

A convenient method for simultaneous quantification of multiple phytohormones and metabolites: application in study of rice–bacterium interaction

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Additional file 1: Supplemental figures and tables

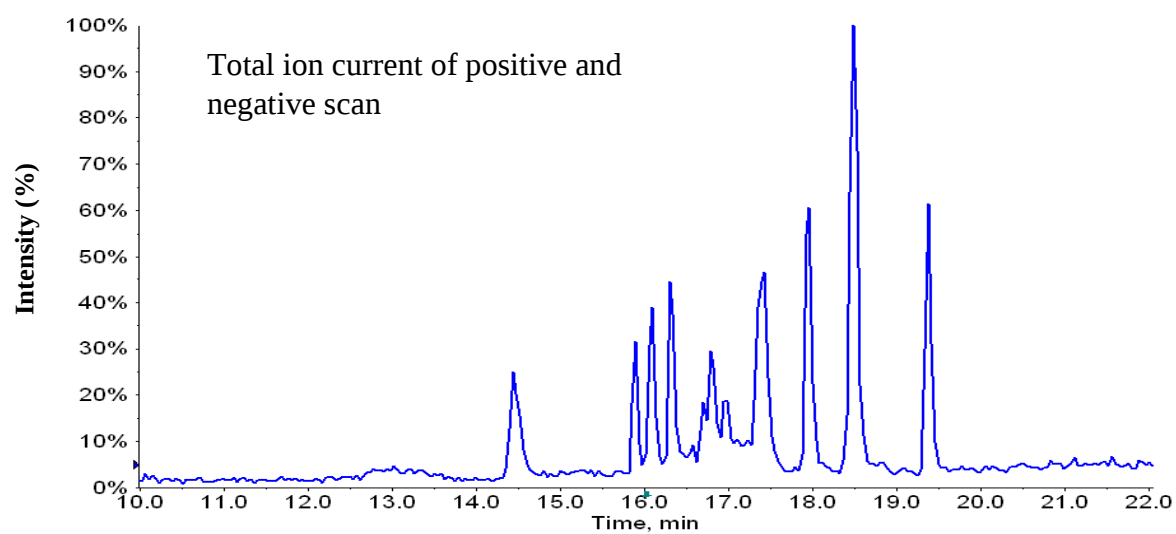


Figure S1. Representative LC chromatograms of analytes and their internal standards.

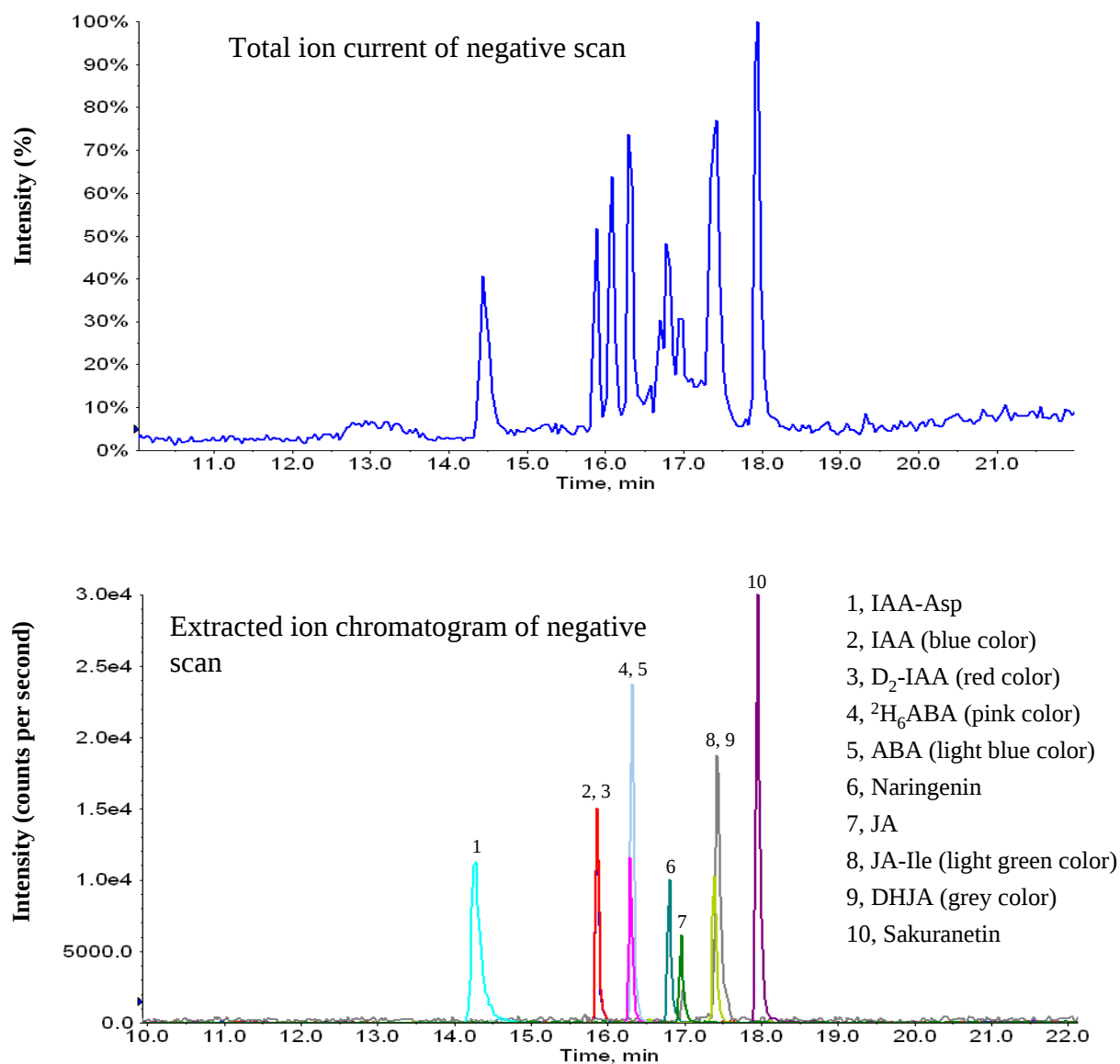


Figure S1 (continued 1). Representative LC chromatograms of analytes and their internal standards.

