Supplemental information, Figure S5

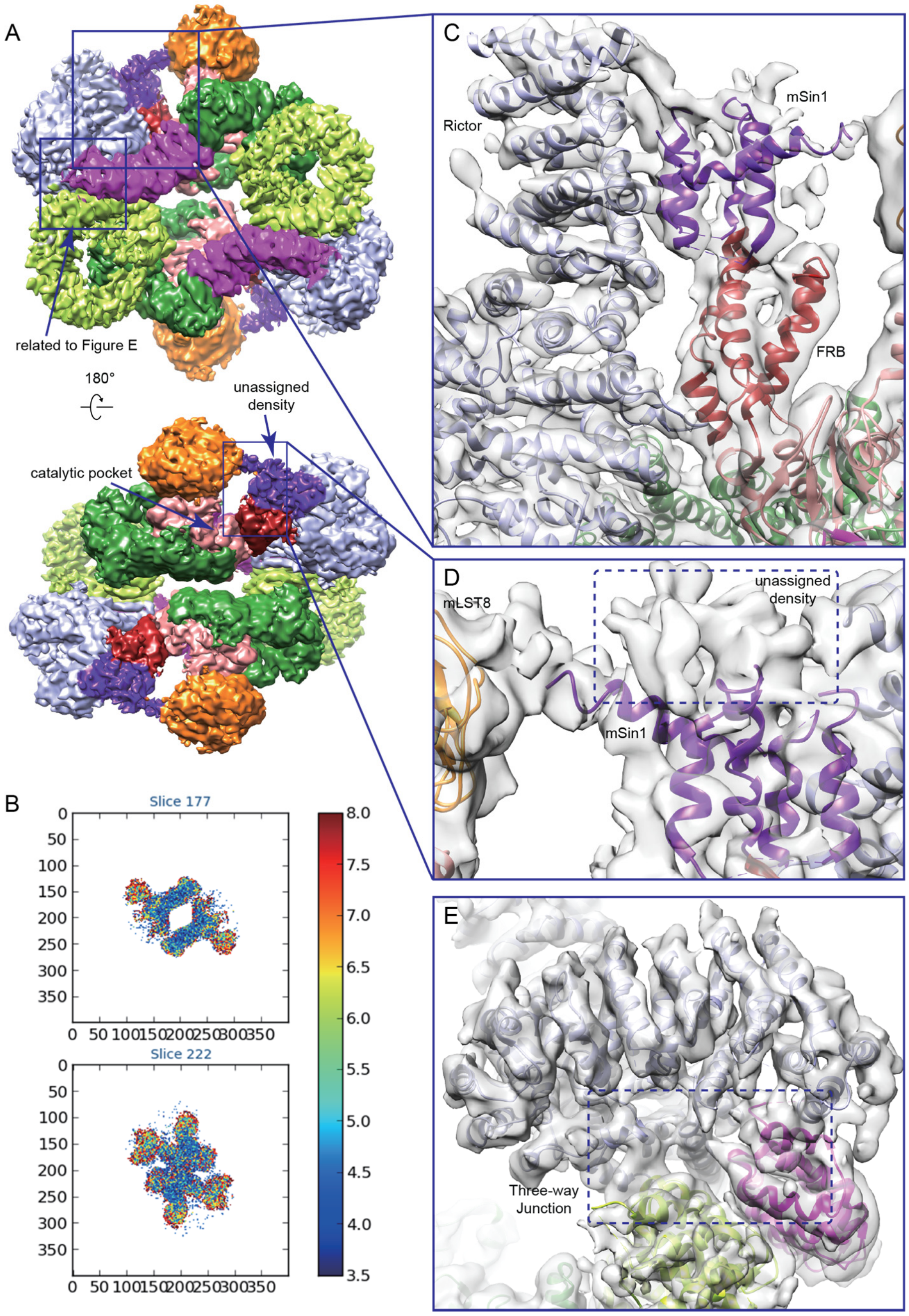

Figure S5 Cryo-EM map and model building of mTORC2 complex. **(A)** Two different views of mTORC2 cryo-EM map. All the domains are colored as in Figure **3B**. **(B)** A local resolution map of mTORC2 calculated by ResMap showed resolution ranging from 3.5 to 8.0 Å, with two slices through the center of the local-resolution map depicted below. **(C-E)** The close-up views of the representative regions within mTORC2 with corresponded model fitted into the cryo-EM map. Note that the unassigned density (flattened stretch) is close to the catalytic cavity of mTOR. The density might be derived from CRIM domain of mSin1 and contribute to substrate recruitment (described in Discussion).