

Table 1S. Differences in GC levels between normal (control) lymphoblasts and N370S/N370S lymphoblasts treated for 10 or 15 days with ABX, IFG or DMSO (Mock) using ABX as the reference category¹.

GC Species	Control (WT)	ABX vs. control	p	ABX vs. IFG	p	ABX vs. Mock	p
	pmol/mg protein	EST (95% CI)²		EST (95% CI)		EST (95% CI)	
GC 16 ³	359 ± 17 ⁴	+324 (+305, +342)	<0.001	-252 (-215, -290)	<0.001	-404 (-362, -447)	<0.001
GC 18	45.5 ± 2	+65 (+58, +71)	<0.001	-48 (-33, -64)	<0.001	-26 (-13, -41)	<0.001
GC 20	59.2 ± 3	+31 (+24, +37)	<0.001	-43 (-33, -54)	<0.001	-24 (-12, -37)	<0.001
GC 22	131 ± 5	+60 (+47, +71)	<0.001	-51 (-33, -70)	<0.001	-30 (-13, -48)	<0.001
GC 24	93.5 ± 4	+80 (+70, +89)	<0.001	-40 (-23, -58)	<0.001	-14 (-30, +2)	0.08
GC 24:1 ⁵	185 ± 6	-22 (-7, -39)	0.003	-39 (-22, -56)	0.001	-28 (-12, -45)	<0.001
GC total	873 ± 32	+539 (+508, +568)	<0.001	-625 (-569, -682)	<0.001	-374 (-324, -508)	<0.001

1. A separate model was created using the mock group as a reference to determine whether there were any differences between the mock- and IFG-group (data not shown). Significant increases were found in all but the GC 24:1 species in the IFG- versus Mock-group.
2. A linear regression model using maximum likelihood algorithm for parameter estimation was used to determine the significance of the differences between all the groups. The first value (EST) represents the average difference between groups, with the 95% confidence interval (95% CI). If all 3 values are positive or all 3 values are negative, the difference is statistically significant. For example, on average the major GC16 form is 324 pmol/mg protein higher in the ABX group than in the control, with a confidence interval of 305 to 342, which is statistically significant. Only the ABX vs. Mock difference for the GC 24 form is not significant.
3. Refers to the carbon chain length of the fatty acid moiety, which defines the individual forms of GC
4. Standard error
5. GC containing a 24-carbon fatty acid chain with 1 double bond

Table 2S. Deuteration levels of specific GCase segments in the presence of IFG, ABX and FNZ as a function of four exchange periods (30, 100, 300, 1,000 and 3,000 s).

numbering					isofagomine						fluphenazine						ambroxol					
-propeptide	+propeptide	Z	30	100	300	1000	3000	avg	30	100	300	1000	3000	avg	30	100	300	1000	3000	avg		
34	37	73	76	1	4%	2%	3%	3%	6%	4%	0%	3%	-3%	-1%	7%	1%	5%	2%	-1%	6%	-1%	2%
39	51	78	90	2	2%	-1%	0%	1%	0%	0%	1%	-1%	1%	0%	0%	0%	2%	-3%	-1%	5%	-1%	1%
69	91	108	130	2	-1%	-3%	-1%	0%	-5%	-2%	-4%	-1%	0%	-1%	-2%	-2%	-1%	-3%	0%	1%	-5%	-2%
97	103	136	142	1	-3%	-3%	-3%	0%	-1%	-2%	-4%	-3%	-4%	-6%	0%	-3%	-5%	-1%	-4%	-2%	-2%	-3%
108	117	147	156	2	-7%	1%	-1%	4%	8%	1%	-3%	1%	-1%	8%	6%	2%	-6%	-3%	-5%	8%	3%	-1%
119	127	158	166	1	-10%	-8%	-13%	-9%	-22%	-12%	-1%	-2%	0%	-5%	-8%	-3%	2%	0%	-3%	-2%	-9%	-2%
130	134	169	173	1	-6%	-16%	-4%	2%	-2%	-5%	-7%	-14%	-2%	4%	5%	-3%	-2%	-9%	-5%	1%	-6%	-4%
135	142	174	181	1	-4%	-6%	-6%	-1%	-3%	-4%	-4%	-11%	-5%	-8%	-6%	-7%	-1%	-7%	-4%	5%	-7%	-3%
156	167	195	206	2	1%	-2%	-2%	3%	-3%	0%	3%	0%	-2%	1%	-3%	0%	-1%	-1%	-1%	3%	-1%	0%
170	174	209	213	1	4%	-3%	1%	3%	-3%	1%	-1%	-4%	0%	1%	-2%	-2%	3%	-3%	4%	1%	-12%	-2%
177	185	216	224	1	1%	-7%	-11%	-12%	-18%	-9%	0%	-4%	-7%	-6%	-5%	-4%	-1%	-6%	-7%	-3%	-8%	-5%
187	197	226	236	1	-18%	-18%	-9%	-6%	-9%	-12%	-11%	-11%	-3%	-4%	-2%	-6%	-15%	-12%	-8%	-1%	-8%	-9%
200	212	239	251	2	1%	-1%	-3%	-3%	-6%	-2%	3%	1%	-3%	-1%	-4%	-1%	4%	-2%	-3%	2%	-1%	0%
215	219	254	258	1	0%	0%	0%	-1%	0%	0%	0%	0%	0%	-1%	0%	0%	-1%	0%	-1%	-1%	-1%	-1%
222	227	261	266	1	0%	-4%	1%	1%	-1%	-1%	-3%	-4%	1%	-3%	-1%	-2%	0%	-1%	-2%	3%	-2%	-1%
230	240	269	279	1	-4%	-8%	-13%	-14%	-14%	-10%	-4%	-8%	-11%	-16%	-17%	-11%	-3%	-6%	-12%	-10%	-8%	-8%
243	249	282	288	1	-15%	-31%	-45%	-48%	-51%	-38%	-21%	-35%	-37%	-25%	-9%	-26%	-17%	-29%	-35%	-11%	-6%	-19%
252	259	291	298	2	-1%	-6%	-6%	-3%	-1%	-4%	-1%	-7%	-8%	-5%	-4%	-5%	-1%	0%	-1%	2%	-3%	-1%
281	283	320	322	1	-3%	-3%	-3%	3%	-4%	-2%	0%	-6%	5%	3%	1%	1%	4%	0%	6%	3%	2%	3%
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315	336	354	375	2	-8%	-15%	-3%	3%	-4%	-6%	-13%	-20%	-7%	2%	-3%	-8%	-2%	-8%	-1%	5%	-3%	-2%
343	347	382	386	1	1%	-6%	-6%	-11%	-22%	-9%	5%	-2%	-4%	-7%	-7%	-3%						
350	362	389	401	2	-7%	-9%	-7%	-7%	-10%	-8%	-4%	-7%	-5%	-3%	-1%	-4%	2%	-7%	-4%	4%	-5%	-2%
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374	383	413	422	1	0%	-2%	-2%	-2%	-9%	-3%	-1%	-4%	-1%	-2%	-5%	-3%	-1%	-1%	-3%	-1%	-5%	-2%
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399	405	438	444	1	-1%	-4%	-2%	-1%	-2%	-2%	0%	-4%	-1%	-2%	-2%	-2%	-1%	-2%	-2%	0%	-1%	-1%
408	411	447	450	1	0%	-1%	0%	3%	0%	0%	1%	1%	3%	-1%	1%	1%	7%	1%	5%	7%	8%	6%
414	417	453	456	1	-5%	-14%	-20%	-28%	-31%	-19%	-2%	-10%	-5%	-3%	-1%	-4%	3%	0%	-4%	4%	8%	2%
420	426	459	465	1	1%	-6%	3%	5%	0%	1%	-2%	-4%	1%	2%	1%	-1%	3%	-2%	-3%	4%	0%	0%
429	436	468	475	2	4%	-2%	1%	1%	0%	1%	0%	0%	-1%	1%	1%	0%	2%	-1%	1%	2%	-4%	0%
435	446	474	485	2	2%	-3%	-1%	3%	1%	1%	0%	-3%	0%	0%	1%	-1%	1%	-5%	-2%	7%	-1%	0%
449	457	488	496	1	-3%	-3%	-1%	1%	0%	-1%	-3%	-4%	1%	-1%	1%	-1%	-1%	0%	0%	4%	0%	0%
459	461	498	500	1	2%	2%	0%	-1%	1%	1%	-1%	4%	2%	-1%	2%	1%	-4%	3%	-1%	-5%	-2%	-2%
464	480	503	519	2	1%	-2%	-1%	-1%	1%	0%	1%	-2%	-1%	-1%	3%	0%	0%	-3%	0%	1%	1%	0%
482	493	521	532	2	-2%	-6%	-2%	-2%	0%	-2%	0%	-2%	0%	-3%	-5%	-2%	-1%	0%	-2%	0%	-9%	-2%

