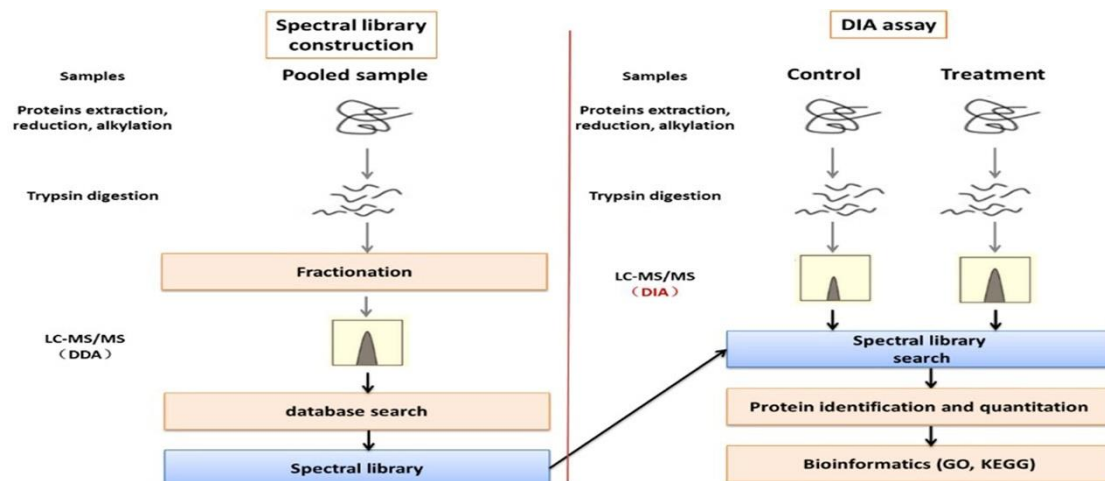
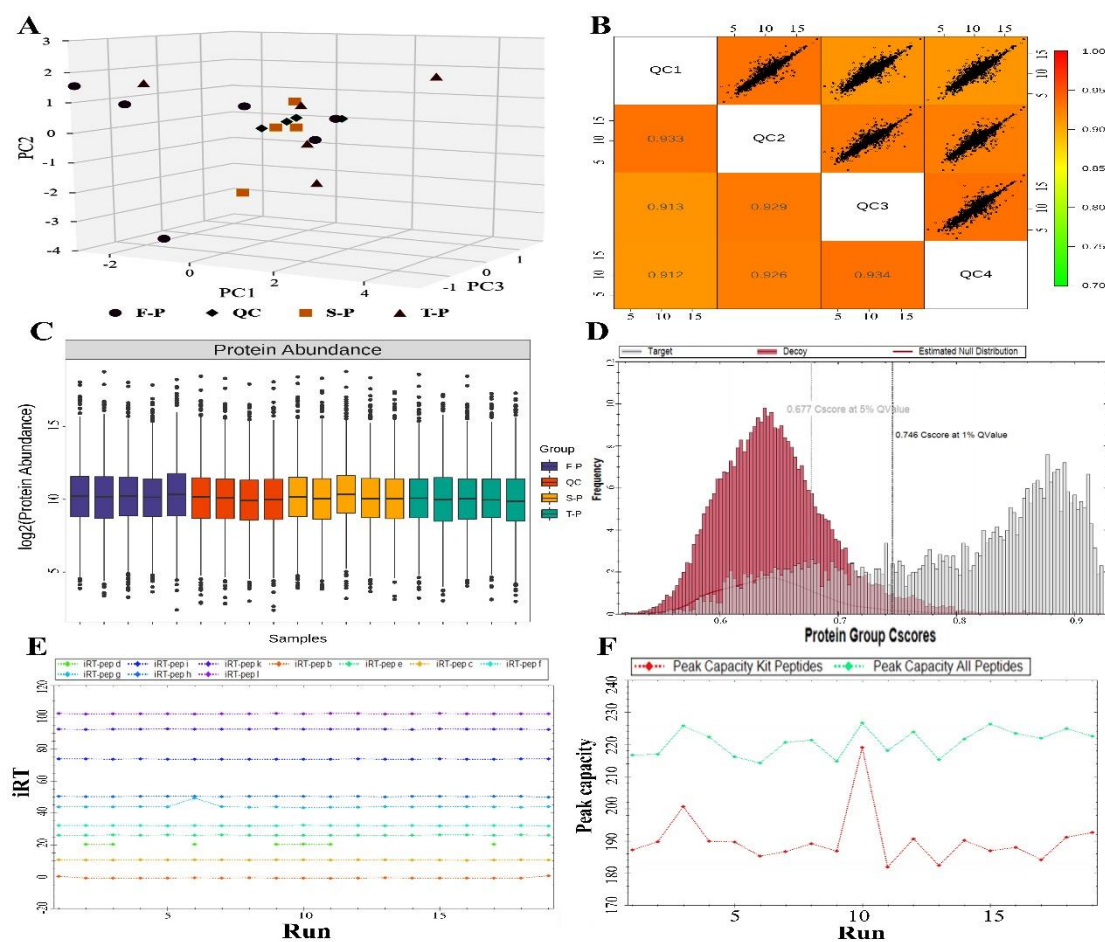
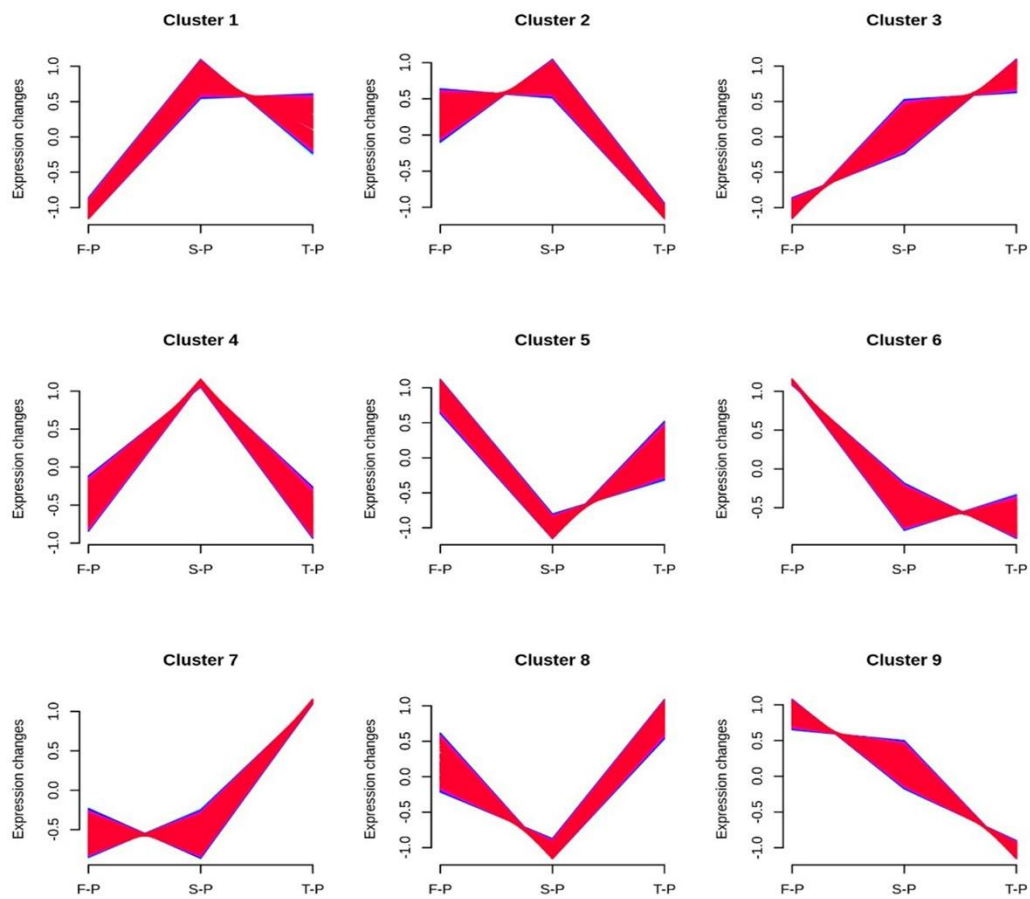




