

A proteo-transcriptomic map of non-alcoholic fatty liver disease signatures

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Supplementary Table S1. Patient demographics discovery cohort.

Clinical feature	Discovery cohort (n=191)	T2DM			F3-F4			NAS≥4			
		yes	no	p-value	yes	no	p-value	yes	no	p-value	Test
Age (years)	55.24 +/- 11.04	57.16 +/- 10.13	52.28 +/- 11.77	0.005194	56.86 +/- 10.37	54.1 +/- 11.39	0.086267	55.09 +/- 10.96	55.57 +/- 11.3	0.735964	Mann-Whitney U Test
Sex (% female)	38.7	39.66	37.33	0.747709	36.71	40.18	0.627849	42.75	30.00	0.093217	chi-square
BMI	33.47 +/- 6.67	34.7 +/- 6.6	31.56 +/- 6.35	0.000455	33.47 +/- 6.29	31.85 +/- 6.48	0.000009	34.32 +/- 6.43	31.62 +/- 6.87	0.004339	Mann-Whitney U Test
T2DM (%)	60.73	-	-		82.28	45.54	3.04E-07	67.18	46.67	0.007058	chi-square
Plts *10 ⁹	224.08 +/- 67.57	222.1 +/- 64.96	227.15 +/- 71.76	0.643818	216.71 +/- 79.28	229.29 +/- 57.73	0.117157	228.48 +/- 73.27	214.48 +/- 52.32	0.196513	Mann-Whitney U Test
AST (u/L)	43.27 +/- 21.80	45.49 +/- 22.33	39.83 +/- 20.63	0.083272	53.15 +/- 22.24	36.29 +/- 18.64	5.76E-09	48.85 +/- 22.34	31.08 +/- 14.53	5.55E-10	Mann-Whitney U Test
ALT (u/L)	59.70 +/- 33.47	60.84 +/- 34.29	57.93 +/- 32.33	0.490027	68.20 +/- 33.58	53.71 +/- 32.22	0.000935	66.52 +/- 34.37	44.82 +/- 26	0.000001	Mann-Whitney U Test
Steatosis				0.453791			0.62781			3.91E-19	chi-square
1	72	41	31		27	45		21	51		
2	82	54	28		37	45		73	9		
3	37	21	16		15	22		37	0		
Ballooning				0.000077			1.31E-08			1.14E-11	chi-square
0	26	7	19		1	25		5	21		
1	108	65	43		38	70		71	37		
2	57	44	13		40	17		55	2		
Lobular Inflammation				0.074619			0.000319			1.15E-13	chi-square
0	19	7	12		3	16		1	18		
1	109	66	43		37	72		68	41		
2	61	41	20		38	23		60	1		
3	2	2	0		1	1		2	0		
Brunt Fibrosis				8.56E-08			3.23E-40			0.000024	chi-square
0	30	7	23		0	30		13	17		
1	56	26	30		0	56		30	26		
2	26	18	8		0	26		23	3		
3	56	46	10		56	0		47	9		
4	23	19	4		23	0		18	5		
NASH (%)	82.2	91.38	68.00	0.000037	72.32	96.20	0.000021	95.42	53.33	1.69E-12	chi-square
NAS≥4 (%)	68.59	75.86	57.33	0.007058	82.28	58.93	0.000617	-	-		chi-square
F3-4 (%)	41.14	56.03	18.67	3.04E-07	-	-		49.62	23.33	0.000617	chi-square

Supplementary Table S2. Proteomics analysis of 191 NAFLD plasma comparing fibrosis stage F3-4 vs baseline F0-2, corrected for sex, centre and T2DM (Benjamini-Hochberg false discovery rate)

Seq_ID	Prot_ID	logFC	AveExpr	t	P.Value	adj.P.Val
6379-62	ADAMTSL2	0.811499	5.441107	11.94999	5.62E-25	2.96E-21
3339-33	THBS2	1.110356	9.459685	10.9796	4.36E-22	1.15E-18
18882-7	CLSTN2	0.713373	4.826478	10.76768	1.84E-21	2.57E-18
4430-44	COLEC11	1.108784	7.924007	10.75937	1.95E-21	2.57E-18
3320-49	IGFBP7	0.380736	10.55276	10.02049	2.78E-19	2.93E-16
5636-10	MFAP4	0.654039	5.902806	9.632734	3.6E-18	3.17E-15
7179-69	NFASC	0.433402	5.362726	9.072233	1.37E-16	1.04E-13
2844-53	TIE1	0.354911	8.133766	8.326696	1.53E-14	1.01E-11
9377-25	KITLG	-0.40869	6.446717	-7.83701	3.07E-13	1.67E-10
13682-47	CSF1R	0.471703	7.48062	7.831953	3.16E-13	1.67E-10
3470-1	SELE	0.508595	10.16049	7.127598	2E-11	8.81E-09
11646-4	CHST9	0.472917	4.958641	7.055498	3.03E-11	1.19E-08
6527-1	TRIL	0.400859	6.811331	7.048804	3.15E-11	1.19E-08
16818-200	CDCP1	0.57152	7.203658	6.951237	5.48E-11	1.7E-08
5028-59	CD163	0.408776	6.976311	6.950896	5.49E-11	1.7E-08
3311-27	FCGR3B	0.43408	7.471102	6.885696	7.94E-11	2.33E-08
17456-53	GOLM1	0.54749	7.706002	6.84212	1.01E-10	2.82E-08
15431-31	OTC	1.025538	7.691387	6.72079	2E-10	5.27E-08
13133-73	LTBP4	0.388172	9.177252	6.710255	2.12E-10	5.32E-08
18173-11	AKR7A3	0.879792	7.708759	6.598203	3.93E-10	9.44E-08
6576-1	ART4	0.407154	6.324532	6.574332	4.48E-10	1.03E-07
13717-15	FCN2	-0.42638	9.275241	-6.41835	1.05E-09	2.21E-07
2952-75	IGF1	-0.55997	8.143833	-6.39075	1.22E-09	2.38E-07
5737-61	SEMA4D	0.361268	6.229998	6.247696	2.62E-09	4.74E-07
19581-15	IGFBP5	-0.40109	7.085282	-6.2424	2.69E-09	4.74E-07
3284-75	BGN	0.371897	7.898085	6.158789	4.2E-09	6.92E-07
11109-56	SVEP1	0.414864	6.424363	6.144155	4.53E-09	7.13E-07
6077-63	CECR1	0.546389	9.469767	6.133105	4.8E-09	7.13E-07
11178-21	SVEP1	0.42747	6.421544	6.127931	4.94E-09	7.13E-07
9715-15	IGSF3	0.373138	4.412386	6.120484	5.13E-09	7.13E-07
17782-23	ACAA1	0.678144	8.783432	6.06029	7.03E-09	9.28E-07
15475-4	PLTP	0.325208	8.833601	6.053069	7.3E-09	9.31E-07
14079-14	IL18R1	0.40612	8.262083	6.016041	8.86E-09	1.04E-06
11241-8	ASL	0.657557	9.16099	5.981263	1.06E-08	1.22E-06
7019-13	SEMA7A	0.397113	5.93514	5.97212	1.11E-08	1.22E-06
3503-4	ITGA1 ITGB1	0.521772	9.78422	5.972027	1.11E-08	1.22E-06
12370-30	APOF	-0.646	7.753566	-5.92775	1.4E-08	1.45E-06
8304-50	TNFRSF11B	0.420184	7.988973	5.927248	1.4E-08	1.45E-06
16081-38	AKR1B10	0.913563	8.894256	5.903732	1.58E-08	1.61E-06
8337-65	PTPRU	0.391917	7.472262	5.803305	2.64E-08	2.53E-06
5121-3	SEMA6B	0.370983	5.975784	5.692961	4.61E-08	4.27E-06
15533-97	MSR1	0.431639	8.681483	5.628836	6.35E-08	5.68E-06
8923-94	GALNT16	0.373142	7.018788	5.614127	6.83E-08	5.92E-06

