

Supplement:

Increased lipogenesis and impaired β -oxidation predict type 2 diabetic kidney disease progression in American Indians

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Supplement Table 1: Identified lipids by adducts, mass, and retention time in positive and negative modes. The mass accuracy was ± 0.001 Da in positive mode and ± 0.005 Da in negative mode, with overall mass error of less than 2 parts per million. CE, cholesterol Esters; DAG, diacylglycerol; LPC, lysophosphatidylcholine; LPE, lysophosphatidylethanolamine; MAG, monoacylglycerol; PC, phosphatidylcholine; pPC, plasmeyn-yl-phosphatidylcholine; PE, phosphatidylethanolamine; pPE: plasmeyn-yl-phosphatidylethanolamine; PA, phosphatidic acid; SM, sphingomyelin; TAG, triacylglycerol; FFA, free Fatty Acid; CerP, ceramide-phosphates; PG, phosphatidylglycerol; PI, phosphatidylinositol; x:y, number of carbons:number of double bonds.

Lipids in Positive Mode				
Class	Compound name	Type of adducts	m/z	RT/min
CE	CE 16:0	[M+NH ₄]	642.6189	10.92
	CE 16:1	[M+NH ₄]	640.6032	10.65
	CE 17:0	[M+NH ₄]	656.6345	11.11
	CE 18:0	[M+NH ₄]	670.6502	11.28
	CE 18:1	[M+NH ₄]	668.6345	10.89
	CE 18:2	[M+NH ₄]	666.6189	10.72
	CE 18:3	[M+NH ₄]	664.6032	10.48
	CE 20:3	[M+NH ₄]	692.6345	10.74
	CE 20:4	[M+NH ₄]	690.6189	10.52
	CE 20:5	[M+NH ₄]	688.6032	10.37
	CE 22:4	[M+NH ₄]	718.6502	10.82
	CE 22:5	[M+NH ₄]	716.6345	10.64
	CE 22:6	[M+NH ₄]	714.6189	10.48
	DAG	DAG 26:0	[M+NH ₄]	502.4469
DAG 30:0		[M+NH ₄]	558.5094	7.38
DAG 30:1		[M+NH ₄]	556.4938	6.89
DAG 31:0		[M+NH ₄]	572.5251	7.69
DAG 32:0		[M+NH ₄]	586.5407	7.90
DAG 32:1		[M+NH ₄]	584.5251	7.48
DAG 32:2		[M+NH ₄]	582.5094	7.03
DAG 33:0		[M+NH ₄]	600.5564	8.12
DAG 33:1		[M+NH ₄]	598.5407	7.76
DAG 34:0		[M+NH ₄]	614.5720	8.40
DAG 34:1		[M+NH ₄]	612.5564	7.96
DAG 34:2		[M+NH ₄]	610.5407	7.58
DAG 34:3		[M+NH ₄]	608.5251	7.19
DAG 35:1		[M+NH ₄]	626.5720	8.20
DAG 35:2		[M+NH ₄]	624.5564	7.83
DAG 36:0		[M+NH ₄]	642.6033	8.86
DAG 36:1		[M+NH ₄]	640.5877	8.47
DAG 36:2		[M+NH ₄]	638.5720	8.07
DAG 36:3	[M+NH ₄]	636.5564	7.68	

Lipids in Positive Mode				
Class	Compound name	Type of adducts	m/z	RT/min
	DAG 36:4	[M+NH4]	634.5407	7.33
	DAG 36:5	[M+NH4]	632.5251	6.94
	DAG 38:1	[M+NH4]	668.6189	8.93
	DAG 38:2	[M+NH4]	666.6033	8.52
	DAG 38:4	[M+NH4]	662.5720	7.90
	DAG 38:5	[M+NH4]	660.5564	7.61
	DAG 38:6	[M+NH4]	658.5407	7.25
	DAG 38:7	[M+NH4]	656.5251	6.89
	DAG 40:6	[M+NH4]	686.5720	7.68
	DAG 40:7	[M+NH4]	684.5564	7.52
LPC	LPC 14:0	[M+H]	468.3090	1.10
	LPC 14:0	[M+Na]	490.2910	1.16
	LPC 15:0	[M+H]	482.3246	1.36
	LPC 15:0	[M+Na]	504.3066	1.37
	LPC 16:0	[M+H]	496.3403	1.62
	LPC 16:0	[M+Na]	504.3430	2.11
	LPC 16:1	[M+H]	494.3246	1.33
	LPC 16:1	[M+Na]	516.3066	1.25
	LPC 17:0	[M+H]	510.3560	2.05
	LPC 17:0	[M+Na]	532.3379	2.01
	LPC 17:1	[M+H]	508.3403	1.49
	LPC 18:0	[M+H]	524.3716	2.49
	LPC 18:0	[M+Na]	546.3535	2.38
	LPC 18:1	[M+Na]	544.3379	1.69
	LPC 18:2	[M+H]	520.3403	1.60
	LPC 18:2	[M+Na]	542.3223	1.43
	LPC 18:3	[M+H]	518.3246	1.12
	LPC 18:3	[M+Na]	540.3066	1.15
	LPC 19:0	[M+H]	538.3873	2.96
	LPC 20:0	[M+H]	552.4029	3.44
	LPC 20:1	[M+H]	550.3873	2.64
	LPC 20:1	[M+Na]	572.3692	2.62
	LPC 20:2	[M+H]	548.3716	20
	LPC 20:3	[M+H]	546.3560	1.61
	LPC 20:3	[M+Na]	568.3379	1.60
	LPC 20:4	[M+H]	544.3403	1.45
	LPC 20:4	[M+Na]	566.3223	1.34
	LPC 20:5	[M+H]	542.3246	1.08
	LPC 22:4	[M+H]	572.3716	1.86
	LPC 22:4	[M+Na]	594.3535	1.88
	LPC 22:5	[M+H]	570.3560	1.51
	LPC 22:6	[M+H]	568.3403	1.30
	LPC 24:0	[M+H]	608.4655	5.30

Lipids in Positive Mode				
Class	Compound name	Type of adducts	m/z	RT/min
LPE	LPE 16:0	[M+H]	454.2934	1.69
	LPE 18:0	[M+H]	482.3246	2.48
	LPE 18:0	[M+Na]	504.3066	2.62
	LPE 18:1	[M+H]	480.3090	1.87
	LPE 18:2	[M+H]	478.2934	1.40
	LPE 20:4	[M+H]	502.2934	1.34
	LPE 22:6	[M+H]	526.2933	1.29
MAG	MAG 17:0	[M+Li]	351.3087	3.19
	MAG 18:1	[M+NH ₄]	374.3270	2.90
PA	PA 34:0	[M+Na]	699.4941	8.37
PC	PC 30:0	[M+Na]	728.5206	6.07
	PC 30:1	[M+Na]	726.5050	5.54
	PC 32:0	[M+Na]	756.5519	6.75
	PC 32:1	[M+Na]	754.5363	6.23
	PC 32:2	[M+Na]	752.5206	5.75
	PC 32:3	[M+H]	728.5230	5.37
	PC 33:2	[M+Na]	766.5363	6.09
	PC 34:0	[M+Na]	784.5832	7.43
	PC 34:2	[M+Na]	780.5519	6.42
	PC 34:3	[M+H]	756.5543	6.78
	PC 34:3	[M+Na]	778.5363	5.93
	PC 34:4	[M+Na]	776.5206	5.68
	PC 36:1	[M+Na]	810.5989	7.57
	PC 36:2	[M+Na]	808.5832	7.16
	PC 36:3	[M+H]	784.5856	7.45
	PC 36:4	[M+H]	782.5700	7.86
	PC 36:4	[M+Na]	804.5519	6.08
	PC 36:5	[M+H]	780.5543	5.60
	PC 36:5	[M+Na]	802.5363	5.73
	PC 36:6	[M+H]	778.5387	5.89
	PC 38:4	[M+H]	810.6013	7.56
	PC 38:4	[M+Na]	832.5832	7.02
	PC 38:5	[M+H]	808.5856	5.09
	PC 38:6	[M+H]	806.5700	6.03
	PC 38:6	[M+Na]	828.5519	5.44
	PC 38:6	[M+Na]	828.5519	6.14
	PC 38:8	[M+H]	802.5387	5.86
	PC 40:10	[M+H]	826.5387	5.62
	PC 40:4	[M+Na]	860.6145	7.55
	PC 40:9	[M+H]	828.5543	6.09
PC 42:10	[M+H]	854.5700	5.83	
PE	PE 32:1	[M+H]	690.5074	6.27
	PE 34:0	[M+H]	720.5543	7.38

Lipids in Positive Mode				
Class	Compound name	Type of adducts	m/z	RT/min
	PE 34:1	[M+H]	718.5387	6.90
	PE 34:2	[M+H]	716.5230	6.46
	PE 35:2	[M+H]	730.5387	6.79
	PE 36:0	[M+H]	748.5856	7.91
	PE 36:1	[M+H]	746.5700	7.50
	PE 36:2	[M+H]	744.5543	7.01
	PE 36:2	[M+H]	744.5543	7.12
	PE 36:3	[M+H]	742.5387	6.59
	PE 36:4	[M+H]	740.5230	6.40
	PE 36:5	[M+H]	738.5074	5.88
	PE 38:3	[M+H]	770.5700	7.28
	PE 38:4	[M+H]	768.5543	7.04
	PE 38:5	[M+H]	766.5387	6.54
	PE 40:6	[M+H]	792.5543	6.94
pPC	pPC 18:0	[M+Na]	544.3379	1.89
pPE	pPE 34:1	[M+H]	702.5438	7.22
	pPE 34:2	[M+H]	700.5281	6.75
	pPE 34:2	[M+H]	700.5281	6.82
	pPE 36:1	[M+H]	730.5751	7.80
	pPE 36:2	[M+H]	728.5594	7.37
	pPE 36:4	[M+H]	724.5281	6.72
	pPE 36:5	[M+H]	722.5125	6.34
	pPE 38:1	[M+H]	758.6063	8.27
	pPE 38:2	[M+H]	756.5907	7.95
	pPE 38:3	[M+H]	754.5751	7.58
	pPE 38:4	[M+H]	752.5594	7.33
	pPE 38:6	[M+H]	748.5281	6.64
	pPE 40:4	[M+H]	780.5907	7.78
	pPE 40:5	[M+H]	778.5751	7.46
	pPE 40:6	[M+H]	776.5594	7.25
SM	SM 21:0	[M]	523.3876	1.87
	SM 30:1	[M]	647.5128	4.46
	SM 30:1	[M+Na]	669.4948	4.41
	SM 31:1	[M]	661.5284	4.84
	SM 32:0	[M]	677.5597	5.53
	SM 32:0	[M+Na]	699.5417	5.47
	SM 32:1	[M+Na]	697.5261	2.13
	SM 32:1	[M+Na]	697.5261	5.23
	SM 32:2	[M]	673.5284	4.66
	SM 33:0	[M]	691.5754	5.86
	SM 33:1	[M]	689.5597	4.41
	SM 33:1	[M+Na]	711.5417	5.60
	SM 33:2	[M]	687.5441	5.05

