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Title:

The role of DNA methylation in the accumulation of iridoid glycosides in *Rehmannia glutinosa*

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Tables

Table S1 The preimer and its base sequence

Preimer	Sequence (5' to 3')
<i>DXS-F</i>	AAAAAAGTAGAAACTGTTGGTATC
<i>DXS-R</i>	CTTTTCCGATTACCAGAGTT
<i>DXR-F</i>	ACTTCCAACAGTTACTTCAG
<i>DXR-R</i>	TTAATCCCCACCACAATC
<i>10HGO-F</i>	TGAGAATCAAATCAAAAAAAG
<i>10HGO-R</i>	AAACAAGAAAATAAAAAACGG
<i>G10H-F</i>	GCGACGTAAACGGCCACAAG
<i>G10H-R</i>	GAAGTAACCATTTCAGCCAAG
<i>GPPS-F</i>	ATGATGTCTGTAAGGGGGCTG
<i>GPPS-R</i>	TTCATTGTCTTGTGATGACTCTC
<i>qDXS-F</i>	CCTCGGACGAGGCAGAACTAT
<i>qDXS-R</i>	CCACTCTCTCCCCTTCAATCAG
<i>qDXR-F</i>	ATTTGGCTTACGCTGCTGG
<i>qDXR-R</i>	TTCTGCTCGGTGCTTATCG
<i>q10HGO-F</i>	GCCTGGGCACGAGATTG
<i>q10HGO-R</i>	TGAGTATTTGTTGGGGCAGTA
<i>qG10H-F</i>	GTAATGCTTGGTTCGCTTTTG
<i>qG10H-R</i>	GGAGTGGTTGAGCCTTCTGC
<i>qGPPS-F</i>	TCCTGCTATCTAGAGCTTGTGTGGC
<i>qGPPS-R</i>	ACGCTGATCTGATGTAGTTGTCATT
<i>qTIP41-F</i>	TGGCTCAGAGTTGATGGAGTGCT
<i>qTIP41-R</i>	CTCTCCAGCAGCTTTCTCGGAGA

Table S2 The co-occurrence on DXS/DXR/10HGO/G10H/GPPS synthase family of *R. glutinosa*

No.of queries matched	Plant Organism	Gene Co-occurrence				
		DXS	DXR	10HGO	G10H	GPPS
5	<i>Aquilegia coerulea</i>	✓	✓	✓	✓	✓
	<i>Citrus clementine</i>					
	<i>Citrus sinensis</i>					
	<i>Erythranthe guttata</i>					
	<i>Eucalyptus grandis</i>					
	<i>Gossypium raimondii</i>					
	<i>Malus domestica</i>					
	<i>Morus notabilis</i>					
	<i>Nelumbo nucifera</i>					
	<i>Nicotiana sylvestris</i>					
	<i>Nicotiana tomentosiformis</i>					
	<i>Populus trichocarpa</i>					
	<i>Prunus mume</i>					
	<i>Prunus persica</i>					
	<i>Pyrus x bretschneideri</i>					
	<i>Ricinus communis</i>					
	<i>Solanum lycopersicum</i>					
	<i>Theobroma cacao</i>					
	<i>Vitis vinifera</i>					
4	<i>Beta vulgaris</i>	✓	✓		✓	✓
	<i>Cicer arietinum</i>	✓	✓	✓		✓
	<i>Cucumis sativus</i>	✓	✓	✓		✓
	<i>Fragaria vesca</i>	✓	✓	✓		✓
	<i>Glycine max</i>	✓	✓	✓		✓
	<i>Linum usitatissimum</i>	✓	✓	✓		✓
	<i>Manihot esculenta</i>	✓	✓	✓		✓
	<i>Phaseolus vulgaris</i>	✓	✓	✓		✓
	<i>Solanum tuberosum</i>	✓	✓	✓	✓	
3	<i>Aegilops tauschii</i>	✓	✓			✓
	<i>Amborella trichopoda</i>	✓	✓			✓
	<i>Arabidopsis lyrata</i>	✓	✓			✓
	<i>Arabidopsis thaliana</i>	✓	✓			✓
	<i>Boechera stricta</i>	✓	✓			✓
	<i>Brachypodium distachyon</i>	✓	✓			✓
	<i>Brassica oleracea</i>	✓	✓			✓
	<i>Brassica rapa</i>	✓	✓			✓
	<i>Camelina sativa</i>	✓	✓			✓
	<i>Capsella grandiflora</i>	✓	✓			✓
	<i>Capsella rubella</i>	✓	✓			✓
	<i>Carica papaya</i>	✓	✓			✓
	<i>Cucumis melo</i>	✓	✓			✓
	<i>Eutrema salsugineum</i>	✓	✓			✓
	<i>Hordeum vulgare</i>	✓	✓			✓
	<i>Leersia perrieri</i>	✓	✓			✓
	<i>Medicago truncatula</i>	✓	✓	✓		
	<i>Musa acuminata</i>	✓	✓			✓
	<i>Oryza barthii</i>	✓	✓			✓
	<i>Oryza brachyantha</i>	✓	✓			✓
	<i>Oryza glaberrima</i>	✓	✓			✓
	<i>Oryza glumipatula</i>	✓	✓			✓
	<i>Oryza nivara</i>	✓	✓			✓
	<i>Oryza punctata</i>	✓	✓			✓
	<i>Oryza rufipogon</i>	✓	✓			✓
	<i>Oryza sativa</i>	✓	✓			✓
	<i>Panicum virgatum</i>	✓	✓			✓
	<i>Phoenix dactylifera</i>	✓	✓			✓
	<i>Physcomitrella patens</i>	✓	✓			✓
	<i>Selaginella moellendorffii</i>	✓	✓			✓
	<i>Setaria italic</i>	✓	✓			✓
	<i>Sorghum bicolor</i>	✓	✓			✓
	<i>Tarenaya hassleriana</i>	✓	✓			✓
	<i>Zea mays</i>	✓	✓			✓

2	<i>Arabis alpina</i>	✓	✓			
	<i>Triticum aestivum</i>		✓			✓
1	<i>Chlorella variabilis</i>		✓			
	<i>Coccomyxa subellipsoidea</i>		✓			
	<i>Micromonas pusilla</i>					✓
	<i>Oryza meridionalis</i>					✓
	<i>Ostreococcus lucimarinus</i>					✓
	<i>Ostreococcus tauri</i>					✓
	<i>Triticum urartu</i>		✓			
	<i>Volvox carteri</i>		✓			
Rate of gene co-occurrence (%)		87.5%	94.4%	38.9%	30.6%	90.3%

The symbol ✓ indicates the presence of relative genes for DXS, DXR, 10HGO, G10H, GPPS of *R. glutinosa*.

Table S3 Some homologous proteins on DXS/DXR/10HGO/G10H/GPPS synthase family of *R. glutinosa*

Species	Accession Number	Identity (%)				
		DXS	DXR	10HGO	G10H	GPPS
<i>Aquilegia coerulea</i>	Aquca_026_00112.1	85.2				
	Aquca_002_00164.1		82.2			
	Aquca_026_00015.1			66.5		
	Aquca_152_00005.1				55.9	
	Aquca_007_00559.1					72.3
<i>Citrus clementina</i>	XP_006419702.1	88.1				
	XP_006439818.1		79.5			
	XP_006426239.1			67.7		
	XP_006440464.1				56.3	
	XP_006448990.1					73.5
<i>Citrus sinensis</i>	XP_006489186.1	88.1				
	XP_006476776.1		79.3			
	XP_006466345.1			68.0		
	XP_006477330.1				55.9	
	XP_006468063.1					73.1
<i>Erythranthe guttata</i>	Migut.G00229.1.p	88.9				
	Migut.I00013.1.p		85.0			
	Migut.H02275.1.p			71.7		
	Migut.H00477.1.p				79.9	
	Migut.G00061.1.p					87.3
<i>Eucalyptus grandis</i>	XP_010024490.1	87.2				
	XP_010027708.1		83.8			
	XP_010052660.1			66.1		

	XP_010050611.1			56.4	
	XP_010056939.1				74.5
<i>Gossypium raimondii</i>	Gorai.011G184200.1	83.2			
	Gorai.006G189200.1		83.5		
	Gorai.008G089500.1			67.8	
	Gorai.006G211100.1				56.2
	Gorai.011G047900.1				80.9
<i>Malus domestica</i>	XP_008340868.1	86.6			
	XP_008374435.1		82.9		
	XP_008384197.1			65.6	
	XP_008389841.1				58.1
	XP_008371630.1				70.3
<i>Morus notabilis</i>	XP_010105036.1	87.1			
	XP_010101212.1		82.4		
	XP_010095885.1			69.5	
	XP_010108078.1				56.6
	XP_010090457.1				76.7
<i>Nelumbo nucifera</i>	XP_010279602.1	85.9			
	XP_010243034.1		83.9		
	XP_010244709.1			67.1	
	XP_010277464.1				54.6
	XP_010275055.1				73.8

The homologs for DXS, DXR, 10HGO, G10H, GPPS of *R. glutinosa* were searched from 72 species of plants, and were all obtained from 19 species of plants. The homologs in the above 9 species had high similarity with DXS/DXR/10HGO/G10H/GPPS synthase of *R. glutinosa*

Table S4 Correlation analysis between the content of total iridoid glycosides and expression levels of related enzymes genes

Gene name	85-5 total iridoid glycosides		Jinjiu total iridoid glycosides	
	Correlation coefficient	Significance	Correlation coefficient	Significance
<i>DXS</i>	0.265	0.666	0.365	0.557
<i>DXR</i>	-0.415	0.487	-0.991	0.001**
<i>10HGO</i>	0.110	0.860	-0.517	0.372
<i>G10H</i>	0.275	0.654	-0.155	0.804
<i>GPPS</i>	-0.906	0.034*	-0.447	0.450

statistical significance was determined by a two-sided t-test: * P < 0.05, ** P < 0.01.

Table S5 The genomic DNA methylation levels of *R. glutinosa* root

Band Type (MSAP)	Growth periods				
	I	II	III	IV	V
I	45	29	35	29	24
II	19	22	31	20	20
III	17	19	18	18	16
Total bands	81	70	84	67	60
Methylation bands	36	41	49	38	36
Total methylation%	20.99%	27.14%	21.43%	26.87%	26.67%
MSAP%	44.44%	58.57%	58.33%	56.72%	60.00%

Note: I belts were present in both EcoRI/Hpa II and EcoRI/Msp I digestion combination. II belts were present only in EcoRI/Hpa II. III belts were present only in EcoRI/Msp I.

Total bands= I +II+III, methylated bands= II+ III, total methylated ratio(%)=III/(I +II+ III)*100%, MSAP(%)=(II+III)/(I +II+ III) *100%.

Table S6 The genomic DNA methylation levels of *R. glutinosa* leaf

Band Type (MSAP)	Growth periods				
	I	II	III	IV	V
I	36	53	37	31	37
II	22	25	19	23	28
III	19	21	21	19	28
Total bands	77	99	77	73	93

Methylation bands	41	46	40	42	56
Total methylation%	24.68%	21.21%	27.27%	26.03%	30.11%
MSAP%	53.25%	46.46%	51.95%	57.53%	60.22%

Note: I belts were present in both EcoRI/Hpa II and EcoRI/Msp I digestion combination. II belts were present only in EcoRI/Hpa II. III belts were present only in EcoRI/Msp I.

Total bands= I +II+III, methylated bands= II+ III, total methylated ratio(%)=III/(I+II+ III)*100%, MSAP(%)=(II+III)/(I +II+ III) *100%.

Table S7 Effects of 5-azaC on the levels of genomic DNA methylation in *R. glutinosa* root

Band Type (MSAP)	I					
	CK	15μM	30μM	50μM	100μM	250μM
I	56	54	54	50	59	66
II	29	27	36	38	47	33
III	18	23	27	24	30	47
Total bands	103	104	117	112	136	146
Methylation bands	47	50	63	62	77	80
Total methylation%	17.48%	22.12%	23.08%	21.43%	22.06%	32.19%
MSAP%	45.63%	48.08%	53.85%	55.36%	56.62%	54.79%

Band Type (MSAP)	II					
	CK	15μM	30μM	50μM	100μM	250μM
I	26	24	38	29	33	29
II	27	26	30	33	30	29
III	23	21	29	23	18	30
Total bands	76	71	97	85	81	88
Methylation bands	50	47	59	56	48	59
Total methylation%	30.26%	29.58%	29.90%	27.06%	22.22%	34.09%
MSAP%	65.79%	66.20%	60.82%	65.88%	59.26%	67.05%

Band Type (MSAP)	III					
	CK	15μM	30μM	50μM	100μM	250μM
I	44	27	30	33	35	27
II	44	30	20	24	20	30

III	18	32	32	29	14	14
Total bands	106	89	82	86	69	71
Methylation bands	62	62	52	53	34	44
Total methylation%	16.98%	35.96%	39.02%	33.72%	20.29%	19.72%
MSAP%	58.49%	69.66%	63.41%	61.63%	49.28%	61.97%
Band Type (MSAP)	IV					
	CK	15μM	30μM	50μM	100μM	250μM
I	29	23	24	27	39	41
II	32	45	23	26	33	29
III	15	29	23	32	26	21
Total bands	76	97	70	85	98	91
Methylation bands	47	74	46	58	59	50
Total methylation%	19.74%	29.90%	32.86%	37.65%	26.53%	23.08%
MSAP%	61.84%	76.29%	65.71%	68.24%	60.20%	54.95%
Band Type (MSAP)	V					
	CK	15μM	30μM	50μM	100μM	250μM
I	26	33	36	42	30	39
II	23	23	11	18	32	20
III	12	18	20	26	26	20
Total bands	61	74	67	86	88	79
Methylation bands	35	41	31	44	58	40
Total methylation%	19.67%	24.32%	29.85%	30.23%	29.55%	25.32%
MSAP%	57.38%	55.41%	46.27%	51.16%	65.91%	50.63%

Table S8 Effects of 5-azaC on the levels of genomic DNA methylation in *R. glutinosa* leaf

Band Type (MSAP)	I					
	CK	15μM	30μM	50μM	100μM	250μM
I	47	48	48	39	65	66
II	27	30	26	18	15	21
III	17	29	23	24	12	20

