Supplemental Figure 1. Alignment of the genomic sequences with similarity to dhs genes identified from Convolvulus arvensis. Exons are numbered according to Reimann et al. (2004). carv-1 is interpreted as functional DHS-coding gene, carv-2 and carv-3 are most likely pseudogenes. In the first line the amino acid sequence encoded by the exon sequences of carv-1 is given. Predicted exon regions are boxed, the respective coding sequences are given in upper case characters. Lower case characters indicate intron sequences. Hyphens indicate sequence gaps. Of intron 5 of carv-3 with a total length of 2949 bp only 334 bp are shown in this alignment. The putatively modified splicing cite within exon5 of carv-3 is indicated by an arrow.
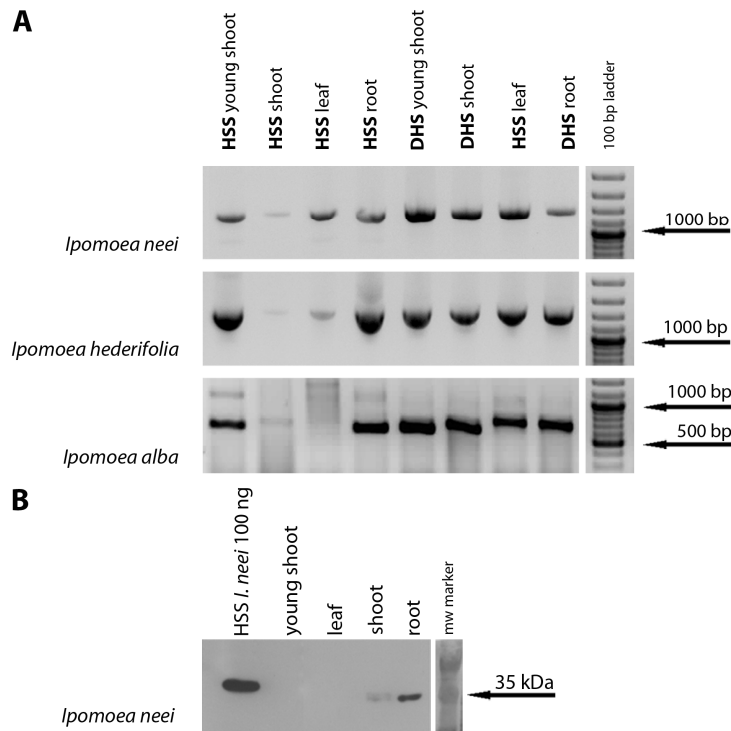
Supplemental Figure 2. Tissue-specific expression of DHS and HSS in various plant organs. A. Transcript detection by RT-PCR of the PA-producing species *I. neei*, *I. hederifolia*, and the PA-free species *I. alba*. 1 µg total RNA of various plant organs was reverse-transcribed and DHS- and HSS-coding cDNAs were amplified by PCR with gene-specific primers. The expected size of PCR products was 1200 bp for HSS and DHS of *I. hederifolia* and *I. neei* and 600 bp for HSS and DHS of *I. alba*. A 100-bp DNA size marker is shown. **B.** Protein gel-blot analysis for HSS of *I. neei*. 20 µg of soluble protein extracted from the same plant organs as used for RT-PCR were separated by SDS-PAGE and blotted onto a polyvinylidene difluoride membrane. HSS was detected with an affinity-purified antibody against HSS of *I. neei*. As a positive control, 100 ng of purified recombinant HSS protein was applied. The recombinant HSS protein contained a 6xHis tag resulting in a slightly increased protein size in comparison with the native HSS. mw marker, molecular weight marker.

Supplemental Table 1. Genomic organization of *dhs* and *hss* genes of the Convolvulaceae species *I. neei*, *I. alba*, *I. purpurea*, *C. tricolor*, and *C. arvensis*. Numbering of introns follows the genomic organization of the *dhs* gene from *H. sapiens*. The number, position, length, and phase of the introns are given. Introns 3 and 7 are missing in all Convolvulaceae genes. Pseudogenes *carv-2* and *carv-3* are shaded in gray. Variation of the exon lengths is only observable in exon 1 and 9 (framed in gray).

