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Supplemental figures, Table and movie legends

Figure S1.

Representative fluorescence images showing RFP-tagged KLC1 is not associated with the WD/AA or WEWD/AAAA mutant viruses (yellow arrows) at 11 hours post infection. Pink arrows highlight association RFP-KLC1 with DAPI positive WT and WE/AA viruses. Scale bars indicate 10μm.

Figure S2.

RFP-tagged KLC2 is recruited by the wildtype (WT), WE/AA and WD/AA viruses, which were unambiguously identified using DAPI to stain viral DNA at 8 hours post infection. Pink arrows highlight examples of virus particles recruiting RFP-KLC2. Scale bar = 10μm.

Figure S3

Analysis of IEV composition for viruses used in this study. **(A)** Schematic illustrating the composition of authentic IEV as well as aberrant forms of the virus that can include various combinations of B5, A36 or hybrid-GFP and DNA. **(B)** Cells infected with the indicated viruses were stained using anti-B5 (an integral IEV membrane protein) and DAPI to show viral DNA. IEV are identified by the presence of A36 (or GFP fusion protein), B5 and DNA (white arrows). The orange arrows highlight rare 'IEV' that have A36 (or GFP fusion protein) and DNA but lack detectable B5. The yellow arrows indicate A36 (or GFP fusion protein) and B5 positive structures that lack viral DNA, which are likely to be vesicular in nature give A36 and B5 are integral membrane proteins. The green arrow highlights DAPI positive structures that presumably represent IMV, which are known to lack A36 and B5. **(C)** Graphs showing ratio of aberrant forms of IEV compared to those possessing all three markers. A value of 0.9 would indicate a 9-1 ratio of authentic IEV compared to the aberrant form indicated. No difference in the ratio of IEV to non-IEV structures between the different recombinant viruses was detected. Error bars show s.e.m. from 2 randomly selected 20 x20 μm areas in the periphery of 40 infected cells.

