Supplementary Information for:

Functionally overlapping pathways promote bis(monoacylglycero)phosphate synthesis in mammalian cells

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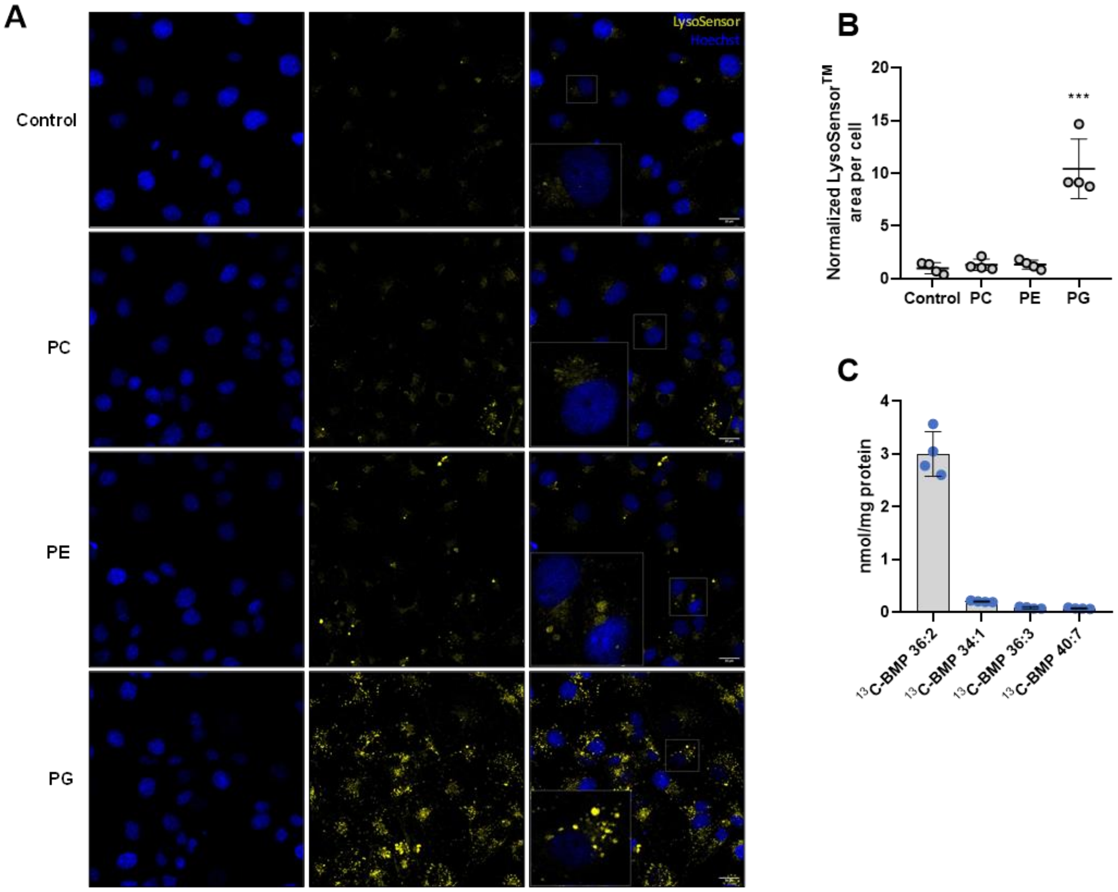

Figure S1. (**A**) Live cell imaging of COS-7 cells supplemented with indicated phospholipids for 18 h (50 µM, all esterified with oleic acid). LE/Lysosomes were stained with LysoSensor^{TM} and nuclei were stained with Hoechst. (**B**) Quantification of LysoSensor^{TM} signal. The fluorescent signal of four randomly picked sections was determined in ImageJ and normalized to cell number (n=4). (**C**) ^{13}C-labeled BMP subspecies formed during ^{13}C-PG loading (n=4 biological replicates). Data are presented as mean ± SD. Statistically significant differences in (A) were determined by one-way ANOVA and corrected for multiple comparisons against control by Bonferroni post hoc test (levels of statistically significant differences are: ***$p < 0.001$). Source data are provided as a Source Data file.

