

Label-Free Quantitative Proteomics for Investigating the Therapeutic Mechanism of Sijunzi Decoction on Spleen Deficiency Syndrome

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Supplementary Table S1. The model group compared the normal control group up-regulate differentially expressed proteins of spleen deficiency syndrome in liver tissue

Supplementary Table S2. The model group compared the normal control group down-regulate differentially expressed proteins of spleen deficiency syndrome in liver tissue

Supplementary Table S3. The model group compared the Sijunzi decoction-treated group up-regulate differentially expressed proteins in liver tissue

Supplementary Table S4. The model group compared Sijunzi decoction-treated group down-regulate differentially expressed proteins in liver tissue

Supplementary table S1. The model group compared the normal control group up-regulate

differentially expressed proteins of spleen deficiency syndrome in liver tissue

Protein IDs	Protein name	Mol. Weight [kDa]	M/NC	P value
P02803	Metallothionein-1	6.0061	7.86900444	0.00252558
P03889	NADH-ubiquinone oxidoreductase chain 1	36.145	1.592723575	0.025804023
Q642C0	DnaJ homolog subfamily C member 8	29.812	2.985640203	0.017126266
Q9QZA6	CD151 antigen	28.355	7.653816199	0.001192592
A1A5S4	Protein Sephs2	35.61	5.579461135	0.005316635
F1LY38	Protein Cwc22	105.03	3.821536145	0.020605251
D3ZML4	Protein Trabd	42.114	5.293102332	0.001953997
D3ZZ20	Protein Afg311	87.202	1.557188905	0.000305998
D4A4W6	Protein Slirp	12.576	1.629983324	0.006928597
F1M6Q3	Protein Col4a2	166.25	2.767910315	0.026596744
G3V7Q6	Proteasome subunit beta type	28.559	1.929639432	0.009199381
M0RCP9	Protein Pin4	13.815	1.52560294	0.01631365
P62749	Hippocalcin-like protein 1	22.338	3.844765343	0.010597404
5M9G9	Protein TBRG4	71.18	2.172970189	0.017991998
99J86	Attractin	158.67	2.964898222	0.00087568
D4A4P4	Protein Flad1	54.604	1.701285126	0.00564803
D4A8H5	Protein Ppp4r2	45.943	3.342909895	0.025182036
F1LR71	Protein Aspscr1	50.973	1.700430674	0.018602222
F1LYI7	Protein LOC100913000	11.776	1.862797414	0.028103495
G3V8Z5	Protein LOC680329	14.283	3.005639271	0.015067294
Q6TUG7	LRRGT00077	32.144	2.150441962	0.009285663
Q9JHL6	Carcinoembryonic antigen-related cell adhesion molecule 1	51.414	1.65193883	0.006301062

G3V798	Protein Srsf4	55.674	1.512620748	0.010419826
O35760	Isopentenyl-diphosphate Delta-isomerase 1	26.396	1.684814682	7.96018E-05
O88900	Growth factor receptor-bound protein 14	60.592	1.621000341	0.042781496
P00697	Lysozyme C-1	16.729	1.669097473	0.007407416
P07483	Fatty acid-binding protein, heart	14.775	2.897660238	0.00317745
P39069	Adenylate kinase isoenzyme 1	21.584	3.874898848	0.022709801
Q01129	Decorin	39.805	2.596990346	0.045278669
Q63042	FAD-linked sulfhydryl oxidase ALR [Pyruvate dehydrogenase (acetyl-transferring)]	22.836	2.589395765	0.019570769
Q63065	kinase isozyme 1, mitochondrial	49.08	1.808443017	0.046470365
Q6P747	Heterochromatin protein 1-binding protein 3	60.806	1.571212331	0.03026128
Q9R0T4	Cadherin-1	98.714	2.209895489	0.001272409
D3ZA93	Protein Acot13	15.27	2.816492649	0.011743618
F1LN42	Protein Tns1	203.91	2.366348865	0.02379845
G3V8Q8	Protein Sec23ip	110.94	2.411724437	0.032455517
D3ZXP3	Protein H2afx	15.114	2.246380523	0.035582588
F1MAM0	Cationic amino acid transporter 2	76.904	6.760989734	0.0008825
O88453	Scaffold attachment factor B1	104.57	1.560353331	0.046505299
O88496	Vitamin K-dependent gamma-carboxylase	87.478	1.813169999	0.002387759
P43165	Carbonic anhydrase 5A, mitochondrial	34.499	1.608450399	0.000258691
Q00566-2	Isoform B of Methyl-CpG-binding protein 2	55.082	1.95196271	0.048110111

D3ZD11	Protein Spcs2	24.973	1.531271945	0.031246936
	NADH dehydrogenase (Ubiquinone) 1,			
D3ZF13	alpha/beta subcomplex,	17.514	1.613689859	0.002237569
	1 (Predicted), isoform CRA_a			
	Mitochondrial ribosomal			
D4A3E8	protein S27 (Predicted),	47.648	2.109671721	0.036814471
	isoform CRA_b			
	N-acetylglutamate synthase			
D4A904	(Predicted), isoform CRA_a	57.42	2.008700987	0.039645513
F1LYK3	Protein LOC685707	202.35	1.951955701	0.045038237
G3V7F6	Protein RGD1561590	19.586	1.96579534	0.028675275
Q4V8N0	Lipocalin 7, isoform CRA_a	52.764	1.659692842	0.005186358
E9PSI7	Alpha-amylase	57.166	4.771636815	0.000221395
	Isocitrate dehydrogenase			
P41565	[NAD] subunit gamma 1,	42.851	1.5591858	0.031498869
	mitochondrial			
P43278	Histone H1.0	20.885	2.279054534	0.006740616
	Elongation factor G,			
Q07803	mitochondrial	83.456	1.681918328	0.011136309
	Peripheral plasma membrane			
Q62915	protein CASK	103.26	1.607955881	0.038775892
	2-amino-3-carboxymuconate-			
Q8R5M5	6-semialdehyde decarboxylase	38.091	6.77653758	0.033863436
	Nuclear ubiquitous casein and			
Q9EPJ0	cyclin-dependent kinase	27.14	3.248567769	0.00058542
	substrate 1			
Q6T5E8	Protein LOC100912040	59.571	1.507563275	0.006807089
D4A147	Protein Ugt2a3	51.412	2.357811213	0.00012672
P07340	Sodium/potassium-transporting	35.201	2.145019856	0.005146678

