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Supplementary Materials for

Phospholipid remodeling is critical for stem cell pluripotency by facilitating mesenchymal-to-epithelial transition

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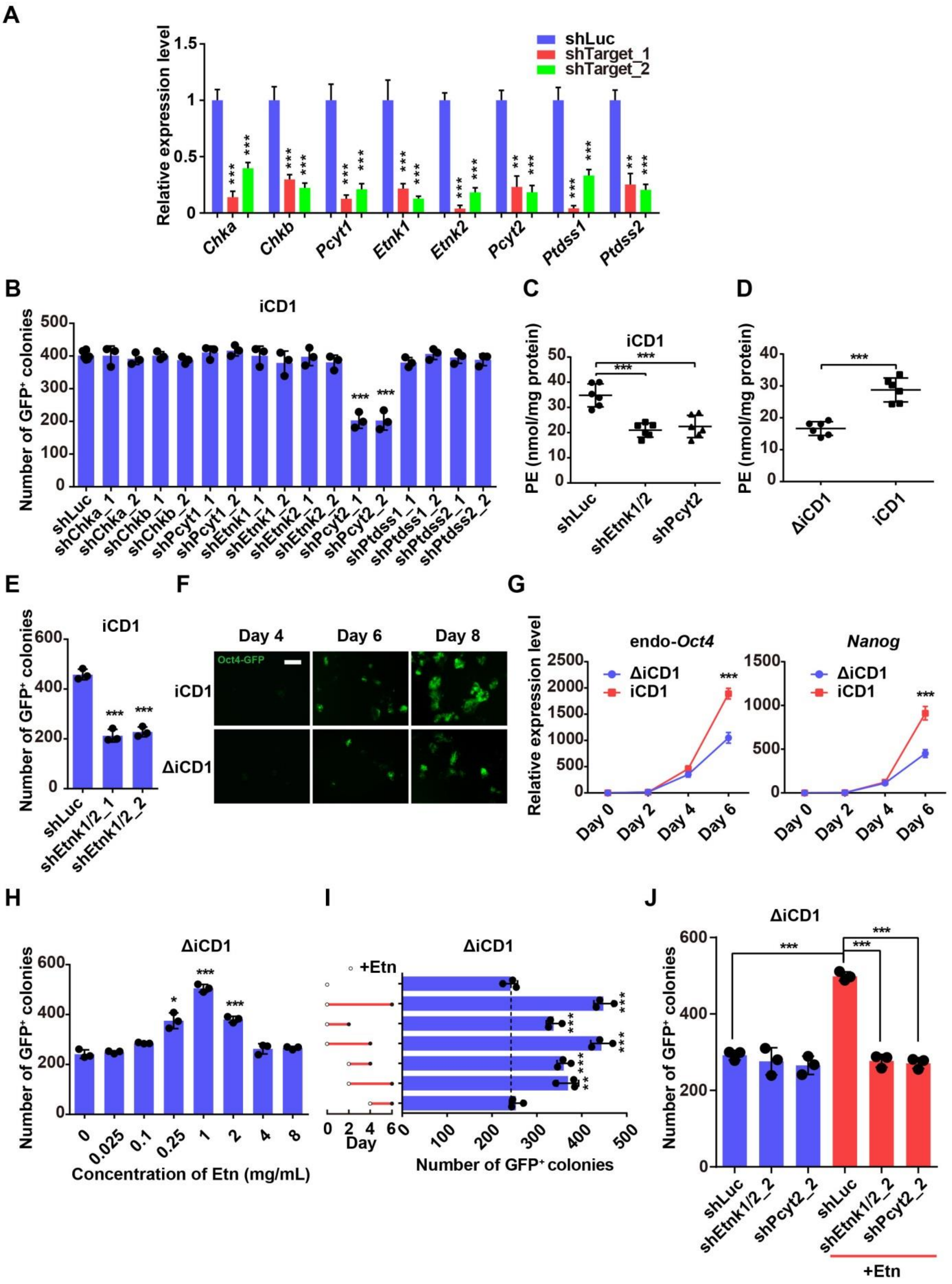
This PDF file includes:

Figure S1



A
Relative expression level
shLuc
shTarget_1
shTarget_2
Chka
Chkb
Pcyt1
Etnk1
Etnk2
Pcyt2
Ptdss1
Ptdss2
B
iCD1
Number of GFP⁺ colonies
shLuc
shChka_1
shChka_2
shChkb_1
shChkb_2
shPcyt1_1
shPcyt1_2
shEtnk1_1
shEtnk1_2
shEtnk2_1
shEtnk2_2
shPcyt2_1
shPcyt2_2
shPtdss1_1
shPtdss1_2
shPtdss2_1
shPtdss2_2
C
iCD1
PE (nmol/mg protein)
shLuc
shEtnk1/2
shPcyt2
D
PE (nmol/mg protein)
ΔiCD1
iCD1
E
iCD1
Number of GFP⁺ colonies
shLuc
shEtnk1/2_1
shEtnk1/2_2
F
Day 4
Day 6
Day 8
Oct4-GFP
iCD1
ΔiCD1
G
endo-Oct4
Nanog
Relative expression level
ΔiCD1
iCD1
Day 0
Day 2
Day 4
Day 6
H
ΔiCD1
Number of GFP⁺ colonies
Concentration of Etn (mg/mL)
0
0.025
0.1
0.25
1
2
4
8
I
ΔiCD1
+Etn
Day
Number of GFP⁺ colonies
J
ΔiCD1
Number of GFP⁺ colonies
shLuc
shEtnk1/2_2
shPcyt2_2
shLuc
shEtnk1/2_2
shPcyt2_2
+Etn

Fig. S1. The CDP-Etn pathway is required for somatic cell reprogramming. (**A**) qRT-PCR analysis of expression of genes encoding rate-limiting enzymes in phospholipid synthesis pathways in MEFs transduced with shRNAs against indicated genes (two shRNAs were used for each gene). Data are represented as mean ± SD, n=3. $^{**}P<0.01$, $^{***}P<0.001$. (**B**) Knocking down *Pcyt2* impaired reprogramming efficiency. The numbers of *Oct4*-GFP$^+$ colonies were counted on day 6 in MEFs transduced with SKO and shRNAs against indicated genes in iCD1 medium (two shRNAs were used for each gene). shRNA against *Luciferase* (shLuc) was used as control. Data are represented as mean ± SD, n=3. $^{***}P<0.001$. (**C** and **D**) Cellular PE levels in MEFs transduced with SKO and shEtnk1/2 or shPcyt2 in iCD1 medium on day 2. shLuc was used as control (C). Cellular PE levels in MEFs transduced with SKO in ΔiCD1 or iCD1 medium on day 2 (D). Data are represented as mean ± SD, n=6. $^{***}P<0.001$. (**E**) Simultaneous knock-down of *Etnk1* and *Etnk2* impaired reprogramming efficiency. The numbers of *Oct4*-GFP$^+$ colonies were counted on day 6 in MEFs transduced with SKO and shRNAs against indicated genes in iCD1 medium (two shRNAs were used for each gene). shLuc was used as control. Data are represented as mean ± SD, n=3. $^{***}P<0.001$. (**F**) Representative Oct4-GFP images of MEFs transduced with SKO inΔiCD1 or iCD1 medium on days 4, 6 and 8. Scale bar, 250 μm. (**G**) qRT-PCR analysis of endogenous pluripotency genes *Oct4* and *Nanog* in MEFs transduced with SKO in ΔiCD1 or iCD1 medium on days 4, 6 and 8. $^{***}P<0.001$. (**H**) Dose-dependent effects of Etn on reprogramming. The numbers of *Oct4*-GFP$^+$ colonies were counted on day 6 in MEFs transduced with SKO in ΔiCD1 medium supplemented with different concentrations of Etn. Data are represented as mean ± SD, n=3. $^{*}P<0.05$, $^{***}P<0.001$. (**I**) Addition of Etn at the early phase of reprogramming was sufficient to achieve optimal reprogramming efficiency. The numbers of *Oct4*-GFP$^+$ colonies were counted on day 6 in MEFs transduced with SKO in ΔiCD1 medium supplemented with Etn during different time frames as indicated. Data are represented as mean ± SD, n=3. $^{**}P<0.01$, $^{***}P<0.001$. (**J**) Etn had no effect on reprogramming when *Etnk1/2* or *Pcyt2* was blocked by shRNAs. The numbers of *Oct4*-GFP$^+$ colonies were counted on day 6. shLuc was used as control. Data are represented as mean ± SD, n=3. ***P<0.001.

Figure S2

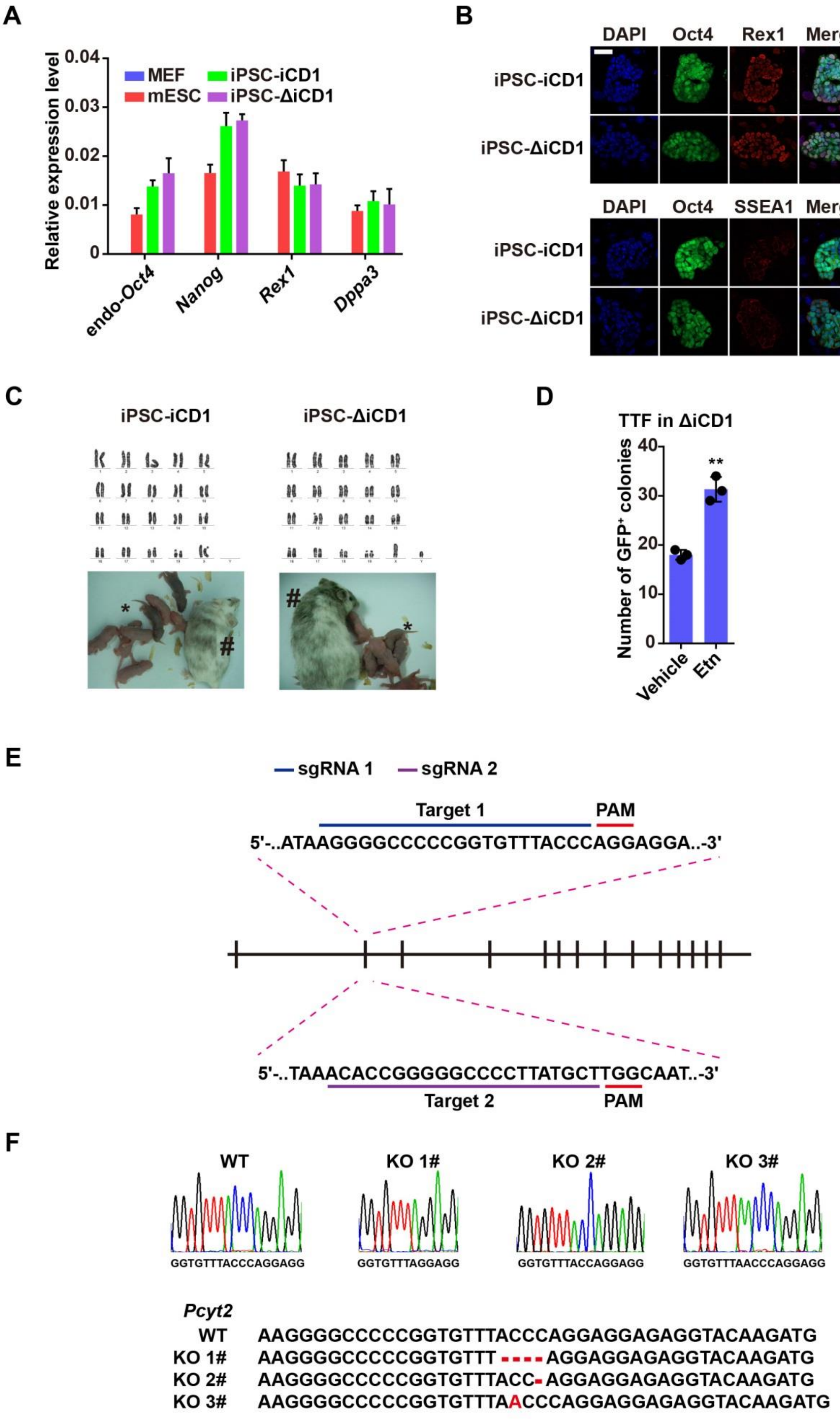

A
Relative expression level
0.04
0.03
0.02
0.01
0
MEF
mESC
iPSC-iCD1
iPSC-ΔiCD1
endo-Oct4
Nanog
Rex1
Dppa3
B
DAPI
Oct4
Rex1
Merge
iPSC-iCD1
iPSC-ΔiCD1
DAPI
Oct4
SSEA1
Merge
iPSC-iCD1
iPSC-ΔiCD1
C
iPSC-iCD1
iPSC-ΔiCD1
*
#
#
*
D
TTF in ΔiCD1
Number of GFP⁺ colonies
40
30
20
10
0
**
Vehicle
Etn
E
sgRNA 1
sgRNA 2
Target 1
PAM
5'-..ATAAGGGGCCCCCGGTGTTTACCCAGGAGGA..-3'
5'-..TAAACACCGGGGGCCCCTTATGCTTGGCAAT..-3'
Target 2
PAM
F
WT
KO 1#
KO 2#
KO 3#
GGTGTTTACCCAGGAGG
GGTGTTTAGGAGG
GGTGTTTACCAGGAGG
GGTGTTTAACCCAGGAGG
Pcyt2
WT AAGGGGCCCCCGGTGTTTACCCAGGAGGAGAGGTACAAGATG
KO 1# AAGGGGCCCCCGGTGTTT----AGGAGGAGAGGTACAAGATG
KO 2# AAGGGGCCCCCGGTGTTTACC-AGGAGGAGAGGTACAAGATG
KO 3# AAGGGGCCCCCGGTGTTTAACCCAGGAGGAGAGGTACAAGATG

Fig. S2. Characterization of iPSCs generated from iCD1 or ΔiCD1 and generation of *Pcyt2* knockout mESCs. (**A**) qRT-PCR analysis of activation of endogenous pluripotency genes. (**B**) Immunofluorescence staining (red) of pluripotency markers (Rex1 and SSEA1) in iPS colonies generated from iCD1 or ΔiCD1. Scale bar, 100 μm. (**C**) Karyotype analysis (up) of iPS colonies generated from iCD1 or ΔiCD1. Germline transmission of chimeric mice (down) generated from iPS colonies generated from iCD1 or ΔiCD1. #: chimeric mice; *: germline transmission mice. (**D**) Supplementation of Etn promoted reprogramming efficiency of mouse tail-tip fibroblasts (TTFs). The numbers of *Oct4*-GFP$^+$ colonies were counted on day 14 in TTFs transduced with SKO with or without Etn. Data are represented as mean ± SD, n=3. **P<0.01. (**E**) Schematic of the two single guide RNAs (sgRNAs, blue and purple bars) designed to target *Pcyt2* loci. Protospacer adjacent motifs (PAM) are indicated by red bars. (**F**) Sequencing results showing three indel mutations in the *Pcyt2* knockout ESCs.