3447-64	CXCL8	0.346502	5.664041	5.613587	6.85E-08	5.92E-06
9931-20	KRT1	0.462207	6.961084	5.537313	9.98E-08	8.36E-06
7999-23	ENTPD1	0.395724	6.072204	5.478358	1.33E-07	1.08E-05
17768-50	HAO1	0.651885	5.847291	5.472537	1.37E-07	1.1E-05
7551-33	LRRC32	0.322405	6.786715	5.454053	1.5E-07	1.16E-05
12663-1	TST	0.458216	6.358902	5.417554	1.79E-07	1.35E-05
6448-36	SEMA3C	0.348941	5.115991	5.372088	2.23E-07	1.59E-05
6605-17	IGFALS	-0.384	9.602472	-5.34777	2.51E-07	1.74E-05
7959-34	CDH7	-0.33073	8.583032	-5.33277	2.7E-07	1.83E-05
3293-2	CD5L	0.483307	8.509954	5.308513	3.03E-07	2.02E-05
10866-60	SMEK1	0.341144	9.642082	5.235261	4.29E-07	2.83E-05
18901-26	HSPA1B	0.386688	8.948832	5.23184	4.37E-07	2.84E-05
5508-62	CTSD	0.42652	6.873863	5.210118	4.84E-07	3.08E-05
18188-12	GATM	0.590158	8.771284	5.204006	4.98E-07	3.13E-05
19617-5	PTGR1	0.549043	10.64063	5.188201	5.36E-07	3.29E-05
3050-7	VWF	0.611651	9.224145	5.173732	5.74E-07	3.48E-05
3049-61	PRSS1	-0.45488	7.329822	-5.14831	6.47E-07	3.77E-05
18893-26	GPR56	0.413794	6.245587	5.078277	8.97E-07	5.05E-05
9580-5	LAMC2	0.373289	6.331564	5.077743	8.99E-07	5.05E-05
9772-153	NLGN2	0.333421	4.103729	5.023255	1.16E-06	6.36E-05
19120-33	DAO	0.324642	4.21669	4.995785	1.31E-06	6.99E-05
11287-14	CYB5A	0.366264	6.012359	4.990105	1.35E-06	7.1E-05
10803-22	HSPA1A	0.344874	7.273378	4.874337	2.28E-06	0.000111
10749-18	HSPA1A	0.366057	7.532547	4.793865	3.27E-06	0.000151
8983-7	GOLM1	0.54904	6.740157	4.783226	3.43E-06	0.000157
5000-52	LGALS3BP	0.357532	8.771033	4.740097	4.15E-06	0.000184
9829-91	SULT2A1	0.597237	3.314615	4.739584	4.16E-06	0.000184
19197-95	ACAT1	0.574738	8.362384	4.737606	4.19E-06	0.000184
6359-50	POMGNT2	0.326125	5.508461	4.650638	6.14E-06	0.000257
18397-5	AKR1C4	0.711662	8.230998	4.598674	7.69E-06	0.000313
4546-27	ADGRE2	0.3754	7.663681	4.596416	7.77E-06	0.000313
9969-8	SLC22A16	-0.41783	8.280028	-4.57368	8.57E-06	0.00034
18185-118	ALDOB	0.569289	8.510528	4.559488	9.11E-06	0.000356
13492-44	HSPA9	0.428561	7.808643	4.550267	9.48E-06	0.000368
2731-29	POR	0.433381	7.837501	4.546331	9.64E-06	0.000371
5430-66	SIRPA	0.536741	7.309928	4.5041	1.15E-05	0.000426
13983-27	CRYZ	0.601128	7.950211	4.494313	1.2E-05	0.000441
18917-53	AMY2A	-0.39577	8.43842	-4.45967	1.39E-05	0.000497
2681-23	HGF	0.41172	5.984086	4.436016	1.54E-05	0.000533
13392-13	ATP1B1	-0.34427	6.654994	-4.42278	1.63E-05	0.000558
5353-89	IL1RN	0.330123	7.032045	4.321998	2.48E-05	0.000797
3069-52	IGHM IGI IGK@ IGL@	0.389893	7.599814	4.285678	2.88E-05	0.000904
3343-1	ACY1	0.654256	8.123984	4.216201	3.82E-05	0.001146
16620-26	LY75	0.334699	7.919238	4.212885	3.87E-05	0.001155
15556-49	AMY2B	-0.33726	5.591009	-4.12582	5.5E-05	0.001527

