

SUPPORTING INFORMATION

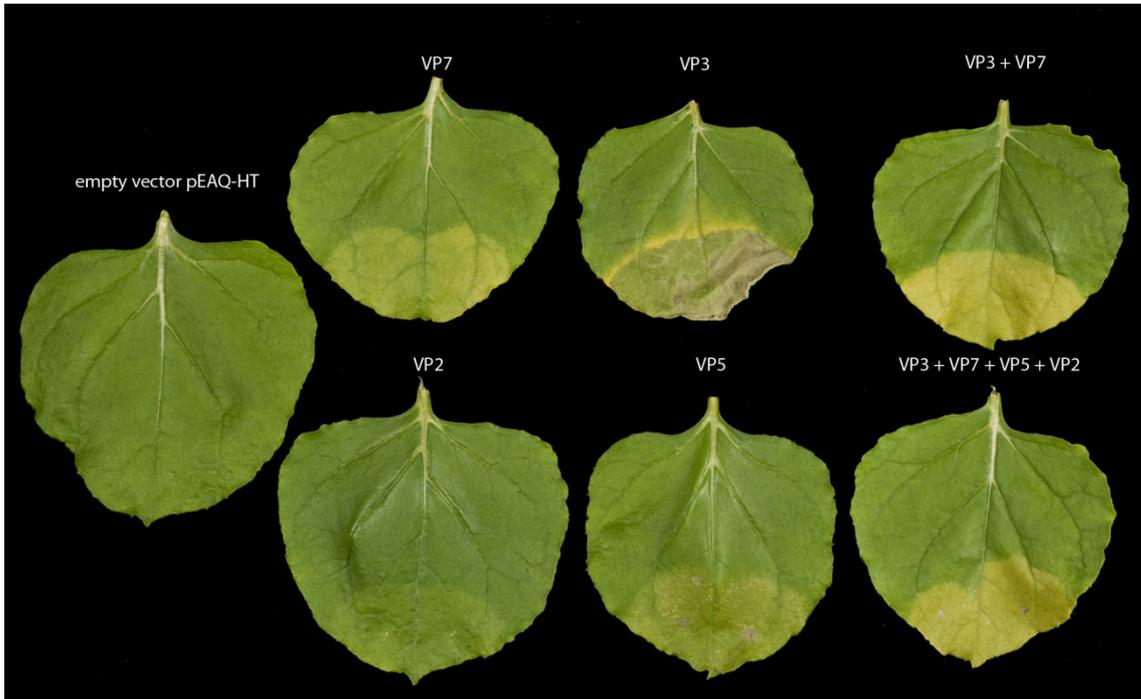


Figure S1: Some BTV8 structural proteins cause symptoms when expressed in plants individually, but not when expressed in combination with their structural neighbouring proteins. Plants were infiltrated with suspensions of *Agrabacterium tumefaciens* harbouring pEAQ-*HT*-based plasmids for expression of BTV-8 structural proteins, either individually or in combinations as indicated. Leaf tissue was harvested 8 days post infiltration and a digital photograph taken.

Supporting Information: Figure S2

(a) VP2

Protein View: B4E549
 SubName: Full=Outer capsid protein VP2
 Database: SPtrEMBL
 Score: 323
 Taxonomy: Bluetongue virus 8

