Supplemental Materials

Novel Victorivirus from a Pakistani Isolate of *Alternaria alternata* Lacking a Typical Translational Stop/Restart Sequence Signature

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Supplementary Table S1

Supplementary Figures S1 to S4

Supplementary Table S1 Primer list

Figure S1. Multiple alignments of victorivirus nucleotide and amino acid sequences. A. Presence of Octanucleotide sequence along with an extra seven conserved nucleotides (5′-AGGGUUCC**GUUGAUC**-3′, bold letters) in the 5’UTR of AalVV1 and several other victoriviruses. The numbers in the parenthesis indicate the start of Octanucleotide sequence in the 5’UTR of the respective viruses. **B**. Comparison of the eight conserved motifs of RNA-dependent RNA polymerase of AalVV1 with those of other victoriviruses **C**. Comparison of C-terminal region of AalVV1 with prototype victorivirus HVv190S showing a Ala/Gly/Pro-rich region.

Figure S2. The Mascot search result of the LC-MS/MS analysis of the major 80 kDa protein band of AalVV1. The peptides predicted by LC-MS/MS analysis were mapped onto the deduced amino acid sequence of AalVV1 under the assumption that ribosomes were slipped on repeated A sequences followed with the stop codon of the ORF1. The light cyan and the light magenta indicate the amino acid sequence of frame +3 and frame +1, respectively, on the positive strands of AalVV1 genome.

Figure S3. Colony morphology of *Cryphonectria parasitica* infected AalVV1. Protoplasts of two strains of *C. parasitica*, the standard RNA silencing-proficient EP155 and RNA silencing-deficient strain Ddcl2, were transfected by partially purified virions of AalVV1. Obtained transfectants and virus-free counterparts were grown on PDA for one week, and photographed.

Figure S4. Predicted secondary structure of the ORF1/ORF2 junction sequences of the two AalVV1 related victoriviruses. Pseudoknot structures were predicted by DotKnot program [Sperschneider and Datta, 2010] and schematically represented for Phomopsis vexans RNA virus (PvRV, accession number KP090346) and Nigrosopra oryzae victorivirus 1 (NoVV1, accession number KT428155). The ORF1 termination codon and the ORF2 AUG codon are denoted in blue and red, while the upstream in-frame ORF2 stop codons are shown in bold. PvRV could utilize the -2 /+1 frameshift and the possible slippery site (blue bracket) is shown. A predicted RNA pseudoknot structure is depicted near the 3′ end of the ORF1, and the nucleotide positions are indicated (2511–2538), whereas NoVV1 could utilize the terminitation-reinitiation strategy and the position of overlapping start codon of the ORF2 and the stop codon of the ORF1 in the tetranucleotide sequence *AUG*A (map position 2554, highlighted red/blue) as indicated.

Sperschneider, J.; Datta, A., DotKnot: pseudoknot prediction using the probability dot plot under a refined energy model. *Nucleic Acids Res* **2010,** 38, (7), e103.

Table S1. List of primers used in the confirmation and completion of the AalVV1 sequence.

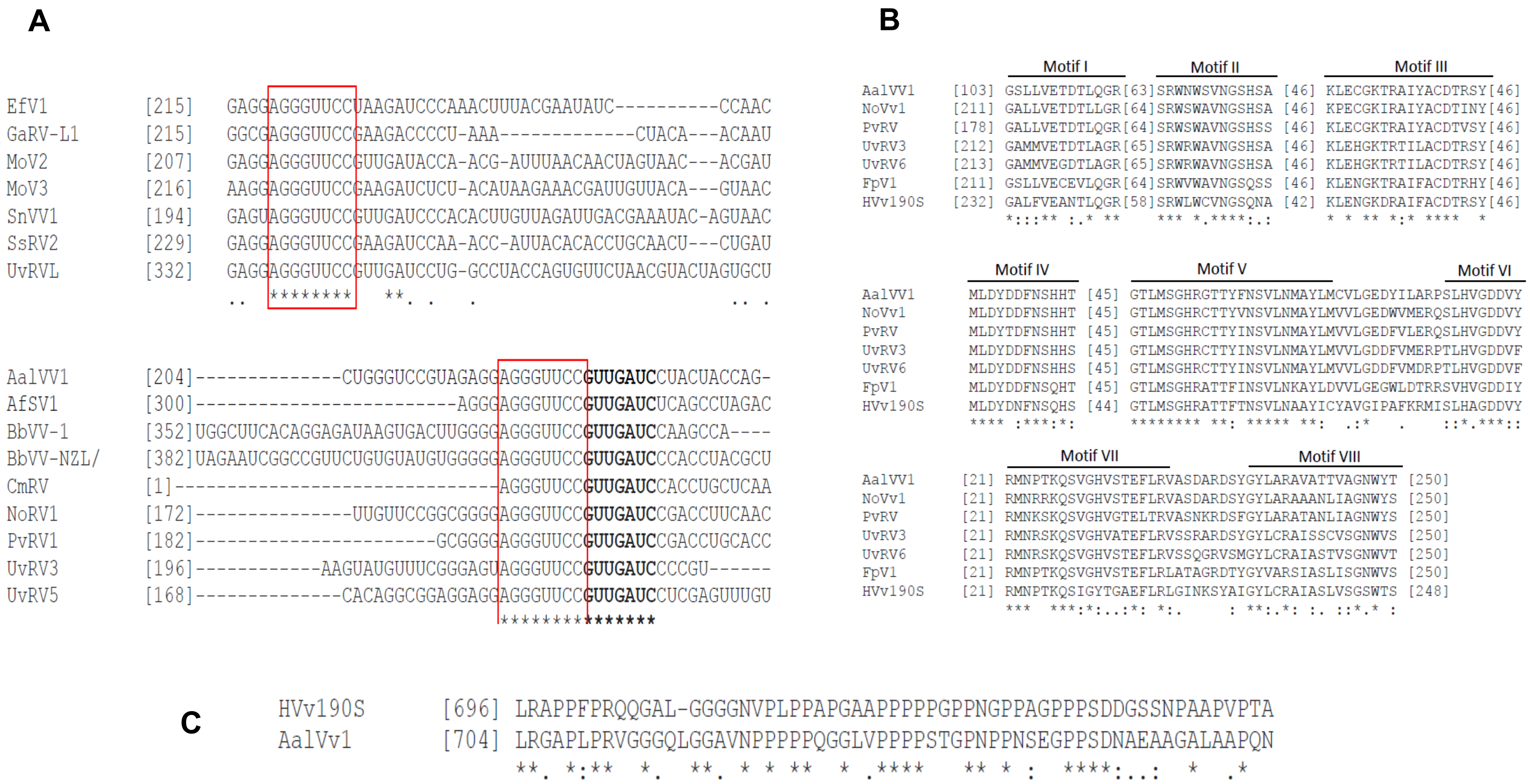
Primer name	Oligonucleotide sequence (5'-3')	Position	Usage
AJ- 19F (1)	CCGATGGCCGATGAGAACAGG	2244-2264	RT-PCR
AJ- 19R (1)	TCTCCAGCAATCCCGCGCTAC	2973-2953	RT-PCR
AJ- 19F (2)	CGCATCCCTTCAAGTTCCGGG	2035-2055	RT-PCR
AJ- 19R (2)	AGATCGTAGGGAGTCAACCGC	2645-2625	RT-PCR
AJ- 19 (E1)	GTAGCGTCGGTATTGGTCGTC	374-353	RLM-RACE
AJ- 19 (E1)	GCACCGTCGGGTGTGCTCACC	4812-4792	RLM-RACE
AJ- 19 (E2)	TGAGTGTAGGCCATCGCCTCG	493-473	RLM-RACE
A2- 19 (E2)	GATGGTCATGTCTAGTTGGTC	4662-4681	RLM-RACE
LIG-For primer	CCGCTCTAGAACTAGTTGGATC		RLM-RACE
LIG-Rev [5'-phosphorylated; 3'-amino-linked]	GATCCAACTAGTTCTAGAGCGG		RLM-RACE
ITS1	TCCGTAGGTGAACCTGCGG		For rDNA amplifiction
ITS2	TCCTCCGCTTATTGATATGC		For rDNA amplifiction

