

Fig. S1

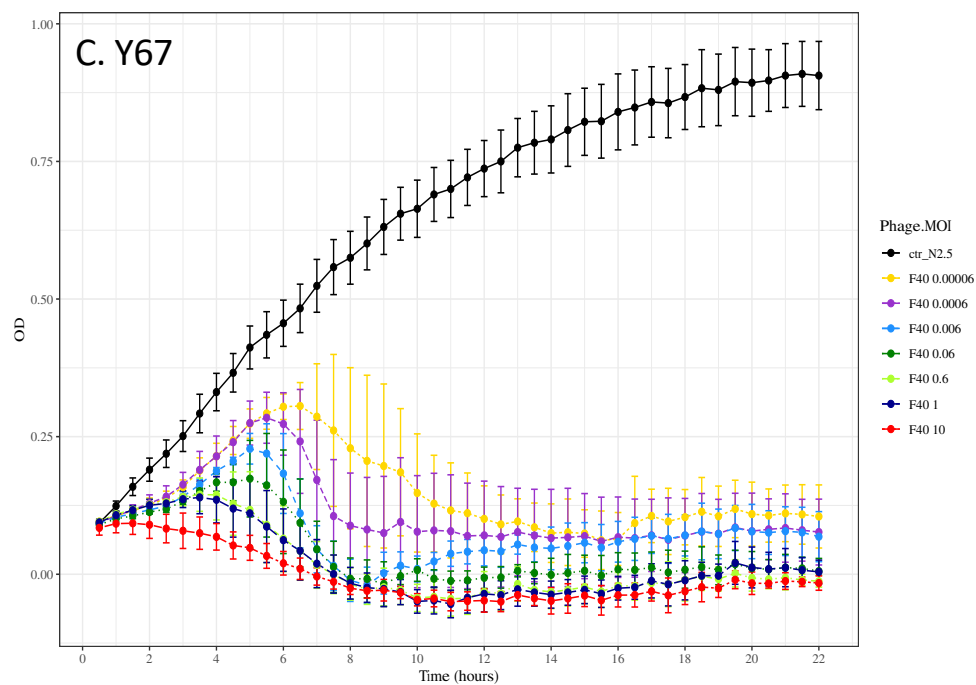
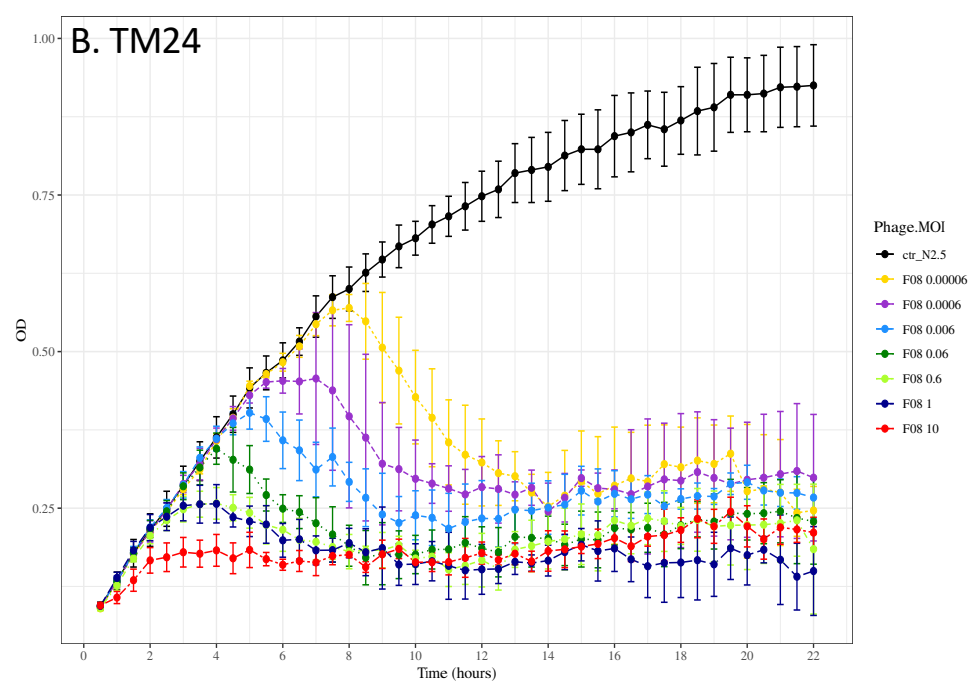
