lipotype
Lipidomics for a better life

TECHNICAL NOTE

Lipotype Blood Lipidomics – Coverage

Lipotype Blood Lipidomics technology provides the broadest coverage of blood lipids ranging from signaling lipids and storage lipids to membrane lipids. Our analysis routinely covers 40 different lipid classes (FFA, TAG, PC, Cer, Chol, etc).

Your lipidomics results will be provided on the level of lipid species (TAG 48:2;0) or lipid subspecies (PC 16:0;0_18:1;0 + fatty acid information).

Here, we present the potential coverage of Lipotype Lipidomics technology, as the exact lipids identified and quantified in your sample depend on the organism, sample type, experiment, and further parameters.

LIPID CLASS	STRUCTURAL DETAILS	RANGES COVERED	EXAMPLE
Free Fatty Acids – FFA	*Molecular Species*	FA length from 2 to 24 FA DB from 0 to 6	FFA 15:1;0
Linear Fatty Acids – LiFA	*Molecular Species*	FA length from 4 to 24 FA DB from 0 to 6	LiFA 14:0;0
Short Chain Fatty Acids – SCFA	*Molecular Species*	FA length from 2 to 5	SCFA 4:0;0
Medium Chain Fatty Acids – MCFA	*Molecular Species*	FA length from 6 to 12	MCFA 12:0;0
Long Chain Fatty Acids – LCFA	*Molecular Species*	FA length from 13 to 24 FA DB from 0 to 6	LCFA 18:0;0
Saturated Fatty Acids – SFA	*Molecular Species*	FA length from 4 to 24	SFA 16:0;0
Unsaturated Fatty Acids – UFA	*Molecular Species*	FA length from 14 to 24 FA DB from 1 to 6	UFA 18:1;0
Acylcarnitines – CAR	*Molecular Species*	FA length from 10 to 22 FA DB from 0 to 6	CAR 18:2;0
Endocannabinoids – NAE	*Molecular Species*	FA length from 16 to 22 FA DB from 0 to 6	NAE 20:4;0
Oxidized Octadecaenoic Acids – oxiOME	*Molecular Species*	molecular structure can be derived from lipid name FA Oxi ≥ 1	12,13-DiHOME

Oxidized Octadecadienoic Acids – oxiODE	*Molecular Species*	molecular structure can be derived from lipid name FA Oxi ≥ 1	13-HpODE
Prostaglandins – Pgd	*Molecular Species*	molecular structure can be derived from lipid name FA Oxi ≥ 1	PGB2
Leukotrienes – LT	*Molecular Species*	molecular structure can be derived from lipid name FA Oxi ≥ 1	LTB4
Thromboxanes – TX	*Molecular Species*	molecular structure can be derived from lipid name FA Oxi ≥ 1	TXB2
Lipoxins – LX	*Molecular Species*	molecular structure can be derived from lipid name FA Oxi ≥ 1	LXA4
Isoprostanes – IsoP	*Molecular Species*	molecular structure can be derived from lipid name FA Oxi ≥ 1	8-iso-PGF1a
Oxidized Eicosatrienoic Acids – oxiETrE	*Molecular Species*	molecular structure can be derived from lipid name FA Oxi ≥ 1	8-HETrE
Oxidized Eicosatetraenoic Acids – oxiETE	*Molecular Species*	molecular structure can be derived from lipid name FA Oxi ≥ 1	5-oxo-ETE
Oxidized Eicosapentaenoic Acids – oxiEPE	*Molecular Species*	molecular structure can be derived from lipid name FA Oxi ≥ 1	18-HEPE
Maresins – MaR	*Molecular Species*	molecular structure can be derived from lipid name FA Oxi ≥ 1	Maresin 1
Resolvin Ds – RvD	*Molecular Species*	molecular structure can be derived from lipid name FA Oxi ≥ 1	Resolvin D5
Protectins – PD	*Molecular Species*	molecular structure can be derived from lipid name FA Oxi ≥ 1	NPD-1
Oxidized Docosapentaenoic Acids – oxiDPA	*Molecular Species*	molecular structure can be derived from lipid name FA Oxi ≥ 1	7,8-DiHDPA
Oxidized Docosahexaenoic Acids – oxiDHA	*Molecular Species*	molecular structure can be derived from lipid name FA Oxi ≥ 1	16-HDHA
Triacylglycerol – TAG	*Species*	Total length from 30 to 78 Total DB from 0 to 18	TAG 48:2;0
Diacylglycerol – DAG	*Subspecies*	FA length from 10 to 26 FA DB from 0 to 6	DAG 18:2;0_20:0:0

