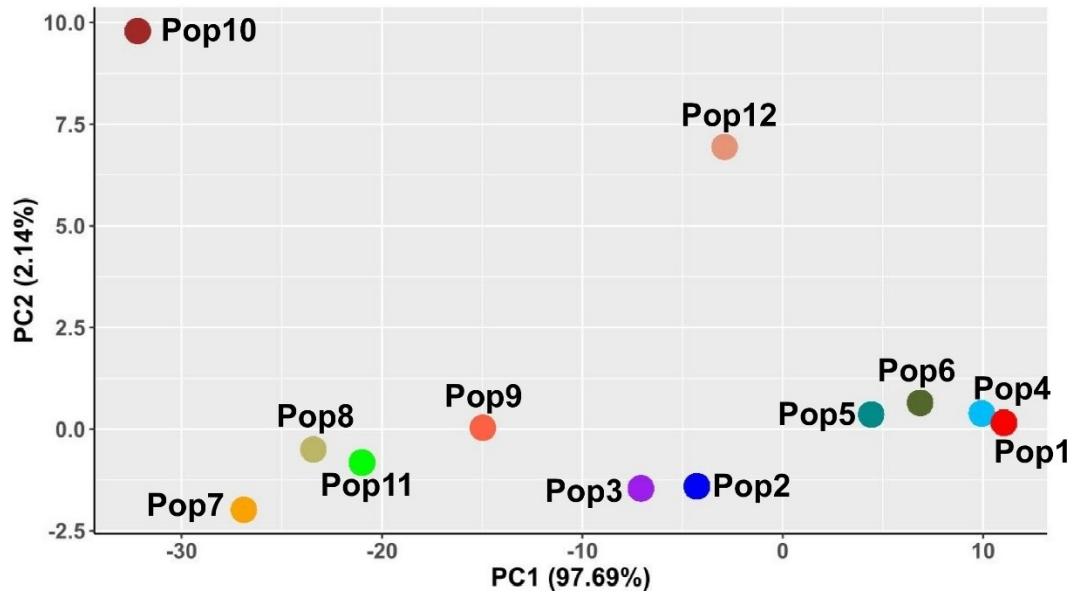


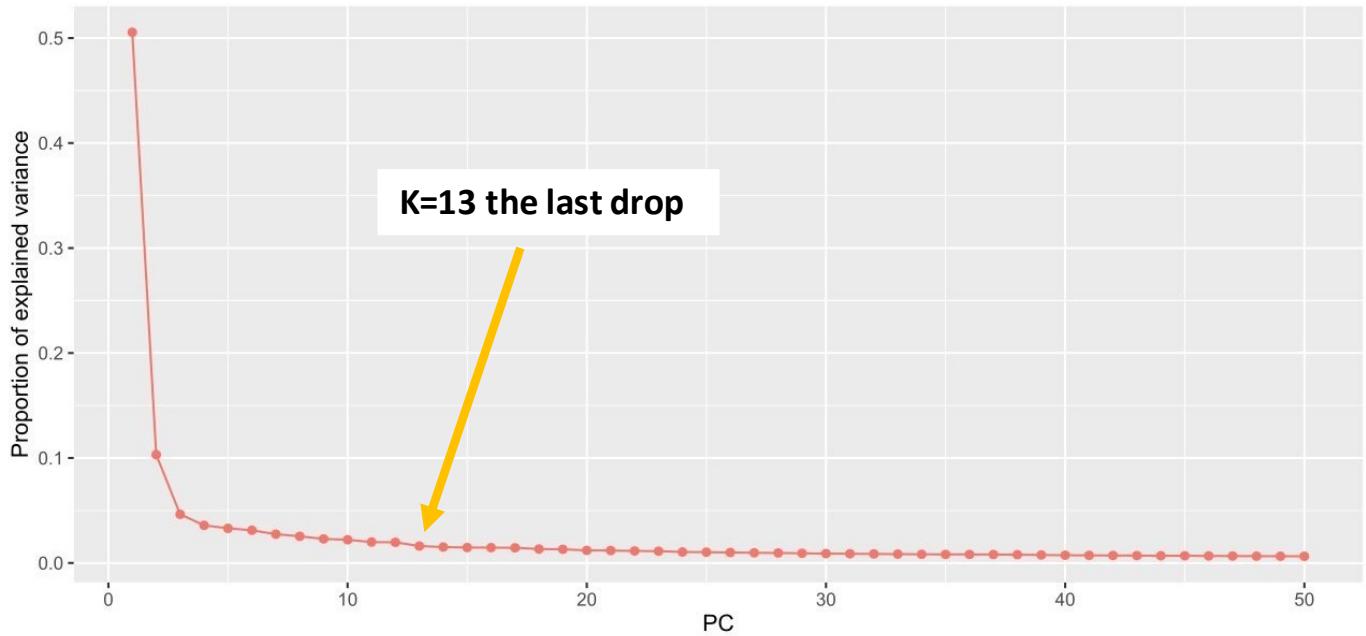
Supplementary Figs



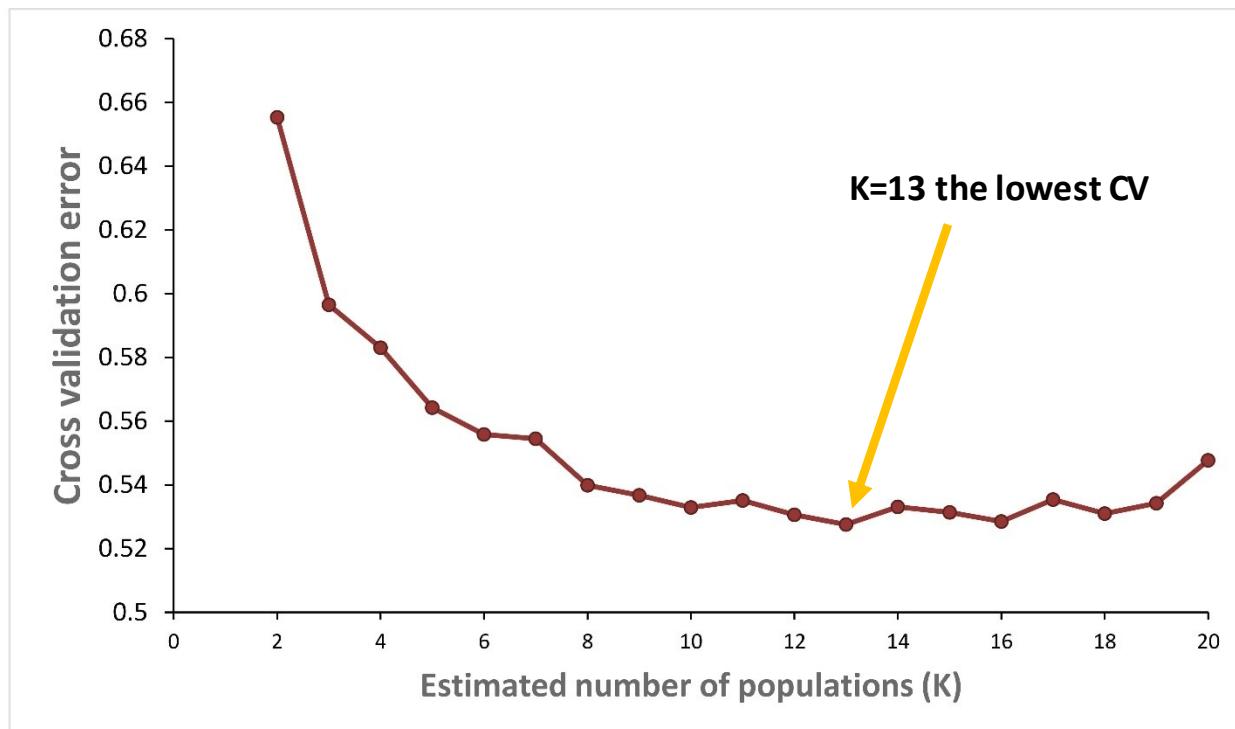
Supplementary Fig. 1. Correlation of environmental factors and their PC1 for latitude, temperature and daylength during the cropping seasons.



