

Table 2 Predicted ORFs located in the candidate region.

ORF	ID ^z	Protein size	Description	Query coverage (%)	E value	Identity	GenBank ID	Re-seq ^y	RNA-seq (TPM) ^x			
									SCM334		PG1-1	
									Uninoculated	PepYLCIV	Uninoculated	PepYLCIV
1	Capana07g000158	148	hypothetical protein	100	4.00E-97	96.6	KAF3666006	13	0.0	0.0	0.0	0.0
2	Capana07g000160	298	pentatricopeptide repeat-containing protein	100	0	100.0	XP_016579749	14	0.8	1.7	0.3	0.8
3	Capana07g000161	197	pentatricopeptide repeat-containing protein	100	1.00E-141	100.0	XP_016578755	6	0.3 ^c	1.5 ^b	0.3 ^b	2.7 ^a
4	Capana07g000162	297	F-box protein SKIP1-like	100	0	100.0	XP_016579750	10	2.7 ^c	5.1 ^{bc}	7.3 ^b	19.1 ^a
5	Capana07g000163	410	putative pentatricopeptide repeat-containing protein-like	100	0	98.8	KAF3645095	7	0.0	0.0	0.0	0.0
6	Capana07g000164	361	shikimate O-hydroxycinnamoyltransferase-like	100	0	100.0	XP_016579751	7	1.0	2.2	2.8	3.3
7	Capana07g000165	793	putative eukaryotic translation initiation factor isoform 4G-2-like	100	0	99.8	KAF3670779	16	0.0 ^b	2.0 ^a	0.4 ^{ab}	0.5 ^{ab}
8	Capana07g000166	964	putative eukaryotic translation initiation factor isoform 4G-2-like	100	0	100.0	KAF3630015	19	0.7	2.6	1.3	1.8
9	Capana07g000167	195	probable RNA-dependent RNA polymerase	87	4.00E-107	95.0	XP_016579761	10	0.3	0.6	0.7	1.4
10	Capana07g000168	471	probable RNA-dependent RNA polymerase	90	0	100.0	XP_016579761	15	2.3 ^b	3.1 ^b	13.5 ^a	12.3 ^a
11	Capana07g000169	874	putative receptor-like protein kinase	96	0	92.0	XP_016579762	5	0.1	1.4	0.0	0.7
12	Capana07g000170	176	eukaryotic translation initiation factor-like	100	5.00E-127	100.0	XP_016579295	7	0.0	0.3	0.0	0.0
13	Capana07g000171	114	60S acidic ribosomal protein P2-like	100	1.00E-69	100.0	XP_016579297	4	0.0	0.0	0.0	0.0
14	Capana07g000173	431	uncharacterized protein	93	0	100.0	XP_016579766	8	15.7 ^{ab}	20.9 ^a	16.4 ^{ab}	11.3 ^b
15	Capana07g000174	293	uncharacterized protein	100	0	100.0	XP_016579767	6	26.6 ^b	35.9 ^b	47.2 ^b	112.4 ^a
16	Capana07g000175	205	ER membrane protein complex subunit 8/9 homolog	100	8.00E-147	100.0	XP_016579768	4	34.9 ^{ab}	60.6 ^a	28.5 ^{ab}	52.1 ^b
17	Capana07g000176	396	serine carboxypeptidase 24 isoform X1	100	0	93.6	XP_016579770	10	5.3	2.7	3.6	0.7

^z ID for genes predicted in the reference genome of *Zunla*.^y Predicted nonsynonymous substitution between PG1-1 and SCM334 from whole-genome resequencing.^x Average values for transcripts per kilobase million (TPM) of candidate ORFs. Three each for uninoculated and PepYLCIV-infected individuals were used for RNA-seq analysis. Different letters indicate significant differences between means (Tukey–Kramer test, $p < 0.05$).