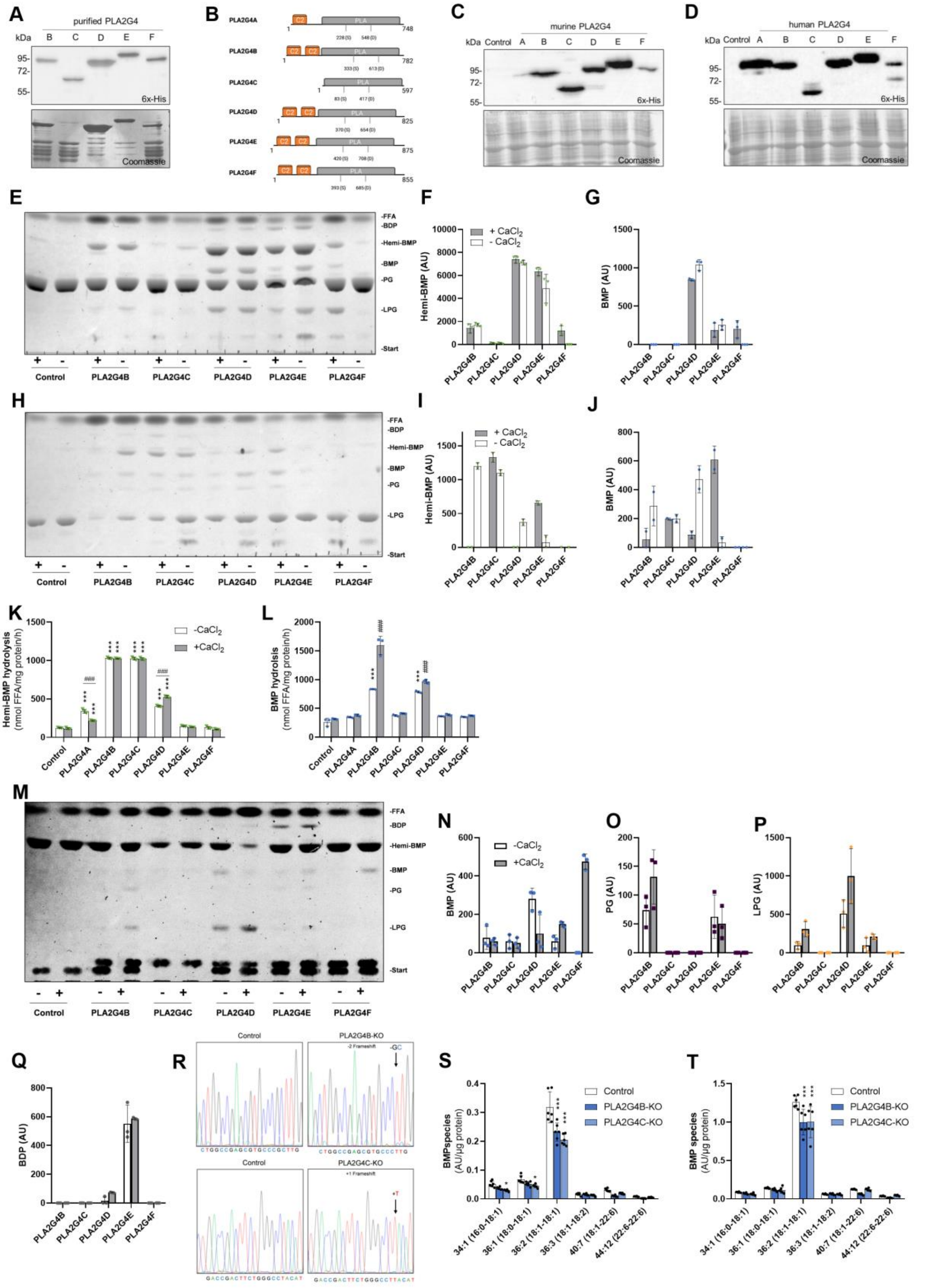

Figure S2. (**A**) Western blotting analysis of PLA2G4 enzymes enriched from lysates of Expi293F cells by affinity chromatography. Coomassie staining indicates that enzymes were partially purified. (**B**) Graphical illustrations of the domains and active sites of the murine PLA2G4 family. (**C, D**) Western blotting analysis of mouse and human PLA2G4A-F expression in Expi293F cells. The lower image shows the Coomassie-stained blot as loading control. (**E**) Representative TLC showing reaction products of semi-purified PLA2G4B-F incubated with di-oleoyl PG in the presence and absence of $CaCl_2$, respectively. (**F, G**) Densitometric analysis of hemi-BMP and BMP formation shown in (E) (n=3 biological replicates). (**H**) Representative TLC showing reaction products of purified PLA2G4B-F incubated with 1-oleoyl LPG in the presence and absence of $CaCl_2$. (**I, J**) Densitometric analysis of hemi-BMP and BMP formation shown in (H) (n=2 biological replicates). In (E) – (G), the reaction mix contained 1 µg protein/assay, 1 mM phospholipid substrate, 1% FA-free BSA (pH 7.4). Samples were incubated for 1 h at 37°C. (**K, L**) Hydrolysis of tri-oleoyl hemi-BMP and di-oleoyl BMP without and with $CaCl_2$ (n=3 biological replicates). Lysates of Expi293F cells expressing recombinant murine PLA2G4 enzymes were used as source of enzymatic activity. The reaction mix (40 µl total) contained 40 µg cell protein, 0.5 mM tri-oleoyl hemi-BMP or BMP, and 1% FA-free BSA (pH 7.4). Samples were incubated for 30 min at 37°C. (**M**) Representative TLC showing the reaction products formed upon the hydrolysis of tri-oleoyl hemi-BMP using semi-purified PLA2G4 enzymes. (**N-Q**) Densitometric analysis of (M) (n=3 biological replicates). Assays were performed under conditions described in (K, L) using 1 µg recombinant protein/assay. (**R**) Verification of the CRISPR-Cas9 mediated deletion of *PLA2G4B* and *PLA2G4C*. Chromatograms of control cells and KO cells are shown. Black arrow bars highlight the region where a frameshift was introduced. (**S, T**) BMP FA-composition of control, *PLA2G4B*-KO, and *PLA2G4C*-KO cells under basal conditions and after 8 h PG supplementation (n=6 biological replicates). The labeling on the x-axis indicates the FA composition of the respective BMP subspecies (number of carbon atoms: degree of saturation). Data are shown as mean ± SD. Statistically significant differences were determined by two-way ANOVA, followed by corrections for multiple comparisons (* = compared to the respective control, $^{\#}$ = comparison between groups) using Bonferroni post hoc test (levels of statistically significant differences are: $^{**,\#\#}p < 0.01$, and $^{***,\#\#\#}p < 0.001$). Source data are provided as a Source Data file.

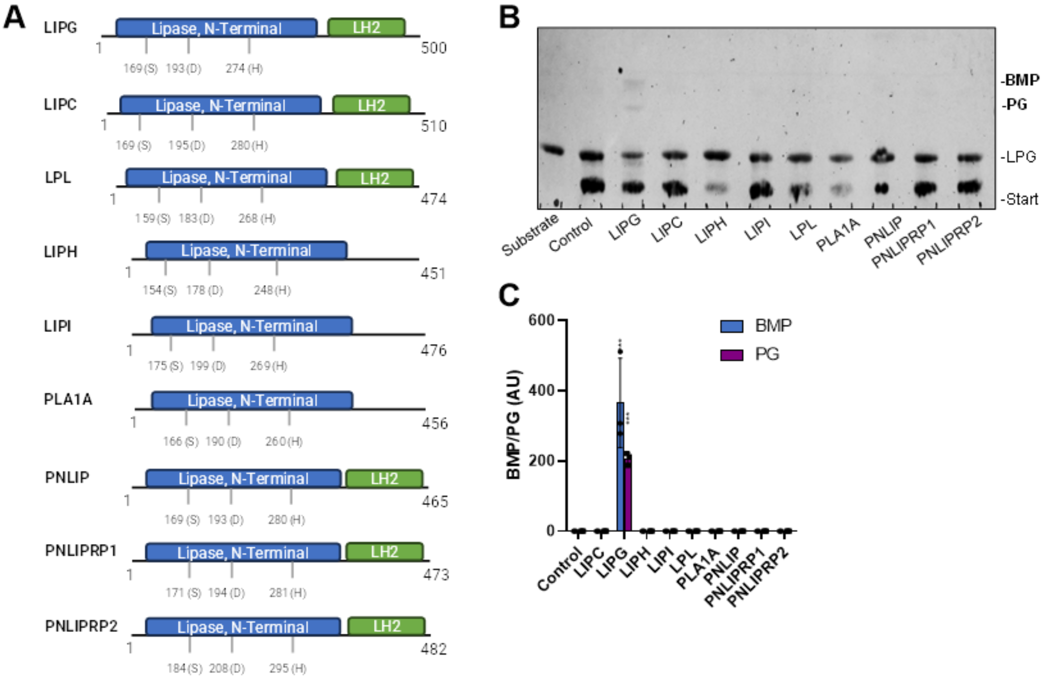

Figure S3. (**A**) Graphical illustrations of the domains and active sites of the murine PNLIP enzyme family. (**B**) Representative TLC showing LPG transacylase activity of PNLIP family members using 1-oleoyl LPG as substrate. The reaction mix (40 µl total) contained 20 µl conditioned supernatant, 0.5 mM sn-1-oleoyl LPG substrate, 1% FA-free BSA, and 20 mM HEPES (pH 7.4). Samples were incubated for 1 h at 37°C. (**C**) Densitometric analysis of BMP and PG formation shown in (B) (n=3 biological replicates). Data are presented as mean ± SD. Statistically significant differences were determined by two-way ANOVA, followed by corrections for multiple comparisons versus control using Bonferroni post hoc test (levels of statistically significant differences are: ***$p < 0.001$). Source data are provided as a Source Data file.

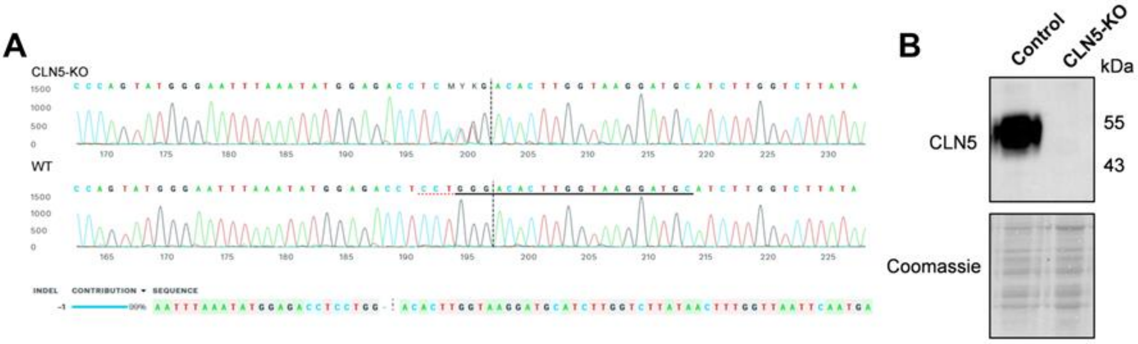

Figure S4. (**A**) Verification of CLN5 knockout in HEK293 cells by Sanger sequencing. The sequence was analyzed using the ICE CRISPR analysis tool by Synthego. (**B**) Verification of CLN5 knockout in HEK293 cells by Western blotting analysis. The Coomassie-stained blot was used as loading control. Source data are provided as a Source Data file.

