

Table S1. Measurement of physical capacity and functional tests of muscle strength, and pressure pain threshold (PPT) as a measure of pain sensitivity before (baseline) and after (post) 15 weeks of resistance exercise in fibromyalgia (FM) patients and healthy controls (CON). Data are presented as mean \pm 1 standard deviation (SD).

Variables	CON Baseline <i>n</i> = 28	FM Baseline <i>n</i> = 26	FM vs CON Baseline P-value	CON Post Exercise <i>n</i> = 26	FM Post Exercise <i>n</i> = 25	FM vs CON Post Exercise P-Value	FM Baseline vs Post Exercise P-value
	Physical capacity						
6-minute walking test (meter)	626.3 (\pm 59.6)	566 (\pm 73.4)	0.001	650 (\pm 52.7)	571.4 (\pm 65.3)	<0.001	0.192
Knee extension right (Steve Strong), (kg))	378.5 (\pm 86.9)	323.8 (\pm 85.5)	0.021	394.5 (\pm 70.2)	351.4 (\pm 105)	0.89	0.101
Knee extension left (Steve Strong), (kg))	351.5 (\pm 80.3)	314.2 (\pm 96)	0.134	360.3 (\pm 66.0)	351.5 (\pm 90.7)	0.693	0.029
Handgrip fore Max Right (Grippit, (N))	262.5 (\pm 35.5)	175.2 (\pm 69.9)	<0.001	277.3 (\pm 42.7)	214.4 (\pm 61.7)	<0.001	0.005
Handgrip fore Max left (Grippit, (N))	239.5 (\pm 43.9)	180.3 (\pm 65.9)	<0.001	256.2 (\pm 45.0)	206.5 (\pm 61.4)	0.002	0.037
Elbow flexion right (Isobex, (kg))	17.2 (\pm 4.4)	12.2 (\pm 4.2)	<0.001	17.6 (\pm 4.1)	14.9 (\pm 4.8)	0.035	0.001
Elbow flexion Left (Isobex (kg))	16.7 (\pm 4.0)	12.4 (\pm 4.5)	<0.001	17.1 (\pm 2.8)	14.5 (\pm 4.9)	0.024	0.012
Location measured PPT	Pressure pain thresholds (PPT)						
Supraspinatus right	327.8 (\pm 119.3)	190.4 (\pm 97.9)	<0.001	299.7 (\pm 102.4)	214.5 (\pm 86.1)	<0.001	0.166
Supraspinatus left	310.0 (\pm 112)	201.2 (\pm 95.6)	<0.001	314.1 (\pm 86.5)	196.2 (\pm 110.7)	<0.001	0.764
Vastus lateralis right	246.3 (\pm 105.2)	136.3 (\pm 72.4)	<0.001	267.3 (\pm 112.4)	156.9 (\pm 84.5)	<0.001	0.270
Vastus lateralis left	272.1 (\pm 104.4)	147.5 (\pm 100.3)	<0.001	255.4 (\pm 106.4)	151.3 (\pm 86.9)	<0.001	0.778
Gluteus right	369.1 (\pm 133.9)	199.3 (\pm 125.1)	<0.001	601.0 (\pm 1131)	211.2 (\pm 132)	<0.001	0.778
Gluteus left	397.0 (\pm 113.5)	203.9 (\pm 106.9)	<0.001	404.9 (\pm 182.3)	245.6 (\pm 166.7)	<0.001	0.271
Knee right	363.6 (\pm 163.3)	168.8 (\pm 84.7)	<0.001	346.8 (\pm 167.0)	180.5 (\pm 116.3)	<0.001	0.677
Knee left	349.4 (\pm 158.5)	167.0 (\pm 88.4)	<0.001	340.7 (\pm 149.7)	184.0 (\pm 116.3)	<0.001	0.382
Mean PPT right side	326.7 (\pm 106.8)	173.7 (\pm 80.2)	<0.001	378.7 (\pm 318.9)	190.8 (\pm 92.7)	0.007	0.412
Mean PPT left side	332.1 (\pm 95.7)	178.6 (\pm 95.7)	<0.001	328.7 (\pm 111.5)	194.3 (\pm 96.9)	<0.001	0.581

Table S2. Identified biological processes from STRING analysis tool (version 11.0). Bold marked biological processes are visualized in the protein-protein network in Figure 3.