Figure S3

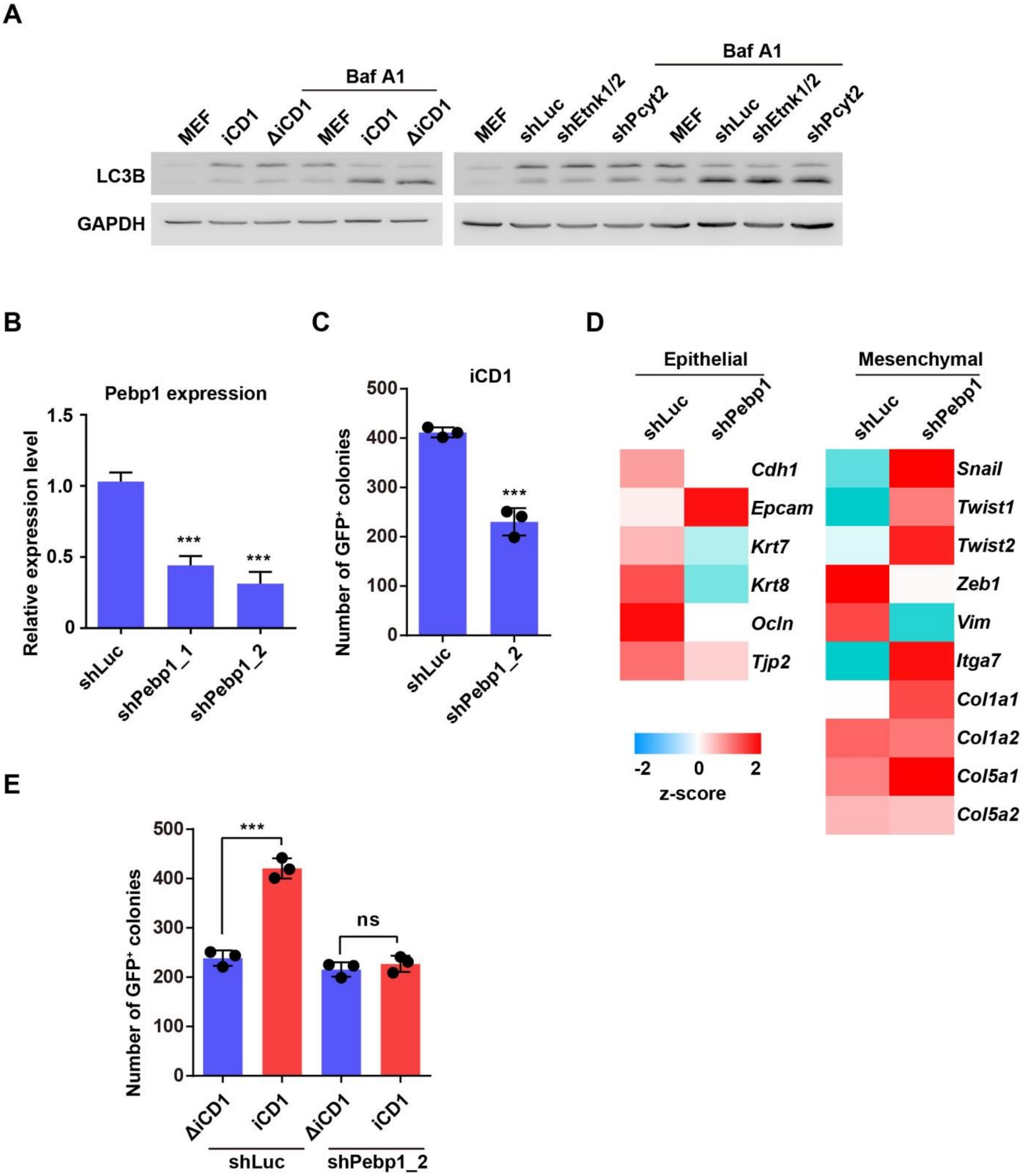

A
Baf A1
MEF
iCD1
ΔiCD1
MEF
iCD1
ΔiCD1
Baf A1
MEF
shLuc
shEtnk1/2
shPcyt2
MEF
shLuc
shEtnk1/2
shPcyt2
LC3B
GAPDH
B
Pebp1 expression
Relative expression level
1.5
1.0
0.5
0
***
***
shLuc
shPebp1_1
shPebp1_2
C
iCD1
Number of GFP⁺ colonies
500
400
300
200
100
0
***
shLuc
shPebp1_2
D
Epithelial
shLuc
shPebp1
Cdh1
Epcam
Krt7
Krt8
Ocln
Tjp2
Mesenchymal
shLuc
shPebp1
Snail
Twist1
Twist2
Zeb1
Vim
Itga7
Col1a1
Col1a2
Col5a1
Col5a2
-2
0
2
z-score
E
Number of GFP⁺ colonies
500
400
300
200
100
0
***
ns
ΔiCD1
iCD1
ΔiCD1
iCD1
shLuc
shPebp1_2

Fig. S3. The CDP-Etn pathway acceleration of MET depends on Pebp1. (**A**) Western blot analysis of LC3B on day 2 in MEFs transduced with SKO in ΔiCD1 or iCD1 medium (left) and in MEFs transduced with SKO and shLuc, shEtnk1/2 or shPcyt2 in iCD1 medium (right) in the absence or presence of bafilomycin A1 (Baf A1). MEFs transfected with empty vector were used as control. (**B**) qRT-PCR analysis of expression of *Pebp1* in MEFs transduced with shRNAs against *Pebp1* (two shRNAs were used, shPebp1_1 or shPebp1_2). Data are represented as mean ± SD, n=3. ***P<0.001. (**C**) *Pebp1* silencing impaired reprogramming efficiency. The numbers of *Oct4*-GFP$^+$ colonies were counted on day 6 in MEFs transduced with SKO and shLuc or shPebp1_2. Data are represented as mean ± SD, n=3. ***P<0.001. (**D**) Heatmaps showing the expression of selected epithelial (left) and mesenchymal (right) genes on day 2 in MEFs transduced with SKO and shLuc or shPebp1 in iCD1 medium.(**E**) The numbers of *Oct4*-GFP$^+$ colonies on day 6 in MEFs transduced with SKO and shLuc or shPebp1_2 in ΔiCD1 or iCD1 medium. Data are represented as mean ± SD, n=3. ***P<0.001. ns: not significant.

Figure S4

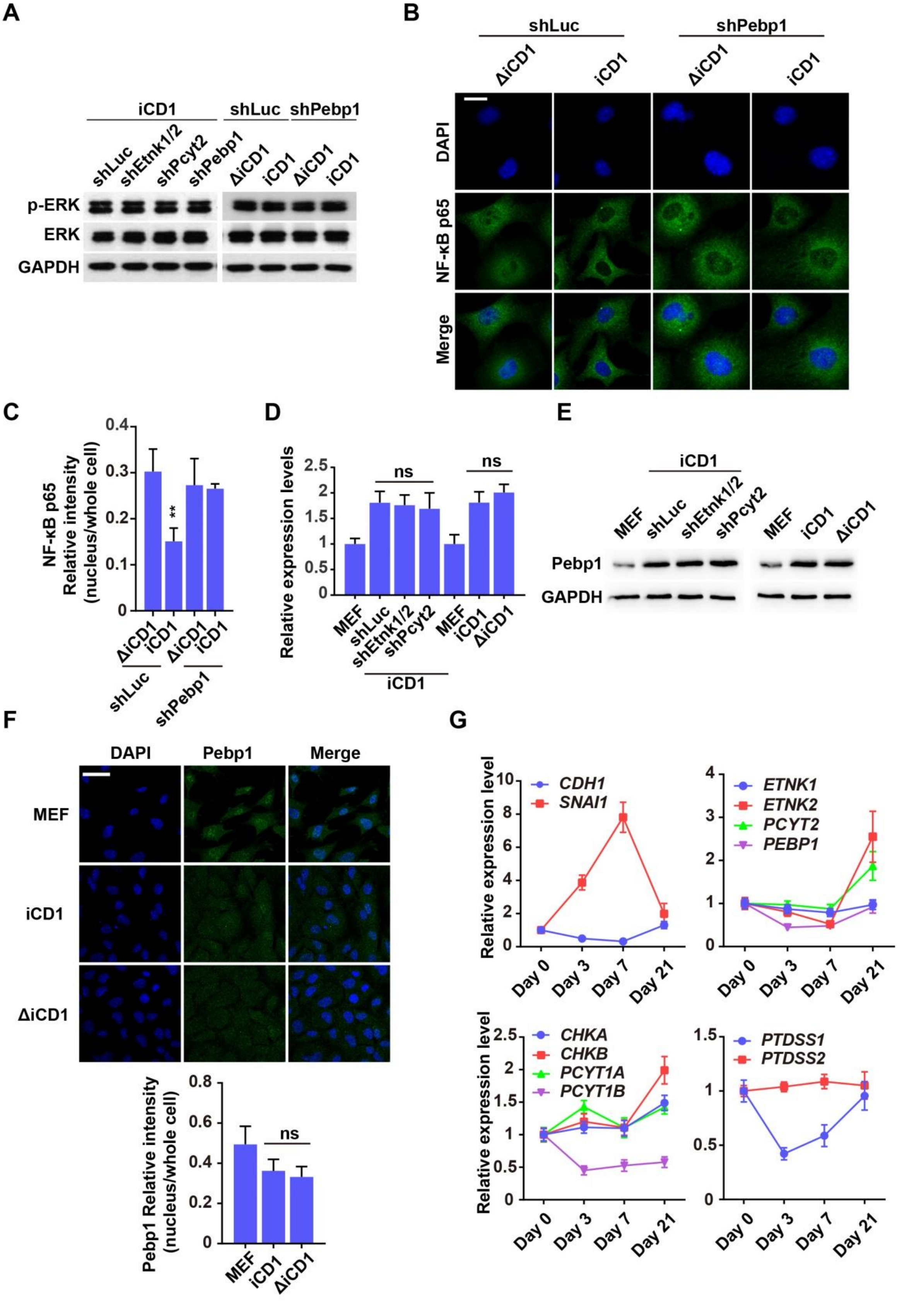

A
iCD1
shLuc
shPebp1
shLuc
shEtnk1/2
shPcyt2
shPebp1
ΔiCD1
iCD1
ΔiCD1
iCD1
p-ERK
ERK
GAPDH
B
shLuc
shPebp1
ΔiCD1
iCD1
ΔiCD1
iCD1
DAPI
NF-κB p65
Merge
C
NF-κB p65 Relative intensity (nucleus/whole cell)
0.4
0.3
0.2
0.1
0
**
ΔiCD1
iCD1
ΔiCD1
iCD1
shLuc
shPebp1
D
Relative expression levels
2.5
2
1.5
1
0.5
0
ns
ns
MEF
shLuc
shEtnk1/2
shPcyt2
MEF
iCD1
ΔiCD1
iCD1
E
iCD1
MEF
shLuc
shEtnk1/2
shPcyt2
MEF
iCD1
ΔiCD1
Pebp1
GAPDH
F
DAPI
Pebp1
Merge
MEF
iCD1
ΔiCD1
Pebp1 Relative intensity (nucleus/whole cell)
0.8
0.6
0.4
0.2
0
ns
MEF
iCD1
ΔiCD1
G
Relative expression level
10
8
6
4
2
0
CDH1
SNAI1
Day 0
Day 3
Day 7
Day 21
4
3
2
1
0
ETNK1
ETNK2
PCYT2
PEBP1
Day 0
Day 3
Day 7
Day 21
Relative expression level
2.5
2
1.5
1
0.5
0
CHKA
CHKB
PCYT1A
PCYT1B
Day 0
Day 3
Day 7
Day 21
1.5
1
0.5
0
PTDSS1
PTDSS2
Day 0
Day 3
Day 7
Day 21