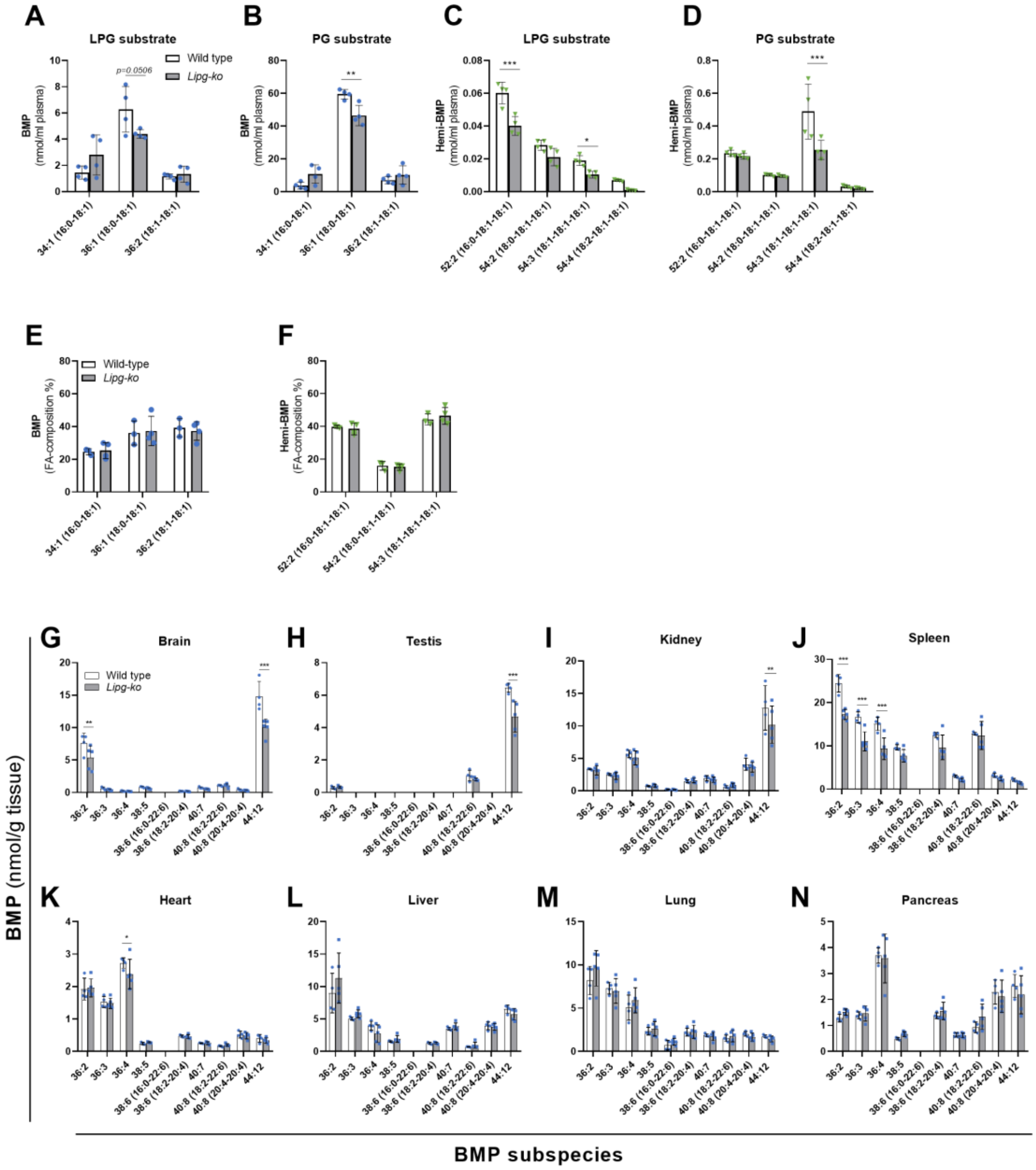

Figure S5. (**A, B**) BMP and (**C, D**) hemi-BMP subspecies formed in heparin-plasma of wild-type and *Lipg*-ko mice using *sn*-1-oleoyl-LPG or di-oleoyl PG as substrate (n=4). (**E&F**) Relative composition of plasma BMP and hemi-BMP subspecies of PG-treated wild-type and *Lipg*-ko mice (n=3 and 4, respectively). Blood samples were collected one hour after injection of di-oleoyl PG (5mg/mouse). (**G-N**) BMP composition of the indicated tissues obtained from wild-type (n=4) and *Lipg*-ko mice (n=5). The labeling on the x-axis indicates the FA composition of the respective BMP subspecies (number of carbon atoms: degree of saturation). Data are shown as mean ± SD. Statistically significant differences were evaluated by two-way ANOVA, followed by corrections for multiple comparisons using Bonferroni post hoc test (levels of statistically significant differences are: *p < 0.05, **p < 0.01, ***p < 0.001). Source data are provided as a Source Data file.

Table S1: **List of qPCR primers, gRNAs, and sequencing primers**

qPCR primer (5‘-3‘)

Primer name	**Sequence**	**Reference**
PLA2G4A Forward	TACCAGCACATTATAGTGGAGCA	PrimerBank ID 113722110c1
PLA2G4A Reverse	GCTGTCAGGGGTTGTAGAGAT	PrimerBank ID 113722110c1
PLA2G4B Forward	AAGCTGACAGTCCTTGATCCTG	This paper
PLA2G4B Reverse	CTTAGAGGGTAGGCGATGGG	This paper
PLA2G4C Forward	TGCCGGAGTCTCATTTGTCC	PrimerBank ID 226693353c2
PLA2G4C Reverse	GGGTGAACTCGAACCAGGTC	PrimerBank ID 226693353c2
PLA2G4D Forward	GCTGACCTGTTGAGTGAGGC	PrimerBank ID 116174753c1
PLA2G4D Reverse	TCGGTGAGCGTCTTGGTCTTA	PrimerBank ID 116174753c1
PLA2G4E Forward	GCCAGACAGACTGTTTTGTGA	PrimerBank ID 331284216c2
PLA2G4E Reverse	ACTCAACTCTAGCACGTTCTTCA	PrimerBank ID 331284216c2
PLA2G4F Forward	GGCGGGAAACCTACCCATAC	PrimerBank ID 281371375c1
PLA2G4F Reverse	CCACAGTTGCACATAGCAGT	PrimerBank ID 281371375c1

Guide RNAs (5‘-3‘)

gRNA name	**Sequence**	**Reference**
PLA2G4B gRNA1 FW	CACCGGCGCCTTTAGTTGCTCCTCG	This paper
PLA2G4B gRNA1 REV	AAACCGAGGAGCAACTAAAGGCGCC	
PLA2G4B gRNA2 FW	CACCGCTGGCCGAGCGTGCCCGCTT	
PLA2G4B gRNA2 REV	AAACAAGCGGGCACGCTCGGCCAGC	
PLA2G4C gRNA1 FW	CACCGTGCCGTCACGTACCTCGCAG	
PLA2G4C gRNA1 REV	AAACCTGCGAGGTACGTGACGGCAC	
PLA2G4C gRNA2 FW	CACCGGACCGACTTCTGGGCCTACA	
PLA2G4C gRNA2 REV	AAACTGTAGGCCCAGAAGTCGGTCC	
CLN5 gRNA_1 FW	CACCGGCATCCTTACCAAGTGTCCC	
CLN5 gRNA_1 REV	AAACGGGACACTTGGTAAGGATGCC	
CLN5 gRNA_2 FW	CACCGAATAAGGATCAGGTTTTGGA	
CLN5 gRNA_2 REV	AAACTCCAAAACCTGATCCTTATTC	
CLN5 gRNA_3 FW	CACCGCATCATCACCCTCCATAACT	
CLN5 gRNA_3 REV	AAACAGTTATGGAGGGTGATGATGC	

Sequencing primers for knock-out validation (5’-3’)

Primer name	**Sequence**	**Reference**
PLA2G4B gRNA1 Left	GCTAGGAGTGGAAGCGTAAAGA	This paper
PLA2G4B gRNA1 Right	CAGAGGACACTCCCCAAAGAG	
PLA2G4B gRNA2 Left	AAGACCCAGGTGACCAAGAAC	
PLA2G4B gRNA2 Right	GATGCGTAGAACCTAAACCCAC	
PLA2G4C gRNA1 Left	AGGTACCCTTCTTCTTGTTCCC	
PLA2G4C gRNA1 Right	CCCATTTATGTGTCAGAAAGCA	

