

Comparative phospholipid membrane compositions of bacterial and cancer cell lines

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Tables of data

Table S1 – Phospholipid membrane composition of bacterial cell lines. Inner refers to the inner leaflet of the cell membrane, whereat outer refers to the outer leaflet of the cell membrane. Herein, CM = cytoplasmic membrane and OM = outer membrane.

	Phospholipid	Phase of growth (%)		Analysis Method	Growth Media	Specific Notes	
		Unknown	Log				Stationary
<i>Enterococcus faecium</i> (Gram +ve)							
S447 ¹ (Daptomycin sensitive)	L-PG inner			8.12	2D TLC, LC/ESI-MS/MS	BHI broth	Sat - 14:0 (8 %), 16:0 (26 %), 18:0 (5 %) Unsat - 16:1,7c (13 %), 18:1,6,9c (6 %), 18:1,9c (4 %), 18:1,7c (34 %) Cyclic - 19:0 (3 %)
	L-PG outer			6			
	PG whole cell			34			
	CL whole cell			29			
	DAG whole cell			13			
R446 ¹ (Daptomycin resistant)	L-PG inner			7	2D TLC, LC/ESI-MS/MS	BHI broth	Sat - 14:0 (9 %), 16:0 (26 %), 18:0 (5 %) Unsat - 16:1,7c (14 %), 18:1,6,9c (6 %), 18:1,9c (3 %), 18:1,7c (29 %) Cyclic - 19:0 (7 %)
	L-PG outer			9			
	PG whole cell			15			
	CL whole cell			47			
	DAG whole cell			23			
<i>Staphylococcus aureus</i> (methicillin resistant) (Gram +ve)							
DSM 20233 ²	PG whole cell			50	TLC	Difco, antibiotic medium III	Lipoteichoic acid was isolated, but quantitative results were not provided. Information relating to alkyl chain composition not provided.
	L-PG whole cell			20			
	CL whole cell			1			
USA300 ³	PG whole cell			60	ESI-MS/MS	TSB	PC – 30:0 (8 %), 31:0 (9 %), 32:0 (27 %), 33:0 (25 %), 34:0 (11 %), 35:0 (20 %), 36:0 (2 %) L-PG – 30:0 (6 %), 31:0 (5 %), 32:0 (28 %), 33:0 (27 %), 34:0 (18 %), 35:0 (21 %), 36:0 (2 %), 37:0 (1%), 38:1 (2 %)
	L-PG whole cell			30			
	CL whole cell			2			
	DAG whole cell			4			
<i>fakA</i> mutant ³	PG whole cell			70	ESI-MS/MS	TSB	PC - 30:0 (4 %), 31:0 (5 %), 32:0 (20 %), 33:0 (21 %), 34:0 (16 %), 35:0 (32 %), 36:0 (4 %) L-PG – 30:0 (4 %), 31:0 (3 %), 32:0 (19 %), 33:0 (20 %), 34:0 (15 %), 35:0 (21 %), 36:0 (3 %), 37:0 (2%), 38:1 (2 %)
	L-PG whole cell			25			
	CL whole cell			1			
	DAG whole cell			3			
CB1118 (USA400) ⁴	PG whole cell	84			2D TLC, spectrophotometry	MHA	Parental strain to produce daptomycin-nonsusceptibility (resistance) Information relating to alkyl chain composition not provided.
	L-PG inner	11					
	L-PG outer	1					
	CL whole cell	5					
CB2205 (20-day DAP-nonsusceptibility) ⁴	PG whole cell	84			2D TLC, spectrophotometry	MHA	CB2201 – day 1 (O-LPG 11 %, I-LPG 1 %, PG 86 %, CL 4 %) CB2202 – day 5 (O-LPG 12 %, I-LPG 2 %, PG 81 %, CL 9 %) CB2203 – day 14 (O-LPG 15 %, I-LPG 3 %, PG 73 %, CL 13 %) Information relating to alkyl chain composition not provided.
	L-PG inner	19					
	L-PG outer	6					
	CL whole cell	7					

<i>Staphylococcus auerus</i> (methicillin sensitive) (Gram +ve)							
209P ⁵	PG whole cell	76.5		TLC, radiolabelling	Nutrient broth	Information relating to alkyl chain composition not provided.	
	L-PG whole cell	16					
	CL whole cell	7					
209P ⁶	PG whole cell		79.3	65.9	TLC, radiolabelling	Synthetic broth 1	CL – 14:0 (22.2 %), 15:0 (24.6 %), 16:0 (12.1 %), 17:0 (15.6 %), 18:0 (6.8 %), 19:0 (4.7 %), 20:0 (1.3 %), 22:0 (12.3 %) PG – 14:0 (1.2 %), 15:0 (51.0 %), 16:0 (4.8 %), 17:0 (23.2 %), 18:0 (3.2 %), 19:0 (13.9 %), 20:0 (2.9 %) L-PG – 14:0 (4.7 %), 15:0 (37.0 %), 16:0 (4.1 %), 17:0 (25.0 %), 18:0 (4.9 %), 19:0 (13.5 %), 20:0 (7.1 %)
	L-PG whole cell		14.3	10			
	CL whole cell		3.6	13.7			
U-71 ⁷	PG whole cell	80			TLC, radiolabelling	Synthetic media 2	Information relating to alkyl chain composition not provided.
	L-PG whole cell	12					
	CL whole cell	5					
<i>Klebsiella pneumonia</i> (Gram -ve)							
Smooth mutant ⁸	PE whole cell	82			TLC, radiolabelling	Synthetic media 3	Information relating to alkyl chain composition not provided.
	PG whole cell	4.5					
	PA whole cell	5					
	CL whole cell	6.5					
005 ⁹	PG whole cell	35			FAB-MS	Nutrient broth	PG – 27:3 (3.7 %), 28:3 (1.4 %), 29:4 (0.4 %), 29:3 (2.7 %), 29:2 (0.3 %), 30:2 (5.2 %), 31:3 (4.8 %), 31:2 (4.3 %), 32:4 (4.2 %), 32:3 (4.1 %), 32:2 (3.9 %), 34:3 (5.9 %) PE – 30:1 (2.4 %), 31:1 (4.2 %), 32:2 (4.6 %), 32:1 (15.9 %), 32:0 (3.6 %), 33:1 (6.8 %), 34:2 (9.4 %), 34:1 (1.3 %), 34:0 (5.3 %), 35:2 (0.7 %), 35:1 (4.5 %), 36:1 (0.3 %)
	PE whole cell	59					
<i>Acinetobacter baumannii</i> (Gram -ve)							
ATCC17978 ¹⁰	PE whole cell				LC-MS	G56 minimal	PG – 16:0/18:3, 18:1/18:3, 16:0/22:6 PE – 16:0/18:3, 18:1/18:3, 16:0/22:6, 18:1/22:6
	PG whole cell						
	CL whole cell						
H01-N ¹¹	PE CM	70			TLC/GC	Non-specific broth	Information relating to alkyl chain composition not provided.
	PE OM	51					
	L-PE CM	3					
	L-PE outer	3					
	CL CM	7					
	CL outer	19					
	L-CL CM	10					
	L-CL outer	15					
	PG CM	10					
	PG outer	11					
<i>Pseudomonas aeruginosa</i> (Gram -ve)							
PAO1 ¹²	PC whole cell		32-30 [a]	5-17 [b]	LC-MS	LB	PC – 35:1, 35:2,

