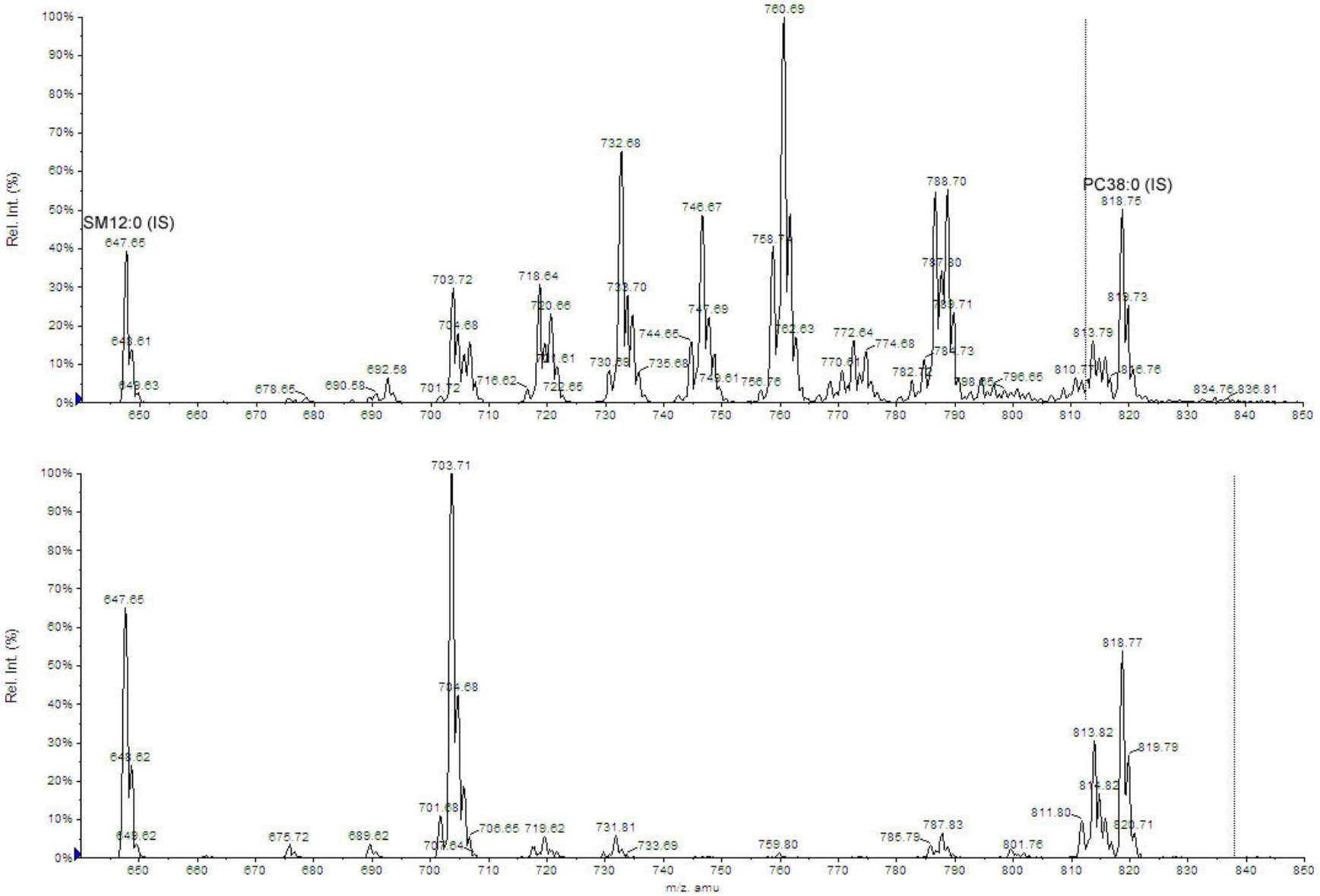
Supplementary Figures

Figure S1. An ESI-MS/MS mass spectrum (positive ion precursor scan of *m/z* 184.15) showing PC and SM detected in lipid extracts from Cav$^{-/-}$ MEFs without (top) and with (bottom) the addition of sodium hydroxide. The even *m/z* ions are PCs and the odd *m/z* ions are SM. PC, phosphatidylcholine; SM sphingomyelin; IS, internal standards

