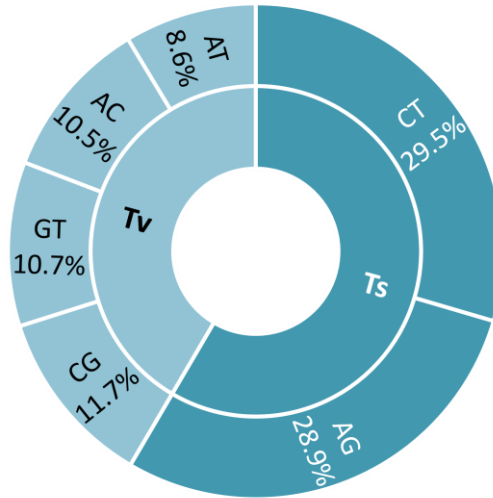
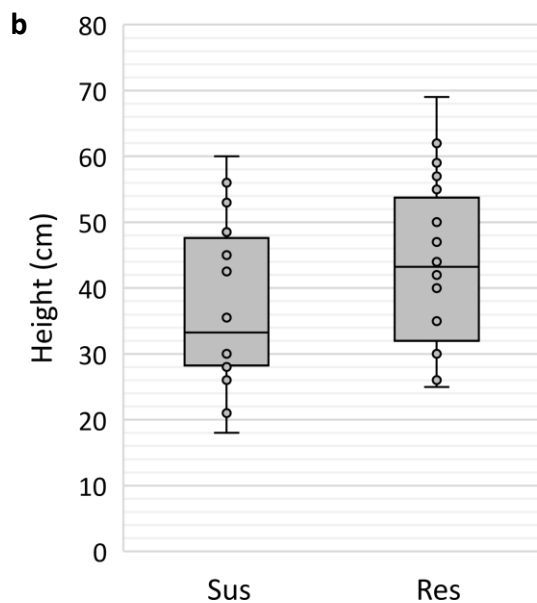
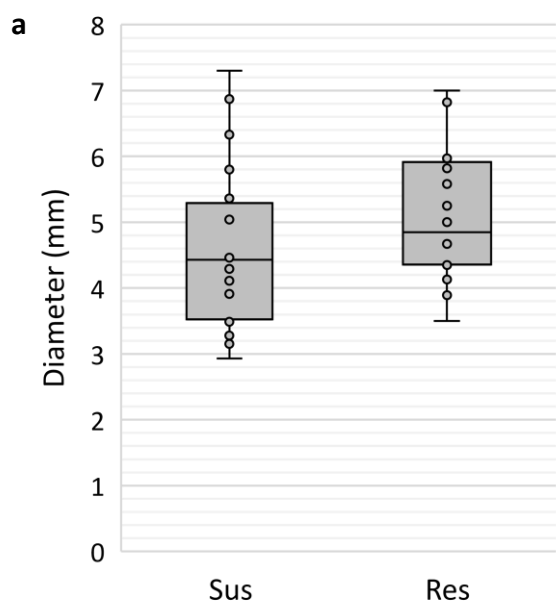


Transitions and Transversions



Supplementary Figure S1. Type of SNPs identified in *P. pinaster* RNA-seq analysis. Ts – transitions; Tv – transversions.



