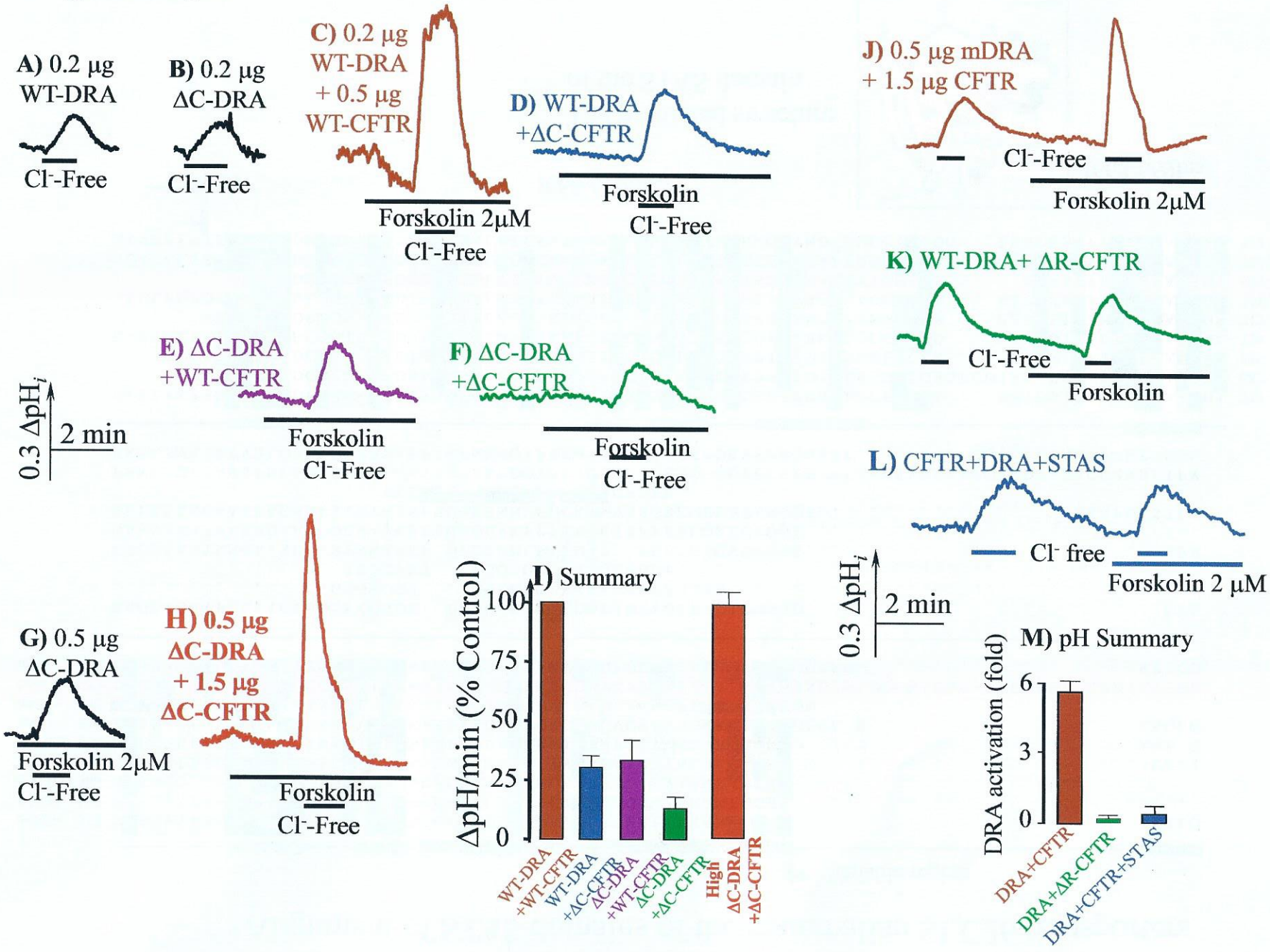
Figure 1, supplement: The PDZ ligands of CFTR and DRA promote their functional interaction, but activation of DRA by CFTR requires the R domain.

HEK293 cells were transfected with 0.2 μg (A-F) or 0.5 μg (G, H) mDRA and 0.5 μg (C-F) or 1.5 μg (H) CFTR constructs. In (A) the cells were transfected with WT-DRA, in (B) with ΔC-mDRA, in (C) the cells were transfected with the WT proteins, in (D) with WT-mDRA and ΔC-CFTR, in (E) with ΔC-mDRA and WT-CFTR and in (F) and (H) with ΔC-mDRA and ΔC-CFTR. The cells were used to measure Cl^-/OH^- exchange activity by mDRA after stimulation of CFTR with forskolin. The results of 4-7 experiments are summarized in (I). In (J) HEK293 cells were transfected with 0.5 μg mDRA+ 1.5 μg CFTR, in (K) with 0.5 μg mDRA+1.5 μg ΔR-CFTR and in (L) with 0.5 μg mDRA+ 1.5 μg CFTR and 1 μg STAS domain and Cl^-/OH^- exchange activity was measured in HEPES-buffered media. Panel (M) summarizes the results of 7 experiments similar to (J, K) and 4 experiments similar to (L). The time and pH scales are given next to the traces. All differences from the respective control are statistically significant ($P<0.01$ or better).

