

**Supplementary Table 1.** Sequence variations of ZmAV1

Position	Con <sup>a</sup>	Alt <sup>b</sup>	Quality <sup>c</sup>	Con #	Alt #	Con %	Alt %
349	T	C	222	62	40	60.8	39.2
359	C	T	222	66	44	60	40
550	A	G	119	54	14	79.4	20.6
868	G	A	49.1317	80	12	87	13
1163	A	G	165	72	22	76.6	23.4
1922	C	T	19.959	82	12	87.2	12.8
2798	A	G	79	104	20	83.9	16.1
2924	A	G	121	112	26	81.2	18.8
2930	A	G	126	114	28	80.3	19.7
2975	C	T	174	112	36	75.7	24.3
2993	G	A	148	122	32	79.2	20.8
3059	G	A	42.6287	128	24	84.2	15.8
3131	G	A	90	56	12	82.4	17.6

<sup>a</sup>Sequence of the assembled contig

<sup>b</sup>Alternative sequence observed in RNA-seq reads

<sup>c</sup>Phred-scaled quality score for the assertion made in Alt by BCFtools

**Supplementary Table 2.** Sequence variations of ZmAV2

Position	Con <sup>a</sup>	Alt <sup>b</sup>	Quality <sup>c</sup>	Con #	Alt #	Con %	Alt %
106	C	T	131	8	8	50	50
632	A	G	222	60	36	62.5	37.5
635	G	A	222	58	36	61.7	38.3
761	G	A	222	50	32	61	39
773	T	C	222	48	34	63	37
824	G	A	222	42	34	55.3	44.7
845	C	T	222	46	38	54.8	45.2
1082	T	G	222	42	32	56.8	43.2
1107	G	A	222	42	38	52.5	47.5
1148	A	G	222	36	30	54.5	45.5
1283	A	G	210	26	14	65	35
1455	C	T	222	28	20	58.3	41.7
1466	G	A	222	28	22	56	44
1596	A	G	193	18	12	60	40
1674	G	A	222	8	20	28.6	71.4
1809	T	C	112	18	8	69.2	30.8
1854	G	A	33.001	12	4	75	25
2154	T	C	212	22	14	61.1	38.9
2163	T	C	203	28	14	66.7	33.3
2199	T	C	180	24	12	66.7	33.3
2241	A	G	222	24	18	57.1	42.9
2252	A	G	222	24	22	52.2	47.8
2268	C	T	222	24	24	50	50
2286	T	C	222	20	18	52.6	47.4
2364	T	C	222	20	16	55.6	44.4
2433	C	T	174	18	12	60	40
2512	C	T	158	14	8	63.6	36.4
2514	A	G	159	14	8	63.6	36.4
2538	G	A	117	26	8	76.5	23.5
2604	C	T	215	46	20	69.7	30.3
2641	T	C	103	52	14	78.8	21.2
2742	C	T	222	34	22	60.7	39.3
3236	A	G	203	24	20	54.5	45.5
3243	T	C	136	20	16	55.6	44.4

<sup>a</sup>Sequence of the assembled contig<sup>b</sup>Alternative sequence observed in RNA-seq reads<sup>c</sup>Phred-scaled quality score for the assertion made in Alt by BCFtools

ZmAV1	-----MAEDLRS-QQTL-----DDRDLNKLTTDAFKAYPEGGLSVVDVSELEGIAACNYTVSRAVKVMKIKPLTKNEHLIKLFHYANDVSNISSILPMLTETNFK	94
ZmAV2	-----MFRCRCEMANEDGSSVPLKT-QAQV-----DEERDVAQLNKALSYDLGGMPIAPWALQDVADCSYTVARALRKLIKLPHYDNKHLQKLFHCEENAVIDSTLPLKLSSFR	107
BLV	-----MAGASGSLPVE-----TTEQTQARVSTALAPLTGVLGNIERFSVEAIIINSNTVDIFLKAIKSLVAYAQDQDILENIAASAANTAGIQHVINMTPKDLFD	95
FpAV2	-----MSVDPPLRF-LEDAAT-----AQAAADAIKLRPLMLELSGSKVLAKECDIEHLLNAGFTVDDVEKLSKSLPKLIDQGVFDDAWTMAKGSGIILSAQEMTFPDLFM	97
FpAV3	-----MPRDPLLNLTANAD-----VSEEQREKLAELLDGIIKAGLNLVNCTYEDMLGANITDDEVEKALKGLAPHYDNGVLADWVTVAANGVVTSQAQNFTLKSFR	97
LpAV1	-----MPRDPLLNLTADAD-----VSEAQRERKLADLLDGVIKAGLNLVNCTYEDMIGANITVDDVEKALKGLAPHYDNGVLADWVTVAANGVVTSQAQNFTLKSFR	97
AcAV1	-----MSAEDFTPRTGLVDTEL-LV-----DPAEAEELHDALMPLEVNLINVKAFTRANIFALRMTVPQYIKEVRVLQNLQDVLQRLKVNWTAEISHKCATLPDEADAGVCLS	102