Total bands	91	107	97	81	92	107
Methylation bands	44	59	49	42	27	41
Total methylation%	18.68%	27.10%	23.71%	29.63%	13.04%	18.69%
MSAP%	48.35%	55.14%	50.52%	51.85%	29.35%	38.32%

Band Type (MSAP)	II					
	CK	15μM	30μM	50μM	100μM	250μM
I	57	39	42	42	36	32
II	35	39	33	36	29	20
III	33	44	39	18	36	20
Total bands	125	122	114	96	101	72
Methylation bands	68	83	72	54	65	40
Total methylation%	26.40%	36.07%	34.21%	18.75%	35.64%	27.78%
MSAP%	54.40%	68.03%	63.16%	56.25%	64.36%	55.56%

Band Type (MSAP)	III					
	CK	15μM	30μM	50μM	100μM	250μM
I	32	41	27	39	53	41
II	23	30	18	30	23	26
III	30	14	39	36	29	26
Total bands	85	85	84	105	105	93
Methylation bands	53	44	57	66	52	52
Total methylation%	35.29%	16.47%	46.43%	34.29%	27.62%	27.96%
MSAP%	62.35%	51.76%	67.86%	62.86%	49.52%	55.91%

Band Type (MSAP)	IV					
	CK	15μM	30μM	50μM	100μM	250μM
I	26	23	26	26	47	47
II	32	21	27	24	26	24
III	20	18	18	23	18	18
Total bands	78	62	71	73	91	89
Methylation bands	52	39	45	47	44	42
Total methylation%	25.64%	29.03%	25.35%	31.51%	19.78%	20.22%

MSAP%	66.67%	62.90%	63.38%	64.38%	48.35%	47.19%
Band Type (MSAP)	V					
	CK	15μM	30μM	50μM	100μM	250μM
I	47	42	41	39	45	38
II	38	18	23	20	17	12
III	32	30	30	21	21	29
Total bands	117	90	94	80	83	79
Methylation bands	70	48	53	41	38	41
Total methylation%	27.35%	33.33%	31.91%	26.25%	25.30%	36.71%
MSAP%	59.83%	53.33%	56.38%	51.25%	45.78%	51.90%

Figures

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1      AAAAAAGTAGAAAACTGTTGGTATCTCTTTTGGATATATGAGATTTCATTGGTTTTAAGTGTGGTTTAGACAGAATACTTAGAGAAAACAT
91     ATATTTTGAATGGCTCTGTTTGCATTTCCCATTTCTGGGAATTTGAGCAAGGGAATGGGTGTTGATGCTCAAAGACACTCCCAATTTATGC
1      M A L F A F P I S G N L S K G M G V D A Q R H S N L C
181    TCTCAGTGGATACATGGGTGCGGTCTACAGTGTCTCTTTTCTGCAAGAATAACCGGTAAGGAAAAAGATCAGCTGGGATTTGTGCATCA
28     S Q W I H G S G L Q C L F F C K N N Q V R K R S A G I C A S
271    TTATCAGAAAGAGGAGAGTATTTCTCACAGAAGCCTGCTACTCCTCTTTTAGACACTATCAACTATCCAATTCACATGAAAAATCTCTCA
58     L S E R G E Y F S Q K P A T P L L D T I N Y P I H M K N L S
361    ATAAAGGAATGAAACAACTTGCAGATGAACGCGATCCGATGTTATTTTCAATGTGTCTAAACTGGGGGTCACTTGGTTCGAGCGCTT
88     I K E L K Q L A D E L R S D V I F N V S K T G G H L G S S L
451    GGCGTTATCGAGCTGACTGTGGCTCTGCATTACATTTGCAATGCTCCTCAAGATAGAATACTTTGGGATGTCGGCCACCGCTCTTATCCT
118    G V I E L T V A L H Y I C N A P Q D R I L W D V G H Q S Y P
541    CATAAGATTTTAACTGGACGAAGACACAAAATCCCGACTTTGAGACAAACAGAAGGACITTTCTGGTTTTACGAAACGGTCTGAGAGTGAA
148    H K I L T G R R H K M P T L R Q T E G L S G F T K R S E S E
631    TACGATTGCTTTGGCACCCTGTCAGTCTACGACTATCTCGGCAGGATTAGGGATGGCTGTAGGAAGAGATATAAAGGAAGAAAT
178    Y D C F G T G H S S T T I S A G L G M A V G R D I K G R S N
721    CATGTAGTGGCCGTAATAGGTGATGGTCTATGACAGCAGGTGAGGCATATGAAGCAATGAACAACGCGCGCTACCTTGATTCTGACATG
208    H V V A V I G D G A M T A G Q A Y E A M N N A G Y L D S D M
811    ATTGTGATTCTTAATGACAAACAAAGITTTCTTGGCCACTGCTAATTTAGACGGTCCAATTCCTCCCGTTGGAGCATTAAAGTAGTGT
238    I V I L N D N K Q V S L P T A N L D G P I P P V G A L S S A
901    TTGAGCAGGTTGCAATCTAATCGACCACTCAGAGAACTAAGAGAAGTTGCCAAGGGAGTTACAAAGCAGATCGGAGGCGCTATGCACGAG
268    L S R L Q S N R P L R E L R E V A K G V T K Q I G G P M H E
991    CTCGGGGCTAAAGTGGACGAATATGCTCGTGGGCTCATCAGTGGTTCGGGTGACACTGTTTGAAGAAGTTGGACTTTACTATATTGGT
298    L A A K V D E Y A R G L I S G S G S T L F E E L G L Y V I G
1081   CCAGTTGATGGTCACAATAICGATGACCTGACGACCAITTCITAGAGAAGTAAAGAACTAAACACGACGGTCCCGTGTGATCCATGTG
328   P V D G H N I D D L T A I L R E V K N T K T T G P V L I H V
1171   GTGACGGAGAAAGCAGAGGATATCCATATGCTGAAAAAGCTGCTGACAAGTACCATGGTGTGGCCAAGTTCGATCCGGGCACAGGAAAG
358   V T E K G R G Y P Y A E K A A D K Y H G V A K F D P A T G K
1261   CAATTTAAATCCAGTGTCCAACCTCAGTCTTACACAACTACTTTGCGAGGGCTTTAATTGCGAAGCTGAAGCAGACAGGATATTATT
388   Q F K S S A P T Q S Y T T Y F A E A L I A E A E A D K D I I
1351   GCCATCCATGCTCAATGGGAGGTGGGACCGGCTTGAACCTCTTCCAAAGCGCTTTTCCAAACAGATGTTTCGATGTCGGAATAGCCGAA
418   A I H A A M G G G T G L N L F Q R R F P T R C F D V G I A E
1441   CAGCACTCTGTAACTTTTGCTGAGGTTTGGCATGTGAAGGCATCAAAACCTTTTGGCAATCTACTCGTCTCTATACAAAGGGCTTAT
448   Q H S V T F A A G L A C E G I K P F C A I Y S S F I Q R A Y
1531   GATCAGGTAGTGATGTGGAATTTGCAGAAGCTGCCTGTGAGGTTTGAATGGACAGAGCTGGCTTAGTTCGGAGCAGATGGTCTCTACA
478   D Q V V H D V D L Q K L P V R F A M D R A G L V G A D G P T
1621   CATTGTGGGGCTTTTGTATGTTACTTTTATGGCATGCCCTCCCAACATGGTGGTGTGGTCTCTTCGGACGAGGAGCAACTATTTCACATG
508   H C G A F D V T F M A C L P N M V V M A P S D E A E L F H M
1711   GTTGCAACTGCCGCTGCTATAGATGACAGACCAAGCTGTTCCGTTATCCGAGAGGTAACGGAATAGGCGTTGAGTTGCCACCTGGAAAC
538   V A T A A A I D D R P S C F R Y P R G N G I G V E L P P G N
1801   AAAGGCATTCTCTTGGAGTTGGTAAGGGGCGAATACTGATTGAAGGGGAGAGAGTGGCTCTGTTGGGGTATGGAACAGCTGTTTCAGAGC
568   K G I P L E V G K G R I L I E G E R V A L L G Y G T A V Q S
1891   TGTTTGGCTGCAGTGTCTTTGGTAGAACCCCATGGTTTACAGTTGACGATCGCAGATGCTCGTTTTGCAAGCCGTTGGATCATGCTCTT
598   C L A A A A L V E P H G L Q L T I A D A R F C K P L D H A L
1981   ATCCGCAGCTTGGCTAAATCAGATGAGGTCCTGATCACTGTGAAGAAGGTTCAATTGGTGGCTTTGGATCTCATGTTGCTCAGTTTATG
628   I R S L A K S H E V L I T V E E G S I G G F G S H V A Q F M
2071   GCGCTGGATGGACTTTTGTATGGAATAAAGTGGAGGCGCACTGGTTCTTCTGATCGATACATCGACCCGCTTCCCGAGCTGACCAA
658   A L D G L L D G K L K W R P L V L P D R Y I D H G S P A D Q
2161   CTGATGCAAGCTGGGCTTACACCGTCCCATATCGCGGCAACAATTTTTAATATACTCGGAAAACTAGGGAAGCTCTGGCGATTATGTCT
688   L M Q A G L T P S H I A A T I F N I L G K T R E A L A I M S
2251   TAGATATCAGAAAAATCGAACAAATGACATTCTCAATGTCTCTTATATTTTCAATTTGTGACTTTAAAAATCCGGTCTTATATTAGCCG
718   +
2341   TGCTTTGATTAAATTATATTGCAACTCTGGTAATCGGAAAG

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(a)DXS

1 ACTTCCAACAGTTACTTCAGTTTCGCGCAGCTTGGCGGCTTTTGTATGGCTTTGAATTTGCTTTGCGCCAATCGCAATCAAGTCCCTCTCT
1 M A L N L L S P I A I K S L S
91 TTCTTCGATTCTCAAATTACAACCTTAATTTTCTCAGGCTCGAAGGTGAGTTTGTCTTTGAAGAGGAAAGGAAATGGATGCACCTTATGCA
16 F F D S S N Y N L N F L E G E F A L K R K G N G C T Y A
181 AAGAGAGTCCATTGTTTCGGCACAACAACCTCTCCGGCGTGGCGGGCGGGCTGTTTCTGAACCAAGTTCGGAAGAGTTGGGACGGCCCG
46 K R V H C S A Q Q P P P A W P G R A V S E P G R K S W D G P
271 AAGCCCAATTCAGTTGTTGGATCAACAGGCTCTATTGGAAGTCTCAGACATTGGACATAGTCGCGGAGAATCCTGGTAAATTTAAAGTTGTT
76 K P I S V V G S T G S I G T Q T L D I V A E N P G K F K V V
361 GCACCTTGCAAGTTCGAACTGACTCTTCTGCTGATCAGGTAAGAAACATTAAACCTAAATAGTTGCGGTCCGAAATGAGACCTTA
106 A L A A G S N V T L L A D Q V K T F K P K L V A V R N E T L
451 TATGATGAGCTCAAAGAGGCTCTGGCTGATATGGAAGAGAAGCCTGAAATTAATCTGGAAGACAGGAGTATCGAGGTAGCCCGCCAT
136 Y D E L K E A L A D M E E K P E I I P G E Q G V I E V A R H
541 CCAGATGTTGTTAGTACAGGAATTGTTGGCTGCGCGGTTTGAAGCCTACAGTGGCTGCCATAGAAGCTGGAAGACATTGCG
166 P D V V T V V T G I V G C A G L K P T V A A I E A G K D I A
631 CTGGCCAATAAGAGAGCGTAATTGCTGGAGTCCCTTTATCCTCCCTCTTGCACACAAGTATGGAGTGAAGATTCTTCTCGCAGATTCT
196 L A N K E T L I A G G P F I L P L A H K Y G V K I L P A D S
721 GAACATTCTGCTATATTTAGTGTATACAAGGCTTCCCGTAGGTGCTCTCAGGCGGATACCTTTGACTGCATCAGGGGGTCTTTTCAAG
226 E H S A I F Q C I Q G L P V G A L R R I L L T A S G G A F R
811 GATTGGCCCATGATAAATTAAGAAGTGAAGTTGCCGATGCTTTAAAGCATCCTAATGGAATATGGGAAGAAGATTACAGTGGAC
256 D W P I D K L K E V K V A D A L K H P N W N M G K K I T V D
901 TCTGCCACACTCTTTAACAAGGACTAGAAGTTATTGAAGTCTCACTATCTGTTTGGGGCTGAATATGATGACATTGATATCGTAATTCTAT
286 S A T L F N K G L E V I E A H Y L F G A E Y D D I D I V I H
991 CCCATCTATCGTACATTCAATGATTGAGACACAGGATTCACTGTTATTGGCACAATTGGGGTGGCTGATATGCGTTTGGCTATTCTA
316 P Q S I V H S M I E T Q D S S V L A Q L G W P D M R L P I L
1081 TACACCTTATCTTGGCCGACAGAATTTCTGTTCTGAGATCACATGGCTCGCCTTGATCTTTGCAAGCTTGGGCTCTTACATTCAAG
346 Y T L S W P D R I F C S E I T W P R L D L C K L F K
1171 ATTCTGACAATGTTAAGTATCCATCGATAGATTAGCTTATGCTGCTGGGCGAGCTGGGGGACCATGACAGGGGTTCTTAGTGACGT
376 I P D N V K Y P S I D L A Y A A G R A G G T M T G V L S A A
1261 AACGAGAAAGCTGTAGAAATGTTTATCAATGAGGAAATAGCTACTTGGACATATTTAAAGTTGTGAACGAACCTGTGAAAGCATCAA
406 N E K A V E M F I N E E I S Y L D I F K V V E R T C E K H Q
1351 GCAGAAGTGTATCACTCTCTTCCGTTGAGGAAATCATGCACTATGACTTGTGGGCACGGGATTATGCCGCCACTTTCGACGCCATTAGCT
436 A E L V S S P S L E E I M H Y D L W A R D Y A A T L Q P L A
1441 GGCTTAAGTCTATTATTGCAATGGCGGAGCCAGCACACGACATGGGGTGGGTGAGCAGATGAAAGTGGGGTGGGTGGATAGAACTC
466 G L S P I I A M A E P A H D N G V G Q H M K V G W V G *
1531 AATTTTTTTTATATAAACTCTAAATTTTTTAAATTTCTAAGTGAATTTTTTTGAAACAAAATGGAGGGGAGAGGGAGGGGCGAGCATG
1621 GCCCCCTAGCTCCGCAATGTGTTCTGTATAGCTGATTGATGGGTGGTGGAGAGGTTAAGTGGGAGATGAGATGCATCTTTTTGA
1711 GGTTTTTTTCATCTTTGCTGGGAGATTGTGGTGGGGATTAA

