Supplementary information, Figure S3

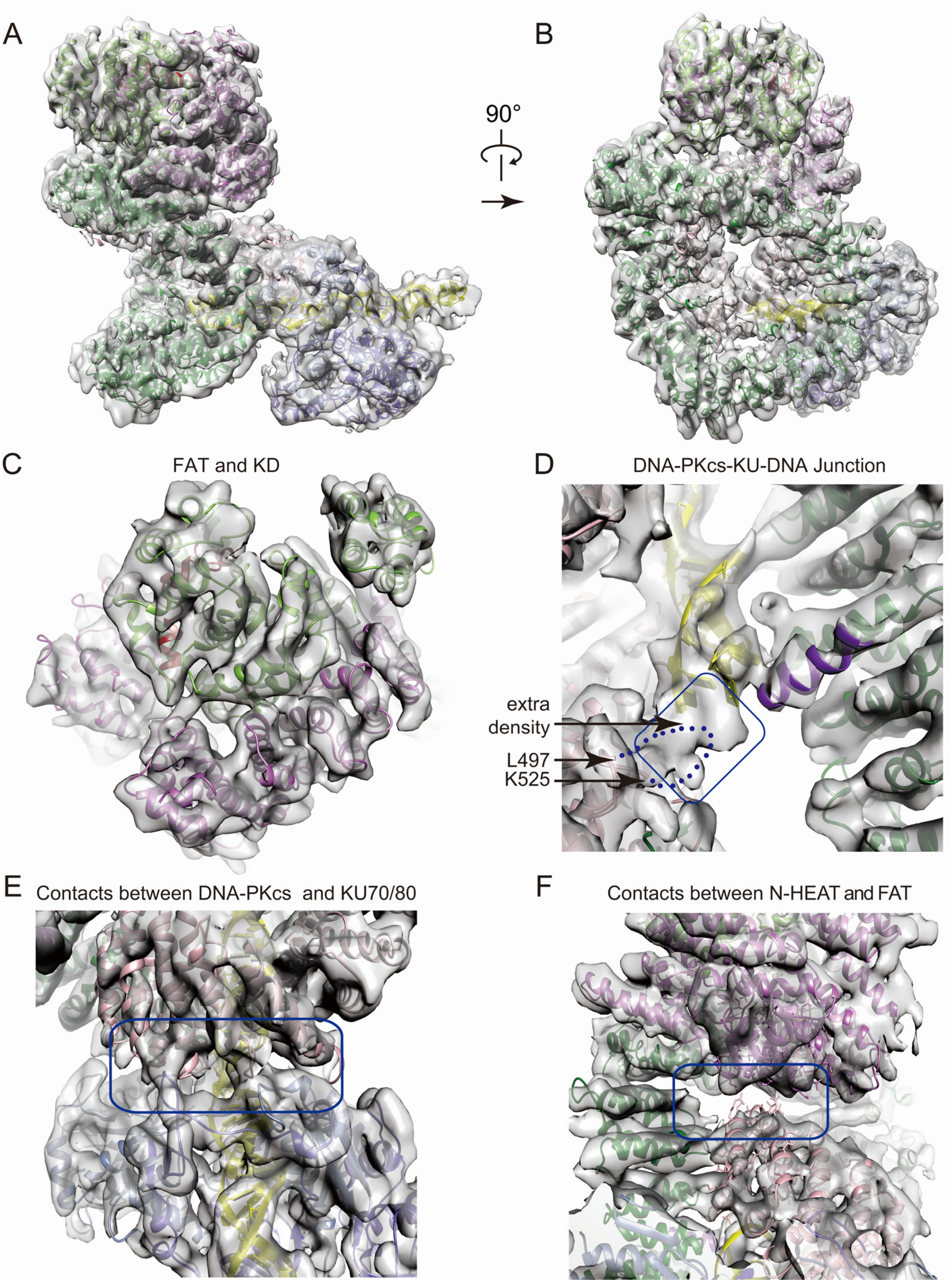

Figure S3 Cryo-EM map for the DNA-PK complex. (**A-B**) Two different views of ribbon representations of the DNA-PK structure fitted into the cryo-EM map. All the domains are colored as in Figure 1A. (**C**-**F**) Close-up views of the structural model and the corresponding cryo-EM map for intermolecular or intramolecular contacts between the FAT and the kinase domain (**C**), DNA-PKcs-KU70/80 and the free DNA end (**D**), DNA-PKcs and KU70/80 heterodimer (**E**), and the FAT and the N-terminus of the N-HEAT (**F**). As shown in **D**, no structural model was built in the density proximal to the free DNA end; this electron density might be derived from residues 497-525, which are connected by dashed lines. Note that the contacts between N-HEAT and FAT (**F**) might be dynamic. The corresponding EM densities do not directly contact each other, but some of the side chains are close enough to mediate intramolecular interactions. This is consistent with their role in regulating the allosteric activation, as a strong interaction in this area would prevent the apo form of DNA-PKcs.