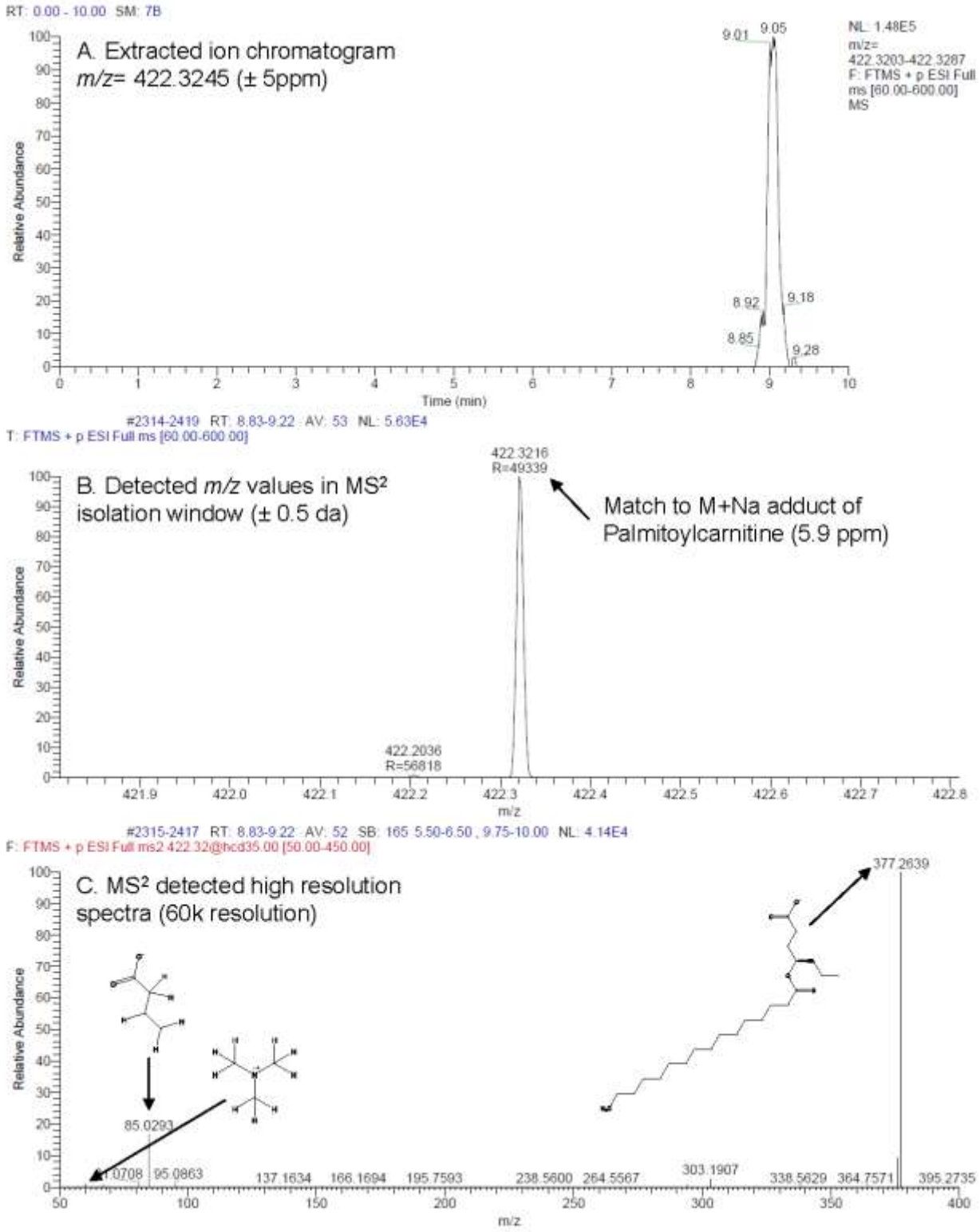

Supp Figure 1. MS/MS chromatograph of palmitoylcarnitine. Within the NIST standard, only one peak was present matching the *m/z* of the sodium adduct form of palmitoylcarnitine, which eluted at ~540 sec. The later retention time most likely occurred due to the use of a different LC frontend than was used for the non-targeted metabolomic profiling. The mass spectra contained

fragments that were consisted with fragmentation of a carnitine ester. Fragments were observed that corresponded to loss of trimethylamine minus a methyl group (377.2637) and oxonium (85.0293, loss of neutral trimethylamine from the palmitoyl head group). Fragments matching the MS/MS mass spectra in METLIN were also present, including 60.0817 and 95.0863. The presence of these adducts suggests that palmitoylcarnitine is the correct identification. Panel A contains the extracted ion chromatogram (EIC) for the *m/z* corresponding to the +Na adduct match of palmitoylcarnitine (*m/z* 422.3245). Panel B contains the high resolution detected masses (60,000 resolution) within the 1 *m/z* isolation window selected for MS^2. Panel C contains the MS^2 fragmentation pattern used for the confirmation of palmitoylcarnitine.

