Supplemental Table 1. Primers used for the construction of expression vectors.

Name	Direction	Sequence (Restriction site and tag sequence contained)
Pex3p-HA	forward	5'-CGCGGTACCCCACCATGCTGAGGTCTGTATGGAATTTTCTG-3' (*Acc*65I site)
	reverse	5'-CGCGCGGCCGCTCAAGCGTAATCTGGAACATCGTATGGGTATTTCTCCAGTTGCTGAGGGGTACT-3' (*Not*I site, in-frame HA sequence)
Pex16p-V5	forward	5'-CGCGGTACCCCACCATGGAGAAGCTGCGGCTCCTGGGCCTC-3' (*Acc*65I site)
	reverse	5'-CGCGCGGCCGCTCACGTAGAATCGAGACCGAGGAGAGGGTTAGGGATAGGCTTACCGCCCCAACTGTAGAAGTAGATTTT-3' (*Not*I site, in-frame V5 sequence)
Myc-Pex19p	forward	5'-CGCGGATCCCCACCATGGAACAAAAACTCATCTCAGAAGAGGATCTGGCCGCCGCTGAGGAAGGCTGTAG-3' (*Bam*HI site, in-frame Myc sequence)
	reverse	5'-CGCGCGGCCGCTCACATGATCAGACACTGTTCACC-3' (*Not*I site)
HA-Pex19p	forward	5'-CGCGGATCCCCACCATGTACCCATACGATGTTCCAGATTACGCTGCCGCCGCTGAGGAAGGCTGTAG-3' (*Bam*HI site, in-frame HA sequence)
	reverse	5'-CGCGCGGCCGCTCACATGATCAGACACTGTTCACC-3' (*Not*I site)
Myc-Pex11βp	forward	5'-CGCGGTACCCCGCCATGGAACAAAAACTCATCTCAGAAGAGGATCTGGACGCCTGGGTCCGCTTCAGTGCT-3' (*Acc*65I site, in-frame Myc sequence)
	reverse	5'-CGCGCGGCCGCTCAGGGCTTGAGTCGTAGCCAGGG-3' (*Not*I site)
ADHAPS-Myc	forward	5'-CGCAAGCTTGGAAGATGGCGGAGGCGGCG

		GCTGCAG-3' (*Hind*III site)
	reverse	5'-CCGCGGCCGCTTACAGATCCTCTTCTGAGATGAGTTTTTGTTCTAAAAGGTTTCTGTTTCCAAAG-3' (*Not*I site, in-frame Myc sequence)
Thiolase-Myc	forward	5'-CGCAAGCTTGGAAGATGCATCGGCTGCAGGTAGTGCTGGGC-3' (*Hind*III site)
	reverse	5'-CCGCGGCCGCTTACAGATCCTCTTCTGAGATGAGTTTTTGTTCGTTCCCAGGGTATTCAAAGACCGCAGC-3' (*Not*I site, in-frame Myc sequence)
Pex19p-NLS-Myc	forward	5'-CGCCTCGAGATGGCCGCCGCTGAGGAAGGCTGTAG-3' (*Xho*I site)
	reverse	5'-CGCGCGGCCGCCATGATCAGACACTGTTCACCACTGGC-3' (*Not*I site)
Pex3p-EGFP	forward	5'-CGCAGATCTGCCACCATGCTGAGGTCTGTATGGAATT-3' (*Bgl*II site)
	reverse	5'-AAAAGTCGACTTCTCCAGTTGCTGAGGGGTAC-3' (*Sal*I site)
Pex16p-EGFP	forward	5'-CGCAGATCTGCCACCATGGAGAAGCTGCGGCTCCTGGGC-3' (*Bgl*II site)
	reverse	5'-AAAAGTCGACGTAGAATCGAGACCGAGGAGAGG-3' (*Sal*I site)
Citrine-Pex11βp	forward	5'-CGCGGTACCATGGAACAAAAACTCATCTCAGAA-3' (*Acc*65I site)
	reverse	5'-CGCGGATCCTCAGGGCTTGAGTCGTAGCCAGGG-3' (*Bam*HI site)
Citrine-Pex19p	forward	5'-CGCGGTACCATGTACCCATACGATGTTCCAGAT-3' (*Acc*65I site)
	reverse	5'-CGCGGATCCTCACATGATCAGACACTGTTCACC-3' (*Bam*HI site)
PLA/AT-3-FL and PLA/AT-3-C113S-FL	forward	5'-CGCACTAGTGGAAAATGCTAGCACCCATACCAGAAC-3' (*Spe*I site)

