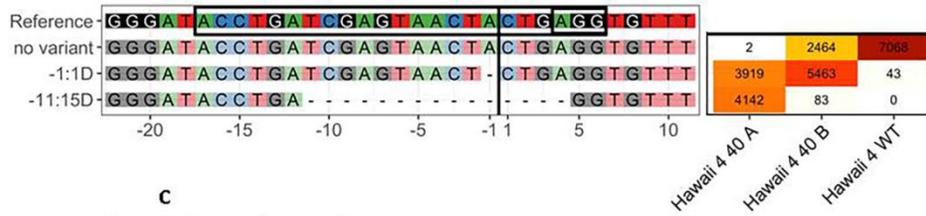
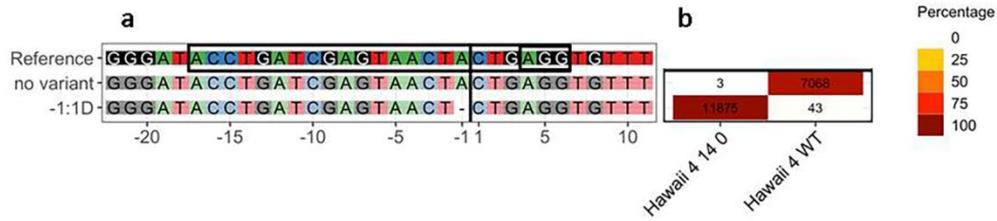


9 (Fv9)	A	Pale green shoot, leaf, mostly albino shoot cluster
9 (Fv9)	B	Albino shoot, leaf, mostly albino shoot cluster
12	A	Albino shoot, leaf
12	B	Albino shoot, leaf
12	C	Albino shoot, leaf