	ATPase subunit beta-1			
P16232	Corticosteroid 11-beta -dehydrogenase isozyme 1	31.883	2.68878794	9.35621E-06
P21588	5-nucleotidase	63.968	1.649890548	0.000483551
P40615	H/ACA ribonucleoprotein complex subunit 4	56.614	1.841063026	0.00439754
Q64536	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2,mitochondrial	46.105	1.669714846	0.011346334
D4A9A3	Protein Cenpv	27.382	1.647391494	0.002626617
E9PST1	Protein RGD1310507	50.86	1.568116643	0.000230282
Q9Z2Y0	Glycine N-acyltransferase -like protein Keg1	34.016	2.001978808	2.34486E-06
P19225	Cytochrome P450 2C70	56.156	1.667037449	0.005334213
P47853	Biglycan	41.706	1.561342567	0.000746489
B2RYS2	Protein LOC685596	13.558	1.512765718	0.015445714
O35913	Solute carrier organic anion transporter family member 1A4	73.251	1.862894404	0.000433362
Q08201	Multidrug resistance protein 3	140.65	1.600782895	0.001538112
G3V9N7	Protein Pacsin3	48.726	1.513556857	0.002259842
P48450	Lanosterol synthase	83.3	1.894981686	0.00219603
D3ZPY8	Protein Akr1c13	36.9	4.945567475	0.000975027
P42123	L-lactate dehydrogenase B chain	36.612	1.633949965	0.001687601
P04694	Tyrosine aminotransferase	50.635	5.430597843	0.000603442
Q562C4	Methyltransferase-like protein 7B	27.904	5.10051254	0.000468522
Q6AXV4	Sorting and assembly machinery component 50 homolog	51.96	1.91123889	0.000976582
G3V9J8	Glycerol-3-phosphate acyltransferase 1,	93.726	1.534943737	0.000595706

	mitochondrial			
M0R9J5	Adenylosuccinatesynthetase isozyme 1	52.607	1.663075596	0.000939859
O08557	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	31.426	1.524294497	0.038565592
P04466	Myosin regulatory light chain 2, skeletal muscle isoform	18.969	13.89125635	0.003943536
P15083	Polymeric immunoglobulin receptor	84.797	1.512837046	0.012985494
Q05096	Unconventional myosin-Ib	131.92	1.667151781	0.00074859
Q68G31	Phenazine biosynthesis-like domain-containing protein	31.687	1.694405473	0.00349124
M0R7F6	Protein Etnppl	55.53	5.558657599	0.003018288
Q63610-2	Isoform 2 of Tropomyosin alpha-3 chain	28.72	2.407296132	0.021682178
Q6T5E9	Protein LOC100912040	60.235	1.839230385	1.63489E-05
Q6SKG1	Acyl-coenzyme A synthetase ACSM3, mitochondrial	65.712	3.447753494	1.27245E-06
P09367	L-serine dehydratase/L -threonine deaminase	38.432	1.803323175	0.000718242
P21643	Tryptophan 2,3-dioxygenase	47.856	3.655035882	0.00055951
P36365	Dimethylaniline monooxygenase [N-oxide-forming] 1	59.825	1.937525706	0.000461734
P02600	Myosin light chain 1/3, skeletal muscle isoform	20.679	2.892572221	0.000743198
O70490	Acyl-coenzyme A synthetase ACSM2, mitochondrial	64.144	3.190975601	0.000137235
D3Z9X1	Uncharacterized protein (Fragment)	55.496	6.134354744	0.000681906
P13697	NADP-dependent malic enzyme	64.002	2.383748079	6.73332E-05
Q8VHT6	Arsenite methyltransferase	41.056	1.806785621	0.000639889

	Glutamic pyruvate transaminase			
G3V872	(Alanine aminotransferase)	57.841	3.683052589	3.65708E-05
	2 (Predicted), isoform CRA_b			
Q5BJQ0	Atypical kinase ADCK3, mitochondrial	72.225	1.507506227	0.001658332
M0RBL9	Protein Vwa8 (Fragment)	78.996	1.622156013	0.021467575
Q920F5	Malonyl-CoA decarboxylase, mitochondrial	54.761	1.570999632	0.001248936
Q68FT5	S-methylmethionine--homocysteine S-methyltransferase BHMT2	39.928	1.572561375	1.35967E-05
Q6AYT9	Acyl-coenzyme A synthetase ACSM5, mitochondrial	64.622	2.443861434	7.36817E-05
Q4QQW3	Hydroxyacid-oxoacid transhydrogenase, mitochondrial	50.225	1.550164439	0.0003284
P17425	Hydroxymethylglutaryl-CoA synthase, cytoplasmic	57.433	2.095735211	4.66021E-06
P07824	Arginase-1	34.973	1.732703013	0.000395114
P17178	Sterol 26-hydroxylase, mitochondrial	60.732	1.503312259	0.000140337
F1LQZ8	Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial	103.92	1.535981091	0.002442188
Q6Q0N1	Cytosolic non-specific dipeptidase	52.693	1.516254876	0.001214572
F1MAR6	Protein ProdH	68.094	2.007368914	0.00026533
P13444	S-adenosylmethionine synthase isoform type-1	43.697	1.608238457	0.000539823
O35547	Long-chain-fatty-acid--CoA ligase 4	74.326	1.648236095	0.001837988
P13221	Aspartate aminotransferase, cytoplasmic	46.428	2.424507234	0.000184369
P25409	Alanine aminotransferase 1	55.109	2.040542166	1.04119E-05
P68136	Actin, alpha skeletal muscle	42.051	3.221609195	2.78478E-06
Q64578	Sarcoplasmic/endoplasmic	109.41	6.784292072	0.00178769

	reticulum calcium ATPase 1			
O09171	Betaine--homocysteine S-methyltransferase 1	44.976	1.81764852	0.000120599
Q5SGE0	Leucine-rich PPR motif-containing protein, mitochondrial	156.65	1.651239501	0.000653068
F1LNW3	Acyl-coenzyme A oxidase	76.746	1.98048518	1.20115E-06
O70127	Bile salt export pump	146.26	1.788362177	0.002186722
P06685	Sodium/potassium-transporting ATPase subunit alpha-1	113.05	1.516655294	0.005935222
P11497	Acetyl-CoA carboxylase 1	265.19	1.826247492	8.48805E-05
G3V8B0	Myosin-7	222.9	3.297894359	0.000180864
F1LRV9	Protein Myh2	223.28	36.37199804	0.000112819
P12785	Fatty acid synthase	272.65	2.09306676	7.04479E-06