Appendix 1. Overall technical route of this project.



Appendix 2. The qualities of the proteome dataset. (A) Scores of Principle Component Analysis (PCA). (B) The scatterplot of QC. (C) Sample Quantitative Intensity Jitter Profile (D) Protein scores of FDR. (E) Chart of iRT elution time. (F) Column peak capacity statistics.



Appendix 3. The protein expression changes of three groups in nine clusters based on trends analysis

Appendix 4. Differentially expressed proteins of serum samples between 12th week of treatment (S-P) and pretreatment (F-P)

Protein	Protein Description	Sequence Number	S-P/F-P	P value
A0A5C2G267	IGL c3259_light_IGKV3-11_IGKJ5 (Fragment)	1	8.04	0.00
A0A024R6R4	Matrix metalloproteinase 2 (Gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase), isoform CRA_a	4	2.83	0.02
A0A5C2GG03	IGH + IGL c101_light_IGLV1-47_IGLJ3 (Fragment)	1	2.53	0.02
A0A5C2G3P6	IGL c3918_light_IGKV1-9_IGKJ3 (Fragment)	1	1.90	0.02
A0A0S2Z3Y1	Lectin galactoside-binding soluble 3 binding protein isoform 1 (Fragment)	16	1.89	0.02
A0A5C2GUD9	IG c1125_light_IGKV1D-17_IGKJ1 (Fragment)	2	1.85	0.01
A0A5F9ZHM4	L-lactate dehydrogenase	3	1.69	0.03
A0A087WXI2	IgG Fc-binding protein	50	1.62	0.01
L8E853	von Willebrand factor	2	1.60	0.02
A0A024R145	Fructose-bisphosphate aldolase	9	1.54	0.05
C0JYY2	Apolipoprotein B (Including Ag(X) antigen)	229	0.67	0.04
A0A5C2GYN0	IG c850_light_IGKV3-15_IGKJ3 (Fragment)	1	0.67	0.00
A0A5C2GPS6	IG c873_heavy_IGHV3-23_IGHD5-24_IGHJ4 (Fragment)	1	0.66	0.00
A0A5C2GER5	IG c1063_heavy_IGHV3-33_IGHD1-1_IGHJ3 (Fragment)	2	0.66	0.03
A0A5C2GC36	IGL c261_light_IGKV1-5_IGKJ2 (Fragment)	2	0.65	0.00
Q13790	Apolipoprotein F	3	0.65	0.02
A0A5C2GKC6	IG c262_light_IGKV3-20_IGKJ1 (Fragment)	2	0.65	0.01
A0A5C2GIP8	IGH + IGL c575_heavy_IGHV3-23_IGHD3-3_IGHJ3 (Fragment)	3	0.64	0.01
A0A5C2G8T5	IGL c225_light_IGKV3-15_IGKJ4 (Fragment)	2	0.62	0.02
B7Z8A2	cDNA FLJ51671, highly similar to Prenylcysteine oxidase	9	0.62	0.05
A0A5C2GDW0	IGH + IGL c207_heavy_IGHV3-53_IGHD2-8_IGHJ2	1	0.62	0.01

