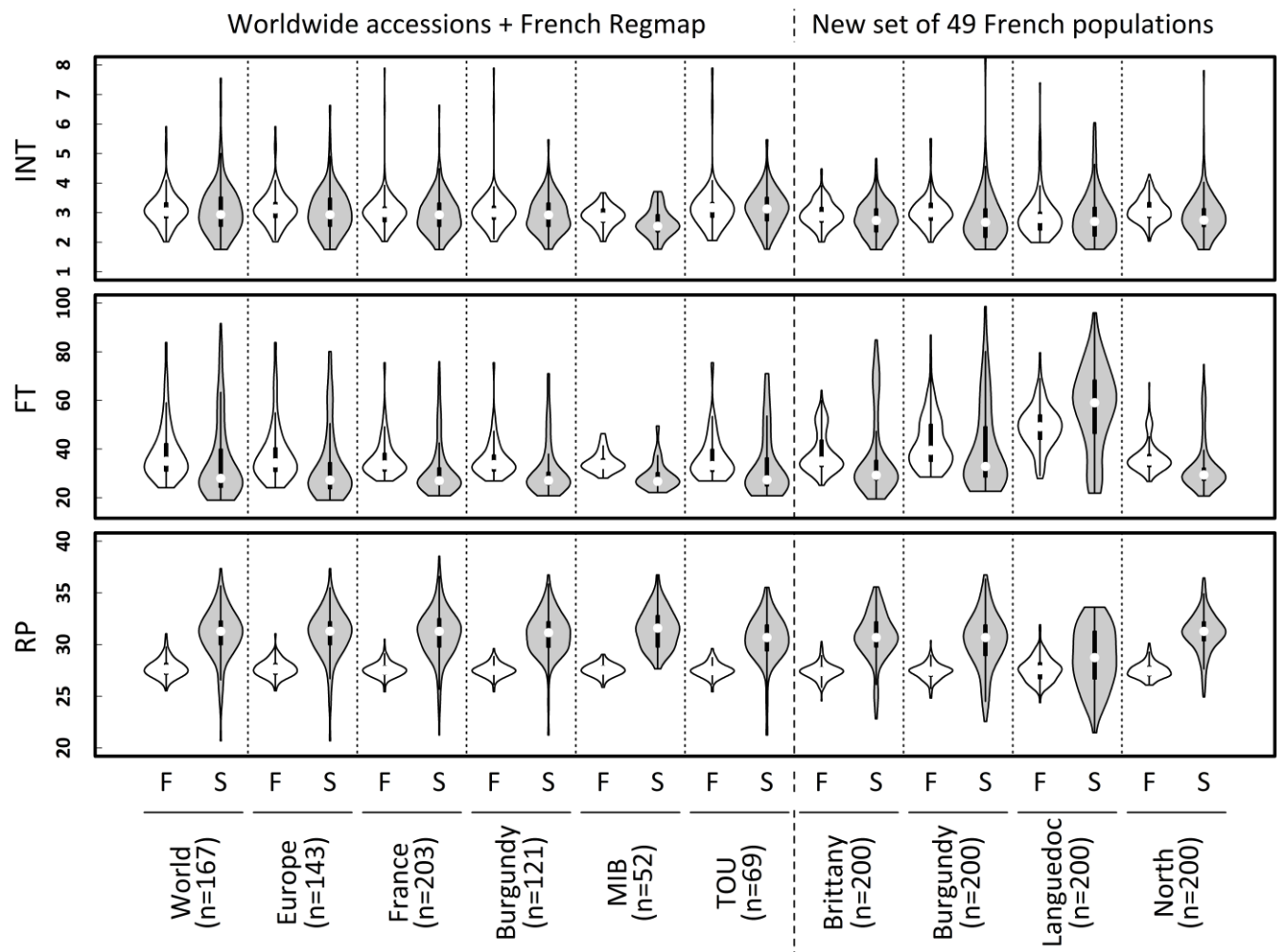


Figure S1. Violin plots of natural variation for the interval between bolting and flowering (INT), flowering time (FT) and reproductive period (RP). White circles indicate the median value and height corresponds to the interquartile range, with the width representing the probability density of the data at different values. INT, FT and RP are expressed in days. ‘F’ and ‘S’ denote Fall and Spring germination cohorts, respectively. Violin plots are based on BLUPs calculated for each of the 352 natural accessions or 800 families.



temperature ($^{\circ}\text{C} \times 10$); **Bio 2**, mean diurnal range (mean of monthly temperature range (max temp - min temp)); **Bio 3**, isothermality ($\text{Bio 2}/\text{Bio 7} \times 100$); **Bio 4**, temperature seasonality (standard deviation $\times 100$); **Bio 5**, max temperature of warmest month ($^{\circ}\text{C} \times 10$); **Bio 6**, min temperature of coldest month ($^{\circ}\text{C} \times 10$); **Bio 7**, temperature annual range ($\text{Bio 5} - \text{Bio 6}$); **Bio 8**, mean temperature of wettest quarter ($^{\circ}\text{C} \times 10$); **Bio 9**, mean temperature of driest quarter ($^{\circ}\text{C} \times 10$); **Bio 10**, mean temperature of warmest quarter ($^{\circ}\text{C} \times 10$); **Bio 11**, mean temperature of coldest quarter ($^{\circ}\text{C} \times 10$); **Bio 12**, annual precipitation (mm); **Bio 13**, precipitation of wettest month (mm); **Bio 14**, precipitation of driest month (mm); **Bio 15**, precipitation seasonality (coefficient of variation); **Bio 16**, precipitation of wettest quarter (mm); **Bio 17**, precipitation of driest quarter (mm); **Bio 18**, precipitation of warmest quarter (mm); **Bio 19**, precipitation of coldest quarter (mm).

Edaphic variables: **OC**, organic carbon (g.kg^{-1}); **N**, total nitrogen (g.kg^{-1}); **C/N**, carbon/nitrogen ratio; **SOM**, soil organic matter (g.kg^{-1}); **P2O5**, phosphorus (P_2O_5) (g.kg^{-1}); **Ca**, exchangeable calcium (cmol+.kg^{-1}); **Mg**, exchangeable magnesium (cmol+.kg^{-1}); **Na**, exchangeable sodium (cmol+.kg^{-1}); **K**, exchangeable potassium (cmol+.kg^{-1}); **Fe**, exchangeable iron (cmol+.kg^{-1}); **Mn**, exchangeable manganese (cmol+.kg^{-1}); **Al**, exchangeable aluminium (cmol+.kg^{-1}); **WHC**, soil water holding capacity (ml.g^{-1}); **pH**.

Competition variables: **Herb**, interspecific competition with herbs which are not grasses; **Grass**, interspecific competition with grasses; **Thal**, intraspecific competition.

Figure S3. Box-and-whiskers plots of ecological variation in French stands. In brackets, significance of the ‘Region’ effect after Bonferroni correction (***: $P < 0.001$, **: $P < 0.01$, *: $P < 0.05$, ns: $P > 0.05$) and percentage of ecological variance explained by the ‘Region’ effect. See legends of Figure S2 for description of the variables.

