Supplementary Table 1: Baseline Characteristics by LRS Category

	Index Cohort				**Validation Cohort**			
Characteristic	**LRS <6**	**LRS 6–10**	**LRS >10**	**P value**	**LRS <6**	**LRS 6–10**	**LRS >10**	**P value**
N (% of cohort)	**157 (24.2%)**	**395 (61.0%)**	**96 (14.8%)**		**168 (19.0%)**	**562 (63.6%)**	**153 (17.3%)**	
DEMOGRAPHICS								
Age, years	63.9 ± 13.3	67.4 ± 11.9**	67.2 ± 10.7	0.017	71.4 ± 12.4	74.9 ± 10.2**	74.6 ± 9.9	0.011
Male sex, n (%)	98 (62.4%)	326 (82.5%)***	81 (84.4%)***	0.000	73 (43.5%)	412 (73.3%)***	123 (80.4%)***	0.000
BMI, kg/m²	27.6 ± 5.3	27.7 ± 5.1	28.8 ± 6.3	0.439	28.2 ± 6.9	29.2 ± 6.0*	29.1 ± 6.1	0.043
Waist circumference, cm	--	--	--	--	98.5 [85.8–108.0]	102.0 [95.0–113.0]***	103.0 [96.0–115.0]***	0.000
Hip circumference, cm	--	--	--	--	105.0 [95.0–112.2]	106.0 [100.0–112.0]	105.0 [99.0–113.0]	0.404
Waist-to-hip ratio	--	--	--	--	0.9 [0.9–1.0]	1.0 [0.9–1.0]***	1.0 [0.9–1.1]***	0.000
Systolic BP, mmHg	127.0 ± 23.5	124.8 ± 21.0	126.9 ± 24.5	0.637	125.7 ± 22.9	126.6 ± 23.2	127.2 ± 22.3	0.781
Diastolic BP, mmHg	76.5 ± 13.8	75.0 ± 13.0	76.2 ± 14.7	0.485	70.1 ± 11.7	69.3 ± 12.8	67.6 ± 12.2	0.227
Heart rate, bpm	79.5 ± 18.7	80.0 ± 18.9	90.6 ± 27.9**	0.008	72.1 ± 13.1	72.7 ± 17.7	76.4 ± 17.8	0.050
NYHA functional class, n (%)								
Class I	18 (11.5%)	34 (8.6%)	2 (2.1%)**	0.031	4 (2.4%)	5 (0.9%)	2 (1.3%)	0.311
Class II	65 (41.4%)	169 (42.8%)	42 (43.8%)	0.928	89 (53.0%)	238 (42.3%)*	57 (37.3%)**	0.012
Class III	45 (28.7%)	111 (28.1%)	31 (32.3%)	0.717	67 (39.9%)	256 (45.6%)	78 (51.0%)	0.136
Class IV	4 (2.5%)	19 (4.8%)	4 (4.2%)	0.487	8 (4.8%)	62 (11.0%)*	16 (10.5%)	0.052
CONGESTION ASSESSMENT								

	Index Cohort				Validation Cohort			
Characteristic	**LRS <6**	**LRS 6–10**	**LRS >10**	**P value**	**LRS <6**	**LRS 6–10**	**LRS >10**	**P value**
Congestion score (0–3)	0.0 [0.0–0.3]	0.3 [0.0–1.0]***	1.0 [0.3–1.7]***	0.000	--	--	--	--
Peripheral oedema, n (%)	55 (35.0%)	182 (46.1%)	64 (66.7%)***	0.000	63 (37.5%)	303 (53.9%)***	95 (62.1%)***	0.000
None	72 (45.9%)	158 (40.0%)	22 (22.9%)***	0.000	78 (46.4%)	194 (34.5%)***	42 (27.5%)***	0.000
Ankle	41 (26.1%)	87 (22.0%)	21 (21.9%)	0.296	40 (23.8%)	153 (27.2%)	45 (29.4%)	0.719
Below knee	10 (6.4%)	73 (18.5%)**	27 (28.1%)***	0.000	21 (12.5%)	122 (21.7%)*	40 (26.1%)**	0.014
Above knee	4 (2.5%)	22 (5.6%)	16 (16.7%)***	0.000	2 (1.2%)	28 (5.0%)*	10 (6.5%)*	0.063
Jugular venous distention, n (%)	16 (10.2%)	91 (23.0%)**	30 (31.2%)***	0.001	27 (16.1%)	153 (27.2%)**	52 (34.0%)***	0.001
Hepatomegaly, n (%)	14 (8.9%)	85 (21.5%)***	26 (27.1%)***	0.000	2 (1.2%)	19 (3.4%)	5 (3.3%)	0.361
Orthopnoea, n (%)	14 (8.9%)	85 (21.5%)***	26 (27.1%)***	0.000	--	--	--	--
Rales/crackles, n (%)	17 (10.8%)	53 (13.4%)	10 (10.4%)*	0.088	5 (3.0%)	37 (6.6%)***	5 (3.3%)**	0.000
ECHOCARDIOGRAPHY								
LVEF, %	30.4 ± 8.7	30.1 ± 10.0	29.4 ± 10.0	0.785	40.1 ± 14.4	41.2 ± 13.1	41.3 ± 13.1	0.813
LVEDD, mm	63.6 ± 9.0	62.7 ± 9.4	61.3 ± 9.6	0.336	53.6 ± 10.1	55.1 ± 9.3	54.8 ± 8.1	0.294
Left atrial diameter, mm	46.3 ± 7.2	49.1 ± 8.2***	48.9 ± 7.8	0.004	43.7 ± 7.8	45.7 ± 6.8**	45.4 ± 6.6*	0.023
IVS thickness, mm	10.0 ± 2.1	10.2 ± 2.7	10.0 ± 2.2	0.901	11.6 ± 2.6	13.0 ± 5.4**	12.3 ± 3.0	0.013
Mitral regurgitation, n (%)	69 (43.9%)	193 (48.9%)	38 (39.6%)	0.282	55 (32.7%)	165 (29.4%)	48 (31.4%)	0.797
Dilated IVC, n (%)	--	--	--	--	27 (16.1%)	106 (18.9%)	37 (24.2%)	0.199
Right atrial pressure, mmHg	--	--	--	--	7.5 [7.0–10.0]	10.0 [7.0–12.5]*	10.0 [7.5–13.1]**	0.008
Tricuspid regurgitation gradient, mmHg	--	--	--	--	29.5 [25.8–39.2]	33.0 [27.0–41.0]	36.0 [29.5–47.0]**	0.005

