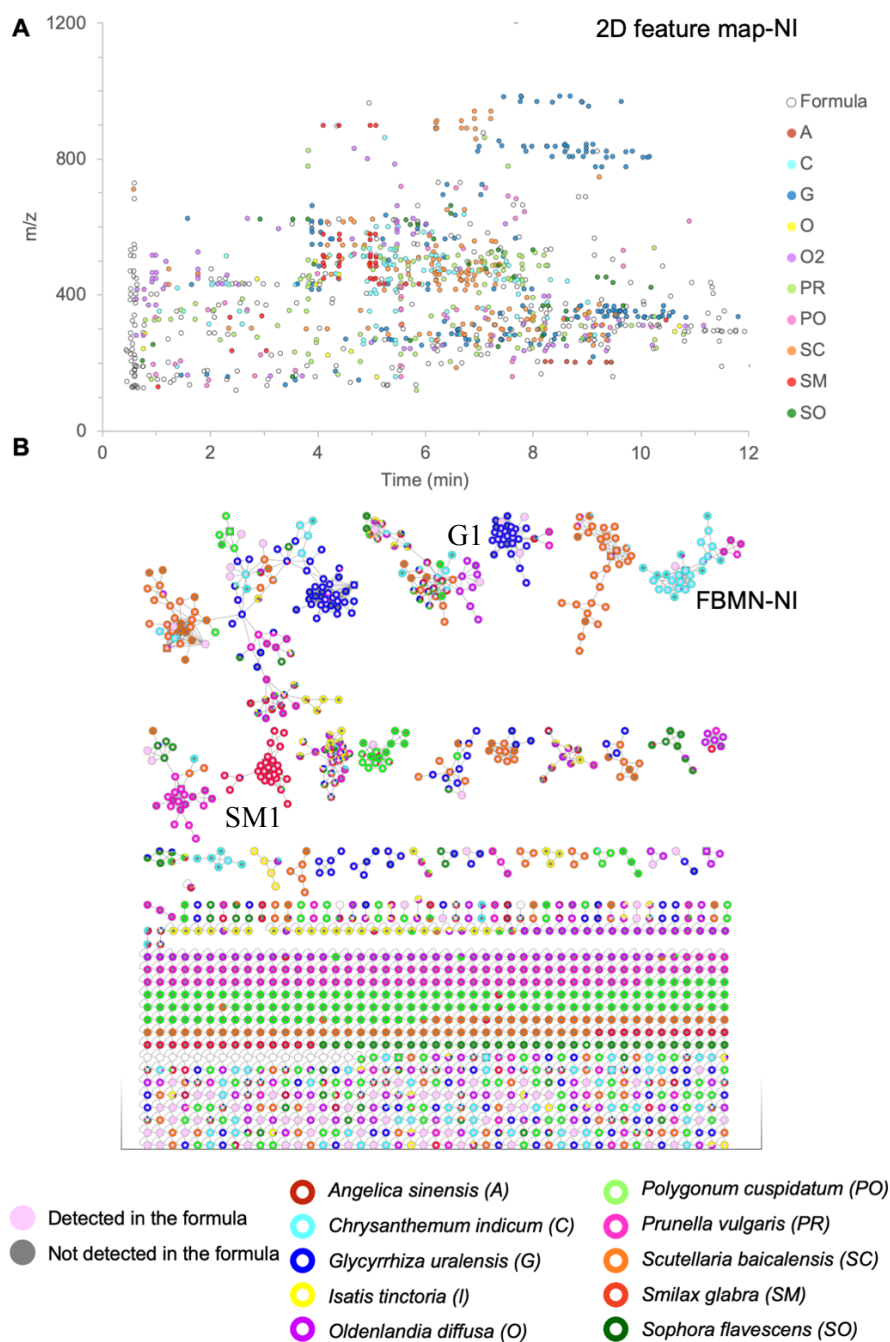


Supplementary Material

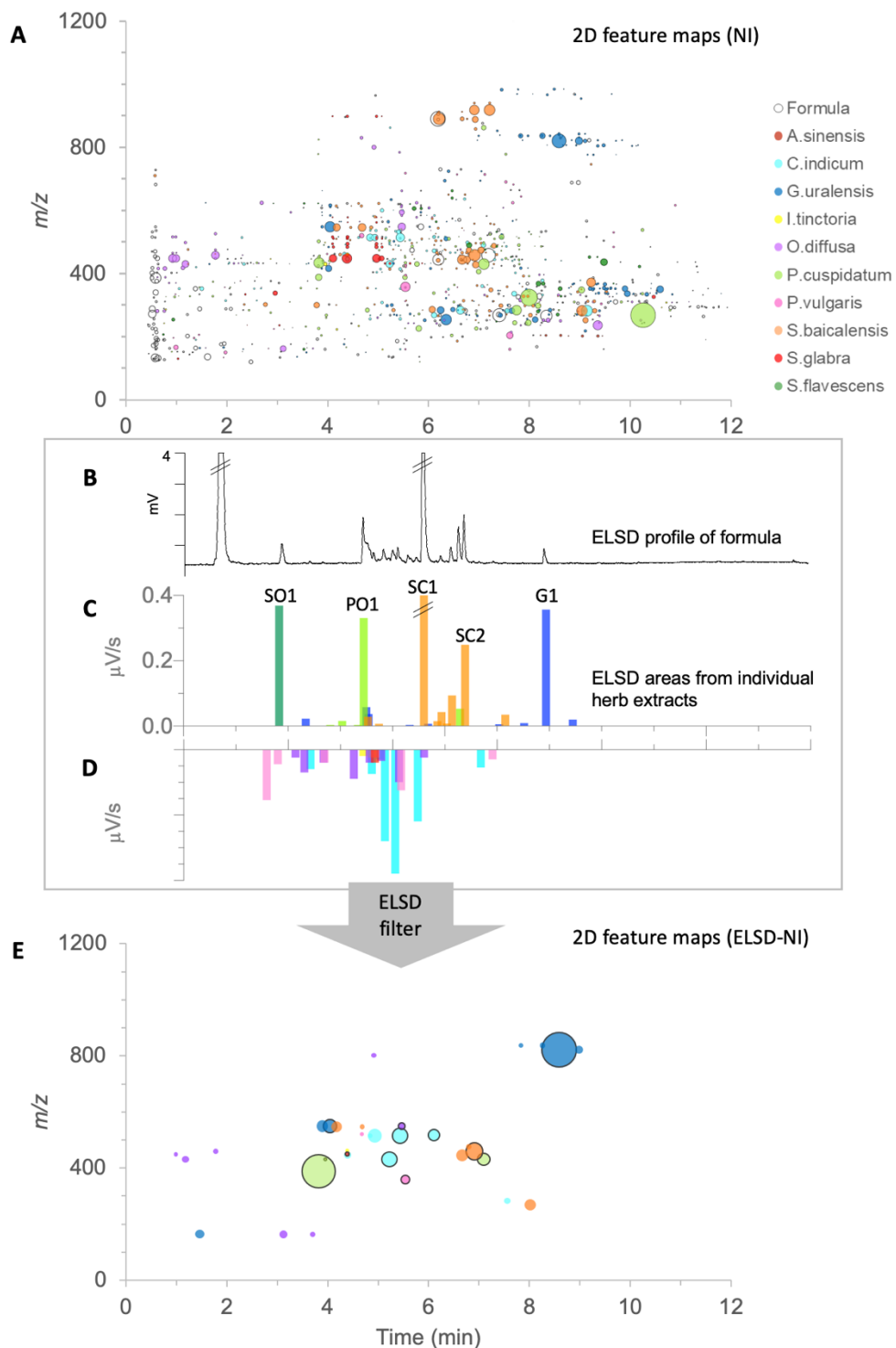
1	<i>Visualization of the contribution of each herb to the formula and ELSD filtering.....</i>	2
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1 Visualization of the contribution of each herb to the formula and ELSD filtering

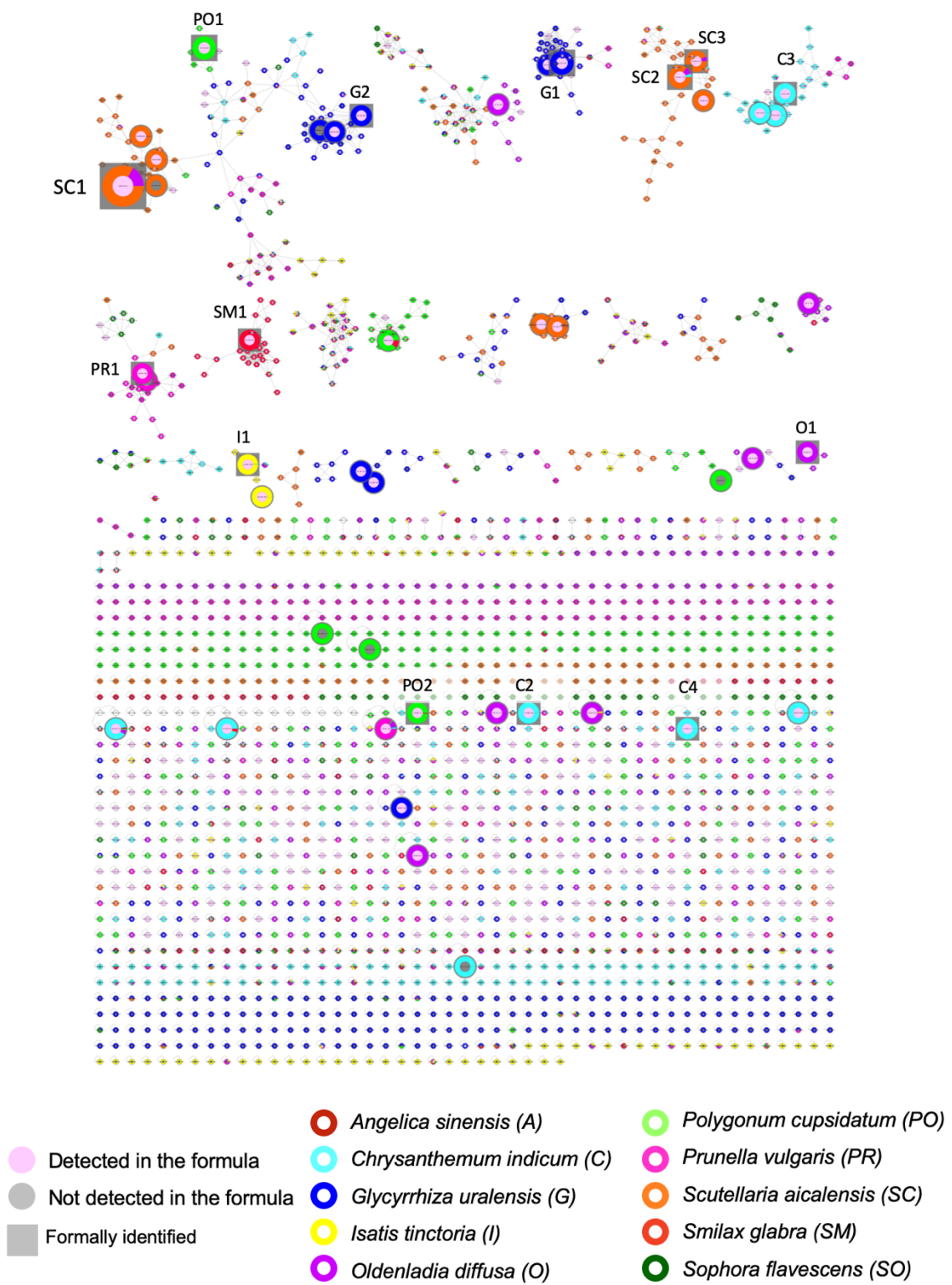
These are additional figures for sections 2.2. and 2.3.



Supplementary Figure 1: Visualization of the contribution of the ten herbs to the formula, in which each herb is represented by a different color: A) 2D feature map in NI: each black circle represents a feature detected in the formula, the size of the circles is fixed and equal for all features. The inner color of the circle indicates that the feature is specifically detected in one of the ten herbs (90% specificity threshold). B) FBMN in NI for the organization of the MS/MS spectra of all features presented in A, which the same color coding and fixed node size.

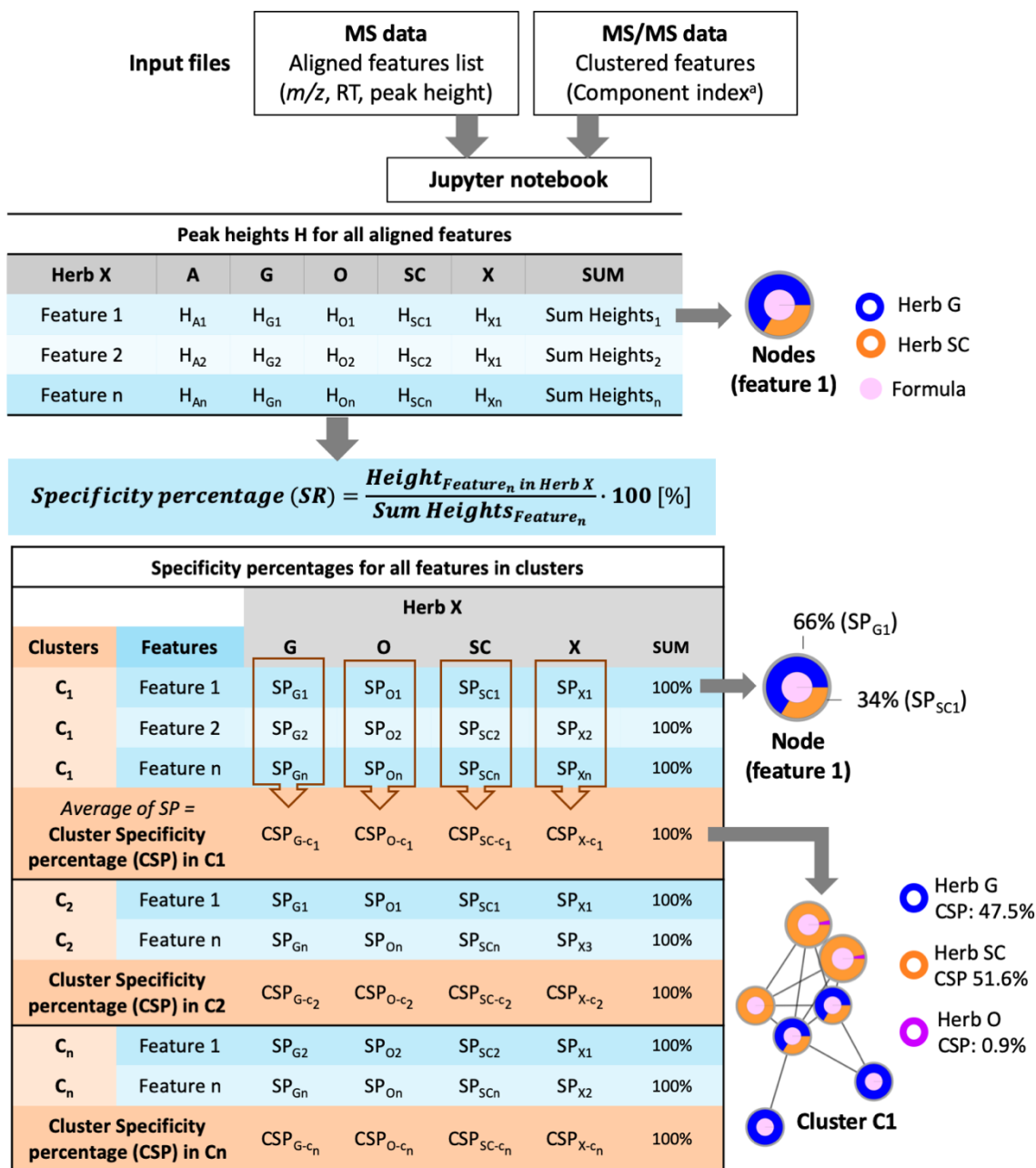


Supplementary Figure 2: A) 2D feature map of HRMS processed data in negative ionization, B) ELSD profiling of the formula, C) and D) bar plot with superimposed ELSD area of the single herb extracts adjusted to their proportion into the formula, divided into high (C) and low areas (D). E) 2D feature map (NI) with attributed ELSD areas. Dots with black circle represents the components that were further identified.



Supplementary Figure 3: Visualization of the ELSD detected peaks in the FBMN-NI. Each herb is represented by a different color, the size of the node is proportional to ELSD areas. See table 2 for the name of the components.