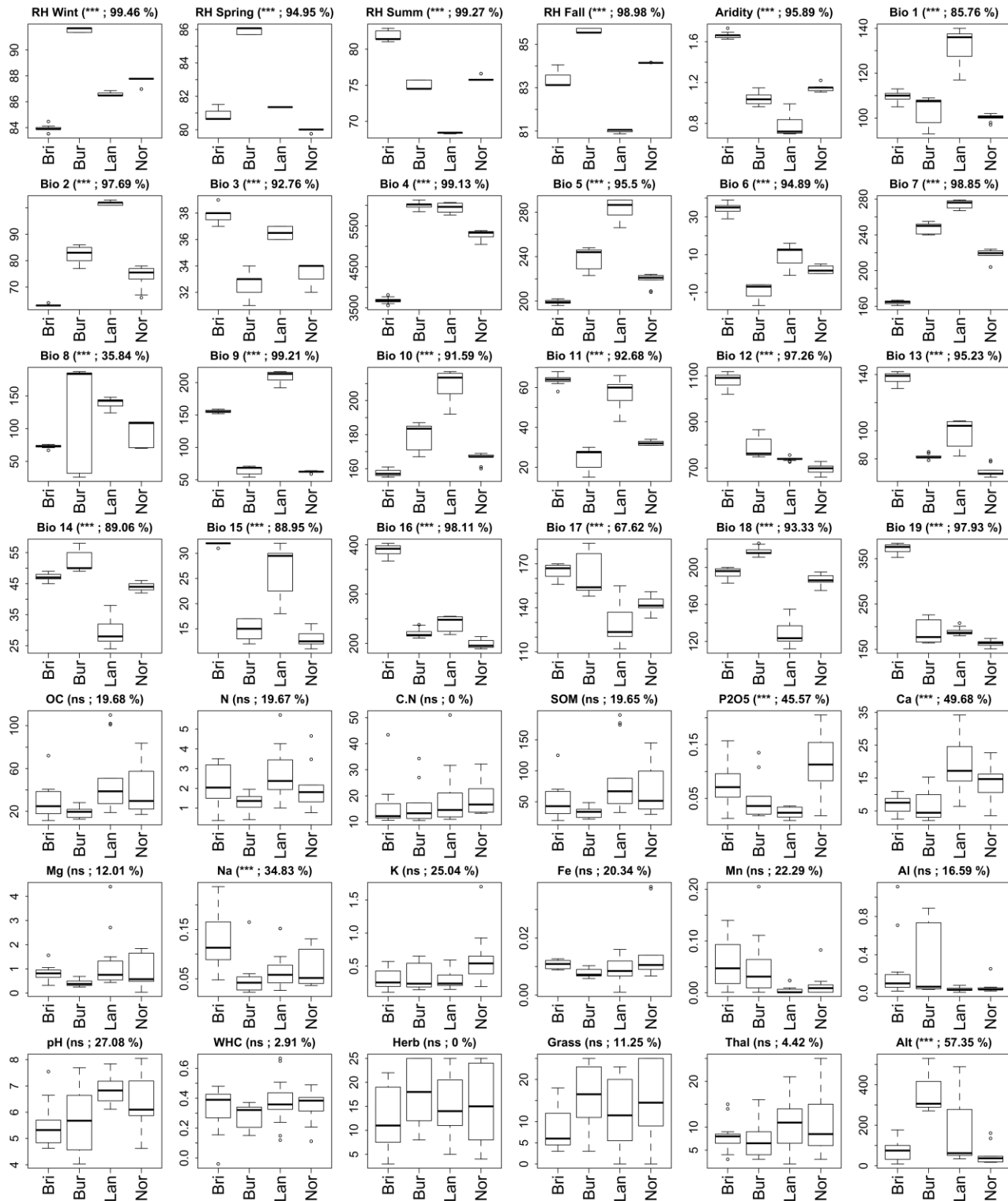
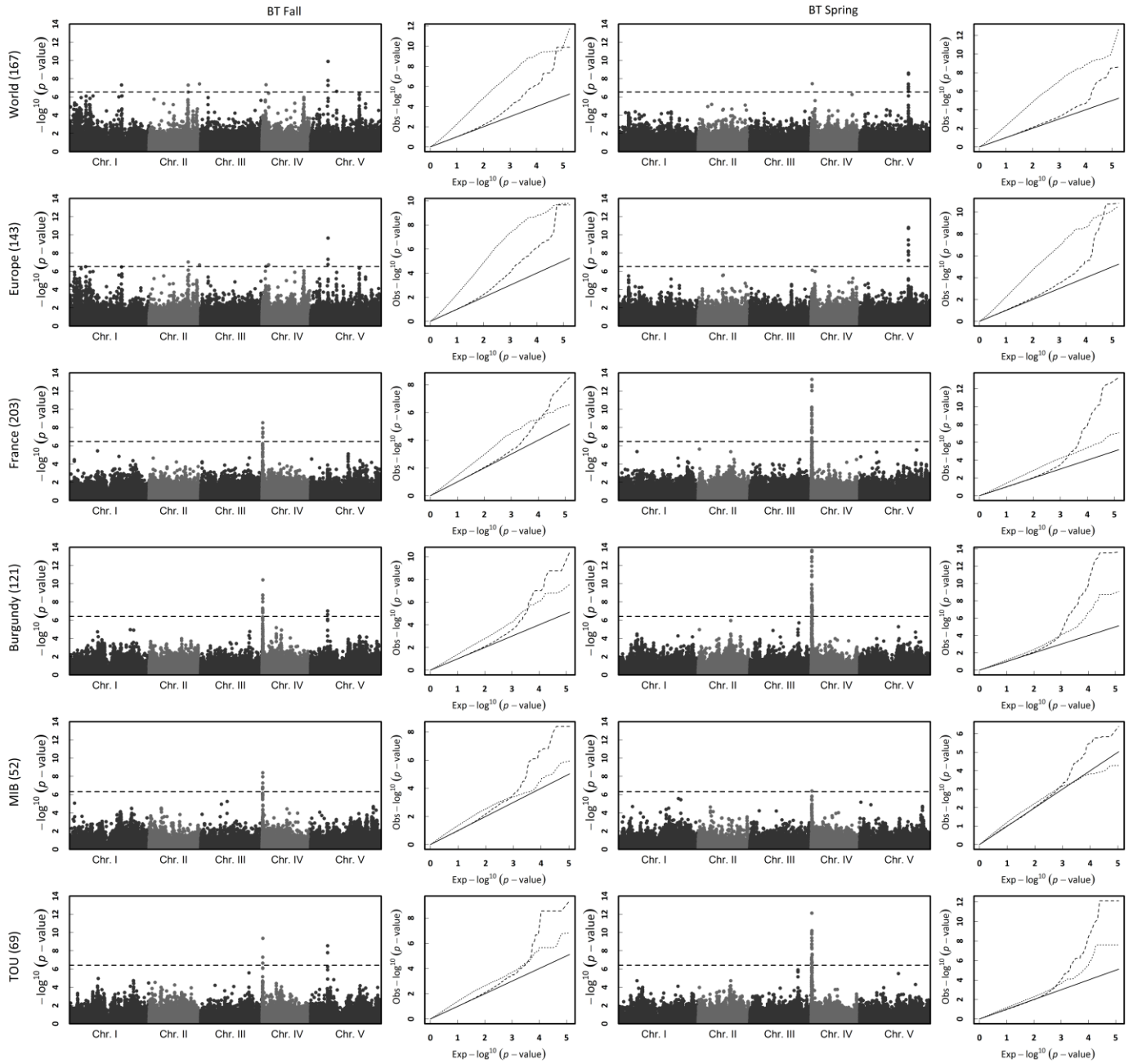


Figure S4. Manhattan plots of the genome-wide association mapping (EMMAX) results and quantile-quantile plot of p-values (negative logarithm, Wilcoxon and EMMAX) for BT, INT, FT, FP, RP and FRR in each cohort and at different geographic scales.



Manhattan plots: The x -axis indicates the position along each chromosome. The five chromosomes are presented in a row along the x -axis in different shades of grey. The y -axis indicates the $-\log_{10} p$ -values using the EMMAX method. The dashed line denotes the Bonferroni threshold. MARF > 10%.

Quantile-quantile plots: The different curves of the Q-Q plots correspond to different analyses of GWA mapping. Solid line: expected; dotted line: Wilcoxon with minor allele relative frequency (MARF) > 10%; dotted line: EMMAX with MARF > 10%.

Figure S4. (continued)

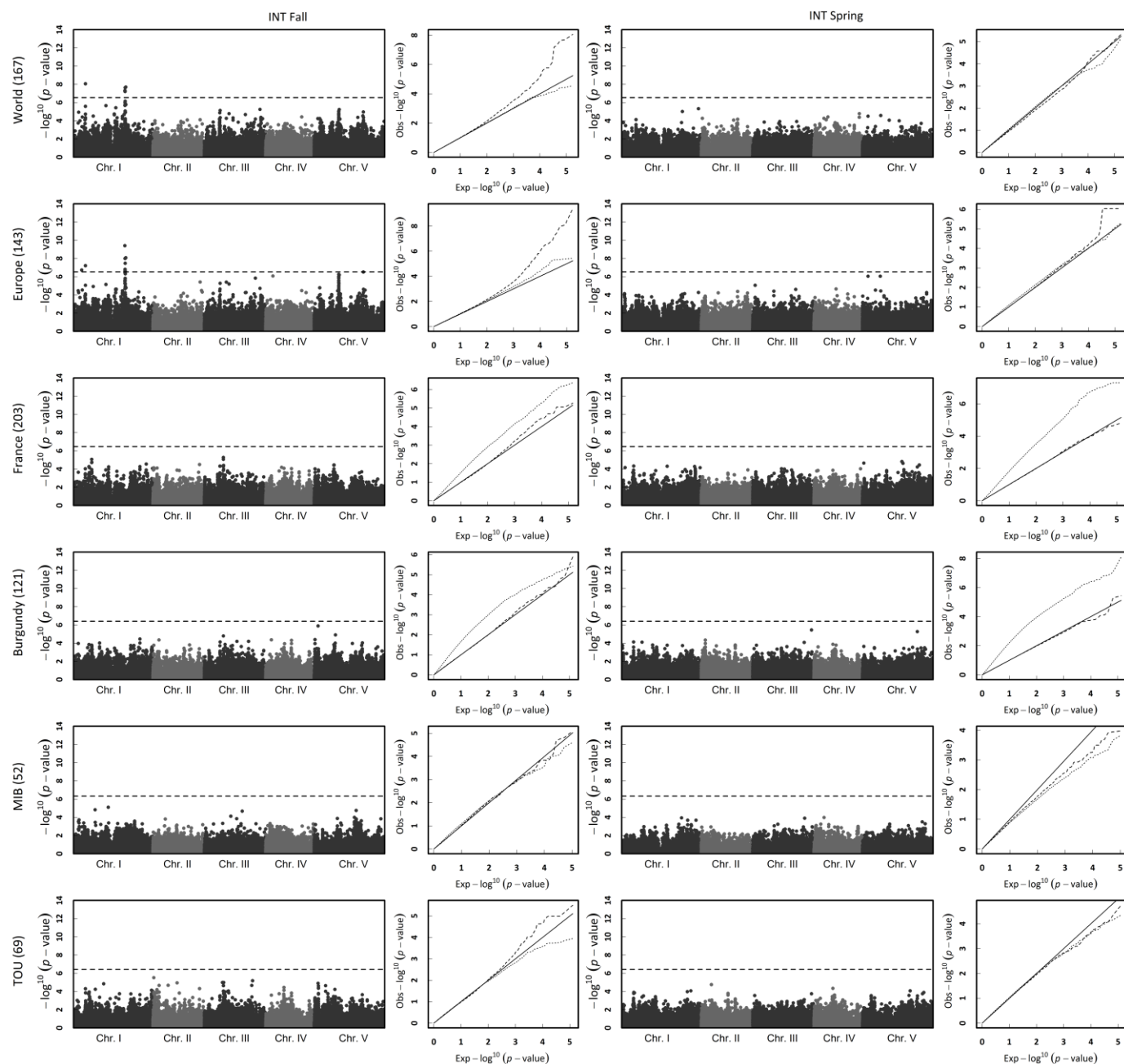


Figure S4. (continued)