	(Fragment)			
A0A5C2GWZ7	IG c1107_heavy_IGHV3-74_IGHD3-3_IGHJ4 (Fragment)	1	0.62	0.05
A0A5C2H0H1	IG c1570_light_IGKV3-11_IGKJ3 (Fragment)	2	0.61	0.05
A0A5C2GE58	IG c273_heavy_IGHV3-23_IGHD3-22_IGHJ5 (Fragment) IGH + IGL	1	0.60	0.02
A0A5C2GAN6	c142_heavy_IGHV3-48_IGHD4-11_IGHJ6 (Fragment)	2	0.60	0.04
P35542	Serum amyloid A-4 protein	1	0.60	0.01
Q9UL92	Myosin-reactive immunoglobulin heavy chain variable region (Fragment)	4	0.58	0.05
A0A5C2GHA2	IG c1208_heavy_IGHV3-30_IGHD3-3_IGHJ3 (Fragment)	2	0.57	0.02
A0A5C2FT85	IGL c29_light_IGKV3D-15_IGKJ2 (Fragment)	2	0.57	0.01
A0A5C2G0C4	IGL c1856_light_IGKV3-20_IGKJ1 (Fragment)	3	0.56	0.02
A0A5C2GLX4	IG c356_heavy_IGHV4-59_IGHD4-17_IGHJ4 (Fragment)	2	0.56	0.03
A0A5C2GN64	IG c618_heavy_IGHV3-15_IGHD1-26_IGHJ4 (Fragment)	2	0.56	0.04
A0A5C2G9T7	IGH c33_heavy_IGHV3-33_IGHD3-10_IGHJ4 (Fragment)	2	0.56	0.01
A8K104	cDNA FLJ78726, highly similar to Homo sapiens olfactomedin 1 (OLFM1), transcript variant 1, mRNA	4	0.55	0.01
A0A5C2G773	IGH c452_heavy_IGHV3-7_IGHD3-3_IGHJ4 (Fragment)	1	0.55	0.00
A0A5C2GA89	IGH c185_heavy_IGHV3-7_IGHD3-16_IGHJ4 (Fragment)	1	0.53	0.03
A0A5C2G7M9	IGL c504_light_IGKV3-15_IGKJ1 (Fragment)	1	0.53	0.03
A0A5C2GXS3	IG c510_light_IGKV3-11_IGKJ5 (Fragment)	2	0.50	0.04
A0A5C2GP10	IG c1165_heavy_IGHV3-30_IGHD7-27_IGHJ4 (Fragment)	1	0.49	0.01
A0A5C2GWD7	IG c759_light_IGKV1D-33_IGKJ3 (Fragment)	1	0.48	0.02
A0A5C2GP39	IG c593_heavy_IGHV3-48_IGHD3-3_IGHJ4 (Fragment)	1	0.48	0.00
A0A5C2GLW6	IG c505_heavy_IGHV4-34_IGHD1-26_IGHJ6 (Fragment)	2	0.47	0.03
A0A5C2FW17	IGL c1012_light_IGKV1-5_IGKJ1 (Fragment)	1	0.45	0.01

A0A5C2GVU1	IG c1453_light_IGKV3-11_IGKJ5 (Fragment)	2	0.45	0.00
Q0ZCJ1	Immunoglobulin heavy chain variable region (Fragment)	2	0.44	0.02
A0A5C2GQE4	IG c100_light_IGKV1D-33_IGKJ2 (Fragment)	2	0.43	0.04
A0A5C2GQ71	IG c912_heavy_IGHV4-61_IGHD2-2_IGHJ6 (Fragment)	2	0.43	0.01
A0A5C2G1H9	IGL c2982_light_IGKV4-1_IGKJ1 (Fragment)	4	0.42	0.04
A0A5C2FZ01	IGL c2181_light_IGKV3-20_IGKJ3 (Fragment)	2	0.37	0.01
A0A5C2FUJ1	IGL c668_light_IGKV3-20_IGKJ1 (Fragment)	2	0.34	0.01
	IGH			
A0A5C2G830	c558_heavy_IGHV3-43_IGHD3-10_IGHJ1 (Fragment)	1	0.29	0.01
A0A5C2GB45	IGH + IGL c305_light_IGKV2-28_IGKJ1 (Fragment)	3	0.27	0.01
A0A5C2FVW7	IGL c1218_light_IGKV1D-39_IGKJ5 (Fragment)	2	0.26	0.02
A2IPI4	HRV Fab 025-VL (Fragment)	1	0.23	0.04

Notes: Red labeling indicates the upregulated proteins with at least 1.5-fold and green labeling indicates the downregulated proteins with at least 1.5-fold.

Appendix 5. Differentially expressed proteins of serum samples between 24th week of treatment (T-P) and pretreatment (F-P)

Protein	Protein Description	Sequence Number	T-P/F-P	P value
Q9UL89	Myosin-reactive immunoglobulin heavy chain variable region (Fragment)	2	4.90	0.03
A0A5C2G080	IGL c1940_light_IGKV3-20_IGKJ5 (Fragment)	1	3.73	0.04
A0A5C2GXL1	IG c378_light_IGKV1-9_IGKJ4 (Fragment)	2	3.14	0.00
A0A5C2GJ52	IG c1284_light_IGKV1-5_IGKJ2 (Fragment)	1	3.10	0.02
A0A5C2GL87	IG c1157_light_IGKV3-20_IGKJ2 (Fragment)	2	2.52	0.03
A0A5C2G4T4	IGL c3550_light_IGLV3-19_IGLJ3 (Fragment)	1	2.51	0.03
A0A5C2FVH4	IGL c1031_light_IGLV1-40_IGLJ1 (Fragment)	2	2.48	0.04
A0A5C2GUW4	IG c1311_heavy_IGHV4-39_IGHD6-19_IGHJ4	1	2.43	0.04