2 Script to evaluate the specificity of nodes and clusters

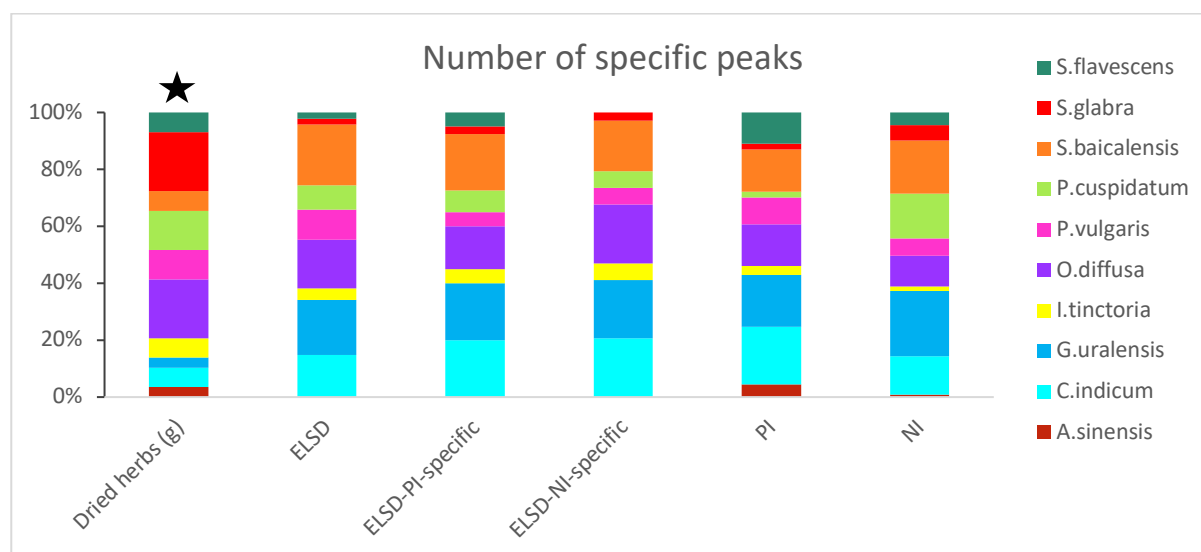


- Counting the numbers of specific features: (SP_X) > selected threshold, visualization of these numbers (histograms), and export as a text file.
- Selection of specific clusters for an herb X: (CSP_{X-cn}) > selected threshold
- Counting the numbers of clusters at a chosen CSP_{X-cn} and visualization of these numbers (histograms)
- Export data from a selected cluster as a text file

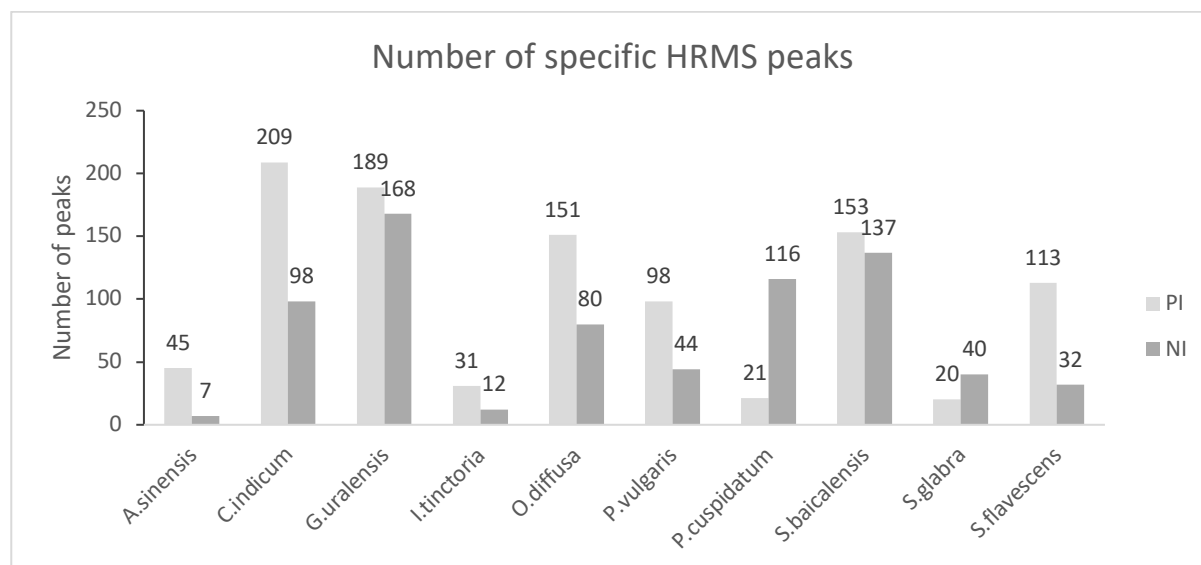
Supplementary Figure 4: Main steps of the script developed to express numerically the specificity of nodes and clusters. The *specificity percentage* is the relative height intensity of one feature in a multi-herb formula. The peak height of one aligned feature in one herb is divided by the sum of the heights in all herbs. The *cluster specificity percentage* is the average of the specificity percentages of the features grouped in a cluster for a given herb. ^a component index is a number that designates a cluster in GNPS terminology

3 Features and clusters specificity

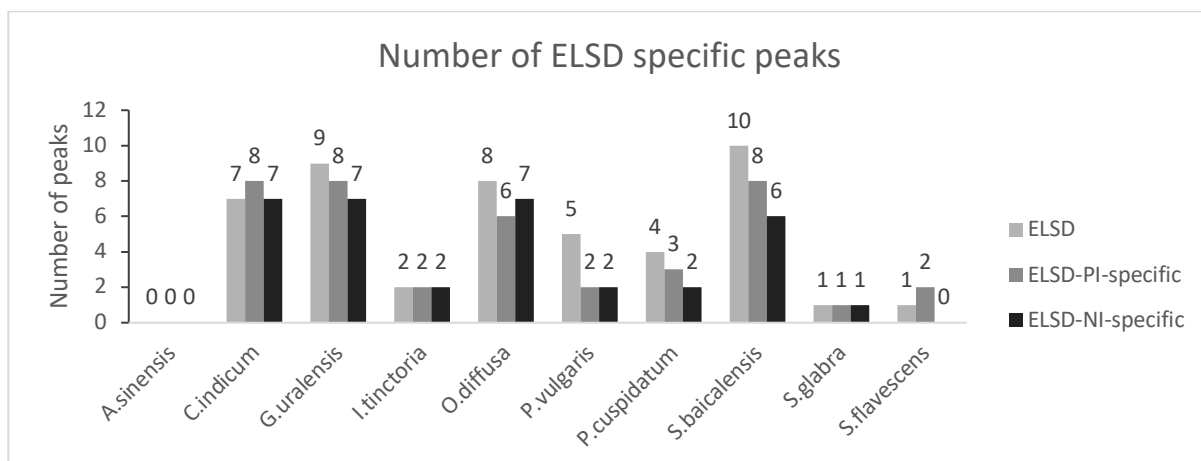
These are additional figures for section 2.2. and 2.3



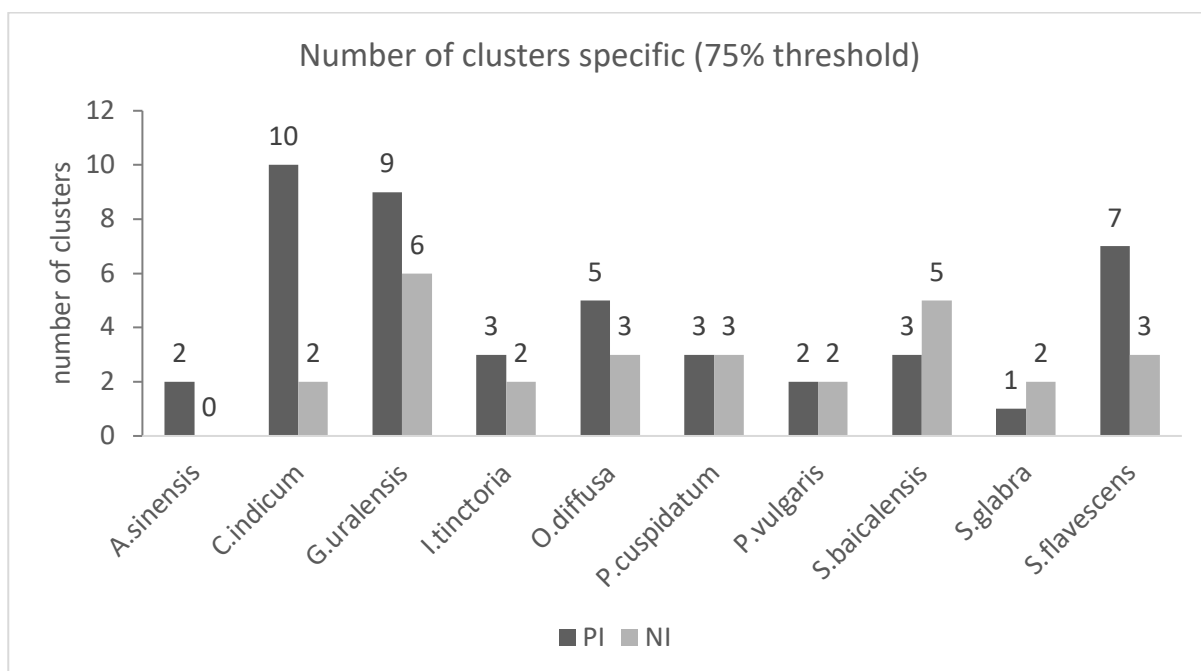
Supplementary Figure 5: Comparison of the numbers of specific peaks (90% threshold) in regard of the herbal drug proportion (★) in the formula before decoction. PI: positive ionization. NI: negative ionization.



Supplementary Figure 6: Comparison of the numbers of specific peaks (90% threshold) for each herb in UHPLC-HRMS. PI: positive ionization. NI: negative ionization.

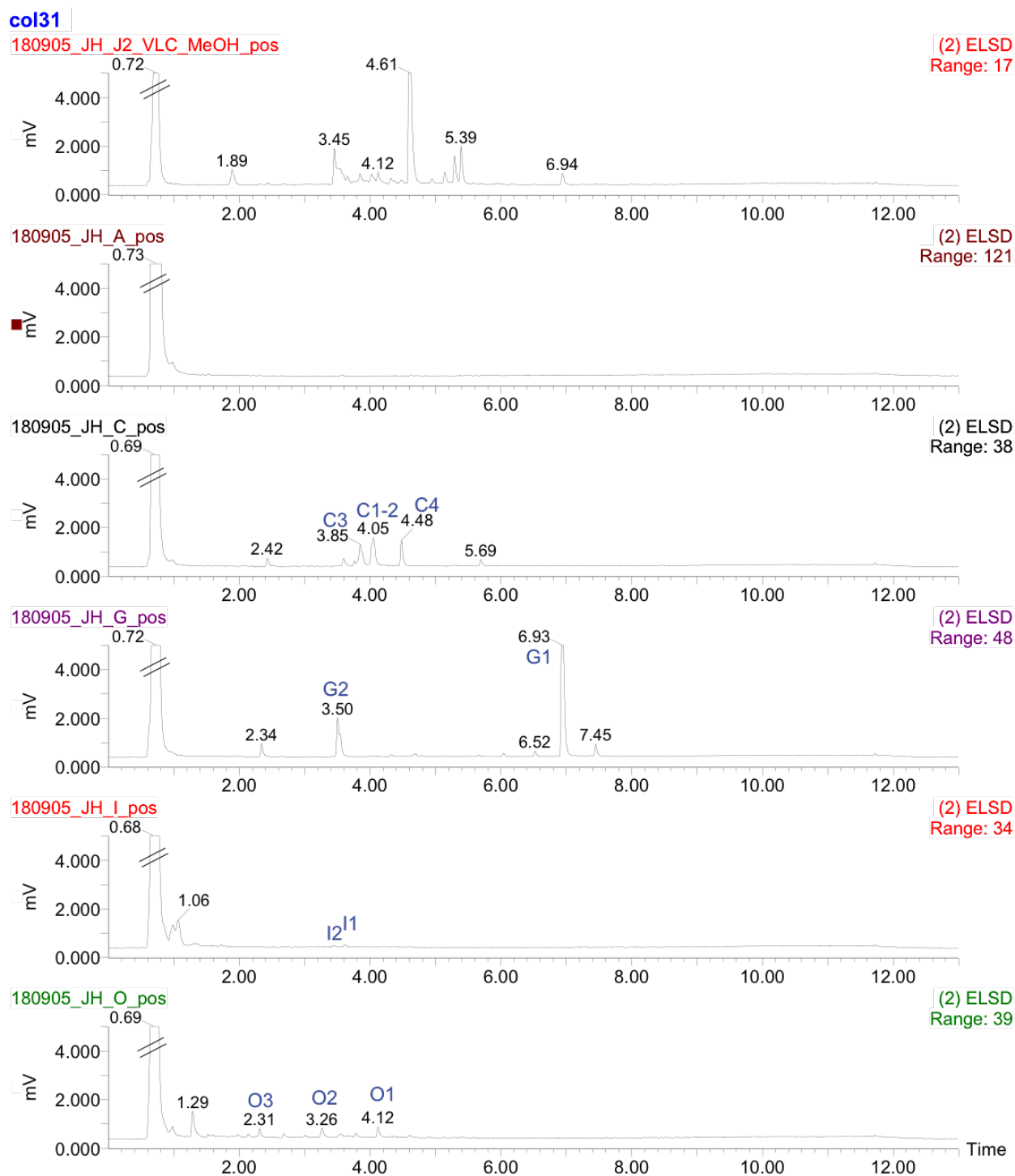


Supplementary Figure 7: Comparison of the numbers of specific peaks ELSD detected for each herb. PI: positive ionization. NI: negative ionization.



Supplementary Figure 8: number of specific clusters to each herb in both ionization mode in the FBMN (75% threshold).

4 ELSD chromatograms of the TCM formula and individual herb extracts

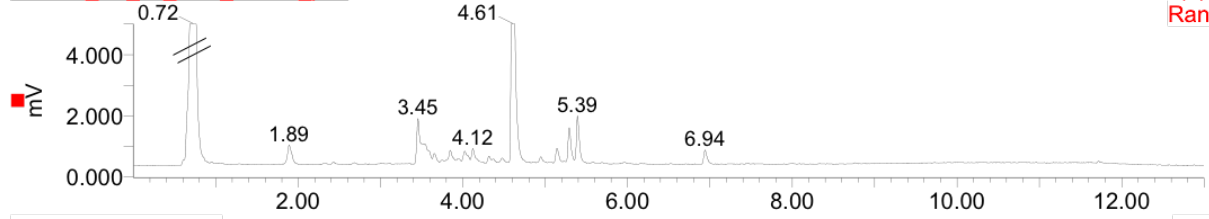


Supplementary Figure 9: ELSD chromatograms of the enriched extract (J2-VLC-MeOH) and single herb extract (*A.sinensis* (A), *C.indicum* (C), *G.uralensis* (G), *I.tinctoria* (I), *O.diffusa* (O)) with ELSD peak numbering corresponding to subsequent annotations and identifications.