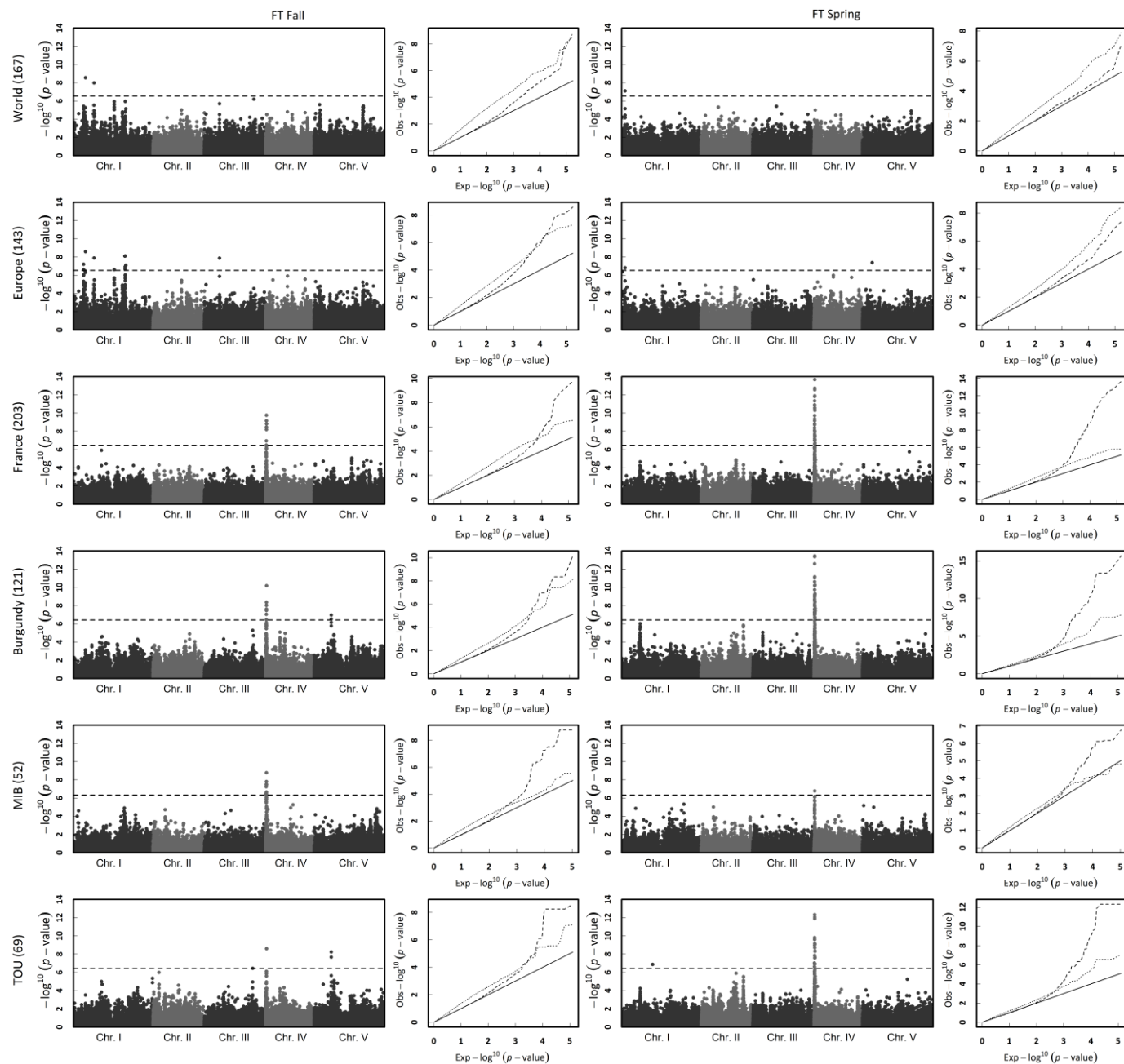


Figure S4. (continued)

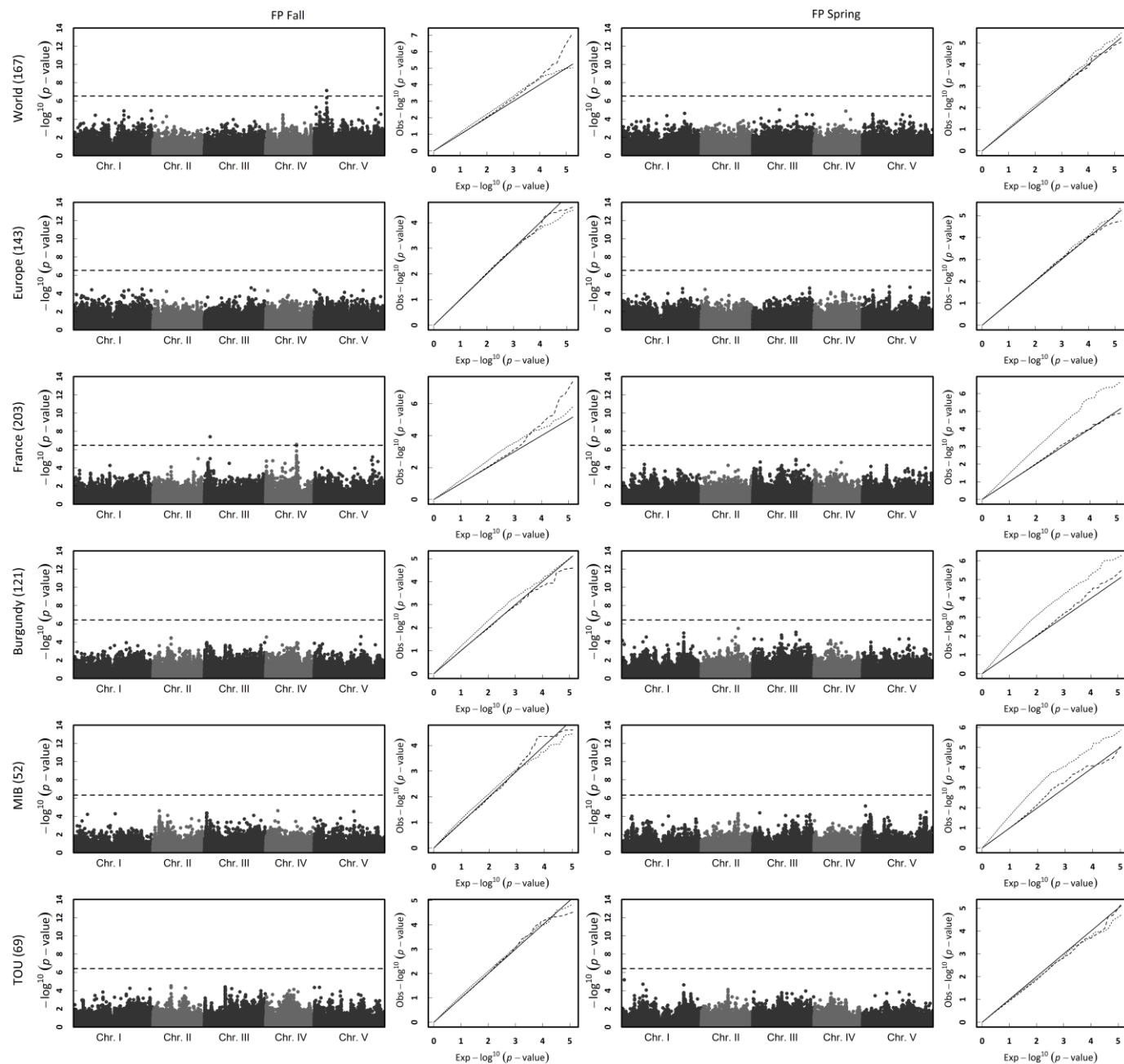


Figure S4. (continued)