	(Fragment)			
A0A5C2GA71	IGL c292_light_IGKV1D-39_IGKJ2 (Fragment)	2	2.40	0.01
A0A0S2Z3Y1	Lectin galactoside-binding soluble 3 binding protein isoform 1 (Fragment)	16	2.25	0.00
A0A5C2GH93	IG c1022_light_IGLV1-44_IGLJ2 (Fragment)	1	2.08	0.03
	IG			
A0A5C2GPV2	c32_heavy_IGHV4-59B_IGHD3-3_IGHJ4 (Fragment)	1	1.92	0.05
A0A2U8J8Q0	Ig heavy chain variable region (Fragment)	1	1.89	0.05
A0A5C2GTJ7	IG c771_light_IGKV1-5_IGKJ2 (Fragment)	1	1.84	0.02
	IG			
A0A5C2GNY5	c384_heavy_IGHV4-34_IGHD1-26_IGHJ4 (Fragment)	1	1.67	0.04
	IGH + IGL			
A0A5C2GAK5	c201_heavy_IGHV4-39_IGHD3-10_IGHJ2 (Fragment)	1	1.67	0.05
	IGH			
A0A5C2G721	c108_heavy__IGHV4-39_IGHD4-23_IGHJ4 (Fragment)	1	1.66	0.05
	IG			
A0A5C2GIE4	c1217_heavy_IGHV4-61_IGHD4-23_IGHJ1 (Fragment)	1	1.66	0.05
	IG			
A0A5C2GJ11	c574_heavy_IGHV4-61_IGHD3-16_IGHJ6 (Fragment)	1	1.66	0.05
A0A5C2GBB1	IGH + IGL c492_light_IGKV1D-33_IGKJ2 (Fragment)	1	1.64	0.01
	IGH			
A0A5C2G6T6	c8_heavy__IGHV3-74_IGHD1-26_IGHJ1 (Fragment)	1	1.63	0.05
A0A5C2G1U7	IGL c3139_light_IGKV1-5_IGKJ4 (Fragment)	1	1.61	0.01
A0A5C2G0F0	IGL c2642_light_IGKV1D-33_IGKJ3 (Fragment)	1	1.60	0.01
	IG			
A0A5C2GF74	c376_heavy_IGHV3-21_IGHD3-9_IGHJ4 (Fragment)	3	1.59	0.01
Q569I7	Uncharacterized protein	2	1.56	0.01
A0A5C2FZ58	IGL c1964_light_IGKV1-39_IGKJ5 (Fragment)	1	1.55	0.05

A0A5C2GKS2	IG c1329_heavy_IGHV4-39_IGHD2-8_IGHJ6 (Fragment)	1	1.55	0.03
O75882	Attractin	24	0.66	0.01
A0A5C2FVY4	IGL c346_light_IGKV1-12_IGKJ4 (Fragment)	2	0.66	0.04
A0A5C2GJ22	IG c699_heavy_IGHV3-23_IGHD3-10_IGHJ4 (Fragment)	3	0.66	0.03
Q6UXB8	Peptidase inhibitor 16	2	0.66	0.03
B2R701	cDNA, FLJ93202, Homo sapiens protease inhibitor 16 (PI16), mRNA	5	0.66	0.04
A0A5C2GC36	IGL c261_light_IGKV1-5_IGKJ2 (Fragment)	2	0.65	0.00
A0A5C2FWU2	IGL c656_light_IGKV1-27_IGKJ4 (Fragment)	3	0.65	0.03
A0A5C2FWA3	IGL c1368_light_IGKV1D-39_IGKJ1 (Fragment)	2	0.65	0.00
A0A5C2GWN8	IG c987_heavy_IGHV4-59B_IGHD3-10_IGHJ6 (Fragment)	2	0.65	0.02
A6XGL1	Transthyretin	14	0.65	0.01
A0A5C2GR94	IG c4_light_IGKV3-20_IGKJ3 (Fragment)	3	0.65	0.04
A0A5C2GGH5	IG c1305_heavy_IGHV3-23_IGHD3-9_IGHJ4 (Fragment)	2	0.65	0.03
A0A5C2GTE2	IG c617_light_IGKV3-15_IGKJ5 (Fragment)	2	0.64	0.01
A0A384NKM6	Apolipoprotein H (Beta-2-glycoprotein I), isoform CRA_a	19	0.64	0.02
A0A5C2GMF2	IG c998_light_IGKV4-1_IGKJ2 (Fragment)	2	0.64	0.04
A0A5C2G9Q1	IGH c116_heavy_IGHV4-59_IGHD1-14_IGHJ5 (Fragment)	2	0.64	0.03
A0A5C2GNZ7	IG c280_heavy_IGHV3-23_IGHD2-21_IGHJ2 (Fragment)	1	0.63	0.04
A0A5C2GHT7	IG c1037_heavy_IGHV3-53_IGHD5-24_IGHJ4 (Fragment)	1	0.63	0.01
A0A5C2GT99	IG c577_light_IGKV3-11_IGKJ4 (Fragment)	2	0.63	0.03

	IG			
A0A5C2GE65	c1144_heavy_IGHV3-23_IGHD6-13_IGHJ3 (Fragment)	1	0.62	0.05
	IG			
A0A5C2GDN3	c481_heavy_IGHV3-11_IGHD3-22_IGHJ4 (Fragment)	3	0.62	0.00
A0A5C2G1J4	IGL c2326_light_IGKV1-39_IGKJ1 (Fragment)	1	0.61	0.04
A0A182DWH7	Selenoprotein P (Fragment)	7	0.61	0.01
	IG			
A0A5C2GED6	c847_heavy_IGHV3-30_IGHD3-22_IGHJ4 (Fragment)	1	0.61	0.05
A0A5C2G045	IGL c917_light_IGKV3-20_IGKJ1 (Fragment)	2	0.61	0.02
A0A5C2GC11	IGL c231_light_IGKV1-5_IGKJ3 (Fragment)	1	0.60	0.01
B7Z9B1	cDNA FLJ52398, highly similar to Cadherin-13	4	0.60	0.01
A0A5C2FT85	IGL c29_light_IGKV3D-15_IGKJ2 (Fragment)	2	0.60	0.03
B7ZW00	COL6A3 protein	16	0.60	0.00
A0A5C2G710	IGL c178_light_IGKV1D-39_IGKJ2 (Fragment)	2	0.60	0.02
A0A5C2FYG7	IGL c1216_light_IGKV3-20_IGKJ2 (Fragment)	2	0.60	0.00
B7Z8A2	cDNA FLJ51671, highly similar to Prenylcysteine oxidase	9	0.59	0.04
A0A5C2FXP5	IGL c17_light_IGKV2D-28_IGKJ4 (Fragment)	3	0.59	0.04
	IG			
A0A5C2GF48	c1070_heavy_IGHV3-74_IGHD2-15_IGHJ2 (Fragment)	2	0.58	0.03
A0A5C2G229	IGL c2506_light_IGKV1-33_IGKJ4 (Fragment)	1	0.58	0.02
A0A5C2FVL3	IGL c216_light_IGKV3-20_IGKJ1 (Fragment)	3	0.58	0.04
A0A5C2FT75	IGL c19_light_IGKV3-15_IGKJ2 (Fragment)	2	0.58	0.01
A0A5C2GKC6	IG c262_light_IGKV3-20_IGKJ1 (Fragment)	2	0.58	0.00
A0A5C2FY76	IGL c575_light_IGKV1-12_IGKJ4 (Fragment)	2	0.57	0.01
A0A5C2GDW0	IGH + IGL c207_heavy_IGHV3-53_IGHD2-8_IGHJ2	1	0.57	0.00