Negative perturbations $\leq -9\%$ are highlighted in blue.

Figure 1S

A) Histogram showing the total amounts (pmol/mg total protein) of different lipid species found in extracts from Wild Type (WT) (black bars), and ABX- (hatched), IFG- (grey) or Mock, DMSO- (white) treated N370S/N370S patient lymphoblasts grown for 10 days in culture. The total amount of each lipid is derived by summing the amounts of each of the lipid's isoforms, which were determined by triplicate assays (see accompanying figure showing levels of all isoforms that could be detected and quantified for each lipid). Standard error (n=3) is shown. The higher levels of lipids SM, PE and PC are shown on the right Y-axis, levels of other lipids are displayed on the left Y-axis. The abbreviations of individual lipid species used in this and accompanying supplementary figures are as follows: Glucosylceramide (GC), Ceramide (CER), Phosphatidylserine (PS), Phosphatidylinositol (PI), Lactosylceramide (LC), Ceramide TriHexoside (CTH), Sphingomyelin (SM), Phosphatidylcholine (PC) and Phosphatidylethanolamine (PE).

B) Histogram showing amount (pmol/mg) of different GC isoforms from extracts of Wild Type (WT) (black bars), and ABX (hatched), IFG (grey) or DMSO (white) treated N370S/N370S patient lymphoblasts grown in the presence of the drug for 10 days. The amount of each isoform represents the average of three independent analyses. The total amount of GC is derived by summing the amounts of the different GC isoforms for the triplicate determinations. Standard error (n=3) is shown. The higher levels of lipids GC C16 and GC (total level) are shown on the right Y-axis, levels of the other GC isoforms are displayed on the left Y-axis.

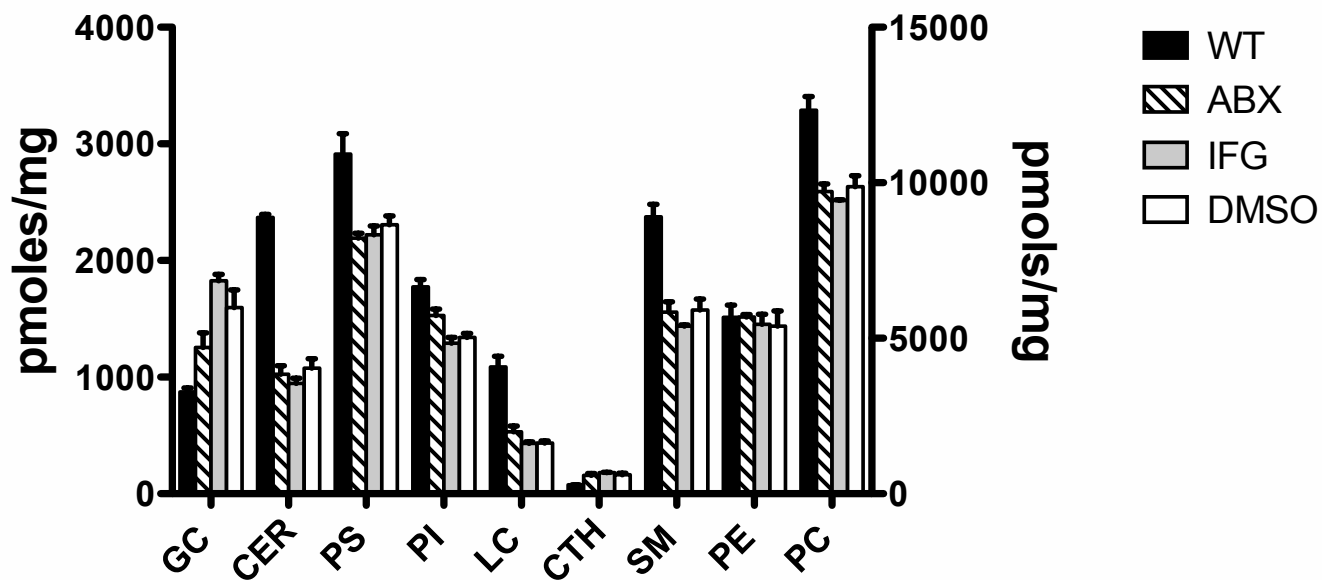
Figure 2S.

