Supporting Information for:

RyR2 Disease Mutations at the C-terminal Domain Inter-subunit Interface Alter Closed-state Stability and Channel Activation

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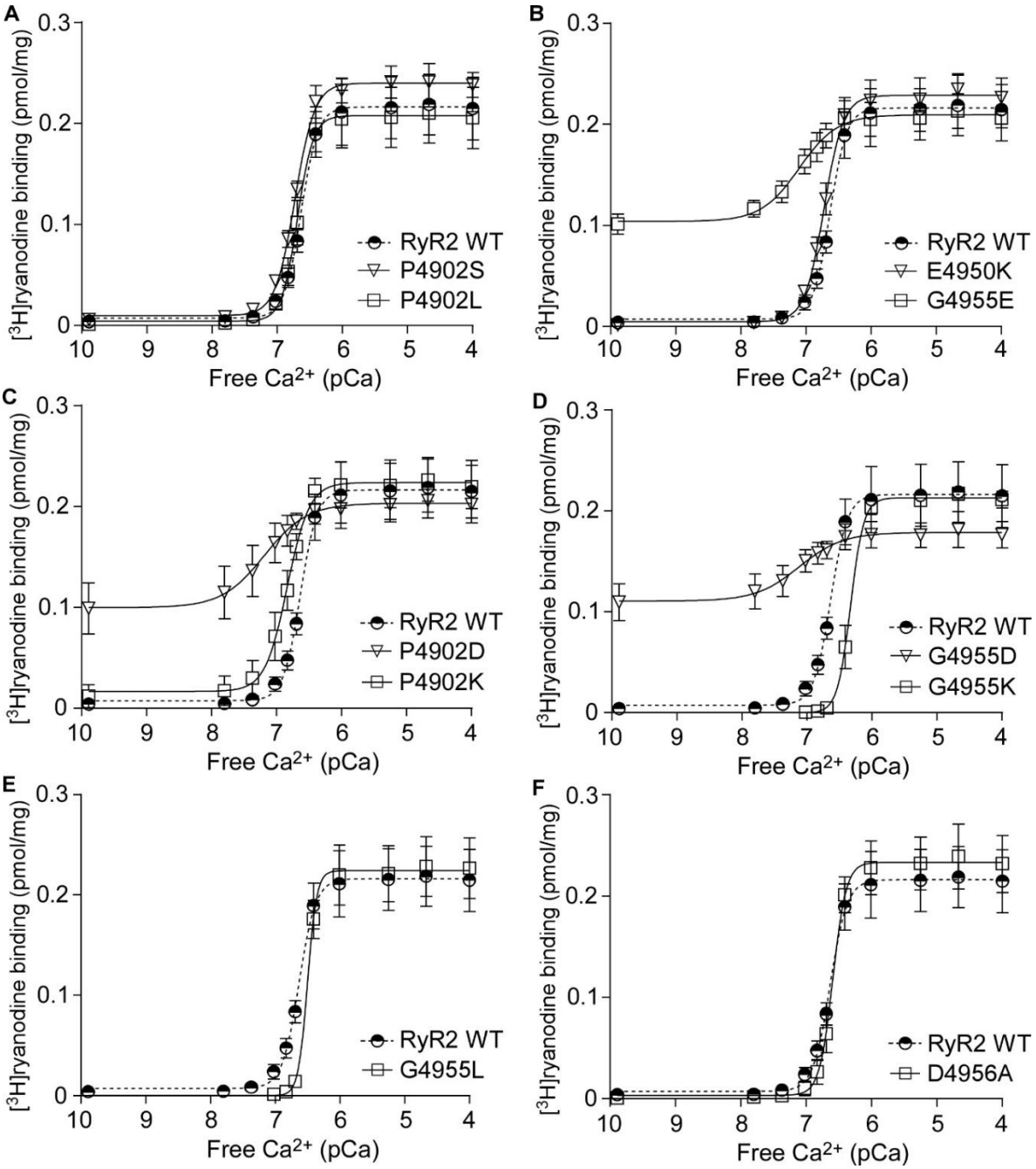
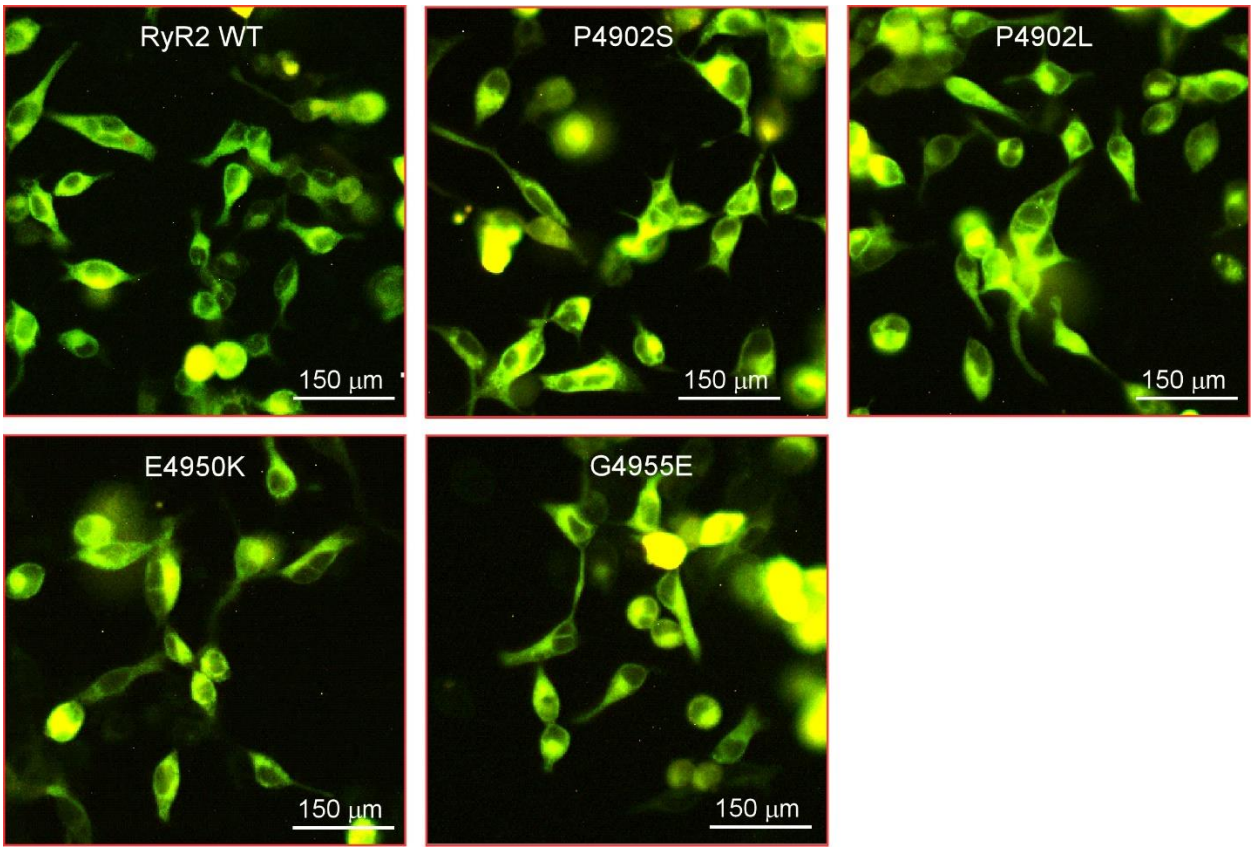
Supplementary Figure 1



