

VvTPS9	491	ATGGTGTCAAGATCATCATATACAAGTTTCTTGGATGCGG
VaTPS9	1	
VvTPS9	531	CATCTGGGGACCTGTTGAATTCCTCAAAACACCTAGAAC
VaTPS9	41	
VvTPS9	571	CCTCCAAGGGTGATGACAGTTCAGGAATATTTCTGAT
VaTPS9	81	
VvTPS9	611	GGTGATGGAAACGGAAGTAACGATGAGGATTCAGACATT
VaTPS9	121	C.....
VvTPS9	651	TCTCATCCAAATGTCGTGAGAAGAAAATTATAGTGGCAA
VaTPS9	161	
VvTPS9	691	TTTTCTTCCTCTGCTTGCTCAAAAAGATTAAACACCGGC
VaTPS9	201	
VvTPS9	731	AGATGGTGCTTCAGTTTGTATGAAGATGCGCTTTGTGTAC
VaTPS9	241	
VvTPS9	771	AAATGAAGGATGGTTTCTCATCTGAACTGATGTTGTTTA
VaTPS9	281	
VvTPS9	811	TGTGGGATCTCTGAAGGTTGATGTAGATACCAGTGAGCAA
VaTPS9	321	
VvTPS9	851	GAAGAAGTTGCTGAGAGACTACTAGCAGAAATTAATTGTG
VaTPS9	361	
VvTPS9	891	TGCCACTTTTCTCTCCTGACCTTCAGAAAAAGTTTTA
VaTPS9	401	
VvTPS9	931	TCATGGGTTCTGCAACAATATCTGTGGCTCTCTCCAT
VaTPS9	441	
VvTPS9	971	TATATGCTCCCCATGTCACCAGAGCACTGCAATCGCTTGG
VaTPS9	481	
VvTPS9	1011	ATAGGTTTCTTTGGCAGGCCTATGTTTCAGCCAATAAAAT
VaTPS9	521	
VvTPS9	1051	ATTTGCAGATAAGGTCATGGAGGTGATCAATCCTGAAGAA
VaTPS9	561	
VvTPS9	1091	GATTATGTATGGATTCATGACTATCACCTTATGATTCTCC
VaTPS9	601	
VvTPS9	1131	CTACTTTTAAAGAAAGCGCTTCATCGAGTTAAGCTTGG
VaTPS9	641	
VvTPS9	1171	ATTCTTCCTCCACAGTCATTCCCCTCATCAGAAATCTAC
VaTPS9	681	
VvTPS9	1211	CGAACTCTGCCAGTCAGAGATGATATTCTAAAAGCATTGC
VaTPS9	721	
VvTPS9	1251	TGAATGCAGACTTAGTTGGTTTTCATACATTGATTATGC
VaTPS9	761	
VvTPS9	1291	TCGCCACTTTTGTCTTGTGCAGTAGAATGCTAGGCCTG
VaTPS9	801	
VvTPS9	1331	AACTATGAATCCAAGAGAGGTACATTGGACTTGAGTATT
VaTPS9	841	

VvTPS9 1371 TTGGCCGCACGGTTTATGTCAAATTTTGCCTGTGGGAAT
VaTPS9 881

VvTPS9 1411 TCATATGGGCCAACTTGAATCCGCACTAAATCTCCCTCT
VaTPS9 921

VvTPS9 1451 ACATCCATCAAGGTCAAAGAAATCCAAGAACAAATTC AAGG
VaTPS9 961

VvTPS9 1491 GAAAAAGATTATCTGGGTGTTGATGATATGGACATATT
VaTPS9 1001

VvTPS9 1531 TAAAGGACTAAGTCTAAAATTACTAGCCATGGAACACCTT
VaTPS9 1041

VvTPS9 1571 CTGCAGCATTATGAAGAGTTGCGGGTGAAC TAGTCTTGG
VaTPS9 1081

VvTPS9 1611 TTCAAATTGTAATCCTGCAAGGAGCACAGGTAAAGATGT
VaTPS9 1121

VvTPS9 1651 TCAGGAAGCAAAAAGGGAGACATATGCTATTACCGAAAGG
VaTPS9 1161

VvTPS9 1691 ATAAATGCAAATTTTGGTTTCCAGGCTATGAACCGGTGG
VaTPS9 1201

VvTPS9 1731 TCCTGATTGATCATCCTGTGCCTTCTATGAGAAGACTGC
VaTPS9 1241

VvTPS9 1771 CTATTATGCTTGGCTGAATGTTGCATAGTAAATGCTGTG
VaTPS9 1281 C.....