Supplementary table S2. The model group compared the normal control group down-regulate differentially expressed proteins of spleen deficiency syndrome in liver tissue

Protein IDs	Protein name	Mol. Weight [kDa]	M/NC	P value
B2GV54	Neutral cholesterol ester hydrolase 1	45.821	0.248846103	0.016854715
P01681	Ig kappa chain V region S211	11.433	0.206984865	0.011303672
R9PXZ7	Leukosialin	39.739	0.210976039	0.002196645
Q6AXR5	UDP-N-acetylglucosamine transporter	36.078	0.279948034	0.021483172
Q8K1P8	Monocarboxylate transporter 8	60.118	0.399502578	0.003647242
Q920L7	Elongation of very long chain fatty acids protein 5	35.235	0.348276861	0.025026164
D3ZQL7	Protein Tppp	23.546	0.30304237	0.021820104
F7EQ04	Protein RGD1312005	21.682	0.608794822	0.016572735
Q4KM87	Actin-like 6A	47.42	0.362962893	0.038983071
F1LZH0	Protein LOC100912707 (Fragment)	13.611	0.624371998	0.010928068

M0R684	Protein Ces2a (Fragment)	15.398	0.43052685	0.02087412
O55166	Vacuolar protein sorting-associated protein 52 homolog	82.102	0.537924545	0.028594845
P11466	Peroxisomal carnitine O-octanoyltransferase	70.302	0.236092764	0.004328215
P23764	Glutathione peroxidase 3	25.442	0.665230607	0.033705903
Q5XID1	Anamorsin	33.041	0.633630081	0.047497067
Q62967	Diphosphomevalonate decarboxylase	43.902	0.597196959	0.023662828
Q66HA6	ADP-ribosylation factor-like protein 8B	21.539	0.392930953	0.028208424
Q6AY20	Cation-dependent mannose-6-phosphate receptor	31.095	0.469656717	0.000667669
Q6MG48	Protein PRRC2A	229.04	0.314534444	0.033304172
D3ZIK1	Protein Lin28b	30.078	0.5660099	0.033800334
D3ZWS2	Protein LOC690000	15.07	0.611814665	0.034347305
D4A238	Protein Rtp4	27.75	0.277661162	0.009134091
D4A4L6	Uncharacterized protein	12.969	0.339763859	0.02146447
G3V8D4	Apolipoprotein C-II (Predicted)	10.695	0.531657341	0.027745926
M0RBD5	Uncharacterized protein (Fragment)	11.023	0.551511679	0.003980072
Q66H18	Protein Syp11	28.628	0.349571287	0.042514203
Q6MGA3	Antigen peptide transporter 2	77.749	0.294381948	0.0196733
P17078	60S ribosomal protein L35	14.552	0.665942732	0.007109502
P50115	Protein S100-A8	10.238	0.422221164	0.000147093
P62268	40S ribosomal protein S23	15.807	0.611748393	0.013748901
Q9QUH3	Apolipoprotein A-V	41.426	0.292311476	0.003814709
B5DEJ6	Protein Tpk1	27.207	0.381019321	0.032033734
D4A8T3	Coatomer protein complex, subunit zeta 1 (Predicted)	20.198	0.385721415	0.037289039
D4A9Z8	Protein Chmp4b	25.109	0.602261757	0.002517689
E9PTI1	Protein Atp6v1h	50.825	0.441148149	0.021465152

Q5M860	Protein Arhgdib	22.884	0.283725847	0.016841594
Q5XI04	Protein Stom	31.378	0.387526831	0.043531584
Q7TPJ4	Ac2-202	54.292	0.584453765	0.048162366
P05371	Clusterin	51.375	0.481551841	0.002890924
P50116	Protein S100-A9	13.145	0.299046045	0.019425805
Q63184	Interferon-induced, double-stranded RNA-activated protein kinase	58.258	0.384442052	0.047197721
Q8K5B3	Multiple coagulation factor deficiency protein 2 homolog	16.148	0.427822769	0.025027891
Q8R431	Monoglyceride lipase	33.499	0.433175516	0.000240599
Q91ZN1	Coronin-1A	51.065	0.430521199	0.006213905
D3ZD09	Cytochrome c oxidase subunit 6B1	10.071	0.660003004	0.047775158
D4A3X3	Interferon, alpha-inducible protein (Clone IFI-15K) (Predicted)	18.225	0.403478038	0.000612181
E9PSZ7	Protein Cyp2t1	56.111	0.176356707	0.00392333
Q6IN37	GM2 ganglioside activator	21.493	0.575360507	0.024565491
D3ZE31	Protein Ces2a	61.932	0.241997079	0.000960401
Q9Z269	Vesicle-associated membrane protein-associated protein B	26.916	0.536190295	0.006057777
O70513	Galectin-3-binding protein	63.742	0.353828571	0.022595259
P04916	Retinol-binding protein 4	23.22	0.598632848	0.020431291
P08011	Microsomal glutathione S-transferase 1	17.471	0.558083436	0.006132445
P61459	Pterin-4-alpha-carbinolamine dehydratase	11.999	0.567874886	0.012923936
P63174	60S ribosomal protein L38	8.2178	0.3892662	0.007802612
Q01579	Glutathione S-transferase theta-1	27.468	0.633697156	0.006251487
Q4KM35	Proteasome subunit beta type-10	29.038	0.552341628	0.024415878
Q9QZH8	Arylacetamide deacetylase	45.692	0.610044581	0.013845286
D3ZV91	Protein L3hypdh	37.914	0.530662443	0.0242775
D4A3I4	Protein Btf3l4	17.27	0.379704164	0.006866617