Table S2. Some properties of reported victoriviruses

SNo	Virus name	Abbreviations	Accession	Genome length (nt)	CP coding region	RdRp coding region	Host	Conserved octanucleotide sequence in 5'UTR	Reference
1	Aspergillus foetidus slow virus 1	AfSV1	NC_038928	5194	374-2599	2599-5188	Fungi	**AGGGTTCCGTTGATC**	Kozlakidis *et al*., 2013
2	Beauveria bassiana victorivirus 1	BbVV-1	NC_038929	5288	444-2672	2672-5176	Fungi	**AGGGTTCCGTTGATC**	Herrero *et al*., 2012
3	Beauveria bassiana victorivirus NZL/1980	BbVV-NZL/ 1980	NC_024151	5327	459-2735	2735-5266	Fungi	**AGGGTTCCGTTGATC**	Khalifa. (unpublished)
4	Botryosphaeria dothidea victorivirus 1	BdV1	NC_025214	5322	512-2743	2743-5265	Fungi	----------	Zhai et al. (unpublished)
5	Chalara elegans RNA Virus 1	CeRV1	NC_005883	5310	329-2641	2619-4067	Fungi	----------	Park *et al*., 2005
6	Coniothyrium minitans RNA virus	CmRV	NC_007523	4975	62-2389	2386-4875	Fungi	**AGGGTTCCGTTGATC (start of UTR)**	Cheng *et al*., 2003
7	Eimeria tenella RNA virus 1	EtV 1	NC_026140	6006	350-2716	2713-5928	Protozoa	----------	Wu *et al*., 2016
8	Epichloe festucae virus 1	EfV1	NC_038930	5109	271-2571	2568-5051	Fungi	**AGGGTTCC**	Romo *et al*., 2007
9	Fusarium poae victorivirus 1	FpV 1	NC_030867	5124	164-2572	2572-5055	Fungi	**AGGGTTCC (in ORF1)**	Osaki *et al*., 2016
10	Gremmeniella abietina RNA virus L1	GaRV-L1	NC_003876	5133	276-2603	2603-5080	Fungi	**AGGGTTCC**	Tuomivirta and Hantula, 2003
11	Helicobasidium mompatotivirus 1-17	HmTV1-1-17	NC_005074	5207	200-2566	2563-5100	Fungi	----------	Nomura *et al*., 2003
12	Helminthosporium victoriae virus 190S	HvV190S	NC_003607	5179	290-2608	2605-5112	Fungi	----------	Huang and Ghabrial, 1996
13	Magnaporthe oryzae virus 1	MoV1	NC_006367	5359	575-2815	2818-5316	Fungi	----------	Yokoi *et al*., 2007
14	Magnaporthe oryzae virus 2	MoV2	NC_010246	5139	275-2641	2638-5130	Fungi	**AGGGTTCC**	Maejima *et al*., 2008
15	Magnaporthe oryzae virus 3	MoV3	NC_027209	5181	283-2634	2631-5108	Fungi	**AGGGTTCC**	Tang *et al*., 2015
16	Nigrospora oryzae victorivirus 1	NoRV1	NC_030224	5100	236-2554	2554-5037	Fungi	**AGGGTTCCGTTGATC**	Zhong *et al*., 2016
17	Phomopsis vexans RNA virus	PvRV1	NC_026135	5076	243-2543	2642-5026	Fungi	**AGGGTTCCGTTGATC**	Zhang *et al*., 2015
18	Rosellinia necatrix victorivirus 1	RnVV1	NC_021565	5329	373-2664	2664-5192	Fungi	----------	Chiba *et al*., 2013
19	Sclerotinia nivalis victorivirus 1	SnVV1	NC_030392	5162	286-2583	2580-5081	Fungi	**AGGGTTCC**	Wu and Li. (unpublished)
20	Sphaeropsis sapinea RNA virus 1	SsRV1	NC_001963	5163	80-2581	2574-5090	Fungi	**AGGGTTCCGTTGATC (in ORF1)**	Preisig *et al*., 1998
21	Sphaeropsis sapinea RNA virus 2	SsRV2	NC_001964	5202	296-2665	2658-5135	Fungi	**AGGGTTCC**	Preisig *et al*., 1998
22	Tolypocladium cylindrosporum	TcV1	NC_014823	5196	327-2603	2604-5126	Fungi	----------	Herrero and

