

**Supplemental Table S1** Nucleotide sequences from cDNA clones of eight grass species.

<b>Grass species</b>	<b>No. of clones</b>	<b>Seq. identity among clones*</b>	<b>Homologous Cyn d 1 sequence<sup>#</sup></b>
<i>Zo. matrella</i>	4	99.76-100.0%	Cyn d 1.0203; AF177380.1 (85%)
<i>P. indica</i>	3	99.88-100.00%	Cyn d 1.0203; AF177380.1 (85%)
<i>B. pertusa</i>	4	99.33-99.51%	Cyn d 1.0203; AF177380.1 (85%)
<i>S. halepense</i>	4	99.20-99.30%	Cyn d 1.0203; AF177380.1 (86%)
<i>S. spontaneum</i>	2	100%	Cyn d 1.0203; AF177380.1 (85%)
<i>Ze. mays</i>	4	95.24-99.02%	Cyn d 1.0203; AF177380.1 (83%)
<i>E. procera</i>	4	97.43-100.00%	Cyn d 1.0203; AF177380.1 (85%)
<i>M. repens</i>	3	99.39-99.51%	Cyn d 1.0202; AF177378.1 (85%)

\*; Sequence identity among clones was analyzed using Clustal Omega. <sup>#</sup>; Homologous sequences were analyzed using nucleotide Blastn analysis with more than 80% sequence identity. Percentages of sequence identities are presented in parentheses.