	(Fragment)			
	IG			
A0A5C2GPS6	c873_heavy_IGHV3-23_IGHD5-24_IGHJ4 (Fragment)	1	0.56	0.00
	IG			
A0A5C2GNB0	c1181_heavy_IGHV3-30_IGHD3-10_IGHJ6 (Fragment)	2	0.56	0.00
	IG			
A0A5C2GG43	c988_heavy_IGHV3-23_IGHD4-17_IGHJ4 (Fragment)	1	0.56	0.02
A0A5C2FVK1	IGL c644_light_IGKV3-20_IGKJ4 (Fragment)	3	0.56	0.03
A0A5C2GD97	IGL c583_light_IGKV3D-20_IGKJ2 (Fragment)	1	0.55	0.00
A0A5C2FU97	IGL c322_light_IGKV3-20_IGKJ1 (Fragment)	2	0.55	0.02
A0A5C2G2I1	IGL c3481_light_IGKV3D-20_IGKJ4 (Fragment)	2	0.55	0.01
A0A0S2Z4I5	Complement factor properdin isoform 1 (Fragment)	9	0.55	0.00
	IGH + IGL			
A0A5C2GH42	c55_heavy_IGHV4-34_IGHD3-3_IGHJ4 (Fragment)	2	0.55	0.00
A8K104	cDNA FLJ78726, highly similar to Homo sapiens olfactomedin 1 (OLFM1), transcript variant 1, mRNA	4	0.55	0.01
	IGH + IGL			
A0A5C2GAN6	c142_heavy_IGHV3-48_IGHD4-11_IGHJ6 (Fragment)	2	0.55	0.03
	IG			
A0A5C2GFV3	c503_heavy_IGHV3-21_IGHD1-26_IGHJ4 (Fragment)	4	0.54	0.00
	IG			
A0A5C2GLX4	c356_heavy_IGHV4-59_IGHD4-17_IGHJ4 (Fragment)	2	0.54	0.01
P35542	Serum amyloid A-4 protein	1	0.54	0.00
	IGH			
A0A5C2G9W8	c63_heavy_IGHV3-30_IGHD2-21_IGHJ3 (Fragment)	2	0.54	0.02
A0A5C2G164	IGL c1217_light_IGKV3-20_IGKJ3 (Fragment)	1	0.54	0.01
	IGH			
A0A5C2G614	c410_heavy_IGHV3-20_IGHD3-10_IGHJ6	2	0.54	0.04

	(Fragment)			
A0A5C2GTS4	IG c1123_light_IGKV3-15_IGKJ4 (Fragment)	2	0.53	0.03
A0A5C2GSM3	IG c401_light_IGKV1-12_IGKJ5 (Fragment)	2	0.52	0.01
A6NLG9	Biglycan	1	0.52	0.01
A0A5C2FUQ0	IGL c748_light_IGKV4-1_IGKJ1 (Fragment)	2	0.51	0.00
P0DOX7	Immunoglobulin kappa light chain	3	0.51	0.02
	IGH + IGL			
A0A5C2GCU8	c568_heavy_IGHV3-23_IGHD2-21_IGHJ3 (Fragment)	2	0.51	0.05
	IGH + IGL			
A0A5C2GBK4	c412_heavy_IGHV1-2_IGHD3-3_IGHJ5 (Fragment)	1	0.51	0.05
	IGH			
A0A5C2GDZ7	c221_heavy__IGHV3-48_IGHD4-23_IGHJ6 (Fragment)	2	0.51	0.00
A0A5C2GVA0	IG c1247_light_IGKV1D-13_IGKJ4 (Fragment)	2	0.51	0.03
A0A5C2GJY0	IG c758_light_IGKV3-20_IGKJ3 (Fragment)	2	0.51	0.01
	IG			
A0A5C2GL50	c46_heavy_IGHV4-34_IGHD2-15_IGHJ6 (Fragment)	2	0.50	0.03
A0A5C2G7M9	IGL c504_light_IGKV3-15_IGKJ1 (Fragment)	1	0.50	0.01
	IG			
A0A5C2GRS7	c589_heavy_IGHV3-30_IGHD5-5_IGHJ4 (Fragment)	2	0.50	0.01
A0A5C2GYE9	IG c1409_light_IGKV3-20_IGKJ2 (Fragment)	2	0.50	0.00
A0A5C2FXH8	IGL c900_light_IGKV3-20_IGKJ2 (Fragment)	1	0.50	0.01
A0A5C2G8T5	IGL c225_light_IGKV3-15_IGKJ4 (Fragment)	2	0.49	0.00
Q13790	Apolipoprotein F	3	0.49	0.00
	IG			
A0A5C2GE58	c273_heavy_IGHV3-23_IGHD3-22_IGHJ5 (Fragment)	1	0.49	0.00
	IG			
A0A5C2GNN4	c150_heavy_IGHV3-48_IGHD1-26_IGHJ3 (Fragment)	1	0.49	0.03