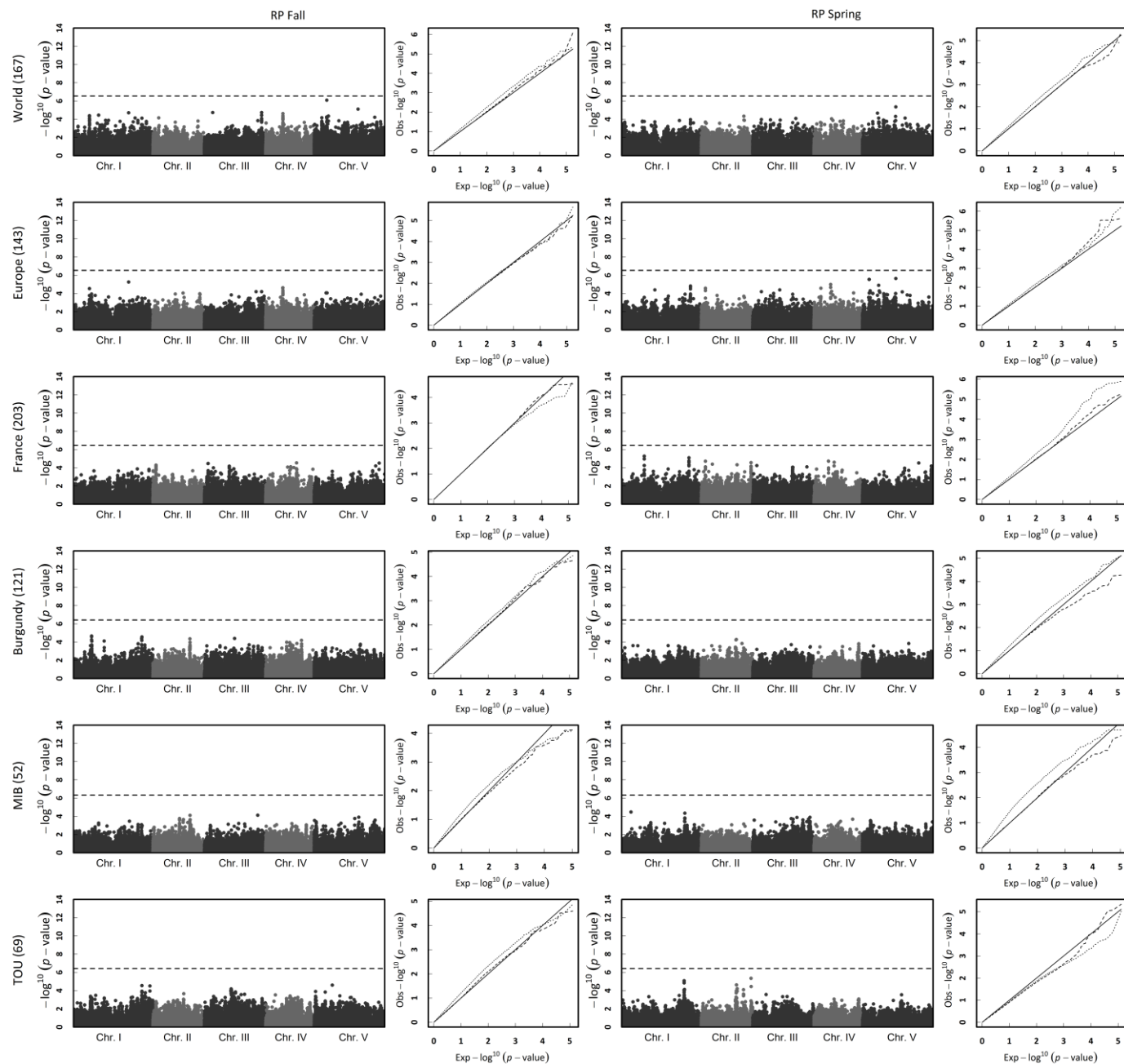


Figure S4. (continued)

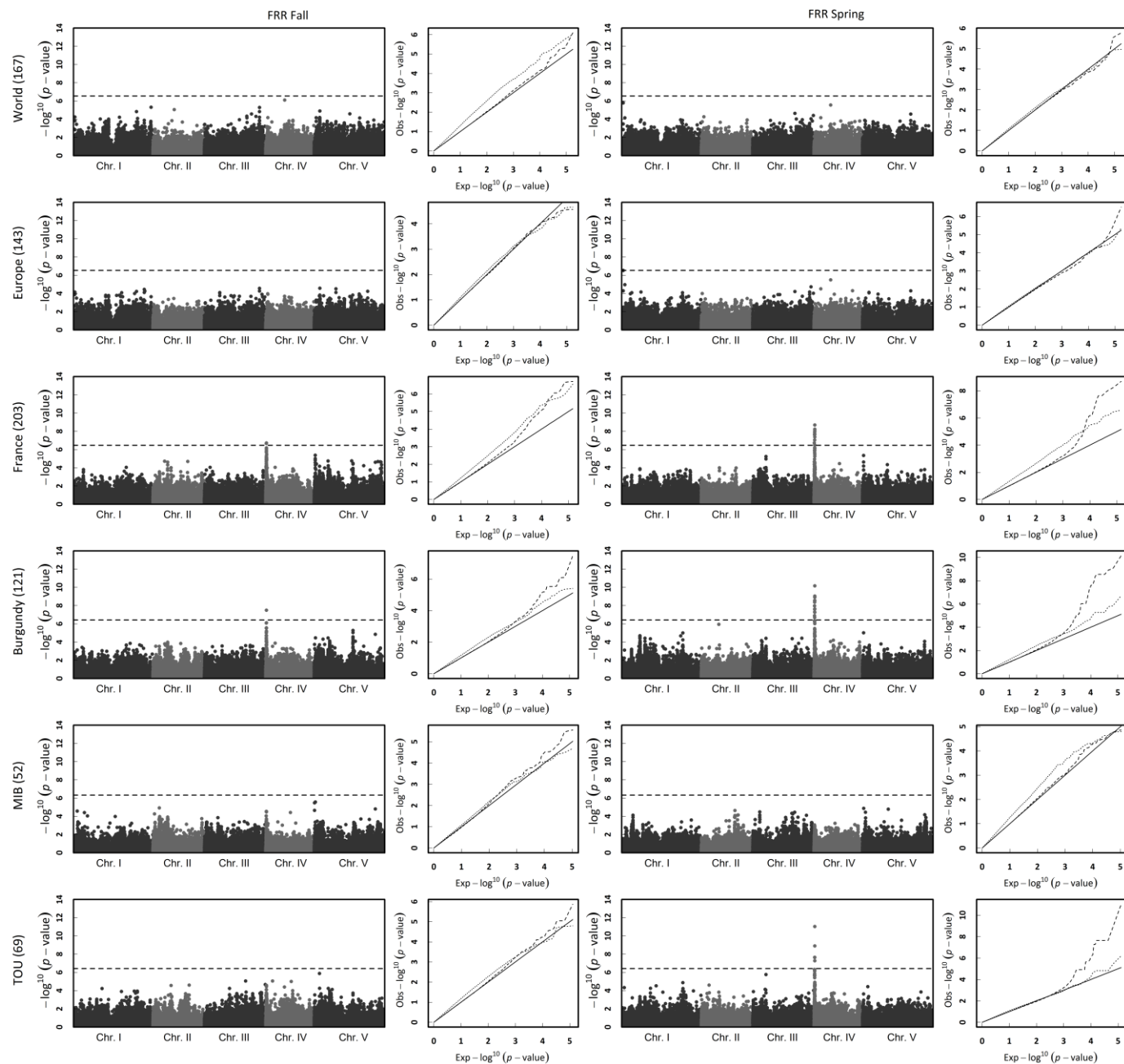


Figure S5. Close up of the association peaks at the beginning of chromosome 5 (left) and around *FRIGIDA* (right) at three different geographical scales for bolting time. Moccasin colored area indicates the genomic position of *FRIGIDA*. Method = EMMAX, MARF > 10%.

