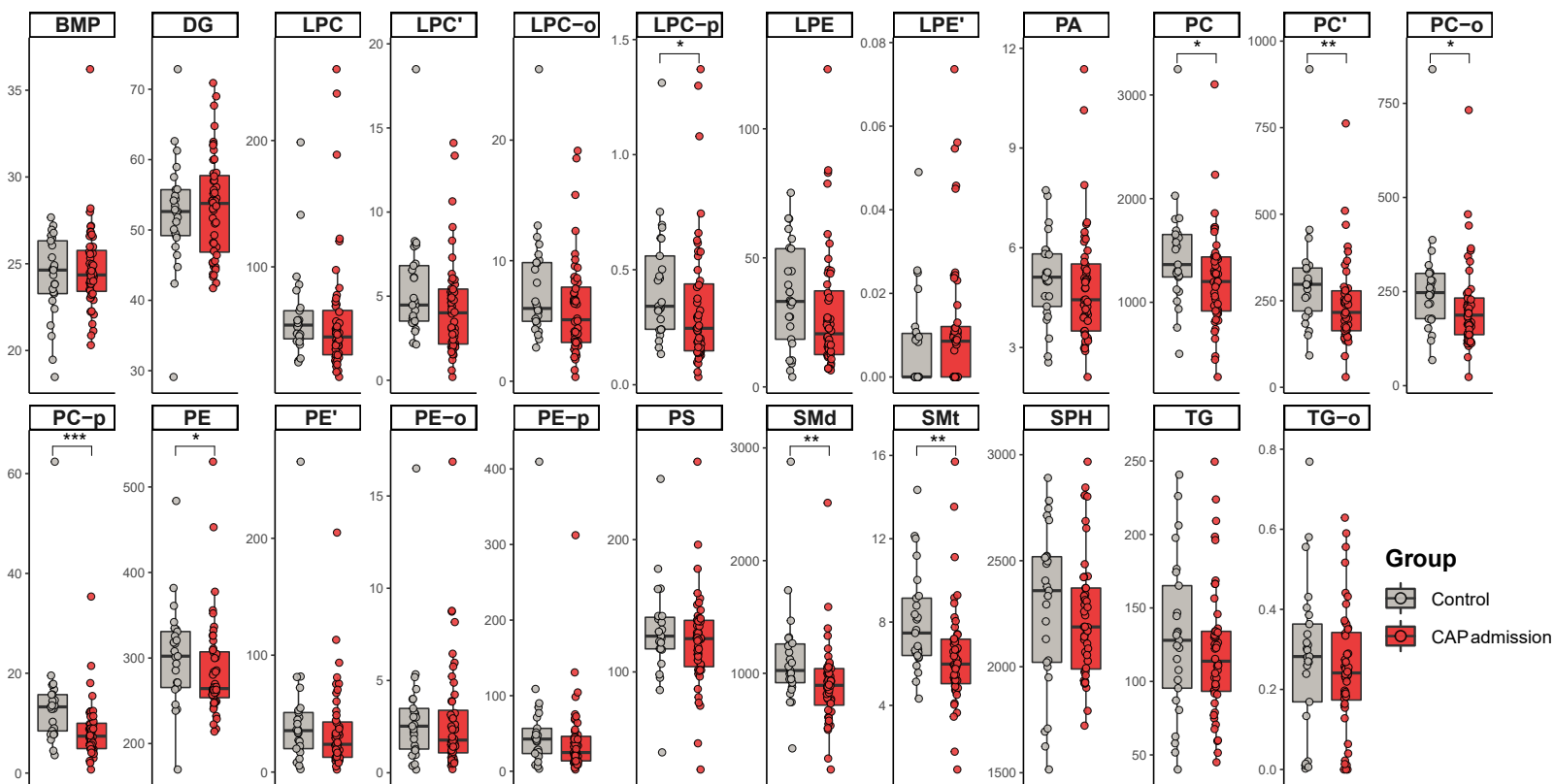


Supplemental Table 2

ID	Common name	Abbr.	Synonyms	Category	Main class
BMP	Lysobisphosphatidic acid	LBPA	BMP, bis(monoacylglycero)phosphate	[GP]	Glycerophosphoglycerols [GP04]
CE	Cholesteryl ester	CE		[ST]	Sterols [ST01]
Cer	Ceramide	Cer		[SP]	Ceramides [SP02]
DG	Diacylglycerol	DG	DAG	[GL]	Diacylglycerols [GL02]
Hex2Cer[d]	Dihexosylceramide	Hex2Cer	Glc2Cer; Gal2Cer; LacCer	[SP]	Neutral glycosphingolipids [SP05]
Hex2Cer[t]	Hydroxy-dihexosylceramide	Hex2Cer		[SP]	Neutral glycosphingolipids [SP05]
HexCer[d]	Hexosylceramide	HexCer	GlcCer; GalCer	[SP]	Neutral glycosphingolipids [SP05]
HexCer[t]	Hydroxy-hexosylceramide	HexCer		[SP]	Neutral glycosphingolipids [SP05]
LPC	Lysophosphatidylcholine	LysoPC	LPC	[GP]	Glycerophosphocholines [GP01]
LPC-O	Alkyllysophosphatidylcholine	LysoPC(O)		[GP]	Glycerophosphocholines [GP01]
LPC'	Alkyl/alkenyllysophosphatidylcholine	LysoPC(')		[GP]	Glycerophosphocholines [GP01]
LPC-P	Alkenyllysophosphatidylcholine	LysoPC(P)		[GP]	Glycerophosphocholines [GP01]
LPE	Lysophosphatidylethanolamine	LysoPE	LPE	[GP]	Glycerophosphoethanolamines [GP02]
LPE-O	Alkyllysophosphatidylethanolamine	LysoPE(O)		[GP]	Glycerophosphoethanolamines [GP02]