AcAV2	-----MASSSGDPYQYLDITL-LS-----DPVAESVLSQDAVQHLASIGVRVERFTRDSIHMRMSVPAYVKEIRILGNISDRRELLNKVNLQGVKNVLSLPEDVTPOMVLS	102
PeAV1	-----MSGPSQRVVFH-PG-----GRADPTVELSVESEARVANEGFRVHTWTPGILARSFIPVKRFIDAVERVLNPNEPDEVFNRLNLLGVRDGWWETNTCTVSQFYK	96
CaAV1	-----MSGTSPRTPGSSGVKTVPLTA-RE-----KETAMIEEIDEIGVTFIELGVSAFFDSDRVYTKNLLPAQYRLRLLRQFGKG-KDAGEVELTFSAAIAKQVRASRGIGWNWKIQ	106
STV	-----MAGVGGSAGRVPNAAVPLTA-KE-----KERTVMREIVEIGETFVELGIDKRYFQRTTYVSHMILLPNQYFKLKQFKG-KTAEELDLALGAAVAHVGLSRMGITFKKFD	106
AoAV1	-----MAEPRTTQATAEVDYVANL-----PADEADAFFVYARWFVTTYHLAAGGLDPTATYPREGYSKDKMAARLRLRFFKGD-KDVAVIDTIFAVGVRKSFFTAKESATFEQFAN	104
FpAV1	-----MAEVKVRTQTPAPTGDYVANL-----PEGDDARFVYYAGWVPLTTVYHAFAALPQGTYRLEGYTDFKDALRFLYFKG-KDWNVIETIVAVGIRRNFTTAADSATFENFAN	104
RHV-A	MEDRRAEE-DRLDDLLPAGGGAPPPLRG-LPPLPRAEPTDAELOQAIDEAVAVVYEAAGMPAGRFTVQRVHEIGLTVFVKQARAVFGGKNDQADLIFTTIGIMGVCGSLRTMEAGFW	118
MsAV1	-----MADFEAQRDDNIAANAPIGG-LS-----SKQQEIDVTAAITPLLAAGFPQAIFNYDDLLRGYTAFTCFDFIKPLSITAERRELISLCALG-NNRFDMSVVAELDEFLN	104
VCV-M	-----MAQFETSDPANVGEAGIGG-IR-----SKEAEQATVNQAMNAIVRLLGFPDFIDIDALLERGFTAKSWDCYRATSITSERRDMDSALLG-GTRFWELPIDATLENID	104
CdAV1	-----MAEHQDPOAQAGGAVGDDVEEVLN-LEGGIGP-TAAEERNRLQEARLRLPIANGVNIERITVNDCLRLGFTVQLARALRVLTSIASDEMDRLIISQAHLSRLAPAARSVTDLHILA	114
CoAV1	-----MANAGGNGAPRVQPLQPQPVYY-FQOH-----TPAENQARITEAVFTLAQCGVNVGLFTDAVNVQGMTTDQFIKAVKPLQTHAEQGVINPLFTEAIRARVFVDVMMELNVQVVN	110
GaAV1	MSHSEEEVRFEGFPIDRTAAAGPSAQL-HGTT-----TERAEQEVTRMVPQLRNQGQLNTEVFTLASTYDVGTLTDGFCKLARGFLSITDEDIQESESSLAGQKKGKLGPLRRVSVREFVD	115
EbAV1	-----MGEPLPTEVLY-VL-----TPAEEQEAELTRLAALPQIQLPAGLFDRTAVLRLANRANTYKGFKLHQLQTVSRLVDQDIIIVALSGLVKKDFFPLPVRNMNISQFCR	95
EbAV2	-----MTGZTGPSNQVH-LGL-----TPDQEQQELTALSAGLVAEQGPAAIFSRTAIDCGYDFARFVYRVRVKMSDDLKLMDLFDEVLTLAVTGLFFFVSPRLCTKFCF	99
ScAV1	-----MSETSGNSGTESEKMERIRKELEADQENLELTLEEQQAEAMDKLVPPFRARIPEEINFNVEQAQLDGHFSKNYKLKVTVHNLEKDHGLKAISKGGALGFWELEYTEMTRAEFVK	113
SpAV1	-----MAGLEGEGSEGIIHL-VEK-----TPKQEQEELFTASEKLREAGIPLGFADRNATIKAHGHSFNGYMKMVKVNTYTEGGFFDTLLVMGGSKLYPIHSMKMDHFGFVR	100
PpAV1	-----ITL-V-----ISIMSNLSCAQIVQKLRDGGRLRLVANLVEELPRNNIREDVLAANCRRGVSVLLDQGMLDVALGQAAKGIGLSQLSVTREISGPELLA	87
ZmAV1	FCKWLTPVAKKIIAQLNADRRLRRGSVDVTPPEAAMILLESQAQDRTEYTESKARARYDIDVAKYKKIAKRTRQLEEDLDKVQASYPLQLIERPDEHSVMASAWHRYVDFCTSNNFE	215
ZmAV2	FCDWLLSPVAKRRIEQQLVNAIDLKKRSRDAITPAETALVAILEVAQNDCVADVSVRVITYDEEIKKKRICKLQKLEEHKARKIEKARKKYPGLLLERPSESDVCNQAHHKVVECNASGIK	228
BLV	LSRWVTKTAAGMEAISKITTQRRRLRQGGAGRSAQSVAWNLFTQQQADYQAEEKKRKMTRFERKREDLKQLQALQDTEAASMERLAQYPTQVAPATMETEVLVACWAAYVADCRGGIT	216
FpAV2	FRRWLTTPOGAQALSLVQARRKMTKAGKVLGHQDVALLRLQHYEDDARRELDKARVETEAAVAQLOQAEIDKLKKYAKAEEKQKRDPLIANYVPLTDNEVRNQAWDMYCQCINEGSV	218
FpAV3	FKVWITKDGOSTALRQAQQKAKLAKAGKDAPEADMELLRLWKAQQDQMDSQFVKRERVPIDAKIASLRAKIVEQEELELLAKGKEMMVKYPLLSAYVAPDLSELRLDLCWKVYLQICNSEKGK	218
LpAV1	FKVWITKDGATRALRQAQQKAKLAKAGKDAPEADMETLRLWKAQQDQMDSQFVKRERVPIDAKIASLRAKIVEQEELELLAKGKEMMVKYPLLSAYVAPDLSELRLDLCWKVYLQICNSEKGK	218