3310-62	FCGR2B	0.490749	6.210732	4.122495	5.57E-05	0.001532
4374-45	GDF15	0.402443	9.909949	4.11272	5.79E-05	0.001575
4234-8	IL1RL1	0.322473	6.944597	3.964429	0.000104	0.002545
15363-32	APOA5	-0.35482	8.081196	-3.95375	0.000108	0.00264
16300-4	TREM2	0.354218	9.66672	3.940584	0.000114	0.002743
6471-53	CFHR4	-0.78972	9.577361	-3.90195	0.000132	0.003093
11104-13	CHI3L1	0.681666	8.051781	3.702931	0.000278	0.00576
3313-21	FCN2	-0.33154	11.64123	-3.69323	0.000288	0.005923
4535-50	BST1	0.353099	8.560208	3.673036	0.000311	0.006256
7206-20	FBP1	0.41975	8.95545	3.587905	0.000423	0.007913
4929-55	SHBG	0.467472	7.481542	3.559987	0.000467	0.008623
2212-69	PLAT	0.344	8.226273	3.543018	0.000496	0.009034
6213-10	CGB2	0.356431	6.270862	3.537301	0.000507	0.009125
9986-14	NPW	0.570931	7.506144	3.462564	0.000659	0.011116
19335-2	HN1	-0.42133	6.558972	-3.41963	0.000766	0.012467
12627-97	ATG7	-0.34016	4.810903	-3.32592	0.001056	0.015914
8048-9	FTMT	-0.36616	7.239857	-3.29616	0.001167	0.017109
9253-52	ABO	1.216839	9.193858	3.194467	0.001637	0.022499
17787-1	ECHS1	0.419809	9.639293	3.182374	0.001704	0.023169
18381-16	ALDH2	0.376943	7.066654	3.181302	0.00171	0.023191
4435-66	ENPP7	0.477713	8.20253	3.180055	0.001717	0.023226
17758-79	DCXR	0.333853	6.820472	3.174597	0.001747	0.023524
8300-82	PEX14	0.3354	4.951527	3.168901	0.00178	0.023724
17396-23	ADH1A	0.388407	9.117731	3.152978	0.001875	0.024677
10700-10	IGSF11	-0.57418	4.403175	-3.12046	0.002084	0.026496
7859-21	PCDHGC3	-0.4138	6.087429	-3.03689	0.002722	0.031989
14150-7	IL36A	-0.38983	6.655166	-3.02386	0.002836	0.03304
9739-4	MSH2	0.340458	5.0584	3.007958	0.002982	0.034431
12394-53	C16orf54	0.345842	4.304297	2.979696	0.003258	0.036968
9213-24	FTCD	0.696501	10.54269	2.967442	0.003384	0.037836
9832-33	HGD	0.326008	6.96329	2.932773	0.003767	0.041161
6580-29	PZP	-0.72495	5.579797	-2.86449	0.004641	0.04737
16828-8	COL6A1	0.402965	8.476906	2.846112	0.004906	0.049122

Supplementary Table S3. Proteomics analysis of 191 NAFLD plasma comparing NAS $\geq$ 4 to NAS $<$ 4, corrected for sex, centre and T2DM (Benjamini-Hochberg false discovery rate)

Seq_ID	Prot_ID	logFC	AveExpr	t	P.Value	adj.P.Val
19617-5	PTGR1	0.709834	10.65149	6.597547	3.95E-10	2.08E-06
18398-1	AKR1D1	0.692049	5.654246	6.25448	2.53E-09	6.67E-06
17138-8	GSTA1	0.59826	6.716996	6.164578	4.07E-09	7.16E-06
18173-11	AKR7A3	0.856029	7.661145	6.056098	7.19E-09	9.48E-06
18397-5	AKR1C4	0.897977	8.215337	5.635281	6.15E-08	6.49E-05
11313-100	PCBD1	0.475933	6.902215	5.437433	1.63E-07	0.000125
8325-37	ADH4	0.675213	9.441038	5.430993	1.68E-07	0.000125
7206-20	FBP1	0.645228	8.988682	5.40629	1.89E-07	0.000125
17396-23	ADH1A	0.664929	9.163206	5.30882	3.03E-07	0.000177
3503-4	ITGA1 ITGB1	0.487272	9.756303	5.232775	4.35E-07	0.000211
14636-25	HRSP12	0.472088	8.968137	5.230079	4.4E-07	0.000211
6379-62	ADAMTSL2	0.438272	5.33044	5.177044	5.65E-07	0.000232
18185-118	ALDOB	0.671969	8.51564	5.174509	5.72E-07	0.000232
9829-91	SULT2A1	0.678077	3.30708	5.157223	6.2E-07	0.000234
12370-30	APOF	-0.59518	7.809011	-5.12113	7.35E-07	0.000258
19241-31	RBP5	0.384945	7.686203	5.031741	1.11E-06	0.000367
3339-33	THBS2	0.605059	9.309428	4.914384	1.9E-06	0.000589
17758-79	DCXR	0.528901	6.856828	4.902244	2.01E-06	0.000589
18901-26	HSPA1B	0.379854	8.930734	4.853145	2.51E-06	0.000673
15562-24	GUSB	0.497407	7.678665	4.839487	2.66E-06	0.000673
9832-33	HGD	0.544487	6.992119	4.77752	3.51E-06	0.000806
10749-18	HSPA1A	0.379269	7.521161	4.713613	4.66E-06	0.001025
16818-200	CDCP1	0.424651	7.143365	4.695979	5.04E-06	0.001063
3470-1	SELE	0.359238	10.10873	4.542707	9.79E-06	0.001913
13967-14	TXNRD1	0.396184	7.901958	4.482931	1.26E-05	0.002222
10803-22	HSPA1A	0.332643	7.257642	4.431744	1.57E-05	0.002669
2731-29	POR	0.438189	7.822986	4.349006	2.22E-05	0.003341
11424-4	FAH	0.413774	8.566145	4.286742	2.87E-05	0.0042
9931-20	KRT1	0.379708	6.926123	4.220593	3.75E-05	0.005078
3343-1	ACY1	0.684509	8.095875	4.183478	4.36E-05	0.005746
18342-2	PSAT1	0.503414	9.654546	4.177686	4.46E-05	0.005746
11241-8	ASL	0.498862	9.102031	4.168514	4.63E-05	0.00582
16300-4	TREM2	0.390028	9.65984	4.126519	5.48E-05	0.006573
13939-14	UGP2	0.335935	4.797654	4.107597	5.91E-05	0.00678
3216-2	PIGR	0.469805	7.562641	4.024141	8.22E-05	0.008671
9213-24	FTCD	0.978389	10.57104	4.004959	8.86E-05	0.009043
17755-5	UGDH	0.643968	9.510802	3.956313	0.000107	0.010652
11265-8	ALDH1A1	0.558853	7.884879	3.913553	0.000126	0.012326
13983-27	CRYZ	0.555098	7.912424	3.898565	0.000134	0.012496
15447-45	SORD	0.435121	11.05304	3.895862	0.000135	0.012496
16616-137	ENO3	0.400336	6.769721	3.815639	0.000183	0.016094
12663-1	TST	0.343984	6.325106	3.749249	0.000235	0.018472
17377-1	AKR1C3	0.325198	6.182696	3.71762	0.000264	0.019877

16081-38	AKR1B10	0.622579	8.784872	3.673698	0.00031	0.021968
13998-26	ADSSL1	0.419586	6.180073	3.6716	0.000312	0.021968
3050-7	VWF	0.466392	9.170541	3.648013	0.00034	0.023319
15675-3	CEBPB	-0.33984	5.340598	-3.63751	0.000354	0.023613
15431-31	OTC	0.608183	7.556523	3.570082	0.000451	0.027658
9933-49	ATP1B4	-0.49831	4.562781	-3.52839	0.000523	0.030325
6471-53	CFHR4	-0.75381	9.618786	-3.50797	0.000562	0.031896
15525-294	ADH1C	0.667872	8.7253	3.481571	0.000617	0.032881
18449-33	PPIG	-0.34373	5.868784	-3.44375	0.000704	0.036072
5102-55	MICB	0.384082	3.901227	3.421671	0.00076	0.038573

Supplementary Table S4. Pearson Correlation analysis of circulating proteins with hepatic mRNA.