Supplementary Table 1. Internal standards for mass spectrometry analysis.

1. [$^{13}C_6$]-D-glucose
2. [^{15}N]-indole
3. [2-^{15}N]-L-lysine dihydrochloride
4. [$^{13}C_5$]-L-glutamic acid
5. [$^{13}C_7$]-benzoic acid
6. [3,4-$^{13}C_2$]-cholesterol
7. [^{15}N]-L-tyrosine
8. [trimethyl-$^{13}C_2$]-caffeine
9. [$^{15}N_2$]-uracil
10. [3,3-$^{13}C_2$]-cystine
11. [1,2-$^{13}C_2$]-palmitic acid
12. [^{15}N,$^{13}C_5$]-L-methionine
13. [^{15}N]-choline chloride
14. 2'-deoxyguanosine-$^{15}N_2$,$^{13}C_{10}$-5'monophosphate

Supplementary Table 2. Optimized operating conditions for the LTQ Velos Orbitrap.

HESI probe with S-lens combination for ESI
MS^1 mode scanning *m/z* range of 85-2000
Resolution - 60,000
Maximum number of ions collected - 5.00×10^5
Maximum injection time - 5 µL/s
Capillary temperature - 275°C
Source heater - 45°C
Voltage - 4.6 kV
Sheath gas - 45
Auxiliary gas flow - 5
Sweep gas flow – 0

Supplementary Table 3: Ocular health and treatments in POAG patients and controls

	POAG	Control	p-value
Antihypertensives	44 (61.1)	43 (59.7)	1.000
Statins	28 (38.9)	26 (36.1)	0.863
Diabetes medications	12 (16.7)	19 (26.4)	0.610
Insulin	1 (1.4)	2 (2.8)	1.000
Corticosteroids	7 (9.7)	10 (13.9)	0.607
Thyroid hormone	14 (19.4)	9 (12.5)	0.363
Estrogen	5 (6.9)	5 (6.9)	1.000
Testosterone	3 (4.2)	2 (2.8)	1.000
Vitamin D	38 (52.8)	31 (34.1)	0.320

* Best Corrected Visual Acuity (BCVA) in better-seeing eye. † In either eye.
Any ocular surgery defined as any penetrating ocular surgery, e.g. cataract surgery, trabeculectomy, vitrectomy, and globe repair.

Supplementary Table 4: Systemic medications in POAG patients and controls

	POAG	Control	p-value
BCVA < 20/40* (%)	9 (12.5)	0 (0)	0.003
Macular drusen† (%)	0 (0)	4 (5.6)	0.120
Cataract surgery† (%)	42 (58.3)	55 (76.4)	0.034
Any ocular surgery† (%)	49 (68.1)	55 (76.4)	0.352

Supplementary Table 5. The 41 differentially expressed m/z features with associated p-values.

m/z	Retention Time	Mean Intensity POAG	Mean Intensity Control	P-Value	Adjusted P-Value
422.3200	399	0.6056	10.0655	4.48E-22	1.09E-18
272.2938	370	0.2037	-8.5473	1.60E-19	1.96E-16
290.2953	344	0.3069	-7.0356	2.95E-17	1.99E-14
421.3158	394	-7.1719	3.4103	3.26E-17	1.99E-14
288.2884	345	0.4213	-4.0571	2.37E-15	1.15E-12
289.2918	345	0.4422	-4.2332	1.34E-14	5.44E-12
286.2728	350	-0.2550	-8.1016	3.06E-14	1.07E-11
316.3200	368	0.4292	-3.1932	3.92E-14	1.20E-11
376.2584	398	-8.1885	1.9576	1.94E-13	5.26E-11