Scatterplots showing the levels (n=3) of each of the Lipid's isoforms that could be identified and measured in extracts from Wild Type (Control_1, black bars), and ABX (ABX_1, hatched), IFG (IFG_1, grey) or DMSO (Mock_1, white) treated N370S/N370S patient fibroblasts, grown in culture for 10 days. Horizontal line denotes the average amount. The size of the lipid alkyl chains are prefixed with the abbreviation for chain(C) followed by the number of carbon atoms. The presence of double bonds in the alkyl chain is denoted by the number prefixed with a backslash.

Fig. 1.Suppl.

A.

Lipid Species



B.

GC isoforms

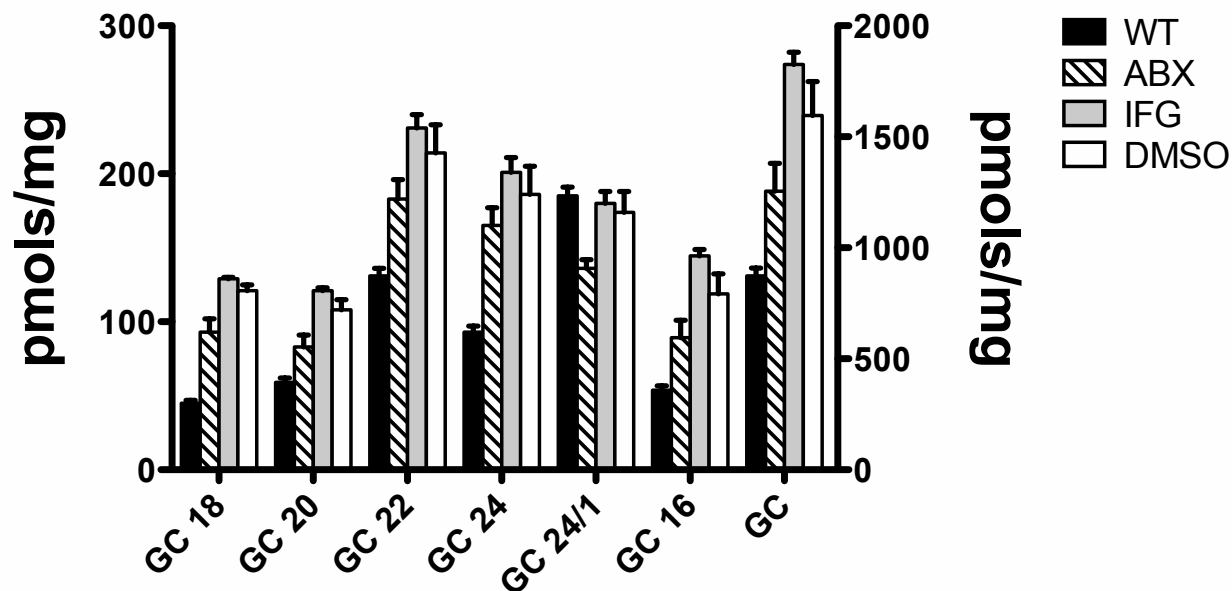
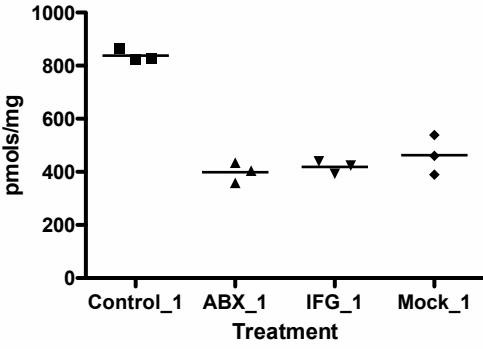
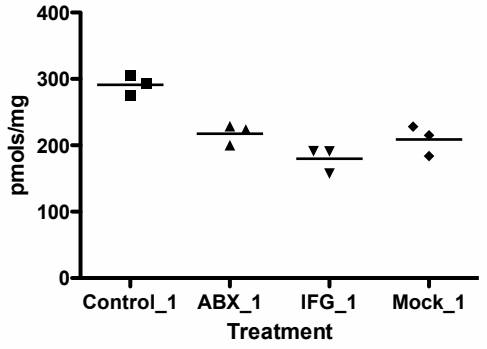


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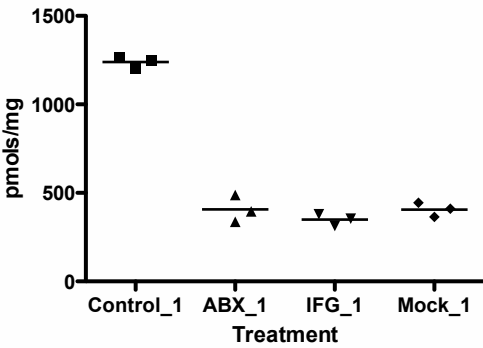
CER C16



