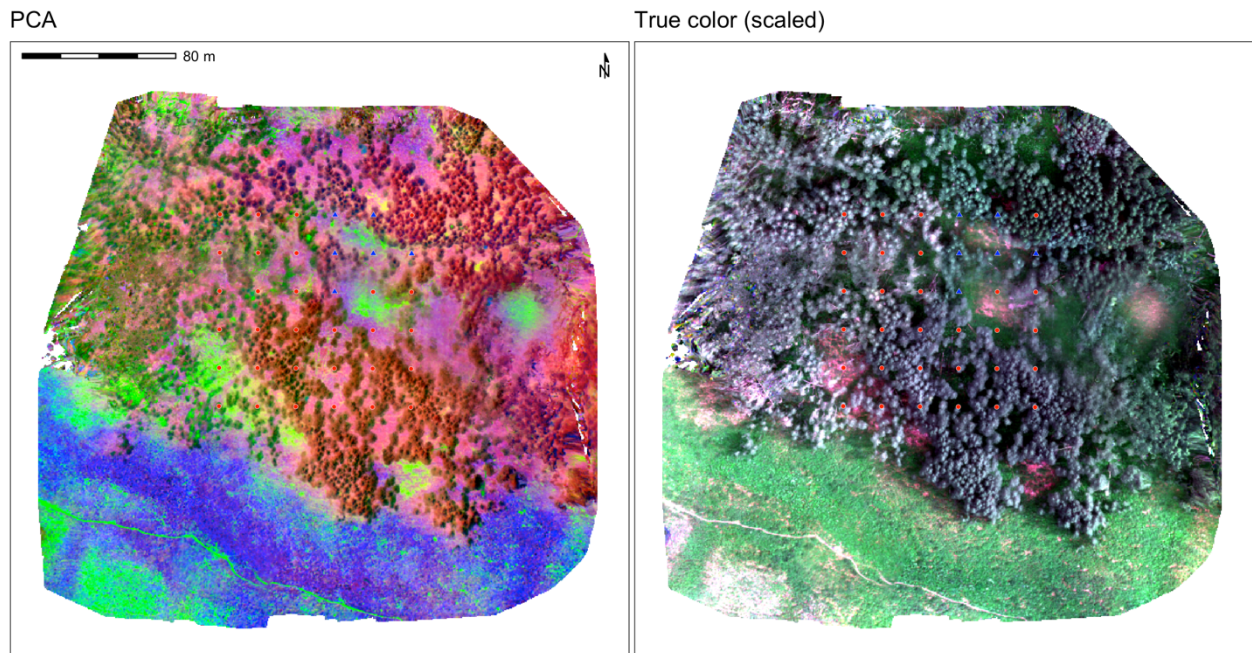1 **Supporting Information**
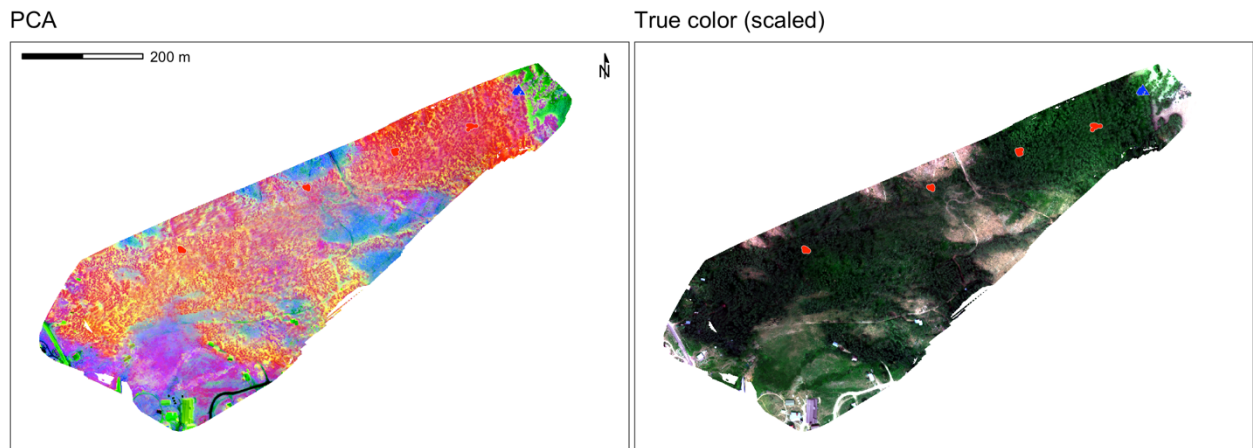
2

3 **Figure S1.** False color multispectral imagery for the *Ben-1ha* site. Triploid and diploid plots are

4 labeled as red and blue points respectively.

