Figure S1. Hydrogen-Deuterium Exchange results

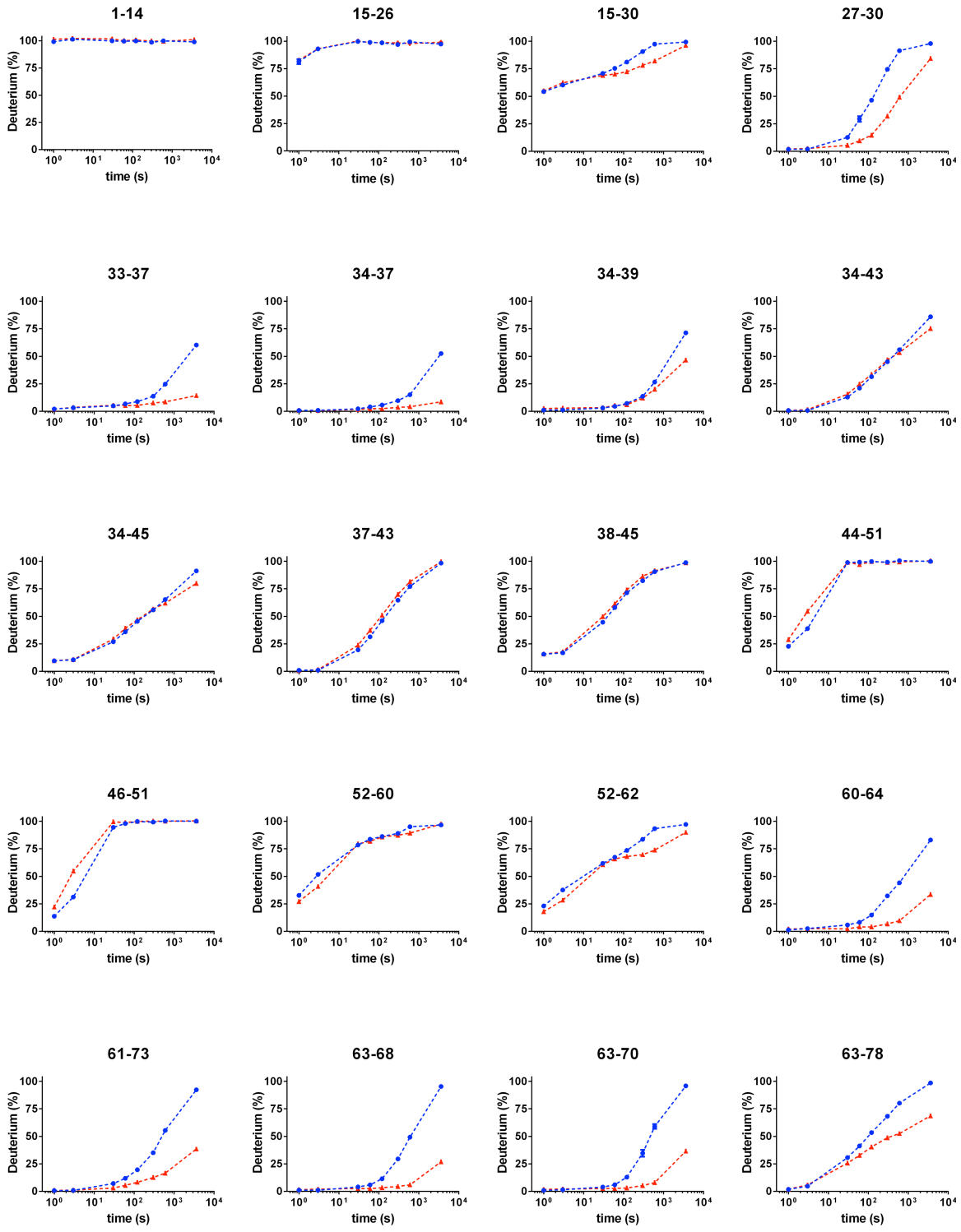

Figure 1S A. Hydrogen deuterium exchange data