Seq_ID	Target	Ensembl_ID	Official_gene_name	p value	corr.coef	95_conf_int	95_conf_int.1
4929-55	SHBG	ENSG00000129214	<i>SHBG</i>	1.78E-17	0.876268	0.79300049	0.927396253
15395-15	GST M1-1	ENSG00000134184	<i>GSTM1</i>	1.3E-15	0.851284	0.753413109	0.9122534
6580-29	Pregnancy zone protein	ENSG00000126838	<i>PZP</i>	2.67E-15	0.846576	0.746031835	0.909381085
3504-58	LEAP-1	ENSG00000105697	<i>HAMP</i>	2.27E-14	0.831597	0.722710503	0.9002024
7145-1	ITIH3	ENSG00000162267	<i>ITIH3</i>	4.69E-11	0.763398	0.619575237	0.857627716
8323-163	TFF3	ENSG00000160180	<i>TFF3</i>	5.07E-11	0.762557	0.618333775	0.857094558
3339-33	TSP2	ENSG00000186340	<i>THBS2</i>	5.66E-11	0.761361	0.616568015	0.856335353
4435-66	ENPP7	ENSG00000182156	<i>ENPP7</i>	7E-11	0.75903	0.613133366	0.854855619
4874-3	Angiogenin	ENSG00000214274	<i>ANG</i>	2.92E-10	0.742664	0.58917403	0.844422774
8960-3	LRAP	ENSG00000164308	<i>ERAP2</i>	2.26E-09	0.716896	0.551986859	0.827837191
3060-43	C9	ENSG00000113600	<i>C9</i>	6.57E-09	0.702246	0.531133563	0.818320615
3367-8	FETUB	ENSG00000090512	<i>FETUB</i>	7.36E-09	0.700632	0.528848957	0.817268357
11646-4	Carbohydrate sulfotransferase 9	ENSG00000154080	<i>CHST9</i>	1.37E-08	0.691603	0.516113511	0.811367127
6551-94	Vaspin	ENSG00000165953	<i>SERPINA12</i>	2.6E-08	0.681964	0.502601781	0.805039693
12370-30	Apo F	ENSG00000175336	<i>APOF</i>	3.83E-08	0.675931	0.494189475	0.801065208
15594-47	HTRA1	ENSG00000166033	<i>HTRA1</i>	5.35E-08	0.670618	0.48680924	0.79755591
4721-54	TFF3	ENSG00000160180	<i>TFF3</i>	5.46E-08	0.670297	0.486364744	0.797343879
4337-49	CRP	ENSG00000132693	<i>CRP</i>	6.78E-08	0.666798	0.481519571	0.795027669
8248-222	SIG14	ENSG00000254415	<i>SIGLEC14</i>	9.35E-08	0.661515	0.474225613	0.791523503
16900-29	MDGA1	ENSG00000112139	<i>MDGA1</i>	1.29E-07	0.656064	0.466726394	0.78789884
8469-41	IGFBP-2	ENSG00000115457	<i>IGFBP2</i>	2.32E-07	0.645962	0.452899796	0.781157056
6605-17	IGFALS	ENSG00000099769	<i>IGFALS</i>	5.82E-07	0.629297	0.430293484	0.76996692
18895-54	GSTM4	ENSG00000168765	<i>GSTM4</i>	6.79E-07	0.626426	0.426423196	0.768029947
3320-49	IGFBP-7	ENSG00000163453	<i>IGFBP7</i>	1.27E-06	0.614275	0.410126032	0.759804512
13717-15	FCN2	ENSG00000160339	<i>FCN2</i>	2.34E-06	0.602088	0.393911294	0.751508057
6081-52	PCOC2	ENSG00000163710	<i>PCOLCE2</i>	2.71E-06	0.599013	0.3898397	0.74940686
13676-46	Inhibin bB chain	ENSG00000163083	<i>INHBB</i>	3.47E-06	0.593869	0.38304822	0.745885843
8356-88	NEU1	ENSG00000101405	<i>OXT</i>	3.91E-06	0.591349	0.379728647	0.744157413
8690-25	CAV3	ENSG00000182533	<i>CAV3</i>	9.78E-06	0.571164	0.353339281	0.730241233
3484-6	Angiotensinogen	ENSG00000135744	<i>AGT</i>	0.000016	0.559836	0.338678335	0.722372371
4842-62	Glypican 3	ENSG00000147257	<i>GPC3</i>	2.28E-05	0.551278	0.32767417	0.716400175
6379-62	ATL2	ENSG00000197859	<i>ADAMTSL2</i>	2.52E-05	0.548819	0.32452411	0.714680018
9748-31	GSTM3-3	ENSG00000134202	<i>GSTM3</i>	0.000026	0.548133	0.323645349	0.714199308
3173-49	ASAH1	ENSG00000138744	<i>NAAA</i>	3.53E-05	0.540526	0.313934481	0.708862516
6471-53	FHR4	ENSG00000134365	<i>CFHR4</i>	3.56E-05	0.540307	0.313654882	0.708708185
3313-21	FCN2	ENSG00000160339	<i>FCN2</i>	4.85E-05	0.532445	0.303669776	0.703171761
10565-19	SLIK3	ENSG00000121871	<i>SLITRK3</i>	0.000049	0.532156	0.303303038	0.70296749
2925-9	PAI-1	ENSG00000106366	<i>SERPINE1</i>	5.23E-05	0.530498	0.301203803	0.701796958
9754-33	Quinone reductase 2	ENSG00000124588	<i>NQO2</i>	5.57E-05	0.528851	0.299120361	0.700633088
7179-69	NFASC	ENSG00000163531	<i>NFASC</i>	6.24E-05	0.52586	0.295344067	0.698518084
16300-4	TREM2	ENSG00000095970	<i>TREM2</i>	6.25E-05	0.525831	0.295306511	0.698497015
18893-26	GPR56	ENSG00000205336	<i>ADGRG1</i>	7.34E-05	0.521554	0.289918744	0.695467122
11237-49	PCOC1	ENSG00000106333	<i>PCOLCE</i>	7.58E-05	0.5207	0.288844782	0.694861435
16081-38	Aldose reductase-like	ENSG00000198074	<i>AKR1B10</i>	8.06E-05	0.51907	0.286794938	0.693703774

