

Supplementary information, Figure S3

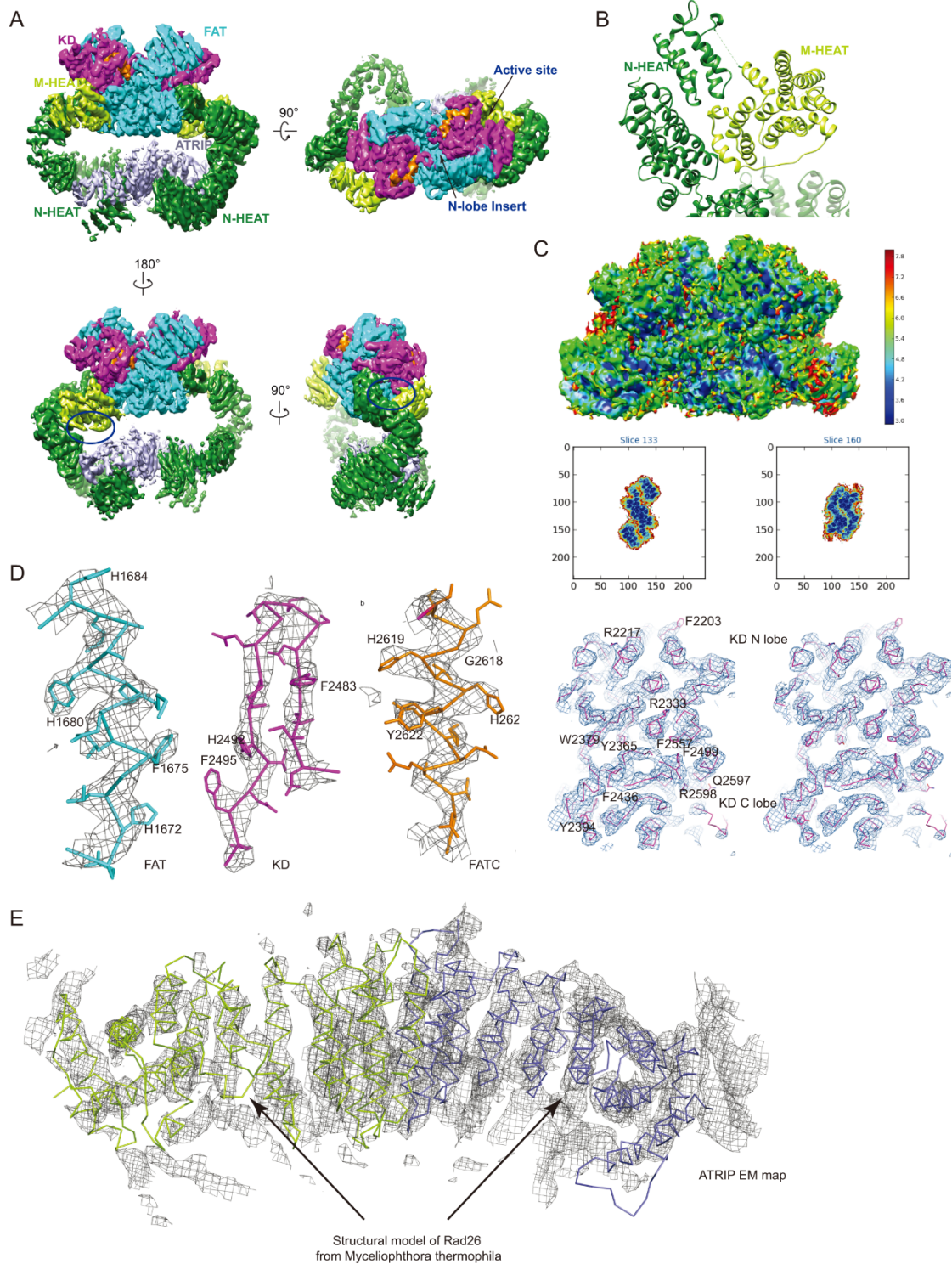


Figure S3 Cryo-EM map for the ATR-ATRIP complex. (A) Four different views of ATR-ATRIP cryo-EM map. All the domains are colored as in Figure 1A. Cryo-EM map corresponding to the connection within M-HEAT (lower left) and connection between

N-HEAT and M-HEAT (lower right) are indicated in blue circles, respectively. (B) Ribbon representations of close-up view of the connection between N-HEAT and M-HEAT. (C) A local resolution map of ATR N-terminal part calculated by ResMap showed resolution ranging from 3.0 to 7.0 Å, with two slices through the center of the local-resolution map depicted below. (D) The close-up view of the representative regions of the FAT, KD and FATC domain of ATR with corresponding cryo-EM map shown as black mesh. Representative residues are shown as stick representations. The bulk side chains fit into the cryo-EM map properly, indicating the side chains of the model were assigned correctly. (E) Docking structure of Rad26 (373-841) from *Myceliophthora thermophila* (PDB: 5LOI) into the EM map corresponding to ATRIP. Two Rad26 molecules can be symmetrically docked into the EM map with some extra fragments extrude out, suggesting a 2:2 stoichiometry of ATR and ATRIP in the complex.