Supplemental Figure 1. Intermolecular interfaces in different $Vps4_{\Delta MIT}$ crystal forms. Note that in some cases similar, but non-identical interfaces have been grouped together.

Supplemental Figure 2. Comparative models for Vps4 protein oligomerization. Representative equilibrium sedimentation profiles for full length Vps4 (panel 1), $Vps4_{\Delta MIT}$ (panel 2), $Vps4_{\Delta MIT,Q216A}$ (panel 3, Interface 1 mutant), $Vps4_{\Delta MIT,L151D}$ (panel 4, Interface 2 mutant) fit to monomer, dimer and trimer single species models with fixed molecular weights. Sedimentation data are plotted as absorbance versus the distance from the center of the axis of rotation (radius). To simplify the plot, the radius was normalized so the data from all three sectors (i.e. three different concentrations) overlap. In each case, data from three protein concentrations and one speed are displayed (gray) along with the indicated single ideal species fit (black lines). The fits for each protein were globally fit to three concentrations and two speeds. The residuals (differences between the raw absorbance data and the fit) are shown below each panel. A good fit is indicated by random and small residuals.

Supplemental Figure 3. $Vps4_{\Delta MIT,Q216A}$ dimerizes and dodecamerizes normally. Gel filtration chromatograms of the mutant $Vps4_{\Delta MIT,Q216A}$ protein in the absence (black) or presence (green) of ATP. For reference, elution positions of dimeric (2) and dodecameric (12) proteins are shown as dotted vertical lines, and the elution positions of molecular weight standards are shown below the chromatograms. Note