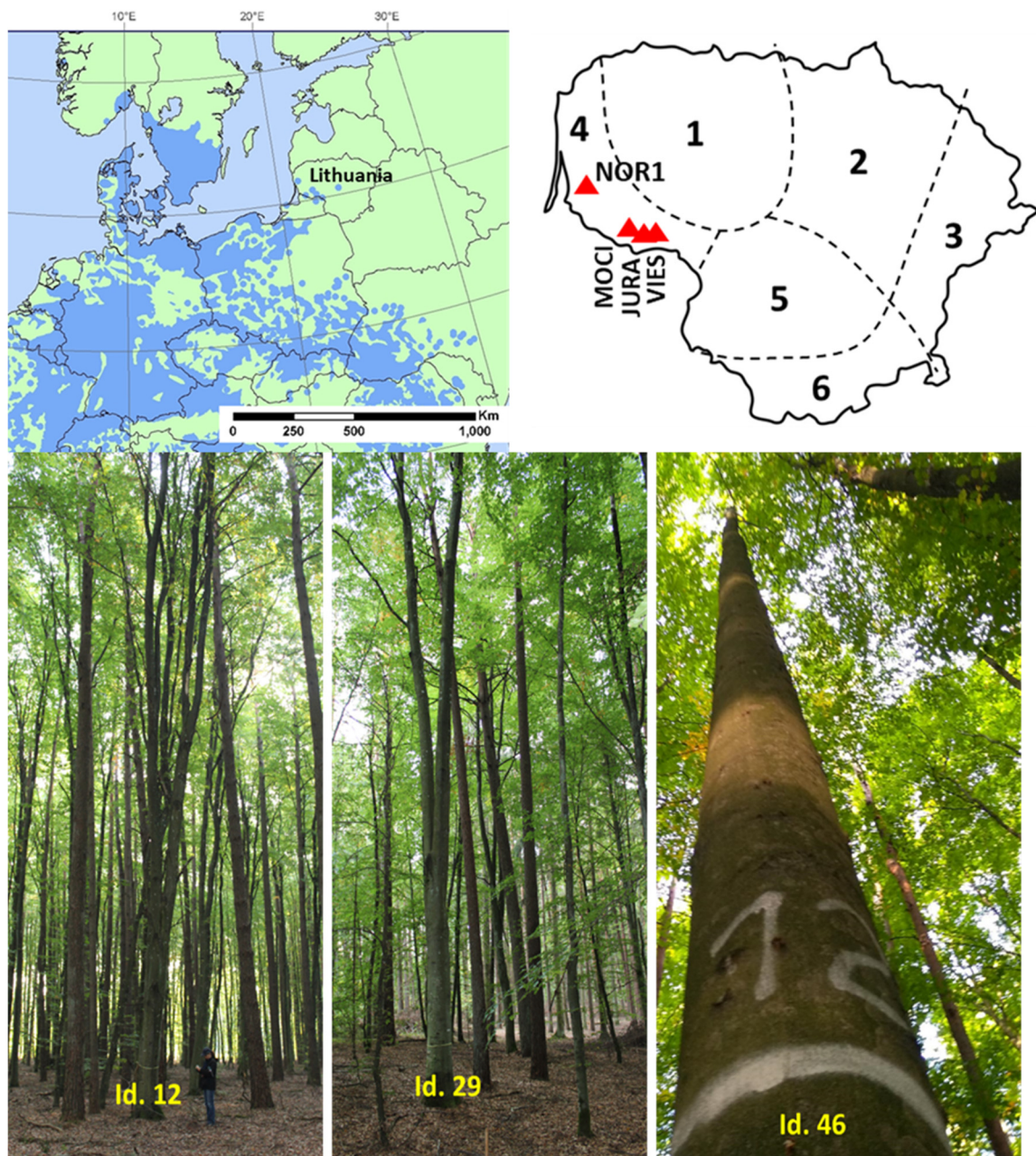


# Supplementary Materials

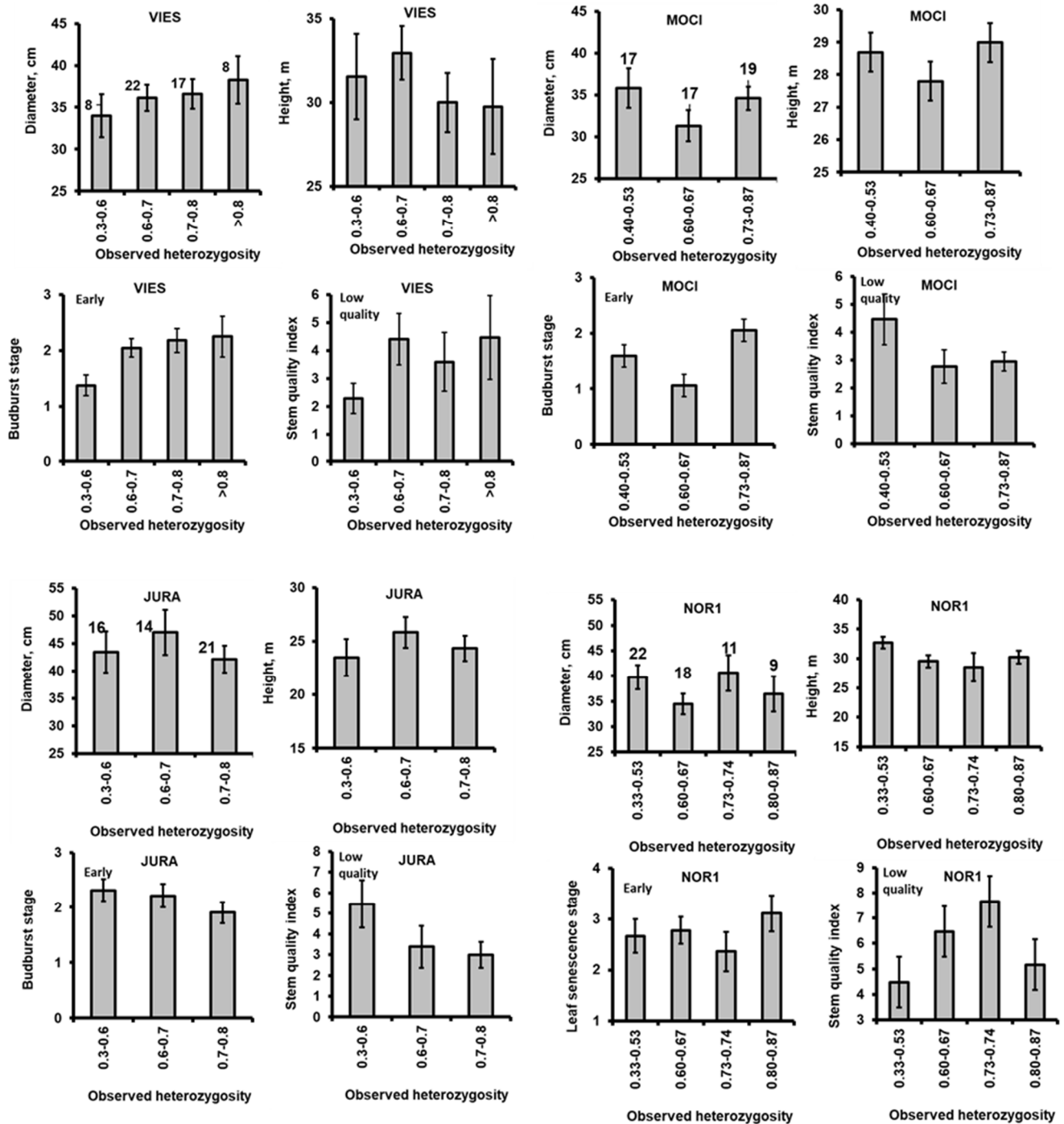
**Table S1.** genetic diversity characteristics of the nuclear microsatellite loci based sample size of 208 individuals in four European beech stands of VIES, NORK1, MOCI and JURA.