6 **Figure S2.** False color multispectral imagery for the *Jolanta-1* site. Triploid and diploid plots are

7 labeled as red and blue points respectively.
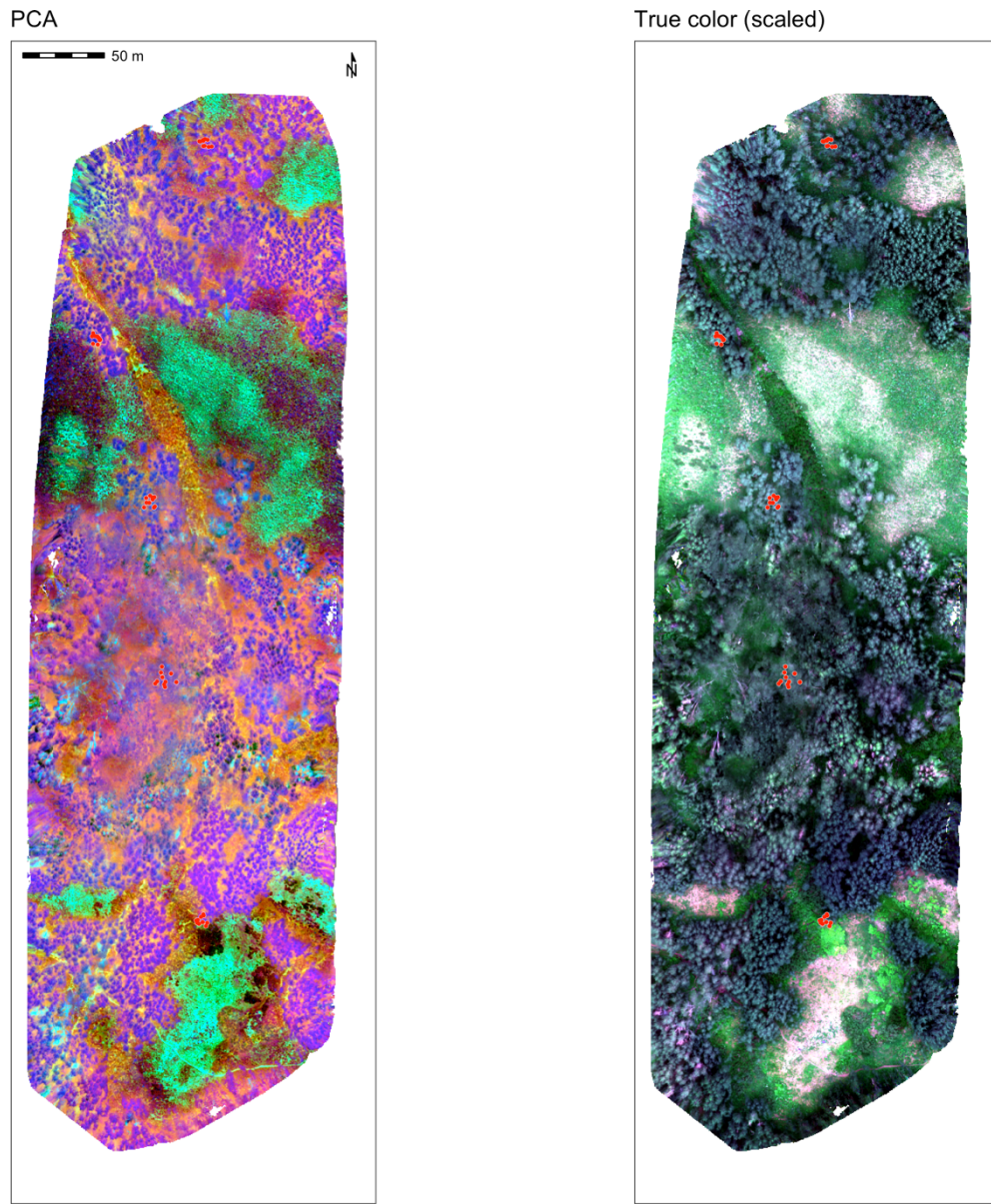
PCA

True color (scaled)