Fig. S4. The CDP-Etn-Pebp1 axis modulates NF-κB signaling to inhibit mesenchymal genes. (**A**) Western blot analysis of Erk and phosphorylated Erk (p-Erk) on day 2 in MEFs transduced with SKO and shLuc, shEtnk1/2, shPcyt2 or shPebp1 in iCD1 medium (left) and in MEFs transduced with SKO and shLuc or shPebp1 in ΔiCD1 or iCD1 medium (right). (**B** and **C**) Immunofluorescence staining (green) of NF-κB P65 on day 2 in MEFs transduced with SKO in ΔiCD1 or iCD1 medium (B). Scale bar, 25 μm. Quantification of relative fluorescence intensity of NF-κB P65 (nucleus/whole cell) on day 2 in MEFs transduced with SKO in ΔiCD1 or iCD1 medium (C). Data are shown as mean ± SD, and acquired from at least 30 cells from 3 independent experiments. (**D** and **E**) qPCR analysis (D) and western blot analysis (E) of Pebp1 expression on day 2 in MEFs transduced with SKO and shLuc, shEtnk1/2 or shPcyt2 in iCD1 medium (left) and in MEFs transduced with SKO in ΔiCD1 or iCD1 medium (right). MEFs transfected with empty vector were used as control. (**F**) Immunofluorescence staining (green) of Pebp1 on day 2 in MEFs transduced with SKO in ΔiCD1 or iCD1 medium (up). Scale bar, 100 μm. Quantification of relative fluorescence intensity of Pebp1 (nucleus/whole cell) on day 2 in MEFs transduced with SKO in ΔiCD1 or iCD1 medium (down). Data are shown as mean ± SD, and acquired from at least 30 cells from 3 independent experiments. (**D**) qRT-PCR analysis of expression of EMT markers (*CDH1* and *SNAI1*), key genes of phospholipids synthesis (*ETNK1*, *ETNK2*, *PCYT2*, *CHKA*, *CHKB*, *PCYT1A*, *PCYT1B*, *PTDSS1*, *PTDSS2*) and *PEBP1* on days 0, 3, 7 and 21 in hepatocyte differentiation. Data are represented as mean ± SEM, n=2.

Table S1. Lipid species identified MEFs, mESCs, and MEFs undergoing SKO reprogramming on days 2, 4, 6, and 8. Lipids are divided into two categories: lipids with successful matching of MS^2 and lipids with no matching of MS^2. To the molecules with successful matching of MS^2, all information of t_R, MS^1 and MS^2 was employed for more accurate characterization of lipids, including the length of structure chain and position of double bond (e.g., PE (22:1/20:4)). To the molecules with no matching of MS^2, the information of t_R and MS^1 was employed to annotate the class of lipids, such as the length of chain and position of double bond (e.g., PE 48:6).

Lipid molecules with successful matching of MS^2

Name	MEF	Day 2	Day 4	Day 6	Day 8	mESC
PE(22:1/20:4)	3919137	8736843	10157376	3556863	2390636	1549751
PE(20:1p/22:6)	14528843	28806459	42561264	22071777	19930756	9228402
PE(20:1/20:4)	17834119	55935834	46486017	15325420	12962004	8289760
PE(20:1/18:1)	58778088	59203663	87759308	69370357	83224468	50115700
PE(20:0p/22:6)	27989655	50601144	60064072	29030353	25348002	19402011
PE(20:0p/22:5)	8846952	16201550	22731057	12339573	11063036	9425591
PE(20:0p/20:5)	1.17E+08	2.05E+08	2.51E+08	1.51E+08	1.34E+08	54807656
PE(20:0p/20:4)	92694926	2.21E+08	3.59E+08	2.69E+08	3.05E+08	69029647
PE(20:0p/18:1)	43874237	91836134	1.57E+08	1.24E+08	1.31E+08	3.21E+08
PE(20:0p/16:0)	1.36E+08	1.44E+08	2.4E+08	2.33E+08	2.73E+08	4.91E+08
PE(20:0/20:4)	17163013	45009428	74254650	25228912	40915196	4892858
PE(20:0/18:1)	15303795	37726651	65884330	52950706	74982404	1.55E+08
PE(18:2p/22:6)	24155788	33889956	37248367	21260825	17793382	528469.3
PE(18:1p/24:6)	2850091	6235141	7490725	3390032	3385144	2678962
PE(18:1p/22:6)	15194790	25028931	26086336	12955501	11109474	893618.8

PE(18:1p/22:5)	3417293	5362454	10220984	9220013	10759638	6837920
PE(18:1p/22:4)	33790738	53203331	81244796	51385275	49443839	12983423
PE(18:1p/22:2)	18097517	37081150	59840362	49559843	55415050	10689067
PE(18:1p/22:1)	12477122	21133360	40085992	40164555	47665276	15988729
PE(18:1p/20:5)	36730716	49494924	59605528	34530482	30442963	728553
PE(18:1p/20:4)	42268634	76113355	88668621	42076474	37454616	20021854
PE(18:1p/20:1)	21073659	33084461	74907618	59536747	64839145	39439072
PE(18:1p/18:2)	1.83E+08	3.71E+08	4.81E+08	2.82E+08	2.58E+08	80442764
PE(18:1p/18:1)	37235407	54645815	95132136	66029437	74981301	61836387
PE(18:1p/16:0)	86871788	1.1E+08	2.13E+08	1.84E+08	2.28E+08	1.51E+08
PE(18:1p/15:0)	17080699	37822021	56925912	33968328	33307959	19611560
PE(18:1p/14:0)	3616143	1739310	3201102	2320482	3194613	1937437
PE(18:1/24:2)	6268398	14096925	22150633	20152830	16324214	2581106
PE(18:1/24:1)	7086618	11402398	15542604	10607822	10300313	4089966
PE(18:1/24:0)	3516775	3976354	4571926	2744775	2267573	3913041
PE(18:1/22:6)	7374209	7822538	39407891	47408943	53296827	9916206
PE(18:1/22:4)	15178482	31966595	38921399	16989392	12549380	1823355
PE(18:1/22:1)	20887633	42464020	73021194	61790927	60895696	45182174
PE(18:1/19:1)	15477681	6326372	6378073	5204297	5952293	2828320
PE(18:1/18:3)	8014412	9909136	10058454	4765649	4866091	6244527
PE(18:1/18:2)	5696619	5564245	9502282	8777127	8797155	8704111
PE(18:1/18:1)	30905207	32543602	52087908	47526653	46074799	19769651
PE(18:0p/24:6)	3870712	8291546	13246113	6225032	6382890	5547880
PE(18:0p/22:6)	5.17E+08	9.5E+08	1.4E+09	8.38E+08	8.84E+08	3.03E+08
PE(18:0p/22:4)	26736709	53736251	63714750	27515648	35691566	29679098

PE(18:0p/22:3)	59821126	1.32E+08	2.65E+08	3.02E+08	3.2E+08	84667990
PE(18:0p/22:1)	4262642	11072634	18462505	13812435	15002058	30008553
PE(18:0p/20:5)	2.12E+09	4.52E+09	7.16E+09	4.23E+09	4.68E+09	9.9E+08
PE(18:0p/20:4)	2.92E+08	9.76E+08	1.29E+09	5.22E+08	9.32E+08	6.7E+08
PE(18:0p/20:3)	51272832	99888747	1.65E+08	1.6E+08	1.63E+08	2.36E+08
PE(18:0p/18:1)	5.59E+08	6.89E+08	1.35E+09	1.26E+09	1.66E+09	3.18E+09
PE(18:0p/16:0)	7943528	9579749	16153291	18512006	16995481	23405715
PE(18:0/22:4)	18249595	39532505	76547078	27748013	27179561	4907377
PE(18:0/22:3)	27511866	75091967	1.3E+08	1.04E+08	1.04E+08	19400482
PE(18:0/21:3)	2104591	4267503	4944360	2959658	2768000	6556682
PE(18:0/20:5)	88501568	1.75E+08	2.14E+08	1.14E+08	90235784	13344412
PE(18:0/20:4)	1.11E+08	1.39E+08	1.91E+08	2.02E+08	2.32E+08	74584202
PE(18:0/20:3)	12755945	19270335	29539771	23946246	26312856	6465905
PE(18:0/20:2)	1.01E+08	2.1E+08	4.06E+08	2.61E+08	3.11E+08	5.42E+08
PE(18:0/18:1)	8114130	12598637	31030857	26143113	25594506	17761077
PE(18:0/16:1)	1.13E+09	1.92E+09	3.17E+09	2.24E+09	2.61E+09	3.35E+09
PE(17:1/20:4)	10728601	14342118	13836576	7469663	4832595	10914107
PE(17:0/20:4)	24485887	39343099	42336782	28456704	23936286	2460001
PE(17:0/19:0)	50259167	1.25E+08	1.96E+08	1.25E+08	1.35E+08	3.57E+08
PE(17:0/17:0)	8681979	9653140	13191987	8347471	9928233	7311010
PE(16:1/18:1)	7.35E+08	9.26E+08	1.84E+09	1.69E+09	2.09E+09	3.78E+08
PE(16:1/16:1)	45894678	39427344	74307835	86259120	1.18E+08	14047568
PE(16:1/14:0)	5776206	5144693	12217595	8852499	9359428	3597973
PE(16:0p/22:4)	3.51E+08	6.88E+08	9.94E+08	5.72E+08	6.77E+08	1.48E+08
PE(16:0p/22:3)	75357078	1.74E+08	1.78E+08	68494297	1.35E+08	1.05E+08

PE(16:0p/22:1)	63959226	78751132	1.68E+08	1.4E+08	2.12E+08	66064297
PE(16:0p/21:3)	12234659	53013177	58245868	36235931	35928098	1333073
PE(16:0p/20:4)	45366774	77005590	96219532	47133840	47119328	20588558
PE(16:0p/20:3)	3E+08	4.73E+08	7.85E+08	5.59E+08	6.3E+08	5.22E+08
PE(16:0p/18:2)	7.63E+08	7.63E+08	1.83E+09	1.76E+09	2.01E+09	1.33E+09
PE(16:0p/18:1)	9790503	11751639	12534568	11990741	12386820	25116331
PE(16:0p/16:0)	4410047	3642109	6612572	7176423	7964239	5554591
PE(16:0/22:6)	2.48E+08	2.4E+08	2.29E+08	1.15E+08	79639508	16498754
PE(16:0/22:5)	51601984	1.74E+08	3.83E+08	3.48E+08	4.8E+08	3.17E+08
PE(16:0/22:1)	21111934	28443903	37238579	24569949	28002767	28814254
PE(16:0/20:5)	66276266	95648580	97923859	36735732	48149153	4741000
PE(16:0/20:4)	55019055	52661463	73123088	56982497	63979493	7445580
PE(16:0/20:3)	99018257	97156123	2.44E+08	2.94E+08	3.19E+08	39011071
PE(16:0/20:1)	60961593	72107774	1.05E+08	53257578	84969355	47449889
PE(16:0/18:1)	35477383	44602944	66978637	47033229	56403562	28538592
PE(16:0/16:1)	3.98E+08	4.37E+08	7.36E+08	6.33E+08	8.82E+08	1.72E+08
PE(16:0/16:0)	38316223	42124833	72046822	63879594	85529875	15606010
PE(16:0/14:0)	18472327	31964397	66469092	50799051	61700768	63760050
PC(19:0/19:0)	19438105	12597157	11694990	20215749	13091335	19956215
PC(26:2/16:0)	3253866	2297150	2147692	2599821	4300262	2879604
PC(26:1/18:1)	11147323	3888439	2133831	2028107	2552979	29762931
PC(26:1/16:1)	51363593	25930561	21492650	24903806	40192834	1.22E+08
PC(24:5/18:1)	897958.5	1689857	1285448	2184584	5936022	7834870
PC(20:1/18:1)	6574952	5686745	4807147	6622628	10503639	37741924
PC(20:0e/16:0)	1199996	859085.3	557631.5	300921.8	603961.8	29517835

