FIGURE S4  Proposed interactions between the UNC-17 and SUP-1 proteins. UNC-17 is a twelve-pass transmembrane protein; the e245, e359, and p300 alleles are associated with identical missense mutations (G347R) that introduce a positive charge in the ninth TMD. SUP-1 is a Type I single-transmembrane protein; suppressing alleles of sup-1 are associated with identical missense mutations (G84E) that introduce a negative charge in the transmembrane segment. We propose that the TMDs of the two proteins interact (inset), and the negatively charged glutamic acid of SUP-1(G84E) neutralizes the positively charged arginine of UNC-17(G347R), facilitating proper conformation and function of the transporter. The N- and C-termini of each protein are indicated, and the predicted SUP-1 signal peptide is shown in green. The curved arrows in the inset represent the direction of translation of each protein; note that the interacting TMDs are anti-parallel.