

# Single-cell Electrical Lysis of Erythrocytes Detects Deficiencies in the Cytoskeletal Protein Network

*Ning Bao<sup>a,d</sup>, Gayani C. Kodippili<sup>b</sup>, Katie M. Giger<sup>b</sup>, Velia M. Fowler<sup>c</sup>, Philip S. Low<sup>b,\*</sup>, Chang Lu<sup>a,\*</sup>*

<sup>a</sup>Department of Chemical Engineering, School of Biomedical Engineering and Sciences, Virginia Tech, Blacksburg, Virginia 24061, USA. Email: changlu@vt.edu; Fax: +1-540-231-5022; Tel: +1-540-231-8681

<sup>b</sup>Department of Chemistry, Purdue University, West Lafayette, Indiana 47907, USA. Email: plow@purdue.edu

<sup>c</sup>Department of Cell Biology, The Scripps Research Institute, La Jolla, California 92037, USA.

<sup>d</sup>School of Public Health, Nantong University, Nantong 226019, P. R. China

## Supporting information

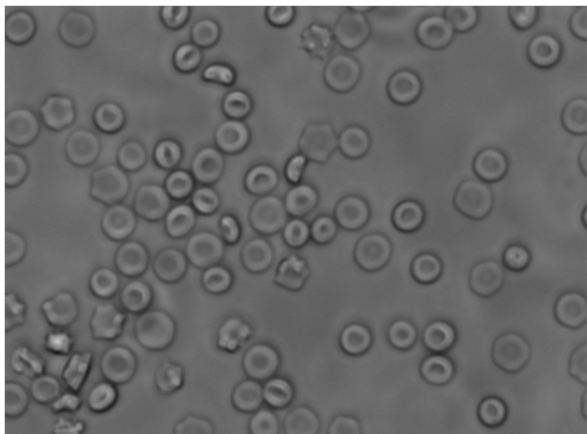
Table S1	Wilcoxon signed ranks tests for the histograms of the lysis time
Figure S1	The optical images of red blood cells from normal, $\beta$ -adducin-null, nb/nb and Tmod1-null mice.
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**Table S1. Wilcoxon signed ranks tests for the histograms of the lysis time**

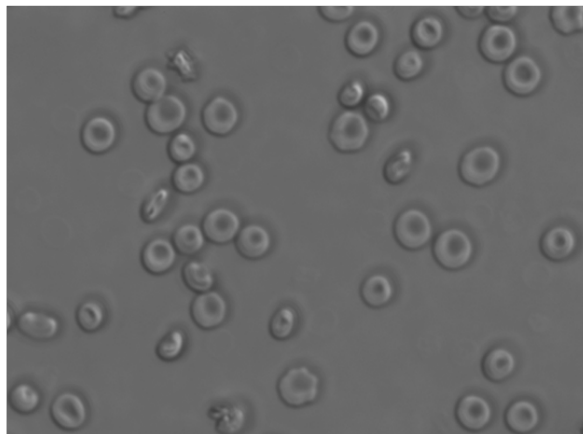
Electroporation field intensity	RBC samples (from 5 normal mice, 3 $\beta$ -adducin null mice, 2 nb/nb mice and 2 Tmod1 null mice)		Wilcoxon signed rank test		Statistical significance §
			P	H	
1200 V/cm	Normal 1	$\beta$ -adducin null 1	$1.1702 \times 10^{-4}$	1	***
	Normal 1	nb/nb 1	$4.8345 \times 10^{-4}$	1	***
	$\beta$ -adducin null 1	nb/nb 1	0.0092	1	**
	nb/nb 1	nb/nb 2	0.6154	0	ns
	Normal 1	Normal 2	0.7652	0	ns
1100 V/cm	Normal 3	Tmod1 null 1	0.2091	0	ns
	Normal 3	$\beta$ -adducin null 2	0.0281	1	*
	$\beta$ -adducin null 2	Tmod1 null 1	0.0426	1	*
	Normal 3	Normal 4	0.6926	0	ns
	Normal 3	Normal 5	0.0778	0	ns
	Normal 4	Normal 5	0.4002	0	ns
	$\beta$ -adducin null 2	$\beta$ -adducin null 3	0.6080	0	ns
Tmod1 null 1	Tmod1 null 2	0.8293	0	ns	

§ The statistical significance is obtained according to the P value of Wilcoxon signed rank test. When the P value is over 0.05, there is no statistical significance (ns) between the two samples. When the P value is between 0.01 and 0.05, the difference between the two samples is significant (\*). When the P value is between 0.001 and 0.01, the difference between the two samples is very significant (\*\*). When the P value is less than 0.001, the difference between the two samples is extremely significant (\*\*\*).

