Supplementary Table S1. Identified allergens of the kiwi extracts.

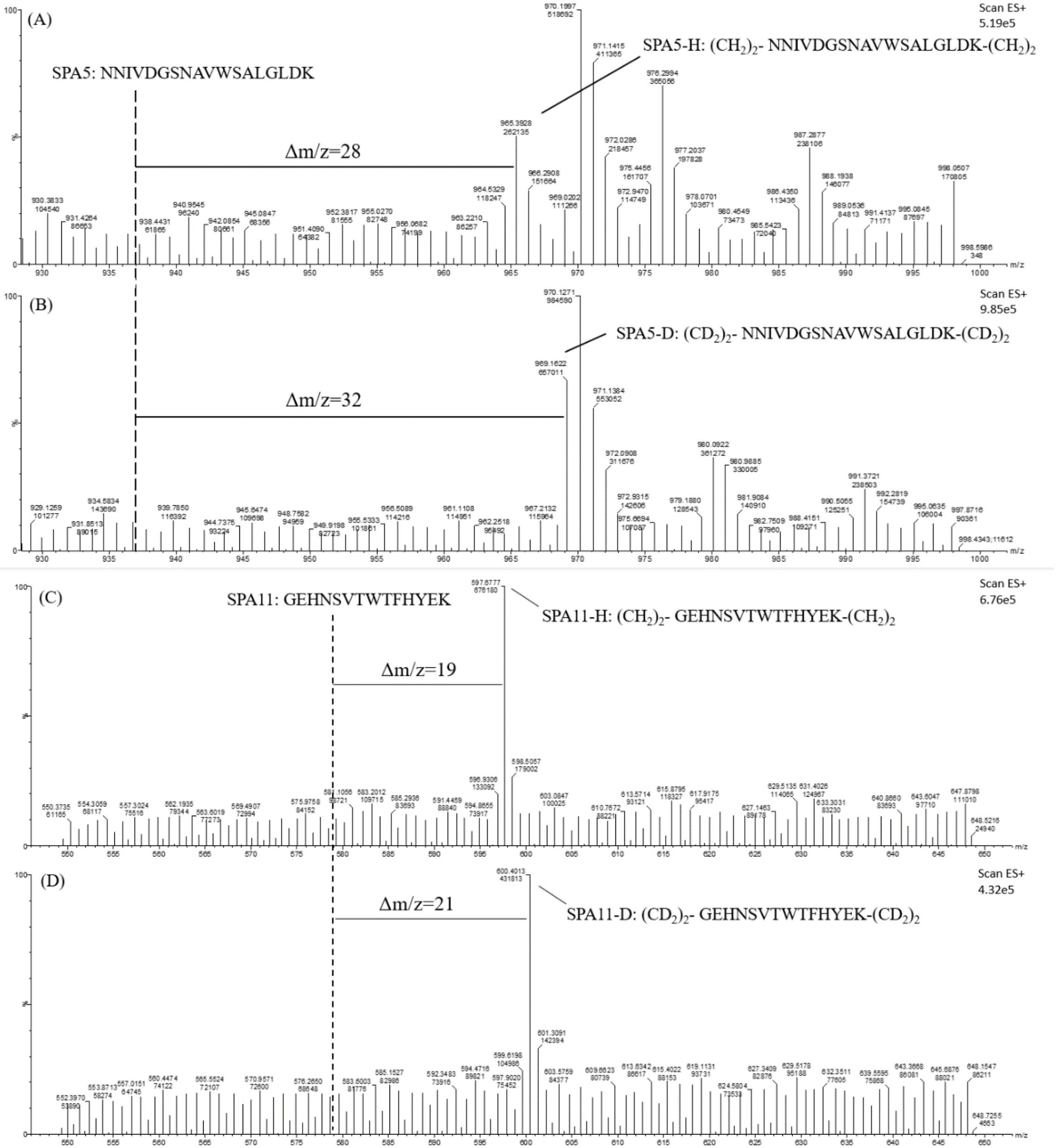
Protein ID	IUIS name	Protein name	MASCOT score	Coverage
P00758	Act d 1	Actinidian	1577	47.9
P81370	Act d 2	Thaumatin-like protein	906	60.9
Q6TPK4	Act d 4	Cysteine proteinase inhibitor 1	287	71.4
P84527	Act d 5	Kiwellin	1469	42.7
P83326	Act d 6	Pectinesterase inhibitor	511	26.2
P85076	Act d 7	Pectinesterase	320	14.1
P86137	Act d 10	Non-specific lipid-transfer protein 1	41	14.1
P85524	Act d 11	Kirola	437	58.7

