

Supplements:

Table S1. Characterization of the satDNAs revealed in repeatomes of *S. officinalis* and *S. sclarea*

Tandem Repeat/ Genome Proportion, %	Repeat Length, bp	Sequence
<i>Salvia officinalis</i>		
SO3/ 1.3	687	<p>GAAATCCAACCTTTAGACCGCAGCGCTCGACCCACCATGTGCCAGGCTATTTTGGCCACATCTCATTCCCCGGGGTAGGATCCGGTGGATCTTTACGTCGTCGGGGCTCATATACGAGGGGGAAGCTATCACGGAGTTCTACCCCGTTCTGAGCCGGCCGAAAAATAAGGATACCTTACGTGAGCTTGAATAGGCTATATTAAGCCATATTTCTATCGATACGAAAAATATCGACCGAGCCGAATGTCAAATCAAACCATCCCAAGTCCTTGGTCTATAAAAAAGGATCCTAACGCCGTGTTAATCACTCCAAAAGACCGGATAAAGAAGGAGATATGGCCAAAACGGTGTTCGCGTTGAACGCAACCGTAGCACA CTCCAATTTTTTGGCCATATCTCATTGTTTCTAGTCTGCTCACAACGGTCTTTATACCGTTGGA AAGCCACTTCAGAGGGGTACAATTTTTCTGAGTTAGTTTCTCAAATCGAGCACTAAAAATGGTC CCGAAATCCAACCTTTTCCGACCACAGCGCACGATGCAACGTGTACCTGGCTGATTTCTTGGCC ATATGTAATTCGTGAGTGTCTTCTCCAGCGGTCTTTTACCCTGGAAAGCTTACTCACAGGG TTATGACTCTAGTACAGACAACCTTCGAATTGGGCCCTTTTCGAGCTTG</p> <p>CAAAAACTTCTCGGCTTTGGAAGGTGGGAAGTATTTCTCCAAGAACAATCGGCACATATCCTTC CAAGTGGTGACCTTCTCTCGATCAAGCTCCTTGTACCATTTCTAGCTTCTACACAACATCAACC TATGTGCTTGATGGTTAGGAATCCATAAATTACCTCCAACACCTCTATCATCCGTTTAAACA AGAAAAAGGCGGGCTAAGGCTCAAAGAGGCTAAATCAAAGGATAGTGGGTATGTGGGGTTAG TGTATAGGATATGTCCATGGTTGGTGAAAGTGGCGGTGACAAAGGATGGCCTAAGATCACTT CCTAGTTCAAACACACACATGTGGTCTCGACGGAGAACCAAGGCAAGTTCTAGAATCCATATG CATGTATGATATCCCTCAAGCAAGAAAAATAGGCATAAAAATGCACAAAGGCTCAAATCTCAC GGGATAATCAAATAGTTCTCAAAATCAAAGGCAACTAATCCAAATTCATCATGCAATGCGTCA CTTCCGCAAGGTTCCAATCATAATAAGCCAAAAATGCTATGAAATCTTATCAATCGCCGGCGCC AAAATTTGATAGCACTTTTTCTAACACAAAAATATGCAAGAAAAATAGGGCAAGTATTATATATC GTATCCACAGAGACTGAATATCGAAATTACAGCAAGTAATCCTAGTTGAGACTTCACCTCTCTC CCCCCAAACTTATTCCACACAATACAAGGGGAATAAGGTTGGAAAAAGAAAAAGTGGCTATCT TAAGCAACTTAATAAAAGAGAGAGAAAAATAGATATAAAAAATCAAAGATTAAGGTTGACCC TAGGCAAGTGCTACTTTTAACCAAAATTCACACAATTAACCTATTAATCTATTTACCAATTTAAT CCAAATTCATATGAAGGATCACACATGCAACCATAAAATTCGCTAGGATAGATTATGATAGT AGGCTAGTCTAAACCTATCTCCGCTAGGTCTCAAGGGAAGTAAACTAGTTACCAAAAAGCTCC