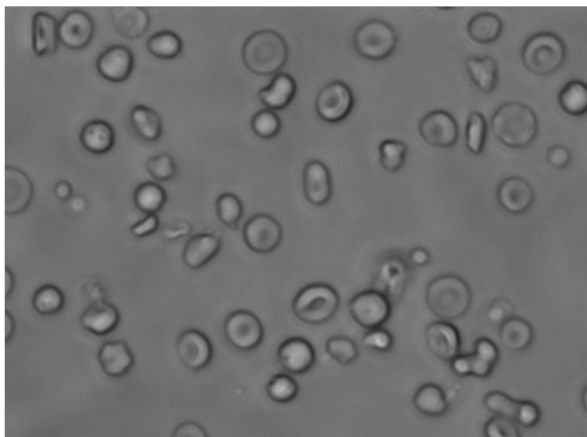
Normal



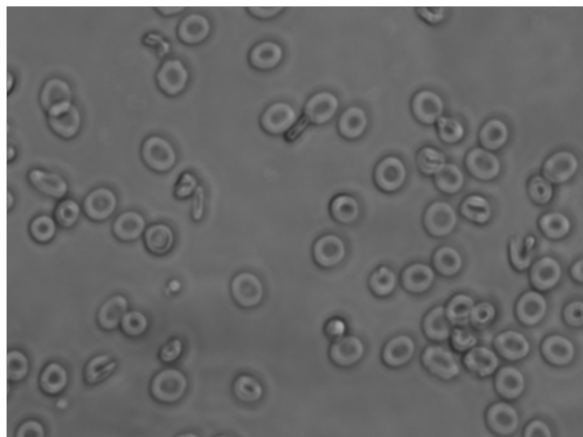
$\beta$ -adducin null