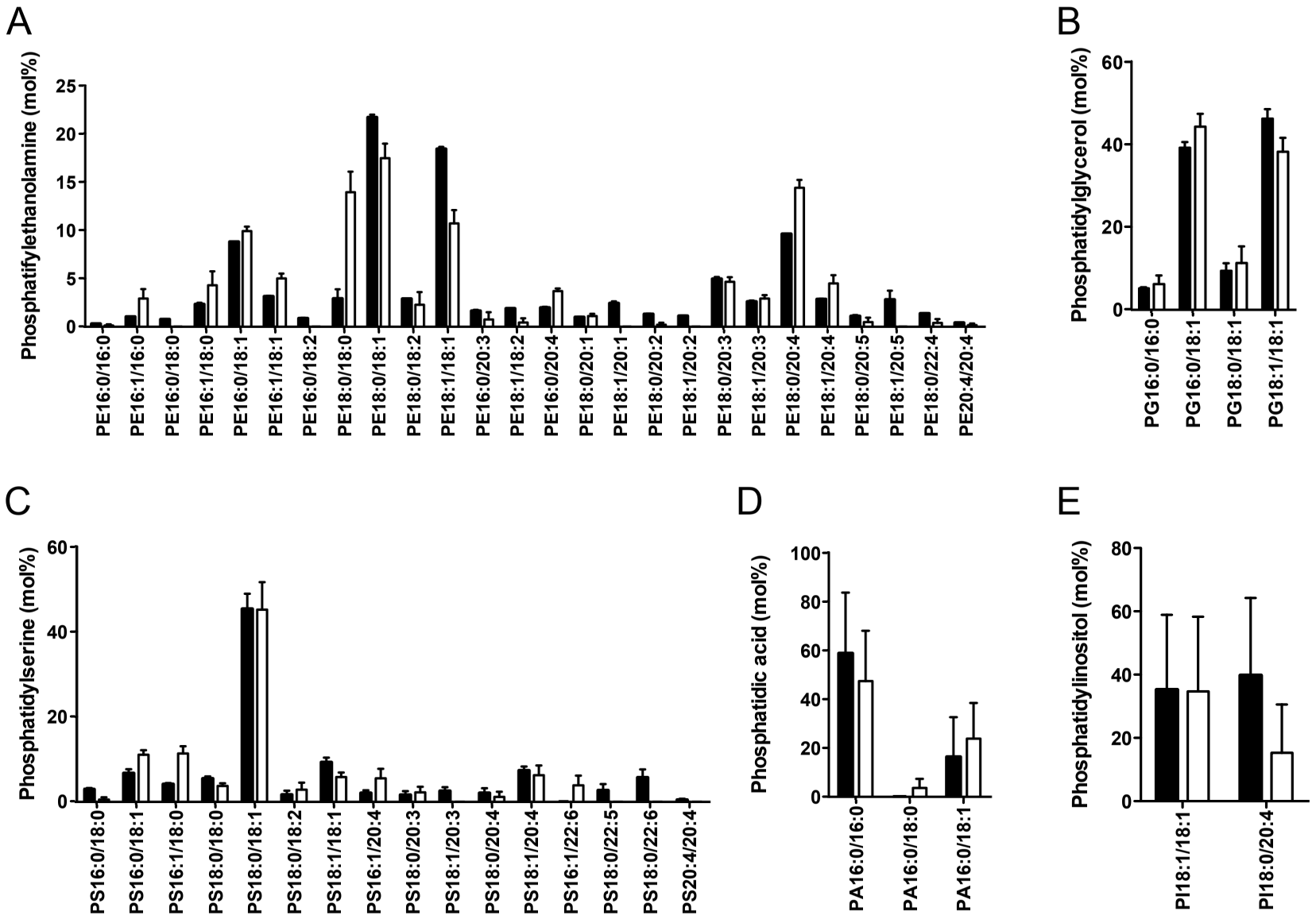
Figure S2. The levels of individual phosphatidylethanonamine (PE, A), phosphatidylglycerol (PG, B), phosphatidylserine (PS, C), phosphatidic acid (PA, D) and phosphatidylinositol (PI, E) in WT (filled bars) and Cav1$^{-/-}$ (hollow bars) MEFs. Data are presented as mean + standard error (n=4).

Figure S3. Protein distribution and lipid contents of DRMs from WT and Cav1$^{-/-}$ MEFs. MEF cell homogenates labeled with [^{14}C]-acetate were extracted with 1% Triton, floated on Optiprep step gradients and eight fractions were collected from the top of the gradients.
A. 20 l of each fraction was analyzed by immunoblotting for marker proteins YES, Cav1 and Cav2.
B. Lipids from DRM fractions were separated by TLC and ^{14}C-cholesterol counted for each fraction. Results are presented as the percentage of ^{14}C-cholesterol present in each fraction. The data show mean ± standard deviation of three independent experiments.