#Term ID	Term Description	Observed Gene Count	Back-ground Gene Count	FDR	Matching Proteins in Your Network (Labels)
GO:0003012	muscle system process	9	291	6.09×10^{-8}	ACTA1,GSN,MYH7,MYOM1,MYOT,NEB, SMPX,TPM2,TTN
GO:0002576	platelet degranulation	7	129	1.45×10^{-7}	APOA1,FGA,FGB,KNG1,ORM2,PLG,TTN
GO:0006936	muscle contraction	8	244	1.91×10^{-7}	ACTA1,MYH7,MYOM1,MYOT, NEB,SMPX,TPM2,TTN
GO:0030049	muscle filament sliding	5	38	5.72×10^{-7}	ACTA1,MYH7,NEB,TPM2,TTN
GO:0003008	system process	14	1827	7.31×10^{-7}	ACTA1,FGA,FGB,GSN,KNG1,MYH7,MYOM1, MYOT,NEB,RBP4,SMPX,SYNPO,TPM2,TTN
GO:0072376	protein activation cascade	5	74	7.43×10^{-5}	C3,C4A,FGA,FGB,KNG1
GO:0045055	regulated exocytosis	9	691	1.19×10^{-5}	APOA1,C3,FGA,FGB,GSN,KNG1,ORM2, PLG,TTN
GO:0030029	actin filament-based process	8	493	1.23×10^{-5}	ACTA1,GSN,MYH7,MYOM1,MYOZ1,NEB, TPM2,TTN
GO:0050714	positive regulation of protein secretion	6	240	4.38×10^{-5}	FGA,FGB,MYOM1,ORM2,RBP4,TTN
GO:0030195	negative regulation of blood coagulation	4	48	4.46×10^{-5}	FGA,FGB,KNG1,PLG
GO:0050708	regulation of protein secretion	7	422	4.91×10^{-5}	APOA1,FGA,FGB,MYOM1,ORM2,RBP4,TTN
GO:0030239	myofibril assembly	4	59	6.81×10^{-5}	ACTA1,MYOM1,MYOZ1,TTN
GO:0032879	regulation of localization	13	2524	0.00010	APOA1,APOA4,C3,C4A,FGA,FGB,GSN,MYOM1, ORM2,PLG,RBP4,SYNPO2,TTN
GO:0048518	positive regulation of biological process	18	5459	0.00013	ACTA1,APOA1,APOA4,C3,C4A,FGA,FGB, GSN,KNG1,MYOM1,NACA,ORM2,PLG,RBP4, SYNPO,SYNPO2,TTN,UBA52
GO:0009611	response to wounding	7	547	0.00015	APOA1,FGA,FGB,GSN,KNG1,NACA,PLG
GO:0034114	regulation of heterotypic cell-cell adhesion	3	21	0.00015	APOA1,FGA,FGB

GO:0042730	fibrinolysis	3	21	0.00015	FGA,FGB,PLG
GO:0048522	positive regulation of cellular process	17	4898	0.00015	APOA1,APOA4,C3,C4A,FGA,FGB,GSN, KNG1,MYOM1,NACA,ORM2,PLG,RBP4, SYNPO,SYNPO2,TTN,UBA52
GO:0007015	actin filament organization	5	200	0.00018	ACTA1,GSN,MYOM1,TPM2,TTN
GO:0032501	multicellular organismal process	19	6507	0.00020	ACTA1,APOA1,APOA4,C3,FGA,FGB, GSN,KNG1,MYH7,MYOM1,MYOT, NACA,NEB,PLG,RBP4,SMPX,SYNPO,TPM2,TTN
GO:0014888	striated muscle adaptation	3	26	0.00021	ACTA1,GSN,MYH7
GO:0022607	cellular component assembly	12	2343	0.00021	ACTA1,APOA1,APOA4,FGA,FGB,GSN, MYOM1,MYOZ1,SYNPO,SYNPO2,TTN,UBA52
GO:0072378	blood coagulation, fibrin clot formation	3	27	0.00021	FGA,FGB,KNG1
GO:0097435	supramolecular fiber organization	6	383	0.00021	ACTA1,GSN,MYOM1,MYOZ1,TPM2,TTN
GO:0051050	positive regulation of transport	8	892	0.00022	C3,C4A,FGA,FGB,MYOM1,ORM2,RBP4,TTN