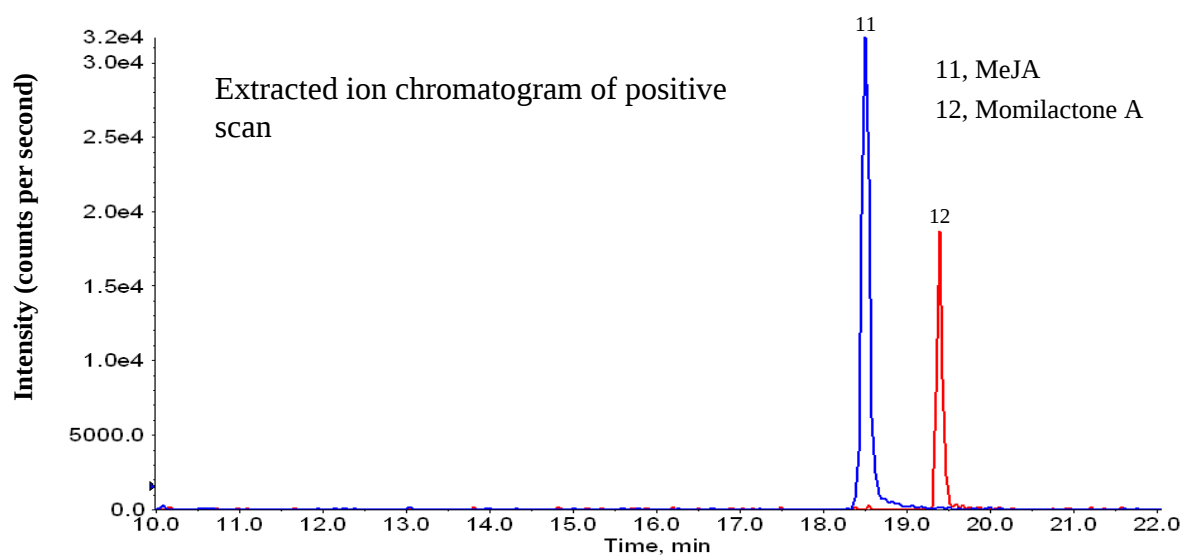
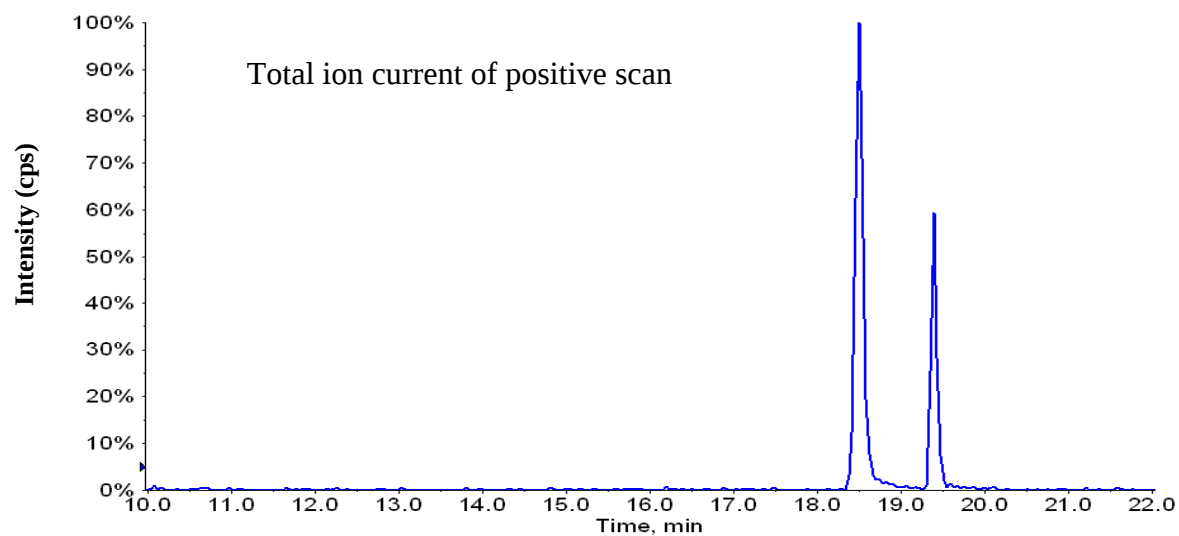


Figure S1 (continued 2). Representative LC chromatograms of analytes and their internal standards.

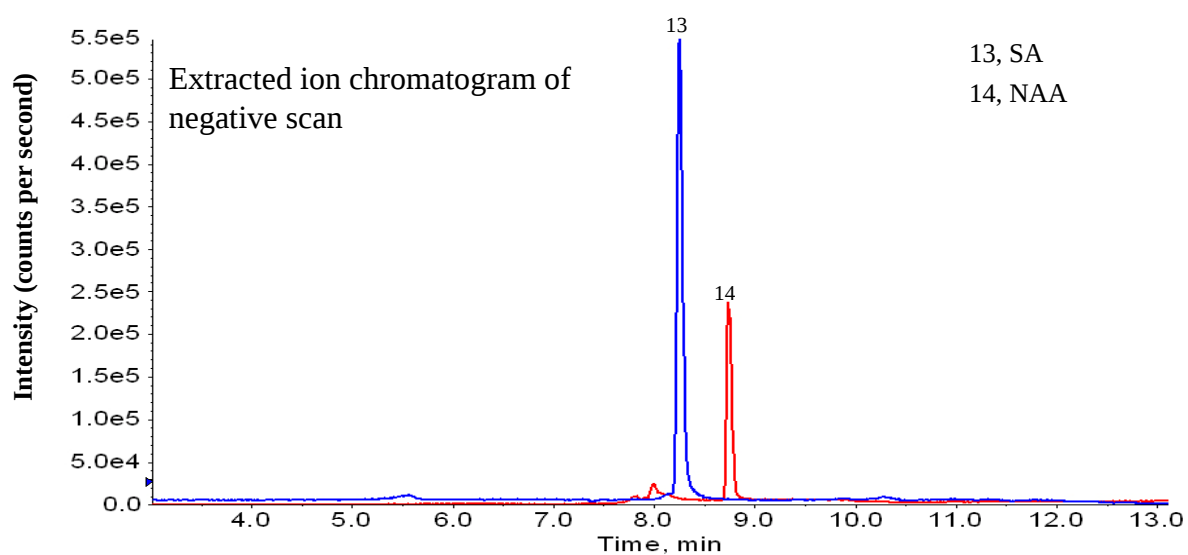
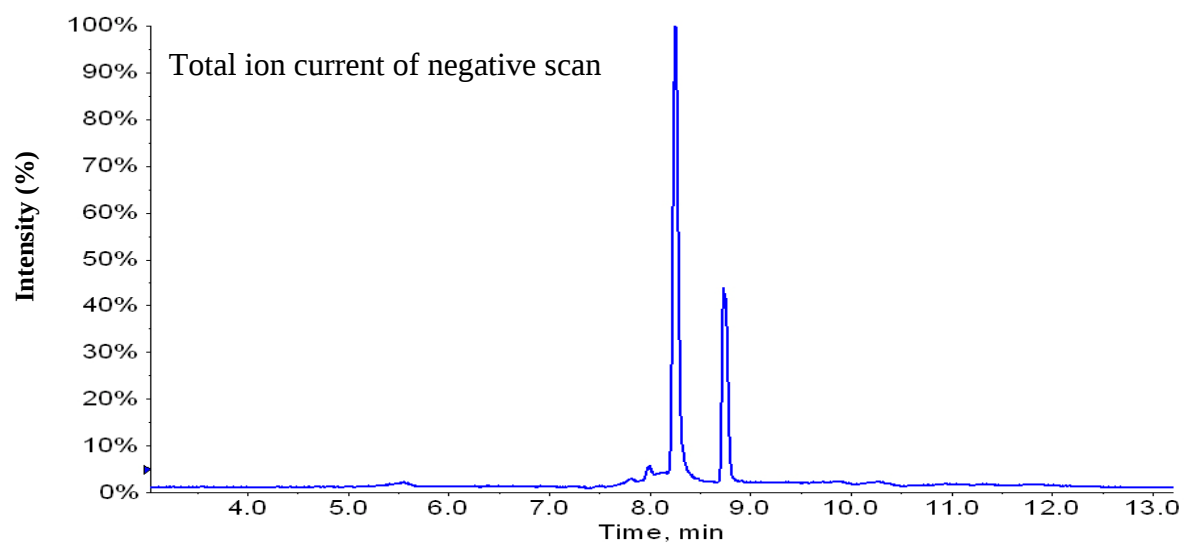


Figure S1 (continued 3). Representative LC chromatograms of analytes and their internal standards.