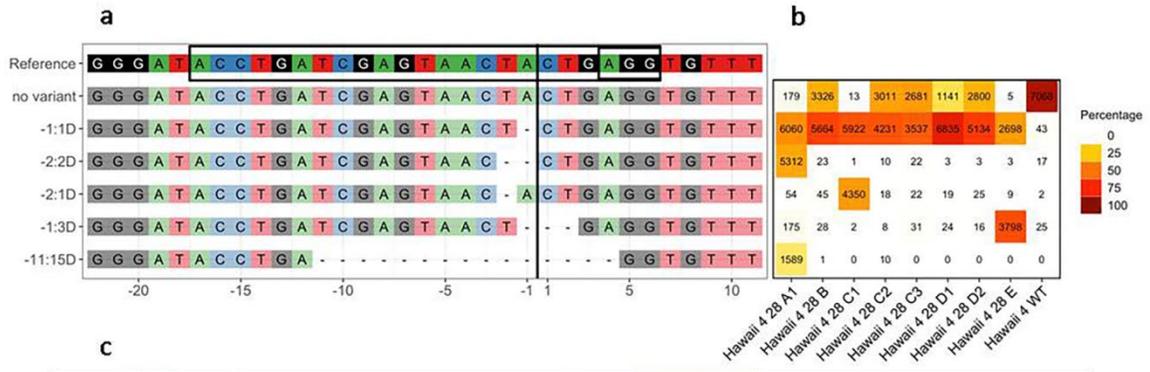
Hawaii 4 9, 12



**c**

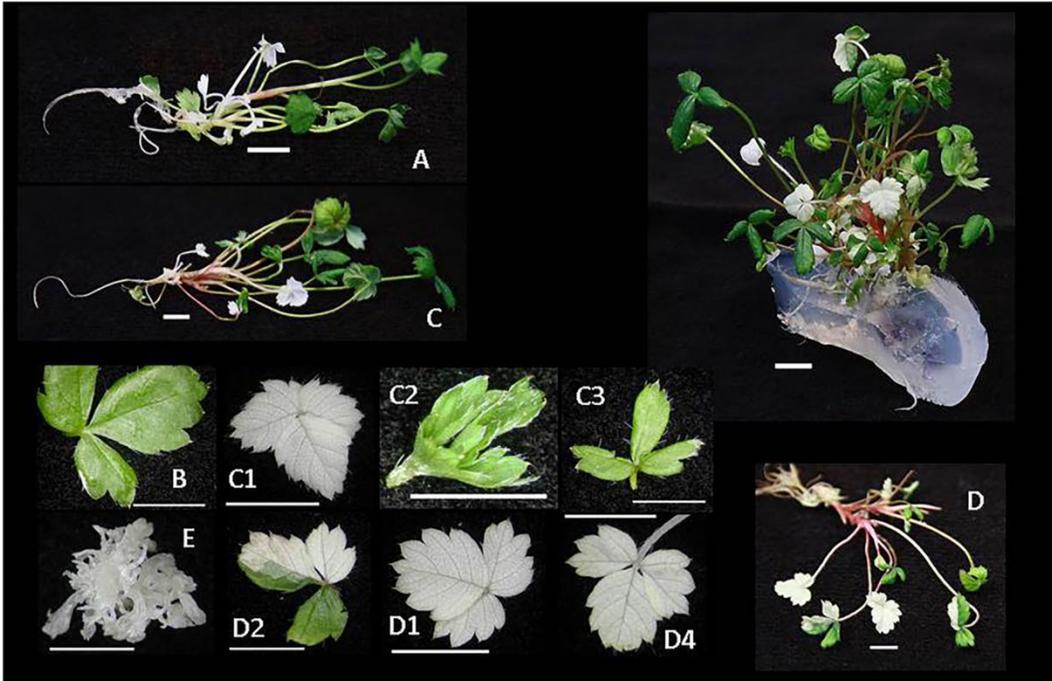
14		Albino shoot, leaf
40	A	Albino shoot
40	B	Variegated (mottled), separate rooted shoot