8465-52	Cathepsin H	ENSG00000103811	CTSH	0.00010 5	0.51183 3	0.277724543	0.688555856
11104-13	YKL-40	ENSG00000133048	CHI3L1	0.00010 6	0.51151 6	0.277329131	0.688330493
19557-3	KLOTB	ENSG00000134962	KLB	0.00010 7	0.51148 4	0.277288441	0.688307297
6364-7	TPSNR	ENSG00000139192	TAPBPL	0.00010 8	0.51111 4	0.276821205	0.688040887
3449-58	Kallistatin	ENSG00000100665	SERPINA4	0.00010 9	0.51086 4	0.276514468	0.68786593
13123-3	FLRT3	ENSG00000125848	FLRT3	0.00011 7	0.50885 7	0.274007354	0.686434129
15363-32	Apo A-V	ENSG00000110243	APOA5	0.00012	0.50817 2	0.273152328	0.685945095
14006-36	GNMT	ENSG00000124713	GNMT	0.00013 1	0.50576 4	0.270150248	0.684225091
3195-5	Granulysin	ENSG00000115523	GNLY	0.00015 5	0.50103 9	0.26427428	0.680845144
8989-4	SCUB1	ENSG00000159307	SCUBE1	0.00016	0.50014 6	0.263165423	0.680205315
14624-51	CTCF	ENSG00000102974	CTCF	0.00016 6	-0.49913	0.679477233	0.261904954
12400-25	UBE2T	ENSG00000077152	UBE2T	0.00017 1	-0.49826	-0.67885016	0.260820497
18882-7	CSTN2	ENSG00000158258	CLSTN2	0.00019 4	0.49459	0.256281105	0.676218684
15513-108	Prostasin	ENSG00000052344	PRSS8	0.00019 5	0.49448 1	0.256146276	0.67614036
8304-50	OPG	ENSG00000164761	TNFRSF11B	0.00022 6	0.49014	0.250783938	0.673017578
3028-36	Ck-b-8-1	ENSG00000274736	CCL23	0.00024 1	0.48821 8	0.24841488	0.671633135
3708-62	a2-Macroglobulin	ENSG00000175899	A2M	0.00025 2	0.48690 2	0.246794701	0.670684622
15516-12	SAA-4	ENSG00000148965	SAA4	0.00027	0.48484 5	0.244263832	0.669200176
9370-69	GGH	ENSG00000137563	GGH	0.00029 8	0.48189 3	0.240638902	0.667068101
15486-126	ABP1	ENSG00000002726	AOC1	0.0003	0.48170 7	0.240411008	0.666933826
13728-19	ERP29	ENSG00000089248	ERP29	0.00030 1	-0.48154	0.666813554	-0.24020692
5636-10	MFAP4	ENSG00000166482	MFAP4	0.00031 7	0.47995 9	0.238267179	0.665669333
2888-49	C7	ENSG00000112936	C7	0.00032 9	0.47888 2	0.236947684	0.664889834
11363-58	AQP4	ENSG00000171885	AQP4	0.00035 6	-0.47645	0.663129908	0.233974368
2913-1	MPIF-1	ENSG00000274736	CCL23	0.00037 3	0.47508	0.232296637	0.662134749
17456-53	GOLM1	ENSG00000135052	GOLM1	0.00038 4	0.47417	0.231185621	0.661474906
13672-3	HSP76	ENSG00000173110	HSPA6	0.00041 5	-0.47176	0.659727089	0.228248133
5742-14	PPA6	ENSG00000162836	ACP6	0.00043 1	0.47054 4	0.226763214	0.658841776
6227-1	kallikrein 10	ENSG00000129451	KLK10	0.00043 3	0.47042 1	0.226612392	0.658751789
5934-1	Ferritin	ENSG00000167996	FTH1	0.00044	-0.46991	0.658380542	-0.22599039
5000-52	LG3BP	ENSG00000108679	LGALS3BP	0.00047 4	0.46755 1	0.223119493	0.656664297
4481-34	C4	ENSG00000224389	C4B	0.00048 2	0.46702 8	0.22248392	0.656283738
12635-9	TRDMT	ENSG00000107614	TRDMT1	0.00050 3	-0.46569	0.655309564	0.220858626
13496-19	HMCS1	ENSG00000112972	HMGCS1	0.00050 8	0.46540 1	0.220506996	0.655098612
3184-25	Coagulation Factor VII	ENSG00000057593	F7	0.00055 4	0.46263 2	0.217147444	0.653079713
5601-2	PGRP-L	ENSG00000161031	PGLYRP2	0.00059 3	0.46044 3	0.214495647	0.651481746
19377-14	NOE2	ENSG00000105088	OLFM2	0.00068 5	0.45580 4	0.208887438	0.648089432
4971-1	CATZ	ENSG00000101160	CTSZ	0.00068 9	0.45558 1	0.208617595	0.647925768
14249-68	TRIM1	ENSG00000080561	MID2	0.00074	0.45327 2	0.205832359	0.646234102
3607-71	DKK3	ENSG00000050165	DKK3	0.00084 3	0.44893 4	0.200611665	0.643051513
9191-8	Trefoil factor 2	ENSG00000160181	TFF2	0.00087 1	0.44785 9	0.199319131	0.642261204
19376-74	NNMT	ENSG00000166741	NNMT	0.00097 4	0.44409 5	0.19480341	0.63949269
8975-26	RCD1	ENSG00000144580	CNOT9	0.00105 2	0.44147 3	0.191663617	0.637560913
12345-4	APC10	ENSG00000164162	ANAPC10	0.00107 6	-0.4407	0.636994752	0.190745141
11109-56	SVEP1	ENSG00000165124	SVEP1	0.00113 3	0.43895 3	0.188651838	0.635702613
16914-104	sCD14	ENSG00000170458	CD14	0.00113 9	0.43877 2	0.188435511	0.635568937