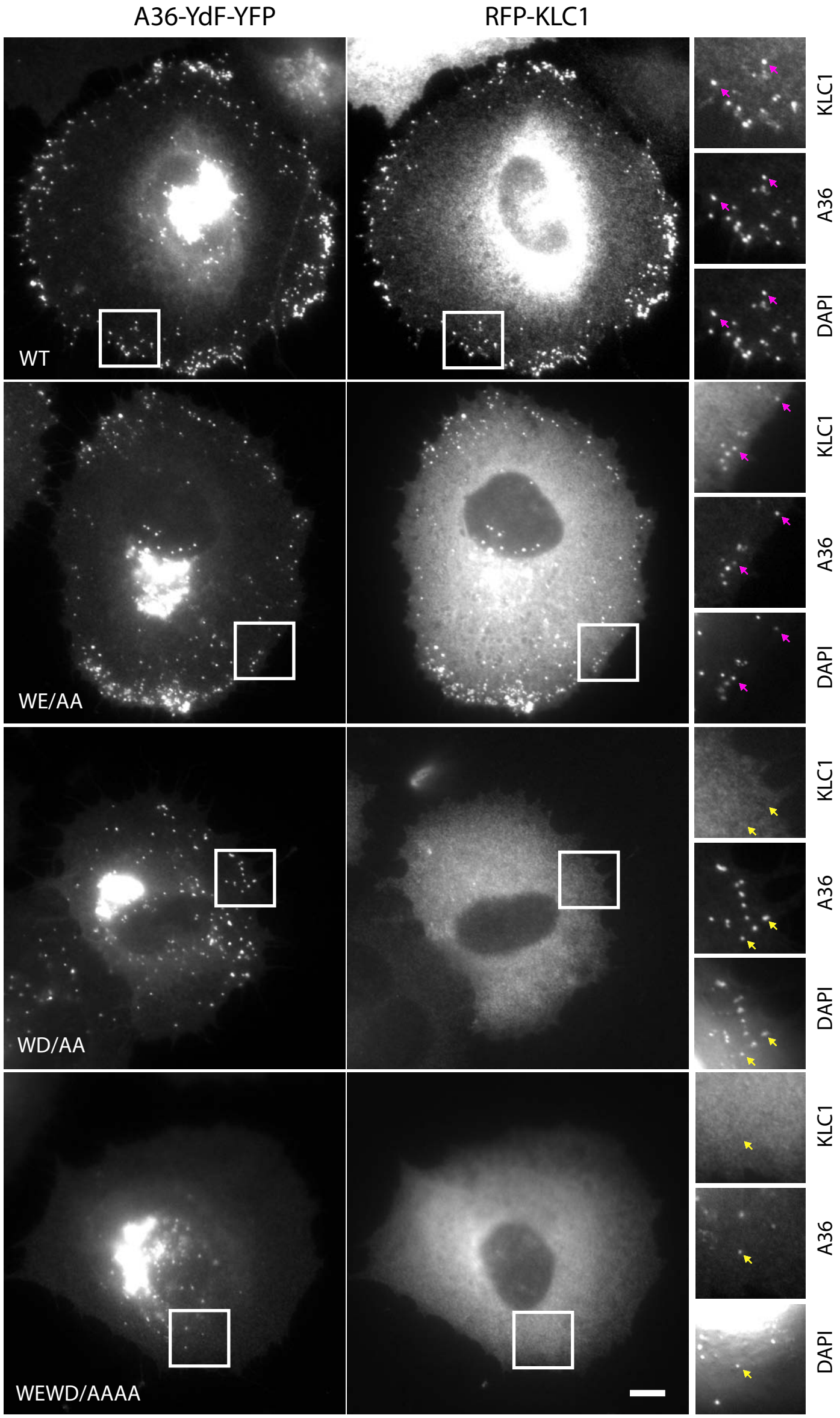
Table S1

Table shows the filtered output of the search patterns described in figure 3A applied to the human RefSeq protein database. Motifs overlapping with predicted transmembrane or conserved functional domains were removed, as were records that lacked homologues in the NCBI Homologene database. 'GI', 'GeneID', 'Homologene group' and 'Symbol' identify the gene and protein sequence. Length indicates the predicted number of amino acids in