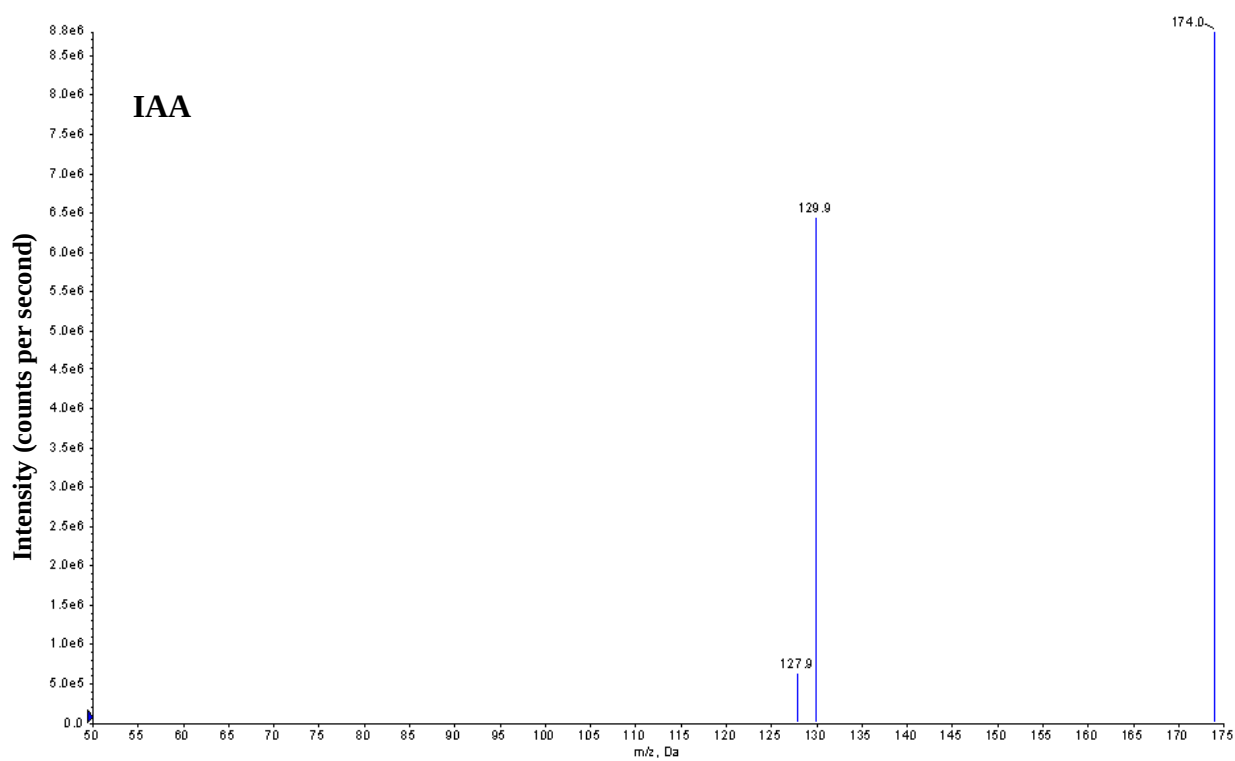
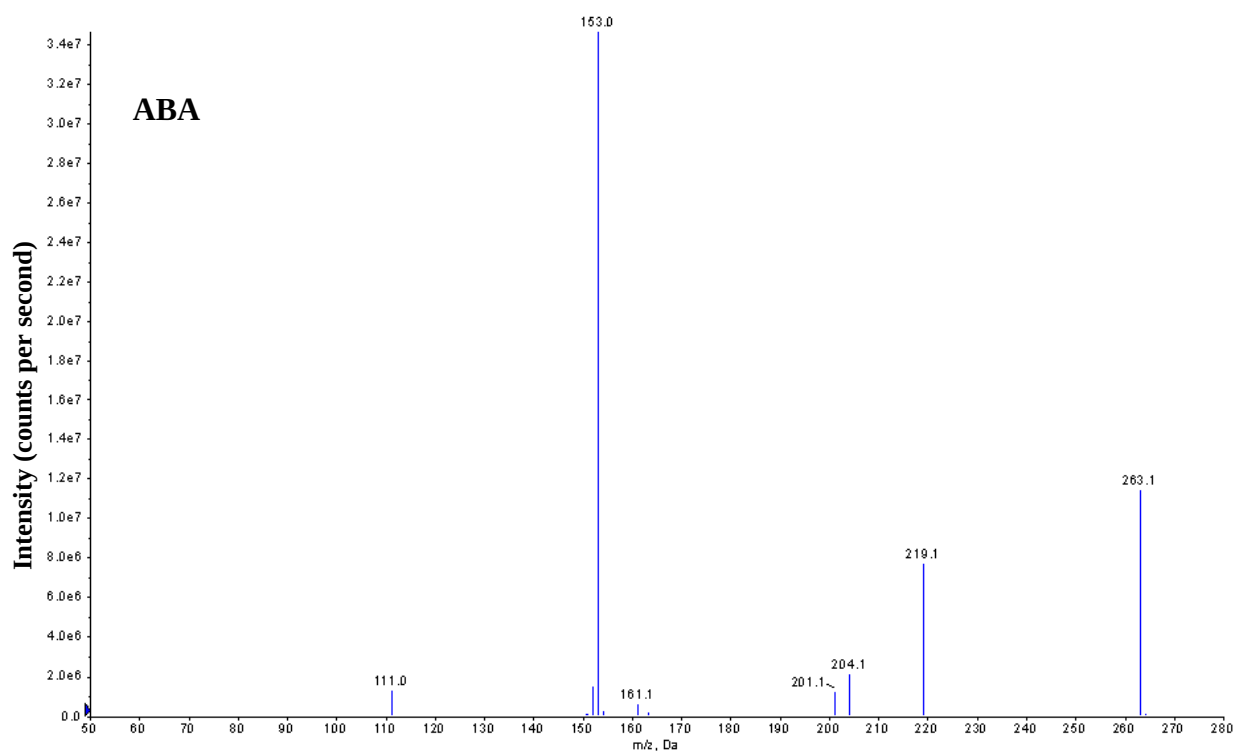


Figure S2. Representative MS fragmentation patterns of analytes.