	Index Cohort				Validation Cohort			
Characteristic	**LRS <6**	**LRS 6–10**	**LRS >10**	**P value**	**LRS <6**	**LRS 6–10**	**LRS >10**	**P value**
Right ventricular systolic pressure, mmHg	--	--	--	--	38.8 [33.0–50.4]	45.0 [36.0–54.6]**	46.5 [39.0–60.4]***	0.001
LFTS & LIVER NITS								
ALT, U/L	20.0 [15.0–26.5]	26.0 [18.0–39.5]***	41.5 [25.0–99.0]***	0.000	19.0 [15.0–24.2]	22.0 [17.0–32.0]***	34.0 [22.0–47.0]***	0.000
AST, U/L	21.0 [17.0–25.0]	26.0 [20.0–34.0]***	38.0 [26.0–77.0]***	0.000	20.0 [16.0–24.0]	23.0 [18.0–30.0]***	32.0 [21.0–45.0]***	0.000
Platelet count, ×10^9/L	255.4 ± 79.5	210.2 ± 69.2***	205.0 ± 73.3***	0.000	293.2 ± 94.7	235.9 ± 89.2***	224.2 ± 88.4***	0.000
GGT, U/L	27.0 [17.0–36.0]	61.0 [31.0–101.0]***	189.0 [98.0–338.2]***	0.000	26.0 [18.0–35.2]	45.0 [28.0–74.0]***	124.0 [53.0–273.0]***	0.000
Alkaline phosphatase, U/L	74.0 [58.0–101.0]	87.0 [69.0–117.0]***	131.0 [91.0–193.0]***	0.000	83.5 [67.8–100.2]	86.0 [71.0–109.0]*	112.0 [79.0–157.0]***	0.000
Total bilirubin, μmol/L	11.7 [8.1–15.8]	14.0 [10.3–20.4]***	19.3 [13.7–29.4]***	0.000	9.0 [6.0–12.0]	10.0 [7.0–15.0]***	13.0 [8.0–18.0]***	0.000
Albumin, g/L	32.9 ± 9.1	32.1 ± 8.8	30.9 ± 7.4	0.195	39.5 ± 4.9	37.6 ± 5.9***	36.2 ± 6.2***	0.000
FIB-4 index	1.2 [0.8–1.7]	1.6 [1.2–2.4]***	2.3 [1.3–3.9]***	0.000	1.2 [0.9–1.6]	1.7 [1.2–2.4]***	2.2 [1.4–3.1]***	0.000
Hepatic steatosis index	36.9 ± 6.3	38.1 ± 7.2	39.9 ± 7.9**	0.020	37.6 ± 8.1	38.9 ± 7.7*	40.2 ± 8.3**	0.005
LABORATORY VALUES								
NT-proBNP, ng/L	2664.0 [1415.5–6780.0]	4919.5 [2372.8–9372.0]*	4182.0 [2995.0–9354.5]*	0.055	609.0 [263.0–1674.0]	1328.0 [555.0–3173.2]***	2285.0 [657.0–6060.0]***	0.000
Creatinine, μmol/L	91.0 [77.3–106.1]	105.2 [88.0–129.5]***	116.3 [89.2–141.4]***	0.000	86.0 [72.8–111.0]	97.0 [82.0–128.0]***	100.0 [82.0–132.0]***	0.000
eGFR, mL/min/1.73m²	75.3 ± 23.4	64.4 ± 22.6***	60.2 ± 24.7***	0.000	65.7 ± 22.0	61.0 ± 25.4**	60.3 ± 22.2*	0.023

	Index Cohort				**Validation Cohort**			
Characteristic	**LRS <6**	**LRS 6–10**	**LRS >10**	**P value**	**LRS <6**	**LRS 6–10**	**LRS >10**	**P value**
Haemoglobin, g/dL	13.3 ± 1.9	13.4 ± 2.0	13.6 ± 1.9	0.622	16.9 ± 21.1	15.4 ± 16.9	13.9 ± 10.6	0.169
Sodium, mmol/L	140.4 ± 3.0	139.5 ± 3.9*	136.8 ± 5.2***	0.000	139.1 ± 3.6	139.3 ± 3.3	138.0 ± 3.3***	0.000
COMORBIDITIES, n (%)								
Diabetes mellitus	25 (15.9%)	142 (35.9%)***	53 (55.2%)***	0.000	13 (7.7%)	155 (27.6%)***	97 (63.4%)***	0.000
Hypertension	95 (60.5%)	245 (62.0%)	53 (55.2%)	0.471	84 (50.0%)	323 (57.5%)	99 (64.7%)*	0.028
Atrial fibrillation	42 (26.8%)	182 (46.1%)***	47 (49.0%)***	0.000	66 (39.3%)	265 (47.2%)	73 (47.7%)	0.163
Prior myocardial infarction	44 (28.0%)	143 (36.2%)	38 (39.6%)	0.106	66 (39.3%)	277 (49.3%)*	76 (49.7%)	0.060
Prior stroke	9 (5.7%)	36 (9.1%)	7 (7.3%)	0.402	15 (8.9%)	108 (19.2%)**	36 (23.5%)***	0.002
COPD	27 (17.2%)	62 (15.7%)	16 (16.7%)	0.903	28 (16.7%)	81 (14.4%)	24 (15.7%)	0.734
Chronic kidney disease	25 (15.9%)	118 (29.9%)**	36 (37.5%)***	0.000	61 (36.3%)	249 (44.3%)	71 (46.4%)	0.105
HEART FAILURE MEDICATIONS								
ACE inhibitor/ARB, n (%)	112 (71.3%)	227 (57.5%)**	59 (61.5%)	0.010	126 (75.0%)	410 (73.0%)	112 (73.2%)	0.869
ACEi/ARB % of target dose, mean ± SD	49.1 ± 41.8	46.6 ± 39.0	53.1 ± 38.7	0.359	42.1 ± 27.0	46.0 ± 31.3	47.3 ± 30.5	0.545
Beta-blocker, n (%)	119 (75.8%)	281 (71.1%)	60 (62.5%)*	0.077	127 (75.6%)	402 (71.5%)	111 (72.5%)	0.585
Beta-blocker % of target dose, mean ± SD	26.7 ± 20.2	29.6 ± 22.6	32.3 ± 23.4	0.327	47.1 ± 31.8	46.4 ± 32.6	51.8 ± 30.8	0.134
Loop diuretic, n (%)	151 (96.2%)	386 (97.7%)	92 (95.8%)	0.462	164 (97.6%)	547 (97.3%)	150 (98.0%)	0.879
Dose, mg/day (furosemide equiv.)	40.0 [40.0–60.0]	40.0 [40.0–100.0]***	80.0 [40.0–141.2]***	0.000	40.0 [40.0–40.0]	40.0 [40.0–50.0]**	40.0 [40.0–80.0]***	0.000
MRA, n (%)	85 (54.1%)	200 (50.6%)	45 (46.9%)	0.524	57 (33.9%)	188 (33.5%)	50 (32.7%)	0.972

	Index Cohort				Validation Cohort			
Characteristic	**LRS <6**	**LRS 6–10**	**LRS >10**	**P value**	**LRS <6**	**LRS 6–10**	**LRS >10**	**P value**
Dose, mg/day (spironolactone equiv.)	25.0 [25.0–25.0]	25.0 [25.0–50.0]	25.0 [25.0–50.0]	0.232	25.0 [25.0–25.0]	25.0 [25.0–25.0]	25.0 [25.0–25.0]	0.108

Table 1: Baseline Characteristics Stratified by LiverRisk Score Category | Index cohort N=157 | Validation cohort N=168

Values presented as mean ± SD, median [IQR], or n (%)

** P<0.05, ** P<0.01, *** P<0.001 vs LRS <6 reference group (pairwise comparisons)*

Overall P values from Kruskal-Wallis test (continuous) or Chi-square/Fisher's exact test (categorical)