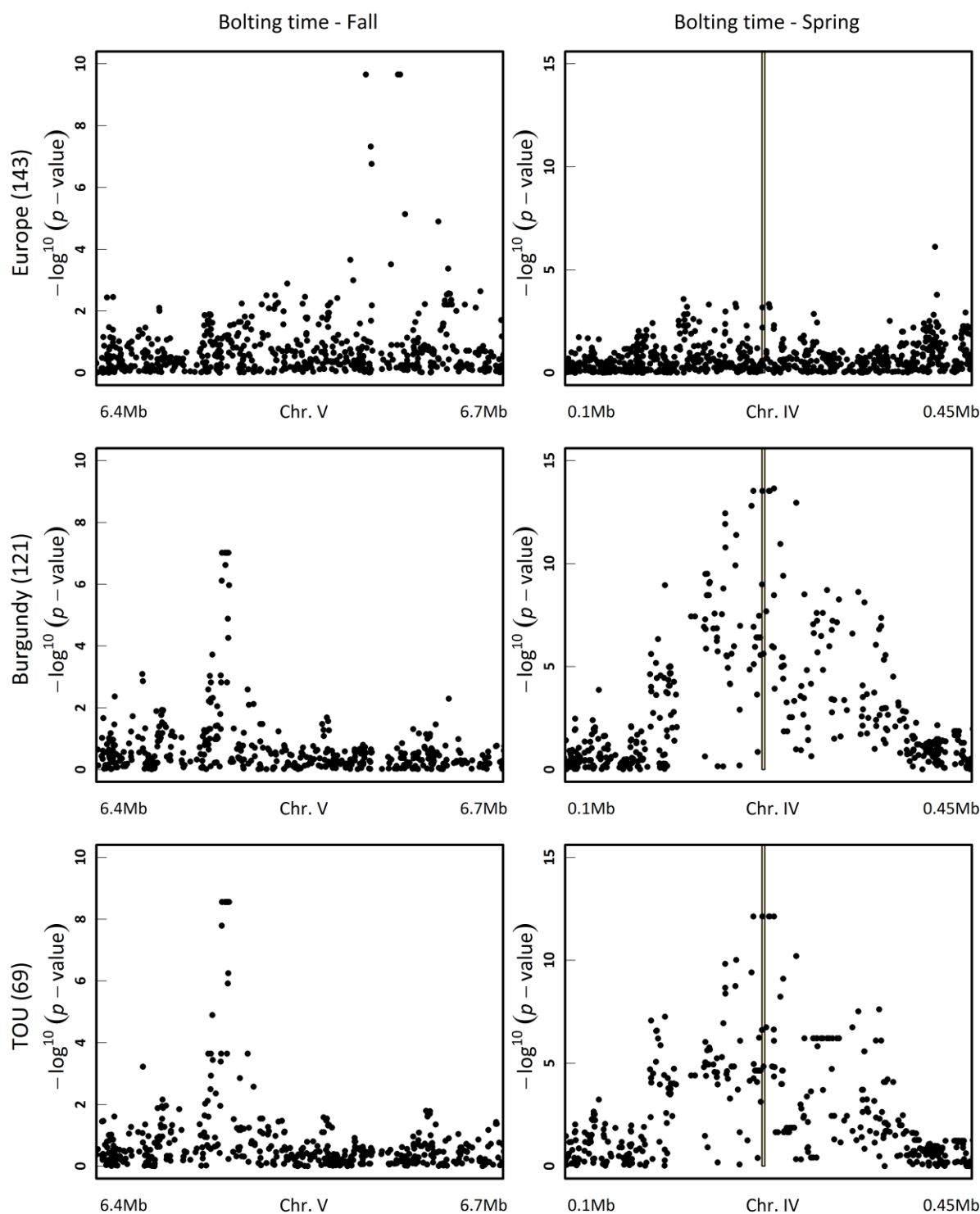


Table S1: Plant material.**A. French stands**

Stand	Region	Town	Latitude	Longitude	Habitat	Sub-habitat	Families (N)	149 SNPs ^a
CIRY	Burgundy	Ciry-le-Noble	46°36.257'N	4°17.971'E	grassland	railway station	21	17
CON	Burgundy	Conforgien	47°14.011'N	4°11.893'E	grassland	river bank	20	20
ETA-1	Burgundy	Etang sur Arroux	46°52.060'N	4°11.078'E	grassland	railway station	10	10
ETA-2	Burgundy	Etang sur Arroux	46°52.060'N	4°11.078'E	hoed land	railway station	10	8
LIE	Burgundy	Liernais	47°12.879'N	4°16.036'E	grassland	parking lot	20	18
MAR-3	Burgundy	Marigny l'Eglise	47°21.333'N	3°56.183'E	grassland	roadside	20	20
MAR-4	Burgundy	Marigny l'Eglise	47°21.356'N	3°56.024'E	meadow	perennial meadow	18	18
MOL	Burgundy	Saint- Léger sous Beauvray	46°54.732'N	4°06.425'E	meadow	meadows-footpath	20	19
RAD	Burgundy	Sainte-Radegonde	46°41.010'N	4°04.982'E	meadow	perennial meadow	23	22
TOU-J2	Burgundy	Toulon sur Arroux	46°39.060'N	4°06.466'E	hoed land	perennial meadow	21	21
TOU-M1	Burgundy	Toulon sur Arroux	46°39.071'N	4°06.758'E	hoed land	meadows-footpath	17	17
ABA	Brittany	Abaty	48° 16.599'N	4° 11.367'W	grassland	courtyard	20	19
BRE	Brittany	Brendaouez	48° 36.909'N	4° 25.129'W	grassland	roadside, along a stone wall	22	22
DIR-2.8	Brittany	Dirinon	48° 23.571'N	4° 17.134'W	grassland	railway station	11	11
DIR-8.5	Brittany	Dirinon	48° 23.571'N	4° 17.134'W	grassland	railway station	11	10
FOR	Brittany	La Forest Landerneau	48° 25.560'N	4° 18.413'W	meadow	parking lot	20	19
MIL	Brittany	Milizac	48° 28.176'N	4° 33.526'W	meadow	roadside	20	16
PLO	Brittany	Plougastel-Daoulas	48° 21.839'N	4° 22.348'W	hoed land	garden	20	20
PLY	Brittany	Ploudiry	48°27.502'N	4° 8.383'W	hoed land	perennial meadow	14	14
ROC	Brittany	La Roche Maurice	48° 28.450'N	4° 12.269'W	grassland	railway station	20	20
RUM	Brittany	Rumiqueal	48° 38.989' N	4° 21.607'W	hoed land	roadside	23	23
TRE	Brittany	Treflaouenan	48° 37.868'N	4° 5.047'W	hoed land	cultivated field	19	19
ARR-1	Languedoc	Arrigas	43° 59.254'N	3° 28.813' E	meadow	river bank	7	7
ARR-2	Languedoc	Arrigas	43° 59.254'N	3° 28.813' E	meadow	river bank	7	7
ARR-3	Languedoc	Arrigas	43° 59.254'N	3° 28.813' E	meadow	river bank	7	7
BEZ	Languedoc	Bez et Esparon	43° 58.551'N	3° 31.895' E	grassland	roadside	21	21
ISS	Languedoc	Issensac	43° 50.296'N	3° 42.036'E	grassland	clearing in forest (<i>Quercus ilex</i>)	6	3

Stand	Region	Town	Latitude	Longitude	Habitat	Sub-habitat	Families (N)	149 SNPs ^a
LEC	Languedoc	Lecques	43° 50.280'N	4° 04.259' E	grassland	waste ground	20	20
MOU1-1	Languedoc	Moussac 1	43° 57.694'N	4° 14.900'E	grassland	river bank -fluvial deposit	7	7
MOU1-2	Languedoc	Moussac 1	43° 57.694'N	4° 14.900'E	grassland	river bank -fluvial deposit	9	9
MOU1-3	Languedoc	Moussac 1	43° 57.694'N	4° 14.900'E	meadow	river bank -fluvial deposit	4	4
MOU2	Languedoc	Moussac 2	43° 58.064'N	4° 14.265'E	hoed land	cultivated field	22	22
NOZ	Languedoc	Nozières-Brignon	43° 58.548'N	4° 12.474'E	grassland	railway station	20	18
PCH	Languedoc	Puechredon	43° 57.500'N	4° 02.603' E	grassland	garrigue	10	4
QUI	Languedoc	Quissac	43° 54.600' N	4° 00.285' E	grassland	waste ground (railway station)	20	20
SAL	Languedoc	Salinelles	43° 47.646'N	4° 04.462' E	grassland	rocky hillside	20	20
VED	Languedoc	St Jean de Vedas	43° 33.686'N	3° 49.268' E	grassland	garrigue	8	5
VEN	Languedoc	Vendargue	43° 39.259'N	3° 57.657' E	grassland	railway	12	12
BAU	North	Bauvin	50° 30.358'N	2° 54.095'E	grassland	railway	20	20
BRI	North	Brillon	50° 25.947'N	3° 19.719'E	hoed land	flower bed	21	21
CAT-S	North	Mont des Cats	50° 47.010'N	2° 40.101'E	hoed land	perennial meadow	20	19
CAT-T	North	Mont des Cats	50° 46.904'N	2° 39.961'E	hoed land	roadside	20	18
ENC-1	North	Mont de l'Enclus	50° 45.195'N	3° 29.501'E	hoed land	roadside	21	21
ENC-2	North	Mont de l'Enclus	50° 45.400'N	3° 28.480'E	hoed land	roadside	21	21
ESP1	North	Esplechin	50° 34.569'N	3° 18.601'E	meadow	perennial meadow	11	11
ESP2	North	Esplechin	50° 34.569'N	3° 18.601'E	hoed land	meadow, old gravel deposit	11	11
GEN	North	Genech	50° 32.217'N	3° 13.283'E	hoed land	cultivated field	15	15
LCL	North	Lecelles	50° 28.021'N	3° 24.222'E	grassland	roadside	20	20
WAV	North	Wavrin	50° 33.366'N	2° 55.251'E	hoed land	garden	20	19

^a Number of families genotyped for 149 SNPs

B. Worldwide accessions and French accessions from the French RegMap panel
(<http://bergelson.uchicago.edu/>).

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100000	WORLD,EUROPE

^a Accession identities have been retrieved from Horton *et al.* (2012).

^b Six different geographical scales. Grey cases correspond to natural accessions that were likely to be contaminants, *i.e.* accessions for which geographical origin is suspicious (Anastasio *et al.* 2011).

Table S2. List of the 328 *a priori* candidate genes for flowering time.