<b>Locus</b>	<b>N</b>	<b>Na</b>	<b>Ne</b>	<b>Ho</b>	<b>He</b>	<b>Fis</b>
<b>mfs11</b>	207	12	3.83	0.63	0.74	0.15
<b>mfc5</b>	206	26	10.90	0.69	0.91	0.24
<b>mfc7</b>	207	17	2.68	0.59	0.63	0.06
<b>sfc0036</b>	207	10	4.64	0.73	0.78	0.06
<b>DE576A0</b>	207	7	3.29	0.68	0.70	0.02
<b>mfc11<sup>a</sup></b>	207	12	3.12	0.39	0.68	0.43
<b>FS3-04</b>	207	4	1.62	0.41	0.38	-0.07
<b>FS1-15</b>	207	19	6.17	0.76	0.84	0.09
<b>csolf19</b>	207	14	5.72	0.75	0.83	0.09
<b>csolf31</b>	207	12	7.13	0.83	0.86	0.04
<b>DUCT</b>	207	8	2.38	0.56	0.58	0.04
<b>EEU75</b>	207	12	5.46	0.78	0.82	0.05
<b>EJV8T</b>	207	9	3.94	0.71	0.75	0.05
<b>EMILIY</b>	207	8	4.63	0.70	0.78	0.11
<b>ERHBI</b>	207	5	2.22	0.55	0.55	0.01

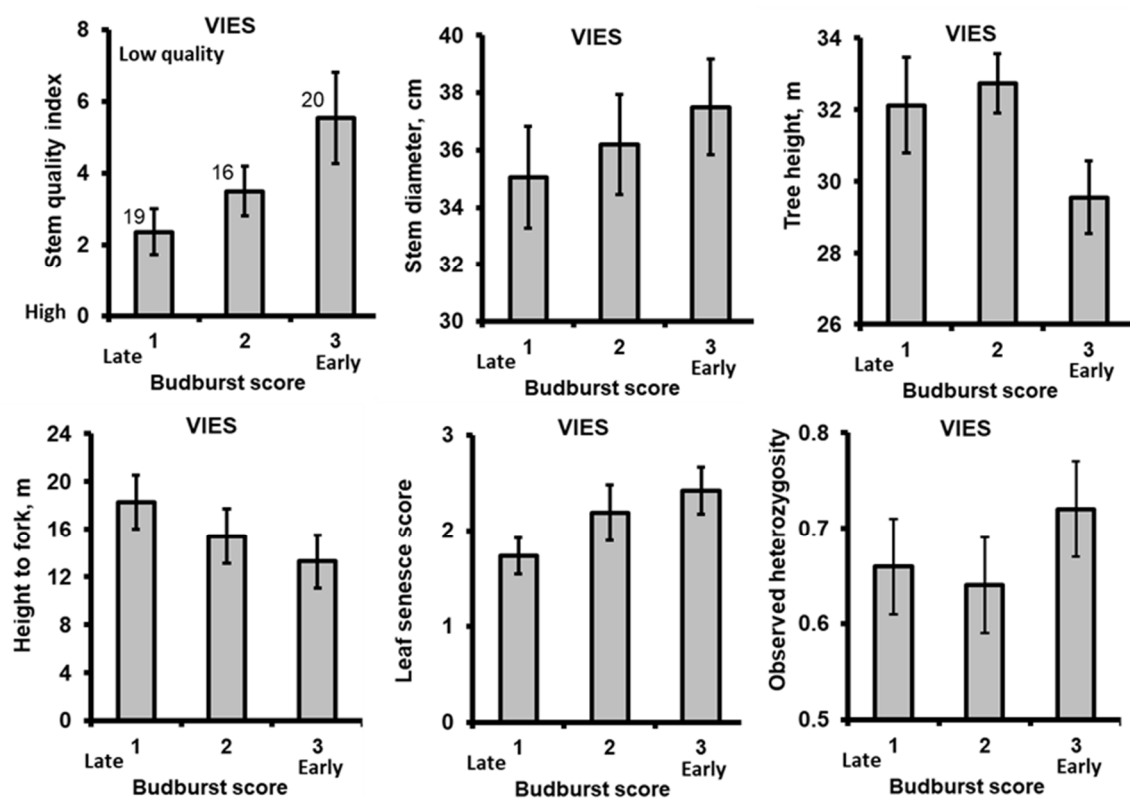
<sup>a</sup>— removed from further analysis due to high freq. of null alleles.