(b)DXR

1 TGAGAATCAAAATCAAAAAAGCAAAAAAATGGCGGAATCAGTAAAGCTGTAGGGTGGGGAGCGAGGGACAGCTCGGGTTTTT
1 M A E S V K A V G W G A R D T S G F
91 TGCTCCTCTGAATTTACACAGACGGGCCACCGGCGAGCGGGAATGTCAGTTCAAGGTTTTGTACTGTGGTGTCTGTCATTCCGATATTC
19 L S P L N F T R R A T G S R D V Q F K V L Y C G V C H S D I
181 ACATGATCAAGAACGATTGGGGCTTCGCCATTACCGGATGATCCCGGTCACGAGATCGTCGGCGTCTGACCGAAGTCGGGTGGAAGG
49 H M I K N D W G F A H Y P M I P G H E I V G V V T E V G S K
271 TTCATAAATTCAAGGTCGGAGACAATGTCGGCGTCGGAGTTATAGTAGACGCGTGGCGGAAATGCGATCAATGTGTTAACGACCTGGAGA
79 V H K F K V G D N V G V G V I V D A C R K C D Q C V N D L E
361 ATTACTGTCCCGAACGGATCGACACCTATAACGGCGTTTTACCGGACGGGTCCCTCACCTACGGCGGTTACTCTGACATTATGGTGGCTG
109 N Y C P E R I D T Y N G V L P D G S L T Y G G Y S D I M V A
451 ACGAGGAGTTCGTATCCGCTGGCCGACAATTTCCCGATGGATAAAGCGCCCTTTAGTCTGCGCAGAAATCACCACTTACAGCCCGT
139 D E E F V I R W P D N F P M D K G A P L V C A R I T T Y S P
541 TGAGATACTACGGGCTCGACAAGCCCGGCTACACGTCGGGGTGGCGGGCTAGGGGGCTGGGCCACGTGGCGGTCAAATTCCTCAAGG
169 L R Y Y G L D K P G L H V G V A G L G G L G H V A V K F L K
631 CTTTCGGAACAAAGGTAACGGTTTTGGACATTTCCCTGATAAGAAAAGTTATGCCATTGATACCTCGGCGCGGACGGCTTTTACTGA
199 A F G T K V T V L D I S P D K K S Y A I D T L G A D G F I L
721 GCAATAGGCCGGCTGAAATGGAAGCCCGGCTGGGACTTTGGATGGTATTTTGGATTGTCTCTGTTGTTCACTCTCTTCAGGGGTTGT
229 S N R P A E M E A A A G T L D G I L D C V S V V H S L Q G L
811 TGGATTTGTTGAAGCCACATGGGAAGTTGGTTGGTTGGCTTGGCGGAGAAGCCGCTTGAGCTGCCATTTTTTCGTTGACTCTGGGAC
259 L D L L K P H G K L V V V G L P E K P L E L P I F S L T L G
901 GGAAATGATGGGCGGAGTATGATTGAGGGCTAAAAAGACACAGGAGATGATTGATTTTGTGCGAAACATAATATATTGCCTGAAG
289 R K M M G G S M I G G L K E T Q E M I D F A A K H N I L P E
991 TTGAGTTTATTTCCATGGATTATATTAATCTGCCATGAAGAGGCTTGCAAGAGGTGATGTGAAATTTAGGTTTGTATTGATGTCGGGA
319 V E V I S M D Y I N T A M K R L A R G D V K F R F V I D V G
1081 AAACACTTAAAGCCGACTGATTGGACTCGCGGCTGGCTTACGCGCAATCTGGAACAGGGGAGCTTTTTAGTTTGGGTTATATTGTGT
349 K T L K A D *
1171 CATCCGTTTTTATTTCTGTT

(c)10HGO

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1      CTCCACACCATTTTCAACACCAATGGATTTCCTCACAATTCGTCTAGGACTGTTATTTGCTCTGACCTTAATCCATGGCCTCCAAACACTA
1      M D F L T I L L G L L F A L T L I H G L Q T L
91     TCCACCAGGGGCAAAAAGCTTCCACCTGGCCCAACGCCGCTGCGCCCTCATCGGCAGTCTCCACTTACTCGGCGATCAACCCCAAAATCT
24     S T R G K K L P P G P T P L P L I G S L H L L G D Q P H K S
181    CTCGCCGCTCTCGCCAAAATTTATGGCCCCCTAATGTGCCTCCGCTTGGGTTTATAAACACGGTGGTGATTTCTCCGCCGCCATGGCT
54     L A R L A K T Y G P L M C L R L G F I N T V V I S S A A M A
271    AAGGAGTTTCTGCAAAAACAGGACCTCCAGTTTTCGAGCAGGACTGTCCCGACGCCATCCACGCTCAGCAGCAGTTCAAATACTCCGTC
84     K E V L Q K Q D L Q F S S R T V P D A I H A H D Q F K Y S V
361    GTCTGGCTTCCGGTGGCTAACAGGTGGCGCAGCCTCTGGAAGCTCTGAACCTCGAATATGTTCTCCGGCAACCGTCTCGACCGGAATCAG
114    V W L P V A N R W R S L W K A L N S N M F S G N R L D A N Q
451    CATCTCCGGTGTAGAAAAGTGCAGGAGCTCATCGCTTATTCGCGAAAAACAGTCAGACCGGCGACGCGTGGATGTTGGCCGCGCGGCG
144    H L R C R K V Q E L I A Y C R K N S Q T G D A V D V G R A A
541    TTCAGAACTTCCITGAATTTACTGTGCAACAGATTTTCTCCAAGGATTGACGGAATCCGTTTTCCGATTCCGCTAAGGAATCAAGGAT
174    F R T S L N L L S N T I F S K D L T D P F S D S A K E F K D
631    CTGGTGGGAATATCATGGTGGAGGCGCGCAAGCCCAACCTGGTTGATTTTTTCCCTTTCTCGAGAAAATTGATCCCCAGGGGAATACGA
204    L V R N I M V E A G K P N L V D F F P F L E K I D P Q G I R
721    CGCCGTATGACTATTGATTTCGGAAGGTGATTGACCTTTTCAGTGGTTTAAATCAATGAAGATTAGAAAAGGGGAAATCCCAAAACAGT
234    R R M T I H F G K V I D L F S G L I N E R L E K G K S Q T S
811    GATGTAATTTGACGTCTCTCCTCACCAGCAACCAAGAAACCCCGAAGAAATGACCGGACTCAGATCGAACGCATGTGCTTGGACCTGTTT
264    D V I D V L L T A T K E T P E E I D R T H I E R M C L D L F
901    GTTCGGGGACTGACACAACTTCAAGCACTGGAGTGGGCAATGGCAGAGCGCTCAAAAACCCAGAGACAATGAAAAAGCCCAAGCA
294    V A G T D T T S S T L E W A M A E A L K N P E T M K K A K A
991    GAGCTCGAAGAAATGTAATCGGAAAAGGTAAAGTACTAGACGAGCAGATATCTCCGCTTACCTTATCTCCGATGCATGGTGAAGAAACT
324    E L E V I G K G K V L D E A D I S R L P Y L R C M V K E T
1081   CTCGGAATCCACCCGCGGTGCGCTTCTAATCCCGCGCAGAGTCGAGCAAGAGTCGAGGTTTGGGGCTACACAGTGCCCAAAACTCA
354    L R I T H P P V P F L I P R R V E Q D V E V C G Y T V P K N S
1171   CAAGTTTTCGTCAACGCTGGGCAATCGGAAGGACCCCGATATCTGGAATAATCCCTGGAATTCAAACCCGAGAGGTTCTCTGGAATC
384    Q V F V N A W A I G R D P I W K N P L E F K P E R F L E S
1261   GAGGTGACATGCGTGGACGGGACTTCGAGCTGATCCGCTTCGCGCGCGGAGAGGATTGCGCTGGAATGCGCTCTCGCTGTGAGAATG
414    E V D M R G R D F E L I P F G A G R R I C P G L P L A V R M
1351   GTGCTGTAAATGCTTGGTTGCTTTGAATTCGTTTGAAGCTTGAAGGTGGGATGGGCCCAAGGATTGGATATCGAGGAGAAAA
444    V P V M L G S L L N S F D W K L E G G I G P K D L D M E E K
1441   TTTGGAATCAGGTTGCAAGGCTCAACCACTCCGGGCTGTCCTGTCTGCTGTAAG
474    F G I T L Q K A Q P L R A V P V T L *

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(d)G10H

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1      ACGAGGGGCGTATAGGATATGATGCTCTGAAGGGGGCTGACCCGGATATCGAGGTGCGGGTACGCGCGTCTGATGGGTTTACTCTTTG
1      M M S V R G L T R I S R S G Y A R R R W V Y S L
91     TTGGGCACTAATAATAGCCTGCCATTGCTCGAGCAACCTACTCACTTTCGTTCCCTGTTCAATCTTCCCAAGAGGTTTGGGTTGCAGA
25     L G S N N S L P L L E Q P T H F R S P V Q S Q E V L G C R
181    GTTATTTATTTCTGGGTTTCAAGTGCCTTAAGCAGTGTGCGGCAACAGGCTCATTCTCAGAGCAGCACCGCGGTTGAGGAGCACTAGAT
55     V I Y S W V S S A L S S V G Q Q A H S Q S S T A V E E Q L D
271    CCATTTCTCTAGTTGCTGATGAATTTCTCTGTGCGGATGCTTAAGTCCATGGTAGTCGCGGAGGTTCCCAACTTGCCTCTGCT
85     P F T S L V A D E F S L V A D R L R S M V V A E V P K L A S A
361    GCGGAATATTTTTCAAATTTGGGAGTTGAAGGAAAAAGATTCCGACCCACTGTTCTATTGTTGATGGCAACGGCTTTAAATGTATCGGTG
115    A E Y F F K L G V E G K R F R P T V L L L M A T A L N V S V
451    CCAAGGCACTACCTGTGGCTGCGGTTGATACCTTGTCTGTGGAGTTGCGTTCAAGACAACAGTGTATCGCTGAGATCACAGAAATGATC
145    P R Q L P V A A V D T L S V E L R S R Q Q C I A E I T E M I
541    CATGTTGCTAGCCTCCTCCATGATGACGTGTTGGATGATCCGATACAAGGAGGGAATCGGTTCTTTGAATTTGTGATGGGAAATAAG
175    H V A S L L H D D V L D D A D T R R G I G S L N F V M G N K
631    CTAGCTGATTTGGCCGGAGATTTCCTGCTATCTAGAGCTTGTGTGGCCCTTGCCTCATTAAAAAACACTGAGGTGGTATCCCTCTTGCT
205    L A V L A G D F L L S R A C V A L A S L K N T E V V S L A V
721    AAAATTGTGGAGCATCTAGTTACTGGTGAACCATGCAAACTGACAACTACATCAGATCAGCGTTGCGCATGGAATACTATATGCAGAA
235    K V V E H L V T G E T M Q M T T T S D Q R C S M E Y Y M Q K
811    ACATACTACAAAAGTCATCAATTGATTTCAAATAGCTCAAGGCTATTGCCCTTCTTGTGAGACAACTGCAGAAAGTTTCGATTTTGGCT
265    T Y Y K T A S L I S N S C K A I A L L A G Q T A E V S I L A
901    TATGAGTATGGCAAAATTTGGGTTTGGCTTTTCAGTTAATTGATGACGTACTTGAATTCAGTGGCACATCAACATCCCTTGGGAAGGGC
295    Y C T Y G K N L G L A F Q L I D D V L D F T G T S T S L G K G
991    TCCTTGTGACATTCGACATGGGATTGTTACTGCTCTATATTATTCGCAATGGAGGAGTTCCCTGAGCTGCGGGATGTTGTTGATCAG
325    S L S D I R H G I V T A P I L F A M E E F P E L R D V V D Q
1081   GGATTTGACAATTCGAAATGTGACCGTGCTCTAGAGTATCTTGGAAAGAGTCGTGGAATTCAGAGAACTAGGGAGCTGGCAGCAAG
355    G F T D N S A N V D R A L E Y L G K S R G I Q R T R E L A K
1171   CATGCTAGCCTTGCCTCAGCTGCGATTGATTCATTTCCGGAGAACGATGATGAGGATGTCCAAAGGTCAAGAGGGGCACTTGTAGAATTA
385    H A S L A S A A A I D S F P E N D D E D V Q R S R R A L V E L
1261   ACACAGAGAGTCAACAGAACAAAGTAAGACACACAGTGATTAAATCAGGTT
415    T Q R V I T R T K *

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(e)GPPS

Fig. S1 The CDS and amino acid sequences of DXS/DXR/10HGO/G10H/GPPS synthase genes in *R.glutinosa*

(a), (b), (c), (d) and (e) represent the CDS and amino acid sequences of DXS(MG764508), DXR (MG764509), 10HGO (MH102394), G10H (MK559439) and GPPS (MG770219), respectively.

