

Table S1. Kemerovo virus (KEMV) genome: lengths of dsRNA genome segments, encoded proteins, 5' and 3' NCRs, terminal conserved sequences for KEMV smb1/Vero2/BSR3 (a) and KEMV Ps.IRE1 (b).

a)

Segment	Protein	Accession	5' NCR	5' termini-----3' termini	3' NCR
1: 3896 bp	VP1(Pol); 1285 AA; 145,956 Da	PP278971	11 bp	5' - GUAAAAUGUC-----UAAGGAUAC - 3'	28 bp
2: 2792 bp	VP2(T2); 908 AA; 102,750 Da	PP278972	18 bp	5' - GUAAAACUUC-----UAAGGAUAC - 3'	47 bp
3: 1934 bp	VP3(Cap); 632 AA; 72,416 Da	PP278973	5 bp	5' - GUAAAAUGUU-----AUAACUUAC - 3'	26 bp
4: 1730 bp	VP4(OC1); 554 AA; 62,562 Da	PP278974	17 bp	5' - GUAAAAUCUUA-----CCAAGAUAC - 3'	54 bp
5: 1719 bp	NS1(TuP); 529 AA; 60,037 Da	PP278975	39 bp	5' - GUAAAAAUUU-----UUAAGAUAC - 3'	96 bp
6: 1667 bp	VP5(OC2); 537 AA; 59,444 Da	PP278976	22 bp	5' - GUAAAAUUUC-----AUAGGUUAC - 3'	37 bp
7: 1197 bp	NS2(ViP); 368 AA; 40,934 Da	PP278977	45 bp	5' - GUAAAAUUUU-----AUAAGAUAC - 3'	51 bp
8: 1183 bp	VP7(T13); 357AA; 39,479 Da	PP278978	18 bp	5' - GUAAAAUUCU-----AUAAGUUAC - 3'	97 bp
9: 1049 bp	VP6(Hel); 317 AA; 34,198 Da NS4; 151 AA; 17,622 Da	PP278979	58 bp	5' - GUAAAAUUC-----UAAAGAUAC - 3'	43 bp
10: 707 bp	NS3; 214 AA; 23,410 Da NS5; 62 AA; 7,743 Da	PP278980	18 bp	5' - GUAAAAUUUC-----AUAGGAUAC - 3'	50 bp
Consensus				5' - GUAAAA ^A / _U ^G / _U ^C / _U ⁻⁻⁻ / _A ^U / _A ^A / _G ^A / _C ^A / _U UAC - 3'	

b)

Segment	Protein	Accession	5' NCR	5' termini-----3' termini	3' NCR
1: 3896 bp	VP1(Pol); 1285 AA; 145,904 Da	PP278981	11 bp	5' - GUAAAAUGUC-----UAAGGAUAC - 3'	28 bp
2: 2792 bp	VP2(T2); 908 AA; 102,750 Da	PP278982	18 bp	5' - GUAAAACUUC-----UAAGGAUAC - 3'	47 bp
3: 1934 bp	VP3(Cap); 632 AA; 72,402 Da	PP278983	5 bp	5' - GUAAAAUGUU-----AUAACUUAC - 3'	26 bp
6: 1667 bp	VP5(OC2); 537 AA; 59,444 Da	PP278984	22 bp	5' - GUAAAAUUUC-----AUAGGUUAC - 3'	37 bp
7: 1197 bp	NS2(ViP); 368 AA; 40,934 Da	PP278985	45 bp	5' - GUAAAAUUUU-----AUAAGAUAC - 3'	51 bp
8: 1183 bp	VP7(T13); 357AA; 39,507 Da	PP278986	18 bp	5' - GUAAAAUUCU-----AUAAGUUAC - 3'	97 bp
9: 1049 bp	VP6(Hel); 317 AA; 34,198 Da NS4; 151 AA; 17,622 Da	PP278987	58 bp	5' - GUAAAAUUC-----UAAAGAUAC - 3'	43 bp
Consensus				5' - GUAAAA ^A / _U ^G / _U ^C / _U ⁻⁻⁻ / _A ^U / _A ^A / _G ^A / _C ^A / _U UAC - 3'	

AA: amino acid, Da: dalton, NCR: non-coding region.