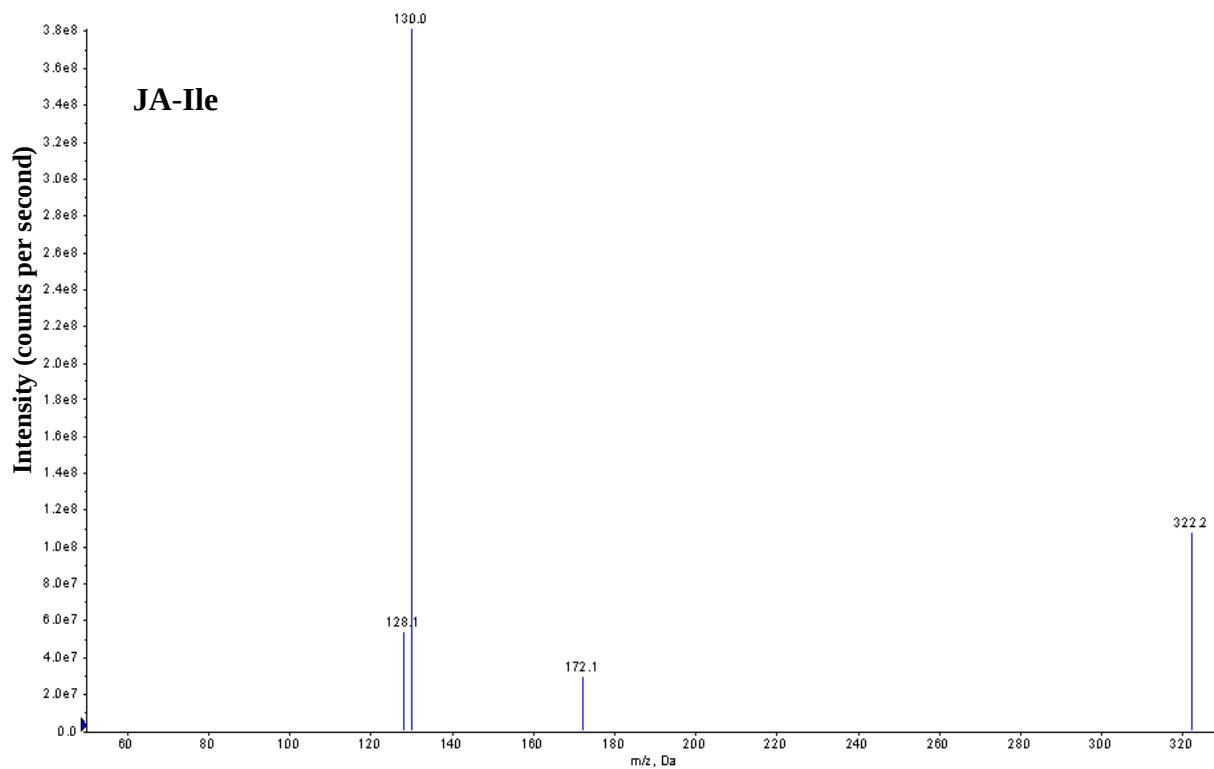
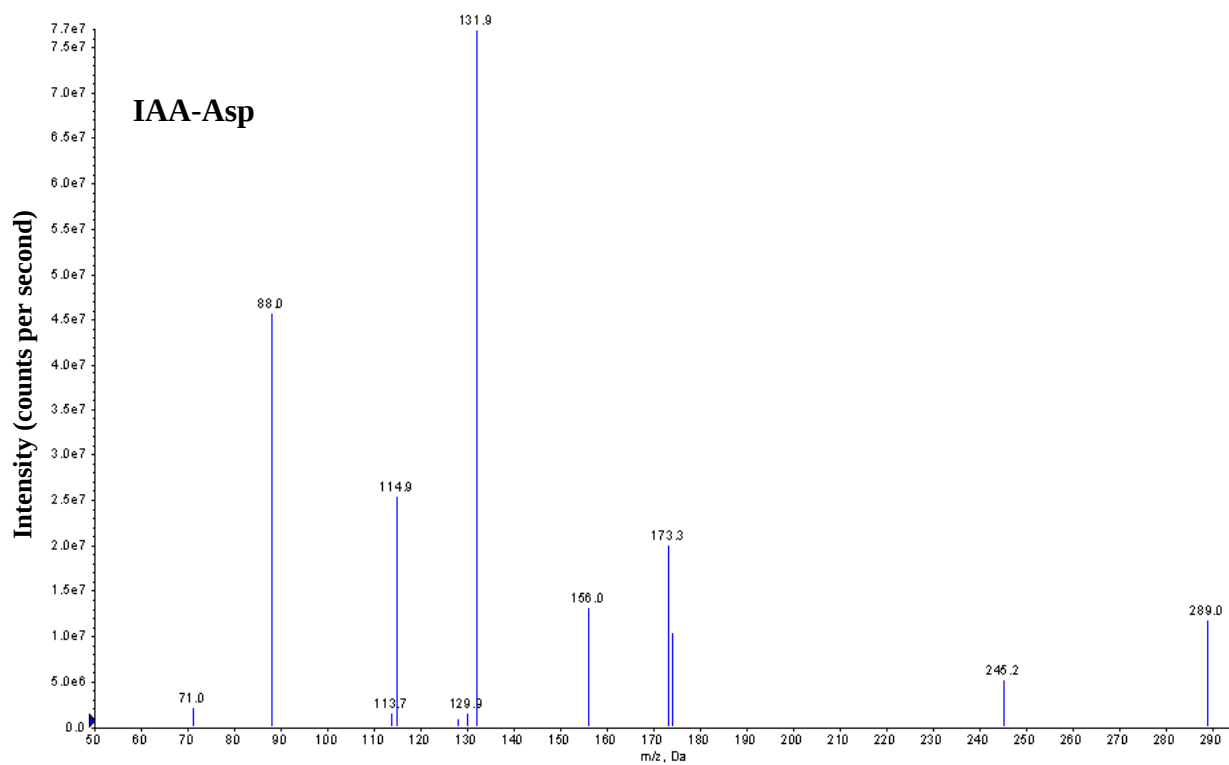


Figure S2 (continued 1). Representative MS fragmentation patterns of analytes.

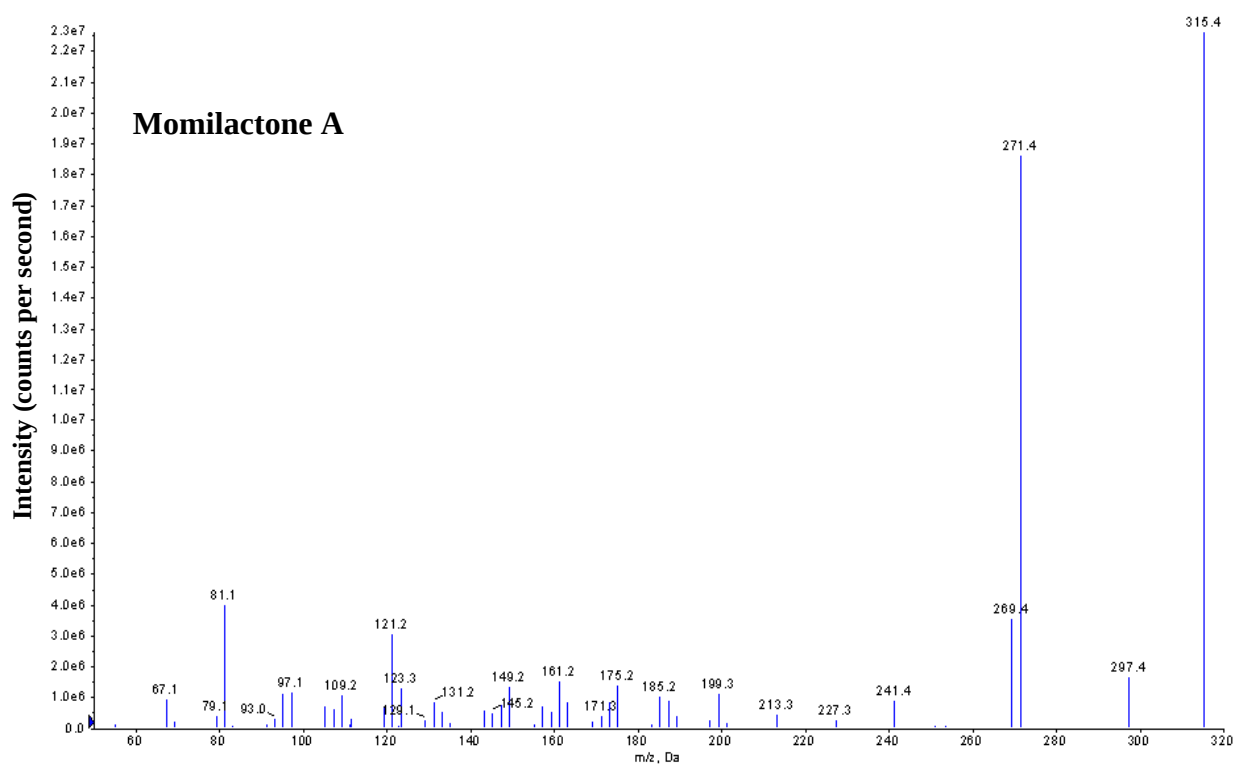
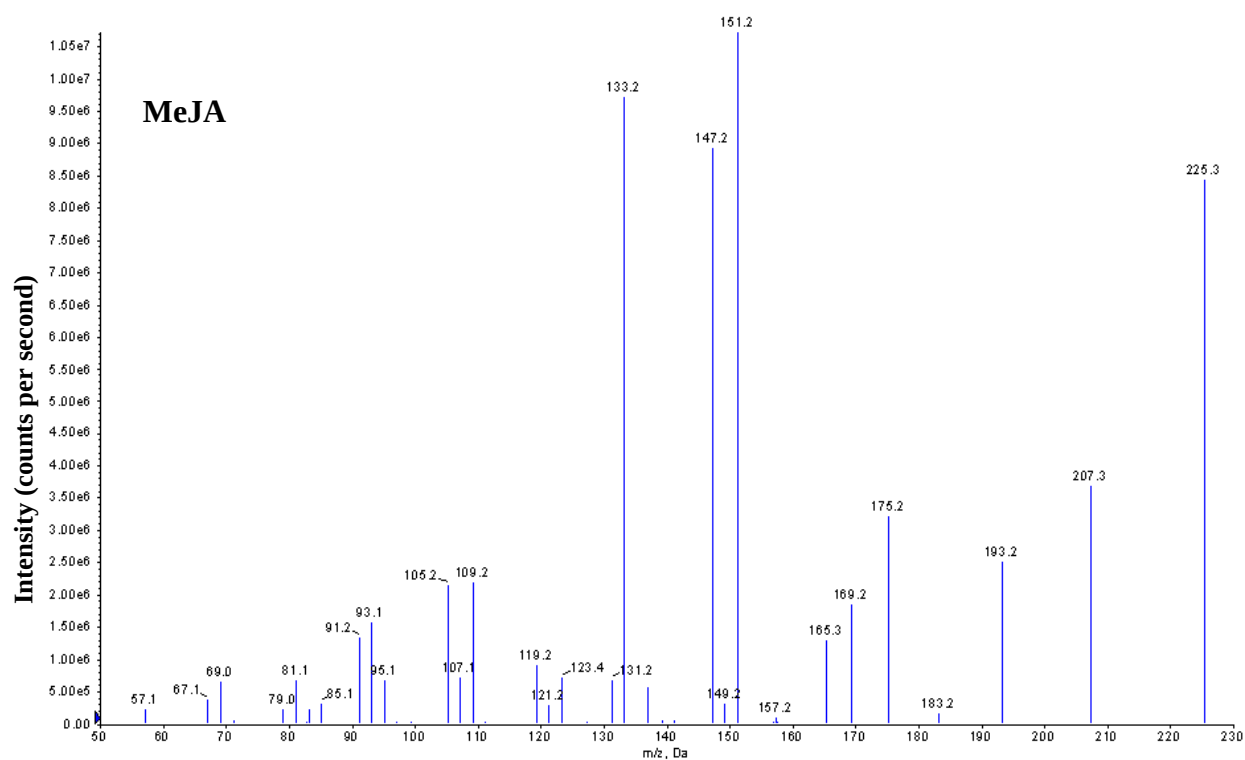