Ploidy • triploid ▲ diploid

8

9

10   **Figure S3.** False color multispectral imagery for the *Jolanta-2* site. Triploid and diploid plots are

11   labeled as red and blue points respectively.
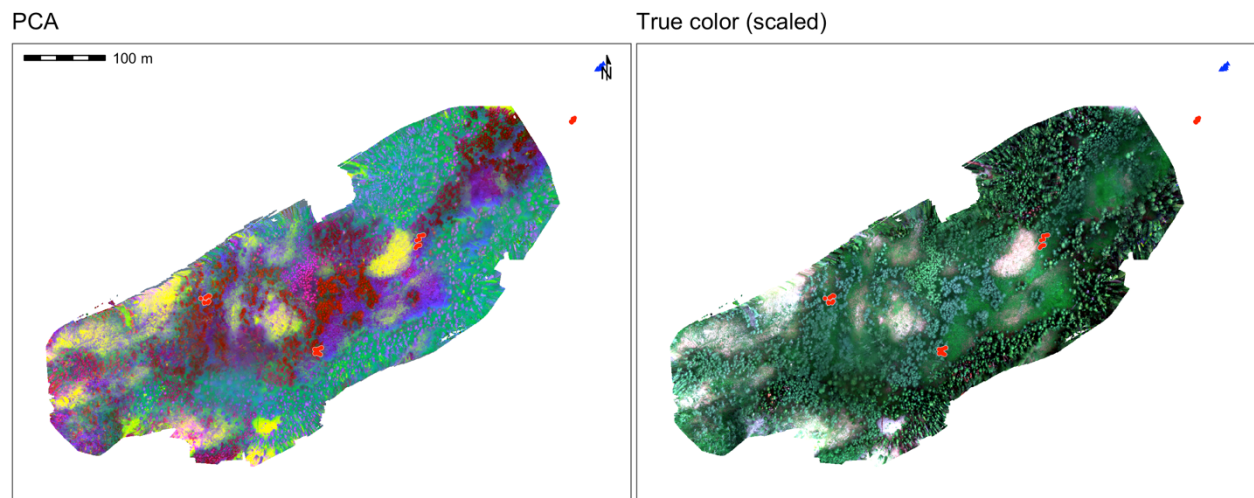

12

13   **Figure S4.** False color multispectral imagery for the *Jolanta-3* site. Triploid and diploid plots are

14   labeled as red and blue points respectively. The two clusters of genetic samples at the top right of

15   the image were not covered by the imagery.

16

17   **Figure S5.** Classification error rate for predictions of ploidy level. In this analysis, models were

18   trained on data from one site (columns) and tested on data from another site (rows). Error rates at

19   each train-test combination reflect mean values across an ensemble of ten random forest

20   classifiers. Gray cells indicate cases where data were not available for the cross-validation, e.g. if

21   training data did not include points in both diploid and triploid classes.
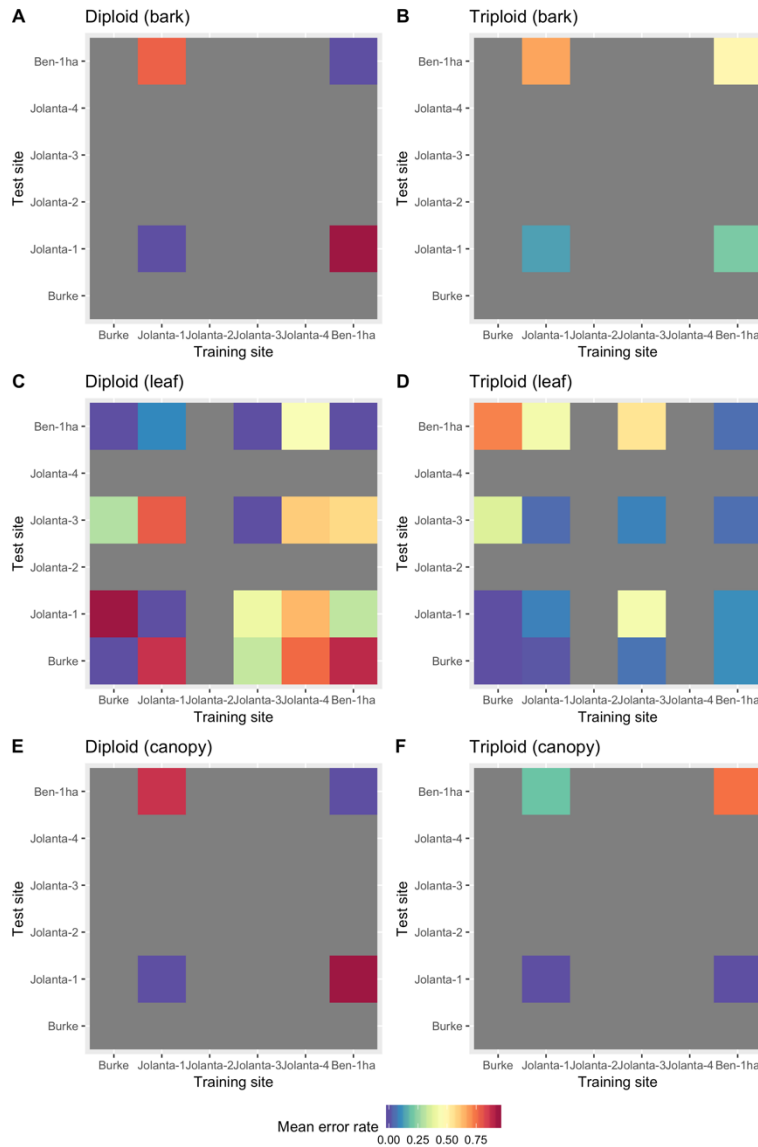