PLA2G4C gRNA2 Left	AGAGCCTACAGAAAACCATCCA
PLA2G4C gRNA2 Right	AAGTGCCCAGATTTTGATGACT
CLN5 Left	TTTGAATGGTCCCCTAAAAATG
CLN5 Right	CTCACCTTCCAGGAGCTAGGTA

Primers for site-directed mutagensis (5’-3’)

Primer name	**Sequence**	**Reference**
mLipg_S169A_fw	GATTGGCTACgcgCTTGGAGCACAC	This paper
mLipg_S169A_re	AAGTGAACGTTCCCAAG	
mPla2g4d_S370A_fw	CAGTGGCATCgcgGGCTCTACAT	
mPla2g4d_S370A_re	AAGTAGGTCACACAGTCC	
mPla2g4e_S420A_fw	CACCGGCTTGgcgGGTGCAACCT	
mPla2g4e_S420A_re	ATGTAAGTAGAAGCGTCCAGAAAGTTCAGC	

Table S2: **List of recombinant proteins**

Nr	Full Name	Gene Name	Acession Number	Expression vector	No WB	no WB/no activity
1	patatin-like phospholipase domain containing 1	Pnpla1	NM_001034885.3	pcDNA™4/HisMaxC		
2	patatin-like phospholipase domain containing 2	Pnpla2	NM_001163689.1	pcDNA™4/HisMaxC		
3	patatin-like phospholipase domain containing 3	Pnpla3	NM_054088	pcDNA™4/HisMaxC		
4	patatin-like phospholipase domain containing 6	Pnpla6	NM_001122818.2	pcDNA™4/HisMaxC		
5	patatin-like phospholipase domain containing 7	Pnpla7	NM_146251.4	pcDNA™4/HisMaxC		
6	patatin-like phospholipase domain containing 8	Pnpla8	NM_026164.2	pcDNA™4/HisMaxC	x	x
7	phospholipase A2, group VI	Pla2g6	NM_001199023.1	pcDNA3.1(+)/myc-HisB		
8	Pancreatic Lipase	Pnlip	NM_026925.4	pcDNA3.1(+)/myc-HisB		
9	Pancreatic Lipase Related Protein 2	Pnliprp2	NM_11128.2	pFlag-CMV-5.1		
10	Phospholipase A2 Group VII	Pla2g7	NM_013737.5	pcDNA3.1(+)/myc-HisB		
11	Predicted gene 13124 (AADACL4 family member 2)	Aadacl4fm2	NM_001085542.1	pcDNA3.1(+)/myc-HisB	x	
12	arylacetamide deacetylase like 4	Aadacl4	NM_001081248.1	pcDNA3.1(+)/myc-HisB		
13	Predicted gene 13178 (AADACL4 family member 3)	Aadacl4fm3	NM_001085536.2	pcDNA3.1(+)/myc-HisB		
14	Predicted gene 436 (AADACL4 family member 4)	Aadacl4fm4	NM_001085504.1	pcDNA3.1(+)/myc-HisB	x	
15	Predicted gene 438 (AADACL4 family member 5)	Aadacl4fm5	NM_001126316.1	pcDNA3.1(+)/myc-HisB	x	
16	Predicted gene 5538 (AADACL2 family member 2)	Aadacl2fm2	NM_001101531.1	pcDNA3.1(+)/myc-HisB	x	
17	Predicted gene 5709	Gm5709	XM_888144.5	pcDNA3.1(+)/myc-HisB		
18	Predicted gene 8298 (AADACL2 family member 3)	Aadacl2fm3	NM_001243003.1	pcDNA3.1(+)/myc-HisB		
19	Protein Phosphatase Methylesterase 1	Ppme1	NM_028292.2	pcDNA3.1(+)/myc-HisB	x	x
20	Retinoblastoma Binding Protein 9	Rbbp9	NM_015754.2	pcDNA™4/HisMaxC	x	x
21	Lipid droplet associated hydrolase	Ldah	NM_172401	pcDNA™4/HisMaxC		
22	RIKEN cDNA 3110057O12 Gene (abhydrolase domain containing 18)	Abhd18	BC092533.1	pcDNA3.1(+)/myc-HisB	x	

23	RIKEN cDNA 9430007A20 Gene (AADACL4 family member 1)	Aadacl4fm1	NM_198662.3	pcDNA3.1(+)/myc-HisB		
24	RIKEN cDNA C130079G13 Gene (AADACL2 family member 1)	Aadacl2fm1	NM_177661.3	pcDNA3.1(+)/myc-HisB	x	
25	Spastic Paraplegia 21 Homolog (SPG21, maspardin)	Spg21	NM_138584.2	pcDNA3.1(+)/myc-HisB		
26	Testis Expressed 30	Tex30	NM_029368.2	pcDNA3.1(+)/myc-HisB	x	x
27	α/β Hydrolase Domain Containing 14a	Abhd14a	NM_001110271.2	pcDNA™4/HisMaxC	x	x
28	α/β Hydrolase Domain Containing 14b	Abhd14b	NM_029631	pcDNA™4/HisMaxC		
29	α/β Hydrolase Domain Containing 4	Abhd4	NM_134076.3	pcDNA™4/HisMaxC		
30	α/β Hydrolase Domain Containing 10	Abhd10	NM_172511.4	pcDNA™4/HisMaxC	x	x
31	α/β Hydrolase Domain Containing 13	Abhd13	NM_026868.1	pcDNA™4/HisMaxC	x	
32	α/β Hydrolase Domain Containing 11	Abhd11	NM_145215.2	pcDNA™4/HisMaxC		
33	Bile Acid-CoA: Amino Acid N-Acyltransferase	Acnat1	NM_001164565.1	pcDNA3.1(+)/myc-HisB		
34	Acyl-CoA Amino Acid N-Acyltransferase 2	Acnat2	NM_145368.3	pcDNA3.1(+)/myc-HisB		
35	Acyl-Coenzyme A Amino Acid N-Acyltransferase 3	Baat	NM_007519.3	pcDNA3.1(+)/myc-HisB		
36	Carboxypeptidase, vitellogenic-like	Cpvl	NM_027749.2	pcDNA3.1(+)/myc-HisB		
37	Carboxymethylenebutenolidase-like	Cmbl	NM_181588.4	pcDNA3.1(+)/myc-HisB		
38	Cathepsin A (Lysosomal protective protein (Mo54)	Ctsa	NM_001038492.2	pcDNA3.1(+)/myc-HisB		
39	Serine carboxypeptidase 1	Scpep1	NM_029023.3	pcDNA3.1(+)/myc-HisB		
40	Acetylcholinesterase	Ache	NM_001290010.1	pcDNA3.1(+)/myc-HisB	x	
41	Transmembrane protein 53	Tmem53	NM_001285812.1	pcDNA3.1(+)/myc-HisB		
42	α/β Hydrolase Domain Containing 1	Abhd1	NM_021304.3	pcDNA™4/HisMaxC	x	
43	Carboxylesterase 2F	Ces2f	NM_001079865.2	pcDNA3.1(+)/myc-HisB	x	
44	neuroligin 2	Nlgn2	NM_198862.2	pcDNA3.1(+)/myc-HisB		
45	Prolyl Endopeptidase	Prep	NM_011156.3	pcDNA3.1(+)/myc-HisB		
46	phospholipase D family, member 3	Pld3	NM_001317355.1	pcDNA3.1(+)/myc-HisB		