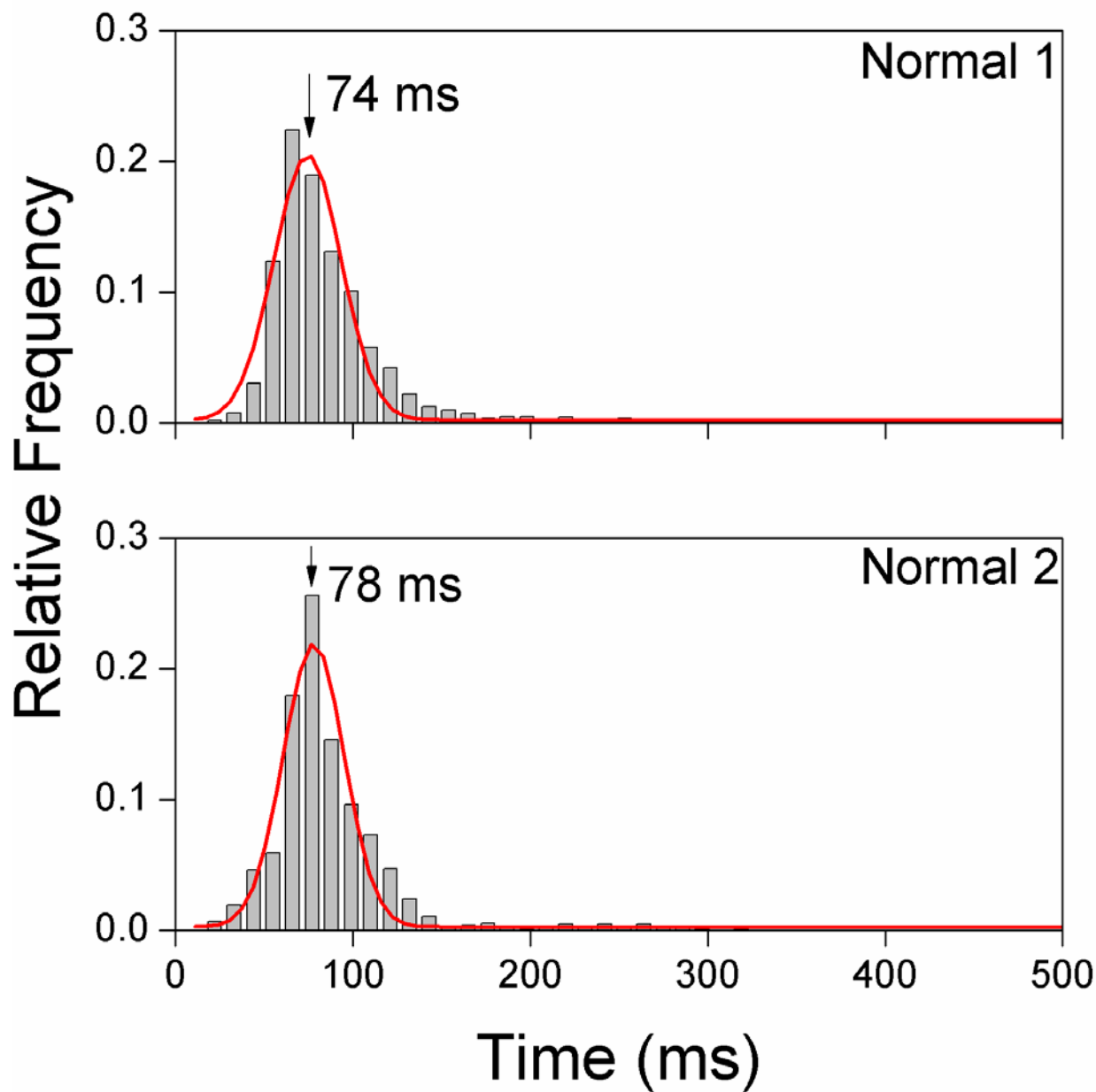
nb/nb



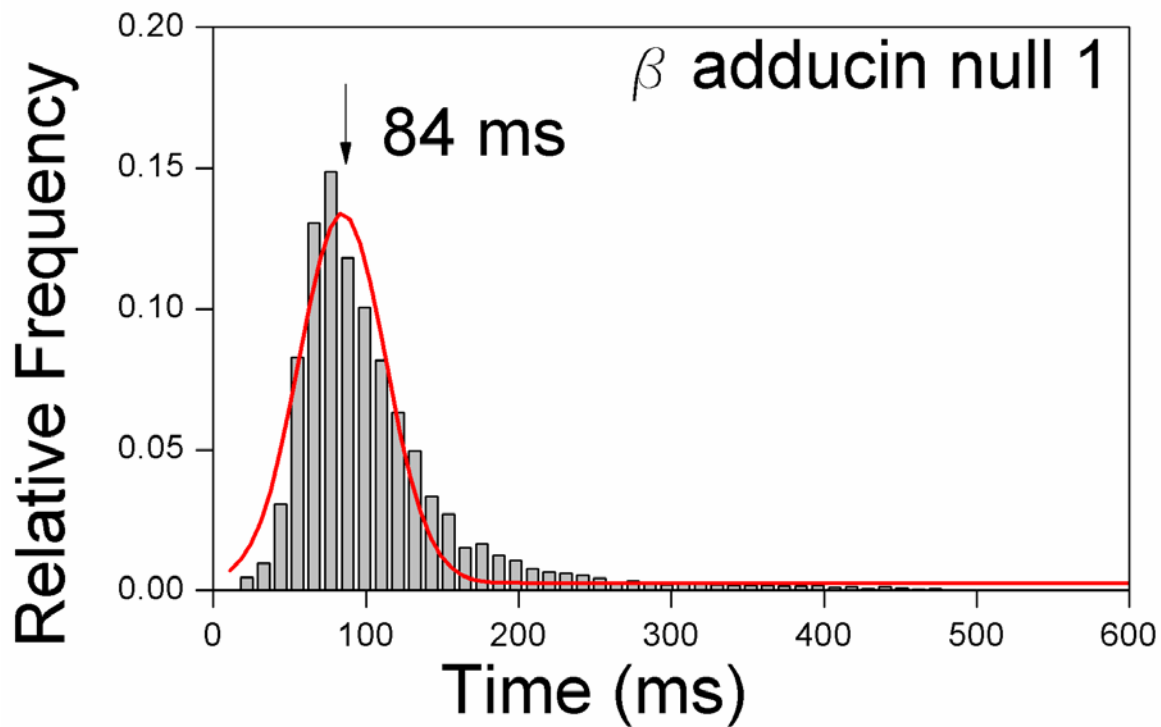
Tmod1 null



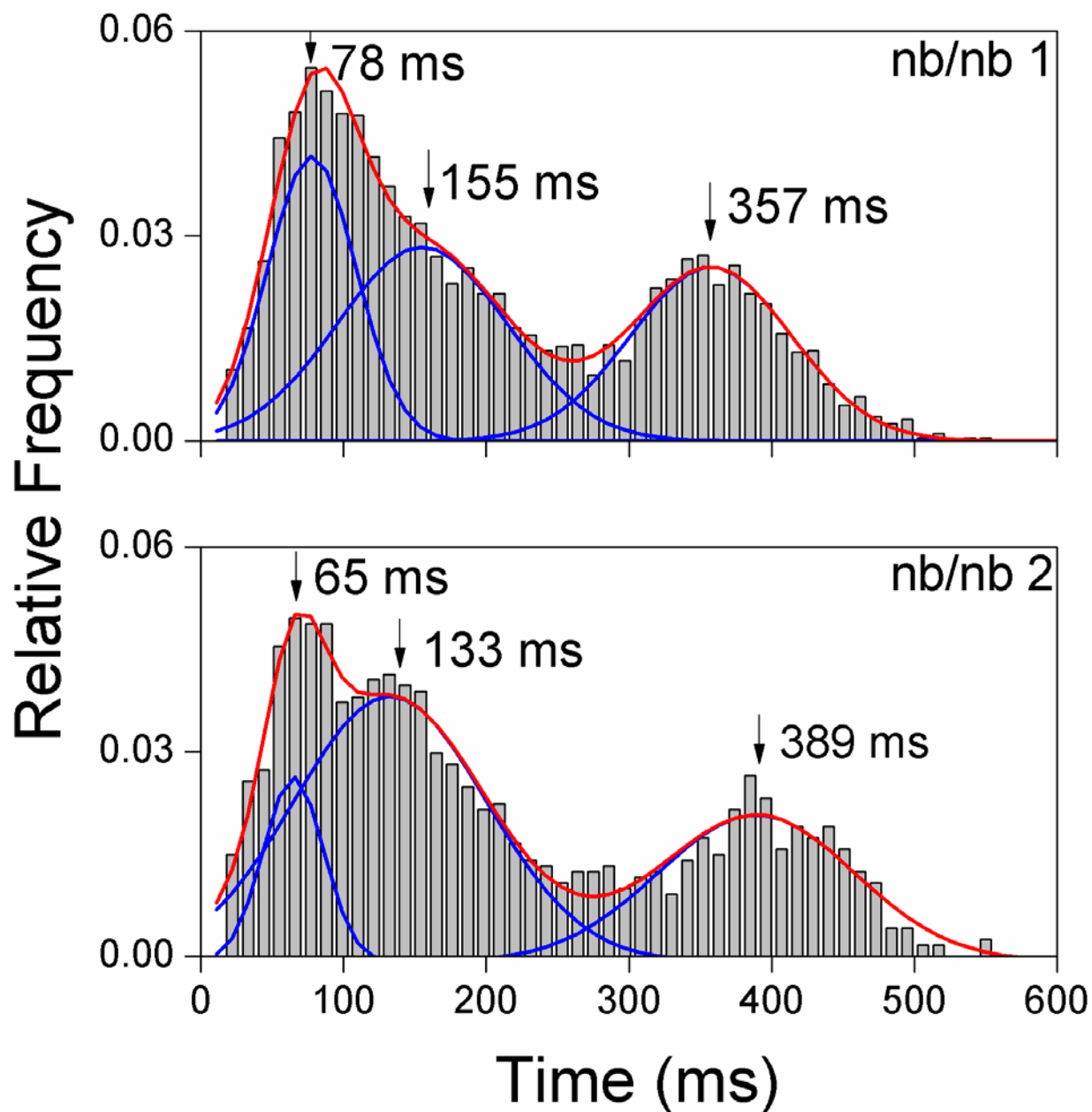
**Figure S1.** The optical images of red blood cells from normal,  $\beta$ -adducin-null, nb/nb and Tmod1-null mice.