A0A5C2GMM8	IG c951_light_IGKV1-12_IGKJ3 (Fragment)	2	0.49	0.05
A0A2U8J8Z6	Ig heavy chain variable region (Fragment)	2	0.48	0.04
A0A5C2GUD3	IG c363_light_IGKV2D-28_IGKJ2 (Fragment)	1	0.48	0.01
A0A5C2G7U8	IGL c548_light_IGKV4-1_IGKJ4 (Fragment)	2	0.48	0.00
A0A5C2GKG3	IG c273_light_IGKV1-6_IGKJ1 (Fragment)	2	0.48	0.03
A0A5C2GRH3	IG c1314_heavy_IGHV3-53_IGHD3-10_IGHJ6 (Fragment)	2	0.48	0.03
A0A1W6IYK2	N90-VRC38.06 light chain variable region (Fragment)	2	0.47	0.00
A0A5C2GGM0	IG c55_heavy_IGHV3-48_IGHD3-10_IGHJ3 (Fragment)	2	0.47	0.01
A0A5C2GHA2	IG c1208_heavy_IGHV3-30_IGHD3-3_IGHJ3 (Fragment)	2	0.47	0.01
A0A5C2GJL5	IG c1251_light_IGKV1-5_IGKJ1 (Fragment)	2	0.47	0.05
A0A5C2FW17	IGL c1012_light_IGKV1-5_IGKJ1 (Fragment)	1	0.47	0.01
A0A5C2G0F4	IGL c2659_light_IGKV1D-16_IGKJ5 (Fragment)	2	0.47	0.04
A0A5C2G7K3	IGL c464_light_IGKV4-1_IGKJ5 (Fragment)	1	0.47	0.04
A0A5C2GKA2	IG c756_light_IGKV1-12_IGKJ3 (Fragment)	2	0.46	0.01
A0A5C2G1H9	IGL c2982_light_IGKV4-1_IGKJ1 (Fragment)	4	0.46	0.04
A0A5C2GP39	IG c593_heavy_IGHV3-48_IGHD3-3_IGHJ4 (Fragment)	1	0.46	0.00
A0A5C2G2X3	IGL c1767_light_IGKV3-20_IGKJ3 (Fragment)	2	0.45	0.02
A0A5C2GFZ1	IGL c319_light_IGKV3D-20_IGKJ5 (Fragment)	2	0.45	0.05
B4DZM1	cDNA FLJ58310, highly similar to Homo sapiens trinucleotide repeat containing 15 (TNRC15), mRNA	1	0.43	0.01
A0A5C2GIP8	IGH + IGL c575_heavy_IGHV3-23_IGHD3-3_IGHJ3 (Fragment)	3	0.43	0.00

A0A0S2Z3L8	Decorin (Fragment)	2	0.43	0.00
A0A5C2FUJ1	IGL c668_light_IGKV3-20_IGKJ1 (Fragment)	2	0.43	0.01
A0A5C2G0C4	IGL c1856_light_IGKV3-20_IGKJ1 (Fragment)	3	0.42	0.01
B2R6V9	cDNA, FLJ93141, highly similar to Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA IGH + IGL	5	0.42	0.03
A0A5C2G966	c217_heavy_IGHV3-48_IGHD2-15_IGHJ4 (Fragment) IGH	2	0.42	0.04
A0A5C2G9T7	c33_heavy_IGHV3-33_IGHD3-10_IGHJ4 (Fragment) IGH	2	0.42	0.00
A0A5C2GVU1	IG c1453_light_IGKV3-11_IGKJ5 (Fragment) IGH	2	0.41	0.00
A0A5C2G7Y9	c508_heavy_IGHV3-33_IGHD1-7_IGHJ4 (Fragment) IG	1	0.41	0.03
A0A5C2GLW6	c505_heavy_IGHV4-34_IGHD1-26_IGHJ6 (Fragment) IGH	2	0.40	0.02
A0A5C2GA89	c185_heavy_IGHV3-7_IGHD3-16_IGHJ4 (Fragment) IG	1	0.40	0.01
A0A5C2GF46	c1011_heavy_IGHV3-7_IGHD3-3_IGHJ1 (Fragment) IGL c1933_light_IGKV3-11_IGKJ4 (Fragment)	2	0.40	0.01
A0A5C2G6A0	IGH + IGL c635_light_IGKV1D-39_IGKJ1 (Fragment)	3	0.39	0.02
A0A5C2GC09	IG c376_light_IGLV3-21_IGLJ2 (Fragment)	1	0.38	0.05
A0A5C2G7J4	IGL c454_light_IGKV3-11_IGKJ2 (Fragment) IGH + IGL	2	0.37	0.04
A0A5C2GBS8	c198_heavy_IGHV3-20_IGHD1-26_IGHJ4 (Fragment) IGH + IGL	2	0.36	0.03
A0A5C2GCK5	c478_heavy_IGHV3-21_IGHD6-19_IGHJ6 (Fragment) IGL c3692_light_IGKV1D-39_IGKJ1 (Fragment)	1	0.35	0.03
A0A5C2G3F9		2	0.34	0.03

	IGH				
A0A5C2G773	c452_heavy__IGHV3-7_IGHD3-3_IGHJ4 (Fragment)	1	0.33	0.00	
A0A5C2GWD7	IG c759_light_IGKV1D-33_IGKJ3 (Fragment)	1	0.33	0.00	
	IG				
A0A5C2GD14	c725_heavy_IGHV1-18_IGHD6-6_IGHJ4 (Fragment)	2	0.32	0.00	
	IG				
A0A5C2GUN0	c217_heavy_IGHV3-49_IGHD4-23_IGHJ6 (Fragment)	2	0.31	0.04	
	IGH				
A0A5C2G830	c558_heavy__IGHV3-43_IGHD3-10_IGHJ1 (Fragment)	1	0.30	0.02	
	IGH + IGL				
A0A5C2GHS8	c295_heavy_IGHV3-21_IGHD2-15_IGHJ4 (Fragment)	1	0.28	0.01	
	IG c1186_light_IGKV3-20_IGKJ2 (Fragment)	2	0.27	0.05	
	IG				
A0A5C2GQ71	c912_heavy_IGHV4-61_IGHD2-2_IGHJ6 (Fragment)	2	0.22	0.00	
	IGL c1204_light_IGKV3-20_IGKJ2 (Fragment)	1	0.21	0.01	
A0A5C2FX06	IGL c1949_light_IGKV4-1_IGKJ1 (Fragment)	1	0.17	0.02	
A0A5C2FYI7	IGH + IGL c305_light_IGKV2-28_IGKJ1 (Fragment)	3	0.15	0.00	
A0A5C2GB45	IG c1430_light_IGKV3-15_IGKJ4 (Fragment)	2	0.15	0.02	
A0A5C2H035	IGL c1528_light_IGKV3-15_IGKJ1 (Fragment)	1	0.14	0.04	