for peptides from 1-14 to 63-78

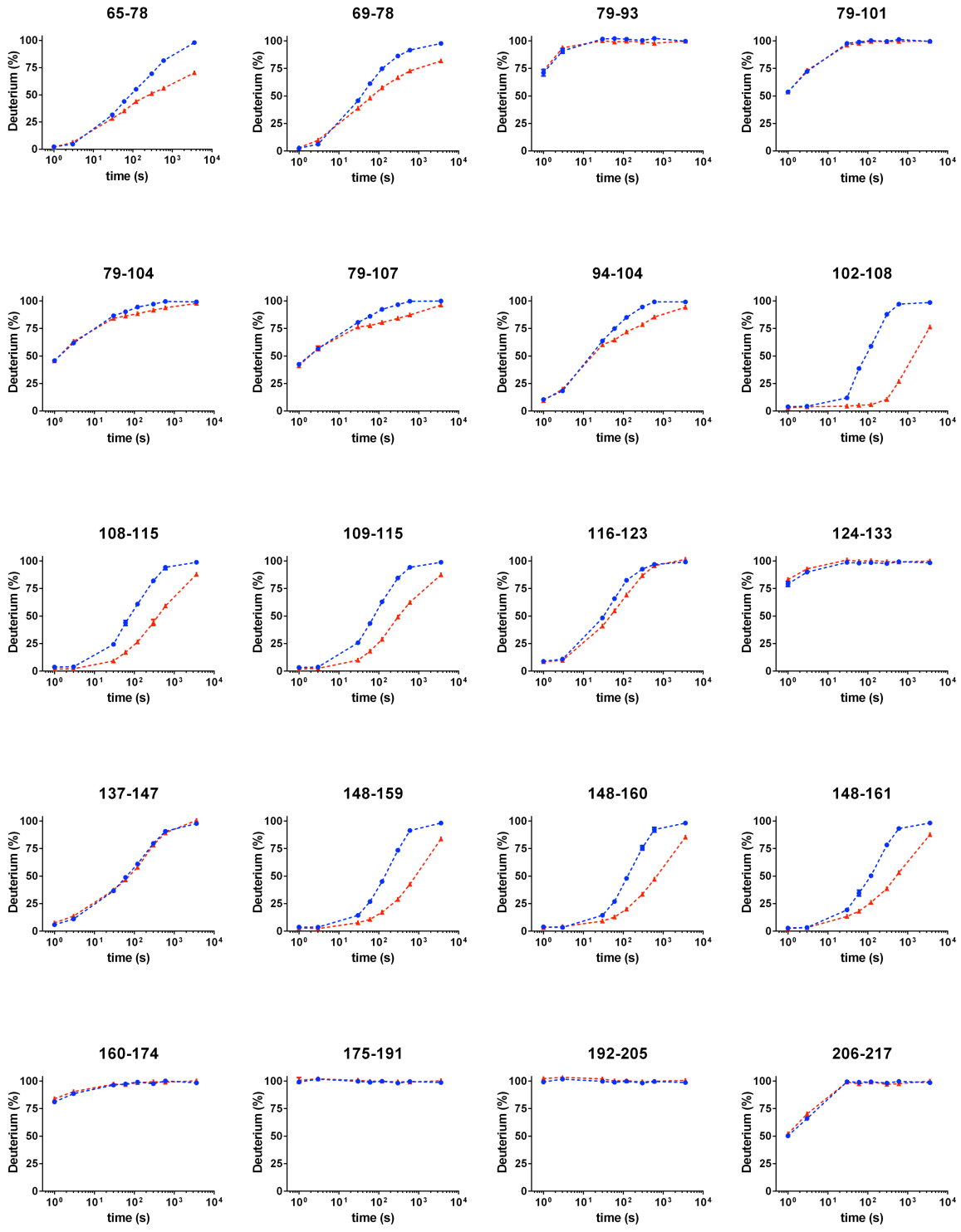

Figure 1S B Hydrogen deuterium exchange data for peptides from 65-217