PC(19:0/19:0）	10806100	9465531	9132346	9754931	20731168	86593461
PC(18:2/20:4)	8141172	9044582	6594314	4908467	6901260	53473392
PC(18:1p/20:4)	1724482	1356882	735148.6	496029.8	585816.2	5076214
PC(18:1p/20:3)	6834503	12276217	9497213	8032846	12878504	9357384
PC(18:1p/16:1)	3712605	3191529	3042247	3455122	8376093	6054604
PC(18:1p/16:0)	68983165	58807188	67090306	90635942	1.82E+08	4.98E+08
PC(18:1/24:0)	4689382	2168923	1450098	1554740	2480920	4641038
PC(18:1/22:1)	6133919	5373651	5717797	7711639	14331632	3640410
PC(18:1/20:4)	19174615	21731802	13819760	9352125	15327064	11058450
PC(18:1/14:0)	1.88E+09	1.53E+09	1.51E+09	1.96E+09	3.88E+09	5.22E+09
PC(18:0p/22:6)	2744161	3603077	2555972	2243257	3622007	3222357
PC(18:0p/22:5)	1504066	2554833	1658957	1282887	1761353	3595963
PC(18:0p/22:4)	2778083	4665439	3562376	2952911	4916853	1898936
PC(18:0p/18:2)	4314205	4538374	4658229	5091945	8712402	35413229
PC(18:0p/18:1)	1.26E+08	1.27E+08	1.32E+08	1.81E+08	3.25E+08	1.24E+09
PC(18:0p/16:0)-2	8519136	5499800	4176725	6172930	9107249	53288522
PC(18:0p/16:0)	2968429	2040831	2903777	3779525	6821068	6504161
PC(18:0e/20:4)	3381820	3956099	4134239	4336411	7330248	8078507
PC(18:0e/18:1)	48768234	41276773	35985505	43218000	77481776	1.1E+09
PC(18:0/20:3)	5864130	5853932	5363119	5670829	12352331	7607917
PC(18:0/18:0)	6288949	3205987	2569545	3224947	5527820	59568939
PC(18:0/17:0)	2972673	3046749	2344197	3140765	1912796	8192589
PC(18:0/16:0)	1.21E+08	70495266	55160307	67106891	1.17E+08	3.82E+08
PC(17:1/18:3)	5195888	5015818	6153761	7725150	27218499	5059974
PC(17:0/18:1)	13188087	14106420	10954966	13211642	23606228	12241453

PC(16:1/18:1)	2.01E+09	1.92E+09	1.88E+09	2.49E+09	5.15E+09	4.09E+09
PC(16:1/16:1)	7.75E+08	5.93E+08	4.62E+08	7.28E+08	1.25E+09	2.45E+08
PC(16:1/12:0)	7660870	2828219	4092578	7786403	7463590	8962357
PC(16:0e/20:4)	11298388	14062549	10338652	7630153	17647816	16726566
PC(16:0e/20:1)	16168139	16649193	17691758	24465895	43124410	1.69E+08
PC(16:0e/18:1)	4.25E+08	3.24E+08	3.1E+08	3.98E+08	8.05E+08	3.79E+09
PC(16:0e/16:1)	1.33E+08	88854507	88883443	1.13E+08	2.27E+08	1.68E+09
PC(16:0e/16:0)	15355149	10087579	9750080	12990559	26100429	2.04E+08
PC(16:0e/14:0)	19423190	10435220	6362422	7882278	14057282	5.66E+08
PC(16:0/24:1)	29812745	19879349	14085333	16765260	23089752	1.03E+08
PC(16:0/24:0)	3141972	1320582	763613.2	732657.8	1153267	14284556
PC(16:0/22:4)	42430106	38739241	43406404	48530288	92616707	59522784
PC(16:0/22:1)	66794603	62360246	58130958	65886055	1.44E+08	5.6E+08
PC(16:0/21:1)	12217167	12379638	9166616	8604409	14047553	18212500
PC(16:0/20:4)	10407287	9215015	6312671	7841796	21982810	13718829
PC(16:0/20:1)	18909526	20364774	30148073	24945711	48416994	63461648
PC(16:0/18:1)	1.25E+08	1.36E+08	1.25E+08	1.42E+08	2.43E+08	1.27E+08
PC(16:0/17:1)	8584299	9547260	11276540	10988865	26272963	29218795
PC(16:0/17:0)	16064375	17656130	15571081	18471311	32055966	13485803
PC(16:0/16:1)	69122755	61119171	60785055	69972978	1.29E+08	47674227
PC(16:0/16:0)	23837857	21076839	18282889	21001501	34751541	67322082
PC(16:0/14:0)	18742578	15799582	12565565	15196578	24756488	29208091
PC(14:0/18:3)	7542069	5564499	6035955	6651722	16664792	1916359
PC(12:0/18:2)	51695324	32707262	36019737	48559371	98683187	2900663
TG(15:0/15:0/15:0)	12627677	18969949	14797720	17178152	17173782	79457311

PS(20:3/22:6)	7810553	4987188	6366211	9137733	11052272	67871.82
PS(20:3/20:4)	1319801	2106517	2227553	1603449	1364365	1969960
PS(20:1/18:1)	1438391	802963.7	1590354	1440729	296123.7	5156059
PS(19:1/22:5)	2969365	2986587	2091091	920643.4	465735.6	121459.9
PS(18:1/24:1)	20380397	21072113	21540839	24103213	24634982	707581.5
PS(18:1/22:5)	6682605	6772121	8841743	2988531	1803951	10698093
PS(18:1/22:2)	88301973	1.17E+08	78166262	63498561	50198985	4184798
PS(18:1/22:1)	2.97E+08	2.97E+08	2.22E+08	2.11E+08	2.42E+08	47214590
PS(18:1/19:1)	77419084	1.44E+08	2.04E+08	3.08E+08	3.25E+08	8016935
PS(18:1/18:1)	4202587	3794347	3120679	1291103	978670.2	8633308
PS(18:0/22:5)	4476424	4934100	5784692	2594395	1562031	17823432
PS(18:0/20:4)	7743049	3048386	2427717	2577413	602163.4	1509666
PS(18:0/20:1)	7077040	6563098	6959273	7188183	9658870	246507
PS(18:0/19:1)	1.03E+08	1.55E+08	1.7E+08	1.52E+08	2.88E+08	58662390
PS(18:0/18:1)	25830717	19121207	24365225	28388863	46599499	2800485
PS(18:0/16:1)	13391697	11974322	6943554	4745315	3788350	7283276
PS(17:1/18:1)	7939960	9192164	9680138	8652459	8944725	2564433
PS(17:0/20:4)	3681682	5224659	5610956	5469917	5039970	673680.8
PS(17:0/18:1)	6324557	6361685	12310326	29861208	21908634	64508501
PS(16:1/18:1)	5243427	2061939	3384277	4428354	2052460	4239936
PS(16:0/20:2)	24288871	20546428	12113915	24009568	23007500	168457.1
PS(16:0/17:1)	36268166	21799443	27747362	28919018	27932143	10013433
PI(19:0/20:4)	3872509	4270281	3382973	5739657	4790474	3445968
PI(18:1/22:2)	1456298	1042056	862029.6	850214.9	734592.4	2197913
PI(18:1/18:2)	4707917	4070233	3122088	3321015	2562634	461904.1

PI(18:0/20:4)	3828041	2052676	1510208	330999	544105.1	3124339
PI(18:0/20:3)	13371668	13559340	9361254	3365750	2655301	5932684
PI(18:0/18:2)	65782464	37763192	51729958	19999128	15085380	2.72E+08
PI(18:0/18:1)	9714901	5964069	7694821	2810483	2124074	39954187
PI(17:1/18:1)	1408218	719626.2	1353994	1103480	545982.6	312486.3
PI(17:0/18:1)	1860851	1349728	1394288	847357.8	515524.5	79764.15
PI(16:1/18:1)	19425765	11431550	11658898	7532332	5899753	17526009
PI(16:1/17:0)	13747233	12304312	10026708	7508384	6858570	1025428
PI(16:0/18:1)	13423741	9795613	9849705	5570997	3193812	29721365
PI(16:0/16:1)	5119663	4131053	4963437	2238288	1919297	2710092
PG(20:2/22:6)	50315235	56595698	36148793	29048481	19922380	4834857
PG(20:2/22:5)	5322584	4331978	3122283	1008201	1310431	378228.8
PG(18:2/18:2)	4021682	2656224	4457394	3871994	5382463	656410.1
PG(18:1/22:4)	50724309	35571376	22753643	18719997	15517762	337842.4
PG(18:1/20:4)	3.17E+08	2.08E+08	1.49E+08	1.56E+08	1.34E+08	1312868
PG(18:1/20:3)	89688943	69688695	76850781	1.16E+08	1.16E+08	5023671
PG(18:1/20:2)	29700860	19521322	25691828	18648761	30764079	1261950
PG(18:1/18:3)	21451220	8380041	12084970	22951156	12770387	624537.7
PG(18:1/18:2)	2.3E+09	1.11E+09	1.21E+09	1.67E+09	1.98E+09	9887178
PG(18:1/18:1)	1.44E+09	1.58E+09	2.27E+09	2.35E+09	2.75E+09	5E+08
PG(18:1/14:0)	95075975	27012394	26015820	19395890	23694259	10670771
PG(18:0/18:1)	3.51E+08	2.35E+08	2.6E+08	2.62E+08	2.68E+08	2.3E+08
PG(18:0/16:0)	2128979	1494810	1544453	1551970	1159146	3451328
PG(17:1/18:1)	64350995	36126779	40467465	29278836	56049391	482085.2
PG(16:1/22:6)	8750071	6753150	4216879	4331048	3503844	145401.9

PG(16:1/18:2)	13321792	12569316	11878207	14327809	28040020	248255.2
PG(16:1/18:1)	54969256	38293271	47639343	46163918	49413513	16768369
PG(16:0/18:1)	94240561	61852514	87475898	1.26E+08	1.62E+08	2589452
PG(16:0/16:0)	2792714	2331873	2538416	2078257	1677610	7026914

Lipid molecules with no matching of MS^2

Name	**MEF**	**Day 2**	**Day 4**	**Day 6**	**Day 8**	**mESC**
PE O-45:1	5158339	12327585	21624031	22903130	15055618	6693326
PE O-42:7-2	1525056	3518864	4815956	2445144	2042380	13623941
PE O-42:7-1	1943471	3036053	6221959	4631096	3605214	24277963
PE O-42:3	3.19E+08	4.79E+08	6.22E+08	5.28E+08	2.65E+08	18385977
PE O-42:2	2.59E+09	4.56E+09	5.98E+09	4.65E+09	3.25E+09	3.57E+09
PE O-42:1-3	92103881	1.92E+08	1.92E+08	1.2E+08	57894642	2.96E+08
PE O-41:3	12123435	20197201	27485182	27202768	24798239	80871096
PE O-40:9	2367957	4665009	9102095	4295200	2216412	17236096
PE O-40:8-1	3849264	4955111	8011401	11438101	6964743	27184857
PE O-40:7-2	43895261	69202703	70352851	53798801	32509350	1.92E+08
PE O-40:6-7	11464673	20082915	25689610	13230008	9361424	13830601
PE O-40:6-6	3888296	6259681	8640037	4574604	2983321	35728284
PE O-40:4	4187961	16913626	21067647	15470926	9092872	10399621
PE O-40:3	34508356	34158948	22725837	10066741	7503666	1.61E+08
PE O-40:2-1	9747800	12757799	16562141	18445596	12831175	13197529
PE O-40:2	1423974	4692452	3893263	3428154	2234238	11119420
PE O-40:1	2770898	6525579	6898615	6157703	8215555	10982120
PE O-39:3-1	28792033	48499048	47662305	27098055	20883472	1.28E+08

PE O-39:2-1	36411790	33616457	77950947	45195808	43002005	3.31E+08
PE O-38:7-1	746879.3	1790444	2837354	1929721	1545265	12240558
PE O-38:6-2	9173616	24270061	27218089	13480989	7651420	36389548
PE O-38:6	2200882	7733127	10695960	7551283	3400019	25831636
PE O-38:5-2	821448.4	2857125	5548772	2863018	2630844	3781309
PE O-38:4-1	18808460	25941726	43533584	27824305	15758386	25568128
PE O-38:4	2075490	10704289	20054355	12778919	10674409	16846795
PE O-38:3-2	16292508	36859940	51778160	50459135	28339540	61779587
PE O-37:4	35379210	43575850	64732527	40622214	34366288	3.02E+08
PE O-37:3-1	10072894	9774739	10033116	6494759	5237227	2.32E+08
PE O-37:2	46508029	52378927	1.29E+08	1.32E+08	1.2E+08	5.17E+08
PE O-37:1-1	3340043	5492705	8754440	7786810	6965063	11688563
PE O-37:1	46178725	56280807	1.35E+08	89058591	82879694	2.99E+08
PE O-37:0	68902401	55153822	48270929	40473415	19676401	1.78E+09
PE O-36:5-1	8104618	15267070	22455989	11976582	12187887	25638947
PE O-36:4-1	17987986	1.01E+08	1.26E+08	45598518	35444560	55008684
PE O-36:4	45388678	1.04E+08	1.45E+08	1.19E+08	85430581	2.51E+08
PE O-36:3-2	12434439	38047048	45867948	41855347	50278592	1.23E+08
PE O-36:3-1	8813790	14709021	21469500	27581082	22122818	56344925
PE O-36:3	3035780	6873231	11191089	10271550	6344537	19124686
PE O-36:2-2	1.69E+08	1.89E+08	3.46E+08	3.11E+08	1.98E+08	7.31E+08
PE O-36:1-1	9681386	8156752	13937266	7994519	10612821	45839856
PE O-36:1	8570096	28344927	29101509	21306176	7854340	40209414
PE O-36:0	10263949	9749479	8293636	5568931	2178469	39585465
PE O-35:4-1	1845633	2182894	3361727	3043995	2137080	9249886