	PE whole cell		32-30 [a]	5-17 [b]			PE – 16:0/17:1, 16:0/19:1, 16:1/19:1, 17:1/18:1, 17:1/19:1, PG – 16:0/17:1, 16:0/19:1, 17:1/18:1, 17:1/19:1 PC - 32:0, 32:1, 34:2 PE - 16:0/16:0, 16:0/16:1, 16:1/18:1, 18:1/18:1 PG - 16:0/16:0, 16:0/18:1, 16:1/18:1 Lipids that were present, but had different profiles: PC - 34:1, PE - 14:0/18:1, 15:0/18:1, 16:0/16:0/18:1, PG - 16:1/19:1, 18:0/18:1
	PG whole cell		32-30 [a]	5-17 [b]			
	PC whole cell		6-13 [a]	33-13 [b]			
	PE whole cell		6-13 [a]	33-13 [b]			
	PG whole cell		6-13 [a]	33-13 [b]			
PAO1 (outer membrane) ¹³	PE whole cell		60	33 [c]	TLC	LB	Information relating to alkyl chain composition not provided.
	PG whole cell		27	63 [c]			
	PC whole cell		13	3.9 [c]			
B-219 ¹⁴	PA whole cell	0.1			LC-MS/MS	Universal medium	PA – 34:1 (0.1 %) PE – 32:0 (4 %), 32:1 (18 %), 32:2 (2 %), 33:1 (19 %), 33:2 (3 %), 34:1 (8 %), 34:2 (5 %), 36:2 (4 %) PG – 31:2 (3 %), 32:1 (5 %), 32:2 (4 %), 33:1 (19 %), 34:2 (10 %), 35:2 (6 %), 36:2 (2 %)
	PE whole cell	59					
	PG whole cell	41					
PAK (MHB) ¹⁵	PC		2.2 [d]			MH	PC – 32:0, 32:1, 34:1, 34:2, 36:1 PE – 32:1 34:1, 36:2 PG – 22:1, 34:1, 36:2 CL – 66.2, 70.3
	PE		17.9 [d]				
	PG		6.7 [d]				
	CL		1.0 [d]				
PAK (SCFM) ¹⁵	PC		0 [d]			SCFM	PC – 32:0, 32:1, 34:1, 34:2, 36:1 PE – 32:1 34:1, 36:2 PG – 22:1, 34:1, 36:2 CL – 66.2, 70.3
	PE		13.6 [d]				
	PG		7.4 [d]				
	CL		0.8 [d]				
PAK (SCFM-PC) ¹⁵	PC		22.0 [d]			SCFM-PC	PC – 32:0, 32:1, 34:1, 34:2, 36:1 PE – 32:1 34:1, 36:2 PG – 22:1, 34:1, 36:2 CL – 66.2, 70.3
	PE		24.9 [d]				
	PG		15.5 [d]				
	CL		1.1 [d]				
<i>Enterobacter cloacae</i> (<i>E. cloacae</i>) (Gram -ve)							
<i>E. cloacae</i> (012) ⁹	PE whole cell	65			FAB-MS	Nutrient broth	PE – 30:0 (3.0 %), 32:2 (6.3 %), 32:1 (20.2 %), 32:0 (0.9 %), 33:1 (6.1 %), 33:0 (1.3 %), 34:2 (9.9 %), 34:1 (12.3 %), 35:2 (1.7 %), 35:1 (2.4 %) PG – 27:3 (5.0 %), 28:3 (3.0 %), 29:4 (2.8 %), 29:3 (1.6 %), 30:2 (7.7 %), 31:2 (8 %), 32:3 (1.0 %), 32:2 (3.7 %), 32:1 (0.9 %), 34:1 (1.1%)
	PG whole cell	35					
<i>E. cloacae</i> (008) ⁹	PE whole cell	50.3			FAB-MS	Nutrient broth	PE – 30:1 (1.4 %), 30:0 (1.5 %), 31:1 (1.1 %) 32:2 (4.3 %), 32:1 (13.8 %), 32:0 (6.1 %), 33:1 (2.6 %), 34:2 (7.3 %), 34:1 (7.4 %), 34:0 (2.2 %), 35:2 (1.2 %), 35:1 (0.8 %), 38:0 (0.6 %) PG – 27:3 (2.1 %), 28:3 (0.7 %), 29:4 (1.5 %), 29:3 (1.9 %), 30:2 (6.6 %), 30:1 (0.7 %), 31:2 (7.6 %), 32:3 (0.5 %), 32:2 (5.9 %), 32:1 (2.3 %), 33:3 (0.8 %), 33:2 (1.6 %), 33:1 (1.4 %), 34:3 (2.8 %), 34:2 (2.3 %), 34:1 (3.3 %) PS – 34:1 (4.1 %), 32:0 (0.4 %), 33:0 (3.2 %)
	PG whole cell	42					
	PS whole cell	7.7					
<i>E. cloacae</i> S _{w1} ¹⁶	PE CM		73		TLC	Soy broth	Information relating to alkyl chain composition not provided.