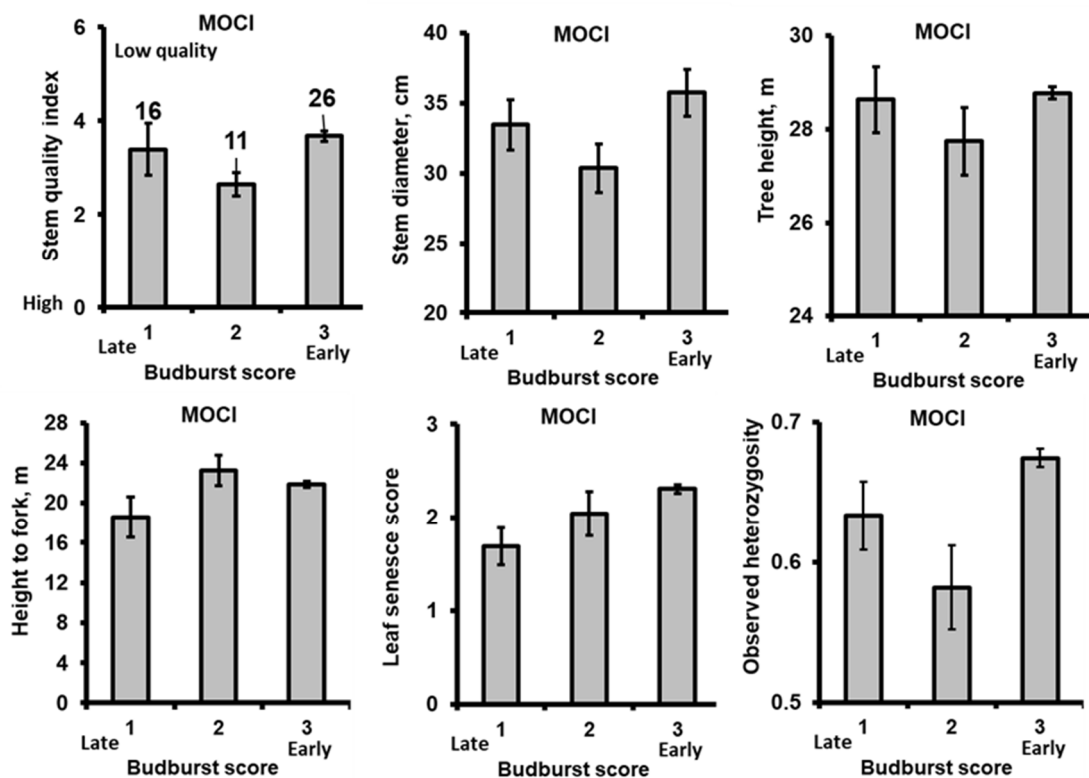
**Figure S1.** Upper maps: north-eastern natural range of European beech and location of Lithuania (left), six forest natural regions of Lithuania and location of the studied stand (right). Photos: European beech tree stem morphotypes in a densely stocked MOCI stand, illustrating in general the stand structure and the stem morphotypes. The Ids refer to ids. of the sampled trees and points at the trees in the photos: id 12 – multiple forking at the base and in midsection of the stem (one of the worst stem quality index (SQI) of 10.5 in MOCI stand (the worst was 15.0, best 1); id.29 – the SQI = 7; and id 46 – one of the best trees at the site with SQI= 1).



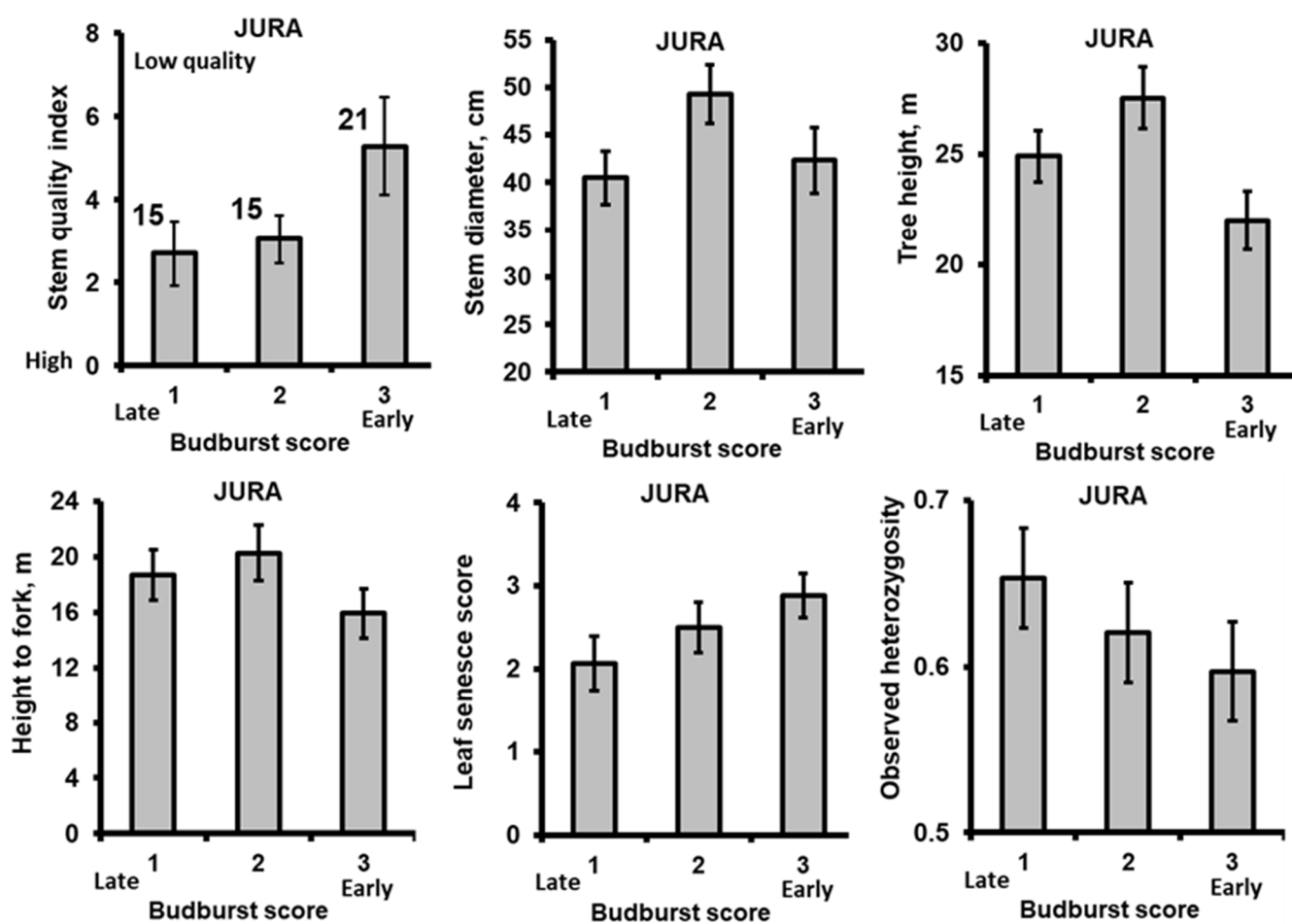
**Figure S2.** Associations between observed heterozygosity (Ho) and main four phenotypic traits of European beech trees in the four studied stands (four plots per stand defined by the id at the top of each plot). The error bars show the standard error. The Ho is presented in intervals delayed on X axis. The Ho values differed along the stands, so does the interval values. The number of trees in Ho intervals is shown at the top of the bars in the upper leftmost plot for each stand.