VvTPS9 1811 AGGGATGGAATGAACTTAATGCCATACAATTACATAGTTT
VaTPS9 1321

VvTPS9 1851 GCAGGCAGGGGACTCCAAAAATAGATGAAGCTTTGGGAAT
VaTPS9 1361

VvTPS9 1891 TACCTCTGGGTCTCTCGTACTAGTACACTTGTGTCTCA
VaTPS9 1401

VvTPS9 1931 GAATTCATAGGTTGCTACCGTCACTTAGTGGTGCAATAA
VaTPS9 1441

VvTPS9 1971 GAGTCAACCCATGGGATATTGATGCTGTGGCTGATGCACT
VaTPS9 1481

VvTPS9 2011 AAACATAGCCATCACAATGCCTGGTTTAGAGAAGCAGTTG
VaTPS9 1521

VvTPS9 2051 CGGCATGAGAAGCACTATCGGTACGTCAGCTCTCATGATG
VaTPS9 1561 T.....

VvTPS9 2091 TGGCATATTGGGCATGCAGTTTTATGCAGGATTTGGAGCG
VaTPS9 1601

VvTPS9 2131 GG CATGCAAAGATCACTACAGTAAACGTTGCTGGAGCATT
VaTPS9 1641

VvTPS9 2171 GGT TTTGGTCTGAGTTTCAGAATTGTTGCTCTTCTCCCA
VaTPS9 1681

VvTPS9 2211 ATTTTAGGAACTTCCCTTGACCATATTGTCAAAGCATA
VaTPS9 1721

VvTPS9	2251	TAAGAGGGCGAATAGAAGGGCGATATTTTGGATTATGAT
VaTPS9	1761	
VvTPS9	2291	GGAAACAGTGGTTCCGCAATCTCCATTGTTAAACCTCCTA
VaTPS9	1801	
VvTPS9	2331	GCCCTGAGGTTATCTCTATTCTAAATGACCTTTGCAATGA
VaTPS9	1841	
VvTPS9	2371	CCCTAAGAACACTGTGTTTATTGTTAGTGGCAGGGGGAAA
VaTPS9	1881	
VvTPS9	2411	AACTCTCTGAGTGACTGGTTCGCTCAATGT CAGAATTGG
VaTPS9	1921	
VvTPS9	2451	GAATAGCAGCTGAGCATGGATAC TTCATTAGGTGGAGTCA
VaTPS9	1961	
VvTPS9	2491	GAGT TCCAATTGGGAATCAAGACCTTTACTCATGGACTTT
VaTPS9	2001	
VvTPS9	2531	GACTGGAAAAGAATTGCAGATCCGTATGCAATTATATA
VaTPS9	2041	
VvTPS9	2571	CTGAGGCAACTGATGGCTCCTACATAGAGACTAAGGAGAG
VaTPS9	2081	
VvTPS9	2611	TGCC TTGGTATGGCACCACCAAGATGCTGACCTGATTTT
VaTPS9	2121	
VvTPS9	2651	GGATCCTGCCAGGCAATGGAGTTGCTGGATCATCTTGAGA
VaTPS9	2161	C.....
VvTPS9	2691	ATGTTCTTGCAATGAACCTGTGGAAGTTAAGAGGGGCCA
VaTPS9	2201	
VvTPS9	2731	TCATATTGTTGAGGTTAAGCCACAGGGAGTCAGTAAAGGT
VaTPS9	2241	
VvTPS9	2771	CAGGTTACAGAGAAAATCTTTCCACAATGATCAGTGATG
VaTPS9	2281	
VvTPS9	2811	GGAAACCACCAGATTTTGTGATGTGCATTGGGGACGATAG
VaTPS9	2321	
VvTPS9	2851	GT CAGATGAGGACATGTTTGAGAGCATATCAAGCACCATT
VaTPS9	2361	
VvTPS9	2891	TATAGTCCATCACTGCCTGCACCCAGAGATCTTTGCAT
VaTPS9	2401	G.....
VvTPS9	2931	GCACGGTCGGC AAAAAACCAAGCAAAGCTAGGTACTACCT
VaTPS9	2441	
VvTPS9	2971	TGATGATTCTGCAGATGTTTGAAACTGCTCCAGGGCCTG
VaTPS9	2481	
VvTPS9	3011	GCCAGAGCTTCTAGTATGAAGCCCAAGGTAGCACACAAA
VaTPS9	2521	
VvTPS9	3051	TACAGTTCTCCTTTGAAAGTGTTGCTTGA
VaTPS9	2561	.G.....