GO:0032880	regulation of protein localization	8	901	0.00023	APOA1,FGA,FGB,GSN,MYOM1, ORM2,RBP4,TTN
GO:0030036	actin cytoskeleton organization	6	418	0.00027	ACTA1,GSN,MYOM1,MYOZ1,TPM2,TTN
GO:1900026	positive regulation of substrate adhesion-dependent cell spreading	3	32	0.00027	APOA1,FGA,FGB
GO:0006941	striated muscle contraction	4	111	0.00029	MYH7,MYOM1,SMPX,TTN
GO:0070925	organelle assembly	7	666	0.00029	ACTA1,GSN,MYOM1,MYOZ1,SYNPO,SYNPO2,TTN
GO:0006959	humoral immune response	5	252	0.00030	C3,C4A,FGA,FGB,KNG1
GO:0032101	regulation of response to external stimulus	8	955	0.00030	APOA1,C3,C4A,FGA,FGB,KNG1,PLG,UBA52
GO:0090207	regulation of triglyceride metabolic process	3	34	0.00030	APOA1,APOA4,C3
GO:0016192	vesicle-mediated transport	10	1699	0.00035	APOA1,C3,FGA,FGB,GSN,KNG1,ORM2, PLG,TTN,UBA52
GO:0061061	muscle structure development	6	457	0.00035	ACTA1,MYH7,MYOM1,MYOZ1,NEB,TTN
GO:0042060	wound healing	6	461	0.00036	FGA,FGB,GSN,KNG1,NACA,PLG

GO:0014706	striated muscle tissue development	5	271	0.00038	ACTA1,MYH7,MYOM1,RBP4,TTN
GO:0051049	regulation of transport	10	1732	0.00038	APOA1,APOA4,C3,C4A,FGA,FGB,MYOM1,ORM2,RBP4,TTN
GO:0002682	regulation of immune system process	9	1391	0.00046	APOA1,C3,C4A,FGA,FGB,GSN,ORM2,RBP4,UBA52
GO:0007517	muscle organ development	5	287	0.00046	ACTA1,MYH7,MYOM1,NEB,TTN
GO:0010035	response to inorganic substance	6	491	0.00046	ACTA1,APOA4,FGA,FGB,GSN,TTN
GO:0032956	regulation of actin cytoskeleton organization	5	297	0.00053	APOA1,GSN,NEB,SYNPO,SYNPO2
GO:0006950	response to stress	13	3267	0.00057	APOA1,APOA4,C3,C4A,FGA,FGB,GSN,KNNG1,MYH7,NACA,ORM2,PLG,UBA52
GO:0032102	negative regulation of response to external stimulus	5	310	0.00061	APOA1,FGA,FGB,KNNG1,PLG
GO:0031099	regeneration	4	151	0.00062	APOA1,APOA4,GSN,NACA
GO:0030240	skeletal muscle thin filament assembly	2	6	0.00069	ACTA1,TTN
GO:0043152	induction of bacterial agglutination	2	6	0.00069	FGA,FGB
GO:0051130	positive regulation of cellular component organization	8	1128	0.00069	APOA1,C3,C4A,FGA,FGB,GSN,SYNPO,SYNPO2
GO:0016043	cellular component organization	16	5163	0.00071	ACTA1,APOA1,APOA4,C3,FGA,FGB,GSN,MYOM1,MYOZ1,NEB,PLG,SYNPO,SYNPO2,TPM2,TTN,UBA52
GO:2000257	regulation of protein activation cascade	3	54	0.00075	C3,C4A,FGA
GO:0010038	response to metal ion	5	339	0.00084	ACTA1,FGA,FGB,GSN,TTN
GO:0030300	regulation of intestinal cholesterol absorption	2	7	0.00084	APOA1,APOA4
GO:0043062	extracellular structure organization	5	339	0.00084	APOA1,APOA4,FGA,FGB,PLG
