

Supplementary Information

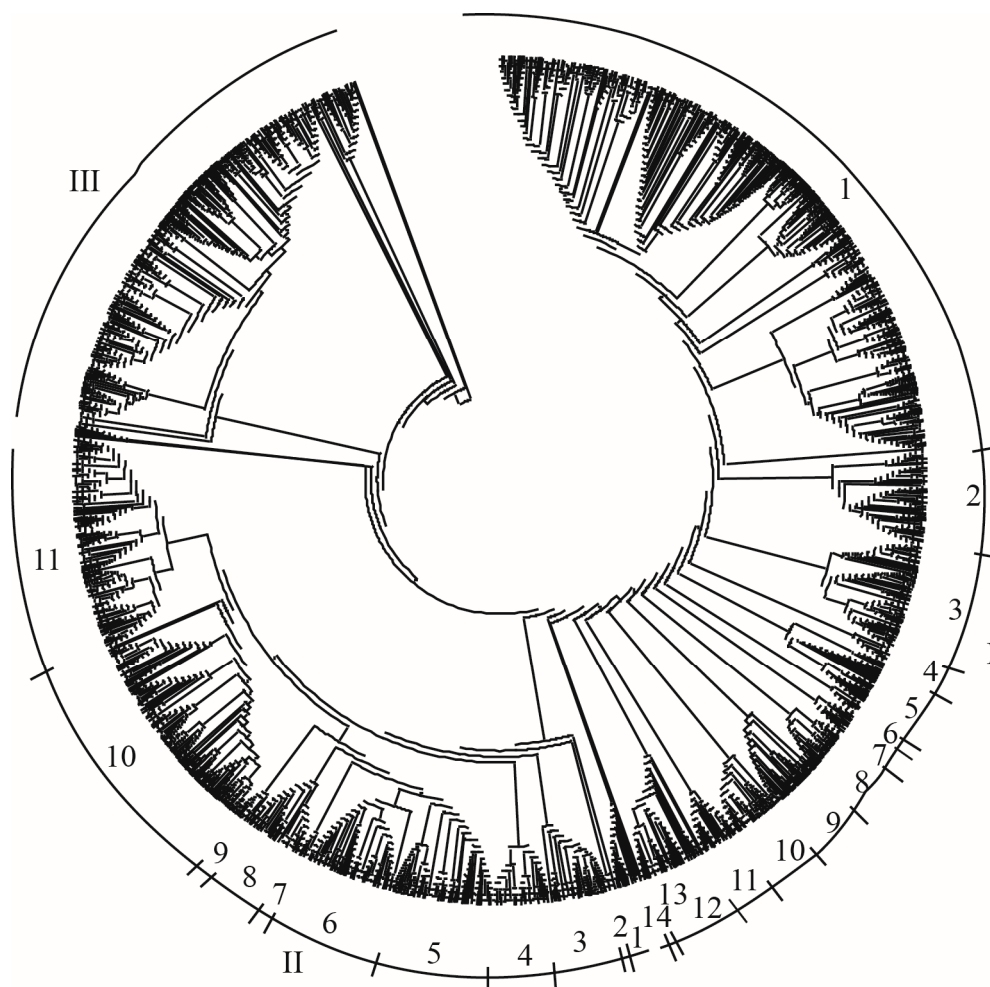


Figure S1. Phylogeny tree of *S*-adenosyl-L-methionine-dependent methyltransferases (SCOP53335). A neighbor-joining tree containing 2,354 sequences was generated based on the *S*-adenosyl-L-methionine-dependent methyltransferases domain sequences by Mega 5.02. A bootstrap value of 1000 replications was applied and all of sequences were classified into three clusters, 14 subgroups in the first cluster and 11 subgroups in the second cluster.