AcAV1	FARWLKRGVGAKVLSDAQHLLQKRAVGSEVPKVLAFVQDQDQIAJDMHAERKKIQAEGQAKIDELREIREQVREYDEKAKASSKRFKPARKYVPPTKAKIDEECWNAYLNQVKQSGKT	223
AcAV2	FARWLKRGAGARVLADQHQHLLKINKKAVGDSTPDIVFAHLLDQVQDLTNAKKRVOHSSQVRIDELELRQKQIAEEHNLRLRDLAATRQFTPANDYAPPSSAALDNECMELYCARADGRA	223
PeAV1	FCNWLSKSAEGTTRLNEIRKARLQKQGPQGTLEDVSLVAALDEQVAEFLQRRKKETRLEFESPKLIDLRQJIALVQQEMSAITMKAHADFSPASIYPMDDLEFGEACWNLYRAECAARNQD	217
CaAV1	FLNWAKSPAGHKAIQEVMNIEKLERGGDFDVTVEAALNFLDVRDNIGHQKEARAIEHEIAELERQKINLRRDLDELDREIAHDQHPRVSPGVYPLTDAELNRCMNFFRAQHGVGV	227
STV	FLNWVTKTKEKDALGETMYAQKLEQKGRGDFSFIAEVALLHCFETQRNDMLRDEKDVRVLAKEEEIADLQRKIVKRREKLEEDIATKSNYEPVSRVYGLSDYELNCKCWSLYQQNPDKVTA	227
AoAV1	FLEFLRTADAAAETDLRDRSFAQAGGKGVNAEISSVVAQTLVQQLADLEQHARMIAQSKRDLFELAIAKEESELTKLMSDEEFFPASITYKLNPMLQKECWMVRAKASSTELAAV	225
FpAV1	FLEFLKTPEGASAITEDLRRAFLAAGKGVFTAVDIAAVSPLTVQAADEQHARMIAQSKRDLFELAIAKEESELTKLMSDEEFFPASITYKLNPMLQKECILAKAADPVLSAV	225
RHV-A	VIRWARSNVGRQALETGQKVKVEDKRAFTPQNEVALCQIFTMTOQGIMAEVKEARASTQIDEELTRLRLRQKQIAEVQKPVYPLTDAELNRCMNFFRAQHGVGV	239
MsAV1	FVKWLKSPEGRDAQTAAKKRSLQKRAVGGLSTADVAIQMGNMIAQYKERKARAPIEQQRHRERLRLDDEALTELSVKEFGRQIATYQEPGDNHTVSREAYKLYEYCRENVR	225
VCV-M	FVKWIKSPEGRDAQTAAKKRSLQKRAVGGLSTADVAIQMGNMIAQYKERKARAPIEQQRHRERLRLDDEALTELSVKEFGRQIATYQEPGDNHTVSREAYKLYEYCRENVR	225
CdAV1	ICEWMKTERGAQAIRNLTSQAKSRAVGGRTVADVMSLQAFNQVADWWSAQVKEARIEEEEMAELRQALQKQLNDSLNAAINESYWPASSYKAPALNQVQSYALYAADCRRSGTV	235
CoAV1	CVEWLKSRRGGNAISTVYTRKLQAKVLPPTTAADWAVASLWQQLSDLGSKRKEIRVEDEAELREIREQLETEKGLDLAIDAEMVPMASMYNELNAEIAARRSFNLYTQRALQGVV	231
GaAV1	FLKWLDKDTGGQEAARAIHQGKLLKKAQEGSQADELTLLQVNFNLMLQDMSQAIKKERSIRDEEYIALRSMRRLERQDAKILEIREESPASPNFKEPESDVEGRLSYDIVVQRAKEAHT	236
EbAV1	FSEWLRSKDKGQNSLHEVQRHKKLEKAQAGLVEPREVALEQIFSAQRADWAAKEERSAYDQFQKQDQFQKQDQFQFELDEALNERAYAMYVHDQCVKWR	216
EbAV2	FGAYLTTKKGQEEALHGAQMKYKQAVKIGEFPDKVLEQIIFNAQDRAEYVLEKERSYDREIEALKKQIRLLEAKERERLQIAAGFAPASPYSEPPDADVAVEAWEEMYQNDARAKGVK	228
ScAV1	FARWLSTTEGVDFVFGLQMKKTYTSKAKDSVTPRQIAISGVFTHMLQKYSSEVKETRSKEYDEIARMERELRLRKEKEEREIGKLIDQYKPAULYVPPKDEEGLVAREYLEADERGKGA	234
SpAV1	FARWLQSKEGDEIYTLLQREQKLRLKAGESLTPQMIKNDVFNLIRTEFSRAMKAEREKFEEQKDELRLRLRQKEREERQAFKLNQEKFAPISFYREPTDEEVGIAAYEMYNEARAKNGKT	221
PpAV1	FARWCKDKDKNRDLAQAQKVSIRRKAGASLATDDVAFVSLFDQMYADWSHAACEVRVTHERRIQLAEELRIVRQLRVLAVALENALAYRAVSSRAPNEEEFVSRCDWKLATFIGTPPA	208
ZmAV1	VPQKNDGNLARAYQFERENCELTLEIKNTACQPKEVERDYLQYCKEKFVKGFLVNSKTKELKLIGDTMCHARLEYFLTRIPPLERRRLDQIPVGRLTRK-GKMTPNIP-LSQIFSTPALGTMV	334
ZmAV2	QEKRNSASLEKAISMFNDIILRLEIKAKCCEKPEVDRDYLQYCKEKFVKGFLVTPPKISALTHSRDTILQRLRESHFLKAPLEREELLPLIPVGTVNPM-GHLNATMS-LREILWTESLKNRQV	347
BLV	PSAKTNASLTEAVKHYSANVRDQILTTYCEQENQVADLTRYAREKIOSFTVQETREEPVLEISIQRQLEQRLRISLPLELRLKHFHMVKQVPGIPPLHK-RGRPSCKP-LLTKLSPPELLRRQ	335
FpAV2	PMGRSTSTNLKIVGDKFRDHIVQAHKLTYCQCPDHTDALIEFGKQKILRCQEGAGSKLESSFTYSLSSIQRMMLRQYPLAQRQKQMMWEMIPGMVPPTR-PSLRTQM-LSQLPTNPLLLKPRV	337