	virus 1								Zabalgogeazcoa, 2011
23	Ustilaginoidea virens RNA virus 1	UvRV1	NC_020997	5142	274-2604	2904-5075	Fungi	----------	Zhong *et al.*, 2014
24	Ustilaginoidea virens RNA virus 3	UvRV3	NC_023547	5075	259-2532	2532-5021	Fungi	**AGGGTTCCGTTGATC**	Zhong *et al.*, 2014
25	Ustilaginoidea virens RNA virus 5	UvRV5	NC_028477	5221	314-2584	2584-5166	Fungi	**AGGGTTCCGTTGATC**	Zhong *et al.* (unpublished)
26	Ustilaginoidea virens RNA virus L	UvRVL	NC_025366	5654	421-2661	2661-5144	Fungi	**AGGGTTCC**	Jiang et al., 2015
27	Alternaria arborescens victorivirus 1	AaVV1	NC_040793	5206	327-2657	2654-5143	Fungi	**AGGGTTCCGTTGATC**	Komatsu *et al.*, 2016
28	Botryosphaeria dothidea victorivirus 2	BdVV2	MH301088	5,090	284-2505	2512-5019	Fungi	**AGGGTTCCGTTGATC**	Yang *et al.*, 2019
29	Fusarium asiaticum victorivirus 1	FaVV1	NC_040653	5281	378-2657	2657-5185	Fungi	-----------	Li *et al.*, 2019
30	Nigrospora oryzae victorivirus 2	NoRV2	MH823900	5166	327-2597	2597-5095	Fungi	----------	Liu *et al.*, 2019
31	Ustilaginoidea virens RNA virus M	UvRVM	NC_025367	2714	731-2239		Fungi	--------	Jiang *et al.*, 2014

Figure S1



A

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EfV1        [215]  GAGGAGGGUUCCUAAGAUCCCAAACUUUACGAAUAUC----------CCAAC
GaRV-L1     [215]  GGCGAGGGUUCCGAAGACCCCU-AAA-------------CUACA---ACAAU
MoV2        [207]  GAGGAGGGUUCCGUUGAUACCA-ACG-AUUUAACAACUAGUAAC---ACGAU
MoV3        [216]  AAGGAGGGUUCCGAAGAUCUCU-ACAUAAGAAACGAUUGUUACA---GUAAC
SnVV1       [194]  GAGUAGGGUUCCGUUGAUCCCACACUUGUUAGAUUGACGAAAUAC-AGUAAC
SsRV2       [229]  GAGGAGGGUUCCGAAGAUCCAA-ACC-AUUACACACCUGCAACU---CUGAU
UvRVL       [332]  GAGGAGGGUUCCGUUGAUCCUG-GCCUACCAGUGUUCUAACGUACUAGUGCU
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AalVV1      [204]--------------CUGGGUCCGUAGAGGAGGGUUCCGUUGAUCCUACUACCAG-
AfSV1       [300]-------------------------AGGGAGGGUUCCGUUGAUCUCAGCCUAGAC
BbVV-1      [352]UGGCUUCACAGGAGAUAAGUGACUUGGGGAGGGUUCCGUUGAUCCAAGCCA----
BbVV-NZL/   [382]UAGAAUCGGCCGUUCUGUGUAUGUGGGGGAGGGUUCCGUUGAUCCCACCUACGCU
CmRV        [1]-------------------------------AGGGUUCCGUUGAUCCACCUGCUCAA
NoRV1       [172]---------------UUGUUCCGGCGGGGAGGGUUCCGUUGAUCCGACCUUCAAC
PvRV1       [182]-----------------------GCGGGGAGGGUUCCGUUGAUCCGACCUGCACC
UvRV3       [196]------------AAGUAUGUUUCGGGAGUAGGGUUCCGUUGAUCCCCGU------
UvRV5       [168]--------------CACAGGCGGAGGAGGAGGGUUCCGUUGAUCCUCGAGUUUGU
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B

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                      Motif I            Motif II                 Motif III
AalVV1    [103] GSLLVETDTLQGR[63]SRWNWSVNGSHSA [46] KLECGKTRAIYACDTRSY[46]
NoVv1     [211] GALLVETDTLLGR[64]SRWSWAVNGSHSA [46] KPECGKIRAIYACDTINY[46]
PvRV      [178] GALLVETDTLQGR[64]SRWSWAVNGSHSS [46] KLECGKTRAIYACDTVSY[46]
UvRV3     [212] GAMMVETDTLAGR[65]SRWRWAVNGSHSA [46] KLEHGKTRTILACDTRSY[46]
UvRV6     [213] GAMMVEGDTLAGR[65]SRWRWAVNGSHSA [46] KLEHGKTRTILACDTRSY[46]
FpV1      [211] GSLLVECEVLQGR[64]SRWVWAVNGSQSS [46] KLENGKTRAIFACDTRHY[46]
HVv190S   [232] GALFVEANTLQGR[58]SRWLWCVNGSQNA [42] KLENGKDRAIFACDTRSY[46]
                *:::** :.* **    *** *.****:.:      * * ** *:* ****  *
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                  Motif IV                 Motif V                     Motif VI
AalVV1        MLDYDDFNSHHT [45] GTLMSGHRGTTYFNSVLNMAYLMCVLGEDYILARPSLHVGDDVY
NoVv1         MLDYDDFNSHHT [45] GTLMSGHRCTTYVNSVLNMAYLMVVLGEDWVMERQSLHVGDDVY
PvRV          MLDYTDFNSHHT [45] GTLMSGHRCTTYINSVLNMAYLMVVLGEDFVLERQSLHVGDDVY
UvRV3         MLDYDDFNSHHS [45] GTLMSGHRCTTYINSVLNMAYLMVVLGDDFVMERPTLHVGDDVF
UvRV6         MLDYDDFNSHHS [45] GTLMSGHRCTTYINSVLNMAYLMVVLGDDFVMDRPTLHVGDDVF
FpV1          MLDYDDFNSQHT [45] GTLMSGHRATTFINSVLNKAYLDVVLGEGWLDTRRSVHVGDDIY
HVv190S       MLDYDNFNSQHS [44] GTLMSGHRATTFTNSVLNAAYICYAVGIPAFKRMISLHAGDDVY
              **** :***:*:      ******** **: ***** **:  .:*   .    ::*.***::
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                       Motif VII                  Motif VIII
AalVV1     [21] RMNPTKQSVGHVSTEFLRVASDARDSYGYLARAVATTVAGNWYT [250]
NoVv1      [21] RMNRRKQSVGHVSTEFLRVASDARDSYGYLARAAANLIAGNWYS [250]
PvRV       [21] RMNKSKQSVGHVGTELTRVASNKRDSFGYLARATANLIAGNWYS [250]
UvRV3      [21] RMNRSKQSVGHVATEFLRVSSRARDSYGYLCRAISSCVSGNWVS [250]
UvRV6      [21] RMNRSKQSVGHVSTEFLRVSSQGRVSMGYLCRAIASTVSGNWVT [250]
FpV1       [21] RMNPTKQSVGHVSTEFLRLATAGRDTYGYVARSIASLISGNWVS [250]
HVv190S    [21] RMNPTKQSIGYTGAEFLRLGINKSYAIGYLCRAIASLVSGSWTS [248]
                ***  ***:*:..:*: *:.     : **:.*: :. ::*.* :
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C