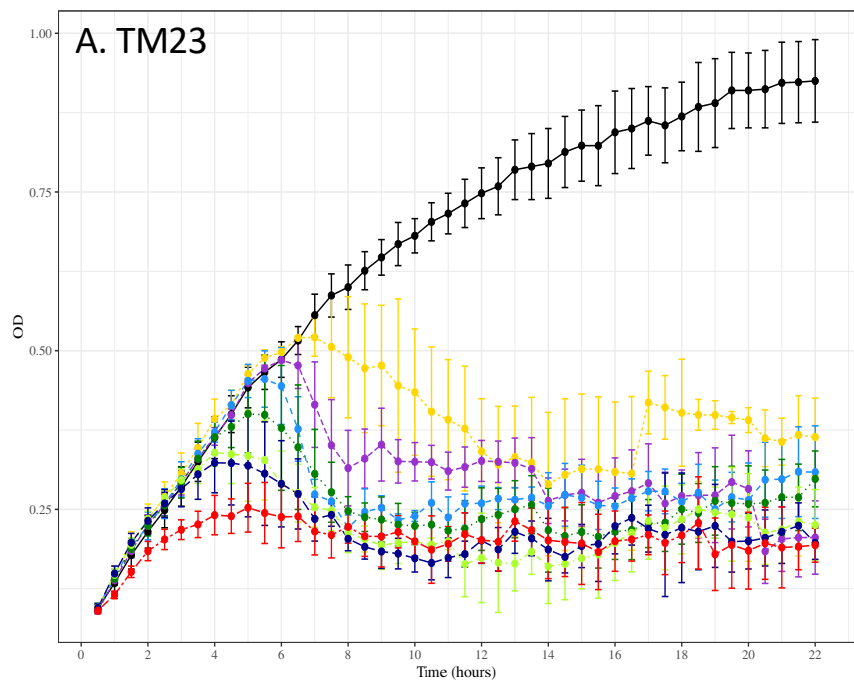
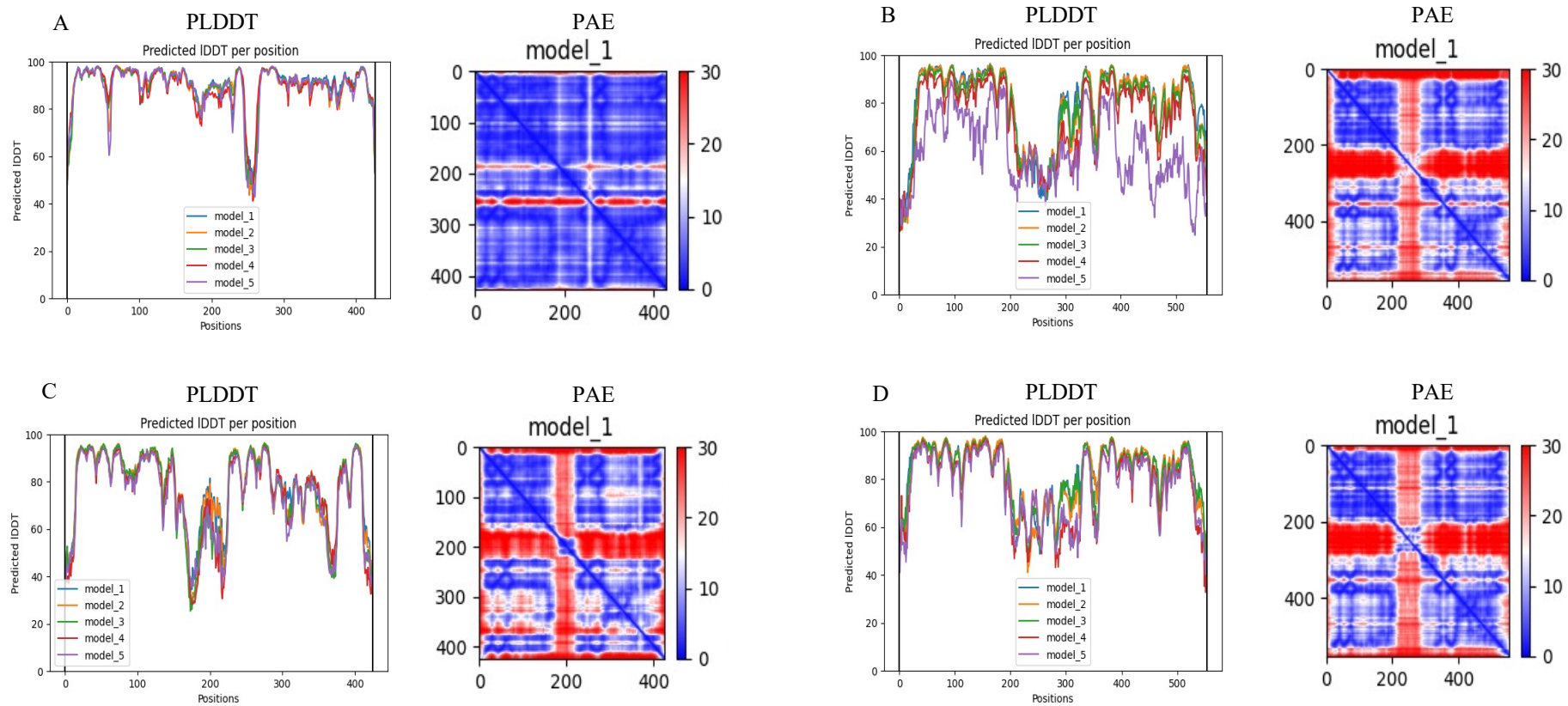