Supplementary Table S2. BLAST results of candidate peptides with 100% identity and 100% query coverage

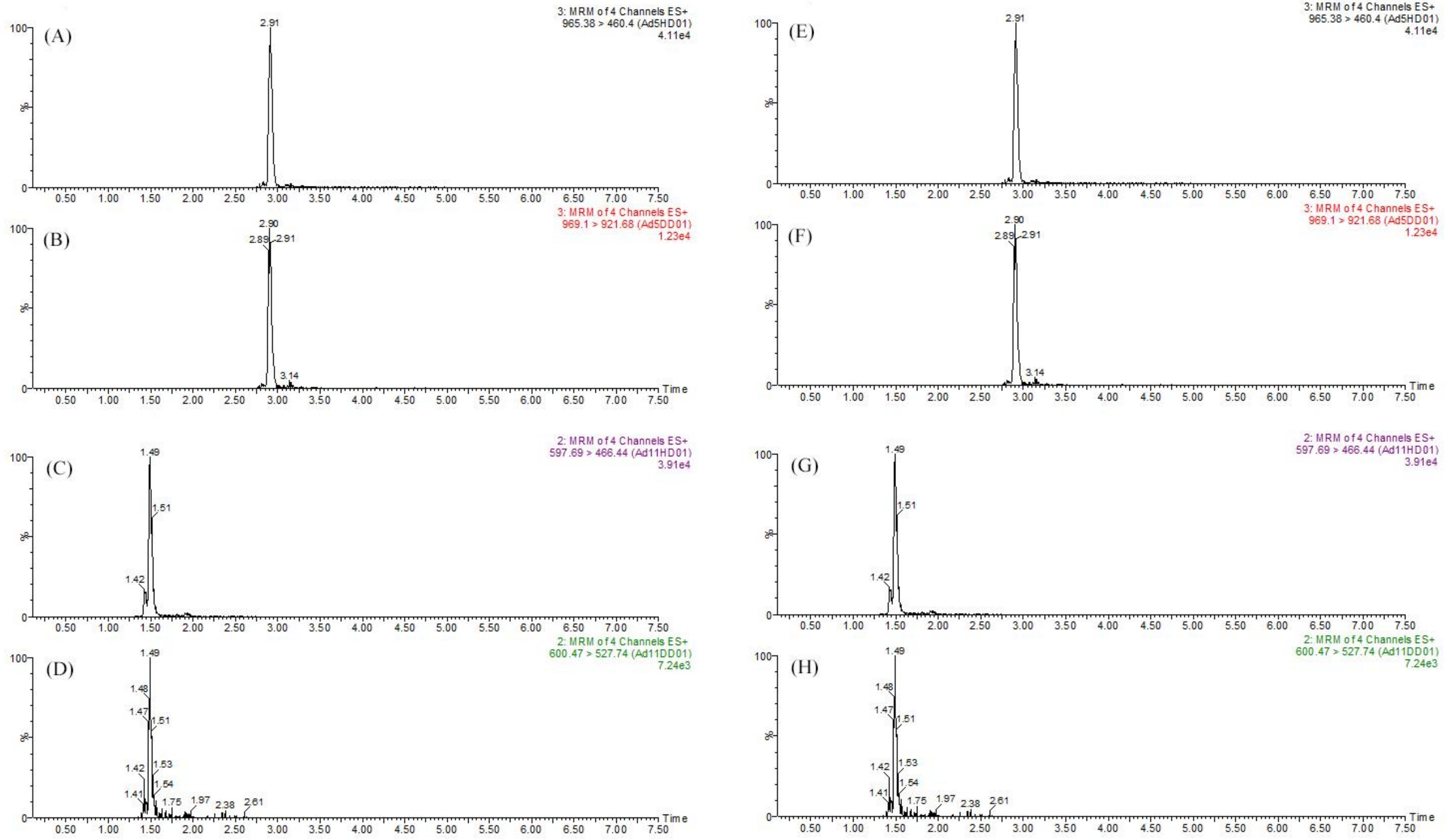
Protein	Peptide sequence	Protein in non-*Actinidia* species (species)	Protein ID
Act d 1	SAGAVVDIK	—[a]	—
Act d 5	NNIVDGSNAVWSALGLDK	—	—
	IVALSTGWYNGGSR	Ripening-related protein grip22 (Vitis vinifera)	Q9M4H4
		Uncharacterized protein (Citrus unshiu)	A0A2H5Q537
		Uncharacterized protein (Vitis vinifera)	F6GU22
		Grip22-like protein (Vitis quinquangularis)	A0A163HAW5
		Uncharacterized protein (Cucumis sativus)	A0A0A0KBF2
		Uncharacterized protein (Cucumis sativus)	A0A0A0KGH1
		Kiwellin-like (Cucumis melo)	A0A1S3CI58
		Uncharacterized protein (Citrus clementina)	V4SG37
		Ripening-related protein (Siraitia grosvenorii)	K7NBR3
		Uncharacterized protein (Gossypium barbadense)	A0A2P5Q249
		Uncharacterized protein (Cucumis sativus)	A0A0A0KDC3
		Kiwellin-like (Gossypium hirsutum)	A0A1U8J808
		kiwellin-like (Cucumis melo)	A0A1S3CNR1
		Uncharacterized protein (Cucumis sativus)	A0A0A0K532
Act d 11	GEHNSVTWTFHYEK	—	—

