

**Supplemental table 1 Proteins whose content is significantly modified in hepatocytes by Aramchol. See text for experimental details**

Accession	Protein name	P value	Fold change (Log <sub>2</sub> ) achol/ctrl
Fibrosis			
P20152	Vimentin GN = Vim PE = 1 SV = 3	6.29E-04	0.13
Q8BTM8	Filamin-A GN = Flna PE = 1 SV = 5	2.02E-02	0.45
Q80X90	Filamin-B GN = Flnb PE = 1 SV = 3	1.13E-02	0.50
P05784	Keratin type I cytoskeletal 18 GN = Krt18 PE = 1 SV = 5	4.89E-02	0.78
Translation			
Q5SFM8	RNA-binding protein 27 GN = Rbm27 PE = 1 SV = 3	1.08E-02	0.32
Q9D7S7	60S ribosomal protein L22-like 1 GN = Rpl22l1 PE = 1 SV = 1	3.86E-02	0.42
Q64737	Trifunctional purine biosynthetic protein adenosine-3 GN = Gart PE = 1 SV = 3	2.33E-03	0.50
P23116	Eukaryotic translation initiation factor 3 subunit A GN = Eif3a PE = 1 SV = 5	3.10E-03	0.59
Q9CZD3	Glycine--tRNA ligase GN = Gars PE = 1 SV = 1	6.87E-03	0.63
Q8JZQ9	Eukaryotic translation initiation factor 3 subunit B GN = Eif3b PE = 1 SV = 1	4.13E-02	0.67
Q9D8N0	Elongation factor 1-gamma GN = Eef1g PE = 1 SV = 3	2.47E-02	0.71
Q922B2	Aspartate--tRNA ligase cytoplasmic	2.02E-	0.72

	GN = Dars PE = 1 SV = 2	02	
Q9D0I9	Arginine--tRNA ligase cytoplasmic	1.47E-	0.72
	GN = Rars PE = 1 SV = 2	02	
B2RY56	RNA-binding protein 25 GN = Rbm25	1.28E-	1.92
	PE = 1 SV = 2	02	
Q80XI3	Eukaryotic translation initiation factor 4	7.92E-	3.90
	gamma 3 GN = Eif4g3 PE = 1 SV = 2	03	
Lipid metabolism			
Q91YR9	Prostaglandin reductase 1 GN = Ptgr1	4.55E-	0.42
	PE = 1 SV = 2	02	
Q9DBG5	Perilipin-3 GN = Plin3 PE = 1 SV = 1	3.09E-	0.51
		02	
Q80XL6	Acyl-CoA dehydrogenase family	3.98E-	1.21
	member 11 GN = Acad11 PE = 1 SV = 2	02	
Q9DBG1	Sterol 26-hydroxylase mitochondrial	2.98E-	1.31
	GN = Cyp27a1 PE = 1 SV = 1	02	
P97742	Carnitine O-palmitoyltransferase 1	3.02E-	1.32
	liver isoform GN=Cpt1a PE=1 SV=4	02	
Q07417	Short-chain specific acyl-CoA	3.13E-	1.36
	dehydrogenase mitochondrial GN =	02	
	Acads PE = 1 SV = 2		
P54869	Hydroxymethylglutaryl-CoA synthase	2.19E-	1.37
	mitochondrial GN = Hmgcs2 PE = 1 SV	03	
	= 2		
Q99JY0	Trifunctional enzyme subunit beta	1.40E-	1.38
	mitochondrial GN = Hadhb PE = 1 SV	02	
	= 1		
P51660	Peroxisomal multifunctional enzyme	9.10E-	1.39
	type 2 GN = Hsd17b4 PE = 1 SV = 3	03	
Q8VCH6	Delta(24)-sterol reductase GN = Dhcr24	2.69E-	1.41
	PE = 1 SV = 1	02	

P50544	Very long-chain specific acyl-CoA dehydrogenase mitochondrial GN = Acadvl PE = 1 SV = 3	2.65E-02	1.42
Q8BMS1	Trifunctional enzyme subunit alpha mitochondrial GN = Hadha PE = 1 SV = 1	1.78E-02	1.42
P16332	Methylmalonyl-CoA mutase mitochondrial GN = Mut PE = 1 SV = 2	1.21E-02	1.43
Q9R0H0	Peroxisomal acyl-coenzyme A oxidase 1 GN = Acox1 PE = 1 SV = 5	1.83E-02	1.43
P53395	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex mitochondrial GN = Dbt PE = 1 SV = 2	4.62E-02	1.45
Q3UNX5	Acyl-coenzyme A synthetase ACSM3 mitochondrial GN = Acsm3 PE = 1 SV = 2	2.96E-02	1.46
P08249	Malate dehydrogenase mitochondrial GN = Mdh2 PE = 1 SV = 3	6.58E-03	1.46
P51174	Long-chain specific acyl-CoA dehydrogenase mitochondrial GN = Acadl PE = 1 SV = 2	4.07E-02	1.47
Q9EQ20	Methylmalonate-semialdehyde dehydrogenase [acylating] mitochondrial GN = Aldh6a1 PE = 1 SV = 1	2.26E-04	1.47
Q80XN0	D-beta-hydroxybutyrate dehydrogenase mitochondrial GN = Bdh1 PE = 1 SV = 2	1.38E-02	1.50
P41216	Long-chain-fatty-acid--CoA ligase 1 GN = Acsl1 PE = 1 SV = 2	1.94E-02	1.56