6558-5	COL10	ENSG00000184374	COLEC10	0.00117 7	0.43763 6	0.187078251	0.634729628
11178-21	SVEP1	ENSG00000165124	SVEP1	0.00129 9	0.43420 4	0.182986636	0.632193027
11510-31	Apo L1	ENSG00000100342	APOL1	0.00131 3	0.43384	0.182553138	0.631923714
10666-7	GNPTG	ENSG00000090581	GNPTG	0.00131 7	0.43372 4	0.182414517	0.631837572
17341-89	THIC	ENSG00000120437	ACAT2	0.00132	0.43364 4	0.182319682	0.631778634
14133-93	IL-1 sRII	ENSG00000115590	IL1R2	0.00146	0.43012 6	0.178135076	0.629172768
2692-74	NPS-PLA2	ENSG00000188257	PLA2G2A	0.00148 8	0.42943 9	0.177319297	0.628663576
6049-64	PTPRS	ENSG00000105426	PTPRS	0.00156 8	0.42759 9	0.175135379	0.627298516
7854-38	NR3L1	ENSG00000188211	NCR3LG1	0.00157 9	-0.42734	-	-
5018-68	Peroxioredoxin-6	ENSG00000117592	PRDX6	0.00165 5	-0.42568	0.625870543	0.172855561
9829-91	SULT 2A1	ENSG00000105398	SULT2A1	0.00171 2	0.42444 9	0.17140306	0.624959176
16892-23	ENPP2	ENSG00000136960	ENPP2	0.00181 5	0.42236 2	0.168932842	0.623406403
19491-11	DHB8	ENSG00000204228	HSD17B8	0.00201 9	-0.41848	-	-
13998-26	PURA1	ENSG00000185100	ADSS1	0.00204 6	0.41800 5	0.163788373	0.620161052
3283-21	BGH3	ENSG00000120708	TGFB1	0.00213 1	0.41650 2	0.162017019	0.61903998
12695-62	KLH12	ENSG00000117153	KLHL12	0.00221	-0.41517	-	-
14747-9	CRLF1	ENSG00000006016	CRLF1	0.00228 8	0.41387 9	0.158929476	0.617081442
6480-1	CANT1	ENSG00000171302	CANT1	0.00233 4	-0.41315	-	-
3326-58	Nectin-like protein 2	ENSG00000182985	CADM1	0.00238 5	0.41233 8	0.1571173	0.615929264
10558-26	PCDH9	ENSG00000184226	PCDH9	0.00252 5	0.41020 6	0.154613801	0.61433431
15391-114	GAS-6	ENSG00000183087	GAS6	0.00271 1	0.40754 1	0.151489036	0.612338268
9335-28	PSG9	ENSG00000183668	PSG9	0.00277 9	0.40659 7	0.150383216	0.611630481
3212-3	ASAH2	ENSG00000188611	ASAH2	0.00280 4	0.40626 6	0.149996051	0.611382499
10704-91	LRMP	ENSG00000118308	IRAG2	0.00288 7	-0.40516	-	-
8099-42	SPON2	ENSG00000159674	SPON2	0.00289	0.40511 7	0.148651209	0.610520412
6086-15	CRDL2	ENSG00000054938	CHRD2	0.00300 2	0.40367	-	-
15548-35	SERA	ENSG00000092621	PHGDH	0.00339 3	-0.39896	0.605892006	0.141460053
17460-51	Mx1	ENSG00000157601	MX1	0.00345 8	0.39821 6	0.14059425	0.605332625
5649-83	PSG4	ENSG00000243137	PSG4	0.00350 4	0.39770 5	0.139999413	0.604948044
4763-31	Afamin	ENSG00000079557	AFM	0.00353 5	0.39735 9	0.139596442	0.604687388
15556-49	Alpha-amylase 2B	ENSG00000240038	AMY2B	0.00361	-0.39654	-	-
3070-1	IL-2	ENSG00000109471	IL2	0.00361 9	0.39644 4	0.13853176	0.603998232
9313-27	CBLN1	ENSG00000102924	CBLN1	0.00372 8	0.39528 3	0.137180959	0.603122873
18380-78	Albumin	ENSG00000163631	ALB	0.00375 8	0.39497	0.136817263	0.602886995
9002-36	SPA11	ENSG00000186910	SERPINA11	0.00376	0.39495 1	0.13679481	0.602872431
4374-45	MIC-1	ENSG00000130513	GDF15	0.00382 3	0.39429 6	0.136032968	0.602378057
19553-14	STX1a	ENSG00000106089	STX1A	0.00383 9	-0.39414	-	-
8843-34	MRF	ENSG00000124920	MYRF	0.00386 1	-0.39391	-0.60208588	0.135582974
3580-25	a1-Antitrypsin	ENSG00000197249	SERPINA1	0.00394 2	0.39309 7	0.134640604	0.601473601
13463-1	PXDN	ENSG00000130508	PXDN	0.00413 6	0.39119	0.132426985	0.600033204
15585-304	fibulin 5	ENSG00000140092	FBIN5	0.00429 9	0.38965 6	0.130648527	0.598873765
7211-2	RNase 1	ENSG00000129538	RNASE1	0.00432 7	0.38939 7	0.130348686	0.598678094
2994-71	IL-1Rrp2	ENSG00000115598	IL1RL2	0.00439 4	0.38878 1	0.129634335	0.598211697
3447-64	IL-8	ENSG00000169429	CXCL8	0.00441 4	0.38860 6	0.129431752	0.598079374
4153-11	alpha-1-antichymotrypsin complex	ENSG00000196136	SERPINA3	0.00454 9	0.38739 6	0.12803175	0.597164219
15515-2	SAA	ENSG00000173432	SAA1	0.00463 3	0.38666 2	0.127182025	0.596608174

