

Supplementary Table 2

Total fraction new at end of labeling period - % new (F)

	Fibrosis Score	Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011
		3	0	2	1	4	0
Liver Proteins	Uniprot Accession						
1,4-alpha-glucan-branching enzyme	Q04446			30.88%			
14-3-3 protein epsilon	P62258						72.43%
14-3-3 protein eta	Q04917					34.39%	36.91%
17-beta-hydroxysteroid dehydrogenase 13	Q7Z5P4		75.91%	79.19%	97.87%		74.13%
17-beta-hydroxysteroid dehydrogenase type 6	O14756			62.68%	74.18%		73.86%
2,4-dienoyl-CoA reductase, mitochondrial	Q16698	93.15%	51.27%	51.38%	84.89%		64.27%
3-hydroxyacyl-CoA dehydratase 3	Q9P035			57.24%			
3-hydroxyacyl-CoA dehydrogenase type-2	Q99714	52.52%	42.53%	42.53%	52.36%		47.27%
3-hydroxyanthranilate 3,4-dioxygenase	P46952			40.76%			
3-ketoacyl-CoA thiolase, mitochondrial	P42765	81.48%	46.94%	45.07%	78.16%	79.03%	53.81%
3-ketoacyl-CoA thiolase, peroxisomal	P09110	100.67%	76.45%	67.06%	84.66%	90.61%	68.38%
3-mercaptopyruvate sulfurtransferase	P25325	95.52%	57.54%	54.17%	78.49%		58.36%
40S ribosomal protein S7	P62081		70.49%	62.69%	89.55%		68.47%
40S ribosomal protein S8	P62241	23.12%	5.75%	5.39%	36.76%	31.51%	8.73%
40S ribosomal protein SA	P08865	86.45%	54.32%	52.22%	74.14%	71.14%	54.13%
4-aminobutyrate aminotransferase, mitochondrial	P80404	90.42%	58.38%	48.13%	76.79%	94.46%	59.39%
4-hydroxyphenylpyruvate dioxygenase	P32754		91.59%	77.97%			77.07%
4-trimethylaminobutyraldehyde dehydrogenase	P49189		46.09%	44.96%			
60 kDa heat shock protein, mitochondrial	P10809	87.05%	50.39%	45.29%	73.48%		53.91%
60S acidic ribosomal protein P0	P05388			52.12%			
60S ribosomal protein L6	Q02878	79.22%	51.32%	51.69%	68.00%	55.20%	53.24%
60S ribosomal protein L7	P18124	95.32%					
78 kDa glucose-regulated protein	P11021	102.49%	76.33%	62.58%	87.18%	96.40%	79.34%
Abhydrolase domain-containing protein 14B	Q96IU4		77.95%				

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	Fibrosis Score	3	0	2	1	4	0
Acetyl-CoA acetyltransferase, cytosolic	Q9BWD1		51.96%	52.67%	67.44%		80.75%
Acetyl-CoA acetyltransferase, mitochondrial	P24752	83.72%	52.77%	41.38%	78.63%	70.53%	49.96%
Aconitate hydratase, mitochondrial	Q99798		70.22%				
Actin, alpha skeletal muscle	P68133						9.48%
Actin, aortic smooth muscle	P62736	93.33%	50.79%	48.98%	72.21%	37.71%	12.67%
Actin, cytoplasmic 1	P60709	84.88%	55.94%	49.63%	74.02%	51.79%	54.80%
Acyl-coenzyme A synthetase ACSM2A, mitochondrial	Q08AH3		55.43%	53.26%			
Acyl-coenzyme A thioesterase 1	Q86TX2		60.49%				57.38%
Adenylate kinase 2, mitochondrial	P54819		45.40%	50.51%			
ADP/ATP translocase 1	P12235		54.57%	68.90%	85.58%		54.53%
Aflatoxin B1 aldehyde reductase member 3	O95154		76.54%				
Agmatinase, mitochondrial	Q9BSE5			33.69%			
Alanine aminotransferase 1	P24298			28.31%			
Alcohol dehydrogenase [NADP+]	P14550			68.08%			
Alcohol dehydrogenase 1A	P07327	95.49%	59.93%	43.79%	78.37%	70.39%	56.61%
Alcohol dehydrogenase 1B	P00325	95.13%	58.48%	40.30%	74.17%	84.42%	57.70%
Alcohol dehydrogenase 1C	P00326	96.31%	61.22%		84.16%		59.47%
Alcohol dehydrogenase 4	P08319	100.36%	61.47%	46.73%	76.33%	86.49%	61.52%
Alcohol dehydrogenase 6	P28332		46.82%	48.70%	70.01%		55.40%
Alcohol dehydrogenase class-3	P11766		46.93%	32.23%			
Aldehyde dehydrogenase family 8 member A1	Q9H2A2		70.12%	55.80%			60.83%
Aldehyde dehydrogenase X, mitochondrial	P30837	100.77%	61.21%		96.02%	96.53%	61.46%
Aldehyde dehydrogenase, mitochondrial	P05091	101.68%	68.33%	60.89%	83.66%	99.04%	69.34%
Aldehyde oxidase	Q06278		70.58%	72.00%	84.03%		65.25%
Aldo-keto reductase family 1 member C1	Q04828		63.01%	46.66%	68.73%	88.52%	55.57%
Aldo-keto reductase family 1 member C3	P42330			47.71%			
Aldo-keto reductase family 1 member C4	P17516			49.18%			
Alpha-1-antitrypsin	P01009		75.45%			93.00%	86.47%

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Alpha-2-macroglobulin	P01023	85.17%	62.74%	54.75%	71.62%	73.84%	51.44%
Alpha-actinin-1	P12814	95.48%	73.65%		84.87%	68.06%	38.76%
Alpha-actinin-2	P35609						22.31%
Alpha-actinin-4	O43707	83.31%	58.67%	57.48%		58.97%	48.70%
Alpha-enolase	P06733	101.49%	65.36%	42.36%	83.52%	98.20%	70.52%
Amine oxidase [flavin-containing] A	P21397		45.47%	44.71%	68.98%		
Amine oxidase [flavin-containing] B	P27338	99.60%	47.94%	26.88%	82.90%		
Aminoacylase-1	Q03154		59.00%	50.50%	71.90%	96.25%	66.55%
Annexin A1	P04083					69.27%	
Annexin A2	P07355		58.01%			55.55%	49.55%
Annexin A4	P09525					89.70%	
Annexin A5	P08758		65.23%	64.06%	82.47%	77.25%	60.28%
Annexin A6	P08133	98.52%	76.68%	72.19%	96.40%	88.56%	70.84%
Apolipoprotein A-I	P02647					73.97%	
Apoptosis-inducing factor 1, mitochondrial	O95831		42.18%	27.52%	65.88%		39.30%
Arginase-1	P05089	87.95%	54.91%	44.15%	72.12%		57.40%
Argininosuccinate lyase	P04424	83.63%	56.97%	57.44%	65.16%	75.70%	57.40%
Argininosuccinate synthase	P00966		66.41%	50.21%	75.61%		73.25%
Arylacetamide deacetylase	P22760						77.43%
Aspartate aminotransferase, cytoplasmic	P17174	98.70%	63.08%	53.48%	83.87%		57.55%
Aspartate aminotransferase, mitochondrial	P00505	81.36%	49.94%	43.66%	73.66%	71.63%	46.22%
ATP synthase subunit alpha, mitochondrial	P25705	100.10%	57.25%	52.56%	85.48%	75.65%	57.08%
ATP synthase subunit b, mitochondrial	P24539		45.19%		71.06%		
ATP synthase subunit beta, mitochondrial	P06576	92.60%	48.87%	41.53%	81.60%	80.44%	49.27%
ATP synthase subunit delta, mitochondrial	P30049				81.37%		
ATP synthase subunit f, mitochondrial	P56134		43.11%				
ATP synthase subunit O, mitochondrial	P48047	86.82%	42.31%	71.45%	58.51%		59.94%
ATP-binding cassette sub-family D member 3	P28288		64.73%	57.52%	81.42%		76.65%
Beta-actin-like protein 2	Q562R1			39.83%			

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Beta-enolase	P13929						52.95%
Betaine--homocysteine S-methyltransferase 1	Q93088	98.02%	64.46%	54.88%	80.63%		64.57%
Betaine--homocysteine S-methyltransferase 2	Q9H2M3			59.24%			51.03%
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	Q3LXA3	90.94%	57.04%	54.42%	71.57%		57.30%
Biglycan	P21810					32.65%	
Bile acid-CoA:amino acid N-acyltransferase	Q14032		59.23%	41.37%			73.80%
Bile acyl-CoA synthetase	Q9Y2P5		74.76%	57.47%	85.30%		70.56%
Bile salt sulfotransferase	Q06520	98.88%	62.24%	54.68%	83.23%		64.58%
C-1-tetrahydrofolate synthase, cytoplasmic	P11586	72.35%	51.57%	41.35%	58.76%		58.65%
Calcium-binding mitochondrial carrier protein Aralar1	O75746		46.85%		63.14%		50.34%
Calcium-binding mitochondrial carrier protein Aralar2	Q9UJS0	86.73%	46.01%	34.66%	75.48%		53.02%
Caldesmon	Q05682					81.10%	
Calmodulin	P62158					95.70%	89.22%
Calnexin	P27824	103.89%	74.55%	64.24%			70.29%
Calreticulin	P27797	109.41%	66.82%	61.52%	75.87%	84.77%	71.89%
Calsequestrin-1	P31415						15.37%
Carbamoyl-phosphate synthase [ammonia], mitochondrial	P31327	87.63%	47.79%	41.85%	77.01%	80.08%	51.03%
Carbonic anhydrase 1	P00915			26.51%		58.57%	
Carbonic anhydrase 2	P00918	89.24%	57.72%	45.82%	75.87%	73.82%	55.03%
Carbonic anhydrase 3	P07451				87.41%		22.35%
Carbonyl reductase [NADPH] 1	P16152	93.21%	59.10%	52.55%	72.11%	77.01%	58.59%
Catalase	P04040	97.82%	66.35%	65.82%	83.43%	81.49%	70.16%
Cathepsin D	P07339	103.88%	68.31%	58.14%	86.91%	92.44%	74.94%
Clathrin heavy chain 1	Q00610						65.23%
Cocaine esterase	O00748		47.67%	34.09%			

