Tadross et al., http://www.jgp.org/cgi/content/full/jgp.200910308/DC1

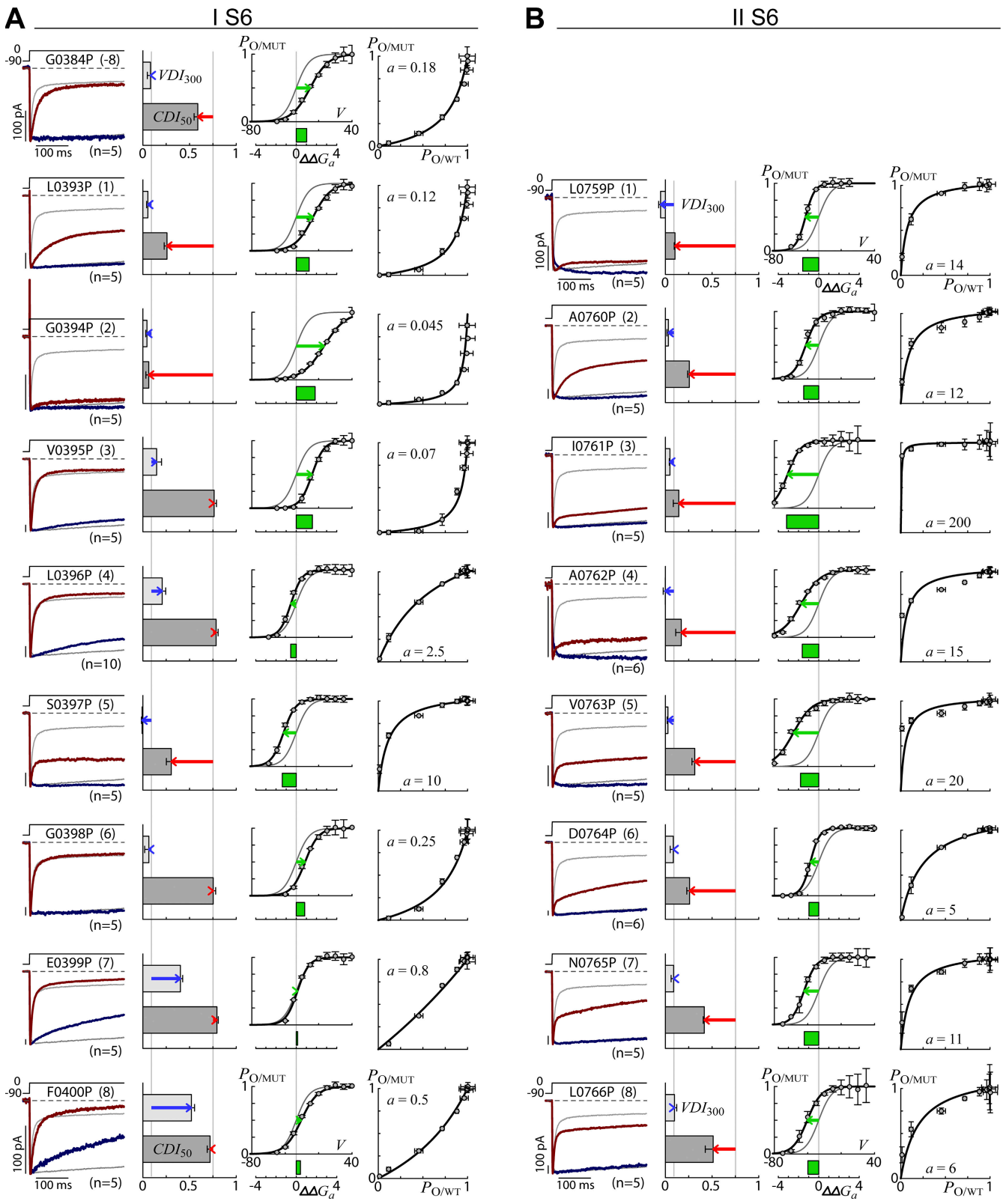
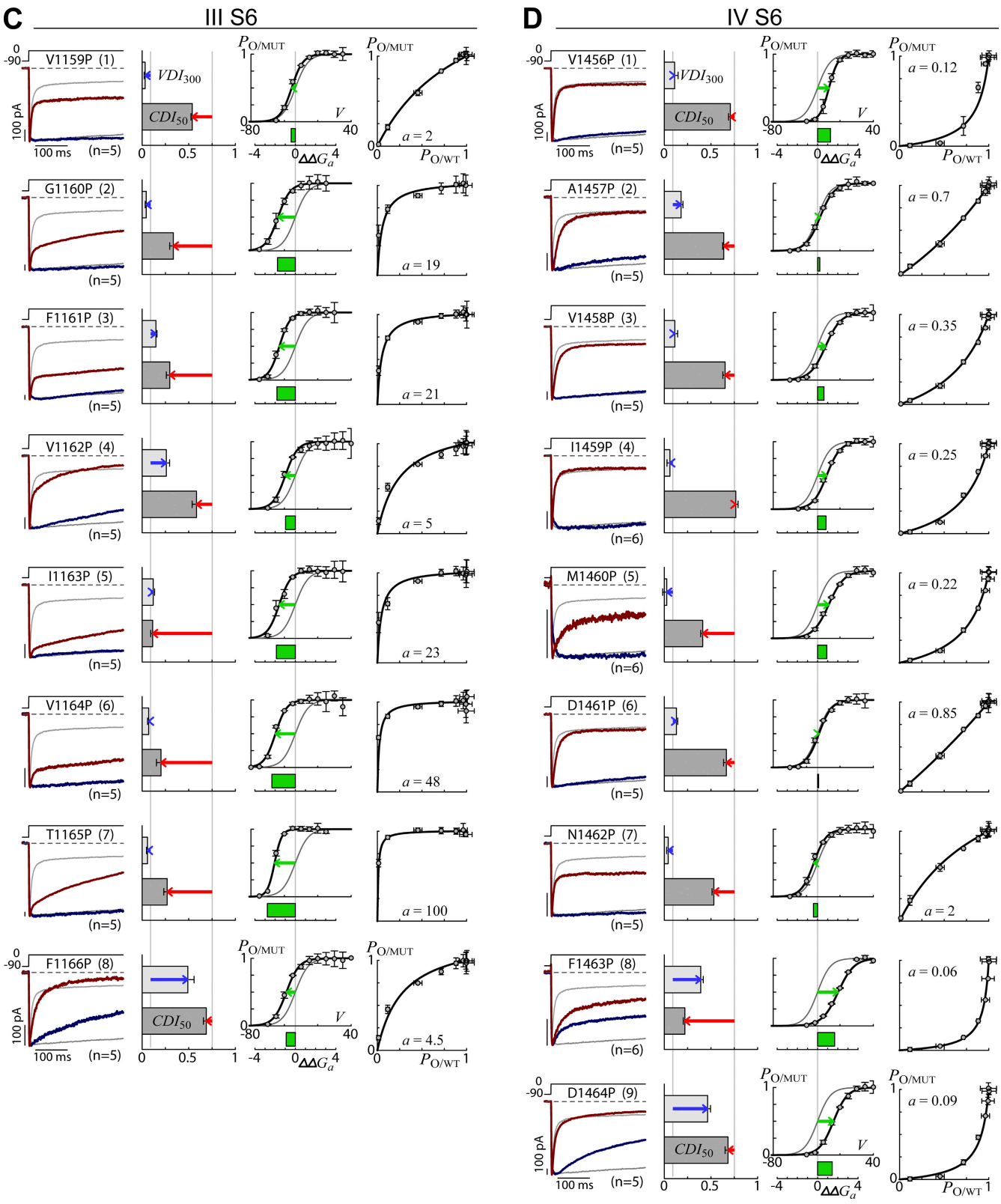


Figure S1. Functional profiles for systematic S6 mutagenesis scan. This figure is an extended version of Fig. 3 that includes all constructs from our mutagenesis screen. Data are organized into four columns, where each column corresponds to a channel domain (IS6, IIS6, IIIS6, and IVS6). Within a column, each row corresponds to data from a $Ca_V1.3$ proline mutant coexpressed with $\alpha_2\delta$ and β_{2a}. Format for each construct follows that in Fig. 2. Exemplar traces (left column) show Ba^{2+} (blue) and Ca^{2+} (red) currents for the mutant channel,



with the native channel behavior overlaid in light gray for reference. Voltage pulse protocol and mutated residue (identified by name and common S6 coordinate) are indicated above data traces. For *VDI* and *CDI* metrics (second column), native channel values are indicated by the vertical gray lines, and deviation from native channel behavior is indicated by colored arrows. This is also done for the voltage activation relations (third column), which show both $\Delta\Delta G_a$ (bars) and $\Delta V_{1/2}$ (arrows). The fourth column shows fits for $\Delta\Delta G_a$ determination, as done in Fig. 2 E (left). Axis labels are shown only for top and bottom rows, with identical format throughout.