1	MEELAIPIYT	NVFPALLDG	YDYIIDVSSR	VEEEDPEVK	RHDVTEIPRN
51	SMFDIKDEHI	RDALIKPVN	NDGYVLPV	DITLKAFFDR	KRVVLNDGHS
101	EFHTKTNWVQ	WMIDDAMDVQ	PLKVDIAHTR	SRISHALFNC	TVRLHSHKAD
151	TASYHVEPVE	IESWGCNHTW	LSRIHHLVNV	ELFHCSQEA	YTLKPTYKII
201	SNAER ASTSD	SFNGTMIELG	RNHQIQMGDQ	GYQKLKEGLV	QVRIEGKTPL
251	VIQEEITALN	KIREQWIARN	FDQREIKVLD	LCRLLSTIGR	KMCNTEEEPK
301	NEADLSVK FQ	MELDEIFRPG	NNERTNIMGG	GVHRKNEDRF	YVLIMIAASD
351	TNKGR IWWSN	PYPCLRGALI	AAEVQLGDVY	NLLRNWFQWS	VRPTYVPYDR
401	NR ESDKYIYS	RINLFDSTLR	PGDKIVHWEY	KLLNEVREVS	INKGNECDLF
451	PEDEEFTTKF	HEARYTEMKN	QIIQSGWNQR	DFKMHKILED	GANVLTIDFE
501	KDAHIGTGSA	LSLPDYYNKW	IIAPMFNAKL	RITEVVIGTA	HTDDPAVGRS
551	AK AFTHDPFD	LQRYCLARYY	DVRPGMMGRA	LSKQQNMSSM	TDKLSK QEDY
601	AGIVSRRLLEY	KERENRCLTE	TAQYVFEKTC	LYVLELLSRH	TMPSEDSEVT
651	FEHPTIDPSV	DIETWKIIDV	SQLIIFVFDY	LFENRKIVRD	TTEARWTLFK
701	IRSEVGRARI	DAIEMTFPRF	GRMLRNASQA	KINQDIACLN	FLPLLFIIIGD
751	NISYHRQWS	IPVLLYAHI	RIIPLEVGAY	NNRFGLTSYL	EYMAFFPSYA
801	TRVAKIDESI	KCAIAMAEF	YMNTDIHSGS	VMSNVITTKR	LLYETYLASL
851	CGGYSDDLW	YLPITHPSKC	LVAFEVADDV	VPLSVRRERI	LSRFPLSSRH
901	VK GIALISVD	RNQKVSQTE	GIVTHRLCKK	NLLKYVCDVI	LFKFSGHVFG
951	NDEMLTKLLN	V			

(b) VP3

Protein View: B4E550
SubName: Full=Inner capsid protein VP3
Database: SPtrEMBL
Score: 476
Taxonomy: Bluetongue virus 8

1	MAAQNEQRPE	RIK TPYLEG	DVLSSDSGPL	LSVFALQEIM	QKVRQVQADY
51	MTATREVDFT	VPDVQKILDD	IKALAAEQVY	KIVKVPSISF	RHIVMQSRDR
101	VLR VDTYEE	MSQVGDVITE	DEPEK FYSTI	IKKVR FIRGK	GSFILHDIPT
151	RDHR GMEVAE	PEVLGVEFKN	VLPVLTAEHR	AMIQNALDGS	IIENGNVATR
201	DVDV FIGACS	EPIYRIYNRL	QGYIEAVQLO	ELRNSIGWLE	RLGQRKRITY
251	SQEVLTDFRR	QDTIWVLALQ	LPVNPQVVWD	VPRSSIANLI	MNIATCLPTG
301	EYIAPNPRIS	SITLTQRITT	TGPFALITGS	TPTAQQLNDV	RKIYLALMFP
351	GQIILD LKID	PGERMDPAVR	MVAGVVG HLL	FTAGGR FTNL	TQNMAR QLDI
401	ALNDYLLMY	NTRVQVNYGP	TGEPLDFQIG	RNQYDCNVFR	ADFATGTGYN
451	GWATIDVEYR	DPAPYVHAQR	YIRYCGIDSR	ELINP TTYGI	GMTYHCYNEM
501	LRMLVAAGKD	SEAA YFRSML	PFHMVRFARI	NQIINEDLHS	VFSLPDDMFN
551	ALLPDLIAGA	HQNADPVVLD	VSWISLWFAF	NR SFEP THR N	EMLEIAP LIE
601	SVYASELSVM	KVDMRHLSLM	QRRFPD VLIQ	ARPSHF WKAV	LND SPEAVKA
651	VMNLSHSHNF	INIRDMMRWV	LLPSLQ PSLK	LAL EEEEAWAA	AN DFEDLMLT
701	DQVY MHRDML	PEPRLDDIER	FRQEGF YYTN	MLEAP PEIDR	VVQYTYE IAR
751	LQANMGQFRA	ALRRIMDDDD	WVREGGV LRT	VR VKFFDARP	PDDILQ GLPF
801	SYDTNEK GGL	SYATIKYATE	TTIFYLIYNV	EF SNT PDSL V	LINPT YTM TK
851	VFINKRIVER	VRVGQILAVL	NR RFVAYK GK	MR IMDITQ SL	KMGTK LAA PT
901	V				