22

23

24   **Figure S6.** Distribution of error rates of random forest classifiers trained on a single site and

25   tested at all other sites. Boxes indicate interquartile ranges and are shown in blue for diploids and

26   red for triploids. Error rates at each train-test combination reflect mean values across an

27   ensemble of ten random forest classifiers. Missing bars indicate cases where data were not

28   available for the cross-validation, e.g. if training data did not include points in both diploid and
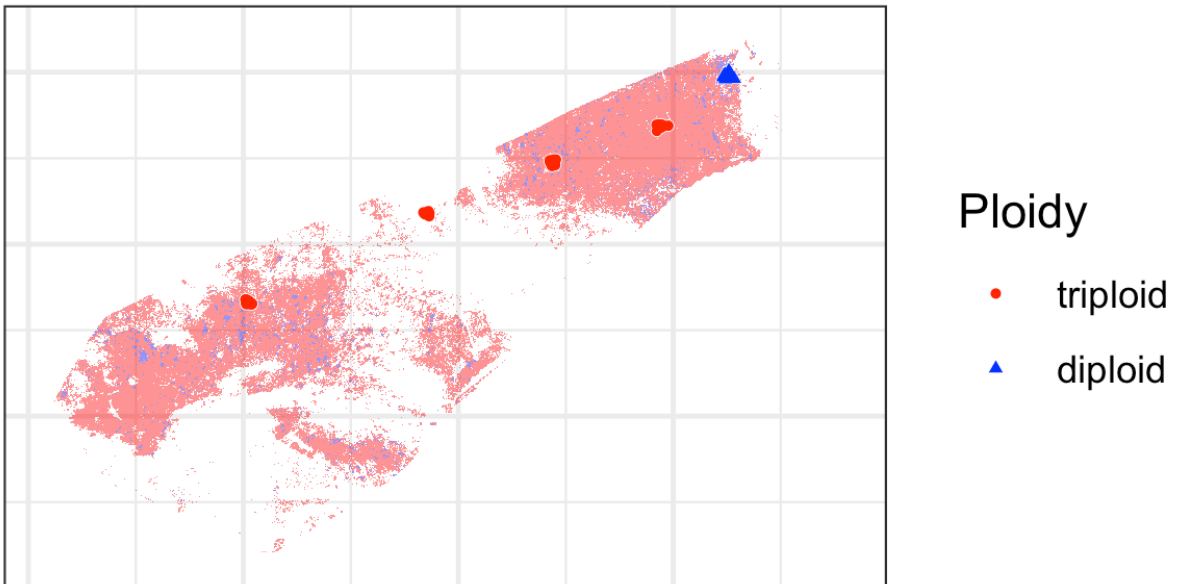
29   triploid classes.
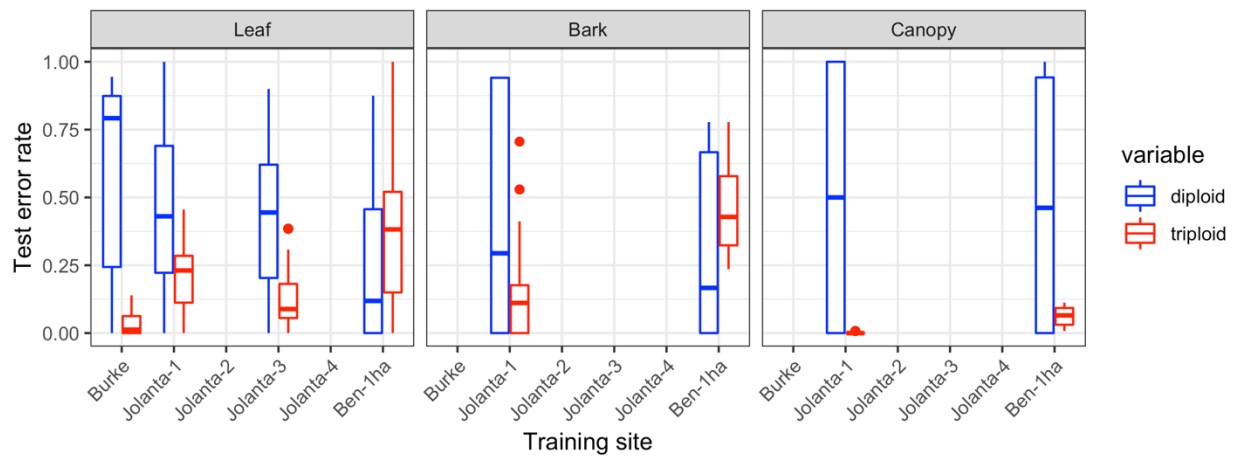
30