	PE OM		77			
	L-PE CM		0.4			
	L-PE OM		9			
	PG CM		23			
	PG OM		6			
	CL CM		3.6			
	CL OM		8			
<i>E. cloacae</i> AZT-R ¹⁶	PE CM		80	TLC	Soy broth	Information relating to alkyl chain composition not provided.
	PE OM		7			
	L-PE CM		1			
	L-PE OM		10			
	PG CM		17			
	PG OM		5			
	CL CM		2			
	CL OM		9			
<i>E. cloacae</i> AMA-R ¹⁶	PE CM		79	TLC	Soy broth	Information relating to alkyl chain composition not provided.
	PE OM		82			
	L-PE CM		1			
	L-PE OM		6			
	PG CM		17			
	PG OM		5			
	CL CM		2			
	CL OM		6			
<i>Bacillus subtilis</i> (Gram +ve)						
I'1a ¹⁷	PG whole cell	70	75	LC-MS/MS	LB	PE – 28:0 (2 %), 29:0 (4 %), 30:0 (6 %), 32:1 (1 %), 32:0 (2 %), 33:0 (2 %)
	PE whole cell	22	17			PG – 29:0 (5 %), 30:0 (38 %), 31:0 (15 %), 32:0 (15 %)
	CL whole cell	4	7			CL – 61:0 (1 %), 62:0 (1 %), 63:0 (1 %), 64:0 (1 %)
	L-PG whole cell	3	2			L-PG – 32:0 (3 %)
DSM 3257 ¹⁷	PG whole cell	65	30	LC-MS/MS	LB	PE – 28:0 (4 %), 29:0 (10 %), 30:0 (9 %), 32:1 (5 %), 32:0 (2 %), 33:0 (4 %)
	PE whole cell	35	70			PG – 29:0 (11 %), 30:0 (24 %), 31:0 (9 %), 32:0 (9 %)
	CL whole cell	4	10			CL – 61:0 (1 %), 62:0 (1 %), 63:0 (1 %), 64:0 (1 %)
	L-PG whole cell	2	2			L-PG – 32:0 (2 %)
<i>Escherichia coli</i> (Gram -ve)						
B ¹⁸	PE whole cell	75	decreases	TLC/radioactivity	LB	Information relating to alkyl chain composition not provided.
	PG whole cell	20	9			
	CL whole cell	5	50			
BL21AI Api ¹⁹	PE (odd)		decreased	RP-HPLC-ESI- iontrap-MS	TSB/M9 minimal	PE – 28:0, 30:1, 30:0, 32:1, 33:1, 34:1, 35:1, 34:2, 35:2, 36:2
	PG (odd)		decreased			PG – 30:0, 32:1, 33:1, 34:1, 35:1, 34:2, 35:2, 36:2, 37:2
	Lipid A					No change in quantity of lipid A between wild type and resistant <i>E. coli</i> .

[a] – From 0 minutes to 20 minutes.

[b] – From 3 hours to 24 hours.

[c] – Membrane vesicles.

[d] – Relative area under mass spec peak.

Table S2 – Phospholipid membrane composition in cancer samples.