Right heart parameters and anthropometrics available for Validation cohort only

Supplementary Table 2: Baseline Characteristics by HSI Category

	Index Cohort				**Validation Cohort**			
Characteristic	**HSI <30**	**HSI 30–36**	**HSI >36**	**P value**	**HSI <30**	**HSI 30–36**	**HSI >36**	**P value**
N (% of cohort)	**198 (12.8%)**	**507 (32.8%)**	**839 (54.3%)**		**189 (11.4%)**	**474 (28.6%)**	**993 (60.0%)**	
DEMOGRAPHICS								
Age, years	72.6 ± 11.8	70.2 ± 11.8**	66.0 ± 11.6***	0.000	78.4 ± 10.4	75.5 ± 10.4***	71.6 ± 10.3***	0.000
Male sex, n (%)	153 (77.3%)	388 (76.5%)	611 (72.8%)	0.208	136 (72.0%)	327 (69.0%)	648 (65.3%)	0.116
BMI, kg/m²	21.6 ± 2.4	25.3 ± 2.4***	30.8 ± 5.0***	0.000	21.5 ± 2.4	25.2 ± 2.6***	32.6 ± 5.7***	0.000
Waist circumference, cm	--	--	--	--	90.0 [83.0–97.0]	96.0 [90.0–103.0]***	109.0 [101.0–118.0]***	0.000
Hip circumference, cm	--	--	--	--	94.5 [90.0–100.0]	102.0 [95.0–107.0]***	110.0 [104.0–118.0]***	0.000
Waist-to-hip ratio	--	--	--	--	0.9 [0.9–1.0]	1.0 [0.9–1.0]	1.0 [0.9–1.1]***	0.000
Systolic BP, mmHg	122.3 ± 21.9	123.8 ± 21.7	126.8 ± 21.8**	0.001	124.4 ± 23.7	123.5 ± 21.7	127.7 ± 22.2*	0.002
Diastolic BP, mmHg	72.7 ± 12.0	73.8 ± 13.1	76.6 ± 13.6***	0.000	66.8 ± 12.9	68.5 ± 12.6	70.5 ± 13.2***	0.000
Heart rate, bpm	78.7 ± 19.4	79.7 ± 20.0	81.7 ± 20.0	0.038	73.0 ± 16.0	73.2 ± 16.3	74.5 ± 17.1	0.171
NYHA functional class, n (%)								
Class I	16 (8.1%)	42 (8.3%)	63 (7.5%)	0.869	2 (1.1%)	6 (1.3%)	8 (0.8%)	0.696
Class II	87 (43.9%)	228 (45.0%)	395 (47.1%)	0.622	63 (33.3%)	211 (44.5%)*	426 (42.9%)*	0.025
Class III	67 (33.8%)	158 (31.2%)	218 (26.0%)*	0.029	88 (46.6%)	200 (42.2%)	435 (43.8%)	0.584
Class IV	4 (2.0%)	15 (3.0%)	42 (5.0%)	0.057	36 (19.0%)	57 (12.0%)*	123 (12.4%)*	0.033
CONGESTION ASSESSMENT								
Congestion score (0–3)	0.3 [0.0–1.0]	0.3 [0.0–1.0]	0.3 [0.0–1.0]	0.366	--	--	--	--

	Index Cohort				Validation Cohort			
Characteristic	**HSI <30**	**HSI 30–36**	**HSI >36**	**P value**	**HSI <30**	**HSI 30–36**	**HSI >36**	**P value**
Peripheral oedema, n (%)	87 (43.9%)	245 (48.3%)	418 (49.8%)	0.166	88 (46.6%)	228 (48.1%)	574 (57.8%)**	0.000
None	82 (41.4%)	186 (36.7%)	286 (34.1%)	0.166	76 (40.2%)	196 (41.4%)	312 (31.4%)**	0.000
Ankle	50 (25.3%)	131 (25.8%)	187 (22.3%)	0.347	47 (24.9%)	115 (24.3%)	282 (28.4%)	0.201
Below knee	31 (15.7%)	84 (16.6%)	173 (20.6%)	0.061	34 (18.0%)	86 (18.1%)	240 (24.2%)	0.014
Above knee	6 (3.0%)	30 (5.9%)	58 (6.9%)	0.103	7 (3.7%)	27 (5.7%)	52 (5.2%)	0.621
Jugular venous distention, n (%)	42 (21.2%)	121 (23.9%)	172 (20.5%)	0.122	60 (31.7%)	127 (26.8%)	242 (24.4%)	0.382
Hepatomegaly, n (%)	29 (14.6%)	83 (16.4%)	131 (15.6%)	0.850	5 (2.6%)	25 (5.3%)	31 (3.1%)	0.105
Orthopnoea, n (%)	29 (14.6%)	83 (16.4%)	131 (15.6%)	0.850	--	--	--	--
Rales/crackles, n (%)	29 (14.6%)	60 (11.8%)	101 (12.0%)	0.395	10 (5.3%)	23 (4.9%)	53 (5.3%)	0.366
ECHOCARDIOGRAPHY								
LVEF, %	30.4 ± 10.5	30.7 ± 10.8	30.8 ± 10.3	0.838	39.1 ± 15.1	39.1 ± 13.3	41.5 ± 13.5	0.017
LVEDD, mm	60.7 ± 10.7	61.2 ± 10.4	62.5 ± 9.3*	0.052	53.1 ± 11.1	54.4 ± 9.0	55.7 ± 9.1*	0.053
Left atrial diameter, mm	46.3 ± 8.9	47.9 ± 8.2	48.3 ± 7.3**	0.004	43.9 ± 7.5	44.9 ± 7.4	45.9 ± 7.1**	0.008
IVS thickness, mm	10.4 ± 2.5	10.2 ± 2.3	10.6 ± 2.5	0.064	12.8 ± 7.0	12.0 ± 3.1	12.6 ± 3.9	0.024
Mitral regurgitation, n (%)	100 (50.5%)	256 (50.5%)	386 (46.0%)	0.239	81 (42.9%)	171 (36.1%)	255 (25.7%)***	0.000
Dilated IVC, n (%)	--	--	--	--	43 (22.8%)	96 (20.3%)	173 (17.4%)	0.167
Right atrial pressure, mmHg	--	--	--	--	10.0 [7.5–15.0]	10.0 [7.0–12.5]	10.0 [7.0–12.5]	0.531
Tricuspid regurgitation gradient, mmHg	--	--	--	--	35.0 [29.0–43.0]	33.2 [26.0–43.0]	33.0 [26.0–41.0]	0.199
Right ventricular systolic pressure, mmHg	--	--	--	--	45.0 [38.0–56.0]	44.5 [35.8–56.5]	43.0 [35.0–53.5]	0.203
LFTS & LIVER NITS								

	Index Cohort				Validation Cohort			
Characteristic	**HSI <30**	**HSI 30–36**	**HSI >36**	**P value**	**HSI <30**	**HSI 30–36**	**HSI >36**	**P value**
ALT, U/L	17.0 [13.0–25.0]	21.0 [15.0–30.6]***	29.0 [20.0–45.0]***	0.000	18.0 [14.0–26.0]	20.5 [16.0–29.0]**	24.0 [18.0–35.0]***	0.000
AST, U/L	27.0 [21.0–36.8]	25.0 [20.0–34.1]	25.0 [19.0–34.5]**	0.007	26.0 [21.0–38.0]	24.0 [20.0–33.0]*	22.0 [17.0–29.0]***	0.000
Platelet count, $\times 10^9$/L	219.1 ± 76.0	223.8 ± 93.7	225.9 ± 74.8	0.135	241.7 ± 100.3	243.9 ± 92.0	247.8 ± 91.7	0.114
GGT, U/L	51.5 [28.0–97.0]	50.0 [25.0–94.0]	56.0 [29.0–111.0]	0.095	38.0 [23.0–113.2]	43.0 [23.8–86.8]	47.0 [29.0–87.0]	0.023
Alkaline phosphatase, U/L	88.5 [64.8–119.5]	84.0 [64.7–116.0]	83.0 [64.0–117.0]	0.818	93.0 [74.0–129.0]	89.0 [69.0–116.8]	89.0 [71.0–114.0]	0.216
Total bilirubin, µmol/L	13.7 [9.2–23.8]	14.0 [10.0–22.0]	13.6 [9.4–20.0]	0.187	11.0 [7.0–16.0]	11.0 [8.0–16.0]	10.0 [7.0–14.0]**	0.000
Albumin, g/L	30.8 ± 8.7	31.6 ± 9.1	32.1 ± 8.4	0.156	36.9 ± 6.5	38.2 ± 6.2*	38.0 ± 5.8*	0.089
LiverRisk Score	6.7 [5.9–7.7]	7.0 [6.0–8.2]	7.2 [6.1–9.2]*	0.044	7.2 [6.0–8.9]	6.9 [6.2–8.4]	7.4 [6.4–9.1]	0.016
FIB-4 index	2.4 [1.7–3.4]	1.9 [1.3–2.6]***	1.4 [1.0–2.0]***	0.000	2.3 [1.6–3.2]	1.8 [1.3–2.5]***	1.4 [1.0–1.9]***	0.000
OTHER LABORATORY VALUES								
NT-proBNP, ng/L	7055.5 [3662.0–12418.8]	5459.5 [2762.0–10184.8]*	3636.0 [2153.8–7061.5]***	0.000	2907.0 [1318.8–7699.5]	1777.0 [667.0–3964.2]***	1023.0 [393.0–2613.0]***	0.000
Creatinine, µmol/L	106.0 [87.0–128.0]	105.0 [84.0–132.6]	99.0 [83.1–126.0]	0.187	103.0 [82.0–135.0]	98.0 [79.2–124.0]	96.0 [79.0–122.0]	0.149
eGFR, mL/min/$1.73m^2$	62.6 ± 22.4	62.9 ± 23.3	67.3 ± 23.0*	0.001	57.2 ± 22.8	60.4 ± 23.3	62.7 ± 25.2**	0.007
Haemoglobin, g/dL	12.8 ± 1.7	13.2 ± 1.9*	13.4 ± 1.9***	0.000	16.2 ± 20.3	14.6 ± 13.6*	14.5 ± 13.1***	0.001
Sodium, mmol/L	138.7 ± 4.3	139.2 ± 4.0	139.5 ± 4.0*	0.035	137.5 ± 9.9	139.0 ± 3.3**	139.1 ± 3.3***	0.002