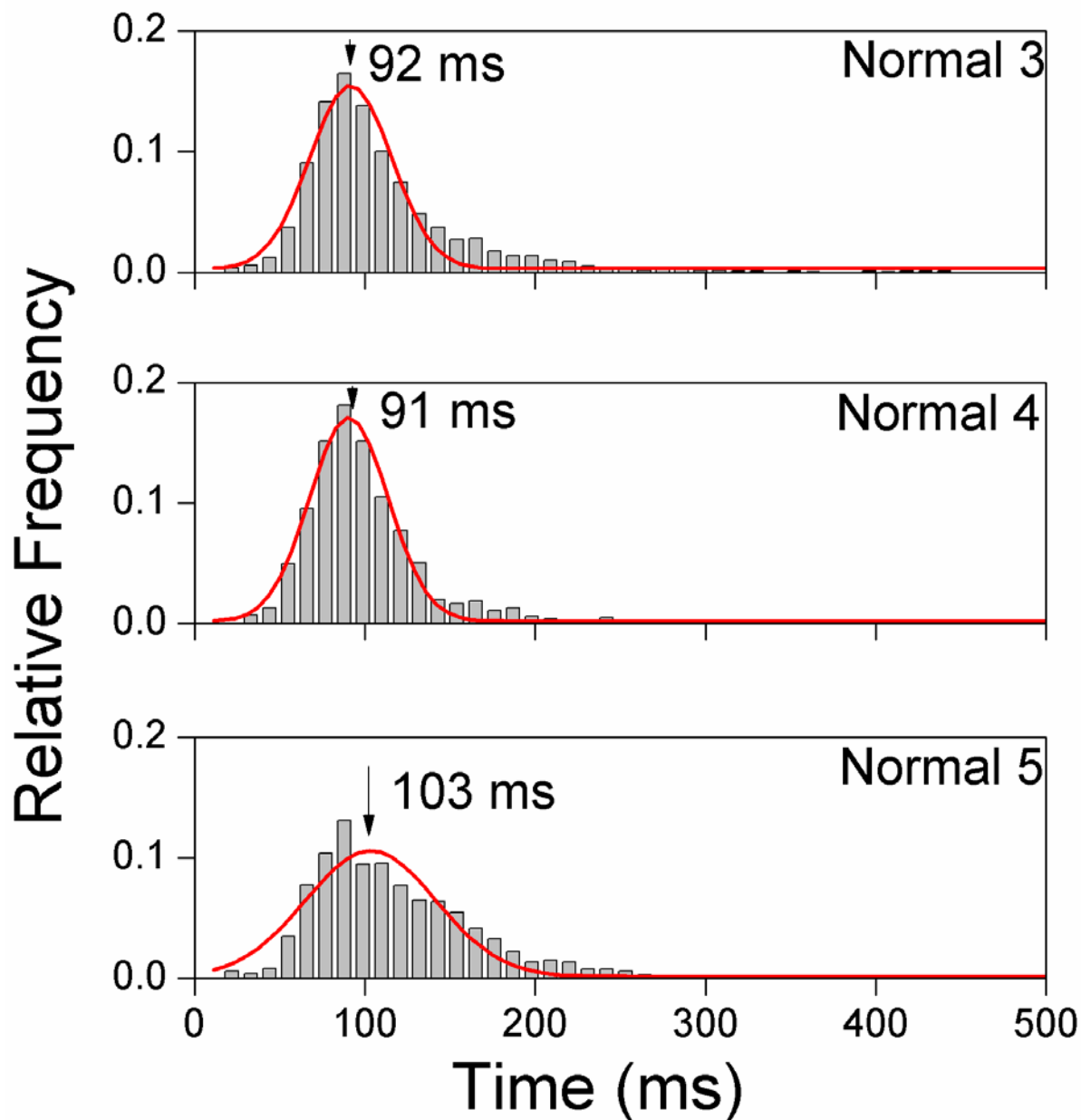
**Figure S2.** The lysis time histograms compiled based on data taken using RBCs from two normal mice. Fitting by a Gaussian (outlined in red) reveals the centroid lysis time. The field intensity for lysis (in the narrow section) was 1200 V/cm. Each histogram consists of data from ~2000-3000 cells.