31

32   **Figure S7.** Spatial predictions of an ensemble of random forest classifiers at the *Ben-1ha* site,

33   with canopy pixels shaded light red (triploids) or light blue (diploids). Georeferenced genetic

34   samples are shown as red circles (triploids), or blue triangles (diploids).
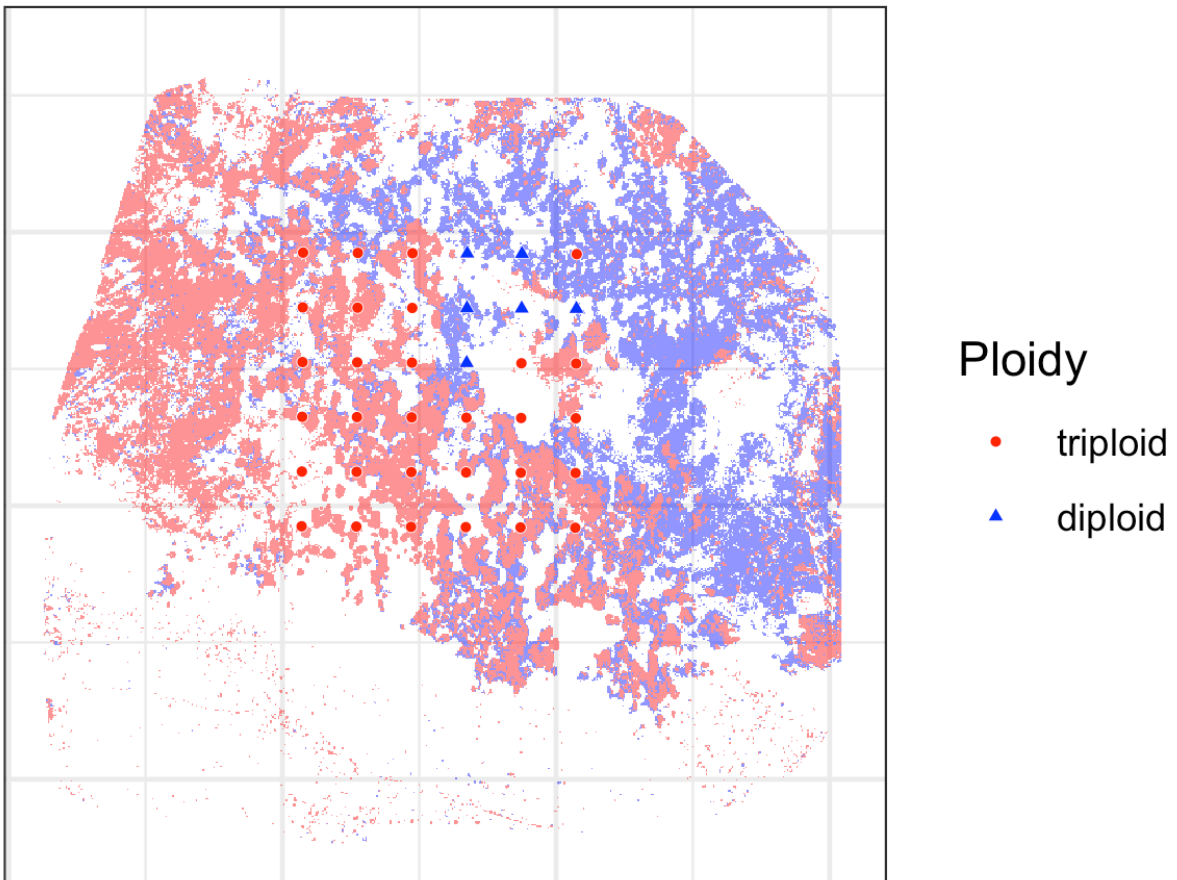
35