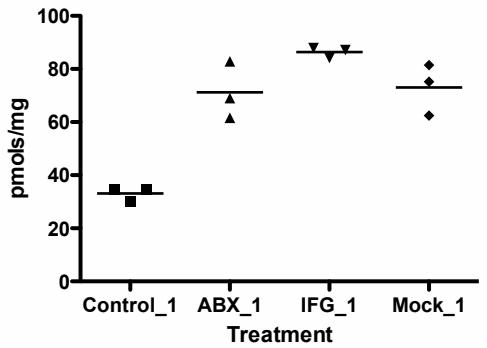
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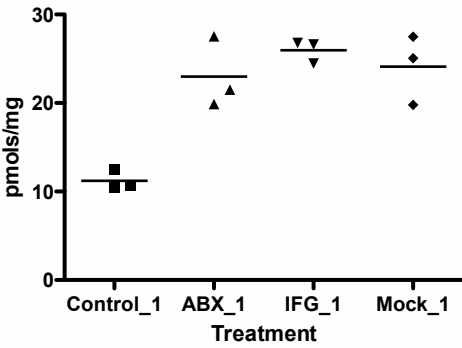
CER C24/1



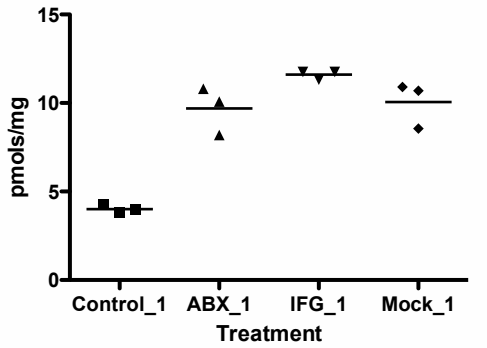
CTH C16



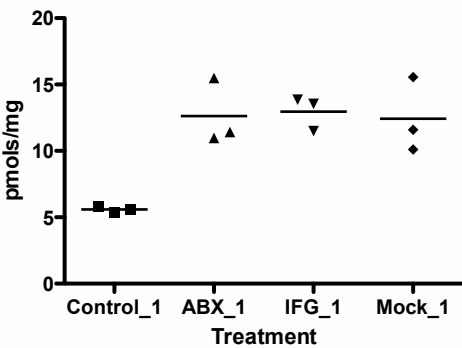
CTH C18



CTH C20



CTH C22



CTH C24

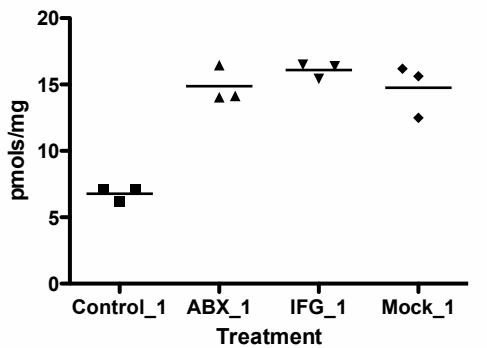


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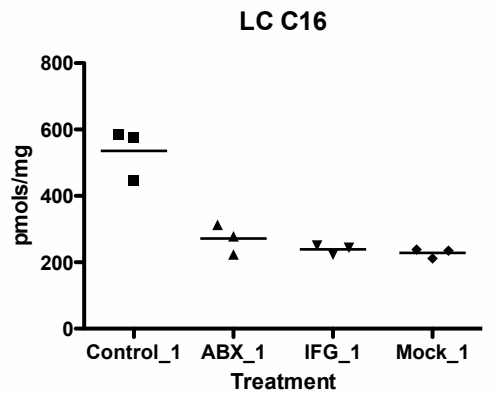
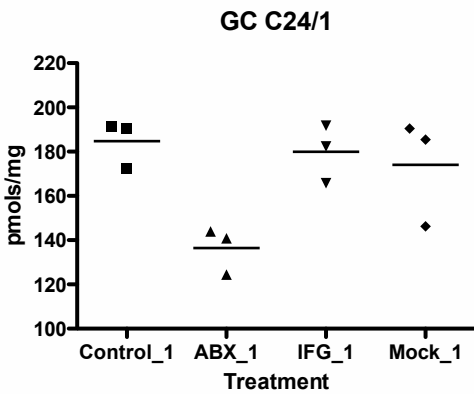
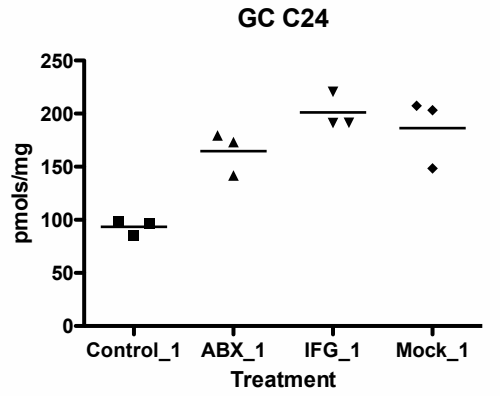
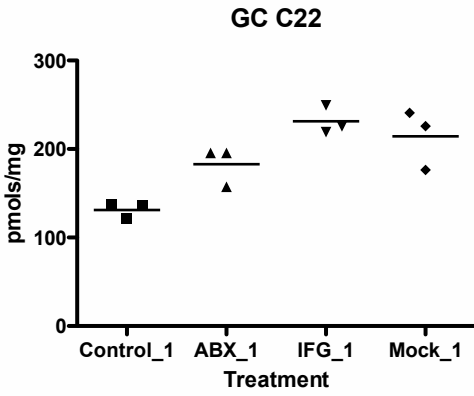
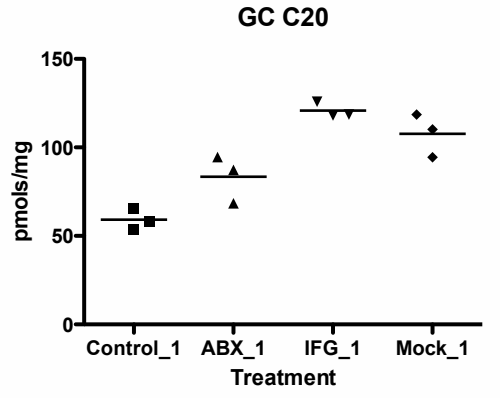
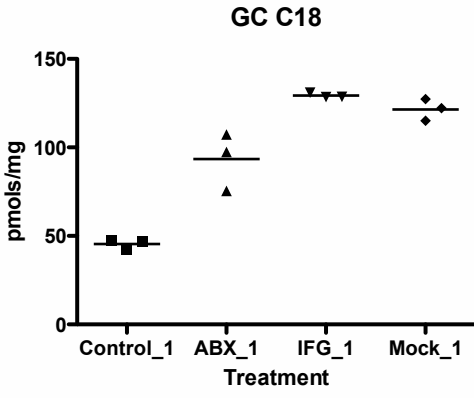
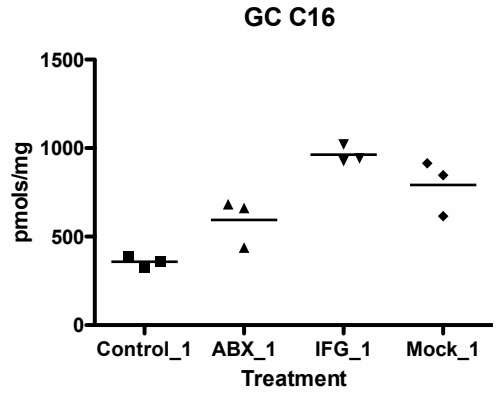
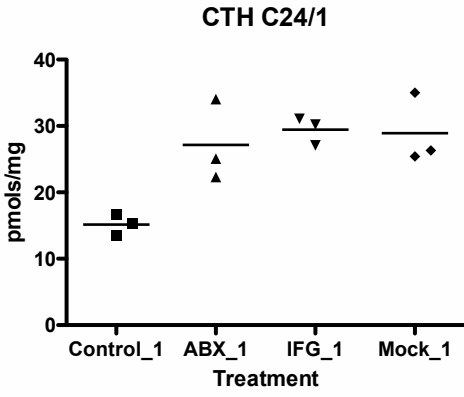