D4A605	Nicotinamide N-methyltransferase (Predicted)	29.515	0.377675636	0.042829871
G3V778	Pyruvate dehydrogenase kinase, isoenzyme 4	46.609	0.115987859	5.89192E-06
G3V8L1	PYD and CARD domain containing Proteasome (Prosome, macropain)	21.673	0.636249344	0.040558423
Q6MGA6	subunit, beta type 9 (Large multifunctional peptidase 2)	23.343	0.587157308	0.003594072
Q99JC6	Protein Tapbp	50.044	0.592858851	0.002738996
P84083	ADP-ribosylation factor 5	20.529	0.656914682	0.01565525
Q5U1Y2	Protein Rac2	21.441	0.543714186	0.015149291
P20759	Ig gamma-1 chain C region	35.945	0.210717248	1.2365E-05
G3V645	2-5-oligoadenylate synthase-like protein 1	58.968	0.567406408	0.00937891
P01835	Ig kappa chain C region, B allele	11.601	0.653147605	0.001606562
Q5M891	C4b-binding protein alpha chain	67.201	0.5547618	0.000291286
Q9Z1Y3	Cadherin-2	99.685	0.658866403	0.005659034
A0JN30	Canopy 2 homolog (Zebrafish)	20.709	0.66600546	0.04462009
F1M9V7	Protein Npepps	103.34	0.542749579	0.03515551
G3V680	Beta-galactoside alpha-2,6-sialyltransferase 1	46.753	0.494535618	0.000862966
Q499V1	Protein Upp1	34.114	0.483215454	0.002909164
P29457	Serpin H1	46.517	0.540151061	0.04554475
Q6AYC2	Immunity-related GTPase family M protein	46.337	0.553007535	0.00355286
Q6MG61	Chloride intracellular channel protein 1	26.98	0.664911108	0.048735056
D3ZFD0	Uncharacterized protein	232.66	0.666307389	0.024257548
D3ZV82	Protein LOC685067	71.481	0.381836535	0.047371562
F1LPW0	Uncharacterized protein (Fragment)	54.871	0.284270721	0.00393899

O70535	Leukemia inhibitory factor receptor	122.39	0.557960637	0.026042362
P07335	Creatine kinase B-type	42.725	0.596445958	0.015251171
P50237	Sulfotransferase 1C1	35.764	0.654274181	0.007538158
Q3MID3	ADP-ribosylation factor GTPase-activating protein 2	56.556	0.663616054	0.042994642
Q9EPH1	Alpha-1B-glycoprotein	56.478	0.347336171	0.000122315
D3ZUX1	Protein Hykk	42.475	0.321813107	0.000690993
F1LPS6	Protein Ifit1 (Fragment)	53.479	0.1259678	0.000693161
Q5VLR5	BWK4	46.878	0.641723967	0.001759977
M0RAS6	Protein LOC100910979	93.889	0.081647069	0.04462841
B5DEY0	Pls1 protein	51.65	0.28878695	0.034206193
Q498D5	Regulator of microtubule dynamics protein 2	47.217	0.589203174	0.000610116
Q6P6S9	Ectonucleoside triphosphate diphosphohydrolase 5	47.372	0.588320978	0.008513699
Q7TP52	Carboxymethylenebutenolidase homolog	27.903	0.581144949	0.003564879
Q62669	Protein Hbb-b1	16.022	0.666164752	0.002348918
A0JPJ7	Obg-like ATPase 1	44.535	0.587964135	0.000275489
Q63083	Nucleobindin-1	53.506	0.544701049	0.028779095
Q68G31	Phenazine biosynthesis-like domain-containing protein	31.687	1.694405473	0.00349124
G3V7V6	All-trans-13,14-dihydroretinol saturase, isoform CRA_b	67.477	0.437420286	0.007616376
Q4V797	Interferon-gamma-inducible GTPase Ifgga1 protein	48.271	0.204258001	0.001783896
B0BNN3	Carbonic anhydrase 1	28.299	0.648301141	0.006641146
B2RYT7	Haloacid dehalogenase-like hydrolase domain containing 3	27.794	0.59599985	0.001662908
Q9Z0V5	Peroxiredoxin-4	31.007	0.549858875	0.005253869

P14141	Carbonic anhydrase 3	29.431	0.516539893	5.02999E-06
Q5RJP0	Aldose reductase-related protein 1	36.121	0.515438904	0.001005849
Q64563	Alcohol dehydrogenase 4	40.276	0.610293011	0.000781243
Q6XQN1	Nicotinate phosphoribosyltransferase	58.564	0.472134548	3.25532E-06
B0BN46	Grhpr protein	35.937	0.630415267	0.00012184
P01048	T-kininogen 1	47.775	0.482908546	0.025821982
F7F3M3	Protein Ces2a	44.35	0.465986512	0.000260702
Q6DGG0	Peptidyl-prolyl cis-trans isomerase D	40.765	0.626242131	0.000273678
Q68G19	RCG57123	61.026	0.616572095	0.00068558
D4ABY2	Coatomer subunit gamma-2	80.488	0.647508336	0.003219493
Q5I0H9	Protein disulfide-isomerase A5	59.399	0.456726023	0.000711883
F7F469	Protein Igtp	157.77	0.482632869	0.000656987
M3ZCQ0	Sulfotransferase	33.12	0.360937073	0.002673091
P02680	Fibrinogen gamma chain	50.632	0.590993265	0.001698773
P20059	Hemopexin	51.35	0.553350607	0.000103684
Q5BKC4	C9 protein	63.774	0.35413409	4.56806E-05
D4AAV1	Protein Amdhd1	46.57	0.610169643	0.000292219
F1M9D6	Protein Stat1	87.249	0.511505278	0.004840624
P55006	Retinol dehydrogenase 7	35.736	0.450894154	0.00309931
Q5XI38	Lymphocyte cytosolic protein 1	70.121	0.632779528	0.001155858
F8WFT7	Band 3 anion transport protein	103.24	0.645952	0.001022492
P08932	T-kininogen 2	47.704	0.423230808	1.09196E-05
Q5RKI1	Eukaryotic initiation factor 4A-II	46.402	0.528005206	0.000562501
G3V9R2	Protein Cfh	140.23	0.639115781	0.004791174
F1MAC0	Protein Ifi47	47.432	0.590704909	0.000233376
Q63010	Liver carboxylesterase B-1	62.494	0.588861294	0.000652947
P08541	UDP-glucuronosyltransferase 2B2	60.985	0.306563434	6.1891E-05
P31000	Vimentin	53.732	0.617884625	0.004803407
P06399	Fibrinogen alpha chain	86.685	0.550842898	8.97217E-05