Notes: Red labeling indicates the upregulated proteins with at least 1.5-fold and green labeling indicates the downregulated proteins with at least 1.5-fold.

Appendix 6. GO analysis of serum differential proteins between 12th week of treatment (S-P) and pretreatment (F-P)

GO_Term	Category	Test Number	Over_Under	TestSeqs	p.value	FDR
carboxylic acid metabolic process	P	3	over	A0A024R145,B7Z8A2,A0A5F9ZHM4	0.01	0.39
organic acid metabolic process	P	3	over	A0A024R145,A0A5F9ZHM4,B7Z8A2	0.01	0.39

oxoacid metabolic process	P	3	over	A0A024R145,A0A5F9ZHM4,B7Z8A2	0.01	0.39
small molecule metabolic process	P	4	over	A0A024R145,Q13790,A0A5F9ZHM4,B7Z8A2	0.01	0.39
direct ossification	P	1	over	A0A024R6R4	0.02	0.39
head morphogenesis	P	1	over	A0A024R6R4	0.02	0.39
face morphogenesis	P	1	over	A0A024R6R4	0.02	0.39
face development	P	1	over	A0A024R6R4	0.02	0.39
sulfur amino acid metabolic process	P	1	over	B7Z8A2	0.02	0.39
prenylcysteine metabolic process	P	1	over	B7Z8A2	0.02	0.39
intramembranous ossification	P	1	over	A0A024R6R4	0.02	0.39
bone trabecula morphogenesis	P	1	over	A0A024R6R4	0.02	0.39
bone trabecula formation	P	1	over	A0A024R6R4	0.02	0.39
cellular modified amino acid catabolic process	P	1	over	B7Z8A2	0.02	0.39
sulfur amino acid catabolic process	P	1	over	B7Z8A2	0.02	0.39
prenylcysteine catabolic process	P	1	over	B7Z8A2	0.02	0.39
chemoattractant activity	F	1	over	P35542	0.02	0.39
prenylcysteine oxidase activity	F	1	over	B7Z8A2	0.02	0.39
fructose-1-phosphate aldolase activity	F	1	over	A0A024R145	0.02	0.39
lipid transporter activity	F	2	over	C0JYY2,Q13790	0.02	0.39
high-density lipoprotein particle	C	2	over	P35542,Q13790	0.03	0.39
collagen catabolic process	P	1	over	A0A024R6R4	0.03	0.39
body morphogenesis	P	1	over	A0A024R6R4	0.03	0.39

trabecula morphogenesis	P	1	over	A0A024R6R4	0.03	0.39
trabecula formation	P	1	over	A0A024R6R4	0.03	0.39
response to immobilization stress	P	1	over	L8E853	0.03	0.39
sulfur compound catabolic process	P	1	over	B7Z8A2	0.03	0.39
skeletal system morphogenesis	P	1	over	A0A024R6R4	0.03	0.39
blood vessel maturation	P	1	over	A0A024R6R4	0.03	0.39
cellular response to amino acid stimulus	P	1	over	A0A024R6R4	0.03	0.39
protein homooligomerization	P	1	over	L8E853	0.03	0.39
on lactate dehydrogenase activity	F	1	over	A0A5F9ZHM4	0.03	0.39
aldehyde-lyase activity	F	1	over	A0A024R145	0.03	0.39
L-lactate dehydrogenase activity	F	1	over	A0A5F9ZHM4	0.03	0.39
fructose-bisphosphate aldolase activity	F	1	over	A0A024R145	0.03	0.39
sarcomere	C	1	over	A0A024R6R4	0.03	0.39
Weibel-Palade body	C	1	over	L8E853	0.03	0.39
myofibril	C	1	over	A0A024R6R4	0.03	0.39
protein-lipid complex	C	2	over	Q13790,P35542	0.04	0.39
plasma lipoprotein particle	C	2	over	Q13790,P35542	0.04	0.39
lipoprotein particle	C	2	over	Q13790,P35542	0.04	0.39
carbohydrate metabolic process	P	2	over	A0A024R145,A0A5F9ZHM4	0.05	0.39
transporter activity	F	2	over	C0JYY2,Q13790	0.05	0.39

Appendix 7. GO analysis of serum differential proteins between 24th week of treatment (T-P) and pretreatment (F-P)

GO_Term	Category	Test Number	Over_Under	TestSeqs	p.value	FD R
sulfur compound catabolic process	P	2	over	A6NLG9,B7Z8A2	0.00	0.39
multicellular organism growth	P	2	over	O75882,B4DZM1	0.01	0.39
sulfur compound metabolic process	P	2	over	A6NLG9,B7Z8A2	0.01	0.39
developmental growth	P	3	over	B4DZM1,O75882,Q6UXB8	0.03	0.39
peptide cross-linking	P	2	over	A6NLG9,B2R6V9	0.04	0.39
pigmentation	P	1	over	O75882	0.05	0.39
multicellular organismal movement	P	1	over	B4DZM1	0.05	0.39
muscle adaptation	P	1	over	Q6UXB8	0.05	0.39
musculoskeletal movement	P	1	over	B4DZM1	0.05	0.39
negative regulation of muscle hypertrophy	P	1	over	Q6UXB8	0.05	0.39
negative regulation of cardiocyte differentiation	P	1	over	Q6UXB8	0.05	0.39
ventral spinal cord development	P	1	over	B4DZM1	0.05	0.39
regulation of muscle adaptation	P	1	over	Q6UXB8	0.05	0.39
sulfur compound biosynthetic process	P	1	over	A6NLG9	0.05	0.39
sulfur amino acid metabolic process	P	1	over	B7Z8A2	0.05	0.39
chondroitin sulfate metabolic process	P	1	over	A6NLG9	0.05	0.39
dermatan sulfate metabolic process	P	1	over	A6NLG9	0.05	0.39
prenylcysteine metabolic process	P	1	over	B7Z8A2	0.05	0.39
regulation of cell growth involved in cardiac muscle	P	1	over	Q6UXB8	0.05	0.39