LPE'	Alkyl/alkenyllysophosphatidylethanolamine	LysoPE(')		[GP]	Glycerophosphoethanolamines [GP02]
LPE-P	Alkenyllysophosphatidylethanolamine	LysoPE(P)		[GP]	Glycerophosphoethanolamines [GP02]
PA	Phosphatidic acid	PA		[GP]	Glycerophosphates [GP10]
PC	Phosphatidylcholine	PC		[GP]	Glycerophosphocholines [GP01]
PC-O	Alkylphosphatidylcholine	PC(O)		[GP]	Glycerophosphocholines [GP01]
PC'	Alkyl/alkenylphosphatidylcholine	PC(')		[GP]	Glycerophosphocholines [GP01]
PC-P	Alkenylphosphatidylcholine	PC(P)		[GP]	Glycerophosphocholines [GP01]
PE	Phosphatidylethanolamine	PE		[GP]	Glycerophosphoethanolamines [GP02]
PE-O	Alkylphosphatidylethanolamine	PE(O)		[GP]	Glycerophosphoethanolamines [GP02]
PE'	Alkyl/alkenylphosphatidylethanolamine	PE(')		[GP]	Glycerophosphoethanolamines [GP02]
PE-P	Alkenylphosphatidylethanolamine	PE(P)		[GP]	Glycerophosphoethanolamines [GP02]
SM[d]	Sphingomyelin/Ceramide phosphocholines	SM[d]		[SP]	Phosphosphingolipids [SP03]
SM[t]	Hydroxysphingomyelin	SM[t]		[SP]	Phosphosphingolipids [SP03]
SPH	Sphingosine, Sphinganine	SPH[d]		[SP]	Sphingoid bases [SP01]
TG	Triacylglycerols	TG	TAG	[GL]	Triacylglycerols [GL03]
TG-O	Alkyldiacylglycerol	TG-O		[GL]	Triacylglycerols [GL03]

Supplemental Table 2: Nomenclature overview of lipid classes.