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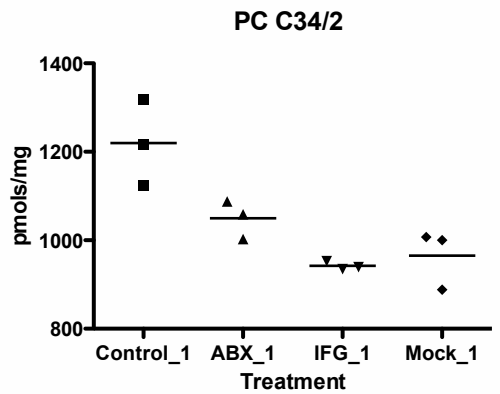
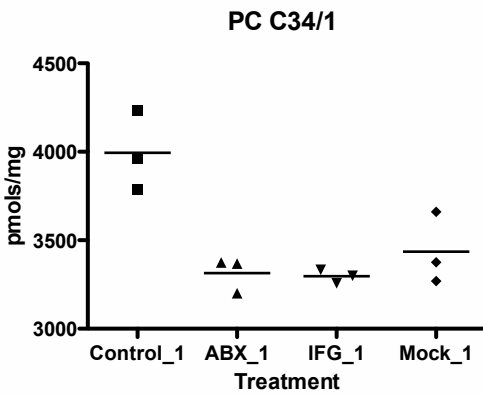
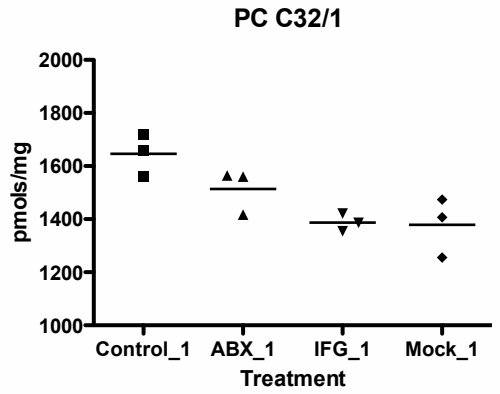
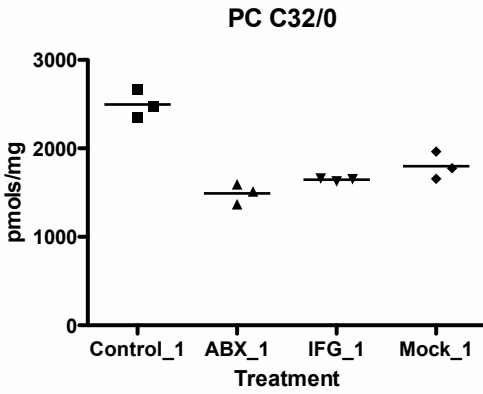
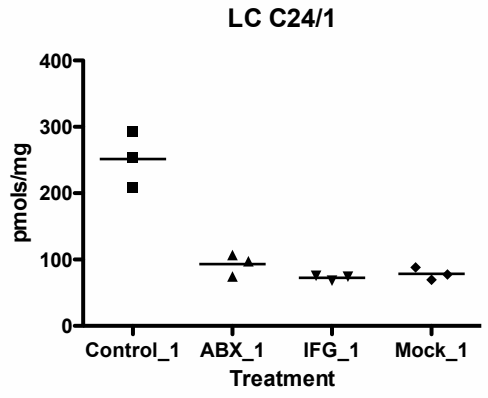
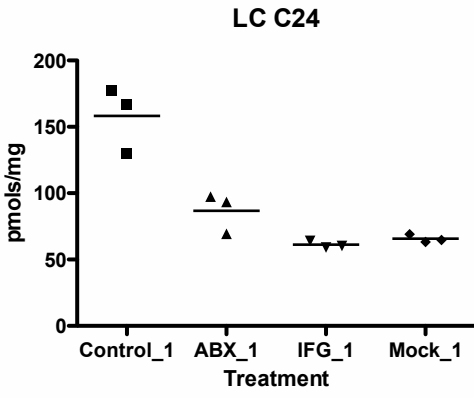
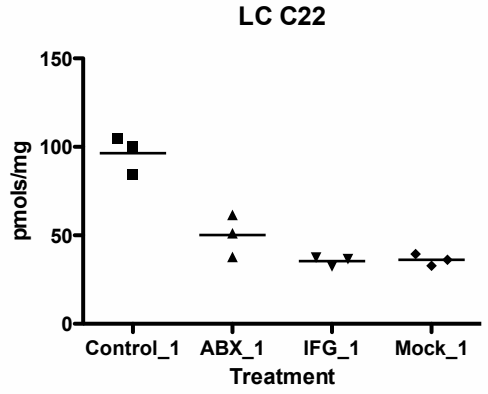
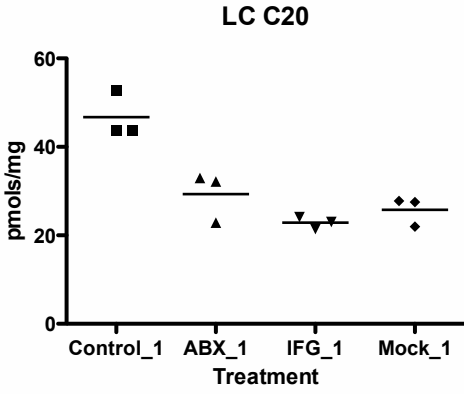