FpAV3	VFPKNDNEILRVEEYKYLVNNRHLNRLPQKNQMLNYGKLKIKLLESEKSKRELSTVQASSQSLIHRVMSRPLQKQRLKMAIPMVGPTLP-LSQIQLRQDLMMSRT	337
LpAV1	AFPKNEENLRLVEEYKYLVNNRHLNRLPQKNQMLNYGKLKIKLLESEKSKRELSTVQASSQSLIHRVMSRPLQKQRLKQRMKEMMVAIPMVGPTLP-LNLQITTVP-LSSQLQRLDLMRMRT	337
AcAV1	APEWNAVQLEQANTMQYQQLTQHQDQFCGLESQNPQIPLKVMADSKLKELADNHEFVQASRPSEWSVRSVESHLLRHLPLPQVRQFQANNVPVGPVSQLVMQNSRNMRA-LRTLLNPOLLTWKSQ	343
AcAV2	LPPWNAIQEQAQTTALSNEVINKHRQDFCKIPSQNRLLQQTWAASKIQLDRLNTQEFVQASQSSNDWSLQSVQETHLLWRLPLPLRLLKQWANTIPVGVKVS-RKRNGNII-LRSMLGADLNPNPMQ	342
PeAV1	EAPLDDGLLEAVLTHGNAQLKQKKAQEGSQADELTLLQVNFNLMLQDMSQAIKKERSIRDEEYIALRSMRRLERQDAKILEIREESPASPNFKEPESDVEGRLSYDIVVQRAKEAHT	336
CaAV1	GVHPMTMSQKMEADFTYVHVKARARVEYMRHDIVPLLQYEEINQKIAHDFAVGDKRQVRHLVNWQEWVMKVMVKWDVTRVLKLRDIPVGTNLPRN-GNQTLCSR-LSEQIPMNRLL	346
STV	GAKPTRKQVKEAFDMYAEFVAKTNRLEFLKHGNVKELEQAFQAFQIAKILGYEQLGDKGKSRVLYGSWQQWVLRWIMKWNQTRKRLKLNLPVGLRKG-KEMTPCRP-LSEIIPMEREEKRT	346
AoAV1	AVPTND-QLADALKNFKEEVERRHADFLQAOQNRLTALREYVNNKILSFLVVENTGSRPALTSLWLPWTAKELEKQYPLPERISATAMIPMGRRTSP-TTSVSCRNLLEVMRSPALLAVRQ	344
FpAV1	AVPTNE-QISDQKFREEVERQDMVTLSQODDLRHLRREYVGKKILSFLVVEGSRPLDTSWLPWTAKELEKQYPLPERISATAMIPMGRRTSP-TTSVSCRNLLEVMRSPALLAVRQ	344
RHV-A	APIKTEAFKLAIDAYKKNFDTFKEFTRFIRSDHEQVQLRKFADERIHLFDGIGEPKKAGTFAAWSQSVNLLNLLRPLRLLRQKEMMVRMMPVGVKMLP-GERSQNL-LEEVLPVPLLEGVQ	358
MsAV1	AIAQYQGGFEKAVELFGNKVREAHFCAYLSDPARSDFVDRDYYNQKIVHLERSGEKKQAGSFAVSMLPMEKWLMLMFPPLSTRLTLMKIPVGVKVKH-GETPTNRP-LRKGADKSRVLNVRQ	344
VCV-M	AIASHQGGDFKAVEMFGAKVRETHFRDYLTDATRAEFIRDYNNQKVLHLDRSGEKKQAGTFVTSWNPDVKEWLLMLPLSQRQLSLMEKIPVGVKVPSP-GOLPENOP-LRRSVEGPLVLEKQ	344
CdAV1	PLPAGSLGYSKAVLFGQQVREHDQFLSEYLQRLVGLKAGQGRRREVENFVPSWQEWVSQLLMRPLYRPLERWLLRPLVGRINPP-GREPRTRL-LREVMPAELMKAKRQ	354
CoAV1	PLPRNDGDKMADVLFNGEVNRQHMQEFGQEVQVQQLMQLFQRLKQILEDQHIERQKQASTFVPLWQSVVRLRHSPLRQLRLEMMEMLIPVGPVNP-KENNVRMP-LSLFLPEWLKSEKGQ	350
GaAV1	WLPKNAAGLKAARDLYQGEVNRQMMTCAAVTPARPLMFYERLKKIQLQFDAADTQKAETFVTTWQQLVVAQALMHRPLVERQLKLANLVPVGRPPL-GTLLGTWP-LRRNLSPDILKEARQ	355
EbAV1	PRSKEHGGVQLAVEAFGGQVKKQQAEEFARPEAVKLFEYAKRKLISFEEMTSNRPKIGFTWMPRVETYLLSRPVKLRKICSMCPVGLPPP-GVAPGCP-LSKFVREELVSGVV	335
EbAV2	AMSRYDGGDKYAVANFGNKVRLHCLEYCGDASRTLLEYCKKKLIAFGPIRISDKPHPSRVCWLEQVETWLLSRPVALRREICLSPVLPVGFPHLP-QORPCEFE-LSSLLVSRDVERKRNQ	339
ScAV1	KKTVATGLLEYAKQLFGQEARNRFEIIFASKEEYQDALKYLAQEVQLCLFEATQTPREMENTTLLSLSVERSALWPLPQKRSVLSVGLPGRPLP-HQRPQCRP-LCQIINPEISLNPQRQ	353
SpAV1	PMSRYHGGDVYARQHFSQARELAQVYFASNPENQDIMERFMKERFFLFGRRPPMNLGSQECWSLALVERKLWKLMPQLRQRLRLLTGMIPIGILQAP-GRRGRCRE-LRRKLSPDLASPRQ	340
PpAV1	RAALTSANLEVACTTYGAEVASEWKAHHCRTPDVREALQNYCMRKIKHFEQESNEKQARNFVPSWMLQVSLRPLSTREREARGIPVGVRPL-PLAVRSKP-LWQLISQELKSSLRQ	327

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**Supplementary Fig. 1.** Multiple sequence alignment of the ORF1+2 fusion proteins. The first amino acids of the ORF2 are highlighted in yellow.

