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1
psy62 TTGGGGTTTCGTTTTGGGTATCACGTATACAAATTTTTTATCGCTTGTGATTGATTTCTCTCTTGGTTTGTCTTTACTTT
lshi-1 TTGGGGTTTCGTTTTGGGTATCACGTATACAAATTTTTTATCGCTTGTGATTGATTTCTCTCTTGGTTTGTCTTTACTTT
AHCA1 TTGGGGTTTCGTTTTGGGTATCACGTATACAAATTTTTTATCGCTTGTGATTGATTTCTCTCTTGGTTTGTCTTTACTTT
JXGC TTGGGGTTTCGTTTTGGGTATCACGTATACAAATTTTTTATCGCTTGTGATTGATTTCTCTCTTGGTTTGTCTTTACTTT
A4 TTGGGGTTTCGTTTTGGGTATCACGTATACAAATTTTTTATCGCTTGTGATTGATTTCTCTCTTGGTTTGTCTTTACTTT
gxpsy TTGGGGTTTCGTTTTGGGTATCACGTATACAAATTTTTTATCGCTTGTGATTGATTTCTCTCTTGGTTTGTCTTTACTTT
                the encoding sequence of the putative signal peptide
91
psy62 CTTTATTGATTGGTGATGTTTCGCTTAAGGACATGTGATTTCAAATGACCTTTTTTTGTAAGTAA
lshi-1 CTTTATTGATTGGTGATGTTTCGCTTAAGGACATGTGATTTCAAATGACCTTTTTTTGTAAGTAA
AHCA1 CTTTATTGATTGGTGATGTTTCGCTTAAGGACATGTGATTTCAAATGACCTTTTTTTGTAAGTAA
JXGC CTTTATTGATTGGTGATGTTTCGCTTAAGGACATGTGATTTCAAATGACCTTTTTTTGTAAGTAA
A4 CTTTATTGATTGGTGATGTTTCGCTTAAGGACATGTGATTTCAAATGACCTTTTTTTGTAAGTAA
gxpsy CTTTATTGATTGGTGATGTTTCGCTTAAGGACATGTGATTTCAAATGACCTTTTTTTGTAAGTAA
156

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FIGURE S1. ClustalW alignment of the nucleotide sequences of CLIBASIA_03875 from six CLas strains for which the complete genome or chromosome was available, including psy62 (NC_012985.3), lshi-1 (NZ_AP014595.1), AHCA1 (NZ_CP029348.1), JXGC (NZ_CP019958.1), A4 (NZ_CP010804.1) and gxpsy (NC_020549.1). The coding sequence of the putative signal peptide is underlined.

Table S1. The primers used in this study¹

Construct/Gene Name	Primer Name	Primer Sequence (5' -3')
pMD3875	3875F	TTGGGGTTTCGTTTTTGGGTA
	3875R	TTACTTACAAAAAAGGTCATTG
pET-3875SP-mphoA	3875SP-F	AAGGAGATATACATATGTTGGGGTTTCGTTTTTGGGTA
	3875SP-R	AGGCATTCTGGAGCTTATAAAGCAAAGTAAAAACAAACCA
pm3875-GFP	m3875gfp-F	GACGAGCTCGGGTACCATGTTGCTTTATTGATTGGTGA
	m3875gfp-R	TGGTGTGACTCTAGACTTACAAAAAAGGTCATTGA
pPVX-m3875	m3875-F	GAGCACCAGCTAGCATCGATATGTTGCTTTATTGATTGG
	m3875-R	CAAGCTTATCGGCGTTCGACTTACTTACAAAAAAGGTCATT
pPVX-eGFP	eGFP-F	GAGCACCAGCTAGCATCGATATGTTGAGCAAGGGCGAGGA
	eGFP-R	CAAGCTTATCGGCGTTCGACTCAAAGATCTACCATGTACA
pPVX-A7	ES34m1-F	GAGCACCAGCTAGCATCGATATGTTGCTTTATTGATTGGTGTCTGT
	m3875-R	--
pPVX-A9	ES34m2-F	GAGCACCAGCTAGCATCGATATGTTGCTTTATTGATTGGTGATGTT
		GCCTTAAG
pPVX-A11	m3875-R	--
	ES34m3-F	GAGCACCAGCTAGCATCGATATGTTGCTTTATTGATTGGTGATGTT
		CGCTTAGCG
pPVX-A7-11	m3875-R	--
	ES34m4-F	GAGCACCAGCTAGCATCGATATGTTGCTTTATTGATTGGTGCTGTT
		GCCTTAGC
pPVX-A22	m3875-F	--
	ES34m5-R	CAAGCTTATCGGCGTTCGACTTACGCACAAAAAAGGTCATT
qPCR assay		
<i>Nbactin</i>	NbActin-F	GCAGGAATCCACGAGACTACA
	NbActin-R	AACCTCCAATCCAGACACTGT
<i>NbCNGC23</i>	NbCNGC23-F	CAGTTATCGTCACGGTGATAC
	NbCNGC23-R	CCTGAGGGACAGGTAGGACGAC

<i>NbCNGC24</i>	NbCNGC24-F	AATCATCGTTCTTACTAGTGGGCT
	NbCNGC24-R	CATCCTCTGCTTGTAATCCTGTGG
<i>NbCNGC25</i>	NbCNGC25-F	CGTTCTTACCTCTGGGTAAAT
	NbCNGC25-R	GTTCTCTGCTTTAATTCTCGAGG
<i>NbCNGC26</i>	NbCNGC26-F	GAGAGGCTTAAGCGAACAGCA
	NbCNGC26-R	CCCATTCTCCATTACCTGATTCAC
<i>NbBI-1</i>	NbBI1-F	CTTTTCTGGTTGCACTTTGCG
	NbBI1-R	AAAGAGGGTCAGAGCATGCTTC
<i>NbBI-2</i>	NbBI2-F	GCACTCTTTGAAGGGGCTTCTG
	NbBI2-R	CCCAAGGTACAAGTACTCTCTGC
<i>NbWRKY9</i>	NbWRKY9-F	CATCCAAAGCCTCAGTCCAC
	NbWRKY9-R	CCTTCCATCTCTTCGCCTCA

1. The restriction recognition sequences of *Nde* I (CATATG), *Hind* III (AAGCTT), *Kpn* I (GGTACC), *Xba* I (TCTAGA), *Cla* I (ATCGAT) and *Sal* I (GTCGAC) within the primers are in bold and underlined. Genes included in qPCR assay are *Nbactin* (GenBank No. JQ256516.1), *NbBI-1* (GenBank No. JX481914.1), *NbWRKY9* (GenBank No. AB711130.1), as well as five additional ones *NbCNGC23* (Niben101Scf08863g01010.1), *NbCNGC24* (Niben101Scf08680g02015.1), *NbCNGC25* (Niben101Scf04528g09004.1), *NbCNGC26* (Niben101Scf08157g02012.1) and *NbBI-2* (Niben101Scf02705g01020.1) from *N. benthamiana* draft genome sequence V1.0.1 (https://solgenomics.net/organism/Nicotiana_benthamiana/genome).