PE O-35:3-1	4623550	5622272	5403932	4240077	2262286	1.14E+08
PE O-35:2-2	11010419	22006214	31216593	17618113	11410607	49689249
PE O-35:2	1.59E+08	1.03E+08	1.42E+08	89567083	1.11E+08	46054482
PE O-35:1-1	1.88E+08	1.69E+08	1.86E+08	1.45E+08	1.05E+08	3.75E+08
PE O-35:1	1.39E+08	1.62E+08	2.73E+08	1.93E+08	1.48E+08	1.25E+09
PE O-35:0	5.98E+08	4.11E+08	3.49E+08	2.85E+08	1.5E+08	5.82E+09
PE O-34:2-1	5093659	12868284	24139976	23142971	16517026	1.19E+08
PE O-34:2	2520105	5139904	7069896	6764692	3601643	23896889
PE O-34:1-1	1.17E+08	1.33E+08	2.11E+08	1.47E+08	96759634	7.55E+08
PE O-34:1	11087145	6833756	5616821	2489684	1621207	3364729
PE O-34:0	9247217	17015608	13580548	7927150	4106050	65860152
PE O-33:2-4	9735362	23023128	27448535	14260160	9279448	21031451
PE O-33:1	33492760	28348100	32095423	17997616	18162863	1.06E+08
PE O-33:0	1.99E+08	1.61E+08	1.42E+08	1.02E+08	55434908	2.34E+09
PE O-32:4	3951971	6089875	10809286	5693106	3213753	37861816
PE O-32:0	16162481	15194565	8704625	4593198	1622503	75664385
PE O-31:0	28085954	18783409	14381215	8647533	3257548	1.7E+08
PE O-27:0	43555091	32924251	30982783	24310820	12290387	27047759
PE 48:6	1393364	4142959	5239641	4020203	2713398	23897068
PE 44:9	1349977	2404159	3818624	3920989	1675544	3288138
PE 44:1	1605127	1414123	1994147	1852821	981094	3486692
PE 43:6	1.67E+08	3.35E+08	3.37E+08	1.12E+08	52796252	31178738
PE 43:5	31462092	1.72E+08	1.43E+08	49750165	21689600	14341876
PE 43:4-1	1.5E+08	3.08E+08	4.21E+08	2.43E+08	1.45E+08	35376007
PE 42:9	24718460	38535664	60264511	33549009	19261069	8517503

PE 42:8	5651376	12925997	25012540	25572418	18539719	34074081
PE 42:7	1375463	2732350	12675688	25142512	13189636	12853652
PE 42:5	3374491	15831501	7286619	2839106	551330	7893112
PE 42:4	12018874	34898366	48516571	22771168	15397771	1.18E+08
PE 42:3	11475206	25335474	35255625	21896687	8884556	49554832
PE 41:7	35879841	68217665	73233665	30582780	8789182	15378187
PE 41:6	44254132	85037611	1.31E+08	73748134	64309257	56304083
PE 41:5	48621883	1.57E+08	1.7E+08	2.26E+08	2.21E+08	1.38E+09
PE 41:4	4.36E+08	1.17E+09	1.33E+09	4.26E+08	3.03E+08	2.58E+08
PE 41:3	1.97E+08	3.67E+08	5.17E+08	4.56E+08	3.05E+08	1.47E+08
PE 41:2	2.31E+08	1.55E+08	2.32E+08	1.39E+08	1.01E+08	1.11E+09
PE 41:1	2.4E+08	2.45E+08	2.89E+08	2.95E+08	2.51E+08	6.25E+09
PE 40:7	1222887	1131833	3215426	2828896	409622.9	14691892
PE 40:6-2	82766565	2.39E+08	2.47E+08	1.13E+08	49455052	59125188
PE 40:5	16656542	43859189	51764058	28509829	22023010	35285331
PE 40:4-2	22019305	57316219	63185784	41560295	19143879	39648902
PE 40:4-1	17150263	35535592	74607310	26827517	16384563	23745346
PE 40:3	6853449	36943189	52667644	26426496	14204018	35010897
PE 40:2	1.62E+08	2.97E+08	3.19E+08	2.08E+08	99501412	1.61E+08
PE 40:1	32117080	63563220	80976917	42819208	19534147	39692769
PE 39:6	16057313	20522652	27347596	22243284	17407787	13276687
PE 39:5-1	1.13E+08	4.35E+08	6.1E+08	3.38E+08	1.81E+08	6.21E+08
PE 39:4-1	76326432	1.54E+08	1.52E+08	1.42E+08	1.45E+08	2.35E+09
PE 39:3	3.04E+08	5.6E+08	9.22E+08	6.34E+08	4.55E+08	88458764
PE 39:2	4846483	6716933	13877411	12233010	8050391	51229679

PE 39:1	3.43E+08	4.42E+08	5.59E+08	4.47E+08	3.38E+08	6.27E+08
PE 39:0	72783115	43011810	48963759	46637498	25895419	3.77E+08
PE 38:5-1	35361466	95342838	1.24E+08	59477933	46174624	3.48E+08
PE 38:4-3	78045220	1.57E+08	1.57E+08	86295667	48025434	24946188
PE 38:3-1	9052148	18961578	27853913	24469736	12810906	5361387
PE 38:2	17411373	14650093	19710904	16733422	12491496	23823567
PE 38:1	3.83E+08	7.35E+08	7.08E+08	4.53E+08	2.08E+08	3.17E+08
PE 38:0	16335974	22593126	23759643	17764224	8489474	33137507
PE 37:4	1.99E+08	3.38E+08	7.28E+08	4.12E+08	3.76E+08	8.32E+08
PE 37:3	2.12E+08	4.15E+08	7.48E+08	6.08E+08	3.54E+08	88273583
PE 37:2	47306547	55011291	86251143	72799618	1.27E+08	27984598
PE 37:1	1.34E+10	3.81E+10	6.71E+10	3.22E+10	3.3E+10	5.19E+10
PE 37:0	1.35E+09	1.04E+09	1.27E+09	9.72E+08	5.55E+08	3E+09
PE 36:4	7562982	14768415	19516495	15992180	8332670	64114614
PE 36:3-1	5484186	16301224	25882481	17591056	15810870	35770213
PE 36:2-1	1.27E+08	1.9E+08	2.51E+08	1.22E+08	1.15E+08	17355924
PE 36:1-2	6040531	6711157	4770750	4633710	2034035	13684400
PE 36:1-1	9.91E+08	1.83E+09	2.26E+09	1.27E+09	7.01E+08	3.31E+08
PE 36:0	65021485	1.19E+08	1.71E+08	1.29E+08	76586384	8.76E+08
PE 35:5	1449430	2466131	4199288	2490853	2938765	461298.2
PE 35:4	9428717	20352157	24130935	7915315	6216439	31342971
PE 35:3	23749152	10209645	20560198	19435180	15752531	1269296
PE 35:1	4.81E+09	6.18E+09	7.43E+09	5.69E+09	7E+09	2.12E+09
PE 35:0	6.41E+09	5.24E+09	5.98E+09	4.46E+09	2.83E+09	4.66E+09
PE 34:4	3914546	11611234	25691978	14903728	16991462	50798585

PE 34:3-1	2534290	3437714	4714285	2424640	2308116	4611580
PE 34:1	15151549	24720689	40715262	22689023	12255570	918237.1
PE 33:0	1.69E+09	2.64E+09	3.61E+09	2.15E+09	1.32E+09	4.22E+09
PE 32:0	51771326	71369900	96255090	65634097	31314285	22448039
PE 31:1	66575709	82764402	1.76E+08	1.23E+08	72219622	6914284
PE 31:0	2.38E+08	2.19E+08	3.37E+08	2.38E+08	1.27E+08	4.68E+08
PE 28:0	1328346	1971200	1686942	704635.1	387092.4	8992956
PC O-45:1	13712739	12131875	17120909	15183130	34722179	2520212
PC O-45:0	1.41E+08	49320554	58418881	1.19E+08	2.42E+08	6587933
PC O-44:3-2	4503198	3451615	2599472	2867566	3801607	12967669
PC O-44:2-1	1034233	717432.5	472642	533440.2	747258.3	2760448
PC O-44:0	72635011	49975599	79716969	1.18E+08	1.99E+08	1816965
PC O-42:8	8579400	6599594	5285786	6618710	6587023	18401318
PC O-42:7-2	2376906	2120348	1709841	1850182	1212064	2222629
PC O-42:6-1	652378.6	1546822	1355924	498202.9	762461.1	2110062
PC O-42:5-2	2471471	3034346	1939189	1234188	850119.2	533055.4
PC O-42:3-1	10349141	12794560	13549691	22046758	18662773	3923444
PC O-42:2-2	9002331	11889675	8363920	8934734	7997744	5242280
PC O-42:1-1	1519666	1789432	867698.5	773460.4	462133	1106728
PC O-42:0	19328025	9970307	18949742	28025160	56820728	663425.7
PC O-40:8	4793904	3819429	3469988	5280162	4347988	3540833
PC O-40:7	23549448	34459555	19965916	13790467	12685096	3002999
PC O-40:6-2	11156857	32127507	24032289	27889843	36512849	26836934
PC O-40:6-1	1120258	3227776	5874403	6973163	6558810	12951029
PC O-40:5-2	6331650	5714364	5614062	6812476	7825414	842103.6

PC O-40:5-1	21795847	41344350	31384316	16467343	14958729	4196513
PC O-40:4-1	10283238	30318854	25105824	29484858	24326569	5532667
PC O-40:3-1	38172359	53700001	57119508	75378292	83828053	29287843
PC O-40:2-1	39687521	36737659	33724736	72512876	52227546	17806565
PC O-40:1-1	10514627	10463927	6892394	6177885	5477085	7486045
PC O-39:3	1.33E+08	1.72E+08	1.46E+08	1.62E+08	1.76E+08	25946372
PC O-39:2	5001868	7399500	4557298	4116546	3040859	3691322
PC O-39:1	10720115	11949091	9962459	11351356	16375399	9241158
PC O-38:4-2	6823062	6337580	10179782	7694701	6171552	6091008
PC O-38:4-1	6349455	22799275	17953809	9054123	5724980	5590590
PC O-38:3-2	26454404	50115440	48564892	67860454	53309296	47593938
PC O-38:2-2	3950737	3998525	3831560	5819388	5729273	4804149
PC O-38:2-1	1921176	5379529	5781257	8385897	6690383	5633908
PC O-38:1-1	26583906	22412957	15717334	22612628	16565855	42546237
PC O-38:0	2091653	2381738	854069.9	486278.3	237317.9	3363384
PC O-37:1-2	737323.7	1159568	948172.5	1061169	1021685	1830699
PC O-36:7	2116968	1643572	1487114	584833.2	409799.7	929062.5
PC O-36:6-1	10514402	9168383	11074303	11678829	10459426	6024544
PC O-36:5-1	993230.2	1310986	2727349	2556054	1569638	3774333
PC O-36:3-2	1.46E+08	75377038	1.14E+08	1.63E+08	2.02E+08	78171302
PC O-36:3-1	9907077	21244933	10785965	8103328	6809028	3095949
PC O-36:2-2	1.18E+09	1.31E+09	1.44E+09	1.62E+09	1.57E+09	2.61E+09
PC O-36:2-1	78383718	1E+08	1.07E+08	93653431	1.08E+08	1.57E+08
PC O-36:1-2	1.9E+08	1.58E+08	1.3E+08	1.46E+08	1.2E+08	1.34E+09
PC O-36:1-1	1.49E+08	1.69E+08	1.84E+08	2.1E+08	2.01E+08	3.38E+08

PC O-36:0	5882990	4093681	2166961	2726436	1564416	26602770
PC O-35:2-1	8.2E+08	2.42E+09	1.43E+09	7.13E+08	1.42E+09	1.43E+08
PC O-35:1-2	24347377	17710622	13799045	12622062	16774585	20666482
PC O-35:1-1	2.94E+08	1.17E+08	1.4E+08	2E+08	1.58E+08	5790835
PC O-34:5-1	6692156	4288667	1975333	2890173	1275615	5301506
PC O-34:3-2	11023027	14910820	10941964	10950618	9161525	4348875
PC O-34:1-2	3.44E+09	2.78E+09	2.44E+09	2.69E+09	2.39E+09	5.71E+09
PC O-34:1-1	65199193	51920473	51757655	35758500	57755643	54388643
PC O-34:0	4.12E+08	3.32E+08	2.89E+08	3.23E+08	2.81E+08	6.86E+08
PC O-33:4	4558150	4445621	5724796	6519236	4796958	6410624
PC O-33:2-2	48495825	54427380	64064726	68880061	44329530	9104757
PC O-33:1-2	2.19E+08	3.5E+08	3.34E+08	2.31E+08	3.46E+08	63698320
PC O-33:0	5011225	3224330	4729091	6973052	8560215	2132450
PC O-32:4	1053398	2938859	2815097	2640599	3040578	3878908
PC O-32:1-2	3011791	1891056	1614542	3454288	1986506	509607.1
PC O-32:0	1.03E+08	74258758	60905395	68153945	61350907	1.22E+08
PC O-31:1-1	26454716	14244168	21058015	17894405	19775923	40237769
PC O-31:0	47379035	93026841	87356359	80774856	84519232	25672056
PC O-30:1-2	53457410	69139999	44537833	37175768	26540259	2678823
PC 46:5	1609487	1398895	1237931	1535653	1582402	2073505
PC 46:4	1324506	2723927	3178117	2402421	3385640	4743009
PC 46:3	1440733	1048419	1043635	1125059	1079405	1787859
PC 44:3	11853863	7010070	5266993	5099814	3727755	1871099
PC 44:2	16120427	7655866	3848350	2914737	2305866	8656573
PC 44:12	2310691	2299348	3842125	3885106	4346705	2279407