Intron position

	219 bp	387 bp	509 bp	606 bp	693 bp	826 bp	936 bp	1026 bp

Intron phase

	0	0	-	0	0	1	-	0

Species (gene)	E 1	I 1	E 2	I 2	E 3	(I 3)	E 4	I 4	E 5	I 5	E 6	I 6	E 7	(I 7)	E 8	I 8	E 9
I. neei (dhs)	219	358	168	588	122	0	97	293	87	176	133	76	110	0	126	117	87
I. alba (dhs)	219	369	168	794	122	0	97	422	87	338	133	78	110	0	126	96	87
I. purpurea (dhs)	a)	a)	a)	630	122	0	97	405	87	176	130	80	110	0	a)	a)	a)
I. purpurea (dhs)	216	443	168	227	122	0	97	407	87	163	130	79	110	0	126	223	87
C. tricolor (dhs)	a)	105	168	291	122	0	97	340	87	109	133	76	110	0	126	192	a)
C. arvensis (dhs)	a)	300	168	593	122	0	97	432	87	343	133	85	110	0	126	236	a)
I. neei (hss)	210	2736	168	538	122	0	97	76	87	943	133	82	110	0	126	118	78
I. hederifolia (hss)	210	2971	168	521	122	0	97	77	87	584	133	82	110	0	126	114	78
I. alba (hss)	210	1164	168	756	122	0	97	78	87	1158	133	85	110	0	126	121	78
C. arvensis (*carv*-2)	a)	a)	a)	582	122	0	97	160	x	x	133	80	110	0	126	405	a)
C. arvensis (*carv*-3)	213	1319	168	1001	122	0	97	139	67	2948	132	80	110	0	126	91	78
dhs/H. sapiens [b]	207	1233	165	238	122	80	97	79	87	2060	106	79	104	965	126	83	96

[a] 5' and 3' ends are missing because of amplification with degenerate primers that bind within the sequence
[b] GenBank accession number NC_000019.8

Supplemental Table 2. Distances from pairwise comparisons of selected pairs of DHS- and HSS-coding cDNA sequences from the Convolvulaceae. d_{aa}, amino acid distance; d_{na}, nucleotide distance. Distances for paralogous sequences are given in bold.

d_{aa} / d_{na}	DHS *I. hederifolia*	DHS *I. meyeri*	DHS *I. alba*	DHS *I. purpurea*	DHS *Merremia quinquefolia*	HSS *I. neei*	HSS *I. hederifolia*	HSS *I. meyeri*	HSS *I. alba*	HSS *M. quinquefolia*
DHS *I. neei*	0.0141 0.0226	0.0249 0.0312	0.0248 0.0311	0.0285 0.0287	0.0503 0.0560	**0.1409** **0.1370**				
DHS *I. hederifolia*		0.0177 0.0324	0.0177 0.0312	0.0177 0.0275	0.0357 0.0509		**0.1250** **0.1257**			
DHS *I. meyeri*			0.0177 0.0287	0.0285 0.0227	0.0433 0.0510			**0.1299** **0.1492**		
DHS *I. alba*				0.0285 0.0239	0.0321 0.0472				**0.0975** **0.1296**	
DHS *I. purpurea*					0.0467 0.0422					
DHS *M. quinquefolia*										**0.1448** **0.1537**
HSS *I. neei*							0.0141 0.0083	0.0508 0.0487	0.0772 0.0512	0.1249 0.1296
HSS *I. hederifolia*								0.0581 0.0550	0.0772 0.0550	0.1290 0.1338
HSS *I. meyeri*									0.0731 0.0642	0.1198 0.1421
HSS *I. alba*										0.1298 0.1439

Supplemental Table 3. Analyses of codon substitution patterns. Dataset A. The log-likelihood values and parameter estimates for various models of evolution are given. Numbering of the amino acid positions is based on the amino acid sequence of the DHS from *I. hederifolia*, position 1 is defined as the start codon in the open reading frame.

