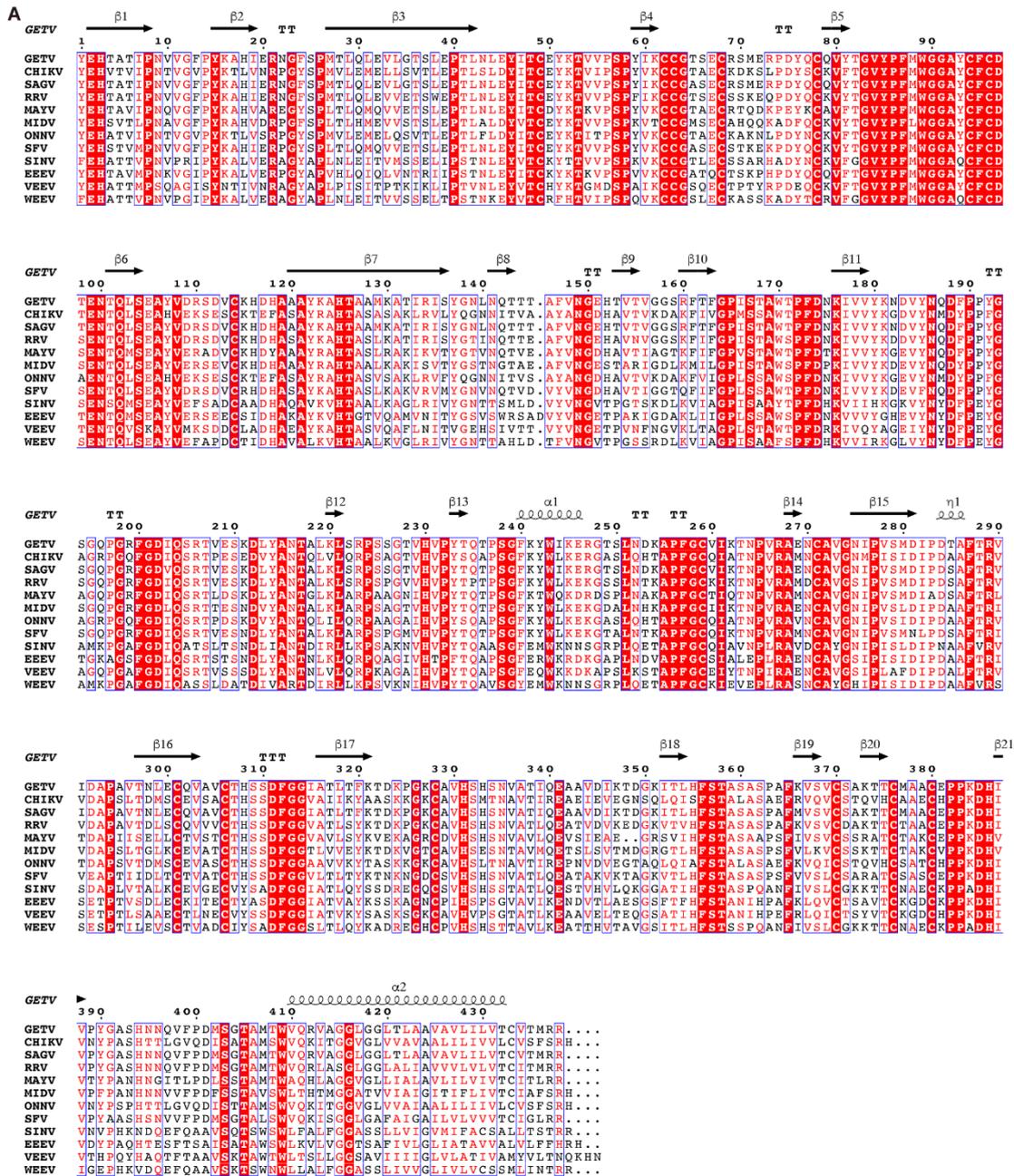


Figure S1. Cryo-EM reconstruction of GETV virions. (A) Cryo-EM micrographs of purified GETV virions. (B) Two-dimensional classification scheme of GETV virions. (C) Location of the three blocks (B1-3) selected for conducting the Block-based reconstruction. B1, B2, and B3 are indicated by a red, black, and yellow dashed circle, respectively. (D) Fourier Shell Correlation (FSC 0.143) profile of GETV Cryo-EM density map. The primary resolution curve is colored grey, and the final resolution curves of three blocks and CP are colored red, black, yellow, and blue, respectively. (E) Local resolution of the three blocks B1 (left), B2 (middle), and B3 (right).