	Phospholipid	Cancer vs control	Method	Control comparison	
Lung cancer					
NSCLC Tissue	PC - 32:3, 34:1, 36:2, 36:3 ²⁰ SM - 16:0 ²⁰	Upregulated Upregulated	MALDI-MS MALDI-MS	Adjacent normal lung tissue – 2 cm apart Adjacent normal lung tissue – 2 cm apart	
	PC - 40:4, 40:5, 40:6, 40:7, 42:5, 42:6, 42:7, 42:8, 42:9 ²¹ PE - 38:3, 40:3, 40:4, 40:5, 40:6, 42:6, 42:7, 42:8, 42:9, 44:12 ²¹ PI - 36:4, 38:2, 38:3, 38:4, 40:3, 40:4, 40:5, 42:2 ²¹ PS - 42:9, 44:9 ²¹ PI - 32:0, 34:0, 34:1, 36:1, 36:2, 38:6 ²¹ PC - 28:1, 32:0, 32:1, 32:3, 34:0, 34:2, 34:3, 34:4, 36:5, 36:6, 40:8, 44:3, 44:9, 44:10 ²¹ PE - 32:0, 34:0, 34:3, 34:4, 36:3, 36:4, 36:5, 38:1, 38:7 ²¹ PS - 32:0, 32:1, 34:0, 34:1, 34:2, 34:3 36:1, 36:2, 36:3, 36:4, 38:1, 38:2, 38:3, 38:4, 38:5, 38:6, 38:7, 40:1, 40:2, 40:7, 40:8, 42:2, 42:3, 42:4, 42:5, 42:8 ²¹ SM - 34:1, 34:2, 36:1, 36:2, 40:1, 42:1, 42:2 ²¹	Upregulated Upregulated Upregulated Upregulated Downregulated Downregulated Downregulated Downregulated	ESI-MS ESI-MS ESI-MS ESI-MS ESI-MS ESI-MS ESI-MS ESI-MS	Matched distant lung tissue – > 5 cm apart Matched distant lung tissue – > 5 cm apart Matched distant lung tissue – > 5 cm apart Matched distant lung tissue – > 5 cm apart Matched distant lung tissue – > 5 cm apart Matched distant lung tissue – > 5 cm apart Matched distant lung tissue – > 5 cm apart Matched distant lung tissue – > 5 cm apart	
	PC - 32:2, 32:3-1, 32:3-2, 33:1, 33:2, 34:3, 34:4, 35:2, 35:3, 36:1, 36:2, 36:3, 36:4-1, 36:4-2, 36:5, 38:1, 38:2, 38:3, 38:4, 38:5, 38:6 ²² PE - 32:0, 32:1, 34:0, 34:1, 34:2, 36:3, 36:4, 38:1, 38:4, 38:6 ²² LPA - 18:1(9Z)/0:0 ²² LPC - 14:0sn-1, 14:0sn-2, 15:0sn-1, 15:0sn-2, 16:0sn-1, 16:0sn-2, 16:1sn-1, 17:0sn-1, 18:0sn-1, 18:1sn-1, 18:1sn-2, 18:2sn-1, 19:0sn-1, 20:1sn-1, 20:1sn-2, 20:5sn-1, 22:4sn-1, 22:4sn-2, 22:5sn-1, 22:6sn-1 ²² LPE - 16:0sn-1, 16:0sn-2, 16:1sn-1, 18:0sn-1, 18:0sn-2, 18:1sn-1, 18:1sn-2, 18:2sn-2, 20:0sn-1, 20:1sn-1, 20:2sn-1, 20:2sn-2, 20:3sn-1, 20:4sn-2, 20:5sn-1, 22:4sn-2, 22:6sn-1, 22:6sn-2 ²² Sphingosine-1-phosphate ²²	Upregulated Upregulated Upregulated Upregulated Upregulated Upregulated	LC-MS LC-MS LC-MS LC-MS LC-MS LC-MS	Distal noncancerous tissue Distal noncancerous tissue Distal noncancerous tissue Distal noncancerous tissue Distal noncancerous tissue Distal noncancerous tissue	
	Tissue	PC - 34:1, 36:1 ²³ PA - 36:2 ²³ PC - 38:6 ²³ PE - 38:4 ²³ PI - 38:4 ²³ SM - 22:0, 24:1 ²³ PC - 16:0/18:1, 34:1/Na ⁺²⁴	Upregulated Upregulated Downregulated Downregulated Downregulated Downregulated Upregulated	MS MS MS MS MS MS MSI	Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue
	Adenocarcinoma Tissue	PC - 16:0/18:1, (16:0/16:1)/(16:0/16:0), (16:0/18:1)/(16:0/18:0), (16:0/18:1)/(16:0/16:0), 36:4 ²⁵ PC - 16:0/16:0 ²⁵	Upregulated Downregulated	LC-MS LC-MS	Normal lung tissue Normal lung tissue

	SM - 42:2 ²⁵	Downregulated	LC-MS	Normal lung tissue
Breast cancer				
Cell lines[e]	PC - 32:1, 34:0, 38:5, 38:6 ²⁶ PE - 32:1, 34:0, 34:1, 34:2, 36:0, 36:4, 38:1, 38.5, 38:6, 40:5, 40:6 ²⁶ PI - 32:0, 32:1, 34:0, 34:1, 38:5, 40:6 ²⁶ SM - 36:2, 36:3, 41:1 ²⁶ PE - 34:5 ²⁶ PI - 38:3 ²⁶ SM - 40:1 ²⁶	Upregulated Upregulated Upregulated Upregulated Downregulated Downregulated Downregulated	HILIC-HPLC/ESI-MS HILIC-HPLC/ESI-MS HILIC-HPLC/ESI-MS HILIC-HPLC/ESI-MS HILIC-HPLC/ESI-MS HILIC-HPLC/ESI-MS HILIC-HPLC/ESI-MS	MCF10A Cell line MCF10A Cell line MCF10A Cell line MCF10A Cell line MCF10A Cell line MCF10A Cell line MCF10A Cell line
T-47D	PC - 14:0/18:1 ²⁶ PE - 16:1/18:0, 16:0/18:1, 18:0/18:2, 18:1/18:1 ²⁶ PI - 18:1/18:1, 18:2/18:0, 18:0/18:1 ²⁶ CL - 16:1/18:1/18:1/18:2 ²⁶ PC - 18:1/18:1, 18:0/18:1 ²⁶ PI - 22.5/18:0 ²⁶ CL - 16:1/18:1/18:2/20:3, 18:2/18:2/18:2/20:2 ²⁶ SM - 18:1/22:0, 18:1/24.1, 18:1/24:0 ²⁶	Upregulated Upregulated Upregulated Upregulated Downregulated Downregulated Downregulated Downregulated	TLC, ESI-MS TLC, ESI-MS TLC, ESI-MS TLC, ESI-MS TLC, ESI-MS TLC, ESI-MS TLC, ESI-MS TLC, ESI-MS	MCF10A cell line MCF10A cell line MCF10A cell line MCF10A cell line MCF10A cell line MCF10A cell line MCF10A cell line MCF10A cell line
MDA-MB-231	PC - 14:0/18:1, 16:0/16:1, 18:1/18:1, 18:0/18:1 ²⁶ PI - 18:1/18:1, 18:2/18:0, 18:0/18:1, 22.5/18:0 ²⁶ SM - 18:1/22:0, 18:24:0 ²⁶	Upregulated Upregulated Upregulated	TLC, ESI-MS TLC, ESI-MS TLC, ESI-MS	MCF10A cell line MCF10A cell line MCF10A cell line
	PC - 16:1/18:1, 18:1/18:2, 18:1/18:1, 18:2/20:3, 18:0/20:4, 18:0/20:0, 18:1/20:0, 18:1/22:5 ²⁷ PE - 17:0/19:0, 18:1/20:4, 18:1/22:4 ²⁷ PI - 16:0/16:1, 16:1/18:1, 16:0/18:1, 16:0/22:6, 18:1/20:4, 18:0/20:4, 18:0/20:3 ²⁷ PS - 16:1/18:1, 16:0/18:0, 16:0/18:1, 17:0/18:1, 18:0/18:0, 18:1/20:0, 18:0/22:6, 18:1/22:4, 18:1/22:0 ²⁷ PE - 18:1/18:1 ²⁷ PG - 16:0/18:1, 18:1/18:1 ²⁷ PI - 18:1/18:1, 18:0/18:1 ²⁷	Upregulated Upregulated Upregulated Upregulated Downregulated Downregulated Downregulated	DI-MS DI-MS DI-MS DI-MS DI-MS DI-MS DI-MS	MCF10A cell line MCF10A cell line MCF10A cell line MCF10A cell line MCF10A cell line MCF10A cell line MCF10A cell line
MCF-7	PC - 16:1/18:1, 18:1/18:2, 18:1/18:1, 18:2/20:3, 18:0/20:4, 18:1/20:1, 18:1/20:0, 18:1/22:5 ²⁷ PE - 18:1/18:1, 17:0/19:0, 18:1/20:4, 18:1/22:4 ²⁷ PG - 16:0/18:1, 18:1/18:1 ²⁷ PI - 16:0/16:1, 16:1/18:1, 16:0/18:1, 18:1/20:4 ²⁷ PS - 16:1/18:1, 16:0/18:0, 16:0/18:1, 17:0/18:1, 18:0/18:0, 18:1/20:0, 18:0/22:6, 18:1/22:4, 18:1/22:0 ²⁷ PI - 18:1/18:1, 18:0/20:4, 18:0/20:3 ²⁷ PS - 18:1/18:2, 18:0/18:1, 18:1/22:1 ²⁷	Upregulated Upregulated Upregulated Upregulated Upregulated Downregulated Downregulated	DI-MS DI-MS DI-MS DI-MS DI-MS DI-MS DI-MS	MCF10A cell line MCF10A cell line MCF10A cell line MCF10A cell line MCF10A cell line MCF10A cell line MCF10A cell line