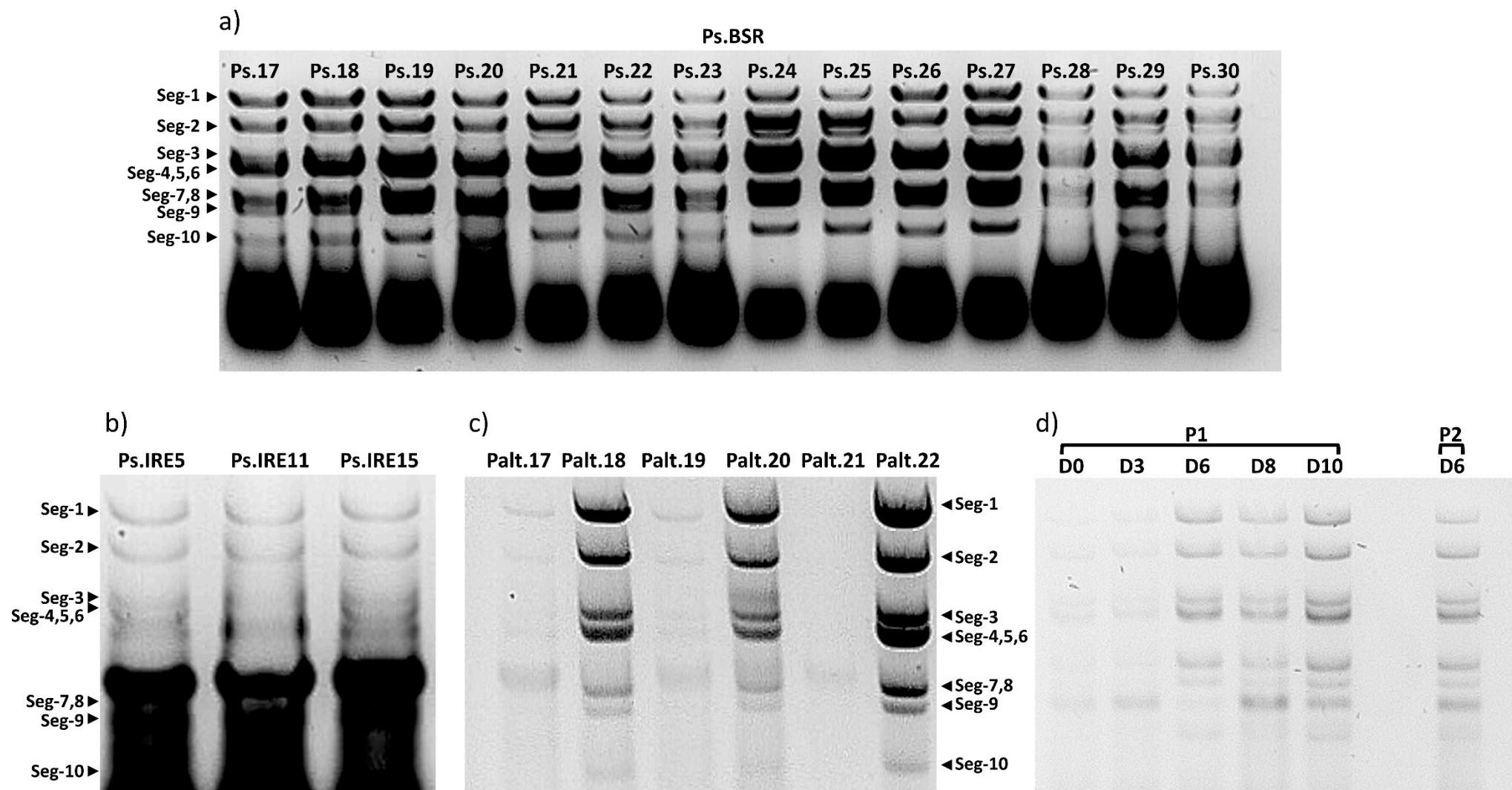


Figure S1. Electropherotypes of the Kemerovo virus (KEMV) dsRNA genome from various cell culture passages. dsRNA extracts were analysed by agarose gel electrophoresis (1% agarose in TAE buffer: 400 mM Tris-Acetate pH 8.0, 10 mM EDTA).

