Table S8. Selected predicted off-targets against members of the *PpKAI2L* gene family clade i.i-iii for the analysis of off-target activity.

On-target gene	Predicted off-targets sequence[a,b]	Off-target annotation[c]
PpKAI2L-F	AGA**G**G**CG**TTTCCACACCGTC*CGG*	OffT1*: 5’ UTR of Pp3c15_18460 locus
	A**A**ACGTATTTCCACA**T**C**C**T**G***TGG*	OffT2*: Exon of Pp3c16_12790
PpKAI2L-J	ACGTT**CC**GAGCC**C**TCAGG**C**A*AGG*	OffT2*: 3’ UTR of Pp3c15_11920 locus
	ACGTTG**A**GAGCC**G**T**G**A**T**GTA*GGG*	OffT5*: Exon of Pp3c15_4920
PpKAI2L-K	A**G**GTGGC**C**AA**G**TACATGGT**G***AGG*	OffT1*: Exon of Pp3c5_23900
	AA**A**TGG**A**G**C**ATTACAT**A**GTA*TGG*	OffT2*: 3’ UTR of Pp3c2_2130 locus
	AA**A**TGGCGAA**A**T**C**CAT**T**GTA*AGG*	OffT3*: Exon of Pp3c15_5520

[a]: Protospacer adjacent motif (PAM) sequence preceded by crRNA sequence is shown in italics and underlined. SS; Specificity score data from CRISPOR (Hsu *et al.*, 2013),

[b]: Mismatch of off-target sequence with respect to the crRNA sequence is shown in red,

[c]: Identifier and annotation of genomic elements from Phytozome V11 - *P. patens* genome V3.3

*Off-targets for which the activity of the sgRNA was measured by sequencing PRC fragments of the surrounding predicted site in eight mutants