(c) VP5

Protein View: B4E553
 SubName: Full=Outer capsid protein VP5
 Database: SPtrEMBL
 Score: 131
 Taxonomy: Bluetongue virus 8

1	MGKIIKLSLR	FGKKVGNALT	SNTAKKIYST	IGKAAERFAE	SEIGSAAIDG
51	LVQGSVHSLM	TGESYGESVK	QAVLLNVMGS	GEELPDPLSP	GERGMQTKIR
101	ELEDEQRNEL	IRLKYNDKIK	QKFGKELEEV	YEFMNGVAKQ	EEDEEKHYDV
151	LKK AVNSYDK	ILTEEEKQMR	ILATALQKEV	KERTGTEAVM	VKEYRNKIDA
201	LK EAIEVERD	GMQEEAIQEI	AGMTADVLEA	ASEEVPLIGA	GMATAVATGR
251	AIEGAYKLKK	VINALSGIDL	THLRTPKIEP	TIVSTVLDHK	FKDIPDEMLA
301	VSVLSKNRAI	EENHKEIIHL	KNEILPRFCK	AMDEEKEICG	IEDKKIHPKV
351	MMKFKIPRTQ	QPQIHIYSAP	WSDDDVFFFH	CISHHHANES	FFIGFDLGD
401	LVHYEDLTAH	WHALGAAQAA	VGRSLNEVYK	EFLNLAINNT	YSSQMHARM
451	IRSK TVHPIY	LGSLHYDISF	STLRSNAQRI	VYDEELQMI	LRGPLHFQRR
501	AILGAIKHGV	KILGTEVDIP	LFLRNA		

(d) VP7

Protein View: B4E554
 SubName: Full=VP7 core protein
 Database: SPtrEMBL
 Score: 177
 Taxonomy: Bluetongue virus 8

1	MDTIAARALT	VMR ACATLQE	ARIVLEANVM	EILGIAINRY	NGLTLRGV TM
51	RPTSLAQRNE	MFFMCLD MML	SAAGIN VGPI	SPDY TQHMAT	IGVLAT PEIP
101	FTTEA ANEIA	R VTGETSTWG	PARQPYGFFL	ETEETFQPGR	WFM RAAQAVT
151	AVVCGPDMIQ	VSLNAGARGD	VQQIFQGRND	PMMIYLVWRR	IENFAMAQGN
201	SQQTQAGVTV	SVGGVDMRAG	RIIA WDGQAA	LHVH NPTQON	AMVQ IQVVFY
251	ISMDK TLNQY	PALTAEIFNV	YSFRDHTWHG	LRTAILNRTT	LPNMLPPIFP
301	PNDRDSILTL	LLLSTL ADVY	TVLR PEFAIH	GVNP MPGLT	RAIAR AAVY

Figure S2: Mass spectrometry analysis of 4 main protein bands recovered from SDS-PAGE analysis of a density gradient fractions from leaf tissue co-infiltrated with constructs for co-expression of BTV-8 VP2, VP3, VP5 and VP7. The major protein hit of each band is presented (a-d). Matched peptides are shown in **red**. Scores >75 are considered significant ($p < 0.05$).

