Supporting Information for:

Probing Structural Dynamics and Topology of the KCNE1 Membrane Protein in Lipid Bilayers via Site-directed Spin Labeling and EPR Spectroscopy

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Figure S1: CW-EPR spectral simulation of KCNE1 mutants in liposomes using Multicomponent LabVIEW program. The mutants V50C and I66C are along the transmembrane domain, F12C is along N-terminus and D76C is along C-terminus of KCNE1.

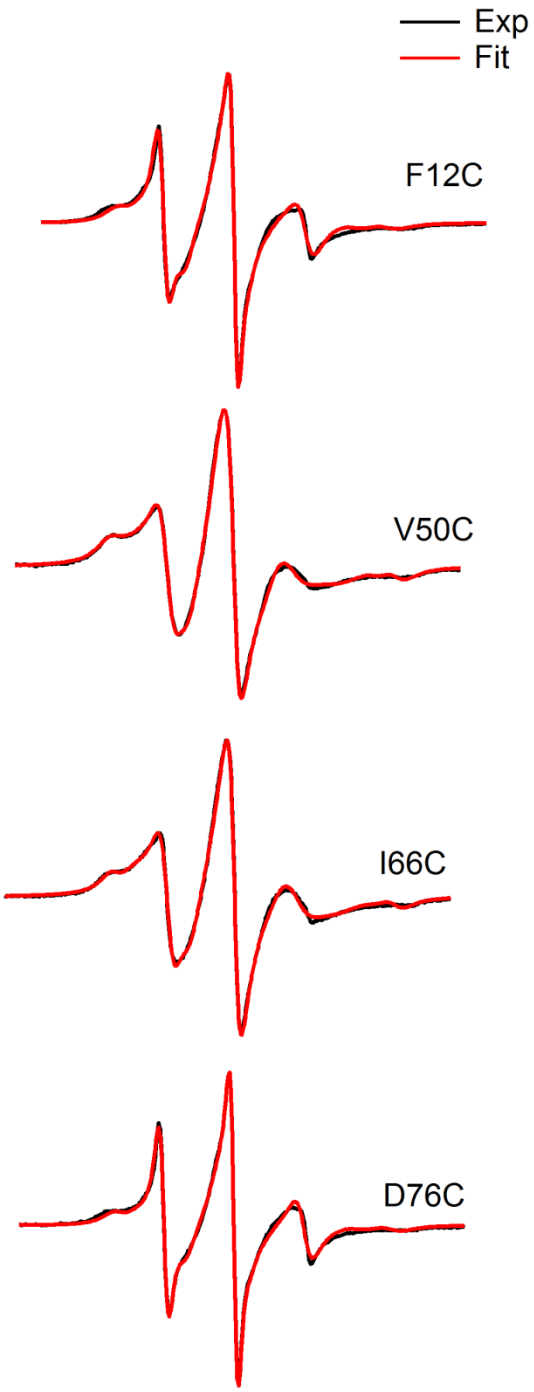

Figure S2: CW-EPR spectra on KCNE1 mutants in 7.5% LMPG micelles (black) and POPC/POPG liposomes (red).

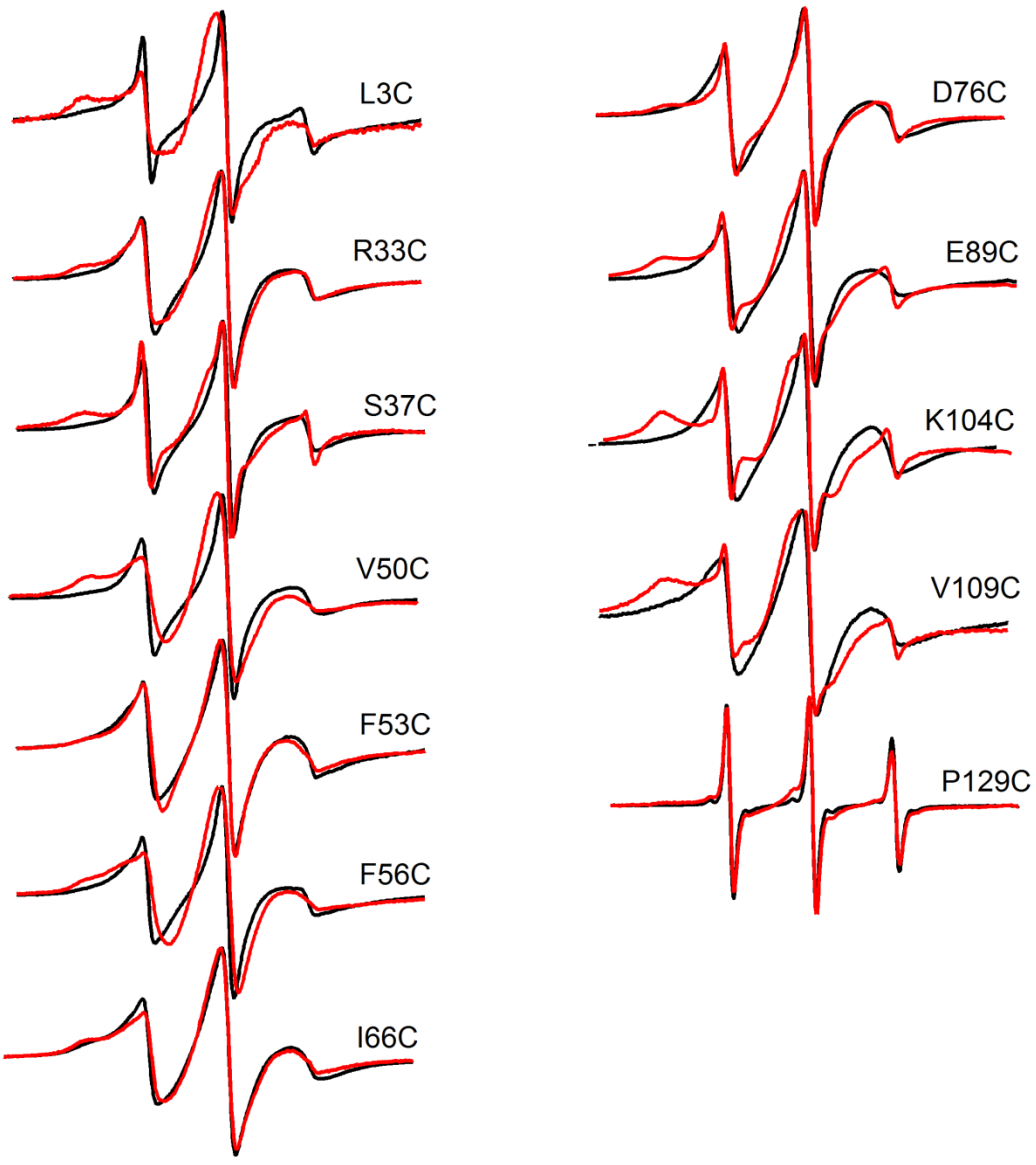

Table S1: Rotational Correlation times and relative population of two spectral components of EPR spectra (Figure S1) obtained from the best fit spectral simulation.

Mutants		Rotational Correlation Time (ns)	Relative Population (%)
F12C	site1	0.8	55
	site2	8.2	45
V50C	site1	1.2	74
	sute2	13.7	26
I66C	site1	1.1	76
	site2	16.1	24
D76C	site1	0.8	55
	site2	8.2	45