Figure S2 (continued 2). Representative MS fragmentation patterns of analytes.

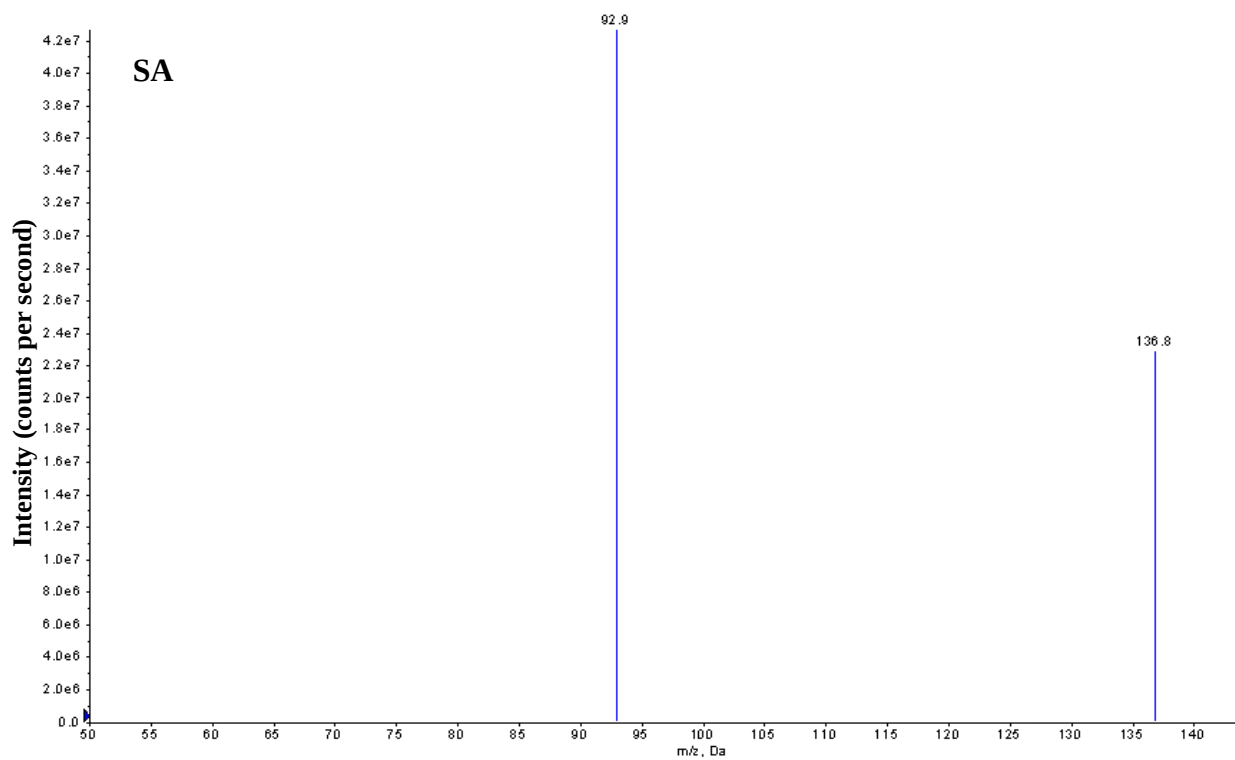
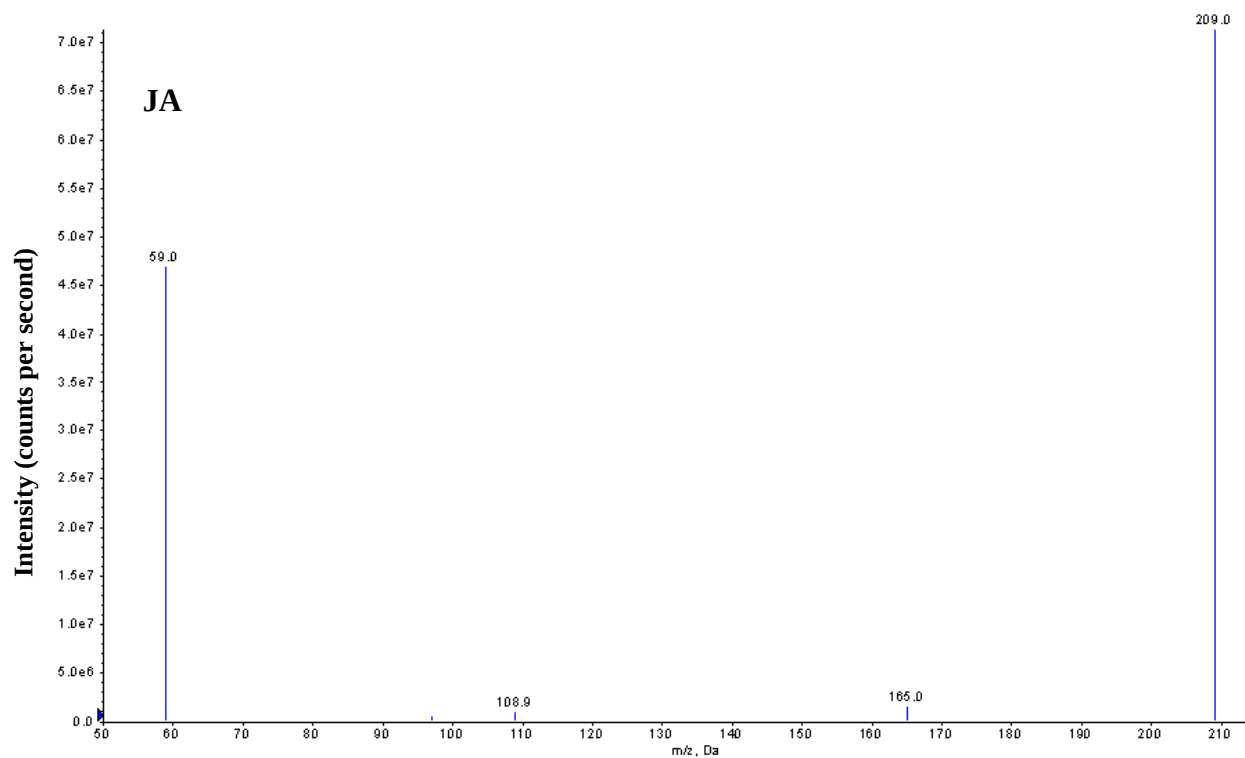


Figure S2 (continued 3). Representative MS fragmentation patterns of analytes.