Model Code	Likelihood (lnL)	ts/tv	Estimates of Parameters	Positively selected sites [b]
M0 (one ratio)	-3535.17	2.443	$\omega = 0.12284$	Not calculated
Site Models				
M1a (Nearly Neutral)	-3498.75	2.604	$p_0 = 0.887$ ($p_1 = 0.113$) $\omega_0 = 0.063$ ($\omega_1 = 1,000$)	Not calculated
M2a (Positive Selection)	-3498.75	2.604	$p_0 = 0.887$ $p_1 = 0.068$ ($p_2 = 0.044$) $\omega_0 = 0.063$ ($\omega_1 = 1,000$) $\omega_2 = 1,000$	No sites identified
Branch Model	-3525.32	2.452	$\omega_0 = 0.091$ [a] $\omega_a = 0.202$ [a] $\omega_B = 0.094$ [a] $\mathbf{\omega_C = 1.919}$ [a] $\omega_D = 0.165$ [a]	Not calculated
Branch-Site Model A [c]				
Clade a	-3483.06	2.565	$p_0 = 0.811$ $p_1 = 0.064$ $p_2 = 0.126$ ($0.11642 + 0.00917$) $\omega_0 = 0.044$ ($\omega_1 = 1.000$) $\omega_2 = 1.140$	E89 D119 T120 H128 P159 L175 D186 I189 L246 D259 P260 P263 **N266** I271 **I277** **N281** G288 I295 A316 G348 G349
Branch A	-3498.75	2.604	$p_0 = 0.887$ $p_1 = 0.113$, $p_2 = 0.000$ ($0.000 + 0.000$) $\omega_0 = 0.063$ ($\omega_1 = 1.000$) $\omega_2 = 1.000$	No sites identified
Branch B	-3498.15	2.606	$p_0 = 0.812$ $p_1 = 0.103$ $p_2 = 0.086$ ($0.076 + 0.010$) $\omega_0 = 0.060$ ($\omega_1 = 1.000$) $\omega_2 = 1.000$	V113 P337
Branch C	-3493.17	2.607	$p_0 = 0.884$ $p_1 = 0.108$ $p_2 = 0.008$ ($0.008 + 0.0009$) $\omega_0 = 0.062$ ($\omega_1 = 1.000$) $\mathbf{\omega_2 = 95.074}$	**N281** G349
Branch D	-3497.59	2.645	$p_0 = 0.883$ $p_1 = 0.106$ $p_2 = 0.011$ ($0.010 + 0.001$) $\omega_0 = 0.062$ ($\omega_1 = 1.000$) $\mathbf{\omega_2 = 22.923}$	T120 P159 L175
Branch-Site Model A with $\omega_2 = 1$				
Clade a	-3483.15	2.556	$p_0 = 0.789$ $p_1 = 0.064$ $p_2 = 0.134$ ($0.124 + 0.001$) $\omega_0 = 0.043$ ($\omega_1 = 1.000$) ($\omega_2 = 1.000$)	Not calculated
Branch A	-3498.75	2.604	$p_0 = 0.887$ $p_1 = 0.113$ $p_2 = 0.000$ ($0.000 + 0.000$) $\omega_0 = 0.063$ ($\omega_1 = 1.000$) ($\omega_2 = 1.000$)	Not calculated
Branch B	-3498.15	2.606	$p_0 = 0.812$ $p_1 = 0.103$ $p_2 = 0.086$ ($0.076 + 0.010$) $\omega_0 = 0.060$ ($\omega_1 = 1.000$) ($\omega_2 = 1.000$)	Not calculated
Branch C	-3495.86	2.590	$p_0 = 0.553$ $p_1 = 0.064$ $p_2 = 0.384$ ($0.344 + 0.040$) $\omega_0 = 0.062$ ($\omega_1 = 1.000$) ($\omega_2 = 1.000$)	Not calculated
Branch D	-3497.87	2.591	$p_0 = 0.841$ $p_1 = 0.103$ $p_2 = 0.056$ ($0.050 + 0.006$) $\omega_0 = 0.059$ ($\omega_1 = 1.000$) ($\omega_2 = 1.000$)	Not calculated

[a] omega ratios were calculated for the branches, labeled in Fig. 3, (ω_a branches in the HSS clade, ω_B HSS branch B, ω_C HSS branch C, ω_D HSS branch D)

[b] Numbering of the amino acid positions is based on the amino acid sequence of the DHS from *I. hederifolia*. Position 1 is defined as the start codon in the open reading frame.

[c] The models assume four site classes. In site class 0, all lineages are under purifying selection with a small ω ratio ω_0. In site class 1, all lineages are undergoing weak purifying selection or neutral evolution with ω_1 close to 1. In site class 2 (2a + 2b), a proportion of class-0 and class-1 sites come under positive selection with $\omega_2 \geq 1$ on the foreground lineages (Yang et al., 2005).

Supplemental Table 4. Likelihood Ratio Test (LRT) statistics and *P* values for various tests of positive selection. Dataset A.