PC 44:11-2	317554.3	464405.1	887024.6	422613.5	174648.8	3486168
PC 43:6	2508399	5456718	4576626	2992771	2697303	2685500
PC 42:6	5944017	6475162	4972298	6233553	6871349	2404917
PC 42:3-1	73417470	61004218	56010399	76067055	57562251	7141238
PC 42:2-2	1.47E+08	86101428	66063467	69121409	61508085	42570040
PC 42:1	50084368	26759437	15410151	11829907	9953515	51268367
PC 41:4	4997144	3450813	2055386	3351641	4240148	5050746
PC 41:2-1	6487007	5822105	3838238	3162563	2077795	291957.9
PC 40:6-2	6611363	11188592	13591210	26387177	27603079	7109776
PC 40:6-1	12423331	64719784	21905774	9140669	5318677	2439752
PC 40:5-3	16226148	12885933	8160405	4955110	2742448	1473534
PC 40:3	1.29E+08	1.73E+08	1.62E+08	2E+08	1.56E+08	18885195
PC 40:2-1	5.49E+08	3.95E+08	3.51E+08	3.96E+08	4.07E+08	3.1E+08
PC 40:1-2	71615588	31642651	29272934	39990633	29896965	13162790
PC 40:1-1	51694742	23339167	8842448	10809304	14124749	52377319
PC 40:0	8088316	3407056	1832763	1685209	1157074	6153961
PC 39:8	4017968	5631348	6341249	6658526	5920321	7710177
PC 39:6	1373466	2411276	1910932	5228084	5926408	436787
PC 39:3	1402012	8014427	5428029	4355026	3157133	659643.9
PC 38:8	4767757	8799732	6914560	6444970	5560338	7550228
PC 38:5-1	12771796	20897778	12122601	6116327	4315086	527640.7
PC 38:4-2	33242932	1.91E+08	1.44E+08	47235712	39052974	1577520
PC 38:3	32792521	37801354	40276512	26840679	38344936	6054648
PC 38:2-2	71430185	1.04E+08	1.21E+08	1.63E+08	1.01E+08	25069640
PC 38:1-1	2.24E+08	2.91E+08	2.55E+08	2.49E+08	3.26E+08	4.01E+08

PC 37:7	52262973	1.02E+08	1.17E+08	1.74E+08	1.72E+08	9802153
PC 37:6	11599079	22241631	26223835	30477733	42777648	46789307
PC 37:5	16689861	22364097	27217233	42516839	37127062	11836488
PC 37:2-2	3077786	4594720	3327238	3988236	5786103	845546.6
PC 37:1-2	19447888	22553122	27145990	27248210	42107349	14938910
PC 37:1-1	16551600	31645196	37727114	35345281	45102740	41925632
PC 37:0	5263902	6862985	5720771	5083752	4182576	1710081
PC 36:4-1	19667725	39566593	24978781	14288154	11599729	2798811
PC 36:2-2	1.88E+08	2.99E+08	2.49E+08	3.07E+08	1.93E+08	32557971
PC 36:0	2448647	2494264	2424746	3003088	2179281	2793802
PC 35:5-2	7511702	10251816	10881865	16376474	15790970	12381510
PC 35:5-1	9574529	18563579	27599788	30980216	46691351	13545992
PC 35:4	552807	808527.4	960251.1	1116733	1340645	855272.4
PC 35:1	3468981	3634703	4244698	3433403	5409481	2116770
PC 35:0-1	11748405	7539245	10640297	10744060	11148203	19218738
PC 34:2	76855057	43270984	1.56E+08	36216272	1.44E+08	1503452
PC 34:1	1039119	473197.1	357314.5	466922.8	384899.6	5825466
PC 34:0	38123431	22090915	26513341	28284613	32228380	4916871
PC 33:5	2470440	1925046	2266653	2182317	3318836	815972.9
PC 33:4	1694323	630307.8	661743.6	684008.8	972886.6	925801.3
PC 33:1	4410130	5487052	4576164	2599462	3154355	4014733
PC 33:0-1	5147807	2327418	1262248	2126367	1074277	2968482
PC 32:3	12105236	12943719	16365424	12964159	14727897	1001072
PC 32:1	3.02E+08	1.35E+08	2.54E+08	3.05E+08	1.92E+08	6997214
PC 30:2	87421446	63508355	1.14E+08	1.37E+08	1.3E+08	5005190

PC 29:1	4420692	5358652	7096782	4562332	4260276	5115764
PC 29:0	7641258	4351472	3176714	4721392	1933188	559982.7
PC 28:1	14060808	8970601	13641241	14821398	9520901	2846611
PC 26:0	18231033	1625497	1637443	1455670	727451.7	1975268
LPE O-20:1	989379.1	2103777	2275393	1468844	1225409	1146683
LPE O-18:2	79846254	4.81E+08	3.43E+08	2.8E+08	5.17E+08	94319632
LPE O-16:1	2041030	1926979	1743325	1366958	913184.5	1016674
LPE 24:1	1172833	1336626	1439894	1008821	839296.8	797600.6
LPE 22:2	1843897	3687842	3832383	3188737	1999020	255572.4
LPE 22:1	2917465	6016894	14184991	4277349	7296743	12814255
LPE 21:0	17982781	5979904	5213690	2847233	4219445	864981.2
LPE 20:5	3666525	3836802	2313007	970771.3	571370.6	381482.9
LPE 20:4	56658567	65651415	47793841	18964351	13859114	1419637
LPE 20:1	6181803	12510369	15711818	7560446	5352720	1383111
LPE 20:0	448459	590249.4	791175.1	395799.5	392574.7	1092561
LPE 18:4	7.1E+08	1.29E+09	8.42E+08	1.01E+09	9.82E+08	9.43E+08
LPE 17:2	3891328	19908628	8178863	4206025	3191641	11686558
LPE 16:1	42185253	28746709	32459805	19882650	22958938	2855733
LPE 14:0	876215.2	786443.9	1116053	519081.6	603584.4	305273.1
LPE 12:0	1.02E+08	2.5E+08	2.93E+08	1.6E+08	1.92E+08	1.36E+08
LPC O-20:2	717744.1	887042	761767.2	727869.8	480531.5	6639026
LPC O-18:2-2	2314389	1311252	1311551	1197544	877479.8	1888049
LPC O-18:2-1	2595252	935701.7	538417.7	499998.7	334755.5	957274
LPC O-18:1	1842642	5813942	1983658	1108793	604724.1	33018382
LPC O-18:0	473389.9	724066.8	398825.8	388482.2	290497.4	11984573

LPC O-16:1	1.79E+08	1.54E+08	1.24E+08	91204624	49817332	50832204
LPC O-16:0	32108992	13959948	14461134	17307393	15607341	16448179
LPC 26:0	7873540	3569697	1579157	980721.1	213935.1	5656838
LPC 24:1	49783729	22603628	12892105	17831079	8192159	2936292
LPC 24:0	21014315	3833134	1340081	1070884	710930.5	2040433
LPC 22:5-1	9892216	9086702	6218800	2928467	1444110	709663.4
LPC 22:4	7594307	7142666	6977123	4874529	3726801	9650761
LPC 22:3	5114283	7390399	6627143	3271895	2050985	265008.6
LPC 22:1	9275394	7131051	7439543	9969957	3316243	1459207
LPC 22:0	24585276	7710736	10338485	11833434	7504292	25463273
LPC 20:3	28073982	21612873	22620823	28997196	8655026	8260784
LPC 20:2	25609268	14790577	23050859	10193674	7114974	2588982
LPC 20:1	47139125	52026495	47263210	30755142	20815685	18167568
LPC 20:0	3764992	2944230	2585211	3545557	1373564	6170592
LPC 19:1	2428349	4741976	4557708	5401827	4633873	9604686
LPC 18:4-1	17799047	12282939	11794615	11229931	8172542	1666435
LPC 18:1	1.83E+09	1.65E+09	1.38E+09	1.23E+09	8.15E+08	6.3E+08
LPC 18:0	4.24E+08	4.83E+08	3.28E+08	4.05E+08	2.13E+08	63154435
LPC 17:1	15579956	15433298	9958423	8418434	5178219	1065060
LPC 17:0	8459687	10951254	7815665	5092918	4449365	1068475
LPC 16:1	3.89E+08	3.09E+08	2.75E+08	2.66E+08	2E+08	38919559
LPC 14:1	2559335	1813817	2718179	2279926	1311499	236171.1
LPC 14:0	46038787	39511133	33458152	30889708	18916379	9927217
LPC 12:0	48577816	78007052	75194684	65127840	39830825	1.11E+08
DG 33:0-1	493854.3	2072075	1760270	980370.7	1447781	7564437

DG 34:0-3	61680000	48805671	56749750	58592165	96464188	14148514
DG 34:1-2	15508398	19679736	22663784	32644965	79888263	2383410
DG 34:2-1	1.69E+08	1.2E+08	2.67E+08	3.7E+08	9.5E+08	51668799
DG 35:0-3	43583189	71735107	66205759	44308207	33447310	1183726
DG 35:1-1	5523282	8212679	9189818	7802079	8440289	2429573
DG 35:2-1	15769654	13601268	16247340	15705366	19276061	2212434
DG 36:0-1	1101701	1229799	1046724	641965.8	605151.6	7034909
DG 36:0-2	39550070	34757436	40822801	45016960	47778012	86789277
DG 36:1-1	3.99E+08	3.56E+08	4.12E+08	4.49E+08	4.82E+08	8.61E+08
DG 36:1-2	7808073	6963072	9402991	8753430	8963028	9480688
DG 36:1-3	14748061	10566471	15019691	28968448	28251993	3282849
DG 36:1-4	2.05E+08	1.35E+08	1.81E+08	2.46E+08	3.54E+08	2.14E+08
DG 36:2-1	10423674	4583799	7265817	9209241	9309387	6087132
DG 36:2-2	1.48E+08	1.06E+08	1.54E+08	2.77E+08	2.84E+08	31050614
DG 36:2-5	18335437	7038848	8874090	17672518	15954296	1753737
DG 36:3-1	1.24E+08	70890418	95107912	1E+08	1.61E+08	29969597
DG 36:3-2	1.86E+08	70335819	96147017	1.86E+08	1.66E+08	3705694
DG 37:1-1	3260168	1626150	1496769	936998.2	1233356	1059617
DG 37:2-1	11826918	13914629	14299242	13168586	12895483	3348312
DG 37:2-3	6960194	13205550	4639382	4893672	4350807	33578356
DG 37:3-2	1644375	1823328	2289247	2335558	3240552	2969601
DG 38:0-2	2016454	1889694	1917664	1330524	1708625	9786499
DG 38:1-1	14382484	21039523	22903083	15119659	18394084	1E+08
DG 38:1-2	4144169	4547814	6714169	10838374	8396925	6649552
DG 38:1-3	19223279	18102141	24628617	24446363	32162571	38154567

DG 38:2-1	41206860	44306090	60995304	1E+08	78915216	75840803
DG 38:2-2	1.72E+08	1.7E+08	2.07E+08	2.15E+08	2.95E+08	3.42E+08
DG 38:2-3	25304326	19223152	25141595	35979890	30913074	6782456
DG 38:2-4	1.04E+08	56843339	65297062	1.68E+08	1.27E+08	6715017
DG 38:3-1	9.61E+08	5.22E+08	5.95E+08	1.5E+09	1.11E+09	53894281
DG 38:3-2	2.37E+08	1.67E+08	2.04E+08	3.38E+08	3.05E+08	61920974
DG 38:4-1	1.71E+08	84610811	1.24E+08	1.42E+08	90216009	15002075
DG 38:4-2	1.79E+09	1.19E+09	8.92E+08	9.12E+08	8.08E+08	66876859
DG 38:5-1	2.91E+08	1.8E+08	1.54E+08	1.61E+08	1.21E+08	9080892
DG 40:1-1	7294556	7363899	7754495	4355334	4798519	7310700
DG 40:1-2	3806725	4257099	6030288	4400697	7111950	4571545
DG 40:2-1	32217266	36018933	47116333	37273118	56982221	37444760
DG 40:3-1	18433983	24034401	31414892	41525667	51354110	11831508
DG 40:4-1	78351116	71449525	63383731	66836020	43558672	8396137
DG 40:5-2	77955121	65382142	50038555	73055266	33063579	2083561
DG 40:9-1	26561218	17372713	18581252	12110502	8591358	23764070
DG 41:2-1	3675715	2352858	3728996	729237.8	1458701	38572359
DG 41:5-1	9302153	6199504	6055615	4981125	3923979	9372697
DG 41:6-1	37701850	72508186	65923286	44257040	39318205	1.73E+08
DG 42:10-1	1.23E+08	58997176	70415344	78928080	39138190	19842345
DG 42:1-1	5284952	2997473	2360753	1581273	1568247	16873531
DG 42:1-2	3354027	2786229	3314367	2537139	3100986	2457045
DG 42:2-1	26287832	22932293	25533401	19561168	22972658	23760446
DG 42:3-1	10041658	11557274	17798969	16783766	22007314	2268732
DG 42:9-2	1.73E+08	1.87E+08	1.64E+08	1.17E+08	94876833	2.14E+08