R.glutinosa	MALPFAEPISGNLSKG.MGVDAQRHSNLCSWVHESG..LCLFCKNNQVRKRSACI..LSERGEYFSQKRP..TPLLDTINYPIHMKNLS..RELKOLADE	97
Salvia splendens	MLKSTLISLSGYMEQIYPTFSAR..TTRKNTTGICAILSERGEYFSQKRP..TPLLDTINYPIHMKNLS..RELKOLADE	77
Sesamum indicum	MALCTEAVPGNLSGVVGADAKQTSLSGSMWRGSD..LOPHSFSSKNNQIRKRSIGV..LSERGEYFSQKRP..TPLLDTINYPIHMKNLS..RELKOLADE	98
Salvia officinalis	MALCPFXFCGNLSKGLAAADAQKHTNFCSWLLGADLPFOFHPFFCKNNQVRKRSSTGICAILSERGEYFSQKRP..TPLLDTINYPIHMKNLS..RELKOLADE	100
Salvia pomifera	MALCPFAFCGNLSKGLAAADAQKHTNFCSWLLGADLPFOFHPFFCKNNQVRKRSSTGICAILSERGEYFSQKRP..TPLLDTINYPIHMKNLS..RELKOLADE	100
Salvia fruticosa	MALCPFAFCGNLSKGLAAADAQKHTNFCSWLLGADLPFOFHPFFCKNNQVRKRSSTGICAILSERGEYFSQKRP..TPLLDTINYPIHMKNLS..RELKOLADE	100
Consensus	s rk g ca l ergeyfsqkp tpiltdinypihmknls kel qlade	
R.glutinosa	LRSDVFNVSKTGGHLGSSSLGVIELTVALHYV..NAPQDRHLWDVGHC..SYPHKILTGRRH..KMB..LRQT..GLSGFTKRSESDYCFG..GHSSTTISAGLGMA	197
Salvia splendens	LRSDVFNVSKTGGHLGSSSLGVIELTVALHYV..NAPQDRHLWDVGHC..SYPHKILTGRRDKMBS..LRQT..GLSGFTKRSESDYCFG..GHSSTTISAGLGMA	177
Sesamum indicum	LRSDVFNVSKTGGHLGSSSLGVIELTVALHYV..NAPQDRHLWDVGHC..SYPHKILTGRRDKM..LRQT..GLSGFTKRSESDYCFG..GHSSTTISAGLGMA	198
Salvia officinalis	LRSDVFNVSKTGGHLGSSSLGVIELTVALHYV..NAPQDRHLWDVGHC..SYPHKILTGRRDKMBS..LRQT..GLSGFTKRSESDYCFG..GHSSTTISAGLGMA	200
Salvia pomifera	LRSDVFNVSKTGGHLGSSSLGVIELTVALHYV..NAPQDRHLWDVGHC..SYPHKILTGRRDKMBS..LRQT..GLSGFTKRSESDYCFG..GHSSTTISAGLGMA	200
Salvia fruticosa	LRSDVFNVSKTGGHLGSSSLGVIELTVALHYV..NAPQDRHLWDVGHC..SYPHKILTGRRDKMBS..LRQT..GLSGFTKRSESDYCFG..GHSSTTISAGLGMA	200
Consensus	lrsvdfnvsktgghlgssslgvieiltvalhy nappd ilwdvgqh yphkiltgrr m lrqt glsgftkrsees ydcfg ghssttisaglgma	
R.glutinosa	VGRDKGRKNNVAVIGDGAMTAGQAYEAMNNAGYLDSDMIVILNDNKQVSLPTANLDGPI..PVGALSALSRLQSNRPLRELREVAKVTKQIGGPMHE	297
Salvia splendens	VGRDKGRKNNVAVIGDGAMTAGQAYEAMNNAGYLDSDMIVILNDNKQVSLPTANLDGPI..PVGALSALSRLQSNRPLRELREVAKVTKQIGGPMHE	277
Sesamum indicum	VGRDKGRKNNVAVIGDGAMTAGQAYEAMNNAGYLDSDMIVILNDNKQVSLPTANLDGPI..PVGALSALSRLQSNRPLRELREVAKVTKQIGGPMHE	298
Salvia officinalis	VGRDKGRKNNVAVIGDGAMTAGQAYEAMNNAGYLDSDMIVILNDNKQVSLPTANLDGPI..PVGALSALSRLQSNRPLRELREVAKVTKQIGGPMHE	300
Salvia pomifera	VGRDKGRKNNVAVIGDGAMTAGQAYEAMNNAGYLDSDMIVILNDNKQVSLPTANLDGPI..PVGALSALSRLQSNRPLRELREVAKVTKQIGGPMHE	300
Salvia fruticosa	VGRDKGRKNNVAVIGDGAMTAGQAYEAMNNAGYLDSDMIVILNDNKQVSLPTANLDGPI..PVGALSALSRLQSNRPLRELREVAKVTKQIGGPMHE	300
Consensus	vgrd kgr n vvavigdgamttagqayeamnnagylsdmivilndnkqvsldptanldgp pvgalssalsrlqsnrplrelrevakgvtkqigggpmhe	
R.glutinosa	IAAKVDEYARG..ISGSGSTLFEELGLYYIGPVDGHN..DDLTAILREVK..TKTTGPVLIHVVTEKGRGYPYAEKAADKYHG..KFDPATGKQFKS..APTQS	397
Salvia splendens	IAAKVDEYARG..ISGSGSTLFEELGLYYIGPVDGHN..DDLTAILREVK..TKTTGPVLIHVVTEKGRGYPYAEKAADKYHG..KFDPATGKQFKS..APTQS	377
Sesamum indicum	IAAKVDEYARG..ISGSGSTLFEELGLYYIGPVDGHN..DDLTAILREVK..TKTTGPVLIHVVTEKGRGYPYAEKAADKYHG..KFDPATGKQFKS..APTQS	398
Salvia officinalis	IAAKVDEYARG..ISGSGSTLFEELGLYYIGPVDGHN..DDLTAILREVK..TKTTGPVLIHVVTEKGRGYPYAEKAADKYHG..KFDPATGKQFKS..APTQS	400
Salvia pomifera	IAAKVDEYARG..ISGSGSTLFEELGLYYIGPVDGHN..DDLTAILREVK..TKTTGPVLIHVVTEKGRGYPYAEKAADKYHG..KFDPATGKQFKS..APTQS	400
Salvia fruticosa	IAAKVDEYARG..ISGSGSTLFEELGLYYIGPVDGHN..DDLTAILREVK..TKTTGPVLIHVVTEKGRGYPYAEKAADKYHG..KFDPATGKQFKS..APTQS	400
Consensus	aakvdeyarg isgsgstlfeelgllyigpvdghn ddltail evk tkttgpvliahvvttekgrygyaekaadkyhgv kfdpatgkqfks aptqs	
R.glutinosa	YTTYFAEALIAEAEADKDI..AIIHAAMGGGTGLNLFQRRFPTRCFVDGIAEQHS..VTFAGLACE..IKPFCAIYSSF..QRAYDQVVHVDLQKLPVRFAMDR	497
Salvia splendens	YTTYFAEALIAEAEADKDI..AIIHAAMGGGTGLNLFQRRFPTRCFVDGIAEQHS..VTFAGLACE..IKPFCAIYSSF..QRAYDQVVHVDLQKLPVRFAMDR	477
Sesamum indicum	YTTYFAEALIAEAEADKDI..AIIHAAMGGGTGLNLFQRRFPTRCFVDGIAEQHS..VTFAGLACE..IKPFCAIYSSF..QRAYDQVVHVDLQKLPVRFAMDR	498
Salvia officinalis	YTTYFAEALIAEAEADKDI..AIIHAAMGGGTGLNLFQRRFPTRCFVDGIAEQHS..VTFAGLACE..IKPFCAIYSSF..QRAYDQVVHVDLQKLPVRFAMDR	500
Salvia pomifera	YTTYFAEALIAEAEADKDI..AIIHAAMGGGTGLNLFQRRFPTRCFVDGIAEQHS..VTFAGLACE..IKPFCAIYSSF..QRAYDQVVHVDLQKLPVRFAMDR	500
Salvia fruticosa	YTTYFAEALIAEAEADKDI..AIIHAAMGGGTGLNLFQRRFPTRCFVDGIAEQHS..VTFAGLACE..IKPFCAIYSSF..QRAYDQVVHVDLQKLPVRFAMDR	500
Consensus	ytytfaealiaeaeadkdi aiihaamgggtglnlfqrrfptrcfdvgiaeqh vtfaglace ikpfcaiysf qraydqvvhvdldqklpvrfamdr	
R.glutinosa	AGLVGADGPTHCGAFDVTFMACLPNMVVMAPSDEAELFHMVATAAAIDDRPSCFRYPGRNG..GVELPPGNKG..PLE..GKGRIL..EGERVALLGYG..SAVQS	597
Salvia splendens	AGLVGADGPTHCGAFDVTFMACLPNMVVMAPSDEAELFHMVATAAAIDDRPSCFRYPGRNG..GVELPPGNKG..PLE..GKGRIL..EGERVALLGYG..SAVQS	577
Sesamum indicum	AGLVGADGPTHCGAFDVTFMACLPNMVVMAPSDEAELFHMVATAAAIDDRPSCFRYPGRNG..GVELPPGNKG..PLE..GKGRIL..EGERVALLGYG..SAVQS	598
Salvia officinalis	AGLVGADGPTHCGAFDVTFMACLPNMVVMAPSDEAELFHMVATAAAIDDRPSCFRYPGRNG..GVELPPGNKG..PLE..GKGRIL..EGERVALLGYG..SAVQS	600
Salvia pomifera	AGLVGADGPTHCGAFDVTFMACLPNMVVMAPSDEAELFHMVATAAAIDDRPSCFRYPGRNG..GVELPPGNKG..PLE..GKGRIL..EGERVALLGYG..SAVQS	600
Salvia fruticosa	AGLVGADGPTHCGAFDVTFMACLPNMVVMAPSDEAELFHMVATAAAIDDRPSCFRYPGRNG..GVELPPGNKG..PLE..GKGRIL..EGERVALLGYG..SAVQS	600
Consensus	aglvgadgpthcgafdvtfmaclpnmvmapsdeaelfhmvataaaiddrpscfryprng g elppgnkg ple gkgril egervallgyg avqs	
R.glutinosa	CAAAAALVE..RGL..LT..ADARFCKPLD..ALIRSLAKSHEVLITVEEGSIGGFGSHVA..FMALDGLLDG..LKWRLPLVLPDRYIDHG..SADQLMOAGL..E..ESH	697
Salvia splendens	CAAAAALVE..RGL..LT..ADARFCKPLD..ALIRSLAKSHEVLITVEEGSIGGFGSHVA..FMALDGLLDG..LKWRLPLVLPDRYIDHG..SADQLMOAGL..E..ESH	677
Sesamum indicum	CAAAAALVE..RGL..LT..ADARFCKPLD..ALIRSLAKSHEVLITVEEGSIGGFGSHVA..FMALDGLLDG..LKWRLPLVLPDRYIDHG..SADQLMOAGL..E..ESH	698
Salvia officinalis	CAAAAALVE..RGL..LT..ADARFCKPLD..ALIRSLAKSHEVLITVEEGSIGGFGSHVA..FMALDGLLDG..LKWRLPLVLPDRYIDHG..SADQLMOAGL..E..ESH	700
Salvia pomifera	CAAAAALVE..RGL..LT..ADARFCKPLD..ALIRSLAKSHEVLITVEEGSIGGFGSHVA..FMALDGLLDG..LKWRLPLVLPDRYIDHG..SADQLMOAGL..E..ESH	700
Salvia fruticosa	CAAAAALVE..RGL..LT..ADARFCKPLD..ALIRSLAKSHEVLITVEEGSIGGFGSHVA..FMALDGLLDG..LKWRLPLVLPDRYIDHG..SADQLMOAGL..E..ESH	700
Consensus	c aaaaalve gl lt adarfckpld alirslakshevlitveegsiggfgshva fmaldgldg lkwrlplvpdryidhg p dq agl p h	
R.glutinosa	IAATVFNILGK..REAL..IMS	717
Salvia splendens	IAATVFNILGK..REAL..IMS	697
Sesamum indicum	IAATVFNILGK..REAL..IMS	718
Salvia officinalis	IAATVFNILGK..REAL..IMS	720
Salvia pomifera	IAATVFNILGK..REAL..IMS	720
Salvia fruticosa	IAATVFNILGK..REAL..IMS	720
Consensus	iaat fnilg real ims	