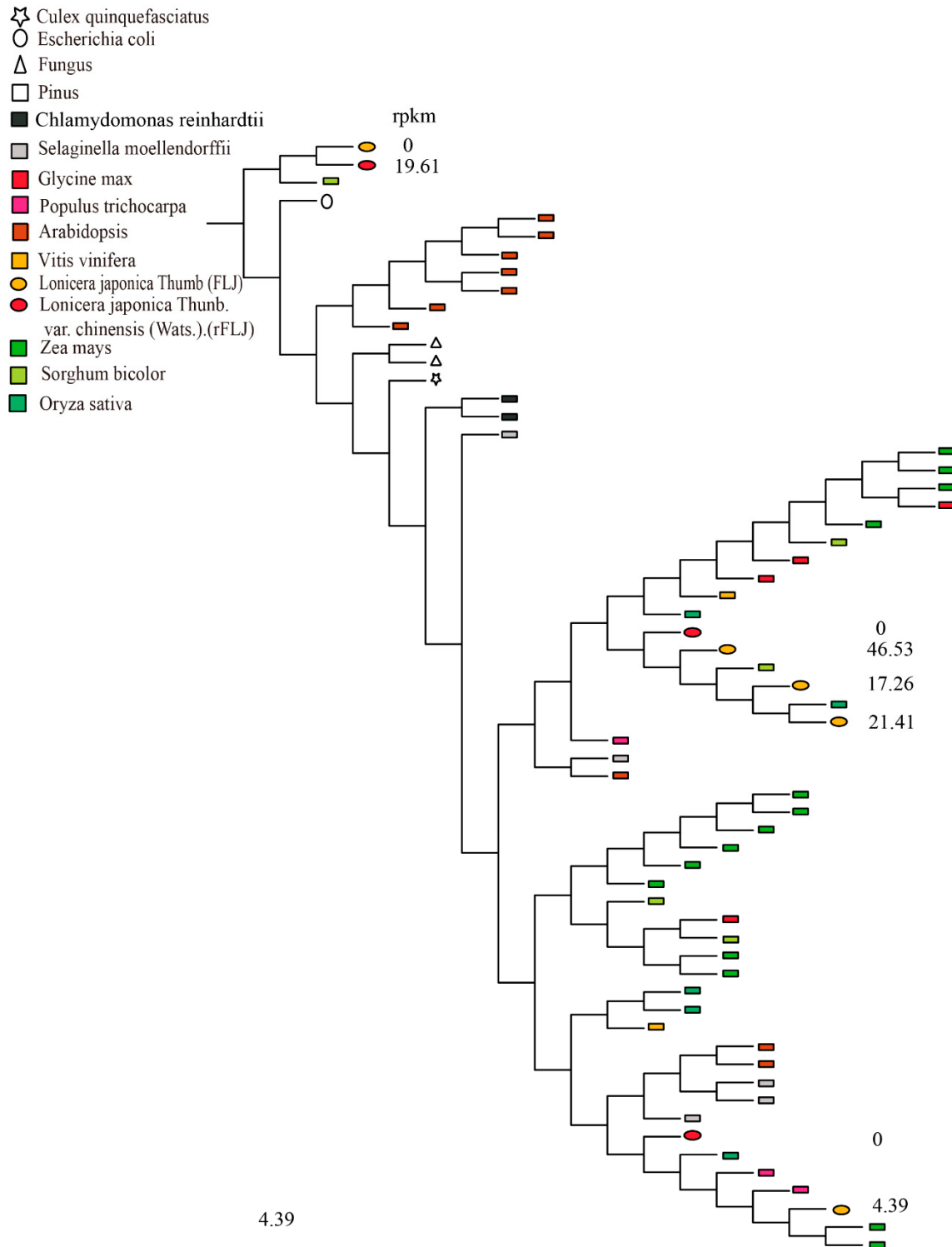


Figure S2. Phylogeny and expression of *S*-adenosyl-L-methionine-dependent methyltransferases sequences in subgroups 12 in the first cluster. A neighbor-joining tree containing 62 sequences was generated based on the *S*-adenosyl-L-methionine-dependent methyltransferases domain sequences. A bootstrap value of 1000 replications was applied. The rpk value of sequences in flowers of *Lonicera japonica* is shown.