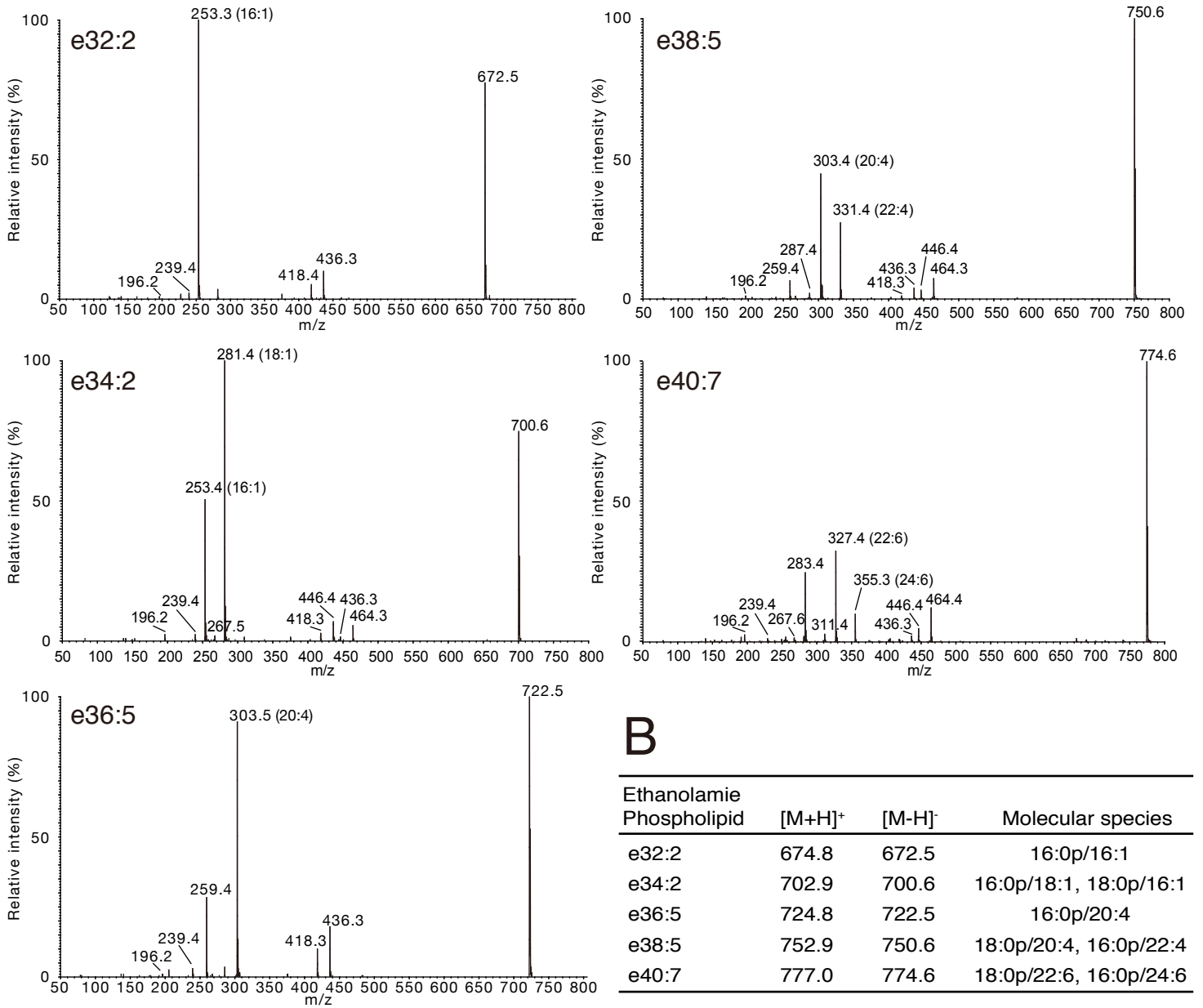|		
	reverse	5'-CGCGCGGCCGCTCACTTATCGTCGTCATCC TTGTAATCTTGCTTCTGTTTCTTGTTTC-3' (*Not*I site, in-frame FLAG sequence)
	forward	5'-CGCACTAGTGGAAAATGGGAGACCTGATT GAGATTTTCC-3' (*Spe*I site)
PLA/AT-3-ΔN10-FL	reverse	5'-CGCGCGGCCGCTCACTTATCGTCGTCATCC TTGTAATCTTGCTTCTGTTTCTTGTTTC-3' (*Not*I site, in-frame FLAG sequence)
	forward	5'-CGCACTAGTGGAAAATGCTAGCACCCATAC CAGAAC-3' (*Spe*I site)
PLA/AT-3-ΔC27-FL	reverse	5'-CGCGCGGCCGCTCACTTATCGTCGTCATCC TTGTAATCCTTGACCGCATCTCTGACCTGATC-3' (*Not*I site, in-frame FLAG sequence)
	forward	5'-CGCACTAGTCCAAGATGGCTTTGGCCAGAC CAAG-3' (*Spe*I site)
PLA/AT-2-FL	reverse	5'-CGCGCGGCCGCCTACTTATCGTCGTCATCC TTGTAATCTTGCCTTTCCCGCTTGCTTCTGG-3' (*Not*I site, in-frame FLAG sequence)