GACGTATTTAAATCCCTATGAACAAGTTTTCCTCGGGTAGGATAAACAAGTATCATATCATGCT TCAATCATTCAATTATGCAGCATTGTAAATAGACATAAACTACACAACCTAGGCATGCAAGACT AGTGATCAATTAATCATGCATGAGAATAAGCTCATTGAAACATAGAATCCAAATTGGAAAGCA TGACGAAGTCAAAAGGAATAATCCATACAAAGCTCAACTAGTTCAACCAACCTAGGATCAT GAGAAGTTTAGCTACTCATGATGAGGAGAAAGACATAAAGTAAATAATACTCCCCTGTATTGA GCTAATGGTAGAACTTGCATAAACTTGAAGTAAGCCAAGATCACACAACACCTTGGAGAAGG TTTGAATCTAAAACTCCAAAGAAAACTCCCCGGATCCTTTTGCTTTGATGGGAGCTTGTTTT GAAGTATGACACTACACTCCTCGGTGAGGTGATCGTCTCAAACCTTGCCCAATGCCACCGCATC CTTGAGGAACCTTCACATACCCCGGCCATGAGGGATGACGAGAAGAGGGGGTTTGAGGCCTATT TATAGAGAGATGTCCAAGAACTTCTGCAACTTCTCGTCGTAATTCGCTTGGCTAGGCATTGAG GAAACGGAGCTCTGGGAGGAAAGTCTTGGGCTCAAAGTAGGTCTCGCCGCCAAGCCTCTCGGT CTGGGTCTCGGTGAGACCTGGACCGAGAGGGCACTGGCGGAGTTTTCGTTTTGGCTCGTTCTC CCTCGTCCGGAATCCAAATCACGAACGGTTTTCGCTACGGACTCCTATCGAGATGGACTTCAA TCCTATGCATTCCAAACTCCTCAAATGATCCATCATGTTTCTGTAATTTTCTAAACTTTGAGGC TTGAATCCATTGGTGTAGTTTCTTGGTCTCTTCGAGTCTTCTTCAACACTTGGGTGTCTTTTC ATCTAAAAACCTACAAAACATACCAAAACAACCAAAAGCATAACAAAGCTCGACAAATGATA AAACATATCCTAAACGAGCTAAAAGACCTTGAAAACCAACAAAACCTAAATAGGTAATAAATA GGGCTCTATCAACTCCCCAACTTAACCATTTGCTCGTCCGAGCAACAAAGAAAAACAAAAC AAA</p>
SO4/ 1.2	2884	<p>CGCGGGCAATGCCGCTCGCACACCTTGTCCCTCCCGGTTTTCTGTGTCCAAGCGTACCCAATGCT CGGGTGTGCTAGCTTGTGTTTTGCTTCCGGAGATGCTACGCATACCGGTGGCGGAGCGCGGGC TTGTGCTCCCGGCATTGTGTGCGTGGCGATGCGTGGTGTGT</p> <p>CGGCACCAGCACGGGCGCCGCTCGACGGGACACGGCACAGCACGGGCGGCCGCTCGACGGG GCACGAGTCTCGCGCACGGGCGCGCGCATCGTCGGGGGTGCCCCGCGCAGGGGCGCCCGCT CGACGTGACT</p>
SO44/0.37	170	<p>GCGCGGGCAATGCCGCTCGCACACCTTGTCCCTCCCGGTTTTCTGTGTCCAAGCGTACCCAATGCT CGGGTGTGCTAGCTTGTGTTTTGCTTCCGGAGATGCTACGCATACCGGTGGCGGAGCGCGGGC TTGTGCTCCCGGCATTGTGTGCGTGGCGATGCGTGGTGTGT</p>
SO46/ 0.36	135	<p>CGGCACCAGCACGGGCGCCGCTCGACGGGACACGGCACAGCACGGGCGGCCGCTCGACGGG GCACGAGTCTCGCGCACGGGCGCGCGCATCGTCGGGGGTGCCCCGCGCAGGGGCGCCCGCT CGACGTGACT</p>
SO48/ 0.34	9722	<p>CACACTAGATCACAAAGCGGATAAGCATCACACACAACAAGATGTATATCATATAAGATCATAG AGATAGGAAAAGATTGATGATAAATCAATAAAGTCTCTGAAAGATAGACATGCAGAAAG</p>

