

Supplementary Information for

A computational method for predicting the most likely evolutionary trajectories in the stepwise accumulation of resistance mutations

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This PDF file includes:

Figures S1 to S4 (not allowed for Brief Reports)

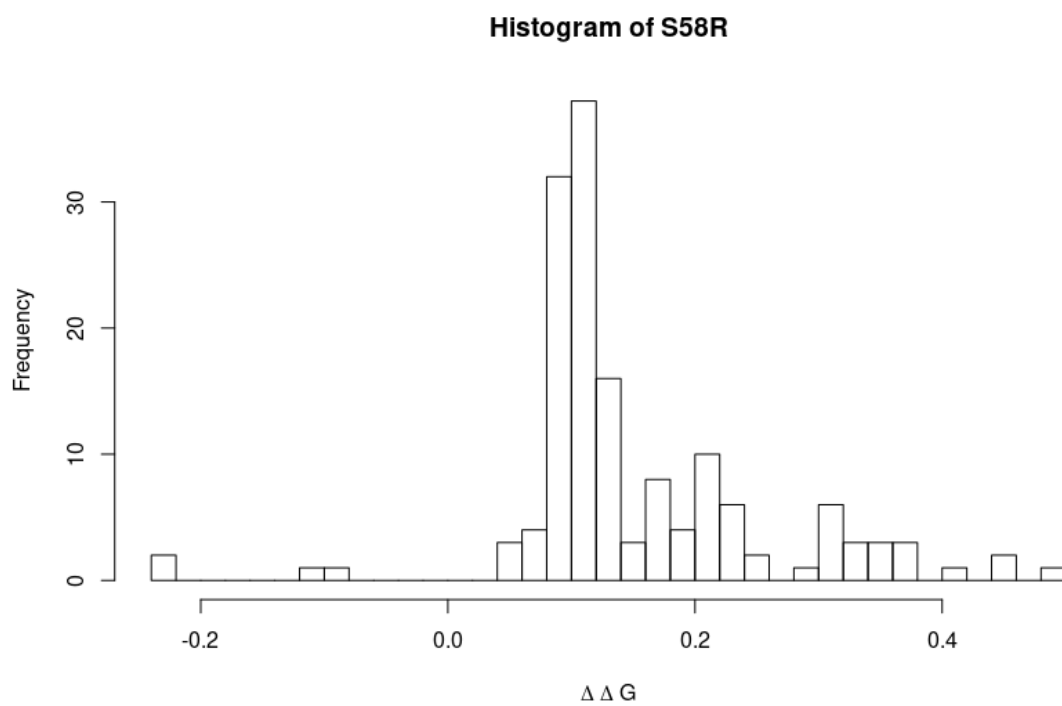


Fig. S1. Distribution of 150 Flex-ddG predictions of *Pv*DHFR-pyrimethamine binding free energy change upon single mutation S58R

Histogram of S117N

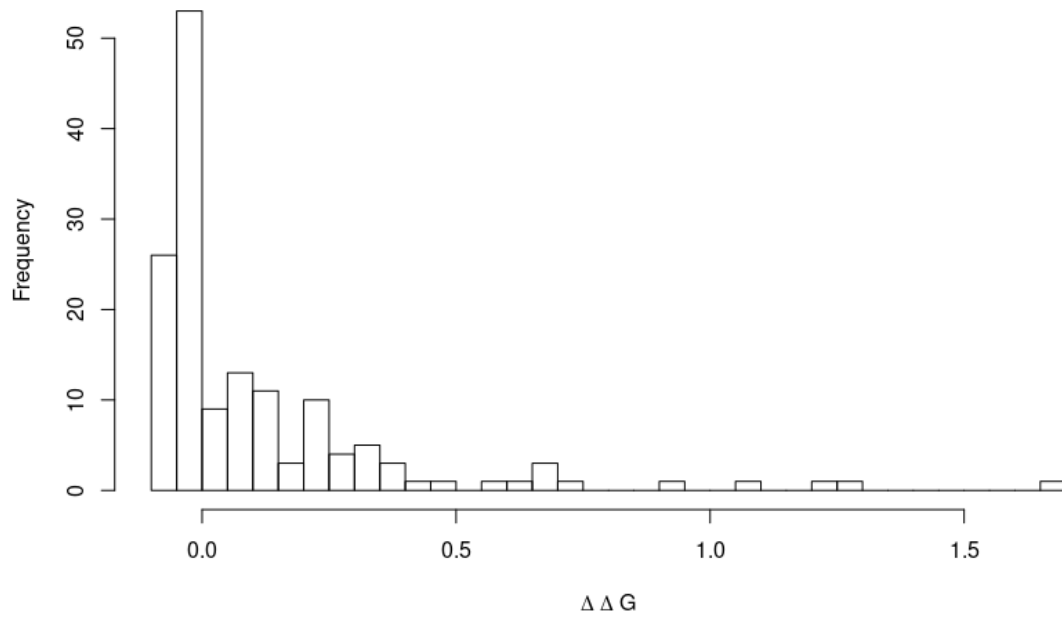


Fig. S2. Distribution of 150 Flex-ddG predictions of *Pv*DHFR-pyrimethamine binding free energy change upon single mutation S118N

