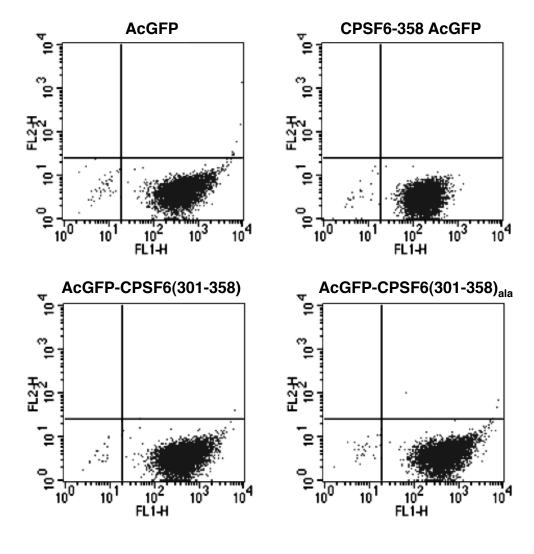
SUPPLEMENTAL FIGURES

S1. FACS profiles for HeLa cells transduced with AcGFP, CPSF6-358-AcGFP, AcGFP-CPSF6(301-358), and AcGFP-CPSF6(301-358)_{ala} followed by WT HIV or N74D HIV infection. A) HeLa cells stably expressing AcGFP, CPSF6-358-AcGFP, AcGFP-CPSF6(301-358), and AcGFP-CPSF6(301-358)_{ala} after transduction using the non-selectable pMX vector were enriched by FACS twice to adjust protein expression levels. FL-1 axis measures GFP fluorescence levels with arbitrary logarithmic units. FL-2 axis measurements are compared to screen for auto fluorescence characteristic of dead cells. Cell populations are over 99% pure for GFP expression. CPSF6-358-AcGFP population has lower mean fluorescence on the FL-1 channel. B) HeLa cells stably expressing AcGFP, CPSF6-358-AcGFP, AcGFP-CPSF6(301-358), and AcGFP-CPSF6(301-358)_{ala} were infected with WT HIV-RFP or N74D HIV-RFP. 2 days later, HIV infection was assayed by FACS by enumerating GFP/RFP double-positive cells (R2).

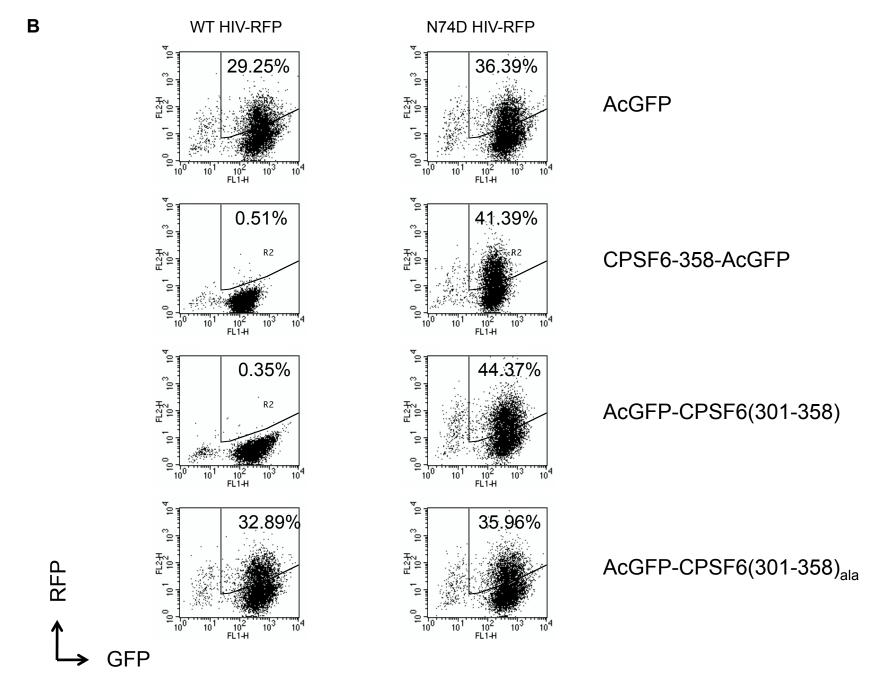
S2. Single tryptophan substitutions of CPSF6-358 residues 316-321 impairs antiviral activity. HeLa cells were stably transduced with LPCX vectors encoding CPSF6-358 with single residue tryptophan mutations. Empty vector control, CPSF6-358 expressing vector, and tryptophan mutant cell lines were infected with WT or N74D HIV-RFP and assayed 2 days later.

S3. Analysis of TRIM5-CPSF6 fusion proteins transiently expressed in 293T cells. A) TRIM5-CPSF6 fusion proteins described in Figure 3 were ectopically expressed in 293T cells. As controls, empty vector, rhTRIM5(1-299), CPSF6(261-358), and CPSF6(301-358) constructs were also transiently transfected in 293T cells. The expression of controls and TRIM5-CPSF6 fusion proteins were examined by western analysis at 2 days post-transfection. B) 293T cells expressing control protein or TRIM5-CPSF6 fusion proteins were infected with WT HIV-RFP or N74D HIV-RFP at 2 days post-transfection and then assayed by FACS analysis at 2 days post-infection.