(a)DXS

R. glutinosa	MALNLLSPETIKSLSEFDS...SNYNLNLFLRLKEGFALKRKKGNGCHYAKRVHCSAQ.QPPPAWPGRVSEPGRKSSWDGPKPISVVGSTGSIGTQTLDIVAE	97
Olea europaea var. sylvestris	MALNELSPETIKSLSEFLDTSKSSYNLNLKNOGVFALKRKKDE.TTIAKRVHCSAQQPPPAWPGRVSEPGRKIWDGPKPISVVGSTGSIGTQTLDIVAE	99
Handroanthus impetiginosus	MALNLLSPETIKTLSEFLDSNKSSNYNRNLSLKFOGGFALKRKKENGCTAAKRTHCSAQ.PPPPAWPGRVSEPGRKIWDGPKPISVVGSTGSIGTQTLDIVAE	99
Osmanthus fragrans	MALNLLSPETDIKSSSEFLDISKSNHNLNLKFOGGFALKRKKDCGRTAARVQCLAQ.PPPPAWPGRVSEPGRKSSWDGPKPISVVGSTGSIGTQTLDIVAE	99
Olea europaea subsp. europaea	MALNELSPETINSLSEFLDTSKSSYNLNLKNEGVFALKRKKDA.NTVAKRVHCSAQQPPPAWPGRVSEPGRKSSWDGPKPISVVGSTGSIGTQTLDIVAE	99
Camellia sinensis	MALNLLSPETIKATSEFLDSSKSNH..QLLKLOGGFALKRKKDYGATFCRKTHCSAQ.QPPPAWPGRVSEPGRKSSWDGPKPISVVGSTGSIGTQTLDIVAE	97
Consensus	maln lsp i sf d s l g falk k t kr c aq pppawpgr v ep rk wdgpkpis vgstgsigtqtldivae	
R. glutinosa	NPCKKVVVALAAGSNVTLADQVKTFKFKLVAVRNETLYDELKEALADMEKPEIIPGEGVIEVARHPDAITVVTGIVGCAGLKPTVAAIEAGKDIALA	197
Olea europaea var. sylvestris	NPDKKVVVALAAGSNVTLADQVKRFEPQLVAVRNBESLVDELKEALADMEKPEIIPGEGVIEVARHPDAITVVTGIVGCAGLKPTVAAIEAGKDIALA	199
Handroanthus impetiginosus	NENKPKVVVALAAGSNVTLADQVKTFKFKLVAVRNBESLVDELKEALADVDEKPEIIPGEGVIEVARHPDAITVVTGIVGCAGLKPTVAAIEAGKDIALA	199
Osmanthus fragrans	NPDKKRVVALAAGSNVTLADQVKTFKFKLVAVRNBESLVDELKEALADVDEKPEIIPGEGVIEVARHPDAITVVTGIVGCAGLKPTVAAIEAGKDIALA	199
Olea europaea subsp. europaea	NPDKKVVVALAAGSNVTLADQVKRFEPQLVAVRNBESLVDELKEALADMEKPEIIPGEGVIEVARHPDAITVVTGIVGCAGLKPTVAAIEAGKDIALA	199
Camellia sinensis	NPDKKRVVALAAGSNVTLADQVKTFKFKLVAVRNBESLVDELKEALADVDEKPEIIPGEGVIEVARHPDAITVVTGIVGCAGLKPTVAAIEAGKDIALA	197
Consensus	np kf valaagsnv lladq k f p lv vrne l elkealad e kpeiipge g evarhpd tvvtgivgcaglkptvaaieagkdiala	
R. glutinosa	NKETLIAGGPFVLPPLAHKKVYKILPADSEHSAIFQCIQGLPFGALRRRIILTASGGAFRDLPVDKLKQVKVADALKHPNWNMGKKITVDSATLFNKGLEVI	297
Olea europaea var. sylvestris	NKETLIAGGPFVLPPLARKENIKILPADSEHSAIFQCIQGLPFGALRRRIILTASGGAFRDLPVDKLKQVKVADALKHPNWNMGKKITVDSATLFNKGLEVI	299
Handroanthus impetiginosus	NKETLIAGGPFVLPPLAQKHKKVYKILPADSEHSAIFQCIQGLPFGALRRRIILTASGGAFRDLPVDKLKQVKVADALKHPNWNMGKKITVDSATLFNKGLEVI	299
Osmanthus fragrans	NKETLIAGGPFVLPPLAHKKVYKILPADSEHSAIFQCIQGLPFGALRRRIILTASGGAFRDLPVDKLKQVKVADALKHPNWNMGKKITVDSATLFNKGLEVI	299
Olea europaea subsp. europaea	NKETLIAGGPFVLPPLAHKKVYKILPADSEHSAIFQCIQGLPFGALRRRIILTASGGAFRDLPVDKLKQVKVADALKHPNWNMGKKITVDSATLFNKGLEVI	299
Camellia sinensis	NKETLIAGGPFVLPPLAHKKVYKILPADSEHSAIFQCIQGLPFGALRRRIILTASGGAFRDLPVDKLKQVKVADALKHPNWNMGKKITVDSATLFNKGLEVI	297
Consensus	nketliaggpf lpla k kilpadsehsaifqciqgl galrrri ltasggafrd p dklk kvvadalkhpnwnmgkkitvdsatlfnkglevi	
R. glutinosa	EAHYLFGAEYDDIEIVIHQPSIIHSMIETQDSSVLAQLGWPDMLRPILYTLSPDRISCSEITWPRLDLCKLGSALTFFKAPDNVKYPSMDLAYAAGRAGGT	397
Olea europaea var. sylvestris	EAHYLFGAEYDDIEIVIHQPSIIHSMIETQDSSVLAQLGWPDMLRPILYTLSPDRISCSEITWPRLDLCKLGSALTFFKAPDNVKYPSMDLAYAAGRAGGT	399
Handroanthus impetiginosus	EAHYLFGAEYDDIEIVIHQPSIIHSMIETQDSSVLAQLGWPDMLRPILYTLSPDRISCSEITWPRLDLCKLGSALTFFKAPDNVKYPSMDLAYAAGRAGGT	399
Osmanthus fragrans	EAHYLFGAEYDDIEIVIHQPSIIHSMIETQDSSVLAQLGWPDMLRPILYTLSPDRISCSEITWPRLDLCKLGSALTFFKAPDNVKYPSMDLAYAAGRAGGT	399
Olea europaea subsp. europaea	EAHYLFGAEYDDIEIVIHQPSIIHSMIETQDSSVLAQLGWPDMLRPILYTLSPDRISCSEITWPRLDLCKLGSALTFFKAPDNVKYPSMDLAYAAGRAGGT	399
Camellia sinensis	EAHYLFGAEYDDIEIVIHQPSIIHSMIETQDSSVLAQLGWPDMLRPILYTLSPDRISCSEITWPRLDLCKLGSALTFFKAPDNVKYPSMDLAYAAGRAGGT	397
Consensus	eahylfgaeydd ivihqpsi hsmietqdssvlaqlgwpdmrlpilytlswp ri cse twprldlcklgsaltfk pdnvkyps dlayaagrsgt	
R. glutinosa	MTGVLSAANEKAVEMFINEEISYLEIFKVVVELTCCKHQAEIVSSPSLEEIIHYDLNWARDYAATLQPLAGLSPFIAMAEPAHDNGVQHMKVGVWG	492
Olea europaea var. sylvestris	MTGVLSAANEKAVELFINEEISYLEIFKIVVELTCDKHQSELVSSPSLEEIIHYDLNWARDYAATLQPLAGLSPALV.....	474
Handroanthus impetiginosus	MTGVLSAANEKAVEMFINEEISYLEIFKVVVELTCDKHRAELVSSPSLEEIIHYDLNWARDYAATLQPLAGLSPALV.....	474
Osmanthus fragrans	MTGVLSAANEKAVEMFINEEISYLEIFKVVVELTCCKHQAEIVSSPSLEEIIHYDMWARDYAATLQPSAGLSPALV.....	474
Olea europaea subsp. europaea	MTGVLSAANEKAVELFINEEISYLEIFKIVVELTCDKHRSSELVSSPSLEEIIHYDLNWARDYAATLQPSAGLSPALV.....	474
Camellia sinensis	MTGVLSAANEKAVEMFINEEISYLEIFKIVVELTCDKHQAEIVTAPSLLEEIIHYDLNWARDYAATLQPSGLSPVPV.....	472
Consensus	mtgvlsaanekave fi e i yl if ve tc kh elv psleei hyd war yaa q glsp	

(b)DXR

R._glutinosa	MAES.....VKAVGWGARDTSGFLSPINFTRRATGSRDVQKVKLYCGVCHSDHMKNDWGFAYHFMIPGHEIVGVVTEVGSKVHKFKVGDNVGVGVTV	94
Striga_asiatica	MAKT.....VKALGWGARDSSGILLSPLEFTRRATGSRDVRKQVLYCGVCHSDHLVKNWGFARYPMIPGHEIVGVVTEVGSKVDFKFKVGDKVAVGVVMV	94
Handroanthus impetiginosus	MAEG.....VKATGWGARDSSGILLSPLKFTRRATGERDVQKVKLYCGICHSDLHSIRNEWGNAQYPLIPGHEIVGVVTEVGSKVNKVKVGDKVGVGCLV	94
Sesamum indicum	MAGSS.....VKAFGWGARDPSGVLSPFDPSRRPTRDHDVQKVKLYCGICHSDLHAIKNEWGCFSTYFVVPGHEIVGVVTEVGSKVQKQVQVGDVGVGCLV	95
Pogostemon cablin	MAKSPETEHPVKACGWAARDTSGVFSPTFNSRRATGEHDVQKVKLYCGVCHSDHLMVRNEWGFTQYPIVPGHEIVGVVTEVGSKVQKFKVGDVGVGCLV	100
Phtheirospermum japonicum	MAKT.....VKAAAGWAARDSSGILLSPLKFTRRATGDRDVQKVKLYCGICHSDLHAIKNEWGFAQYPLVPGHEIVGVVTEVGSKVQKFKVGDVGVGCMV	94
Consensus	ma vka gw a d sg sp f rr t dv f vlycg chsd h n wg yp pgheivgvvtevgskv k vgd v vg v	
R._glutinosa	DACRKCDDQCVNDLENYCP.ERIDTYNGVLPDGSITYGGYSDLMVADEEFVIRWPDNFFEMDKGAPLVCARITTYSPRLYYGLDKPGLHVGVAAGLGGLGHVA	193
Striga_asiatica	GSCRLCDQCENNLENYCP.EKLDITYNGVQADGSITYGGYSDLMVADEEFVIRWPDNFFEMDRGAPLVCAGITTYSPRLYYGLDKPGLHVGVAAGLGGLGHVA	193
Handroanthus impetiginosus	DSCRKCDQCCANNLENYCG.QPVFTYGSNLPDGTVTGGYSDLMVADEEFFIRWPDNFFEMDKGAPLVCAGITTYSPRLYYGLDKPGLHVGVAAGLGGLGHVA	193
Sesamum indicum	DSCRKCDQCTNNLENYCP.QTVLTYNTILPDGTVTGGYSDLMVVADEEFFAIRWPDNFFEMDKGAPLVCAGITTYSPRLYYGLDKPGLHVGVAAGLGGLGHVA	194
Pogostemon cablin	GSCRCDDQCNNDLENYCP.KQILTYSMFYIDGITTYGGYSDLMVADEEFVIRWPDNFFEMDKGAPLVCAGITTYSPRLHFGGLDKPGLHVGVAAGLGGLGHVA	199
Phtheirospermum japonicum	NSCRKCDQCAKDLNLYCGGGATFTYNSVDSGGSVTYGGYSDLMVVADEEFVIRWPDNFFEMDKGAPLVCAGITTYSPRLSFGGLDKPGLHVGVAAGLGGLGHVA	194
Consensus	cr cdqc lenyc ty dg t ggysd mv e f irwp n p d gapl ca ittysplr gldkpg gv glgglghva	
R._glutinosa	VKFLKAEGETKVTVLDISPKKSYAIDTLGADGFIILSNRPAEMEAAGTLDGILDCVSVVHSLQGLLDLLKPHGKLVVGLPEKPLELEPFISLTIGRKMVG	293
Striga_asiatica	VKFLKAEGAKVTVMDIAPEKKRAYALETLGADQELLSH...ELESAGTLDGILDCVSAFHSIQAYLSLLKPHGKLVVGLPERPLELEPMFSLATERKMIG	290
Handroanthus impetiginosus	VKFAKAEGLKVTVISTSVGKKKEALETLGADAFLVSRPEEQQAAGTMDGIIIDTVSASHPILPLLKPHGKLVVGLPEKPLELEPFISLTRRAVA	293
Sesamum indicum	VKFAKAEGETKVTVISTSVGKKKEALEGLGADTFLVSRDPAEMKAAAGSLOGIIDTVSAQHPIEPLLSLLKPHGKMIMVGAPEKPLELEPFISLIMTRKMA	294
Pogostemon cablin	VKFAKAEGETKVTVISTSLSKKEEAIKNLGADEIVSRDPEQLQAAGTLDGIIIDTVSATHPLLPLVSLKENGKLVVGLPEKPLELEPFISLLQGRKSIS	299
Phtheirospermum japonicum	VKFAKAEGLKVTIISTSAKKKAEALETLGADAFLLISREPAELAAAGTLDGIIIDTVSAPHPIQPLLNLLKPDGKLVVGLPEKPLELEPFISLVMGRKIVA	294
Consensus	vkf ka g kv t kk a lgad f s a g dgi d vs h llkp gk vg p p e p f l r	
R._glutinosa	GSMIGGLKETQEMIDFAAKHNILPEVEVISM DYINTAMKRLARGDVKERFVIDVGKTLKAD	354
Striga_asiatica	GSMIGGLKETQEMIDFAAKHNILPEVEIISM DYINTAMERLARADVKYRFVIDVGNLSKSK	351
Handroanthus impetiginosus	GSMIGGLKETQEMIDFAAKHQILPEVEIVPM DYVNTAMERLVKADVKYRFVIDVGKTLKAD	354
Sesamum indicum	GSMIGGLKETQEMIDFAAKHNILPEVEMISM DYVNTAMERLAKADVKYRFVIDIGKTLKKE	355
Pogostemon cablin	GSAIGGLKETQEMIDFAAKHNILPEVEMIPIDYVNTAMERLAKSDVKYRFVIDVAKTLKPE	360
Phtheirospermum japonicum	GSMIGGLKETQEMIDFAAEHNILPEVEIVSV DYVNTAMERLAIGDVKYRFVIDIGNTLKAE	355
Consensus	gs igg ketqem dfaa h ilp ve dy n am rl dvk rfv d k	