P16303	Carboxylesterase 1D	62.146	0.470279714	5.7086E-06
O88813	Long-chain-fatty-acid--CoA ligase 5	76.404	0.652692519	0.013565763
Q4AEF8	Coatomer subunit gamma-1	97.613	0.659518725	0.003299395
P51647	Retinal dehydrogenase 1	54.458	0.614263357	8.9587E-06
P14480	Fibrinogen beta chain Isoform 2 of Fibrinogen beta chain	54.235	0.576746966	0.000303983
D3ZCF8	Protein Abca8	184.06	0.620925854	0.000309357
P08649	Complement C4	192.16	0.631221497	0.00049511
P14046	Alpha-1-inhibitor 3	163.77	0.494398594	2.64357E-05
Q63041	Alpha-1-macroglobulin	167.12	0.575008756	0.000124181

Supplementary table S3. The model group compared the Sijunzi decoction-treated group up-regulate differentially expressed proteins in liver tissue

Protein IDs	Protein name	Mol. weight [kDa]	M/SJZD	P. value
P18437	Non-histone chromosomal protein HMG-17	9.3654	1.844233555	0.014590434
Q07066	Peroxisomal membrane protein 2	22.577	1.838902271	0.04096295
A1A5S4	Protein Sephs2	35.61	2.675991194	0.004670811
D3ZBJ0	LSM5 homolog, U6 small nuclear RNA associated (<i>S. cerevisiae</i>) (Predicted), isoform CRA_c	9.9374	1.898019831	0.005721734
D3ZML4	Protein Trabd	42.114	7.370587352	0.002925881
D4ACG8	Protein Fuom	16.83	4.66187473	0.005034431
Q05175	Brain acid soluble protein 1	21.79	2.807682261	0.046841672
Q5U3Y7	Transmembrane protein 97	20.946	1.610618032	0.014391369
Q5XIE0	Acidic leucine-rich nuclear phosphoprotein 32 family member E	29.418	2.155420998	0.019223592
Q63619	Ubiquinone biosynthesis protein COQ7 homolog (Fragment)	20.14	1.874693192	0.045829175

Q68FV1	Trimeric intracellular cation channel type B	32.444	1.678641207	0.026338189
D3ZF45	Protein Larp4b	81.084	1.758776496	0.000844879
D4A197	Methylmalonyl CoA epimerase (Predicted), isoform CRA_d	18.816	2.433878824	0.002817391
G3V7K5	Protein Npc1	142.95	1.686845727	0.029562903
P01015	Angiotensinogen	51.981	1.519021293	0.007237224
P80385	5-AMP-activated protein kinase subunit gamma-1	37.386	1.764654068	0.027972245
Q5BK32	FAS-associated factor 2	41.079	1.540103189	0.02303191
Q9JHW0	Proteasome subunit beta type-7	29.927	1.566214409	0.000537786
D3ZQM0	Protein Sf3a1	88.587	1.514706156	0.002403205
G3V8Q8	Protein Sec23ip	110.94	2.02446079	0.048860437
Q5I0K1	Pipecolic acid oxidase	43.89	3.80557468	0.038957626
Q99PV2	Protein Stxbp3	68.02	4.667025282	0.00391088
D3ZXP3	Protein H2afx	15.114	2.022923649	0.010882446
F1MAM0	Cationic amino acid transporter 2	76.904	3.591693728	0.00117466
O35078	D-amino-acid oxidase	38.82	1.62248411	0.049267318
P28073	Proteasome subunit beta type-6	25.289	1.768733169	0.000598677
Q5HZE4	Methylthioribose-1-phosphate isomerase	39.587	1.754946505	0.011513417
F1LYK3	Protein LOC685707	202.35	1.948249738	0.043762841
M0R907	Protein Snrpd3	13.916	1.561597566	0.049184812
D3ZE31	Protein Ces2a	61.932	1.709662317	0.000179827
F1M3H8	Protein Hnrnpa0	30.296	1.708566723	0.003611077
P43278	Histone H1.0	20.885	1.539787841	0.001329149
Q9EPJ0	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	27.14	2.959195146	0.000948182
D3ZJ32	Protein Esyt2	94.414	3.859124844	0.030830218
F1LPR6	Uncharacterized protein (Fragment)	41.307	6.555579838	0.011680996
D4A147	Protein Ugt2a3	51.412	5.662867211	2.96668E-06

Q06884	Cytochrome P-450	57.675	2.505292721	8.18116E-05
M0R9D0	Acidic leucine-rich nuclear phosphoprotein 32 family member A	28.305	1.842160108	0.037435081
B0BN63	LOC681996 protein	38.104	1.55463543	0.005161955
G3V816	Non-metastatic cell expressed protein 3	19.119	1.513010401	0.005238988
Q5U3Y8	Basic transcription factor 3	17.699	1.682303618	0.009525401
Q07439	Heat shock 70 kDa protein 1A/1B	70.184	1.540547438	0.025233431
Q9Z2Y0	Glycine N-acyltransferase-like protein Keg1	34.016	1.499698152	0.001061032
O35821	Myb-binding protein 1A	152.28	1.924879499	0.001235728
P19225	Cytochrome P450 2C70	56.156	1.601995368	0.015904456
Q7TQM4	Sterol O-acyltransferase 2	60.497	1.694132335	0.01859851
A3KN98	Bco2 protein	60.19	1.693874936	0.000105273
O70196	Prolyl endopeptidase	80.741	1.698267556	0.000383507
P16970	ATP-binding cassette sub-family D member 3	75.315	1.755281199	0.003420393
P48450	Lanosterol synthase	83.3	1.64309453	0.003921828
Q64638	UDP-glucuronosyltransferase 1-5	59.993	1.501716686	0.009810376
D3ZPY8	Protein Akr1c13	36.9	3.093205265	0.023569905
P04694	Tyrosine aminotransferase	50.635	3.422314374	0.001921661
P97584	Prostaglandin reductase 1	35.718	1.536076449	0.001204787
Q562C4	Methyltransferase-like protein 7B	27.904	2.035629703	0.002827715
D3ZUF9	Pitrilysinmetallepetidase 1 (Predicted)	108.54	1.539831881	0.00036756
G3V9J8	Glycerol-3-phosphate acyltransferase 1, mitochondrial	93.726	1.535337502	4.14775E-06
Q64550	UDP-glucuronosyltransferase 1-1	59.662	1.501069017	0.019843831
P57093	Phytanoyl-CoA dioxygenase, peroxisomal	38.588	1.584174231	0.00296807
M0R7F6	Protein Etnppl	55.53	5.445312243	0.002965803
P09367	L-serine dehydratase/L-threonine deaminase	38.432	2.675890841	0.000254416
P21643	Tryptophan 2,3-dioxygenase	47.856	2.529168645	5.49252E-05