GO:2000427	positive regulation of apoptotic cell clearance	2	7	0.00084	C3,C4A

GO:0032233	positive regulation of actin filament bundle assembly	3	60	0.00093	APOA1,SYNPO,SYNPO2
GO:0010898	positive regulation of triglyceride catabolic process	2	8	0.00097	APOA1,APOA4
GO:0034371	chylomicron remodeling	2	8	0.00097	APOA1,APOA4
GO:1902905	positive regulation of supramolecular fiber organization	4	180	0.00099	APOA1,GSN,SYNPO,SYNPO2
GO:0006952	defense response	8	1234	0.0010	APOA4,C3,C4A,FGA,FGB,GSN,KNNG1,ORM2
GO:0043687	post-translational protein modification	5	365	0.0010	APOA1,C3,C4A,FGA,KNNG1
GO:0008015	blood circulation	5	373	0.0011	FGA,FGB,KNNG1,MYH7,TTN
GO:0010810	regulation of cell-substrate adhesion	4	189	0.0011	APOA1,FGA,FGB,PLG
GO:0010873	positive regulation of cholesterol esterification	2	9	0.0011	APOA1,APOA4
GO:0030155	regulation of cell adhesion	6	623	0.0011	APOA1,FGA,FGB,GSN,KNNG1,PLG
GO:0051006	positive regulation of lipoprotein lipase activity	2	9	0.0011	APOA1,APOA4
GO:0065008	regulation of biological quality	13	3559	0.0011	APOA1,APOA4,C3,FGA,FGB,GSN,KNNG1,MYH7,NEB,PLG,RBP4,SYNPO,UBA52
GO:0034378	chylomicron assembly	2	10	0.0012	APOA1,APOA4
GO:0002253	activation of immune response	5	393	0.0013	C3,C4A,FGA,FGB,UBA52
GO:0051495	positive regulation of cytoskeleton organization	4	203	0.0013	APOA1,GSN,SYNPO,SYNPO2
GO:0080134	regulation of response to stress	8	1299	0.0013	APOA1,C3,C4A,FGA,FGB,KNNG1,PLG,UBA52
GO:0009605	response to external stimulus	10	2152	0.0014	ACTA1,APOA1,APOA4,C3,C4A,FGA,FGB,GSN,KNNG1,TTN
GO:0010737	protein kinase A signaling	2	11	0.0014	MYOM1,TTN
GO:0031639	plasminogen activation	2	11	0.0014	FGA,FGB
GO:0033700	phospholipid efflux	2	12	0.0015	APOA1,APOA4

GO:1904035	regulation of epithelial cell apoptotic process	3	78	0.0015	FGA,FGB,GSN
GO:0031347	regulation of defense response	6	676	0.0016	APOA1,C3,C4A,FGA,FGB,UBA52
GO:0045087	innate immune response	6	676	0.0016	APOA4,C3,C4A,FGA,FGB,GSN
GO:0034116	positive regulation of heterotypic cell-cell adhesion	2	13	0.0017	FGA,FGB
GO:0034380	high-density lipoprotein particle assembly	2	13	0.0017	APOA1,APOA4
GO:0051258	protein polymerization	3	83	0.0017	FGA,FGB,GSN
GO:0071688	striated muscle myosin thick filament assembly	2	13	0.0017	MYOM1,TTN
GO:0050790	regulation of catalytic activity	10	2249	0.0018	APOA1,APOA4,C3,C4A,GSN,KNK1, SYNPO2,TPM2,TTN,UBA52
GO:0001523	retinoid metabolic process	3	87	0.0019	APOA1,APOA4,RBP4
GO:0002224	toll-like receptor signaling pathway	3	87	0.0019	FGA,FGB,UBA52
GO:0110053	regulation of actin filament organization	4	235	0.0020	APOA1,GSN,SYNPO,SYNPO2