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SO107/ 0.058	362	TTGGAGGATCCGCCAAAAATACGGAAAAATTTGACCGAGCCAAATGTCGAATCCGACCTCCC AGACCTTAGGGCTATGCATAAGGATCACGAGGATGCGTTATGGGCCCCGAGACGGCTACGAA GAAGGAGATATGGCCAAAAACAGTGTCTGGCAAAGGCCAATCGGAGCGACGCCGGCGTTTATG CCATATCTCAATCGTTTGTGGTCTGTGCGAGCGGTCTATATACCGTTGGAAAGCCAATTCAGA GAGCTACGACTTTGCTGGATGGTATTGGCAAACGGGATCTGCATCGGCCCAAAAATCGAC TTGAAGAGCTTGCCGTGAAAATGAGATTTTCTCAAAGGGGTACCC
SO108/ 0.056	352	CAGAAATTTTTCTGATTTTTTGGGCCCTTGTCTATTGCGTCGACCCAAGCAAATATTCTCATTTTT ACGAAAGGCTTTTCGAGACCCGAAAAGGGTCCGAATCGAAAAATGTCTTCACCAAAGTCGTA GCCCTCTGAATTATCTTTCCAACAGCATAAAGATGACCGTGACAGGACCACAAGCGAATGAGA TATGGCCAATAAACAGGGCTATTCTTCAATTACCTTTCACCCGAACACTGTTTTGACCATATCTC CTTAGATATGGGCTGTCTTGGGCCAATTAACACGGCCTAGTGATCCTTATTGCGTGCCCTACGG CTTGGTAGAGTCAGATTTACATTGGCTCGG
SO113/ 0.052	178	CAAATCCTAAACCCTAATTGTAGATTTTAACCAAATGTCTTATTGGTATGCTTTATTTGTCTCA TTTTGACTTCATATTAGCCTCATTTGAGACTTCATATTGTCTCGTTATAGAAATTGTGGACAC TTGTACCGTAGGAGTATATATGCTTCTCTAAGCCCTAAACCCTAATTT
SO145/ 0.032	1564	TTCTTTTCAGGCATGGAAGTGCAGCTATGAGTTCTTGAGCTAATGAGCTAGGCTGCTCTGAGCT AACGGCCCGTCAATTCTGAGTCATCGATGGAATTGAATAAGGGCCTACCGATCCTGTTGCTAG AAGCTAATGAGCTAATGTAGCTACCCGCTCCTACCATTCCGAAGGCATCCAAGGAATGGAATA AGGAGCGACCTTCTCTCTTCTATGAAGCTATGAGTTATTGTAGCTTCTTGTGTTTATGAGCTCT TAGCTACTCCTTTCCTTTGTCTTATCTTATCTTGCTTTCTATGGCTTTAGAGTTGCTATTAAAGAG CTATAAGAGGCAGCTAAGGACTTGTGTTTGAACCTCTTTAGCTGCTAACTATCTCTATAGCC CGGACCATGAACACAATCTGAACTCGGACTTGTGACAACGACAACGAGGGCTCTGCTTCTC TCTGTTTTCTCCTGGGTAAGTACTAGAACTTGAGAGTCAGGATTTGAAGACTCTCAAGGACG AGGAAAGCAGCTCAGTATGAACTACAGTGATTACACCGTCAGAACAACTCGAACCAAGAGA GGGGATATCCACTGATATGCCGAACGATAGAGCTCCCGAACTTGTCGTACATCGAACGAAC CCTCGGATAGGAACTCCTTGTGTTTCTGTTCTTTTCACAAACAAACATGTAACCTTTTCTCTTC CTTACTGAAAGCCAGAGAGTGACCTACTAGTTGTAGGGCAGGATCGACTTAGAGTTGCTAAGA GCGCCCCCAGTCCCGTACACAAAAAGGGAGGGATGGGGGGTGCAGCTCAGAGTGAAGAAAG GAATGGAACCAAGTGATGGACTGTGAGGTGACAGGCCAGAACGATATGGTACCAGGAGTTAC GCGCGCGCACGAGGAGTTCCAAAAATGGCTTTCCTCGATAAACTCTGTTGTTTTATTGCGCGCC CTTACAAGTTGTTGTAGCTGTCTTATTGCTGCTTCTAGTCAAGTACCTGTACCAAGTATGG AGCCAACGTCGATCGCTTTCAGCTTGGGAACCTCTATTTTCGCTCGATGAGAGGATTTCCCGCTA TCATCTAGGGCCTTTATGGGTTTGAAGCAAGCCACCCCAAGTTCTAGCACACTACTGCCTTC TTGTCCCTTCGTTTCATAGCTAGGAGTTCATAGGTAAACCCAAGATAGTCTCACTTCCAGCAGTA TTCAATCGACTGATGCTACACTTGCTAACCATCTCACTAACTAGACCGAAGGGGTTCACTAGTC ATCTACGACATTTCCAATTGAACTCTAACTCCTCATTTGTTGCTTGTGTTTTTAAAAACAGAC ATGTAAACTTGTCTCTCATGAGCTGTTTGGCAGTGAGTGACCCATCGAAATGGGGCAGCAAC CCTAAGAGTCTCTTTACTGAGCTCCTGTTTACAGTTGTTACTGAGTTCTGTAGCTATGAGCT AAGGAAGCTAGCTGCTAGAACGCGCTAAAACACGAGTTTAACAGGCCTCACGATAGATTGTAT TCCAAGATCTGAAACCTTGCTTTTAAAGCTC
SO202/ 0.021	181	GGAAATAGTTACCAAGTACATCACCATAAGTATTGGAAATTTCCACGGTAGGCGTTACCGTGG AAATTATTCTAAGTGTAAGAAATTTTCACGAAACGAGTTTTCGTGGACATAACCATTAGTATTAG AGATTTTCATGCTAGGAATTATGCTAGAAAGCACTGTATGTGTAGAAATTCAAC
SO342/ 0.01	133	ATATAGAATATAATATATGGAGTTTCATTATATTAATATACTCTATCATATAATATAAGTGAAT ACATTATACTTATTCATAATATTAAGATATGAGACTATACTTTAGTCTTTTTCTTATTACTTTATT TAA
<i>Salvia sclarea</i>		
SS1 /1.9	362	GAAAGTCGTAGCCCTCTGAACTGGCTTTCCAACGATATGCTGACCGCTGCGGGGCGACCTCGTA CCAATGAGATATGGCCGAAACGCCGGCGTCCATTGCGCTCTACCGGAACACTGTTTTGG CCATATCTCCTTCCCCGTAGGTGCGTCTCGGGGCCATAACGCGTCCATTTGATCCTTATGTATAG CACTAGGCCATGGCAGGGTCGAATCCGACATCTGGCTAGGTCGAAATTTTCCGTATTTTCGGCC AAACCTCAAAGGGGGTACCTTGGGGAAAAATCTCATTTTCAAGGAGAGCTATTACGGTCAAT TTCAGGGCCCTTGACGCCCCGCTCTCGAAAAGTCCATCCAG
SS8 /1.3	158	GAAGATTAGAGTGCGAAGGAACGGCCTCGTTCTCGTCGGAATTGCTCCGAAATCGTGGTCTCTC GTTGAAGGCCTAACTACCGGAGTTGCCGTTTTCTTGAGAATTGCTCGCTTTTTTCGACCAAAGC GCACCAAACATACCTTATTATGATGTGTC