col31

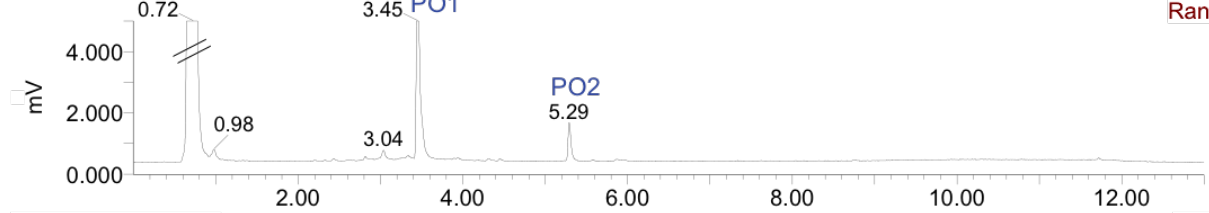
180905_JH_J2_VLC_MeOH_pos

(2) ELSD
Range: 17



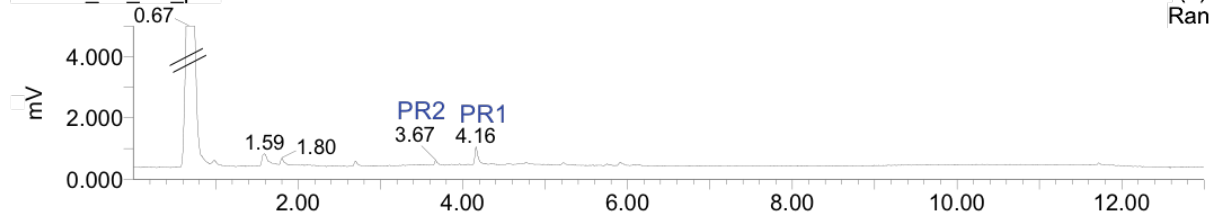
180905_JH_PO_pos

(2) ELSD
Range: 29



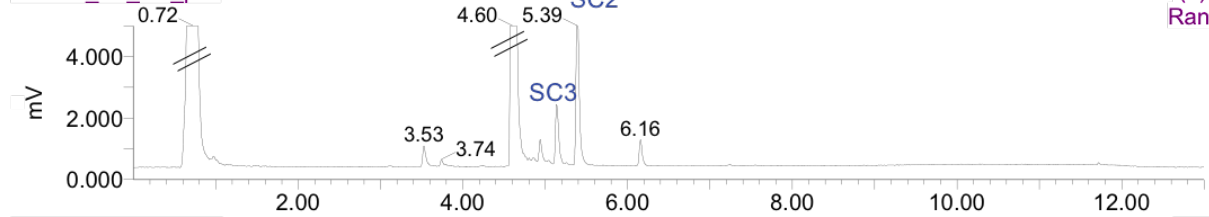
180905_JH_PR_pos

(2) ELSD
Range: 20



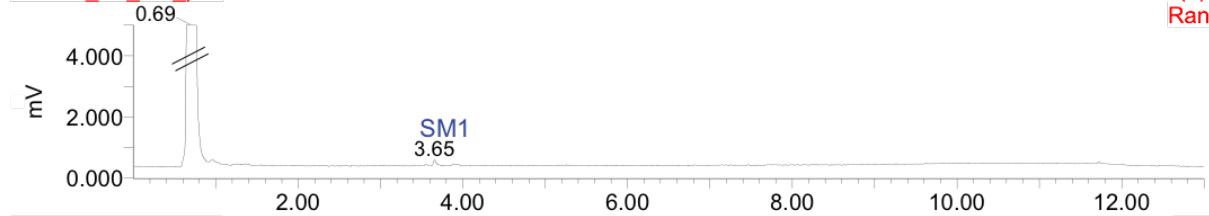
180905_JH_SC_pos

(2) ELSD
Range: 53



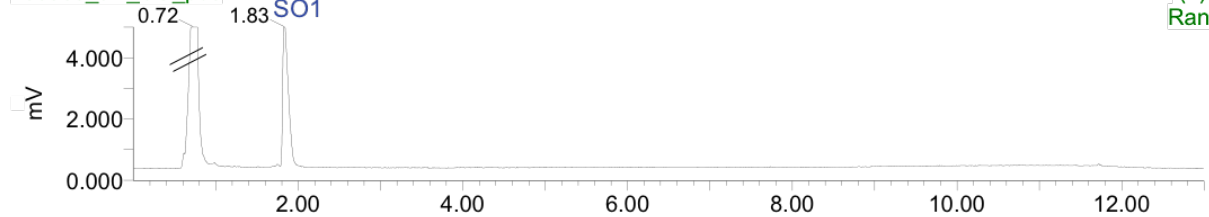
180905_JH_SM_pos

(2) ELSD
Range: 23



180905_JH_SO_pos

(2) ELSD
Range: 36

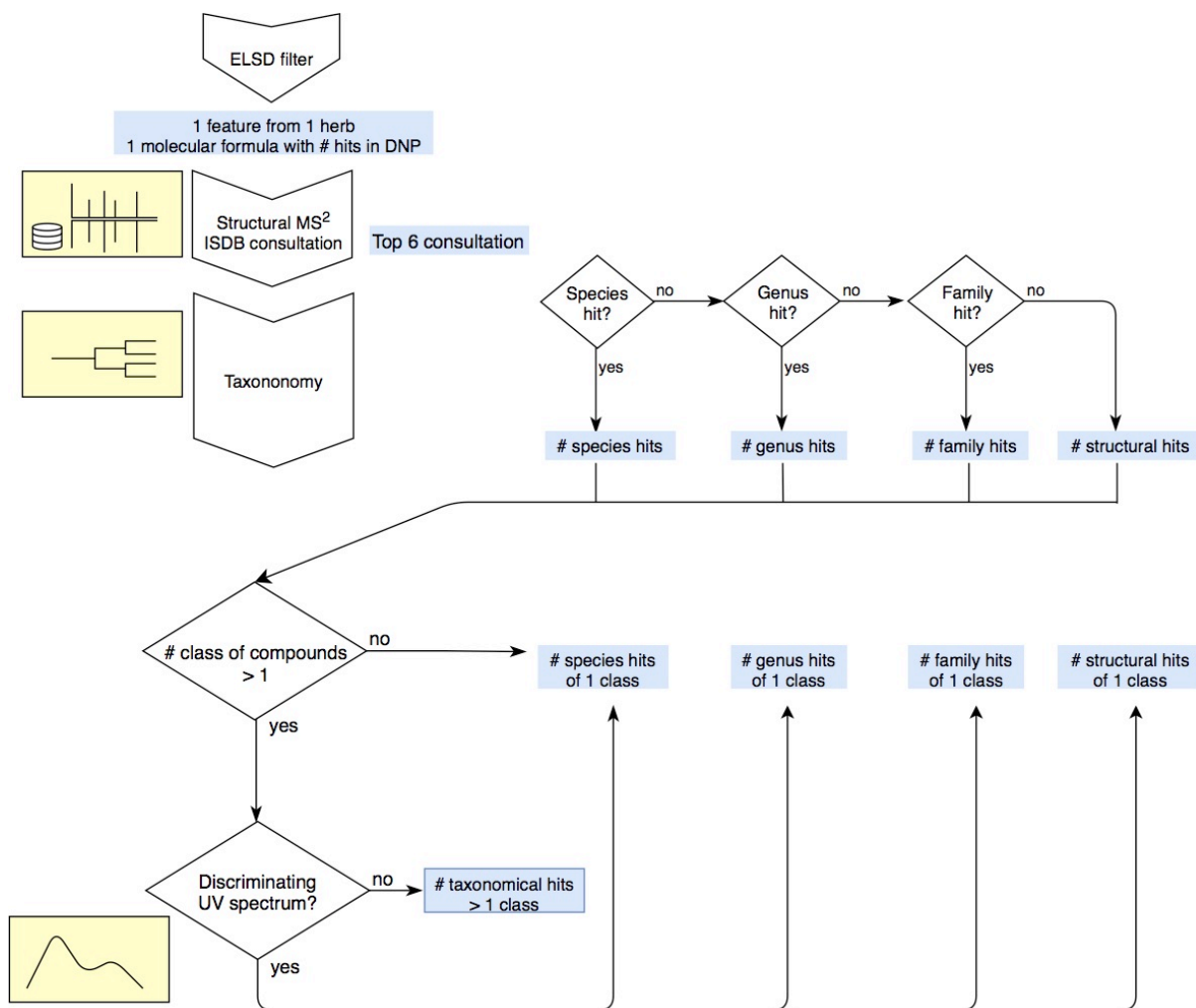


Supplementary Figure 10: ELSD chromatograms of the enriched extract (J2-VLC-MeOH) and single herb extract (*P.cuspidatum* (PO), *P.vulgaris* (PR), *S.baicalensis* (SC), *S.glabra* (SM), *S.flavescens* (SO)), with ELSD peak numbering corresponding to subsequent annotations and identifications.

5 Detailed annotations of the specific and abundant components

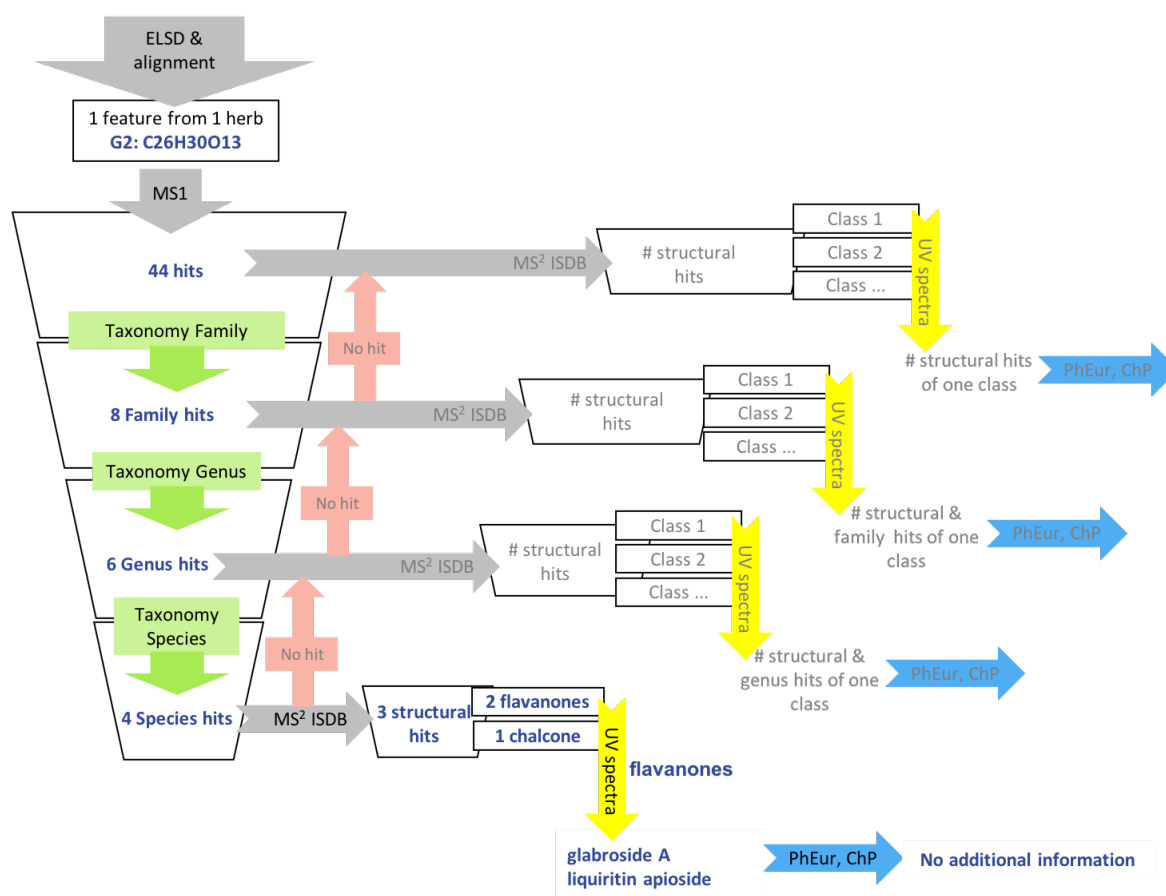
5.1 Annotation workflow

For the features selected by ELSD filtering, their ISDB annotations obtained in the FBMN were verified and completed in detail. The annotation strategy combined MF assignment with taxonomic data since most of the constituting herbs were rather well documented from a phytochemical point of view. HRMS/MS and UV spectra were used for checking annotation consistency (Main text Fig. 1.6 and Suppl. Mat. Fig.5). The number of potential structures for the MF retrieved from HRMS data were reduced by applying a taxonomic filter (from the species to the family taxa level) (Suppl. Mat. Fig. 5). The annotation consistency was checked between the hits obtained by MF assignment from HRMS and filtering by taxonomy and ISDB spectral scoring (Top 6 hits) (Suppl. Mat. Fig. 5). When necessary, UV spectra were used as orthogonal information to confirm or discriminate the classes of compounds. Finally, a comparison with the markers referenced in the European and Chinese Pharmacopoeias was performed. Three detailed examples of this annotation process are presented in Suppl. Mat. Fig. 6 to 8. The annotation presented below were obtained from a first batch of metabolites profiling (data not shown). This workflow resulted in the thorough annotation of 22 potential markers among the features selected by ELSD, which included between 2 to 4 potential markers per herb, at the exception of *Angelica sinensis* for which no ELSD peak were detected. The combination of MF assignment, taxonomic filter, MS/MS scoring and orthogonal UV check provided in half of the cases a single highly probable structure, and in the other half up to 4 putative structures belonging to the same chemical class of components (Suppl. Mat., Table S1). Interestingly, the results of the taxonomic filtering and ISDB annotations were consistent in 80% of cases. Furthermore, orthogonal control by UV spectra permitted the discrimination of all annotated structures belonging to more than one class of compounds even after taxonomic filtering. Finally, the verification of the annotations against the Pharmacopoeias permitted to discriminate between 2 annotations and to modify a case.

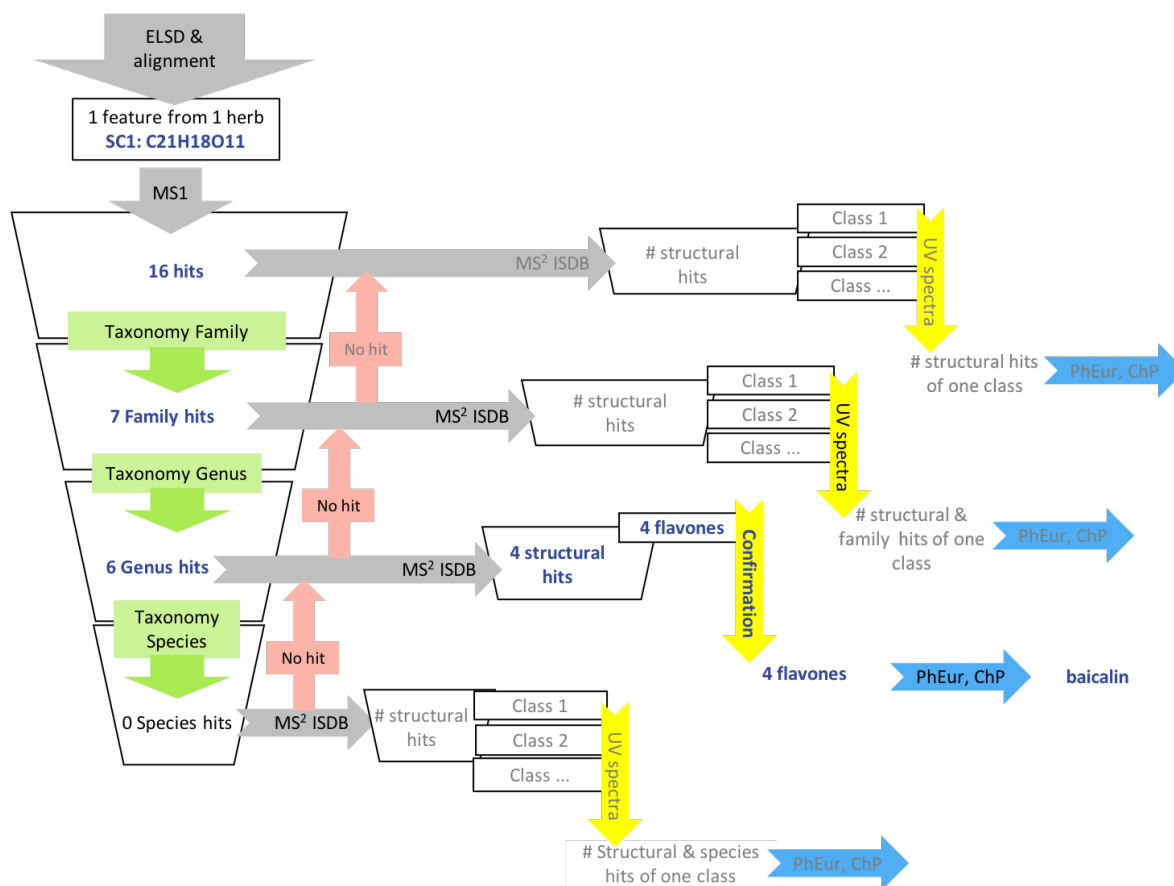


Supplementary Figure 11: scheme of the annotation strategy.

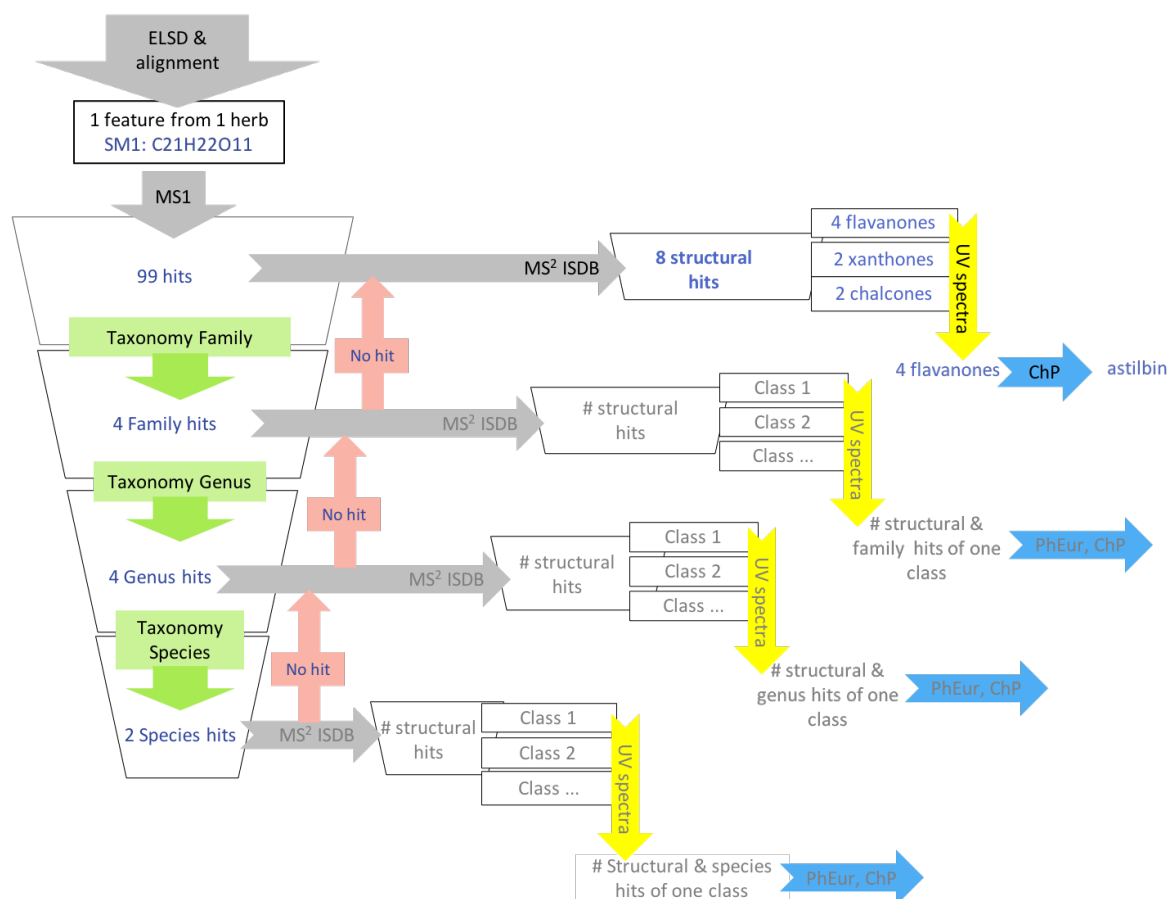
5.2 Example of annotations



Supplementary Figure 12: annotation scheme for G2, (formally identified as liquiritin apioside): for G2 molecular formula, the DNP listed 4 possible structures for the species, three of which were proposed by the ISDB consultation. Among them, the UV spectrum eliminated the chalcone, resulting in two possible structures of the same chemical class at the end of the annotation.