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Cofilin-1	P23528			28.58%		79.22%	
Collagen alpha-1(I) chain	P02452	18.65%	4.26%	7.41%	12.13%	11.66%	6.41%
Collagen alpha-1(III) chain	P02461	17.60%	5.28%	4.68%	9.37%	8.77%	6.69%
Collagen alpha-1(IV) chain	P02462			1.81%		18.48%	
Collagen alpha-1(VI) chain	P12109	34.81%	16.54%	17.33%	34.35%	22.13%	16.80%
Collagen alpha-1(XIV) chain	Q05707					38.24%	
Collagen alpha-2(I) chain	P08123	19.58%	8.65%	9.37%	12.68%	11.59%	8.35%
Collagen alpha-3(VI) chain	P12111	28.21%	24.51%	12.37%	25.41%	18.63%	19.25%
Complement C3	P01024		97.13%		81.81%		
Complement C4-A	P0C0L4		82.13%				
Corticosteroid 11-beta-dehydrogenase isozyme 1	P28845		78.97%				
Creatine kinase M-type	P06732						16.36%
Creatine kinase S-type, mitochondrial	P17540						39.94%
Cullin-associated NEDD8-dissociated protein 1	Q86VP6		50.56%	47.48%			
Cystathionine gamma-lyase	P32929	107.46%	75.44%	55.98%	96.23%		66.98%
Cytochrome b5	P00167	106.58%	65.41%	57.12%	84.83%	89.46%	67.84%
Cytochrome b-c1 complex subunit 2, mitochondrial	P22695						57.17%
Cytochrome c oxidase subunit 2	P00403	85.35%	57.55%	43.35%	91.81%	81.64%	55.12%
Cytochrome c oxidase subunit 5A, mitochondrial	P20674		42.35%	34.92%	65.14%		41.99%
Cytochrome P450 1A2	P05177		73.40%		65.12%		
Cytochrome P450 2A6	P11509		101.36%				
Cytochrome P450 2C8	P10632		97.51%	101.84%			
Cytochrome P450 2C9	P11712	94.02%	83.99%	63.08%	86.00%		80.84%
Cytochrome P450 2E1	P05181				85.61%		
Cytochrome P450 3A4	P08684			75.74%			
Cytochrome P450 3A5	P20815		76.90%		75.72%	93.98%	77.39%

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Cytoplasmic aconitate hydratase	P21399		61.12%	52.86%	81.05%		
Cytosol aminopeptidase	P28838		67.20%				74.02%
Cytosolic 10-formyltetrahydrofolate dehydrogenase	O75891		53.49%	60.92%	93.43%		57.97%
Cytosolic non-specific dipeptidase	Q96KP4	70.97%	57.18%	31.06%			80.80%
D-beta-hydroxybutyrate dehydrogenase, mitochondrial	Q02338	96.54%	48.47%	57.34%			52.22%
D-dopachrome decarboxylase	P30046		60.38%	47.92%	81.59%	81.27%	60.69%
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	Q13011	88.13%	49.83%		75.09%	73.56%	57.22%
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	P30038	92.90%	55.33%	50.84%	83.61%	49.54%	59.35%
Delta-aminolevulinic acid dehydratase	P13716			37.26%			
Desmin	P17661					61.67%	61.98%
Dihydropyrimidinase	Q14117			62.10%	91.70%		70.09%
Dimethylaniline monooxygenase [N-oxide-forming] 3	P31513		69.67%	55.11%	77.93%		
Dimethylglycine dehydrogenase, mitochondrial	Q9UI17		48.99%	62.73%			
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	P04843	89.46%	50.88%		70.20%		
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	P04844		65.99%	54.69%	75.44%		55.86%
Elastin	P15502					7.86%	
Electron transfer flavoprotein subunit alpha, mitochondrial	P13804	89.84%	49.58%	46.01%	75.94%	77.93%	49.71%
Electron transfer flavoprotein subunit beta	P38117	67.15%	48.44%	42.74%	85.22%		59.50%
Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	Q16134		68.59%	59.55%			76.79%

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	<b>Score</b>	<b>3</b>	<b>0</b>	<b>2</b>	<b>1</b>	<b>4</b>	<b>0</b>
Elongation factor 1-alpha 1	P68104	90.45%	61.96%	55.87%	69.03%	77.40%	55.06%
Elongation factor 2	P13639		85.18%	75.04%			
Endoplasmic reticulum chaperone protein	P14625	102.60%	73.35%	65.52%	87.97%	95.42%	77.69%
Enoyl-CoA hydratase domain-containing protein 2, mitochondrial	Q86YB7		53.38%	58.12%	96.52%		80.40%
Enoyl-CoA hydratase, mitochondrial	P30084	86.48%	44.92%	41.81%	72.24%	72.59%	48.89%
Epoxide hydrolase 1	P07099	98.15%	63.71%	52.81%	82.49%	86.46%	66.28%
Epoxide hydrolase 2	P34913		67.44%	52.54%	80.70%		73.63%
Ester hydrolase C11orf54	Q9H0W9		54.78%	67.96%			
Estradiol 17-beta-dehydrogenase 11	Q8NBQ5			62.89%			
Fatty acid synthase	P49327	105.87%	86.59%	91.38%	79.43%		82.10%
Fatty acid-binding protein, liver	P07148	93.26%	73.50%	47.63%	78.45%	83.61%	59.10%
Ferritin light chain	P02792	95.31%	70.40%	77.45%	83.76%	97.61%	65.16%
Fibronectin	P02751	104.52%	60.85%			81.85%	80.44%
Filamin-A	P21333				108.52%	53.81%	80.16%
Filamin-B	O75369			60.70%			
Filamin-C	Q14315						26.46%
Flavin reductase (NADPH)	P30043		53.46%	54.53%	69.77%		65.26%
Formimidoyltransferase-cyclodeaminase	O95954	91.20%	62.17%	54.44%	80.74%	87.14%	59.95%
Fructose-1,6-bisphosphatase 1	P09467	104.22%	68.29%	52.19%	86.82%	80.55%	65.05%
Fructose-bisphosphate aldolase A	P04075						42.13%
Fructose-bisphosphate aldolase B	P05062	111.24%	77.15%	65.90%	84.37%	95.51%	74.32%
Fumarate hydratase, mitochondrial	P07954		50.49%	45.47%	76.69%		51.00%
Fumarylacetoacetase	P16930	89.91%	56.58%	42.86%	71.22%	69.76%	50.09%
Galactokinase	P51570		50.23%	42.12%			51.13%
Galectin-1	P09382					58.98%	61.11%
Gamma-glutamyltransferase 5	P36269	98.64%		58.23%		60.85%	
Gelsolin	P06396		57.90%	64.72%			
Glucose-6-phosphate isomerase	P06744	77.30%	52.15%	45.38%	75.83%	72.33%	50.52%

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Glutamate dehydrogenase 1, mitochondrial	P00367	87.26%	43.79%	38.33%	76.89%		43.42%
Glutathione S-transferase A1	P08263	93.75%	58.45%	41.51%	74.62%	86.92%	57.54%
Glutathione S-transferase kappa 1	Q9Y2Q3		67.96%				74.51%
Glutathione S-transferase Mu 1	P09488	91.49%		52.38%	65.98%		65.08%
Glutathione S-transferase omega-1	P78417			35.67%			
Glyceraldehyde-3-phosphate dehydrogenase	P04406	95.24%	59.62%	50.23%	79.11%	64.22%	50.29%
Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic	P21695		60.22%	46.27%			
Glycine amidinotransferase, mitochondrial	P50440	104.05%	69.98%	68.17%	81.68%	90.24%	66.90%
Glycine dehydrogenase [decarboxylating], mitochondrial	P23378			15.99%			
Glycogen debranching enzyme	P35573			19.89%			35.83%
Glycogen phosphorylase, brain form	P11216						37.80%
Glycogen phosphorylase, liver form	P06737	75.62%	46.99%	30.22%	60.46%		32.21%
Glycogen phosphorylase, muscle form	P11217						26.70%
Glyoxylate reductase/hydroxypyruvate reductase	Q9UBQ7	87.44%	56.97%	46.20%	73.77%	75.96%	55.26%
Heat shock 70 kDa protein 1A/1B	P08107		73.34%	69.27%		72.62%	59.46%
Heat shock cognate 71 kDa protein	P11142		80.69%		89.96%		
Heat shock protein beta-1	P04792	99.56%	69.28%	63.57%	80.61%	76.66%	58.63%
Heat shock-related 70 kDa protein 2	P54652			59.33%	88.25%		82.67%
Hemoglobin subunit alpha	P69905	30.42%	10.13%	12.24%	37.10%	40.45%	11.75%
Hemoglobin subunit beta	P68871	29.17%	9.63%	6.63%	39.31%	36.81%	14.35%
Hemoglobin subunit delta	P02042	39.52%	20.27%	25.79%	54.39%	51.01%	21.29%
Hemoglobin subunit gamma-1	P69891			15.67%			
Heterogeneous nuclear ribonucleoprotein K	P61978	101.01%	77.56%	88.93%		97.46%	
Histone H2A type 1-A	Q96QV6		35.68%	24.45%	51.89%	30.27%	28.63%
Histone H2A type 1-B/E	P04908	54.67%	26.91%	10.42%	41.99%	24.35%	20.52%
Histone H2B type 1-A	Q96A08					25.82%	

