

**A**

e.g:  
>ptc-miR156k  
TGACAGAAGAGAGGGAGCAC

AlternativeSplicingtype:  genomeFeature:  tarPred:  tarScore:  misMat:  wob:

**B**

miRName	Target	BindSite	miRseq	tarSeq	Score	Mismatch	CIGAR	TargetGene	SeqDescription
ptc-miR156k	Chr05:21776451-21777282	24-43	CACGAGGGAGAGAAGACAGT	GTGCCCTTATTTCTGTCA	3.5	HC1T0T1A1T8	20M	Potri.005G203100	hypothetical protein POPTR_0005s22470g [Populus trichocarpa]
ptc-miR156k	Chr07:2840217-2840420	77-96	CACGAGGGAGAGAAGACAGT	GTGCAACCTCTATATTTCA	5	HA0A5A2A1T3	20M	Potri.007G036600	hydroxyproline-rich glyco family [Theobroma cacao]
ptc-miR156k	Chr03:11109734-11110241	13-22	CACGAGGGAGAGAAGACAGT	GTGCTCCCTCCTTCTCACT	5.5	10C0T4C0A1T0	20M	Potri.009G083600	(S)-ureidoglycine aminohydrolase isoform X1
ptc-miR156k	Chr05:21777185-21777282	24-43	CACGAGGGAGAGAAGACAGT	GTGCCCTTATTTCTGTCA	3.5	HC1T0T1A1T8	20M	Potri.005G203100	hypothetical protein POPTR_0005s22470g [Populus trichocarpa]
ptc-miR156k	Chr05:21777185-21777282	9-28	CACGAGGGAGAGAAGACAGT	GTGTCCTATCTCTCTAGTA	5.5	BA3A8A0G0T1	20M	Potri.015G004000	AA-amino acid hydrolase ILR1-like 5
ptc-miR156k	Chr11:11170279-11171213	311-330	CACGAGGGAGAGAAGACAGT	GTGCTGCTCTTTCTGCCA	3.0	5G1T3T5C2	20M	Potri.011G092200	Serine threonine phosphatase PP-X isozyme 1 [Populus trichocarpa]
ptc-miR156k	Chr02:157591-157937	81-100	CACGAGGGAGAGAAGACAGT	GTGCTCTCTCTCACTGTAA	5.5	6T5A0C4A1	20M	Potri.002G002400	squamosa promoter-binding 14
ptc-miR156k	Chr02:20429882-20429882	371-890	CACGAGGGAGAGAAGACAGT	CAGCTTCCTTTCTGTGTCA	4.0	DC0A3T3T4G5	20M	Potri.002G219500	(S)-oxoacyl-(acyl-carrier) mitochondrial
ptc-miR156k	Chr01:37003041-37003223	342-61	CACGAGGGAGAGAAGACAGT	CTTCTCTCTCTCTCTGTCA	4.0	DC1T3T6C7	13M1D7M	Potri.001G359700	DNA topoisomerase 1-like [Populus euphratica]
ptc-miR156k	Chr05:21776676-21777282	24-43	CACGAGGGAGAGAAGACAGT	GTGCCCTTATTTCTGTCA	3.5	HC1T0T1A1T8	20M	Potri.005G203100	hypothetical protein POPTR_0005s22470g [Populus trichocarpa]
ptc-miR156k	Chr17:1427413-1428017	4-23	CACGAGGGAGAGAAGACAGT	GCTCTCCCTCTCTCCACTCA	5	1C0T10C1A0C3	20M	Potri.017G016800	Guanylate-binding family isoform 1 [Theobroma cacao]
ptc-miR156k	Chr17:1427413-1428017	4-23	CACGAGGGAGAGAAGACAGT	GCTCTCCCTCTCTCCACTCA	5	1C0T10C1A0C3	20M	Potri.017G016800	Guanylate-binding family isoform 1 [Theobroma cacao]
ptc-miR156k	Chr05:21776462-21777282	24-43	CACGAGGGAGAGAAGACAGT	GTGCCCTTATTTCTGTCA	3.5	HC1T0T1A1T8	20M	Potri.005G203100	hypothetical protein POPTR_0005s22470g [Populus trichocarpa]
ptc-miR156k	Chr11:3857278-3858622	428-447	CACGAGGGAGAGAAGACAGT	CTTTCCCTCTATTTCTGCCA	5.5	6C1T0T7A5C2	20M	Potri.011G045500	katanin p80 WD40 repeat-containing subunit B1 homolog isoform X2
ptc-miR156k	Chr01:15775287-15775287	14-33	CACGAGGGAGAGAAGACAGT	GTGCTATATCATTCTGTCA	6.0	5A0T0A2A0T8	20M	Potri.001G181200	methyltransferase 22 isoform X1
ptc-miR156k	Chr13:12487243-12487850	815-334	CACGAGGGAGAGAAGACAGT	GTGGTGTGTCTCTCTCTCT	5.5	3G2T0G8C2T0	20M	Potri.013G111300	CCA tRNA nucleotidyltransferase 2 isoform X1 [Eucalyptus grandis]
ptc-miR156k	Chr18:13861809-13862189	89-108	CACGAGGGAGAGAAGACAGT	GTGATCCCTCTCTCTCTCT	4.5	5A9C3C2T0	13M1D7M	Potri.018G113100	ENHANCED DISEASE RESISTANCE 2-like isoform X1
ptc-miR156k	Chr08:12201780-12203225	175-194	CACGAGGGAGAGAAGACAGT	GTGGTCCCTTCTCTCTCTTT	5.0	3G5T6C1T0T0	20M	Potri.008G178600	dentin sialophospho -like
ptc-miR156k	Chr01:15775312-15775291	14-33	CACGAGGGAGAGAAGACAGT	GTGCTATATCATTCTGTCA	6.0	5A0T0A2A0T8	20M	Potri.001G181200	methyltransferase 22 isoform X1
ptc-miR156k	Chr07:2840199-2840420	95-114	CACGAGGGAGAGAAGACAGT	GTGCAACCTCTATATTTCA	5	HA0A5A2A1T3	20M	Potri.007G036600	hydroxyproline-rich glyco family [Theobroma cacao]