Hawaii 4 14, 40

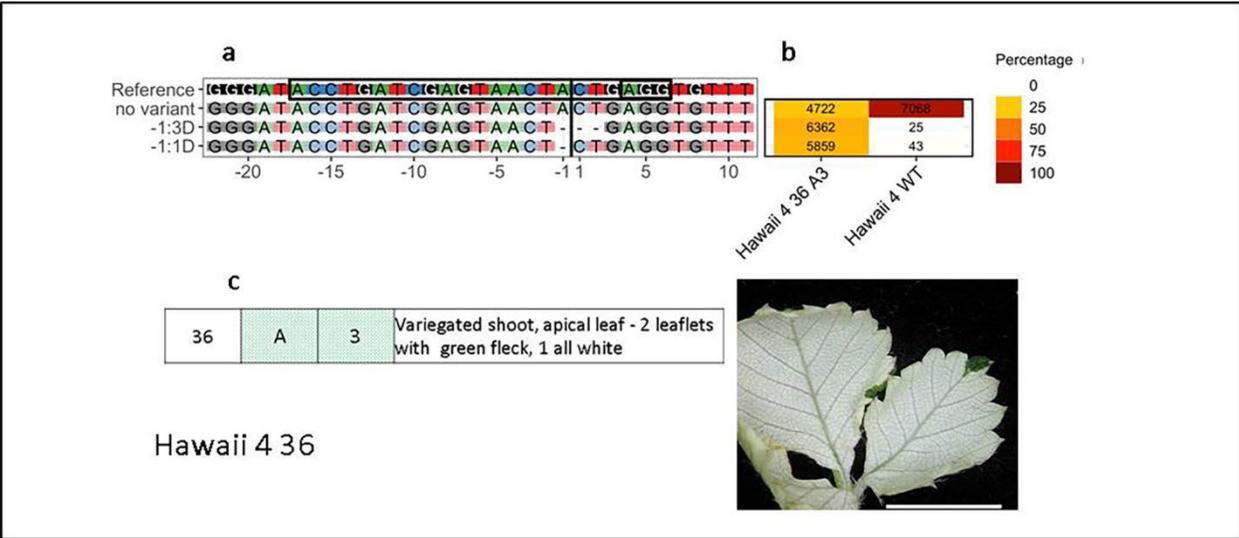
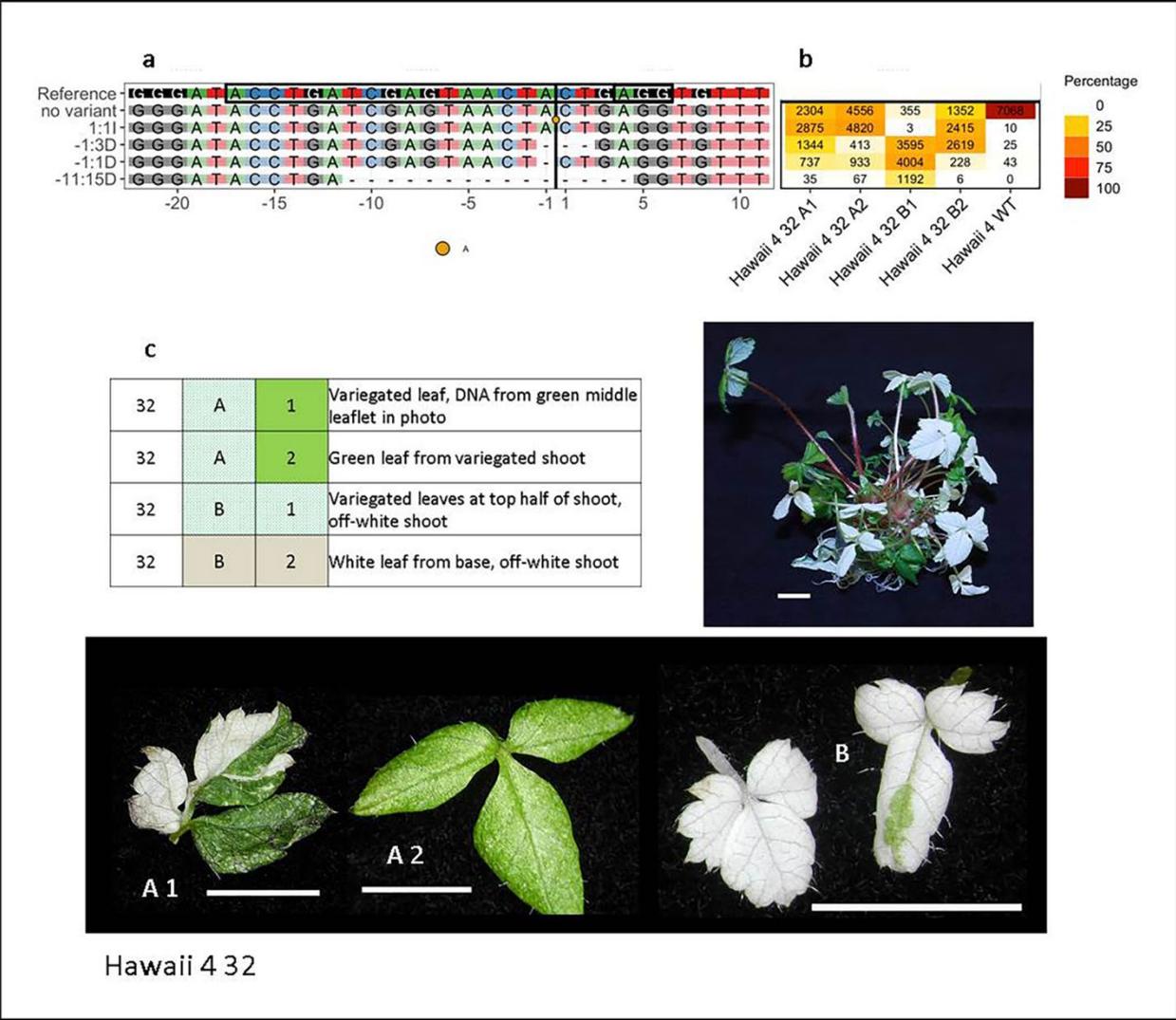