Phosphatidylcholine – PC	*Subspecies*	FA length from 10 to 26 FA DB from 0 to 6	PC 16:0;0_18:1;0
Phosphatidylethanolamine – PE	*Subspecies*	FA length from 10 to 26 FA DB from 0 to 6	PE 16:0;0_18:1;0
Phosphatidylinositol – PI	*Subspecies*	FA length from 10 to 26 FA DB from 0 to 6	PI 16:0;0_18:1;0
Lyso-phosphatidylcholine – LPC	*Species*	Total length from 10 to 26 Total DB from 0 to 6	LPC 18:2;0
Lyso-phosphatidylethanolamine – LPE	*Species*	Total length from 10 to 26 Total DB from 0 to 6	LPE 18:2;0
Ether-linked PC – PC O-	*Subspecies*	FA length from 10 to 26 FA DB from 0 to 6	PC O-18:1;0/22:5;0
Ether-linked PE – PE O-	*Subspecies*	FA length from 10 to 26 FA DB from 0 to 6	PE O-18:1;0/22:5;0
Ether-linked LPC – LPC O-	*Species*	Total length from 10 to 26 Total DB from 0 to 6	LPC O-20:2;0
Ether-linked LPE – LPE O-	*Species*	Total length from 10 to 26 Total DB from 0 to 6	LPE O-20:2;0
Ceramide – Cer	*Species*	Total length from 30 to 46 Total DB from 0 to 2 Total OH from 2 to 4	Cer 36:1;2
Hexosylceramide – HexCer	*Species*	Total length from 30 to 46 Total DB from 0 to 2 Total OH from 2 to 4	HexCer 36:1;2
Sphingomyelin – SM	*Species*	Total length from 30 to 46 Total DB from 0 to 2 Total OH from 2 to 4	SM 34:2;2
Cholesterol – Chol	*Class*	–	Chol
Cholesterol esters – CE	*Species*	Total length from 10 to 26 Total DB from 0 to 6	CE 18:2;0

Abbreviations

FA = fatty acid, **DB** = double bonds, **OH** = hydroxyl groups, **Oxi** = oxygen containing substituents

Lipid species

Lipid species are annotated according to their molecular composition as follows:
CLASS <sum of carbon atoms>:<sum of DB>;<sum of OH>

For example, PI 34:1;0 denotes phosphatidylinositol with a total length of its fatty acids equal to 34 carbon atoms, total number of double bonds in its fatty acids equal to 1 and 0 hydroxylations. In case of sphingolipids, SM 34:1;2 denotes a sphingomyelin species with a total of 34 carbon atoms, 1 double bond, and 2 hydroxyl groups in the ceramide backbone.

Lipid subspecies

Lipid subspecies annotation contains additional information on the exact identity of their acyl moieties and their *sn*-position (if available) as follows:
CLASS <sum of carbon atoms>:<sum of DB>;<sum of OH>_<sum of carbon atoms>:<sum of DB>;<sum of OH>

For example, PI 18:1;0_16:0;0 denotes phosphatidylinositol with octadecenoic (18:1;0) and hexadecanoic (16:0;0) fatty acids, for which the exact position (*sn*-1 or *sn*-2) in relation to the glycerol backbone cannot be discriminated (underscore "_" separating the acyl chains).

When the information on *sn*-position is available, it is annotated with "/" sign as follows:
CLASS <sum of carbon atoms>:<sum of DB>; sum of OH>/<sum of carbon atoms>:<sum of DB>;<sum of OH>

For example, PC O-18:1;0/16:0;0 denotes an ether-phosphatidylcholine, where an alkyl chain with 18 carbon atoms and 1 double bond (O-18:1;0) is ether-bound to *sn*-1 position of the glycerol and a hexadecanoic acid (16:0;0) is connected via an ester bond to the *sn*-2 position of the glycerol (slash "/" separating the chains signifies that the *sn*-position on the glycerol can be resolved). In that case, the first part of the syntax refers to the hydrocarbon chain at *sn*-1 position.

Oxylipins

Molecular species of oxylipins (oxiOME, oxiODE, Pgd, LT, TX, LX, IsoP, oxiETrE, oxiETE, oxiEPE, MaR, RvD, PD, oxiDPA, oxiDHA) are annotated according to the nomenclature proposed by the LIPID MAPS® Lipid Classification System (www.lipidmaps.org/databases/lmsd).

For example, PGB2 denotes 15S-hydroxy-9-oxo-5Z,8(12),13E-prostatrienoic acid.

About Lipotype

Lipotype is the leading lipidomics provider and your access to lipids and lipid metabolism data. Our mass spectrometry-based platform can be applied to all biological samples and covers more than 4200 lipids – the broadest lipidomics coverage. It is robust and reproducible, and combines reliable data quality control with state-of-the-art data visualization and statistical analyses. Contact us, order your lipidomics, send in your samples, and understand your results in as little as two weeks.

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