GO:0051239	regulation of multicellular organismal process	11	2788	0.0021	APOA1,APOA4,C3,FGA,FGB,KNK1, MYH7,NACA,ORM2,PLG,RBP4
GO:0045723	positive regulation of fatty acid biosynthetic process	2	16	0.0022	APOA1,APOA4
GO:0051128	regulation of cellular component organization	10	2306	0.0022	APOA1,APOA4,C3,C4A,FGA,FGB, GSN,NEB,SYNPO,SYNPO2
GO:0090066	regulation of anatomical structure size	5	464	0.0022	FGA,FGB,GSN,KNK1,NEB
GO:0090277	positive regulation of peptide hormone secretion	3	95	0.0022	FGA,FGB,RBP4
GO:0034375	high-density lipoprotein particle remodeling	2	17	0.0024	APOA1,APOA4
GO:0043691	reverse cholesterol transport	2	17	0.0024	APOA1,APOA4
GO:0051241	negative regulation of multicellular organismal process	7	1098	0.0025	APOA1,APOA4,FGA,FGB,KNK1,PLG,RBP4
GO:0032103	positive regulation of response to	5	499	0.0029	C3,FGA,FGB,PLG,UBA52

external stimulus					
GO:0065003	protein-containing complex assembly	8	1514	0.0029	APOA1,APOA4,FGA,FGB,GSN,MYOM1,TTN,UBA52
GO:0002250	adaptive immune response	4	280	0.0033	C3,C4A,FGA,FGB
GO:0044057	regulation of system process	5	516	0.0033	APOA1,APOA4,FGA,FGB,MYH7
GO:0006810	transport	13	4130	0.0034	APOA1,APOA4,C3,FGA,FGB,GSN,KNNG1,NACA,ORM2,PLG,RBP4,TTN,UBA52
GO:0006955	immune response	8	1560	0.0034	APOA4,C3,C4A,FGA,FGB,GSN,KNNG1,ORM2
GO:0007596	blood coagulation	4	288	0.0035	FGA,FGB,KNNG1,PLG
GO:0032268	regulation of cellular protein metabolic process	10	2486	0.0035	APOA1,C3,C4A,FGA,FGB,GSN,KNNG1,SYNPO2,TTN,UBA52
GO:0051707	response to other organism	7	1173	0.0035	APOA4,C3,C4A,FGA,FGB,GSN,KNNG1
GO:0070613	regulation of protein processing	3	116	0.0035	C3,C4A,GSN
GO:0034622	cellular protein-containing complex assembly	6	832	0.0036	FGA,FGB,GSN,MYOM1,TTN,UBA52
GO:0033344	cholesterol efflux	2	24	0.0038	APOA1,APOA4
GO:0010954	positive regulation of protein processing	2	25	0.0040	C3,GSN
GO:0070527	platelet aggregation	2	25	0.0040	FGA,FGB
GO:0031102	neuron projection regeneration	2	26	0.0042	APOA1,APOA4
GO:0035296	regulation of tube diameter	3	129	0.0042	FGA,FGB,KNNG1
GO:0050776	regulation of immune response	6	873	0.0042	APOA1,C3,C4A,FGA,FGB,UBA52
GO:0050896	response to stimulus	18	7824	0.0042	ACTA1,APOA1,APOA4,C3,C4A,FGA,FGB,GSN,KNNG1,MYH7,MYOM1,NACA,ORM2,PLG,RBP4,SYNPO,TTN,UBA52
GO:0051336	regulation of hydrolase activity	7	1238	0.0042	APOA1,APOA4,C3,C4A,GSN,KNNG1,TPM2
GO:0051592	response to calcium ion	3	129	0.0042	FGA,FGB,TTN
GO:1905952	regulation of lipid localization	3	129	0.0042	APOA1,APOA4,C3