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Histone H2B type 1-B	P33778	54.94%	27.23%	17.79%	47.63%	21.19%	23.46%
Histone H3.1t	Q16695	29.73%	18.92%	6.35%	22.39%	11.72%	9.91%
Histone H3.3	P84243	32.61%	12.52%	15.03%	20.92%	11.14%	14.41%
Histone H4	P62805	44.46%	19.22%	13.97%	34.38%	21.86%	18.99%
HLA class I histocompatibility antigen, A-1 alpha chain	P30443	104.57%					
HLA class I histocompatibility antigen, A-25 alpha chain	P18462	106.86%					
Homogentisate 1,2-dioxygenase	Q93099			39.83%	95.44%		75.36%
Hydroxyacid oxidase 1	Q9UJM8	108.55%	74.86%	75.82%	95.38%		73.12%
Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	Q16836	89.11%	43.51%	40.08%	72.34%	62.53%	43.46%
Hydroxymethylglutaryl-CoA synthase, cytoplasmic	Q01581			62.74%	94.04%		73.28%
Hydroxymethylglutaryl-CoA synthase, mitochondrial	P54868	95.07%	65.52%	62.92%	84.23%	98.47%	64.91%
Ig alpha-1 chain C region	P01876					73.25%	
Ig gamma-1 chain C region	P01857	67.12%	57.70%	18.18%	63.15%	48.30%	47.34%
Ig gamma-2 chain C region	P01859					41.73%	
Ig heavy chain V-III region BRO	P01766					59.41%	
Ig kappa chain C region	P01834	63.03%	52.24%	27.84%	49.05%	47.88%	33.83%
Ig lambda-2 chain C regions	P0CG05					57.67%	
Immunoglobulin lambda-like polypeptide 5	B9A064		56.71%			61.82%	
Isochorismatase domain-containing protein 2, mitochondrial	Q96AB3	77.79%	40.66%	35.87%	44.40%		47.26%
Isocitrate dehydrogenase [NADP] cytoplasmic	O75874	110.19%	56.22%	51.49%	80.30%		51.94%
Isocitrate dehydrogenase [NADP], mitochondrial	P48735	80.92%	35.20%	43.45%		61.04%	43.95%
Keratin, type I cytoskeletal 10	P13645				11.99%		

Supplementary Table 2

Total fraction new at end of labeling period - % new (F)

		Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011
	<b>Fibrosis Score</b>	<b>3</b>	<b>0</b>	<b>2</b>	<b>1</b>	<b>4</b>	<b>0</b>
Keratin, type I cytoskeletal 18	P05783	96.59%	59.22%	52.17%	79.83%	74.40%	63.43%
Keratin, type II cytoskeletal 1	P04264				3.51%		
Keratin, type II cytoskeletal 2 epidermal	P35908				20.05%		
Keratin, type II cytoskeletal 7	P08729					95.56%	
Keratin, type II cytoskeletal 8	P05787	106.78%	67.40%	49.77%	85.54%	82.95%	73.75%
Ketohexokinase	P50053			-3.70%			
Lambda-crystallin homolog	Q9Y2S2			35.64%			
Leukotriene-B(4) omega-hydroxylase 1	P78329		78.03%				
Liver carboxylesterase 1	P23141	102.43%	61.68%	55.53%	83.31%	96.40%	67.18%
L-lactate dehydrogenase A-like 6B	Q9BYZ2		62.39%	53.46%	78.65%		46.24%
Long-chain-fatty-acid--CoA ligase 1	P33121	69.44%	68.04%	66.40%	74.73%		61.62%
Lumican	P51884					57.45%	28.15%
L-xylulose reductase	Q7Z4W1	94.48%	53.83%	52.59%	79.05%	75.39%	60.26%
Malate dehydrogenase, cytoplasmic	P40925		55.30%	43.80%	58.63%		52.94%
Malate dehydrogenase, mitochondrial	P40926	84.10%	44.03%	46.84%	69.83%	65.16%	42.33%
Maleylacetoacetate isomerase	O43708		46.69%	37.31%			46.21%
Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	P11310	96.44%	62.43%	77.63%	88.80%		78.87%
Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	Q02252		56.73%	45.74%	73.91%		59.50%
Microfibril-associated glycoprotein 4	P55083					17.15%	
Microsomal glutathione S-transferase 1	P10620	79.70%	49.84%	39.70%	71.12%	67.23%	50.86%
Microsomal triglyceride transfer protein large subunit	P55157	99.42%	72.17%	63.65%	94.45%		91.38%
Mimecan	P20774					16.20%	
Mitochondrial carrier homolog 2	Q9Y6C9		49.09%	49.90%	72.72%		52.62%
Moesin	P26038					93.49%	
Myoglobin	P02144						17.05%
Myomesin-2	P54296						21.00%

**Supplementary Table 2**

**Total fraction new at end of labeling period - % new (F)**

		Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011
	<b>Fibrosis Score</b>	<b>3</b>	<b>0</b>	<b>2</b>	<b>1</b>	<b>4</b>	<b>0</b>
Myosin light chain 1/3, skeletal muscle isoform	P05976						16.24%
Myosin light chain 3	P08590						8.63%
Myosin light chain 6B	P14649					77.16%	49.34%
Myosin light polypeptide 6	P60660		75.51%	71.73%	74.01%	68.40%	73.75%
Myosin regulatory light chain 2, skeletal muscle isoform	Q96A32						21.25%
Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	P10916						18.24%
Myosin-1	P12882						19.94%
Myosin-10	P35580					73.57%	
Myosin-11	P35749					53.13%	
Myosin-13	Q9UKX3						13.61%
Myosin-2	Q9UKX2						25.48%
Myosin-6	P13533		-23.23%		4.93%		19.11%
Myosin-7	P12883						20.75%
Myosin-9	P35579	97.98%	81.39%	79.12%	84.15%	72.33%	74.85%
Myosin-binding protein C, slow-type	Q00872						43.17%
Myozenin-1	Q9NP98						28.36%
NAD kinase domain-containing protein 1	Q4G0N4			8.44%			
NAD(P) transhydrogenase, mitochondrial	Q13423		33.51%	32.59%			
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	Q9P0J0				75.07%		
NADPH--cytochrome P450 reductase	P16435		92.07%				
Neutral alpha-glucosidase AB	Q14697			48.06%			
Nicotinate phosphoribosyltransferase	Q6XQN6			44.45%			
Nucleophosmin	P06748		49.33%	38.91%			
Nucleoside diphosphate kinase A	P15531		60.73%			74.18%	
Omega-amidase NIT2	Q9NQR4				72.23%		
Ornithine carbamoyltransferase, mitochondrial	P00480		54.02%	38.08%	83.87%		56.22%

Supplementary Table 2

Total fraction new at end of labeling period - % new (F)

		Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011
	Fibrosis Score	3	0	2	1	4	0
Peptidyl-prolyl cis-trans isomerase A	P62937			91.67%		88.78%	80.71%
Peroxiredoxin-1	Q06830	113.55%	66.30%	51.23%			75.19%
Peroxiredoxin-2	P32119	74.30%	45.57%	41.66%	67.81%		50.46%
Peroxiredoxin-4	Q13162	101.43%	75.58%	59.61%	83.33%		
Peroxiredoxin-5, mitochondrial	P30044			47.19%			
Peroxiredoxin-6	P30041	96.97%	62.59%	49.23%	71.85%	75.63%	55.24%
Peroxisomal acyl-coenzyme A oxidase 2	Q99424				20.56%		
Peroxisomal bifunctional enzyme	Q08426	98.60%	67.23%	67.82%	86.31%	105.35%	73.26%
Peroxisomal membrane protein 2	Q9NR77				92.93%		
Peroxisomal multifunctional enzyme type 2	P51659	101.43%	70.11%	70.14%	90.40%		68.51%
Peroxisomal sarcosine oxidase	Q9P0Z9	64.13%	53.52%	58.83%	85.88%		61.58%
Peroxisomal trans-2-enoyl-CoA reductase	Q9BY49		42.79%	50.02%			
Phenazine biosynthesis-like domain-containing protein	P30039		38.00%	40.40%			
Phosphate carrier protein, mitochondrial	Q00325	86.50%	57.43%	45.94%	73.58%	67.44%	47.56%
Phosphatidylethanolamine-binding protein 1	P30086	96.65%	60.65%	51.33%	80.16%	82.91%	59.73%
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	Q16822	84.05%	57.55%	49.95%	74.45%	77.66%	57.48%
Phosphoenolpyruvate carboxykinase, cytosolic [GTP]	P35558		63.65%	62.69%	82.29%		
Phosphoglucomutase-1	P36871	96.80%	54.30%	43.81%	79.97%		54.86%
Phosphoglycerate kinase 1	P00558	97.36%	58.09%	36.56%	68.44%	64.62%	40.24%
Phosphoglycerate mutase 1	P18669	95.36%	58.60%	31.96%	71.85%	72.21%	39.35%
Polypyrimidine tract-binding protein 1	P26599		58.03%				
Prelamin-A/C	P02545	5.43%	36.85%	23.08%	48.53%	66.96%	27.89%
Profilin-1	P07737		88.49%	80.22%	88.36%	104.32%	87.28%
Prohibitin	P35232	96.53%	49.02%	51.71%	86.63%	101.28%	58.05%
Prohibitin-2	Q99623	71.15%	46.00%	41.55%	71.91%	18.43%	50.26%
Prolargin	P51888					38.97%	

Supplementary Table 2

Total fraction new at end of labeling period - % new (F)

		Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011
	Fibrosis Score	3	0	2	1	4	0
Proline dehydrogenase 1, mitochondrial	O43272					21.37%	
Prostaglandin reductase 1	Q14914	84.92%	56.61%	46.36%	66.97%	78.71%	
Proteasome activator complex subunit 1	Q06323		74.50%				
Proteasome activator complex subunit 2	Q9UL46		70.84%	58.20%			71.00%
Protein CutA	O60888			7.77%			
Protein disulfide-isomerase	P07237	110.56%	71.56%	64.98%	86.54%	100.77%	76.72%
Protein disulfide-isomerase A3	P30101		71.91%	87.76%	84.34%		79.25%
Protein disulfide-isomerase A4	P13667		74.31%	59.06%			60.18%
Protein disulfide-isomerase A6	Q15084	102.09%	66.69%	62.34%	77.61%	98.38%	71.46%
Protein DJ-1	Q99497		61.06%	57.94%			55.25%
Protein NipSnap homolog 1	Q9BPW8		49.33%	51.90%	83.10%		62.89%
Protein NYNRIN	Q9P2P1	85.22%		41.49%			
Protein-glutamine gamma-glutamyltransferase 2	P21980	101.47%	73.31%	56.47%	88.70%	79.74%	68.45%
Pterin-4-alpha-carbinolamine dehydratase	P61457			49.03%			
Putative beta-actin-like protein 3	Q9BYX7	76.53%	44.32%	40.68%	60.75%	45.26%	28.44%
Putative inactive carboxylesterase 4	Q9UKY3	106.50%	68.23%	62.41%	87.05%	97.52%	69.07%
Pyruvate carboxylase, mitochondrial	P11498	84.02%	52.72%	48.42%	72.71%		47.60%
Pyruvate kinase isozymes R/L	P30613		66.91%	60.74%			67.13%
Quinone oxidoreductase	Q08257		54.30%	56.51%			62.34%
Rab GDP dissociation inhibitor alpha	P31150	99.12%		57.55%			66.03%
Rab GDP dissociation inhibitor beta	P50395		74.85%	65.71%			76.39%
Ras GTPase-activating-like protein IQGAP2	Q13576			59.52%			
Receptor expression-enhancing protein 6	Q96HR9		80.60%	59.88%	85.52%		
Retinal dehydrogenase 1	P00352	97.40%	59.75%	55.09%	84.09%	84.25%	61.17%
Retinol dehydrogenase 16	O75452		63.16%	47.07%			
Ribonuclease UK114	P52758	90.90%	57.47%	47.12%	77.07%	72.55%	58.10%
Ribose-5-phosphate isomerase	P49247			8.50%			

Supplementary Table 2

Total fraction new at end of labeling period - % new (F)

	Fibrosis Score	Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011
		3	0	2	1	4	0
Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	O14983						32.75%
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	P16615						44.23%
Sarcosine dehydrogenase, mitochondrial	Q9UL12			49.87%		55.01%	
Selenium-binding protein 1	Q13228	100.13%	61.51%	49.31%	71.53%	68.26%	57.80%
Serine hydroxymethyltransferase, cytosolic	P34896		65.24%	54.48%			66.30%
Serine--pyruvate aminotransferase	P21549	97.20%	70.56%	64.00%	81.66%	88.47%	70.00%
Serum albumin	P02768	74.70%	42.28%	40.74%	64.77%	34.71%	43.65%
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	P45954		65.41%	66.79%	87.24%		72.42%
Short-chain specific acyl-CoA dehydrogenase, mitochondrial	P16219		50.51%	40.06%	71.11%		46.61%
Sideroflexin-1	Q9H9B4		46.26%	38.92%			
Sorbitol dehydrogenase	Q00796		60.02%	44.98%	81.07%	87.07%	63.64%
Spectrin alpha chain, brain	Q13813		70.25%	65.02%	90.36%		64.46%
Stress-70 protein, mitochondrial	P38646	111.66%	81.66%	80.74%	82.17%		87.68%
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	P31040	75.76%	51.06%	52.81%	81.00%	86.16%	58.93%
Succinate-semialdehyde dehydrogenase, mitochondrial	P51649		38.68%	40.82%			38.61%
Sulfotransferase 1A1	P50225			50.45%	77.33%	69.59%	62.08%
Superoxide dismutase [Cu-Zn]	P00441			77.04%			
Superoxide dismutase [Mn], mitochondrial	P04179	99.13%	48.74%	50.26%	76.52%	84.95%	61.84%
Talin-1	Q9Y490			6.22%			
Thioredoxin-dependent peroxide reductase, mitochondrial	P30048	94.12%	59.17%	63.42%	94.07%	73.70%	60.16%
Thiosulfate sulfurtransferase	Q16762	95.70%	61.43%	45.45%	83.71%		65.91%
Thymidine phosphorylase	P19971	103.48%	64.23%		81.03%	66.82%	66.87%

**Supplementary Table 2**

**Total fraction new at end of labeling period - % new (F)**

		Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011
	<b>Fibrosis Score</b>	<b>3</b>	<b>0</b>	<b>2</b>	<b>1</b>	<b>4</b>	<b>0</b>
Titin	Q8WZ42						28.12%
Transforming growth factor-beta-induced protein ig-h3	Q15582					103.62%	
Transgelin	Q01995					62.94%	
Transgelin-2	P37802					71.02%	
Transketolase	P29401		48.87%			47.36%	39.44%
Tricarboxylate transport protein, mitochondrial	P53007						55.27%
Trifunctional enzyme subunit alpha, mitochondrial	P40939	84.65%	44.90%	37.30%	74.26%	66.14%	46.94%
Trifunctional enzyme subunit beta, mitochondrial	P55084		47.70%	42.83%	78.34%		51.25%
Triosephosphate isomerase	P60174	86.29%	50.76%	41.19%	70.87%	58.56%	45.80%
Tripeptidyl-peptidase 1	O14773		54.05%	30.78%	69.24%	72.00%	
Tropomyosin alpha-1 chain	P09493				75.11%	50.45%	23.08%
Tropomyosin alpha-3 chain	P06753						29.78%
Tropomyosin alpha-4 chain	P67936					54.15%	
Tropomyosin beta chain	P07951						20.82%
Troponin C, slow skeletal and cardiac muscles	P63316						28.16%
Tubulin alpha-1A chain	Q71U36	88.66%	56.89%	43.86%	75.24%	66.14%	58.59%
Tubulin alpha-1B chain	P68363	75.74%	46.92%	40.63%	72.03%	58.64%	38.13%
Tubulin alpha-4A chain	P68366	108.81%	58.55%		95.15%		59.21%
Tubulin beta chain	P07437		66.06%	68.24%			
Tubulin beta-2A chain	Q13885	98.48%	73.68%	36.99%	64.56%	50.43%	46.89%
Tubulin beta-3 chain	Q13509						51.47%
Tubulin beta-4A chain	P04350		65.53%				
Ubiquitin-60S ribosomal protein L40	P62987	124.84%	93.91%	97.14%	94.16%	111.51%	93.48%
UDP-glucose 6-dehydrogenase	O60701		67.65%	54.40%			
UDP-glucuronosyltransferase 1-1	P22309		64.75%				
UDP-glucuronosyltransferase 1-10	Q9HAW8		52.52%				40.34%

Supplementary Table 2

Total fraction new at end of labeling period - % new (F)

		Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011
	<b>Fibrosis</b>						
	<b>Score</b>	<b>3</b>	<b>0</b>	<b>2</b>	<b>1</b>	<b>4</b>	<b>0</b>
UDP-glucuronosyltransferase 1-4	P22310		79.04%				
UDP-glucuronosyltransferase 2A1	Q9Y4X1			60.70%	73.50%		56.13%
UDP-glucuronosyltransferase 2B15	P54855			89.81%			
UDP-glucuronosyltransferase 2B4	P06133			44.70%			
UDP-glucuronosyltransferase 2B7	P16662	111.36%	68.99%	66.76%			95.86%
Urocanate hydratase	Q96N76			53.39%			
UTP--glucose-1-phosphate uridylyltransferase	Q16851	103.20%	61.15%	59.13%	86.37%	102.06%	66.56%
Very long-chain acyl-CoA synthetase	O14975	114.20%	74.30%	68.38%	89.92%		77.31%
Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	P49748			72.56%			67.33%
Vimentin	P08670	101.01%	63.80%	52.31%	93.73%	56.15%	57.56%
Vinculin	P18206		35.15%			35.94%	33.64%
Voltage-dependent anion-selective channel protein 1	P21796		49.24%				

Supplementary Table 2

		Fractional synthesis rate - % new per day (k)						Protein FSR vs Fibrosis Score (r <sup>2</sup> )
		Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011	
Fibrosis Score		3	0	2	1	4	0	
Liver Proteins		Uniprot Accession						
1,4-alpha-glucan-branching enzyme	Q04446			1.85%				
14-3-3 protein epsilon	P62258						6.13%	
14-3-3 protein eta	Q04917					1.92%	2.19%	
17-beta-hydroxysteroid dehydrogenase 13	Q7Z5P4		6.47%	7.85%	≥4.11%		6.44%	
17-beta-hydroxysteroid dehydrogenase type 6	O14756			4.93%	2.42%		6.39%	
2,4-dienoyl-CoA reductase, mitochondrial	Q16698	≥6.98%	3.27%	3.61%	3.37%		4.90%	
3-hydroxyacyl-CoA dehydratase 3	Q9P035			4.25%				
3-hydroxyacyl-CoA dehydrogenase type-2	Q99714	2.26%	2.52%	2.77%	1.32%		3.05%	
3-hydroxyanthranilate 3,4-dioxygenase	P46952			2.62%				
3-ketoacyl-CoA thiolase, mitochondrial	P42765	5.11%	2.88%	3.00%	2.72%	7.10%	3.68%	0.69
3-ketoacyl-CoA thiolase, peroxisomal	P09110	≥6.98%	6.57%	5.55%	3.35%	≥10.47%	5.48%	
3-mercaptopyruvate sulfurtransferase	P25325	≥6.98%	3.89%	3.90%	2.74%		4.17%	
40S ribosomal protein S7	P62081		5.55%	4.93%	4.03%		5.50%	
40S ribosomal protein S8	P62241	0.80%	0.27%	0.28%	0.82%	1.72%	0.44%	0.60
40S ribosomal protein SA	P08865	6.06%	3.56%	3.69%	2.42%	5.65%	3.71%	0.60
4-aminobutyrate aminotransferase, mitochondrial	P80404	≥6.98%	3.98%	3.28%	2.61%	≥10.47%	4.29%	
4-hydroxyphenylpyruvate dioxygenase	P32754		≥10.47%	7.56%			7.01%	
4-trimethylaminobutyraldehyde dehydrogenase	P49189		2.81%	2.99%				
60 kDa heat shock protein, mitochondrial	P10809	6.19%	3.19%	3.02%	2.37%		3.69%	
60S acidic ribosomal protein P0	P05388			3.68%				
60S ribosomal protein L6	Q02878	4.76%	3.27%	3.64%	2.03%	3.65%	3.62%	0.20
60S ribosomal protein L7	P18124	≥6.98%						
78 kDa glucose-regulated protein	P11021	≥6.98%	6.55%	4.91%	3.67%	≥10.47%	7.51%	
Abhydrolase domain-containing protein 14B	Q96IU4		6.87%					