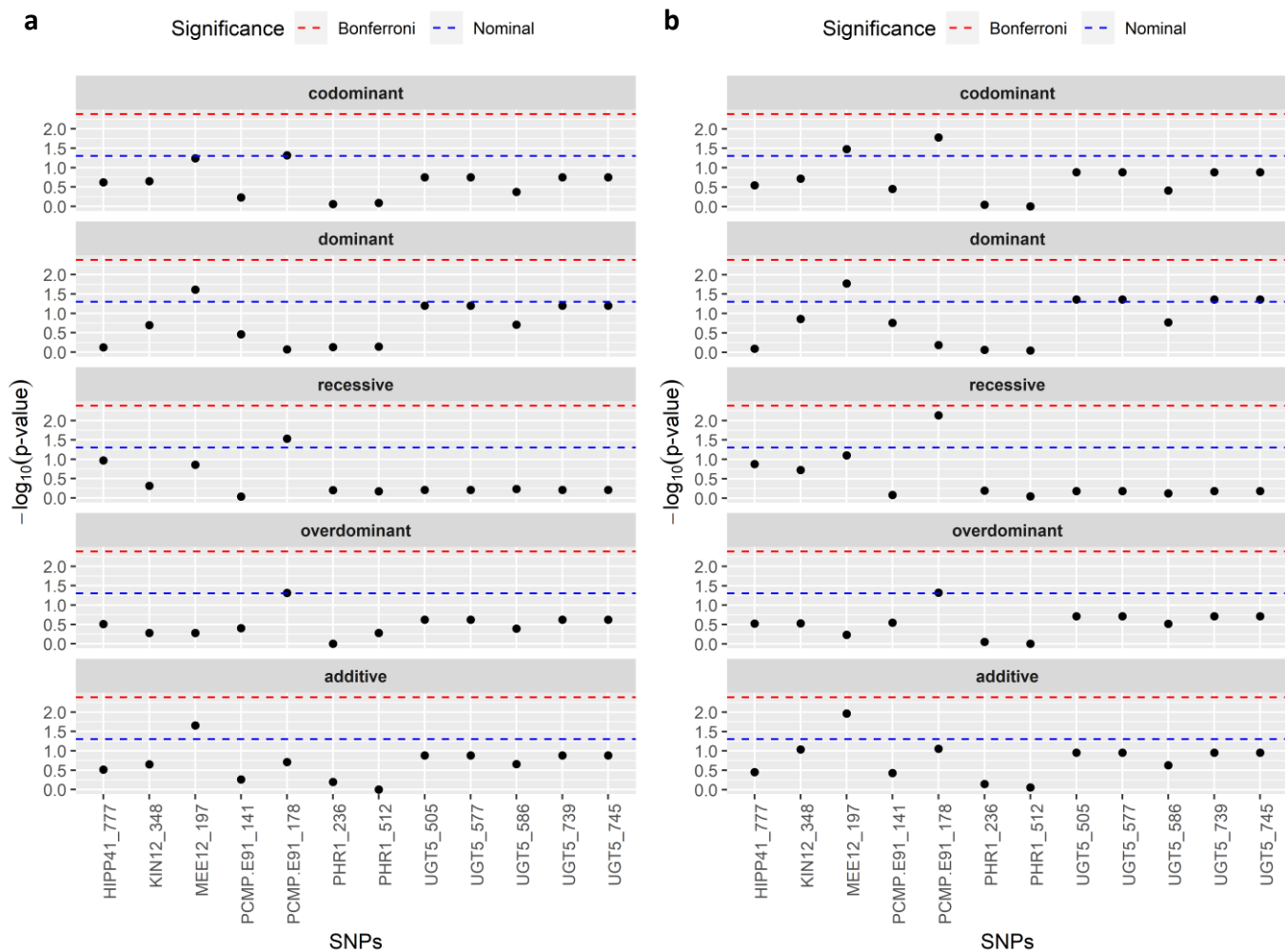
c

	<i>N</i>	Mean (mm)	SD	<i>p</i> -value
Susceptible	20	4.59	1.20	0.13
Resistant	20	5.16	1.01	