Supplementary Figure 13: annotation scheme for SC1 (baicalin): this component was classified as a trihydroxyflavone by taxonomy (6 genus hits), four of which were then proposed by ISDB consultation. Among the 4 final hits, the most relevant was baicalin, which is the marker of both European and Chinese Pharmacopoeias.



Supplementary Figure 14: annotation schema for SM1 (astilbin): no match between taxonomy and ISDB was found. The ISDB consultation retrieved 3 classes of compounds. UV spectrum discriminated them by demonstrating the presence of flavanone and discarding the chalcones and xanthones. If no concordant taxonomical hit was retrieved by the ISDB consultation, three pentahydroxyflavanones were suggested. The consultation of the Chinese Pharmacopoeia (CP) permitted to discriminate between them and to select the official marker, astilbin, which is not referenced in the DNP for *S.glabra*.

5.3 Summary of annotations

Supplementary Table S1: summary of the annotations

HRMS/MS: 21 annotations	Number of cases
	Cases
Taxonomy-ISDB consistency	17 (81%)
1 structure	9
> 1 structure	8
> 1 class of components	4
UV discrimination	4
Taxonomy-ISDB inconsistency	4 (19%)
> 1 class of components	4
UV discrimination	4
Number of structures of 1 class after UV discrimination	
1 hit	11
2 to 4	10
Literature (ChP, PhEur) discrimination	2
Literature (ChP, PhEur) modification	1

+ 1 annotation at HRMS + taxonomic level => 22 annotations

Formal identification		NMR		Spiking
Number of hits of 1 class after annotation		confirmation	modification	confirmation
1 hit	13	6	2	3
2 hits	2	3	2	-
3 hits	3			
4 hits	4			
Number of formally identified components		16		

6 Identification and annotation tables

These tables summarize the identifications and annotations mentioned in the main text. The complete metadata is available in the Cytoscape files in [doi:10.25345/C5516P](https://doi.org/10.25345/C5516P) including IUPAC and InChI key.

Supplementary Table S2 : identification and annotations for *Angelica sinensis*

N°	Co-marker	RT (min)	Molecular formula	m/z	Feature	Spec ^a	Identification/ annotation	Tax ^b	MSI ^c	Chemical family	Cluster specificity			ID ^g
											PI ^d	NI ^e	CI ^f	
A1		10.37	C ₁₂ H ₁₄ O ₂	191.1068	[M+H] ⁺	1	ligustilide	S	1			ND		110
	Co-A1-1	10.11	C ₁₂ H ₁₄ O ₂	191.1068	[M+H] ⁺	1	neoligustilide buthylphtalide	G	3					252
	Co-A1-2	11.87	C ₁₂ H ₁₄ O ₂	191.1068	[M+H] ⁺	1	neoligustilide buthylphtalide	G	3					1270
	Co-A1-3	5.85	C ₁₂ H ₁₄ O ₄	207.102	[M+H] ⁺	1	6, 7-epoxyligustilide 9-hydroxylicustilide	F	2	isobenzofurans	85%	PI-17		502
	Co-A1-4	6.20	C ₁₂ H ₁₄ O ₄	207.102	[M+H] ⁺	1	6, 7-epoxylicustilide 9-hydroxylicustilide	F	2					698
	Co-A1-5	11.87	C ₂₄ H ₂₈ O ₄	381.207	[M+H] ⁺	1	11 potential structures	S	3					721

^a Spec: feature specificity; ^b Tax: taxonomic data referenced in (DNP, 2019a): S: species, G: genus, F: family, ND: not described, ^c MSI: *Metabolomic Standard Initiative*, level of identification proposed in (Sumner et al., 2007). ^d PI: positive ionization; ^e NI: negative ionization; ^f CI: cluster index; ^g: identification number in MZmine and Cytoscape.

Supplementary Table S3 : identification and annotations for *Chrysanthemum indicum*

N°	Co-marker	RT (min)	Molecular formula	m/z	Feature	Spec ^a	Identification/ annotation	Tax ^b	MSI ^c	Chemical family	Cluster specificity			
											PI ^d	NI ^e	CI ^f	ID ^g
C3		4.90	C ₂₅ H ₂₄ O ₁₂	517.1346	[M+H] ⁺	1	1,3-Dicaffeoyl-epi-quinic acid	F	1		8%			148
				515.1196	[M-H] ⁻	1								49
C1	Co-C3-1	5.40	C ₂₅ H ₂₄ O ₁₂	517.1344	[M+H] ⁺	1	trans-Di-O-caffeoylquinic acid	F	3					82
				515.1197	[M-H] ⁻	1								26
C8	Co-C3-2	4.84	C ₂₅ H ₂₄ O ₁₂	517.1347	[M+H] ⁺	1	trans-Di-O-caffeoylquinic acid	F	3	Caffeoylquinic acids	84%	P-I3 NI-34		152
				515.1199	[M-H] ⁻	1								396
				515.1198	[M-H] ⁻	1								854
C6	Co-C3-5	1.37	C ₁₆ H ₁₈ O ₉	355.1024	[M+H] ⁺	0.91	chlorogenic acid	F	2					184
				353.0882	[M-H] ⁻	0.89								102
C2		5.20	C ₂₁ H ₂₀ O ₁₀	433.1131	[M+H] ⁺	1	Cosmosiin	F	1	trihydroxyflavone	selfloop			58
				431.0985	[M-H] ⁻	1								41
C4		6.08	C ₂₄ H ₂₂ O ₁₃	519.1131	[M+H] ⁺	1	Cosmosiin-6''-O-Malonyl	F	1	trihydroxyflavone	selfloop			706
				517.0990	[M-H] ⁻	1								195
C5		4.31	C ₂₁ H ₂₀ O ₁₁	449.1079	[M+H] ⁺	1	3',5,5',7-Tetrahydroxyflavone; 7-O-β-D-Glucopyranoside	NA	3	tetrahydroxyflavone	selfloop			206
				447.0937	[M-H] ⁻	0.94								117
C7		7.55	C ₂₅ H ₂₄ O ₁₃	533.1294	[M+H] ⁺	0.99	QRM00 ^h LHF87 ^h LMY39 ^h	NA		dihydroxymethoxyflavone malonylglucoside	selfloop			71
				531.1147	[M-H] ⁻	ND-F ⁱ								1157
C7-F			C ₁₆ H ₁₂ O ₅	283.0613	[M-malonylhexose] (m/z -248.05321)	0.99								92

^a Spec: feature specificity; ^b Tax: taxonomic data referenced in (DNP, 2019a): S: species, G: genus, F: family, ND: not described, ^c MSI: *Metabolomic Standard Initiative*, level of identification proposed in (Sumner et al., 2007). ^d PI: positive ionization; ^e NI: negative ionization; ^f CI: cluster index; ^g: identification number in MZmine and Cytoscape; ^h CRC number, structure available in (DNP, 2019b); ⁱ ND-F not detected in the formula.

Supplementary Table S4 : identification and annotations for *Glycyrrhiza uralensis*

N°	Co-marker	RT (min)	Molecular formula	m/z	Feature	Spec ^a	Identification/ annotation	Tax ^b	MSI ^c	Chemical family	Cluster specificity					
											PI ^d	NI ^e	CI ^f	ID ^g		
G1		8.57	C ₄₂ H ₆₂ O ₁₆	823.4116	[M+H] ⁺	1	uralsaponin A	S	1						63	
				821.3974	[M-H] ⁻	1									4	
G5	Co-G1-1	8.98	C ₄₂ H ₆₂ O ₁₆	823.4116	[M+H] ⁺	1	licoricesaponin K2 or isomers	S/G	2							230
					821.3973	[M-H] ⁻										1
	Co-G1-2	9.08	C ₄₂ H ₆₂ O ₁₆	823.4116	[M+H] ⁺	1	licoricesaponin K2 or isomers	S/G								
	Co-G1-3	9.17	C ₄₂ H ₆₂ O ₁₆	823.4116	[M+H] ⁺	1	licoricesaponin K2 or isomers	S/G								
G6	Co-G1-4	9.92	C ₄₂ H ₆₄ O ₁₆	825.427	[M+H] ⁺	1	uralsaponin C licoricesaponin J2	S		oleanane triterpenoids	100%	90%	PI-1 NI-8			
	Co-G1-6	8.24	C ₄₂ H ₆₂ O ₁₇	839.4061	[M+H] ⁺	1	uralsaponin U Licoricesaponin G2 or isomers	S/G	2							96
				837.3921	[M-H] ⁻	1										71
	Co-G1-5	8.24	C ₄₂ H ₆₂ O ₁₇	839.4061	[M+H] ⁺	1	uralsaponin U Licoricesaponin G2 or isomers	S/G								
	Co-G1-7	8.61	C ₄₂ H ₆₂ O ₁₇	839.4061	[M+H] ⁺	1	uralsaponin U Licoricesaponin G2 or isomers	S/G								
	Co-G1-8	7.81	C ₄₂ H ₆₂ O ₁₇	839.4061	[M+H] ⁺	1	uralsaponin U Licoricesaponin G2 or isomers	S/G								
G8	Co-G1-9	7.81	C ₄₂ H ₆₂ O ₁₇	839.406	[M+H] ⁺	1	uralsaponin U Licoricesaponin G2 or isomers	S/G	2							584
					837.3922	[M-H] ⁻										1
G2		3.99	C ₂₆ H ₃₀ O ₁₃	551.1762	[M+H] ⁺	1	liquiritin apioside	S	1	flavanones						168
				549.1617	[M-H] ⁻	1										17
G3	Co-G2-2	3.84	C ₂₆ H ₃₀ O ₁₃	551.176	[M+H] ⁺	1	glabroside	S	1	flavanones						1452
					549.1618	[M-H] ⁻										1
G9	Co-G2-1	5.81	C ₂₆ H ₃₀ O ₁₃	551.1759	[M+H] ⁺	0.98	neolicuroside isoliquiritin-aposide	S/G	2			21%	38%	PI-3 NI-5		251
					549.1619	[M-H] ⁻										ND-F ⁱ
	Co-G2-3	5.99	C ₂₆ H ₃₀ O ₁₃	551.1762	[M+H] ⁺	1	neolicuroside isoliquiritin-aposide	S/G	2							1258
	Co-G2-4	3.97	C ₂₁ H ₂₂ O ₉	419.1330	[M+H] ⁺	1	liquiritin neisoliquiritin isoliquiritin	S/G	2							419
	Co-G2-5	6.00	C ₂₁ H ₂₂ O ₉	419.1330	[M+H] ⁺	1	liquiritin neisoliquiritin isoliquiritin	S/G	2	flavanones						764
	Co-G2-6	6.19	C ₂₁ H ₂₂ O ₉	419.1330	[M+H] ⁺	1	liquiritin neisoliquiritin isoliquiritin	S/G	2							1537
G4		1.46		165.0548	[M-?] ⁻	1	unknown									587
G7		6.15	C ₂₂ H ₂₂ O ₉	431.1335	[M+H] ⁺	0.95	isoononin	G	2	isoflavones (2 substituents)	selfloop					106

^a Spec: feature specificity; ^b Tax: taxonomic data referenced in (DNP, 2019a): S: species, G: genus, F: family, ND: not described, ^c MSI: *Metabolomic Standard Initiative*, level of identification proposed in (Sumner et al., 2007). ^d PI: positive ionization; ^e NI: negative ionization; ^f CI: cluster index; ^g: identification number in MZmine and Cytoscape; ^h CRC number, structure available in (DNP, 2019b); ⁱ ND-F not detected in the formula.

Supplementary Table S5 : identification and annotations for *Isatis tinctoria*

N°	Co-marker	RT (min)	Molecular formula	m/z	Feature	Spec ^a	Identification/ annotation	Tax ^b	MSI ^c	Chemical family	Cluster specificity			ID ^g
											PI ^d	NI ^e	CI ^f	
11		3.90	C ₂₁ H ₂₀ O ₁₀	433.1131	[M+H] ⁺	0.99	isovitexin	S	1	flavones				232
				431.0986	[M-H] ⁻	0.99								147
12	Co-I1-1	4.33	C ₂₂ H ₂₂ O ₁₁	463.1235	[M+H] ⁺	1	isoscoparin	S	2	Trihydroxymethoxyflavone -C-glucoside	50%	80%	PI-57 NI-24	195
				461.1095	[M-H] ⁻	1								172
	Co-I1-2	2.08	C ₂₁ H ₂₀ O ₁₁	449.1080	[M+H] ⁺	1	HGS57 ^h LJX37 ^h KRF92 ^h	NA	3	Tetrahydroxyflavone -C-glucoside				1530
				447.0939	[M-H] ⁻	1								719

^a Spec: feature specificity; ^b Tax: taxonomic data referenced in (DNP, 2019a): S: species, G: genus, F: family, ND: not described, ^c MSI: *Metabolomic Standard Initiative*, level of identification proposed in (Sumner et al., 2007). ^d PI: positive ionization; ^e NI: negative ionization; ^f CI: cluster index; ^g: identification number in MZmine and Cytoscape; ^h CRC number, structure available in (DNP, 2019b).

Supplementary Table S6 : identification and annotations for *Oldenlandia diffusa*

N°	Co-marker	RT (min)	Molecular formula	m/z	Feature	Spec ^a	Identification/annotation	Tax ^b	MSI ^c	Chemical family	Cluster specificity			ID ^e
											PI ^d	NI ^e	CI ^f	
O1		5.43	C ₂₆ H ₃₀ O ₁₃	573.1580	[M+Na] ⁺	1	Scandoside; 10-O-(4-Hydroxy-Z-cinnamoyl), Me ester		1	Iridoid monoterpenoids	100%	100%	PI-102 NI-71	189
				549.1611	[M-H] ⁻	1								37
O2		3.07	C ₉ H ₈ O ₃	165.0548	[M+H] ⁺ (?)	ND-F ⁱ	coumaric acid (fragment?)	NA			selfloop			2256
				163.0392	[M-H] ⁻ (?)	0.93								61
O3		1.16	C ₁₈ H ₂₄ O ₁₂	455.1164	[M+Na] ⁺	1	asperulosidic acid	F	2	Iridoid monoterpenoids	100%		PI-186	193
				431.1197	[M-H] ⁻	1								45
O4		3.72	ND	ND	?	ND-F ⁱ	coumaric acid (fragment?)	NA			selfloop			774
				163.0391	[M-H] ⁻ (?)	1								
O5	Co-O-1	4.87	C ₃₇ H ₃₈ O ₂₀	803.203	[M+H] ⁺	1	KBY51 ^h	S	2	flavonol-di-glycoside-cinnamoyl	60%	71%	PI-100	272
				801.1896	[M-H] ⁻	1								116
	Co-O-2	4.63	C ₃₈ H ₄₀ O ₂₁	833.213	[M+H] ⁺	1	OYT10 ^h	S	2				NI-28	508
	Co-O-3	5.38	C ₃₇ H ₃₈ O ₁₉	787.208	[M+H] ⁺	1	JOH23 ^h							1027
O6		1.73	C ₁₈ H ₂₂ O ₁₁	432.1503	[M+NH ₄] ⁺ (m/z +17.0265)	1	6'-Acetyl-deacetylasperuloside.	G	2	Iridoid monoterpenoids	25%		PI-3	224
				415.1235	[M+H] ⁺	1								784
				459.115	[M+FA] ⁻	1								31
O7		0.98	C ₁₇ H ₂₄ O ₁₁	427.1211	[M+Na] ⁺	1	feretoside	G	2	Iridoid monoterpenoids	selfloop			128
				449.1306	[M+FA] ⁻	1								39
SC1 (O8)		6.16	C ₂₁ H ₁₈ O ₁₁	447.0918	[M+H] ⁺	0.06	baicalin	S	1	flavones				3
				445.0780	[M-H] ⁻	0.17								10

^a Spec: feature specificity; ^b Tax: taxonomic data referenced in (DNP, 2019a): S: species, G: genus, F: family, ND: not described, ^c MSI: *Metabolomic Standard Initiative*, level of identification proposed in (Sumner et al., 2007). ^d PI: positive ionization; ^e NI: negative ionization; ^f CI: cluster index; ^g: identification number in MZmine and Cytoscape; ^h CRC number, structure available in (DNP, 2019b); ⁱ ND-F not detected in the formula.