Supplementary Table 2

		Fractional synthesis rate - % new per day (k)						Protein FSR vs Fibrosis Score (r <sup>2</sup> )
		Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011	
Fibrosis Score		3	0	2	1	4	0	
Acetyl-CoA acetyltransferase, cytosolic	Q9BWD1		3.33%	3.74%	2.00%		7.85%	
Acetyl-CoA acetyltransferase, mitochondrial	P24752	5.50%	3.41%	2.67%	2.76%	5.55%	3.30%	0.57
Aconitate hydratase, mitochondrial	Q99798		5.51%					
Actin, alpha skeletal muscle	P68133						0.47%	
Actin, aortic smooth muscle	P62736	≥6.98%	3.22%	3.36%	2.29%	2.15%	0.65%	
Actin, cytoplasmic 1	P60709	5.72%	3.73%	3.43%	2.41%	3.32%	3.78%	0.07
Acyl-coenzyme A synthetase ACSM2A, mitochondrial	Q08AH3		3.67%	3.80%				
Acyl-coenzyme A thioesterase 1	Q86TX2		4.22%				4.06%	
Adenylate kinase 2, mitochondrial	P54819		2.75%	3.52%				
ADP/ATP translocase 1	P12235		3.59%	5.84%	3.46%		3.75%	
Aflatoxin B1 aldehyde reductase member 3	O95154		6.59%					
Agmatinase, mitochondrial	Q9BSE5			2.05%				
Alanine aminotransferase 1	P24298			1.66%				
Alcohol dehydrogenase [NADP+]	P14550			5.71%				
Alcohol dehydrogenase 1A	P07327	≥6.98%	4.16%	2.88%	2.73%	5.53%	3.98%	
Alcohol dehydrogenase 1B	P00325	≥6.98%	4.00%	2.58%	2.42%	8.45%	4.10%	
Alcohol dehydrogenase 1C	P00326	≥6.98%	4.31%		3.29%		4.30%	
Alcohol dehydrogenase 4	P08319	≥6.98%	4.34%	3.15%	2.57%	9.10%	4.55%	
Alcohol dehydrogenase 6	P28332		2.87%	3.34%	2.15%		3.84%	
Alcohol dehydrogenase class-3	P11766		2.88%	1.95%				
Aldehyde dehydrogenase family 8 member A1	Q9H2A2		5.49%	4.08%			4.46%	
Aldehyde dehydrogenase X, mitochondrial	P30837	≥6.98%	4.30%		≥4.11%	≥10.47%	4.54%	
Aldehyde dehydrogenase, mitochondrial	P05091	≥6.98%	5.23%	4.69%	3.24%	≥10.47%	5.63%	
Aldehyde oxidase	Q06278		5.56%	6.37%	3.28%		5.03%	
Aldo-keto reductase family 1 member C1	Q04828		4.52%	3.14%	2.08%	9.84%	3.86%	
Aldo-keto reductase family 1 member C3	P42330			3.24%				
Aldo-keto reductase family 1 member C4	P17516			3.38%				
Alpha-1-antitrypsin	P01009		6.38%			≥10.47%	9.53%	

Supplementary Table 2

		Fractional synthesis rate - % new per day (k)						Protein FSR vs Fibrosis Score (r <sup>2</sup> )
		Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011	
Fibrosis Score		3	0	2	1	4	0	
Alpha-2-macroglobulin	P01023	5.78%	4.49%	3.97%	2.25%	6.10%	3.44%	0.52
Alpha-actinin-1	P12814	≥6.98%	6.06%		3.37%	5.19%	2.34%	
Alpha-actinin-2	P35609						1.20%	
Alpha-actinin-4	O43707	5.43%	4.02%	4.28%		4.05%	3.18%	
Alpha-enolase	P06733	≥6.98%	4.82%	2.75%	3.22%	≥10.47%	5.82%	
Amine oxidase [flavin-containing] A	P21397		2.76%	2.96%	2.09%			
Amine oxidase [flavin-containing] B	P27338	≥6.98%	2.97%	1.57%	3.15%			
Aminoacylase-1	Q03154		4.05%	3.52%	2.27%	≥10.47%	5.22%	
Annexin A1	P04083					5.36%		
Annexin A2	P07355		3.94%			3.69%	3.26%	
Annexin A4	P09525					10.33%		
Annexin A5	P08758		4.80%	5.12%	3.11%	6.73%	4.40%	
Annexin A6	P08133	≥6.98%	6.62%	6.40%	≥4.11%	9.85%	5.87%	
Apolipoprotein A-I	P02647					6.12%		
Apoptosis-inducing factor 1, mitochondrial	O95831		2.49%	1.61%	1.92%		2.38%	
Arginase-1	P05089	6.41%	3.62%	2.91%	2.28%		4.06%	
Argininosuccinate lyase	P04424	5.48%	3.83%	4.27%	1.88%	6.43%	4.06%	0.54
Argininosuccinate synthase	P00966		4.96%	3.49%	2.52%		6.28%	
Arylacetamide deacetylase	P22760						7.09%	
Aspartate aminotransferase, cytoplasmic	P17174	≥6.98%	4.53%	3.83%	3.26%		4.08%	
Aspartate aminotransferase, mitochondrial	P00505	5.09%	3.15%	2.87%	2.38%	5.73%	2.95%	0.70
ATP synthase subunit alpha, mitochondrial	P25705	≥6.98%	3.86%	3.73%	3.45%	6.42%	4.03%	
ATP synthase subunit b, mitochondrial	P24539		2.73%		2.21%			
ATP synthase subunit beta, mitochondrial	P06576	≥6.98%	3.05%	2.68%	3.02%	7.42%	3.23%	
ATP synthase subunit delta, mitochondrial	P30049				3.00%			
ATP synthase subunit f, mitochondrial	P56134		2.56%					
ATP synthase subunit O, mitochondrial	P48047	6.14%	2.50%	6.27%	1.57%		4.36%	
ATP-binding cassette sub-family D member 3	P28288		4.74%	4.28%	3.01%		6.93%	
Beta-actin-like protein 2	Q562R1			2.54%				

**Supplementary Table 2**

**Fractional synthesis rate - % new per day (k)**

		Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011	Protein FSR vs Fibrosis Score (r <sup>2</sup> )
	<b>Fibrosis Score</b>	<b>3</b>	<b>0</b>	<b>2</b>	<b>1</b>	<b>4</b>	<b>0</b>	
Beta-enolase	P13929						3.59%	
Betaine--homocysteine S-methyltransferase 1	Q93088	≥6.98%	4.70%	3.98%	2.93%		4.94%	
Betaine--homocysteine S-methyltransferase 2	Q9H2M3			4.49%			3.40%	
Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	Q3LXA3	≥6.98%	3.84%	3.93%	2.25%		4.05%	
Biglycan	P21810					1.80%		
Bile acid-CoA:amino acid N-acyltransferase	Q14032		4.08%	2.67%			6.38%	
Bile acyl-CoA synthetase	Q9Y2P5		6.26%	4.28%	3.42%		5.82%	
Bile salt sulfotransferase	Q06520	≥6.98%	4.43%	3.96%	3.19%		4.94%	
C-1-tetrahydrofolate synthase, cytoplasmic	P11586	3.90%	3.30%	2.67%	1.58%		4.21%	
Calcium-binding mitochondrial carrier protein Aralar1	O75746		2.87%		1.78%		3.33%	
Calcium-binding mitochondrial carrier protein Aralar2	Q9UJS0	6.12%	2.80%	2.13%	2.51%		3.60%	
Caldesmon	Q05682					7.57%		
Calmodulin	P62158					≥10.47%	10.61%	
Calnexin	P27824	≥6.98%	6.22%	5.14%			5.78%	
Calreticulin	P27797	≥6.98%	5.01%	4.77%	2.54%	8.55%	6.04%	
Calsequestrin-1	P31415						0.79%	
Carbamoyl-phosphate synthase [ammonia], mitochondrial	P31327	6.33%	2.95%	2.71%	2.63%	7.33%	3.40%	0.70
Carbonic anhydrase 1	P00915			1.54%		4.01%		
Carbonic anhydrase 2	P00918	6.76%	3.91%	3.06%	2.54%	6.09%	3.81%	0.49
Carbonic anhydrase 3	P07451				3.70%		1.20%	
Carbonyl reductase [NADPH] 1	P16152	≥6.98%	4.06%	3.73%	2.28%	6.68%	4.20%	
Catalase	P04040	≥6.98%	4.95%	5.37%	3.21%	7.67%	5.76%	
Cathepsin D	P07339	≥6.98%	5.22%	4.35%	3.63%	≥10.47%	6.59%	
Clathrin heavy chain 1	Q00610						5.03%	
Cocaine esterase	O00748		2.94%	2.08%				