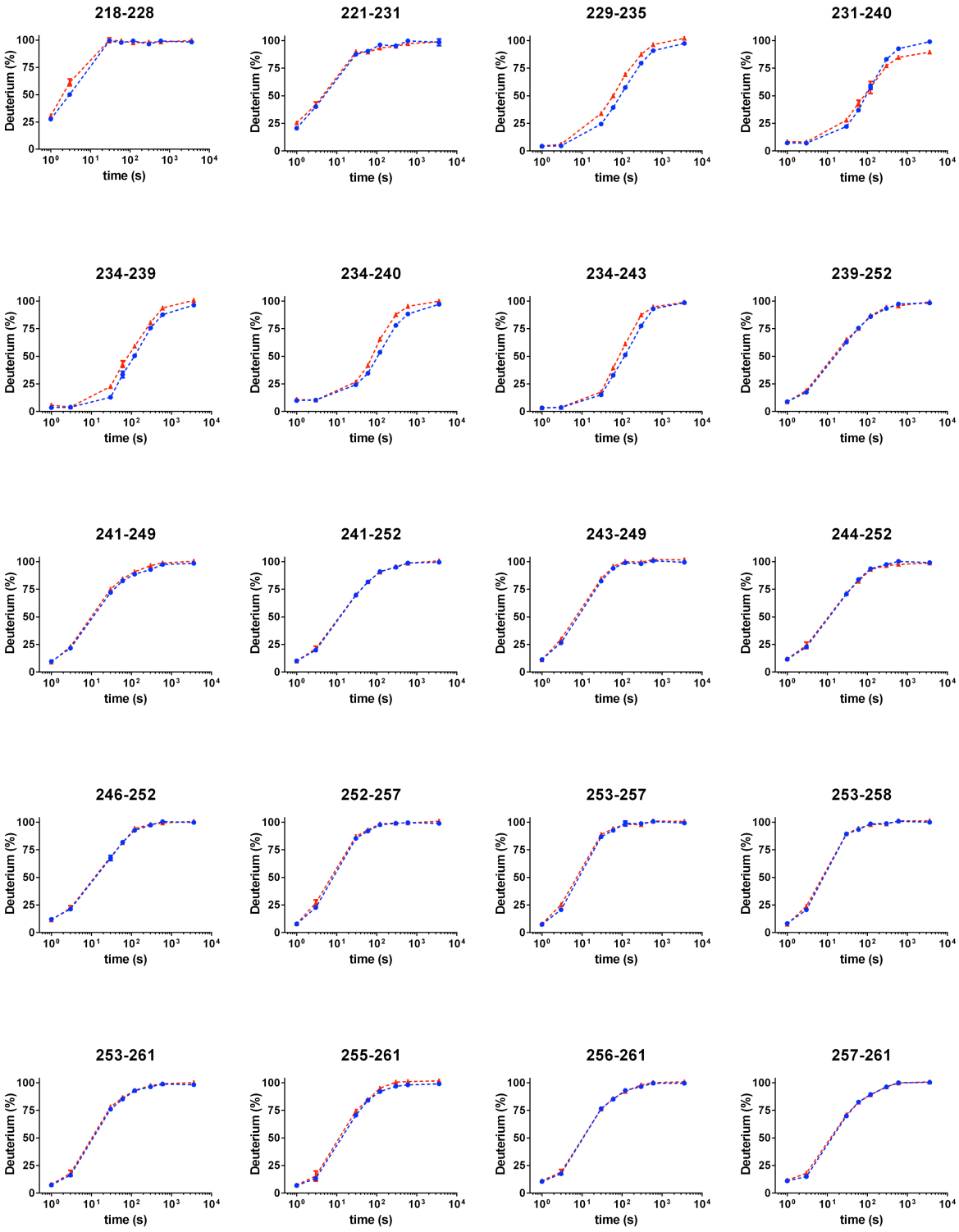

Figure 1S C. Hydrogen deuterium exchange data for peptides from 218-261