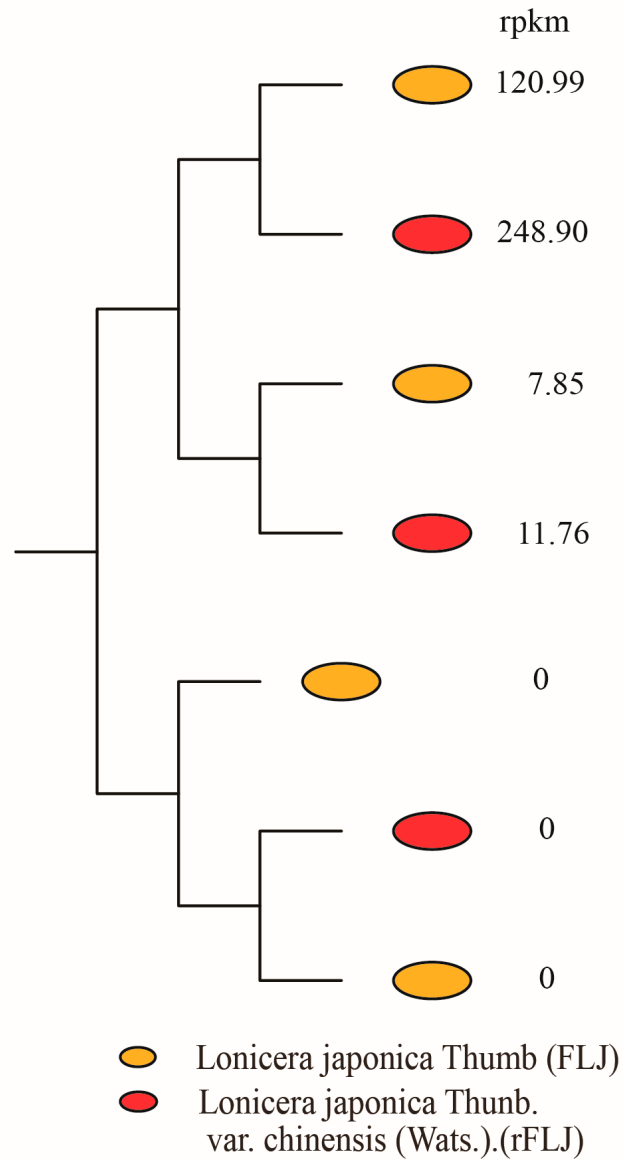


Figure S3. Phylogeny and expression of *S*-adenosyl-L-methionine-dependent methyltransferases sequences in subgroups 2 in the second cluster. A neighbor-joining tree containing 7 sequences was generated based on the *S*-adenosyl-L-methionine-dependent methyltransferases domain sequences. A bootstrap value of 1000 replications was applied. The rpk value of sequences in flowers of *Lonicera japonica* is shown.