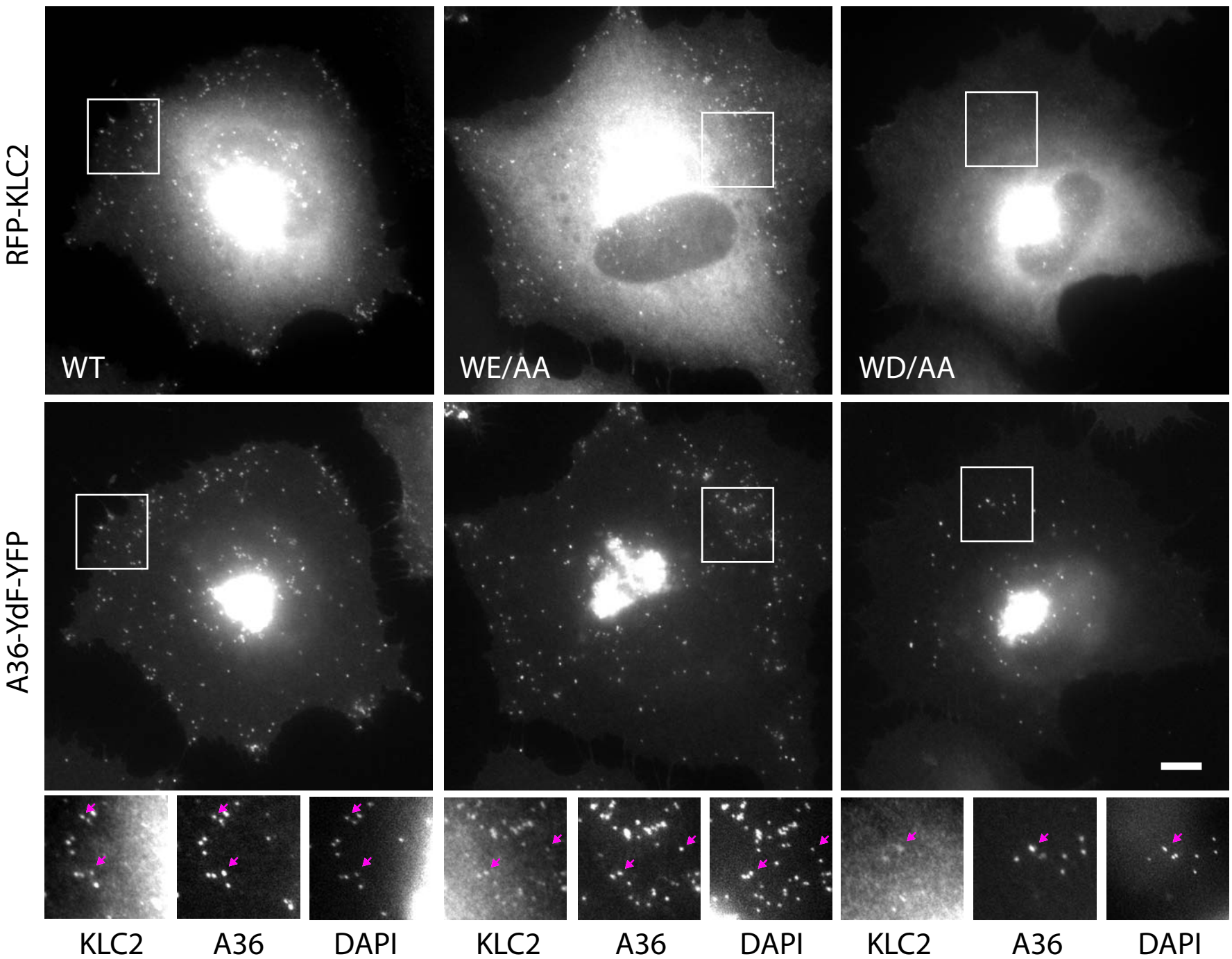
each protein. Motif Sequence shows the two tryptophan residues and the intervening sequence. The amino acid positions of the tryptophan residues are indicated in the 'Motif Start' and 'Motif End' columns. The length of the motif including the tryptophan residues is give by 'Motif Length'. 'P1-P4' indicates match to pattern described in figure 3A. Rows highlighted in green represent proteins where 1 or more W(DENQ) sequences has been implicated in KLC binding. Yellow shows KLC interacting proteins verified in this study.

Movie S1. Movie shows a cell infected with A36-YdF-YFP. Images were captured at 10 frames per second. The total sequence represents 18.4 seconds. The scale bar indicates 10μm. Left panels show YFP fluoresence. Right panel shows paths of virus movement during the course of the movie in red. This was produced by combining the frame in view on the left with a maximum intensity projection of all previous frames.

Movie S2. Movie shows a cell infected with A36-YdF-YFP WD/AA. Images were captured at 10 frames per second. The total sequence represents 18.4 seconds. The scale bar indicates 10μm. Left panels show YFP fluoresence. Right panel shows paths of virus movement during the course of the movie in red. This was produced by combining the frame in view on the left with a maximum intensity projection of all previous frames.