	Index Cohort				Validation Cohort			
Characteristic	**HSI <30**	**HSI 30–36**	**HSI >36**	**P value**	**HSI <30**	**HSI 30–36**	**HSI >36**	**P value**
COMORBIDITIES, n (%)								
Diabetes mellitus	16 (8.1%)	123 (24.3%)***	360 (42.9%)***	0.000	17 (9.0%)	96 (20.3%)***	421 (42.4%)***	0.000
Hypertension	104 (52.5%)	307 (60.6%)	561 (66.9%)***	0.000	81 (42.9%)	259 (54.6%)**	633 (63.7%)***	0.000
Atrial fibrillation	85 (42.9%)	230 (45.4%)	369 (44.0%)	0.811	90 (47.6%)	204 (43.0%)	437 (44.0%)	0.588
Prior myocardial infarction	67 (33.8%)	189 (37.3%)	293 (34.9%)	0.589	93 (49.2%)	241 (50.8%)	482 (48.5%)	0.719
Prior stroke	14 (7.1%)	56 (11.0%)	66 (7.9%)	0.089	41 (21.7%)	89 (18.8%)	154 (15.5%)*	0.063
COPD	42 (21.2%)	86 (17.0%)	139 (16.6%)	0.290	30 (15.9%)	74 (15.6%)	181 (18.2%)	0.382
Chronic kidney disease	54 (27.3%)	153 (30.2%)	215 (25.6%)	0.192	97 (51.3%)	214 (45.1%)	434 (43.7%)	0.125
HEART FAILURE MEDICATIONS								
ACE inhibitor/ARB, n (%)	122 (61.6%)	314 (61.9%)	519 (61.9%)	0.997	122 (64.6%)	338 (71.3%)	732 (73.7%)*	0.034
ACEi/ARB % of target dose, mean ± SD	40.9 ± 26.8	45.8 ± 36.6	51.1 ± 39.7	0.053	38.9 ± 32.6	41.0 ± 29.8	48.3 ± 32.0	0.000
Beta-blocker, n (%)	151 (76.3%)	367 (72.4%)	591 (70.4%)	0.247	132 (69.8%)	350 (73.8%)	737 (74.2%)	0.453
Beta-blocker % of target dose, mean ± SD	31.9 ± 21.8	33.0 ± 25.1	31.5 ± 24.7	0.392	38.7 ± 27.7	44.6 ± 30.9	49.6 ± 32.8	0.000
Loop diuretic, n (%)	193 (97.5%)	491 (96.8%)	822 (98.0%)	0.431	186 (98.4%)	467 (98.5%)	958 (96.5%)	0.047
Dose, mg/day (furosemide equiv.)	40.0 [40.0–80.0]	40.0 [40.0–80.0]	40.0 [40.0–80.0]	0.357	40.0 [40.0–60.0]	40.0 [40.0–50.0]	40.0 [40.0–57.5]	0.607
MRA, n (%)	84 (42.4%)	247 (48.7%)	412 (49.1%)	0.226	55 (29.1%)	137 (28.9%)	357 (36.0%)	0.012
Dose, mg/day (spironolactone equiv.)	25.0 [25.0–50.0]	25.0 [25.0–50.0]	25.0 [25.0–25.0]	0.418	25.0 [25.0–25.0]	25.0 [25.0–25.0]	25.0 [25.0–25.0]**	0.006

Table 1: Baseline Characteristics Stratified by HSI Category | Index cohort N=198 | Validation cohort N=189

Supplementary

	Index Cohort				Validation Cohort			
Characteristic	**HSI <30**	**HSI 30–36**	**HSI >36**	**P value**	**HSI <30**	**HSI 30–36**	**HSI >36**	**P value**

Values presented as mean ± SD, median [IQR], or n (%)

** P<0.05, ** P<0.01, *** P<0.001 vs HSI <30 reference group (pairwise comparisons)*

Overall P values from Kruskal-Wallis test (continuous) or Chi-square/Fisher's exact test (categorical)

6 Supplementary Table 3: baseline differences between patients with LRS and FIB-4 available

	Index Cohort			Validation Cohort		
Characteristic	**LRS Cohort**	**FIB-4 Cohort**	**P value**	**LRS Cohort**	**FIB-4 Cohort**	**P value**
N	**648**	**1336**		**883**	**1681**	
DEMOGRAPHICS						
Age, years	66.5 ± 12.1	68.5 ± 12.1	**0.000**	74.2 ± 10.7	73.6 ± 10.7	0.105
Male sex, n (%)	505 (77.9%)	983 (73.6%)	**0.041**	608 (68.9%)	1123 (66.8%)	0.313
BMI, kg/m²	27.8 ± 5.3	27.7 ± 5.3	0.664	29.0 ± 6.2	29.2 ± 6.4	0.340
Systolic BP, mmHg	125.6 ± 22.2	125.7 ± 22.4	0.980	126.6 ± 23.0	126.1 ± 22.4	0.819
Diastolic BP, mmHg	75.5 ± 13.4	75.3 ± 13.6	0.618	69.2 ± 12.5	69.4 ± 13.0	0.597
Heart rate, bpm	81.4 ± 20.8	81.3 ± 20.4	0.992	73.2 ± 17.0	74.0 ± 16.9	0.207
NYHA functional class, n (%)						
Class I	54 (8.3%)	108 (8.1%)	0.918	11 (1.2%)	16 (1.0%)	0.624
Class II	276 (42.6%)	584 (43.7%)	0.672	384 (43.5%)	710 (42.2%)	0.563
Class III	187 (28.9%)	395 (29.6%)	0.785	401 (45.4%)	735 (43.7%)	0.431
Class IV	27 (4.2%)	56 (4.2%)	1.000	86 (9.7%)	219 (13.0%)	**0.018**
CONGESTION ASSESSMENT						
Congestion score (0–3)	0.3 [0.0–1.0]	0.3 [0.0–1.0]	0.679	--	--	--
Peripheral oedema, n (%)	301 (46.5%)	666 (49.9%)	0.092	461 (52.2%)	905 (53.8%)	0.646
None	252 (38.9%)	465 (34.8%)	0.092	314 (35.6%)	589 (35.0%)	0.646
Ankle	149 (23.0%)	312 (23.4%)	0.826	238 (27.0%)	455 (27.1%)	0.939
Below knee	110 (17.0%)	267 (20.0%)	0.098	183 (20.7%)	363 (21.6%)	0.757
Above knee	42 (6.5%)	87 (6.5%)	1.000	40 (4.5%)	87 (5.2%)	0.579