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HVv190S       [696] LRAPPFPRQQGAL-GGGGNVPLPPAPGAAPPPPPGPPNGPPAGPPPSDDGSSNPAAPVPTA
AalVv1        [704] LRGAPLPRVGGGQLGGAVNPPPPPQGGLVPPPPSTGPNPPNSEGPPSDNAEAAGALAAPQN
                    **. *:**  *.  **. * * **  * .****   ** * :  ****:..:  *  .*
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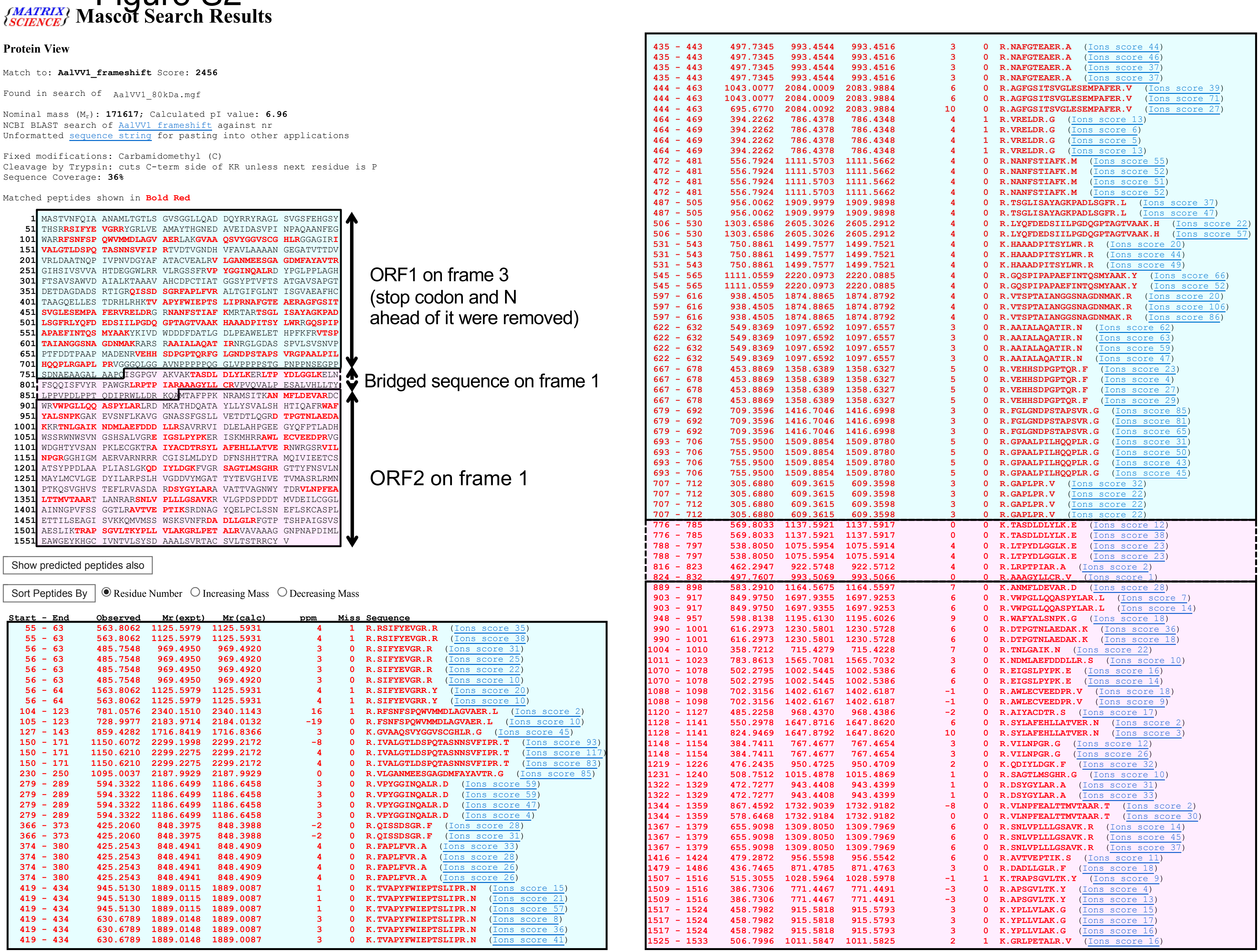
Figure S2