ZmAV1	HGTKPTTPIQRNLLEMTLPPMNLKTKNLRVQLLTHVRGGVRQISIARSKWEAGVRRIIGGGEMRGWEKDSALYRGGGNLHDAIRLALTGRQDPPGSFLFEHSLERATEILLLPCNLEVPD	4558																			
ZmAV2	EGSKVKPPLRKEMLLIPMPLNLLMAMPRVNLLHAFVHSAGRLKIAKSWEAGVRVIIGGGEMRGWNSEDAKSYRGGGNLHDAIRLALTGRHDLPGSFLFQHNFNRSARSILKLPDSLVPD	4681																			
BLV	IGHREKPPLGIRTELQAPPLKAECDSRIGVLRSRAPQADLKIPRSRSKWEAGVRKIIGGGELKDWFKAKSMSYRGGGNLFDALRLLSACDDYDGYTRLKGNVSVEAAREKLLLPSGLRVPD	4566																			
FpAV2	LGPARGPPLKVAEAVISGNSLLSTPNRQIJIHRRSGQGPQGAPIPTRSRWEAGVRHIIIGGGELLEWRDNVNRKYYRGGGNLHDAILLIGSADDVTPTALLSVVEEARRVLLPDPGLAVPD	4588																			
FpAV3	VGGRGPDPQQAESCTSGFLRANKRLVRHRERSLQLRQISIPHARSKWEAGIRHIIGGGELINFRADNCYRGGGNLFDALTLLARADDTEYSTLSVHSVEQARHVLRLPSGLPVPD	4588																			
LpAv1	VGGRGPDPDQLQAESCCVFSSFLRKNRRLRVRSRSLRQLVSPHARSKWEAGIRHIVIGGGELINFRADNCYRGGGNLFDALTLLARADDTEYSTLSVHSVEQARHVLRLPSGLPVPD	4588																			
AcAV1	IGMRKKPPLQKANESRSSKIDDLRNPRILVLRKPERGLGGIPTARSKFEAMVRKVIGGGEMLNWSIDSNSYRGGGNFTDALTLLADARYDAPEMFLSDYLSIEKARSLKLPDSLKVC	4644																			
AcAV2	RGIKNNPKPLARAEVASVTSLSLDINARILVLRSPTRPTSRSGEAVRKVIGGGEMIDWRTVSNQYRGGGNSDFTDALLIDARADTPEGKFLPDYFTLWKARDILRLPSLKVPC	4638																			
PeAV1	LGSKQPAPLSSEIERAFLIPPLWQNQRLSLIRLPRLDLGRIPHSRSRVEAKVRKVIGGGEMRDRAANAMYRGGGSFSDAKLLIIDAREDAPGAILSEKWKVDSARRYLLPCLGPVPR	4577																			
CaAV1	ISYRPAPQLSKMLECKEASLLRANGRVEIIMPIGGCDLRAIPCARSKWEAGIRKIKIGGGEMLNWKVAGNMRYGGCSDAIKLLSSASTIPGRLHQCPGALARGLPSLNSPV	4677																			
STV	LQKLKYRSLTRATEVEAEAVSLLYPNARIEVEPRIGDRTAIFPSRSRWEVGVRKVIGGGEVNLNWIDNGKYYRGGGCFADAIKLLQATGQRPPRQLLEDYTITTAREALGLPSLAVPS	4677																			
AoAV1	RGTGPPRRLGAGVPAAVGTPVLLQGGARLHVTRAPVPRDERRGIPYARSKWEAGVRKIIGGGELSDNQAASSKVRCCGNASDALLLADASDRLPKGTLRLGLFTLRGARDALRLPSLVPD	4655																			
FpAV1	LPSSAPSLRGAWSVPRAGVAPLQLGGARLRLVRAPVAPDTRGIPFARSKWEAGVRKIIGGGEMDNLWQVSSKERCGGNASDALLMLADASDRLPGRILRLGLFTLRGAREARLRLPSLGSVPD	4655																			
RHV-A	AGVKGNARSLRNVEASVQARLQELQTYRFRVREMEHVRVSIAVRSRFEAGIRRIIGGGEMRSWTSYDRSMYRGGGSNDAMKLLSAASVTPGKLLDQCYRVSSARKARLRLPSLGSVPD	4799																			
MsAV1	SYGKSYLSRERLKHQELCGITSQMPGEPRIKIFKSFWESEPMGPIMPMSRKYCEAVRWVIGGGEVNRKWDVSSYRGGGSNDALKLLAANASTVRPGKLLDRYVSFRVARARLRLPGLPSLGSVPD	4655																			
VCV-M	QGIKLTRGLQRNVEMKGTLPSQSLRGRIRIRLPRWPWTDHNRMIPTSMSRVEAGVRWVIGGGETRWRKEASTMYRGGCSNDALKLLANSTVLPGRLLRLDYLSLRVARARLSLPADFCVPD	4655																			
CdAV1	AGIRHRPQLQRKIEEAGGGSRGAEMTGRVRLVWENGERHRTRPTVARGKIRKTIIGGGELNNRDESSYMRGGGSADALRIMLFSADAPPPGRVLTDFWREGSARQFQFIELFEPVD	4751																			
CoAV1	LGIKVQRGLRRQIEVVEGVASEEFLRVRGKVYVEWAAEKARLLPVARSKFETGVRVIGGGEMRNHWASSMYRGGGNNDALRLLSNASFNPMEKYLHECFTIETARRELLTTDQKVPD	4711																			
GaAV1	SGLKGRPGLERFGFLQGGLSEALLETLGTRKLVHFEPEVRSMARSKWEAGVRKIIGGGEMGRWSASSYRGGGNNDALRLLSQAKDFFGRFLTDFTVKDMAREACLESLDALVPD	4767																			