P36365	Dimethylaniline monooxygenase [N-oxide-forming] 1	59.825	1.606979729	0.000457783
D3Z9X1	Uncharacterized protein (Fragment)	55.496	2.526984306	0.014727517
B1H250	Protein RGD1564894	33.986	1.538000025	0.005120152
Q8VHT6	Arsenite methyltransferase	41.056	2.493106218	0.000196181
G3V872	Glutamic pyruvate transaminase (Alanine aminotransferase) 2 (Predicted), isoform CRA_b	57.841	1.743360351	7.11666E-05
F1M7N8	Protein LOC102550717	60.594	4.413196626	0.009047546
M3ZCQ0	Sulfotransferase	33.12	5.251481526	0.001078899
P09118	Uricase	34.934	1.81187644	3.4457E-05
P55006	Retinol dehydrogenase 7	35.736	10.19326574	0.000731884
Q68FT5	S-methylmethionine--homocysteine S-methyltransferase BHMT2	39.928	1.615716156	2.79935E-05
Q63276	Bile acid-CoA:amino acid N-acyltransferase	46.464	1.845951156	0.002413928
P17425	Hydroxymethylglutaryl-CoA synthase, cytoplasmic	57.433	1.856238352	1.81883E-05
P07824	Arginase-1	34.973	1.555837664	0.000549448
P22789	Alcohol sulfotransferase A	33.251	1.705067724	9.64085E-05
P13221	Aspartate aminotransferase, cytoplasmic	46.428	1.528831671	0.001018692
B3DMA2	Acyl-CoA dehydrogenase family member 11	87.37	1.517496635	0.000733774
P80299	Bifunctional epoxide hydrolase 2	62.34	1.789896335	6.22383E-05
P97852	Peroxisomal multifunctional enzyme type 2	79.427	1.560331081	0.000466667
F1LNW3	Acyl-coenzyme A oxidase	76.746	1.998250236	1.08075E-05

Supplementary table S4. The model group compared Sijunzi decoction-treated group down-regulate differentially expressed proteins in liver tissue

Protein IDs	Protein name	Mol. Weight [kDa]	M/SJZD	P. value
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B2GV54	Neutral cholesterol ester hydrolase 1	45.821	0.506429573	0.000807209
O70257	Syntaxin-7	29.85	0.209062099	0.011450329
P01681	Ig kappa chain V region S211	11.433	0.248604265	0.008903793
P02803	Metallothionein-1	6.0061	0.584657587	0.047943417
R9PXZ7	Leukosialin	39.739	0.281582439	0.039900005
P14423	Phospholipase A2, membrane associated	16.294	0.266587273	0.017351127
P55314	Complement component C8 beta chain	66.666	0.310149419	0.018069455
P62744	AP-2 complex subunit sigma	17.018	0.637489744	0.013738598
Q62833	G protein-coupled receptor kinase 5	67.782	0.400271656	0.045364471
P97849	Long-chain fatty acid transport protein 1	71.282	0.277322721	0.010743964
Q498T4	39S ribosomal protein L2, mitochondrial	32.999	0.646850266	0.039166463
Q8K1P8	Monocarboxylate transporter 8	60.118	0.584112602	0.015261584
Q9R0J8	Legumain	49.466	0.664742917	0.036725922
B0BNN4	Complement factor properdin	50.572	0.460375047	0.007801932
D3ZDS2	Protein Msr1	49.247	0.593077039	0.026828122
D3ZGY1	Protein Wibg	22.726	0.39483687	0.047812196
I6L9G5	Protein Rcn3	37.941	0.345425697	0.034863342
M0R8G6	Uncharacterized protein (Fragment)	10.694	0.509161368	0.001256253
M0R9U2	Uncharacterized protein (Fragment)	10.845	0.33959863	7.31146E-07
O08719	Ena/VASP-like protein	42.094	0.547217057	0.045191932
P11654	Nuclear pore membrane glycoprotein 210	204.16	0.639923242	0.033562733
P11762	Galectin-1	14.857	0.586069709	0.004205626
G3V6Z7	Golgi autoantigen, golgin subfamily a, 5, isoform CRA_a	82.405	0.586582693	0.0202909
Q62967	Diphosphomevalonate decarboxylase	43.902	0.579336311	0.000358132
Q6P4Z9	COP9 signalosome complex subunit 8	23.235	0.643209604	0.00431381
G3V9G5	Protein Synm	172.88	0.62587073	0.007448991
B0BMZ1	Protein RGD1305587	13.185	0.608196889	0.000294811
D3ZBB2	Protein LOC100361952	13.383	0.491591577	0.003046348