Fig. S2



Supp. Fig. S3. ClustalW alignment of the complete amino acid sequence of MCP-TM23 and MCP-Y67. The alignment was obtained from UCSF ChimeraX. Conserved b-sheets regions are in yellow. The loop in MCP-TM23 is coloured in magenta from proline-205 to glycine-310.

CLUSTAL W ALN saved from UCSF ChimeraX

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TM23_MCP_unrelaxed_model_1  MGCVWCAPSSSTGEENMTVNDAAIQTRKMTTPVPVERSRRNHKIRNLTSL. 49
Y67_MCP_unrelaxed_model_1  .....MKGVTLARPQKVNRSKIRVPTTNYRLVQ 28
                               ::  ::: *  *:*: .  *  :

TM23_MCP_unrelaxed_model_1  PAGKCVPIAVVPLLREDAASMSVSLAFEMQETVEILLNSVNVNVQCWLF 99
Y67_MCP_unrelaxed_model_1  RPWQIQPFICFPVLPGEILRKTLWTDTAITDPLLNRFGWHCETKFFYVR 78
                               . :  *:::.*:* :  ::  ::::  :::  :::  :.

TM23_MCP_unrelaxed_model_1  NLASTRFRSMDDINLSYAGEPRGTDPPVVPW..FELAAAGAYGTNAIHDR 146
Y67_MCP_unrelaxed_model_1  ARD.TVPASSDTIKNIF.....IDPDANLSSLYE.....AADAKY.. 112
                               *  * * *:  :  ** .  :*  .::: * :

TM23_MCP_unrelaxed_model_1  LGKHAKSTDMVNMAVEAYNAIWNHRATEISPNITQRARLDKTLAQAFWP 196
Y67_MCP_unrelaxed_model_1  ..FHAYGVN.....WLKNCVRQIVENYY.....RAE..... 136
                               ** ..:  *:: :  .  ** .

TM23_MCP_unrelaxed_model_1  KNMFSHIVPDFDQAVMEGEVALNVTNQMLPLVKTGASSGINVKFTGGAER 246
Y67_MCP_unrelaxed_model_1  .....DEAPDD.....YTIDGLWAATVGTD..... 156
                               *: * :  * : *  ...*:.

TM23_MCP_unrelaxed_model_1  TLVINAGDNIVRGAGSNFAGTQSITFEFTNVFAELQDNGITVSLANIELAR 296
Y67_MCP_unrelaxed_model_1  ...NWTDSMV.....LGAQQDAEDVSLTVGVDD...AIGMRELSAQ 192
                               *  *:*  *:* .:*  .. ::*  :::  ::: * :

TM23_MCP_unrelaxed_model_1  KTOAWADIRKQYNGLSEEMLIIDLLMD.GISVPEQMWK.QPILLKAAQTQF 344
Y67_MCP_unrelaxed_model_1  RMYEFLKM....GLLTDMDYSDFLRITYGVKIPAEELPGKPKYLGGVSEWT 238
                               :  :  ::  .  *::  *:*  *:::*  :  :*  *  ...

TM23_MCP_unrelaxed_model_1  GMAKRYASNGEALTQSVVNGAAAVEFRVATPK...VPCGGVIMITAEIAP 391
Y67_MCP_unrelaxed_model_1  MPTNTVEP....TTGVATTACYWSNKDRLDKDHLFKEPGFVVGLRVYRP 283
                               ::  .  *  *..*  .  :  *  .  *:::  *

TM23_MCP_unrelaxed_model_1  EQLFERRLDPY...LHAQGVADLPSYTRDFLDPE.KVDVVPNRYIDIDHD 437
Y67_MCP_unrelaxed_model_1  .KIFRSGIKGSVSGIMDTALEWLPVAVLMD..DPDTSLTRVASGAGPLG.A 329
                               ::* .:  :  ::  **:  *  **:::  ::  *..  :.