GO:0002684	positive regulation of immune system process	6	882	0.0043	C3,C4A,FGA,FGB,RBP4,UBA52
GO:0003300	cardiac muscle hypertrophy	2	28	0.0044	MYH7,TTN
GO:0015850	organic hydroxy compound transport	3	134	0.0044	APOA1,APOA4,RBP4

GO:2000352	negative regulation of endothelial cell apoptotic process	2	28	0.0044	FGA,FGB
GO:0097746	regulation of blood vessel diameter	3	137	0.0046	FGA,FGB,KNNG1
GO:0006911	phagocytosis, engulfment	2	31	0.0051	C3,GSN
GO:0019730	antimicrobial humoral response	3	143	0.0051	FGA,FGB,KNNG1
GO:0045907	positive regulation of vasoconstriction	2	33	0.0057	FGA,FGB
GO:0070328	triglyceride homeostasis	2	33	0.0057	APOA1,APOA4
GO:0009893	positive regulation of metabolic process	11	3280	0.0058	ACTA1,APOA1,APOA4,C3,FGA,FGB,GSN,MYOM1,NACA,TTN,UBA52
GO:0006958	complement activation, classical pathway	2	34	0.0059	C3,C4A
GO:0048738	cardiac muscle tissue development	3	154	0.0059	MYH7,RBP4,TTN
GO:0002697	regulation of immune effector process	4	362	0.0061	APOA1,C3,C4A,RBP4
GO:0061384	heart trabecula morphogenesis	2	35	0.0061	NACA,RBP4
GO:0001932	regulation of protein phosphorylation	7	1370	0.0063	APOA1,C3,FGA,FGB,SYNPO2,TTN,UBA52
GO:0022407	regulation of cell-cell adhesion	4	366	0.0063	APOA1,FGA,FGB,PLG
GO:0031349	positive regulation of defense response	4	365	0.0063	C3,FGA,FGB,UBA52
GO:1902042	negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	2	36	0.0063	FGA,FGB
GO:0050706	regulation of interleukin-1 beta secretion	2	37	0.0066	APOA1,ORM2
GO:0045214	sarcomere organization	2	38	0.0068	MYOM1,TTN
GO:0051180	vitamin transport	2	38	0.0068	APOA1,RBP4
GO:0003205	cardiac chamber development	3	166	0.0069	MYH7,NACA,RBP4
GO:0002758	innate immune response-activating signal transduction	3	168	0.0070	FGA,FGB,UBA52

GO:0006695	cholesterol biosynthetic process	2	41	0.0076	APOA1,APOA4
GO:0046890	regulation of lipid biosynthetic process	3	174	0.0076	APOA1,APOA4,C3
GO:0052548	regulation of endopeptidase activity	4	393	0.0076	C3,C4A,GSN,KNG1
GO:0002376	immune system process	9	2370	0.0078	APOA4,C3,C4A,FGA,FGB,GSN,KNG1,ORM2,UBA52
GO:0048747	muscle fiber development	2	43	0.0080	ACTA1,TTN
GO:0048468	cell development	7	1493	0.0092	ACTA1,APOA1,APOA4,GSN,MYOM1,MYOZ1,TTN
GO:0019538	protein metabolic process	12	4194	0.0102	APOA1,APOA4,C3,C4A,FGA,FGB,GSN,KNG1,NACA,PLG,TTN,UBA52
GO:0044267	cellular protein metabolic process	11	3603	0.0104	APOA1,APOA4,C3,C4A,FGA,GSN,KNG1,NACA,PLG,TTN,UBA52
GO:0051346	negative regulation of hydrolase activity	4	438	0.0104	APOA1,C3,C4A,KNG1