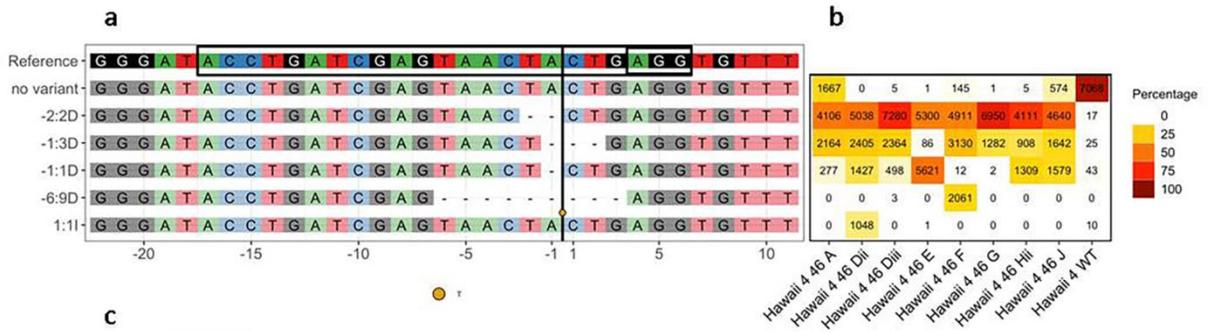
**c**

28	A	1	White axillary, variegated shoot	28	C	3	Green axillary shoot, green leaf
28	B		Variegated leaf, very small white sector	28	D	1	Variegated shoot, variegated leaf (very small green sector leaf edge tip)
28	C	1	Shoot axillary which is half green, half white, albino leaf	28	D	2	Variegated shoot, variegated leaf ('harlequin')
28	C	2	Shoot axillary which is half green, half white, green leaf	28	E		All-albino shoot cluster, leaf



Hawaii 4 28



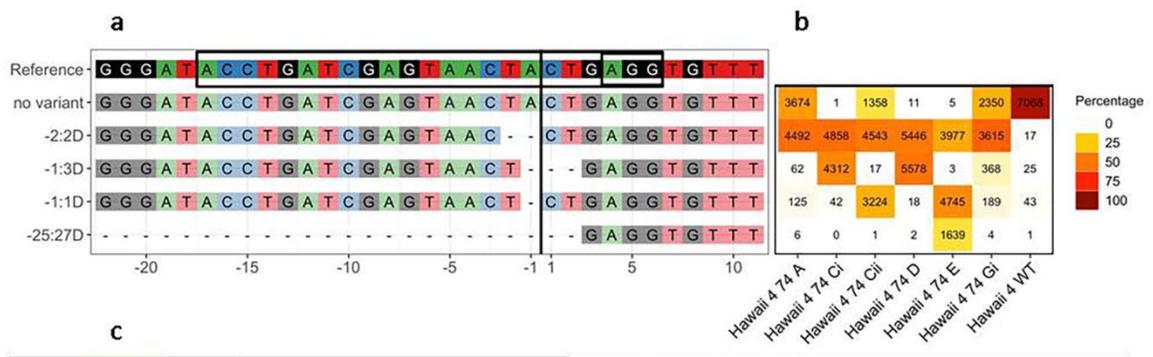


**c**

46	A		Green rooted shoot
46	D	ii	Albino leaf, from shoot with white and green leaves
46	D	iii	Apical albino leaves, green bits at base. Separate shoot from Dii
46	E		Small albino shoot
46	F		Small albino shoot
46	G		Rooted very pale shoot
46	H	ii	Variegated shoot, white basal leaf
46	J		Pale green shoot, leaf