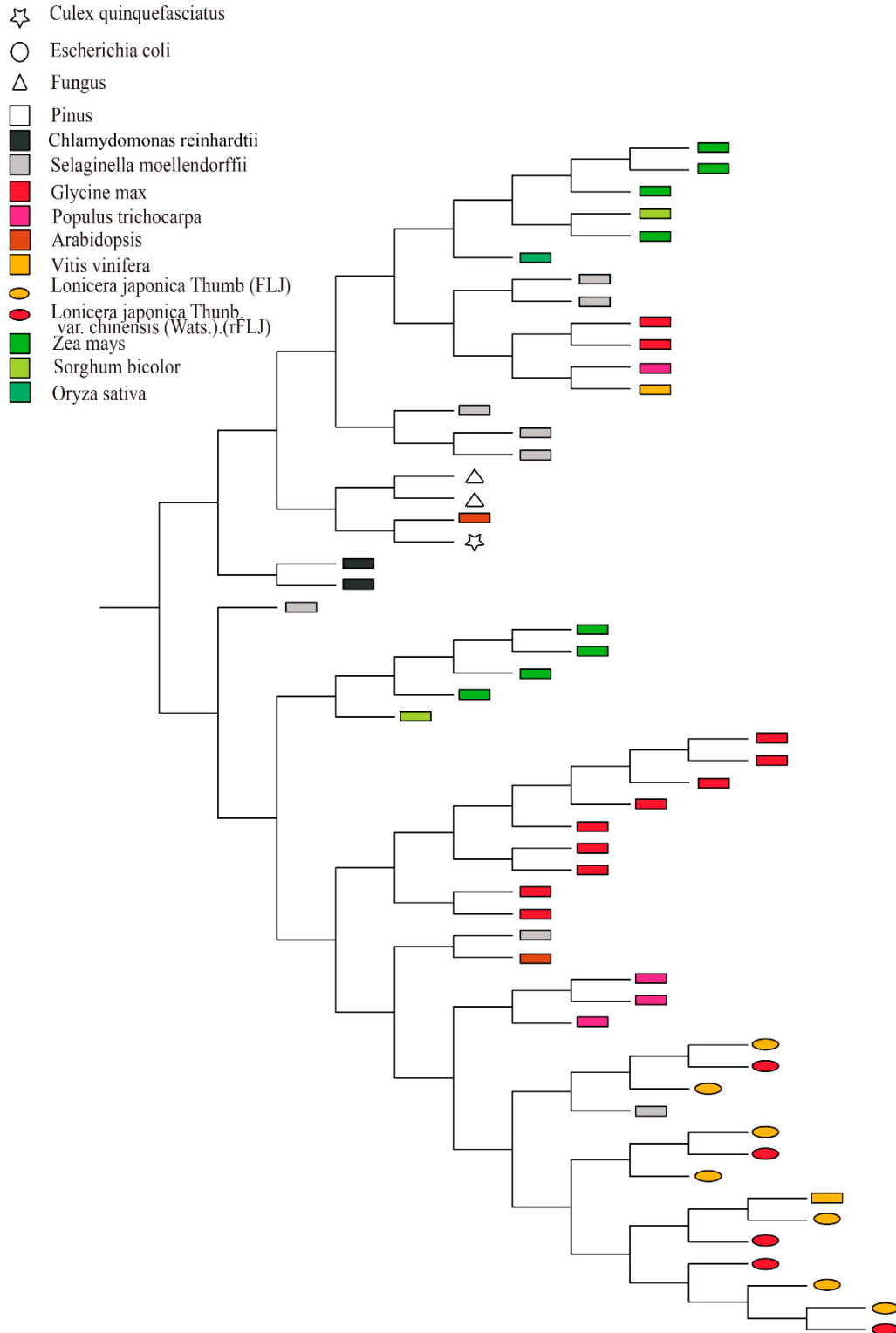


Figure S4. Phylogeny and expression of *S*-adenosyl-L-methionine-dependent methyltransferases sequences in subgroups 8 in the second cluster. A neighbor-joining tree containing 55 sequences was generated based on the *S*-adenosyl-L-methionine-dependent methyltransferases domain sequences. A bootstrap value of 1000 replications was applied.

Table S1. Sequences from twenty-one species in this study.

Species	Genome Database
<i>Arabidopsis lyrata</i>	http://www.phytozome.net/
<i>Arabidopsis thaliana</i>	http://www.phytozome.net/
<i>Aspergillus nidulans</i> FGSC A4	www.broad.mit.edu/annotation/fgi
<i>Chlamydomonas reinhardtii</i>	http://www.ncbi.nlm.nih.gov/
<i>Culex quinquefasciatus</i>	www.vectorbase.org/Culex_quinquefasciatus/Info/Index
<i>Escherichia coli</i> str. K-12 substr. W3110	www.broad.mit.edu
<i>Glycine max</i>	http://www.phytozome.net/
<i>Larixgmelinii</i>	http://dendrome.ucdavis.edu/
<i>Lonicera japonica</i>	Database in our group
<i>Lonicera japonica</i> var. <i>chinensis</i>	Database in our group
<i>Oryza sativa</i>	http://www.phytozome.net/
<i>Penicillium marneffei</i> ATCC 18224	http://fungalgenomes.org/data/PEP/
<i>Pinus pinaster</i>	http://dendrome.ucdavis.edu/
<i>Pinus taeda</i>	http://dendrome.ucdavis.edu/
<i>Populus trichocarpa</i>	http://www.phytozome.net/
<i>Pseudotsugamenziesii</i>	http://dendrome.ucdavis.edu/
<i>Selaginella moellendorffii</i>	http://www.phytozome.net/
<i>Sorghum bicolor</i>	http://www.phytozome.net/
<i>Vitis vinifera</i>	http://www.phytozome.net/
<i>Volvox carterii</i>	http://www.ncbi.nlm.nih.gov/
<i>Zea mays</i>	http://www.phytozome.net/

Table S2. Gene copies and total rpkm of *Lonicera japonica* SAME in subgroups.