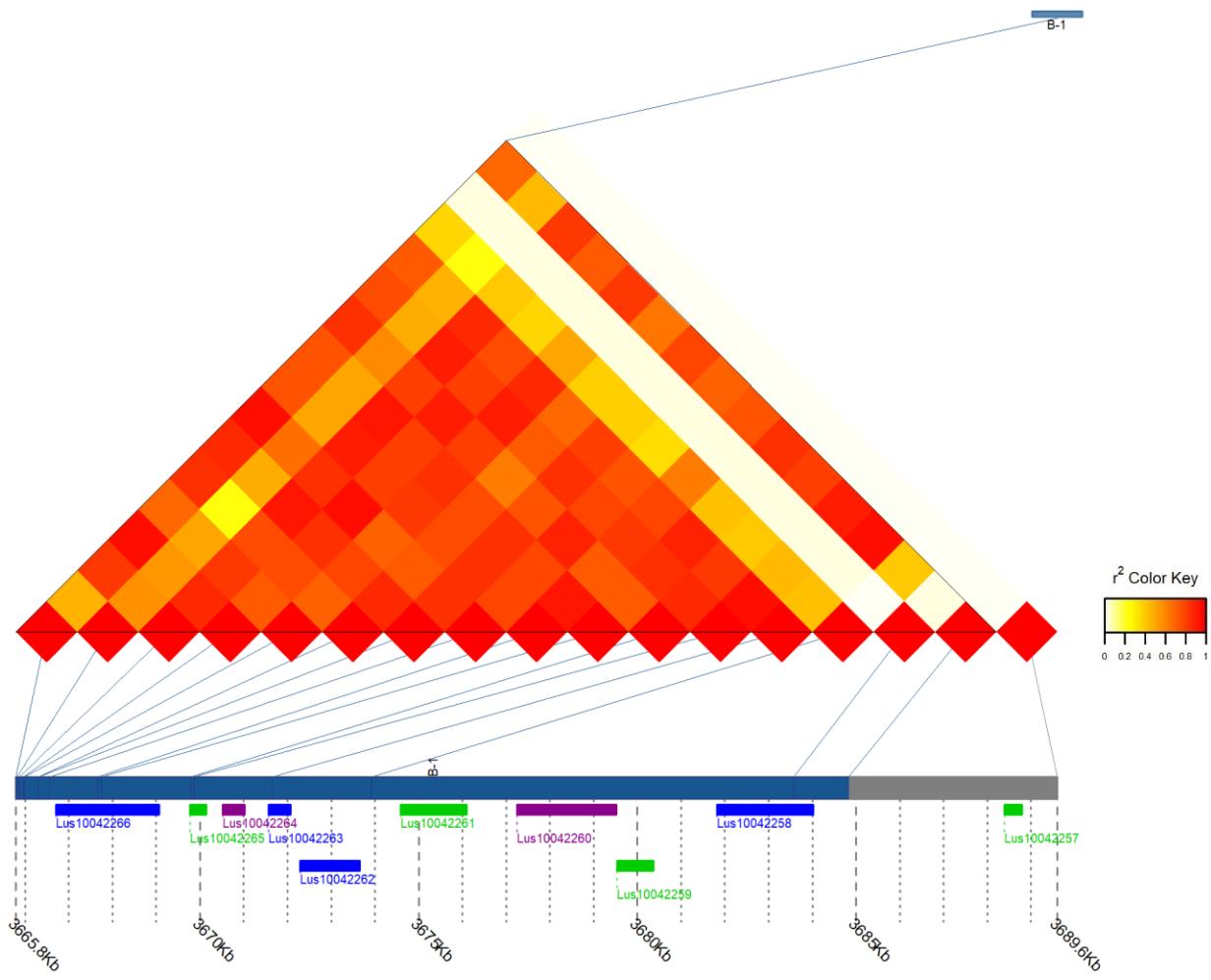
Supplementary Fig. 2. Principal component analysis (PCA) based on latitude, temperature and day-length of the cropping seasons. Values in parentheses indicate the percent variation explained by the principal components (PCs).



Supplementary Fig. 3. Appropriate number of populations (PC-based Kestimate). The K=13 appeared to have the last drop and hence K=12 is assumed to be the estimated number of populations.



Supplementary Fig. 4. Appropriate number of populations (K estimate using cross validation technique in AMIXTURE). The K=13 appeared to have the lowest error which is assumed to be the estimated number of populations



Supplementary Fig. 5. The linkage disequilibrium block at locus Chr1: 36558000-3689600 harboring six UGT87s tandem genes (Lus10042264, Lus10042263, Lus10042262, Lus10042261, Lus10042260, Lus10042259).

Supplementary Tables

Supplementary Table 1. Population and putative geographic origins .