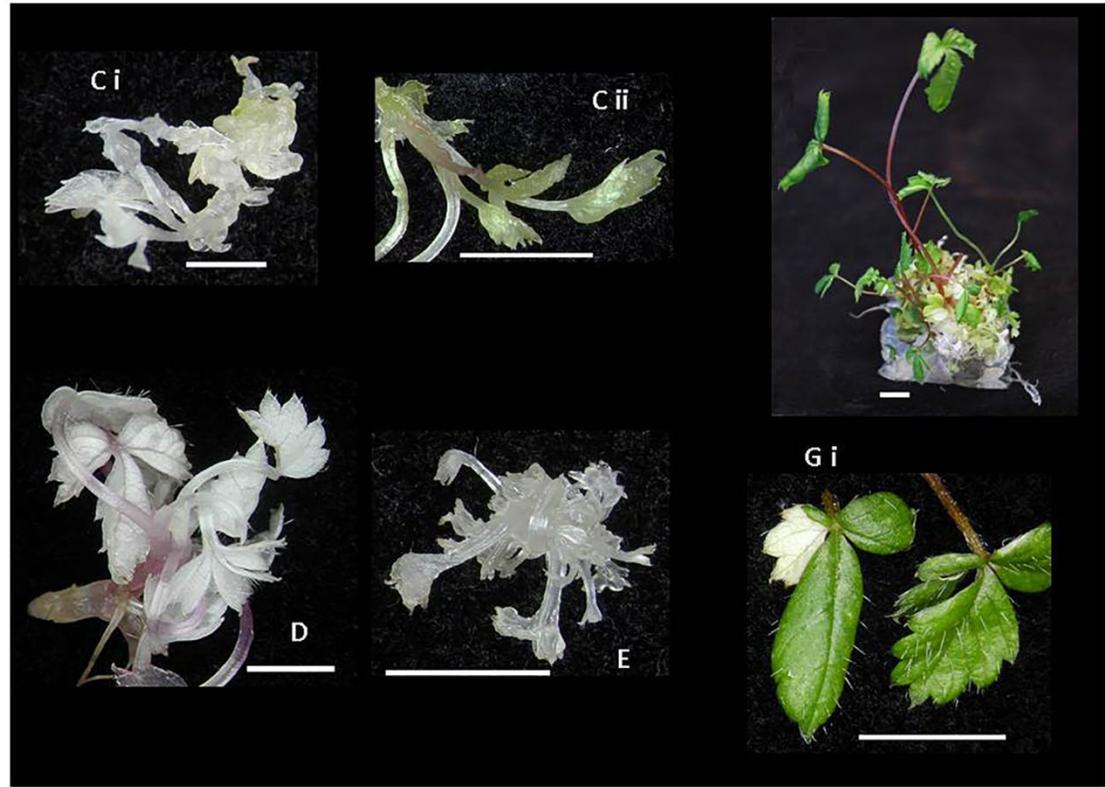


Hawaii 4 46

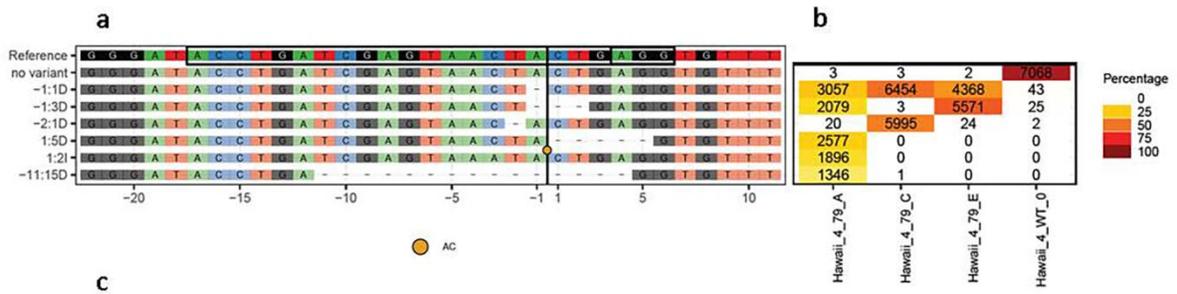


**c**

74	A		Green rooted shoot, leaf	74	D		Rooted albino shoot
74	C	i	Variegated shoot, albino axillary shoot, leaf	74	E		Albino shoot
74	C	ii	Pale green axillary shoot, leaf	74	G	i	Variegated shoot, variegated leaf



