## Supplementary Movie 1. DDK recruitment to the MCM2-7 DH.

The cryo-EM structures of the MCM2-7-DDK (MD) complex in the presence of either ATP $\gamma$ S or ADP:BeF<sub>3</sub> show the recruitment mechanism of DDK to the MCM2-7 DH and the different DDK binding modes. The MD-(ATP $\gamma$ S) state I-III maps reveal initial DDK anchoring to Mcm2 via the Dbf4 HBRCT domain, followed by DDK docking in an Mcm4 DDK targeted conformation. The MD-(ADP:BeF<sub>3</sub>) state I and swiveled state map reveal the different DDK binding modes, explaining DDK targeted phosphorylation of Mcm4 and Mcm2/6.

# Supplementary Movie 2. Flexible analysis of MD-(ATPyS) state III multi-body refinement.

The MD-(ATPγS) state III map was split into three bodies (separating the MCM2-7 DH and each of the two DDK subunits) and subjected to multi-body refinement. The distinct movements of DDK relative to the DH are shown.

## Supplementary Movie 3. Molecular dynamics simulation of Mcm4(N)-Mcm6-DDK model I.

The Mcm4(N)-Mcm6-DDK model I structure, which features an extended Mcm4 N-terminal tail (aa. 134-176), was simulated for a total of 400 ns. The GROMACS molecular dynamics simulation is shown with different views and different frame steps (either 100 or 500 frame steps during the 40,000-frame simulation).

# Supplementary Movie 4. Molecular dynamics simulation of Mcm4(N)-Mcm6-DDK model II.

The Mcm4(N)-Mcm6-DDK model II structure, which features an extended Mcm4 N-terminal tail (aa. 134-176), was simulated for a total of 400 ns. The GROMACS molecular dynamics simulation is shown with different views and different frame steps (either 100 or 500 frame steps during the 40,000-frame simulation).

# Supplementary Movie 5. Molecular dynamics simulation of Mcm4(N)-Mcm6-DDK model III.

The Mcm4(N)-Mcm6-DDK model III structure, which features an extended Mcm4 N-terminal tail (aa. 134-176), was simulated for a total of 400 ns. The GROMACS molecular dynamics simulation is shown with different views and different frame steps (either 100 or 500 frame steps during the 40,000-frame simulation).