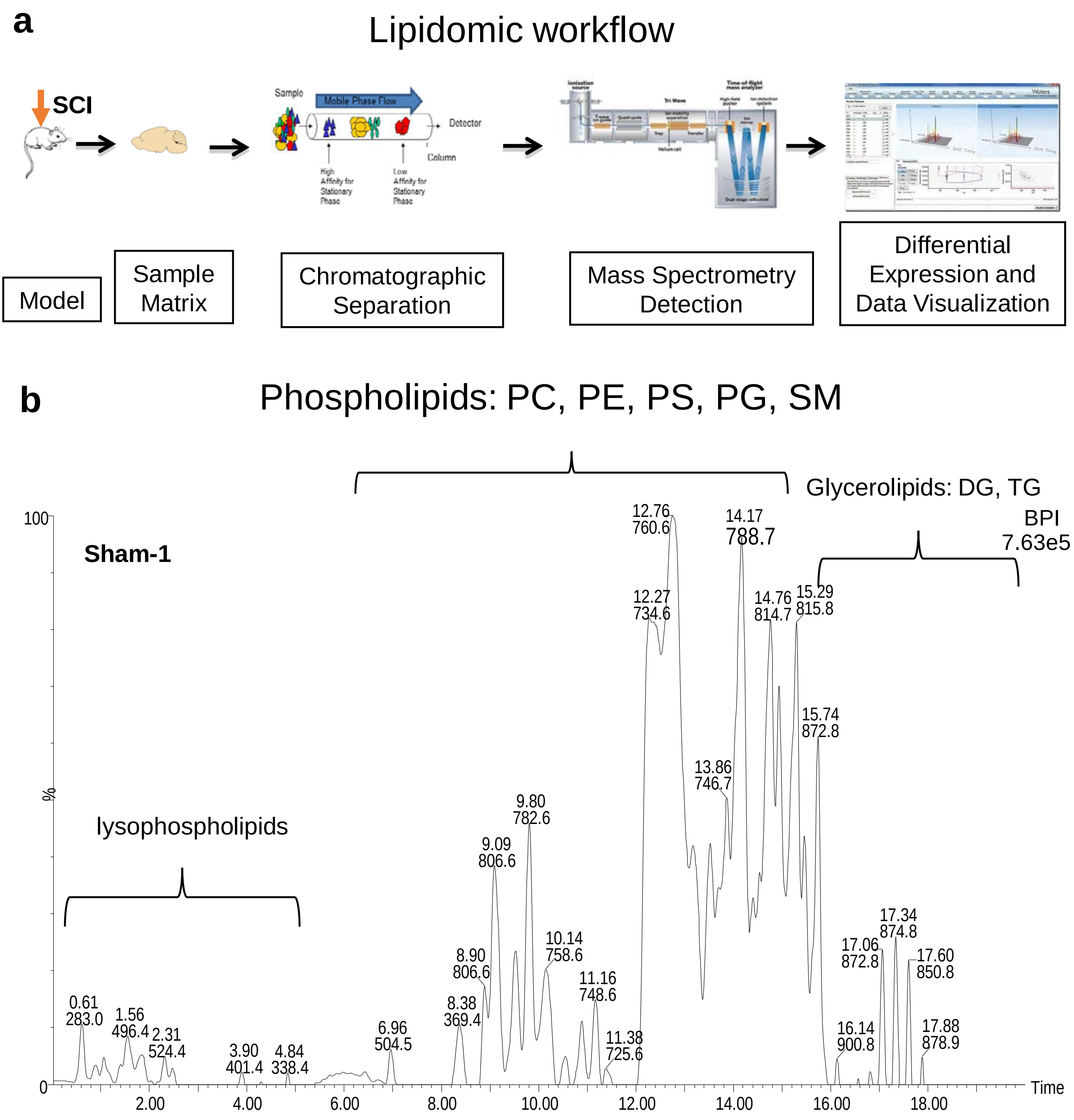

**Supplementary Figure S1.** Lipidomic analysis of lysosomal membranes by LC-MS. Related to Figure 3. (**a**) Lipidomics workflow representing how samples were collected, processed and analyzed to obtain lipid profiles of lysosomal membranes. (**b**) Example UPLC-HDMSE data for identification of LPC (18:0). Base peak ion chromatogram for entire chromatographic run (20 minutes), extracted ion chromatogram for m/z 524.3710, higher-collision energy mass spectrum for m/z 524.3710, and proposed structure for m/z 524.3710 are shown. Identification is based on chromatographic retention, accurate mass precursor ion, and ion mobility aligned tandem mass spectrometry.