36

37   **Figure S8.** Spatial predictions of an ensemble of random forest classifiers at the *Jolanta-1* site,

38   with canopy pixels shaded light red (triploids) or light blue (diploids). Georeferenced genetic

39   samples are shown as red circles (triploids), or blue triangles (diploids).
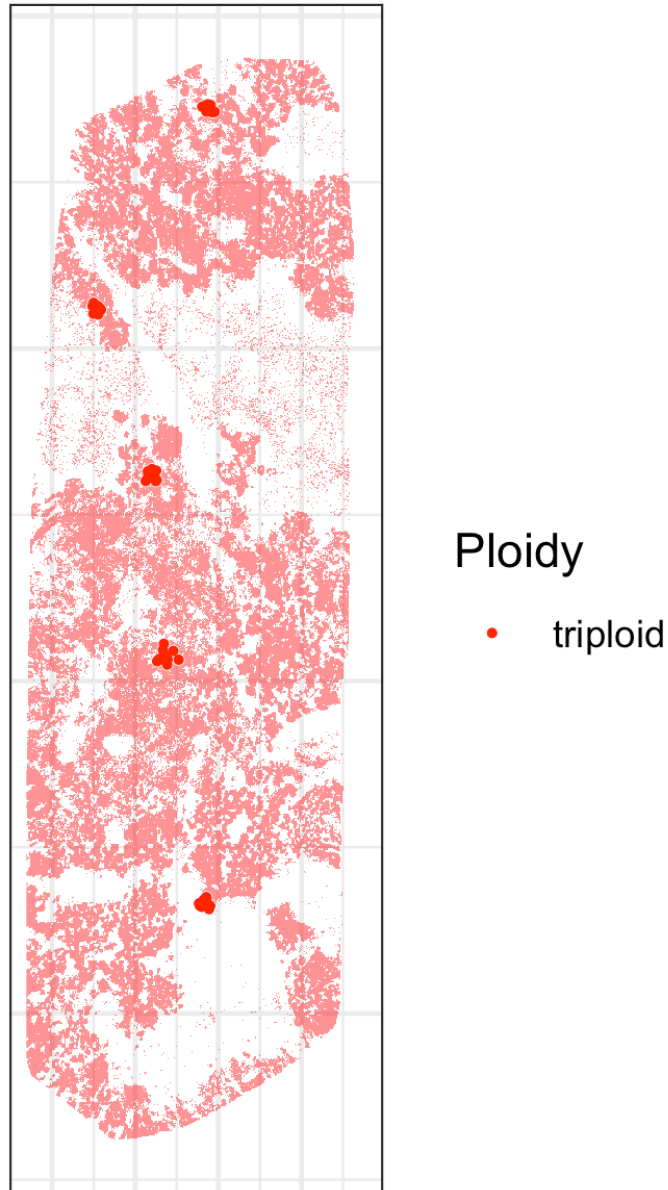

40

41

42   **Figure S9.** Spatial predictions of an ensemble of random forest classifiers at the *Jolanta-2* site,

43   with canopy pixels shaded light red (triploids) or light blue (diploids). Georeferenced genetic

44   samples are shown as red circles (triploids), or blue triangles (diploids).

45

46

47   **Figure S10.** Spatial predictions of an ensemble of random forest classifiers at the *Jolanta-3* site,

48   with canopy pixels shaded light red (triploids) or light blue (diploids). Georeferenced genetic

49   samples are shown as red circles (triploids), or blue triangles (diploids). The two clusters of

50   genetic samples at the top right of the image were not covered by the imagery.

51