Mascot Search Results

Protein View

```
Match to: AalVV1_frameshift Score: 2456

Found in search of  AalVV1_80kDa.mgf

Nominal mass (Mr): 171617; Calculated pI value: 6.96
NCBI BLAST search of AalVV1_frameshift against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 36%

Matched peptides shown in Bold Red

   1 MASTVNFQIA ANAMLTGTLS GVSGGLLQAD DQYRRYRAGL SVGSFEHGSY
  51 THSRRSIFYE VGRRYGRLVE AMAYTHGNED AVEIDASVPI NPAQAANFEG
 101 WARRFSNFSP QWVMMDLAGV AERLAKGVAA QSVYGGVSCG HLRGGAGIRI
 151 VALGTLDSPQ TASNNSVFIP RTVDTVGNDH VFAVLAAAAN GEGATVTTDV
 201 VRLDAATNQP IVPNVDGYAF ATACVEALRV LGANMEESGA GDMFAYAVTR
 251 GIHSIVSVVA HTDEGGWLRR VLRGSSFRVP YGGINQALRD YPGLPPLAGH
 301 FTSAVSAWVD AIALKTAAAV AHCDPCTIAT GGSYPTVFTS ATGAVSAPGT
 351 DETDAGDADS RTIGRQISSD SGRFAPLFVR ALTGIFGLNT ISGVAEAFHC
 401 TAAGQELLES TDRHLRHKTV APYFWIEPTS LIPRNAFGTE AERAGFGSIT
 451 SVGLESEMPA FERVRELDRG RNANFSTIAF KMRTARTSGL ISAYAGKPAD
 501 LSGFRLYQFD EDSIILPGDQ GPTAGTVAAK HAAADPITSY LWRRGQSPIP
 551 APAEFINTQS MYAAKYKIVD WDDDFDATLG DLPEAWELET HPFKFRVTSP
 601 TAIANGGSNA GDNMAKRARS RAAIALAQAT IRNRGLGDAS SPVLSVSNVP
 651 PTFDDTPAAP MADENRVEHH SDPGPTQRFG LGNDPSTAPS VRGPAALPIL
 701 HQQPLRGAPL PRVGGGQLGG AVNPPPPPQG GLVPPPPSTG PNPPNSEGPP
 751 SDNAEAAGAL AAPQISGPGV AKVAKTASDL DLYLKERLTP YDLGGLKELN
 801 FSQQISFVYR PAWGRLRPTP IARAAAGYLL CRVPVQVALP ESALVHLLTY
 851 LPPVPDLPPT QDIPRWLLDR KQAMTAFPPK NRAMSITKAN MFLDEVARDC
 901 WRVWPGLLQQ ASPYLARLRD MKATHDQATA YLLYSVALSH HTIQAFRWAF
 951 YALSNPKGAK EVSNFLKAVG GNASSFGSLL VETDTLQGRD TPGTNLAEDA
1001 KKRTNLGAIK NDMLAEFDDD LLRSAVRRVI DLELAHPGEE GYQFPTLADH
1051 WSSRWNWSVN GSHSALVGRE IGSLPYPKER ISKMHRRAWL ECVEEDPRVG
1101 WDGHTYVSAN PKLECGKTRA IYACDTRSYL AFEHLLATVE RNWRGSRVIL
1151 NPGRGGHIGM AERVARNRRR CGISLMLDYD DFNSHHTTRA MQIVIEETCS
1201 ATSYPPDLAA PLIASLGKQD IYLDGKFVGR SAGTLMSGHR GTTYFNSVLN
1251 MAYLMCVLGE DYILARPSLH VGDDVYMGAT TYTEVGHIVE TVMASRLRMN
1301 PTKQSVGHVS TEFLRVASDA RDSYGYLARA VATTVAGNWY TDRVLNPFEA
1351 LTTMVTAART LANRARSNLV PLLLGSAVKR VLGPDSPDDT MVDEILCGGL
1401 AINNGPVFSS GGTLRAVTVE PTIKSRDNAG YQELPCLSSN EFLSKCASPL
1451 ETTILSEAGI SVKKQMVMSS WSKSVNFRDA DLLGLRFGTP TSHPAIGSVS
1501 AESLIKTRAP SGVLTKYPLL VLAKGRLPET ALRVAVAAAG GNPNAPDIML
1551 EAWGEYKHGC IVNTVLSYSD AAALSVRTAC SVLTSTRRCY V
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ORF1 on frame 3
(stop codon and N
ahead of it were removed)

Bridged sequence on frame 1

ORF2 on frame 1

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Start - End     Observed   Mr(expt)   Mr(calc)      ppm  Miss Sequence
   55 - 63      563.8062  1125.5979  1125.5931        4     1 R.RSIFYEVGR.R  (Ions score 35)
   55 - 63      563.8062  1125.5979  1125.5931        4     1 R.RSIFYEVGR.R  (Ions score 38)
   56 - 63      485.7548   969.4950   969.4920        3     0 R.SIFYEVGR.R  (Ions score 31)
   56 - 63      485.7548   969.4950   969.4920        3     0 R.SIFYEVGR.R  (Ions score 25)
   56 - 63      485.7548   969.4950   969.4920        3     0 R.SIFYEVGR.R  (Ions score 22)
   56 - 63      485.7548   969.4950   969.4920        3     0 R.SIFYEVGR.R  (Ions score 10)
   56 - 64      563.8062  1125.5979  1125.5931        4     1 R.SIFYEVGRR.Y  (Ions score 20)
   56 - 64      563.8062  1125.5979  1125.5931        4     1 R.SIFYEVGRR.Y  (Ions score 10)
  104 - 123     781.0576  2340.1510  2340.1143       16     1 R.RFSNFSPQWVMMDLAGVAER.L  (Ions score 2)
  105 - 123     728.9977  2183.9714  2184.0132      -19     0 R.FSNFSPQWVMMDLAGVAER.L  (Ions score 10)
  127 - 143     859.4282  1716.8419  1716.8366        3     0 K.GVAAQSVYGGVSCGHLR.G  (Ions score 45)