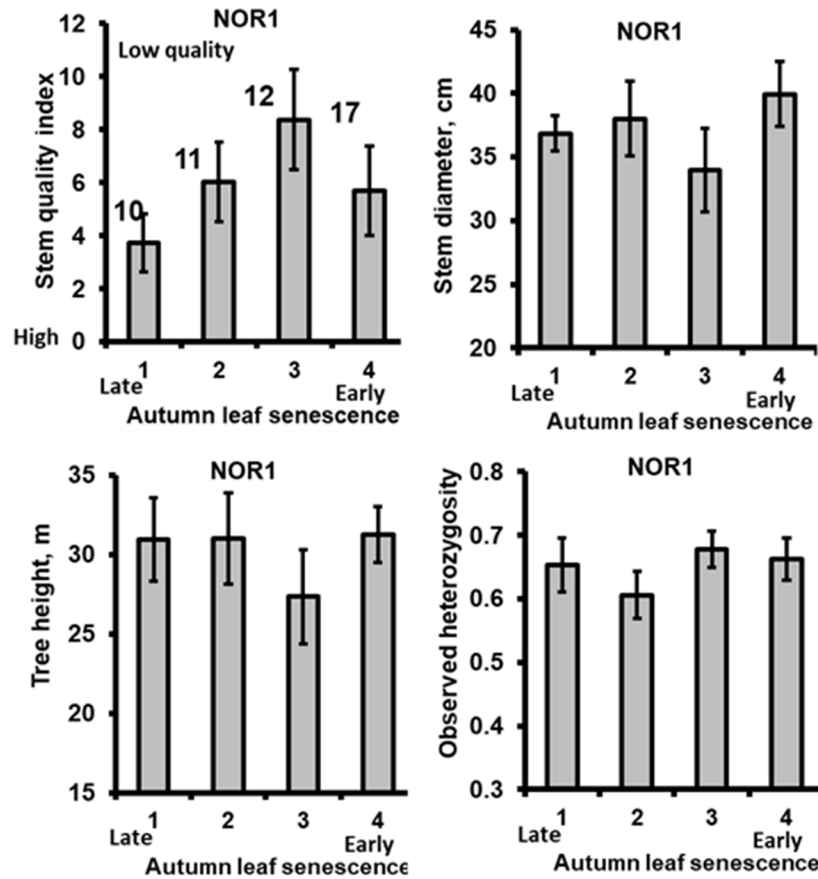
**Figure S3.** Associations between the budburst phenology, autumn leaf senescence, stem quality and observed heterozygosity in VIES stand. The number of trees at a particular budburst stage is given above the bars at upmost left plot. Error bars indicate standard error.