47	phospholipase A2, group IVE	Pla2g4e	NM_177845.4	pcDNA3.1(+)/myc-HisB		
48	N-myc downstream regulated gene 2	Ndrg2	NM_013864.2	pcDNA3.1(+)/myc-HisB		
49	Arylacetamide Deacetylase-like 2	Aadacl2	NM_001128091.1	pcDNA3.1(+)/myc-HisB		
50	family with sequence similarity 83, member C	Fam83c	NM_027788.3	pcDNA3.1(+)/myc-HisB		
51	family with sequence similarity 83, member F	Fam83f	NM_145986.2	pcDNA3.1(+)/myc-HisB		
52	Platelet Activating Factor Acetylhydrolase 2	Pafah2	NM_001285872.1	pcDNA3.1(+)/myc-HisB		
53	Dipeptidylpeptidase 9	Dpp9	NM_172624.3	pcDNA3.1(+)/myc-HisB		
54	Carboxylesterase 1A	Ces1a	NM_001013764.2	pcDNA3.1(+)/myc-HisB		
55	phospholipase D family, member 4	Pld4	NM_178911	pcDNA3.1(+)/myc-HisB		
56	MIT, microtubule interacting and transport, domain containing 1	Mitd1	NM_026913.3	pcDNA3.1(+)/myc-HisB		
57	Fatty acid amide hydrolase	Faah	NM_010173.5	pcDNA3.1(+)/myc-HisB		
58	palmitoyl-protein thioesterase 1	Ppt1	NM_008917.3	pcDNA3.1(+)/myc-HisB		
59	dickkopf WNT signaling pathway inhibitor 4	Dkk4	NM_145592.2	pcDNA3.1(+)/myc-HisB	x	
60	neuroligin 1	Nlgn1	NM_138666.4	pcDNA3.1(+)/myc-HisB		
61	phospholipase A2, group IVB (cytosolic)	Pla2g4b	NM_145378	pcDNA3.1(+)/myc-HisB		
62	N-myc downstream regulated gene 1	Ndrg1	NM_008681.2	pcDNA3.1(+)/myc-HisB		
63	Carboxylesterase 1H	Ces1h	NM_001370830.1	pcDNA3.1(+)/myc-HisB		
64	mesoderm specific transcript	Mest	NM_001252292.1	pcDNA3.1(+)/myc-HisB	x	
65	phospholipase A2, group IVC (cytosolic, calcium-independent)	Pla2g4c	NM_001168504.1	pcDNA3.1(+)/myc-HisB		
66	phospholipase D family, member 6	Pld6	NM_001290283.1	pcDNA3.1(+)/myc-HisB		
67	Esterase D/ Formylglutathione Hydrolase	Esd	NM_001285423.1	pcDNA3.1(+)/myc-HisB		
68	Acetylcholinesterase	Ache	NM_001290010.1	pcDNA3.1(+)/myc-HisB		
69	family with sequence similarity 83, member G	Fam83g	NM_178618.3	pcDNA3.1(+)/myc-HisB		
70	Family with Sequence Similarity 135 Member B	Fam135b	NM_177819.3	pcDNA3.1(+)/myc-HisB	x	x

71	glycosylphosphatidylinositol specific phospholipase D1	Gpld1	NM_008156.2	pcDNA3.1(+)/myc-HisB		
72	lipase, member I	Lipi	NM_001252513.1	pcDNA3.1(+)/myc-HisB	x	x
73	family with sequence similarity 172, member A	Fam172a	NM_138312.1	pcDNA3.1(+)/myc-HisB		
74	malonyl CoA:ACP acyltransferase (mitochondrial)	Mcat	NM_001030014.2	pcDNA3.1(+)/myc-HisB		
75	Acyl-CoA Thioestesterase 1	Acot1	NM_012006.2	pcDNA3.1(+)/myc-HisB		
76	Transmembrane and coiled-coil domain-cont prot 4	Tmco4	NM_001305423.1	pcDNA3.1(+)/myc-HisB		
77	Dipeptidylpeptidase 6	Dpp6	NM_010075.2	pcDNA3.1(+)/myc-HisB		
78	Family with Sequence Similarity 135 Member A	Fam135a	NM_026604.4	pcDNA3.1(+)/myc-HisB	x	x
79	Dipeptidylpeptidase 4	Dpp4	NM_010074.3	pcDNA3.1(+)/myc-HisB		
80	α/β Hydrolase Domain Containing 17c	Abhd17c	NM_133722.2	pcDNA3.1(+)/myc-HisB		
81	Neuroligin 4	Nlgn4l	EF694290.1	pcDNA3.1(+)/myc-HisB		
82	Endothelial Lipase	Lipg	NM_010720.3	pcDNA3.1(+)/myc-HisB		
83	Carboxylesterase 3A	Ces3a	NM_198672.1	pcDNA3.1(+)/myc-HisB		
84	notum palmitoleoyl-protein carboxylesterase	Notum	NM_175263.4	pcDNA3.1(+)/myc-HisB		
85	Pyrophosphatase	Ppa2	NM_146141.2	pcDNA3.1(+)/myc-HisB		
86	Carboxylesterase 5A	Ces5a	NM_001003951.3	pcDNA3.1(+)/myc-HisB	x	
87	Carboxylesterase 4A	Ces4a	NM_146213.2	pcDNA3.1(+)/myc-HisB		
88	neuroligin 3	Nlgn3	NM_172932.4	pcDNA3.1(+)/myc-HisB		
89	lipase, member O2	Lipo2	NM_001322338.1	pcDNA3.1(+)/myc-HisB	x	x
90	phospholipase D1	Pld1	NM_001164056.1	pcDNA3.1/myc-His(-)A		
91	family with sequence similarity 83, member H	Fam83h	NM_001168253.1	pcDNA3.1(+)/myc-HisB		
92	predicted gene 8978	Gm8978	NM_001323251.2	pcDNA3.1(+)/myc-HisB	x	
93	Dipeptidylpeptidase 10	Dpp10	NM_199021.3	pcDNA3.1(+)/myc-HisB		
94	phospholipase D2	Pld2	NM_001302475	pcDNA3.1(+)/myc-HisB		

95	phospholipase A2, group IIA (platelets, synovial fluid)	Pla2g2a	NM_001082531.1	pcDNA3.1(+)/myc-HisB		
96	lipase, member O3	Lipo3	NM_001013770.4	pcDNA3.1(+)/myc-HisB	x	x
97	phospholipase A2, group IVD	Pla2g4d	NM_001024137.1	pcDNA3.1(+)/myc-HisB		
98	family with sequence similarity 83, member A	Fam83a	NM_173862.2	pcDNA3.1(+)/myc-HisB		
99	Post-GPI attachment to proteins 1	Pgap1	NM_001163314.2	pcDNA3.1(+)/myc-HisB		
100	prokineticin 2	Prok2	NM_015768.2	pcDNA3.1(+)/myc-HisB		
101	epoxide hydrolase 2, cytoplasmic	Ephx2	NM_007940.4	pcDNA3.1(+)/myc-HisB		
102	palmitoyl-protein thioesterase 2	Ppt2	NM_001302393.1	pcDNA3.1(+)/myc-HisB		
103	family with sequence similarity 83, member B	Fam83b	NM_001045518.2	pcDNA3.1(+)/myc-HisB		
104	Diacylglycerol Lipase alpha	Dagla	NM_198114.2	pcDNA3.1(+)/myc-HisB		
105	lipase, member O1	Lipo1	NM_001323065.1	pcDNA3.1(+)/myc-HisB	x	x
106	Dipeptidylpeptidase 8	Dpp8	NM_028906.2	pcDNA3.1(+)/myc-HisB		
107	prolylcarboxypeptidase (angiotensinase C)	Prcp	NM_028243.3	pcDNA3.1(+)/myc-HisB		
108	phospholipase A2, group IVA (cytosolic, calcium-dependent)	Pla2g4a	NM_008869	pcDNA3.1(+)/myc-HisB		
109	N-myc downstream regulated gene 3	Ndrg3	NM_180956.1	pcDNA3.1(+)/myc-HisB		
110	family with sequence similarity 83, member E	Fam83e	NM_001033170.4	pcDNA3.1(+)/myc-HisB		
111	N-myc downstream regulated gene 4	Ndrg4	NM_145602.4	pcDNA3.1(+)/myc-HisB		
112	colipase, pancreatic	Clps	NM_025469.3	pcDNA3.1(+)/myc-HisB		
113	protease, serine 16 (thymus)	Prss16	NM_019429.2	pcDNA3.1(+)/myc-HisB		
114	KAT8 regulatory NSL complex subunit 3	Kansl3	NM_001310513.1	pcDNA3.1(+)/myc-HisB		
115	phospholipase D family, member 5	Pld5	NM_176916.4	pcDNA3.1(+)/myc-HisB		
116	Phospholipase A2, group XV	Pla2g15	NM_133792.3	pcDNA3.1(+)/myc-HisB		
117	Acyl-CoA Thioestesterase 6	Acot6	NM_172580.1	pcDNA™4/HisMaxC		
118	Arylacetamide Deacetylase-like 3	Aadacl3	NM_001085503.2	pcDNA3.1(+)/myc-HisB	x	x