Supplemental Table 2. Primers used for RT-PCR.

Name	Direction	Sequence
PLA/AT-1	forward	5'-CTGCCCAGGGGACTTGATCGAAGTG-3'
	reverse	5'-ACTTGGCGCTTGTAAAGGACGCAGG-3'
PLA/AT-2	forward	5'-GGCTATGCACACTGGGCCATCTACG-3'
	reverse	5'-GTTGGTCAGGGCAGACAGGACACTG-3'
PLA/AT-3	forward	5'-GCTGACCAGCGAGAACTGTGAGCAC-3'
	reverse	5'-CTCCAGCGATGCCTACCGCCTTGAC-3'
PMP70	forward	5'-GTCATTGTCGAAAGGTTGGCATCAC-3'
	reverse	5'-AGTTGCCTCTGCCATCCATATGCAG-3'
catalase	forward	5'-AAGGTTTGGCCTCACAAGGACTACCCTC-3'
	reverse	5'-TAGGCAAAAAGGCGGCCCTGAAGCATTTTG-3'
Pex3p	forward	5'-TCAAGTATTCAGCACCTACTTGGAG-3'
	reverse	5'-TAATCCAAGAAGAAGACTTATGCTGC-3'
Pex11βp	forward	5'-CCTCAATCGAGCCTTGTACTTCGCC-3'
	reverse	5'-GCGAATCTCATAAGCATCACGGCTC-3'
Pex16p	forward	5'-GTGGTGCGAACCCTCCAGAACA-3'
	reverse	5'-CCCAGGCTGAGCAAGTGCAGC-3'
Pex19p	forward	5'-GATCACAGAAAAGTATCCAGAATGG-3'
	reverse	5'-AAGTTGAGGCCAGGAGGCATCTC-3'
GAPDH	forward	5'-CGCTGAGTACGTCGTGGAGTCCACT-3'
	reverse	5'-AGCAGAGGGGGCAGAGATGATGACC-3'

Supplemental Figure. **Determination of molecular species of ether-type ethanolamine phospholipids by product ion scanning.**

A, the product ion spectra of the [M-H]⁻ ions of the major ether-type ethanolamine phospholipids form HEK293 cells are shown. B, molecular species determined by product ion scanning (A) are summarized. The prefix "e" indicates an ether-type phospholipid and the postfix "p" indicates a chain with a vinyl ether linkage.

A

e32:2 — peaks labeled: 253.3 (16:1), 672.5, 196.2, 239.4, 418.4, 436.3

e34:2 — peaks labeled: 281.4 (18:1), 253.4 (16:1), 700.6, 196.2, 239.4, 267.5, 418.3, 446.4, 436.3, 464.3

e36:5 — peaks labeled: 303.5 (20:4), 722.5, 259.4, 196.2, 239.4, 418.3, 436.3

e38:5 — peaks labeled: 750.6, 303.4 (20:4), 331.4 (22:4), 287.4, 259.4, 196.2, 436.3, 418.3, 446.4, 464.3

e40:7 — peaks labeled: 774.6, 327.4 (22:6), 283.4, 355.3 (24:6), 239.4, 267.6, 311.4, 196.2, 446.4, 436.3, 464.4

B

Ethanolamie Phospholipid	[M+H]+	[M-H]-	Molecular species
e32:2	674.8	672.5	16:0p/16:1
e34:2	702.9	700.6	16:0p/18:1, 18:0p/16:1
e36:5	724.8	722.5	16:0p/20:4
e38:5	752.9	750.6	18:0p/20:4, 16:0p/22:4
e40:7	777.0	774.6	18:0p/22:6, 16:0p/24:6

Supplemental Figure. Uyama et al.