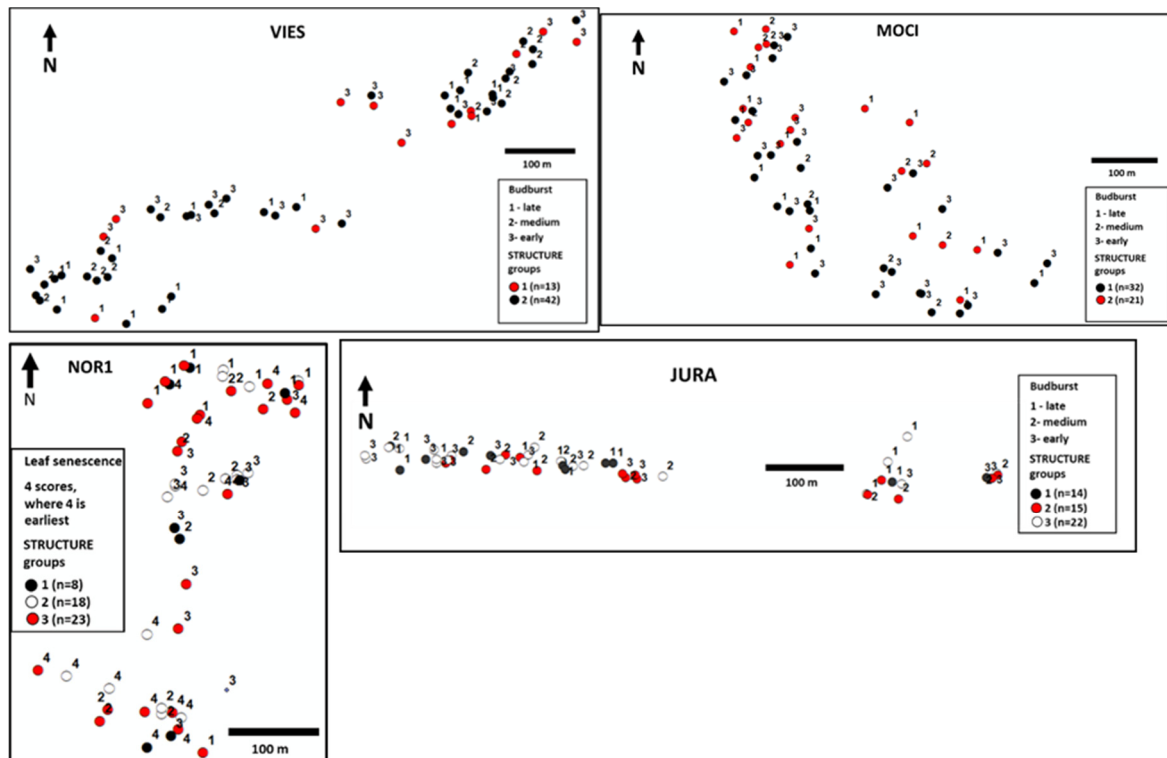
**Figure S4.** Associations between the budburst phenology, autumn leaf senescence, stem quality and observed heterozygosity in MOCI stand. The number of trees at a particular budburst stage is given above the bars at upmost left plot. Error bars indicate standard error.



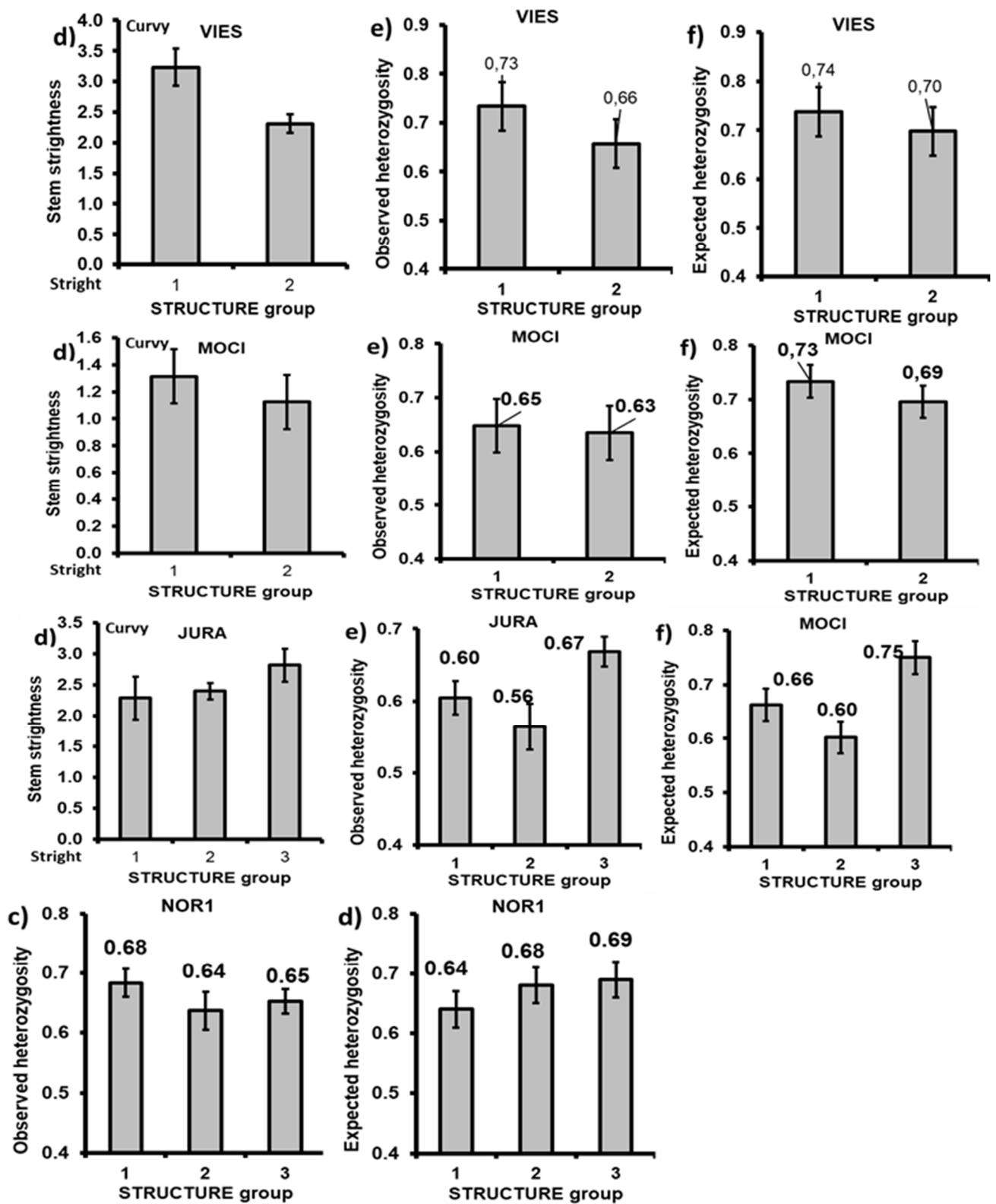
**Figure S5.** Associations between the budburst phenology, autumn leaf senescence, stem quality and observed heterozygosity in JURA stand. The number of trees at a particular budburst stage is given above the bars at upmost left plot. Error bars indicate standard error.