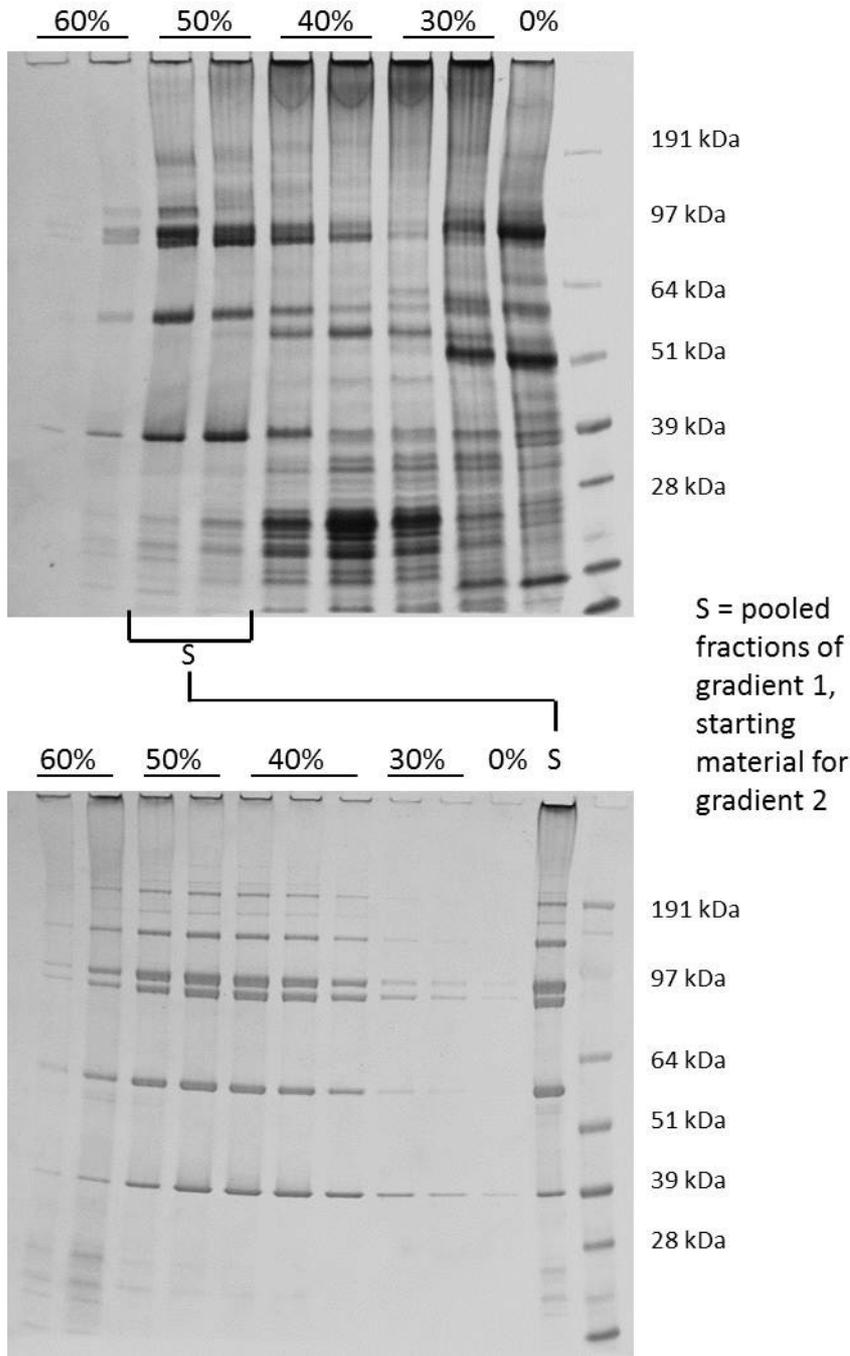


Figure S3: Clarified extract from leaf tissue expression four BTV structural proteins, separated on two consecutive step sucrose gradients. Approximate sucrose concentration of steps indicated in per cent. Two fractions from sucrose gradient 1 (top) were pooled to provide starting material (S) for sucrose gradient 2 (bottom).