Model	Null model	df[a]	LRT (2ΔlnL)	*P* values
LRT 1, site model				
M2a (Positive Selection) -3498.75	M1a (Nearly Neutral) -3498.75	2	0	-
LRT 2, branch model				
Branch model -3525.32	M0 -3535.17	4	19.7	0.0006
LRT 3, branch-site model, positive selection				
Branch-Site Model A	Branch-Site Model A with $\omega_2 = 1$			
Clade a -3483.06	-3483.15	1	0.20	-
Branch A -3498.75	-3498.75	1	0	-
Branch B -3498.15	-3498.15	1	0	-
Branch C -3493.17	-3495.86	1	5.38	0.0204□
Branch D -3497.59	-3497.87	1	0	-
LRT 4, branch-site model, relaxed selection				
Branch-Site Model A with $\omega_2 = 1$	M1a (Nearly Neutral)			
Clade a -3483.15	-3498.75	2	31.2	0.0000*
Branch A -3498.75	-3498.75	2	0	-
Branch B -3498.15	-3498.75	2	1.2	0.5488
Branch C -3495.86	-3498.75	2	5.78	0.0556
Branch D -3497.87	-3498.75	2	1.76	0.4148

[a] df = degrees of freedom

* Significance corrected for multiple hypothesis testing by Bonferroni´s method (Anisimova and Yang, 2007) P ≤ 0.01

□ Significance corrected for multiple hypothesis testing by B-Y method (Narum, 2006, Benjamini and Yekutiele, 2001) P ≤ 0.02190

Supplemental Table 5. Analyses of codon substitution patterns. Dataset B. The log-likelihood values and parameter estimates for various models of evolution are given. Numbering of the amino acid positions is based on the amino acid sequence of the DHS from *I. hederifolia*: position 1 is defined as the start codon in the open reading frame.

Model Code	Likelihood (lnL)	ts/tv	Estimates of Parameters	Positively selected sites [b]
M0 (one ratio)	-3022.60	2.806	$\omega = 0.134$	Not calculated
Site Models				
M1a (Nearly Neutral)	-2988.26	2.890	$p_0 = 0.902$ ($p_1 = 0.098$) $\omega_0 = 0.077$ ($\omega_1 = 1,000$)	Not calculated
M2a (Positive Selection)	-2988.26	2.890	$p_0 = 0.902$ $p_1 = 0.041$ ($p_2 = 0.057$) $\omega_0 = 0.063$ ($\omega_1 = 1,000$) $\omega_2 = 1,000$	No sites identified
Branch Models	-3003.18	2.803	$\omega_0 = 0.074$ [a] $\omega_a = 0.210$ [a] $\omega_B = 0.057$ [a] **$\omega_C = 999.000$** [a] $\omega_D = 0.433$ [a]	Not calculated
Branch-Site Model A				
Clade a	-2974.31	2.845	$p_0 = 0.821$ $p_1 = 0.034$ $p_2 = 0.146$ ($0.140 + 0.006$) $\omega_0 = 0.057$ ($\omega_1 = 1.000$) $\omega_2 = 1.000$	H157 P188 L204 D215 I218 L246 D259 P260 P263 I271 G275 **I277 N281** G288 S289 I295 A316 G348 G349
Branch A	-2988.26	2.890	$p_0 = 0.902$ $p_1 = 0.098$, $p_2 = 0.000$ ($0.000 + 0.000$) $\omega_0 = 0.077$ ($\omega_1 = 1.000$) $\omega_2 = 1.000$	V154 A190
Branch B	-2988.26	2.890	$p_0 = 0.902$ $p_1 = 0.098$, $p_2 = 0.000$ ($0.000 + 0.000$) $\omega_0 = 0.077$ ($\omega_1 = 1.000$) $\omega_2 = 1.000$	V113 P337
Branch C	-2978.59	2.863	$p_0 = 0.837$ $p_1 = 0.075$ $p_2 = 0.087$ ($0.080 + 0.007$) $\omega_0 = 0.075$ ($\omega_1 = 1.000$) **$\omega_2 = 999.000$**	D148 **N266 I277 N281** G421
Clade c	-2984.50	2.884	$p_0 = 0.856$ $p_1 = 0.083$ $p_2 = 0.061$ ($0.056 + 0.005$) $\omega_0 = 0.072$ ($\omega_1 = 1.000$) $\omega_2 = 2.269$	
Branch D	-2988.26	2.890	$p_0 = 0.902$ $p_1 = 0.098$ $p_2 = 0.000$ ($0.000 + 0.000$) $\omega_0 = 0.077$ ($\omega_1 = 1.000$) $\omega_2 = 1.000$	No sites detected
Branch E	-2986.92	2.952	$p_0 = 0.891$ $p_1 = 0.094$ $p_2 = 0.014$ ($0.013 + 0.001$) $\omega_0 = 0.076$ ($\omega_1 = 1.000$) **$\omega_2 = 67.746$**	T149 L204
Branch P	-2988.26	2.890	$p_0 = 0.902$ $p_1 = 0.098$ $p_2 = 0.000$ ($0.000 + 0.000$) $\omega_0 = 0.077$ ($\omega_1 = 1.000$) $\omega_2 = 1.000$	
Clade p	-2985.62	2.905	$p_0 = 0.814$ $p_1 = 0.089$ $p_2 = 0.097$ ($0.087 + 0.010$) $\omega_0 = 0.067$ ($\omega_1 = 1.000$) $\omega_2 = 1.000$	
Branch-Site Model A with $\omega_2 = 1$				
Clade a	-2974.31	2.885	$p_0 = 0.821$ $p_1 = 0.034$ $p_2 = 0.146$ ($0.140 + 0.006$) $\omega_0 = 0.043$ ($\omega_1 = 1.000$) ($\omega_2 = 1.000$)	Not calculated
Branch A	-2988.26	2.890	$p_0 = 0.902$ $p_1 = 0.098$, $p_2 = 0.000$ ($0.000 + 0.000$) $\omega_0 = 0.077$ ($\omega_1 = 1.000$) $\omega_2 = 1.000$	Not calculated
Branch B	-2988.26	2.890	$p_0 = 0.902$ $p_1 = 0.098$, $p_2 = 0.000$ ($0.000 + 0.000$) $\omega_0 = 0.077$ ($\omega_1 = 1.000$) $\omega_2 = 1.000$	Not calculated
Branch C	-2981.73	2.847	$p_0 = 0.000$ $p_1 = 0.000$ $p_2 = 0.384$ ($0.918 + 0.082$) $\omega_0 = 0.075$ ($\omega_1 = 1.000$) ($\omega_2 = 1.000$)	Not calculated
Clade c	-2984.95	2.845	$p_0 = 0.821$ $p_1 = 0.034$ $p_2 = 0.145$ ($0.140 + 0.006$) $\omega_0 = 0.057$ ($\omega_1 = 1.000$) ($\omega_2 = 1.000$)	