Lipids in Positive Mode				
Class	Compound name	Type of adducts	m/z	RT/min
	SM 34:1	[M]	703.5754	5.89
	SM 34:1	[M+Na]	725.5573	5.94
	SM 34:2	[M+Na]	723.5417	5.37
	SM 35:1	[M]	717.5911	5.67
	SM 35:1	[M]	717.5911	6.26
	SM 35:1	[M+Na]	739.5730	6.27
	SM 35:2	[M]	715.5754	5.66
	SM 35:2	[M+Na]	737.5573	5.78
	SM 36:1	[M+Na]	753.5886	6.67
	SM 36:2	[M+Na]	751.5730	6.14
	SM 37:1	[M]	745.6224	6.97
	SM 37:2	[M]	743.6067	6.56
	SM 38:0	[M]	761.6536	7.55
	SM 38:1	[M]	759.6380	7.10
	SM 38:1	[M+Na]	781.6199	7.32
	SM 38:2	[M]	757.6224	6.69
	SM 38:4	[M]	753.5911	5.87
	SM 39:0	[M]	775.6693	7.85
	SM 39:1	[M+Na]	795.6356	7.66
	SM 39:2	[M]	771.6380	7.15
	SM 40:1	[M+Na]	809.6513	7.92
	SM 40:2	[M]	785.6536	7.05
	SM 40:2	[M+Na]	807.6356	7.44
	SM 41:1	[M+Na]	823.6669	8.21
	SM 41:2	[M+Na]	821.6513	7.76
	SM 41:4	[M]	795.6380	6.86
	SM 41:5	[M]	793.6224	6.32
	SM 42:1	[M+Na]	837.6826	8.49
	SM 42:2	[M]	813.6849	11.70
	SM 42:2	[M+Na]	835.6669	7.93
	SM 42:4	[M]	809.6536	7.00
	SM 42:5	[M]	807.6380	6.61
	SM 43:1	[M]	829.7163	8.77
	SM 43:1	[M+Na]	851.6982	8.78
	SM 43:2	[M]	827.7006	8.31
	SM 43:4	[M]	823.6693	7.34
	SM 44:1	[M]	843.7319	9.05
	SM 44:2	[M]	841.7163	8.49
TAG	TAG 40:0	[M+NH4]	712.6451	9.45
	TAG 42:0	[M+NH4]	740.6764	9.77
	TAG 42:1	[M+NH4]	738.6608	9.49
	TAG 44:1	[M+NH4]	766.6921	9.79
	TAG 46:0	[M+NH4]	796.7390	10.31

Lipids in Positive Mode				
Class	Compound name	Type of adducts	m/z	RT/min
	TAG 46:1	[M+Na]	799.6787	10.08
	TAG 46:1	[M+NH4]	794.7233	10.04
	TAG 46:2	[M+NH4]	792.7077	9.80
	TAG 48:0	[M+NH4]	824.7702	10.55
	TAG 48:1	[M+NH4]	822.7546	10.29
	TAG 48:2	[M+NH4]	820.7390	10.07
	TAG 48:3	[M+NH4]	818.7233	9.84
	TAG 49:0	[M+NH4]	838.7859	10.66
	TAG 49:1	[M+NH4]	836.7702	10.45
	TAG 49:2	[M+NH4]	834.7546	10.24
	TAG 50:0	[M+NH4]	852.8015	10.79
	TAG 50:1	[M+NH4]	850.7859	10.53
	TAG 50:2	[M+NH4]	848.7702	10.30
	TAG 50:3	[M+NH4]	846.7546	10.11
	TAG 50:3	[M+NH4]	846.7546	9.20
	TAG 50:4	[M+NH4]	844.7390	8.98
	TAG 50:4	[M+NH4]	844.7390	9.91
	TAG 50:5	[M+NH4]	842.7233	9.73
	TAG 51:1	[M+NH4]	864.8015	10.69
	TAG 51:2	[M+NH4]	862.7859	10.51
	TAG 51:3	[M+NH4]	860.7702	10.31
	TAG 51:4	[M+NH4]	858.7546	10.06
	TAG 52:0	[M+Na]	885.7882	11.02
	TAG 52:0	[M+NH4]	880.8328	11.03
	TAG 52:1	[M+Na]	883.7726	10.82
	TAG 52:1	[M+NH4]	878.8172	10.80
	TAG 52:2	[M+NH4]	876.8015	10.54
	TAG 52:3	[M+Na]	879.7413	10.38
	TAG 52:3	[M+NH4]	874.7859	10.36
	TAG 52:4	[M+NH4]	872.7702	10.17
	TAG 52:4	[M+NH4]	872.7702	9.27
	TAG 52:5	[M+NH4]	870.7546	9.99
	TAG 52:6	[M+Na]	873.6944	9.77
	TAG 52:6	[M+NH4]	868.7390	9.79
	TAG 53:0	[M+NH4]	894.8484	11.14
	TAG 53:1	[M+NH4]	892.8328	10.92
	TAG 53:2	[M+NH4]	890.8172	10.73
	TAG 53:3	[M+NH4]	888.8015	10.54
	TAG 53:4	[M+NH4]	886.7859	10.34
	TAG 53:5	[M+NH4]	884.7702	10.16
	TAG 54:1	[M+Na]	911.8038	11.02
	TAG 54:1	[M+NH4]	906.8484	11.05
	TAG 54:2	[M+NH4]	904.8328	10.84

Lipids in Positive Mode				
Class	Compound name	Type of adducts	m/z	RT/min
	TAG 54:3	[M+NH4]	902.8172	10.63
	TAG 54:4	[M+NH4]	900.8015	10.42
	TAG 54:5	[M+NH4]	898.7859	10.24
	TAG 54:6	[M+Na]	901.7257	10.04
	TAG 54:6	[M+NH4]	896.7702	10.04
	TAG 54:7	[M+Na]	899.7100	9.84
	TAG 54:7	[M+NH4]	894.7546	9.89
	TAG 54:8	[M+NH4]	892.7390	9.67
	TAG 56:0	[M+NH4]	936.8954	11.52
	TAG 56:1	[M+NH4]	934.8797	11.28
	TAG 56:2	[M+NH4]	932.8641	11.06
	TAG 56:3	[M+NH4]	930.8484	10.87
	TAG 56:4	[M+NH4]	928.8328	10.70
	TAG 56:5	[M+NH4]	926.8172	10.54
	TAG 56:6	[M+NH4]	924.8015	10.36
	TAG 56:7	[M+NH4]	922.7859	10.17
	TAG 56:8	[M+NH4]	920.7702	9.99
	TAG 56:9	[M+NH4]	918.7546	9.82
	TAG 58:1	[M+NH4]	962.9110	11.55
	TAG 58:10	[M+NH4]	944.7702	9.91
	TAG 58:3	[M+NH4]	958.8797	11.10
	TAG 58:5	[M+NH4]	954.8484	10.76
	TAG 58:6	[M+NH4]	952.8328	10.60
	TAG 58:7	[M+NH4]	950.8172	10.49
	TAG 58:8	[M+NH4]	948.8015	10.23
	TAG 58:9	[M+NH4]	946.7859	10.10
	TAG 60:12	[M+NH4]	968.7702	10.88
	TAG 62:1	[M+NH4]	1018.9740	12.09

Lipids in Negative Mode				
Class	Compound name	Type of Adducts	m/z	RT/min
FFA	FFA 16:0		255.2329	2.30
	FFA 18:0		283.2642	3.27
	FFA 18:1		281.2486	2.50
	FFA 18:2		279.2329	1.92
	FFA 20:0		311.2955	4.30
	FFA 20:1		309.2799	3.45
	FFA 20:2		307.2642	2.82
	FFA 22:0		339.3268	5.29
	FFA 22:1		337.3112	4.43
	FFA 22:2		335.2955	3.76
	FFA 22:3		333.2799	3.18

Lipids in Negative Mode				
Class	Compound name	Type of Adducts	m/z	RT/min
	FFA 24:0		367.3581	6.21
	FFA 24:1		365.3425	5.36
	FFA 24:2		363.3268	4.70
	FFA 24:3		361.3112	4.07
	FFA 20:4		303.2329	1.85
CerP	CerP 34:1	[M-H]	616.4706	5.91
LPE	LPE 16:0	[M-H]	452.2777	1.71
	LPE 18:0	[M-H]	480.3090	2.49
	LPE 18:1	[M-H]	478.2934	1.88
	LPE 18:2	[M-H]	476.2777	1.40
	LPE 20:3	[M-H]	502.2934	1.68
	LPE 20:4	[M-H]	500.2777	1.37
	LPE 22:4	[M-H]	528.3090	1.91
	LPE 22:5	[M-H]	526.2934	1.62
	LPE 22:6	[M-H]	524.2777	1.33
Spinganine	N-(hexadecanoyl)- sphing-4-enine	[M-H]	536.5041	6.85
PA	PA 34:2	[M-H]	671.4652	6.36
PC	PC 30:0	[M-Ac-H]	764.5442	6.12
	PC 30:1	[M-Ac-H]	762.5285	5.59
	PC 30:2	[M-Ac-H]	760.5129	5.06
	PC 32:0	[M-Ac-H]	792.5754	6.81
	PC 32:1	[M-Ac-H]	790.5598	6.26
	PC 32:2	[M-Ac-H]	788.5442	5.77
	PC 32:3	[M-Ac-H]	786.5285	5.32
	PC 33:1	[M-Ac-H]	804.5754	6.60
	PC 33:2	[M-Ac-H]	802.5598	6.13
	PC 34:1	[M-Ac-H]	818.5911	6.85
	PC 34:2	[M-Ac-H]	816.5754	4.54
	PC 34:3	[M-Ac-H]	814.5598	5.94
	PC 34:4	[M-Ac-H]	812.5442	5.71
	PC 35:1	[M-Ac-H]	832.6068	7.24
	PC 35:2	[M-Ac-H]	830.5911	6.75
	PC 35:3	[M-Ac-H]	828.5754	6.26
	PC 36:1	[M-Ac-H]	846.6224	7.54
	PC 36:2	[M-Ac-H]	844.6068	10.73
	PC 36:2	[M-Ac-H]	844.6068	7.04
	PC 36:3	[M-Ac-H]	842.5911	6.56
	PC 36:4	[M-Ac-H]	840.5754	6.23
	PC 36:5	[M-Ac-H]	838.5598	5.81
	PC 36:6	[M-Ac-H]	836.5442	5.45
	PC 37:2	[M-Ac-H]	858.6224	7.42
	PC 37:3	[M-Ac-H]	856.6068	6.91

Lipids in Negative Mode				
Class	Compound name	Type of Adducts	m/z	RT/min
	PC 37:4	[M-Ac-H]	854.5911	6.68
	PC 37:6	[M-Ac-H]	850.5598	5.91
	PC 38:2	[M-Ac-H]	872.6381	7.71
	PC 38:3	[M-Ac-H]	870.6224	7.30
	PC 38:4	[M-Ac-H]	868.6068	6.92
	PC 38:5	[M-Ac-H]	866.5911	6.55
	PC 38:6	[M-Ac-H]	864.5754	6.19
	PC 38:7	[M-Ac-H]	862.5598	5.65
	PC 39:6	[M-Ac-H]	878.5911	6.58
	PC 40:4	[M-Ac-H]	896.6381	7.53
	PC 40:5	[M-Ac-H]	894.6224	7.21
	PC 40:6	[M-Ac-H]	892.6068	6.83
	PC 40:7	[M-Ac-H]	890.5911	6.31
	PC 40:8	[M-Ac-H]	888.5754	5.90
	PC 42:10	[M-Ac-H]	912.5754	5.78
PE	PE 32:0	[M-H]	690.5074	6.79
	PE 32:1	[M-H]	688.4917	6.28
	PE 33:0	[M-H]	704.5231	7.08
	PE 33:1	[M-H]	702.5074	6.60
	PE 34:1	[M-H]	716.5231	6.90
	PE 34:2	[M-H]	714.5074	6.43
	PE 34:3	[M-H]	712.4917	6.02
	PE 35:1	[M-H]	730.5387	7.14
	PE 35:2	[M-H]	728.5231	6.77
	PE 35:3	[M-H]	726.5074	6.23
	PE 35:4	[M-H]	724.4917	6.09
	PE 36:0	[M-H]	746.5700	7.92
	PE 36:1	[M-H]	744.5543	6.94
	PE 36:1	[M-H]	744.5543	7.49
	PE 36:2	[M-H]	742.5387	7.06
	PE 36:3	[M-H]	740.5231	5.14
	PE 36:3	[M-H]	740.5231	6.58
	PE 36:4	[M-H]	738.5074	6.26
	PE 36:5	[M-H]	736.4917	6.01
	PE 37:4	[M-H]	752.5231	6.72
	PE 38:2	[M-H]	770.5700	7.51
	PE 38:3	[M-H]	768.5543	7.29
	PE 38:4	[M-H]	766.5387	6.96
	PE 38:5	[M-H]	764.5231	6.56
	PE 38:6	[M-H]	762.5074	6.16
	PE 40:4	[M-H]	794.5700	7.47
	PE 40:5	[M-H]	792.5543	7.20
	PE 40:6	[M-H]	790.5387	6.95