Tissue	PC ²⁸ PE ²⁸ PI ²⁸ SM ²⁸	Upregulated Upregulated Upregulated Upregulated	UPLC-MS UPLC-MS UPLC-MS UPLC-MS	Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue
Tissue	PC - 38:6 ²⁹ PE - 34:1, PE 36:1 ²⁹ PI - 36:4 ²⁹ SM - 34:1 ²⁹	Upregulated Upregulated Upregulated Downregulated	HILIC-HPLC/ESI-MS HILIC-HPLC/ESI-MS HILIC-HPLC/ESI-MS HILIC-HPLC/ESI-MS- MALDI- MS	Normal breast tissue Normal breast tissue Normal breast tissue Normal breast tissue
	PC - 32:0, 34:1 ³⁰ SM - d18:1/16:0 ³⁰	Upregulated Upregulated	MALDI-MS MALDI-MS	Adjacent normal breast tissue Adjacent normal breast tissue
	Sphingosine, sphingosine-1-phosphate, dihydro-sphingosine, dihydro-sphingosine-1-phosphate ³¹	Upregulated	LC-ESI-MS/MS	Normal breast tissue
	PC - 32:1, 34:1, 36:1 ²³ PA - 36:2 ²³ PC - 38:4, 38:6 ²³ PA - 38:3, 40:5 ²³ PE - 38:4 ²³ PI - 38:4 ²³ SM - 22:0, 24:1 ²³	Upregulated Upregulated Downregulated Downregulated Downregulated Downregulated Downregulated	MS MS MS MS MS MS MS	Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue
Prostate cancer				
Cell lines DU145, 22RV1, LNCaP	PC - 32:1, 34:1 ³² PC - 36:2 ³² PE - 18:1/16:0 ³² PE - 18:1/18:1 ³² SM - 18:1/20:0 ³² SM - 18:1/16:0 ³² SM - 18:1/22:0 ³² PC - 32:1, 34:1 ³² PC - 36:2 ³² PE - 18:1/16:0 ³² SM - 18:1/20:0, 18:1/22:0 ³²	Upregulated [f] Upregulated [g] Upregulated [h] Upregulated [i] Upregulated [f] Upregulated [h] Upregulated [g] Downregulated [j] Downregulated [k] Downregulated [l] Downregulated [j]	LC-ESI-MS/MS LC-ESI-MS/MS LC-ESI-MS/MS LC-ESI-MS/MS LC-ESI-MS/MS LC-ESI-MS/MS LC-ESI-MS/MS LC-ESI-MS/MS LC-ESI-MS/MS LC-ESI-MS/MS	Cell line PNT1a Cell line PNT1a Cell line PNT1a Cell line PNT1a Cell line PNT1a Cell line PNT1a Cell line PNT1a Cell line PNT1a Cell line PNT1a Cell line PNT1a Cell line PNT1a
Tissue	PI - 18:0/18:1, 18:0/20:3, 18:0/20:2 ³³ LPC - 16:0/OH ³⁴ PE - 44:7, 34:2 ³⁵ PI - 37:2 ³⁵ PI - 37:6, 33:1 ³⁵ LPE - 16:0, 18:0, 18:1 ³⁵	Upregulated Downregulated Upregulated Upregulated Downregulated Downregulated	High res MALDI-MSI High res MALDI-MSI DESI-MSI DESI-MSI DESI-MSI DESI-MSI	Adjacent benign epithelium Adjacent benign epithelium Benign prostate tissue Benign prostate tissue Benign prostate tissue Benign prostate tissue