SS123/0.056	170	TTTTTTCGACCAAAAGCCACACACACCCTTATTGTGACGTGTCCCGGTAAAAAGTGTGCAA GAACGGCATCGTTGTCGTCGAAATTGGTTCGAAATCGAGGTTGTTCCGTAGGAAGCTCATTGCT AGCTTAACCTCCGTGAATCCTCGTTTTCCTTAGAATCGGCTG
SS337/0.0098	397	TTGGGTGGTAACGGCGGTGCAAGATGTACGGATTGTCGTTTCGAGGGGAGGATTGTTGGGGTTG GCAAACCCATCCCACATCGGAAGATAGAAGAAGGAATAACTTCTATATAATAAAGTCCACCAC TAATTAGTATGAGGCCTTTTGGGAAGGAGCCCAAAACAAATCCGTGCGGGCTCGGCCAAAG CGGACAATATCATACTAATGACGGAATGGTGCGGTGGCAGTCCCTAACAGTGGTATCAGAGC CGATGGTTTCGGCTGGGCCCAATATGTGGGCGGGTGGAGACTGCTTCCCGATGATGGAGGTAA ACCCCAAGTGAGCTCACGATTGAATCCGGTGGTTCCTTGTGTCGAAAGTCTTCCTGATAGTGTG GTCAGGCGGCGAGTCCCG