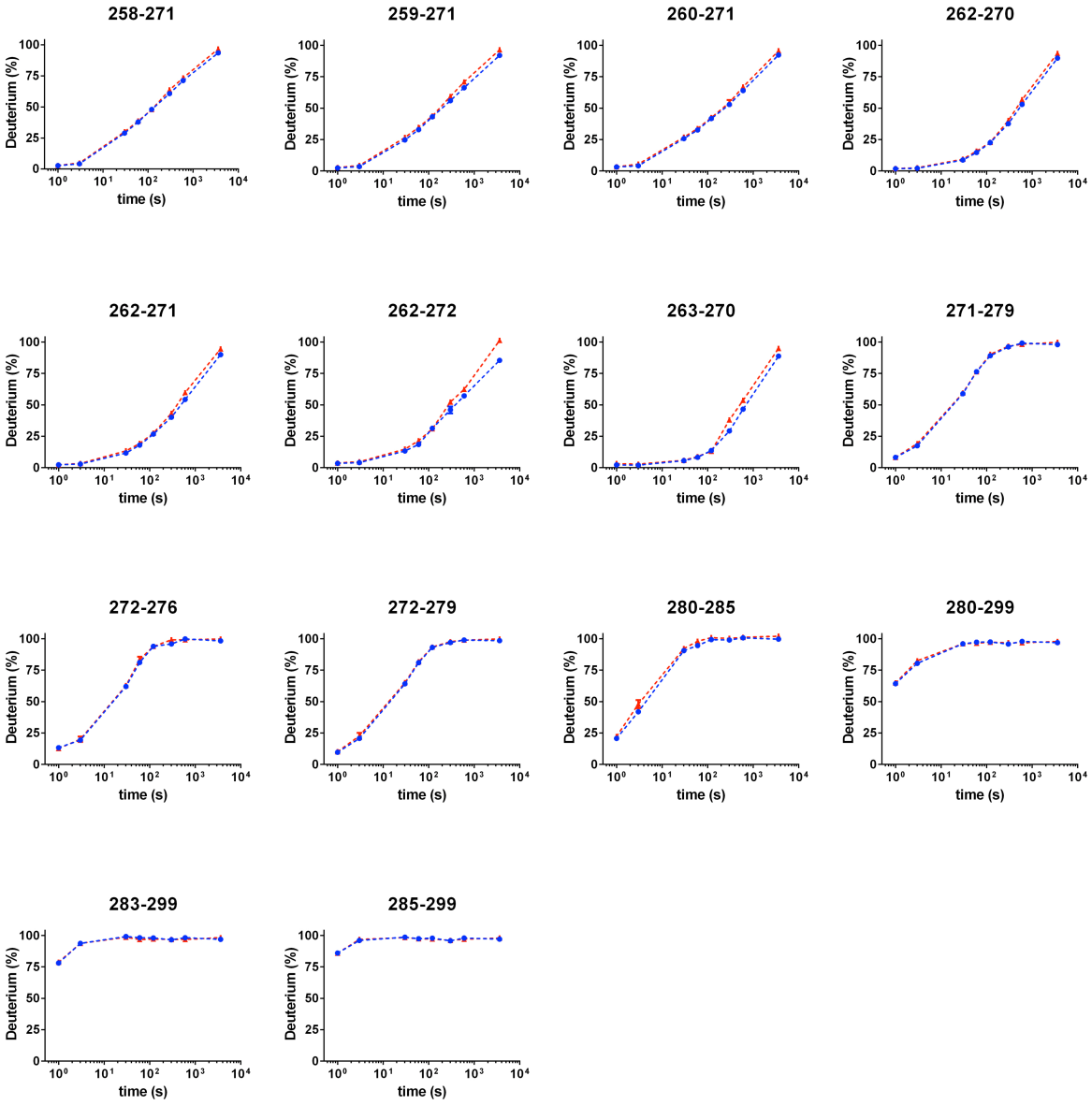

Figure 1S D Hydrogen deuterium exchange data for peptides from 258-299

Figure 1S E. HDX heatmap of E4WT.

