Figure S1

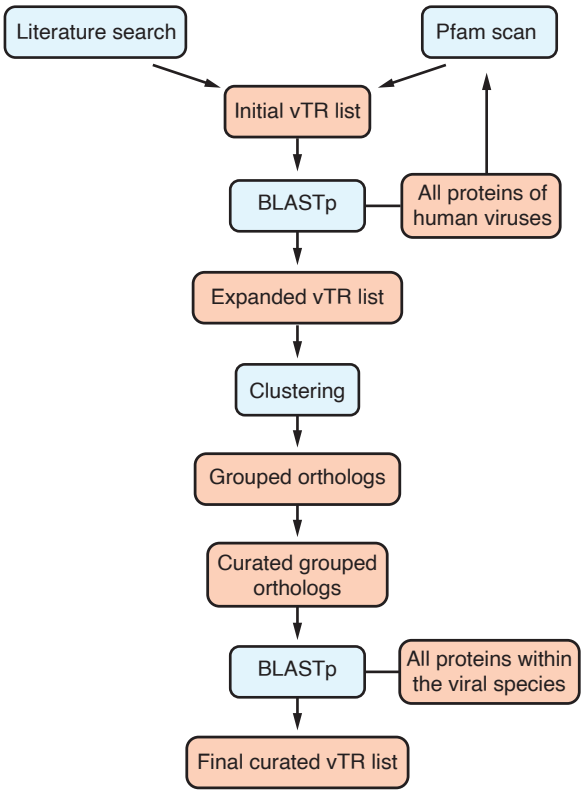
Literature search
Pfam scan
Initial vTR list
BLASTp
All proteins of human viruses
Expanded vTR list
Clustering
Grouped orthologs
Curated grouped orthologs
BLASTp
All proteins within the viral species
Final curated vTR list

Figure S1. Overview of the Procedure Used to Generate the Curated vTR Catalog, Related to Figure 2 and Table S2

A set of candidate vTRs was obtained based on extensive literature searches. A second set of candidate vTRs was obtained by scanning for putative DNA-binding domains using HMMER in the set of 4,026,372 protein sequences encoded by human viruses contained in the UniProt database. Additional candidate vTRs were identified based on orthology using BLASTp to generate an expanded vTR list. Groups of orthologous putative vTRs across the strains of a given viral species were identified by clustering the protein amino acid sequences. The resulting clusters of putative vTRs were manually curated based on available literature evidence. Finally, each putative vTR was used as a BLASTp query to compare to other proteins within the same viral species. The resulting set of putative vTRs was again manually verified and curated to produce the final vTR list.