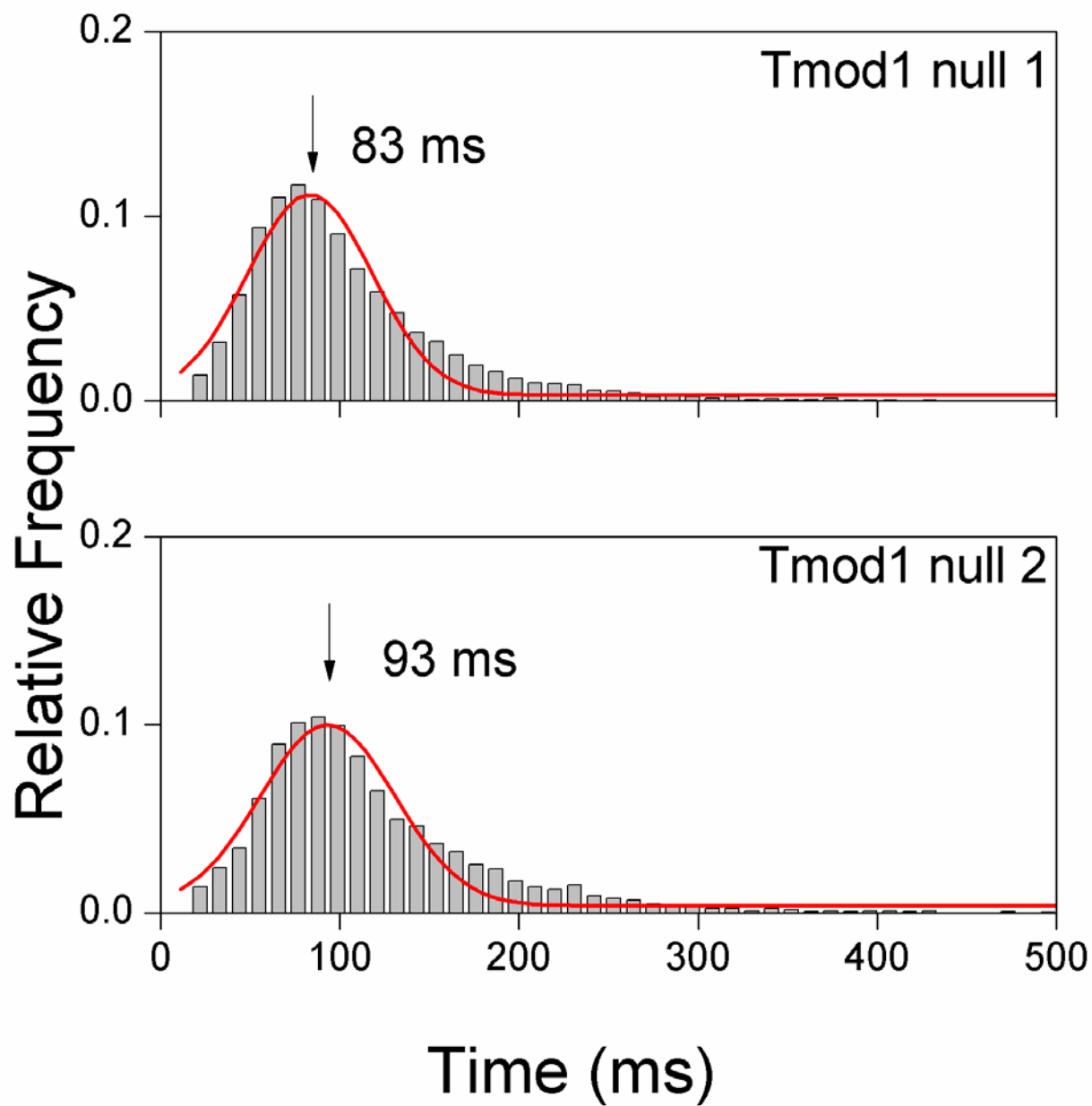
**Figure S3.** The lysis time histogram compiled based on data taken using RBCs from one  $\beta$ -adducin-null mouse. Fitting by a Gaussian (outlined in red) reveals the centroid lysis time. The field intensity for lysis (in the narrow section) was 1200 V/cm. Each histogram consists of data from ~2000-3000 cells.



**Figure S4.** The lysis time histograms compiled based on data taken using RBCs from two nb/nb mice. Fitting by 3 separate Gaussians (with each outlined in blue and the combined outlined in red) reveals the centroid lysis times for various subpopulations. The field intensity for lysis (in the narrow section) was 1200 V/cm. Each histogram consists of data from ~2000-3000 cells.