B

GETV β_1 β_2 β_3 β_4 TT β_5 β_6 β_7 β_8

1 10 20 30 40 50 60 70 80 90

GETV SVTEHFNVYKATRPVLAAYCADGDCGQFYSFVAIEKIRDEASDGMKIKVAAOIGINKGGT...HEHNKIRYIAGHMKKANKRDSQVHTSGVCAIR
 CHIKV SIKDHFNVYKATRPVLAAYCADGDCGQFYSFVAIEKIRDEASDGMKIKVAAOIGINKGGT...HDWTKIRYDNIHPADAERAGLFTSAFCIT
 SAGV SVTEHFNVYKATRPVLAAYCADGDCGQFYSFVAIEKIRDEASDGMKIKVAAOIGINKGGT...HEHNKIRYIAGHMKKANKRDSQVHTSGVCAIR
 RRV SVTEHFNVYKATRPVLAAYCADGDCGQFYSFVAIEKIRDEASDGMKIKVAAOIGINKGGT...HAHTKIRYIAGHMKKANKRDSQVHTSGVCAIR
 MAYV STANHFNVYKATRPVLAAYCADGDCGQFYSFVAIEKIRDEASDGMKIKVAAOIGINKGGT...HDHTKIRYIAGHMKKANKRDSQVHTSGVCAIR
 MIDV GLTEDYKAYKLTTRPVLAAYCADGDCGQFYSFVAIEKIRDEASDGMKIKVAAOIGINKGGT...HSWTKIRYIAGHMKKANKRDSQVHTSGVCAIR
 ONNV NARENFNVYKATRPVLAAYCADGDCGQFYSFVAIEKIRDEASDGMKIKVAAOIGINKGGT...HDWTKIRYIAGHMKKANKRDSQVHTSGVCAIR
 SFV SVSQHFNVYKATRPVLAAYCADGDCGQFYSFVAIEKIRDEASDGMKIKVAAOIGINKGGT...HDYTKIRYIAGHMKKANKRDSQVHTSGVCAIR
 SINV F...T.LTSPVLTGTSYCHHTTEPFSFVKIEQVWDEADNTRIRIQTSAQFCYDQSGAASVNYKIRMSLQKODHTIEEGSMDAIIKISITSGPGRRL
 EEEV DLDTHTQYKLTTRPVLAAYCADGDCGQFYSFVAIEKIRDEASDGMKIKVAAOIGINKGGT...VDLAYMSFNGKTKSIRIDNHLVHTSAFCIT
 VEEV STEELFKYKLTTRPVLAAYCADGDCGQFYSFVAIEKIRDEASDGMKIKVAAOIGINKGGT...LKGRTIRYDNIHPADAERAGLFTSAFCIT
 MEEV S...ITDDFTLTSPLVLPVGRHSAPEFSFVKIEQVWDEADNTRIRIQTSAQFCYDQSGAASVNYKIRMSLQKODHTIEEGSMDAIIKISITSGPGRRL