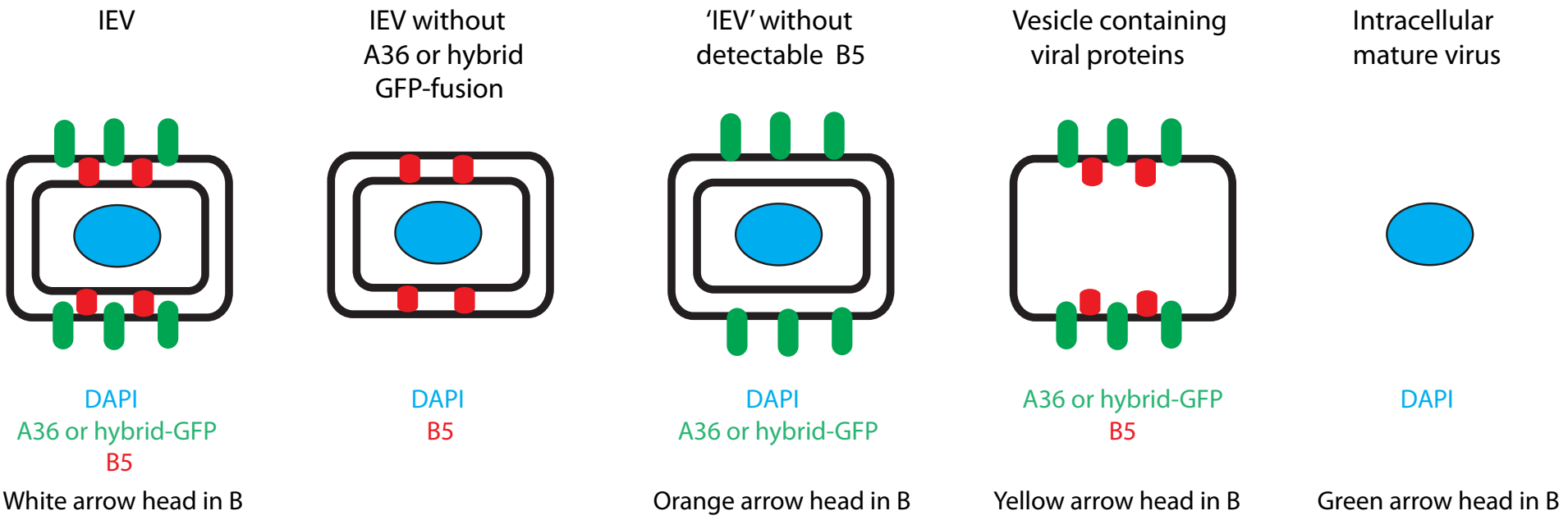


Supplementary Figure 1 Dodding *et al.* 2011

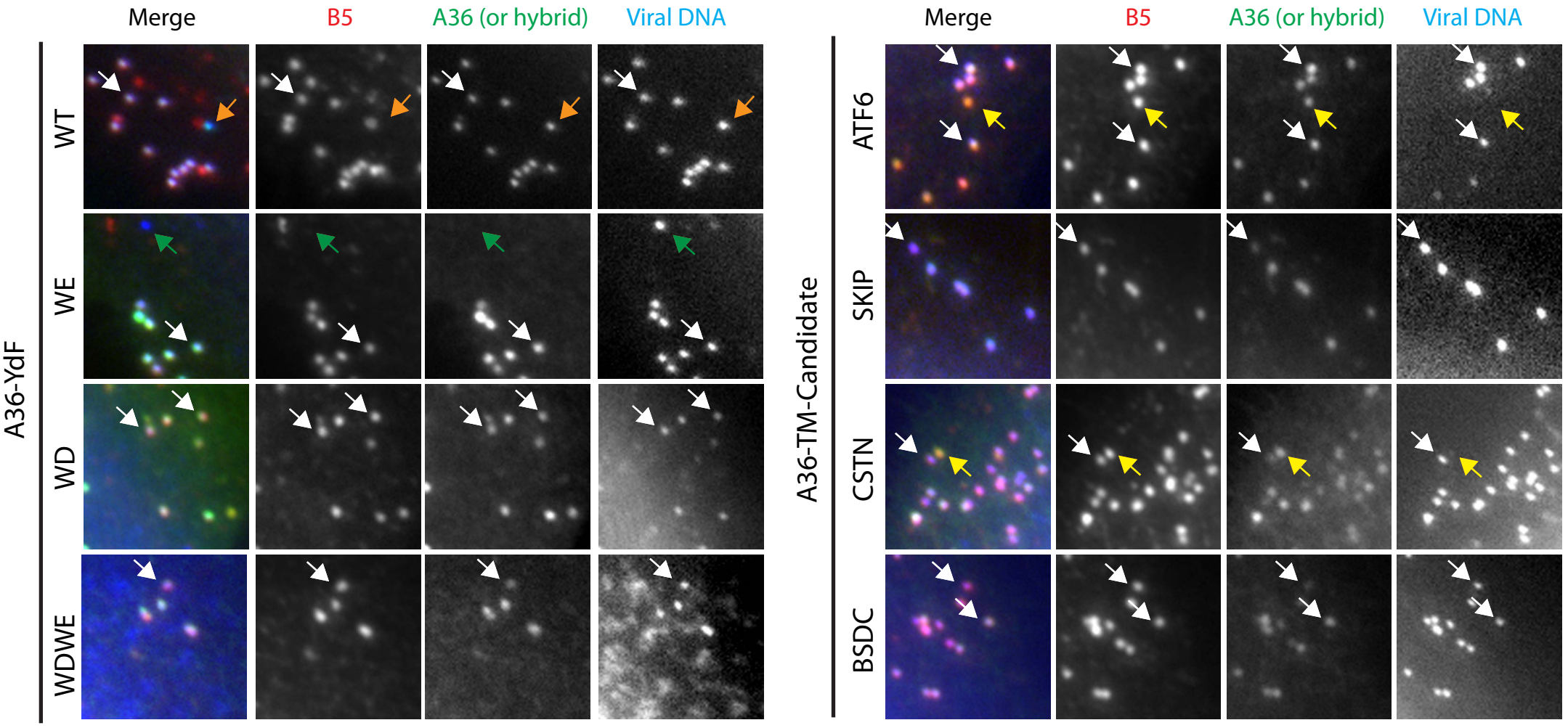