399.3066	533	-0.0533	-8.1268	6.49E-12	1.58E-09
366.3353	575	9.9792	2.7045	8.14E-12	1.81E-09
317.3230	368	0.4813	-3.5052	6.62E-11	1.35E-08
333.2988	531	0.1488	-5.2844	2.84E-10	5.34E-08
422.3245	370	0.3522	-6.1851	3.69E-10	6.44E-08
377.3247	532	-1.0216	-7.8453	5.23E-10	8.50E-08
443.3320	530	-0.5401	-6.8413	7.48E-09	1.14E-06
466.4089	531	-1.4803	-7.8125	8.75E-09	1.26E-06
244.2626	352	0.4986	-3.8047	2.23E-08	3.02E-06
377.2615	398	-6.2669	0.7218	2.67E-08	3.43E-06
422.3820	529	0.3401	-3.6401	1.25E-07	1.53E-05
378.3564	518	0.4488	-2.3766	4.96E-07	5.77E-05
292.2108	22	0.1441	-3.1321	6.21E-07	6.89E-05
398.2532	347	-0.2515	-4.1004	4.22E-06	0.000447
289.2726	531	0.5074	-3.0628	4.45E-06	0.000452
314.3041	370	-0.1226	-3.4051	7.63E-06	0.000745
449.3516	462	-0.0917	-5.0347	7.94E-06	0.000745
211.9866	128	-2.9691	0.0256	7.87E-05	0.007109
422.3271	232	0.8503	-2.3039	0.000133	0.01137
1265.6270	320	-6.3824	-2.0388	0.000135	0.01137
211.9803	49	-2.8617	-7.3872	0.000247	0.020051
1036.6970	501	-4.1712	-0.8063	0.000255	0.020051
350.3247	533	0.1031	-2.2449	0.000337	0.025705
438.3773	531	-0.7070	-3.9830	0.000399	0.029491
180.8937	90	-3.7300	-0.4342	0.000611	0.043842
851.8857	46	-1.5215	-5.3378	0.000636	0.044182
482.4182	565	-5.8526	-2.3188	0.000652	0.044182
182.8876	68	-0.0889	-2.2534	0.000674	0.044421
782.8072	46	-4.2051	-0.8950	0.000708	0.045491
1256.1450	325	-5.2867	-1.7505	0.000767	0.047166
311.2549	534	-0.6330	-2.9864	0.000773	0.047166
167.0700	419	-2.8528	-0.3988	0.000796	0.047397

Supplementary Table 6. The 41 *m/z* features significantly different between POAG cases and controls, including putative matches to METLIN (10 ppm).

Cluster	P Value	*m/z*	Presence in POAG Cohort	Putative Matches
1	7.87E-05	211.9866	Lower	No Match
1	0.000796	167.0700	Lower	3,4-dihydroxyphenylacetone (tyrosine metabolism)
2	0.000611	180.8937	Lower	1,2,4,6-tetrachloro-1,4-cyclohexadiene
2	0.000708	782.8072	Lower	No Match
3	0.000247	211.9803	Higher	No Match
3	0.000636	851.8857	Higher	No Match
3	0.000674	182.8876	Higher	No Match
4	3.69E-10	422.3245	Higher	Palmitoylcarnitine
4	1.60E-19	272.2938	Higher	Heptadecanone
4	2.95E-17	290.2953	Higher	Probable $^{13}C_2$ form of 288.280
4	2.37E-15	288.2884	Higher	C17 Sphinganine
4	1.34E-14	289.2918	Higher	Probable ^{13}C form of 288.280
4	3.06E-14	286.2728	Higher	C17 Sphingosine; heptadecanedione
4	3.92E-14	316.3200	Higher	Possible 288.2884 plus 2(-CH_2-), C19 Sphinganine
4	6.62E-11	317.3230	Higher	Probable ^{13}C form of 316.3200
4	2.23E-08	244.2626	Higher	Pentadecanone
4	6.21E-07	292.2108	Higher	Hydroxytetradecanedioic acid
4	7.63E-06	314.3041	Higher	Heptadecanediol
4	0.000133	422.3271	Higher	Monoglyceride (22:5); Triglyceride (12:0/18:4/22:6), cholane tetrol
5	6.49E-12	399.3066	Higher	FluorohydroxyD3; (Triterpene); DG(24:0/22:6)
5	8.14E-12	366.3353	Higher	Heptadecylbenzenediol
5	2.84E-10	333.2988	Higher	HODE-cholesteryl ester
5	5.23E-10	377.3247	Higher	Hydroxyergocalciferol; DG(24:0/22:6)
5	7.48E-09	443.332	Higher	Dihydroergocalciferol; cholestanediol
5	8.75E-09	466.4089	Higher	Ergostanol
5	1.25E-07	422.3820	Higher	Diapo-zeta-carotene (terpene)
5	4.96E-07	378.3564	Higher	No Match
5	4.45E-06	289.2726	Higher	No Match
5	0.000337	350.3247	Higher	Azacholecalciferol; decaprenol (terpene)
5	0.000399	438.3773	Higher	Ergosterol
5	0.000773	311.2549	Higher	HODE-methyl ester; monoglyceride
6	3.26E-17	421.3158	Lower	Multiple vitamin D analogs; TG (12:0/16:0/20:5)
6	1.94E-13	376.2584	Lower	C19 Sphingosine-1-phosphate
6	4.48E-22	422.3200	Lower	Probable ^{13}C form of 421.3158

6	2.67E-08	377.2615	Lower	Probable ^{13}C form of 376.2584
6	0.000652	482.4182	Lower	MG(24:1); TG (18:0/18:0/20:0)
6	0.000767	1256.1450	Lower	Complex glycosphingolipid
7	4.22E-06	398.2532	Higher	Arg/Gln/Ile/Leu - tripeptides
7	7.94E-06	449.3516	Higher	Squalene, hopane (steroid biosynthesis)
8	0.000135	1265.6270	Lower	Balanitesin, a saponin agent
8	0.000255	1036.6970	Lower	Surfactin (surfactant)