	PC - 16:0/14:0, 16:0/16:1, 16:0/18:2, 16:0/18:1, 16:0/18:0, 18:1/18:2, 18:1/18:1, 18:0/18:1, 18:1/20:4, 18:1/20:218:1/20:1, 18:1/20:0 ³⁵	Upregulated	ESI-QqQ/MS	Tissue from healthy males
	SM - d18:1/24:2, d18:1/24:0 ³⁵	Upregulated	ESI-QqQ/MS	Tissue from healthy males
	PC - 18:0/22:5 ³⁵	Downregulated	MALDI-ToF/MS	Tissue from healthy males
Colorectal cancer				
Tissue	PA - 31:0 ³⁶	Upregulated	REIMS	Normal adjacent mucosa
	PG - 36:1 ³⁶	Upregulated	REIMS	Normal adjacent mucosa
	PS - 41:0, 44:6, 44:8 ³⁶	Upregulated	REIMS	Normal adjacent mucosa
	PS - 43:5 ³⁶	Downregulated	REIMS	Normal adjacent mucosa
	PA - 36:2 ²³	Upregulated	MS	Adjacent normal tissue
	PC - 32:1, PC 34:1 ²³	Upregulated	MS	Adjacent normal tissue
	PA - 38:3, PA 40:5 ²³	Downregulated	MS	Adjacent normal tissue
	PC - 38:4 ²³	Downregulated	MS	Adjacent normal tissue
	PE - 38:4 ²³	Downregulated	MS	Adjacent normal tissue
	PI - 38:4 ²³	Downregulated	MS	Adjacent normal tissue
	SM - 22:0, 24:1 ²³	Downregulated	MS	Adjacent normal tissue
	PC ³⁷	Upregulated	HPLC	Adjacent normal tissue
	PC - 16:0/18:1 ³⁸	Upregulated	MALDI-MSI	Adjacent colorectal mucosa and tumour remote tissue – 10 cm apart
	LPC - 16:0, 18:1 ³⁸	Upregulated	MALDI-MSI	Adjacent colorectal mucosa and tumour remote tissue – 10 cm apart
	PC - 16:0/16:1 ³⁹	Upregulated	Imaging MS	Adjacent non-neoplastic mucosa
	PC ⁴⁰	Upregulated	MS	Adjacent normal mucosa
	PE ⁴⁰	Upregulated	MS	Adjacent normal mucosa
	PC, PE, PI ⁴¹	Upregulated	MRS	Adjacent normal mucosa – 4 cm or greater apart
	PS ⁴¹	Downregulated	MRS	Adjacent normal mucosa – 4 cm or greater apart
	PC - 26:0, 28:1, 30:0, 31:2, 31:4, 32:1, 34:1 ⁴²	Upregulated	LC-MS	Tumour adjacent tissue
	PE - 28:1, 31:4, 33:4 ⁴²	Upregulated	LC-MS	Tumour adjacent tissue
	PG - 37:6 ⁴²	Upregulated	LC-MS	Tumour adjacent tissue
	PS - 16:0, 28:2 ⁴²	Upregulated	LC-MS	Tumour adjacent tissue
	LPC - 24:0 ⁴²	Upregulated	LC-MS	Tumour adjacent tissue
	LPE - 16:1, 18:2 ⁴²	Upregulated	LC-MS	Tumour adjacent tissue
	LPG - 20:4, 21:0 ⁴²	Upregulated	LC-MS	Tumour adjacent tissue
	SM - 24:2, 39:2 ⁴²	Upregulated	LC-MS	Tumour adjacent tissue
	Sphingosine - 14:2, 18:3 ⁴²	Upregulated	LC-MS	Tumour adjacent tissue
Cells isolated from tumour tissue	PC - 32:0, 32:1, 36:5, 38:4 ⁴³	Upregulated	LC-MS/MS	Cells isolated from tumour adjacent normal tissue
	LPC - 14:0, 22:0, 24:0, 26:0, 16:1, 22:1, 24:1, 20:3, 20:4, 22:4, 22:5, 22:6 ⁴³	Upregulated	LC-MS/MS	Cells isolated from tumour adjacent normal tissue

	LPE - 18:0, 22:0, 24:0, 16:1, 22:1, 24:1, 20:3, 20:4, 22:4, 22:5, 22:6 ⁴³ LPS - 16:1, 20:3 ⁴³	Upregulated Upregulated	LC-MS/MS LC-MS/MS	Cells isolated from tumour adjacent normal tissue Cells isolated from tumour adjacent normal tissue
Colorectal Liver Metastasis				
Tumour tissue	PC - 36:2-16:0/20:2, 38:3-18:1/20:2, 38:2-18:1/20:1, 36:2-16:1/20:1 ⁴⁴ PE - 40:1-18:1/22:0, 38:3-18:1/20:2, 38:4-18:2/20:2, 34:1-16:1/18:0 ⁴⁴ PS - 36:2-18:1/18:1 ⁴⁴ SM - 34:1-d18:1/16:0 ⁴⁴ PC - 38:6-16:0/22:6 ⁴⁴ PE - 38:7-16:1/22:6, 34:3-16:0/18:3, 40:7-18:1/22:6, 38:6-16:0/22:6, 36:5-16:0/20:5, 36:4-16:0/20:4, 40:6-18:0/22:6 ⁴⁴ PI - 36:1-16:0/20:1 ⁴⁴ PS - 40:7-18:1/22:6 ⁴⁴	Upregulated Upregulated Upregulated Upregulated Downregulated Downregulated Downregulated Downregulated	LC-ESI-MS LC-ESI-MS LC-ESI-MS LC-ESI-MS LC-ESI-MS LC-ESI-MS LC-ESI-MS LC-ESI-MS	Normal liver parenchyma Normal liver parenchyma Normal liver parenchyma Normal liver parenchyma Normal liver parenchyma Normal liver parenchyma Normal liver parenchyma Normal liver parenchyma
Ovarian cancer				
Tissue sample	PC - 32:3, 34:1, 36:2 ⁴⁵ PI - 38:4 ⁴⁵	Upregulated Upregulated	MALDI-MS MALDI-MS	Adjacent normal tissue Adjacent normal tissue
Urothelial cancer of the bladder				
Tumour tissue	PC ⁴⁶ PE ⁴⁶ PI ⁴⁶ PS ⁴⁶	Upregulated Upregulated Upregulated Upregulated	LC-MS LC-MS LC-MS LC-MS	Benign adjacent tissue, normal bladder tissue Benign adjacent tissue, normal bladder tissue Benign adjacent tissue, normal bladder tissue Benign adjacent tissue, normal bladder tissue
Pancreatic cancer				
Ductal adenocarcinoma tissue	PS ⁴⁷ (detected on the cell surface)	Upregulated	Annexin V-FITC Staining, Flow Cytometry	Adjacent normal tissue
Gastric cancer				
Tissue	PC - 16:0/18:0 ⁴⁸ LPC - 16:0 ⁴⁸ PC - 32:1, 34:1, 36:1 ²³ PA - 36:2 ²³ PC - 38:4, 38:6 ²³ PA - 38:3, 40:5 ²³ PE - 38:4 ²³ PI - 38:4 ²³ SM - 22:0, 24:1 ²³	Upregulated Downregulated Upregulated Upregulated Downregulated Downregulated Downregulated Downregulated Downregulated	MALDI-MSI MALDI-MSI MS MS MS MS MS MS MS	Adjacent non-neoplastic mucosa Adjacent non-neoplastic mucosa Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue
Glioblastoma				