119	Candidate tumor suppressor in ovarian cancer 2	Ovca2	NM_027136.3	pcDNA3.1(+)/myc-HisB		
120	Arylacetamide Deacetylase/Esterase	Aadac	NM_023383.1	pcDNA3.1(+)/myc-HisB	x	
121	Arylformamidase	Afmid	NM_027827.3	pcDNA3.1(+)/myc-HisB		
122	Acyl-CoA Thioesterase 5	Acot5	NM_145444.3	pcDNA™4/HisMaxC		
123	α/β Hydrolase Domain Containing 8	Abhd8	NM_022419.3	pcDNA™4/HisMaxC		
124	Acyl-CoA Thioesterase 4	Acot4	NM_134247.3	pcDNA™4/HisMaxC		
125	Biphenyl Hydrolase-like	Bphl	NM_026512.1	pcDNA3.1(+)/myc-HisB		
126	Butyrylcholinesterase	Bche	NM_009738	pcDNA3.1(+)/myc-HisB	x	
127	Carboxyl Ester Lipase	Cel	NM_009885.2	pcDNA3.1(+)/myc-HisB		
128	Carboxyesterase 2B	Ces2b	NM_198171.3	pcDNA3.1(+)/myc-HisB		
129	Carboxylesterase 1B	Ces1b	NM_001081372.1	pcDNA3.1(+)/myc-HisB		
130	Carboxylesterase 1F	Ces1f	NM_144930.2	pcDNA™4/HisMaxC	x	x
131	Carboxylesterase 2A	Ces2a	NM_133960.5	pFlag-CMV-5.1		
132	Carboxylesterase 1D	Ces1d	NM_053200.2	pFlag-CMV-5.1		
133	Carboxylesterase 2G	Ces2g	NM_197999.2	pFlag-CMV-5.1	x	
134	Carboxylesterase 2C	Ces2c	NM_145603.2	pFlag-CMV-5.1		
135	Carboxylesterase 1E	Ces1e	NM_133660.3	pcDNA™4/HisMaxC	x	
136	Carboxylesterase 2H	Ces2h	NM_001272045.2	pcDNA3.1(+)/myc-HisB	x	x
137	Carboxylesterase 1G	Ces1g	NM_021456.4	pcDNA™4/HisMaxC	x	
138	Carboxylesterase 3B	Ces3b	NM_144511.2	pcDNA™4/HisMaxC	x	
139	Carboxylesterase 1C	Ces1c	NM_007954.4	pcDNA™4/HisMaxC	x	
140	Diacylglycerol Lipase beta	Daglb	NM_144915.3	pcDNA™4/HisMaxC	x	
141	Dipeptidylpeptidase 7	Dpp7	NM_031843.2	pcDNA3.1(+)/myc-HisB	x	x
142	Lipase Family Member K	Lipk	NM_172837.4	pcDNA™4/HisMaxC	x	
143	Lecithin Cholesterol Acyltransferase	Lcat	NM_008490.2	pcDNA3.1(+)/myc-HisB		

144	Lipase Family Member M	Lipm	NM_023903.1	pcDNA™4/HisMaxC	x	
145	Lipase Family Member N	Lipn	NM_027340.2	pFlag-CMV-5.1	x	
146	Gastric Lipase	Lipf	NM_026334.3	pcDNA3.1(+)/myc-HisB		
147	Hepatic Lipase	Lipc	NM_008280.2	pcDNA3.1(+)/myc-HisB		
148	Fibroblast Activation Protein	Fap	NM_007986.3	pcDNA3.1(+)/myc-HisB	x	
149	Lipase Member O4	Lipo4	NM_001323386.1	pcDNA™4/HisMaxC		
150	Lipase Member H	Liph	NM_001083894.1	pcDNA™4/HisMaxC	x	
151	Lipoprotein Lipase	Lpl	NM_008509.2	pcDNA™4/HisMaxC		
152	Lysophospholipase 1	Lypla1	NM_008866.3	pcDNA3.1(+)/myc-HisB		
153	Lysophospholipase-like Protein	Lyplal1	NM_146106.2	pcDNA3.1(+)/myc-HisB		
154	Lysophospholipase 2	Lypla2	NM_011942.1	pcDNA™4/HisMaxC		
155	Lysosomal Acid Lipase A	Lipa	NM_021460.3	pcDNA™4/HisMaxC	x	
156	Monoglycerid Lipase	Mgl	NM_001166251.1	pcDNA™4/HisMaxC		
157	Neutral Cholesterol Ester Hydrolase 1	Nceh1	NM_178772.3	pcDNA™4/HisMaxC		
158	Oleoyl-ACP Hydrolase	Olah	NM_145921.1	pcDNA3.1(+)/myc-HisB		
159	Hormone Sensitive Lipase	Lipe	NM_010719.5	pcDNA™4/HisMaxC		
160	α/β Hydrolase Domain Containing 16a	Abhd16a	NM_178592.3	pcDNA™4/HisMaxC	x	
161	Carboxylesterase 2E	Ces2e	NM_172759.3	pFlag-CMV-5.1	x	
162	phospholipase A2, group IB, pancreas	Pla2g1b	XM_006538948.2	pcDNA3.1(+)/myc-HisB		
163	phospholipase A2, group IIE	Pla2g2e	NM_012044.2 (correct)	pcDNA3.1(+)/myc-HisB		
164	phospholipase A2, group XIIB	Pla2g12b	NM_023530.2	pcDNA3.1(+)/myc-HisB		
165	phospholipase A2, group XIIA	Pla2g12a	NM_001286948.1	pcDNA3.1(+)/myc-HisB		
166	phospholipase A2, group III	Pla2g3	NM_172791.2	pcDNA3.1(+)/myc-HisB		
167	phospholipase A2, group X	Pla2g10	NM_001291009.2	pcDNA3.1(+)/myc-HisB		

168	phospholipase A2, group IIC	Pla2g2c	NM_008868.3	pcDNA3.1(+)/myc-HisB		
169	otoconin 90	Oc90	NM_010953.2	pcDNA3.1(+)/myc-HisB		
170	phospholipase A2, group IIF	Pla2g2f	NM_012045.4	pcDNA3.1(+)/myc-HisB	x	
171	α/β Hydrolase Domain Containing 17a	Abhd17a	NM_145421.2	pcDNA™4/HisMaxC		
172	α/β Hydrolase Domain Containing 17b	Abhd17b	NM_146096.3	pcDNA™4/HisMaxC	x	x
173	α/β Hydrolase Domain Containing 5	Abhd5	NM_026179.2	pcDNA™4/HisMaxC		
174	phospholipase A2, group IID	Pla2g2d	NM_011109.2	pcDNA3.1(+)/myc-HisB		
175	α/β Hydrolase Domain Containing 3	Abhd3	NM_134130.1	pcDNA™4/HisMaxC		
176	α/β Hydrolase Domain Containing 16b	Abhd16b	NM_183181.2	pcDNA™4/HisMaxC		
177	α/β Hydrolase Domain Containing 12b	Abhd12b	NM_001195033.2	pcDNA™4/HisMaxC		
178	Acyl-CoA Thioestesterase 3	Acot3	NM_134246.3	pcDNA™4/HisMaxC		
179	patatin-like phospholipase domain containing 5	Pnpla5	NM_029427.1	pcDNA™4/HisMaxC		
180	Pancreatic Lipase Related Protein 1	Pnliprp1	NM_018874.2	pFlag-CMV-5.1		
181	Phospholipase A1 Member A	Pla1a	NM_134102.4	pcDNA3.1(+)/myc-HisB		
182	α/β Hydrolase Domain Containing 9 (epoxide hydrolase 3)	Ephx3	NM_001033163.4	pcDNA™4/HisMaxC		
183	α/β Hydrolase Domain Containing 7 (epoxide hydrolase 4)	Ephx4	NM_001001804.2	pcDNA™4/HisMaxC		
184	Serine Hydrolase-like	Serhl	NM_023475.3	pcDNA3.1(+)/myc-HisB		
185	epoxide hydrolase 1, microsomal	Ephx1	NM_010145.3	pcDNA3.1(+)/myc-HisB		
186	Serine active site containing 1	Serac1	NM_001111017.1	pcDNA3.1(+)/myc-HisB	x	
187	phospholipase A2, group IVF	Pla2g4f	NM_001024145.3	pcDNA3.1(+)/myc-HisB		
188	prokineticin 1	Prok1	NM_001044382.2	pcDNA3.1(+)/myc-HisB		
189	prolyl endopeptidase-like	Prepl	NM_001163622.1	pcDNA3.1(+)/myc-HisB		
190	family with sequence similarity 83, member D	Fam83d	NM_027975.2	pcDNA3.1(+)/myc-HisB	x	x
191	phospholipase A2, group V	Pla2g5	NM_001122954.1	pcDNA3.1(+)/myc-HisB		