Population	Country	Province	Reference for historical flax production	Locality	Latitude	Longitude
Pop1	Russia	Novgorod	Sherman H, 2008. From Flax to Linen in the Medieval Rus Lands In: Notherton R. and Owen-Crocker GR.(eds.) Medieval Clothing and Textile	Novgorod	56.2965	43.9361
Pop2	Georgia	Javakheti	Akhalkatsi, M., Ekhvaia, J., Asanidze, Z., 2012. Diversity and Genetic Erosion of Ancient Crops and Wild Relatives of Agricultural Cultivars for Food: Implications for Nature conservation in Georgia (Caucasus). In: Tiefenbacher, J., (ed). Perspectives on Nature Conservation – Patterns, Pressures and Prospects. InTech, Rijeka, Croatia, pp 51-92	The province	41.5479	43.7381
Pop3	Turkey	Anatolia	Ertug F., 2015. Linseed oil and oil mills in central Turkey Flax/Linum and Eruca, important oil plants of Anatolia	The province	39.0000	32.000
Pop4	Lithonia	Lithonia	Jankauskien Z., Bačelis K.2008. The new Lithuanian fibre flax variety 'SNAIGIAI'. Latvian Journal of Agronomy 11:67-72	Lithonia	55.1694	23.8813
Pop5	Czech Republic	Bohemia	Strida M. 1985.The influence of flax production in the giant mountains region upon the textile location in Behemia.	Bohemia	49.8175	15.473
Pop6	Canada	Saskatchewan	MacCracken J.A., 1916. A review of the status and possibilities of flax production and manipulation in Canada; Dominion of Canada, Department of Agriculture Hon. Martin Burrell, Minister of Agriculture, Ont. Ottawa	Saskatoon	52.133	-106.67
Pop7	India	Maharashtra	Gill, K.S., 1987. Linseed. Indian council of agricultural research. New Delhi, India. 386 pp.	Aurangabad	19.8762	75.3433
Pop8	India	Madhya Pradesh	Gill, K.S., 1987. Linseed. Indian council of agricultural research. New Delhi, India. 386 pp.	Sukha	22.9734	78.6569

Population	Country	Province	Reference for historical flax production	Locality	Latitude	Longitude
Pop9	Pakistan	Punjab	Amjad, M., 2014. Oilseeds crops of Pakistan. Pakistan agricultural research council, plant sciences division. Islamabad, Pakistan.	Faisalabad	31.1704	72.7097
Pop10	Ethiopia	Amhara	Central statistical agency of Ethiopia, 2013. Area and production of major crops, Addis Ababa, Ethiopia	Lalibela	12.0309	39.0476
Pop11	India	Uttar-Pradesh	Gill, K.S., 1987. Linseed. Indian council of agricultural research. New Delhi, India. 386 pp.	Allahabad	25.4458	81.8463
Pop12	Portugal	Minho	Neto M.S., 2016. Conflicts and decline, 1620-1703. In: Freire, D., Lains, P.(Eds.), an agrarian history of Portugal, 1000-2000 : economic development on the European frontier, Brill, Boston pp 101-131	Braga	41.5511	-8.4283

Supplementary Table 2. Private haplotypes harbored in three or more individuals.

Population	Private haplotype	Frequency within subpopulations (%)	Frequency within the overall population (%)
Pop3	Chr3:Hap1	40.00	3.64
	Chr5:Hap1	18.92	1.82
	Chr11:Hap1	8.57	0.78
Pop5	Chr3:Hap2	7.69	0.78
Pop8	Chr4:Hap1	44.44	1.04
	Chr9:Hap1	33.33	0.78
	Chr12:Hap1	33.33	0.78
	Chr13:Hap1	33.33	0.78
Pop9	Chr8:Hap1	71.43	1.30
Pop10	Chr1:Hap1	57.14	1.04
	Chr2:Hap1	71.43	1.30
	Chr10:Hap1	100.00	1.82
	Chr11:Hap2	85.71	1.56
	Chr12:Hap2	57.14	1.04
	Chr13:Hap2	100.00	1.82
Pop11	Chr1:Hap2	14.71	1.30
	Chr2:Hap2	8.82	0.78
	Chr2:Hap3	58.82	5.19
	Chr2:Hap4	8.82	0.78
	Chr3:Hap3	47.06	4.16
	Chr3:Hap4	8.82	0.78
	Chr4:Hap2	52.94	4.68
	Chr4:Hap3	8.82	0.78
	Chr5:Hap2	70.59	6.23
	Chr7:Hap1	88.24	7.79
	Chr10:Hap2	82.35	7.27
	Chr12:Hap3	76.47	6.75
	Chr13:Hap3	8.82	0.78
	Chr14:Hap1	97.06	8.57
Pop12	Chr2:Hap5	42.86	0.78

Supplementary Table 3. Outlier loci of signatures for adaptation and their candidate genes proposed based on the annotation of their *Arabidopsis* orthologs.

