

#Additional File S3: CAAX/CpAX proteins (<100aa) from *B. cinerea*, *B. sinoalli*, *S. sclerotiorum*, *M. fructicola*, *R. commune*, *A. resinae* & *P. destructans*

>M\_fructicola\_VICG01000013.1\_EYC84\_009782  
MLLFLRFLSWGFFSTVGLGNGHFHASIIISCVPNLCVIHGHDSNQYHLFMGNKFLSLPLR  
PTTMCSAP\*

>M\_fructicola\_VICG01000010.1\_EYC84\_008624  
MRVMVQEYLAGVQEKMLARRAEDSQGLKWPMNQAGDARCLCWFQLPTFINLAYGLLSCSG  
VVMLCCIVLCCVVL\*

>M\_fructicola\_VICG01000011.1\_EYC84\_009873  
MQDEDEDDYALAAMGISNGGGYRPSDSNQNTYTPPPPQPESQLPPLERRASTPPPETLK  
HNKAKRNRNFVCAK\*

>M\_fructicola\_VICG01000002.1\_EYC84\_004913  
MKIRKTLVESGQMESDADDDEEEEEEDGGGGGVDVVKPCRSKRALKRLKLRSSHGKL  
RLKSKRVEYGALYKCTLYCTVE\*

>M\_fructicola\_VICG01000003.1\_EYC84\_005768  
MPYRAIPQLKINNFPLRSLLRPPVKIALWPSLNSLFCPPSPLLVIHLPTSPTAYRYIT  
IRSARGCLLSHYPPPKRTCPIP\*

>M\_fructicola\_VICG01000011.1\_EYC84\_010293  
MVFFKYLLRFVSRSWTFKTSDHVASDFCEFGVSLDDRYIVQCNLTCTTHATGRPVGIGNE  
KSYPIQLSVFTKLCIDIICACNAN\*

>M\_fructicola\_VICG01000016.1\_EYC84\_011744  
MAQQPQKPHRSLWDREPSDVANMPPVYTQEYDNRVSPQPQSQPPANAVKDASETQKEAI  
YVQKQNERKNNEDDVASGCCGCSVM\*

>M\_fructicola\_VICG01000007.1\_EYC84\_002179  
MQFIATTFIAILSAVAASPLQSRSGLCSSALDTAQCCDVSVAGVANLNCASPSSTPTSV  
ENFRSICAAGGQQASCCVLPVAGDALVCVAP\*

>M\_fructicola\_VICG01000007.1\_EYC84\_002586  
MPDNGITLCQYPSIRHLNHWYSTSGIYLCNFSILFLFWPFFKRIPIPIERSPRINEQQSN  
YLSSASGLEIEIMNRRDAAGVVGCTFCAVC\*

>M\_fructicola\_VICG01000004.1\_EYC84\_003548  
MKRKEEKTDKKKKIIIVQQLPSILHSSPQAGTSNPHLTQIHSFHDRFGIPKREQDPCSV  
PLHVTQDQPPSASQTARESMSSLHNHDAPCLPV\*

>M\_fructicola\_VICG01000011.1\_EYC84\_010490  
MIYKLFEPSSRFDWDAGHLYQSRIKELIQDKDGDLETYGMVAQRELSTTRVLVHTKTLF  
YFLPLISIHGWIQSMQGNVRQKARQKAMQCINVA\*

>M\_fructicola\_VICG01000006.1\_EYC84\_000648  
MIRFRMGRSRIRSSALSIFHEEINTVMRLFVYIISSSPLLLSPQLTIYTSILIIILAQR  
HPSHHITGHDIILIIYTQGNAMQRSAAQIEKLLACLLA\*

>C\_cinerea\_NC\_037317.1\_BCIN\_08g01220  
MPADWRDTKSGNVKGFIRRKDPNPLNWGYKVDKVLVSHPKAAMIKTDVSKPKKDDKCKS  
CEKKKKKEEKKKEKKKSAGGCIVS\*

>C\_cinerea\_NC\_037322.1\_BCIN\_13g03330  
MCTSTSTGLVNRNGPGSAASSTISDIVKGTSTTGKTKCLECDGYECCCIPIPTVM\*

>C\_cinerea\_NC\_037319.1\_Bcgg1  
MPQGYSSRDVGDPSQIKKNKQSMADLKLRLTELNRLREDLERERIPVVSQAASIIQYT  
SQTkDFMVPSIWGTVEKKDDPYAPQQSGGCCLVM\*

>C\_cinerea\_NC\_037315.1\_Bhp3  
MQFTTTTLIAILSALAVASPIEPRQNATAQQERLCTSAIDTAMCCQTTLAGVINQTCTTP  
AITPINKQAFRAYCAAQGQDSSCCKTPLVGDGVICTPP\*

>B\_sinoallii\_NW\_024066037.1\_EAF02\_006546  
MPADWRtdKSGNVKGFIRRKDPNPMNWGYKVDDKVLShPKAGMVKTDVSKPKKDDKCKS  
CEKKKEKEKKKKEKKDSAGGCLVS\*

>B\_sinoallii\_NW\_024066059.1\_EAF02\_011438  
MPQGYSSRDVGDPSQIKKNKQSMADLKLRLTELNRLREDLERERIPVVSQAASIIQYT  
SQTkDFMVPSIWGTVDKKDDPYAPQQSGGCCLVM\*

>B\_sinoallii\_NW\_024066033.1\_EAF02\_004193  
MTTSLLEAWIWIWITQCAGKTCKFFAFPTNLPRLPtGNSLLAEAEAPYRSRKSQQQSYDQH  
VEKFRHAWRKKENPAAGLADGCSGICSGFRKGC PAL\*