EbAV1	EGTKTNPRLRAFATVQLGAEVRL-STRVLVWHTFGPETQRIRPVARSRIEAGLRRRIIGGGAMRGWDADSKMFRGGGNSSDALLLLGQCDNDLNLPGGLLREHFSSLSSAKRALSLPGLLGPV	4555																			
EbAV2	LGHRIPIVLAGIRGAQELDSSIMR-NPRLKVVNFQGEGRVPHRSKYEALRRLRRIIGGGAMRSWEDSKMFRGGGTSSDALLLSQADFRLPGLLKEHFSRTRLARECLCPLEDLVPV	4599																			
ScAV1	EVGRPSQDLDLPLERKPKTLEE-NPRLKVVRSVPGPGRDRRIPVRSRGEYAGVRKVIGGGALRSWQDQAMYRGGGNNDALLLMSQASEKRPAGFLRDRYSVLARRALGLPSLDQVPD	4731																			
SpaV1	VGVKLQOGISRKVELTSLGPKMLR-TSRLRVLRLSLGPERPRAVSRFEAGVRKVIGGGAMRSWEVDSSYRGGGSNDALRLLGQARDRPGFAFLSGKFTQASARLLALPNNLDLVPD	4606																			
PpAV1	VGMRKVKGISQPMQHNLVPSLFLQGNGRLDVLVDVSGSKHKGRIPTAMSFMKGVKRVVIGGGEMRDWNRSASFNFVRGGGLDGAALKFSSCKTSPQRFLCDVYSLEVAREILDPLGPV	4488																			
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ZmAV1	GPKAVRMKNFNEDATAQPVRLARCKSKYGLKEGLERIAWDLYDRVGDGKLRRLWQPLPLLARIFRSKLVEQESAIIKIFSGQPIGRAVMMLDAMEQFSSPLYNALCDVSVKLNRVPESG	5766																			
ZmAV2	GRDSVTMRNFNEEATAGPVPLCRAIGCKTGYLKGLEDIVNLYRDRVNGELRWTWELPPLLARIFRSKLIDQDAAKEEKKILTQPLGRAVMMLDASEQFQSSPLYNLVSGVSVRLNCERRSG	5899																			
BLV	GVGCVHKMKNFNDNEASAGPLCRAFGIRKAGLRSRLEQFAWEIYDGGNGDQDGLAIPFPLGRVLLGARVYRTKLTGEKAMRKISTGDGSIRAIMMLDAYEQFQSSPINFVNISDAVTHLHSDP	5777																			
FpAV2	GKACCKVMQFNDDATAGPLLRAFGVFKGKGKLAATQEFQWVLYDVRGSEDLKPRQPLGFLGARVYRTKLTGEKALMELKQDAAKEEKKIOPQFPLGRAVMMLDASEQFQSSPFLNAISEATVHLSNPRSG	5799																			
FpAV3	GAQCCFMQFNDDASAGPLLRAFGVFKNKGKLSMVESFWGMYDRVGSQDLPQLCPCLLARLGFRTRKLVDKDKAAKKIFDVEPVGRAVMMLDVEQEAFQSSPLFNAISEQVTFLHSDP	5799																			
LpAv1	GPQCCFMQFNDDASAGPLLRAFGVFKNKGKLYKLSIIFFWVGMYDRVGSQDLPQLCPCLLARLGFRTRKLVDKDKAAKKIFDVEPVGRAVMMLDVEQEAFQSSPLFNAISEQVTFLHSDP	5799																			
AcAV1	HRNCVSVMFNNEATAGPFPRHAGIRKINYKGMLRQLEDFAWCENAYNNTDGGNSPMLSYIIRRSGFRTRKLVSTTEAFQAKMDKPKIGRCVMMMDAIEQFQSSPLYNLVSLKTTAQAFDIKS	5855																			
AcAV2	NRQALKVSNFNNDATAGPFPRAYGIKSKYGMRLQLEDFAWCENAYNNTDGGNSPMLSYIIRRSGFRTRKLVSTTEAFQAKMDKPKIGRCVMMMDAIEQFQSSPLYNLVSLKTLADLRFDPASG	5849																			
PeAV1	GPEATKMKNFNNDATAGPALRAGFLRKSGLKTSLEEFWAFNCLDAFARGGAEEADCLPFLVAFARVGYRTKLLTLDANSKINSCKPLGRVCVMMMDAIEQFQSSPLYNLVSLNTHLSRFQRNSG	5787																			
CaAV1	GKGCRVKNYNDATTPFLYPSFGIKKGKLYKLDNLQSLMEDITYCHYSISATDRLPYFAARVFRSKLLPMEALRKFRADNPQMGRVCVMMMDAIEQFQSSPLYNLVSKYTS-DSKGAT	5877																			
STV	GKGSCKVKNYNDATTPFLYPSFGIKKGKLYKLDNLQSLMEDITYCHYSISATDRLPYFAARVFRSKLLPMEALRKFRADNPQMGRVCVMMMDAIEQFQSSPLYNLVSKYTS-RSGQTS	5877																			
AoAV1	GRACCNKHFNVNEATAGPFPLRAGVKKKESLEQLLGFVWECFDATNDIIRRLPFFGMRIGFRTRKLKKSEMLTKIIRDFKPLGRVCVMMMDAIEQFQSSPLYNLVSKLSDADALKRDPMSG	5866																			