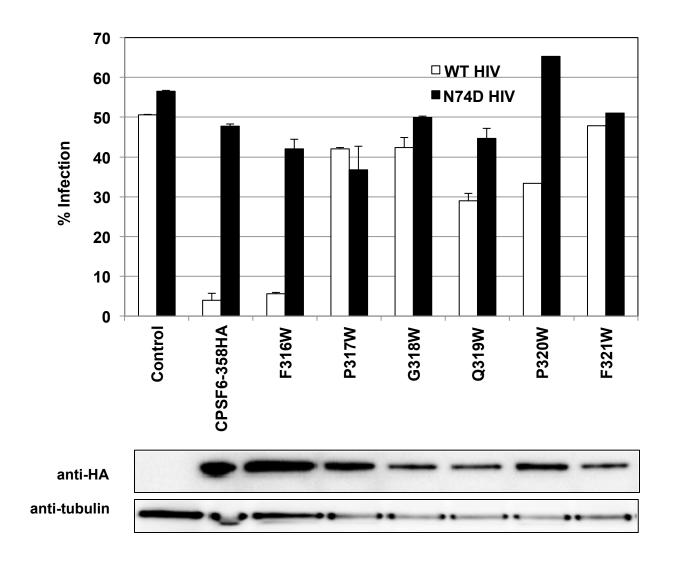
S4. Lack of evidence for positive selection of *CPSF6*. A) Seven orthologous *CPSF6* genes were analysed from the simian primate species shown. B) The molecular evolution of *CPSF6* is compared to that of two primate genes known to evolve under positive selection, *TRIM5* and *APOBEC3G*. For each, an alignment was created of orthologous sequences from the species shown in panel A. These matched-species datasets were then analysed using the PAML software package. Twice the difference in the natural logs of the likelihoods $(2\Delta \lambda)$ of the two models (M7-M8) being compared is shown. The p-value indicates the confidence with which the null model (M7; positive selection of codons disallowed) can be rejected in favor of the model of positive selection (M8; positive selection of some codons allowed). Positive selection is supported in only the latter two genes. In contrast, the very low value of $2\Delta \lambda$ for *CPSF6* suggests that positive selection is not supported. C) A protein alignment of the seven CPSF6 orthologs is shown in the region of the CA-binding domain.



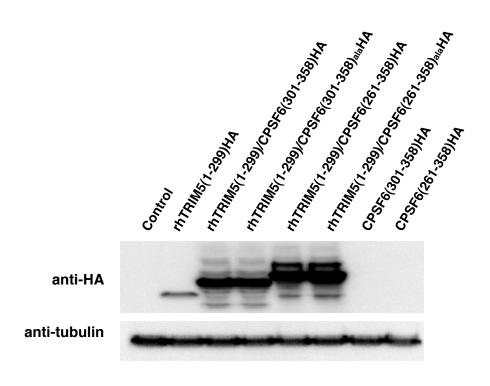
Supplemental Figure 1

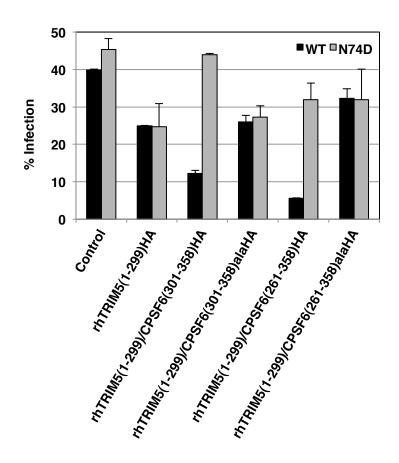


Supplemental Figure 2

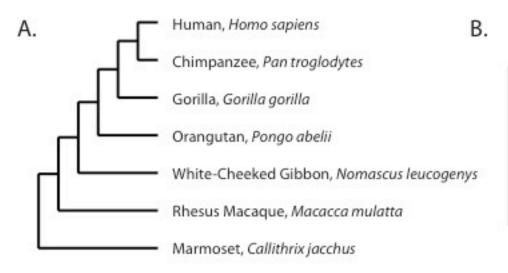


A B





Supplemental Figure 4



Gene	2Δε	p-value
CPSF6	0.00027	not sig.
TRIM5	24	p<0.001
APOBEC3G	40	p<0.001

C.	CA binding
C.	2

Human Chimpanzee Gorilla Rhesus Marmoset WhiteCheekedGibbon

Orangutan

AGPPNRGDRPPPPVLFPGOPFGOPPLGPLPPGPPPPVPGYGPPPPPPOOGPPPPPGPF AGPPNRGDRPPPPVLFPGQPFGQPPLGPLPPGPPPPVPGYGPPPPPQQGPPPPPGPF AGPPNRGDRPPPPVLFPGQPFGQPPLGPLPPGPPPPVPGYGPPPPPQQGPPPPPGPF AGPPNRGDRPPPPVLFPGOPFGOPPLGPLPPGPPPPVPGYGPPPGPPPPOOGPPPPPGPF AGPPNRGDRPPPPVLFPGQPFGQPPLGPLPPGPPPPVPGYGPPPPPQQGPPPPPGPF AGPPNRGDRPPPPVLFPGQPFGQPPLGPLPPGPPPPVPGYGPPPPPQQGPPPPPGPF AGPPNRGDRPPPPVLFPGOPFGOPPLGPLPPGPPPPVPGYGPPPGPPPPOOGPPPPPGPF