Supplementary Table S7 : identification and annotations for *Polygonum cuspidatum*

N°	Co-marker	RT (min)	Molecular formula	m/z	Feature	Spec ^a	Identification/ annotation	Tax ^b	MSI ^c	Chemical family	Cluster specificity			
											PI ^d	NI ^e	CI ^f	ID ^g
PO1		3.76	C ₂₀ H ₂₂ O ₈	391.1395	[M+H] ⁺	1	E-piceid		1					145
				389.1244	[M-H] ⁻	1						52		
				435.1300	[M+FA] ⁻	0.99								
	Co-Po-1	2.55	C ₂₀ H ₂₂ O ₈	391.1395	[M+H] ⁺	1	resveratrolside	NA	3	stilbenes	11%	6%	PI-3 NI-5	1636
	Co-Po-2	5.13	C ₁₄ H ₁₂ O ₃	229.086	[M+H] ⁺	1	resveratrol analog	NA	3					1619
Co-Po-3	5.50		229.086	[M+H] ⁺	1	resveratrol analog			656					
Co-Po-4	5.79		229.0862	[M+H] ⁺	1	resveratrol analog			1067					
PO2		7.07	C ₂₁ H ₂₀ O ₁₀	455.0950	[M+Na] ⁺	1	emodin-8-glucoside	1	1	anthraquinones	selfloop			416
			C ₁₅ H ₁₀ O ₅	271.0599	[M-hexose] ⁺ (m/z -162.0528)	0.99								135
			C ₂₁ H ₂₀ O ₁₀	431.0986	[M-H] ⁻	0.98								13
PO3		2.69	C ₃₇ H ₃₀ O ₁₆	731.1606	[M+H] ⁺	ND-F ⁱ	3'-galloylprocyanidin B1 or B2	G		proanthocyanidin flavonoids				2336
				729.1472	[M-H] ⁻	ND-F ⁱ						1833		
PO4		2.03	C ₁₅ H ₁₄ O ₆	291.0862	[M+H] ⁺	0.87	Catechin epicatechin	G			60%		PI 120	752
			C ₃₇ H ₃₀ O ₁₆	731.1607	[M+H] ⁺	ND-F ⁱ	3'-galloylprocyanidin B1 or B2	G		proanthocyanidin flavonoids				2388
PO4-F			C ₁₅ H ₁₄ O ₆	289.0721	[M-H] ⁻	0.88								171
PO4			C ₃₇ H ₃₀ O ₁₆	729.1472	[M-H] ⁻	ND-F ⁱ								1778
PO5		3.66	C ₄₄ H ₃₀ O ₂₀	883.1716	[M+H] ⁺	ND-F ⁱ	3,3'-digalloylprocyanidin B2			proanthocyanidin flavonoids				2372
				3.73	881.1584	[M-H] ⁻	ND-F ⁱ		G				1777	

^a Spec: feature specificity; ^b Tax: taxonomic data referenced in (DNP, 2019a): S: species, G: genus, F: family, ND: not described, ^c MSI: *Metabolomic Standard Initiative*, level of identification proposed in (Sumner et al., 2007). ^d PI: positive ionization; ^e NI: negative ionization; ^f CI: cluster index; ^g: identification number in MZmine and Cytoscape; ⁱ ND-F not detected in the formula.

Supplementary Table S8 : identification and annotations for *Prunella vulgaris*

N°	Co-marker	RT (min)	Molecular formula	m/z	Feature	Spec ^a	Identification/ annotation	Tax ^b	MSI ^c	Chemical family	Cluster specificity				
											PI ^d	NI ^e	CI ^f	ID ^g	
PR1		5.49	C ₁₈ H ₁₆ O ₈	361.0918	[M+H] ⁺	1	rosmarinic acid	S	1					646	
				359.0778	[M-H] ⁻	1								22	
				C ₉ H ₆ O ₃	163.039	[M-?] ⁺	1								340
PR2	Co-PR1-1	4.63	C ₂₄ H ₂₆ O ₁₃	521.1306	[M-H] ⁻	1	salviaflaside	F	2	rosmarinic/salvianolic acid lignans	6%	69%	PI-3 NI-10	105	
				C ₉ H ₆ O ₃	163.0388	[M-?] ⁺	1								1159
PR3	Co-PR1-2	2.27	C ₁₈ H ₁₈ O ₉	377.0883	[M-H] ⁻	0.93	danshensuan C	F	2					947	
				C ₉ H ₈ O ₄	181.0496		ND-F ⁱ								2405
					179.0341		0.85								

^a Spec: feature specificity; ^b Tax: taxonomic data referenced in (DNP, 2019a): S: species, G: genus, F: family, ND: not described, ^c MSI: *Metabolomic Standard Initiative*, level of identification proposed in (Sumner et al., 2007). ^d PI: positive ionization; ^e NI: negative ionization; ^f CI: cluster index; ^g: identification number in MZmine and Cytoscape; ⁱ ND-F not detected in the formula.

Supplementary Table S9 : identification and annotations for *Scutellaria baicalensis*

N°	Co-marker	RT (min)	Molecular formula	m/z	Feature	Spec ^a	Identification/ annotation	Tax ^b	MSI ^c	Chemical family	Cluster specificity			ID ^g	
											PI ^d	NI ^e	CI ^f		
SC1		6.16	C ₂₁ H ₁₈ O ₁₁	447.0918	[M+H] ⁺	0.94	baicalin	S	1					3	
				445.0780	[M-H] ⁻	0.93								10	
SC4	Co-Sc1-1	6.63	C ₂₁ H ₁₈ O ₁₁	447.0914	[M+H] ⁺	1	2', 5, 7-trihydroxyflavone-7-O-glucoside 5, 7, 8-trihydroxyflavone-7-O-glucoside	G	2	Flavones (3 O substituents)	14%	25%	PI-3 NI-5	18	
					445.0781	[M-H] ⁻								1	23
	Co-Sc1-2	7.11	C ₂₁ H ₁₈ O ₁₁	447.0923	[M+H] ⁺	0.99	2', 5, 7-trihydroxyflavone-7-O-glucoside 5, 7, 8-trihydroxyflavone-7-O-glucoside	G	2					105	
					445.0781	[M-H] ⁻								1	
Co-Sc1-3	7.02	C ₂₂ H ₂₀ O ₁₂	477.1030	[M+H] ⁺	0.98	hispidulin-7-glucuronide NMM41 ^h	S/G	3					31		
SC2		7.16	C ₂₂ H ₂₀ O ₁₁	461.1079	[M+H] ⁺	0.91	wogonoside	S	1	flavones (3 O substituents); O-glucuronides				selfloop	6
				459.0938	[M-H] ⁻	0.85								5	
SC3		6.89	C ₂₂ H ₂₀ O ₁₁	461.1078	[M+H] ⁺	0.97	oroxyloside	S	1					selfloop	7
				459.0938	[M-H] ⁻	0.93								8	
SC8	Co-Sc2-1	6.81	C ₂₂ H ₂₀ O ₁₂	475.0886	[M-H] ⁻	1	hispidulin-7-glucuronide NMM41 ^h	S/G	3	trihydroxymethoxyflavone		96%	NI-1	74	
	Co-Sc2-2	7.04	C ₂₂ H ₂₀ O ₁₂	475.0886	[M-H] ⁻	1	hispidulin-7-glucuronide NMM41 ^h	S/G	3					50	
	Co-Sc2-3	7.29	C ₂₃ H ₂₂ O ₁₂	489.1041	[M-H] ⁻	1	LHK67 ^h	G	2	tetrahydroxymethoxyflavone				79	
	Co-Sc2-4	6.25	C ₂₃ H ₂₂ O ₁₃	505.0992	[M-H] ⁻	1	MWZ53 ^h or isomers	G/NA	3	pentahydroxyflavone				519	
	Co-Sc2-5	6.14	C ₂₃ H ₂₂ O ₁₃	505.0992	[M-H] ⁻	1								357	
	Co-Sc2-6	7.97	C ₁₇ H ₁₄ O ₇	329.0668	[M-H] ⁻	1	thymusin	F	2	trihydroxydimethoxyflavone				209	
	Co-Sc2-7	9.29	C ₁₇ H ₁₄ O ₆	313.0721	[M-H] ⁻	1	velutin	F		dihydroxydimethoxyflavone				216	
SC5		7.99	C ₁₅ H ₁₀ O ₅	271.0602	[M+H] ⁺	1	baicalein norwogonin	S 2G	3	flavones (3 O substituents)	selfloop		selfloop	143	

2',5,7-trihydroxflavone												
			269.0458	[M-H] ⁻	1							139
SC6	4.10	C ₂₆ H ₂₈ O ₁₃	549.1603	[M+H] ⁺	0.96	chrysin 6-C-glucoside 8-C-arabinoside chrysin 6-C-arabinoside 8-C-glucoside	S	2	flavones (3 O substituents) di-C-glycosides	61%	PI-74	35
			547.1463	[M-H] ⁻	0.98							40
SC7	6.52	C ₂₁ H ₂₀ O ₁₁	449.1075	[M+H] ⁺	ND-F ⁱ	<i>dihydrobaicalin</i> or <i>CYL29</i> ^h	S	2	<i>flavones (4 O substituents); O-glucuronides</i>		PI-3 NI-5	2551
			447.0924	[M-H] ⁻	ND-F ⁱ							1888
SC9	4.65	C ₂₆ H ₂₈ O ₁₃	549.1604	[M+H] ⁺	0.97	chrysin 6-C-glucoside 8-C-arabinoside chrysin 6-C-arabinoside 8-C-glucoside	S	2	flavones (3 O substituents) di-C-glycosides	61%	PI-74	42
			547.1464	[M-H] ⁻	0.97							33
SC10	4.98	C ₂₇ H ₃₀ O ₁₄	579.1711	[M+H] ⁺	1	nivyaside RDD41 ^h KRG85 ^h	NA	3	flavones (3 O substituents) di-C-glycosides	50%	PI-57	827
SC11	5.19	C ₂₁ H ₂₀ O ₉	417.118	[M+H] ⁺	1	chrysin 6-C-glucopyranoside chrysin 8-C-glucopyranoside.	S	2	flavones (3 O substituents) C-glycosides	50%	PI-57	588
SC12	6.22	C ₂₁ H ₂₀ O ₉	417.117	[M+H] ⁺	1	chrysin 6-C-glucopyranoside chrysin 8-C-glucopyranoside.	S	2	flavones (3 O substituents) C-glycosides	50%	PI-57	455

^a Spec: feature specificity; ^b Tax: taxonomic data referenced in (DNP, 2019a); S: species, G: genus, F: family, ND: not described, ^c MSI: *Metabolomic Standard Initiative*, level of identification proposed in (Sumner et al., 2007). ^d PI: positive ionization; ^e NI: negative ionization; ^f CI: cluster index; ^g: identification number in MZmine and Cytoscape; ^h CRC number, structure available in (DNP, 2019b); ⁱ ND-F not detected in the formula.

Supplementary Table S10 : identification and annotations for *Smilax glabra*

N°	Co-marker	RT (min)	Molecular formula	m/z	Feature	Spec ^a	Identification/ annotation	Tax ^b	MSI ^c	Chemical family	Cluster specificity			
											PI ^d	NI ^e	CI ^f	ID ^g
SM1		4.33	C ₂₁ H ₂₂ O ₁₁	451.1236	[M+H] ⁺	1	astilbin	S	1					98
				449.1088	[M-H] ⁻	1								19
	Co-SM1-1	4.92	C ₂₁ H ₂₂ O ₁₁	451.1237	[M+H] ⁺	1	OBC08 aceronidin NJL24 ^h	NA	3	pentahydroxyflavanone-O-rhamoside	100%	99%	PI-25 NI22	257
	Co-SM1-2	4.04	C ₂₁ H ₂₂ O ₁₁	451.1237	[M+H] ⁺	1	OBC08 aceronidin NJL24 ^h	NA	3					315
	Co-SM1-3	5.02	C ₂₁ H ₂₂ O ₁₁	451.1237	[M+H] ⁺	1	OBC08 aceronidin NJL24 ^h	NA	3					667
	Co-SM1-4	4.98	C ₂₁ H ₂₀ O ₁₁	449.108	[M+H] ⁺	1	PYZ08 ^h POT37 ^h HBN30 ^h KQW57 ^h NRN98 ^h LHZ69 ^h	NA	3					716
Co-SM1-5	2.90	C ₁₅ H ₁₆ O ₉	341.087	[M+H] ⁺	1	eucryphin	S	2	benzopyran					779

^a Spec: feature specificity; ^b Tax: taxonomic data referenced in (DNP, 2019a): S: species, G: genus, F: family, ND: not described, ^c MSI: *Metabolomic Standard Initiative*, level of identification proposed in (Sumner et al., 2007). ^d PI: positive ionization; ^e NI: negative ionization; ^f CI: cluster index; ^g: identification number in MZmine and Cytoscape; ^h CRC number, structure available in (DNP, 2019b).

Supplementary Table S11 : identification and annotations for *Sophora flavescens*

N°	Co-marker	RT (min)	Molecular formula	m/z	Feature	Spec ^a	Identification/ annotation	Tax ^b	MSI ^c	Chemical family	Cluster specificity			
											PI ^d	NI ^e	CI ^f	ID ^g
SO1-1		0.83	C₁₅H₂₄N₂O₂	265.1911	[M+H]⁺	0.98	oxymatrine	S	1			NA		1
	Co-SO1-1	0.83	C ₁₅ H ₂₂ N ₂ O ₂	263.1756	[M+H] ⁺	0.97	allomatrine isomers	G	3					5
	Co-SO1-2	0.63	C ₁₅ H ₂₀ N ₂ O	245.1644	[M+H] ⁺	1	isosophoramine	G	2					202
	Co-SO1-3	0.77	C ₁₅ H ₂₂ N ₂ O	247.1809	[M+H] ⁺	1	5-episophocarpine	S	2	quinolizidine alkaloid	89%		PI-4	21
	Co-SO1-4	1.04	C ₁₅ H ₂₀ N ₂ O ₂	261.1601	[M+H] ⁺	1	7-hydroxysophoramine	G	2			-		798
	Co-SO1-6	1.1	C ₁₅ H ₂₂ N ₂ O ₂	263.1756	[M+H] ⁺	1	allomatrine isomers	G	3					29
	Co-SO1-7	1.59	C ₁₅ H ₂₄ N ₂ O ₃	281.1859	[M+H] ⁺	1	6,7-dihydroxylupanine	G	2					81
	Co-SO-1	7.67	C ₂₆ H ₃₂ O ₇	457.222	[M+H] ⁺	1	kushenol F	S	2					
	Co-SO-2	7.73	C ₂₆ H ₃₂ O ₇	457.222	[M+H] ⁺	1	kurarinol	S	2					
	Co-SO-3	7.95	C ₂₆ H ₃₂ O ₇	457.2222	[M+H] ⁺	1	PPB59 ^h	S	2					
	Co-SO-3	7.62	C ₂₆ H ₃₀ O ₇	455.2057	[M+H] ⁺	1	kushenol I	S/G	3	prenylated flavanone	97%	15%	PI-26	
	Co-SO-4	9.18	C ₂₆ H ₃₀ O ₇	455.2064	[M+H] ⁺	1	leachianone D	S/G	3					
				453.1927	[M-H] ⁻	1								259
	Co-SO-5	9.48	C ₂₆ H ₃₀ O ₆	437.1976	[M-H] ⁻	1	cyclokaridin	S	2					46
	Co-SO-6	10.18	C ₂₅ H ₂₈ O ₆	423.182	[M-H] ⁻	1	kushenol F	S	2					253

^a Spec: feature specificity; ^b Tax: taxonomic data referenced in (DNP, 2019a): S: species, G: genus, F: family, ND: not described, ^c MSI: *Metabolomic Standard Initiative*, level of identification proposed in (Sumner et al., 2007). ^d PI: positive ionization; ^e NI: negative ionization; ^f CI: cluster index; ^g: identification number in MZmine and Cytoscape; ^h CRC number, structure available in (DNP, 2019b).