TM23_MCP_unrelaxed_model_1  TPTDVYGYAPLN.YLWNDAGPGIGGRFIR....PTVDASFDEDRQAIWA 481
Y67_MCP_unrelaxed_model_1  LGQD.YTFDMRDYFLYGEEFMNFDPTTWSGAVALPAVETAPTDP....K 373
                               *  * :  :  *:::  :..  *:::  :  *

TM23_MCP_unrelaxed_model_1  VETQNPTLS.EDAYLVPADIHLKPFWTSTIDPFDICITIGETVITG...NT 527
Y67_MCP_unrelaxed_model_1  FNKRYPSLAMAKQLFVDATADVK.....TRIETSGRVDMTIAGRVIDT 416
                               .:::  *:*:  .  :*  *  .:*  :  :  :  :*:*  :*

TM23_MCP_unrelaxed_model_1  VFGPRLIEAQAASDYDKVMEKVDVARIEK 556
Y67_MCP_unrelaxed_model_1  TPSVARLEV..... 425
                               . .  :*.

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Fig. S4

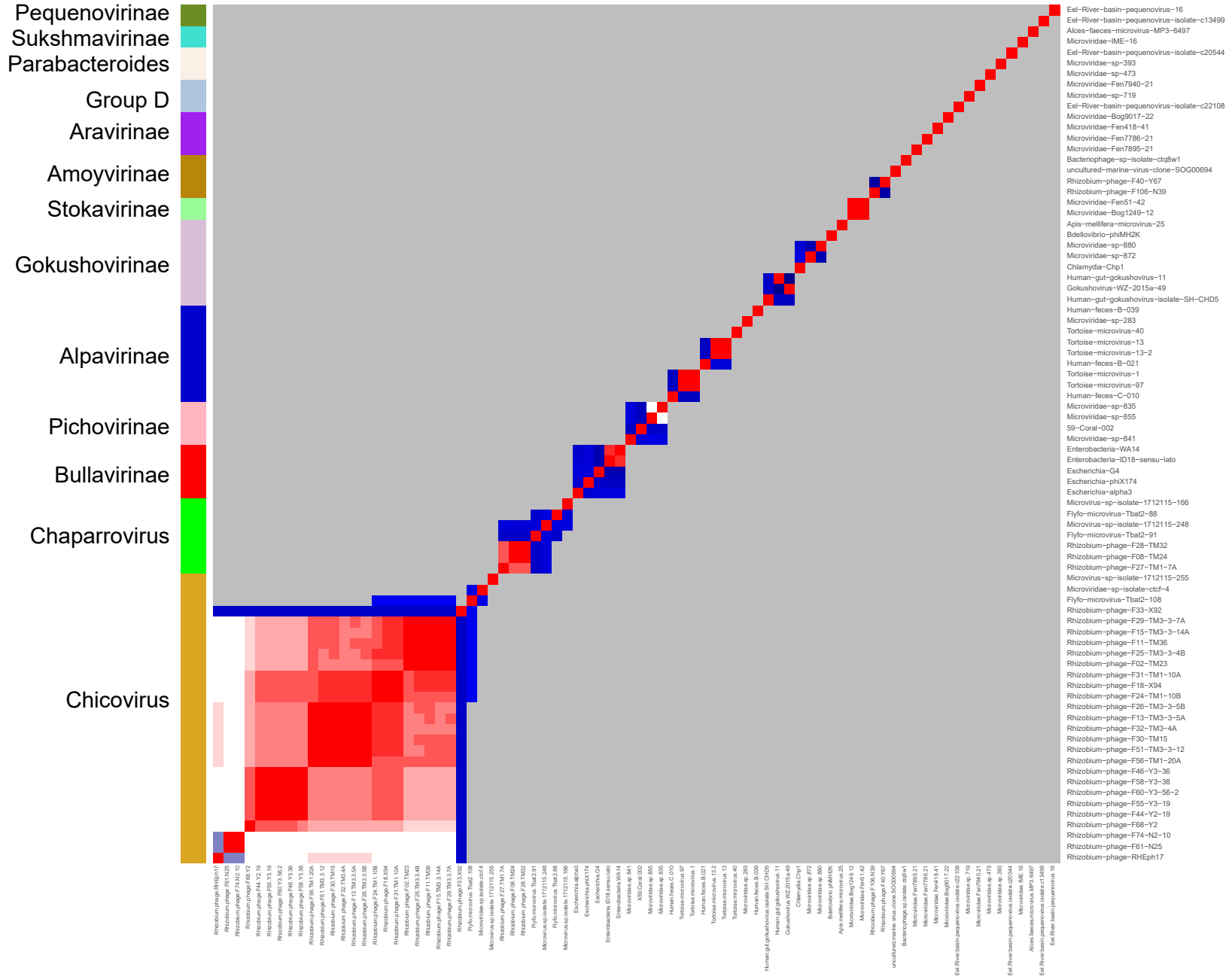
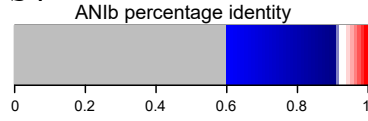