Q4LDG0	Bile acyl-CoA synthetase GN = Slc27a5 PE = 1 SV = 2	2.76E-04	1.56
Q8QZT1	Acetyl-CoA acetyltransferase mitochondrial GN = Acat1 PE = 1 SV = 1	2.82E-02	1.62
Q91W64	Cytochrome P450 2C70 GN = Cyp2c70 PE = 1 SV = 2	4.63E-02	1.63
Q8CIM7	Cytochrome P450 2D26 GN = Cyp2d26 PE = 1 SV = 1	2.50E-02	1.64
E9Q414	Apolipoprotein B-100 GN = Apob 1 SV = 1	3.50E-02	1.65
Q9CZ13	Cytochrome b-c1 complex subunit 1 mitochondrial GN = Uqcrc1 PE = 1 SV = 2	8.45E-04	1.68
Q8K3K7	1-acyl-sn-glycerol-3-phosphate acyltransferase beta GN = Agpat2 PE = 1 SV = 1	7.21E-03	1.69
O88455	7-dehydrocholesterol reductase GN = Dhcr7 PE = 1 SV = 1	4.41E-02	1.69
Q8JZR0	Long-chain-fatty-acid--CoA ligase 5 GN = Acsl5 PE = 1 SV = 1	9.83E-04	1.70
O35488	Very long-chain acyl-CoA synthetase GN = Slc27a2 PE = 1 SV = 2	2.59E-03	1.72
Q9DBW0	Cytochrome P450 4V2 GN = Cyp4v2 = 1 SV = 1	3.39E-02	1.73
P11714	Cytochrome P450 2D9 GN = Cyp2d9 PE = 1 SV = 2	1.44E-02	1.85
Q8VCW8	Acyl-CoA synthetase family member 2 mitochondrial GN = Acsc2 PE = 1 SV = 1	1.39E-04	1.85
Q9R1J0	Sterol-4-alpha-carboxylate	3- 3.84E-	1.92

	dehydrogenase decarboxylating GN = 02		
	Nsdhl PE = 1 SV = 1		
Q5XG73	Acyl-CoA-binding domain-containing protein 5 GN = Acbd5 PE = 1 SV = 1	1.82E-02	2.08
P08226	Apolipoprotein E GN = Apoe PE = 1 SV = 2	8.64E-03	2.59
Q9JHI5	Isovaleryl-CoA dehydrogenase mitochondrial GN = Ivd PE = 1 SV = 1	7.33E-04	2.92
Q64337	Sequestosome-1 GN = Sqstm1 PE = 1 SV = 1	2.90E-02	5.01
1 Carbon metabolism			
Q9D110	5-formyltetrahydrofolate cyclo-ligase GN = Mthfs PE = 2 SV = 2	2.11E-02	0.44
O35490	Betaine--homocysteine S-methyltransferase 1 GN = Bhmt PE = 1 SV = 1	1.54E-02	1.31
Q99LB7	Sarcosine dehydrogenase mitochondrial GN = Sardh PE = 1 SV = 1	8.73E-04	1.33
Q9DBT9	Dimethylglycine dehydrogenase mitochondrial GN = Dmgdh PE = 1 SV = 1	7.80E-03	1.36
Q9DD20	Methyltransferase-like protein 7B GN = Mettl7b PE = 1 SV = 2	3.87E-02	2.33
Q9JIF0	Protein arginine N-methyltransferase 1 GN = Prmt1 PE = 1 SV = 1	3.87E-02	2.62
Carbohydrate metabolism			
P05064	Fructose-bisphosphate aldolase A GN = Aldoa PE = 1 SV = 2	2.59E-02	0.56
Q9DCD0	6-phosphogluconate dehydrogenase decarboxylating GN = Pgd PE = 1 SV = 1	1.90E-02	0.64