(c)10HGO

R. glutinosa	MDFLTILLGLLFALTLIHGLQTLSTRGKKLPFGPTPLPLIGSLHLLGDOPHKSLARLAKTYGPLMCLRLGFTINTVVSSAAMAREVLQKQDLQFSSRTVP	100
Phtheirospermum japonicum	SHPRPPNPLHP.GQKAPPGPTPLPLIGSLHLLGDOPHKSLARLAKTYGPLICLRLGFTINTVVSSAAMAREVLQKQDLQFSSRTVP	85
Handroanthus impetiginosus	MDFLTIVLGLLFALTLIHGLQTLSTRGKKLPFGPTPLPLIGSLHLLGDOPHKSLARLAKIHGPTMCLRLGFTINTVVSSAAMAREVLQKQDLQFSSRTVP	100
Sesamum indicum	MDFLTIVLGLLFTLVLVHGLQTLSSARAKKLPFGPTPLPLIGSLHLLGDOPHQSARLAKTHGPTMCLRLGFTINTVVSSAAMAREVLQKQDLQFSSRTVP	100
Scoparia dulcis	MDFLTIVLGLILSLTIVHILQLLSIKSKKLPFGPTPLPLIGSLHLLGDOPHKSLARLAKTHGPTMCLRLGFTINTVVSSAAMAREVLQKQDLQFSSRTVP	100
Striga asiatica	MDFLTIVLGLLFAATLLHAVQTLSSARRRNLPFGPTPLPLIGSLHLLGDPLHHSARLAKSHGPTMCLRLGFTINTVVSSAAMAREVLQKQDLQFSSRTVP	100
Consensus	1 ppgptplp gslhlldg ph sla lak gp clrlg ntvv saa a e lqkqdl fssrt p	
R. glutinosa	DATHAHDQFKYSVVWLPVANRWRSRLKALNSNMFSGNRLDANOHLRCRKVQELIACRKNSQTCDAVDVGAAAFRTSLNLLSNTIFSKDLTDPFSDSAKE	200
Phtheirospermum japonicum	NATHAHDQFKYSVVWLPVAAWRWSRLKALNSNMFSGNRLDANOHLRCRKVQELIACRKSSQTCDAVDVGAAAFRTSLNLLSNTIFSKDLTDPFSDSAKE	185
Handroanthus impetiginosus	DATHAHDQFKYSVVWLPVASRWGRRLKALNSNMFSGNRLDANOHLRSRKVQELIACRKNSQSCDAVDVGAAAFRTSLNLLSNTIFSKDLTDPFSDSAKE	200
Sesamum indicum	DATHAHDQFKYSVVWLPVASRWRSRLKALNSNMFSGNRLDANOHLRCRKVQELIACRKNSQTCDAVDVGAAAFRTSLNLLSNTIFSKDLTDPFSDSAKE	200
Scoparia dulcis	NATHAHDQFKYSVVWLPVANRWRSRLKALNSNMFSGNRLDANOHLRSRKVQELIACRKNSQTCDAVDVGAAAFRTSLNLLSNTIFSKDLTDPFSDSAKE	200
Striga asiatica	DATHAHDQFKYSVVWLPVAFRWRSRLKALNSNMFSGNRLDANOHLRCRKVQELIACRKNSQSCDAVDVGAAAFRTSLNLLSNTIFSKDLTDPFSDSAKE	200
Consensus	a hahdqfks vwlpva rwr l k lnsn f g rl a qhllr rkvqel a crk sq g vdvgraaf tslnllsntifskdltdpfdsake	
R. glutinosa	FKDLVRNIMVEAGKPNLVDFPFLEKIDPQGIIRRMTHIFGKVIDLFSGLINERLEKKG...SQTSDVIDVLLTATKETPBEIDRTHIERMCLDLFVAGT	297
Phtheirospermum japonicum	FKDLVRNIMVEAGKPNLVDFPFLEKIDPQGIIRRMTHIFGKVIDLFSGLISERLEKGN..SQTSDVIDVLLAASKETPBEIDRTHIERLCLDLFVAGT	283
Handroanthus impetiginosus	FRDLVRNIMVEAGKPNLVDFPFLEKIDPQGIIRRMTHIFGKVIDLFSGLINERLEKKGPPNANTSQSDVIDVLLTATKETPBEIDRTHIERLCLDLFVAGT	300
Sesamum indicum	FKDLVRNIMVEAGKPNLVDFPFLEKIDPQGIIRRMTHIFGKVIDLFSGLINERLEKKGTONAGNSQSDVIDVLLTATSKENPBEIDRTHIERMCLDLFVAGT	300
Scoparia dulcis	FKDLVWGMVEAGKPNLVDFPFLEKIDPQGIIRRMTHIFGKVIDLFSGLINERLEKKGKQSDGASQSDVIDVLLTSEENPBEIDRTHIERMCLDLFVAGT	300
Striga asiatica	FKDLVMSIMVEAGKPNLVDFPFLEKIDPQGIIRRMTHIFGKVIDLFSGLINERLEKKGK..SQSDVIDVLLAASRETPEIDRTHIERLCLDLFVAGT	298
Consensus	f dlv mveagkpnlvdfpf l k dpqg r rmt fgk 1 gli er kg sdivd ll e p eidr hier clldlfvagt	
R. glutinosa	DTTSSTLEWAMAEALKNPETMKKAKAELEEVIGKGVLEADISRLPYLRCMVKETLRIHPPVPFLIPRRVEQDVEVCGYTPVKNSQVFVNAWAIGRDED	397
Phtheirospermum japonicum	DTTSSTLEWAMAEALKNPETMAKAKAELEEVIGKGVLEADISRLPYLRCEVKETLRIHPPVPFLIPRRVEQDVEVCGYTPVKNSQVFVNAWAIGRDED	383
Handroanthus impetiginosus	DTTSSTLEWAMAEALKNPETMKKAKAELEEVIGKGVLEADISRLPYLRCEVKETLRIHPPVPFLIPRRVEQDVEVCGYTPVKNSQVFVNAWAIGRDED	400
Sesamum indicum	DTTSSTLEWAMAEALKNPETVKKAKAELEEVIGKGVLEADISRLPYLRCMVKETLRIHPPVPFLIPRRVEQDVEVCGYTPVKNSQVFVNAWAIGRDED	400
Scoparia dulcis	DTTSSTLEWAMAEALKNPETMKKAKAELEEVIGKGVLEADISRLPYLRCEVKETLRIHPPVPFLIPRRVEQDVEVCGYTPVKNSQVFVNAWAIGRDED	400
Striga asiatica	DTTSSTLEWAMAEALKNPETMKKAKAELEEVIGKGVLEADISRLPYLRCEVKETLRIHPPVPFLIPRRVEQDVEVCGYTPVKNSQVFVNAWAIGRDED	398
Consensus	dttsstlewamaealk p a ele v gkgk e di rlpylrc vketlrihppvpfliplrve d vcgypvknsqvfvnawagrde d	
R. glutinosa	IMKNPLEKFPBRFLESEVDMRGRDFELIPFGAGRRICPGLPLAVRMVPVMLGSLLSNFDWKLEGGIGPKLDMEEKFGITLQKAQPIRAVPIPL..	491
Phtheirospermum japonicum	VMQNPLEKFPBRFMESEVDMRGRDFELIPFGAGRRICPGLPLAVRMVPVMLGSLLSNFDWKLEGGIEPKELDMEEKFGITLQKAQPIRAVPIPLGN	479
Handroanthus impetiginosus	IMKNPLEKFPBRFLESEVDMRGRDFELIPFGAGRRICPGLPLAVRMVPVMLGSLLSNFDWKLEGGIGPKELDMEEKFGITLQKAQPIRAVPIPL..	494
Sesamum indicum	VMKDPLEKFPBRFLESELDMRGRDFELIPFGAGRRICPGLPLAVRMVPVMLGSLLSNFDWKLENGIGPKELDMEEKFGITLQKAQPIRAVPIPL..	494
Scoparia dulcis	TMSNPLEKFPBRFLDSEVDMRGRDFELIPFGAGRRICPGLPLAVRMVPVMLGSLLSNFDWKLDGMSKELDMEEKFGITLQKANPIRAVPIPL..	494
Striga asiatica	VMADPLEKFPBRFLESELDMRGRDFELIPFGAGRRICPGLPLAVRMVPVMLGSLLSNFDWKLP...EGELDMAEKFGITLQKAQPIRAVPIPL..	489
Consensus	w plef p rf se dmrgdrfelipfgagrricpglplavrmvpvmlgsllnsfdwkl ldm ekfgitlqka pl avp	

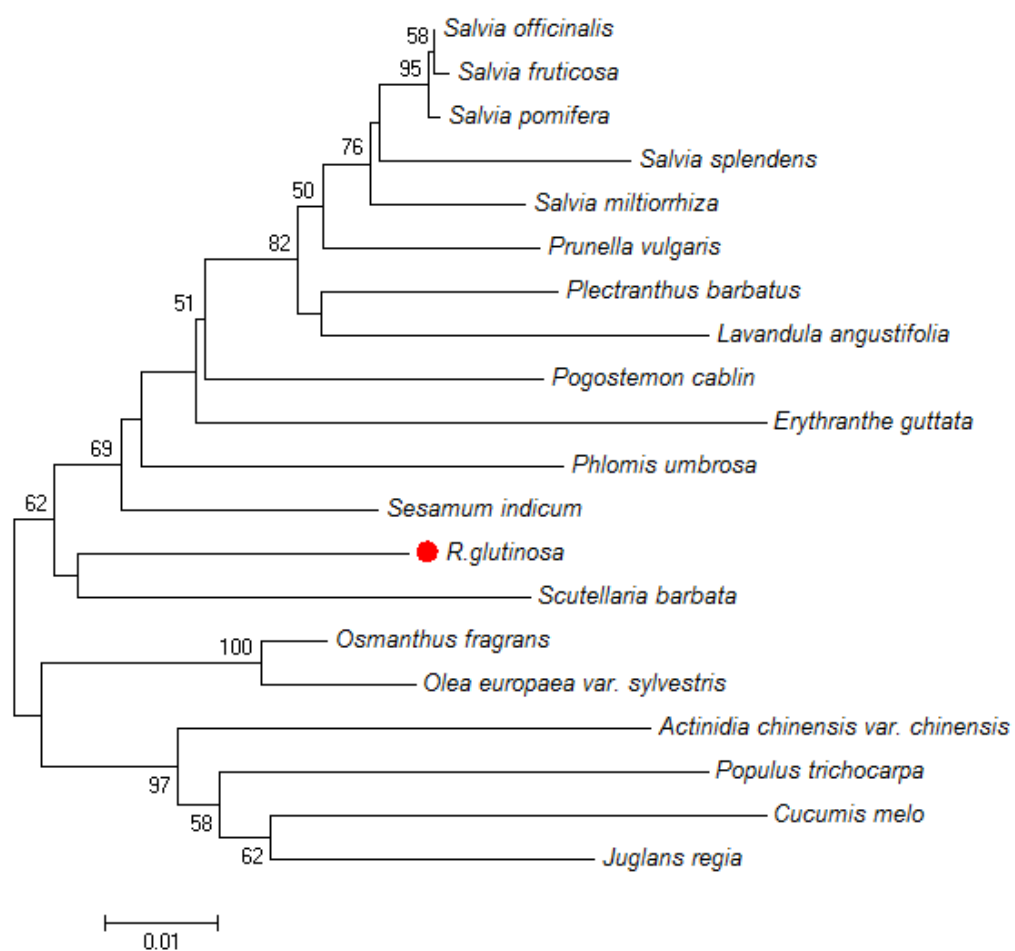
(d) *G10H*

R._glutinosa	MMSVRGLTRISRSGYARRRWVYSLG..SNNSLPILLEQPTHFRSPVQSSQEVLCGRVIYSWVSSALSSVGQQAHSQSSTAVEEQLDPFSLVADEEFLVAD	98
Sesamum_indicum	MMSVRGLTRVSRACARCRWVYSSLG..TYADPPLLQNSSHFRSPVQASQEVLCGRVIYSWVSSALSSVGQQAHIQSSSAVEEQLDPFSLVADELSILAN	98
Handroanthus_impetiginosus	MLSVRGLARLSRSAYTRGRWVYSSLG..SGNSSPILLEQSTHSCSPVQSSQEVLCGRVIYSWVSSNGISSVGQQLQFHSSSAEEQLDPFSLVADELSLLAN	98
Pogostemon_cablin	MISVRGLTLLRSRGYARCRWVYSSLS..SNSSTPILLEHSTHFCSPVQSSKEVLCGRVIYSWVSSNVLNTVGQQAQFQSSSIVEEQLDPFSLVADELSLLAN	98
Dorcoceras_hygrometricum	MYPELLRGLVH.EKVLESQDMVLGCRVFIYSWVSSAIISSIGQQSQHEGTYVVEEQLDPFSLVADELSILAN	69
Centranthera_grandiflora	MFVVRRLKRLSWSGYARQWGHSSSLGGVNSSCLKFLDHCNHSRSPVQSSQEVSGCQGTIYSWVSSNAISSVGQQTQFQSSSTVEEQVDPFSLVADELSVLAN	100
Consensus	1 h v gc yswvs gqq eeq dpfslvade s a	
R._glutinosa	RLRSMVVAEVPKLASAAEYFFKLGVEGKRFRPTVLLLMATALNVSVPRQLPVAAVDT.SVELRSRQOCIETEMIHVASLLHDDVLDADTRRGIGSLN	197
Sesamum_indicum	RLRSMVVAEVPKLASAAEYFFKMGVEGKRFRPTVLLLMATALDVQMPRHADAIDTLSTELRSRQOCIETEMIHVASLLHDDVLDADTRRGIGSLN	198
Handroanthus_impetiginosus	RLRSMVVAEVPKLASAAEYFFKMGVEGKRFRPTVLLLMATALNTPIPRSTPDAIIGTISMELSRQOCIETEMIHVASLLHDDVLDADTRRGIGSLN	198
Pogostemon_cablin	RLRSMVVAEVPKLASAAEYFFKMGVEGKRFRPTVLLLMATALNVMPRPQPSVAAVDSLMELSRQOCIETEMIHVASLLHDDVLDADTRRGIGSLN	198
Dorcoceras_hygrometricum	SLRSMVVAEVPKLASAAEYFFKMGVEGKRFRPTVLLLMATALNVMPRPVPGGAGDTLSMELSRQOCIETEMIHVASLLHDDVLDADTRRGIGSLN	169
Centranthera_grandiflora	RLRTMVVAEVPKLASAAEYFFKMGVEGKRFRPTVLLLMATALNVPIPLQPEAAVDNLMELSRQOCIETEMIHVASLLHDDVLDADTRRGIGSLN	200
Consensus	lr mvva vpklasaaeyffk gvegkrfrptvlllmatal pr a s elr rq c aei emihvasllhddvlddadtrrgigsln	
R._glutinosa	FVMGNKLAVLAGDFLLSRACVALASLKNTEVVSLLAKVVEHLVTGETMQMTTSSDQRCSMEEYMQKTYKKTASLISNSCKAIALLAGQTAEVSTLAYEYG	297
Sesamum_indicum	FVMGNKLAVLAGDFLLSRACVALASLKNTEVVSLLAKVVEHLVTGETMQMTTSSDQRCNMEYMQKTYKKTASLISNSCKAIALLAGQTAEVSTLAYEYG	298
Handroanthus_impetiginosus	FVMGNKLAVLAGDFLLSRACVALASLKNTEVVSLLAKVVEHLVTGETMQMTTSSDQRCSMEEYMQKTYKKTASLISNSCKAIALLAGQTAEVSTLAYEYG	298
Pogostemon_cablin	FVMGNKLAVLAGDFLLSRACVALASLKNTEVVSLLAKVVEHLVTGETMQMTTSSGQRCSMEEYMQKTYKKTASLISNSCKAIALLAGQTAEVSTLAYEYG	298
Dorcoceras_hygrometricum	FVMGNKLAVLAGDFLLSRACVALASLKNTEVVSLLAMVVEHLVTGETMQMTTSSDQRCSMEEYMQKTYKKTASLISNSCKAIALLAGQTAEVSTLAYEYG	269
Centranthera_grandiflora	FVMGNKLAVLAGDFLLSRACVALASLKNTEVVSLLAKVVEHLVTGETMQMTTSSDQRCSMEEYMQKTYKKTASLISNSCKAIALLAGQTAEVSTLAYEYG	300
Consensus	fvmgnklavlagdfllsracvalaslkntevvs la vvehlvtgetmqmtt s qrc smeeymqkty ktaslisnscka allagqt evs layeyg	
R._glutinosa	KNLGLAFQLIDVDLDFGTGSTSLGKGSLSDIRHGIIITAPILFAMEEPELIRDVVDQGFDDNSANVDRALEYLCKSRGIQRTRELAAKHASLASAAIDSLPE	397
Sesamum_indicum	KNLGLAYQLIDVDLDFGTGSTSLGKGSLSDIRHGIIITAPILFAMEEPELIRTVVNEGFDDSSANVDRALEYLCKSRGIQRTRELAAKHASLASAAIDSLPE	398
Handroanthus_impetiginosus	KNLGLAFQLIDVDLDFGTGSTSLGKGSLSDIRHGIIITAPILFAMEEPELIRAVVDQGFDDKSENVNRALEYLAKSRGIQRTRELAAKHANLASAAIDSLPE	398
Pogostemon_cablin	KNLGLAFQLIDVDLDFGTGSTTLGKGSLSDIRHGIIITAPILFAMEEPELIRTVVDQGFDDSSNVDSALDYLAKSRGIQRTRELAAKHASLASAAIDSLPE	398
Dorcoceras_hygrometricum	KNLGLAFQLIDVDLDFGTSSSLGKGSLSDIRHGIIITAPILFAMEEPELIRAVVDQGFDDNSANVDRALEYLCKSHGIERTRELAAKHANLASVAIDSLPE	369
Centranthera_grandiflora	KNLGLAYQLIDVDLDFGTGSASLGKGSLSDIRHGIIITAPILFAMEEPELIRAVVDQGFDDNSANVDRALEYLCKSRGIQRTRELAAKHASLASAAIDSLPE	400
Consensus	knlgla qliddvldftgts lgkgslsdirhgi tapilfamee pelr v gfd s nv al yl ks gi rtrelaakha las aids pe	
R._glutinosa	NDDVDVQSRRALVELTQRVITRTK	422
Sesamum_indicum	NNDENVQSRRALVELTHRIVITRTK	423
Handroanthus_impetiginosus	NDDVDVQSRRALVELTQRVITRTK	423
Pogostemon_cablin	NDDVDVQSRRALVELTQRVITRTK	423
Dorcoceras_hygrometricum	NDDKDVQSRRALVELTHRIVITRTK	394
Centranthera_grandiflora	NDDKNVQSRRALVELTQRVITRTK	425
Consensus	n d vq srralvelt rvitrtk	