Fig. S5

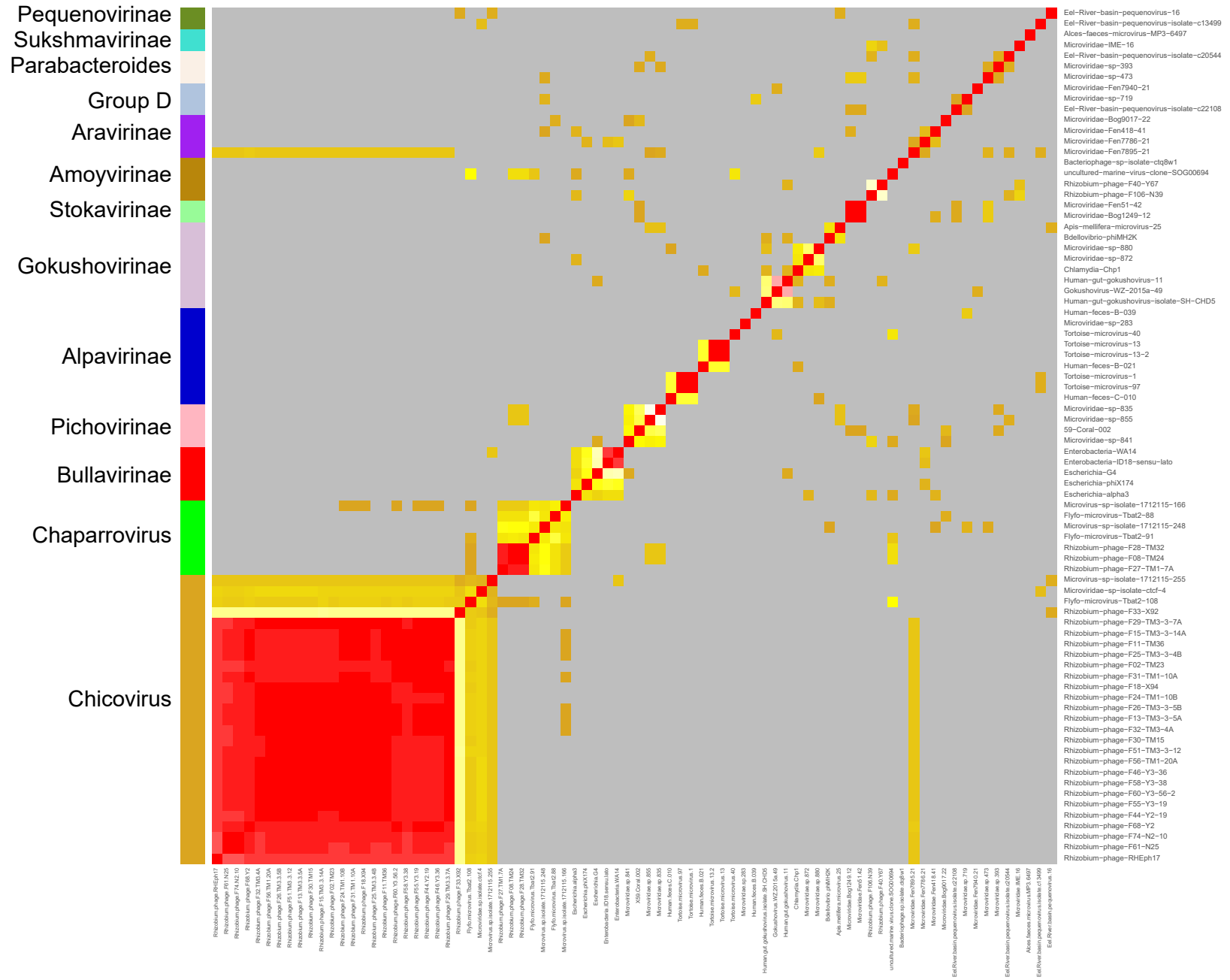
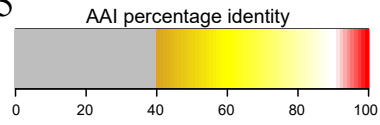


Fig. S6