**Supplementary Table 2**

		Fractional synthesis rate - % new per day (k)						Protein FSR vs Fibrosis Score (r <sup>2</sup> )
		Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011	
Fibrosis Score		3	0	2	1	4	0	
Cofilin-1	P23528			1.68%		7.14%		
Collagen alpha-1(I) chain	P02452	0.63%	0.20%	0.39%	0.23%	0.56%	0.32%	0.79
Collagen alpha-1(III) chain	P02461	0.59%	0.25%	0.24%	0.18%	0.42%	0.33%	0.38
Collagen alpha-1(IV) chain	P02462			0.09%		0.93%		
Collagen alpha-1(VI) chain	P12109	1.30%	0.82%	0.95%	0.75%	1.14%	0.88%	0.66
Collagen alpha-1(XIV) chain	Q05707					2.19%		
Collagen alpha-2(I) chain	P08123	0.66%	0.41%	0.49%	0.24%	0.56%	0.42%	0.48
Collagen alpha-3(VI) chain	P12111	1.00%	1.28%	0.66%	0.52%	0.94%	1.02%	0.04
Complement C3	P01024		≥10.47%		3.04%			
Complement C4-A	P0C0L4		7.83%					
Corticosteroid 11-beta-dehydrogenase isozyme 1	P28845		7.09%					
Creatine kinase M-type	P06732						0.85%	
Creatine kinase S-type, mitochondrial	P17540						2.43%	
Cullin-associated NEDD8-dissociated protein 1	Q86VP6		3.20%	3.22%				
Cystathionine gamma-lyase	P32929	≥6.98%	6.38%	4.10%	≥4.11%		5.28%	
Cytochrome b5	P00167	≥6.98%	4.83%	4.23%	3.37%	10.23%	5.40%	
Cytochrome b-c1 complex subunit 2, mitochondrial	P22695						4.04%	
Cytochrome c oxidase subunit 2	P00403	5.82%	3.90%	2.84%	≥4.11%	7.70%	3.82%	
Cytochrome c oxidase subunit 5A, mitochondrial	P20674		2.50%	2.15%	1.88%		2.59%	
Cytochrome P450 1A2	P05177		6.02%		1.88%			
Cytochrome P450 2A6	P11509		≥10.47%					
Cytochrome P450 2C8	P10632		≥10.47%	≥11.51%				
Cytochrome P450 2C9	P11712	≥6.98%	8.33%	4.98%	3.51%		7.87%	
Cytochrome P450 2E1	P05181				3.46%			
Cytochrome P450 3A4	P08684			7.08%				
Cytochrome P450 3A5	P20815		6.66%		2.53%	≥10.47%	7.08%	

**Supplementary Table 2**

		Fractional synthesis rate - % new per day (k)						Protein FSR vs Fibrosis Score (r <sup>2</sup> )
		Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011	
Fibrosis Score		3	0	2	1	4	0	
Cytoplasmic aconitate hydratase	P21399		4.29%	3.76%	2.97%			
Cytosol aminopeptidase	P28838		5.07%				6.42%	
Cytosolic 10-formyltetrahydrofolate dehydrogenase	O75891		3.48%	4.70%	≥4.11%		4.13%	
Cytosolic non-specific dipeptidase	Q96KP4	3.75%	3.85%	1.86%			7.86%	
D-beta-hydroxybutyrate dehydrogenase, mitochondrial	Q02338	≥6.98%	3.01%	4.26%			3.52%	
D-dopachrome decarboxylase	P30046		4.21%	3.26%	3.02%	7.61%	4.45%	
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	Q13011	6.46%	3.14%		2.48%	6.05%	4.04%	
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	P30038	≥6.98%	3.66%	3.55%	3.23%	3.11%	4.29%	
Delta-aminolevulinic acid dehydratase	P13716			2.33%				
Desmin	P17661					4.36%	4.60%	
Dihydropyrimidinase	Q14117			4.85%	≥4.11%		5.75%	
Dimethylaniline monooxygenase [N-oxide-forming] 3	P31513		5.42%	4.00%	2.70%			
Dimethylglycine dehydrogenase, mitochondrial	Q9UI17		3.06%	4.94%				
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	P04843	6.82%	3.23%		2.16%			
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	P04844		4.90%	3.96%	2.51%		3.89%	
Elastin	P15502					0.37%		
Electron transfer flavoprotein subunit alpha, mitochondrial	P13804	6.93%	3.11%	3.08%	2.54%	6.87%	3.27%	0.71
Electron transfer flavoprotein subunit beta	P38117	3.37%	3.01%	2.79%	3.41%		4.30%	
Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	Q16134		5.26%	4.53%			6.95%	

**Supplementary Table 2**

		Fractional synthesis rate - % new per day (k)						Protein FSR vs Fibrosis Score (r <sup>2</sup> )
		Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011	
Fibrosis Score		3	0	2	1	4	0	
Elongation factor 1-alpha 1	P68104	≥6.98%	4.39%	4.09%	2.09%	6.76%	3.81%	
Elongation factor 2	P13639		8.68%	6.94%				
Endoplasmic	P14625	≥6.98%	6.01%	5.32%	3.78%	≥10.47%	7.14%	
Enoyl-CoA hydratase domain-containing protein 2, mitochondrial	Q86YB7		3.47%	4.35%	≥4.11%		7.76%	
Enoyl-CoA hydratase, mitochondrial	P30084	6.06%	2.71%	2.71%	2.29%	5.88%	3.20%	0.67
Epoxide hydrolase 1	P07099	≥6.98%	4.61%	3.75%	3.11%	9.09%	5.18%	
Epoxide hydrolase 2	P34913		5.10%	3.73%	2.94%		6.35%	
Ester hydrolase C11orf54	Q9H0W9		3.61%	5.69%				
Estradiol 17-beta-dehydrogenase 11	Q8NBQ5			4.96%				
Fatty acid synthase	P49327	≥6.98%	9.13%	≥11.51%	2.82%		8.19%	
Fatty acid-binding protein, liver	P07148	≥6.98%	6.04%	3.23%	2.74%	8.22%	4.26%	
Ferritin light chain	P02792	≥6.98%	5.53%	7.45%	3.25%	≥10.47%	5.02%	
Fibronectin	P02751	≥6.98%	4.26%			7.76%	7.77%	
Filamin-A	P21333				≥4.11%	3.51%	7.70%	
Filamin-B	O75369			4.67%				
Filamin-C	Q14315						1.46%	
Flavin reductase (NADPH)	P30043		3.48%	3.94%	2.14%		5.03%	
Formimidoyltransferase-cyclodeaminase	O95954	≥6.98%	4.42%	3.93%	2.94%	9.32%	4.36%	
Fructose-1,6-bisphosphatase 1	P09467	≥6.98%	5.22%	3.69%	3.62%	7.44%	5.01%	
Fructose-bisphosphate aldolase A	P04075						2.60%	
Fructose-bisphosphate aldolase B	P05062	≥6.98%	6.71%	5.38%	3.31%	≥10.47%	6.47%	
Fumarate hydratase, mitochondrial	P07954		3.20%	3.03%	2.60%		3.40%	
Fumarylacetoacetase	P16930	6.95%	3.79%	2.80%	2.22%	5.44%	3.31%	0.43
Galactokinase	P51570		3.17%	2.73%			3.41%	
Galectin-1	P09382					4.05%	4.50%	
Gamma-glutamyltransferase 5	P36269	≥6.98%		4.37%		4.26%		
Gelsolin	P06396		3.93%	5.21%				
Glucose-6-phosphate isomerase	P06744	4.49%	3.35%	3.02%	2.54%	5.84%	3.35%	0.62

**Supplementary Table 2**

		Fractional synthesis rate - % new per day (k)						Protein FSR vs Fibrosis Score (r <sup>2</sup> )
		Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011	
Fibrosis Score		3	0	2	1	4	0	
Glutamate dehydrogenase 1, mitochondrial	P00367	6.24%	2.62%	2.42%	2.62%		2.71%	
Glutathione S-transferase A1	P08263	≥6.98%	3.99%	2.68%	2.45%	9.25%	4.08%	
Glutathione S-transferase kappa 1	Q9Y2Q3		5.17%				6.51%	
Glutathione S-transferase Mu 1	P09488	≥6.98%		3.71%	1.93%		5.01%	
Glutathione S-transferase omega-1	P78417			2.21%				
Glyceraldehyde-3-phosphate dehydrogenase	P04406	≥6.98%	4.12%	3.49%	2.80%	4.67%	3.33%	
Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic	P21695		4.19%	3.11%				
Glycine amidinotransferase, mitochondrial	P50440	≥6.98%	5.47%	5.72%	3.03%	≥10.47%	5.26%	
Glycine dehydrogenase [decarboxylating], mitochondrial	P23378			0.87%				
Glycogen debranching enzyme	P35573			1.11%			2.11%	
Glycogen phosphorylase, brain form	P11216						2.26%	
Glycogen phosphorylase, liver form	P06737	4.28%	2.89%	1.80%	1.66%		1.85%	
Glycogen phosphorylase, muscle form	P11217						1.48%	
Glyoxylate reductase/hydroxypyruvate reductase	Q9UBQ7	6.29%	3.83%	3.10%	2.39%	6.48%	3.83%	0.55
Heat shock 70 kDa protein 1A/1B	P08107		6.01%	5.90%		5.89%	4.30%	
Heat shock cognate 71 kDa protein	P11142		7.48%		4.10%			
Heat shock protein beta-1	P04792	≥6.98%	5.36%	5.05%	2.93%	6.61%	4.20%	
Heat shock-related 70 kDa protein 2	P54652			4.50%	3.82%		8.35%	
Hemoglobin subunit alpha	P69905	1.10%	0.49%	0.65%	0.83%	2.36%	0.60%	0.72
Hemoglobin subunit beta	P68871	1.04%	0.46%	0.34%	0.89%	2.09%	0.74%	0.55
Hemoglobin subunit delta	P02042	1.52%	1.03%	1.49%	1.40%	3.24%	1.14%	0.70
Hemoglobin subunit gamma-1	P69891			0.85%				
Heterogeneous nuclear ribonucleoprotein K	P61978	≥6.98%	6.79%	11.01%		≥10.47%		
Histone H2A type 1-A	Q96QV6		2.01%	1.40%	1.31%	1.64%	1.61%	
Histone H2A type 1-B/E	P04908	2.40%	1.42%	0.55%	0.97%	1.27%	1.09%	0.09
Histone H2B type 1-A	Q96A08					1.36%		