FpAV1	GRACCNKHFNVNEATAGPFPLRAGVKKKAEALQLLGFDVWFCDFDASNDGARLLPFFGMRIGFRTRKLPPRSEMLTKIIRDFKPLGRVCVMMMDAIEQFQSSPLYNLVNSLSDADALKRDPMSG	5866																			
RHV-A	SLAEQCQTFTNDQASAGPFLRAGFVKKYKGKLYRMLMEEFWMGIYDRYGDGRDERSLFPITGRFTRKLLGEEGALRKRNHRGEPLGRAVMMLDQECCSSPLYNLISGCRNKGW	6000																			
MsAV1	GPDACRVKNFNFTGFSVPLKFVAFGRSKNQLRQLQDEAWWYNFNSGNSDFGVGFLPGRVLRKSLVTEEKARKKISEGDSVGRAVMMDALEQECCSSPLYNLVSTYFTHKLNRSSG	5866																			
VCV-M	GPEACRVKNFNFTGFSVPLKFVAFGRSKNQLRQLLDEAWWYNFNSFADGQDLDVSGPFLPFFGARLGRFRSKLVSEEKARKKISEGDSVGRAVMMDALEQECCSSPLYNLISSTYRRLERE	5866																			
CdAV1	GPGCCVMKNFNNEATAGPFPLRAGFVKKYKGKLYKTLLEQWVQFYDYYANNVESTDATPLFTRAVFRTRKLTERKALKMVNDTYGRVMMMDAIEQAAQSPPLYNLVSSYFTLRLP	5966																			
CoAV1	GPESVKMKNFNNDATAGPFPLRAGFVKKYKGKLYKTLLEQWVQFYDYYANNVESTDATPLFTRAVFRTRKLTERKALKMVNDTYGRVMMMDAIEQAAQSPPLYNLVSSQCFHGRLLRESG	5929																			
GaAV1	GFGCCSTKFNNEATAGPFPLRAGVVKVHGKLTQEFQWMLYDRYGDGEINQKGLPHLTTTRIGFRTRKLVTREREALRKVQQGTFGRAVMMDALEQEAVASSPLYNLSHKTFLMRNNEPGSG	5979																			
EbAV1	GPECLVMKNFNNDATAGPFPLRAGFVKKYKGKLYKLLKEDDEMWYRQQDFAQGRIDERLPGYFAARVFRTRKLSETCAKELAQAGPFRVGRAVMMDALEQEAAQSPPLYNLVMSNSTYQRRLERDCG	5767																			
EbAV2	GKDCRMKNFNNEATAGPFPLRAGFVKKYKGKLYKLLKEDDEMWYRQQDFAQGRIDERLPGYFAARVFRTRKLSETCAKELAQAGPFRVGRAVMMDALEQEAAQSPPLYNLVTFVFTERRLEKECG	5800																			
ScAV1	GPAATKMKNFNNDATAGPFPLRAGFVKKYKGKLYKLLKLEEMWYDYYDAYAKTGEEDHQLPFLTRARLFRTRKLKKAEAMRRIEGKAMGRVMMMDALEQEAAQSPPLYNLVASHYTFERRLEKDCG	5949																			
SpaV1	GAKSTRMKNFNNDATAGPFPLRSGFVGIKKGKLYKLRKLEEMWYRQYDDYAGAIRDSSGLPFTTARVFRTRKLVSVEKAEEKFQGPFRVGRAVMMDALEQEAAQSPPLYNLVSHYTFRRLRDCG	5811																			
PpAV1	GPEACRINKYNDATAGPVPLRAGVRRKAGLKSSLESMLMSWYFIDAVGDGKLLPEDLPYLRSVGRFRTRKLAREAMAKELGKGEPMGRVAVMMDALEQEAAQSPPLYNVMSGLAQAQNHKKERGV	5699																			
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ZmAV1	WRNNMVRASSDWSRFWGDIRDNSCAIEFLDWSKFDRERPKDIEDIEFVINIFVSCFLPKNRERRELLSAYKYMGRKALIDKVIMLDDGCAFTYDGMIPSGSLWTGGLTALNLYINAAVRRLG	6979																			
ZmAV2	WRNNAVRASSDWSRFWGDIRDACIVELDWSKFDRERPRADIOQFCIDVLCSCFRPGRKRORLSSAYKYMELNALIHKVIMLDDGCAFEAYEGIMPSSGLWTGGLTALNLYITAACESG	7101																			
BLV	WRNYLIRASSDWGKMYKEMRKVAKVVELDWWKFKDFRERPADHISFFDVIILSCFAPTRTREKELLYGAYRMANEALHRLVLTDDGGVFLTWDGMVPSGLWTGGLTALNLYIGALSDIG	6989																			
FpAV2	WRNYLVRASSAWADLWELDKSCGTIVELDWSKFDRERPAEDIQFFVIVCSFCQPRTREREERLLLAGYKMMENALVHRRVLTLDNGCFLKVIDMGPMVPSGLWTGGLTALNLYITAALMSLG	7000																			
FpAV3	WRNYLVRASVAWEFWHRLDAKVIVELDWAJKDFRERPAEDIQFFVIVCSFCQPRKTAERERLLLAGYKMMENALVHRRVLTLDNGCFLKVIDMGPMVPSGLWTGGLTALNLYITAALMSLG	7000																			
LpAv1	WRNYLVRASVAWEFWHRLDAKVIVELDWAJKDFRERPAEDIQFFVIVCSFCQPRKTAERERLLLAGYKMMENALVHRRVLTLDNGCFLKVIDMGPMVPSGLWTGGLTALNLYITAALMSLG	7000																			