	Index Cohort			Validation Cohort		
Characteristic	**LRS Cohort**	**FIB-4 Cohort**	**P value**	**LRS Cohort**	**FIB-4 Cohort**	**P value**
Jugular venous distention, n (%)	137 (21.1%)	292 (21.9%)	0.509	232 (26.3%)	432 (25.7%)	0.649
Hepatomegaly, n (%)	125 (19.3%)	219 (16.4%)	0.128	26 (2.9%)	62 (3.7%)	0.479
Orthopnoea, n (%)	125 (19.3%)	219 (16.4%)	0.128	--	--	--
Rales/crackles, n (%)	80 (12.3%)	172 (12.9%)	0.544	47 (5.3%)	90 (5.4%)	0.997
ECHOCARDIOGRAPHY						
LVEF, %	30.1 ± 9.7	31.1 ± 10.9	0.117	33.8 ± 15.7	35.6 ± 16.0	0.411
LVEDD, mm	62.7 ± 9.4	61.2 ± 9.8	**0.001**	54.7 ± 9.3	54.9 ± 9.3	0.466
Left atrial diameter, mm	48.3 ± 8.0	47.8 ± 7.9	0.218	45.3 ± 7.0	45.3 ± 7.3	0.782
IVS thickness, mm	10.1 ± 2.5	10.5 ± 2.6	**0.007**	12.6 ± 4.6	12.4 ± 4.2	0.409
Mitral regurgitation, n (%)	300 (46.3%)	634 (47.5%)	0.490	268 (30.4%)	511 (30.4%)	0.971
LIVER FUNCTION & FIBROSIS SCORES						
ALT, U/L	25.0 [17.0–40.0]	25.0 [16.0–37.2]	0.251	22.0 [17.0–33.0]	22.0 [17.0–32.0]	0.858
AST, U/L	25.0 [19.0–35.0]	25.1 [20.0–35.0]	0.696	23.0 [18.0–31.0]	23.0 [18.0–31.0]	0.583
Platelet count, ×10⁹/L	220.4 ± 75.0	225.5 ± 88.9	0.358	244.8 ± 93.2	245.8 ± 92.5	0.697
GGT, U/L	54.1 [28.0–107.0]	57.0 [28.0–111.0]	0.330	43.0 [25.0–84.0]	45.0 [26.0–90.0]	0.215
Alkaline phosphatase, U/L	87.0 [67.0–122.5]	86.0 [64.8–120.3]	0.498	88.0 [71.0–113.0]	89.0 [71.0–116.0]	0.363
Total bilirubin, μmol/L	13.7 [10.1–20.5]	13.7 [9.6–20.5]	0.687	10.0 [7.0–15.0]	10.0 [7.0–15.0]	0.943
Albumin, g/L	32.1 ± 8.7	31.6 ± 8.7	0.227	37.7 ± 5.8	37.8 ± 6.0	0.459
FIB-4 index	1.5 [1.1–2.3]	1.7 [1.1–2.4]	0.072	1.6 [1.1–2.3]	1.6 [1.1–2.3]	0.720
Hepatic steatosis index	38.1 ± 7.2	37.7 ± 7.3	0.165	38.9 ± 7.9	39.1 ± 8.0	0.573

	Index Cohort			Validation Cohort		
Characteristic	**LRS Cohort**	**FIB-4 Cohort**	**P value**	**LRS Cohort**	**FIB-4 Cohort**	**P value**
OTHER LABORATORY VALUES						
NT-proBNP, ng/L	4159.0 [2189.5–8939.0]	4752.0 [2578.2–8779.2]	0.253	1239.5 [479.5–3089.0]	1323.0 [496.0–3412.0]	0.420
Creatinine, µmol/L	99.9 [84.0–126.8]	101.0 [84.0–128.0]	0.776	95.0 [79.5–124.0]	97.0 [79.0–124.0]	0.672
eGFR, mL/min/1.73m²	66.4 ± 23.7	65.1 ± 23.3	0.264	61.7 ± 24.3	61.4 ± 24.6	0.614
Haemoglobin, g/dL	13.4 ± 1.9	13.2 ± 1.9	0.148	15.4 ± 17.0	14.8 ± 14.4	0.651
Sodium, mmol/L	139.3 ± 4.1	139.3 ± 4.1	0.901	139.0 ± 3.4	138.9 ± 4.6	0.673
Glucose, mmol/L	6.0 [5.1–7.6]	6.3 [5.3–7.9]	**0.013**	6.2 [5.2–8.3]	6.2 [5.2–8.4]	0.451
Cholesterol, mmol/L	4.2 ± 1.3	4.3 ± 1.3	0.585	3.6 ± 9.9	3.9 ± 14.7	0.602
COMORBIDITIES, n (%)						
Diabetes mellitus	220 (34.0%)	425 (31.8%)	0.367	265 (30.0%)	538 (32.0%)	0.343
Hypertension	393 (60.6%)	849 (63.5%)	0.229	506 (57.3%)	984 (58.5%)	0.551
Atrial fibrillation	271 (41.8%)	603 (45.1%)	0.178	404 (45.8%)	742 (44.1%)	0.464
Prior myocardial infarction	225 (34.7%)	472 (35.3%)	0.829	419 (47.5%)	824 (49.0%)	0.458
Prior stroke	52 (8.0%)	119 (8.9%)	0.568	159 (18.0%)	291 (17.3%)	0.694
COPD	105 (16.2%)	222 (16.6%)	0.867	133 (15.1%)	289 (17.2%)	0.189
Chronic kidney disease	179 (27.6%)	368 (27.5%)	1.000	381 (43.1%)	757 (45.0%)	0.482
HEART FAILURE MEDICATIONS						
ACE inhibitor/ARB, n (%)	398 (61.4%)	813 (60.9%)	0.847	648 (73.4%)	1204 (71.6%)	0.368
ACEi/ARB % of target dose, mean ± SD	29.6 ± 39.0	29.0 ± 37.4	0.921	33.4 ± 32.9	32.3 ± 33.6	0.272

	Index Cohort			Validation Cohort		
Characteristic	**LRS Cohort**	**FIB-4 Cohort**	**P value**	**LRS Cohort**	**FIB-4 Cohort**	**P value**
Beta-blocker, n (%)	460 (71.0%)	947 (70.9%)	1.000	640 (72.5%)	1235 (73.5%)	0.625
Beta-blocker % of target dose, mean ± SD	20.7 ± 22.9	23.0 ± 25.6	0.175	34.3 ± 34.6	34.4 ± 34.2	0.940
Loop diuretic, n (%)	629 (97.1%)	1302 (97.5%)	0.724	861 (97.5%)	1636 (97.3%)	0.881
Dose, mg/day (furosemide equiv.)	40.0 [40.0–100.0]	40.0 [40.0–80.0]	0.379	40.0 [40.0–50.0]	40.0 [40.0–50.0]	0.338
MRA, n (%)	330 (50.9%)	629 (47.1%)	0.119	295 (33.4%)	555 (33.0%)	0.876
Dose, mg/day (spironolactone equiv.)	25.0 [25.0–50.0]	25.0 [25.0–50.0]	0.533	25.0 [25.0–25.0]	25.0 [25.0–25.0]	0.518

Supplementary Table: Baseline Characteristics of Cox Proportional Hazards Analysis Cohorts

Values presented as mean ± SD, median [IQR], or n (%)

P values: Wilcoxon rank-sum test (continuous) or Chi-square/Fisher's exact test (categorical)

Significant p-values: p<0.001 (dark red), p<0.01 (orange), p<0.05 (blue)