GO:0030449	regulation of complement activation	2	52	0.0107	C3,C4A
GO:0051704	multi-organism process	9	2514	0.0109	APOA4,C3,C4A,FGA,FGB,GSN,KNG1,PLG,UBA52
GO:0042246	tissue regeneration	2	54	0.0113	GSN,NACA
GO:0048584	positive regulation of response to stimulus	8	2054	0.0123	APOA1,C3,C4A,FGA,FGB,GSN,PLG,UBA52
GO:0060627	regulation of vesicle-mediated transport	4	480	0.0138	C3,C4A,FGA,FGB
GO:0006954	inflammatory response	4	482	0.0140	C3,C4A,KNG1,ORM2
GO:0009888	tissue development	7	1626	0.0140	ACTA1,GSN,MYH7,MYOM1,NACA,RBP4,TTN
GO:0007507	heart development	4	485	0.0141	MYH7,NACA,RBP4,TTN
GO:0010647	positive regulation of cell communication	7	1631	0.0141	APOA1,C3,FGA,FGB,GSN,RBP4,UBA52
GO:0006508	proteolysis	6	1203	0.0142	C3,C4A,FGA,FGB,PLG,UBA52
GO:0023056	positive regulation of signaling	7	1638	0.0142	APOA1,C3,FGA,FGB,GSN,RBP4,UBA52

GO:0055008	cardiac muscle tissue morphogenesis	2	63	0.0144	MYH7,TTN
GO:0003007	heart morphogenesis	3	235	0.0149	MYH7,RBP4,TTN
GO:0044089	positive regulation of cellular component biogenesis	4	498	0.0150	APOA1,GSN,SYNPO,SYNPO2
GO:0048646	anatomical structure formation involved in morphogenesis	5	831	0.0150	ACTA1,MYOM1,MYOZ1,RBP4,TTN
GO:0010951	negative regulation of endopeptidase activity	3	242	0.0158	C3,C4A,KNG1
GO:0048523	negative regulation of cellular process	12	4454	0.0158	APOA1,APOA4,C3,C4A,FGA,FGB,GSN,KNG1,NACA,PLG,RBP4,UBA52
GO:0007162	negative regulation of cell adhesion	3	245	0.0162	APOA1,KNG1,PLG
GO:0010817	regulation of hormone levels	4	511	0.0162	APOA1,FGA,FGB,RBP4
GO:0065007	biological regulation	21	11740	0.0168	ACTA1,APOA1,APOA4,C3,C4A,FGA,FGB,GSN,KNG1,MYH7,MYOM1,NACA,NEB,ORM2,PLG,RBP4,SYNPO, SYNPO2,TPM2,TTN,UBA52
GO:1903522	regulation of blood circulation	3	249	0.0168	FGA,FGB,MYH7
GO:0042632	cholesterol homeostasis	2	71	0.0169	APOA1,APOA4
GO:0046470	phosphatidylcholine metabolic process	2	72	0.0172	APOA1,APOA4
GO:0060048	cardiac muscle contraction	2	73	0.0176	MYH7,TTN
GO:0045921	positive regulation of exocytosis	2	78	0.0192	FGA,FGB
GO:0051492	regulation of stress fiber assembly	2	78	0.0192	APOA1,SYNPO
GO:1901564	organonitrogen compound metabolic process	13	5281	0.0195	APOA1,APOA4,C3,C4A,FGA,FGB,GSN,KNG1,MYH7,NACA,PLG,TTN,UBA52
GO:0006869	lipid transport	3	272	0.0197	APOA1,APOA4,RBP4
GO:0006928	movement of cell or subcellular component	6	1355	0.0221	ACTA1,APOA1,MYH7,NEB,TPM2,TTN
GO:0010628	positive regulation of gene expression	7	1826	0.0225	ACTA1,C3,GSN,MYOM1,NACA,TTN,UBA52
GO:0006066	alcohol metabolic process	3	290	0.0229	APOA1,APOA4,RBP4