Subgroups *	Copies		Total Gene Express rpkm	
	FLJ	rFLJ	FLJ	rFLJ
I-1	30	27	697.68	433.51
I-12	5	3	89.58	19.61
II-2	4	3	128.84	260.66
II-8	7	5	873.05	822.06
II-11	20	17	855.36	112.27

Abbreviations: FLJ, *Lonicera japonica*; rFLJ, *Lonicera japonica* var. *chinensis* (Watts.); * Subgroups were showed in Figure S1; I-1, subgroups 1 in the first cluster; I-12, subgroups 12 in the first cluster; II-2, subgroups 2 in the second cluster; II-8, subgroups 8 in the second cluster; II-11, subgroups 11 in the second cluster.

Table S3. Gene expression of *SAMe* in buds of *L. japonica* and *L. japonica* var. *chinesis*.

Gene	qRT-PCR	FLJ Rpkm	rFLJ Rpkm
<i>SAMT12</i>	5.93	141.97	0
<i>SAMT17</i>	0.54	0	19.61
<i>SAMT21</i>	8.84	2.89	0
<i>SAMT23</i>	5.72	24.57	0
<i>SAMT24</i>	3.35	116.92	23.08
<i>SAMT33</i>	18.25	5.59	0
<i>SAMT36</i>	13.77	77.75	0
<i>SAMT41</i>	1.11	4.39	0
<i>SAMT42</i>	0.64	0	62.14
<i>SAMT51</i>	1.74	68.79	0
<i>SAMT59</i>	0.19	120.99	248.90
<i>SAMT77</i>	3.89	118.24	0
<i>SAMT81</i>	2.83	2.69	0
<i>SAMT84</i>	3.47	202.73	0
<i>SAMT85</i>	0.88	0	110.58
<i>SAMT87</i>	1.84	2.38	0
<i>SAMT88</i>	0.46	1.50	22.64
<i>SAMT103</i>	7.82	31.61	0
<i>SAMT123</i>	1.25	43.84	0

Abbreviations: FLJ, *Lonicera japonica*; rFLJ, *Lonicera japonica* var. *chinensis* (Watts.); qRT-PCR, the relative abundance of genes was determined using the comparative Ct method as suggested in ABI 7500 Software v2.0.1 (ABI).

Table S4. Primers of *SAMe* in buds of *L. japonica* and *L. japonica* var. *chinesis*.