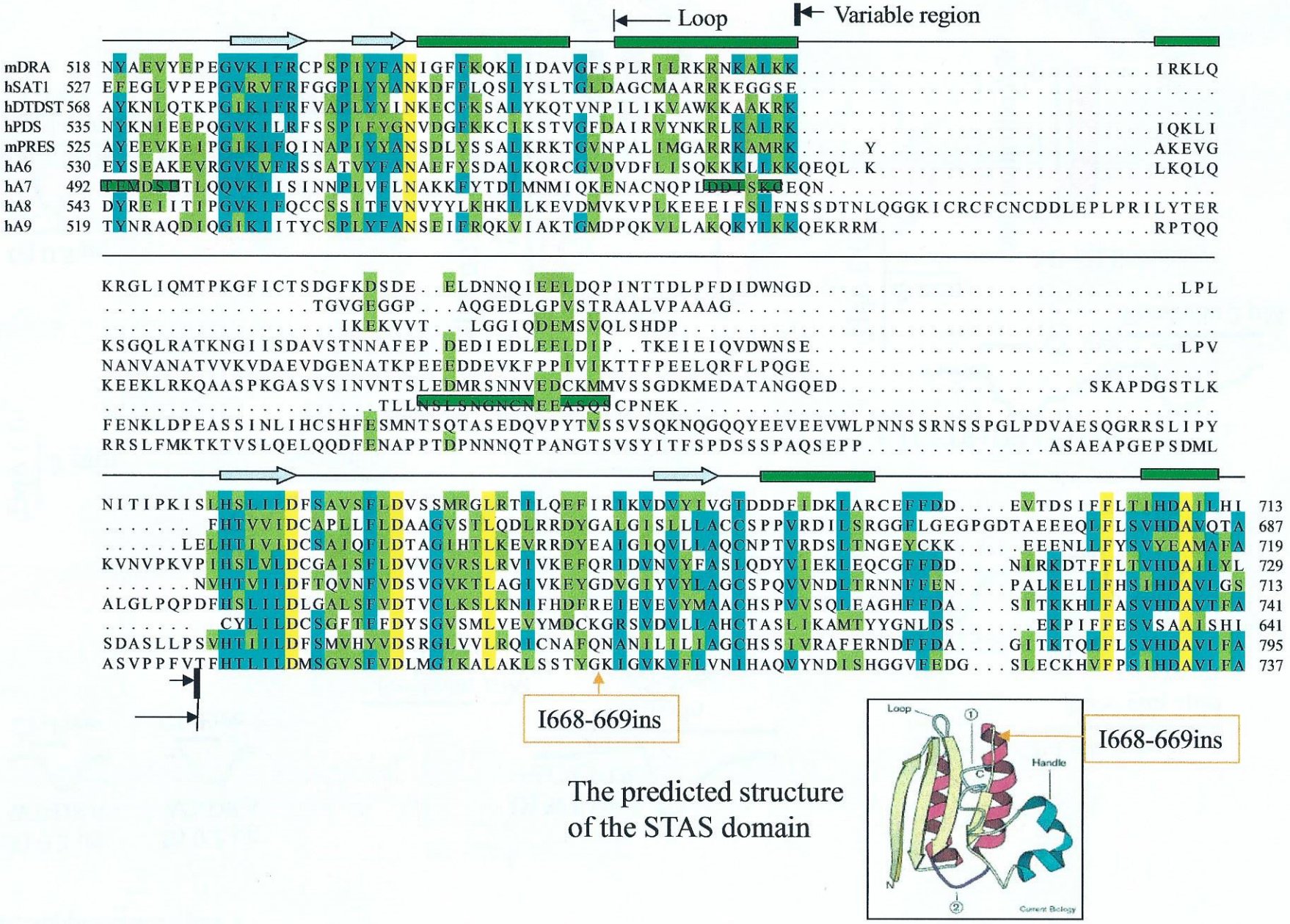
Figure 2, supplement: Alignment of the mammalian STAS domains and its predicted fold. The insertion of Isoleucine between positions 668 and 669 is marked. Residues in yellow boxes are completely conserved, in green boxes are conserved in better than 50% of the sequences and in blue boxes are similar residues. The boundaries of the loop and variable regions are bordered by vertical lines. Predicted α helices are in green bars and β stands are in blue arrows.

Ko et al, Supplement Figure 1



Ko et al, Supplement Figure 2

Alignment of STAS domains of the mammalian SLC26 transporters



The predicted structure of the STAS domain