GETV β_9 β_{10} β_{11} TT β_{12} β_{13} β_{14} TT β_{15} β_{16}

100 110 120 130 140 150 160 170 180 190

GETV GTMCHFLVAVCPGDELLKVOFQDAESHQAQKVOYKHAPAVVGRKFTVRFHFGLVLPCTVYVOLTAPTEEIDMHPDIPDITLLSQSNGVKRIT
 CHIKV GTMCHFLVAVCPGDELLKVOFQDAESHQAQKVOYKHAPAVVGRKFTVRFHFGLVLPCTVYVOLTAPTEEIDMHPDIPDITLLSQSNGVKRIT
 SAGV GTMCHFLVAVCPGDELLKVOFQDAESHQAQKVOYKHAPAVVGRKFTVRFHFGLVLPCTVYVOLTAPTEEIDMHPDIPDITLLSQSNGVKRIT
 RRV GTMCHFLVAVCPGDELLKVOFQDAESHQAQKVOYKHAPAVVGRKFTVRFHFGLVLPCTVYVOLTAPTEEIDMHPDIPDITLLSQSNGVKRIT
 MAYV GTMCHFLVAVCPGDELLKVOFQDAESHQAQKVOYKHAPAVVGRKFTVRFHFGLVLPCTVYVOLTAPTEEIDMHPDIPDITLLSQSNGVKRIT
 MIDV GTMCHFLVAVCPGDELLKVOFQDAESHQAQKVOYKHAPAVVGRKFTVRFHFGLVLPCTVYVOLTAPTEEIDMHPDIPDITLLSQSNGVKRIT
 ONNV GTMCHFLVAVCPGDELLKVOFQDAESHQAQKVOYKHAPAVVGRKFTVRFHFGLVLPCTVYVOLTAPTEEIDMHPDIPDITLLSQSNGVKRIT
 SFV GTMCHFLVAVCPGDELLKVOFQDAESHQAQKVOYKHAPAVVGRKFTVRFHFGLVLPCTVYVOLTAPTEEIDMHPDIPDITLLSQSNGVKRIT
 SINV NHKGYFLVAVCPGDELLKVOFQDAESHQAQKVOYKHAPAVVGRKFTVRFHFGLVLPCTVYVOLTAPTEEIDMHPDIPDITLLSQSNGVKRIT
 EEEV SHHGYFLVAVCPGDELLKVOFQDAESHQAQKVOYKHAPAVVGRKFTVRFHFGLVLPCTVYVOLTAPTEEIDMHPDIPDITLLSQSNGVKRIT
 VEEV DGGYFLVAVCPGDELLKVOFQDAESHQAQKVOYKHAPAVVGRKFTVRFHFGLVLPCTVYVOLTAPTEEIDMHPDIPDITLLSQSNGVKRIT
 MEEV GHRGYFLVAVCPGDELLKVOFQDAESHQAQKVOYKHAPAVVGRKFTVRFHFGLVLPCTVYVOLTAPTEEIDMHPDIPDITLLSQSNGVKRIT

GETV β_{17} β_{18} n_2 β_{19} β_{20} TT β_{21} β_{22} TT β_{23}

200 210 220 230 240 250 260 270 280

GETV A.GGKTRRYNCTCG...SGNVCTSSDKTINSCKIAOCHAAVTHNDKWOYTSFVPR.ADOLSRGKWHVPPFINSFCRVPRARAFQVYVGRREBTV
 CHIKV V.NSQTRRYNCTCG...DSSEGLTDDKVINCKVDQCHAAVTHNDKWOYTSFVPR.ADOLSRGKWHVPPFINSFCRVPRARAFQVYVGRREBTV
 SAGV A.GGKTRRYNCTCG...SGNVCTSSDKTINSCKIAOCHAAVTHNDKWOYTSFVPR.ADOLSRGKWHVPPFINSFCRVPRARAFQVYVGRREBTV
 RRV A.GGKTRRYNCTCG...SGNVCTSSDKTINSCKIAOCHAAVTHNDKWOYTSFVPR.ADOLSRGKWHVPPFINSFCRVPRARAFQVYVGRREBTV
 MAYV V.NGRTRRYNCTCG...SKPSGTTTDDKVINCKVDQCHAAVTHNDKWOYTSFVPR.AEQAERNGKWHVPPFINSFCRVPRARAFQVYVGRREBTV
 MIDV P.KGKSIRRYNCTCG...SKESGVTQDKKEDFNCEVSOCHTAVTHNDKWOYTSFVPR...AGSGKRGKWHVPPFINSFCRVPRARAFQVYVGRREBTV
 ONNV V.DQOTRYNCTCG...GSNEGTLTDDKVINCKVDQCHAAVTHNDKWOYTSFVPR.NSEQGDGRGKWHVPPFINSFCRVPRARAFQVYVGRREBTV
 SFV V.GGKTRRYNCTCG...TGNVCTSSDKTINSCKIAOCHAAVTHNDKWOYTSFVPR.ADEPARNGKWHVPPFINSFCRVPRARAFQVYVGRREBTV
 SINV PPSGKNTIT...YKSDQTKWVNSPDLIR.HADHTAQGKWHVPPFINSFCRVPRARAFQVYVGRREBTV
 EEEV VPSGKNTIT...DVRGTLTSSDHTCTDVKOCRAVLDNCKWVNSGRLEP.GEGDTFNGKWHVPPFINSFCRVPRARAFQVYVGRREBTV
 VEEV PVPVTSALVECECGTKISETINKKQFSCCTKKEOCRAVLDNCKWVNSGRLEP.AAGATLNGKWHVPPFINSFCRVPRARAFQVYVGRREBTV
 MEEV PPSGKNTIT...DYSFGIVSTRTKMNGCTKAKOCIAVKSQTKWVNSPDLIR.HTDHVSQKWHVPPFINSFCRVPRARAFQVYVGRREBTV