8956-96	SREC-II	ENSG00000244486	SCARF2	0.00481	0.38514 9	0.125432875	0.595462141
5752-63	SUSD3	ENSG00000157303	SUSD3	0.0049	0.38439 8	0.124564553	0.594892509
14132-21	HHLA2	ENSG00000114455	HHLA2	0.00497 5	0.38378	0.123850586	0.594423783
19282-3	RAB13	ENSG00000143545	RAB13	0.00504 7	-0.3832	0.593982313	0.123178582
6410-26	INSL4	ENSG00000120211	INSL4	0.00510 8	0.38270 8	0.122614098	0.593611259
9876-2	aldolase C	ENSG00000109107	ALDOC	0.00514 6	0.38240 6	0.122264982	0.593381673
18832-65	SAA2	ENSG00000134339	SAA2	0.00530 7	0.38115 3	0.120820334	0.592430827
2950-57	IGFBP-4	ENSG00000141753	IGFBP4	0.00535 4	0.38078 7	0.120397688	0.592152399
8589-13	CDCP1	ENSG00000163814	CDCP1	0.00535 6	0.38077 3	0.120381661	0.592141838
13427-66	MA1C1	ENSG00000117643	MAN1C1	0.00547 2	0.37989 4	0.119368825	0.59147414
3481-87	XPNPEP1	ENSG00000108039	XPNPEP1	0.00572 3	0.37804 7	0.117242319	0.59007016
13631-1	RB binding protein 5	ENSG00000117222	RBBP5	0.00576 5	-0.37775	0.589843204	0.116898972
8958-51	CHL1	ENSG00000134121	CHL1	0.00580 8	0.37744 2	0.116546547	0.58961017
18435-4	UBX2B	ENSG00000215114	UBXN2B	0.00589 3	-0.37683	0.589148121	0.115848129
11406-82	ACAD8	ENSG00000151498	ACAD8	0.00609	0.37547	0.114279026	0.588108928
11167-6	MTMR1	ENSG00000063601	MTMR1	0.00630 6	-0.37402	0.587001965	0.112610192
12956-4	KBP	ENSG00000198954	KIFBP	0.00632 3	0.37390 7	0.112484564	0.586918562
15310-61	PRC1	ENSG00000198901	PRC1	0.00638 7	0.37348 4	0.111998781	0.586595963
17748-21	QORX	ENSG00000115129	TP53I3	0.00643 7	0.37315 7	0.111623513	0.58634665
10890-135	LCTL	ENSG00000188501	LCTL	0.00646 1	0.37300 3	0.111447293	0.586229547
12815-9	SYIC	ENSG00000196305	IARS1	0.00658 1	-0.37223	0.585641792	0.110563281
19617-5	LTB4DH	ENSG00000106853	PTGR1	0.00658 3	0.37221 8	0.110547069	0.585631008
9986-14	Neuropeptide W	ENSG00000183971	NPW	0.00665 3	0.37177 1	0.110034732	0.585290136
3143-3	sCD4	ENSG00000010610	CD4	0.00670 1	0.37146 7	0.109685786	0.585057875
5092-51	JAG1	ENSG00000101384	JAG1	0.00676 9	0.37104 4	0.109201304	0.584735273
18876-77	CHST4	ENSG00000140835	CHST4	0.00679 2	0.37089 9	0.109035231	0.584624655
8252-2	NOTUM	ENSG00000185269	NOTUM	0.00680 5	0.37082 2	0.108946712	0.584565686
5029-3	SEPR	ENSG00000078098	FAP	0.00690 5	0.37020 2	0.108237006	0.584092726
11667-29	TENC1	ENSG00000111077	TNS2	0.00704 6	0.36934 9	0.107259688	0.583440895
8245-27	sICAM-5	ENSG00000105376	ICAM5	0.0071	0.36902 3	0.106886569	0.583191877
18880-81	Collagen Type III	ENSG00000168542	COL3A1	0.00713 4	0.36882 2	0.106656522	0.583038301
13098-93	VEGF-D	ENSG00000165197	VEGFD	0.00728	0.36795 6	0.105666058	0.58237669
16616-137	ENOB	ENSG00000108515	ENO3	0.00744	0.36703 4	0.104611798	0.581671771
9758-17	RS4X	ENSG00000198034	RPS4X	0.00754 1	-0.36646	0.581230085	0.103951769
18202-22	CD37	ENSG00000104894	CD37	0.00762 8	-0.36596	-0.58085396	0.103390042
15606-19	Keratin 19	ENSG00000171345	KRT19	0.00770 4	0.36553 8	0.102902973	0.58052766
10037-98	SIG12	ENSG00000254521	SIGLEC12	0.00771 1	0.36550 2	0.102861978	0.580500189
6039-24	CRHBP	ENSG00000145708	CRHBP	0.00793 2	0.36428 5	0.101472237	0.579568285
3000-66	MBL	ENSG00000165471	MBL2	0.00803 8	0.36371 1	0.100817601	0.579128879
14151-4	UCRP	ENSG00000187608	ISG15	0.00865 6	0.3605	0.097158515	0.576667691
3890-8	LDH-H 1	ENSG00000111716	LDHB	0.00879 1	-0.35983	0.576152409	0.096394074
8459-1	BMP-6	ENSG00000153162	BMP6	0.00879 4	-0.35981	0.576139183	0.096374461
2190-55	Coagulation Factor XI	ENSG00000088926	F11	0.00881 8	0.35969 6	0.096242483	0.576050182
4557-61	KIRR3	ENSG00000149571	KIRREL3	0.00882 1	0.35968	0.096224916	0.576038334
4276-1	prostatic binding protein	ENSG00000089220	PEBP1	0.00894 4	-0.35907	0.575572704	0.095534736
9583-17	RNF24	ENSG00000101236	RNF24	0.00894 9	0.35905 1	0.095509317	0.575555549

17835-28	ANX13	ENSG00000104537	<i>ANXA13</i>	0.00902 8	-0.35866	-	-
11454-87	EIF3G	ENSG00000130811	<i>EIF3G</i>	0.00923 1	-0.35769	-0.57450809	-
6367-66	fibromodulin	ENSG00000122176	<i>FMOD</i>	0.00923 1	0.35768	0.09395768	0.093958445
11372-2	ZNF18	ENSG00000154957	<i>ZNF18</i>	0.00925 6	-0.35757	-	-
10514-5	PGD2 synthase	ENSG00000107317	<i>PTGDS</i>	0.00941 7	0.35680 8	0.574418404	0.093825762
14051-54	FOXC2	ENSG00000176692	<i>FOXC2</i>	0.00959 9	0.35596 6	0.09295992	0.573832853
9837-6	NAD(P)H dehydrogenase	ENSG00000181019	<i>NQO1</i>	0.00963 7	0.35579 2	0.09200331	0.573185347
7928-183	TPST1	ENSG00000169902	<i>TPST1</i>	0.00966 4	0.35566 7	0.091805691	0.573051508
13961-18	KIF3A	ENSG00000131437	<i>KIF3A</i>	0.00977 8	0.35514 8	0.091664184	0.572955656
14107-1	MTHFS	ENSG00000136371	<i>MTHFS</i>	0.00981 4	-0.35499	0.091075141	0.572556516
9125-23	MASP3	ENSG00000127241	<i>MASP1</i>	0.00992 7	0.35448	-	-
11383-41	Keratin 7	ENSG00000135480	<i>KRT7</i>	0.00998 8	0.35420 6	0.572432914	-0.0908928
						0.090316473	0.5720421
						0.090006022	0.571831489

Supplementary Table S5. Proteo-transcriptomics signature and differential gene expression in cohort of 206 NAFLD patients (Govaere et al 2020; Benjamini-Hochberg false discovery rate)