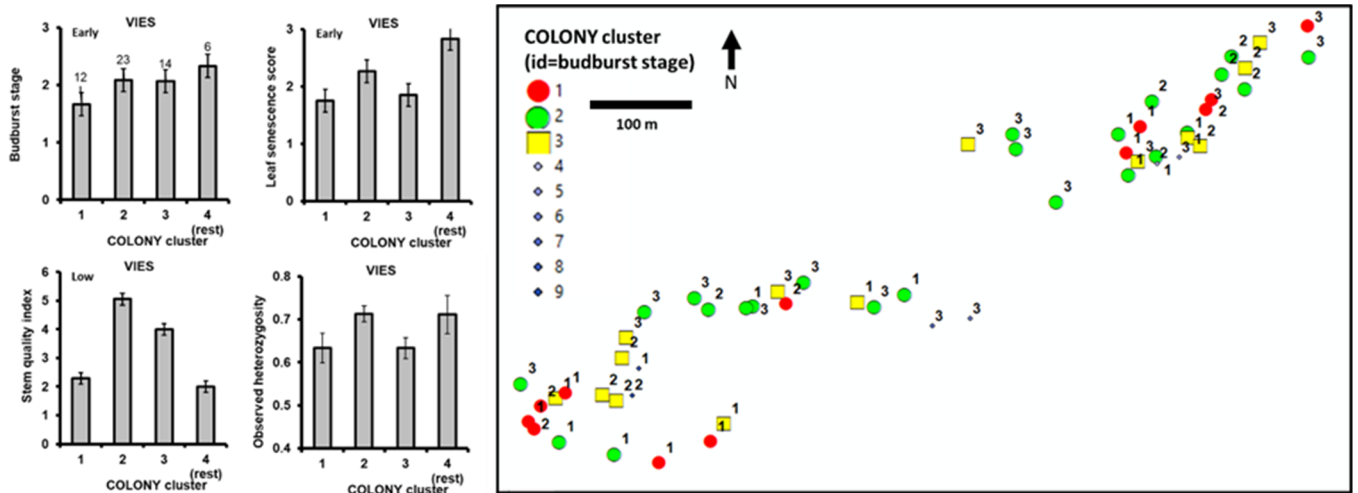
**Figure S6.** Associations between the budburst phenology, autumn leaf senescence, stem quality and observed heterozygosity in NOR1 stand. The number of trees at a particular autumn leaf senescence stage is given above the bars at upmost left plot. Error bars indicate standard error.



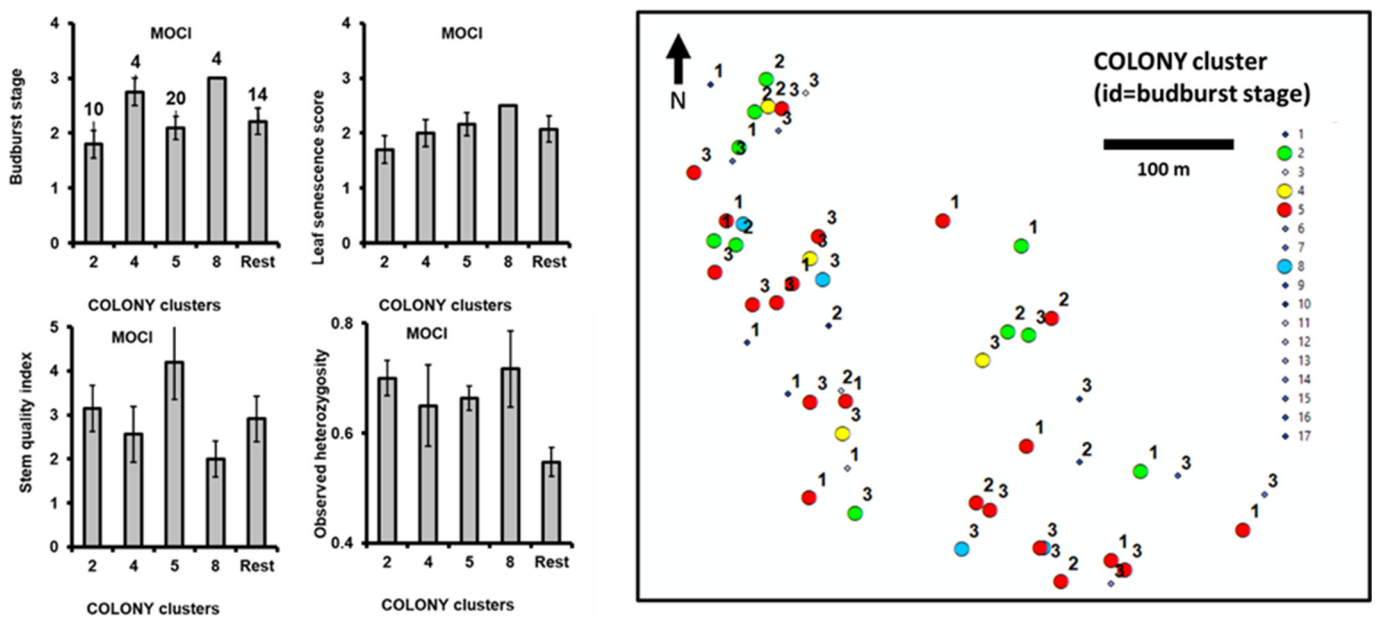
**Figure S7.** Spatial distribution of the STRUCTURE genetic groups in the four stands studied. Size of the STRUCTURE groups is given in the legend. The ids show phenology stages (spring for VIES, JURA, MOCI and autumn for NOR1).