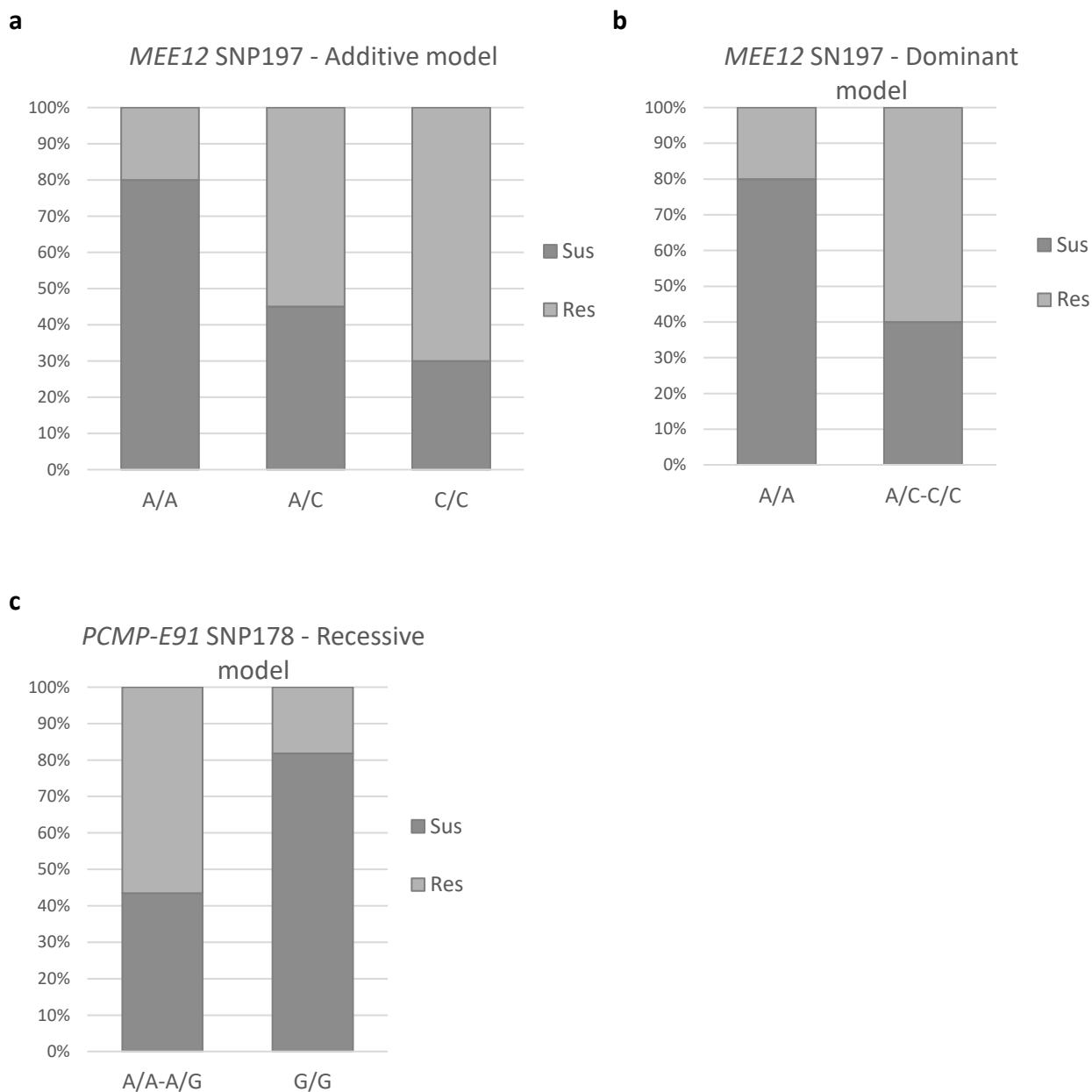
d

	<i>N</i>	Mean (cm)	SD	<i>p</i> -value
Susceptible	20	37.3	12.4	0.11
Resistant	20	43.9	12.4	

Supplementary Figure S2. Boxplots of the height and diameter at the base of the stem of inoculated plants (half-sib family 440) and *t*-test results for the comparison of these parameters' means between susceptible and resistant plants. (a) Boxplot of diameter at the base of the stem and (b) of height. Both measurements were made before inoculations. (c) Results of the two-sample unpaired *t*-test between the mean diameter of susceptible and resistant plants. (d) Results of the two-sample unpaired *t*-test between the mean height of susceptible and resistant plants. *N*, number of plants; SD, standard deviation.



Supplementary Figure S3. Association analysis of the SNPs in the six sequenced gene fragments under different genetic models with resistance to PWN. All analyses were performed with SNPAssoc using a logistic regression model (a) or a logistic regression model adjusted for diameter at the basis of the stem and plant height (b).



Supplementary Figure S4. Genotypes distribution for SNPs associated with phenotype. (a) *MEE12* SNP 197 genotypes distribution following the additive genetic model and (b) following the dominant genetic model. (c) *PCMP-E91* SNP 178 genotypes distribution following the recessive genetic model. Susceptible (Sus) plants are represented in dark grey, while resistant (Res) plant are in light grey.