Figure S1. Nucleotide sequence alignment between *VaTPS9* and *VvTPS9*.

```
#####

# Program: needle

# Rundate: Thu  5 Feb 2026 14:55:16

# Commandline: needle

#   -auto

#   -stdout

#   -asequence emboss_needle-I20260205-145513-0725-23276111-
p2m.asequence

#   -bsequence emboss_needle-I20260205-145513-0725-23276111-
p2m.bsequence

#   -datafile EBL0SUM62

#   -gapopen 10.0

#   -gapextend 0.5

#   -endopen 10.0

#   -endextend 0.5

#   -aformat3 pair

#   -sprotein1

#   -sprotein2

# Align_format: pair

# Report_file: stdout

#####

#=====

#
```

```
# Aligned_sequences: 2
# 1: VvTPS9
# 2: VaTPS9
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 863
# Identity:      862/863 (99.9%)
# Similarity:    863/863 (100.0%)
# Gaps:          0/863 ( 0.0%)
# Score: 4553.0
#
#
#=====
```

```
VvTPS9          1
MVSRSYTSFLDAASGDLNFPQTPRTLPRVMTVPGIISDGDGNGSNDED      50
```

```
|||||
```

```
VaTPS9          1
MVSRSYTSFLDAASGDLNFPQTPRTLPRVMTVPGIISDGDGNGSNDED      50
```

```
VvTPS9          51
```