**C**

ID	Locus	Asregion	Strand	Type	Coordinate	Position	Sequence Description	Sequencing Platform	Inparanoid
1	Potri.009G083600	Chr03:11109734-11110241	+	IntronR	Chr03:11109657-11109733;Chr03:11109734-11110241;Chr03:11110242-11110281	overlap(sense)	(S)-ureidoglycine aminohydrolase isoform X1	Illumina	AT4G17050

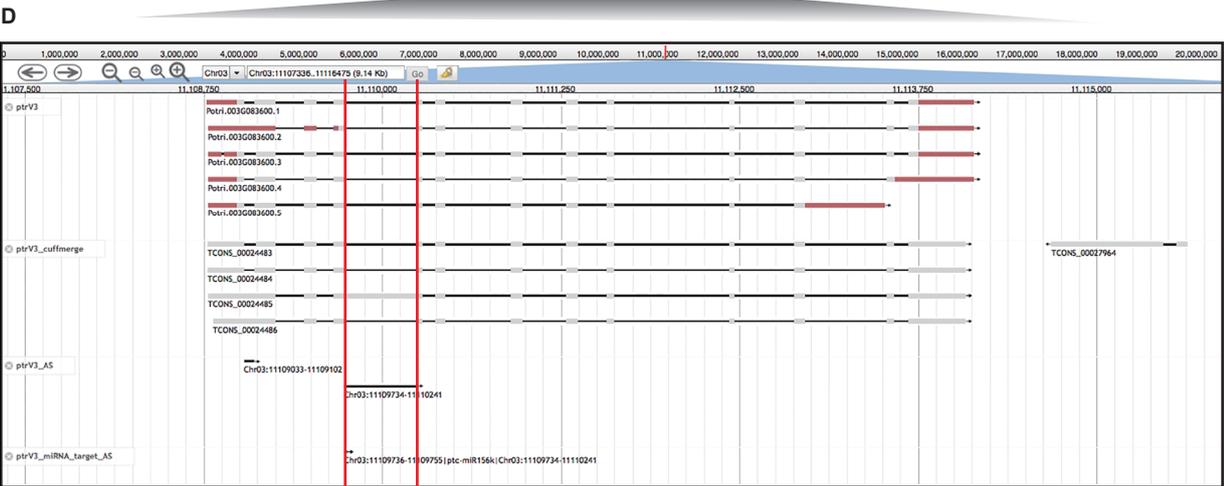


Figure S5. Screenshot of online submission system for *Populus trichocarpa*. (A) The online submission interface for pasting user's own miRNA sequences. (B) The summarized table for prediction results with hyperlinks to more detailed information. (C) and (D) The prediction results for Potri.009G160500, which contains a target site for miR156k in the retained intron.