

1	M	G	T	L	S	A	V	T	H	T	A	C	A	G	Y	H	L	P	E	T	G	S	L
1	<u>atg</u> gggactctgagcgccgtcacacacacagcttgtgcgggatatcatttgcctgaaaccggttcctt																						
24	K	A	K	S	P	P	T	Q	S	S	A	M	E	D	E	I	A	A	L	V	V	D	N
70	aaagcgaaaagcccccccacccaaagtccagccatggaagatgaaatcgccgcactgggtgttgacaac																						
47	G	S	G	M	C	K	A	G	F	A	G	D	D	A	P	R	A	V	F	P	S	I	V
139	ggatccggtatgtgcaaagccggatttgccggagacgatgcccctcgtgctgtcttccccctccatcgtc																						
70	G	R	P	R	H	Q	G	V	M	V	G	M	G	Q	K	D	S	Y	V	G	D	E	A
208	ggtcgccccaggcatcagggagtgtggtgggtatgggccagaaggacagctacgttgggtgacgaagcc																						
93	Q	S	K	R	G	I	L	T	L	K	Y	P	I	E	H	G	I	V	T	N	W	D	D
277	cagagcaagagaggtatcctgaccctgaagtaccccatcgagcacggtattgtgaccaactgggatgac																						
116	M	E	K	I	W	H	H	T	F	Y	N	E	L	R	V	A	P	E	E	H	P	V	L
346	atggagaagatctggcatcacaccttctacaatgagctgagagttgcccctgaggagcaccctgtcctg																						
139	L	T	E	A	P	L	N	P	K	A	N	R	E	K	M	T	Q	I	M	F	E	T	F
415	ctcacagagggccctctgaaccccaaagccaacagggagaagatgacccagatcatgttcgagaccttc																						
162	N	T	P	A	M	Y	V	A	I	Q	A	V	L	S	L	Y	A	S	G	R	T	T	G
484	aacacccccgccatgtacgttgccatccaggctgtgctgtccctgtatgcctctggctcgtaaccacgggt																						
185	I	V	M	D	S	G	D	G	V	T	H	T	V	P	I	Y	E	G	Y	A	L	P	H
553	attgtcatggactccgggtgatgggtgacccacagtgcccattctacgagggctacgccctgccccac																						
208	A	I	L	R	L	D	L	A	G	R	D	L	T	D	Y	L	M	K	I	L	T	E	R
622	gccatcctgcgtctggacttggccggccgcgacctcacagactacctcatgaagatcctgacagagcgt																						
231	G	Y	S	F	T	T	T	A	E	R	E	I	V	R	D	I	K	E	K	L	C	Y	V
691	ggctactccttcaccaccacagccgagagggaaatcgtgcgtgacatcaaggagaagctctgctatgtc																						
254	A	L	D	F	E	Q	E	M	G	T	A	A	S	S	S	S	L	E	K	S	Y	E	L
760	gccctggacttcgagcaggaatgggcactgctgcctcctcctcctcctggagaagagctacgagctg																						
277	P	D	G	Q	V	I	T	I	G	N	E	R	F	R	C	P	E	A	L	F	Q	P	S
829	cctgacggacaggtcatcaccattggcaatgagaggttccgttgccccgagggccctcttccagccttcc																						
300	F	L	G	M	E	S	C	G	I	H	E	T	T	Y	N	S	I	M	K	C	D	V	D
898	ttcctcggatggagtcctgcggaatccacgagaccacctacaacagcatcatgaagtgcgacgtcgat																						
323	I	R	K	D	L	Y	A	N	T	V	L	S	G	G	T	M	Y	P	G	I	A	D	
967	atccgtaaggacctgtacgccaacacccgtgctgtctgtgaggtaccaccatgtaccccggcacgcggac																						
346	R	M	Q	K	E	I	T	A	L	A	P	S	T	M	K	I	K	I	I	A	S	P	E
1036	aggatgcagaaggagatcacagccctggccccatccaccatgaagatcaagatcattgcctcacctgag																						
369	R	K	Y	S	V	W	I	G	G	S	I	L	A	S	L	S	T	F	Q	Q	M	W	I
1105	cgtaaatactctgtctggatcggaggctccatcctggcctccctgtccaccttccagcagatgtggatc																						
392	S	K	Q	E	Y	D	E	S	G	P	S	I	V	H	R	K	C	F	*				
1174	agcaagcaggagtacgatgagtcgggcccctccatcgtccaccgcaaagtcttctaa																						

Cagactgttctcctccccctccccaaacgccccaaacaacttcagctctgtgcaaaacaaccacacacaccacatttctcata  
 cacactcaggcgagagcctagacgaccaactcattggcatggcttcagttatTTTTTggcgcttgactcaggattttaaaaaactgg  
 aacgatgaaggagacagtaaatgtTTTTTggctagggttaaaaaatagaccccagggttctgcagttgcacatctggggacttaaaaaatg  
 tacattttgtttttctttgagtcattccaaatgtttgttaactgcatattgt

**Figure S5.** A complete nucleotide sequence along with translated amino acid sequence of kawakawa *beta-actin* gene. The number on left side represent the corresponding position of the amino acid and cDNA residues, respectively. x – Start codon; x – stop codon; x – 3' untranslated region.