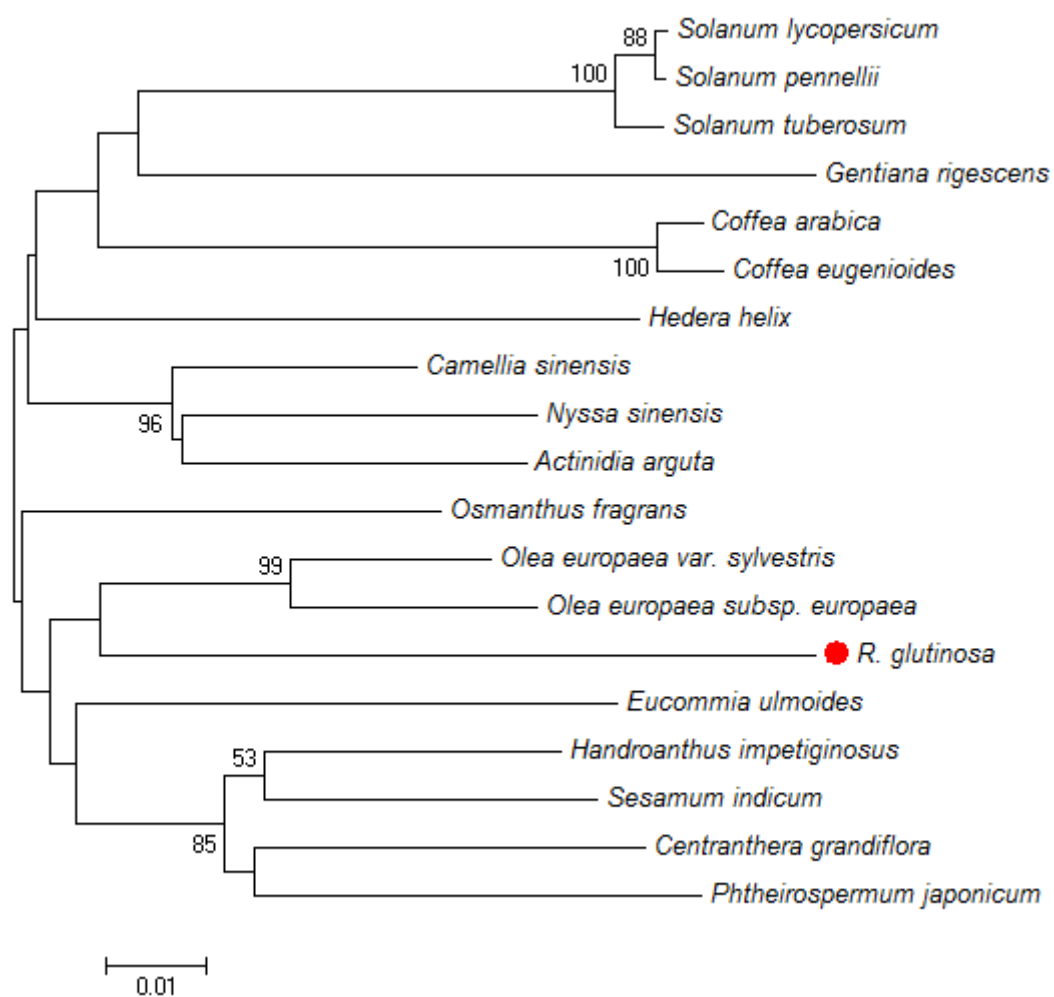
(e) GPPS

Fig.S2 Sequence alignment of DXS/DXR/10HGO/G10H/GPPS synthase in *R. glutinosa*,

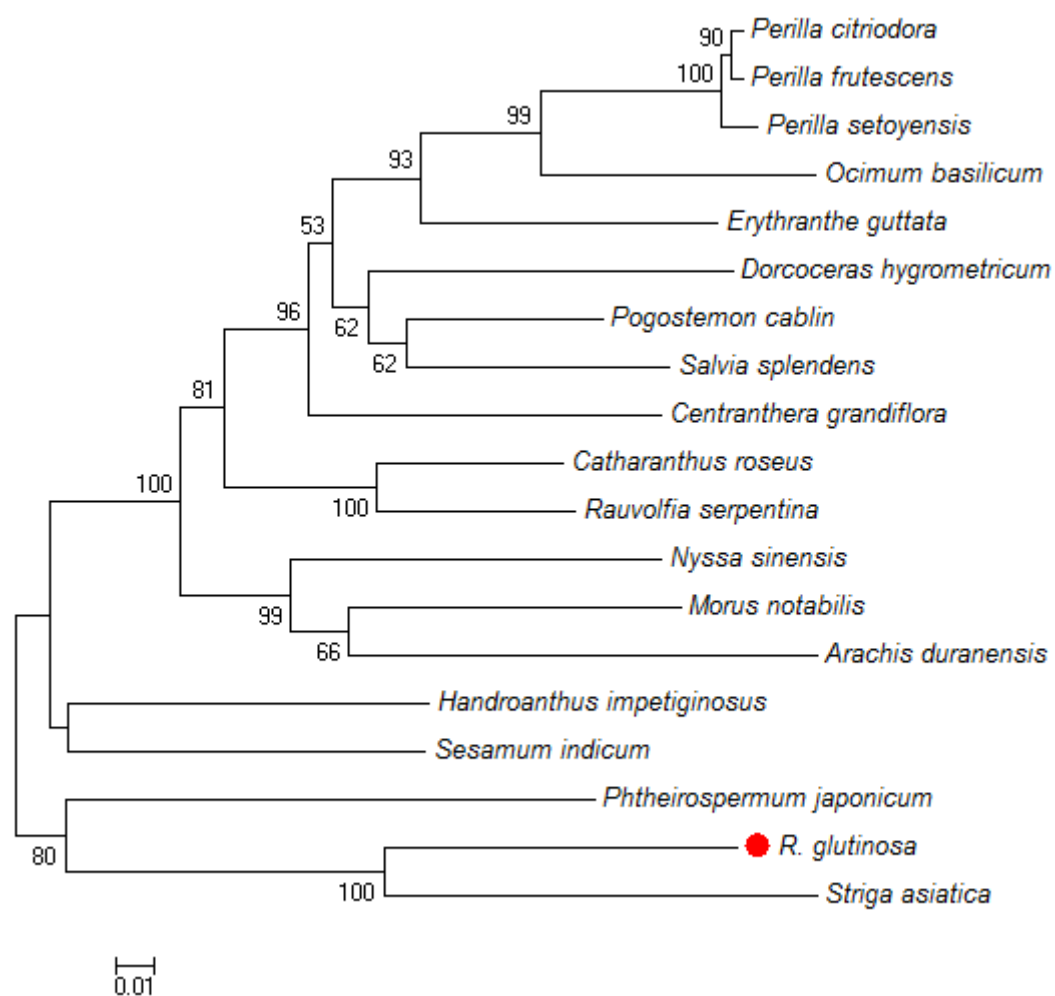
(a) DXS, (b) DXR, (c) 10HGO, (d) G10H and (e) GPPS