Outlier locus ¹	Dataset ²	Method ³	Candidate gene	Candidate gene position	Arabidopsis ortholog	Gene product
Chr1:5466653 (1-1)	1,2,3	PC, F _{ST}	Lus10011967	5444945-5448479	AT4G18130	PHYE
Chr1: 8153987 (1-3)	1	F _{ST}	Lus10035570	8161477- 8163952	AT5G03680	PTL
Chr1:10413007 (1-2)	1,2,3	PC, F _{ST}	Lus10022628	10391933-10394080	AT2G36780	UGT73C3
			Lus10022627	10394469-10394831	AT2G36800	UGT73C5
Chr1:3669787	3	F _{ST}	Lus10042264	3670524-3671021	AT2G30140	UGT87A2
Chr1:3668590	3	F _{ST}	Lus10042263	3671574-3672074	AT2G30140	UGT87A2
			Lus10042262	3672286-3673654	AT2G30150	UGT87A1
			Lus10042261	3674591-3676105	AT2G30140	UGT87A2
			Lus10042260	3677249-3679513	AT2G30140	UGT87A2
			Lus10042259	3679540-3680369	AT2G30140	UGT87A2
Chr3:21893053 (3-1)	1,2	PC, F _{ST}	Lus10023069	21877049-21878326	AT1G64480	CBL8
Chr6:4608251 (6-1)	3	F _{ST}	Lus10032586	4607496-4614198	AT4G26590	OPT5
Chr6:2060851 (6-2)	3	F _{ST}				
Chr6:1640065 (6-3)	3	F _{ST}				
Chr7:10407650 (7-1)	1,2	PC, F _{ST}	Lus10000371	10375359-10375742	AT1G17455	ELF4-L4
Chr7:6193339 (7-2a)	1,3	PC, F _{ST}	Lus10035484	6173436-6176207	AT1G63690	SPPL2
Chr7:6194202 (7-2b)	1,3	PC, F _{ST}	Lus10035485	6181237-6181966	AT1G63690	SPPL2
Chr7:5688679 (7-3)						
Chr8:2932993 (8-1)	1,2,3	PC, F _{ST}	Lus10012356	2916416-2917586	AT3G07870	FBX92
			Lus10012357	2917692-2918078	AT3G07870	FBX92
			Lus10012358	2919119-2920648	AT3G07870	FBX92
Chr8:20674643 (8-2)	1,2	PC, F _{ST}	Lus10024706	20671439-20671648	AT5G25610	RD22
Chr8:21168573 (8-3)	1,2,3	PC, F _{ST}				
Chr9:9316330 (9-1)	1,2,3	PC, F _{ST}				
Chr10:8866967 (10-1)			Lus10039971	8888401-8891236	AT2G12550	NUB1
			Lus10039972	8915052-8917138	AT5G35080	OS9
Chr11:16356168 (11-1)	1,2	PC, F _{ST}	Lus10009925	16347024-16350652	AT2G30360	CIPK11,SNRK3
			Lus10009926	16352838-16353850	AT3G58170	BS14A

			Lus10009928	16371145-16374252	AT2G38290	AMT2
Chr11:7085390 (11-2)	1	F _{ST}				
Chr12:6648172 (12-1)	1,2	PC, F _{ST}	Lus10000500	6658543-6659097	AT2G47770	TSPO
			Lus10000501	6660424-6661533	AT4G15802	HSBP
			Lus10000502	6663419-6663787	AT4G15800	RALFL33
Chr12:15557091 (12-2)	1,2,3	PC, F _{ST}				
Chr13:2709522 (13-1)	1,3	PC, F _{ST}	Lus10006830	5416843-5418512	AT1G17070	STIPL1
Chr14:5404030 (14-1)	1,2	PC, F _{ST}	Lus10006831	5418618-5418878	AT1G17070	STIPL1

¹ Chromosome number: position; numbers in parenthesis indicate the code in Fig. 4

² Datasets 1 = 277K, 2 = 23K and 3 = 34K-exon

³ PC = Principal component from pcadapt; F_{ST} = Fixation index