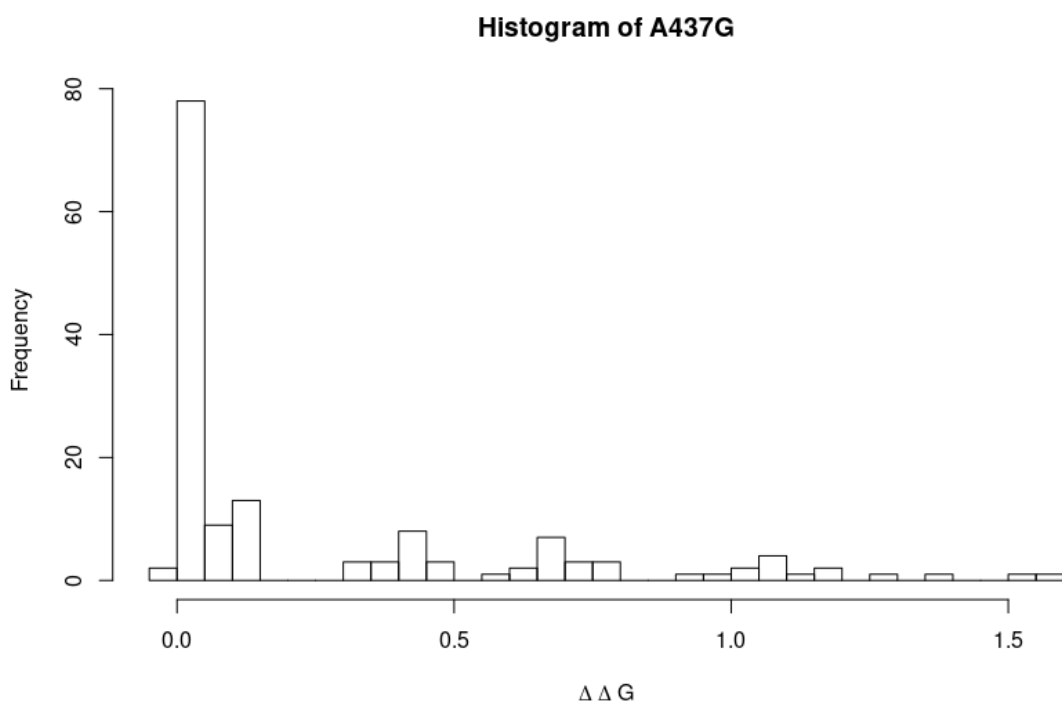


Fig. S3. Distribution of 150 Flex-ddG predictions of *Pf*DHPS-sulfadoxine binding free energy change upon single mutation A437G

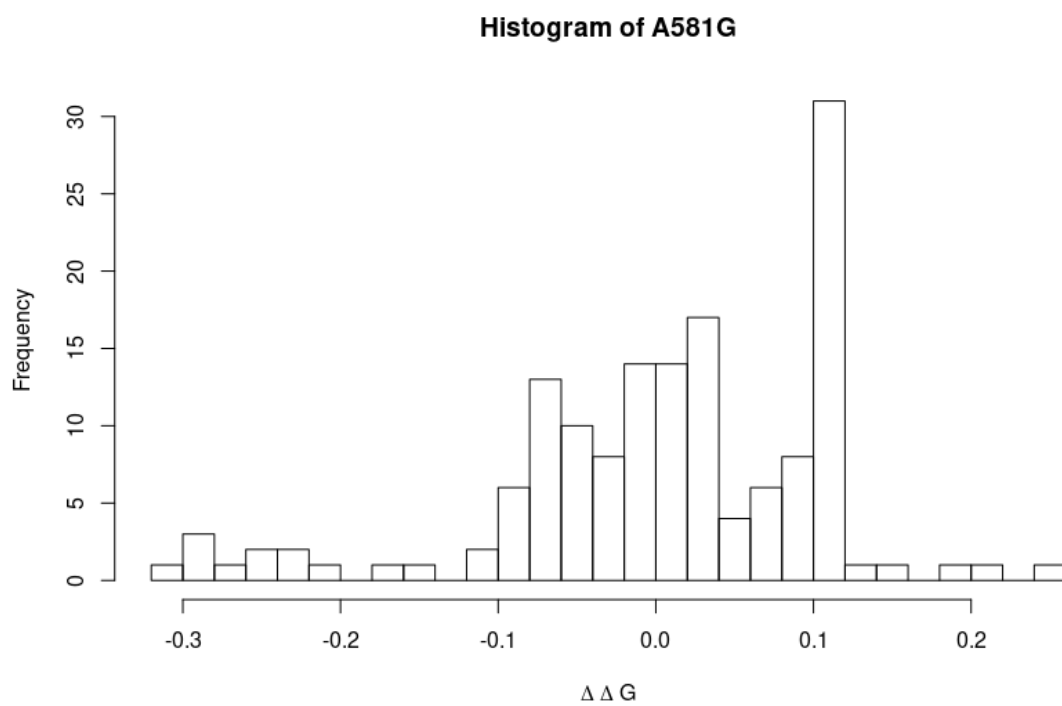


Fig. S4. Distribution of 150 Flex-ddG predictions of *Pf*DHPS-sulfadoxine binding free energy change upon single mutation A581G