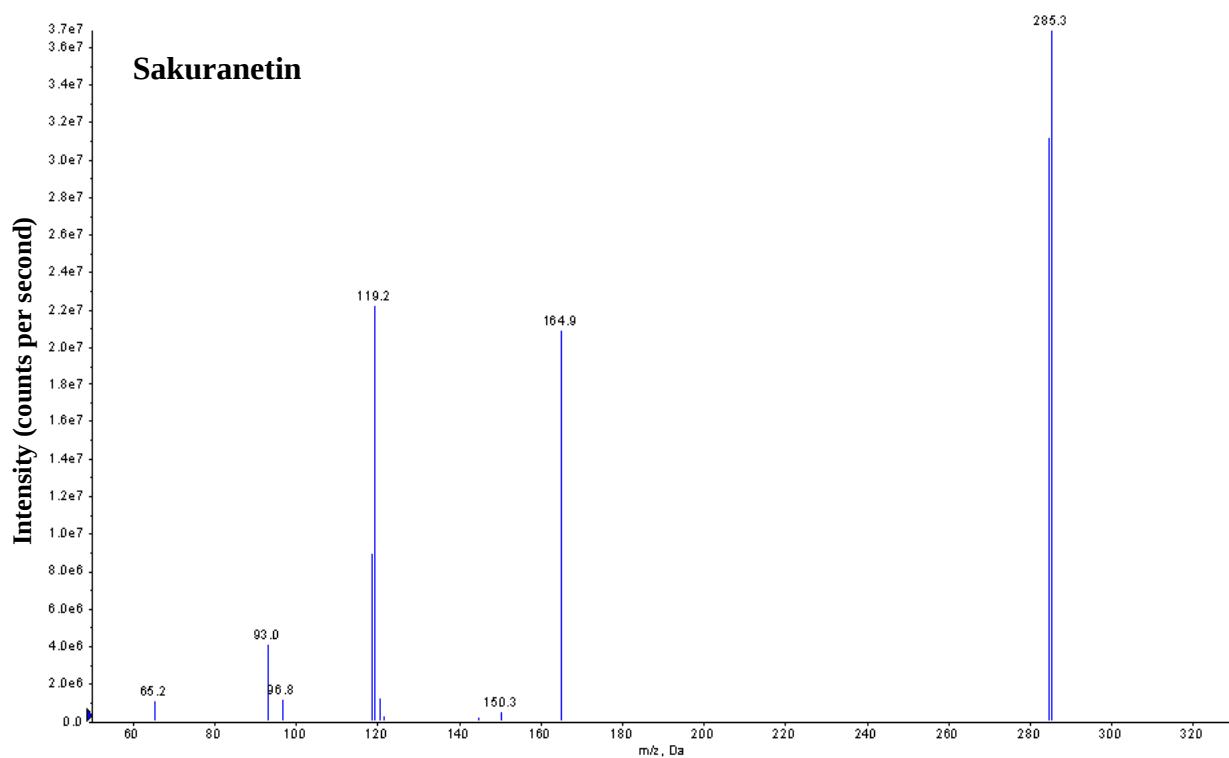
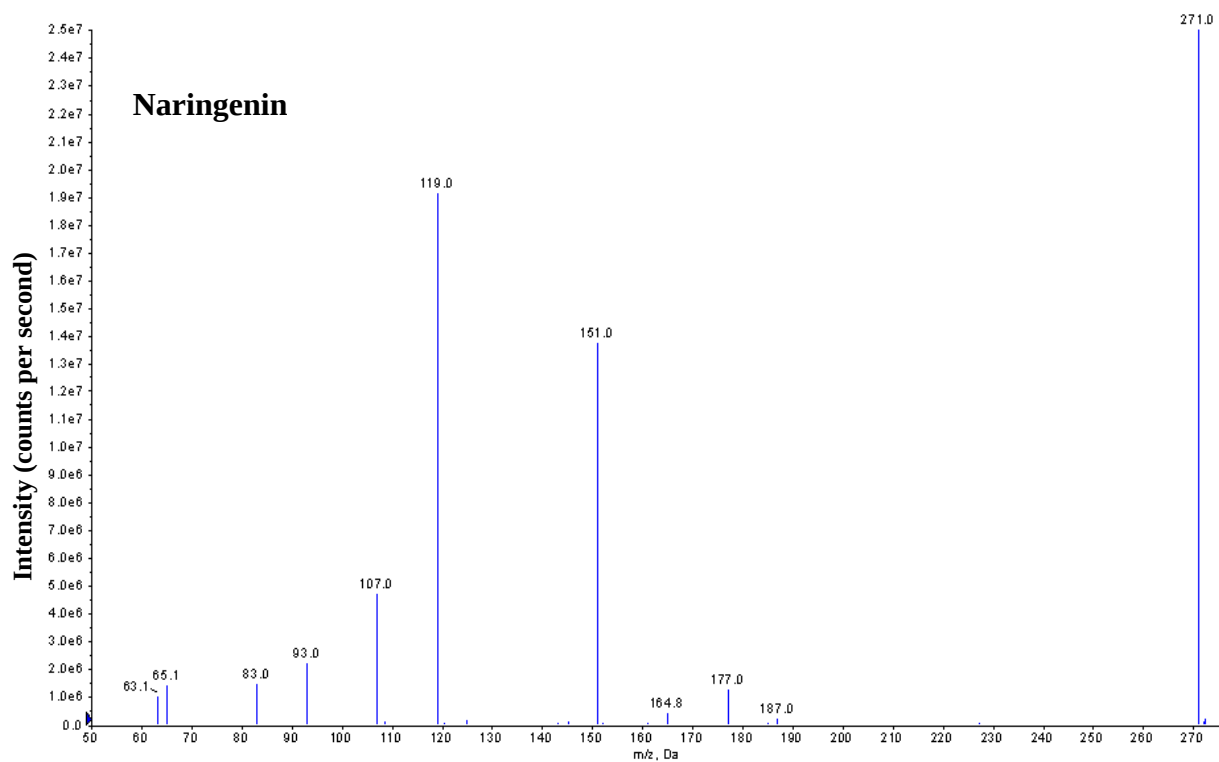


Figure S2 (continued 4). Representative MS fragmentation patterns of analytes.