Branch D	-2988.26	2.890	$p_0 = 0.902\ p_1 = 0.098\ p_2 = 0.000\ (0.000 + 0.000)\ \omega_0 = 0.077\ (\omega_1 = 1.000)\ (\omega_2 = 1.000)$	No sites detected
Branch E	-2987.58	2.880	$p_0 = 0.856\ p_1 = 0.090\ p_2 = 0.054\ (0.0490 + 0.005)\ \omega_0 = 0.073\ (\omega_1 = 1.000)\ (\omega_2 = 1.000)$	Not calculated
Branch P	-2988.26	2.890	$p_0 = 0.902\ p_1 = 0.098\ p_2 = 0.000\ (0.000 + 0.000)\ \omega_0 = 0.077\ (\omega_1 = 1.000)\ \omega_2 = 1.000$	
Clade p	-2985.62	2.905	$p_0 = 0.814\ p_1 = 0.089\ p_2 = 0.097\ (0.087 + 0.010)\ \omega_0 = 0.067\ (\omega_1 = 1.000)\ \omega_2 = 1.000$	

[a] omega ratios were calculated for the branches, labeled in Fig. 3, (ω_a branches in the HSS clade, ω_B HSS branch B, ω_C HSS branch C, ω_D HSS branch D)

[b] Numbering of the amino acid positions is based on the amino acid sequence of the DHS from *I. hederifolia*. Position 1 is defined as the start codon in the open reading frame.

Supplemental Data. Kaltenegger et al. (2013). Plant Cell 10.1105/tpc.113.109744

Supplemental Table 6. Likelihood Ratio Test (LRT) statistics and *P* values for various tests of positive selection. Dataset B.