Name	LocusTag	Start	End	Name	LocusTag	Start	End
LHY	AT1G01060	33379	37840	LDL1	AT1G62830	23264490	23267202
GA2ox6	AT1G02400	486801	489577	DDF2	AT1G63030	23367407	23368410
CRY2	AT1G04400	1185550	1188517	FT	AT1G65480	24331428	24333934
CKL13	AT1G04440	1202255	1205803	RGL1	AT1G66350	24748195	24750043
STO	AT1G06040	1828413	1829890	FKF1	AT1G68050	25508676	25510889
NFYC3	AT1G08970	2882524	2884337	TEM2	AT1G68840	25880327	25881736
PIF3	AT1G09530	3076582	3079539	AP1	AT1G69120	25982330	25986313
PHYA	AT1G09570	3095256	3100357	CDF5	AT1G69570	26161528	26163496
HYL1	AT1G09700	3137767	3140353	AT1G69935	AT1G69935	26341801	26343126
AT1G10588	AT1G10588	3501145	3501904	MMP	AT1G70170	26423874	26425356
DDF1	AT1G12610	4289944	4291017	AGL12	AT1G71692	26952645	26955127
LWD1	AT1G12910	4394897	4396291	Cstf64	AT1G71800	26999452	27002342
RAV1	AT1G13260	4542168	4543742	AT1G72050	AT1G72050	27115024	27117470
UBC1	AT1G14400	4927011	4928690	HAP2C	AT1G72830	27405456	27407969
GAI	AT1G14920	5149226	5151354	miR159a	AT1G73687	27713234	27713415
GA4	AT1G15550	5344478	5346166	MIF1	AT1G74660	28047576	28048127
Cstf77	AT1G17760	6110107	6116617	AT1G74670	AT1G74670	28053286	28054149
miR159b	AT1G18075	6220648	6220833	ASHH1	AT1G76710	28789729	28792676
ATARP4	AT1G18450	6348107	6351975	FLM	AT1G77080	28955637	28960096
AT1G22690	AT1G22690	8027298	8028125	EFS	AT1G77300	29039922	29048810
GI	AT1G22770	8061844	8067716	ATGA2OX1	AT1G78440	29511599	29513051
SEPALLATA3	AT1G24260	8593642	8596098	NUA	AT1G79280	29819176	29832978
PFT1	AT1G25540	8969065	8974660	GA2	AT1G79460	29890392	29894587
TEM1	AT1G25560	8981677	8983041	ELF7	AT1G79730	30000538	30004005
CAL	AT1G26310	9100153	9103603	ATGA3OX4	AT1G80330	30198061	30199537
ATGA2OX2	AT1G30040	10537648	10539831	GA4H	AT1G80340	30200693	30202200
UFO	AT1G30950	11036180	11037508	MOS3	AT1G80680	30324008	30328769
AT1G30960	AT1G30960	11037612	11040033	RGA1	AT2G01570	255249	257550
SUF4	AT1G30970	11040281	11043751	CAND1	AT2G02560	689788	697596
FRL2	AT1G31814	11412608	11414502	UBC2	AT2G02760	773684	775371
VIP1	AT1G43700	16484231	16486241	PKS1	AT2G02950	854947	856538
ATGA20OX5	AT1G44090	16760677	16762486	SEPALLATA4	AT2G03710	1129268	1131838
CH1	AT1G44446	16848359	16851224	CR88	AT2G04030	1281841	1286104
GA2ox4	AT1G47990	17698655	17700834	ELF8	AT2G06210	2428903	2436687
GCR1	AT1G48270	17827953	17830420	AT2G14900	AT2G14900	6404175	6405330
RTV1	AT1G49480	18314178	18316645	PHYB	AT2G18790	8139881	8144430
ATGA2OX7	AT1G50960	18889549	18891719	LKP2	AT2G18915	8194572	8197483
AT1G52800	AT1G52800	19664044	19665362	miR156g	AT2G19425	8412516	8412618
SPA4	AT1G53090	19783352	19786902	FVE	AT2G19520	8455936	8459525
SPL4	AT1G53160	19806419	19807608	PIL5	AT2G20180	8704024	8706892
NFYC9	AT1G54830	20451083	20452671	FIO1	AT2G21070	9040863	9043528
AT1G55080	AT1G55080	20553011	20554254	ATGRP7	AT2G21660	9265249	9266393
HUB2	AT1G55250	20607214	20612378	SVP	AT2G22540	9579874	9583893
NFYC2	AT1G56170	21024764	21025883	AGL17	AT2G22630	9618372	9621957
ORTH2	AT1G57820	21414170	21417946	CLF	AT2G23380	9955553	9960359
ARR3	AT1G59940	22065617	22066973	COL3	AT2G24790	10566898	10568145
ATGA20OX4	AT1G60980	22452573	22454140	miR156a	AT2G25095	10676472	10676553
VIP5	AT1G61040	22483207	22485969	ELF3	AT2G25930	11059035	11063324
ATSCO1	AT1G62750	23233434	23236447	HAP2C	AT2G26710	11380492	11383612

Table S2. (continued)

Name	LocusTag	Start	End
ATC	AT2G27550	11773251	11774681
PNF	AT2G27990	11921433	11924698
miR172a	AT2G28056	11941661	11943604
SYD	AT2G28290	12056213	12073083
TOE1	AT2G28550	12225951	12228543
AT2G30810	AT2G30810	13127826	13128666
ATX1	AT2G31650	13455272	13462181
COP1	AT2G32950	13977933	13983535
SPL3	AT2G33810	14305001	14306072
FES1	AT2G33835	14311787	14314700
ATGA2OX3	AT2G34555	14556988	14558697
NFYA4	AT2G34720	14649767	14651627
FHY1	AT2G37678	15801465	15802793
NFYB1	AT2G38880	16238476	16240834
SNZ	AT2G39250	16388886	16391073
AT2G39540	AT2G39540	16500866	16501241
HOS1	AT2G39810	16612800	16618057
ELF4	AT2G40080	16734294	16734912
SPL9	AT2G42200	17587407	17589630
SHP2	AT2G42830	17820255	17824013
PIF4	AT2G43010	17886427	17889050
FPA	AT2G43410	18025247	18031243
CKB4	AT2G44680	18426546	18428357
HUB1	AT2G44950	18542213	18548591
SAP18	AT2G45640	18799610	18801383
AGL6	AT2G45650	18804350	18806522
SOC1	AT2G45660	18807538	18811047
miR159c	AT2G46255	18994632	18994856
SPA1	AT2G46340	19022173	19027413
APRR9	AT2G46790	19232649	19235087
CCA1	AT2G46830	19245672	19248914
AT2G47310	AT2G47310	19423684	19427277
RFI2	AT2G47700	19552314	19554584
MBD9	AT3G01460	173316	182454
SEPALLATA2	AT3G02310	464279	467074
COL2	AT3G02380	487236	488693
GASA5	AT3G02885	638021	639055
ATVGT1	AT3G03090	700456	704769
AT3G04510	AT3G04510	1215636	1216958
FLK	AT3G04610	1250553	1254873
WNK1	AT3G04910	1354635	1358219
HST	AT3G05040	1401271	1408197
ATGID1A	AT3G05120	1430471	1432778
ATHAP2B	AT3G05690	1676546	1678932
AT3G06910	AT3G06910	2178630	2181197
AtPRMT4b	AT3G06930	2185143	2189387
COL9	AT3G07650	2441657	2444532
AT3G10185	AT3G10185	3145579	3146199
FLD	AT3G10390	3229293	3232345

Name	LocusTag	Start	End
miR172c	AT3G11435	3599776	3599908
ATMYB65	AT3G11440	3602093	3605104
SPY	AT3G11540	3631887	3637955
PIE1	AT3G12810	4065042	4074078
LDL2	AT3G13682	4479193	4481509
SPL5	AT3G15270	5140365	5141348
SPA3	AT3G15354	5169095	5172837
VRN1	AT3G18990	6548869	6551853
HAF2	AT3G19040	6567157	6575282
ATFYPP3	AT3G19980	6961736	6965108
DDL	AT3G20550	7174464	7177942
FIE	AT3G20740	7248809	7252452
AT3G21320	AT3G21320	7499053	7501841
TIC	AT3G22380	7912905	7919510
VRN5	AT3G24440	8876027	8878171
TEL1	AT3G26120	9546398	9549186
LWD2	AT3G26640	9793220	9794457
FUS3	AT3G26790	9853828	9855989
BR6OX2	AT3G30180	11810737	11813765
ATARP6	AT3G33520	14093656	14095549
PCL1	AT3G46640	17183090	17185218
CDF3	AT3G47500	17504000	17506058
REF6	AT3G48430	17935609	17940746
NFYC1	AT3G48590	18008657	18009982
UBP26	AT3G49600	18380549	18387128
AMP1	AT3G54720	20254725	20257848
SMZ	AT3G54990	20373718	20376522
AGL16	AT3G57230	21177423	21180932
AT3G57300	AT3G57300	21199488	21207885
AGL18	AT3G57390	21233701	21235911
SPL15	AT3G57920	21444321	21446035
GIS	AT3G58070	21506613	21507654
SHP1	AT3G58780	21738460	21741907
PIL6	AT3G59060	21827978	21830507
CKB3	AT3G60250	22270337	22272113
AGL13	AT3G61120	22618259	22620491
PIL2	AT3G62090	22988547	22990709
ATGID1B	AT3G63010	23289425	23291486
CRP	AT4G00450	202416	211003
FRI	AT4G00650	269026	271503
ETC3	AT4G01060	460472	461085
EZA1	AT4G02020	886600	891955
LD	AT4G02560	1123490	1128421
GA1	AT4G02780	1237767	1244813
DFL2	AT4G03400	1497536	1499865
PDF2	AT4G04890	2476489	2482345
CRY1	AT4G08920	5724103	5727253
GASA2	AT4G09610	6074770	6075645
SPA2	AT4G11110	6771605	6777225