Note: Cohorts overlap - patients with both LRS and FIB-4 appear in both columns

Supplementary Table 4: Sensitivity analysis for outcomes – Complete cases with FIB-4 and LRS (FIB-4)

FIB-4

	Index Cohort			Validation Cohort			Combined Cohort		
	HR	**95% CI**	**p-value**	**HR**	**95% CI**	**p-value**	**HR**	**95% CI**	**p-value**
Mortality									
Unadjusted	1.90	(1.18-3.06)	0.008**	1.84	(1.27-2.67)	0.001**	1.88	(1.40-2.51)	<0.001***
NT-proBNP	1.76	(1.09-2.84)	0.020*	1.30	(0.89-1.90)	0.168	1.49	(1.11-2.00)	0.008**
Age + Sex	1.14	(0.67-1.93)	0.634	1.23	(0.83-1.83)	0.312	1.25	(0.91-1.71)	0.163
Age + Sex + NT-proBNP	1.05	(0.62-1.77)	0.866	1.02	(0.69-1.52)	0.904	1.09	(0.79-1.49)	0.602
Age + Sex + NT-proBNP + Alcohol	1.07	(0.63-1.82)	0.792	1.05	(0.70-1.56)	0.816	1.11	(0.81-1.52)	0.518
Composite Outcome									
Unadjusted	1.68	(1.14-2.47)	0.008**	1.74	(1.26-2.38)	<0.001***	1.71	(1.34-2.19)	<0.001***
NT-proBNP	1.50	(1.02-2.21)	0.039*	1.25	(0.91-1.73)	0.175	1.35	(1.06-1.73)	0.017*
Age + Sex	1.22	(0.80-1.88)	0.358	1.34	(0.96-1.88)	0.090	1.33	(1.02-1.72)	0.035*
Age + Sex + NT-proBNP	1.10	(0.72-1.69)	0.655	1.10	(0.78-1.54)	0.584	1.13	(0.87-1.47)	0.367
Age + Sex + NT-proBNP + Alcohol	1.11	(0.72-1.70)	0.629	1.14	(0.81-1.60)	0.454	1.15	(0.89-1.50)	0.285

Sensitivity Analysis - FIB-4 (Category: >2.67 vs Reference)
Index: N=548 (Mort=143, Comp=214) | Val: N=743 (Mort=212, Comp=299) | Combined: N=1291 (Mort=355, Comp=513)

**** p<0.001, ** p<0.01, * p<0.05 | NT-proBNP = P16860 (NPX) | Alcohol = Current_Alcohol*

Supplementary Table 5: Sensitivity analysis for outcomes – Complete cases with FIB-4 and LRS (LRS)

LRS

	Index Cohort			Validation Cohort			Combined Cohort		
	HR	**95% CI**	**p-value**	**HR**	**95% CI**	**p-value**	**HR**	**95% CI**	**p-value**
Mortality									
Unadjusted	2.65	(1.50-4.70)	<0.001***	3.13	(1.97-4.99)	<0.001***	2.98	(2.09-4.27)	<0.001***
NT-proBNP	1.98	(1.11-3.53)	0.021*	1.93	(1.20-3.13)	0.007**	1.98	(1.37-2.86)	<0.001***
Age + Sex	2.21	(1.23-3.98)	0.008**	3.10	(1.91-5.03)	<0.001***	2.66	(1.84-3.86)	<0.001***
Age + Sex + NT-proBNP	1.58	(0.87-2.88)	0.136	2.01	(1.22-3.33)	0.006**	1.81	(1.23-2.65)	0.002**
Age + Sex + NT-proBNP + Alcohol	1.68	(0.92-3.09)	0.092	2.09	(1.26-3.44)	0.004**	1.92	(1.31-2.82)	<0.001***
Composite Outcome									
Unadjusted	2.12	(1.34-3.36)	0.001**	2.59	(1.75-3.83)	<0.001***	2.41	(1.79-3.23)	<0.001***
NT-proBNP	1.49	(0.93-2.38)	0.100	1.73	(1.16-2.59)	0.007**	1.64	(1.21-2.22)	0.001**
Age + Sex	1.90	(1.18-3.04)	0.008**	2.68	(1.78-4.03)	<0.001***	2.28	(1.68-3.09)	<0.001***
Age + Sex + NT-proBNP	1.32	(0.81-2.14)	0.267	1.86	(1.22-2.83)	0.004**	1.59	(1.16-2.18)	0.004**
Age + Sex + NT-proBNP + Alcohol	1.34	(0.82-2.18)	0.244	1.90	(1.25-2.89)	0.003**	1.66	(1.21-2.27)	0.002**

Sensitivity Analysis - LRS (Category: >10 vs Reference)
Index: N=548 (Mort=143, Comp=214) | Val: N=743 (Mort=212, Comp=299) | Combined: N=1291 (Mort=355, Comp=513)

**** p<0.001, ** p<0.01, * p<0.05 | NT-proBNP = P16860 (NPX) | Alcohol = Current_Alcohol*

Supplementary Table 6: Standardised regression coefficient per log increase in NT-pro BNP

	Index Cohort			Validation Cohort		
	Std. β (95% CI)	**R²**	**p-value**	**Std. β (95% CI)**	**R²**	**p-value**
Univariate						
Log (LRS)	0.426 (0.323 to 0.529)	9.4%	<0.001	0.396 (0.298 to 0.494)	7.0%	<0.001
Log (FIB-4)	0.333 (0.258 to 0.407)	5.6%	<0.001	0.339 (0.266 to 0.412)	4.9%	<0.001
Log (HSI)	-0.241 (-0.309 to -0.173)	3.0%	<0.001	-0.383 (-0.455 to -0.310)	6.3%	<0.001
Adjusted for age, sex, current alcohol consumption						
Log (LRS)	0.403 (0.298 to 0.507)	8.3%	<0.001	0.365 (0.265 to 0.464)	6.0%	<0.001
Log (FIB-4)	0.227 (0.145 to 0.309)	2.2%	<0.001	0.212 (0.134 to 0.290)	1.8%	<0.001
Log (HSI)	-0.173 (-0.242 to -0.104)	1.5%	<0.001	-0.289 (-0.364 to -0.213)	3.5%	<0.001