  150 - 171    1150.6072  2299.1998  2299.2172       -8     0 R.IVALGTLDSPQTASNNSVFIPR.T  (Ions score 93)
  150 - 171    1150.6210  2299.2275  2299.2172        4     0 R.IVALGTLDSPQTASNNSVFIPR.T  (Ions score 117)
  150 - 171    1150.6210  2299.2275  2299.2172        4     0 R.IVALGTLDSPQTASNNSVFIPR.T  (Ions score 83)
  230 - 250    1095.0037  2187.9929  2187.9929        0     0 R.VLGANMEESGAGDMFAYAVTR.G  (Ions score 85)
  279 - 289     594.3322  1186.6499  1186.6458        3     0 R.VPYGGINQALR.D  (Ions score 59)
  279 - 289     594.3322  1186.6499  1186.6458        3     0 R.VPYGGINQALR.D  (Ions score 59)
  279 - 289     594.3322  1186.6499  1186.6458        3     0 R.VPYGGINQALR.D  (Ions score 47)
  279 - 289     594.3322  1186.6499  1186.6458        3     0 R.VPYGGINQALR.D  (Ions score 4)
  366 - 373     425.2060   848.3975   848.3988       -2     0 R.QISSDSGR.F  (Ions score 28)
  366 - 373     425.2060   848.3975   848.3988       -2     0 R.QISSDSGR.F  (Ions score 31)
  374 - 380     425.2543   848.4941   848.4909        4     0 R.FAPLFVR.A  (Ions score 33)
  374 - 380     425.2543   848.4941   848.4909        4     0 R.FAPLFVR.A  (Ions score 28)
  374 - 380     425.2543   848.4941   848.4909        4     0 R.FAPLFVR.A  (Ions score 26)
  374 - 380     425.2543   848.4941   848.4909        4     0 R.FAPLFVR.A  (Ions score 26)
  419 - 434     945.5130  1889.0115  1889.0087        1     0 K.TVAPYFWIEPTSLIPR.N  (Ions score 15)
  419 - 434     945.5130  1889.0115  1889.0087        1     0 K.TVAPYFWIEPTSLIPR.N  (Ions score 21)
  419 - 434     945.5130  1889.0115  1889.0087        1     0 K.TVAPYFWIEPTSLIPR.N  (Ions score 57)
  419 - 434     630.6789  1889.0148  1889.0087        3     0 K.TVAPYFWIEPTSLIPR.N  (Ions score 8)
  419 - 434     630.6789  1889.0148  1889.0087        3     0 K.TVAPYFWIEPTSLIPR.N  (Ions score 36)
  419 - 434     630.6789  1889.0148  1889.0087        3     0 K.TVAPYFWIEPTSLIPR.N  (Ions score 41)
  435 - 443     497.7345   993.4544   993.4516        3     0 R.NAFGTEAER.A  (Ions score 44)
  435 - 443     497.7345   993.4544   993.4516        3     0 R.NAFGTEAER.A  (Ions score 46)
  435 - 443     497.7345   993.4544   993.4516        3     0 R.NAFGTEAER.A  (Ions score 37)
  435 - 443     497.7345   993.4544   993.4516        3     0 R.NAFGTEAER.A  (Ions score 37)
  444 - 463    1043.0077  2084.0009  2083.9884        6     0 R.AGFGSITSVGLESEMPAFER.V  (Ions score 39)
  444 - 463    1043.0077  2084.0009  2083.9884        6     0 R.AGFGSITSVGLESEMPAFER.V  (Ions score 71)
  444 - 463     695.6770  2084.0092  2083.9884       10     0 R.AGFGSITSVGLESEMPAFER.V  (Ions score 27)
  464 - 469     394.2262   786.4378   786.4348        4     1 R.VRELDR.G  (Ions score 13)
  464 - 469     394.2262   786.4378   786.4348        4     1 R.VRELDR.G  (Ions score 6)
  464 - 469     394.2262   786.4378   786.4348        4     1 R.VRELDR.G  (Ions score 5)
  464 - 469     394.2262   786.4378   786.4348        4     1 R.VRELDR.G  (Ions score 13)
  472 - 481     556.7924  1111.5703  1111.5662        4     0 R.NANFSTIAFK.M  (Ions score 55)
  472 - 481     556.7924  1111.5703  1111.5662        4     0 R.NANFSTIAFK.M  (Ions score 52)
  472 - 481     556.7924  1111.5703  1111.5662        4     0 R.NANFSTIAFK.M  (Ions score 51)
  472 - 481     556.7924  1111.5703  1111.5662        4     0 R.NANFSTIAFK.M  (Ions score 52)
  487 - 505     956.0062  1909.9979  1909.9898        4     0 R.TSGLISAYAGKPADLSGFR.L  (Ions score 37)
  487 - 505     956.0062  1909.9979  1909.9898        4     0 R.TSGLISAYAGKPADLSGFR.L  (Ions score 47)