GO:0022603	regulation of anatomical structure morphogenesis	5	961	0.0240	APOA1,C3,FGA,FGB,NACA
GO:0030198	extracellular matrix organization	3	296	0.0240	FGA,FGB,PLG
GO:0090130	tissue migration	2	90	0.0240	ACTA1,APOA1
GO:0002673	regulation of acute inflammatory response	2	92	0.0248	C3,C4A
GO:0050789	regulation of biological process	20	11116	0.0249	ACTA1,APOA1,APOA4,C3,C4A,FGA,FGB, GSN,KNG1,MYH7,MYOM1,NACA,NEB, ORM2,PLG,RBP4,SYNPO,SYNPO2,TTN,UBA52
GO:0002443	leukocyte mediated immunity	4	632	0.0291	C3,C4A,GSN,ORM2
GO:0001775	cell activation	5	1024	0.0303	C3,FGA,FGB,GSN,ORM2
GO:0043900	regulation of multi-organism process	4	653	0.0321	FGA,FGB,GSN,UBA52
GO:0048585	negative regulation of response to stimulus	6	1483	0.0321	APOA1,FGA,FGB,KNG1,PLG,UBA52
GO:0009967	positive regulation of signal transduction	6	1493	0.0329	APOA1,C3,FGA,FGB,GSN,UBA52
GO:0050727	regulation of inflammatory response	3	338	0.0329	APOA1,C3,C4A
GO:0010604	positive regulation of macromolecule metabolic process	9	3081	0.0330	ACTA1,C3,FGA,FGB,GSN,MYOM1,NACA, TTN,UBA52
GO:0009653	anatomical structure morphogenesis	7	1992	0.0333	ACTA1,MYH7,MYOM1,MYOZ1,NACA,RBP4,TTN
GO:0042981	regulation of apoptotic process	6	1501	0.0333	FGA,FGB,GSN,KNG1,NACA,UBA52
GO:0042157	lipoprotein metabolic process	2	114	0.0349	APOA1,APOA4
GO:0006996	organelle organization	9	3131	0.0359	ACTA1,GSN,MYOM1,MYOZ1,SYNPO, SYNPO2,TPM2,TTN,UBA52
GO:0007160	cell-matrix adhesion	2	119	0.0376	FGA,FGB
GO:0051240	positive regulation of multicellular organismal process	6	1551	0.0377	C3,FGA,FGB,NACA,ORM2,PLG
GO:0007519	skeletal muscle tissue development	2	122	0.0388	ACTA1,MYOM1
GO:0002700	regulation of production of molecular	2	124	0.0397	APOA1,RBP4

mediator of immune response					
GO:0019222	regulation of metabolic process	14	6516	0.0397	ACTA1,APOA1,APOA4,C3,C4A,FGA, FGB,GSN,KNK1,MYOM1,NACA,SYNPO2, TTN,UBA52
GO:0071347	cellular response to interleukin-1	2	124	0.0397	FGB,UBA52
GO:0003231	cardiac ventricle development	2	125	0.0400	MYH7,NACA
GO:0016202	regulation of striated muscle tissue development	2	127	0.0408	NACA,RBP4
GO:0003206	cardiac chamber morphogenesis	2	128	0.0410	MYH7,RBP4
GO:0045807	positive regulation of endocytosis	2	129	0.0414	C3,C4A
GO:2001233	regulation of apoptotic signaling pathway	3	388	0.0429	FGA,FGB,GSN
GO:0045471	response to ethanol	2	134	0.0437	GSN,RBP4
GO:0048583	regulation of response to stimulus	10	3882	0.0437	APOA1,C3,C4A,FGA,FGB,GSN, KNK1,MYH7,PLG,UBA52
GO:0043902	positive regulation of multi-organ- ism process	3	394	0.0440	FGA,FGB,UBA52