192	α/β Hydrolase Domain Containing 15	Abhd15	NM_026185.4	pcDNA™4/HisMaxC		
193	α/β Hydrolase Domain Containing 12	Abhd12	NM_024465.3	pcDNA™4/HisMaxC		
194	α/β Hydrolase Domain Containing 2	Abhd2	NM_018811.6	pcDNA™4/HisMaxC		
195	Acyl-CoA Thioestesterase 2	Acot2	NM_134188.3	pcDNA™4/HisMaxC	x	
196	androgen-induced gene 1 protein	Aig1	NM_025446.4	pcDNA3.1(+)/myc-HisB		
197	androgen-dependent TFPI-regulating protein	Adtrp	NM_001145875	pcDNA3.1(+)/myc-HisB		
198	Acylpeptide Hydrolase	Apeh	NM_146226.2	pcDNA3.1(+)/myc-HisB		
199	α/β Hydrolase Domain Containing 6	Abhd6	NM_025341.3	pcDNA™4/HisMaxC		
200	phospholipase B domain containing 2 (Plbd2)	Plbd2	NM_023625.4	pcDNA™4/HisMaxC	x	x
201	phospholipase A and acyltransferase 1	Plaat1	NM_020386.4:92-913	pcDNA3.1(+)/myc-His C		
202	phospholipase A and acyltransferase 2	Plaat2	NM_017878.1:60-548	pcDNA3.1(+)/myc-His C	x	
203	phospholipase A and acyltransferase 3	Plaat3	NM_001128203.1:140-628	pcDNA3.1(+)/myc-His C		
204	phospholipase A and acyltransferase 4	Plaat4	NM_004585.4:69-563	pcDNA3.1(+)/myc-His C		
205	phospholipase A and acyltransferase 5	Plaat5	NM_001146728.1:175-936	pcDNA3.1(+)/myc-His C		
206	lecithin-retinol acyltransferase	Lrat	NM_023624.4	pcDNA™4/HisMaxC		
no Westernblot signal no activity						
	total	no wb siganl	no wb no activity			
#	206	53	19			
%	100	25,7	9,2			
		74,3	90,8			
	Human PLA2G4 Constructs					
	Full Name	**Gene Name**	**Acession Number**	**Expression vector**		
	Homo sapiens phospholipase A2 group IVA (PLA2G4A), transcript variant 1	PLA2G4A	NM_024420.3	pcDNA3.1(+)/myc-His C		
	Homo sapiens phospholipase A2 group IVB (PLA2G4B)	PLA2G4B	NM_001114633.2	pcDNA3.1(+)/myc-His C		

	Homo sapiens phospholipase A2 group IVC (PLA2G4C), transcript variant 1	PLA2G4C	NM_003706.3	pcDNA3.1(+)/myc-His C		
	Homo sapiens phospholipase A2 group IVD (PLA2G4D)	PLA2G4D	NM_178034.4	pcDNA3.1(+)/myc-His C		
	Homo sapiens phospholipase A2 group IVE (PLA2G4E), transcript variant 1	PLA2G4E	NM_001206670.1	pcDNA3.1(+)/myc-His C		
	Homo sapiens phospholipase A2 group IVF (PLA2G4F), transcript variant 1	PLA2G4F	NM_213600.4	pcDNA3.1(+)/myc-His C		

Table S3: **MRM-Transition list**

Compound Name	Prec Ion	Prod Ion	Frag (V)	CE (V)	Cell Acc (V)	Polarity
BDP 18_1	1321.1	603.4	120	27	4	Positive
BMP 28:0 (14:0-14:0)	667.4	285.2	135	25	5	Positive
BMP 28:0 (14:0-14:0)	665.4	227.2	250	35	4	Negative
BMP 32:0 (16:0-16:0)	723.5	313.2	135	25	5	Positive
BMP 32:0 (16:0-16:0)	721.5	255.2	250	35	4	Negative
BMP 32:1 (16:0-16:1)	721.5	311.2	135	35	5	Positive
BMP 32:1 (16:0-16:1)	719.5	253.2	250	35	4	Negative
BMP 34:0 (16:0-18:0)	751.5	341.3	135	25	5	Positive
BMP 34:0 (16:0-18:0)	749.5	283.2	250	35	4	Negative
BMP 34:1 (16:0-18:1)	749.5	339.3	135	25	5	Positive
BMP 34:1 (16:0-18:1)	747.51	281.2	250	35	4	Negative
BMP 34:2 (16:0-18:2)	747.5	337.3	135	25	5	Positive
BMP 34:2 (16:0-18:2)	745.5	279.2	250	35	4	Negative
BMP 36:0 (18:0-18:0)	779.5	341.3	135	25	5	Positive
BMP 36:0 (18:0-18:0)	777.5	283.2	250	35	4	Negative
BMP 36:1 (18:0-18:1)	777.5	341.3	135	25	5	Positive
BMP 36:1 (18:0-18:1)	775.5	283.2	250	35	4	Negative
BMP 36:2 (18:1-18:1)	775.5	339.3	135	25	5	Positive
BMP 36:2 (18:1-18:1)	773.5	281.24	250	35	4	Negative
BMP 36:3 (18:1-18:2)	773.5	339.3	135	25	5	Positive
BMP 36:3 (18:1-18:2)	771.5	279.2	250	35	4	Negative
BMP 36:4 (18:2-18:2)	771.5	337.3	135	25	5	Positive
BMP 36:4 (18:2-18:2)	769.5	279.23	250	35	4	Negative
BMP 36:5 (18:2-18:3)	769.5	335.25	135	25	5	Positive
BMP 36:5 (18:2-18:3)	767.5	277.2	250	35	4	Negative
BMP 38:4 (18:0-20:4)	799.5	361.3	135	25	5	Positive
BMP 38:4 (18:0-20:4)	797.5	303.2	250	35	4	Negative
BMP 38:5 (18:1-20:4)	797.5	361.3	135	25	5	Positive
BMP 38:5 (18:1-20:4)	795.5	303.23	250	35	4	Negative
BMP 38:5 (18:2-20:3)	797.5	363.3	135	25	5	Positive
BMP 38:5 (18:2-20:3)	795.5	305.2	250	35	4	Negative
BMP 38:6 (16:0-22:6)	795.5	313.2	135	25	5	Positive
BMP 38:6 (16:0-22:6)	793.5	255.2	250	35	4	Negative
BMP 38:6 (18:2-20:4)	795.5	361.3	135	25	5	Positive
BMP 38:6 (18:2-20:4)	793.5	303.23	250	35	4	Negative
BMP 38:7 (16.1-22:6)	793.5	385.3	135	25	5	Positive
BMP 38:7 (16.1-22:6)	791.48	327.23	250	35	4	Negative
BMP 38:7 (18:3-20:4)	793.5	335.25	135	25	5	Positive
BMP 38:7 (18:3-20:4)	791.48	277.2	250	35	4	Negative
BMP 40:5 (18:1-22:4)	825.5	389.3	135	25	5	Positive
BMP 40:5 (18:1-22:4)	823.5	331.3	250	35	4	Negative
BMP 40:6 (18:1-22:5)	823.5	387.28	135	25	5	Positive
BMP 40:6 (18:1-22:5)	821.5	329.3	250	35	4	Negative
BMP 40:6 (18:2-22:4)	823.5	389.23	135	25	5	Positive
BMP 40:6 (18:2-22:4)	821.5	331.3	250	35	4	Negative
BMP 40:7 (18:1-22:6)	821.5	385.2	135	25	5	Positive
BMP 40:7 (18:1-22:6)	819.5	327.23	250	35	4	Negative
BMP 40:7 (18:2-22.5)	819.5	329.2	250	35	4	Negative
BMP 40:7 (18:2-22:5)	821.5	387.2	135	25	5	Positive
BMP 40:8 (18:2-22:6)	819.5	385.2	135	25	5	Positive
BMP 40:8 (18:2-22:6)	817.5	303.23	250	35	4	Negative
BMP 40:8 (20:4-20:4)	819.5	361.3	135	25	5	Positive
BMP 40:8 (20:4-20:4)	817.5	327.23	250	35	4	Negative

