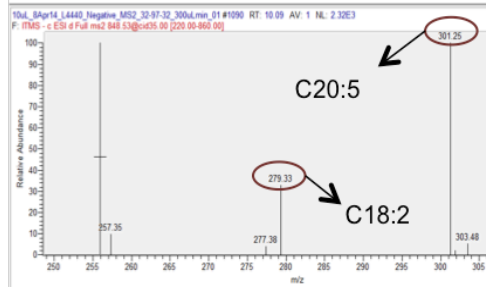
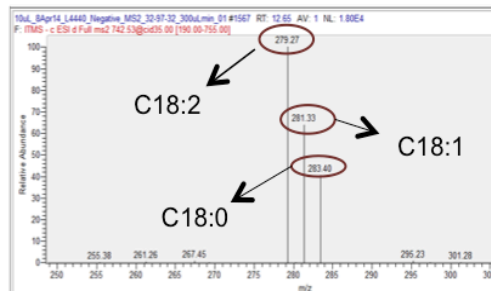


A.



B.



C.

Species	Control RNAi	<i>fat-7</i> RNAi
PtdCho 35:2	(18:2/17:0)60% (18:1/17:1)25% (20:2/15:0)15%	(18:1/17:1)90% (19:1/16:1)10%
PtdCho 36:2	(18:1/18:1)70% (19:1/17:1)30%	(18:1/18:1)70% (18:0/18:2)30%
PtdCho 36:3	(18:2/18:1)70% (20:3/16:0)25% (18:3/18:0)5%	(18:3/18:0)60% (18:2/18:1)30% (20:3/16:0)10%
PtdCho 38:5	(20:4/18:1)70% (20:5/18:0)30%	(20:5/18:0)85% (20:4/18:1)15%
PtdCho 38:6	(20:5/18:1)100%	(20:5/18:1)100%
PtdCho 38:7	(20:5/18:2) 100%	(20:5/18:2)90% (20:4/18:3)10%
PtdCho 40:8	(20:5/20:3)60% (20:4/20:4)40%	(20:5/20:3)65% (20:4/20:4)35%
PtdCho 40:9	(20:5/20:4)100%	(20:5/20:4)100%
PtdEtn 35:2	(18:2/17:0)60% (18:1/17:1)25% (20:2/15:0)15%	(18:1/17:1)90% (19:1/16:1)10%
PtdEtn 36:2	(18:1/18:1)30% (18:2/18:0)70%	(18:1/18:1)40% (18:0/18:2)60%
PtdEtn 37:5	(20:5/17:0)100%	(20:5/17:0)100%
PtdEtn 38:5	(20:5/18:0)100%	(20:5/18:0)100%

S7 Fig. Assessment of Fatty Acid Tail Composition by LC-MS/MS. (A) Mass spectra can be used to identify the fatty acid tails associated with a given phospholipid population using the S2 scan from the LC-MS/MS analysis. For example, phosphatidylcholine (PtdCho) 38:7 shows the mass of two fragments (279.33, 301.25) indicating that the species consists of a C18:2 and a C20:5 fatty acid tail. (B) The MS2 scan of phosphatidylethanolamine (PtdEtn) 36:2 population reveals two different species. Fragment masses 279.27, 281.33, and 283.40 correspond to fatty acid tails C18:2, C18:1, and C18:0. The MS2 scan shows that the PtdEtn 36:2 consists of one molecule with two C18:1 tails and another with C18:0 and C18:2 tails. (C) Table specifying fatty acid tail breakdown estimates for each listed PL species for both control RNAi and *fat-7* RNAi.