Model	Null model	df[a)]	LRT (2ΔlnL)	*P* values
LRT 1, site model				
M2a (Positive Selection) -2988.26	M1a (Nearly Neutral) -2988.26	2	0	-
LRT 2, branch model				
Branch model -3003.18	M0 -3022.60	4	38.84	0.0000
LRT 3, branch-site model, positive selection				
Branch-Site Model A	Branch-Site Model A with $\omega_2 = 1$			
Clade a -2974.31	-2974.31	1	0	-
Branch A -2988.26	-2988.26	1	0	-
Branch B -2988.26	-2988.26	1	0	-
Branch C -2978.59	-2981.73	1	6.28	0.0122□
Clade c -2984.50	-2984.95	1	0.9	0.3428
Branch D -2988.26	-2988.26	1	0	-
Branch E -2986.92	-2987.58	1	1.32	0.2506
Branch P -2988.26	-2988.26	1	0	-
Clade p -2985.62	-2985.62	1	0	-
LRT 4 Branch-site model, relaxed selection				
Branch-Site Model A with $\omega_2 = 1$	M1a (Nearly Neutral)			
Clade a -2974.31	-2988.26	2	27.9	0.0000* □
Branch A -2988.26	-2988.26	2	0	-
Branch B -2988.26	-2988.26	2	0	-
Branch C -2981.73	-2988.26	2	13.1	0.0014* □
Clade c -2984.95	-2988.26	2	6.62	0.0365
Branch D -2988.26	-2988.26	2	0	-
Branch E -2987.58	-2988.26	2	1.4	0.4966
Branch P -2988.26	-2988.26	2	0	-
Clade p -2985.62	-2988.26	2	5.3	0.0707

[a)] df = degrees of freedom

* significance corrected for multiple hypothesis testing by Bonferroni´s method (Anisimova and Yang, 2007) P ≤ 0.0056

□ significance corrected for multiple hypothesis testing by B-Y method (Narum, 2006, Benjamini and Yekutiele, 2001) P ≤ 0.01767

Supplemental Table 7. Nucleotide sequence of primers. For degenerate primers P1-P4, the IUPAC code is used: D = A + G + T; H = A + T + C, K = G + T, M = A + C, N = A + T + C + G, R = A + G, S = C + G, W = A + T and Y = C + T, I = Inosin

Primer	Sequence	Properties and Purpose
P1	5'-dGTC GAC TCG AGA ATT C(T)$_{17}$-3'	oligo(dT) primer
P2	5'-TTH YTD GGI TTY ACD TCI AAY CT-3'	degenerate primer
P3	5'-ATY TTI CCC CAN GAI AYN GCY TC-3'	degenerate primer
P4	5'-GGA AAG AAA TTA ATG ATG AAA GCT CGT ATT TA-3'	3'RACE DHS *I. neei*
P5	5'-GCG ATT TTT CGT TAC CAG GTT CTA TGC-3'	3'RACE HSS *I. neei*
		hss gene of *I. neei*
P6	5'-CCT GGA GCT GCA TTA CGC TCA AAG-3'	3'RACE DHS *M. quinquefolia*
P7	5'-TTC CTT GAA GGG ATC TGT ACT GCG CTC-3'	3'RACE HSS *M. quinquefolia*
P8	5'-TCT GCA CCA TTG CGC ATC AT-3'	5'RACE HSS *I. neei* (GSP1)
P9	5'-AAG CGC TCC GGT CTT CCT AGG ACT G-3'	5'RACE HSS *I. neei* (GSP2)
P10	5'-CTA CAA TGT CAA TGA TTA GAC CAG GAT GA-3'	5'RACE HSS *I. neei* (GSP3)
P11	5'-CCA TTG CGC ATC ATA TT-3'	5'RACE DHS and HSS *M. quinquefolia* (GSP1)
P12	5'-GAC GGT CTG GAT TAT CTC CAG CTT CCT-3'	5'RACE DHS *M. quinquefolia* (GSP2)
P13	5'-CCA TTC TTG TGT GCC CAG TAT AAG TAC G-3'	5'RACE DHS *M. quinquefolia* (GSP3)
P14	5'-CCA GGG TAA CGA TCT GGA TTA TTT GGA TC-3'	5'RACE HSS *M. quinquefolia* (GSP2)
P15	5'-GGG CAG AAG ACA GGA ATT TTG TTC TTG TAT GC-3'	5'RACE HSS *M. quinquefolia* (GSP3)
P16	5'-ATA TAC ATA TGG GAG AAG ATA CCA GAG ATC-3'	expression DHS of *I. neei*, *I. meyeri* (*Nde*I); *dhs* gene of *I. alba*, *I purpurea*, *C. arvensis*
P17	5'-ATA TAC TCG AGT TGA TTG CCT GTG GAA TTT TTA-3'	expression DHS of *I. neei, I. meyeri* (*Xho*I); *dhs* gene of *I. alba*, *I. purpurea*, *C. arvensis*
P18	5'-TAT ACA TAT GGG GGA AGC CAT TAA AGA TGA GAA T-3'	expression HSS of *I. neei*, *I. meyeri* , *I alba*, and *I. hederifolia* (*Nde*I); *hss* gene of *C. arvensis*, *I. neei*
P19	5'-ATA CTC GAG ATG AAA TTT TAT AGC TTT AGT TGC AAA TGT C-3'	expression HSS of *I. neei*, *I. meyeri*, *I alba*, and *I. hederifolia* (*Xho*I); *hss* gene of *C. arvensis*, *I. neei*
P20	5'-TAT ACA TAT GGG AGA AGC CAC GAG AGA TCA GAA C-3'	expression DHS of *M. quinquefolia* (*Nde*I)
P21	5'-TAT ACT CGA GTA GAG TGT CGG TGG ATT TTT TAG CTA TAG TTG C-3'	expression DHS of *M. quinquefolia* (*Xho*I)
P22	5'-TAT ACA TAT GGG AGA AGT CTT CAA TGG CGC T-3'	expression HSS of *M. quinquefolia* (*Nde*I)
P23	5'-TAT ACT CGA GGT GCC TTT TAT TAG CCT TAG CTG C-3'	expression HSS of *M. quinquefolia* (*Xho*I)
P24	5'-GGC RAA GCC ATC MAA ATT GTT AAY G-3'	degenerate primer
P25	5'-CAA AAT CTT YTT RGG STT CAC RTC MAA CC-3'	degenerate primer