Table S2. BLAST homology and FISH chromosome mapping of the satDNAs revealed in repeatomes of *S. officinalis* and *S. sclarea*.

Tandem Repeat	Blast Homology (between the Revealed Tandem Repeats)	BLAST Homology (Available NCBI Data)	FISH Chromosome Localization
<i>Salvia officinalis</i>			
SO3	69% of identity with SO97; 74% of identity with SO107; 71% of identity with SO108, 69.4% of identity with SS1	no	A large cluster was localized in the subtelomeric region of the long arm of chromosome pair 4
SO4		<i>Theobroma cacao</i> genome assembly, chromosome: II, LT594789.1	A large cluster was localized in the subtelomeric region of the long arm of one or two homologs of chromosome pair 5
SO44		no	Small clusters were localized in the pericentromeric region of all chromosomes;
SO46		no	In the NOR region of chromosome pair 3
SO48		Putative LTR elements; <i>Lotus japonicus</i> B-129 DNA, chromosome 2, AP022630.1; <i>Quercus robur</i> genome assembly, chromosome 9, OW028772.1	A large cluster was localized in the subtelomeric region of the long arm of chromosome pair 4
SO97	69% of identity with SO3; 86,5% of identity with SO107; 77% of identity with SS1	<i>Ipomoea trifida</i> cultivar NCNSP0306 chromosome 13 CP025656.199;	A large cluster was localized in the subtelomeric region of the long arm of chromosome pair 4
SO107	74% of identity with SO3; 86,5% of identity with SO97; 80% of identity with SO108; 83.7% of identity with SS1	no	A large cluster was localized in the subtelomeric region of the long arm of chromosome pair 4, and small clusters were detected in the subtelomeric regions of both arms
SO108	71% of identity with SO3; 80% of identity with SO107	<i>Ipomoea trifida</i> cultivar NCNSP0306 chromosome 15 CP025658.1; <i>Jasminum sambac</i> cultivar Hutoumoli linkage group Lg13 CP073644.1	A large cluster was localized in the subtelomeric region of the long arm of chromosome pair 4
SO113		no	Small clusters were localized in the pericentromeric region of all chromosomes
SO145		no	A large cluster was localized in the subtelomeric region of the long arm of chromosome pair 4
SO202		no	A large cluster was localized in the subtelomeric region of the long arm of

			chromosome pair 4, and a minor site was detected in the subtelomeric region of the short arm of one homolog of chromosome pair 6
SO342		no	Dispersed hybridization signals were distributed along all chromosomes
		<i>Salvia sclarea</i>	
SS1	83.7% of identity with SO107; 77% of identity with SO97; 69.4% of identity with SO3	no	Small clusters were localized in the subtelomeric regions of both arms of all chromosomes. In <i>S. officinalis</i> , a large cluster was localized in the subtelomeric region of the long arm of chromosome pair 4
SS8		no	Small polymorphic clusters were localized in the subtelomeric regions of both arms (except chromosome pair 5 and 11) and also in the pericentromeric region of chromosomes
SS123		no	Small clusters were localized in the pericentromeric region of all chromosomes
SS337		<i>Arabidopsis arenosa</i> genome assembly, chromosome: 4-8 LR999455.1	Small clusters were localized in the subtelomeric regions of both arms of all chromosomes

Table S3. List of the oligonucleotide FISH probes.

Tandem Repeat	Oligo FISH probe sequence
SO3	GAAGGAGATA GGCCAAAAC GGTGTTCGCG TTGAACGCAA CCGTAGCACA CTCCAA
SO4	AGAAAACTC CCCGGATCCT TTTGCTTTGA TGGGAGCTTG TTTTGAAGTA TGACA
SO44	TTTGCTT CCGGAGATGC TACGCATCAC CCGTGGCGGA GCGGCGGCTT
SO46	CGCGCATCGT CGGGGGCTGC CCGCGCAGGG GCG
SO48	ATCCAAGGCT TTGGTGAAAA TATCTGCTAT CTGTTTTTCA GTTGGAACAAATTTAATGCA
SO97	AAAGTTGTAG CCCTCTGAGT AAGCTTTCCA ACGGTATAAA GACCGCTGTG AATGGACCA
SO107	TTGGAGGATC CGCCAAAAT ACGGAAAATT TCGACCGAGC CAAATGTCGA ATCCGACCCT
SO108	CCTTTCA CCCGAACACT GTTTTGACCA TATCTCCTTA GATATGGGCT GTCTTGGGCC
SO113	TTGTGGACAC TTGTACCGTA GGAGTATATA TGCTTCTCTA AGCCCTAAAC
SO145	TCGAACAAGA GAGGGGATAT CCACTGATAT GCCCGAACGA TAGAG
SO202	GGAAATAGTT ACCAAGTACA TCACCATAAG TATTGGAAAT TTCCACGGTA GCGTTACCG
SO342	ATATAGAATA TAATATATGG AGTTTCATTA TATTAATATA CTCTATCATA
SS1	GTCGTAGCCC TCTGAAGTGG CTTTCCAACG ATATGCTGAC CGCTGC
SS8	GAATTGCTCG CTTTTTCGAC CAAAGCGCAC CAAACATACC TTTATTATGA TGT
SS123	TCCGTAGGAA GCTCATTGCT AGCTTAACTC CGTGAATCCT CGTTTTTCTT TA

SS337

AGGGGAGGAT TGTGTTGGGGTT GGCAAACCCA TCCCACATCG
GAAGATAGAA GAAGGAA

Figure S1. The raw images from Figure 5.