Relationship between liver scores and NT-pro BNP

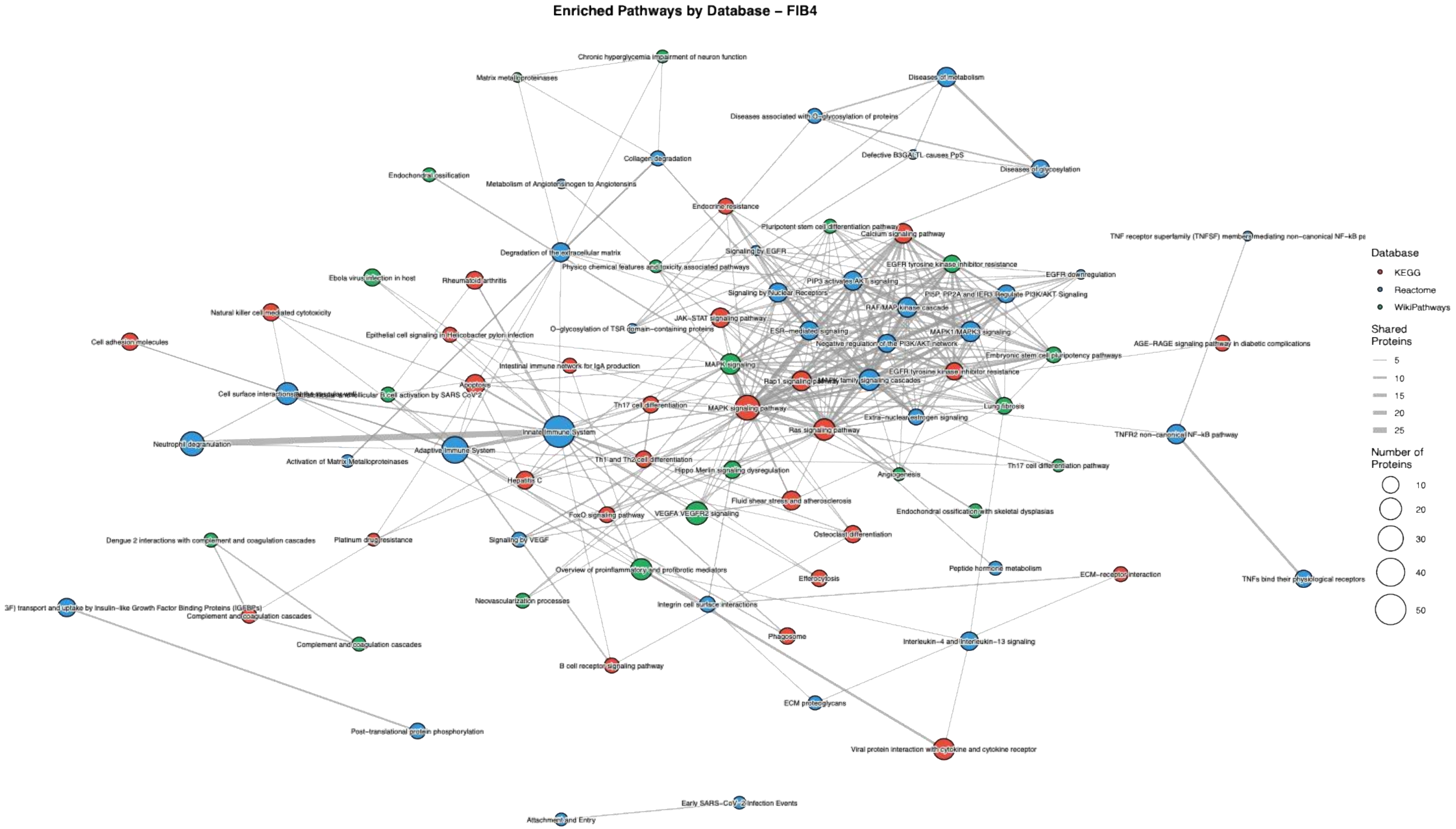
Across both cohorts, log liver fibrosis scores were significantly associated with log NT-pro BNP, with log HSI showing a significant negative association with log NT-pro BNP in both univariate and multi-variate analysis. LRS showed the strongest association with log NT-pro BNP with a standardised β-estimate of 0.403 [95% CI (0.298 to 0.507); $p < 0.001$] in the index cohort and 0.365 [95% CI (0.265 to 0.464); $p < 0.001$] in the validation cohort after adjustment for age, sex, and current alcohol consumption.

Supplementary Table 7: Paired comparison of liver scores at baseline and 9-month follow-up

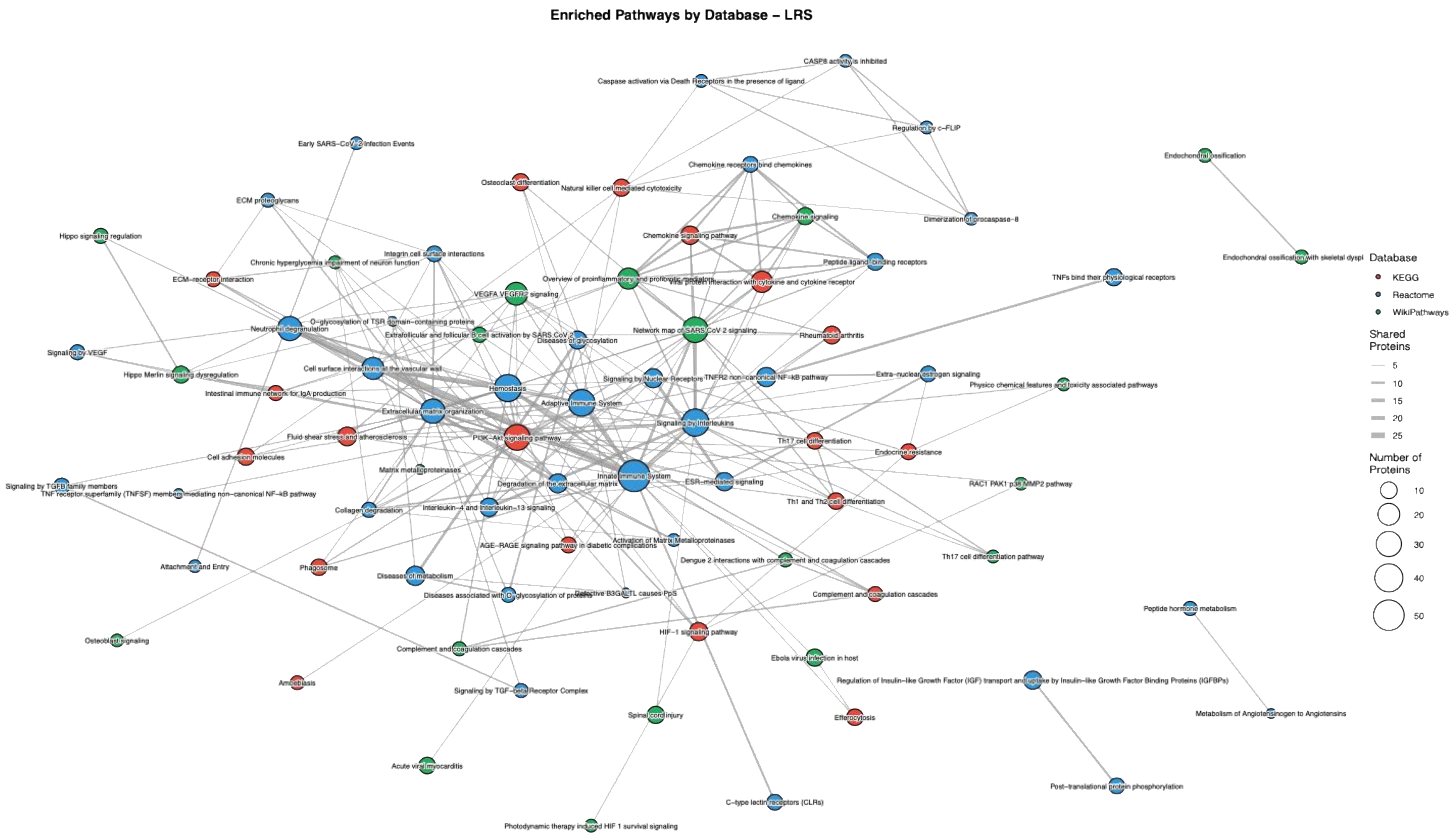
		Median (IQR)			Direction change, n (%)		
Score	**N**	**Baseline**	**Follow-up (9m)**	**Change**	**Increased**	**Decreased**	**p-value**
LRS	152	6.51 (5.65-7.39)	6.26 (5.57-7.35)	-0.03 (-0.69-0.74)	72 (47.4%)	80 (52.6%)	0.764
FIB-4	413	1.54 (1.08-2.27)	1.53 (1.09-2.16)	-0.00 (-0.43-0.32)	206 (49.9%)	207 (50.1%)	0.423
HSI	582	37.08 (32.68-41.70)	36.31 (32.24-41.11)	-0.10 (-1.90-1.43)	271 (46.6%)	301 (51.7%)	0.084