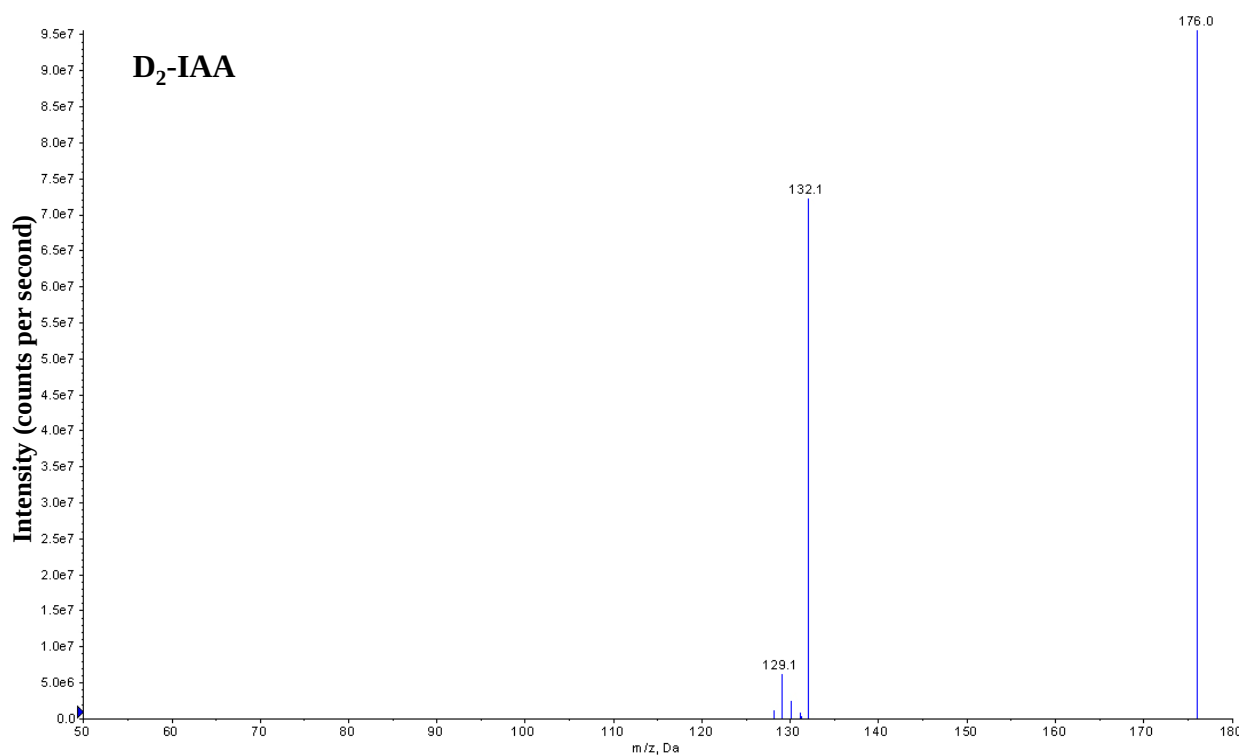
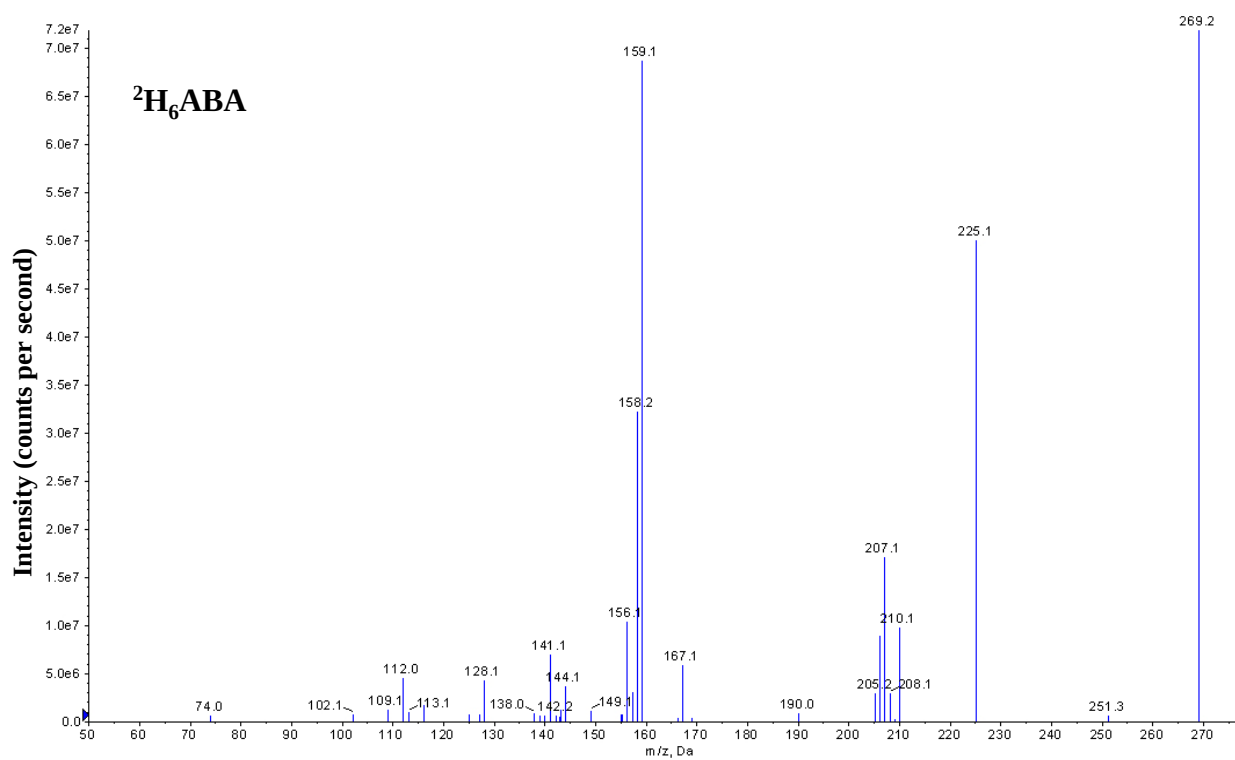


Figure S2 (continued 5). Representative MS fragmentation patterns of analytes.