[a] The query peptide matched to no proteins with 100% identity and 100% coverage after the BLAST search

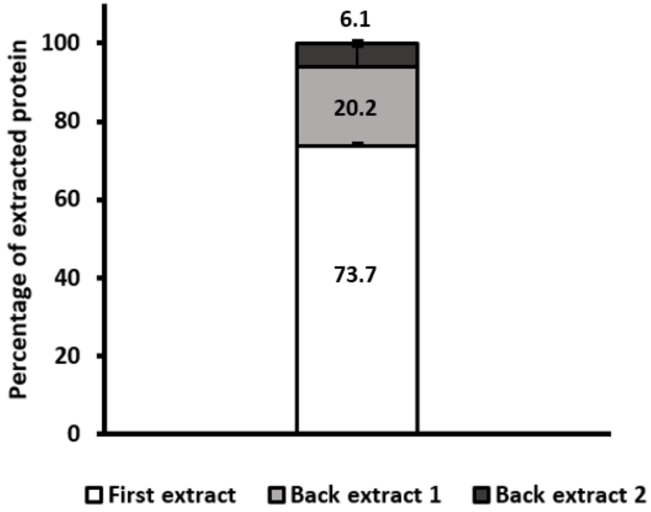
Supplementary Fig S1. Mass spectra of (A) SPA5-H, (B) SPA5-D, (C) SPA11-H and (D) SPA11-D. The dotted line represented the m/z of native signature peptides (SPA5 and SPA11) and Δm/z showed the m/z shift of the signature peptide before and after stable-isotope dimethyl labeling.



Supplementary Fig. S2 MRM chromatograms of (A) SPA5-H (1 μg mL^{-1}), (B) SPA5-D (500 ng mL^{-1}), (C) SPA11-H (1 μg mL^{-1}), and (D) SPA11-D (500 ng mL^{-1}) for the mixture of peptide standards and (E) SPA5-H (568.2 μg mL^{-1}), (F) SPA5-D (500 ng mL^{-1}), (G) SPA11-H (no peak detected), and (H) SPA11-D (500 ng mL^{-1}) for kiwifruit raw extract sample.



Supplementary Fig. S3 Comparison of phenol extraction efficiency.



Supplementary Fig. S4 Comparison of the extraction efficiency of phenol method from reference and the modified phenol method.