**Supplementary Table 2**

		Fractional synthesis rate - % new per day (k)						Protein FSR vs Fibrosis Score (r <sup>2</sup> )
		Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011	
Fibrosis Score		3	0	2	1	4	0	
Histone H2B type 1-B	P33778	2.42%	1.44%	0.98%	1.15%	1.08%	1.27%	0.03
Histone H3.1t	Q16695	1.07%	0.95%	0.33%	0.45%	0.57%	0.50%	0.00
Histone H3.3	P84243	1.20%	0.61%	0.81%	0.42%	0.54%	0.74%	0.07
Histone H4	P62805	1.78%	0.97%	0.75%	0.75%	1.12%	1.00%	0.22
HLA class I histocompatibility antigen, A-1 alpha chain	P30443	≥6.98%						
HLA class I histocompatibility antigen, A-25 alpha chain	P18462	≥6.98%						
Homogentisate 1,2-dioxygenase	Q93099			2.54%	≥4.11%		6.67%	
Hydroxyacid oxidase 1	Q9UJM8	≥6.98%	6.28%	7.10%	≥4.11%		6.26%	
Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	Q16836	6.72%	2.60%	2.56%	2.29%	4.46%	2.71%	0.48
Hydroxymethylglutaryl-CoA synthase, cytoplasmic	Q01581			4.94%	≥4.11%		6.29%	
Hydroxymethylglutaryl-CoA synthase, mitochondrial	P54868	≥6.98%	4.84%	4.96%	3.30%	≥10.47%	4.99%	
Ig alpha-1 chain C region	P01876					5.99%		
Ig gamma-1 chain C region	P01857	3.37%	3.91%	1.00%	1.78%	3.00%	3.05%	0.01
Ig gamma-2 chain C region	P01859					2.46%		
Ig heavy chain V-III region BRO	P01766					4.10%		
Ig kappa chain C region	P01834	3.02%	3.36%	1.63%	1.20%	2.96%	1.97%	0.06
Ig lambda-2 chain C regions	P0CG05					3.91%		
Immunoglobulin lambda-like polypeptide 5	B9A064		3.81%			4.38%		
Isochorismatase domain-containing protein 2, mitochondrial	Q96AB3	4.56%	2.37%	2.22%	1.05%		3.05%	
Isocitrate dehydrogenase [NADP] cytoplasmic	O75874	≥6.98%	3.75%	3.62%	2.90%		3.49%	
Isocitrate dehydrogenase [NADP], mitochondrial	P48735	5.02%	1.97%	2.85%		4.28%	2.76%	
Keratin, type I cytoskeletal 10	P13645				0.23%			

**Supplementary Table 2**

		Fractional synthesis rate - % new per day (k)						Protein FSR vs Fibrosis Score (r <sup>2</sup> )
		Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011	
<b>Fibrosis Score</b>		<b>3</b>	<b>0</b>	<b>2</b>	<b>1</b>	<b>4</b>	<b>0</b>	
Keratin, type I cytoskeletal 18	P05783	≥6.98%	4.08%	3.69%	2.86%	6.19%	4.79%	
Keratin, type II cytoskeletal 1	P04264				0.06%			
Keratin, type II cytoskeletal 2 epidermal	P35908				0.40%			
Keratin, type II cytoskeletal 7	P08729					≥10.47%		
Keratin, type II cytoskeletal 8	P05787	≥6.98%	5.10%	3.44%	3.45%	8.04%	6.37%	
Ketohexokinase	P50053			-0.18%				
Lambda-crystallin homolog	Q9Y2S2			2.20%				
Leukotriene-B(4) omega-hydroxylase 1	P78329		6.89%					
Liver carboxylesterase 1	P23141	≥6.98%	4.36%	4.05%	3.20%	≥10.47%	5.31%	
L-lactate dehydrogenase A-like 6B	Q9BYZ2		4.45%	3.82%	2.76%		2.96%	
Long-chain-fatty-acid--CoA ligase 1	P33121	3.59%	5.19%	5.45%	2.46%		4.56%	
Lumican	P51884					3.88%	1.57%	
L-xylulose reductase	Q7Z4W1	≥6.98%	3.51%	3.73%	2.79%	6.37%	4.39%	
Malate dehydrogenase, cytoplasmic	P40925		3.66%	2.88%	1.58%		3.59%	
Malate dehydrogenase, mitochondrial	P40926	5.57%	2.64%	3.16%	2.14%	4.79%	2.62%	0.71
Maleylacetoacetate isomerase	O43708		2.86%	2.34%			2.95%	
Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	P11310	≥6.98%	4.45%	7.49%	3.91%		7.40%	
Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	Q02252		3.81%	3.06%	2.40%		4.30%	
Microfibril-associated glycoprotein 4	P55083					0.86%		
Microsomal glutathione S-transferase 1	P10620	4.83%	3.14%	2.53%	2.22%	5.07%	3.38%	0.49
Microsomal triglyceride transfer protein large subunit	P55157	≥6.98%	5.81%	5.06%	≥4.11%		≥10.96%	
Mimecan	P20774					0.80%		
Mitochondrial carrier homolog 2	Q9Y6C9		3.07%	3.46%	2.32%		3.56%	
Moesin	P26038					≥10.47%		
Myoglobin	P02144						0.89%	
Myomesin-2	P54296						1.12%	

Supplementary Table 2

		Fractional synthesis rate - % new per day (k)						Protein FSR vs Fibrosis Score (r <sup>2</sup> )
		Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011	
Fibrosis Score		3	0	2	1	4	0	
Myosin light chain 1/3, skeletal muscle isoform	P05976						0.84%	
Myosin light chain 3	P08590						0.43%	
Myosin light chain 6B	P14649					6.71%	3.24%	
Myosin light polypeptide 6	P60660		6.40%	6.32%	2.41%	5.24%	6.37%	
Myosin regulatory light chain 2, skeletal muscle isoform	Q96A32						1.14%	
Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	P10916						0.96%	
Myosin-1	P12882						1.06%	
Myosin-10	P35580					6.05%		
Myosin-11	P35749					3.44%		
Myosin-13	Q9UKX3						0.70%	
Myosin-2	Q9UKX2						1.40%	
Myosin-6	P13533		-0.95%		0.09%		1.01%	
Myosin-7	P12883						1.11%	
Myosin-9	P35579	≥6.98%	7.64%	7.83%	3.29%	5.84%	6.57%	
Myosin-binding protein C, slow-type	Q00872						2.69%	
Myozenin-1	Q9NP98						1.59%	
NAD kinase domain-containing protein 1	Q4G0N4			0.44%				
NAD(P) transhydrogenase, mitochondrial	Q13423		1.86%	1.97%				
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	Q9P0J0				2.48%			
NADPH--cytochrome P450 reductase	P16435		≥10.47%					
Neutral alpha-glucosidase AB	Q14697			3.28%				
Nicotinate phosphoribosyltransferase	Q6XQN6			2.94%				
Nucleophosmin	P06748		3.09%	2.46%				
Nucleoside diphosphate kinase A	P15531		4.25%			6.15%		
Omega-amidase NIT2	Q9NQR4				2.29%			
Ornithine carbamoyltransferase, mitochondrial	P00480		3.53%	2.40%	3.26%		3.93%	

**Supplementary Table 2**

		Fractional synthesis rate - % new per day (k)						Protein FSR vs Fibrosis Score (r <sup>2</sup> )
		Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011	
Fibrosis Score		3	0	2	1	4	0	
Peptidyl-prolyl cis-trans isomerase A	P62937			≥11.51%		9.94%	7.84%	
Peroxiredoxin-1	Q06830	≥6.98%	4.94%	3.59%			6.64%	
Peroxiredoxin-2	P32119	4.12%	2.77%	2.69%	2.02%		3.34%	
Peroxiredoxin-4	Q13162	≥6.98%	6.41%	4.53%	3.20%			
Peroxiredoxin-5, mitochondrial	P30044			3.19%				
Peroxiredoxin-6	P30041	≥6.98%	4.47%	3.39%	2.26%	6.42%	3.83%	
Peroxisomal acyl-coenzyme A oxidase 2	Q99424				0.41%			
Peroxisomal bifunctional enzyme	Q08426	≥6.98%	5.07%	5.67%	3.55%	≥10.47%	6.28%	
Peroxisomal membrane protein 2	Q9NR77				≥4.11%			
Peroxisomal multifunctional enzyme type 2	P51659	≥6.98%	5.49%	6.04%	≥4.11%		5.50%	
Peroxisomal sarcosine oxidase	Q9P0Z9	3.11%	3.48%	4.44%	3.50%		4.55%	
Peroxisomal trans-2-enoyl-CoA reductase	Q9BY49		2.54%	3.47%				
Phenazine biosynthesis-like domain-containing protein	P30039		2.17%	2.59%				
Phosphate carrier protein, mitochondrial	Q00325	6.07%	3.88%	3.08%	2.38%	5.10%	3.07%	0.47
Phosphatidylethanolamine-binding protein 1	P30086	≥6.98%	4.24%	3.60%	2.89%	8.03%	4.33%	
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	Q16822	5.56%	3.89%	3.46%	2.44%	6.81%	4.07%	0.56
Phosphoenolpyruvate carboxykinase, cytosolic [GTP]	P35558		4.60%	4.93%	3.09%			
Phosphoglucomutase-1	P36871	≥6.98%	3.56%	2.88%	2.87%		3.79%	
Phosphoglycerate kinase 1	P00558	≥6.98%	3.95%	2.28%	2.06%	4.72%	2.45%	
Phosphoglycerate mutase 1	P18669	≥6.98%	4.01%	1.93%	2.26%	5.82%	2.38%	
Polypyrimidine tract-binding protein 1	P26599		3.95%					
Prelamin-A/C	P02545	0.17%	2.09%	1.31%	1.19%	5.03%	1.56%	0.17
Profilin-1	P07737		9.83%	8.10%	3.84%	≥10.47%	9.82%	
Prohibitin	P35232	≥6.98%	3.06%	3.64%	3.59%	≥10.47%	4.14%	
Prohibitin-2	Q99623	3.77%	2.80%	2.69%	2.27%	0.93%	3.33%	0.21
Prolargin	P51888					2.24%		