cell development						
negative regulation of cell growth involved in cardiac muscle cell development	P	1	over	Q6UXB8	0.05	0.39
cell growth involved in cardiac muscle cell development	P	1	over	Q6UXB8	0.05	0.39
physiological cardiac muscle hypertrophy	P	1	over	Q6UXB8	0.05	0.39
negative regulation of muscle cell differentiation	P	1	over	Q6UXB8	0.05	0.39
cell differentiation in spinal cord	P	1	over	B4DZM1	0.05	0.39
cardiocyte differentiation	P	1	over	Q6UXB8	0.05	0.39
muscle cell development	P	1	over	Q6UXB8	0.05	0.39
cardiac cell development	P	1	over	Q6UXB8	0.05	0.39
regulation of muscle cell differentiation	P	1	over	Q6UXB8	0.05	0.39
regulation of cardiocyte differentiation	P	1	over	Q6UXB8	0.05	0.39
muscle hypertrophy	P	1	over	Q6UXB8	0.05	0.39
homeostasis of number of cells within a tissue	P	1	over	B4DZM1	0.05	0.39
negative regulation of cardiac muscle hypertrophy	P	1	over	Q6UXB8	0.05	0.39
negative regulation of cardiac muscle cell differentiation	P	1	over	Q6UXB8	0.05	0.39
spinal cord motor neuron differentiation	P	1	over	B4DZM1	0.05	0.39
spinal cord development	P	1	over	B4DZM1	0.05	0.39
regulation of cardiac muscle hypertrophy	P	1	over	Q6UXB8	0.05	0.39
aminoglycan biosynthetic process	P	1	over	A6NLG9	0.05	0.39
cellular modified amino acid catabolic process	P	1	over	B7Z8A2	0.05	0.39
sulfur amino acid catabolic process	P	1	over	B7Z8A2	0.05	0.39
chondroitin sulfate catabolic process	P	1	over	A6NLG9	0.05	0.39

chondroitin sulfate biosynthetic process	P	1	over	A6NLG9	0.05	0.39
dermatan sulfate biosynthetic process	P	1	over	A6NLG9	0.05	0.39
peptide cross-linking via chondroitin 4-sulfate glycosaminoglycan	P	1	over	A6NLG9	0.05	0.39
prenylcysteine catabolic process	P	1	over	B7Z8A2	0.05	0.39
proteoglycan metabolic process	P	1	over	A6NLG9	0.05	0.39
negative regulation of STAT cascade	P	1	over	A6NLG9	0.05	0.39
negative regulation of striated muscle cell differentiation	P	1	over	Q6UXB8	0.05	0.39
cardiac muscle cell differentiation	P	1	over	Q6UXB8	0.05	0.39
striated muscle cell development	P	1	over	Q6UXB8	0.05	0.39
cardiac muscle cell development	P	1	over	Q6UXB8	0.05	0.39
regulation of striated muscle cell differentiation	P	1	over	Q6UXB8	0.05	0.39
regulation of cardiac muscle cell differentiation	P	1	over	Q6UXB8	0.05	0.39
physiological muscle hypertrophy	P	1	over	Q6UXB8	0.05	0.39
regulation of muscle hypertrophy	P	1	over	Q6UXB8	0.05	0.39
striated muscle hypertrophy	P	1	over	Q6UXB8	0.05	0.39
thyroid hormone transport	P	1	over	A6XGL1	0.05	0.39
negative regulation of transferase activity	P	1	over	A6NLG9	0.05	0.39
glycosaminoglycan biosynthetic process	P	1	over	A6NLG9	0.05	0.39
proteoglycan biosynthetic process	P	1	over	A6NLG9	0.05	0.39
chondroitin sulfate proteoglycan metabolic process	P	1	over	A6NLG9	0.05	0.39
dermatan sulfate proteoglycan metabolic	P	1	over	A6NLG9	0.05	0.39

process						
negative regulation of JAK-STAT cascade	P	1	over	A6NLG9	0.05	0.39
cardiac muscle hypertrophy	P	1	over	Q6UXB8	0.05	0.39
negative regulation of kinase activity	P	1	over	A6NLG9	0.05	0.39
chondroitin sulfate proteoglycan biosynthetic process	P	1	over	A6NLG9	0.05	0.39
dermatan sulfate proteoglycan biosynthetic process	P	1	over	A6NLG9	0.05	0.39
negative regulation of protein kinase activity	P	1	over	A6NLG9	0.05	0.39
peptidyl-serine modification	P	1	over	A6NLG9	0.05	0.39
transferase activity, transferring amino-acyl groups	F	1	over	B2R6V9	0.05	0.39
thyroid hormone binding	F	1	over	A6XGL1	0.05	0.39
kinase regulator activity	F	1	over	A6NLG9	0.05	0.39
protein-glutamine gamma-glutamyltransferase activity	F	1	over	B2R6V9	0.05	0.39
kinase inhibitor activity	F	1	over	A6NLG9	0.05	0.39
protein kinase regulator activity	F	1	over	A6NLG9	0.05	0.39
chemoattractant activity	F	1	over	P35542	0.05	0.39
prenylcysteine oxidase activity	F	1	over	B7Z8A2	0.05	0.39