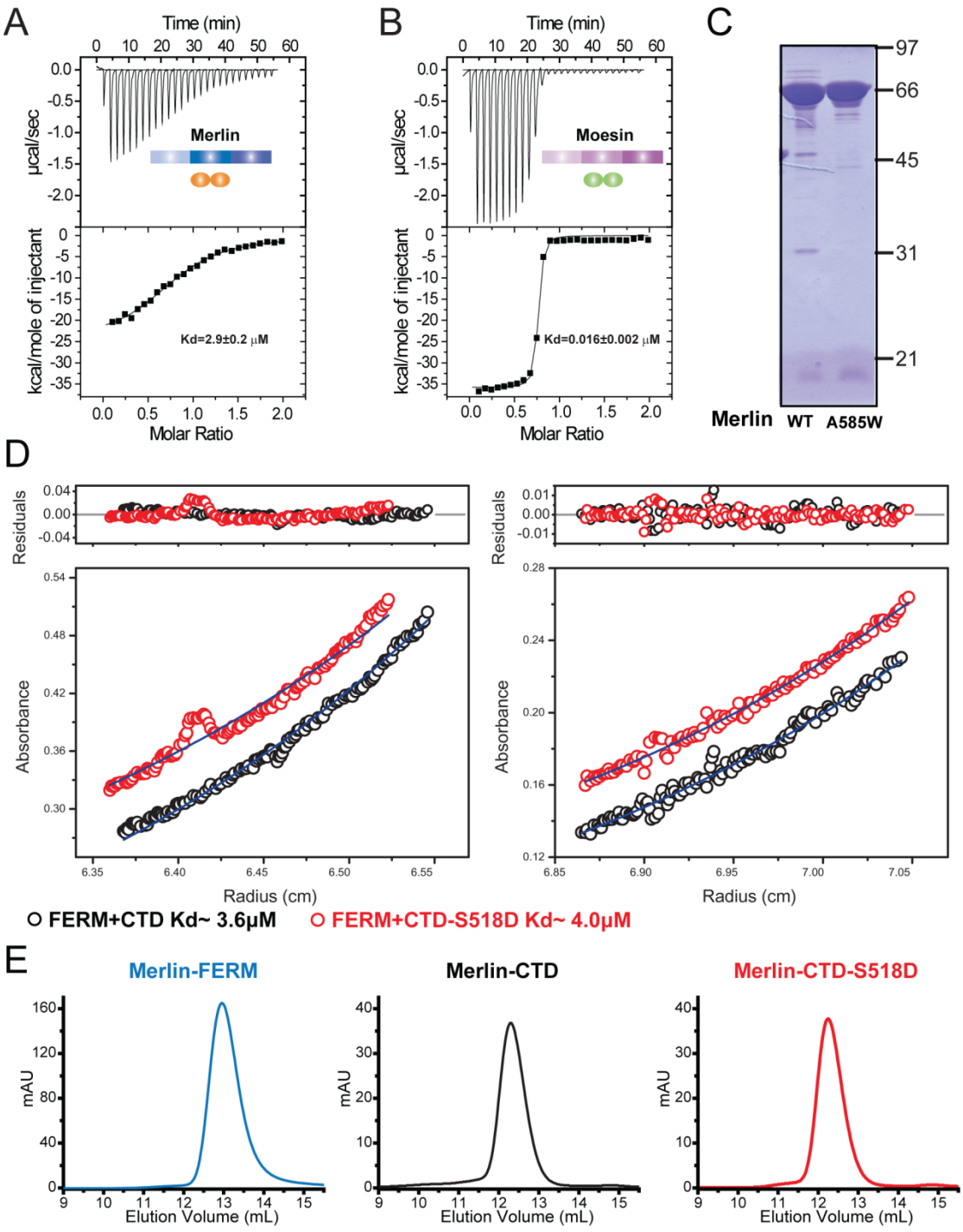

Supplementary information, Figure S1. Head-to-tail auto-inhibition of Merlin and ERMs.

(A-B) ITC-based measurements of the FERM/CTD interaction in Merlin (A) and Moesin (B).

(C) SDS-PAGE with Coomassie blue staining showing the quality of WT-Merlin and

A585W-Merlin used in the biochemical analyses throughout the study.

(D) Analytical ultracentrifugation shows phosphorylation mimetic mutation has no impact on the Merlin FERM/CTD interaction. In this assay, two different protein concentrations are used. Both in high (left panel) and low (right panel) protein concentrations, the Merlin S518D-CTD (labeled in red) displayed an almost identical profile and dissociation constant (K_d of ~4.0 μM) as WT-CTD (labeled in black) in binding to its FERM domain.

(E) The analytical gel filtration profiles of the proteins used for the analytical ultracentrifugation analysis shown in *panel D*.