7 Description of isolated components

1,3-Dicaffeoyl-epi-quinic acid (C1). Pure in M6S8 and S9. UV max: 219; 328 nm. ^1H NMR (DMSO- d_6 , 600 MHz) δ 1.84 (1H, t, $J=11.7$ Hz, H-2''), 2.22 (1H, d, $J=14.2$ Hz, H-6''), 2.32 (1H, d, $J=12.9$ Hz, 2'), 2.36 (1H, m, H-6'), 3.55 (1H, d, $J=8.9$ Hz, H-4), 4.04 (1H, s, H-5), 5.22 (1H, td, $J=9.1, 4.2$ Hz, H-3), 6.17 (1H, d, $J=15.9$ Hz, H-2''), 6.23 (1H, d, $J=15.9$ Hz, H-2'), 6.75 (1H, d, $J=8.1$ Hz, H-8''), 6.75 (1H, d, $J=8.1$ Hz, H-8'), 6.95 (1H, dd, $J=8.1, 2.1$ Hz, H-9''), 6.98 (1H, dd, $J=8.1, 2.1$ Hz, H-9'), 7.03 (1H, d, $J=2.1$ Hz, H-5''), 7.08 (1H, d, $J=2.1$ Hz, H-5'), 7.40 (1H, d, $J=15.9$ Hz, H-3''), 7.47 (1H, d, $J=15.9$ Hz, H-3'); ^{13}C NMR (DMSO- d_6 , 151 MHz) δ 34.6 (C-6), 36.8 (C-2), 68.2 (C-5), 70.3 (C-3), 71.6 (C-4), 114.4 (C-2'), 114.8 (C-5''), 114.9 (C-5'), 115.5 (C-2''), 115.8 (C-8', C-8''), 120.7 (C-9''), 121.3 (C-9'), 125.5 (C-4'), 125.7 (C-4''), 144.1 C- (3''), 144.9 (C-3'), 145.7 (C-6', C-6''), 148.2 (C-7'), 148.6 (C-7''), 165.0 (C-1''), 166.1 (C-1'). ESI-HRMS: m/z 515.1191 (calculated for $\text{C}_{25}\text{H}_{23}\text{O}_{12}$, m/z 515.1190, 1.2 ppm) (Patiny and Borel, 2013) (Kim and Lee, 2005).

Cosmosiin (C2). Impur in M21. UV max: 266, 340 nm. ^1H NMR (MeOD, 600 MHz) δ 3.41 (1H, t, $J=9.6, 8.9$ Hz, H-4''), 3.50 (2H, m, H-2'', H-3''), 3.55 (1H, m, H-5''), 3.73 (1H, dd, $J=12.1, 5.9$ Hz, H-6''b), 3.95 (1H, dd, $J=12.2, 2.3$ Hz, H-6''a), 5.07 (1H, d, $J=7.0$ Hz, H-1''), 6.49 (1H, d, $J=2.1$ Hz, H-6), 6.65 (1H, s, H-3), 6.81 (1H, d, $J=2.1$ Hz, H-8), 6.93 (2H, d, $J=8.4$ Hz, H-3', H-5'), 7.88 (2H, d, $J=8.4$ Hz, H-2', H-6'); ^{13}C NMR (MeOD, 151 MHz) δ 62.5 (C-6''), 71.3 (C-4''), 74.7 (C-2''), 77.9 (C-3''), 78.4 (C-5''), 96.1 (C-8), 101.2 (C-6), 101.6 (C-1''), 104.1 (C-3), 107.1 (C-10), 117.0 (C-3', C-5'), 123.1 (C-1'), 129.6 (C-2', C-6'), 159.0 (C-9), 162.9 (C-5), 162.9 (4'), 164.8 (C-7), 166.8 (C-2), 184.1 (C-4). ESI-HRMS: m/z 431.0988 (calculated for $\text{C}_{21}\text{H}_{19}\text{O}_{10}$, m/z 431.0978, 1.0 ppm) (Redaelli et al., 1980).

Malonylcosmosiin (C4) (Cosmosiin; 6''-*O*-malonyl). Pure in M23S7. UV max: 266; 336 nm. ^1H NMR (DMSO- d_6 , 600 MHz) δ 3.11 (2H, m, H-8''), 3.21 (1H, t, $J=9.3$ Hz, H-4''), 3.28 (1H, overlapped, H-2''), 3.31 (1H, overlapped, H-3''), 3.72 (1H, ddd, $J=9.3, 6.9, 2.0$ Hz, H-5''), 4.12 (1H, dd, $J=12.1, 6.9$ Hz, H-6''b), 4.30 (1H, dd, $J=12.1, 2.0$ Hz, H-6''a), 5.06 (1H, d, $J=7.4$ Hz, H-1''), 6.46 (1H, d, $J=2.3$ Hz, H-6), 6.78 (1H, d, $J=2.3$ Hz, H-8), 6.83 (1H, s, H-3), 6.94 (2H, d, $J=8.6$ Hz, H-3', H-5'), 7.95 (2H, d, $J=8.6$ Hz, H-2', H-6'); ^{13}C NMR (DMSO- d_6 , 151 MHz) δ 44.2 (C-8''), 63.5 (C-6''), 69.6 (C-4''), 73.1 (C-1''), 74.1 (C-5''), 76.0 (C-3''), 94.7 (C-8), 99.6 (C-6), 99.9, 103.2 (C-3), 105.7 (C-10), 116.1 (C-3', C-5'), 121.0 (C-1'), 128.6 (C-2', C-6'), 157.1 (C-9), 161.2 (C-5), 161.4 (4'), 162.7 (C-7), 164.0 (C-2), 167.7 (C-9''), 168.5 (C-7''), 181.6 (C-4). ESI-HRMS: m/z 517.0995 (calculated for $\text{C}_{24}\text{H}_{21}\text{O}_{13}$, m/z 517.0982, 1.5 ppm) (Svehlikova et al., 2004).

Uralsaponin A (G1) (Glycyrrhetic acid; 1'-Epimer). Amorphous powder. Major in M34. UV max 250 nm. ^1H NMR (DMSO- d_6 , 500 MHz) δ 0.71 (1H, m, H-5), 0.71 (3H, s, H-24), 0.75 (3H, s, H-28), 0.95 (3H, s, H-23), 0.96 (2H, m, H-1b, H-16b), 1.03 (6H, s, H-25, H-26), 1.09 (3H, s, H-29), 1.14 (1H, m, H-15b), 1.26 (1H, m, H-22b), 1.34 (4H, m, H-6b, H-7b, H-21b, H-22a), 1.34 (3H, s, H-27), 1.49 (1H, m, H-6a), 1.59 (1H, m, H-2b),

1.62 (1H, m, H-7a), 1.65 (1H, m, H-2a), 1.68 (2H, m, H-19), 1.73 (1H, m, H-15a), 1.80 (1H, m, H-21a), 2.05 (1H, m, H-18), 2.08 (1H, m, H-16a), 2.32 (1H, m, H-9), 2.55 (1H, dt, $J=13.5, 3.4$ Hz, H-1a), 3.04 (2H, m, H-2", H-3), 3.19 (1H, m, H-3"), 3.26 (1H, t, $J=6.5$ Hz, H-4"), 3.31 (1H, m, H-2'), 3.36 (1H, t, $J=9.2$ Hz, H-4'), 3.41 (1H, t, $J=9.2$ Hz, H-3'), 3.55 (1H, d, $J=9.7$ Hz, H-5"), 3.63 (1H, d, $J=9.4$ Hz, H-5'), 4.40 (1H, d, $J=7.5$ Hz, H-1'), 4.49 (1H, d, $J=7.7$ Hz, H-1"), 5.39 (1H, s, H-12); ^{13}C NMR (DMSO- d_6 , 126 MHz) δ 15.5 (C-24), 15.8 (C-25), 16.5 (C-6), 18.0 (C-26), 22.6 (C-27), 25.3 (C-2), 25.4 (C-16), 25.6 (C-15), 26.8 (C-23), 27.4 (C-29), 28.0 (C-28), 30.0 (C-21), 31.1 (C-17), 31.7 (C-7), 35.9 (C-10), 37.2 (C-22), 38.2 (C-1), 38.6 (C-4), 40.3 (C-19), 42.5 (C-14), 42.7 (C-20), 44.5 (C-8), 47.7 (C-18), 53.9 (C-5), 60.7 (C-9), 70.9 (C-4'), 71.1 (C-4"), 74.5 (C-2"), 74.7 (C-5'), 75.3 (C-3"), 75.5 (C-3'), 75.8 (C-5"), 82.2 (C-2'), 87.8 (C-3), 103.0 (C-1'), 104.3 (C-1"), 126.9 (C-12), 169.2 (C-13), 169.6 (C-6"), 169.9 (C-6'), 177.2 (C-30), 198.6 (C-11). ESI-HRMS : m/z 821.3981 [M-H] $^-$, calculated for $\text{C}_{42}\text{H}_{61}\text{O}_{16}$, m/z 821.3960, 2.0 ppm) (Baltina et al., 2005).

Liquiritin apioside (G2) (4'-7-dihydroxyflavanone ; 4'-*O*-[β -D-apiofuranosyl-(1 \rightarrow 2)- β -D-glucopyranoside]). Amorphous powder. Pure in M15S2. UV max: 220; 275; 325 nm. ^1H NMR (DMSO- d_6 , 500 MHz) δ 2.67 (1H, dd, $J=16.7, 2.9$ Hz, H-3b), 3.14 (2H, m, H-3', H-4", 3', 4"), 3.31 (2H, m, H-5", H-5'''a), 3.47 (3H, m, H-2", H-3", H-6''b), 3.64 (1H, d, $J=9.4$ Hz, H-4''b), 3.70 (1H, dt, $J=12.1, 2.5$ Hz, H-6''a), 3.75 (1H, m, H-2''"), 3.95 (1H, d, $J=9.4$ Hz, H-4'''a), 4.95 (1H, d, $J=7.5$ Hz, H-1"), 5.36 (1H, d, $J=1.2$ Hz, H-1''"), 5.52 (1H, dt, $J=12.9, 3.3$ Hz, H-2), 6.35 (1H, d, $J=2.2$ Hz, H-8), 6.51 (1H, dd, $J=8.7, 2.2$ Hz, H-6), 7.06 (2H, d, $J=8.6$ Hz, H-3', H-5'), 7.44 (4H, d, $J=8.6$ Hz, H-2', H-6'), 7.65 (1H, d, $J=8.7$ Hz, H-5); ^{13}C NMR (DMSO- d_6 , 126 MHz) δ 43.0 (C-3), 60.5 (C-6"), 64.2 (C-5''"), 69.7 (C-4"), 73.8 (C-4''"), 75.6 (C-2"), 76.0 (C-2''"), 76.8 (C-5"), 76.9 (C-3"), 78.5 (C-2), 79.2 (C-3''"), 98.5 (C-1"), 102.4 (C-8), 108.6 (C-1''"), 110.5 (C-6), 113.3 (C-10), 115.9 (C-3', C-5'), 127.8 (C-2', C-6'), 128.2 (C-5), 132.2 (C-1'), 157.1 (C-4'), 162.9 (C-7), 164.5 (C-9), 189.7 (C-4). ESI-HRMS : m/z 549.1620 [M-H] $^-$, calculated for $\text{C}_{26}\text{H}_{29}\text{O}_{13}$, m/z 549.50167, 1.2 ppm) (Kitagawa et al., 1994).

10-*O*-*p*-*cis*-Coumaroyl Scandoside Methyl Ester (O1). Major in M20S2. UV max 227; 312 nm. ^1H NMR (DMSO- d_6 , 500 MHz) δ 2.99 (2H, m, H-2', H-9), 3.05 (1H, t, $J=9.4$ Hz, H-4'), 3.16 (3H, m, H-3', H-5', H-5), 3.44 (1H, dd, $J=11.9, 6.2$ Hz, H-6'b), 3.58 (4H, s, H-12), 3.67 (1H, d, $J=11.9$ Hz, H-6'a), 4.04 (1H, d, $J=15.9$ Hz, H-10b), 4.19 (1H, d, $J=15.9$ Hz, 10a), 4.49 (1H, d, $J=8.0$ Hz, H-1'), 5.31 (1H, d, $J=5.9$ Hz, H-1), 5.53 (1H, bs, H-6), 5.74 (1H, s, H-7), 5.76 (1H, d, $J=12.9$ Hz, H-2"), 6.76 (2H, d, $J=8.4$ Hz, H-6", H-8"), 6.86 (1H, d, $J=12.9$ Hz, H-3"), 7.47 (1H, s, H-3), 7.66 (2H, d, $J=8.4$ Hz, H-5", H-9"); ^{13}C NMR (DMSO- d_6 , 126 MHz) δ 39.8 (C-5), 45.6 (C-9), 51.0 (C-12), 58.9 (C-10), 61.0 (C-6'), 70.0 (C-4'), 73.2 (C-2'), 76.6 (C-3'), 77.3 (C-5'), 81.4 (C-6), 94.9 (C-1), 98.4 (C-1'), 108.1 (C-4), 114.9 (C-6", C-8"), 115.4 (C-2"), 124.5 (C-7), 125.3 (C-4"), 132.6 (C-5", C-9"), 143.1 (C-3"), 150.1 (C-8), 152.3 (C-3), 158.9 (C-7"), 165.5 (C-1"), 166.5 (C-11). ESI-HRMS: m/z 549.1623 (calculated for $\text{C}_{26}\text{H}_{29}\text{O}_{13}$, m/z 549.16082, 1.7 ppm) (Otsuka et al., 1991).

E-Piceid (PO1) 1-(3,5-Dihydrophenyl)-2-(4-hydroxyphenyl)-ethylene ; (E)-form, 3-*O*- β -D-glucopyranoside). Amorphous powder. Pure in M14S12. UV max: 221; 281; 425 nm. ^1H NMR (DMSO- d_6 , 600 MHz) δ 3.16 (1H, t, $J=9.0$ Hz, H-4'), 3.21 (1H, t, $J=9.0$, 7.7 Hz, H-2'), 3.27 (1H, t, $J=9.0$ Hz, H-3'), 3.31 (1H, overlapped, H-5'), 3.48 (1H, dt, $J=11.0$, 5.4 Hz, H-6'b), 3.72 (1H, dd, $J=11.0$, 5.4 Hz, H-6'a), 4.61 (1H, t, $J=5.4$ Hz, 6'OH), 4.79 (1H, d, $J=7.7$ Hz, H-1'), 5.01 (1H, s, 4'OH), 5.07 (1H, s, 3'OH), 5.26 (1H, s, 2'OH), 6.33 (1H, t, $J=1.8$ Hz, H-4), 6.56 (1H, t, $J=1.8$ Hz, H-6), 6.72 (1H, t, $J=1.8$ Hz, H-2), 6.75 (2H, d, $J=8.6$ Hz, H-11, H-13), 6.86 (1H, d, $J=16.3$ Hz, H-7), 7.02 (1H, d, $J=16.3$ Hz, H-8), 7.39 (2H, d, $J=8.6$ Hz, H-10, H-14), 9.43 (1H, s, 5OH), 9.57 (1H, s, 12OH); ^{13}C NMR (DMSO- d_6 , 151 MHz) δ 60.7 (C-6'), 69.8 (C-4'), 73.3 (C-2'), 76.7 (C-3'), 77.1 (C-5'), 100.7 (C-1'), 102.7 (C-4), 104.7 (C-2), 107.2 (C-6), 115.5 (C-11, C-13), 125.2 (C-7), 127.9 (C-10, C-14), 128.0 (C-9), 128.5 (C-8), 139.3 (C-1), 157.3 (C-12), 158.4 (C-5), 158.9 (C-3). ESI-HRMS m/z 389.1246 [M-H] $^-$ (calculated for C₂₀H₁₉O₈ m/z 389.1236, 1.1 ppm) (Chen et al., 2001).

Emodin-8-*O*-glucoside (PO2) (1,3,8-trihydroxy-6-methylanthraquinone ; 8-*O*- β -glucopyranoside). Yellow amorphous powder. Pure in M31. UV max: 221; 281; 425 nm. ^1H NMR (DMSO- d_6 , 500 MHz) δ 2.40 (3H, s, 3Me), 3.24 (1H, td, $J=9.3$, 3.9 Hz, H-4'), 3.41 (2H, m, H-2', H-5'), 3.52 (1H, dt, $J=11.3$, 5.0 Hz, H-6'b), 3.72 (1H, bd, $J=11.3$ Hz, H-6'a), 4.59 (1H, t, $J=5.0$ Hz, 6'OH), 5.05 (1H, d, $J=7.4$ Hz, H-1'), 5.05 (2H, overlapped, 2'OH, 4'OH), 5.09 (1H, d, $J=5.0$ Hz, 3'OH), 7.00 (1H, d, $J=2.4$ Hz, H-7), 7.15 (1H, d, $J=1.7$ Hz, H-2), 7.28 (1H, d, $J=2.4$ Hz, H-5), 7.46 (1H, d, $J=1.7$ Hz, H-4), 13.16 (1H, s, 1OH); ^{13}C NMR (DMSO- d_6 , 126 MHz) δ 21.4 (3Me), 60.6 (C-6'), 69.5 (C-4'), 73.3 (C-2'), 76.4 (C-3'), 77.3 (C-5'), 100.8 (C-1'), 108.3 (C-5, C-7), 113.3 (C-8a), 114.4 (C-9a), 119.2 (C-4), 124.1 (C-2), 132.1 (C-4a), 136.5 (C-10a), 146.9 (C-3), 161.0 (C-8), 161.7 (C-1), 164.2 (C-6), 182.1 (C-10), 186.4 (C-9). ESI-HRMS : m/z 431.0990 [M-H] $^-$ (calculated for C₂₁H₁₉O₁₀, m/z 431.0978, 1.5 ppm) (Demirezer et al., 2001).

