

Supplemental Table 1: BLAST search of homologous RNAs, potential targets for theoretical (HSVd)siRNAs-directed RNA silencing in *Nicotiana* genus plants.

<b>&gt;gb AY553216.1 <i>N. tabacum</i> hexokinase 3 (Hxk3) mRNA. Identities: 19/20 (95%) – Gaps: 0/20 (0%)</b>				
HSVd	23	CAAAGGCATGCAAAGAAA	42	
Sbjct	678	CAAAGCCATGCAAAGAAA	697	
<b>&gt;gb AY368905.1 <i>N. benthamiana</i> Hsp90-2 mRNA. Identities: 18/19 (94%) – Gaps: 0/19 (0%)</b>				
HSVd	175	CCCTTCTTCTTACCTTCT	193	
Sbjct	1457	CCCTTCTTCTTAGCTTCT	1439	
<b>&gt;emb AJ617088.1 <i>N. plumbaginifolia</i> cDNA-AFLP fragment. Identities: 18/19 (94%) – Gaps: 0/19 (0%)</b>				
HSVd	170	ATCGTCCCTTCTTCTTAC	188	
Sbjct	110	ATCGTCACTTCTTCTTAC	128	
<b>&gt;gb AY383599.2 <i>N. tabacum</i> proton P-ATPase (nha1) mRNA. Identities: 22/24 (91%) – Gaps: 1/24 (4%)</b>				
HSVd	188	CCTTCTTCTGGCTCTTCTGGAGA	211	
Sbjct	1807	CCTTCTTCTAG-CTTCTTCTGGAGA	1829	
<b>&gt;gb EF421430.1 <i>N. tabacum</i> dihydroflavonol 4-reductase (Dfr2) mRNA. Identities: 18/20 (90%) – Gaps: 0/20 (0%)</b>				
HSVd	183	CTTACCTTCTTCTGGCTCT	202	
Sbjct	171	CTTACCTTCTTCTGTCT	152	
<b>&gt;gb AF211540.1 <i>N. tabacum</i> Avr9/Cf-9 elicited protein 75 (ACRE75) mRNA. Identities: 18/20 (90%) – Gaps: 0/20 (0%)</b>				
HSVd	177	CTTCTTCTTACCTTCTTCT	196	
Sbjct	204	CTTCTTCTTATCTTCTCT	223	
<b>&gt;gb AY169238.2 <i>N. tabacum</i> DNA topoisomerase II mRNA. Identities: 23/26 (88%) – Gaps: 1/26 (3%)</b>				
HSVd	176	CCTTCTTCTTACCTTCT-TCTGGCT	200	
Sbjct	3540	CCTTCTTCTTATCTTCTCTCTAGCT	3515	
<b>&gt;emb AJ718328.1  <i>N. tabacum</i> cDNA-AFLP-fragment BSTT42-135. Identities: 23/26 (88%) – Gaps: 1/26 (3%)</b>				
HSVd	176	CCTTCTTCTTACCTTCT-TCTGGCT	200	
Sbjct	58	CCTTCTTCTTATCTTCTCTCTAGCT	33	
<b>&gt;emb X56263.1 <i>N. tabacum</i> auxin-induced mRNA (pCNT103). Identities: 25/29 (86%) - Gaps: 0/29 (0%)</b>				
HSVd	177	CTTCTTCTTACCTTCTTCTGGCTTCT	205	
Sbjct	392	CTTCTTCTTACCTTCTTCTGGCTTCT	364	