A Relative lipidomic changes in monocytes CAP admission versus controls



B Relative lipidomic changes in monocytes CAP recovery versus controls

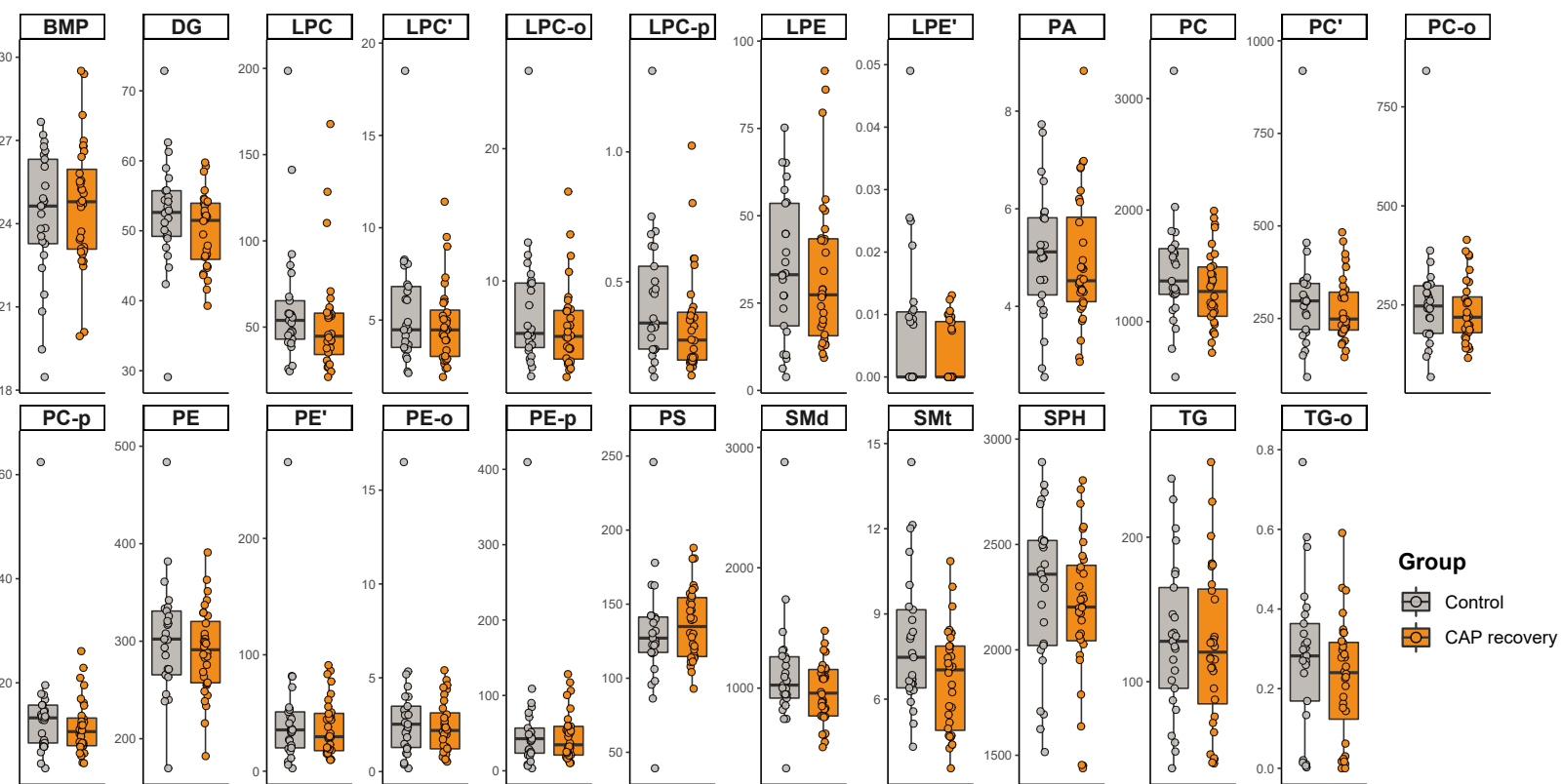
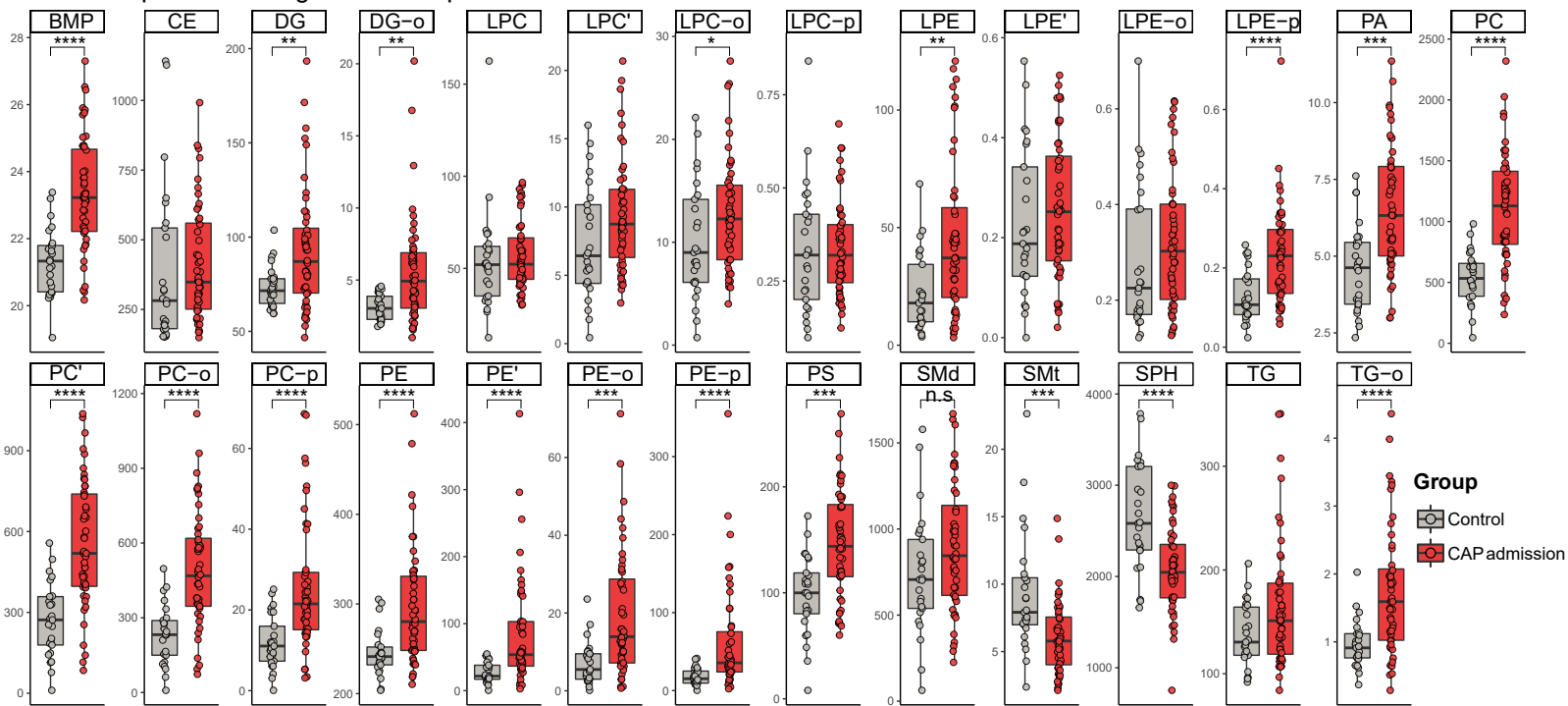