Baicalin (SC1) (5,6,7-trihydroxyflavone ;7-*O*- β -D-glucuronopyranoside). Amorphous powder. Major in M12-13, pure in M20S3. UV max: 220; 276; 318 nm. ^1H NMR (DMSO- d_6 , 500 MHz) δ 3.38 (3H, m, H-2'', H-3'', H-4''), 3.97 (1H, d, $J=9.5$ Hz, H-5''), 5.19 (1H, d, $J=7.5$ Hz, H-1''), 7.00 (1H, s, H-3), 7.04 (1H, s, H-8), 7.60 (3H, m, H-3', H-4', H-5'), 8.08 (2H, d, $J=7.3$ Hz, H-2', H-6'), 8.64 (1H, s, 6OH), 12.57 (1H, s, 5OH); ^{13}C NMR (DMSO- d_6 , 126 MHz) δ 182.4 (C-4), 170.1 (C-6''), 163.5 (C-2), 151.3 (C-7), 149.1 (C-9), 146.6 (C-5), 131.8 (C-4'), 130.6 (C-6), 128.9 (C1', C-3', C-5'), 126.1 (C-2', C-6'), 106.0 (C-10), 105.1 (C-3), 100.0 (C-1''), 93.7 (C-8), 75.2 (C-3''), 75.0 (C-5''), 72.6 (C-2''), 71.2 (C-4''). ESI-HRMS m/z 445.0782 [M-H] $^-$ (calculated for C₂₁H₁₇O₁₁, m/z 445.0771, 1.3 ppm) (Wu et al., 2005) .

Wogonoside (SC2) (5,7-dihydroxy-8-methoxyflavone ; 7-*O*- β -D-glucuronopyranoside). Amorphous powder. Pure in M25. UV max: 220; 276; 355 nm. ^1H NMR (DMSO- d_6 , 500 MHz) δ 3.39 (3H, m, H-2'', H-3'', H-4''), 3.89 (3H, s, 8OMe), 4.01 (1H, d, $J=9.7$ Hz, H-5''), 5.27 (1H, d, $J=7.0$ Hz, H-1''), 6.70 (1H, s, H-6), 7.05 (1H, s,

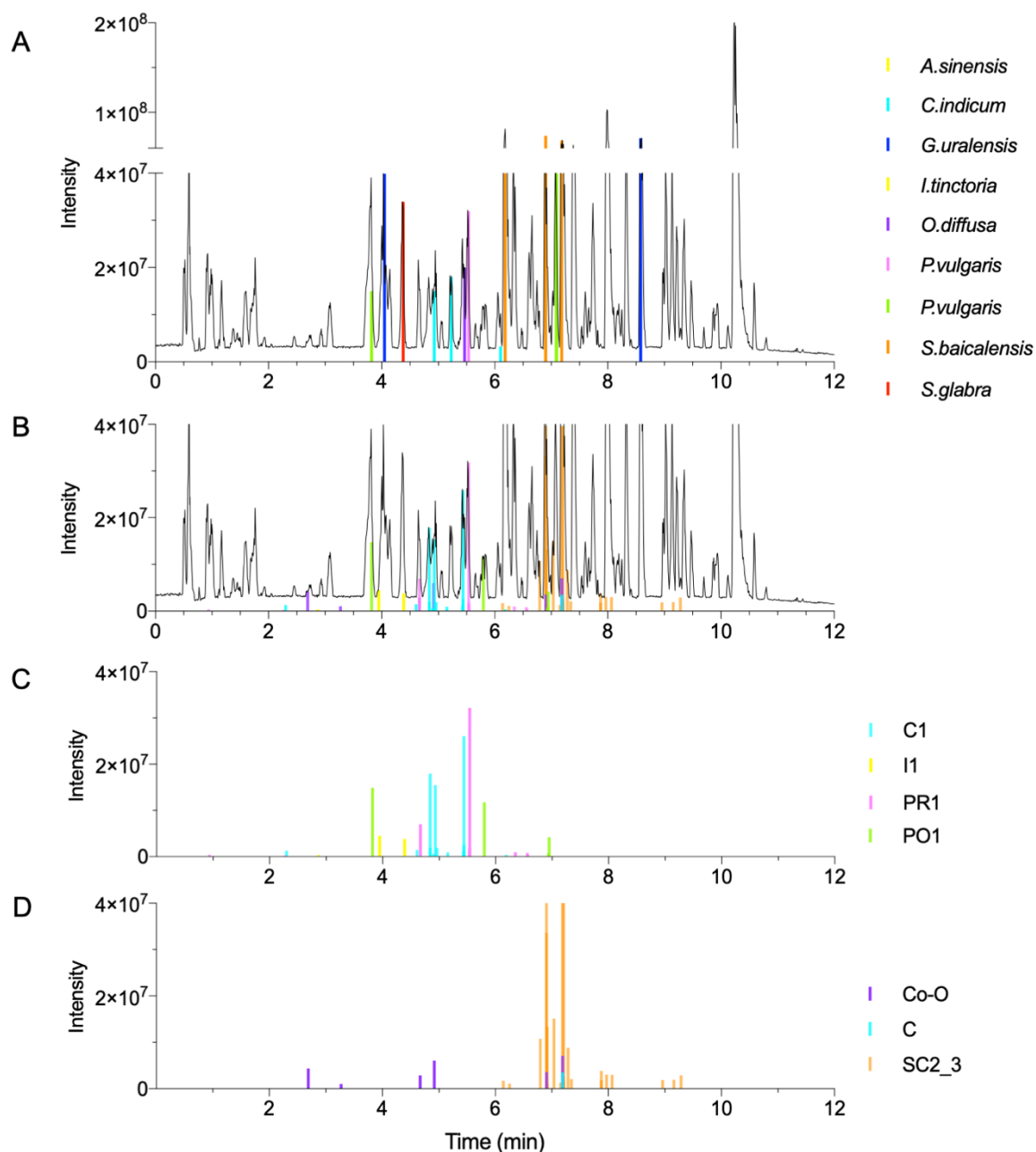
H-3), 7.61 (3H, m, H-3', H-4', H-5'), 8.08 (2H, d, $J=7.6$ Hz, H-2', H-6'), 12.52 (1H, s, 5OH); ^{13}C NMR (DMSO- d_6 , 126 MHz) δ 61.4 (C-8OMe), 71.2 (C-4''), 72.9 (C-2''), 75.3 (C-5''), 75.8 (C-3''), 98.7 (C-6), 99.7 (C-1''), 105.2 (C-3), 105.4 (C-10), 126.4 (C-2', C-6'), 129.3 (C-3', C-5'), 129.3 (C-8), 130.7 (C-1'), 132.2 (C-4'), 149.2 (C-9), 156.0 (C-5, C-7), 163.6 (C-2), 170.0 (C-6''), 182.3 (C-4). ESI-HRMS m/z 459.0941 $[\text{M-H}]^-$ (calculated for $\text{C}_{22}\text{H}_{19}\text{O}_{11}$, m/z 459.0927, 1.8 ppm) (Wu et al., 2005).

Oroxyloside (SC3) (5, 7-dihydroxy-6-methoxyflavone; 7-*O*- β -D-glucuronopyranoside). Amorphous powder. Pure in M23S17. UV max: 214; 271; 310 nm. ^1H NMR (CD_3OD , 600 MHz) δ 3.56 (1H, t, $J=9.1$ Hz, H-3''), 3.62 (2H, t, $J=9.1$ Hz, H-2'', H-4''), 3.91 (3H, s, OCH₃), 4.02 (1H, d, $J=9.8$ Hz, 5''), 5.21 (1H, d, $J=7.5$ Hz, H-1''), 6.82 (1H, s, H-3), 7.03 (1H, s, H-8), 7.58 (3H, m, H-3', H-4', H-5'), 8.04 (2H, d, $J=7.0$ Hz, H-2', H-6'); ^{13}C NMR (CD_3OD , 151 MHz) δ 61.5 (C-OCH₃), 73.1 (C-4''), 74.5 (C-2''), 76.6 (C-5''), 77.5 (C-3''), 96.0 (C-8), 101.9 (C-1''), 105.9 (C-3), 107.9 (C-6), 127.7 (C-2', C-6'), 130.3 (C-3', C-5'), 132.5 (C-10), 133.2 (C-4'), 134.4 (C-1'), 154.2 (C-5), 154.5 (C-9), 158.1 (C-7), 166.4 (C-2), 174.0 (6''), 184.5 (C-4). ESI-HRMS m/z 459.0942 $[\text{M-H}]^-$ (calculated for $\text{C}_{22}\text{H}_{19}\text{O}_{11}$, m/z 459.0927, 2 ppm) (Abe et al., 1990).

Astilbin (SM1), (3, 3', 4', 5, 7-pentahydroxyfavanone; (2R, 3R)-form, 3-*O*- α -L-rhamnopyranoside). Impur in M17. UV max: 200; 220; 290 nm. ^1H NMR (MeOD, 600 MHz) δ 1.19 (3H, d, $J=6.2$ Hz, H-6''), 3.30 (1H, overlapped, H-4''), 3.54 (1H, dd, $J=3.3, 1.7$ Hz, H-2''), 3.66 (2H, dd, $J=9.6, 3.3$ Hz, H-3''), 4.05 (1H, d, $J=1.7$ Hz, H-1''), 4.25 (1H, dq, $J=9.6, 6.2$ Hz, H-5''), 4.58 (1H, d, $J=10.7$ Hz, H-3), 5.07 (1H, d, $J=10.7$ Hz, H-2), 5.90 (1H, d, $J=2.2$ Hz, H-8), 5.92 (1H, d, $J=2.2$ Hz, H-6), 6.80 (3H, d, $J=8.2$ Hz, H-5'), 6.84 (1H, dd, $J=8.2, 2.0$ Hz, H-6'), 6.96 (1H, d, $J=2.0$ Hz, H-2'); ^{13}C NMR (MeOD, 151 MHz) δ 17.9 (C-6''), 70.5 (C-5''), 71.8 (C-2''), 72.2 (C-3''), 73.8 (C-4''), 78.6 (C-3), 84.0 (C-2), 102.2 (C-1''), 102.5 (C-10), 115.5 (C-2'), 116.3 (C-5'), 120.5 (C-6'), 129.2 (C-1'), 146.5 (C-3'), 147.4 (C-4'), 164.1 (C-9), 165.5 (C-5), 168.6 (C-7), 196.0 (C-4). ESI-HRMS: m/z 449.1088 $[\text{M-H}]^-$ (calculated for $\text{C}_{21}\text{H}_{21}\text{O}_{11}$, m/z 449.1083, -0.2 ppm) (Galotta et al., 2008).

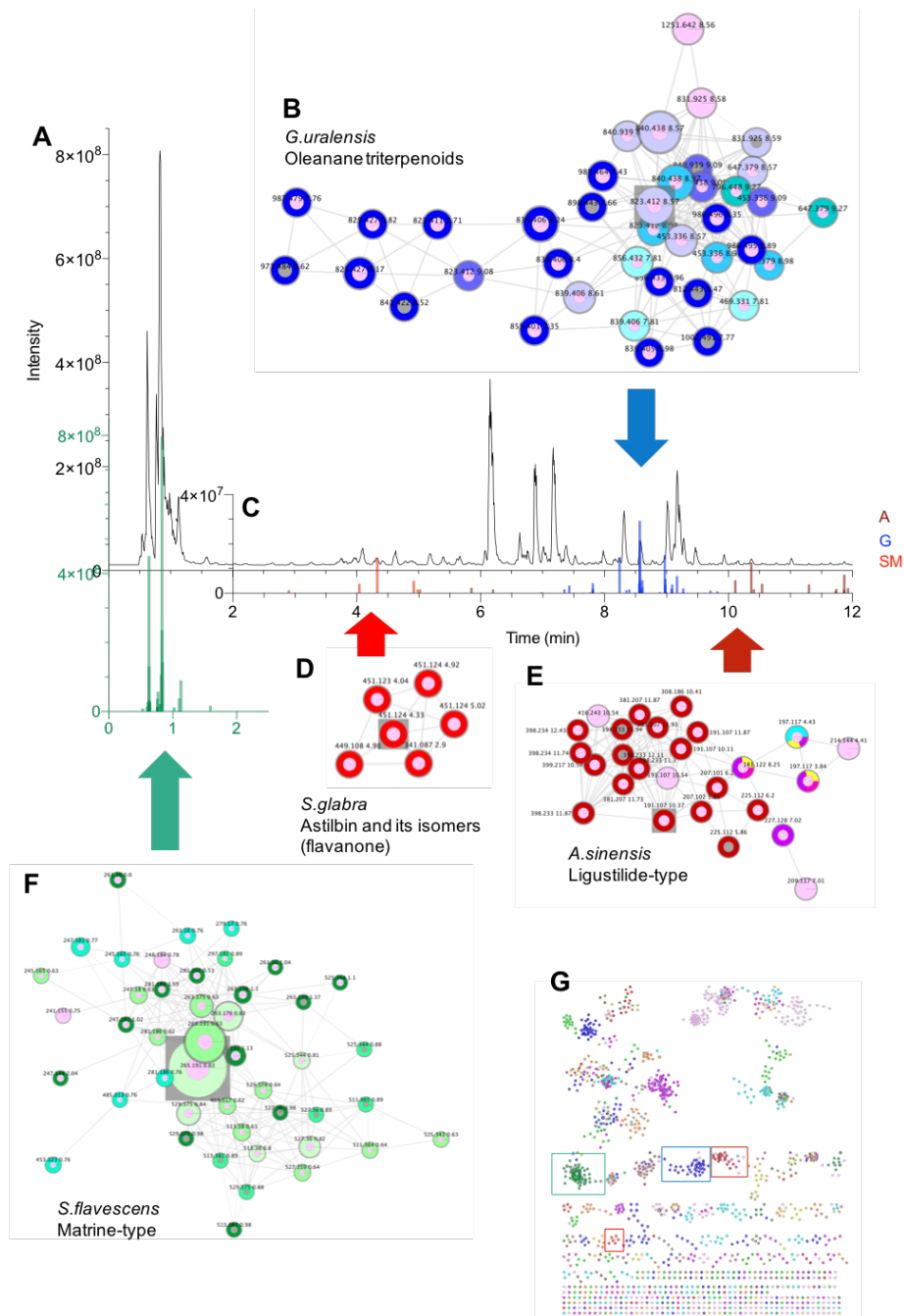
Oxymatrine (SO1) (matrine; N¹-Oxide). Amorphous powder. Pure in M14S6. ^1H NMR (DMSO- d_6 , 600 MHz) δ 1.24 (1H, tdd, $J=12.7, 9.6, 3.1$ Hz, H-12''), 1.53 (1H, m H-13''), 1.56 (2H, m, H-3'', H-9''), 1.58 (1H, m, H-8''), 1.64 (2H, m, H-4'', H-7), 1.71 (2H, m, H-4', H-13'), 1.79 (1H, m, H-5), 1.94 (1H, d, $J=13.8$ Hz, H-8'), 2.15 (2H, m, H-12', H-14''), 2.24 (2H, m, H-9', H-14'), 2.32 (1H, m, H-3'), 3.37 (4H, m, H-2, H-10), 3.45 (1H, bs, H-6), 3.59 (1H, q, $J=11.4$ Hz, H-17''), 4.23 (1H, dd, $J=12.4, 5.3$ Hz, H-17'), 4.49 (1H, bs, H-11); ^{13}C NMR (DMSO- d_6 , 151 MHz) δ 16.6 (C-9), 16.6 (C-3), 18.5 (C-13), 23.3 (C-8), 24.9 (C-4), 27.8 (C-12), 32.6 (C-14), 33.3 (C-5), 41.0 (C-17), 41.1 (C-7), 52.9 (C-11), 66.2 (C-2), 66.4 (C-6), 66.6 (C-10), 168.8 (C-15). ESI-HRMS: m/z 265.1918 $[\text{M+H}]^+$ (calculated for $\text{C}_{15}\text{H}_{25}\text{N}_2\text{O}_2$, m/z 265.1916, 2.7 ppm) (Aslanov et al., 1987)