  506 - 530    1303.6586  2605.3026  2605.2912        4     0 R.LYQFDEDSIILPGDQGPTAGTVAAK.H  (Ions score 22)
  506 - 530    1303.6586  2605.3026  2605.2912        4     0 R.LYQFDEDSIILPGDQGPTAGTVAAK.H  (Ions score 57)
  531 - 543     750.8861  1499.7577  1499.7521        4     0 K.HAAADPITSYLWR.R  (Ions score 20)
  531 - 543     750.8861  1499.7577  1499.7521        4     0 K.HAAADPITSYLWR.R  (Ions score 44)
  531 - 543     750.8861  1499.7577  1499.7521        4     0 K.HAAADPITSYLWR.R  (Ions score 49)
  545 - 565    1111.0559  2220.0973  2220.0885        4     0 R.GQSPIPAPAEFINTQSMYAAK.Y  (Ions score 66)
  545 - 565    1111.0559  2220.0973  2220.0885        4     0 R.GQSPIPAPAEFINTQSMYAAK.Y  (Ions score 52)
  597 - 616     938.4505  1874.8865  1874.8792        4     0 R.VTSPTAIANGGSNAGDNMAK.R  (Ions score 20)
  597 - 616     938.4505  1874.8865  1874.8792        4     0 R.VTSPTAIANGGSNAGDNMAK.R  (Ions score 106)
  597 - 616     938.4505  1874.8865  1874.8792        4     0 R.VTSPTAIANGGSNAGDNMAK.R  (Ions score 86)
  622 - 632     549.8369  1097.6592  1097.6557        3     0 R.AAIALAQATIR.N  (Ions score 62)
  622 - 632     549.8369  1097.6592  1097.6557        3     0 R.AAIALAQATIR.N  (Ions score 63)
  622 - 632     549.8369  1097.6592  1097.6557        3     0 R.AAIALAQATIR.N  (Ions score 59)
  622 - 632     549.8369  1097.6592  1097.6557        3     0 R.AAIALAQATIR.N  (Ions score 47)
  667 - 678     453.8869  1358.6389  1358.6327        5     0 R.VEHHSDPGPTQR.F  (Ions score 23)
  667 - 678     453.8869  1358.6389  1358.6327        5     0 R.VEHHSDPGPTQR.F  (Ions score 4)
  667 - 678     453.8869  1358.6389  1358.6327        5     0 R.VEHHSDPGPTQR.F  (Ions score 27)
  667 - 678     453.8869  1358.6389  1358.6327        5     0 R.VEHHSDPGPTQR.F  (Ions score 29)
  679 - 692     709.3596  1416.7046  1416.6998        3     0 R.FGLGNDPSTAPSVR.G  (Ions score 85)
  679 - 692     709.3596  1416.7046  1416.6998        3     0 R.FGLGNDPSTAPSVR.G  (Ions score 81)
  679 - 692     709.3596  1416.7046  1416.6998        3     0 R.FGLGNDPSTAPSVR.G  (Ions score 65)
  693 - 706     755.9500  1509.8854  1509.8780        5     0 R.GPAALPILHQQPLR.G  (Ions score 31)
  693 - 706     755.9500  1509.8854  1509.8780        5     0 R.GPAALPILHQQPLR.G  (Ions score 50)
  693 - 706     755.9500  1509.8854  1509.8780        5     0 R.GPAALPILHQQPLR.G  (Ions score 43)
  693 - 706     755.9500  1509.8854  1509.8780        5     0 R.GPAALPILHQQPLR.G  (Ions score 45)
  707 - 712     305.6880   609.3615   609.3598        3     0 R.GAPLPR.V  (Ions score 32)
  707 - 712     305.6880   609.3615   609.3598        3     0 R.GAPLPR.V  (Ions score 22)
  707 - 712     305.6880   609.3615   609.3598        3     0 R.GAPLPR.V  (Ions score 22)
  707 - 712     305.6880   609.3615   609.3598        3     0 R.GAPLPR.V  (Ions score 22)
  776 - 785     569.8033  1137.5921  1137.5917        0     0 K.TASDLDLYLK.E  (Ions score 12)
  776 - 785     569.8033  1137.5921  1137.5917        0     0 K.TASDLDLYLK.E  (Ions score 38)
  788 - 797     538.8050  1075.5954  1075.5914        4     0 R.LTPYDLGGLK.E  (Ions score 23)
  788 - 797     538.8050  1075.5954  1075.5914        4     0 R.LTPYDLGGLK.E  (Ions score 23)
  816 - 823     462.2947   922.5748   922.5712        4     0 R.LRPTPIAR.A  (Ions score 2)
  824 - 832     497.7607   993.5069   993.5066        0     0 R.AAAGYLLCR.V  (Ions score 1)
  889 - 898     583.2910  1164.5675  1164.5597        7     0 K.ANMFLDEVAR.D  (Ions score 28)