Figure S1: Relative class-wide lipidomic changes in monocytes during CAP

A) Boxplots showing class-wide lipidomic differences in monocytes between patients with CAP (N=48) and controls (N=25), as determined by a Wilcoxon-ranked sum test of aggregated values per class (a sum of all lipids per class per subject). * p-value < 0.05, ** p-value < 0.01, *** p-value < 0.001, **** p-value < 0.0001. B) Boxplots showing classwide lipidomic differences in monocytes between patients with CAP recovery (N=33) and controls, as determined by a Wilcoxon ranked sum test of aggregated values per class (a sum of all lipids per class per subject). * p-value < 0.05, ** p-value < 0.01, *** p-value < 0.001, **** p-value < 0.0001.

A Relative lipidomic changes in neutrophils CAP admission versus controls



B

Relative lipidomic changes in neutrophils CAP recovery versus controls

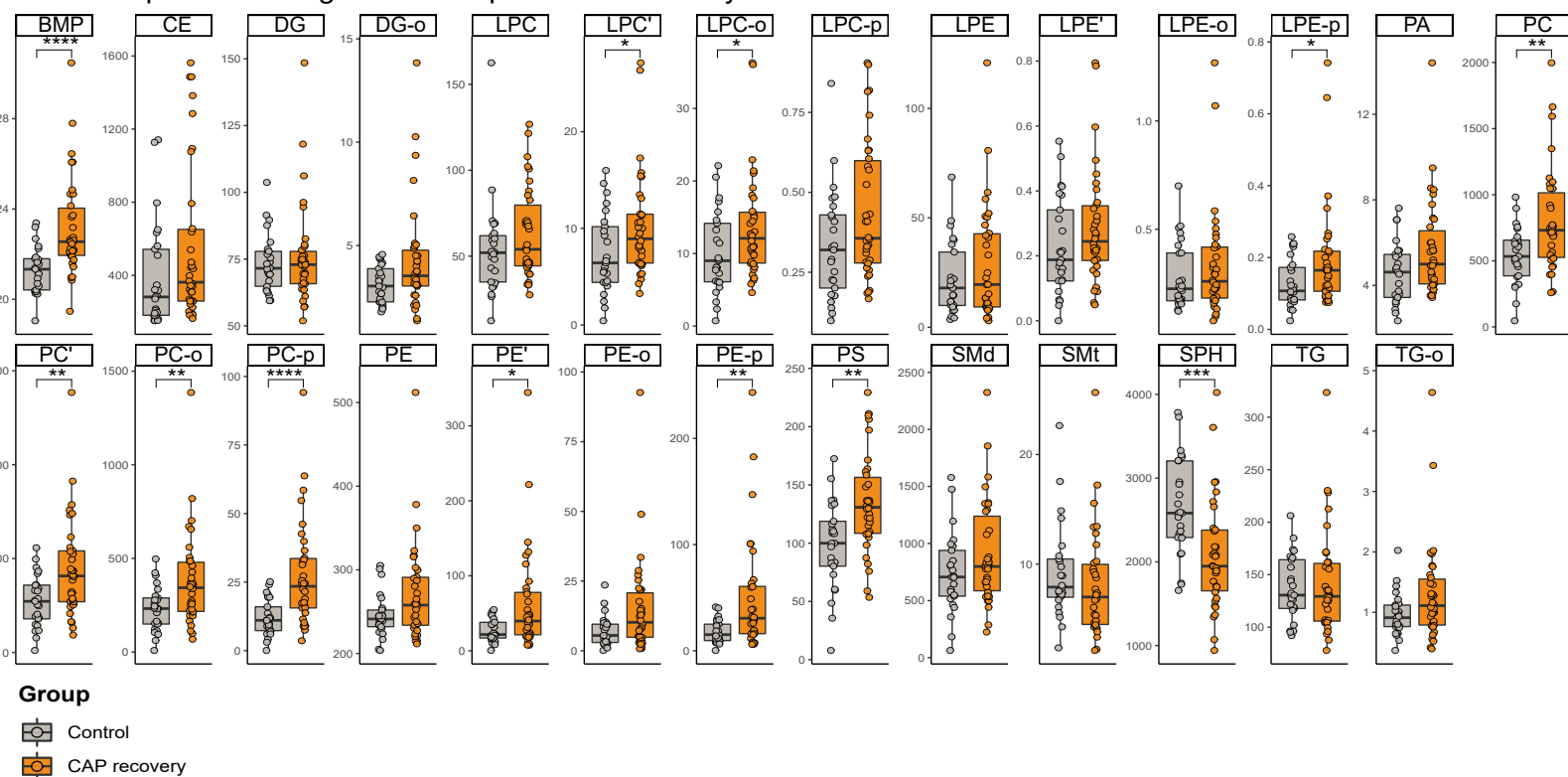


Figure S2: Relative class-wide lipidomic changes in neutrophils during CAP

A) Boxplots showing class-wide lipidomic differences in neutrophils between patients with CAP (N=48) and controls (N=25), as determined by a Wilcoxon-ranked sum test of aggregated values per class (a sum of all lipids per class per subject). * p-value < 0.05, ** p-value < 0.01, *** p-value < 0.001, **** p-value < 0.0001. B) Boxplots showing classwide lipidomic differences in neutrophils between patients with CAP recovery (N=33) and controls, as determined by a Wilcoxon ranked sum test of aggregated values per class (a sum of all lipids per class per subject). * p-value < 0.05, ** p-value < 0.01, *** p-value < 0.001, **** p-value < 0.0001.