(a) dsRNA genome of KEMV that was serially passaged in BSR cells (Ps.BSR), (b) dsRNA genome of KEMV that was serially passaged in IRE/CTVM20 (Ps.IRE), (c) dsRNA genome of KEMV that was passaged by alternation between IRE/CTVM20 and BSR cells (P.alt).

(d) This gel shows the growth kinetics of KEMV in IRE/CTVM20. The cells were infected with KEMV and RNA extraction performed from cell pellets on days 0 (D0), 3 (D3), 6 (D6), 8 (D8) and 10 (D10). The maximum levels of dsRNA genome are reached between days 6 and 10. P1: passage 1 in IRE/CTVM20 and P2: passage 2 in IRE/CTVM20.

```

VP1BSR  MAVVEQRITSANNAIRILPNLPLKDDKTYHDYKYKSKWKDSKATARTTLHGVPVLSENSWRDI PRTTQTFRPRD
VP1IRE  MAVVEQRITSANNAIRILPNLPLKDDKTYHDYKYKSKWKDSKATARTTLHGVPVLSENSWRDI PRTTQTFRPRD
*****

VP1BSR  VVEYYRSQIPVVELQPEEEFLRNYSLDEKDAGPLLAFLRHRSQEEMAVYGDMLRHWYALVQQLSDDYGHAPL
VP1IRE  VVEYYRSQIPVVELQPEEEFLRNYSLDEKDAGPLLAFLRHRSQEEMAVYGDMLRHWYALVQQLSDDYGHAPL
*****

VP1BSR  GLACMERFIDDHGDPFHQSTRDLSKISDERYSSSVLFFEMSICEALHEFNVVLRRESGIPLTTRFGRQEVDR
VP1IRE  GLACMERFIDDHGDPFHQSTRDLSKISDERYSSSVLFFEMSICEALHEFNVVLRRESGIPLTTRFGRQEVDR
*****

VP1BSR  IAIVRELYTLMLTHPKVCNMLRASYSWFVKNWGIAAPEVNLESSESGDDRNSKDITFHRWRRVRNPYSIAIVLA
VP1IRE  IAIVRELYTLMLTHPKVCNMLRASYSWFVKNWGIAAPEVNLESSESGDDRNSKDITFHRWRRVRNPYSIAIVLA
*****

VP1BSR  TEFHKSSLRANLDKVEATAYASKLAGTPMELRVFRAMMANTYTTTFDPRDQSHLQLASLLLAIQTMAGYGRAW
VP1IRE  TEFHKSSLRANLDKVEATAYASKLAGTPMELRVFRAMMANTYTTTFDPRDQSHLQLASLLLAIQTMAGYGRAW
*****

VP1BSR  IVNAGDDPERMLKPSRDNHVTRVARETEKFFVKAYEEARMHGHDIIIPPEDMYSSLLRLAKNTSSGFSSTEVEVKK
VP1IRE  IVNAGDDPERMLKPSRDNHVTRVARETEKFFVKAYEEARMHGHDIIIPPEDMYSSLLRLAKNTSSGFSSTEVEVKK
*****

VP1BSR  KYGPAERDEIVRIKSRQKALYLMREGHKIYSPDMNMSYTTPTCYQTRGTRDVPIKATRTIAINNVNVLAPQH
VP1IRE  KYGPAERDEIVRIKSRQKALYLMREGHKIYSPDMNMSYTTPTCYQTRGTRDVPIKATRTIAINNVNVLAPQH
*****
Motif I

VP1BSR  YILTLPNEYFARAGGSTHPASSEIGGKIIIGDLEATGSRVMDAADTFRNTSDTGVWTLALDYSNYDTHMTQDN
VP1IRE  YILTLPNEYFARAGGSTHPASSEIGGKIIIGDLEATGSRVMDAADTFRNTSDTGVWTLALDYSNYDTHMTQDN
*****
Motif A

VP1BSR  FRRGMISGIRQAVARHHSLLKYEGLWSVDQLIEAGYGAGRVAGTLWNGKRRVCRMDRADYERLPLEDREVPDAPF