**Supplementary Table 2**

		Fractional synthesis rate - % new per day (k)						Protein FSR vs Fibrosis Score (r <sup>2</sup> )
		Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011	
Fibrosis Score		3	0	2	1	4	0	
Proline dehydrogenase 1, mitochondrial	O43272					1.09%		
Prostaglandin reductase 1	Q14914	5.73%	3.80%	3.11%	1.98%	7.03%		
Proteasome activator complex subunit 1	Q06323		6.21%					
Proteasome activator complex subunit 2	Q9UL46		5.60%	4.36%			5.90%	
Protein CutA	O60888			0.40%				
Protein disulfide-isomerase	P07237	≥6.98%	5.72%	5.25%	3.58%	≥10.47%	6.94%	
Protein disulfide-isomerase A3	P30101		5.77%	10.50%	3.31%		7.49%	
Protein disulfide-isomerase A4	P13667		6.18%	4.47%			4.38%	
Protein disulfide-isomerase A6	Q15084	≥6.98%	5.00%	4.88%	2.67%	≥10.47%	5.97%	
Protein DJ-1	Q99497		4.29%	4.33%			3.83%	
Protein NipSnap homolog 1	Q9BPW8		3.09%	3.66%	3.17%		4.72%	
Protein NYNRIN	Q9P2P1	5.79%		2.68%				
Protein-glutamine gamma-glutamyltransferase 2	P21980	≥6.98%	6.00%	4.16%	3.89%	7.26%	5.49%	
Pterin-4-alpha-carbinolamine dehydratase	P61457			3.37%				
Putative beta-actin-like protein 3	Q9BYX7	4.39%	2.66%	2.61%	1.67%	2.74%	1.59%	0.35
Putative inactive carboxylesterase 4	Q9UKY3	≥6.98%	5.21%	4.89%	3.65%	≥10.47%	5.59%	
Pyruvate carboxylase, mitochondrial	P11498	5.56%	3.41%	3.31%	2.32%		3.08%	
Pyruvate kinase isozymes R/L	P30613		5.03%	4.67%			5.30%	
Quinone oxidoreductase	Q08257		3.56%	4.16%			4.65%	
Rab GDP dissociation inhibitor alpha	P31150	≥6.98%		4.28%			5.14%	
Rab GDP dissociation inhibitor beta	P50395		6.27%	5.35%			6.87%	
Ras GTPase-activating-like protein IQGAP2	Q13576			4.52%				
Receptor expression-enhancing protein 6	Q96HR9		7.45%	4.57%	3.45%			
Retinal dehydrogenase 1	P00352	≥6.98%	4.14%	4.00%	3.28%	8.40%	4.51%	
Retinol dehydrogenase 16	O75452		4.54%	3.18%				
Ribonuclease UK114	P52758	≥6.98%	3.89%	3.19%	2.63%	5.88%	4.14%	
Ribose-5-phosphate isomerase	P49247			0.44%				

**Supplementary Table 2**

		Fractional synthesis rate - % new per day (k)						Protein FSR vs Fibrosis Score (r <sup>2</sup> )
		Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011	
Fibrosis Score		3	0	2	1	4	0	
Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	O14983						1.89%	
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	P16615						2.78%	
Sarcosine dehydrogenase, mitochondrial	Q9UL12			3.45%		3.63%		
Selenium-binding protein 1	Q13228	≥6.98%	4.34%	3.40%	2.24%	5.22%	4.11%	
Serine hydroxymethyltransferase, cytosolic	P34896		4.80%	3.94%			5.18%	
Serine--pyruvate aminotransferase	P21549	≥6.98%	5.56%	5.11%	3.03%	9.82%	5.73%	
Serum albumin	P02768	4.16%	2.50%	2.62%	1.86%	1.94%	2.73%	0.02
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	P45954		4.83%	5.51%	3.68%		6.13%	
Short-chain specific acyl-CoA dehydrogenase, mitochondrial	P16219		3.20%	2.56%	2.22%		2.99%	
Sideroflexin-1	Q9H9B4		2.82%	2.46%				
Sorbitol dehydrogenase	Q00796		4.17%	2.99%	2.97%	9.30%	4.82%	
Spectrin alpha chain, brain	Q13813		5.51%	5.25%	≥4.11%		4.93%	
Stress-70 protein, mitochondrial	P38646	≥6.98%	7.71%	8.24%	3.08%		9.97%	
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	P31040	4.29%	3.25%	3.76%	2.97%	8.99%	4.24%	0.55
Succinate-semialdehyde dehydrogenase, mitochondrial	P51649		2.22%	2.62%			2.32%	
Sulfotransferase 1A1	P50225			3.51%	2.65%	5.41%	4.62%	
Superoxide dismutase [Cu-Zn]	P00441			7.36%				
Superoxide dismutase [Mn], mitochondrial	P04179	≥6.98%	3.04%	3.49%	2.59%	8.61%	4.59%	
Talin-1	Q9Y490			0.32%				
Thioredoxin-dependent peroxide reductase, mitochondrial	P30048	≥6.98%	4.07%	5.03%	≥4.11%	6.07%	4.38%	
Thiosulfate sulfurtransferase	Q16762	≥6.98%	4.33%	3.03%	3.24%		5.12%	
Thymidine phosphorylase	P19971	≥6.98%	4.67%		2.97%	5.01%	5.26%	

**Supplementary Table 2**

		Fractional synthesis rate - % new per day (k)						Protein FSR vs Fibrosis Score (r <sup>2</sup> )
		Subject #003	Subject #004	Subject #005	Subject #007	Subject #009	Subject #011	
	Fibrosis Score	3	0	2	1	4	0	
Titin	Q8WZ42						1.57%	
Transforming growth factor-beta-induced protein ig- h3	Q15582					≥10.47%		
Transgelin	Q01995					4.51%		
Transgelin-2	P37802					5.63%		
Transketolase	P29401		3.05%			2.92%	2.39%	
Tricarboxylate transport protein, mitochondrial	P53007						3.83%	
Trifunctional enzyme subunit alpha, mitochondrial	P40939	5.68%	2.71%	2.33%	2.42%	4.92%	3.02%	0.56
Trifunctional enzyme subunit beta, mitochondrial	P55084		2.95%	2.80%	2.73%		3.42%	
Triosephosphate isomerase	P60174	6.02%	3.22%	2.65%	2.20%	4.00%	2.92%	0.34
Tripeptidyl-peptidase 1	O14773		3.53%	1.84%	2.11%	5.79%		
Tropomyosin alpha-1 chain	P09493				2.48%	3.19%	1.25%	
Tropomyosin alpha-3 chain	P06753						1.68%	
Tropomyosin alpha-4 chain	P67936					3.54%		
Tropomyosin beta chain	P07951						1.11%	
Troponin C, slow skeletal and cardiac muscles	P63316						1.57%	
Tubulin alpha-1A chain	Q71U36	6.60%	3.83%	2.89%	2.49%	4.92%	4.20%	0.26
Tubulin alpha-1B chain	P68363	4.29%	2.88%	2.61%	2.28%	4.01%	2.29%	0.66
Tubulin alpha-4A chain	P68366	≥6.98%	4.00%		≥4.11%		4.27%	
Tubulin beta chain	P07437		4.91%	5.73%				
Tubulin beta-2A chain	Q13885	≥6.98%	6.07%	2.31%	1.85%	3.19%	3.01%	
Tubulin beta-3 chain	Q13509						3.44%	
Tubulin beta-4A chain	P04350		4.84%					
Ubiquitin-60S ribosomal protein L40	P62987	≥6.98%	≥10.47%	≥11.51%	≥4.11%	≥10.47%	≥10.96%	
UDP-glucose 6-dehydrogenase	O60701		5.13%	3.93%				
UDP-glucuronosyltransferase 1-1	P22309		4.74%					
UDP-glucuronosyltransferase 1-10	Q9HAW8		3.39%				2.46%	

**Supplementary Table 2**

**Fractional synthesis rate - % new per day (k)**

		<b>Subject #003</b>	<b>Subject #004</b>	<b>Subject #005</b>	<b>Subject #007</b>	<b>Subject #009</b>	<b>Subject #011</b>	<b>Protein FSR vs Fibrosis Score (r<sup>2</sup>)</b>
	<b>Fibrosis Score</b>	<b>3</b>	<b>0</b>	<b>2</b>	<b>1</b>	<b>4</b>	<b>0</b>	
UDP-glucuronosyltransferase 1-4	P22310		7.10%					
UDP-glucuronosyltransferase 2A1	Q9Y4X1			4.67%	2.37%		3.92%	
UDP-glucuronosyltransferase 2B15	P54855			11.42%				
UDP-glucuronosyltransferase 2B4	P06133			2.96%				
UDP-glucuronosyltransferase 2B7	P16662	≥6.98%	5.32%	5.51%			≥10.96%	
Urocanate hydratase	Q96N76			3.82%				
UTP--glucose-1-phosphate uridylyltransferase	Q16851	≥6.98%	4.30%	4.47%	3.56%	≥10.47%	5.22%	
Very long-chain acyl-CoA synthetase	O14975	≥6.98%	6.18%	5.76%	4.10%		7.06%	
Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	P49748			6.47%			5.33%	
Vimentin	P08670	≥6.98%	4.62%	3.70%	≥4.11%	3.75%	4.08%	
Vinculin	P18206		1.97%			2.02%	1.95%	
Voltage-dependent anion-selective channel protein 1	P21796		3.08%					