Lipids in Negative Mode				
Class	Compound name	Type of Adducts	m/z	RT/min
PG	PE 40:7	[M-H]	788.5231	6.44
	PE 40:8	[M-H]	786.5074	6.02
	PG 33:0	[M-H]	735.5176	6.04
	PG 36:0	[M-H]	777.5646	6.88
	PG 36:2	[M-H]	773.5333	6.04
PI	PI 32:1	[M-H]	807.5024	5.05
	PI 34:2	[M-H]	833.5180	5.22
	PI 36:2	[M-H]	861.5493	5.87
	PI 36:3	[M-H]	859.5337	5.36
	PI 36:4	[M-H]	857.5180	5.22
	PI 38:3	[M-H]	887.5649	6.04
	PI 38:4	[M-H]	885.5493	5.85
	PI 38:5	[M-H]	883.5337	5.37
pPE	pPE 32:1	[M-H]	672.4968	6.65
	pPE 34:1	[M-H]	700.5281	7.25
	pPE 34:2	[M-H]	698.5124	6.78
	pPE 34:3	[M-H]	696.4968	6.40
	pPE 36:1	[M-H]	728.5594	7.81
	pPE 36:2	[M-H]	726.5438	7.36
	pPE 36:3	[M-H]	724.5281	6.96
	pPE 36:4	[M-H]	722.5124	6.72
	pPE 36:5	[M-H]	720.4968	6.38
	pPE 38:1	[M-H]	756.5907	8.30
	pPE 38:2	[M-H]	754.5751	7.97
	pPE 38:3	[M-H]	752.5594	7.58
	pPE 38:4	[M-H]	750.5438	7.29
	pPE 38:5	[M-H]	748.5281	6.80
	pPE 38:6	[M-H]	746.5124	6.61
	pPE 40:4	[M-H]	778.5751	7.82
	pPE 40:5	[M-H]	776.5594	7.43
	pPE 40:6	[M-H]	774.5438	7.25
	pPE 42:5	[M-H]	804.5907	7.91
	pPE 42:6	[M-H]	802.5751	7.80
PS	PS 36:1	[M-H]	788.5442	6.43
	PS 38:4	[M-H]	810.5285	6.01

Supplement Table 2: Alignment of various lipid species into different principle components using principle component analysis.

TAG			DAG		pPE			CE		PE	
Short LDB	Int LDB	Int HDB	Short LDB	Long HDB	Short LDB	Short HDB	Long HDB	Short LDB	Long HDB	Saturated	Unsaturated
TAG 40:0	TAG 52:2	TAG 50:4	DAG 30:0	DAG 34:2	pPE 32:1	pPE 36:4	pPE 38:1	CE 16:0	CE 18:2	PE 34:0	PE 32:1
TAG 42:0	TAG 52:3	TAG 50:5	DAG 30:1	DAG 34:3	pPE 34:1	pPE 36:5	pPE 42:5	CE 18:1	CE 18:3	PE 36:0	PE 34:1
TAG 42:1	TAG 54:1	TAG 52:4	DAG 32:0	DAG 36:3	pPE 34:2	pPE 38:3	pPE 42:6		CE 20:3		PE 34:2
TAG 44:1	TAG 54:2	TAG 52:5	DAG 32:1	DAG 36:2	pPE 34:3	pPE 38:4			CE 20:4		PE 36:1
TAG 46:0	TAG 54:3	TAG 52:6	DAG 32:2	DAG 36:3	pPE 36:1	pPE 38:5			CE 20:5		PE 36:2
TAG 46:1	TAG 56:1	TAG 56:8	DAG 34:0	DAG 36:4	pPE 36:2	pPE 38:6			CE 22:4		PE 36:3
TAG 46:2	TAG 56:2	TAG 54:4	DAG 34:1	DAG 36:5	pPE 36:3	pPE 40:4			CE 22:5		PE 36:4
TAG 48:0	TAG 56:3	TAG 54:5	DAG 36:1	DGA 38:4	PE 38:2	pPE 40:5			CE 22:6		PE 36:5
TAG 48:1	TAG 56:4	TAG 54:6		DAG 38:5		pPE 40:6					PE 38:3
TAG 48:2		TAG 54:7		DAG 38:6							PE 38:4
TAG 48:3		TAG 54:8		DAG 40:6							PE 38:5
TAG 50:0		TAG 56:4		DAG 40:7							PE 40:6
TAG 50:1		TAG 56:5									
TAG 50:2		TAG 56:6									
TAG 50:3		TAG 56:7									
TAG 52:0		TAG 56:8									
TAG 52:1		TAG 56:9									
TAG 56:0		TAG 58:5									
TAG 58:1		TAG 58:6									
		TAG 58:7									
		TAG 58:8									
		TAG 58:9									
		TAG 58:10									

FFA		AC	
Saturated	Unsaturated	Intermediate	Long
FFA 16:0	FFA 18:1	AC 8:0	AC 16:0
FFA 18:0	FFA 18:2	AC 8:1	AC 16:1
FFA 20:0	FFA 20:1	AC 10:0	AC 18:0
FFA 22:0	FFA 20:2	AC10:1	AC 18:1
	FFA 20:4	AC 12:0	AC 18:2
	FFA 22:1	AC 12:1	AC 20:0
	FFA 22:2	AC 14:0	AC 20:1
	FFA 22:3	AC 14:1	AC 20:2
		AC 14:2	AC 20:3
			AC 20:4

AC, acylcarnitines; CE, cholesterol esters; DAG, diacylglycerol; FFA, free fatty acids; HDB, high double bond; LDB, low double bond; LPC, lyso-PC; PC, phosphatidylcholine; PE, phosphatidylethanolamine; pPE, plasmenyl-PE; SM, sphingomyelin; TAG, triacylglycerol. ; x:y, number of carbons:number of double bonds.

Supplement Table 3: Categories of chain length and double bond applied for generation of differential networks presented in Figure 7.

lipid	Chain length	Double bond	Double bond and chain length
L-Carnitine (LC)			
AC 2:0	AC bottom	NA	AC bottom
AC 3:0	AC bottom	NA	AC bottom
AC 4:0	AC bottom	NA	AC bottom
AC 5:0	AC bottom	NA	AC bottom
AC 6:0	AC middle	NA	AC middle
AC 8:0	AC middle	NA	AC middle
AC 8:1	AC middle	NA	AC middle
AC 10:0	AC middle	NA	AC middle
AC 10:1	AC middle	NA	AC middle
AC 20:0	AC middle	NA	AC middle
AC 20:0-OH	AC middle	NA	AC middle
AC 12:1	AC middle	NA	AC middle
AC 14:0	AC middle	NA	AC middle
AC 14:0-OH	AC middle	NA	AC middle
AC 14:1	AC middle	NA	AC middle
AC 14:2	AC middle	NA	AC middle
AC 16:0	AC top	NA	AC top
AC 16:0-OH	AC top	NA	AC top
AC 16:1	AC top	NA	AC top
AC 18:0	AC top	NA	AC top
AC 18:1	AC top	NA	AC top
AC 18:2	AC top	NA	AC top
AC 18:2-OH	AC top	NA	AC top
AC 20:0	AC top	NA	AC top
AC 20:1	AC top	NA	AC top
AC 20:2	AC top	NA	AC top
AC 20:3	AC top	NA	AC top
AC 20:4	AC top	NA	AC top
CE 16:0	CE bottom	CE low	CE low bottom
CE 16:1	CE bottom	CE low	CE low bottom
CE 18:0	CE middle	CE low	CE low middle
CE 18:1	CE middle	CE low	CE low middle
CE 18:2	CE middle	CE high	CE high middle
CE 18:3	CE middle	CE high	CE high middle
CE 20:3	CE top	CE high	CE high top
CE 20:4	CE top	CE high	CE high top
CE 20:5	CE top	CE high	CE high top
CE 22:4	CE top	CE high	CE high top
CE 22:5	CE top	CE high	CE high top

lipid	Chain length	Double bond	Double bond and chain length
CE 22:6	CE top	CE high	CE high top
DAG 26:0	DAG bottom	DAG low	DAG low bottom
DAG 30:0	DAG bottom	DAG low	DAG low bottom
DAG 30:1	DAG bottom	DAG low	DAG low bottom
DAG 32:0	DAG bottom	DAG low	DAG low bottom
DAG 32:1	DAG bottom	DAG low	DAG low bottom
DAG 32:2	DAG bottom	DAG high	DAG high bottom
DAG 34:0	DAG middle	DAG low	DAG low middle
DAG 34:1	DAG middle	DAG low	DAG low middle
DAG 34:2	DAG middle	DAG high	DAG high middle
DAG 34:3	DAG middle	DAG high	DAG high middle
DAG 36:0	DAG middle	DAG low	DAG low middle
DAG 36:1	DAG middle	DAG low	DAG low middle
DAG 36:2	DAG middle	DAG high	DAG high middle
DAG 36:3	DAG middle	DAG high	DAG high middle
DAG 36:4	DAG middle	DAG high	DAG high middle
DAG 36:5	DAG middle	DAG high	DAG high middle
DAG 38:1	DAG middle	DAG low	DAG low middle
DAG 38:2	DAG middle	DAG high	DAG high middle
DAG 38:4	DAG middle	DAG high	DAG high middle
DAG 38:5	DAG middle	DAG high	DAG high middle
DAG 38:6	DAG middle	DAG high	DAG high middle
DAG 38:7	DAG middle	DAG high	DAG high middle
DAG 40:6	DAG top	DAG high	DAG high top
DAG 40:7	DAG top	DAG high	DAG high top
FFA 16:0	FFA	FFA low	FFA low NA
FFA 18:0	FFA	FFA low	FFA low NA
FFA 18:1	FFA	FFA low	FFA low NA
FFA 18:2	FFA	FFA high	FFA high NA
FFA 20:0	FFA	FFA low	FFA low NA
FFA 20:1	FFA	FFA low	FFA low NA
FFA 20:2	FFA	FFA high	FFA high NA
FFA 20:4	FFA	FFA high	FFA high NA
FFA 22:0	FFA	FFA low	FFA low NA
FFA 22:1	FFA	FFA low	FFA low NA
FFA 22:2	FFA	FFA high	FFA high NA
FFA 22:3	FFA	FFA high	FFA high NA
FFA 24:0	FFA	FFA low	FFA low NA
FFA 24:1	FFA	FFA low	FFA low NA
FFA 24:2	FFA	FFA high	FFA high NA
FFA 24:3	FFA	FFA high	FFA high NA
lysoPC 14:0	lysoPC bottom	lysoPC low	lysoPC low bottom
lysoPC 16:0	lysoPC bottom	lysoPC low	lysoPC low bottom