>B\_sinoallii\_NW\_024066029.1\_EAF02\_001539  
MTPQPSHFkTFTLSSLYRHHLKPHKLILILNLNLNLIQQLKMCtSTSTGLVNRNGPGSAA  
SSTISDIVKGTSTTGKTKCLECDGYECCCIPIPTVM\*

>B\_sinoallii\_NW\_024066033.1\_EAF02\_004477  
MQFTITTLIAILSAIAAASPIEPRQNGTAQQERLCTSAIDTAMCCQTSLAGVINQTCTSTP  
AITPFTKEQFRAYCAAQGQDSSCCKTPLVGDGVICTPP\*

>S\_sclerotiorum\_NW\_001820814.1\_SS1G\_12764  
MAYDPAMPWILWKSQTTLTDGAISSKSDCLCAAP\*

>S\_sclerotiorum\_NW\_001820822.1\_SS1G\_10003  
MTDTNSSQTKHCEKVIVGGPPVEEINAKTFCIAA\*

>S\_sclerotiorum\_NW\_001820812.1\_SS1G\_13368  
MGIHARCQRIKRADCALRNKSCQRSMRDAAQCVIV\*

>S\_sclerotiorum\_NW\_001820812.1\_SS1G\_13356  
MVEKRDRLLDYAKAHNIAVPTMGAAFEGCSNCSIE\*

>S\_sclerotiorum\_NW\_001820832.1\_SS1G\_03496  
MGHRAVVLPLHFKVSWKPAPVNPIRIMIffSASGDVYCLLD\*

>S\_sclerotiorum\_NW\_001820831.1\_SS1G\_04828  
MVDVEAFGWSGYCTASSKACCPAQLRHLcPTPPVGAVTVPDLAQVSSVTILSSYLcVVV\*

>S\_sclerotiorum\_NW\_001820832.1\_SS1G\_03509  
MSSPDTPGNIEGLLRKGDlnPMNWGFkVDDKILDHPKIGLIKTDVSKPKDDGKCKSCVK  
KQEKAKKKEKNGDAGGCvVS\*

>S\_sclerotiorum\_NW\_001820822.1\_SS1G\_09848  
MCGRCLTKQGVHIDKDFLQeANARRRSEAAEIRQSTILTLKILEQANVfVKEEKRNRRER  
RRRRNTRGGMADRgKIGKQRKCVVM\*

>S\_sclerotiorum\_NW\_001820828.1\_SS1G\_06541  
MTIASVRESLFLQTVRRRRIISALYSISVYGTKVTSRMEGLYVYCGGMGTEGIANGGQSA  
ITDTQRLATKDHRRPHIIVWSNKCSIY\*

>S\_sclerotiorum\_NW\_001820815.1\_SS1G\_12567  
MPQGYSSRDVGDPSQIKKNKQSMADLKLRLTELNRLREDLERERIPVVSQAAKSIIQYT  
SQTkDFMVPSIWGTVDKKDDPYAPQQSGGCCCLVM\*

>S\_sclerotiorum\_NW\_001820824.1\_SS1G\_09095  
MAQNPQEPHRSRWDREPADVANMPPAYTQENETKPPFPQPPLRPTYAMNDGRGGQREV  
YVQQQOVERKHNKDDIALGCCAGCAAGCCCCGCSVM\*

>R\_commune\_FJUW01000046.1\_CZT08289.1  
MSAQQLIYLHPWTGRSQQLEVSPGHGPWIYDIAYCVAN\*

>R\_commune\_FJUW01000014.1\_CZS98287.1  
MARENRFPKVAGYTVNTGPSNPNARYNADYDQRNRPHRPHGGHSSHRPHGGHSSSRKK  
DPCRCVVM\*

>R\_commune\_FJUW01000010.1\_CZS95335.1  
MEASCLPRHDIHPSLGLTTEEFSGSIIILDDRLALATASMYRGLTGEGSPGWSVGRSVDIRP  
EKLRRCPFL\*

>R\_commune\_FJUW01000051.1\_CZT09580.1  
MNLEINLRNSNSLTGTLKSCSIYATPRPILPSHERTPPVKLLDVAAISDSDEIENQTD  
TSTNVNPNPGCTLP\*

>R\_commune\_FJUW01000027.1\_CZT03207.1  
MCGCYVSSRESKVAKSLFENVGISSIYEH LAPS NKSYIVSDWAATALHIFGLSSVQTQAE  
SFRNKKAQGVQPQRHRSSGCVPH\*

>A\_resinae\_NW\_020194476.1\_M430DRAFT\_139873  
MCTATPSAPINHNGPGSAASSTISSIVKPEAGAAGKTKCLECDGFECCEIPIPTVM\*

>A\_resinae\_NW\_020194477.1\_M430DRAFT\_141309  
MPSGYSSRDVGDPSQVKKNKQSMADLKLRLTELNRLREDLERERIPVVSQAAKSIIITYT  
NNTKDFMVPSVWGTVDKKEDPYAPQQSGGCCVVM\*

>P\_destructans\_NW\_020167544.1\_GNG1  
MGYASRDAADPSQIKKNKQSMADLKLRLTELNRLREDLERERIPVVSQAARSIIAYTDT  
TRDFMVPSVWGPVVDKDDPYTPQPTGGCCVVM\*

>P\_destructans\_NW\_020167532.1\_VC83\_05352  
MARSTDPAPLRIAGIQSGTDREAAGHSRISCKPSSSSLADFKEPAYLAINPNGRVPSIH  
DPNTDLTLWESGAIIEYLIIEKYDSGRDQIICPLC\*