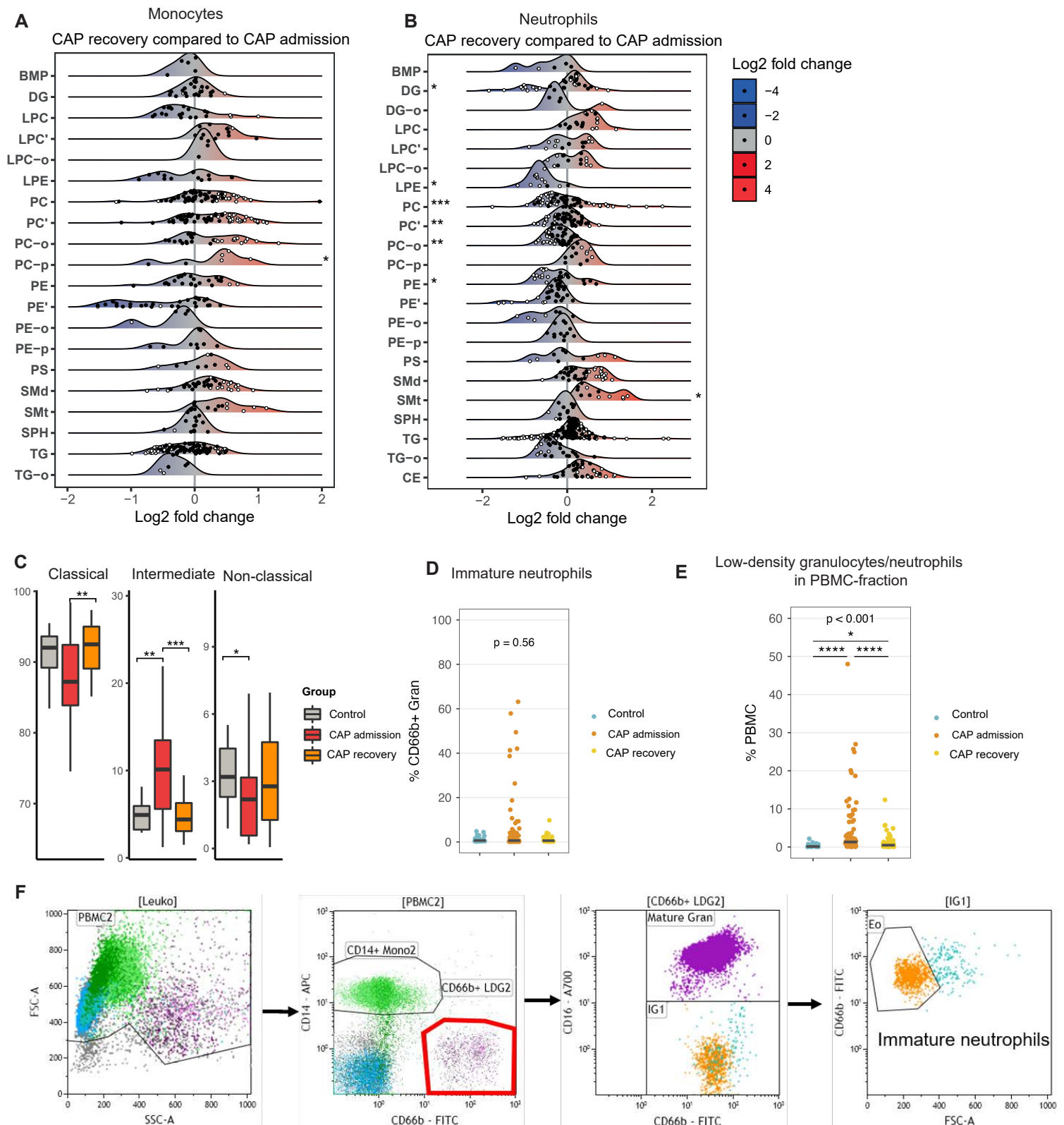


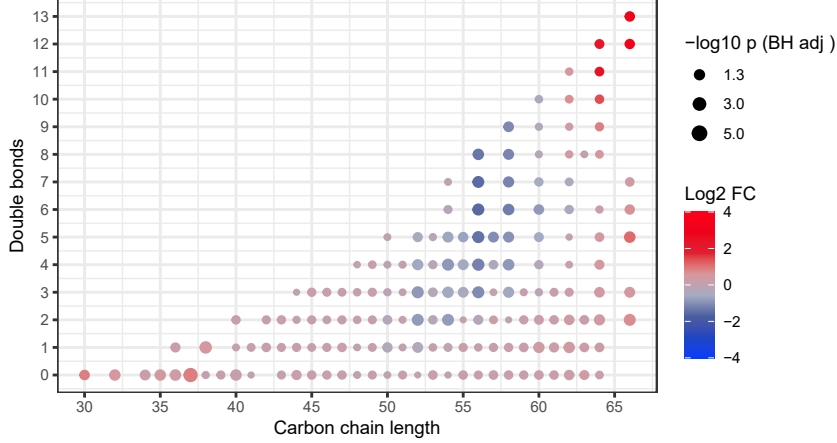
Figure S3: CAP recovery lipid landscapes and monocyte/neutrophils subsets analysis between groups

A) Monocyte lipid landscape plot, comparing CAP recovery samples to CAP admission samples in a paired analysis. Each dot represent a lipid species, which are grouped per lipid class. The color of the dots indicates whether the lipid was significantly different (white) between the groups after Benjamini-Hochberg correction for all annotated lipids. The X-axis shows the log2 fold change between groups for each lipid. The Y-axis indicates the different lipid classes, with a ridge plot per lipid class that shows the distribution of the lipids within their respective classes. On the edges of the plot, stars denote class-wide significant differences as determined by a paired Wilcoxon-ranked sum test of aggregated values per class (a sum of all lipids per class per subject). Stars on the left of the plot indicate a significant class-wide decrease, stars on the right of the plot indicate a significant class-wide increase. A p-value below 0.05 was considered significant. B) Identical to panel A, but here for neutrophils. C) Boxplot comparing the proportion of classical (CD14⁺CD16⁻), intermediate (CD14⁺CD16⁺), and non-classical (CD14^{dim}CD16⁺) monocyte subsets between groups. D) Plot comparing the proportion of immature neutrophils within the neutrophil fraction between the groups. E) Plot comparing the proportion of low-density neutrophils within the polymorphonuclear cell (PBMC) fraction between groups. F) Gating strategy to identify immature low-density neutrophils within the PBMC fraction, defined as CD14⁺ CD66b⁺, CD16^{low/-} cells. * p-value < 0.05, ** p-value < 0.01, *** p-value < 0.001, **** p-value < 0.0001.