lipid	Chain length	Double bond	Double bond and chain length
lysoPC 16:1	lysoPC bottom	lysoPC low	lysoPC low bottom
lysoPC 18:0	lysoPC middle	lysoPC low	lysoPC low middle
lysoPC 18:1	lysoPC middle	lysoPC low	lysoPC low middle
lysoPC 18:2	lysoPC middle	lysoPC high	lysoPC high middle
lysoPC 18:3	lysoPC middle	lysoPC high	lysoPC high middle
lysoPC 20:0	lysoPC middle	lysoPC low	lysoPC low middle
lysoPC 20:1	lysoPC middle	lysoPC low	lysoPC low middle
lysoPC 20:2	lysoPC middle	lysoPC high	lysoPC high middle
lysoPC 20:3	lysoPC middle	lysoPC high	lysoPC high middle
lysoPC 20:4	lysoPC middle	lysoPC high	lysoPC high middle
lysoPC 20:5	lysoPC middle	lysoPC high	lysoPC high middle
lysoPC 22:4	lysoPC middle	lysoPC high	lysoPC high middle
lysoPC 22:5	lysoPC middle	lysoPC high	lysoPC high middle
lysoPC 22:6	lysoPC middle	lysoPC high	lysoPC high middle
lysoPC 24:0	lysoPC top	lysoPC low	lysoPC low top
lysoPE 16:0	lysoPE bottom	lysoPE low	lysoPE low bottom
lysoPE 18:0	lysoPE bottom	lysoPE low	lysoPE low bottom
lysoPE 18:1	lysoPE bottom	lysoPE low	lysoPE low bottom
lysoPE 18:2	lysoPE bottom	lysoPE high	lysoPE high bottom
lysoPE 20:4	lysoPE middle	lysoPE high	lysoPE high middle
lysoPE 22:6	lysoPC top	lysoPE high	lysoPE high top
PC 30:0	PC middle	PC low	PC low middle
PC 30:1	PC middle	PC low	PC low middle
PC 30:2	PC middle	PC high	PC high middle
PC 32:0	PC middle	PC low	PC low middle
PC 32:1	PC middle	PC low	PC low middle
PC 32:2	PC middle	PC high	PC high middle
PC 32:3	PC middle	PC high	PC high middle
PC 34:0	PC middle	PC low	PC low middle
PC 34:1	PC middle	PC low	PC low middle
PC 34:2	PC middle	PC high	PC high middle
PC 34:3	PC middle	PC high	PC high middle
PC 34:4	PC middle	PC high	PC high middle
PC 36:1	PC middle	PC low	PC low middle
PC 36:2	PC middle	PC high	PC high middle
PC 36:3	PC middle	PC high	PC high middle
PC 36:4	PC middle	PC high	PC high middle
PC 36:5	PC middle	PC high	PC high middle
PC 36:6	PC middle	PC high	PC high middle
PC 38:2	PC top	PC high	PC high top
PC 38:3	PC top	PC high	PC high top
PC 38:4	PC top	PC high	PC high top
PC 38:5	PC top	PC high	PC high top

lipid	Chain length	Double bond	Double bond and chain length
PC 38:6	PC top	PC high	PC high top
PC 38:7	PC top	PC high	PC high top
PC 38:8	PC top	PC high	PC high top
PC 40:10	PC top	PC high	PC high top
PC 40:4	PC top	PC high	PC high top
PC 40:5	PC top	PC high	PC high top
PC 40:6	PC top	PC high	PC high top
PC 40:7	PC top	PC high	PC high top
PC 40:8	PC top	PC high	PC high top
PC 40:9	PC top	PC high	PC high top
PC 42:10	PC top	PC high	PC high top
PE 32:1	PE bottom	PE low	PE low bottom
PE 34:0	PE middle	PE low	PE low middle
PE 34:1	PE middle	PE low	PE low middle
PE 34:2	PE middle	PE high	PE high middle
PE 34:3	PE middle	PE high	PE high middle
PE 36:0	PE middle	PE low	PE low middle
PE 36:1	PE middle	PE low	PE low middle
PE 36:2	PE middle	PE high	PE high middle
PE 36:3	PE middle	PE high	PE high middle
PE 36:4	PE middle	PE high	PE high middle
PE 36:5	PE middle	PE high	PE high middle
PE 38:2	PE middle	PE high	PE high middle
PE 38:3	PE middle	PE high	PE high middle
PE 38:4	PE middle	PE high	PE high middle
PE 38:5	PE middle	PE high	PE high middle
PE 38:6	PE middle	PE high	PE high middle
PE 40:4	PE top	PE high	PE high top
PE 40:5	PE top	PE high	PE high top
PE 40:6	PE top	PE high	PE high top
PE 40:7	PE top	PE high	PE high top
PE 40:8	PE top	PE high	PE high top
PI 32:1	PI bottom	PI low	PI low bottom
PI 34:2	PI bottom	PI high	PI high bottom
PI 36:2	PI middle	PI high	PI high middle
PI 36:3	PI middle	PI high	PI high middle
PI 36:4	PI middle	PI high	PI high middle
PI 38:3	PI middle	PI high	PI high middle
PI 38:4	PI middle	PI high	PI high middle
PI 38:5	PI middle	PI high	PI high middle
plasmeylPE 32:1	plasmeylPE bottom	plasmeylPE low	plasmeylPE low bottom
plasmeylPE 34:1	plasmeylPE bottom	plasmeylPE low	plasmeylPE low bottom
plasmeylPE 34:2	plasmeylPE bottom	plasmeylPE high	plasmeylPE high bottom












































lipid	Chain length	Double bond	Double bond and chain length
plasmeylPE 34:3	plasmeylPE bottom	plasmeylPE high	plasmeylPE high bottom
plasmeylPE 36:1	plasmeylPE middle	plasmeylPE low	plasmeylPE low middle
plasmeylPE 36:2	plasmeylPE middle	plasmeylPE high	plasmeylPE high middle
plasmeylPE 36:3	plasmeylPE middle	plasmeylPE high	plasmeylPE high middle
plasmeylPE 36:4	plasmeylPE middle	plasmeylPE high	plasmeylPE high middle
plasmeylPE 36:5	plasmeylPE middle	plasmeylPE high	plasmeylPE high middle
plasmeylPE 38:1	plasmeylPE middle	plasmeylPE low	plasmeylPE low middle
plasmeylPE 38:2	plasmeylPE middle	plasmeylPE high	plasmeylPE high middle
plasmeylPE 38:3	plasmeylPE middle	plasmeylPE high	plasmeylPE high middle
plasmeylPE 38:4	plasmeylPE middle	plasmeylPE high	plasmeylPE high middle
plasmeylPE 38:5	plasmeylPE middle	plasmeylPE high	plasmeylPE high middle
plasmeylPE 38:6	plasmeylPE middle	plasmeylPE high	plasmeylPE high middle
plasmeylPE 40:4	plasmeylPE top	plasmeylPE high	plasmeylPE high top
plasmeylPE 40:5	plasmeylPE top	plasmeylPE high	plasmeylPE high top
plasmeylPE 40:6	plasmeylPE top	plasmeylPE high	plasmeylPE high top
plasmeylPE 42:5	plasmeylPE top	plasmeylPE high	plasmeylPE high top
plasmeylPE 42:6	plasmeylPE top	plasmeylPE high	plasmeylPE high top
SM 30:1	SM bottom	SM low	SM low bottom
SM 32:0	SM bottom	SM low	SM low bottom
SM 32:1	SM bottom	SM low	SM low bottom
SM 32:2	SM bottom	SM high	SM high bottom
SM 34:1	SM bottom	SM low	SM low bottom
SM 34:2	SM bottom	SM high	SM high bottom
SM 36:1	SM middle	SM low	SM low middle
SM 36:2	SM middle	SM high	SM high middle
SM 38:0	SM middle	SM low	SM low middle
SM 38:1	SM middle	SM low	SM low middle
SM 38:2	SM middle	SM high	SM high middle
SM 38:4	SM middle	SM high	SM high middle
SM 40:1	SM top	SM low	SM low top
SM 40:2	SM top	SM high	SM high top
SM 42:1	SM top	SM low	SM low top
SM 42:2	SM top	SM high	SM high top
SM 42:4	SM top	SM high	SM high top
SM 42:5	SM top	SM high	SM high top
SM 44:1	SM top	SM low	SM low top
SM 44:2	SM top	SM high	SM high top
TAG 40:0	TAG bottom	TAG low	TAG low bottom
TAG 42:0	TAG bottom	TAG low	TAG low bottom
TAG 42:1	TAG bottom	TAG low	TAG low bottom
TAG 44:1	TAG bottom	TAG low	TAG low bottom
TAG 46:0	TAG bottom	TAG low	TAG low bottom
TAG 46:1	TAG bottom	TAG low	TAG low bottom

lipid	Chain length	Double bond	Double bond and chain length
TAG 46:2	TAG bottom	TAG high	TAG high bottom
TAG 48:0	TAG bottom	TAG low	TAG low bottom
TAG 48:1	TAG bottom	TAG low	TAG low bottom
TAG 48:2	TAG bottom	TAG high	TAG high bottom
TAG 48:3	TAG bottom	TAG high	TAG high bottom
TAG 50:0	TAG middle	TAG low	TAG low middle
TAG 50:1	TAG middle	TAG low	TAG low middle
TAG 50:2	TAG middle	TAG high	TAG high middle
TAG 50:3	TAG middle	TAG high	TAG high middle
TAG 50:4	TAG middle	TAG high	TAG high middle
TAG 50:5	TAG middle	TAG high	TAG high middle
TAG 52:0	TAG middle	TAG low	TAG low middle
TAG 52:1	TAG middle	TAG low	TAG low middle
TAG 52:2	TAG middle	TAG high	TAG high middle
TAG 52:3	TAG middle	TAG high	TAG high middle
TAG 52:4	TAG middle	TAG high	TAG high middle
TAG 52:5	TAG middle	TAG high	TAG high middle
TAG 52:6	TAG middle	TAG high	TAG high middle
TAG 54:1	TAG middle	TAG low	TAG low middle
TAG 54:2	TAG middle	TAG high	TAG high middle
TAG 54:3	TAG middle	TAG high	TAG high middle
TAG 54:4	TAG middle	TAG high	TAG high middle
TAG 54:5	TAG middle	TAG high	TAG high middle
TAG 54:6	TAG middle	TAG high	TAG high middle
TAG 54:7	TAG middle	TAG high	TAG high middle
TAG 54:8	TAG middle	TAG high	TAG high middle
TAG 56:0	TAG middle	TAG low	TAG low middle
TAG 56:1	TAG middle	TAG low	TAG low middle
TAG 56:2	TAG middle	TAG high	TAG high middle
TAG 56:3	TAG middle	TAG high	TAG high middle
TAG 56:4	TAG middle	TAG high	TAG high middle
TAG 56:5	TAG middle	TAG high	TAG high middle
TAG 56:6	TAG middle	TAG high	TAG high middle
TAG 56:7	TAG middle	TAG high	TAG high middle
TAG 56:8	TAG middle	TAG high	TAG high middle
TAG 56:9	TAG middle	TAG high	TAG high middle
TAG 58:1	TAG top	TAG low	TAG low top
TAG 58:10	TAG top	TAG high	TAG high top
TAG 58:3	TAG top	TAG high	TAG high top
TAG 58:5	TAG top	TAG high	TAG high top
TAG 58:6	TAG top	TAG high	TAG high top
TAG 58:7	TAG top	TAG high	TAG high top
TAG 58:8	TAG top	TAG high	TAG high top

lipid	Chain length	Double bond	Double bond and chain length
TAG 58:9	TAG top	TAG high	TAG high top
TAG 60:12	TAG top	TAG high	TAG high top
TAG 62:1	TAG top	TAG low	TAG low top

AC, acylcarnitines; CE, cholesterol esters; DAG, diacylglycerol; FFA, free fatty acids; PC, phosphatidylcholine; PE, phosphatidylethanolamine; SM, sphingomyelin; TAG, triacylglycerol; x:y, number of carbons:number of double bonds.