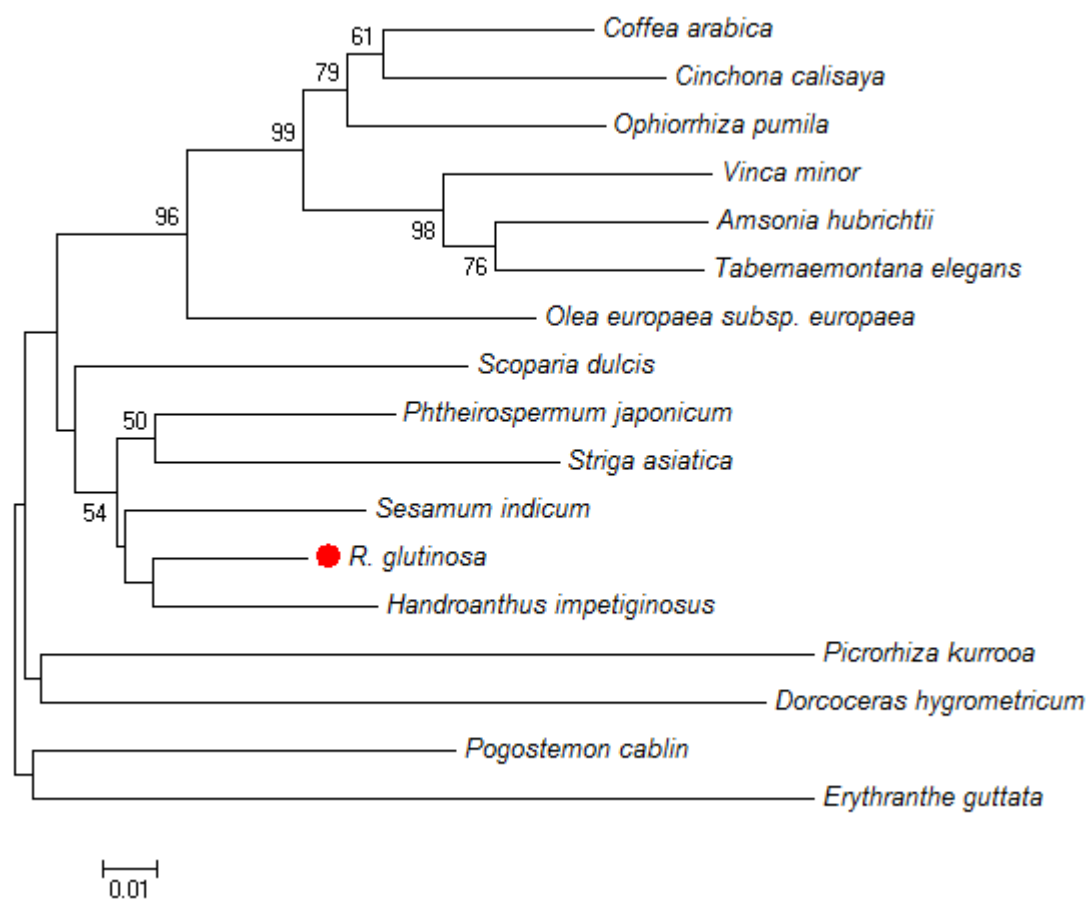
(a) DXS



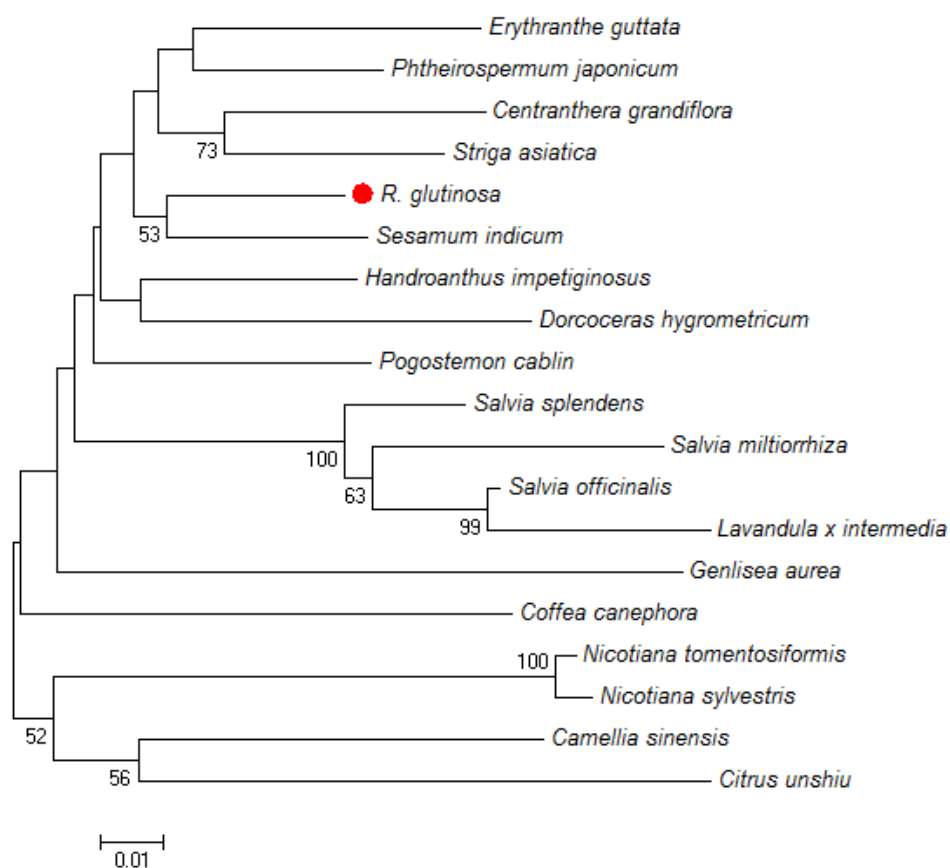
(b) DXR



(c) 10HGO



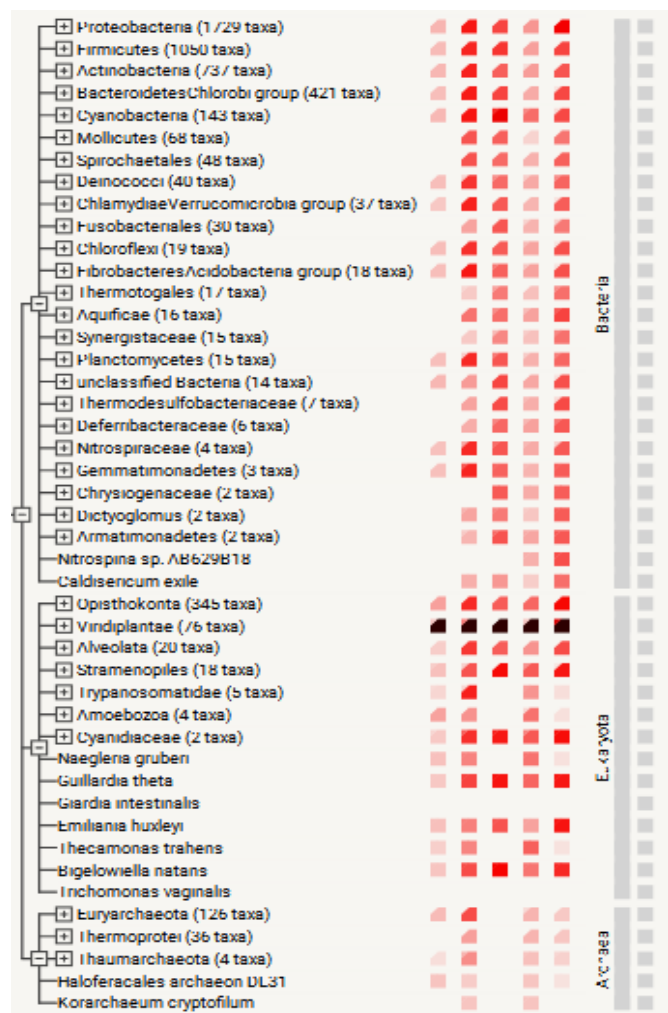
(d) G10H



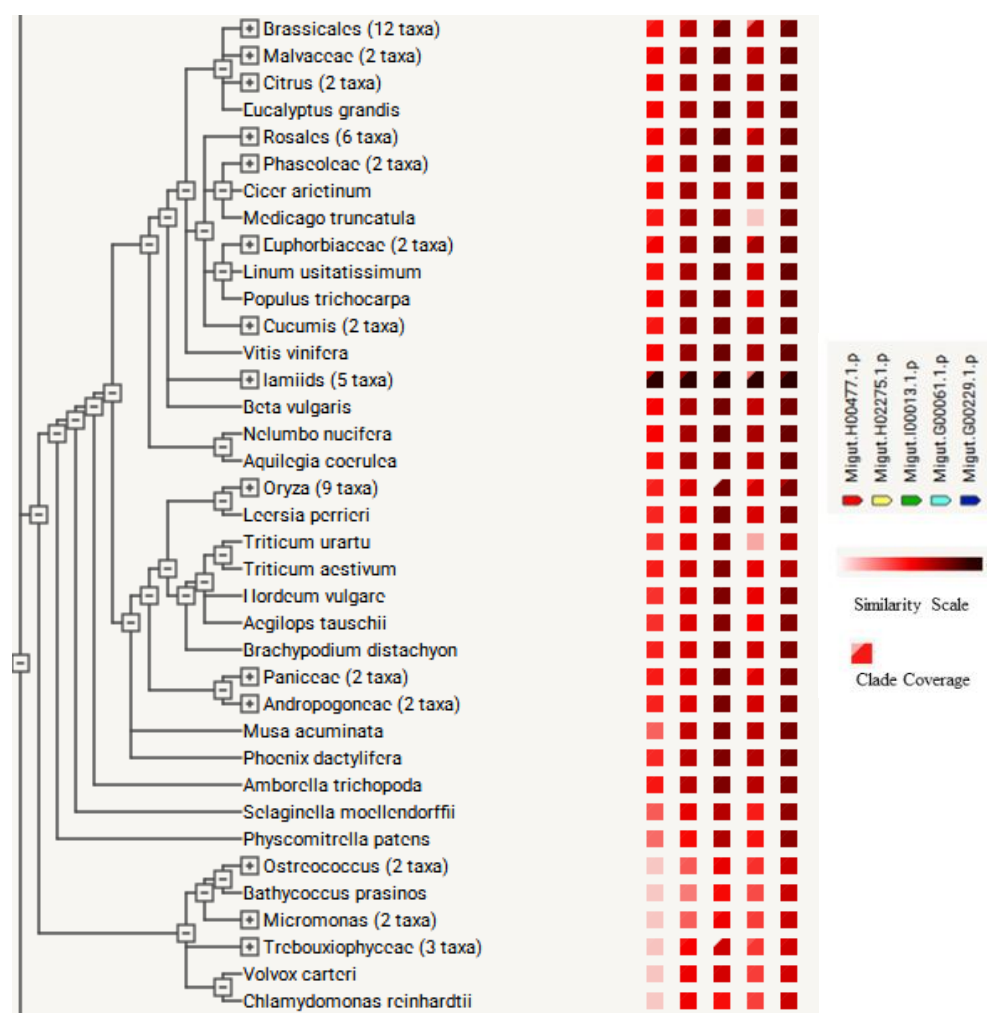
(e) GPPS

Fig.S3 Phylogenetic analysis of DXS/DXR/10HGO/G10H/GPPS synthase in *R. glutinosa*.

(a) DXS, (b) DXR, (c) 10HGO, (d) G10H and (e) GPPS



(a)



(b)

Fig. S4 The co-occurrence on DXS/DXR/10HGO/G10H/GPPS synthase family of *R. glutinosa*

(a) Gene co-occurrence of DXS/DXR/10HGO/G10H/GPPS synthase in the organism, (b) the co-occurrence of DXS/DXR/10HGO/G10H/GPPS synthase in plants. Similarity Scale: the color denotes, for each gene of DXS/DXR/10HGO/G10H/GPPS synthase, the similarity of its best hit in a given STRING genome. Clade Coverage: for groups of genomes that are collapsed in the phylogenetic tree, two distinct colors indicate the lowest and highest similarity observed within that clade.

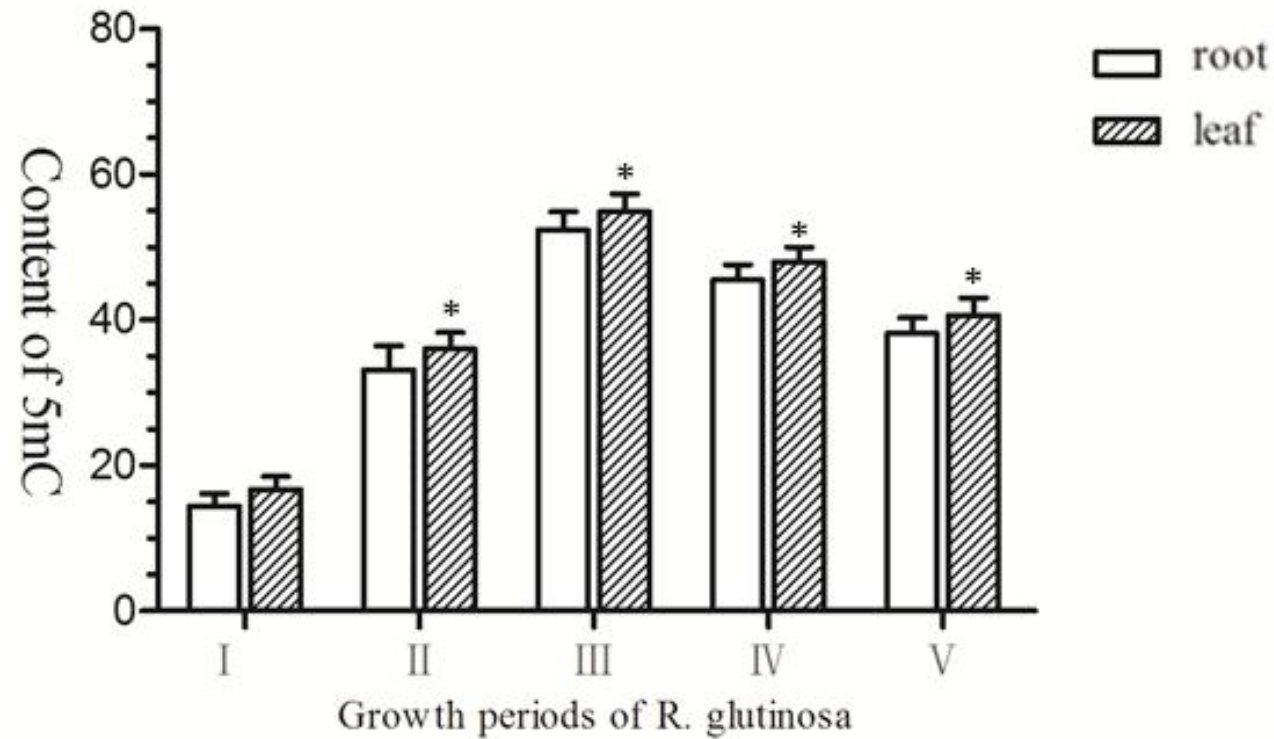


Fig. S5 5mC content of *R. glutinosa*

statistical significance was determined by a two-sided t-test: * $P < 0.05$.

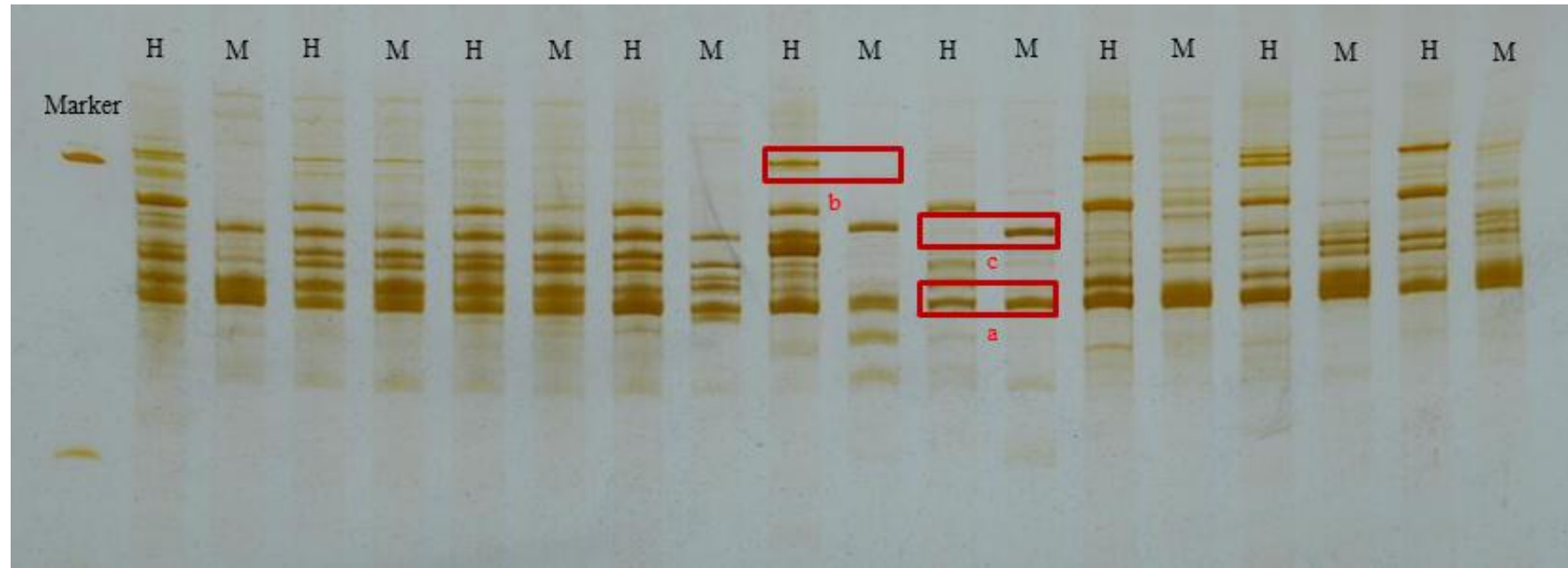


Fig.S6 Methylation banding pattern

a: Both H and M have bands and no methylation occurs; b: *HpaII* has bands and *MspI* no bands, external methylation of single-stranded DNA; III: *HpaII* no bands and *MspI* has bands, internal methylation of double-stranded DNA.