DG 43:6	3246606	4619069	5888967	5341935	3638316	19136219
DG 44:0-1	2996520	1560204	1898333	1661638	1144147	3591241
DG 44:1-1	4151703	1654200	2296944	2285741	2400830	1731949
DG 44:12	2.82E+09	1.42E+09	2.52E+09	2.28E+09	1.41E+09	1.72E+08
DG 44:2-1	6708784	4112879	4061669	2659355	2565345	5479041
DG 44:3-1	2730914	2688349	3547353	2827620	3534568	376233.5
DG 44:5-1	975310.5	874275.7	994895.4	626834.2	823514.7	2745655
DG 44:9-2	7.16E+08	4.9E+08	3.91E+08	2.68E+08	2.24E+08	2.65E+08
DG 45:5-1	5582085	9579600	7840007	5678491	5307375	28481535
DG 46:0-1	11530347	7815995	8640824	7882439	7881571	23265399
DG 46:1-1	29482383	14638018	24242960	23818094	25557681	12781377
DG 47:1-3	907829.9	562798.6	623096.6	596337.9	694130.5	2545997
DG 48:1-3	1.16E+08	71427137	1.12E+08	1.13E+08	1.23E+08	90155741
DG 48:2-3	74447562	38146028	77287325	89852708	1.1E+08	10065961
TG 40:0	745392.7	480712.9	836678.4	626222	734503.8	2147256
TG 42:0-3	6744592	4864252	5651251	6842679	7857406	8631606
TG 42:1-1	3543199	2008413	3356850	4007877	4350444	3938812
TG 43:0-1	1058424	1609002	1751836	1557698	1453377	6671293
TG 43:1	989308.7	1096908	1173484	1083702	1002784	3298901
TG 44:0-1	48875493	35244493	37176549	47983032	62080844	33153444
TG 44:0-2	5183007	3175005	4379702	5756106	7964084	2462757
TG 44:2-2	5927397	5505258	9465772	9887765	13219719	4817377
TG 45:0-2	631817.8	765604.3	919997.9	939443.2	1129018	789128.7
TG 45:1-2	5166685	6316846	7368279	7851100	8441514	19889666
TG 45:2	2119394	2116480	2527058	2725807	2595296	7845994

TG 46:0	1.9E+08	1.74E+08	1.78E+08	2.36E+08	3E+08	92640567
TG 46:1	3.14E+08	1.93E+08	2.48E+08	3.5E+08	5.44E+08	92036769
TG 46:2-2	91081469	55334988	88042290	1.24E+08	1.99E+08	25290819
TG 46:3-4	7009606	6648027	12235753	17843667	25296901	1465843
TG 47:0	11618185	20389779	19620533	21279223	20338665	34299329
TG 47:1-1	24906253	29888147	32782396	41364116	46582477	43023149
TG 47:2-1	11041962	11289326	14437488	17473740	20159408	21864086
TG 48:0-1	3.06E+08	3.74E+08	3.16E+08	4.5E+08	5.02E+08	2.22E+08
TG 48:0-2	2.08E+08	1.72E+08	1.94E+08	2.68E+08	3.91E+08	54577076
TG 48:1-1	1.23E+09	1.01E+09	1.13E+09	1.6E+09	2.32E+09	3.26E+08
TG 48:1-2	1.23E+08	72727489	1.08E+08	1.55E+08	2.66E+08	16322325
TG 48:2-1	6.91E+08	4.05E+08	6.18E+08	9.19E+08	1.57E+09	95266799
TG 49:0-1	10243122	13410386	13502442	17552693	18612564	7194040
TG 49:0-2	9912400	19798221	15348389	16425822	15058391	22220487
TG 49:1-1	56770579	76237779	78209704	98827586	1.11E+08	46983858
TG 49:2-4	47700899	48914822	60723701	81530011	99423551	33387504
TG 49:3-3	10174499	10048153	13274595	18115299	23178546	6101975
TG 50:0-1	2.1E+08	2.56E+08	1.88E+08	2.71E+08	2.61E+08	3.69E+08
TG 50:0-2	3.38E+08	3.43E+08	3.68E+08	4.84E+08	6.49E+08	2E+08
TG 50:1	4.16E+08	3.75E+08	4.79E+08	6.97E+08	9.97E+08	1.17E+08
TG 50:2-1	2.27E+09	2.07E+09	2.61E+09	3.78E+09	5.51E+09	6.37E+08
TG 50:3-1	6.14E+08	3.71E+08	6.1E+08	9.72E+08	1.8E+09	57470674
TG 50:4-1	24330484	13014378	20236690	29737340	55191532	3223413
TG 50:4-2	36235415	23010099	26143453	59282023	56906469	1611123
TG 51:0-1	17200640	14954629	19779245	38587229	32627435	12133902

TG 51:1-1	53851639	75596467	70913830	85649428	85224184	38744725
TG 51:2-1	98935306	1.14E+08	1.23E+08	1.69E+08	1.93E+08	35146593
TG 51:3-1	36631404	38970277	46837896	66205309	82519392	9832768
TG 52:0-1	2.19E+08	2.35E+08	2.2E+08	2.8E+08	3.15E+08	4.21E+08
TG 52:1-1	7.43E+08	7.19E+08	8.75E+08	1.17E+09	1.58E+09	4.88E+08
TG 52:1-2	1.11E+09	1.2E+09	1.13E+09	1.43E+09	1.62E+09	2.15E+09
TG 52:2-1	3.81E+09	3.68E+09	4.45E+09	6.06E+09	7.77E+09	2.48E+09
TG 52:2-2	4.2E+08	2.99E+08	4.28E+08	6.94E+08	1.13E+09	1.07E+08
TG 52:3-1	2E+09	1.54E+09	2.17E+09	3.38E+09	5.37E+09	5.15E+08
TG 52:4-4	2.13E+08	1.04E+08	1.24E+08	1.64E+08	3.81E+08	84023726
TG 53:0	956182.5	1376917	1253542	2635859	3241254	3660227
TG 53:1-1	16531343	23552818	22052677	26808916	29233224	10182345
TG 53:1-3	18466325	27822365	23247631	28085294	26163803	27770640
TG 53:2-3	20760945	24682230	28100471	34143034	38222435	7417009
TG 53:2-4	77915262	99059961	96530454	1.3E+08	1.38E+08	41598568
TG 54:0-1	47624843	49629853	44511879	60191171	60357751	3.61E+08
TG 54:1-1	3.1E+08	2.97E+08	3.29E+08	4.94E+08	5.88E+08	8.84E+08
TG 54:2-1	5.52E+08	5.41E+08	6.46E+08	9.3E+08	1.18E+09	6.03E+08
TG 54:2-2	1.48E+09	1.42E+09	1.56E+09	2.34E+09	2.79E+09	4.25E+09
TG 54:3-2	2.45E+09	2.57E+09	3.08E+09	4.42E+09	5.67E+09	2.91E+09
TG 54:4-1	3.39E+08	2.69E+08	3.35E+08	5.7E+08	6.95E+08	1.59E+08
TG 54:5-1	87584455	61775552	41581687	63470166	36283627	92957559
TG 54:5-2	5177788	4936223	3069640	3021978	2592557	20007743
TG 54:6-3	17733323	16667516	10924306	12508070	9584473	62716760
TG 54:6-6	33921141	34661352	34521701	29822488	32271257	14385479

TG 54:7-4	2030530	1891505	1358375	1340891	1028092	5160351
TG 55:1-3	3291419	4894112	3691380	4331822	3892614	11401042
TG 55:2-1/TG 55:2-4	13200436	24351373	21336835	20872351	28852268	16133525
TG 55:3-2	35183508	45444852	44335864	62532279	67432570	16235429
TG 56:0-1	2694895	2497985	1736691	2214496	1397659	34154860
TG 56:0-2	9593982	9709275	8028006	10854212	10325526	1.24E+08
TG 56:1-1	49962580	52868917	51626050	79304269	90395836	3.84E+08
TG 56:1-4	44199041	43988962	36380931	48771443	46785133	5.68E+08
TG 56:2-1	1.12E+08	1.15E+08	1.34E+08	2.25E+08	2.84E+08	3.93E+08
TG 56:2-3	2.25E+08	2.34E+08	2.32E+08	3.53E+08	4.03E+08	1.71E+09
TG 56:3-1	56810392	47050779	62728092	90673754	1.04E+08	39135941
TG 56:3-2	5.06E+08	5.13E+08	6.03E+08	1E+09	1.27E+09	1.74E+09
TG 56:4-2	1.94E+08	1.98E+08	2.08E+08	3.23E+08	3.73E+08	1.36E+08
TG 56:4-3	36382831	39427739	41159339	45989598	61303128	7970802
TG 56:5-5	1.45E+08	1.47E+08	1.39E+08	1.89E+08	1.98E+08	21200138
TG 56:6-3	68264364	70884687	54853057	57917223	41958119	8313792
TG 57:1	1371602	1751015	1260365	1347536	1074205	3817029
TG 57:2-3	5509749	7069246	6024067	7324425	7156196	6341381
TG 57:3-1	8875469	12661893	11628060	16553442	16610101	4596525
TG 57:3-2	1.4E+08	2.17E+08	2.12E+08	2.81E+08	2.94E+08	5.29E+08
TG 58:0-1	4926955	3722503	2761395	3434955	2870702	43746179
TG 58:1-1	20565906	16238719	11853126	15314192	12840092	1.88E+08
TG 58:2-1	28911145	25566304	34138938	50180439	59203002	88144422
TG 58:2-3	95004072	82498095	74720626	1.09E+08	1.12E+08	5.02E+08
TG 58:3-1	17273384	19248471	22554196	35232663	38355789	17523500

TG 58:3-3	1.32E+08	1.34E+08	1.4E+08	2.36E+08	2.76E+08	5.05E+08
TG 58:4-3	72105586	78706978	89471168	1.44E+08	1.52E+08	71606950
TG 58:5-3	55048223	54916126	60231698	80076150	77974753	14879770
TG 60:1	9729759	7111071	5612173	8066214	6874030	59850607
TG 60:2-2	19291804	15694818	14271457	17620403	23240105	55924723
TG 60:2-3	37906603	27534542	21668085	31369444	27605422	2.31E+08
TG 60:3-1	7973025	7959416	8049890	13498033	13799070	5489686
TG 60:3-3	74573959	59994351	57008388	90568984	92080624	2.2E+08
TG 60:4	30486483	30625224	31987615	52802851	52585380	29662095
TG 62:2-1	6492479	4286319	2993196	3963661	3721623	66908443
TG 62:7	2013452	3184382	2872708	1590306	1228450	31018996
TG 64:3	2408344	1724431	1549046	2240031	1905675	12790879
TG(e) 56:1	5740712	6921577	6535056	15039321	13652634	30829262
TG(e) 56:2	8202508	9669074	14484833	28173379	27982872	18410603
TG(e)48:0	25789044	20268412	21011817	30274004	29088381	2.1E+08
TG(e)50:0	44104443	34163614	43552818	70251957	68271985	1.54E+08
TG(e)50:1	61019993	42912612	66865298	1.21E+08	1.31E+08	53795018
TG(e)52:1	1.36E+08	1.14E+08	1.39E+08	2.25E+08	1.96E+08	9.71E+08
TG(e)52:3	1.85E+08	1.42E+08	2.45E+08	4.83E+08	5.55E+08	95014000
TG(e)54:2/TG(p)54:2	1.24E+08	1.22E+08	1.66E+08	3.03E+08	2.89E+08	5.42E+08
TG(p) 54:1	22904171	23917921	27208223	43551067	35260939	3.04E+08
TG(p) 56:3	39095518	44845566	64777920	1.27E+08	1.28E+08	82903469
TG(P)50:1	2.43E+08	1.94E+08	2.4E+08	3.94E+08	3.82E+08	8.81E+08
TG(P)50:2	15552281	12930635	16529762	34243312	40842518	12655225
TG(P)52:1	1.13E+08	95003023	1.38E+08	2.44E+08	2.56E+08	1.95E+08

