Supplementary Information

System preparation

A total of five systems were constructed and simulated in this study as listed in Table 2 and Fig. 2:

Sys1: isolated FVIIa in solution (109,137 atoms in total);

Sys2: isolated sTF in solution (65,508 atoms);

Sys3: isolated FVIIa on all-DOPS membrane (178,408 atoms);

Sys4: isolated sTF on all-DOPS membrane (135,838 atoms); and

Sys5: the sTF:FVIIa complex on all-DOPS membrane (185,390 atoms).

All systems were derived from the completed model of the complex of sTF and FVIIa, which is described in full in the "*Modeling of sTF and FVIIa"* section of *Materials and Methods* in the main article. For the solution systems, **Sys1** and **Sys2**, the respective parts, i.e., either TF or FVIIa were extracted from the complex model and simulated in solution. The membrane-associated systems, i.e., **Sys3**, **Sys4**, and **Sys5**, were based on the membrane-bound model of the sTF:FVIIa complex, which was constructed by superposition of the the Cα atoms of the GLA domain (residues 1-46 of chain L) of FVIIa in the sTF:FVIIa complex onto our previously reported model of FVIIa-GLA in an all-DOPS lipid bilayer (Y. Z. Ohkubo and E. Tajkhorshid *Structure* 2008; **16**: 72–81). In **Sys5**

all proteins were kept, whereas in order to generate **Sys3** the TF part was removed, that is, only FVIIa and the membrane were kept. Similarly, **Sys4** was constructed by removing FVIIa from the memrbane-bound complex (**Sys5)**.

All systems were respectively solvated in a water box that provided a minimum padding of 12 Å on each side. The systems were then neutralized by randomly replacing several water molecules in the bulk with Na^+ and Cl^- ions to achieve a final ion concentration of 250 mM.

To remove steric clashes that might have arisen from the modeling phase, the solvated and neutralized systems (**Sys1–Sys5)** were subjected to relaxation cycles composed of energy minimizations and short (10 ps) MD simulations. Initially only the modeled parts (absent from the crystal structure) were allowed to move with the rest of the proteins constrained. During the subsequent cycles of relaxation the constraints were gradually removed until a free and stable simulation system was achieved.

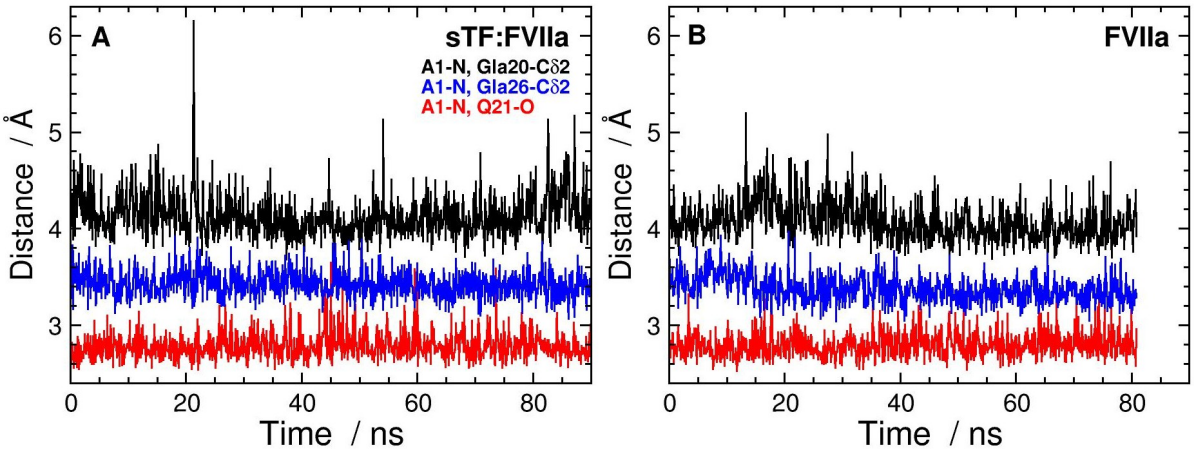

Figure S1. **Distances between the N-terminus of the GLA domain and its main structure**. Distances between N of Ala1 and $C_{\delta 2}$ of Gla20 (black), O of Gln21 (red), and $C_{\delta 2}$ of Gla26 (blue) in the time series are plotted for **(A)** the sTF:FVIIa complex and for **(B)** isolated FVIIa.