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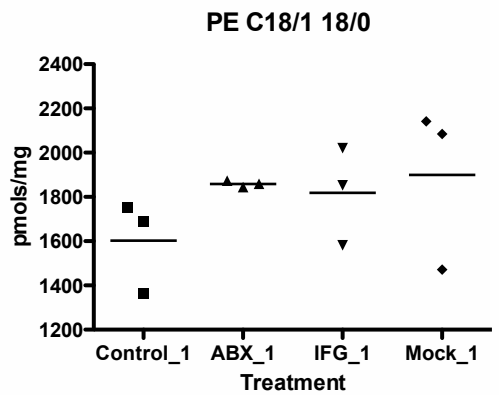
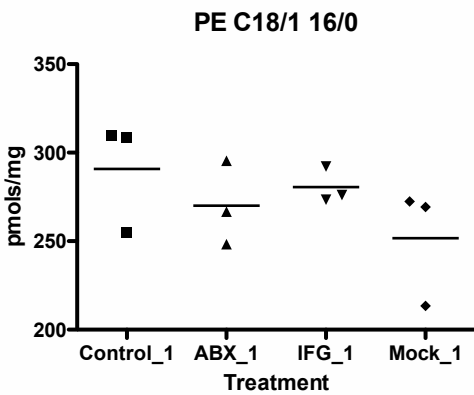
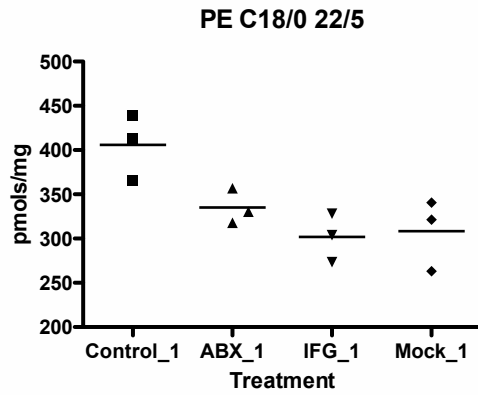
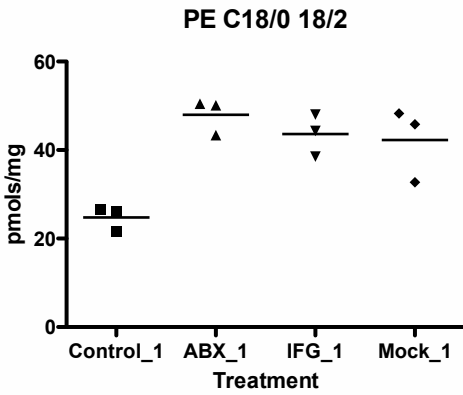
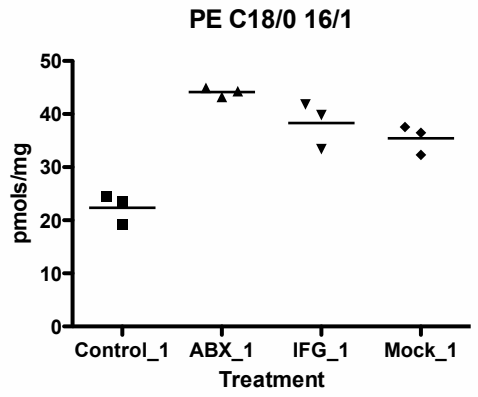
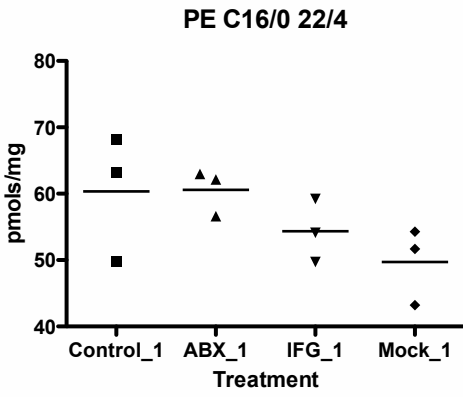
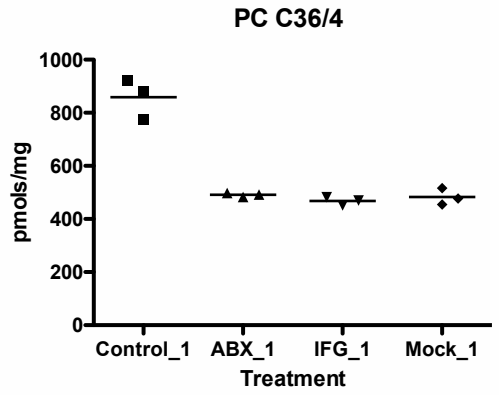
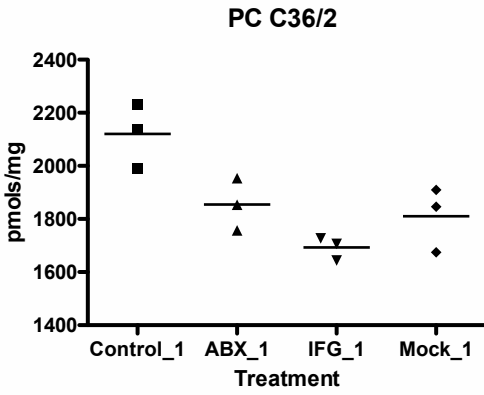