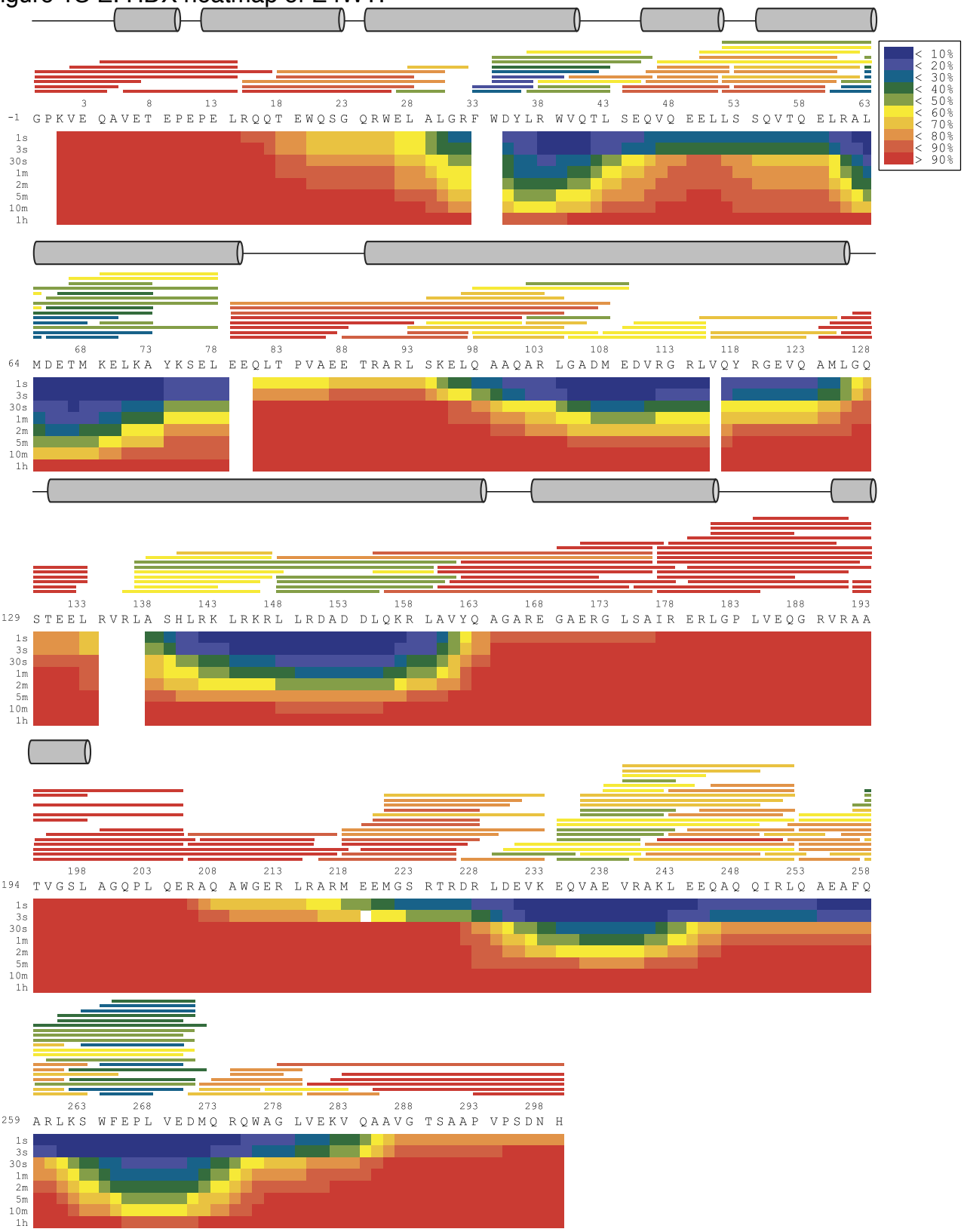

Figure 1S E. HDX heatmap of E4WT. Peptides obtained for apoE4WT are shown at the top of apoE4WT sequence, which are color coded based on the average deuterium uptake across all time points (see color key in the upper-right). Residue-level deuterium uptakes at different time points, located below the apoE4WT sequence, are computed in HDExaminer. The sequence numbering starts at -1 because there are two additional residues (GP) at the N-terminus. Secondary elements of the N-terminal domain (1-198) from a NMR structure of apoE3MM (pdb: 2L7B) are mapped in gray color above apoE4WT peptides (cylinder for α-helix and straight line for disordered region). Heatmap simplifies visualization of HDX results. Locations of α-helices and IDRs can be roughly determined by the color code. Cold color (slower exchange) indicates protection or secondary structure (i.e. α-helix in the case of apoE), whereas warm color represents fast exchange (i.e. unstructured regions). Four major α-helices in the N-terminal domain (29-45, 60-79, 95-127, 138-161), and two α-helices in the C-terminal domain (218-253, 254-284) are observed from the heatmap.