BMP 40:9 (18:3-22:6)	817.48	335.25	135	25	5	Positive
BMP 40:9 (18:3-22:6)	815.48	277.3	250	35	4	Negative
BMP 42:10 (20:4-22:6)	843.5	385.3	135	25	5	Positive
BMP 42:10 (20:4-22:6)	841.5	327.23	250	35	4	Negative
BMP 42:8 (20:4-22:4)	847.5	361.2	135	25	5	Positive
BMP 42:8 (20:4-22:4)	845.5	303.2	250	35	4	Negative
BMP 42:9 (20:3-22:6)	845.5	385.3	135	25	5	Positive
BMP 42:9 (20:3-22:6)	843.5	327.2	250	35	4	Negative
BMP 44:10 (22:4-22:6)	871.5	389.3	135	25	5	Positive
BMP 44:10 (22:4-22:6)	869.5	331.2	250	35	4	Negative
BMP 44:11 (22:5-22:6)	869.5	387.3	135	25	5	Positive
BMP 44:11 (22:5-22:6)	867.5	329.2	250	35	4	Negative
BMP 44:12 (22:6-22:6)	867.5	385.2	135	25	5	Positive
BMP 44:12 (22:6-22:6)	865.5	327.2	250	35	4	Negative
Hemi BMP 14:0	894.67	894.67	135	0	5	Positive
Hemi BMP 14:0	894.67	495.4	135	25	5	Positive
Hemi BMP 14:0 (14:0-14:0-14:0)	875.63	227.2	290	44	4	Negative
Hemi-BMP 52:2 (16:0-18:1-18:1)	1030.8	1030.8	135	0	5	Positive
Hemi-BMP 52:2 (16:0-18:1-18:1)	1030.8	603.4	135	27	5	Positive
Hemi-BMP 52:2 (16:0-18:1-18:1)	1011.76	281.2	290	44	4	Negative
Hemi-BMP 54:2 (18:0-18:1-18:1)	1058.8	1058.8	135	0	5	Positive
Hemi-BMP 54:2 (18:0-18:1-18:1)	1058.8	603.4	135	27	5	Positive
Hemi-BMP 52:2 (16:0-18:1-18:1)	1011.76	255.2	290	44	4	Negative
Hemi-BMP 54:2 (18:0-18:1-18:1)	1039.79	283.2	290	44	4	Negative
Hemi-BMP 54:2 (18:0-18:1-18:1)	1039.79	281.2	290	44	4	Negative
Hemi-BMP 54:3 (18:1-18:1-18:1)	1056.8	1056.8	135	0	5	Positive
Hemi-BMP 54:3 (18:1-18:1-18:1)	1056.8	603.4	135	25	5	Positive
Hemi-BMP 54:3 (18:1-18:1-18:1)	1037.7	281.2	290	44	4	Negative
Hemi-BMP 54:4 (18:2-18:1-18:1)	1054.8	1054.8	135	0	5	Positive
Hemi-BMP 54:4 (18:2-18:1-18:1)	1054.8	603.4	135	27	5	Positive
Hemi-BMP 54:4 (18:2-18:1-18:1)	1035.76	281.2	290	44	4	Negative
Hemi-BMP 54:4 (18:2-18:1-18:1)	1035.76	279.2	290	44	4	Negative
LPG 14:0	455.24	227.2	180	28	4	Negative
LPG 16:0	483.27	255.2	180	28	4	Negative
LPG 16:1	481.25	253.2	180	28	4	Negative
LPG 17:1	495.2	267.2	180	28	4	Negative
LPG 18:0	511.3	283.2	180	28	4	Negative
LPG 18:1	509.28	281.2	180	28	4	Negative
LPG 18:2	507.27	279.2	180	28	4	Negative
LPG 20:4	531.27	303.2	180	28	4	Negative
LPG 22:6	555.27	327.2	180	28	4	Negative
PG 32:0 (16:0-16:0)	740.5	551.5	135	15	5	Positive
PG 32:0 (16:0-16:0)	721.48	255.2	300	45	4	Negative
PG 32:1 (16:0-16:1)	738.5	549.48	135	15	5	Positive
PG 32:1 (16:0-16:1)	719.48	253.2	300	45	4	Negative
PG 34:0 (17:0-17:0)	768.5	579.5	135	15	5	Positive
PG 34:0 (17:0-17:0)	749.5	269.2	300	45	4	Negative

PG 34:1 (16:0-18:1)	766.5	577.5	135	15	5	Positive
PG 34:1 (16:0-18:1)	747.51	255.2	300	45	4	Negative
PG 34:2 (16:0-18:2)	764.5	575.5	135	15	5	Positive
PG 34:2 (16:0-18:2)	745.5	255.2	300	45	4	Negative
PG 34:2 (16:1-18:1)	764.5	575.5	135	15	5	Positive
PG 34:2 (16:1-18:1)	745.5	281.2	300	45	4	Negative
PG 34:3 (16:1-18:2)	762.5	573.4	135	15	5	Positive
PG 34:3 (16:1-18:2)	743.48	253.2	300	45	4	Negative
PG 36:0 (18:0-18:0)	796.6	607.5	135	15	5	Positive
PG 36:0 (18:0-18:0)	777.5	283.2	300	45	4	Negative
PG 36:1(18:0-18:1)	794.5	605.5	135	15	5	Positive
PG 36:1(18:0-18:1)	775.5	281.2	300	45	4	Negative
PG 36:2 (18:1-18:1)	792.5	603.5	135	15	5	Positive
PG 36:2 (18:1-18:1)	773.5	281.28	300	45	4	Negative
PG 36:3 (18:1-18:2)	790.5	601.5	135	15	5	Positive
PG 36:3 (18:1-18:2)	771.5	281.28	300	45	4	Negative
PG 36:4 (16:0-20:4)	788.5	599.5	135	15	5	Positive
PG 36:4 (16:0-20:4)	769.5	255.23	300	45	4	Negative
PG 36:4 (18:2-18:2)	788.5	599.5	135	15	5	Positive
PG 36:4 (18:2-18:2)	769.5	279.23	300	45	4	Negative
PG 38:4 (18:0-20:4)	816.5	627.5	135	15	5	Positive
PG 38:4 (18:0-20:4)	797.5	283.2	300	45	4	Negative
PG 38:5 (18:1-20:4)	814.5	625.5	135	15	5	Positive
PG 38:5 (18:1-20:4)	795.5	281.2	300	45	4	Negative
PG 38:6 (16:0-22:6)	812.5	623.5	135	15	5	Positive
PG 38:6 (16:0-22:6)	793.5	255.23	300	45	4	Negative