



Figure S1. Representative DSSP plots for residues 1202-1282 of (A) Wild type (WT) and (B) W1282X NBD2 as a function of simulation time (500 ns simulation). In these plots residue numbers are given on the y-axis and simulation time on the x-axis. Red, blue, green, yellow, black, and white color correspond to β -sheet, α -helix, bend, turn, β -bridge, and coil secondary structure respectively.

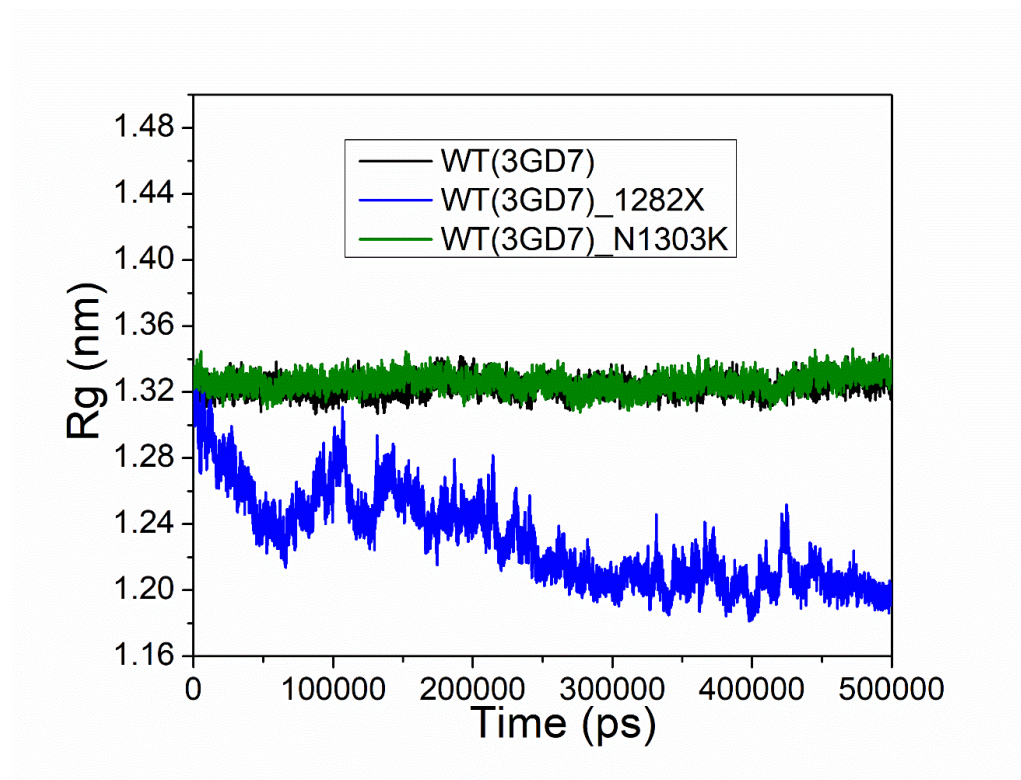
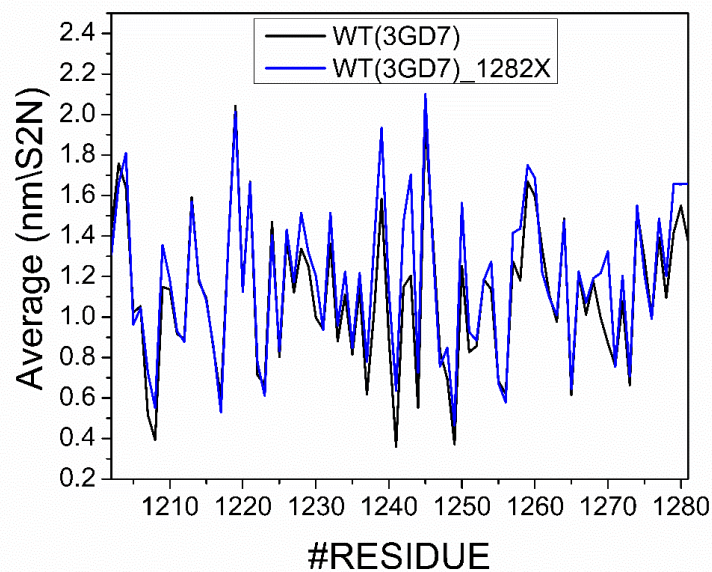


Figure S2. Average Rg values over three 500 ns simulations for residues 1202-1282 are shown. Black, blue and green lines correspond to the wild type, 1282X, and N1303K constructs, respectively. Low Rg values are indicative of a more compact construct.