GETV β_{24} β_{25} β_{26} TT β_{27} α_1 α_2 α_3

290 300 310 320 330 340 350 360 370 380

GETV K.LHDDHPTLLSYSLGADFRPYEENIDRYVERITIPVEGCEISRWGNNDPVRLLWAQLTTECKPHGWPHETILVYGLYPAATAAIVSAAGLAVVLSL
 CHIKV L.LYDDHPTLLSYSLGADFRPYEENIDRYVERITIPVEGCEISRWGNNDPVRLLWAQLTTECKPHGWPHETILVYGLYPAATAAIVSAAGLAVVLSL
 SAGV L.LYDDHPTLLSYSLGADFRPYEENIDRYVERITIPVEGCEISRWGNNDPVRLLWAQLTTECKPHGWPHETILVYGLYPAATAAIVSAAGLAVVLSL
 RRV L.LHDDHPTLLSYSLGADFRPYEENIDRYVERITIPVEGCEISRWGNNDPVRLLWAQLTTECKPHGWPHETILVYGLYPAATAAIVSAAGLAVVLSL
 MAYV L.LHDDHPTLLSYSLGADFRPYEENIDRYVERITIPVEGCEISRWGNNDPVRLLWAQLTTECKPHGWPHETILVYGLYPAATAAIVSAAGLAVVLSL
 MIDV L.LHDDHPTLLSYSLGADFRPYEENIDRYVERITIPVEGCEISRWGNNDPVRLLWAQLTTECKPHGWPHETILVYGLYPAATAAIVSAAGLAVVLSL
 ONNV L.LYDDHPTLLSYSLGADFRPYEENIDRYVERITIPVEGCEISRWGNNDPVRLLWAQLTTECKPHGWPHETILVYGLYPAATAAIVSAAGLAVVLSL
 SFV L.LHDDHPTLLSYSLGADFRPYEENIDRYVERITIPVEGCEISRWGNNDPVRLLWAQLTTECKPHGWPHETILVYGLYPAATAAIVSAAGLAVVLSL
 SINV L.LDHDHPTLLSYSLGADFRPYEENIDRYVERITIPVEGCEISRWGNNDPVRLLWAQLTTECKPHGWPHETILVYGLYPAATAAIVSAAGLAVVLSL
 EEEV L.LHDDHPTLLSYSLGADFRPYEENIDRYVERITIPVEGCEISRWGNNDPVRLLWAQLTTECKPHGWPHETILVYGLYPAATAAIVSAAGLAVVLSL
 VEEV L.LHDDHPTLLSYSLGADFRPYEENIDRYVERITIPVEGCEISRWGNNDPVRLLWAQLTTECKPHGWPHETILVYGLYPAATAAIVSAAGLAVVLSL
 MEEV L.LHDDHPTLLSYSLGADFRPYEENIDRYVERITIPVEGCEISRWGNNDPVRLLWAQLTTECKPHGWPHETILVYGLYPAATAAIVSAAGLAVVLSL