Neutrophils

A

TG saturation CAP recovery compared to CAP admission

**B**

DG saturation CAP admission compared to controls

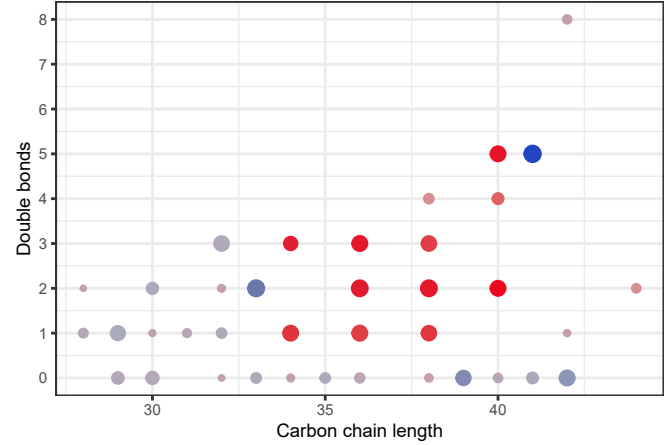


Figure S4. Saturation in neutrophil triacylglycerol and diacylglycerol

A) Dot plots of triacylglycerol saturation differences between neutrophils of CAP recovery and controls. Each dot is a triacylglycerol species. The color of the dots indicates the \log_2 fold change between the groups, the size of the dot is proportional to the Benjamini-Hochberg adjusted $-\log_{10} p$ -value of this change. The X-axis indicates the carbon chain length, the Y-axis shows the amount of double bonds. B) Identical to panel A, but here comparing diacylglycerol saturation between CAP admission and controls.