SDIFSSKREKKIIVANFLPLLAQKDLNTGRWCFSEDEDALLQMKDGFS 100

|||||

VaTPS9 51

SDIFSSKREKKIIVANFLPLLAQKDLNTGRWCFSEDEDALLQMKDGFS 100

VvTPS9 101

SETDVVYVGSCLKVDVDTSEQEEVAERLLAEFNCVPTFLPPDLQKKFYHGF 150

|||||

VaTPS9 101

SETDVVYVGSCLKVDVDTSEQEEVAERLLAEFNCVPTFLPPDLQKKFYHGF 150

VvTPS9 151

CKQYLWPLFHYMLPMSPEHCNRFDRFLWQAYVSANKIFADKVMVINPEE 200

|||||

VaTPS9 151

CKQYLWPLFHYMLPMSPEHCNRFDRFLWQAYVSANKIFADKVMVINPEE 200

VvTPS9 201

DYVWIHDYHLMILPTFLRKRFRVYKLGFFLHSPFPSSEIYRTLPRDDIL 250

|||||

VaTPS9 201

DYVWIHDYHLMILPTFLRKRFRVYKLGFFLHSPFPSSEIYRTLPRDDIL 250

VvTPS9 251
KALLNADLVGFHTFDYARHFLSCCSRMLGLNYESKRGHIGLEYFGRTVYV 300

|||||

VaTPS9 251
KALLNADLVGFHTFDYARHFLSCCSRMLGLNYESKRGHIGLEYFGRTVYV 300

VvTPS9 301
KILPVG IHMQLESALNLPSTSIKVKEIQEQFGKKIILGVDDMDIFKGL 350

|||||

VaTPS9 301
KILPVG IHMQLESALNLPSTSIKVKEIQEQFGKKIILGVDDMDIFKGL 350

VvTPS9 351
SLKLLAMEHLLQHVEELRGELVLVQIVNPARSTGKDVQEA KREYAITER 400

|||||

VaTPS9 351
SLKLLAMEHLLQHVEELRGELVLVQIVNPARSTGKDVQEA KREYAITER 400

VvTPS9 401
INANFGFPGYEPVVLIDHPVPFYEKTAYYALAECCIVNAVRDGMNLPYN 450

|||||

VaTPS9 401
INANFGFPGYEPVVLIDHPVPFYEKTAYYALAECCIVNAVRDGMNMPYN 450

VvTPS9 451
YIVCRQGTPKIDEALGITSGSSRTSTLVVSEFIGCSPSLSGAIRVNPWDI 500

|||||

VaTPS9 451
YIVCRQGTPKIDEALGITSGSSRTSTLVVSEFIGCSPSLSGAIRVNPWDI 500

VvTPS9 501
DAVADALNIAITMPGLEKQLRHEKHYRYVSSHVAYWACSFMQDLERACK 550

|||||

VaTPS9 501
DAVADALNIAITMPGLEKQLRHEKHYRYVSSHVAYWACSFMQDLERACK 550

VvTPS9 551
DHYSKRCWSIGFLSFRIVALSPNFRKLSLDHIVKAYKRANRRAIFLDYD 600

|||||

VaTPS9 551
DHYSKRCWSIGFLSFRIVALSPNFRKLSLDHIVKAYKRANRRAIFLDYD 600

VvTPS9 601
GTVVPQSSIVKTPSPEVISILNDLCNDPKNTVFIVSGRGKNSLSDWFAQC 650

|||||

VaTPS9 601
GTVPQSSIVKTPSPEVISILNDLCNDPKNTVFIVSGRGKNSLSDWFAQC 650

VvTPS9 651
QNLGIAAEHGYFIRWSQSSNWESRPLLMDFDWKRIADPVMQLYTEATDGS 700

|||||

VaTPS9 651
QNLGIAAEHGYFIRWSQSSNWESRPLLMDFDWKRIADPVMQLYTEATDGS 700

VvTPS9 701
YIETKESALVWHHQDADPDFGSCQAMELLDHLENVLANEPVEVKRGHHIV 750

|||||

VaTPS9 701
YIETKESALVWHHQDADPDFGSCQAMELLDHLENVLANEPVEVKRGHHIV 750

VvTPS9 751
EVKPQGVSKGQVTEKILSTMISDGKPPDFVMCIGDRSDEDMFESISSTI 800

|||||

VaTPS9 751
EVKPQGVSKGQVTEKILSTMISDGKPPDFVMCIGDRSDEDMFESISSTI 800

VvTPS9	801	
YSPSLPAPPEIFACTVGQKPSKARYYLLDSADVLKLLQGLARASSMKPKC		850
VaTPS9	801	
YSPSLPAPPEIFACTVGQKPSKARYYLLDSADVLKLLQGLARASSMKPKC		850
VvTPS9	851 STQIQFSFESVA*	863
	:	
VaTPS9	851 STQMQFSFESVA*	863
#	-----	
#	-----	

Figure S2. Amino acid sequence alignment between VaTPS9 and VvTPS9.

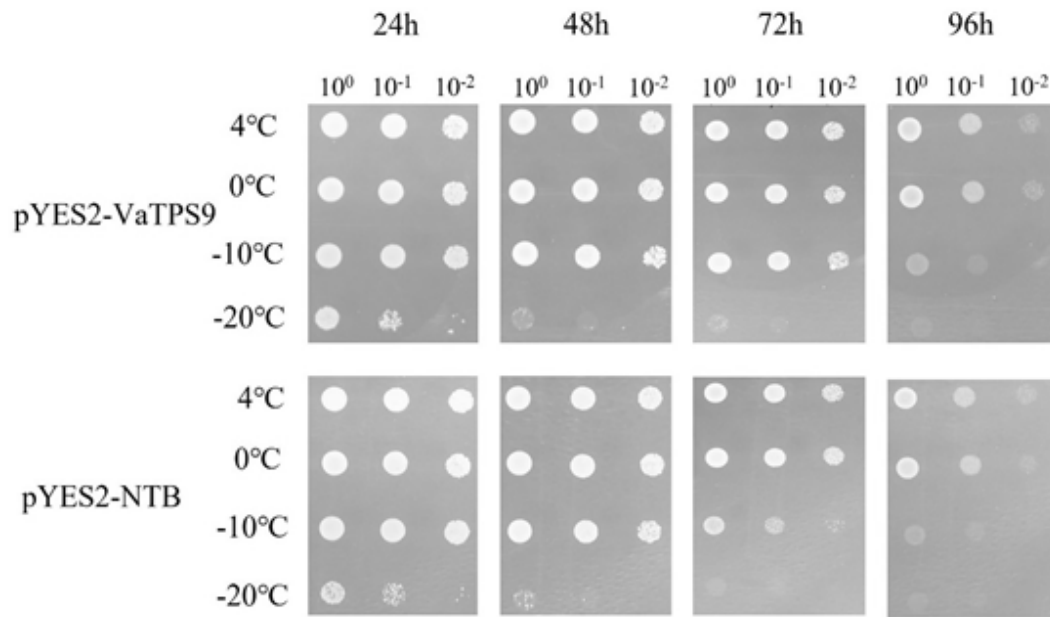


Figure S3. 8-bit grayscale images analyzed using ImageJ (Fiji) (F.6)