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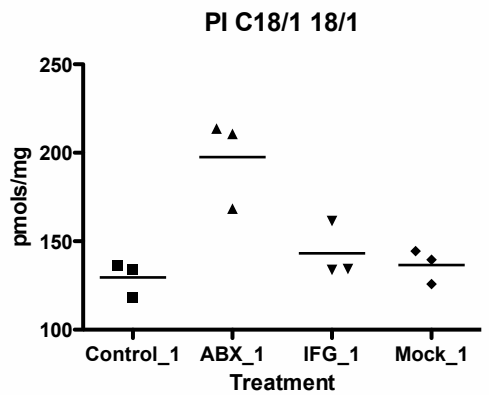
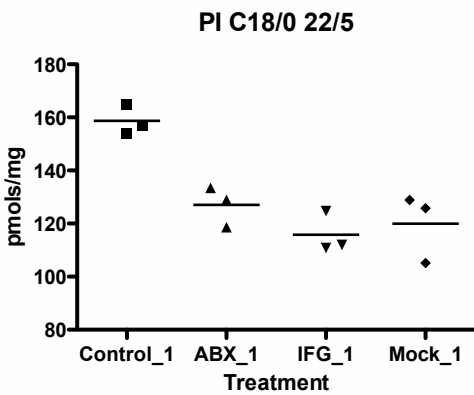
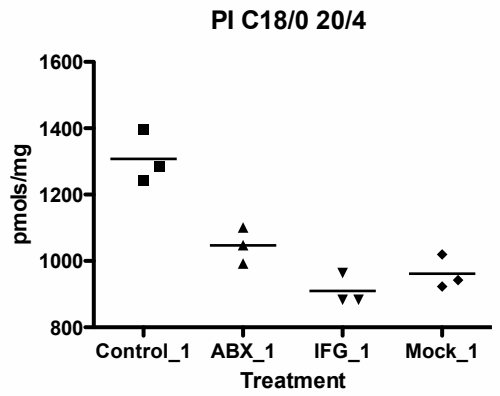
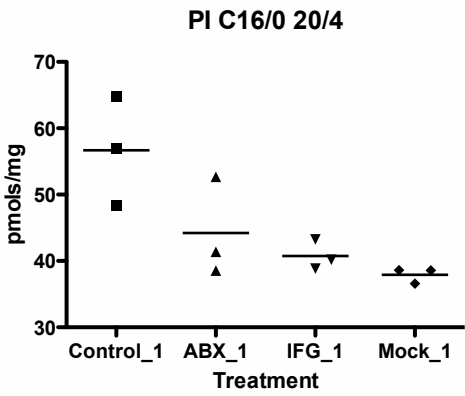
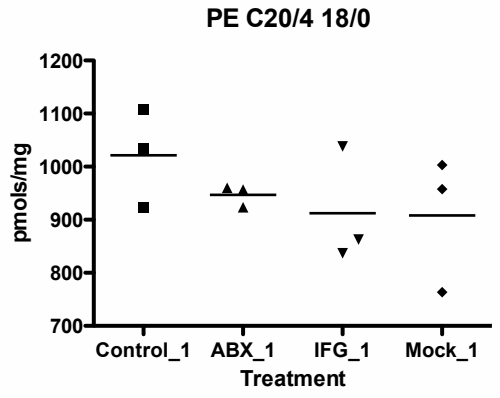
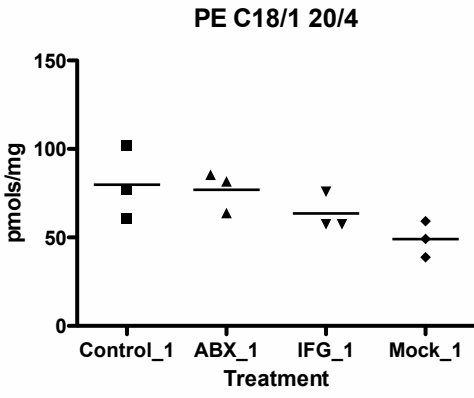
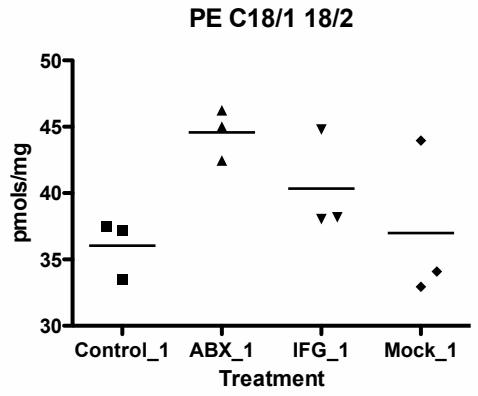
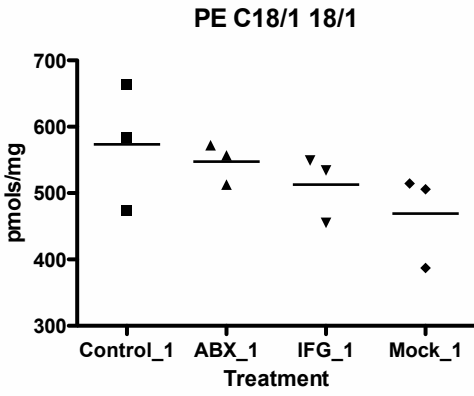