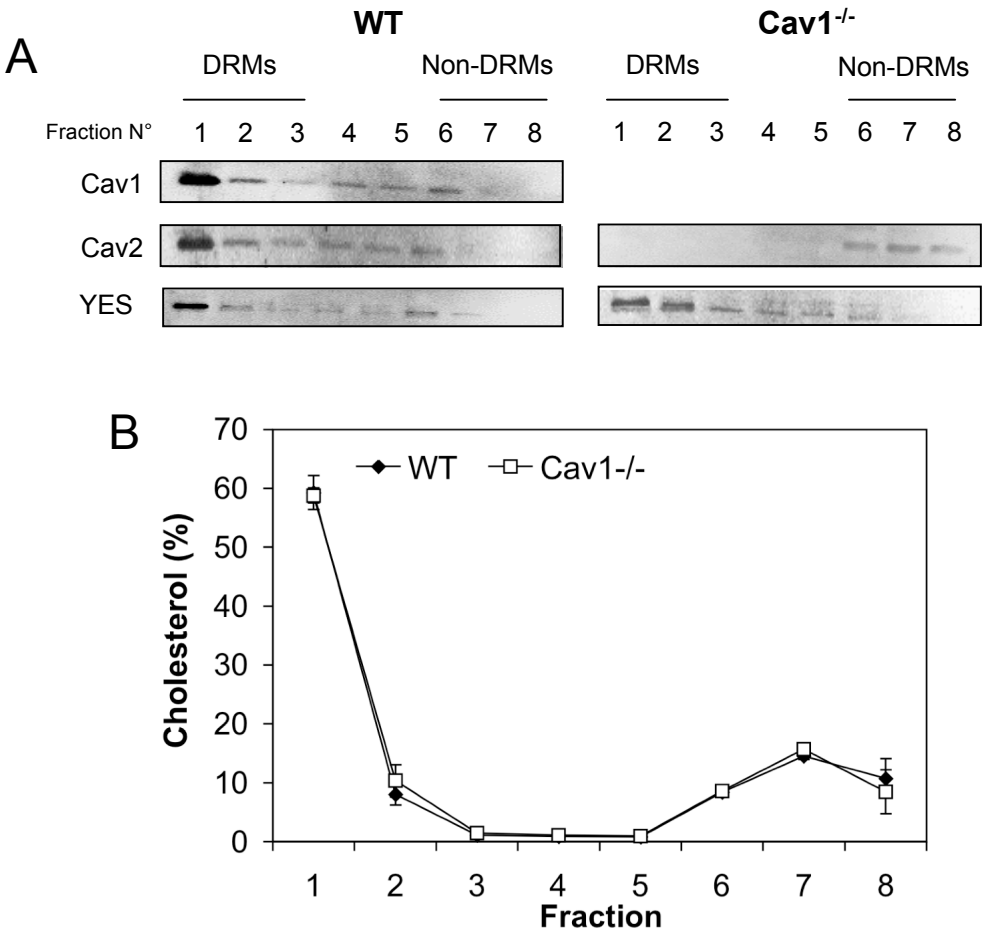
Figure S4. Cholesterol content in NDR and non-raft membranes in WT and Cav1$^{-/-}$ MEFs. Light and heavy membranes were prepared from whole cell homogenate by sonication and separation on a 5-45% sucrose gradient as described in *Methods.* Twelve fractions were collected from the top of the gradient. The distribution of cholesterol across the gradient was determined by fractionating WT (closed diamond) and Cav1$^{-/-}$ MEFs (open squares) with incorporated ^{3}H-cholesterol. The data show mean ± standard deviation of three independent experiments.



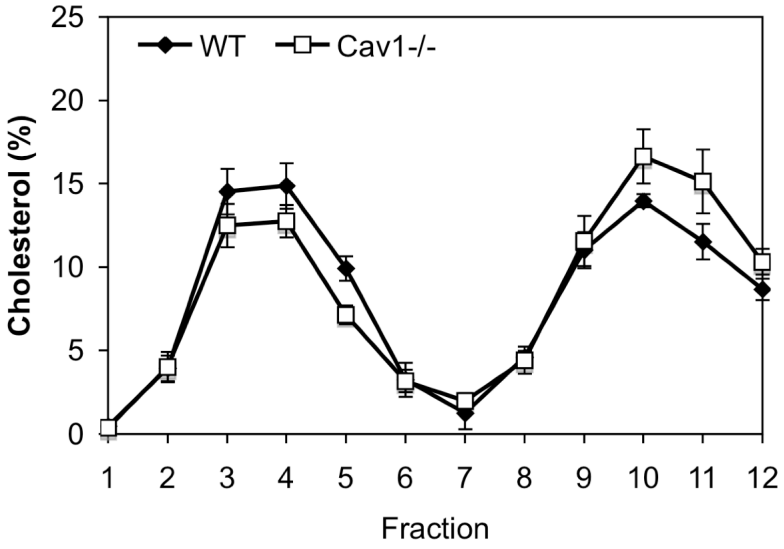
Supplementary Figure 1.



Supplementary Figure S2.



Supplementary Figure S3.



Supplementary Figure S4.