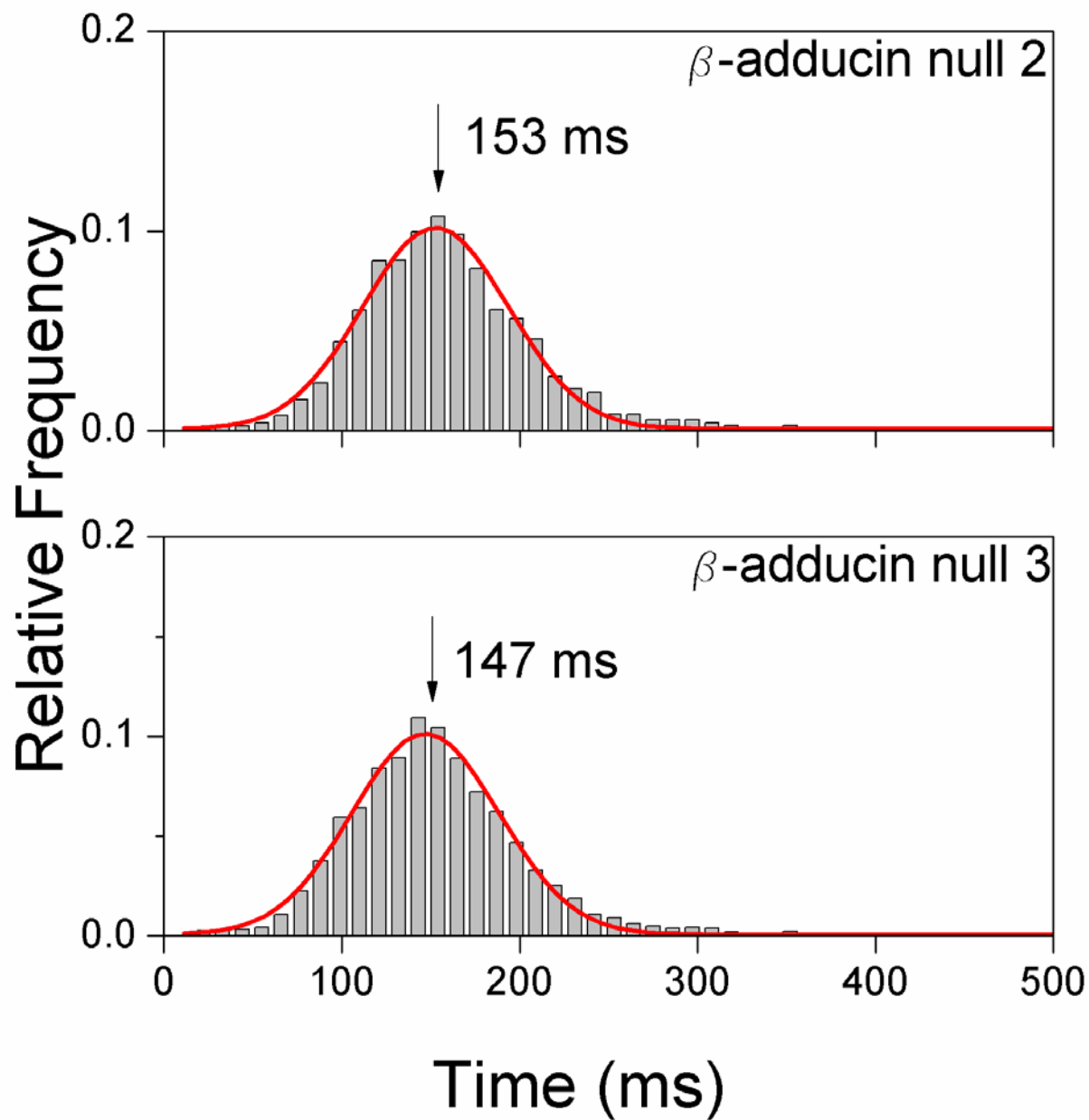


**Figure S5.** The lysis time histograms compiled based on data taken using RBCs from three normal mice. Fitting by a Gaussian (outlined in red) reveals the centroid lysis time. The field intensity for lysis (in the narrow section) was 1100 V/cm. Each histogram consists of data from ~2000-3000 cells.



**Figure S6.** The lysis time histograms compiled based on data taken using RBCs from two Tmod1-null mice. Fitting by a Gaussian (outlined in red) reveals the centroid lysis time. The field intensity for lysis (in the narrow section) was 1100 V/cm. Each histogram consists of data from ~2000-3000 cells.





**Figure S7.** The lysis time histograms compiled based on data taken using RBCs from two  $\beta$ -adducin-null mice. Fitting by a Gaussian (outlined in red) reveals the centroid lysis time. The field intensity for lysis (in the narrow section) was 1100 V/cm. Each histogram consists of data from ~2000-3000 cells.