TG(P)52:2	34880098	28732508	49577680	95633580	1.08E+08	17262080
TG(P)54:4	18268936	20794432	26326535	62539575	72408605	17324039
PS 46:7	763106.6	678942.8	518796.8	582353.3	426493.6	1904887
PS 46:6	1296162	1880048	1090933	470966.2	213034.3	79518.09
PS 46:2	18522654	13434735	12089229	13393643	11041348	2638224
PS 46:0	32257004	14633258	8448462	6605371	5467906	20112193
PS 45:1	1500930	683639	413447.1	459487.5	344756.5	269747.5
PS 44:9	20060807	16354061	8770291	3628209	1868976	4196127
PS 44:8-2	38373573	53313963	31896282	10303181	10587233	11305113
PS 44:7	7568299	5700248	6440171	3790206	2143706	14428835
PS 44:6	21912818	35713852	20211290	11551559	6778257	2954807
PS 44:3	18974546	21987668	20344007	15590920	12676683	666690.1
PS 44:2	38907401	33820755	38496694	41049582	36563393	5395135
PS 44:1	89347484	58130792	52476948	59063174	54969519	19596531
PS 43:1	2292436	1174463	1025568	1002475	769280.5	328828.4
PS 42:6	34070864	27277462	35285935	13093542	9981029	1.77E+08
PS 42:3	13482393	21687927	15308444	10063116	7428134	341832.6
PS 42:1	2.18E+08	2.06E+08	1.81E+08	1.89E+08	1.68E+08	1.92E+08
PS 42:0	7541845	2932839	3224329	3226841	5300596	2690047
PS 41:7	25969611	38889900	24524750	19183709	13672162	3195367
PS 41:3	3794664	6438012	5634570	5323156	4107784	63967.08
PS 41:0	1361570	1245357	1064608	835545	1032292	1383612
PS 40:1-2	39467733	43025268	33115421	31438411	39292733	7038240
PS 40:1-1	2.47E+09	2.27E+09	2.09E+09	2.17E+09	2.06E+09	1.13E+09
PS 40:0	1.21E+09	1.27E+09	1.07E+09	1.03E+09	9.93E+08	8.4E+08

PS 39:7	5239295	5942232	2874065	2715501	3036421	1362270
PS 39:5-1	13694381	9671790	8506059	4546264	5793471	1020364
PS 39:3	1344017	2472519	1474446	1895086	976115.9	137261.5
PS 39:2	12311099	17266649	28872557	35539611	53409200	6250956
PS 39:1	92916906	1.09E+08	86225887	84373728	75026244	13800348
PS 39:0	49125841	72519627	59734622	47899483	39814378	11009001
PS 38:0	2.97E+09	3.04E+09	2.77E+09	2.84E+09	2.74E+09	1.29E+09
PS 37:6	4963449	4489964	2921385	2135894	1914556	65769.57
PS 37:3	9206942	12814798	11620842	15032501	14430089	1467846
PS 36:8	1130795	1022461	952853	934754.4	714104.2	788214.3
PS 36:1-1	41666671	36237723	39621159	76598356	69509209	4820228
PS 36:0-1	1.08E+08	1.22E+08	88196892	48978601	42858946	8921634
PS 35:0	1.86E+08	1.73E+08	1.74E+08	1.62E+08	1.79E+08	1.4E+08
PS 34:1-1	16429658	6569865	14326351	9740151	5573741	15580665
PS 33:0	2.28E+08	1.91E+08	1.67E+08	1.01E+08	1.16E+08	91125300
PS 31:0	40250343	15654756	15287437	11947404	10584435	6020711
PS 30:4	2709215	3229921	3284887	3479674	3003031	3092843
PI 36:0-2	11273152	10335913	5979934	3662885	2491828	887782.6
PI 31:1	5114314	4982897	2075791	2939415	2318806	360302.9
PG 44:1	6320163	4277371	4054606	5644030	5078766	1560726
PG 43:4	44942659	55077868	39923988	24884190	17854694	1263002
PG 42:5	2565332	2661005	2452602	1987914	3684190	213817.6
PG 42:2	225256.8	230298.6	401584.8	325624	334313.2	169355.1
PG 42:1	4771024	5203323	5793216	6778976	6540820	4426659
PG 41:5	6672983	2666908	1847683	1216859	353063.8	1427510

PG 41:3	42711741	46814696	30804374	22901993	20838249	1455696
PG 41:2	53457418	40262389	48498407	77404558	67210011	4755108
PG 41:1	70667846	54135144	53631883	58460736	56245470	22686659
PG 41:0	6008507	4689768	4780433	6128437	5478435	1040355
PG 40:5	3899053	3348792	3507008	4017351	4230259	249169.2
PG 40:4	24432161	33585376	41544503	54550624	62058804	5994210
PG 40:3	19180765	23444974	34952082	55500153	68416186	8414001
PG 40:2	3020705	5615663	6815763	9411423	10977378	1226208
PG 40:1	27120614	20219821	18924983	17327285	18148510	10702073
PG 40:0	2953738	2480340	2619798	3028852	2809365	3153174
PG 39:2	552356.1	1052363	719061.2	655419.5	684120.6	157758.3
PG 39:0	663909.2	714246.9	707610.7	699300.1	722057.9	2134406
PG 38:5-3	6232084	2822042	2589054	2734849	1701600	311158.2
PG 38:3-1	4146663	2732374	3307881	5733939	3756075	1615570
PG 38:2	7526227	3838697	9161703	7741227	5309028	10110854
PG 38:1	1943334	1532828	1383640	1030757	1298667	8240858
PG 38:0-2	59176048	54007412	47927338	44868141	39931079	6055732
PG 38:0-1	2912312	2081749	1068475	500262.2	743622.5	694713.5
PG 37:3	9885020	6765563	6389732	9126875	9223483	254635.8
PG 37:2	4185364	1058743	1964989	2213090	915430.9	6450896
PG 37:1	8615443	3429400	10247083	9738199	3464793	25027422
PG 36:2-1	2.19E+08	1.12E+08	1.17E+08	1.37E+08	1E+08	3.12E+08
PG 35:1	8813477	6164628	4014543	3232876	1845998	861593.9
PG 35:0	47276421	31675219	39348889	50761608	52885782	5907756
PG 33:1	449457.2	503327.4	419679.6	369529.6	108485	350413.7

PG 32:2	5722555	2287695	2609628	2055149	2685466	436882.1

Table S2. shRNA target sequences.

shLuc	5'-CGTACGCGGAATACTTCGA-3'
shChka_1	5'-GAATTTGGGTACATGGAATAT-3'
shChka_2	5'-GTTACTTGACTACATTCCAAA-3'
shChkb_1	5'-GTGAGTGGGTTTATGATTATA-3'
shChkb_2	5'-CCCAGCTTTACGGAGTGTTTC-3'
shPcyt1_1	5'-CCTGTGAGAGTTTATGCGGAT-3'
shPcyt1_2	5'-CCCGAGAGTTCATTGGAAGTT-3'
shEtnk1_1	5'-TTGACATGACTGACTACTTTG-3'
shEtnk1_2	5'-CGACCTGTTGTGTAAGAATAT-3'
shEtnk2_1	5'-CGCCTTAGAAATGGCTAAGAT-3'
shEtnk2_2	5'-CGGCATCACCAACAAGCTATT-3'
shPcyt2_1	5'-GCTCACACAATTCCAAAGGAA-3'
shPcyt2_2	5'-CTGCTATGACATGGTGCATTA-3'
shPtdss1_1	5'-GCCTTGTTGATCCGTAGTTAT-3'
shPtdss1_2	5'-CCTGAACTTCGAGCAGGTTAA-3'
shPtdss2_1	5'-CAAGCTAAAGACGGGCCATTT-3'
shPtdss2_2	5'-CTGTCCCTGAAGACATATAAG-3'
shPebp1_1	5'-GTGGTCAACATGAAGGGTAAT-3'
shPebp1_2	5'-CCCTCTCATTGGGAGTTCTTA-3'

Table S3. Primers for qRT-PCR.

	Forward	Reverse
mGAPDH	5'-AACTTTGGCATTGTGGAAGGGCTCA-3'	5'-TTGGCAGCACCAGTGGATGCAGGGA-3'
mChka	5'-CAGGGGTGGTCTCAGTAACAT-3'	5'-CGCAAGAGCACTTTCCGAG-3'
mChkb	5'-AGGATGCTAAGTGCCCAGAG-3'	5'-TCACGGGACAAACGCTCAG-3'
mPcyt1	5'-GATGCACAGAGTTCAGCTAAAGT-3'	5'-TGGCTGCCGTAAACCAACTG-3'
mEtnk1	5'-CTGTTCACAGATGGGATCACAA-3'	5'-CGCGGAAACTTTTCACTTCCTC-3'
mEtnk2	5'-TTCAGCGTCACGGTGGAAC-3'	5'-GTGATGCCGTCTTTGAAGCG-3'
mPcyt2	5'-CGATGGCTGCTATGACATGGT-3'	5'-GCCCCTTATGCTTGGCAATCT-3'
mPtdss1	5'-GCAGGACTCTGAGCAAGGATG-3'	5'-GGCGAAGTACATGAGGCTGAT-3'
mPtdss2	5'-TGGGACCATTGGATCATGGAC-3'	5'-CCACTCTAATGTTTTGCTTGCC-3'
mCdh1	5'-CAGCCTTCTTTTCGGAAGACT-3'	5'-GGTAGACAGCTCCCTATGACTG-3'
mEpcam	5'-GCGGCTCAGAGAGACTGTG-3'	5'-CCAAGCATTTAGACGCCAGTTT-3'
mKrt7	5'-AGGAGATCAACCGACGCAC-3'	5'-GTCTCGTGAAGGGTCTTGAGG-3'
mOcln	5'-TTGAAAGTCCACCTCCTTACAGA-3'	5'-CCGGATAAAAAGAGTACGCTGG-3'
mSnail	5'-CTTGTGTCTGCACGACCTGT -3'	5'-CTTCACATCCGAGTGGGTTT-3'
mTwist1	5'-CCGGAGACCTAGATGTCATTG-3'	5'-ACGCCCTGATTCTTGTGAA-3'
mZeb1	5'-GCTGGCAAGACAACGTGAAAG-	5'-GCCTCAGGATAAATGACGGC-3'

	3'	
mPebp1	5'-CCAGCAGCATTTCATGGGAC-3'	5'-TGGTGCCACTCCCTGAATTTG-3'
hGAPDH	5'-GGAGCGAGATCCCTCCAAAAT-3'	5'-GCTGTTGTCATACTTCTCATGG-3'
hCDH1	5'-CGAGAGCTACACGTTCACGG-3'	5'-GGGTGTCGAGGGAAAAATAGG-3'
hSNAI1	5'-TCGGAAGCCTAACTACAGCGA-3'	5'-AGATGAGCATTGGCAGCGAG-3'
hETNK1	5'-GTGCCCAAGCTGAACGTCA-3'	5'-TCACCAGGACTACATCCTCCA-3'
hETNK2	5'-GCCCCGGCTTTTCAGGTTAAT-3'	5'-GGCTGGGGTTGATCTCGTT-3'
hPCYT2	5'-TGTCCACCACAGACCTCGT-3'	5'-ATACTCCCGGTACTCAGAGGA-3'
hPEBP1	5'-CCTGCAAGAAGTGGACGAG-3'	5'-ACCAAGGTGTAGAGCTTCCCT-3'
hCHKA	5'-TGGTTCTGGAGAGCGTTATGT-3'	5'-CATTTTCTCGGCGATTTCTGC-3'
hCHKB	5'-GGCTTGCAGCAGTCTAAGTG-3'	5'-GGCACCATTGGTAGGCTCG-3'
hPCYT1A	5'-CTCTGATGCAAGCGAAGAACC-3'	5'-ATCACCGTGAAGCCTTTGAAG-3'
hPCYT1B	5'-TGACATTCCGTATTCCTCTGCT-3'	5'-TCTCTGCGTTGGAACGAACAT-3'
hPTDSS1	5'-GGTCCGTTCACTCGACCTC-3'	5'-TGTGGCGTATCGAAGATTTGG-3'
hPTDSS2	5'-CACCAAGAGAGGTATTGTGGC-3'	5'-AATGGCCCGTCTTTAGCTTGT-3'

Table S4. Primers for ChIP-qPCR.

	Forward	Reverse
S1 (*Snail*, -894,-814)	5'-GCATGTGGCCCGTAGCAC-3'	5'-CGGAGGCCAGTGACTGAATT-3'
S2 (*Snail*, -683,-521)	5'-GGGACCCGAAATCCCCTAAAA-3'	5'-GGAGGACGCCGAGGCTGTT-3'
S3 (*Snail*, -115,+19)	5'-GGGTCTGACTCAGTTACCCC-3'	5'-GGGTCTGACTCAGTTACCCC-3'
T1 (*Twist1*,-147, -47)	5'-ATCCCGCCTCCCTGCGTCC-3'	5'-TAGAGCAGAGGAGCGGGGC-3'
Negative Control (NC)	5'-AGACCTCACCTTGAACTTAC-3'	5'-GACCACCTTATCCGAATGT-3'