Supplement Table 4: False discovery rate (FDR) adjusted serum lipid correlations with lipid regulating gene transcripts in glomerular compartment, which revealed a link between serum lipids and genes involved in fatty acids synthesis and metabolism regulation of complex lipids. Rows that show genes involved in fatty acid metabolism are highlighted.

Pathway	Gene symbol	Lipid	Correlation		p.value	FDR
Linoleate Metabolism	PLA2G4B	AC_Long.PCA	-0.44		0.00047	0.01088
Glycerophospholipid metabolism	PLA2G12A	AC_Long.PCA	0.43		0.00068	0.01409
Butanoate metabolism	HMGCS1	AC_Long.PCA	-0.43		0.00079	0.01551
Glycosphingolipid metabolism	CERK	FFA.Saturated	0.42		0.00094	0.01751
P21 activated kinase	PAK2	AC_Long.PCA	-0.41		0.00161	0.02540
ras homolog family member B	RHOB	DAG.Short.LDB	-0.40		0.00168	0.02623
ras homolog family member B	RHOB	TAG.Short.LDB	-0.39		0.00272	0.03601
De novo fatty acid biosynthesis	PNPLA3	FFA.Saturated	-0.37		0.00382	0.04459
Glycerophospholipid metabolism	PCYT1B	TAG.Int.HDB	0.37		0.00384	0.04467
Phosphatidylinositol phosphate metabolism	PLCB1	DAG.Short.LDB	-0.37		0.00404	0.04607
Glycerophospholipid metabolism	PISD	TAG.Int.HDB	-0.37		0.00426	0.04760
Cholesterol metabolism	NSDHL	TAG.Int.LDB	0.37		0.00428	0.04769
P21 activated kinase	PAK2	DAG.Short.LDB	-0.37		0.00455	0.04955
Butanoate metabolism	HMGCR	AC_Long.PCA	-0.36		0.00523	0.05422
Sphingomyelin metabolism	SMPD3	FFA.Unsaturated	0.36		0.00530	0.05469
Glycerophospholipid metabolism	PAFAH1B1	AC_Long.PCA	-0.36		0.00593	0.05837
Steroid hormone biosynthesis	SULT1E1	AC_Long.PCA	0.36		0.00599	0.05869
Phosphatidylinositol phosphate metabolism	PIK3CB	TAG.Int.LDB	-0.36		0.00600	0.05869
O-Glycan biosynthesis	GALNT2	DAG.Long.HDB	0.36		0.00609	0.05923
De novo fatty acid biosynthesis	ACACA	DAG.Long.HDB	0.36		0.00616	0.05967
Phosphatidylinositol phosphate metabolism	PLCB1	TAG.Short.LDB	-0.35		0.00632	0.06059
Linoleate Metabolism	PLA2G3	AC_Long.PCA	0.35		0.00640	0.06109
Beta-oxidation	PPT1	TAG.Int.LDB	0.35		0.00651	0.06170
Glycerophospholipid metabolism	LYPLA2	AC_Long.PCA	0.35		0.00661	0.06237
Cholesterol metabolism	IDI1	AC_Long.PCA	-0.35		0.00776	0.06923
Butanoate metabolism	HMGCS1	FFA.Saturated	0.34		0.00861	0.07413
Glycerophospholipid metabolism	GLA	DAG.Short.LDB	0.34		0.00924	0.07734
Ceramide metabolism	CERS2	FFA.Saturated	-0.34		0.00984	0.08015
Beta-oxidation	ACOX3	AC_Int.PCA	0.33		0.01031	0.08237
Cholesterol metabolism	FDPS	TAG.Int.LDB	0.33		0.01053	0.08363
Beta-oxidation	ACOX3	FFA.Saturated	0.33		0.01072	0.08467
Butanoate metabolism	HMGCS1	DAG.Long.HDB	0.33		0.01072	0.08471
Glycerophospholipid metabolism	PNPLA6	AC_Long.PCA	-0.33		0.01104	0.08627
De novo fatty acid biosynthesis	ACACA	TAG.Int.HDB	0.33		0.01258	0.09345
Beta-oxidation	ACSL1	TAG.Short.LDB	0.32		0.01284	0.09442
De novo fatty acid biosynthesis	MCAT	TAG.Short.LDB	0.32		0.01289	0.09458
Glycerophospholipid metabolism	LPL	TAG.Int.HDB	-0.32		0.01336	0.09662
Growth factor	PDGFA	FFA.Unsaturated	-0.32		0.01340	0.09675
serine-threonine kinase	AKT1	AC_Long.PCA	-0.32		0.01348	0.09701
Glycerophospholipid metabolism	PCYT1B	DAG.Long.HDB	0.32		0.01349	0.09703
Glycosphingolipid metabolism	FUT2	DAG.Long.HDB	-0.32		0.01370	0.09790
Cholesterol metabolism	CYP51	FFA.Saturated	0.32		0.01410	0.09968
GTPase-activating protein	ARHGAP35	AC_Long.PCA	-0.32		0.01416	0.09987




















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Phosphatidylinositol phosphate metabolism	PIK3CD	FFA.Saturated	-0.32			0.01443	0.10123
Glycerophospholipid metabolism	AGPAT4	AC_Long.PCA	-0.32			0.01496	0.10359
Glycerophospholipid metabolism	GLA	FFA.Unsaturated	0.32			0.01514	0.10424
GTPase-activating protein	ARHGAP1	TAG.Short.LDB	-0.32			0.01531	0.10504
Growth factor	PDGFA	DAG.Long.HDB	-0.32			0.01564	0.10638
Cholesterol metabolism	SC4MOL	AC_Long.PCA	-0.31			0.01651	0.11014
O-Glycan biosynthesis	GALNT2	TAG.Int.HDB	0.31			0.01668	0.11095
Glycerophospholipid metabolism	PAFAH1B3	FFA.Unsaturated	-0.31			0.01669	0.11097
Cholesterol metabolism	PMVK	DAG.Short.LDB	0.31			0.01711	0.11254
Glycerophospholipid metabolism	LCAT	AC_Long.PCA	-0.31			0.01835	0.11761
Cholesterol metabolism	LSS	FFA.Saturated	0.31			0.01855	0.11839
Glycosphingolipid metabolism	FUT1	AC_Long.PCA	-0.31			0.01870	0.11891
Glycosphingolipid metabolism	UGT8	TAG.Int.LDB	-0.30			0.01994	0.12345
Glycosphingolipid metabolism	STT3A	DAG.Short.LDB	-0.30			0.02012	0.12419
P21 activated kinase	PAK2	TAG.Short.LDB	-0.30			0.02014	0.12424
Glycerophospholipid metabolism	GLA	TAG.Int.LDB	0.30			0.02046	0.12549
Glycan biosynthesis	FUT8	DAG.Short.LDB	-0.30			0.02069	0.12617
Beta-oxidation	GCDH	TAG.Short.LDB	0.30			0.02085	0.12665
P21 activated kinase	PAK4	TAG.Int.HDB	0.30			0.02233	0.13228
Phosphatidylinositol phosphate metabolism	PLCG2	FFA.Saturated	-0.30			0.02368	0.13720
Phosphatidylinositol phosphate metabolism	PLCB4	AC_Long.PCA	-0.30			0.02385	0.13763
Beta-oxidation	CPT2	TAG.Short.LDB	0.29			0.02476	0.14053
De novo fatty acid biosynthesis	ACACA	AC_Long.PCA	-0.29			0.02514	0.14176
Glycerophospholipid metabolism	GNPAT	DAG.Short.LDB	0.29			0.02515	0.14179
Sphingomyelin metabolism	S1PR4	AC_Int.PCA	-0.29			0.02561	0.14364
Glycosphingolipid metabolism	CHMP4A	AC_Long.PCA	0.29			0.02566	0.14370
Cholesterol metabolism	FDFT1	AC_Long.PCA	-0.29			0.02642	0.14636
Phosphatidylinositol phosphate metabolism	PLCG2	FFA.Unsaturated	0.29			0.02645	0.14644
Glycosphingolipid metabolism	PTDSS1	FFA.Unsaturated	-0.29			0.02645	0.14644
P21 activated kinase	PAK4	DAG.Long.HDB	0.29			0.02672	0.14728
Butanoate metabolism	HMGCR	FFA.Saturated	0.29			0.02717	0.14868
Glycerophospholipid metabolism	PCYT1A	AC_Int.PCA	0.29			0.02848	0.15301
De novo fatty acid biosynthesis	OXSM	TAG.Short.LDB	0.29			0.02862	0.15343
Glycan biosynthesis	GALNT3	FFA.Unsaturated	-0.29			0.02870	0.15366
GTPase-activating protein	ARHGAP1	DAG.Short.LDB	-0.28			0.03013	0.15889
Glycan biosynthesis	GALNT3	TAG.Int.HDB	0.28			0.03017	0.15895
Cholesterol metabolism	EBP	TAG.Short.LDB	0.28			0.03017	0.15897
Glycosphingolipid metabolism	CERK	AC_Long.PCA	-0.28			0.03067	0.16045
Butanoate metabolism	HMGCS1	DAG.Short.LDB	-0.28			0.03093	0.16118
Linoleate Metabolism	PLA2G4B	FFA.Saturated	0.28			0.03107	0.16164
Beta-oxidation	CPT2	DAG.Short.LDB	0.28			0.03138	0.16254
Glycerophospholipid metabolism	CHPT1	FFA.Saturated	-0.28			0.03141	0.16260
Glycosphingolipid metabolism	PTDSS1	TAG.Int.HDB	-0.28			0.03239	0.16552
Glycerophospholipid metabolism	LPL	DAG.Long.HDB	-0.28			0.03269	0.16647
Fatty acid desaturase	FADS1	AC_Long.PCA	-0.28			0.03275	0.16668
Glycan biosynthesis	GALNT3	DAG.Short.LDB	-0.28			0.03311	0.16775













































