

Table S1 Target gene prediction of VvmiR166s

miRNA_Acc	miRNA_Length	Expectation	UPE	Target_Acc.	Target_Regions	Inhibition
TCGGACCAGGCGTTCATTCC	20	3	22.742	<i>VIT_204s0008g03250.1 (HB-15)</i>	CDS:1205-1223	Cleavage
	20	3	22.742	<i>VIT_204s0008g03250.2 (HB-15)</i>	CDS:1205-1223	Cleavage
	20	3	21.088	<i>VIT_210s0003g04670.1 (HOX32)</i>	CDS:1065-1083	Cleavage
	20	3	21.088	<i>VIT_210s0003g04670.2 (HOX32)</i>	CDS:431-449	Cleavage
	20	3	23.076	<i>VIT_210s0003g04670.3 (HOX32)</i>	CDS:1159-1177	Cleavage
	20	3	23.995	<i>VIT_213s0019g04320.1 (REVOLUTA-like)</i>	CDS:1114-1132	Cleavage
	20	3	23.995	<i>VIT_213s0019g04320.2 (REVOLUTA-like)</i>	CDS:1114-1132	Cleavage
	20	3	23.995	<i>VIT_213s0019g04320.3 (REVOLUTA-like)</i>	CDS:1114-1132	Cleavage
	20	3	23.995	<i>VIT_213s0019g04320.4 (REVOLUTA-like)</i>	CDS:444-462	Cleavage
	20	3	23.995	<i>VIT_213s0019g04320.5 (REVOLUTA-like)</i>	CDS:387-405	Cleavage
	20	3	23.995	<i>VIT_213s0019g04320.6 (REVOLUTA-like)</i>	CDS:1114-1132	Cleavage
	20	3	23.995	<i>VIT_213s0019g04320.7 (REVOLUTA-like)</i>	CDS:1114-1132	Cleavage
	20	3	22.12	<i>VIT_206s0004g02800.1 (REVOLUTA)</i>	CDS:1322-1340	Cleavage

TCGGACCAGGCTTCATTCCCC	20	3	22.12	<i>VIT_206s0004g02800.2 (REVOLUTA)</i>	CDS:1730-1748	Cleavage
	20	3	22.12	<i>VIT_206s0004g02800.3 (REVOLUTA)</i>	CDS:1746-1764	Cleavage
	20	3	18.711	<i>VIT_203s00097g00550.1</i>	CDS:919-938	Translation
	21	2	22.742	<i>VIT_204s0008g03250.1 (HB-15)</i>	CDS:1204-1223	Cleavage
	21	2	22.742	<i>VIT_204s0008g03250.2 (HB-15)</i>	CDS:1204-1223	Cleavage
	21	2	21.088	<i>VIT_210s0003g04670.1 (HOX32)</i>	CDS:1064-1083	Cleavage
	21	2	21.088	<i>VIT_210s0003g04670.2 (HOX32)</i>	CDS:430-449	Cleavage
	21	2	23.076	<i>VIT_210s0003g04670.3 (HOX32)</i>	CDS:1158-1177	Cleavage
	21	2	23.995	<i>VIT_213s0019g04320.1 (REVOLUTA-like)</i>	CDS:1113-1132	Cleavage
	21	2	23.995	<i>VIT_213s0019g04320.2 (REVOLUTA-like)</i>	CDS:1113-1132	Cleavage
	21	2	23.995	<i>VIT_213s0019g04320.3 (REVOLUTA-like)</i>	CDS:1113-1132	Cleavage
	21	2	23.995	<i>VIT_213s0019g04320.4 (REVOLUTA-like)</i>	CDS:443-462	Cleavage
	21	2	23.995	<i>VIT_213s0019g04320.5 (REVOLUTA-like)</i>	CDS:386-405	Cleavage
	21	2	23.995	<i>VIT_213s0019g04320.6 (REVOLUTA-like)</i>	CDS:1113-1132	Cleavage
	21	2	23.995	<i>VIT_213s0019g04320.7 (REVOLUTA-like)</i>	CDS:1113-1132	Cleavage

21	2	22.12	<i>VIT_206s0004g02800.1 (REVOLUTA)</i>	CDS:1321-1340	Cleavage
21	2	22.12	<i>VIT_206s0004g02800.2 (REVOLUTA)</i>	CDS:1729-1748	Cleavage
21	2	22.12	<i>VIT_206s0004g02800.3 (REVOLUTA)</i>	CDS:1745-1764	Cleavage
21	2.5	20.995	<i>VIT_218s0075g00480.1</i>	CDS:3094-3113	Translation
21	2.5	20.995	<i>VIT_218s0075g00480.2</i>	CDS:3094-3113	Translation
21	2.5	20.995	<i>VIT_218s0075g00480.3</i>	CDS:2850-2869	Translation
21	2.5	20.995	<i>VIT_218s0075g00480.4</i>	CDS:2830-2849	Translation
21	2.5	20.995	<i>VIT_218s0075g00480.5</i>	CDS:3094-3113	Translation
21	2.5	20.995	<i>VIT_218s0075g00480.6</i>	CDS:3327-3346	Translation
21	2.5	20.995	<i>VIT_218s0075g00480.7</i>	CDS:2066-2085	Translation
21	3	18.46	<i>VIT_216s0050g01140.1</i>	CDS:357-376	Translation
21	3	17.375	<i>VIT_208s0007g03420.1</i>	CDS:364-383	Cleavage

The sequences of miRNAs and their target genes were compared by BioXM software to predict the mismatch numbers and the target regions.