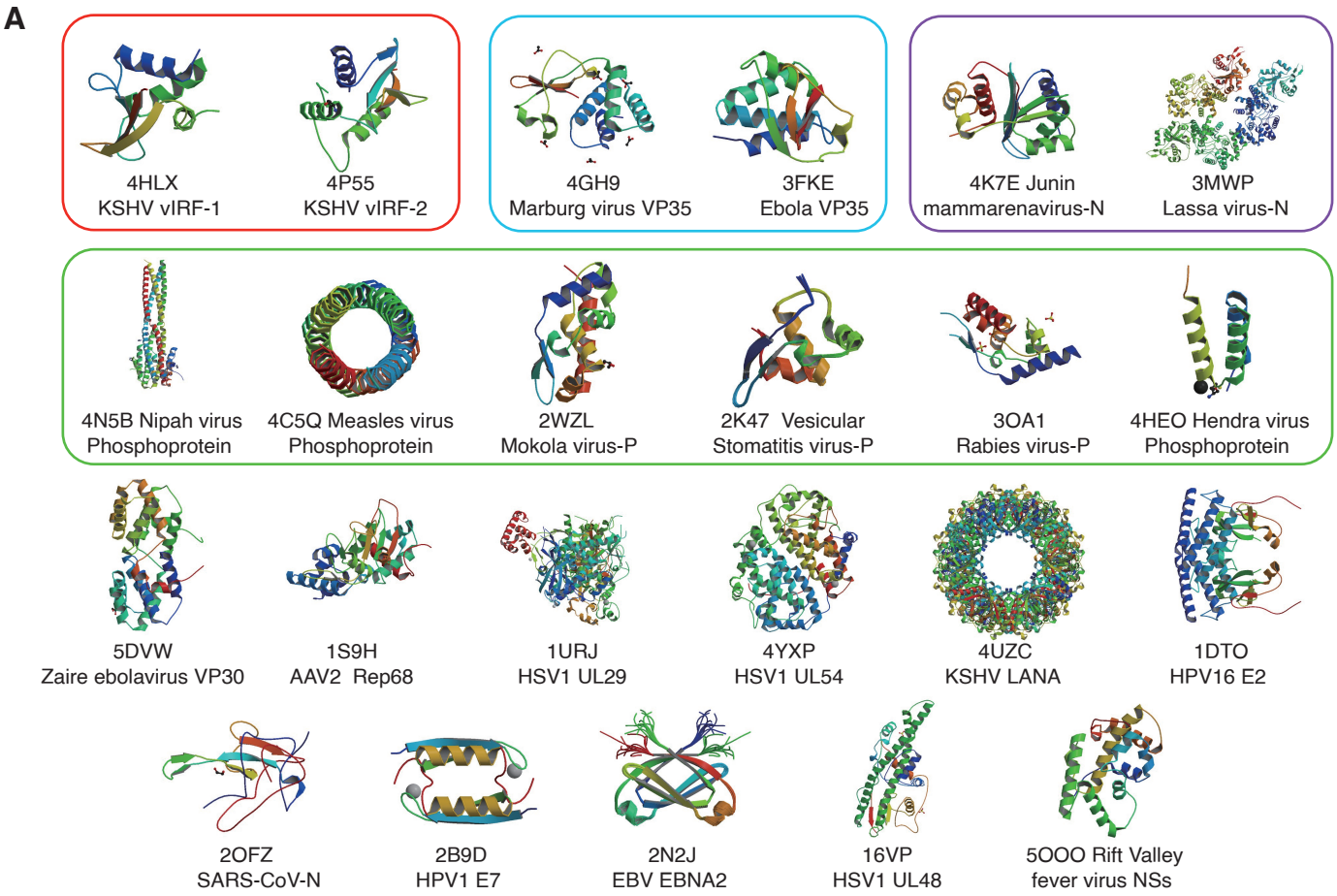
A
4HLX
KSHV vIRF-1
4P55
KSHV vIRF-2
4GH9
Marburg virus VP35
3FKE
Ebola VP35
4K7E Junin
mammarenavirus-N
3MWP
Lassa virus-N
4N5B Nipah virus
Phosphoprotein
4C5Q Measles virus
Phosphoprotein
2WZL
Mokola virus-P
2K47 Vesicular
Stomatitis virus-P
3OA1
Rabies virus-P
4HEO Hendra virus
Phosphoprotein
5DVW
Zaire ebolavirus VP30
1S9H
AAV2 Rep68
1URJ
HSV1 UL29
4YXP
HSV1 UL54
4UZC
KSHV LANA
1DTO
HPV16 E2
2OFZ
SARS-CoV-N
2B9D
HPV1 E7
2N2J
EBV EBNA2
16VP
HSV1 UL48
5OOO Rift Valley
fever virus NSs
B
6SJA
HPV16 E6 with IRF3
LxxLL motif complex
5NT2
Influenza A
NS1 with TRIM25 complex
2XXN
KSHV vIRF-4 with USP7
TRAF domain complex
5T3W
Marburg virus VP30
bound to nucleoprotein
3MI9
HIV-1 Tat with
P-TEFb complex
C
1A1V
HCV NS3
5MHJ
HSV1 RS1
1B3T
EBV EBNA1
2C9L
EBV ZTA
5E5A
HCMV IE1
5BYG
AAV2 Rep68

Figure S2. Protein Structures of vTRs and vTR Complexes, Related to Figure 2

(A) A selection of vTR protein structures available in the Protein Data Bank (https://www.rcsb.org/) (Berman et al., 2002). The longest amino acid sequence protein substructure was chosen to represent each vTR. vTR orthologs are boxed in rectangles of shared color.

(B) Select vTR protein-protein or protein-chemical complex structures.

(C) Select vTR protein-DNA complex structures.