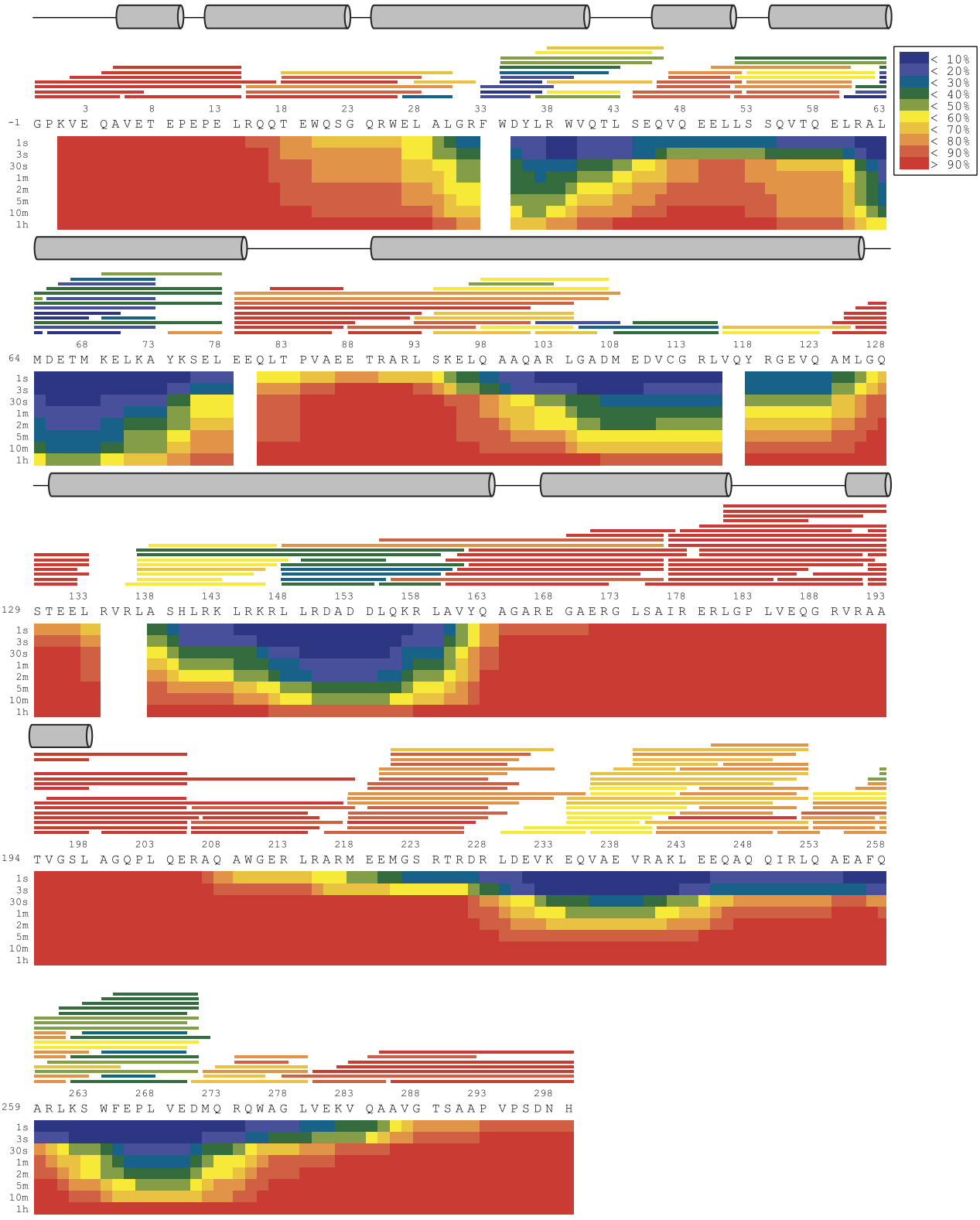

Figure 1S F. HDX heatmap of E3WT. The figure is displayed the same way as Figure 1S E.