Cell line A172 (Single cell analysis)	PC - 32:2/32:1, 32:2/32:0, 32:1/32:0, 33:2/33:1, 33:2/33:0, 33:1/33:0, 34:2/34:1, 34:2/34:0, 34:1/34:0 ⁴⁹ PE - 20:1 ⁴⁹	Upregulated Upregulated	Pico-ESI-MS Pico-ESI-MS	Normal human astrocyte cell line HA (Single cell analysis)
Oesophageal Cancer				
Adenocarcinoma tissue	PE - 38:1, 38:5 ⁵⁰ PG - 40:6, 38:6, PG 38:5, 40:8, 40:7, 36:4, 34:2, 36:3, 36:0, 36:2 ⁵⁰ PI - 37:4, 40:5, 40:4, 38:5 ⁵⁰ PS - 44:9, 42:8 ⁵⁰ PA - 38:1 ⁵⁰ PE - 34:1 ⁵⁰ PS - 36:2 ⁵⁰ PA - 36:2 ⁵⁰	Upregulated Upregulated Upregulated Upregulated Upregulated Downregulated Downregulated Downregulated	DESI-MSI DESI-MSI DESI-MSI DESI-MSI DESI-MSI DESI-MSI DESI-MSI DESI-MSI	Matched healthy oesophageal epithelium - <5 cm apart Matched healthy oesophageal epithelium - <5 cm apart Matched healthy oesophageal epithelium - <5 cm apart Matched healthy oesophageal epithelium - <5 cm apart Matched healthy oesophageal epithelium - <5 cm apart Matched healthy oesophageal epithelium - <5 cm apart Matched healthy oesophageal epithelium - <5 cm apart
Tissue	PC - 32:1, 34:1, 36:1 ²³ PA - 36:2 ²³ PC - 38:4, 38:6 ²³ PA - 38:3, 40:5 ²³ PE - 38:4 ²³ PI - 38:4 ²³ SM - 22:0, 24:1 ²³	Upregulated Upregulated Downregulated Downregulated Downregulated Downregulated	MS MS MS MS MS MS	Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue
Thyroid cancer				
Tissue	PC - 16:0/18:1, 16:0/18:2 ⁵¹ SM - d18:0/16:1 ⁵¹ PC - 34:1, 38:6 ²³ PA - 36:2 ²³ PA - 38:3, 40:5 ²³ PE - 38:4 ²³ PI 38:4 ²³ SM - 22:0, 24:1 ²³	Upregulated Upregulated Upregulated Upregulated Downregulated Downregulated Downregulated Downregulated	MSI MSI MS MS MS MS MS MS	Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue Adjacent normal tissue
Hepatocellular carcinoma				
Tissue	PC - 30:0 ⁵² PC - 34:2 ⁵² PE - 34:2 ⁵² SM - 24:0 ⁵² PC - 34:0, 32:0, 42:2, 34:3, 32:2, 44:3 ⁵³ PC - 26:0, 34:2, 38:6, 40:5 ⁵³	Upregulated Downregulated Downregulated Downregulated Upregulated Downregulated	ESI-MS ESI-MS ESI-MS ESI-MS UPLC-MS UPLC-MS	Benign hepatic tissue Benign hepatic tissue Benign hepatic tissue Benign hepatic tissue Normal liver tissue Normal liver tissue
Renal cell carcinoma				

Tissue	PC - 14:0/16:0, 14:0/18:2, 16:0/16:0, 16:0/16:1, 16:1/16:1, 16:0/18:0, 16:1/18:2, 17:0/18:2, 18:0/18:2, 18:2/18:2, 18:0/20:3, 18:0/20:4, 20:1/18:2, 20:2/18:1 ⁵⁴	Upregulated	LC-TOF/MS	Surrounding normal renal cortex
	PC - 16:0/18:1, 16:0/18:2, 16:0/20:4, 16:0/20:5, 18:1/20:4, 16:0/22:5, 16:0/22:6 ⁵⁴	Downregulated	LC-TOF/MS	Surrounding normal renal cortex

[e] – Nine breast cancer cell lines (ZR-75-1, T-47D, MCF7, MDA-MB-231, MDA-MB-453, MDA-MB-468, SK-BR-3, BT-474 and BT-549).