Table S2. (continued)

Name	LocusTag	Start	End
AGL14	AT4G11880	7143115	7147222
pEARLI1	AT4G12480	7406105	7406937
COP9	AT4G14110	8132886	8134920
NFYB3	AT4G14540	8344616	8345218
ELIP2	AT4G14690	8418283	8419263
FAR1	AT4G15090	8614067	8618145
AT4G15180	AT4G15180	8651406	8662587
ESD4	AT4G15880	9012645	9016116
PHYD	AT4G16250	9195602	9199486
FCA	AT4G16280	9206597	9214825
HAT4	AT4G16780	9449114	9450743
AT4G16810	AT4G16810	9459870	9462253
VRN2	AT4G16845	9476143	9479878
CKB2	AT4G17640	9825197	9827272
PHYE	AT4G18130	10042137	10046082
TSF	AT4G20370	11000771	11002996
Jmj4	AT4G20400	11008666	11013860
ATGA2OX8	AT4G21200	11302685	11306601
ATGA3OX3	AT4G21690	11527229	11529060
EBS	AT4G22140	11727726	11730509
AGL19	AT4G22950	12023915	12027421
AT4G23340	AT4G23340	12195453	12196793
SLY1	AT4G24210	12563553	12564482
AGL24	AT4G24540	12670965	12674072
PGI1	AT4G24620	12708752	12712825
GA5	AT4G25420	12990884	12992458
FWA	AT4G25530	13038360	13042443
TOR1	AT4G27060	13581401	13585155
CIP7	AT4G27430	13718679	13723324
ATHXK1	AT4G29130	14352037	14355103
VIP3	AT4G29830	14597661	14599300
AT4G30200	AT4G30200	14786633	14790503
miR156b	AT4G30972	15074945	15075024
ATPRMT5	AT4G31120	15132011	15136639
FLP1	AT4G31380	15229785	15230718
CYP83B1	AT4G31500	15273471	15275310
miR156c	AT4G31877	15413319	15415873
KNAT5	AT4G32040	15494065	15496356
ATH1	AT4G32980	15914722	15918044
AT4G33280	AT4G33280	16047354	16049355
CIB1	AT4G34530	16498391	16500174
FD	AT4G35900	17004595	17006287
AP2	AT4G36920	17400847	17403332
HLS1	AT4G37580	17658612	17660878
AGL21	AT4G37940	17835695	17838621
BRI1	AT4G39400	18324661	18328826
PNY	AT5G02030	395634	399041
FHL	AT5G02200	437460	438894
PRR7	AT5G02810	637897	641977

Name	LocusTag	Start	End
LCL1	AT5G02840	648704	651972
ATHB51	AT5G03790	1004983	1006373
TFL1	AT5G03840	1024641	1025812
ELF6	AT5G04240	1169544	1174878
miR172b	AT5G04275	1188211	1188299
CPD	AT5G05690	1702688	1706787
MYB33	AT5G06100	1837907	1840727
YAP169	AT5G07200	2243553	2245339
CHE	AT5G08330	2680744	2681813
FLC	AT5G10140	3173497	3179448
AT5G10625	AT5G10625	3358787	3359781
miR156d	AT5G10945	3456647	3456732
HY5	AT5G11260	3593380	3594992
EMF1	AT5G11530	3695862	3701548
miR156e	AT5G11977	3867213	3867308
HAP2A	AT5G12840	4050691	4053606
FY	AT5G13480	4326528	4331699
AGL15	AT5G13790	4449014	4450843
AT5G14920	AT5G14920	4826479	4827980
GASA4	AT5G15230	4944900	4946216
CO	AT5G15840	5171182	5172758
COL1	AT5G15850	5176091	5177897
KIN1	AT5G15960	5209898	5210727
KIN2	AT5G15970	5211911	5212665
FRL1	AT5G16320	5344502	5346019
TFL2	AT5G17690	5827171	5829682
ASP2	AT5G19550	6598017	6601819
NPH4	AT5G20730	7016445	7022113
HUA2	AT5G23150	7785835	7792489
APRR5	AT5G24470	8355951	8358873
FPF1	AT5G24860	8541778	8542449
TNY	AT5G25810	8986771	8987787
GA3	AT5G25900	9036018	9038406
miR156f	AT5G26147	9136126	9136215
AT5G27230	AT5G27230	9584092	9588049
ATGID1C	AT5G27320	9629087	9631210
AT5G28450	AT5G28450	10372938	10374190
LSH1	AT5G28490	10454393	10455196
PHYC	AT5G35840	14007826	14011764
SEF	AT5G37055	14641551	14642440
CIR1	AT5G37260	14751344	14753088
TCH2	AT5G37770	14998854	14999619
PMI15	AT5G38150	15223116	15224947
CDF2	AT5G39660	15878699	15881044
XPB2	AT5G41360	16544340	16549280
CIP1	AT5G41790	16727530	16732847
CUL4	AT5G46210	18731418	18736810
AT5G46910	AT5G46910	19047780	19050880
LBA1	AT5G47010	19072009	19079334

Table S2. (continued)

Name	LocusTag	Start	End
CKB1	AT5G47080	19124612	19126611
NFYB2	AT5G47640	19309227	19310272
PAT1	AT5G48150	19522255	19524698
AtPRMT4a	AT5G49020	19871251	19874920
EMF2	AT5G51230	20823736	20829564
AT5G51310	AT5G51310	20852854	20854718
GA20ox2	AT5G51810	21055188	21056808
PGM	AT5G51820	21063368	21068057
DFL1	AT5G54510	22131093	22133678
miR156h	AT5G55835	22597012	22597117
ZTL	AT5G57360	23241427	23244590
VIN3	AT5G57380	23246395	23249504
COL5	AT5G57660	23355464	23356989
MSI1	AT5G58230	23556012	23558245
SRR1	AT5G59560	24000556	24001957
AT5G59570	AT5G59570	24003888	24005512
VIP2	AT5G59710	24057407	24061918
AT5G59845	AT5G59845	24111324	24112020
APRR3	AT5G60100	24197999	24201364
TOE2	AT5G60120	24207786	24211724
AGL8	AT5G60910	24502482	24506143
VIP4	AT5G61150	24603656	24607725
TOC1	AT5G61380	24675064	24678550
LFY	AT5G61850	24844295	24846933
AT5G62040	AT5G62040	24922810	24923709
CDF1	AT5G62430	25069093	25070934
ELF5	AT5G62640	25149433	25152541
LIP1	AT5G64813	25910279	25912896
MAF2	AT5G65050	25982254	25986326
MAF3	AT5G65060	25987429	25991315
MAF4	AT5G65070	25992260	25996134
MAF5	AT5G65080	25997504	26002465
AT5G65540	AT5G65540	26195689	26198322
ICU2	AT5G67100	26776994	26785104

Table S3. Structure of phenological variation in France in the Fall cohort.

Traits	Model terms	<i>F</i> or LRT	<i>P</i>	Var Comp (%)
BT	Block	18.56	0.0001	0.6
	Region	113.21	0.0001	26.3
	Stand(Region)	22.38	0.0001	37.1
	<i>Family(Stand(Region))</i>	191.10	0.0001	19.0
	Control Bg-2	1.36	0.2441	-
	Error			17.0
INT	Block	0.27	0.6057	0.0
	Region	12.69	0.0001	5.4
	Stand(Region)	2.97	0.0001	6.9
	<i>Family(Stand(Region))</i>	7.40	0.0065	10.5
	Control Bg-2	1.03	0.3109	-
	Error			77.3
FT	Block	20.88	0.0001	0.7
	Region	95.11	0.0001	23.5
	Stand(Region)	22.47	0.0001	38.2
	<i>Family(Stand(Region))</i>	163.30	0.0001	18.8
	Control Bg-2	0.86	0.3544	-
	Error			18.9
FP	Block	4.62	0.0320	0.7
	Region	5.66	0.0008	2.2
	Stand(Region)	4.60	0.0001	13.1
	<i>Family(Stand(Region))</i>	6.30	0.0121	8.8
	Control Bg-2	1.89	0.1700	-
	Error			75.2
RP	Block	14.36	0.0002	1.6
	Region	2.98	0.0308	0.3
	Stand(Region)	3.64	0.0001	9.8
	<i>Family(Stand(Region))</i>	0.30	0.5839	1.6
	Control Bg-2	16.22	0.0001	-
	Error			86.7
FRR	Block	0.02	0.8932	0.0
	Region	15.48	0.0001	8.4
	Stand(Region)	5.76	0.0001	14.4
	<i>Family(Stand(Region))</i>	0.20	0.6547	0.0
	Control Bg-2	0.10	0.7489	-
	Error			77.2

Model random terms were tested with likelihood ratio tests of models with and without these effects. Random effects are in italic. Significant effects are highlighted in bold.