Supplementary Figure 1. Effects of CTD mutations on [^{3}H]ryanodine binding to RyR2. [^{3}H]ryanodine binding to cell lysate prepared from HEK293 cells transiently transfected with the RyR2 WT or CTD mutant cDNAs was carried out at various Ca^{2+} concentrations (0.1 nM to 0.1 mM). [^{3}H]ryanodine binding (shown in pmol/mg) to RyR2 WT, P4902S, P4902L (**A**), to RyR2 WT, E4950K, G4955E (**B**), to RyR2 WT, P4902D, P4902K (**C**), to RyR2 WT, G4955D, G4955K (**D**), to RyR2 WT, G4955L (**E**), or to RyR2 WT, D4956A (**F**). The same sets of [^{3}H]ryanodine binding data (shown in percentage (%) of the maximum binding) can be found in Figs. 2 and 7.

Supplementary Figure 2



Supplementary Figure 2. Representative images of FRET-based D1ER imaging of HEK293 cells
Stable, inducible HEK293 cell lines expressing RyR2 WT and mutants were transfected with the FRET-based ER luminal Ca^{2+}-sensing protein D1ER. Representative images of D1ER protein fluorescence (YFP/CFP) of RyR2 WT, P4902S, P4902L, E4950K, and G4955E expressing HEK293 cells in the presence of 2 mM extracellular Ca^{2+} concentration.