Supplementary Figure 2 Dodding *et al*. 2011

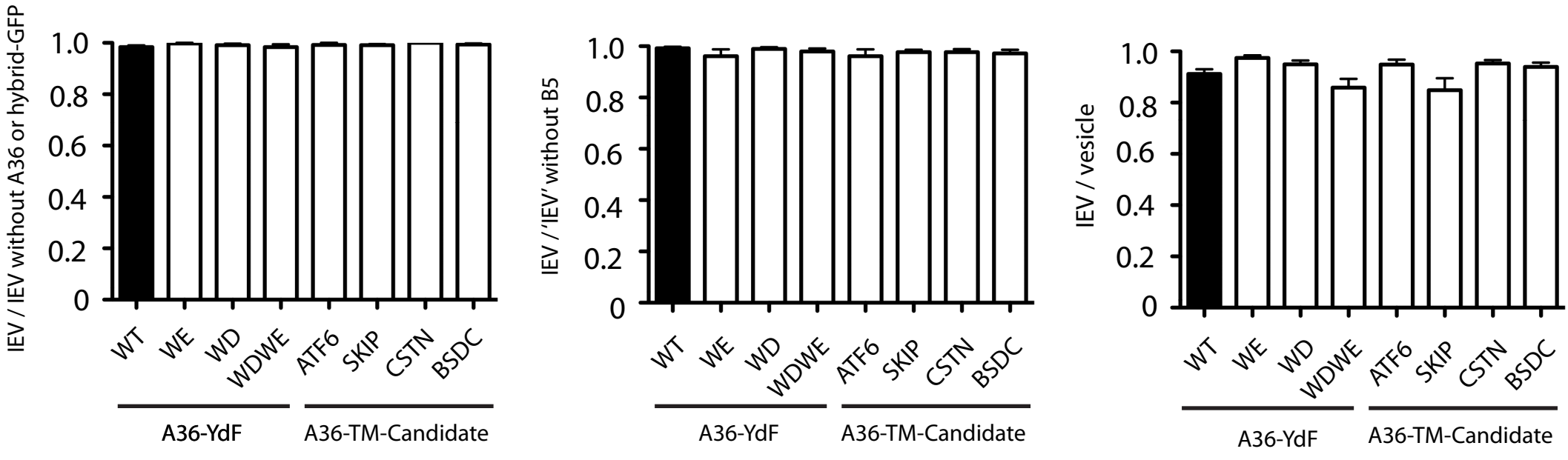
A



B



C



Supplementary Figure 3 Dodding *et al.* 2011