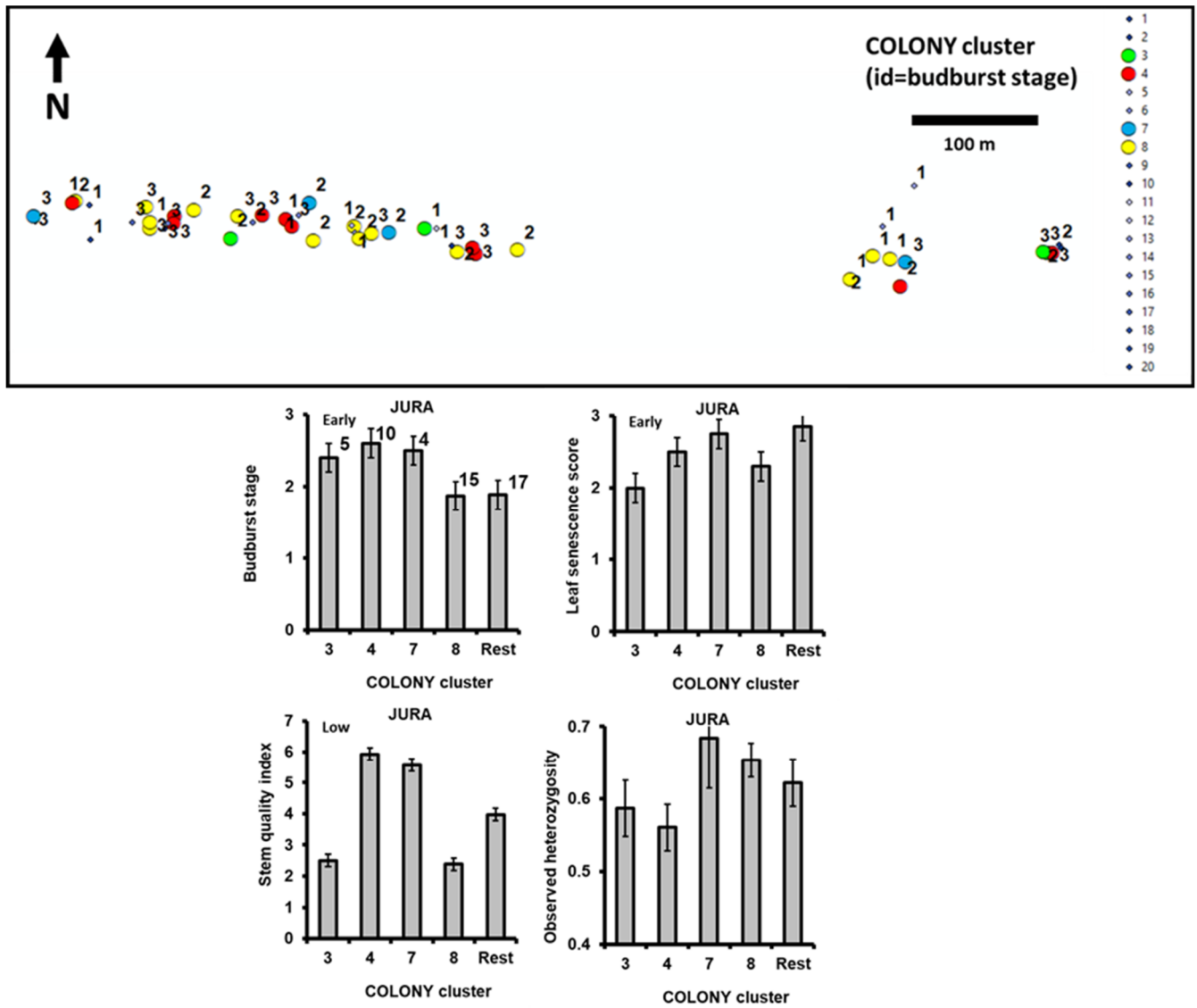
**Figure S8.** Properties of the STRUCTURE genetic groups in the four studied stands of European beech. The size of the genetic groups is 1 given in Figure 4. The error bars show standard errors.



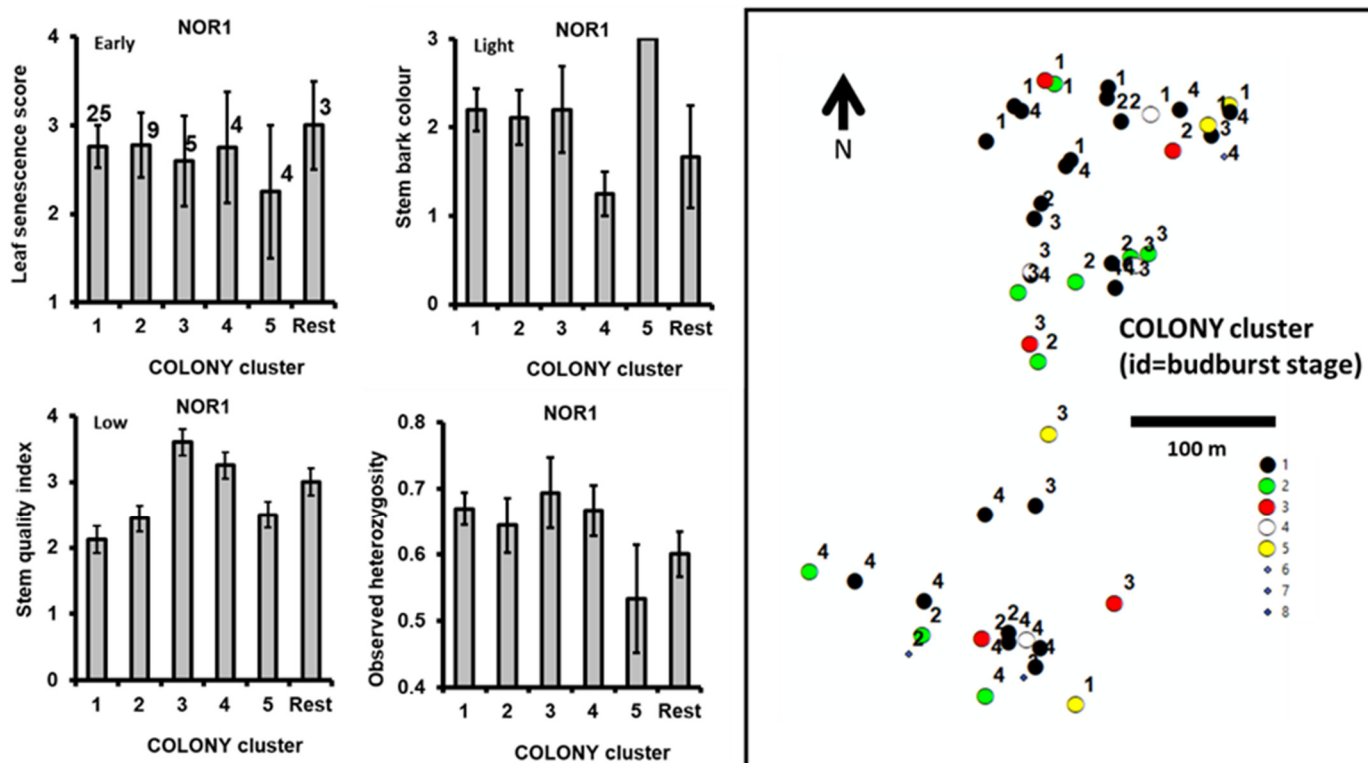
**Figure S9.** Main morphology traits and observed heterozygosity of the Colony genetic clusters (left, Cluster size given above the bars in the leftmost bar plot) in VIES stand. In the bar plots cluster 4 averages the variable for single individual clusters id.s 4 to 9. Right, the spatial arrangement of the Colony cluster, where the id is the budburst stage (3= early budburst).