8 Multi-component signatures



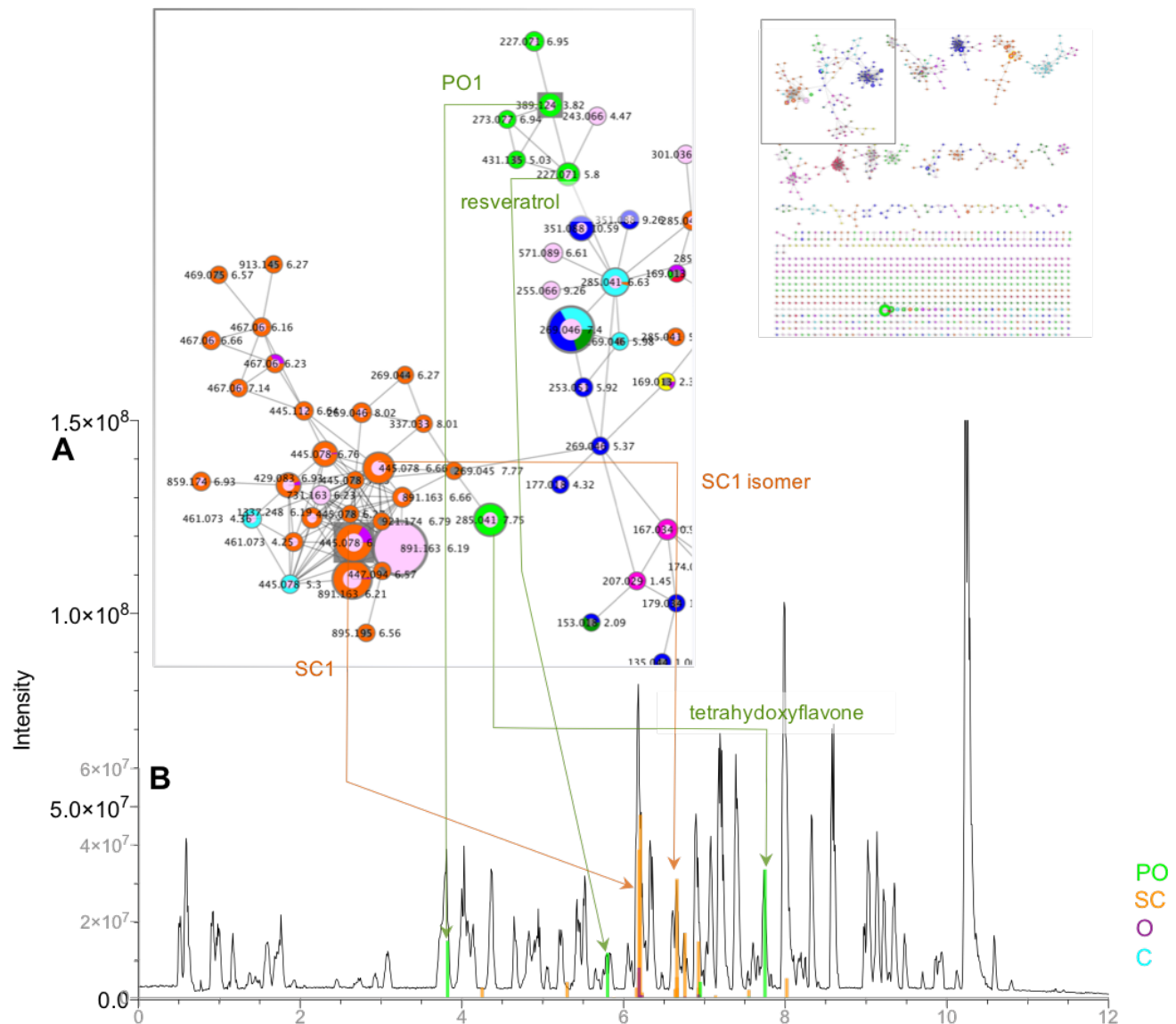
Supplementary Figure 15: multi-component signatures in NI: A) metabolite profile of the formula showing all formally identified components. B) metabolite profile of the formula showing some of the selected multi-component signatures. C) multicomponent signatures for *I. tinctoria* and its marker isovitexin (I1), *P. cuspidatum* and *E-piceid* (PO1), *P.vulgaris* and rosmarinic acid (PR1) and *C.indicum* and C1. D) C)

multicomponent signatures for *S.baicalensis* and wogonoside and oroxyloside (SC2 and SC3), and for *O.diffusa*. See table S3 to S12 for annotations.

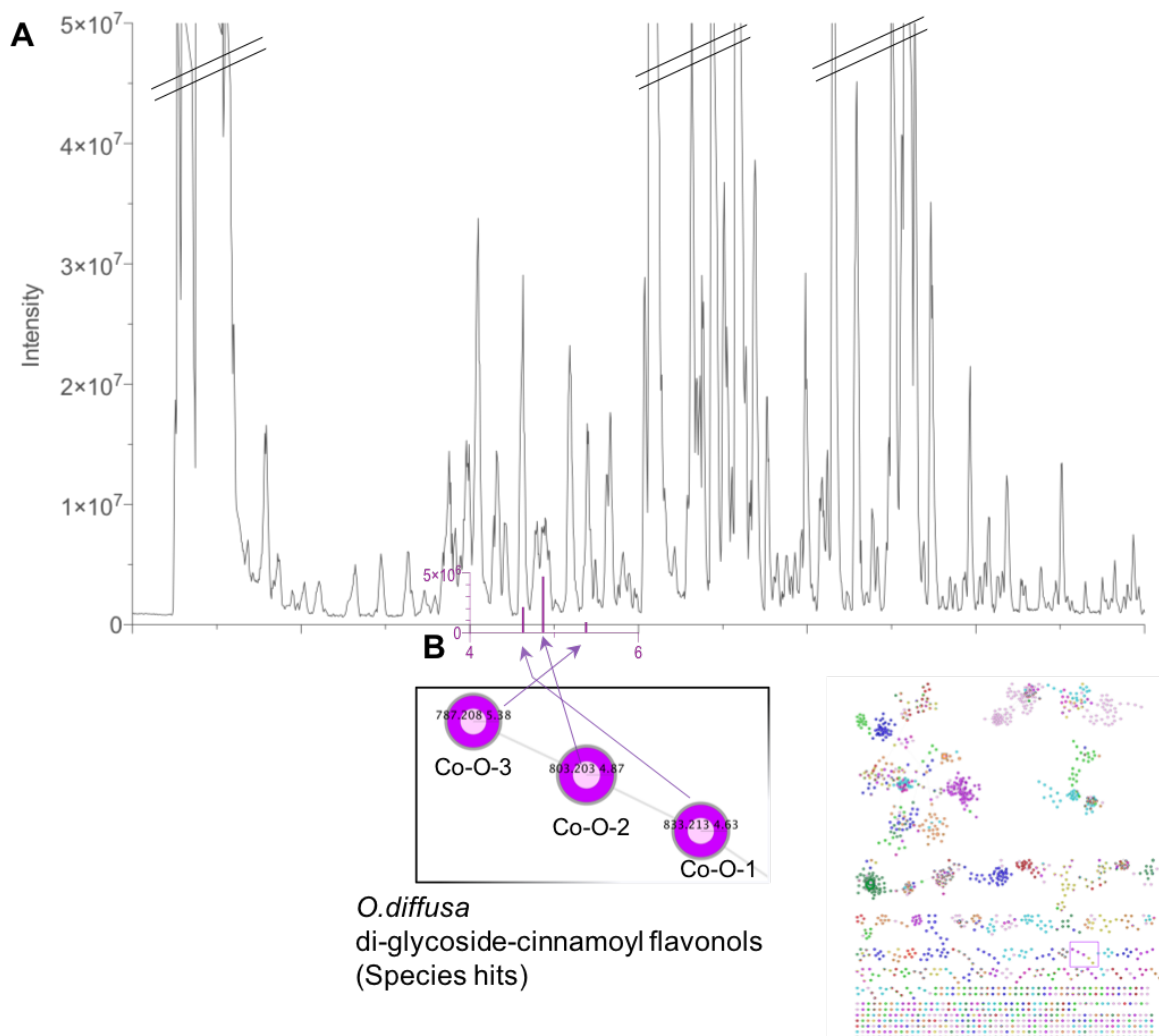


Supplementary Figure 16: representation of clusters from the FBMN-PI in relation to the chromatogram of the formula: A) UHPLC-HRMS metabolite profile of the formula in PI, B) cluster containing potential co-markers for *G. uralensis*, the color tones of the nodes indicate the features with the same retention time, C) bar plot showing the peak height intensity of related clusters, D) cluster with potential co-markers for *S. glabra*, E)

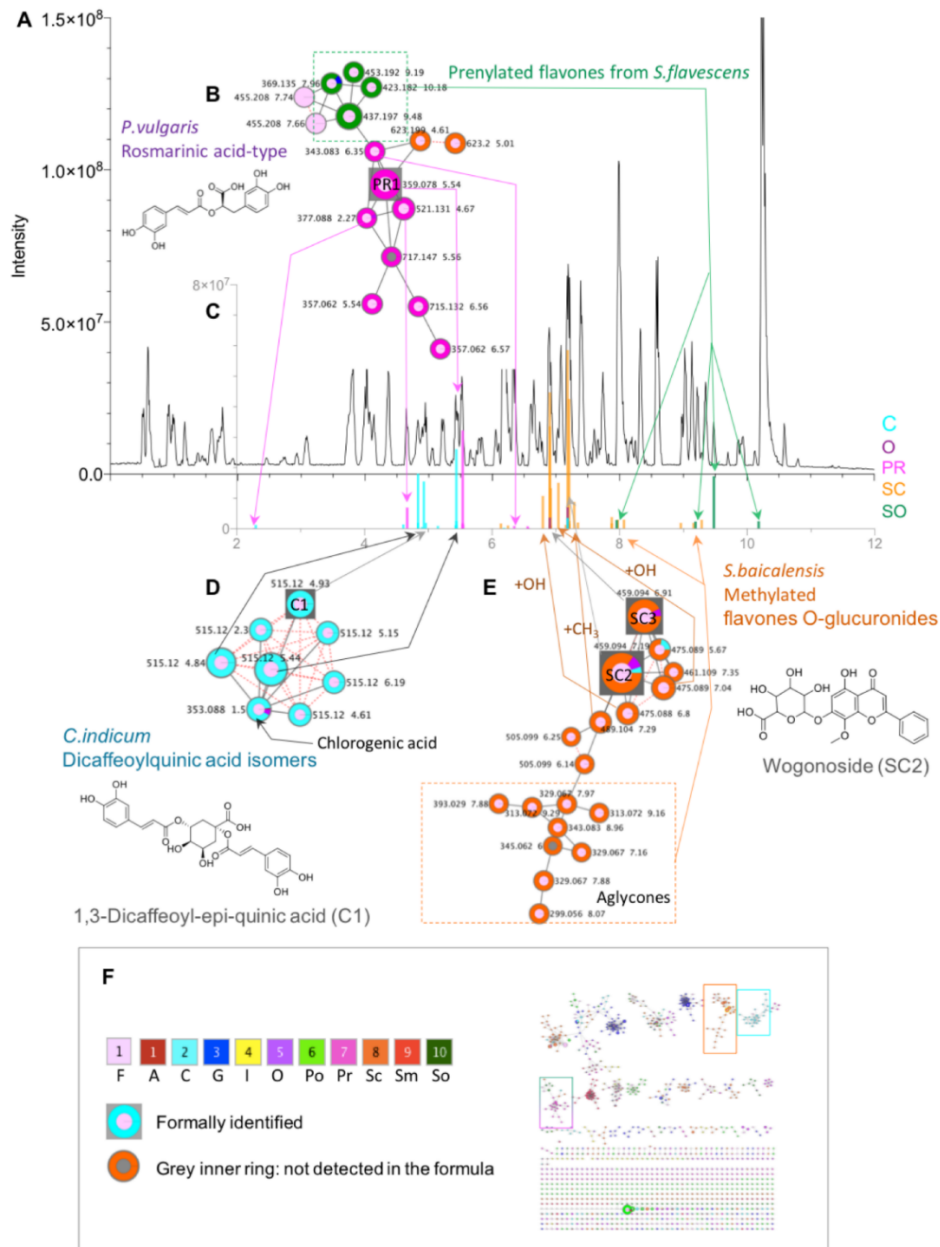
cluster with potential co-markers for *A.sinensis*, F) cluster with potential co-markers for *S.flavescens*, the color tones of the nodes indicate the features with the same retention time. The numbers indicate the m/z ratio of the nodes, followed by their retention time. See table S3, S5, S11 and S12 for related annotation. G) FBMN. See Fig.4 for the node layout legends.



Supplementary Figure 17: representation of a cluster from the FBMN-NI in relation to the chromatogram of the formula: A) UHPLC-HRMS metabolite profile of the formula in NI, B) bar plot showing the peak height intensity of related cluster, which contains potential co-markers for *S.baicalensis* and *P.cuspidatum*. The numbers indicate the m/z ratio of the nodes, followed by their retention time. See table S8 and S10 for related annotation. See Fig.4D for the node layout legends.



Supplementary Figure 18: representation of a cluster from the FBMN-PI in relation to the chromatogram of the formula: A) UHPLC-HRMS/MS metabolite profile of the formula in PI, B) cluster with potential co-markers for *O. diffusa* and the corresponding histogram of the node peak heights as a function of time. The numbers indicate the m/z ratio of the nodes, followed by their retention time. See table S7 for related annotation. See Fig. 4D for the node layout legends.



Supplementary Figure 19: representation of a cluster from the FBMN in NI in relation to the chromatogram of the formula: A) UHPLC-HRMS/MS metabolite profile of the formula in NI, B) cluster with potential co-markers for *P. vulgaris* and *S. flavescens*, C) bar plot showing the peak heights of related nodes in the cluster, D) cluster with potential co-markers for *C. indicum*, E) cluster with potential co-markers for *S. baicalensis*. The

numbers on the nodes indicate the m/z ratio of the nodes, followed by their retention time. See table S4, S8, S8 and S9 for related annotation. See Fig. 4D for the node layout legends.

9 UHPLC-UV-PDA HRMS/MS data acquisition

The analyses were performed on an Acquity UPLC system interfaced to an Orbitrap Q-Exactive Focus mass spectrometer (Thermo Scientific) using a heated electrospray ionization (HESI-II) source and an Acquity UPLC PDA detector. Thermo Scientific Xcalibur 2.1 software was employed for instrument control. PDA detector recorded from 210 to 450 nm (resolution 1.2 nm). The optimized HESI-II parameters were as follows: source voltage, 3.5 kV (PI), 2.5 kV (NI); sheath gas flow rate (N₂), 47.5 units; auxiliary gas flow rate, 11.25 units; spare gas flow rate, 2.25; capillary temperature, 256.25°C, S-Lens RF Level, 45. The mass analyzer was calibrated using a mixture of caffeine, methionine–arginine–phenylalanine–alanine–acetate (MRFA), sodium dodecyl sulfate, sodium taurocholate, and Ultramark 1621 in an acetonitrile/methanol/ water solution containing 1% formic acid by direct injection. The data-dependent MS/MS events were performed on the three most intense ions detected in full scan MS (Top3 experiment). The MS/MS isolation window width was 1 Da, and the stepped normalized collision energy (NCE) was set to 15, 30 and 45 units. In data-dependent MS/MS experiments, full scans were acquired at a resolution of 35,000 FWHM (at m/z 200) and MS/MS scans at 17,500 FWHM both with an automatically determined maximum injection time. After being acquired in a MS/MS scan, parent ions were placed in a dynamic exclusion list for 2.0 s

10 MZmine parameters for peak picking**Supplementary Table S3: MZmine parameters**

MZmine Parameters		HRMS/MS		Fraction control
		PI	NI	NI
1	Mass detection			
	Noise level MS1	1E5	1E5	1E2
	Noise level MS2	1	1	NA
2	Peak detection -> ADAP chromatogram builder			
	Min group size in # of scans	5	5	5
	Group intensity threshold	1E5	5E4	1E2
	Min highest intensity	5E5	2E5	2E2
	m/z tolerance [ppm]	5	5	20
3	Peak detection -> chromatogram deconvolution Wavelets (ADAP)			
	n/z center calculation	MEDIAN		
	S/N threshold	10		
	S/N estimator:	intensity window SN		
	Min feature height	1E5	1E5	2E2
	Coefficient area threshold	100		
	Peak duration range [min]	0.00- 1.50		
	RT wavelet range [min]	0.00 – 0.06		
	m/z range for MS2 scan pairing [Da]	0.025		NA
	RT range for MS2 scan pairing [min]	0.08		NA
4	Isotopic peaks grouper			
	m/z tolerance [ppm]	5		10
	Retention time tolerance absolute [min]	0.01		
	Maximum charge	2		
	Representative isotope	Most intense		
5	Filtering -> Duplicate peak filter			
	m/z tolerance [ppm]	1		
	Retention time tolerance absolute [min]	0.01		
6	Alignment -> JOIN			
	m/z tolerance [ppm]	5		
	Weight for m/z [Da]	1		
	Retention time tolerance absolute [min]	0.02		

	Weight for RT	1	
	Require same charge state	<input checked="" type="checkbox"/>	
	Compare isotope pattern ->	5 ppm 1E3 Min score 70%	20 ppm 1E2 Min score 70%
9	Identification -> Custom Database, adduct search, complex search		
	Retention time tolerance absolute [min]	0.01	0.05
	m/z tolerance [ppm]	5	20
	Max complex/adduct peak height	10000%	
11	Filtering -> peak list rows filter		
	Keep only peaks with MS2 scan (GNPS)	<input checked="" type="checkbox"/>	NA
	Reset the peak number ID		
	Export to .csv		
	Export to .mgf for GNPS		

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