D3ZQR5	Uncharacterized protein	12.767	0.234678928	0.022847464
D3ZYM7	Protein LOC102550385	10.816	0.405837465	7.37118E-05
D4A238	Protein Rtp4	27.75	0.232268512	0.003793661
M0RBD5	Uncharacterized protein (Fragment)	11.023	0.5072364	0.010541204
Q4PP99	Cardiac troponin C	18.42	0.232737682	0.016136546
D3ZE00	Uncharacterized protein	13.104	0.650853026	0.001272435
A1L1K3	Anaphase-promoting complex subunit 5	81.738	0.186603981	0.033115048
D3ZVR7	Prostamide/prostaglandin F synthase	21.607	0.512771872	0.005044219
P02625	Parvalbumin alpha	11.925	0.111492526	0.000164144
P09739	Troponin T, fast skeletal muscle	30.75	0.193529449	0.003626453
P19633	Calsequestrin-1	46.448	0.194045917	0.008750283
P50115	Protein S100-A8	10.238	0.595907118	0.000736044
Q6AYC4	Macrophage-capping protein	38.798	0.532210876	0.031471759
Q920R3	Fatty acid desaturase 1	52.481	0.264087433	0.012109857
	Cytochrome c oxidase subunit VIIa			
D3ZYX8	polypeptide 2 like (Predicted), isoform CRA_e	13.273	0.597472339	0.012125723
M0R6J6	Creatine kinase S-type, mitochondrial	46.34	0.254697141	4.57129E-05
Q56R17	Karyopherin (Importin) alpha 4	57.922	0.398092598	0.041194853
Q5M860	Protein Arhgdib	22.884	0.26442111	0.008136907
Q6TUD3	LRRGT00111	44.779	0.665258496	0.006140774
D3Z8I7	Protein Gstt3	23.381	0.644769728	0.000749031
Q304F3	Protein Tnnc2	18.096	0.083277179	0.000285675
P02764	Alpha-1-acid glycoprotein	23.575	0.154579217	0.000489829
P05371	Clusterin	51.375	0.6191004	0.000925788
P27768	Troponin I, fast skeletal muscle	21.328	0.195077416	0.000396133
Q4KM74	Vesicle-trafficking protein SEC22b	24.74	0.629838261	0.007205084
Q5FWT1	Protein FAM98A	55.07	0.578453773	0.011532041
Q8K5B3	Multiple coagulation factor deficiency	16.148	0.545060152	0.023866613

protein 2 homolog				
Q91ZN1	Coronin-1A	51.065	0.465748031	0.002633947
D3ZWD6	Complement component 8, alpha polypeptide (Predicted)	66.273	0.398011691	0.044423386
D4A3X3	Interferon, alpha-inducible protein (Clone IFI-15K) (Predicted)	18.225	0.519319819	0.002610847
Q5U1W6	Apolipoprotein O-like	28.237	0.588253176	0.000397403
Q6IN37	GM2 ganglioside activator	21.493	0.655910832	0.02371694
O70513	Galectin-3-binding protein	63.742	0.405620945	0.043742138
Q01579	Glutathione S-transferase theta-1	27.468	0.66362458	0.005373374
Q4KM35	Proteasome subunit beta type-10	29.038	0.444382278	0.020543401
Q5I0K3	Citrate lyase subunit beta-like protein, mitochondrial	37.321	0.612279504	0.004441913
Q62638	Golgi apparatus protein 1	133.56	0.664197577	0.012211518
Q5PQW8	Guanylate binding protein 2	67.355	0.086637826	0.037128765
Q8R5M5	2-amino-3-carboxymuconate-6-semialdehyde decarboxylase	38.091	0.378888498	0.005331434
D4A896	Protein Abcg313	73.429	0.60667718	0.024955031
G3V778	Pyruvate dehydrogenase kinase, isoenzyme 4	46.609	0.112563365	4.91474E-06
Q5BK21	Protein Tm7sf2	46.444	0.529396801	0.040129667
Q6MGA6	Proteasome (Prosome, macropain) subunit, beta type 9 (Large multifunctional peptidase 2)	23.343	0.603036901	0.009424686
Q99JC6	Protein Tapbp	50.044	0.551381079	0.000340636
Q6T5E8	Protein LOC100912040	59.571	0.614397098	0.049093563
P16391	RT1 class I histocompatibility antigen, AA alpha chain	41.83	0.124414835	0.000886372
Q5U1Y2	Protein Rac2	21.441	0.531927818	0.010807535
G3V645	2-5-oligoadenylate synthase-like protein 1	58.968	0.555584517	0.014489567

P01835	Ig kappa chain C region, B allele	11.601	0.623671069	0.005288254
P52555	Endoplasmic reticulum resident protein 29	28.574	0.603457832	0.004944053
Q5U2U0	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	69.207	0.664414536	0.026737984
Q5M891	C4b-binding protein alpha chain	67.201	0.264575568	0.000554472
Q9QZ76	Myoglobin	17.157	0.505765154	0.010907694
D3ZUM4	Galactosidase, beta 1 (Mapped)	73.227	0.376039394	0.036157622
F1MAA0	Protein Ttn	401.7	0.351975579	0.030238241
G3V615	Complement factor B, isoform CRA_b	85.352	0.658486182	0.020800933
G3V680	Beta-galactoside alpha-2,6-sialyltransferase 1	46.753	0.536890801	0.003461621
P31977	Ezrin	69.39	0.26134359	0.043424799
F7ERG5	Protein RT1-A2 (Fragment)	41.45	0.658155239	0.015839623
P16290	Phosphoglycerate mutase 2	28.755	0.191807983	0.0067466
P06762	Heme oxygenase 1	33.005	0.396483488	0.042119221
D3ZHZ6	Cytochrome P450 4A10	58.328	0.601489992	0.005923281
P08733	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	18.88	0.292133457	0.000434306
P29457	Serpin H1	46.517	0.490691933	0.011511038
Q6MG61	Chloride intracellular channel protein 1	26.98	0.511890756	0.007051004
Q6P792	Four and a half LIM domains 1	33.578	0.196032807	8.06197E-05
B0BMT9	Protein Sqrdl	50.201	0.387959499	0.009966818
F1LPW0	Uncharacterized protein (Fragment)	54.871	0.388075767	0.000949091
P46418	Glutathione S-transferase alpha-5	25.347	0.560107643	0.002108723
F1LPQ6	Uncharacterized protein (Fragment)	38.698	0.655107924	0.000208687
P50237	Sulfotransferase 1C1	35.764	0.375634495	2.44067E-05
F1LPS6	Protein Ifit1 (Fragment)	53.479	0.068040712	3.77347E-05
M0RAS6	Protein LOC100910979	93.889	0.169887514	0.039985773
Q5I0M4	Aldo-keto reductase family 1, member C13	37.012	0.515292075	0.000470318
P42123	L-lactate dehydrogenase B chain	36.612	0.49352138	0.000695504