  903 - 917     849.9750  1697.9355  1697.9253        6     0 R.VWPGLLQQASPYLAR.L  (Ions score 7)
  903 - 917     849.9750  1697.9355  1697.9253        6     0 R.VWPGLLQQASPYLAR.L  (Ions score 14)
  948 - 957     598.8138  1195.6130  1195.6026        9     0 R.WAFYALSNPK.G  (Ions score 18)
  990 - 1001    616.2973  1230.5801  1230.5728        6     0 R.DTPGTNLAEDAK.K  (Ions score 36)
  990 - 1001    616.2973  1230.5801  1230.5728        6     0 R.DTPGTNLAEDAK.K  (Ions score 18)
 1004 - 1010    358.7212   715.4279   715.4228        7     0 R.TNLGAIK.N  (Ions score 22)
 1011 - 1023    783.8613  1565.7081  1565.7032        3     0 K.NDMLAEFDDDLLR.S  (Ions score 10)
 1070 - 1078    502.2795  1002.5445  1002.5386        6     0 R.EIGSLPYPK.E  (Ions score 16)
 1070 - 1078    502.2795  1002.5445  1002.5386        6     0 R.EIGSLPYPK.E  (Ions score 14)
 1088 - 1098    702.3156  1402.6167  1402.6187       -1     0 R.AWLECVEEDPR.V  (Ions score 18)
 1088 - 1098    702.3156  1402.6167  1402.6187       -1     0 R.AWLECVEEDPR.V  (Ions score 9)
 1120 - 1127    485.2258   968.4370   968.4386       -2     0 R.AIYACDTR.S  (Ions score 17)
 1128 - 1141    550.2978  1647.8716  1647.8620        6     0 R.SYLAFEHLLATVER.N  (Ions score 2)
 1128 - 1141    824.9469  1647.8792  1647.8620       10     0 R.SYLAFEHLLATVER.N  (Ions score 3)
 1148 - 1154    384.7411   767.4677   767.4654        3     0 R.VILNPGR.G  (Ions score 12)
 1148 - 1154    384.7411   767.4677   767.4654        3     0 R.VILNPGR.G  (Ions score 26)
 1219 - 1226    476.2435   950.4725   950.4709        2     0 K.QDIYLDGK.F  (Ions score 32)
 1231 - 1240    508.7512  1015.4878  1015.4869        1     0 R.SAGTLMSGHR.G  (Ions score 10)
 1322 - 1329    472.7277   943.4408   943.4399        1     0 R.DSYGYLAR.A  (Ions score 31)
 1322 - 1329    472.7277   943.4408   943.4399        1     0 R.DSYGYLAR.A  (Ions score 33)
 1344 - 1359    867.4592  1732.9039  1732.9182       -8     0 R.VLNPFEALTTMVTAAR.T  (Ions score 2)
 1344 - 1359    578.6468  1732.9184  1732.9182        0     0 R.VLNPFEALTTMVTAAR.T  (Ions score 30)
 1367 - 1379    655.9098  1309.8050  1309.7969        6     0 R.SNLVPLLLGSAVK.R  (Ions score 14)
 1367 - 1379    655.9098  1309.8050  1309.7969        6     0 R.SNLVPLLLGSAVK.R  (Ions score 45)
 1367 - 1379    655.9098  1309.8050  1309.7969        6     0 R.SNLVPLLLGSAVK.R  (Ions score 37)
 1416 - 1424    479.2872   956.5598   956.5542        6     0 R.AVTVEPTIK.S  (Ions score 11)
 1479 - 1486    436.7465   871.4785   871.4763        3     0 R.DADLLGLR.F  (Ions score 18)
 1507 - 1516    515.3055  1028.5964  1028.5978       -1     1 K.TRAPSGVLTK.Y  (Ions score 9)
 1509 - 1516    386.7306   771.4467   771.4491       -3     0 R.APSGVLTK.Y  (Ions score 4)
 1509 - 1516    386.7306   771.4467   771.4491       -3     0 R.APSGVLTK.Y  (Ions score 13)
 1517 - 1524    458.7982   915.5818   915.5793        3     0 K.YPLLVLAK.G  (Ions score 15)
 1517 - 1524    458.7982   915.5818   915.5793        3     0 K.YPLLVLAK.G  (Ions score 17)
 1517 - 1524    458.7982   915.5818   915.5793        3     0 K.YPLLVLAK.G  (Ions score 16)
 1525 - 1533    506.7996  1011.5847  1011.5825        2     1 K.GRLPETALR.V  (Ions score 16)
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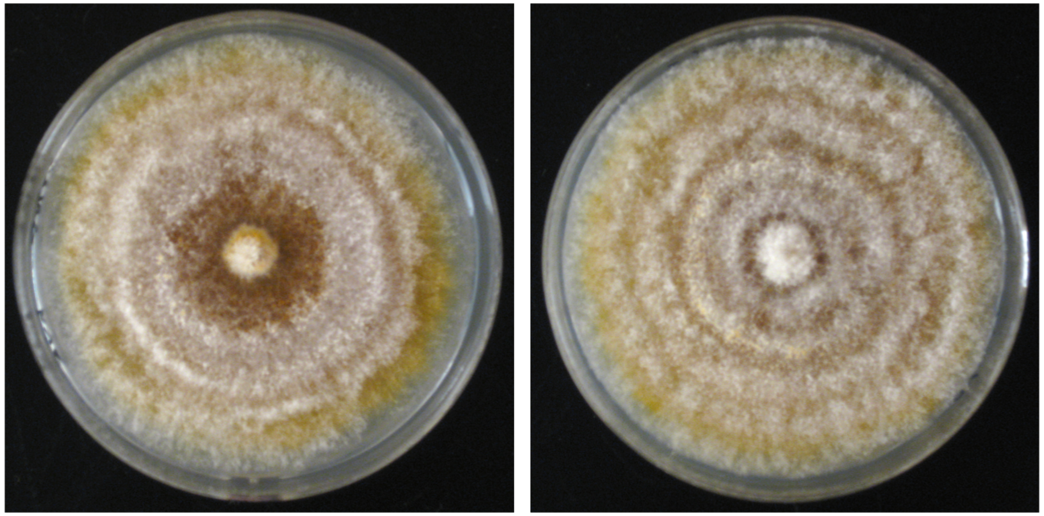
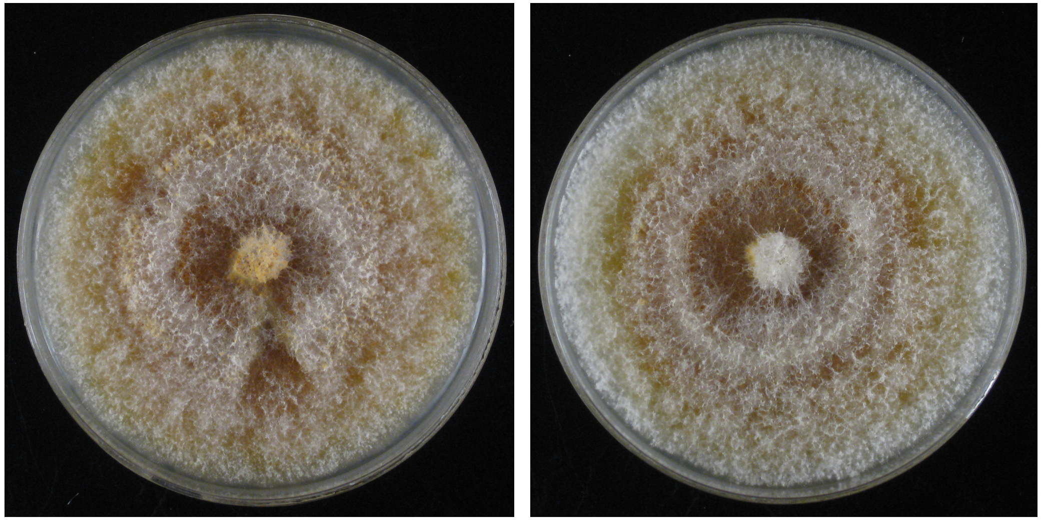
Figure S3



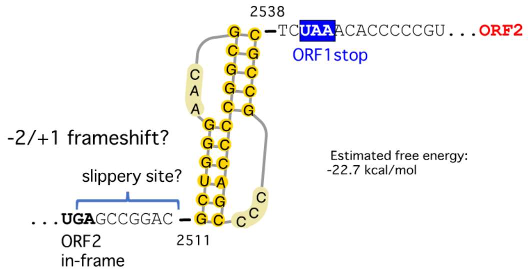
EP155/VF EP155/AalVV1



Δ*dcl2*/VF Δ*dcl2*/AalVV1

Figure S4

Phomopsis vexans RNA virus KP090346



Nigrospora oryzae victorivirus 1 KT428155