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Beta-oxidation	ACSL1	DAG.Short.LDB	0.28			0.03370	0.16919
Beta-oxidation	ACAA2	TAG.Short.LDB	0.28			0.03372	0.16926
Glycerophospholipid metabolism	AGPAT1	FFA.Unsaturated	-0.28			0.03376	0.16940
fucosyltransferase	FUT7	AC_Long.PCA	0.28			0.03471	0.17201
Propanoate Metabolism	MLYCD	DAG.Short.LDB	0.28			0.03477	0.17218
De novo fatty acid biosynthesis	MCAT	DAG.Short.LDB	0.28			0.03478	0.17222
Butanoate metabolism	HMGCS1	TAG.Short.LDB	-0.28			0.03507	0.17309
Phosphatidylinositol phosphate metabolism	PLCB4	FFA.Saturated	0.28			0.03537	0.17386
Glycerophospholipid metabolism	PLA2G7	FFA.Unsaturated	-0.28			0.03599	0.17591
Growth factor	PDGFRB	FFA.Unsaturated	-0.28			0.03623	0.17654
Glycerophospholipid metabolism	PEMT	DAG.Short.LDB	0.27			0.03729	0.17975
Phosphatidylinositol phosphate metabolism	PLCB4	DAG.Long.HDB	0.27			0.03762	0.18055
Glycerophospholipid metabolism	LIPG	TAG.Short.LDB	-0.27			0.03771	0.18072
Glycerophospholipid metabolism	PISD	DAG.Long.HDB	-0.27			0.03772	0.18072
Cholesterol metabolism	LIPE	FFA.Unsaturated	0.27			0.03983	0.18620
Ceramide metabolism	CERS5	TAG.Int.LDB	-0.27			0.04092	0.18897
Glycerophospholipid metabolism	LPL	TAG.Short.LDB	-0.27			0.04100	0.18910
Glycan biosynthesis	GALNT14	TAG.Short.LDB	0.27			0.04147	0.19023
Cholesterol metabolism	DHCR7	DAG.Long.HDB	0.27			0.04163	0.19062
Beta-oxidation	ACOX3	FFA.Unsaturated	0.27			0.04184	0.19123
Cholesterol metabolism	PMVK	TAG.Short.LDB	0.27			0.04258	0.19324
Glycosphingolipid metabolism	STT3A	TAG.Short.LDB	-0.27			0.04274	0.19364
Glycerophospholipid metabolism	DGKG	AC_Int.PCA	0.27			0.04309	0.19437
Beta-oxidation	ACADSB	TAG.Short.LDB	0.27			0.04361	0.19573
Fatty acid metabolism	ACAD8	AC_Long.PCA	0.26			0.04444	0.19782
Linoleate Metabolism	PLA2G1B	TAG.Int.LDB	-0.26			0.04506	0.19930
Cholesterol metabolism	SQLE	DAG.Long.HDB	0.26			0.04551	0.20054
De novo fatty acid biosynthesis	OXSM	DAG.Short.LDB	0.26			0.04588	0.20145
Growth factor	PDGFD	DAG.Short.LDB	-0.26			0.04601	0.20187
Glycosphingolipid metabolism	B4GALT2	AC_Int.PCA	-0.26			0.04624	0.20246
G protein	GNAQ	TAG.Int.LDB	-0.26			0.04630	0.20256
De novo fatty acid biosynthesis	ACACB	AC_Long.PCA	-0.26			0.04716	0.20446
Glycan biosynthesis	FUT8	TAG.Short.LDB	-0.26			0.04746	0.20513
Linoleate Metabolism	PLA2G4A	FFA.Saturated	0.26			0.04747	0.20517
Beta-oxidation	HADHA	TAG.Int.HDB	0.26			0.04755	0.20530
serine-threonine kinase	AKT1	DAG.Short.LDB	-0.26			0.04778	0.20587
Linoleate Metabolism	PLA2G10	FFA.Unsaturated	0.26			0.04814	0.20675
Sphingomyelin metabolism	SMPDL3A	AC_Long.PCA	0.26			0.04817	0.20682
Cholesterol metabolism	CYP51	TAG.Int.LDB	0.26			0.04833	0.20719
Glycerophospholipid metabolism	PAFAH1B3	AC_Int.PCA	-0.26			0.04857	0.20780
Glycosphingolipid metabolism	FUT1	TAG.Short.LDB	-0.26			0.04870	0.20811

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Beta-oxidation	HADHA	TAG.Short.LDB	0.26			0.04899	0.20855
Protein kinase	MAPK14	AC_Long.PCA	-0.26			0.04919	0.20906
Glycosphingolipid metabolism	B4GALT2	AC_Long.PCA	-0.26			0.04922	0.20915
GTPase-activating protein	ARHGAP1	FFA.Saturated	0.26			0.04982	0.21080
Sphingomyelin metabolism	SMPD3	AC_Long.PCA	0.26			0.05004	0.21132
GTPase-activating protein	ARHGAP35	AC_Int.PCA	-0.26			0.05026	0.21194
De novo fatty acid biosynthesis	LYPLA3	TAG.Int.LDB	0.26			0.05032	0.21209
Glycerophospholipid metabolism	PNLIP	AC_Long.PCA	0.26			0.05063	0.21275
Growth factor	PDGFRB	DAG.Long.HDB	-0.26			0.05111	0.21373
Phosphatidylinositol phosphate metabolism	CHKB	TAG.Int.LDB	0.26			0.05127	0.21405
Butanoate metabolism	HMGCR	DAG.Long.HDB	0.26			0.05140	0.21442
Glycerophospholipid metabolism	CDS2	AC_Long.PCA	-0.26			0.05150	0.21462
Phosphatidylinositol phosphate metabolism	PLCG1	TAG.Short.LDB	-0.26			0.05180	0.21521
Cholesterol metabolism	SQLE	FFA.Saturated	0.26			0.05271	0.21744
Growth factor	PDGFA	DAG.Short.LDB	-0.26			0.05331	0.21917
Glycerophospholipid metabolism	ETNK1	AC_Int.PCA	0.25			0.05376	0.22038
Glycerophospholipid metabolism	PEMT	TAG.Int.LDB	0.25			0.05378	0.22040
Phosphatidylinositol phosphate metabolism	PIK3R1	DAG.Long.HDB	-0.25			0.05380	0.22044
Glycosphingolipid metabolism	FUT5	TAG.Int.LDB	0.25			0.05467	0.22276














































Supplement Table 5: False discovery rate (FDR) adjusted serum lipid correlations with lipid regulating gene transcripts in tubulointerstitial compartment, which revealed a link between serum lipids and genes involved in fatty acid synthesis and β -oxidation and metabolic regulation of complex lipids. Rows that show genes involved in fatty acid metabolism are highlighted.

Pathway	Gene symbol	Lipid	Correlation		p.value	FDR
Cholesterol metabolism	DHCR7	AC_Long.PCA	-0.59		0.00003	0.001735
Beta-oxidation	ACAT2	AC_Long.PCA	-0.56		0.00013	0.004339
Phosphatidylinositol phosphate metabolism	GALNT7	DAG.Short.LDB	0.55		0.00014	0.004457
Glycerophospholipid metabolism	PCYT2	TAG.Short.LDB	-0.55		0.00015	0.004666
Phosphatidylinositol phosphate metabolism	SPHK2	TAG.Short.LDB	-0.54		0.00022	0.006133
Cholesterol metabolism	IDI1	AC_Long.PCA	-0.53		0.00033	0.008047
De novo fatty acid biosynthesis	ACACA	TAG.Int.LDB	0.52		0.00042	0.009434
Glycerophospholipid metabolism	LIPA	DAG.Short.LDB	0.52		0.00043	0.009621
Phosphatidylinositol phosphate metabolism	GALNT7	TAG.Short.LDB	0.48		0.00115	0.018668
Beta-oxidation	ACAT1	DAG.Short.LDB	-0.48		0.00131	0.020254
Beta-oxidation	ACAD10	TAG.Short.LDB	-0.47		0.00152	0.022385
Glycerophospholipid metabolism	PLA2G5	TAG.Int.HDB	0.47		0.00156	0.022801
Glycerophospholipid metabolism	LIPA	TAG.Short.LDB	0.47		0.00189	0.025859
Glycerophospholipid metabolism	DGKB	FFA.Unsaturated	-0.46		0.00197	0.026591
Fatty acid desaturase	DEGS1	FFA.Unsaturated	0.46		0.00239	0.030017
Fatty acid elongase	ELOVL1	TAG.Int.HDB	-0.46		0.00240	0.030127
Apoptosis	CASP1	DAG.Short.LDB	0.45		0.00262	0.031781
Cholesterol metabolism	NSDHL	TAG.Short.LDB	-0.45		0.00275	0.032812
Glycerophospholipid metabolism	PNLIPRP1	DAG.Short.LDB	-0.45		0.00284	0.033513
Beta-oxidation	ACAD10	FFA.Saturated	0.45		0.00286	0.033648
Fatty acid elongase	ELOVL4	FFA.Saturated	-0.45		0.00315	0.035725
Fatty acid desaturase	DEGS1	DAG.Short.LDB	0.44		0.00323	0.036203
G protein	GNAI2	DAG.Short.LDB	0.44		0.00329	0.036646
Fatty acid elongase	ELOVL5	DAG.Short.LDB	0.44		0.00336	0.037161
Beta-oxidation	ACAT2	FFA.Unsaturated	-0.44		0.00338	0.037247
Phosphatidylinositol phosphate metabolism	SPHK2	DAG.Short.LDB	-0.44		0.00388	0.040539
De novo fatty acid biosynthesis	HMGCS1	AC_Long.PCA	-0.43		0.00400	0.041401
ras homolog family member C	RHOC	FFA.Unsaturated	0.43		0.00459	0.045033
Beta-oxidation	DECR2	DAG.Short.LDB	-0.43		0.00465	0.045394
serine-threonine kinase	AKT2	FFA.Unsaturated	-0.43		0.00479	0.046154
GTPase-activating protein	ARHGAP32	DAG.Short.LDB	-0.42		0.00514	0.048448
Glycerophospholipid metabolism	LPL	DAG.Short.LDB	-0.42		0.00527	0.049273
ras homolog family member D	RHOD	DAG.Short.LDB	-0.42		0.00543	0.050316
G protein subunit protein 13	GNA13	TAG.Short.LDB	0.42		0.00578	0.052083
Bile acid biosynthesis	SOAT2	DAG.Short.LDB	-0.42		0.00584	0.052435
P21 activated kinase	PAK2	DAG.Short.LDB	0.42		0.00588	0.052699
De novo fatty acid biosynthesis	ACSL5	FFA.Unsaturated	0.42		0.00593	0.052934
GTPase-activating protein	ARHGAP32	TAG.Short.LDB	-0.42		0.00600	0.053324
Fatty acid elongase	ELOVL1	DAG.Short.LDB	0.42		0.00602	0.053442
De novo fatty acid biosynthesis	LYPLA3	FFA.Saturated	0.42		0.00604	0.05347
Glycerophospholipid metabolism	PCYT2	DAG.Short.LDB	-0.42		0.00607	0.053573
Glycerophospholipid metabolism	PLA2G2D	TAG.Short.LDB	0.41		0.00653	0.056053
Fatty acid desaturase	FADS1	AC_Long.PCA	-0.41		0.00692	0.058022
Glycerophospholipid metabolism	MGLL	TAG.Int.LDB	0.41		0.00744	0.060804














