GETV α_4 n_3 α_5

390 400 410 420

GETV L.ASCYMFATARRRCHTPYALDPAVVPVTLGLVLCAPRAHA
 CHIKV G.VAVGCMCAARRRCHTPYALDPAVVPVTLGLVLCAPRAHA
 SAGV L.ASCYMFATARRRCHTPYALDPAVVPVTLGLVLCAPRAHA
 RRV AATCCMLATARRRCHTPYALDPAVVPVTLGLVLCAPRAHA
 MAYV AASVYMCVAVARRRCHTPYALDPAVVPVTLGLVLCAPRAHA
 MIDV SASCCLCVSAARRRCHTPYALDPAVVPVTLGLVLCAPRAHA
 ONNV SLSLGMVICARRRCHTPYALDPAVVPVTLGLVLCAPRAHA
 SFV F.ASCYMLVAVARRRCHTPYALDPAVVPVTLGLVLCAPRAHA
 SINV SVASVYVARRRCHTPYALDPAVVPVTLGLVLCAPRAHA
 EEEV VTSVWLLCRRRCHTPYALDPAVVPVTLGLVLCAPRAHA
 VEEV AASVWLLCRRRCHTPYALDPAVVPVTLGLVLCAPRAHA
 MEEV ASSAACIKARRRCHTPYALDPAVVPVTLGLVLCAPRAHA

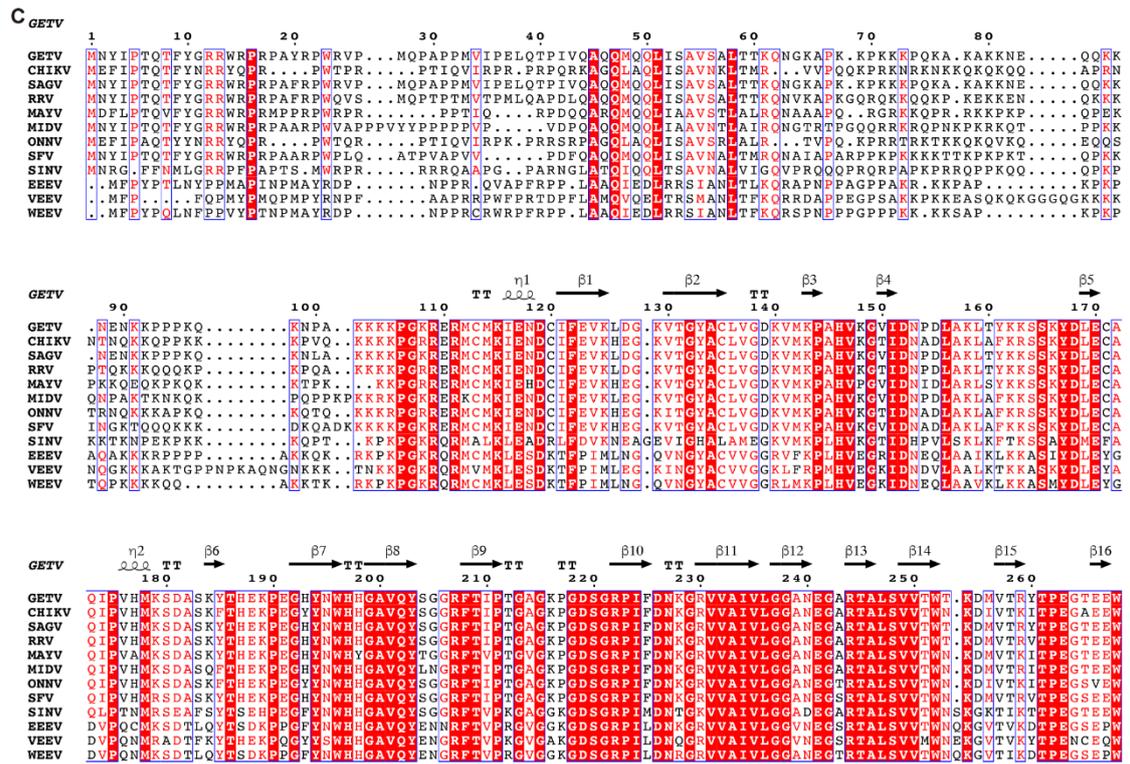


Figure S2. Multiple sequence alignment of the structural proteins from 12 alphaviruses. The alignment was done using the ClustalW and displayed with ESPrpt. The red background highlights the strictly conservative residues. The secondary structure determined by the Cryo-EM atomic structure model of the GETV is shown with linear diagram. (A) Alignment of E1. (B) Alignment of E2. (C) Alignment of CP.