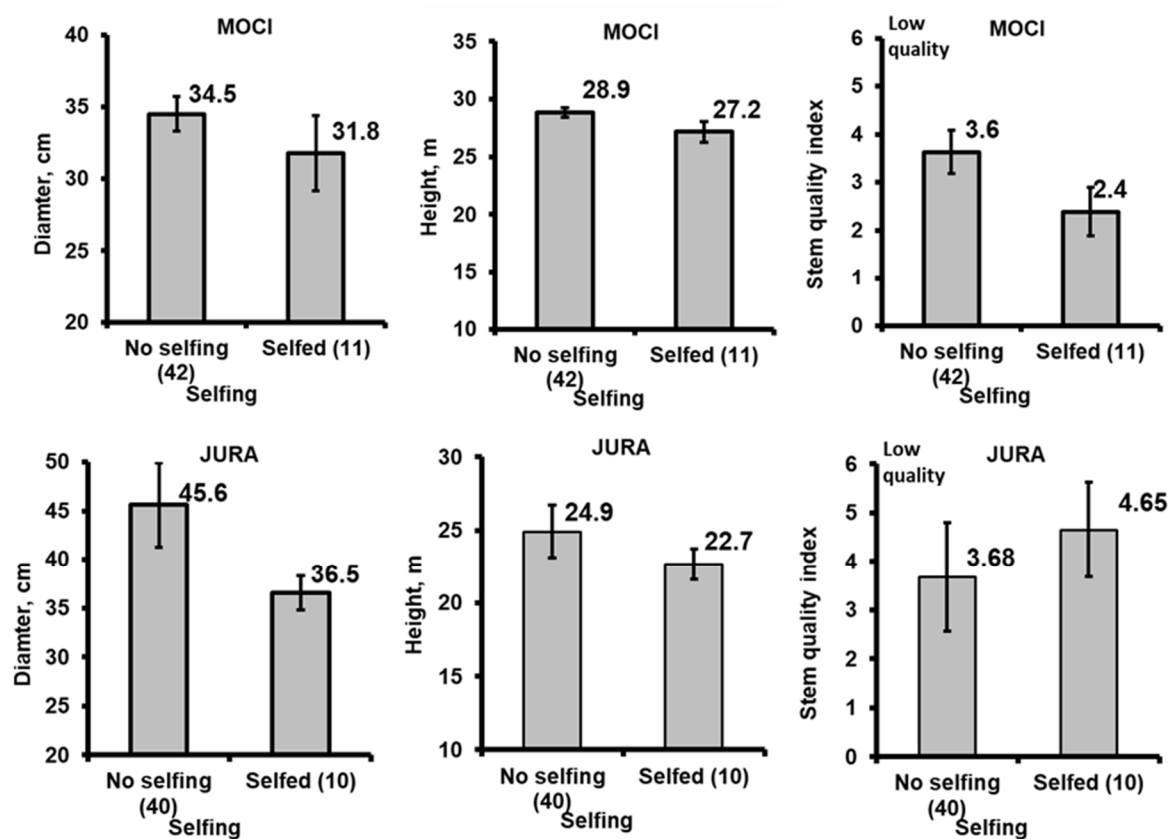
**Figure S10.** Main morphology traits and observed heterozygosity of the Colony genetic clusters (left, Cluster size given above the bars in the leftmost bar plot) in MOCI stand. In the bar plots cluster "Rest" averages the variable for single individual clusters. Right, the spatial arrangement of the Colony cluster, where the id is the budburst stage (3= early budburst).



**Figure S11.** Main morphology traits and observed heterozygosity of the Colony genetic clusters (left, Cluster size given above the bars in the leftmost bar plot) in JURA stand. In the bar plots cluster "Rest" averages the variable for single individual clusters. Above, the spatial arrangement of the Colony cluster, where the id is the budburst stage (3= early budburst).



**Figure S12.** Stem morphology traits and observed heterozygosity of the Colony genetic clusters (left, Cluster size given above the bars in the leftmost bar plot) in NOR1 stand. In the bar plots cluster "Rest" averages the variable for single individual clusters (ids. 6, 7, 8). Right, the spatial arrangement of the Colony clusters, where the id is the leaf senescence stage (4= early senescence).



**Figure S13.** Phenotypes of the selfed trees in MOCI and JURA stands. Numbers at the X axis labels indicate numbers of not selfed and selfed trees. NOR1 and JURA are not shown because there were 1 and 2 selfed trees.