VP1IRE  FRRGMISGIRQAVARHHSLLKYEGLWSVDQLIEAGYGAGRVAGTLWNGKRRVCRMDRADYERLPLEDREVPDAPF
*****

VP1BSR  RFRPPGTSPIRSLALVKEARTLDFVLVTPWDGSDLARVSTHLSGENSTLVANSLNHMA MGRVIQDEVQTRHPGT
VP1IRE  RFRPPGTSPIRSLALVKEARTLDFVLVTPWDGSDLARVSTHLSGENSTLVANSLNHMA MGRVIQDEVQTRHPGT
*****
Motif B

VP1BSR  FEVLSEMYVDDTLHYVKLLTLDQAIDRAINTIFQTIELCGHEASAAKTTFAPFSAEKTQTHAKQGVYIPQDR
VP1IRE  FEVLSEMYVDDTLHYVKLLTLDQAIDRAINTIFQTIELCGHEASAAKTTFAPFSAEKTQTHAKQGVYIPQDR
*****
Motif C Motif D

VP1BSR  MMVISSERRKEIEDVQGYMRAQATTFTVTKVSRGFSDEL AHRILLKASLGYRRFKATIFDGTKFRRRKFFSEE
VP1IRE  MMVISSERRKEIEDVQGYMRAQATTFTVTKVSRGFSDEL AHRILLKASLGYRRFKATIFDGTKFRRRKFFSEE
*****

VP1BSR  DGYTLCRLNPAVLVYAPVECNQYGVHPFALNVVQTCETHLDSIQLFPTYADLVSRNVIRTAFAPPPWNETDVDSR
VP1IRE  DGYTLCRLNPAVLVYAPVECNQYGVHPFALNVVQTCETHLDSIQLFPTYADLVSGNVIRTAFAPPPWNETDVDSR
*****

VP1BSR  LLSTQTPMGLYSRIVRPTVRMALTPDIAALVTQIPLGEHAPDRLSSTMMHSALLKESRARALLAPAYEDRFIE
VP1IRE  LLSTQTPMGLYSRIVRPTVRMALTPDIAALVTQIPLGEHAPDRLSSTMMHSALLKESRARALLAPAYEDRFIE
*****

VP1BSR  SMNKWRPHDFKPTAGVELTAAYAKVLDLQISARDAPTPLFPDMNLSPAFLAQKQCVGHRTTVRPSRTYMDHID
VP1IRE  SMNKWRPHDFKPTAGVELTAAYAKVLDLQISARDAPTPLFPDMNLSPAFLAQKQCVGHRTTVRPSRTYMDHID
*****

VP1BSR  RILRGDVVMRGIIITANTIMTLEKIGFDHDPADLAIIFELLNLD RRVARRLAEFVTGDRLRFDVHALNKRIGIG
VP1IRE  RILRGDVVMRGIIITANTIMTLEKIGFDHDPADLAIIFELLNLD RRVARRLAEFVTGDRLRFDVHALNKRIGIG
*****

VP1BSR  DEFTMSLDVCTDGSRDQRITFPPEFTLAERDAALHAEQIQLLFAAHQGRSVRVALQVRPEHRSALRKARIKMR
VP1IRE  DEFTMSLDVCTDGSRDQRITFPPEFTLAERDAALHAEQIQLLFAAHQGRSVRVALQVRPEHRSALRKARIKMR
*****

VP1BSR  TPRLRVIRSAARAIRSASLALAEQGFL
VP1IRE  TPRLRVIRSAARAIRSASLALAEQGFL
*****

```

Figure S2: alignment of the amino acid sequences of the RNA-dependent RNA polymerase of parental KEMV smb1/Vero2/BSR3 (VP1BSR) and KEMV Ps.IRE1 (VP1IRE).

The 5 amino acid differences resulting from the 5 non-synonymous nucleotide mutations are highlighted in cyan. The motifs of the active polymerase site are shown in red, light-blue, green, purple and dark-blue letters and identified as motifs I, A, B, C and D. The asterisks denote identical amino acids.