						F3-4 vs F0-2 (RNAseq n=206)			NAS4>=4 vs <4 (RNAseq n=206)		
Circulating Proteome	Soma ID	Protein ID	Ens ID	Gene ID	Name	log2FC	p- value	adj p- value	log2FC	p- value	adj p- value
F34 and NAS4	3339-33	TSP2	ENSG00000186340	THBS2	thrombospondin 2	1.15	3.05E-16	8.23E-13	0.88	4.43E-08	6.55E-05
F34 and NAS4	12370-30	Apo F	ENSG00000175336	APOF	apolipoprotein F	-0.25	2.60E-03	2.62E-02	-0.38	1.46E-05	2.24E-03
F34 and NAS4	6379-62	ATL2	ENSG00000197859	ADAMTSL2	ADAMTS-like 2	0.54	3.82E-08	3.57E-06	0.28	8.14E-03	9.67E-02
F34 and NAS4	6471-53	FHR4	ENSG00000134365	CFHR4	complement factor H-related 4	-0.42	6.66E-04	9.58E-03	-0.27	4.08E-02	2.31E-01
F34 and NAS4	16300-4	TREM2	ENSG00000095970	TREM2	triggering receptor expressed on myeloid cells 2	0.83	5.59E-04	8.42E-03	1.59	7.71E-11	8.30E-07
F34 and NAS4	16081-38	Aldose reductase-like	ENSG00000198074	AKR1B10	aldo-keto reductase family 1, member B10 (aldose reductase)	1.88	9.94E-08	7.78E-06	1.95	2.94E-07	2.21E-04
F34 and NAS4	9829-91	SULT 2A1	ENSG00000105398	SULT2A1	sulfotransferase family, cytosolic, 2A, DHEA-preferring, member 1	0.14	1.25E-01	3.63E-01	-0.01	9.48E-01	9.84E-01
F34 and NAS4	19617-5	LTB4DH	ENSG00000106853	PTGR1	prostaglandin reductase 1	-0.03	5.26E-01	7.67E-01	0.06	2.88E-01	6.17E-01
NAS4 only	13998-26	PURA1	ENSG00000185100	ADSSL1	adenylosuccinate synthase like 1	-0.23	4.72E-03	4.10E-02	0.00	9.92E-01	9.97E-01
NAS4 only	16616-137	ENOB	ENSG00000108515	ENO3	enolase 3 (beta, muscle)	-0.17	6.53E-02	2.45E-01	0.03	7.51E-01	9.09E-01
F34 only	4929-55	SHBG	ENSG00000129214	SHBG	sex hormone-binding globulin	0.35	1.97E-02	1.12E-01	-0.26	1.03E-01	3.74E-01
F34 only	6580-29	PZP	ENSG00000126838	PZP	pregnancy-zone protein	-1.04	7.31E-04	1.02E-02	-0.87	7.22E-03	9.02E-02
F34 only	4435-66	ENPP7	ENSG00000182156	ENPP7	ectonucleotide pyrophosphatase/phosphodiesterase 7	0.40	2.38E-03	2.46E-02	0.18	2.10E-01	5.32E-01
F34 only	11646-4	CHST9	ENSG00000154080	CHST9	carbohydrate (N-acetyl)galactosamine 4-0) sulfotransferase 9	0.89	4.48E-10	8.88E-08	0.77	9.77E-07	4.83E-04
F34 only	6605-17	IGFALS	ENSG00000099769	IGFALS	insulin-like growth factor binding protein, acid labile subunit	-0.65	1.82E-06	8.58E-05	-0.48	8.87E-02	2.59E-02
F34 only	3320-49	IGFBP-7	ENSG00000163453	IGFBP7	insulin-like growth factor binding protein 7	0.62	2.26E-11	7.86E-09	0.42	3.18E-05	3.53E-03
F34 only	13717-15	FCN2	ENSG00000160339	FCN2	ficolin (collagen/fibrinogen domain containing lectin) 2	-0.64	1.43E-12	6.34E-10	-0.20	5.07E-02	2.60E-01
F34 only	7179-69	NFASC	ENSG00000163531	NFASC	neurofascin	0.89	3.04E-17	1.97E-13	0.33	5.88E-03	8.02E-02
F34 only	18893-26	GPR56	ENSG00000205336	ADGRG1	adhesion G protein-coupled receptor G1	0.87	4.54E-09	6.24E-07	0.47	4.98E-03	7.28E-02
F34 only	11104-13	YKL-40	ENSG00000133048	CHI3L1	chitinase 3-like 1 (cartilage glycoprotein-39)	1.07	5.56E-05	1.37E-03	0.90	1.85E-03	4.04E-02
F34 only	15363-32	Apo A-V	ENSG00000110243	APOA5	apolipoprotein A-V	-0.32	9.09E-05	2.01E-03	-0.22	1.09E-02	1.14E-01
F34 only	18882-7	CSTN2	ENSG00000158258	CLSTN2	calsyntenin 2	0.84	2.74E-07	1.81E-05	0.53	3.00E-03	5.41E-02
F34 only	8304-5	OPG	ENSG00000164761	TNFRSF11B	tumor necrosis factor receptor superfamily, member 11b	0.26	6.13E-03	4.95E-02	0.23	2.43E-02	1.75E-01
F34 only	5636-10	MFAP4	ENSG00000166482	MFAP4	microfibrillar-associated protein 4	0.77	2.46E-10	5.40E-08	0.60	6.16E-06	1.41E-03
F34 only	17456-53	GOLM1	ENSG00000135052	GOLM1	golgi membrane protein 1	0.68	2.44E-06	1.10E-04	0.54	5.39E-04	1.91E-02
F34 only	5000-52	LG3BP	ENSG00000108679	LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein	0.19	3.36E-02	1.61E-01	0.16	9.68E-02	3.63E-01
F34 only	11178-21	SVEP1	ENSG00000165124	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	0.55	2.09E-09	3.33E-07	0.37	2.92E-04	1.32E-02
F34 only	15556-49	Alpha-amylase 2B	ENSG00000240038	AMY2B	amylase, alpha 2B (pancreatic)	0.03	6.14E-01	8.22E-01	-0.11	1.26E-01	4.17E-01
F34 only	4374-45	MIC-1	ENSG00000130513	GDF15	growth differentiation factor 15	0.79	3.77E-09	5.28E-07	0.58	6.76E-05	5.41E-03
F34 only	3447-64	IL-8	ENSG00000169429	CXCL8	chemokine (C-X-C motif) ligand 8	1.57	2.86E-10	6.07E-08	1.00	2.89E-04	1.32E-02
F34 only	9986-14	Neuropeptide W	ENSG00000183971	NPW	neuropeptide W	0.73	2.64E-04	4.67E-03	0.23	2.81E-01	6.10E-01

Supplementary Table S6. Performance of the proteome classification model in comparison with other scores
cut-off >0.4491 (Sensitivity 0.84 and 1-Specificity 0.14 in Discovery Cohort, Sensitivity 0.91 and 1-Specificity 0.49 in Validation Cohort)

Discovery_cohort (n=191)				
Classification model	Rule-in	positive predictive value	74/97	0.76
	Rule-out	negative predictive value	14/94	0.85
FIB-4 (>1.3)	Rule-in	positive predictive value	74/97	0.59
	Rule-out	negative predictive value	14/94	0.68

Subset_Discovery_cohort (n=35)				
Classification model	Rule-in	positive predictive value	12/15	0.80
	Rule-out	negative predictive value	2/20	0.90
FAST	Rule-in (>0.67)	positive predictive value	12/18	0.67
	Rule-out (<=0.35)	negative predictive value	2/17	0.88

Validation_cohort (n=115)				
Classification model	Rule-in	positive predictive value	39/74	0.53
	Rule-out	negative predictive value	4/41	0.90
FIB-4 (>1.3)	Rule-in	positive predictive value	25/54	0.46
	Rule-out	negative predictive value	18/61	0.70

Subset_Validation_cohort (n=15)				
Classification model	Rule-in	positive predictive value	5/9	0.56
	Rule-out	negative predictive value	4/4	1.00
FAST	Rule-in (>0.67)	positive predictive value	5/8	0.63
	Rule-out (<=0.35)	negative predictive value	5/5	1.00

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