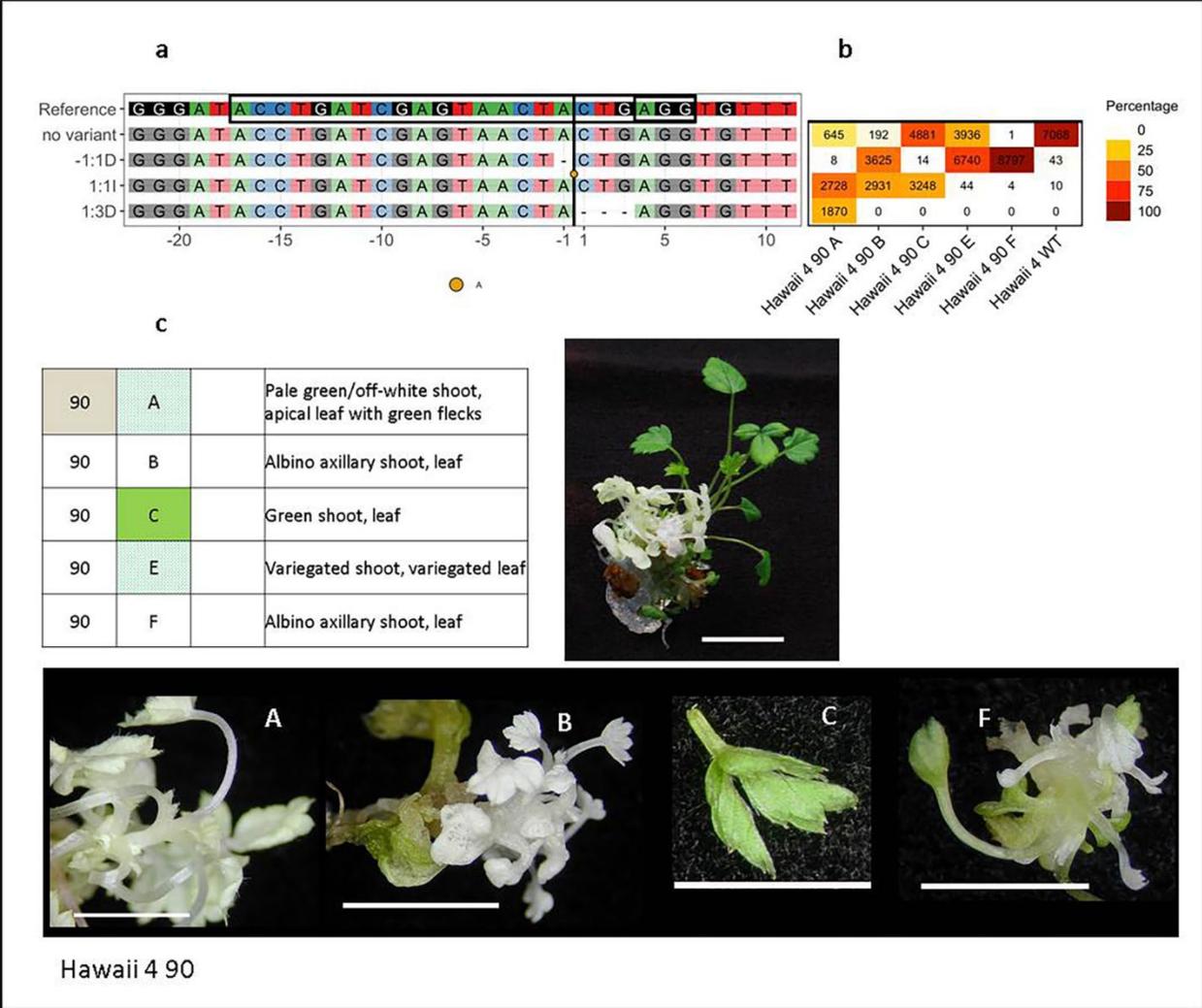
Hawaii 4 74

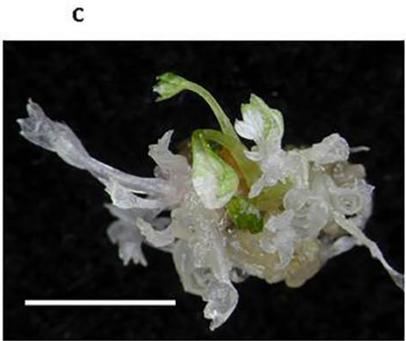
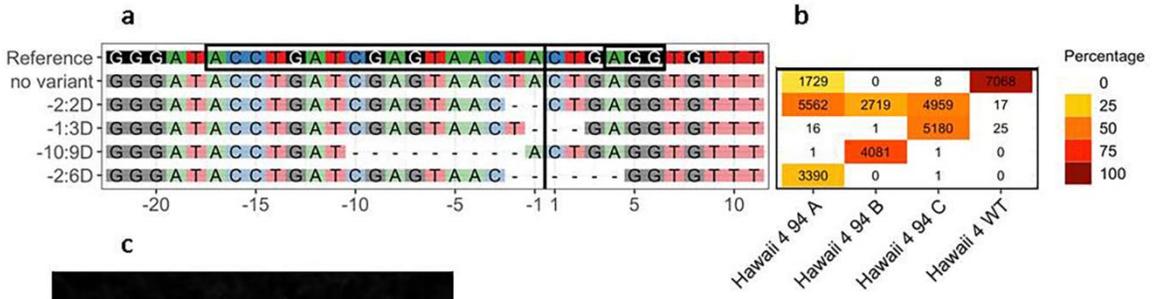