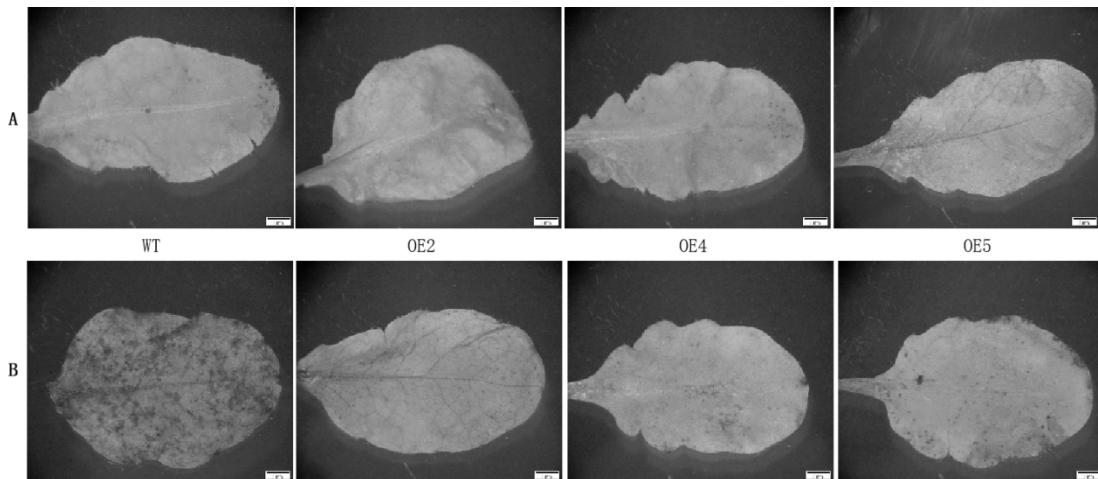


Figure S4. 8-bit grayscale images analyzed using ImageJ (Fiji) (F.11)

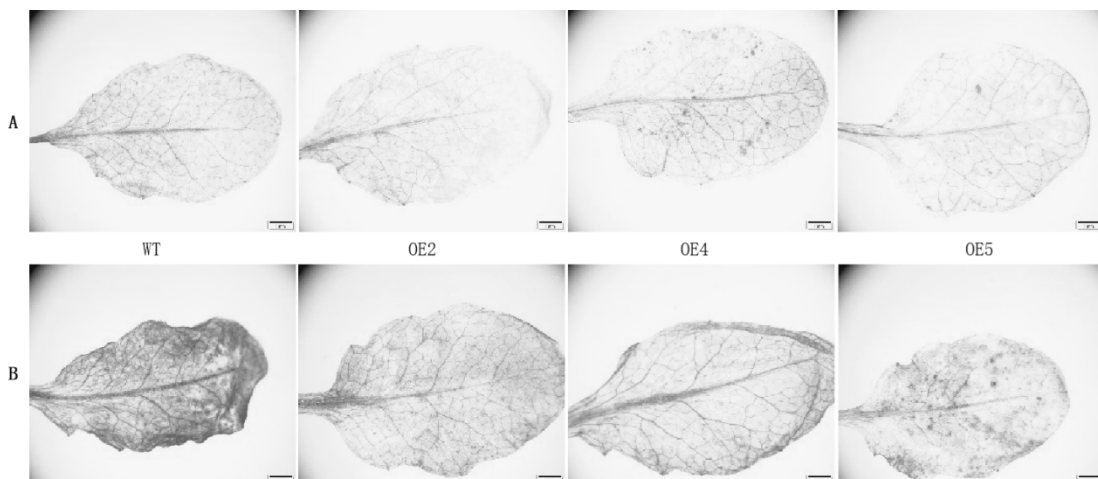


Figure S5. 8-bit grayscale images analyzed using ImageJ (Fiji) (F.12)