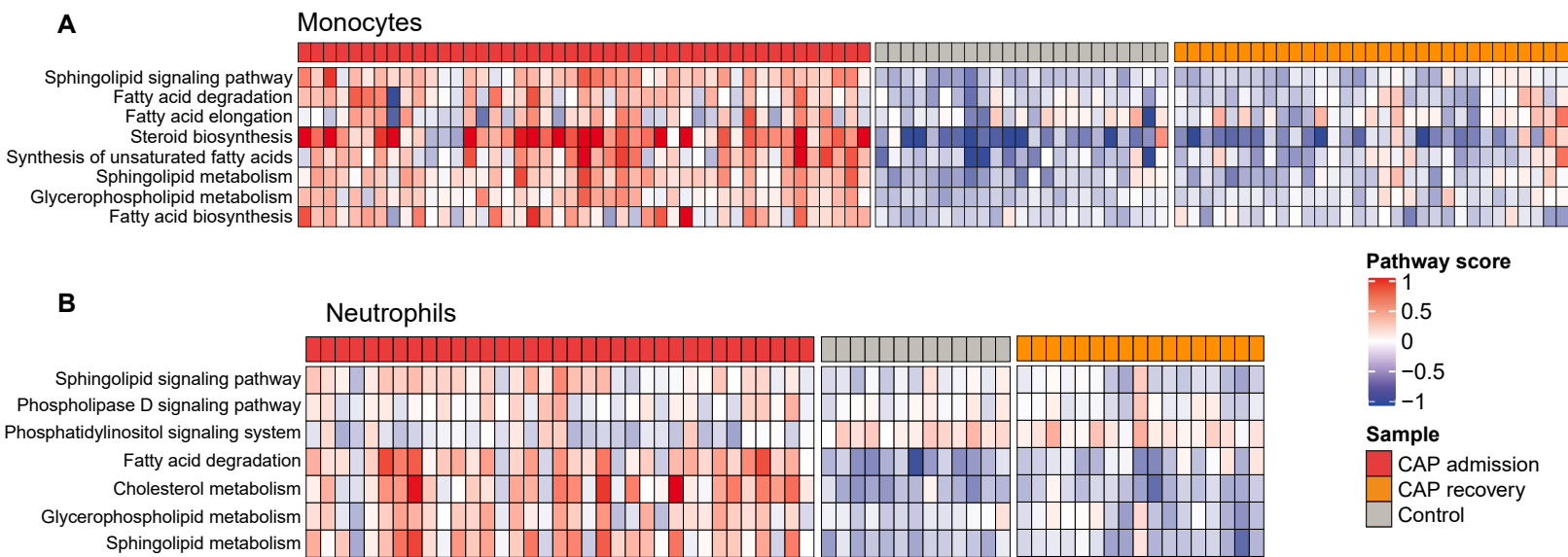


Figure S5: Mean pathway score of enriched lipid-related pathways per subject

A) Heatmap depicting the average Z-score of all genes within each enriched pathway in monocytes, per subject. The heatmap is split per group: CAP admission, CAP recovery and control samples. B) Heatmap depicting the average Z-score of all genes within each enriched pathway in neutrophils, per subject. The heatmap is split per group: CAP admission, CAP recovery and control samples.

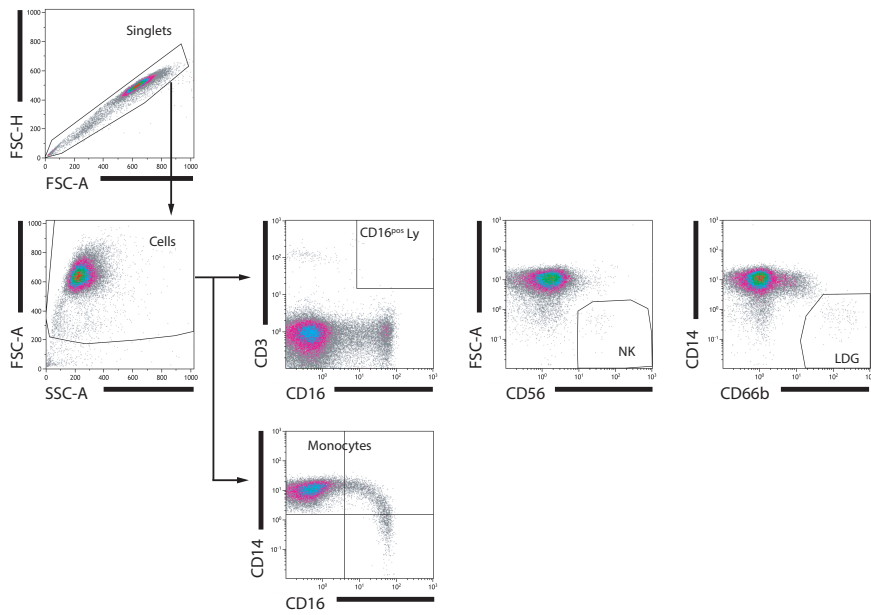
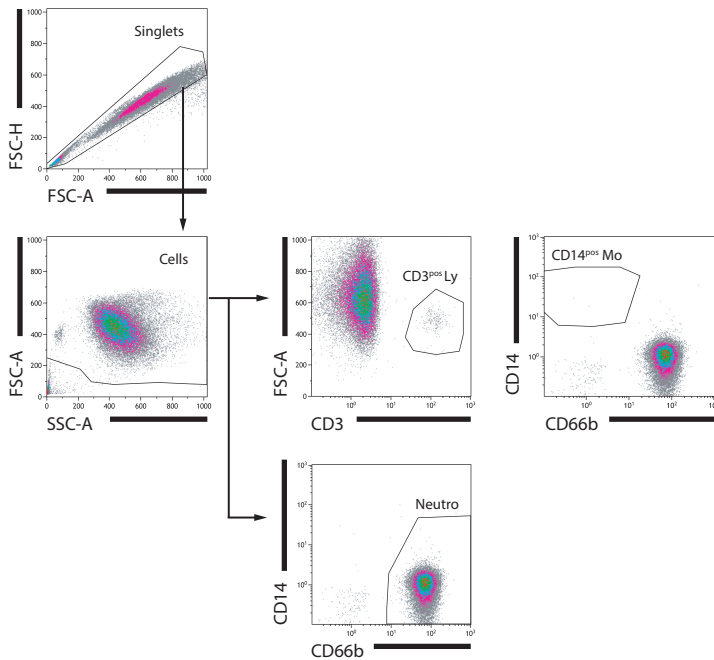
A**B**

Figure S6: Gating strategy

A) Gating strategy for monocytes: all cells in the CD14/CD16 plot were identified as monocytes, consisting of classical (CD14⁺CD16⁻), intermediate (CD14⁺CD16⁺), and non-classical (CD14^{dim}CD16⁺) monocyte subsets. B) Gating strategy for neutrophils.