AcAV1	FRNTIVRASSDWKAFWKEVAKAIVELDWAJKDFRERPAEDIQFFVIVCSFCQPRKTAERERLLLAGYKMMENALVHRRVLTLDNGCFLKVIDMGPMVPSGLWTGGLTALNLYITAALMSLG	7066																			
AcAV2	FRNTIVRASSDWKAFWKEVAKAIVELDWAJKDFRERPAEDIQFFVIVCSFCQPRKTAERERLLLAGYKMMENALVHRRVLTLDNGCFLKVIDMGPMVPSGLWTGGLTALNLYQSVMSLIG	7059																			
PeAV1	FCNSIVRASSDWMLNKDVDSAASCVVELDWWKFDRERPADDISFMIDVIISCEAKYDDEYERLLGYYRILRNLIERCFCVTFDDGGVFFHIDGMVPSGLWTGGLTALNLYLNAALLSLG	6999																			
CaAV1	FRNSVVRASSDWMLWDEKVEASCVVELDWWKFDRERPSADLFMIDVIISCEAKYDDEYERLLGYYRILRNLIERCFCVTFDDGGVFFHIDGMVPSGLWTGGLTALNLYLNAALLSLG	7089																			
STV	FRNTVVRASSDWMLWDEKVEASCVVELDWWKFDRERPSADLFMIDVIISCEAKYDDEYERLLGYYRILRNLIERCFCVTFDDGGVFFHIDGMVPSGLWTGGLTALNLYLNAALLSLG	7089																			
AoAV1	FRNTAVRASSDWSYMEEIKEAKVCMELDWSKFDRERPRCDLEFMDVVDVVISCFAPKNEREQRLLRGYEVCMRRAVERVALLLDGGDALFEIDGMVPSGLWTGGLTALNLYLAASELSEAG	7077																			
FpAV1	FRNTAVRASSDWSYMEEIKEAKVCMELDWSKFDRERPRCDLEFMDVVDVVISCFAPKNEREQRLLRGYEVCMRRAVERVALLLDGGDALFEIDGMVPSGLWTGGLTALNLYLAASELSEAG	7077																			
RHV-A	FRNTTWRASSDWGLYLYSEVERAKAIVELDWAJKDFRERPAEDIQFFVIVCSFCQPRKTAERERLLLAGYKMMENALVHRRVLTLDNGCFLKVIDMGPMVPSGLWTGGLTALNLYLAASELSEAG	7211																			
MsAV1	FKNAVVKASSDWAHHWNGVKDAAVIVELDWSKFDRERPREDEFLEMVMSLISSCFNPKSAEERLLHAYTTSNFRALVERPVFLDGGGVFGIEGMVPSGLWTGGLTALNLYLMAKCAEIG	7079																			
VCV-M	FKNAVVKASSDWAHHWNGVKDAAVIVELDWSKFDRERPREDEFLEMVMSLISSCFNPKSAEERLLHAYTTSNFRALVERPVFLDGGGVFGIEGMVPSGLWTGGLTALNLYLMAKCAEIG	7079																			
CdAV1	FKNGVVRASSDWGLWLRVWQPKQAVKIELDWSKFDRERPREDEFLEVIVKVVCSFCRPRDGRRLQAYQEMMRRALVERALITDGGGVFLVDMGPMVPSGLWTGGLTALNLYLKAICAEIG	7117																			
CoAV1	FRNALIRASSDWHMEEVEQAAVIVELDWSKFDRERPAEDIFFINVLSCFPTKPRERELRLLRAYGIMMRRALIERMLTDNAGVFGISGMVPSGLWTGGLTALNLYLKAICAEIG	7134																			
GaAV1	FRNATIRASSDWGKMWEEVRAQATIVELDWSKFDRERPREDLFLFIVILSCFPLKRNREKRLLRAYGIMMRRALIERLLMDGGVFTIDGMVPSGLWTGGLTALNLYLIAACREIG	7189																			
EbAV1	FKNGIVKASSDWAHKINEDREKAAIEFLDWSKFDRERPADDIFLVIEWLSCFCEPNTDRRERLLRAFGLMMRRALVERIIVMDGGVFFIDGMVPSGLWTGGLTALNLYLNAACMVNG	6979																			
EbAV2	FKNQVIRASSDWNRWWEYLRDSKVIIEFLDWAJKDFRERPREDEFLEMVMSLISSCFNPKSAEERLLHAYTTSNFRALVERPVFLDGGGVFGIEGMVPSGLWTGGLTALNLYLAAACVEG	7019																			
ScAV1	FKNTIIRRASSDWQOAIWHAKEAIEFLDWAJKDFRERPREDEFLEMVMSLISSCFNPKSAEERLLHAYTTSNFRALVERPVFLDGGGVFGIEGMVPSGLWTGGLTALNLYLKAACLEIN	7154																			
SpaV1	FKNAVIRASSDWNEIWKGVRREAIEFLDWSKFDRERPAEDIFFIVDVSFVSCFKPRERLLRAYGIMMRRALIERLLMDGGVFTIDGMVPSGLWTGGLTALNLYLRSACLEVG	7029																			
PpAV1	FRNYVVRASSQWQLDNEVSSCKVLEIWLDSKFDRERPREDLFLMIDLVSCFCEPKSLRERLLRAYGIMMRRALIERLLMDGGVFTIDGMVPSGLWTGGLTALNLYLHQAFCVQDGL	6909																			
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**Supplementary Fig. 1.** Continued

**Supplementary Fig. 1** Continued