Gene	Primers
<i>SAMT12</i>	5'-TGGCTGAGGGATTTCTGGG-3' 5'-TGATGGAAGGCTAGGGTGGC-3'
<i>SAMT17</i>	5'-TGGGGATTAGCATTCCTTTTGT-3' 5'-AATGGCATCAGCATAACAGTCAGA-3'
<i>SAMT21</i>	5'-CTCGGCATCCAGCAAAGTA-3' 5'-TGGTCACGCTCAAATGGTTCA-3'
<i>SAMT23</i>	5'-AGATTTGGGAAGGTGTTGGTG-3' 5'-AGGATGACATAAGAGGGCAGGA-3'
<i>SAMT24</i>	5'-CCTTTTTCCTTCCACTTGCG-3' 5'-GAGCGGGATTACTGCCTATGT-3'
<i>SAMT33</i>	5'-GATGAGCTTCAGGAGCATG-3' 5'-CGAGGTGACCGCAAAACA-3'
<i>SAMT36</i>	5'-TTTGGGACATTATGCGTTGC-3' 5'-CCTTCTTTGCCTGTGCCTTG-3'
<i>SAMT41</i>	5'-CGGAAGCGGGAATGGA-3' 5'-ACTGGAACTATGGAACGGAAT-3'
<i>SAMT42</i>	5'-AATGCGAGGCCAGTTCAA-3' 5'-GCTTCTCCGCCACTACCAC-3'
<i>SAMT51</i>	5'-CTTGTTGGTGCTGCTTTAGTTG-3' 5'-CCTCTGGTAAATCGCCTGAAC-3'
<i>SAMT59</i>	5'-CGCTGGAAGCCCTGAGTATTG-3' 5'-TGCCCGATGTGGCGTTGA-3'
<i>SAMT77</i>	5'-CGAGGGTAAGTGCTGAACG-3' 5'-CAATCATTTACGAACGAGGTCTA-3'
<i>SAMT81</i>	5'-AGCCATATTGTCCTTGTCTGC-3' 5'-ACTCACCACCACGCTCTCC-3'
<i>SAMT84</i>	5'-TTTCTGTTCCCTCGGTTCCC-3' 5'-TATTCTTGCTCCTTACTCCTATCTC-3'
<i>SAMT85</i>	5'-TTCCGCTAACGCTTCTGC-3' 5'-CCTCACCTCCATCCCAATC-3'
<i>SAMT87</i>	5'-TGTGGTGCTTTGCCTTCATC-3' 5'-CGTGGCTACTTTGCTCGTTG-3'
<i>SAMT88</i>	5'-GCTCCATCATTAACCTTTATGTCTAT-3' 5'-TCTTCTACCCTCATTCTCCCT-3'
<i>SAMT103</i>	5'-ATCAGATAGGCATAGACCAAGG-3' 5'-TGTCAGGAGGCACAGAGTTTC-3'
<i>SAMT123</i>	5'-TGCGTATTCATCCGAGTTCA-3' 5'-TCGTCCGCCTCTACACCA-3'
<i>18S</i>	5'-TGGTGGTCGTAACATTCC-3' 5'-TGGTGATTTTGCCTGCT-3'

Table S5. Gene expression of *SAMe* in buds of *L. japonica* and *L. japonica* var. *chinesis*.

Subgroups *	Gene	BLASTP	Orthologs Interpro	Orthologs Pfam	GO Term Prediction
I-2	<i>FLJSAMT59</i> <i>rFLJSAM40</i>	Putative methyltransferase	IPR004159	PF03141	GO:0008168
II-8	<i>FLJSAMT53</i> <i>rFLJSAMT30</i>	Putative methyltransferase	IPR004159	PF03141	GO:0008168
II-11	<i>FLJSAMT51</i> <i>rFLJSAMT28</i>	Putative methyltransferase	IPR004159	PF03141	GO:0008168
	<i>FLJSAMT73</i> <i>rFLJSAMT87</i>	Putative methyltransferase	IPR004159	PF03141	GO:0008168
	<i>FLJSAMT77</i> <i>rFLJSAMT97</i>	Putative methyltransferase	IPR004159	PF03141	GO:0008168
I-1	<i>FLJSAMT12</i> <i>rFLJSAMT2</i>	Putative protein-L-isoaspartate O-methyltransferase	IPR000682	PF01135	GO:0006464 GO:0004719
	<i>FLJSAMT36</i>	probable			GO:0008033
	<i>rFLJSAMT45</i>	N(2),N(2)-dimethylguanosine tRNA methyltransferase	IPR002905	PF02005	GO:0003723 GO:0004809
	<i>FLJSAMT37</i> <i>rFLJSAMT24</i>	phosphoethanolamine n-methyltransferase, putative	IPR003333	PF02353	GO:0008610

* Subgroups were showed in Figure S1; II-2, subgroups 2 in the second cluster; II-8, subgroups 8 in the second cluster; II-11, subgroups 11 in the second cluster; I-1, subgroups 1 in the first cluster.

Sequences data

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>FLJSAMT53

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>FLJSAMT73

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>FLJSAMT77

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>FLJSAMT12

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>FLJSAMT36

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>FLJSAMT37

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