P26	5'-CRC CAT TKC GCA TCA TAT TSG-3'	degenerate primer
P27	5'-AKD GGR AAW GCA ATK GTT GCA TCA C-3'	degenerate primer
P28	5'-GGG ACA TTA CCT TAT GAT GTG TTT TCT CTT-3'	*hss* gene of *I. neei* by inverse PCR
P29	5'-AGT GTG TTG TGT GCC ATA GAA GAC CAT TA-3'	*hss* gene of *I. neei* by inverse PCR
P30	5'-TAA CTC TAT ATG TAT TCA CAT TGT TCA AAT TTA-3'	*hss* gene of *I. neei*
P31	5'-CCA AAT AAT CCA GAC CAC CAC CCT GGT CTA ATC ATT G-3'	site-specific mutagenesis of DHS of *I. neei* (mutation N266H) forward
P32	5'-CAA TGA TTA GAC CAG GGT GGT GGT CTG GAT TAT TTG G	site-specific mutagenesis of DHS of *I. neei* (mutation N266H) reverse
P33	5'-GAT ATT GTG GGA GAT GTC AGG GCC ATG GAT GGT GAG GCT G-3'	site-specific mutagenesis of DHS of *I. neei* (mutations I277V and N281D) forward
P34	5'-CAG CCT CAC CAT CCA TGG CCC TGA CAT CTC CCA CAA TAT C-3'	site-specific mutagenesis of DHS of *I. neei* (mutations I277V and N281D) reverse
P35	5'-TTT TCT TTA CCT GGA GCT GTA TTA CGC-3'	RT-PCR *I. alba* DHS
P36	5'-CCT TCA CTG TTT TTG CTC CAC CAC G-3'	RT-PCR *I. alba* DHS
P37	5'-TCG TTA CCA GGC TCT ATG CTA CGC-3'	RT-PCR *I. alba* HSS
P38	5'-CTT CAC AGC TTT CGC TCC ATT GCG-3'	RT-PCR *I. alba* HSS

Supplemental Table 8. Amplification strategy of DHS- and HSS-coding cDNAs and genes, the length of the identified open reading frame (ORF), the 3'- and 5'-untranslated regions (UTRs), and the accession numbers of sequences identified in this project and taken from the databases. --, not determined