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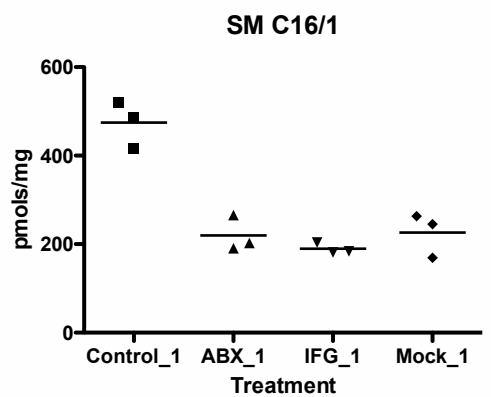
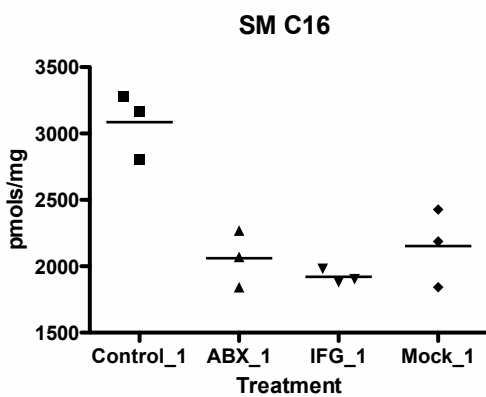
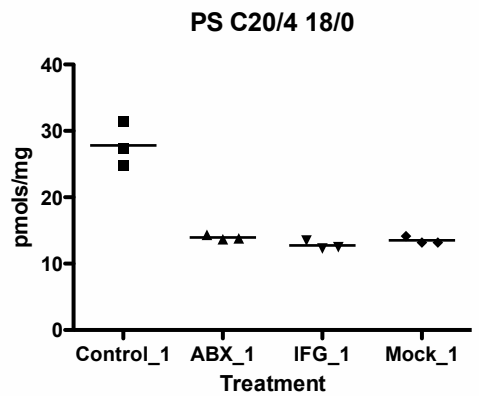
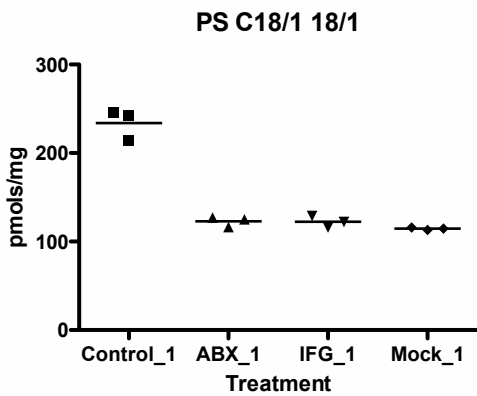
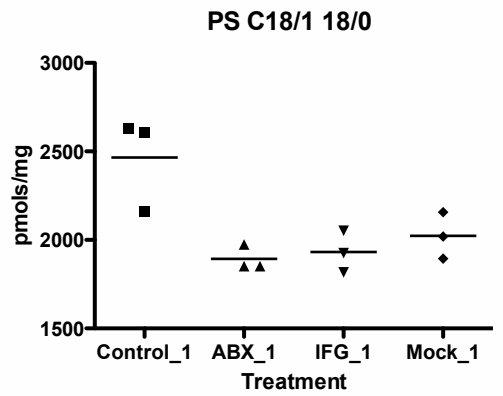
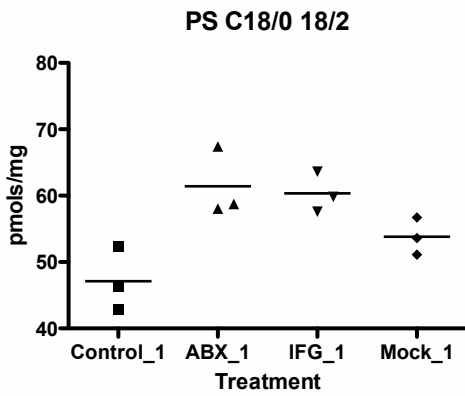
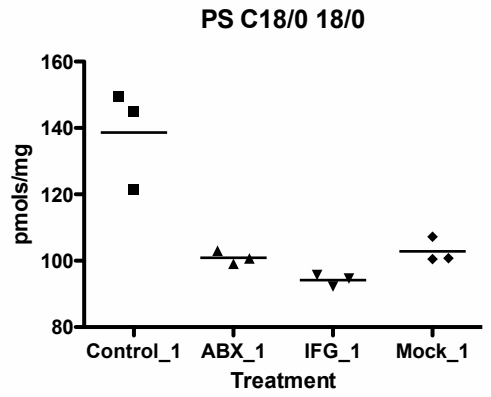
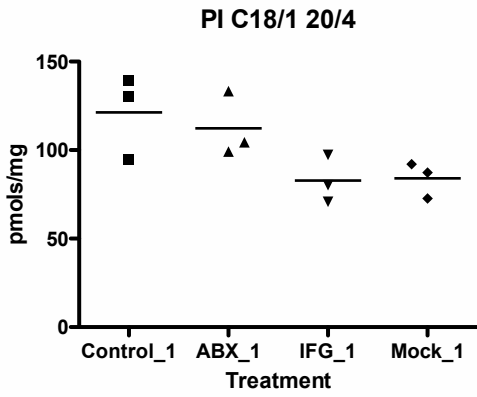


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