	3		
Q8VC28	Aldo-keto reductase family 1 member C13 GN = Akr1c13 PE = 1 SV = 2	3.44E-02	0.68
Q924M7	Mannose-6-phosphate isomerase GN = Mpi PE = 1 SV = 1	1.49E-02	0.71
P09411	Phosphoglycerate kinase 1 GN = Pgk1 PE = 1 SV = 4	1.31E-02	0.77
Q9DBJ1	Phosphoglycerate mutase 1 GN = Pgam1 PE = 1 SV = 3	5.04E-03	0.77
Q64435	UDP-glucuronosyltransferase 1-6 GN = Ugt1a6 PE = 1 SV = 1	4.02E-02	1.35
Q64521	Glycerol-3-phosphate dehydrogenase mitochondrial GN = Gpd2 PE = 1 SV = 2	4.87E-03	1.49
Urea cycle			
Q61176	Arginase-1 GN = Arg1 PE = 1 SV = 1	4.35E-02	1.16
Q8C196	Carbamoyl-phosphate synthase [ammonia] mitochondrial GN = Cps1 PE = 1 SV = 2	3.81E-02	1.29
P25688	Uricase GN = Uox PE = 1 SV = 2	2.62E-03	1.70
P29758	Ornithine aminotransferase mitochondrial GN = Oat PE = 1 SV = 1	4.76E-02	2.00
TCA cycle			
P26443	Glutamate dehydrogenase 1 mitochondrial GN = Glud1 PE = 1 SV = 1	1.18E-02	1.23
O35423	Serine--pyruvate aminotransferase mitochondrial GN = Agxt PE = 1 SV = 4	4.10E-04	1.38

	3				
P05202	Aspartate aminotransferase mitochondrial GN = Got2 PE = 1 SV = 1	3.48E-02	1.39		
Q8BWF0	Succinate-semialdehyde dehydrogenase mitochondrial GN = Aldh5a1 PE = 1 SV = 1	2.18E-03	1.50		
Q9Z2I8	Succinate-CoA ligase (GDP-forming) subunit beta mitochondrial GN = Suc1g2 PE = 1 SV = 3	1.52E-03	1.55		
Q571F8	Glutaminase liver isoform mitochondrial GN = GlS2 PE = 1 SV = 2	1.23E-02	1.59		
Q9Z2I9	Succinate-CoA ligase (ADP-forming) subunit beta mitochondrial GN = Sucla2 PE = 1 SV = 2	5.11E-03	1.87		
OxPhos & antioxidant response					
P24270	Catalase GN = Cat PE = 1 SV = 4	4.84E-03	1.28		
Q9DCN2	NADH-cytochrome b5 reductase 3 GN = Cyb5r3 PE = 1 SV = 3	4.08E-03	1.32		
P67778	Prohibitin GN = Phb PE = 1 SV = 1	2.41E-02	1.35		
Q03265	ATP synthase subunit alpha mitochondrial GN = Atp5a1 PE = 1 SV = 1	4.41E-03	1.38		
P56480	ATP synthase subunit beta mitochondrial GN = Atp5b PE = 1 SV = 2	1.68E-03	1.39		
Q91VD9	NADH-ubiquinone oxidoreductase 75 kDa subunit mitochondrial GN =	4.28E-03	1.41		

	Ndufs1 PE = 1 SV = 2		
Q9DB77	Cytochrome b-c1 complex subunit 2 mitochondrial GN = Uqcrc2 PE = 1 SV = 1	6.36E-03	1.41
Q921G7	Electron transfer flavoprotein-ubiquinone oxidoreductase mitochondrial GN = Etfdh PE = 1 SV = 1	3.06E-02	1.43
Q9DCM2	Glutathione S-transferase kappa 1 GN = Gstk1 PE = 1 SV = 3	3.31E-02	1.43
O35129	Prohibitin-2 GN = Phb2 PE = 1 SV = 1	2.88E-02	1.45
Q05421	Cytochrome P450 2E1 GN = Cyp2e1 PE = 1 SV = 1	2.20E-02	1.51
Q9DC69	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9 mitochondrial GN = Ndufa9 PE = 1 SV = 2	1.26E-02	1.54
P33267	Cytochrome P450 2F2 GN = Cyp2f2 PE = 1 SV = 1	1.13E-02	1.57
Q91YT0	NADH dehydrogenase [ubiquinone] flavoprotein 1 mitochondrial GN = Ndufv1 PE = 1 SV = 1	1.92E-03	1.58
O09111	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11 mitochondrial GN = Ndufb11 PE = 1 SV = 2	4.61E-02	1.89
P20852	Cytochrome P450 2A5 GN = Cyp2a5 PE = 2 SV = 1	9.73E-03	4.29