‘VarComp (%)’ Percentage of variance explained by the corresponding term of the model. Because ‘Control Bg-2’ is a covariate, this term was not included in the variance component analysis.

Table S4. Structure of phenological variation in France in the Spring cohort.

Traits	Model terms	F or LRT	P	Var Comp (%)
BT	Block	1.14	0.2864	0.0
	Region	134.26	0.0001	28.7
	Stand(Region)	22.26	0.0001	37.6
	<i>Family(Stand(Region))</i>	209.40	0.0001	19.0
	Control Bg-2	5.73	0.0168	-
	Error			14.8
INT	Block	0.74	0.3912	0.0
	Region	1.86	0.1350	0.0
	Stand(Region)	3.84	0.0001	10.5
	<i>Family(Stand(Region))</i>	10.90	0.0010	14.4
	Control Bg-2	0.00	0.9661	-
	Error			75.1
FT	Block	3.88	0.0493	0.0
	Region	73.24	0.0001	22.1
	Stand(Region)	20.70	0.0001	43.7
	<i>Family(Stand(Region))</i>	230.40	0.0001	21.7
	Control Bg-2	6.71	0.0098	-
	Error			12.6
FP	Block	6.04	0.0143	0.6
	Region	8.72	0.0001	1.6
	Stand(Region)	6.14	0.0001	25.1
	<i>Family(Stand(Region))</i>	26.00	0.0001	20.0
	Control Bg-2	0.09	0.7630	-
	Error			52.7
RP	Block	2.84	0.0928	0.1
	Region	17.62	0.0001	9.5
	Stand(Region)	5.80	0.0001	22.2
	<i>Family(Stand(Region))</i>	18.50	0.0001	17.9
	Control Bg-2	0.49	0.4838	-
	Error			50.3
FRR	Block	3.28	0.0706	0.9
	Region	4.55	0.0036	1.5
	Stand(Region)	4.86	0.0001	17.5
	<i>Family(Stand(Region))</i>	9.40	0.0022	14.3
	Control Bg-2	3.03	0.0820	-
	Error			65.7

Random terms were tested with likelihood ratio tests of models with and without these effects. Random effects are in italics. Significant effects are highlighted in bold.

‘VarComp (%)’ Percentage of variance explained by the corresponding term of the model. Because ‘Control Bg-2’ is a covariate, this term was not included in the variance component analysis.

Table S5. Genetic coefficient of phenological variation for BT, INT, FT, FP, RP and FRR for each region and cohort.

Cohort	Trait	Brittany	Burgundy	Languedoc	North	<i>P</i>
Fall	BT	0.062 ^b	0.231 ^a	0.143 ^{ab}	0.091 ^b	0.0020
	INT	0.165 ^b	0.215 ^b	0.589 ^a	0.095 ^b	0.0006
	FT	0.050 ^c	0.186 ^a	0.152 ^{ab}	0.054 ^{bc}	0.0009
	FP	0.086	0.133	0.150	0.077	0.3706
	RP	0.035	0.039	0.080	0.048	0.4668
	FRR	0.048	0.091	0.085	0.028	0.1734
Spring	BT	0.124 ^b	0.296 ^a	0.198 ^{ab}	0.074 ^b	0.0096
	INT	0.287	0.549	0.286	0.178	0.1956
	FT	0.072 ^b	0.265 ^a	0.216 ^a	0.059 ^b	0.0004
	FP	0.136	0.185	0.153	0.062	0.1859
	RP	0.037 ^b	0.120 ^{ab}	0.148 ^a	0.032 ^b	0.0037
	FRR	0.089	0.135	0.081	0.038	0.1853

Bold *p*-values indicate a significant ‘region’ effect after Bonferroni correction. When a ‘region’ effect is significant, different letters indicate different coefficients of variation among regions based on a Tukey’s test of multiple comparisons of means ($P = 0.05$).

Table S6. Mean values for genetic diversity parameters of the 49 French stands.

Region	Stands	Habitat	Alt ^a	H_s ^b	PL ^c	n_a ^d	R_s ^e	HG ^f	PHG ^g
Brittany	ABA	grassland	95	0.008	1.48	1.01	1.01	1	1
	BRE	grassland	41	0.264	83.70	1.84	1.26	5	2
	DIR-2.8	grassland	105	0.230	55.56	1.56	1.22	5	5
	DIR-8.5	grassland	105	0.138	60.00	1.60	1.13	1	1
	FOR	meadow	9	0.184	75.56	1.76	1.18	4	2
	MIL	meadow	75	0.092	57.78	1.58	1.09	3	2
	PLO	hoed land	86	0.215	56.30	1.56	1.21	4	2
	PLY	hoed land	177	0.177	75.56	1.76	1.17	3	1
	ROC	grassland	22	0.005	1.48	1.01	1.00	1	0
	RUM	hoed land	14	0.114	33.33	1.33	1.11	2	1
	TRE	hoed land	42	0.233	85.19	1.85	1.23	5	3
			mean	0.15	53.27	1.53	1.15	3.09	1.82
			SD	0.09	29.63	0.30	0.09	1.64	1.33
Burgundy	CIRY	grassland	271	0.268	77.04	1.77	1.26	7	6
	CON	grassland	508	0.081	41.48	1.41	1.08	2	2
	ETA-1	grassland	300	0.240	56.30	1.56	1.23	5	5
	ETA-2	hoed land	300	0.187	59.26	1.59	1.17	3	3
	LIE	grassland	530	0.308	81.48	1.81	1.30	7	6
	MAR-3	grassland	439	0.003	0.74	1.01	1.00	1	1
	MAR-4	meadow	416	0.005	0.74	1.01	1.00	1	1
	MOL	meadow	344	0.241	64.44	1.64	1.24	10	9
	RAD	meadow	289	0.314	87.41	1.87	1.31	16	16
	TOU-J2	hoed land	279	0.151	56.30	1.56	1.15	4	4
	TOU-M1	hoed land	312	0.332	88.15	1.88	1.32	11	11
			mean	0.19	55.76	1.56	1.19	6.09	5.82
			SD	0.12	30.84	0.31	0.12	4.72	4.62
Languedoc	ARR-1	meadow	489	0.007	2.22	1.02	1.01	1	0
	ARR-2	meadow	489	0.192	34.07	1.34	1.18	2	1
	ARR-3	meadow	489	0.124	37.04	1.37	1.11	2	1
	BEZ	grassland	357	0.038	36.30	1.36	1.04	1	1
	ISS	grassland	199	0.316	48.15	1.48	1.26	2	1
	LEC	grassland	43	0.037	34.07	1.34	1.04	2	2
	MOU1-1	grassland	61	0.183	32.59	1.33	1.17	2	0
	MOU1-2	grassland	61	0.077	34.07	1.34	1.07	2	0
	MOU1-3	meadow	61	0.363	64.44	1.64	1.31	4	3
	MOU2	hoed land	63	0.306	81.48	1.81	1.30	12	10
	NOZ	grassland	78	0.185	55.56	1.56	1.18	3	1
	PCH	grassland	59	0.267	45.19	1.45	1.23	3	1
	QUI	grassland	88	0.029	28.15	1.28	1.03	2	0
	SAL	grassland	34	0.043	38.52	1.39	1.04	2	0
	VED	grassland	39	0.350	70.37	1.70	1.31	4	3
	VEN	grassland	42	0.098	18.52	1.19	1.09	2	1
			mean	0.163	41.296	1.413	1.147	2.875	1.563
			SD	0.125	19.601	0.196	0.109	2.579	2.449
North	BAU	grassland	26	0.046	11.11	1.11	1.05	4	4
	BRI	hoed land	19	0.192	66.67	1.67	1.19	3	3
	CAT-S	hoed land	161	0.110	60.00	1.60	1.11	2	0
	CAT-T	hoed land	135	0.027	22.96	1.23	1.03	1	0
	ENC-1	hoed land	74	0.287	72.59	1.73	1.28	7	7
	ENC-2	hoed land	39	0.197	57.78	1.58	1.19	3	3
	ESP1	meadow	47	0.042	43.70	1.44	1.04	1	0
	ESP2	hoed land	47	0.153	66.67	1.67	1.15	3	1
	GEN	hoed land	34	0.207	64.44	1.64	1.20	5	5
	LCL	grassland	17	0.288	64.44	1.64	1.28	3	1
	WAV	hoed land	19	0.000	0.00	1.00	1.00	1	1
			mean	0.14	48.22	1.48	1.14	3.00	2.27
			SD	0.10	25.28	0.25	0.10	1.84	2.33

^a Alt: Altitude (m), ^b H_s : Mean gene diversity, ^c PL : percentage of polymorphic loci, ^d n_a : mean number of observed alleles per locus, ^e R_s : mean allelic richness per locus, ^f HG : number of haplogroups, ^g PHG : number of private haplogroups. SD: standard deviation.

Table S7. List of flowering time candidate genes close to the 100 most associated SNPs for each ‘trait x cohort x geographical scale’ combination.

^a SNP: number of top SNPs close to the candidate gene.

^b Top rank: the highest rank among the top SNPs close to the candidate gene.