**c**

79	A		Albino shoot, leaf
79	C		Albino shoot, leaf
79	E		Albino shoot, leaf

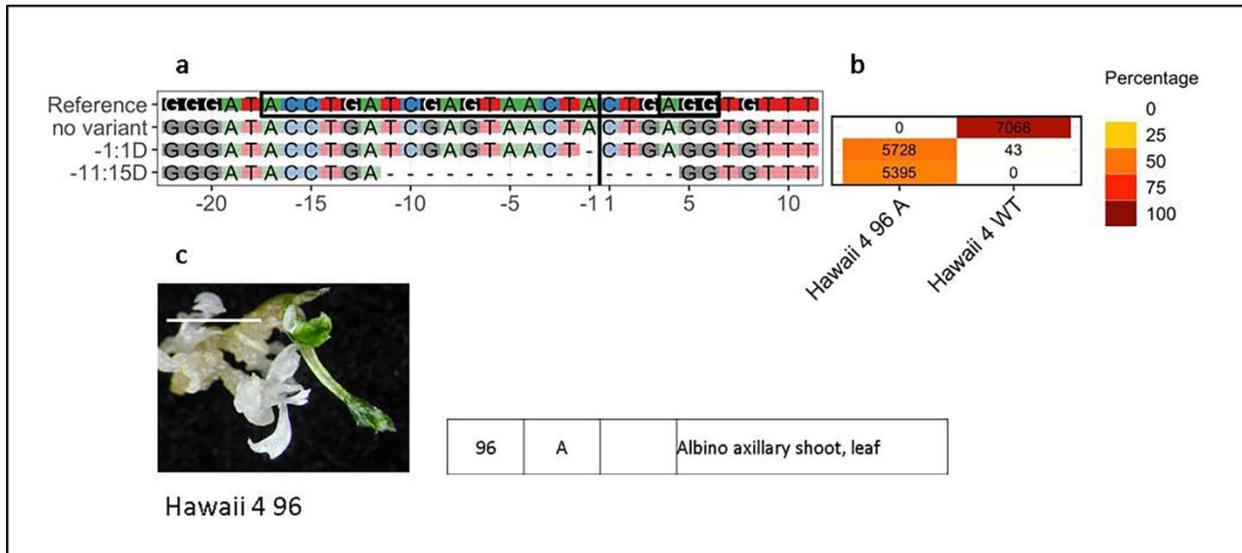
Hawaii 4 79





94	A	Variegated shoot, variegated leaf
94	B	Albino shoot, leaf
94	C	Albino shoot, leaf

Hawaii 4 94



**Fig. S1.** Sequence mutations and corresponding phenotypes of CRISPR/Cas9 transgenic lines of ‘Hawaii 4’.

Sequence mutations and allelic variants with corresponding phenotypes in transgenic shoot lines of *Fragaria* ‘Hawaii 4’. **a** Alignment of the sequence for each variant to the reference sequence. To the left of the panel, each sequence variant type is identified by the location of the mutation relative to the cut site:number bases deleted (D), inserted (I), or substituted (SNV:location relative to cut site and base substitution). Insertion positions are indicated by an orange circle with the inserted base/s shown. Deletions of 3 bases or multiples of 3 result in amino acid loss. Other deletions and insertions cause frameshift and generate stop codons within exon 7, resulting in truncated PDS protein. Insertions and substitutions result in amino acid substitutions. The cut site is shown by a black vertical line; the target site and PAM site (AGG) are within the box in the reference sequence. **b** Heat map showing the number and percentage of variant reads for each sample. Samples are arranged in columns and identified below the panel. **c** Images of phenotypes and an accompanying table giving descriptions for each sequenced sample. Numbers in the first column refer to the shoot line. In subsequent columns individual shoots from a shoot line are designated using a letter (A, B, etc.) and numbers indicate individual leaves from individual shoots. White, pale green or dark green box shading indicates albino, pale green/variegated or green phenotype respectively, for shoots and leaves. WT=wild type. Scale bars are 5 mm.