A. cDNA	Organ for RNA isolation	Degenerate Primer	RACE Primer (3' and 5' RACE)	ORF Primer	length of ORF [bp]	5'UTR [bp]	3'UTR [bp]	accession numbers
DHS *I. neei*	Shoot	P2/P3	P4	P16/P17	1149 bp	--	260	HF911515
HSS *I. neei*	Shoot	P2/P3	P5, P8-P10	P18/P19	1131 bp	80	283	HF911516
DHS *M. quinquefolia*	Seedling	P2/P3	P6, P11-P13	P20/P21	1143 bp	120	308	HF911517
HSS *M. quinquefolia*	Seedling	P2/P3	P7, P11, P14, P15	P22/P23	1122 bp	43	133	HF911518
DHS *I. meyeri*	Leaf	-	-	P16/P17	1149 bp	--	--	HF911519
HSS *I. meyeri*	Leaf	-	-	P18/P19	1131 bp	--	--	HF911520
DHS *I. hederifolia*	Shoot	-	-	P16/P17	1149 bp	--	--	AJ704845
HSS *I. hederifolia*	Root	-	-	P18/P19	1131 bp	--	--	HF911521
DHS *I. alba*	Shoot	-	-	P16/P17	1155 bp	--	--	HF911522
HSS *I. alba*	Shoot	-	-	P18/P19	1131 bp	--	--	HF911523
B. Gene	-	Degenerate Primer	Additional Primer	ORF Primer	length of genomic fragment			
dhs I. neei				P16/P17	2757 bp			HF911504
hss I. neei[a)]			P5, P28-P30	P18/P19	5625 bp			HF911505
hss I. hederifolia				P18/P19	5476 bp			HF911506
dhs I. alba (*ialb-1*)				P16/P17	3072 bp			HF911507
hss I. alba (*ialb-2*)				P18/P19	4492 bp			HF911508
dhs I. purpurea (*ipurp-1*)		P25/P26			1919 bp			HF911509
dhs I. purpurea (*ipurp-2*)				P16/P17	2736 bp			HF911510
dhs C. arvensis (*carv-1*)		P24/P27			2894 bp			HF911512
hss C. arvensis (*carv-2*)		P25/P27			1639 bp			HF911513
hss C. arvensis (*carv-3*)				P18/P19	6691 bp			HF911514
dhs C. tricolor (*ctri-1*)		P24/P27			2018 bp			HF911511

C. cDNA sequences taken from the database	cited in	
DHS *Heliotropium indicum*	(Reimann et al., 2004)	AJ704844
HSS *Heliotropium indicum*	(Reimann et al., 2004)	AJ704843
DHS *Symphytum officinale*	(Reimann et al., 2004)	AJ704852
HSS *Symphytum officinale*	(Reimann et al., 2004)	AJ704851
DHS *Cynoglossum officinale*	(Reimann et al., 2004)	AJ704839
HSS *Cynoglossum officinale*	(Reimann et al., 2004)	AJ704840
DHS *Nicotiana tabacum*	(Ober and Hartmann, 1999b)	AJ242017
DHS *Solanum lycopersicum*		AF296077_1
DHS *Crotalaria retusa*	(Reimann et al., 2004)	AJ704838
HSS *Phalaenopsis* sp.	(Reimann et al., 2004)	AJ704848
DHS *Eupatorium cannabinum*	(Reimann et al., 2004)	AJ704841
HSS *Eupatorium cannabinum*	(Reimann et al., 2004)	AJ704842
DHS *Petasites hybridus*	(Reimann et al., 2004)	AJ704846
HSS *Petasites hybridus*	(Reimann et al., 2004)	AJ704847
DHS *Senecio vernalis*	(Ober and Hartmann, 1999a)	AJ238622
HSS *Senecio vernalis*	(Ober and Hartmann, 1999a)	AJ238623
DHS *Arabidopsis thaliana*		NP_196211
DHS *Zea mays*	(Nurhayati et al., 2009)	AM411617
DHS *Musa acuminata*	(Wang et al., 2001)	AF296079_1

[a] hss gene of *I. neei* was amplified via three PCRs: P18/P30, P28/P29 (inverse PCR) P5/P19

Supplemental Table 9. Species studied in this project with year and country of collection.

Species Location (year) of seed collection	References
Convolvulus arvensis L.	Seed collection Botanical Garden Kiel
Convolvulus tricolor L.	Seed collection Botanical Garden Kiel
Ipomoea hederifolia L. Ella, Sri Lanka (1985)	(Jenett-Siems et al., 1993, 1998, 2005a)
Ipomoea neei (SPRENG.) O'DONELL Boquete, Panama (1995)	(Jenett-Siems et al., 1998, 2005a)
Ipomoea meyeri (SPRENG.) G.DON 93 km to the west of Santiago, Panama (1995)	(Tofern, 1999)
Ipomoea alba L. Tonosi, Panama (1997)	(Tofern, 1999)
Ipomoea purpurea L. Antsirabe, Madagascar (1990)	(Henrici, 1996)
Merremia quinquefolia (L.) H.HALL. Taboga Island, Panama (1997)	(Jenett-Siems et al., 2005a)