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De novo fatty acid biosynthesis	ACSL5	DAG.Short.LDB	0.41			0.00772	0.062275
Glycerophospholipid metabolism	DGKB	DAG.Short.LDB	-0.40			0.00786	0.063063
Glycosphingolipid metabolism	CERK	FFA.Saturated	0.40			0.00798	0.063733
Cholesterol metabolism	EBP	FFA.Saturated	0.40			0.00803	0.063973
Cholesterol metabolism	TM7SF2	AC_Long.PCA	-0.40			0.00843	0.066053
Glycerophospholipid metabolism	PLA2G7	DAG.Short.LDB	0.40			0.00858	0.066873
De novo fatty acid biosynthesis	PTGS2	AC_Long.PCA	0.40			0.00864	0.067158
Cholesterol metabolism	MVD	TAG.Short.LDB	-0.40			0.00866	0.067222
Beta-oxidation	DECR2	FFA.Unsaturated	-0.40			0.00866	0.067222
ras homolog family member B	RHOB	TAG.Int.HDB	-0.40			0.00873	0.06754
serine-threonine kinase	PAK3	DAG.Short.LDB	-0.40			0.00906	0.069057
Ceramide metabolism	CERS4	TAG.Short.LDB	-0.40			0.00926	0.070041
Apoptosis	CASP1	TAG.Short.LDB	0.40			0.00929	0.070225
Protein kinase	MAPK3	DAG.Short.LDB	-0.40			0.00936	0.070552
Bile acid biosynthesis	SOAT2	AC_Long.PCA	-0.39			0.00973	0.072185
Glycerophospholipid metabolism	PAFAH1B1	TAG.Short.LDB	0.39			0.01024	0.074242
De novo fatty acid biosynthesis	PLA2G2E	DAG.Short.LDB	-0.39			0.01027	0.074402
Glycerophospholipid metabolism	CLCF1	TAG.Short.LDB	-0.39			0.01049	0.075286
Glycerophospholipid metabolism	PTDSS2	TAG.Short.LDB	-0.39			0.01071	0.076241
P21 activated kinase	PAK4	DAG.Short.LDB	-0.39			0.01100	0.077591
Glycosphingolipid metabolism	UGCG	DAG.Short.LDB	0.39			0.01101	0.077646
Glycosphingolipid metabolism	NT5C	AC_Long.PCA	-0.39			0.01157	0.080118
Glycerophospholipid metabolism	AGPS	TAG.Short.LDB	0.39			0.01168	0.080512
Beta-oxidation	ACSL1	AC_Long.PCA	-0.39			0.01168	0.080527
Cholesterol metabolism	GGPS1	FFA.Saturated	0.39			0.01173	0.080687
Cholesterol metabolism	IDI1	FFA.Saturated	0.38			0.01288	0.0859
Fatty acid desaturase	FADS3	DAG.Short.LDB	0.38			0.01305	0.086585
Cholesterol metabolism	TM7SF2	FFA.Unsaturated	-0.38			0.01351	0.088627
Glycosphingolipid metabolism	FUT1	TAG.Int.HDB	0.38			0.01362	0.089019
Glycan biosynthesis	GALNT1	DAG.Short.LDB	0.38			0.01385	0.089938
De novo fatty acid biosynthesis	PLA2G4B	DAG.Short.LDB	-0.38			0.01393	0.0902
Beta-oxidation	DECR2	AC_Long.PCA	-0.38			0.01419	0.09123
Glycosphingolipid metabolism	PPAP2C	DAG.Long.HDB	-0.38			0.01426	0.091485
Beta-oxidation	ACAD10	AC_Long.PCA	-0.38			0.01433	0.091733
Glycosphingolipid metabolism	CHMP4A	FFA.Saturated	0.37			0.01451	0.092342
Glycerophospholipid metabolism	CHKA	DAG.Short.LDB	-0.37			0.01463	0.092588
Glycosphingolipid metabolism	PPAP2C	TAG.Int.HDB	-0.37			0.01466	0.092686
Glycerophospholipid metabolism	AGPAT2	FFA.Unsaturated	0.37			0.01488	0.09349
Fatty acid desaturase	FADS2	AC_Long.PCA	-0.37			0.01532	0.095347
G protein	GNAI1	DAG.Long.HDB	-0.37			0.01548	0.095888
Glycosphingolipid metabolism	NT5M	DAG.Short.LDB	-0.37			0.01558	0.096284
Glycerophospholipid metabolism	PLA2G2D	DAG.Short.LDB	0.37			0.01591	0.09763
Glycerophospholipid metabolism	LIPA	FFA.Unsaturated	0.37			0.01631	0.099207
Fatty acid elongase	ELOVL6	AC_Long.PCA	0.37			0.01637	0.099495
De novo fatty acid biosynthesis	FASN	FFA.Unsaturated	-0.37			0.01645	0.099759
























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serine-threonine kinase	AKT3	FFA.Saturated	-0.37		0.01652	0.100115
Glycerophospholipid metabolism	DGKB	TAG.Int.HDB	0.37		0.01667	0.100717
Cholesterol metabolism	SQLE	AC_Long.PCA	-0.37		0.01724	0.102716
P21 activated kinase	PAK6	DAG.Short.LDB	-0.36		0.01783	0.105188
Glycerophospholipid metabolism	PLD1	FFA.Unsaturated	-0.36		0.01798	0.105721
Cholesterol metabolism	LSS	TAG.Short.LDB	-0.36		0.01874	0.108574
Beta-oxidation	ACAT1	TAG.Short.LDB	-0.36		0.01956	0.111823
ras homolog family member D	RHOD	TAG.Short.LDB	-0.36		0.01990	0.113049
Glycerophospholipid metabolism	DUSP11	TAG.Int.HDB	0.36		0.02016	0.114053
ras homolog family member D	RHOD	FFA.Unsaturated	-0.36		0.02039	0.11474
Cholesterol metabolism	SC5D	AC_Long.PCA	-0.36		0.02054	0.115354
G protein	GNAQ	FFA.Unsaturated	-0.36		0.02067	0.115726
De novo fatty acid biosynthesis	ALOX5	DAG.Short.LDB	0.35		0.02169	0.119225
ras homolog family member D	RHOD	AC_Long.PCA	-0.35		0.02180	0.119546
Glycerophospholipid metabolism	LPL	TAG.Short.LDB	-0.35		0.02190	0.119872
Fatty acid desaturase	FADS2	AC_Int.PCA	-0.35		0.02225	0.121057
Glycerophospholipid metabolism	PNPLA6	TAG.Int.HDB	-0.35		0.02254	0.122069
Glycosphingolipid metabolism	FUT1	DAG.Long.HDB	0.35		0.02347	0.125147
Phosphatidylinositol phosphate metabolism	PLCD1	AC_Long.PCA	-0.35		0.02348	0.125147
Glycan biosynthesis	GALNT8	FFA.Saturated	-0.35		0.02361	0.1256
Cholesterol metabolism	DHCR7	TAG.Short.LDB	-0.35		0.02379	0.126194
Glycerophospholipid metabolism	PLA2G5	DAG.Long.HDB	0.35		0.02398	0.126919
Phosphatidylinositol phosphate metabolism	PIK3CD	FFA.Unsaturated	0.35		0.02406	0.127265
Glycerophospholipid metabolism	PTDSS2	DAG.Short.LDB	-0.35		0.02466	0.129305
Phosphatidylinositol phosphate metabolism	PLCL2	DAG.Short.LDB	-0.35		0.02469	0.12937
Steroid hormon biosynthesis	CYP11A1	FFA.Unsaturated	-0.34		0.02596	0.133657
G protein	GNAI2	TAG.Short.LDB	0.34		0.02619	0.134557
Glycosphingolipid metabolism	UGCG	TAG.Short.LDB	0.34		0.02634	0.135071
Fatty acid elongase	ELOVL1	FFA.Unsaturated	0.34		0.02747	0.138795
Sphingomyelin metabolism	S1PR1	TAG.Short.LDB	0.34		0.02749	0.138843
Cholesterol metabolism	SQLE	DAG.Long.HDB	-0.34		0.02797	0.14039
Apoptosis	CASP1	FFA.Unsaturated	0.34		0.02813	0.14083
Beta-oxidation	ACAT2	DAG.Short.LDB	-0.34		0.02845	0.141746
Phosphatidylinositol phosphate metabolism	PIK3CG	TAG.Short.LDB	0.34		0.02874	0.142549
Cholesterol metabolism	NSDHL	DAG.Short.LDB	-0.34		0.02925	0.144284
Glycosphingolipid metabolism	ASAH1	AC_Long.PCA	-0.34		0.02945	0.144956
Bile acid biosynthesis	SOAT2	FFA.Unsaturated	-0.34		0.02959	0.145422
Steroid hormon biosynthesis	CYP11A1	AC_Int.PCA	-0.33		0.03012	0.147224
Sphingomyelin metabolism	SGMS1	TAG.Short.LDB	0.33		0.03012	0.147224
Cholesterol metabolism	GGPS1	AC_Long.PCA	-0.33		0.03020	0.147496
Beta-oxidation	PPT1	FFA.Unsaturated	0.33		0.03037	0.147914
G protein	GNAI2	FFA.Unsaturated	0.33		0.03102	0.149772
Glycerophospholipid metabolism	LPL	AC_Long.PCA	-0.33		0.03123	0.150524
Cholesterol metabolism	MVK	FFA.Unsaturated	-0.33		0.03134	0.150783
Beta-oxidation	ACOX2	FFA.Saturated	0.33		0.03134	0.150784