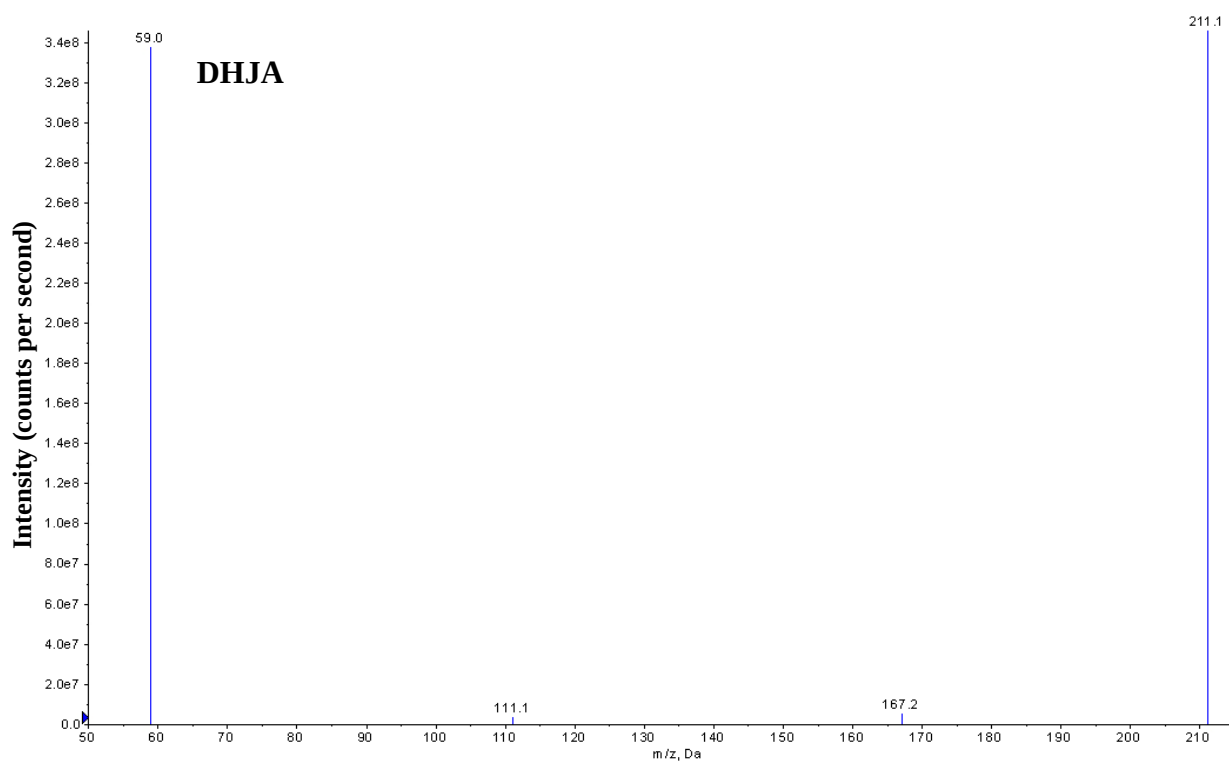
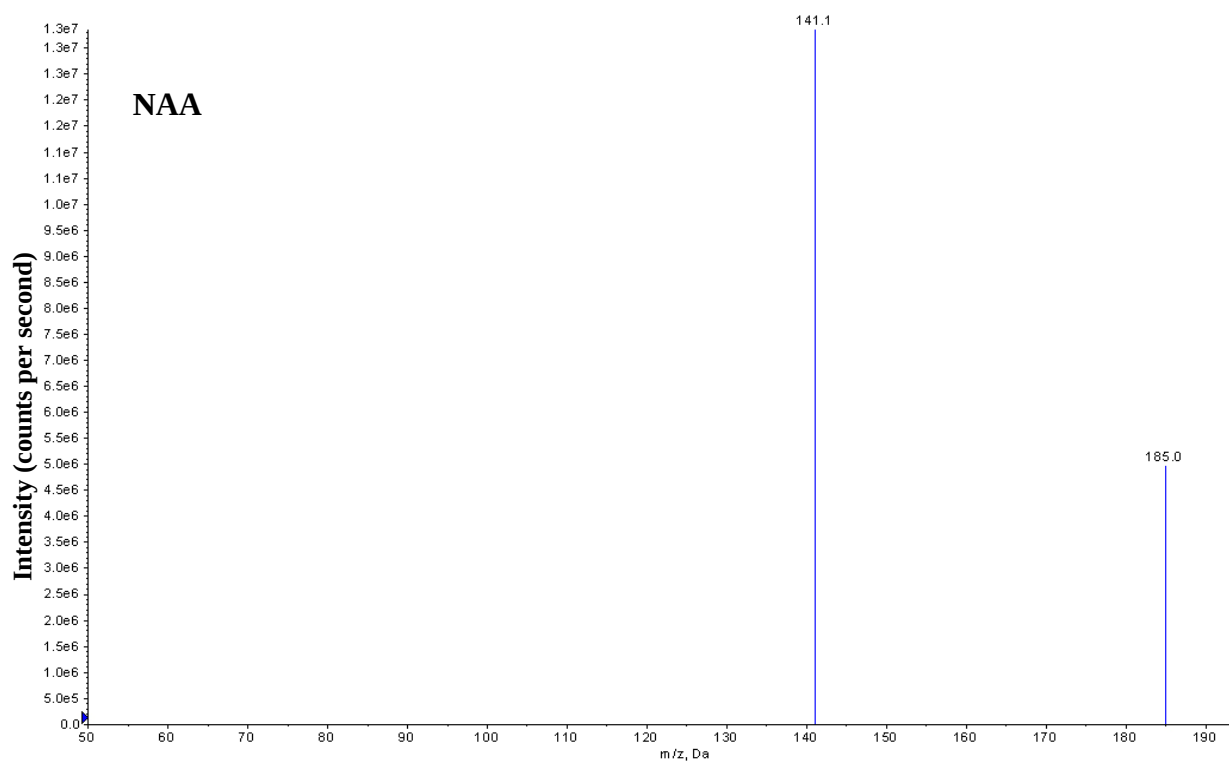


Figure S2 (continued 6). Representative MS fragmentation patterns of analytes.

Table S1. Recovery of analytes in standard-containing samples prepared using different filters and in rice samples

Analyte	Retention time (min)	Recovery rate (%)			Recovery rate (%)	
		Standard after nylon filter-filtration	Standard after cellulose filter-filtration	<i>P</i> value ^a	Rice sample	<i>P</i> value ^b
IAA	15.86	92.4 ± 2.1	90.3 ± 6.2	0.7238	89.8 ± 1.3	0.2808
JA	16.95	90.9 ± 1.7	85.9 ± 8.8	0.5741	89.5 ± 1.4	0.4827
JA-Ile	17.38	91.3 ± 3.9	89.6 ± 7.5	0.8033	89.5 ± 1.4	0.4827
ABA	16.32	93.6 ± 1.1	90.6 ± 3.2	0.4259	92.7 ± 0.9	0.4443
SA	8.28	91.2 ± 4.9	92.2 ± 5.8	0.8665	95.2 ± 1.3	0.7577
IAA-Asp	14.27	91.6 ± 1.7	93.7 ± 2.7	0.4626	89.8 ± 1.3	0.2808
MeJA	18.53	90.2 ± 1.0	90.6 ± 0.4	0.6921	89.5 ± 1.4	0.4827
Momilactone A	19.40	92.5 ± 5.6	90.3 ± 2.7	0.7041		
Sakuranetin	17.95	95.3 ± 1.7	90.3 ± 1.1	0.0741		
Naringenin	16.8	94.5 ± 3.1	91.2 ± 0.4	0.3764		

^aComparison between standard phytohormones and metabolites after nylon filter-filtration and cellulose filter-filtration.

^bComparison between standards after nylon filter-filtration and phytohormones and metabolites in rice samples.

Table S2. Primers used for quantitative reverse-transcription-PCR analysis

Gene (GenBank accession number or RGAP locus number) ^a	Primer name	Forward primer (5'-3')	Reverse primer (5'-3')
<i>ZEP</i> (Os04g37619)	ZEP-F/ R	GGATGCCATTGAGTTT GGTT	TGGCTGACTGAAGTCTC TCG
<i>NCED1</i> (AY838897)	NCED1- F/R	CTCACCATGAAGTCCA TGAGGCTT	GTTCTCGTAGTCTTGGTC TTGGCT
<i>NCED3</i> (AY838899)	NCED3- F/R	CGCAACAGTAAAAAG AATTAACAGC	TATACACACACGCGGTC GTT
<i>NIT1</i> (AK104033)	NIT1F/ R	CACCCCGGCCACTCTA GATA	GATAGCCGCCAACAAAA GCT
<i>AAO3</i> (AK065990)	AAO3F/ R	TTCACCAGCTGAAGGC ACAA	GCTCATCCAAGCCATTA GCAA
<i>CHS</i> (X89859)	CHSF/R	CCGGCGAACTGCGTGT AC	TTCCTGATCTGCGACTTG TCA
<i>AOS2</i> (AY062258)	AOS2-F /R	CAATACGTGTACTGGT CGAATGG	AAGGTGTCGTACCGGAG GAA
<i>ICS1</i> (AK120689)	ICS1-F/ R	TATGGTGCTATCCGCT TCGAT	CGAGAACCGAGCTCTCT TCAA
<i>LOX</i> (D14000)	LOX-F/ R	GCATCCCCAACAGCAC ATC	AATAAAGATTTGGGAGT GACATATTGG
<i>PAL1</i> (X16099)	PAL1-F/ R	GGGCAACCCAGTGAC CAA	CGATTGCCTCGTCGGTC TT
<i>KSL4</i> (AK119327)	KSL4-F/ R	CAACAATGGAGGAATA CA	AACAACCTCATCATACTCT G
<i>CPS4</i> (AK100631)	CPS4-F/ R	TGCCAAGATTCCAAGA GA	GTCCAAGTCAACCATTC C
<i>Actin</i> (X15865)	Actin-F/ R	TGTATGCCAGTGGTCG TACCA	CCAGCAAGGTCGAGAC GAA

^aGenBank, <http://ncbi.nlm.nih.gov>; RGAP, Rice Genome Annotation Project (<http://rice.plantbiology.msu.edu>).