

a) Sample #: SD-1  
 Database: Uniprot  
 Accession #: A0A0U2DCT9  
 Protein Identity: AHSV-5 VP2  
 Protein Score: 655.7  
 False Discovery Rate: 0.5%  
 Peptides: 158

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1 YVFDASEPC YLITDVEGD ALERTWCEVI LTRSGVSRK EVDGVDYEV EPTDRLGLC
41 EIDRHMAG PPYNGRCKD AVPIFFHYT DLKDYKRVG RHHQVYKH DAKLSEIL
121 QPTGKATP PPTTITSLA KGLAQKQVH LARVYDVA FYEDHNSG YINDWIGL
181 QAKKADLQ RSRGSHGDS CVHMADVTI QHWLFLQL LYHYVYKLP EYVVEKSG
241 GLIANNLVR EAGKAEKPT RYGVQPLMT LKRIEDEL DEVIQKIIA YGRFETTAG
301 VRTGQTLME LAKYCELTQ FVSRKQGE DETAFFTEK ENIQGKNS FSRHGKSR
361 SRATYKPKI LKPKHMY EIDPDRHW DYKRFVQQL DEAGKSMK PYVNDIHW
421 IHNKSGDV EHWVDVVTI IGLSVERLY RDIFFKALD DMLSGHEL VGALKYATC
481 LILALYVFG EDIQQFPTI SARGIVETG QHPQPKKQ SETPGITLH EDVYKLFIA
541 RHWASADQ GQVSKPQVQ WHETQKYE DYADLSEKV FALYQALSG RHWDLAQT
601 ERTFDGLVY RQGVVFERA GLDGRHLYV KYNHLLTY FSRFIEYH EITVSAHG
661 LITLDGDA RSTQDFPD KPMAYKLG AHARTYVH LILRHPKX IDDAKSIWY
721 DLSLTFGCS KGLDCHWGS VAKSELKAF KLSAIFPK QDAKRESPT EITPDKSR
781 ERIFPKYH YVALLQHTS DQGLTWDI CEKAEFETK KALLRQDF RHWVEKFA
841 FLDKHALW VLADHEDI NYHKNPLI LSTEDLAVI EIMFQHLG VYDHWYFL
901 EHCIEVNLQ RHLADELK KHWIYAT SEVENRSP RFFKMLD VEGHCGVQ
961 SYVALIPK RPKNLLFL YADGQVWV AMLSDVIG RSLGKPIK RHPVWIKL
1021 EVKTLKTH GMLRLLIS QKQYFFKRY LKRLAKTE R*DCGK*1 KL
  
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c) Sample #: SD-3  
 Database: Uniprot  
 Accession #: A0A0N7CZK8  
 Protein Identity: AHSV-5 VP5  
 False Discovery Rate: 0.4%  
 Protein Score: 973.7

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1 RDKGTFEL KMGKATEA LTEDAEMV KMGKTLQY YSEVGEAL DQNGQTIQ
41 EIQGHGAD INQVTLVA QLESAPUL RPKGLLHV VKELEAKI DVLLETWER
121 IIRVQDGL KIKKHPGA RAGLQREI EYVENALGH LKIQGQSR EYGLYALQY
181 EEDLVEETI EHWYKEP KALQALEL QQATSEAVQ EHLGSAVI EYAEVYFIF
241 GAGAAVAT TRAVDQLEL KRIDKTLTI DLNLEVADI RPKIKKML EKIFQWELA
301 RAIKRYEVI RQNTKSTY IKKINLQK EYKKNKRY VNIQVLEK RRTPKVMT
361 EYHGDDEV ICACIAPKQ QKSNLQFL EIEFVYEDT SVEDHNSG AVSIDRQF
421 QATSEYMA WRPETPEL KPLQRELS EPIYKSDT TVSDQLVH RMLVYDTEL
481 QKCLKPLR FQSTLHNL LFGVLA*LE
  
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b) Sample #: SD-2  
 Database: Uniprot  
 Accession #: A0A0N7CXD3  
 Protein Identity: AHSV-5 VP3  
 Protein Score: 929.2  
 False Discovery Rate: 0.7%  
 Peptides: 160

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1 NQCHRIQK KEKKAATP LQGAIVTIN GPILSVFALQ EIKQKIQK DMMKADPV
41 KGLPFWTI IRIKHLER EDYVIMAPY RFPYTPMGI TRVLDQWY YEMKIQDF
121 VDTDFDPT ALILKRLPL EYHAPILQI ITRDYGKAS IADPELQV FQNALGKAA
181 EIKQIQQTL NQKIKMLV ADHYVYKQ AKSDFTSKH RVLQGVYKQ QYGLRSHW
241 MRLRLKLR IKFAMFLYI FRAKTIKI SGLPIMAYI DNVFQCHIA RLITVALLC
301 FQCELDWY RIGITIQK ITQDPTLII SGLPTAVQK RYRMLYAL RFINQILDI
361 KPSKHAQV VLKRVVGL EHWYVQVH TRITPNAEL LDAALDYLL EYHNSIPH
421 EYPTQPLQF RARQKIDC RIAFRDQVQ RHWKQVDS VQVQDSDP RQVYKTC
481 IDREIIEF EYKHMVYI FRLKSLVA AGDQKAYL RQKLYKHK FAKIQIIE
541 DLKAPSLQ QMFDVLRH IDDFKDTF VVLEYKAI WFAVREKQ IAKSLKAA
601 PLKARTAA LETHMDVQ LHWKRVYI TVDAPKQC KAVLEKAP FIKHLGK
661 RSPYVYD VHWQKQVQ ERLAVLKH AKALHDFD LHLVHYTIQ RHWKPKL
721 EYDFRQCF FTHKIDGAP FIDVYRTH AIANLQAHQ QPAALRKL DQGVQKQ
781 KLRKIEYF ESRFHELE ADYVYKLE RQVWYAK TATATAYL LYVYKHTF
841 DYLIVNPF THKIMNK IWRVYKAV LQKRLVA THQWRLVY TQKTYQGL
901 RPTI
  
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d) Sample #: SD-4  
 Database: Uniprot  
 Accession #: A0A0U2DHE9  
 Protein Identity: AHSV-5 VP7  
 False Discovery Rate: 0.3%  
 Protein Score: 765.1  
 Peptides: 68

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1 *HVMKATA ARLVYKAC YVYDARVH DQWVTEGI ADRHRLW RYVENIQK
41 RERKHPYK TIMVLAALV QIQVDFDQ QALAYWALA VTEIYVQA RHDVRYTQ
121 NQYSPKQY TQYMAVAV QSGEYVYFQ RYKQIIEH KLAQYKAG ANQYNALLA
181 FRSQAVHT FVNRFLATC SPQAGLEA PQTYYVYDQ SVAGQVYVW RTIAPVWQ
241 RARRKIQF EMLVYELH SLYVPEAF TLNRYAYV FTHALKAVI FQKQKQV
301 FVFFPTER EIVATLVAV LADYVALEP DFHWYVAV VQVTRALV AAK*HLKQ
361 VYAFIDKQ VLALHYA*V IQVYEL
  
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**Figure S4** Mass spectrometry analysis of the 4 protein bands recovered from SDS-PAGE separation of density gradient fractions from leaves co-infiltrated with *Agrobacterium* AGL1 pEAQ recombinants for co-expression of AHSV capsid proteins VP2, VP3, VP5 and VP7<sub>mu</sub>.