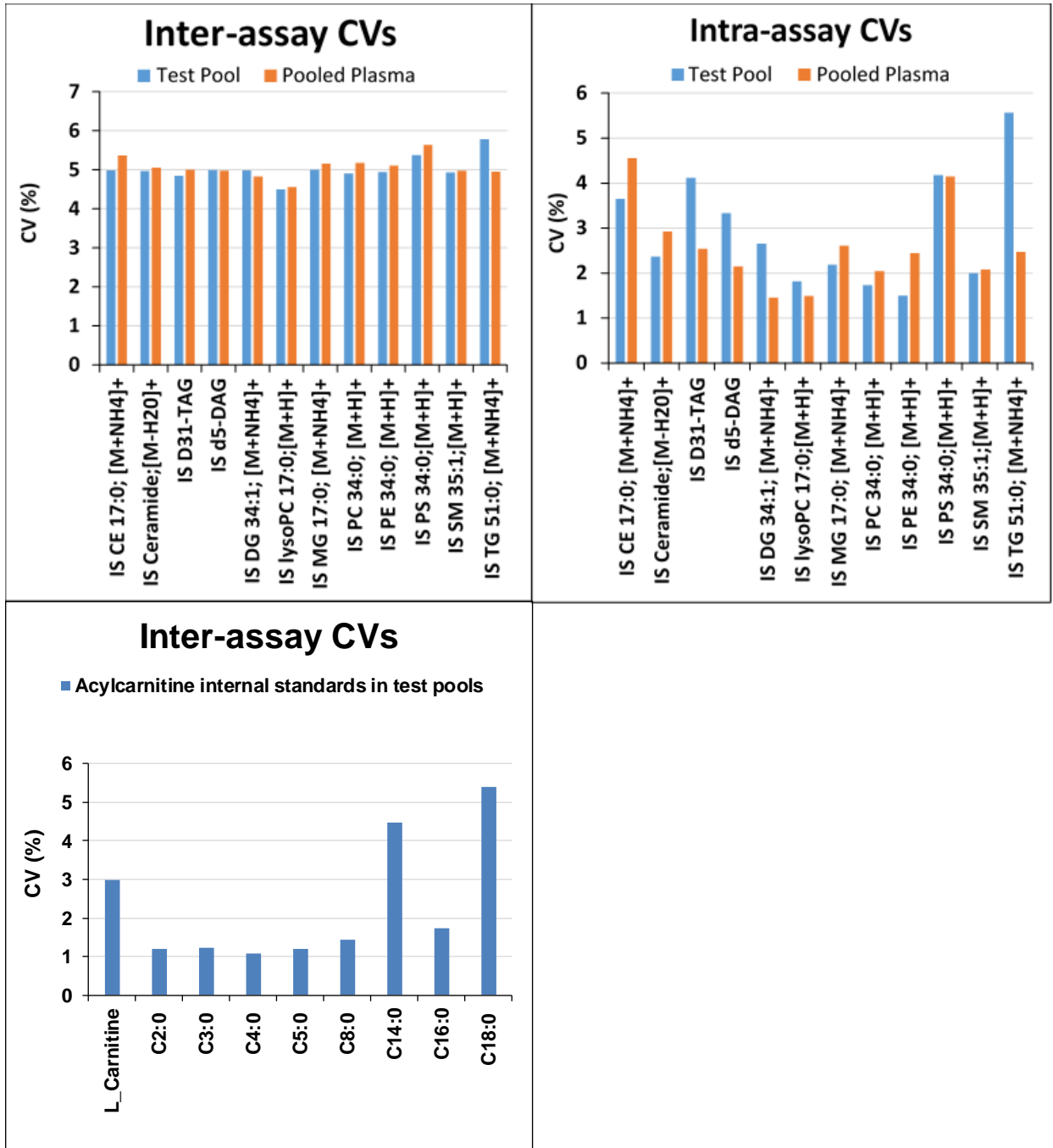
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P21 activated kinase	PAK4	FFA.Unsaturated	-0.33		0.03194	0.152615
Cholesterol metabolism	DHCR7	DAG.Short.LDB	-0.33		0.03269	0.154508
Sphingomyelin metabolism	S1PR1	DAG.Short.LDB	0.33		0.03287	0.155008
P21 activated kinase	PAK2	TAG.Short.LDB	0.33		0.03356	0.157036
Ceramide metabolism	CERS2	FFA.Saturated	0.33		0.03363	0.157274
Glycerophospholipid metabolism	DGKA	DAG.Short.LDB	0.33		0.03364	0.157324
GTPase-activating protein	ARHGAP32	FFA.Saturated	-0.33		0.03398	0.158183
Glycerophospholipid metabolism	PCYT1B	DAG.Short.LDB	-0.33		0.03417	0.15869
Beta-oxidation	CPT1A	DAG.Long.HDB	-0.33		0.03425	0.158929
Glycerophospholipid metabolism	PLA2G7	AC_Long.PCA	0.33		0.03449	0.159551
Glycerophospholipid metabolism	AGPAT1	AC_Int.PCA	0.33		0.03504	0.161026
Cholesterol metabolism	TM7SF2	DAG.Short.LDB	-0.33		0.03519	0.161481
Glycosphingolipid metabolism	SMPD1	AC_Int.PCA	0.33		0.03554	0.162488
Phosphatidylinositol phosphate metabolism	PLCL2	TAG.Short.LDB	-0.32		0.03597	0.163639
Steroid hormone biosynthesis	STS	DAG.Short.LDB	0.32		0.03634	0.164786
Fatty acid desaturase	FADS3	AC_Long.PCA	0.32		0.03640	0.164966
Glycosphingolipid metabolism	B4GALT7	DAG.Long.HDB	0.32		0.03640	0.164966
Glycosphingolipid metabolism	CERK	DAG.Short.LDB	0.32		0.03660	0.165606
Fatty acid desaturase	DEGS1	TAG.Short.LDB	0.32		0.03680	0.166146
Bile acid biosynthesis	SOAT2	FFA.Saturated	-0.32		0.03716	0.167291
fucosyltransferase	FUT7	AC_Long.PCA	-0.32		0.03751	0.16827
Bile acid biosynthesis	SOAT1	FFA.Unsaturated	0.32		0.03770	0.168925
Glycerophospholipid metabolism	CHKA	TAG.Short.LDB	-0.32		0.03772	0.168927
Fatty acid desaturase	SCD5	AC_Long.PCA	-0.32		0.03844	0.171015
Apoptosis	CASP1	AC_Long.PCA	0.32		0.03882	0.171931
De novo fatty acid biosynthesis	PLA2G10	AC_Int.PCA	-0.32		0.03942	0.173625
Glycerophospholipid metabolism	DGKA	FFA.Unsaturated	0.32		0.03986	0.174923
Cholesterol metabolism	NSDHL	AC_Long.PCA	-0.32		0.03987	0.174957
serine-threonine kinase	AKT2	DAG.Short.LDB	-0.32		0.04040	0.176337
Glycan biosynthesis	GALNT1	TAG.Short.LDB	0.32		0.04081	0.1772
Glycerophospholipid metabolism	PLA2G5	DAG.Short.LDB	-0.32		0.04095	0.177517
ras homolog family member A	RHOA	TAG.Short.LDB	0.32		0.04136	0.178774
Protein kinase	MAPK1	TAG.Short.LDB	0.32		0.04137	0.178774
Phosphatidylinositol phosphate metabolism	PLCH2	DAG.Short.LDB	-0.32		0.04193	0.180302
Glycerophospholipid metabolism	PNLIPRP1	FFA.Unsaturated	-0.32		0.04216	0.180811
Glycerophospholipid metabolism	DGKZ	TAG.Int.HDB	-0.31		0.04291	0.1827
Phosphatidylinositol phosphate metabolism	PLCB3	DAG.Short.LDB	0.31		0.04369	0.184313
Phosphatidylinositol phosphate metabolism	CHKB	FFA.Saturated	-0.31		0.04397	0.185068
G protein	GNAI1	TAG.Int.HDB	-0.31		0.04472	0.187126
Glycerophospholipid metabolism	PAFAH1B2	AC_Long.PCA	-0.31		0.04480	0.187393
Cholesterol metabolism	MVK	DAG.Short.LDB	-0.31		0.04486	0.187493
Fatty acid desaturase	FADS2	FFA.Unsaturated	-0.31		0.04521	0.188317
De novo fatty acid biosynthesis	PNPLA3	FFA.Unsaturated	-0.31		0.04521	0.188317
Glycerophospholipid metabolism	LIPA	TAG.Int.HDB	-0.31		0.04570	0.189539
De novo fatty acid biosynthesis	PLA2G4A	AC_Long.PCA	0.31		0.04577	0.189599

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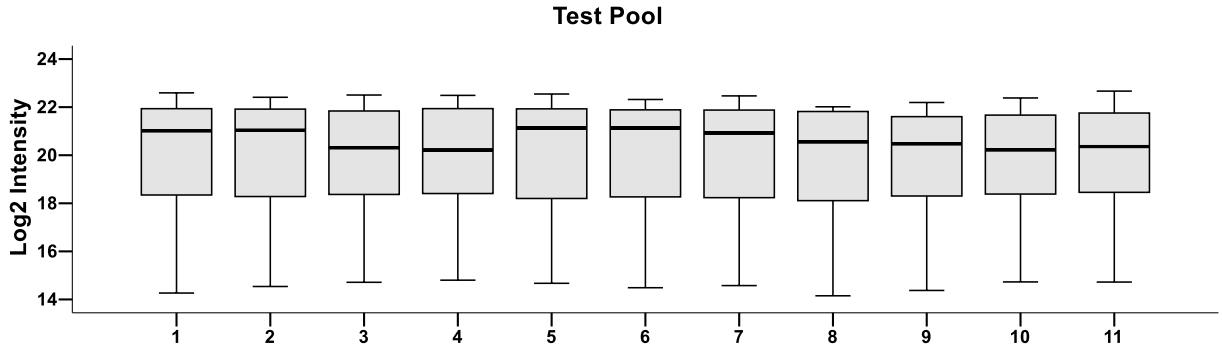
Glycerophospholipid metabolism	PNLIP	FFA.Unsaturated	-0.31		0.04593	0.189927
De novo fatty acid biosynthesis	ACACB	TAG.Short.LDB	-0.31		0.04596	0.189954
O-Glycan biosynthesis	GALNT2	DAG.Short.LDB	0.31		0.04678	0.191743
Glycerophospholipid metabolism	GPLD1	TAG.Short.LDB	-0.31		0.04700	0.192344
De novo fatty acid biosynthesis	ACACB	DAG.Short.LDB	-0.31		0.04748	0.193575
Glycerophospholipid metabolism	PNLIPRP1	TAG.Short.LDB	-0.31		0.04772	0.194282
Cholesterol metabolism	MVK	AC_Int.PCA	-0.31		0.04803	0.194936
Glycosphingolipid metabolism	FUT2	AC_Long.PCA	0.31		0.04855	0.196195
Glycosphingolipid metabolism	NT5M	TAG.Short.LDB	-0.30		0.04962	0.198723
Glycerophospholipid metabolism	PCYT1B	TAG.Short.LDB	-0.30		0.04970	0.19882
Glycerophospholipid metabolism	PLD1	AC_Long.PCA	-0.30		0.05050	0.200858
Cholesterol metabolism	MVD	DAG.Short.LDB	-0.30		0.05076	0.201301
Glycerophospholipid metabolism	LYPLA2	AC_Long.PCA	0.30		0.05084	0.201422
De novo fatty acid biosynthesis	PLA2G4B	AC_Int.PCA	-0.30		0.05164	0.203158
P21 activated kinase	PAK2	FFA.Unsaturated	0.30		0.05200	0.203986
Sphingomyelin metabolism	SGPP1	TAG.Int.LDB	-0.30		0.05348	0.207474
Glycerophospholipid metabolism	PLD1	DAG.Short.LDB	-0.30		0.05353	0.207599
Cholesterol metabolism	TM7SF2	TAG.Short.LDB	-0.30		0.05358	0.207712
Glycan biosynthesis	GALNT10	FFA.Unsaturated	-0.30		0.05364	0.207816
De novo fatty acid biosynthesis	SCD	FFA.Unsaturated	-0.30		0.05383	0.208317
Sphingomyelin metabolism	S1PR5	DAG.Long.HDB	0.30		0.05405	0.208705
Protein kinase	MAPK3	AC_Long.PCA	-0.30		0.05483	0.210543
Prostaglandin synthesis	PTGDS	TAG.Int.HDB	-0.30		0.05484	0.210557

Supplement Figure 1: Comparing inter- and intra-assay coefficients of variation of internal standards in test pools and pooled plasma.

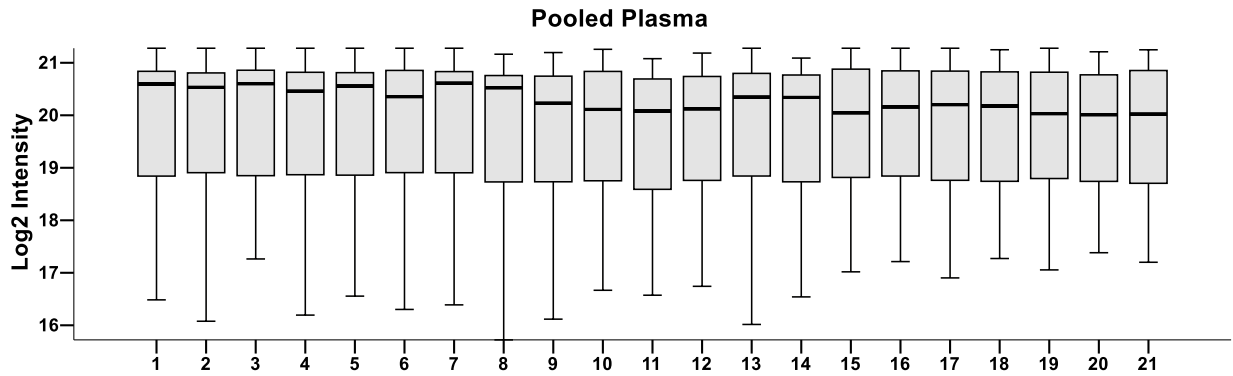


Supplement Figure 2: Illustration of minimal batch to batch variation.

A) Distribution of lipidomic platform internal standards in test pools in sequential runs across different batches



B) Distribution of lipidomic platform internal standards in pooled plasma in sequential runs across different batches



C) Distribution of acylcarnitine internal standards in pooled plasma in sequential runs across different batches