A



B

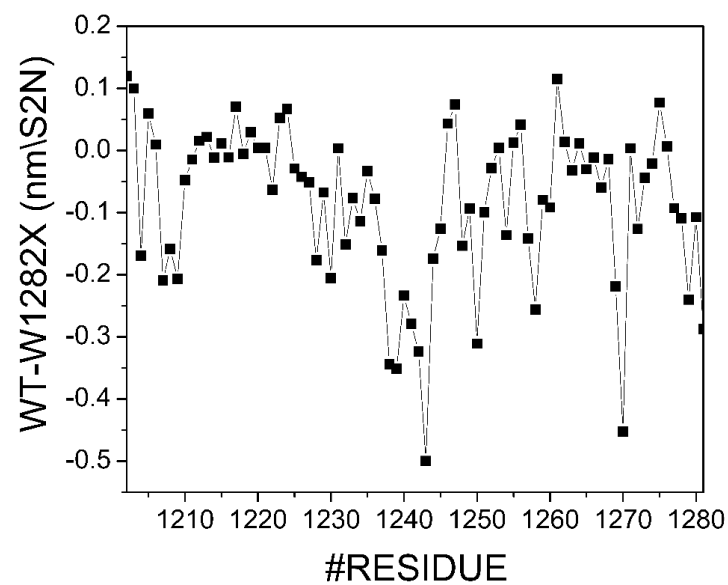
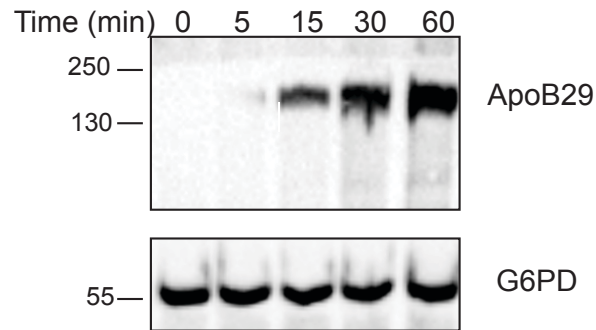


Figure S3. (A) SASA values averaged over three 500 ns simulations for residues 1202-1282 are shown. Black and blue lines correspond to the wild type and 1282X constructs, respectively. Low SASA values are indicative of a less exposed surface area. (B) Average differences plots (WT-1282X) over three 500 ns simulations are shown. Negative values indicate a more exposed SASA in the truncation mutant.

A



B

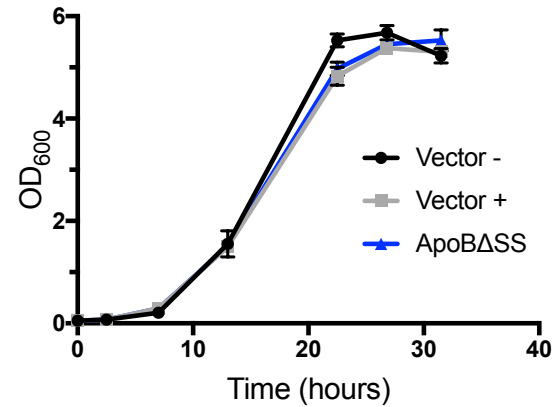


Figure S4. (A) Induction time-course for full-length ApoB29 expression in yeast transformed with the pYES2-ApoB29 expression vector. ApoB29 expression was monitored following the addition of β -estradiol at the indicated time-points. G6PD serves as a loading control. (B) Overnight yeast cultures transformed with an empty vector (Vector) or ApoB Δ SS were diluted to OD_{600} = 0.05 and growth was monitored over the indicated times in the presence (+) or absence (-) of β -estradiol.