P55053	Fatty acid-binding protein, epidermal	15.059	0.455979445	0.000164936
Q68FT3	Pyridine nucleotide-disulfide oxidoreductase domain-containing protein 2	62.878	0.377322954	0.00024077
Q7TP52	Carboxymethylenebutenolidase homolog	27.903	0.660620872	0.003830057
P58775-2	Isoform 2 of Tropomyosin beta chain	32.957	0.400425737	0.004307111
P16409	Myosin light chain 3	22.156	0.278343569	2.69433E-05
P04466	Myosin regulatory light chain 2, skeletal muscle isoform	18.969	0.115451248	0.000477634
Q63083	Nucleobindin-1	53.506	0.499603362	0.004435559
G3V7V6	All-trans-13,14-dihydroretinol saturase, isoform CRA_b	67.477	0.503052739	0.001596896
M0RBP9	Coatomer subunit beta (Fragment)	56.778	0.661221585	0.007221242
Q63610-2	Isoform 2 of Tropomyosin alpha-3 chain	28.72	0.504663685	0.026028882
Q5BK56	Glutathione S-transferase mu 4	25.553	0.482209363	0.001106501
Q05962	ADP/ATP translocase 1	32.989	0.131782551	0.000983913
P50235	Alcohol sulfotransferase	33.531	0.104572522	0.000311871
Q4V797	Interferon-gamma-inducible GTPase Ifgga1 protein	48.271	0.275803615	0.01104296
Q6P725	norvegicus	53.422	0.380600382	0.002117866
P00564	Creatine kinase M-type	43.044	0.242268009	1.29955E-05
P02600	Myosin light chain 1/3, skeletal muscle isoform	20.679	0.170714174	4.57311E-06
P04692	Tropomyosin alpha-1 chain	32.68	0.156932219	0.001775003
P14141	Carbonic anhydrase 3	29.431	0.569524785	7.1588E-06
Q64563	Alcohol dehydrogenase 4	40.276	0.648419439	0.000185663
P01048	T-kininogen 1	47.775	0.443955445	0.02525825
F7F3M3	Protein Ces2a	44.35	0.642246559	0.001825105
G3V8J2	Cytochrome P450, family 8, subfamily b, polypeptide 1	57.725	0.662717761	0.000273963

Q8R4I6	Actinin alpha 3, isoform CRA_a	103.01	0.380082297	0.033495768
P15429	Beta-enolase	47.013	0.162737878	9.85839E-07
F7F469	Protein Igtp	157.77	0.566910887	0.000248698
G3V9U0	Acyl-CoA synthetase short-chain family member 2 (Predicted)	78.887	0.652569211	0.004338938
P11980-2	Isoform M2 of Pyruvate kinase PKM	57.78	0.520656116	0.002018273
P10867	L-gulonolactone oxidase	50.615	0.60670674	0.000201585
P02680	Fibrinogen gamma chain	50.632	0.571597876	3.63834E-05
P20059	Hemopexin	51.35	0.560300451	1.49923E-05
Q5BKC4	C9 protein	63.774	0.245730364	7.91656E-06
F1M9D6	Protein Stat1	87.249	0.563184335	0.010471562
Q5XI38	Lymphocyte cytosolic protein 1	70.121	0.564061465	0.000799117
P06866-2	Isoform 2 of Haptoglobin	42.474	0.626094243	4.43262E-05
P08932	T-kininogen 2	47.704	0.399286047	7.08981E-05
G3V7Q7	IQ motif containing GTPase activating protein 1 (Predicted), isoform CRA_b	188.83	0.503930008	0.038475658
F1LN61	Uncharacterized protein	36.563	0.645804557	3.3331E-05
P05065	Fructose-bisphosphate aldolase A	39.351	0.476594107	0.000373967
P12939	Cytochrome P450 2D10	57.076	0.664530152	0.006126168
G3V9R2	Protein Cfh	140.23	0.473486191	0.000394068
F1MAC0	Protein Ifi47	47.432	0.497709187	0.000280065
P08541	UDP-glucuronosyltransferase 2B2	60.985	0.273898058	3.06689E-05
P68136	Actin, alpha skeletal muscle	42.051	0.248912406	4.4322E-06
D3ZCV0	Protein Actn2	103.83	0.162769912	0.000217593
P31000	Vimentin	53.732	0.62625	0.007020618
Q64578	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	109.41	0.122561436	2.96179E-05
P06399	Fibrinogen alpha chain	86.685	0.478647352	0.000125004
P07687	Epoxide hydrolase 1	52.581	0.545357252	3.22855E-05

Q499N5	Acyl-CoA synthetase family member 2, mitochondrial	67.886	0.651483023	0.000572944
F1LPB3	Long-chain-fatty-acid--CoA ligase 5	76.526	0.638772823	0.000247152
P11507	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	114.77	0.665883562	0.001131511
A0A096P6L8	Fibronectin	209.52	0.556993614	0.007614056
P51647	Retinal dehydrogenase 1	54.458	0.626108444	0.000118694
P14480	Fibrinogen beta chain	54.235	0.534874142	2.66206E-05
P12928-2	Isoform L-type of Pyruvate kinase PKLR	58.793	0.66300202	0.000331485
Q63342	Dimethylglycine dehydrogenase, mitochondrial	96.046	0.595637814	0.011701365
G3V888	ATP citrate lyase, isoform CRA_a	120.78	0.362355684	3.10627E-05
M0RBF1	Complement C3	186.32	0.548635708	0.000163671
F1LMU0	Myosin-4	222.85	0.112028579	0.03672935
G3V8B0	Myosin-7	222.9	0.207928071	2.9602E-07
G3V6E1	Uncharacterized protein	219.63	0.147042847	4.17814E-05
F1LRV9	Protein Myh2	223.28	0.110151917	5.11352E-06