[f]- Upregulated in LNCaP, 22RV1

[g]- Upregulated in 22RV1

[h]- Upregulated in LNCaP

[i]- Upregulated in all 3 cell lines

[j]- Downregulated in DU145

[k]- Downregulated in LNCaP, DU145

[l]- Downregulated in 22RV1

Abbreviations

2D TLC – Two-dimensional thin layer chromatography.

AB – Agrobacterium medium, derivative of M9 minimal medium.

BHI – Brain heart infusion.

DESI – Desorption electron spray ionization.

DESI-MS - Desorption electron spray ionization mass spectrometry.

DESI-IMS - Desorption electron spray ionization imaging mass spectrometry.

DI-ESI(±)-FTICR MS – Direct-infusion positive and negative ion electrospray ionization Fourier transform ion cyclotron resonance mass spectrometry.

DI MS – Direct-infusion electrospray ionization mass spectrometry.

ESI-MS – Electron spray ionization mass spectrometry.

ESI-MS/MS – Electron spray ionization tandem mass spectrometry.

FAB-MS – Fast atom bombardment mass spectrometry.

GC – Gas chromatography.

GC-MS – Gas chromatography coupled with mass spectrometry.

High res – High resolution.

HILIC-HPLC/ESI-MS – Hydrophilic interaction chromatography coupled with high performance liquid chromatography coupled with electron spray ionization mass spectrometry.

HILIC-HPLC/ESI-MS-MALDI-MS – Hydrophilic interaction chromatography coupled with high performance liquid chromatography coupled with electron spray ionization tandem mass spectrometry and matrix-assisted laser desorption.

HPLC – High performance liquid chromatography.

IHC – Immunohistochemistry.

MSI – Mass spectrometry imaging.

LC/ESI-MS/MS – Liquid chromatography coupled with electron spray ionization tandem mass spectrometry.

LC-MS – Liquid chromatography coupled with mass spectrometry.

LC-MS/MS - Liquid chromatography coupled with tandem mass spectrometry.

LC-TOF/MS – Liquid chromatography coupled with time-of-flight mass spectrometry.

MALDI-FTICR-MS – Matrix-assisted laser desorption/ionization Fourier transform ion cyclotron mass spectrometry.

MALDI-MS – Matrix-assisted laser desorption/ionization mass spectrometry.

MALDI-MSI – Matrix-assisted laser desorption mass spectrometry imaging.

MHA – Mueller-Hinton agar.

MS – Mass spectrometry.

MRS – Magnetic resonance spectroscopy.

nLC/ESI-MS/MS – Nano-scale liquid chromatography coupled with electron spray ionization tandem mass spectrometry.

NMR – Nuclear magnetic resonance spectroscopy.

Non-specific broth (per L) – $(\text{NH}_4)_2\text{SO}_4$ 2 g; KH_2PO_4 4 g; $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$ 4 g; $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ 0.2 g; $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$, 0.001 g; and $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, 0.001 g, pH 7.8.

REIMS – Rapid evaporative ionization mass spectrometry.

RP-HILIC – Reverse phase hydrophilic interaction liquid chromatography.

RP-HPLC-ESI-iontrap-MS – Reverse phase high performance liquid chromatography coupled with electron spray ionization, iontrap mass spectrometry.

RRLC-MS – Rapid resolution liquid chromatography coupled with mass spectrometry.

Synthetic broth 1 (per L) – $\text{Na}_2\text{HPO}_4 \cdot 12\text{H}_2\text{O}$ 13.9 g; KH_2PO_4 2.1 g; NH_4Cl 1.0 g; CaCl_2 0.0146 g; MgSO_4 0.22 g; $\text{FeCl}_3 \cdot 4\text{H}_2\text{O}$ 0.24 mg; sodium lactate 2.5 g; peptone 5 g; yeast extract 1.0 g and NaCl 0.5 g, 50 g or 100 g.

Synthetic media 2 (per L) – 19 mM KCl , 0.49 mM K_2HPO_4 , 79 mM NaCl , 20 mM NH_4Cl , 1.4 mM Na_2SO_4 , 0.1 mM adenine, 0.1 mM xanthine, 0.1 mM uracil, 1.8 mM alanine, 1.4 mM arginine, 0.75 mM asparagine, 1.5 mM cysteine, 0.75 mM glutamic acid, 0.3 mM glycine, 1.1 mM histidine, 2 mM isoleucine, 4 mM leucine, 3.5 mM lysine, 1.1 mM methionine, 0.09 mM phenylalanine, 4.6 mM proline, 2.8 mM serine, 1.9 mM threonine, 0.08 mM tyrosine, 2.5 mM valine, and 0.1 M tris(hydroxymethyl) aminomethane, pH 7.4.

Synthetic media 3 (per L) – Substrate Substrate (glucose or succinate) 5 g; NH_4NO_3 6 g; K_2HPO_4 5 g; KH_2PO_4 2 g; 0.5 mL of 1 % $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$ solution in water; 1 mL of trace elements solution containing (g/L): $\text{MnCl}_2 \cdot 4\text{H}_2\text{O}$ 0.004 g; $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$ 2.0 g; $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$ 2.2 g; ammonium molybdate, 0.22 g; and $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$ 1.0 mL of 1.0 %, pH 6).

TLC – Thin layer chromatography.

TSB – Tryptic soy broth (enriched with chloramphenicol or erythromycin).

UHPLC-ESI-TOF/MS – Ultra high-performance liquid chromatography coupled with electron spray ionization time-of-flight mass spectrometry.

UPLC-ESI-MS - Ultra high-performance liquid chromatography coupled with electron spray ionization mass spectrometry.

UHPLC-MS – Ultra high-performance liquid chromatography coupled with mass spectrometry.

UPLC – Ultra high-performance liquid chromatography.

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