Supporting Information: Figure S4

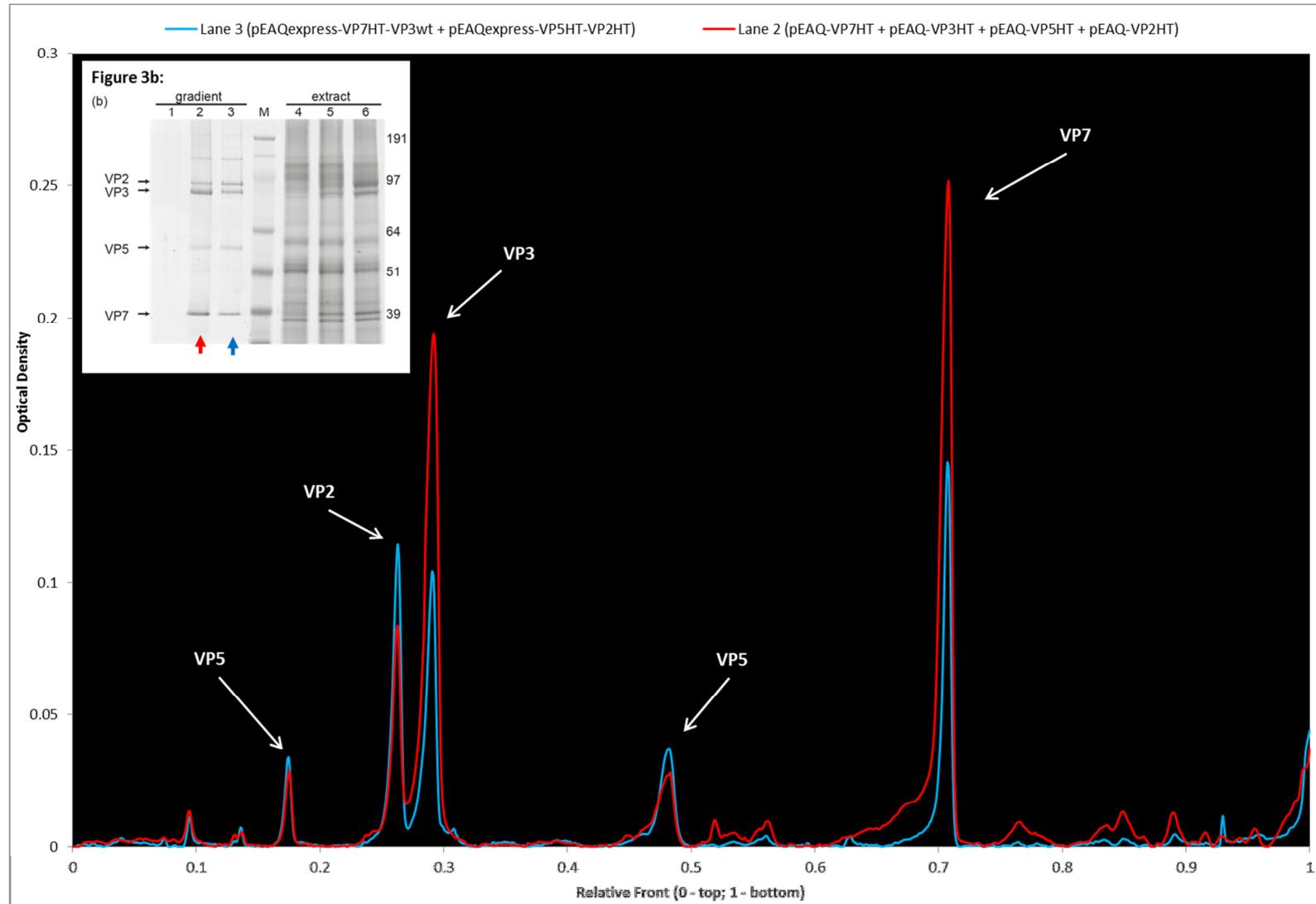


Figure S4: Densitometric analysis of Coomassie-stained gel of Figure 3b (inset). Two lanes were analysed: purified VLP preparations prepared by co-infiltration of four pEAQ-*HT* constructs all under the control of a *HyperTrans* 5'UTR (red), or purified VLP preparation prepared by co-infiltration of two pEAQexpress constructs with VP3 under control of a wild-type 5'UTR (blue).