Wilcoxon signed-rank test

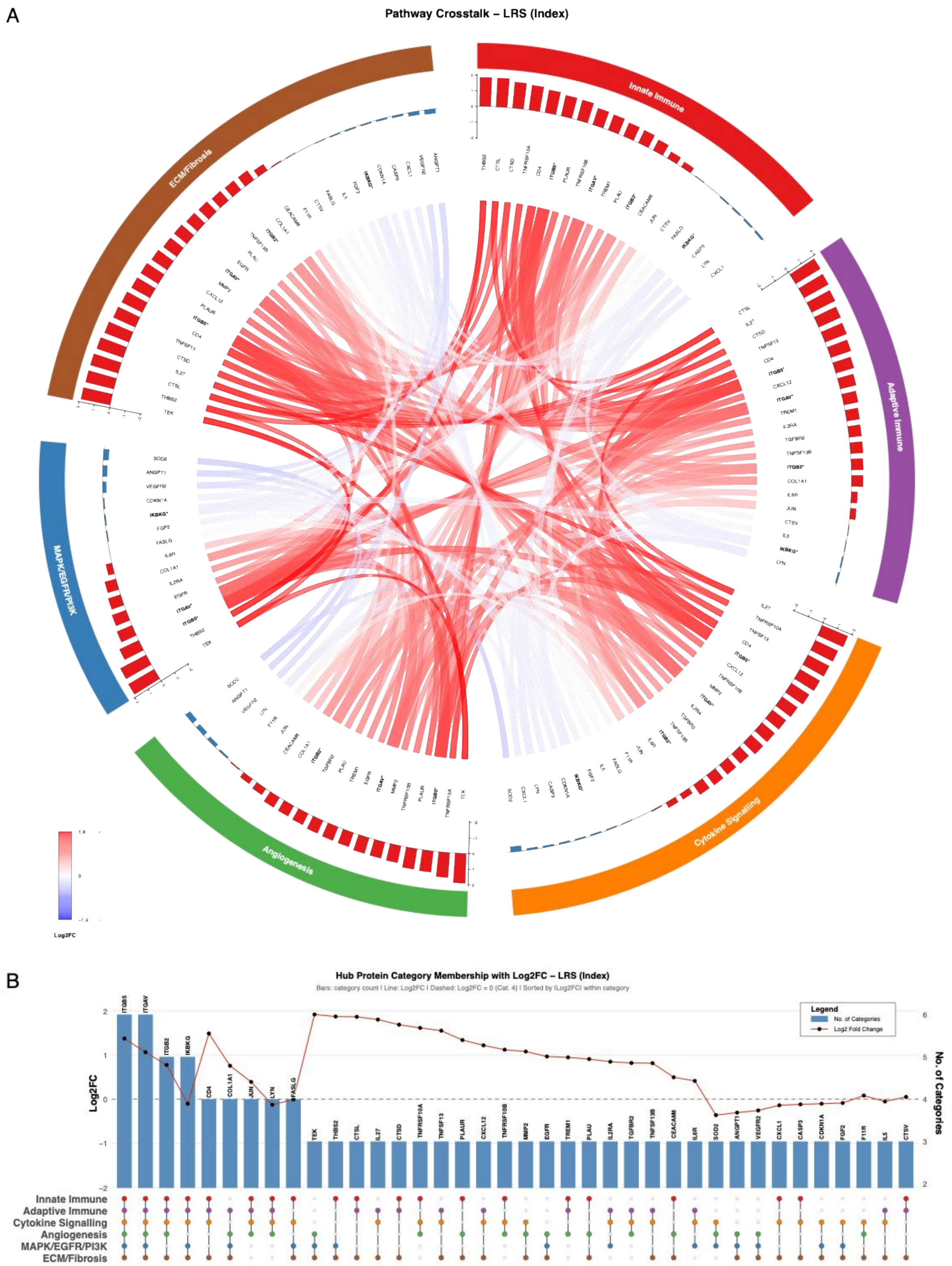
**** p<0.001, ** p<0.01, * p<0.05*



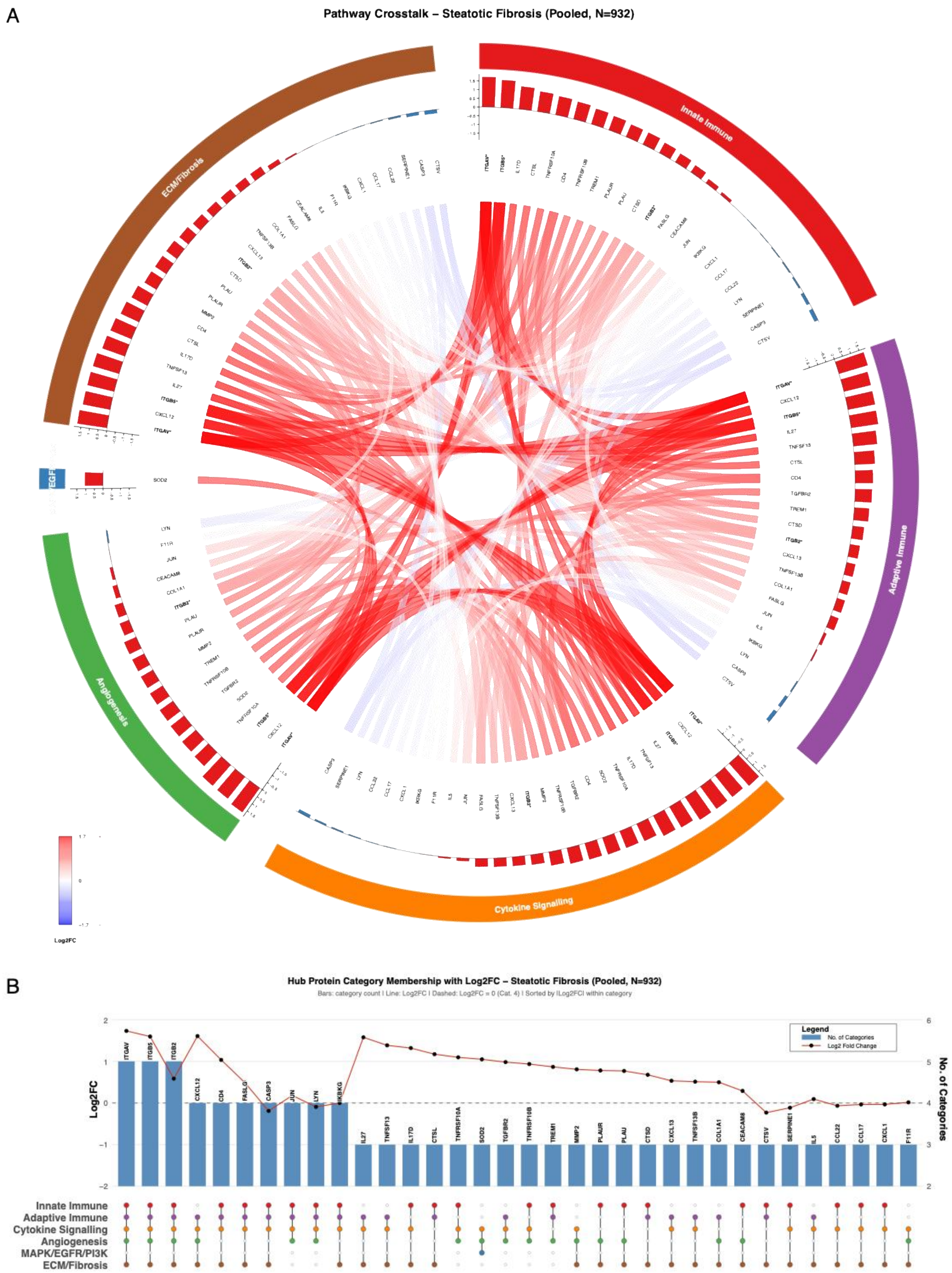
Supplementary Figure 1: Network graph showing shared proteins between significant pathways in liver fibrosis (FIB-4) (KEGG, Reactome, WP)



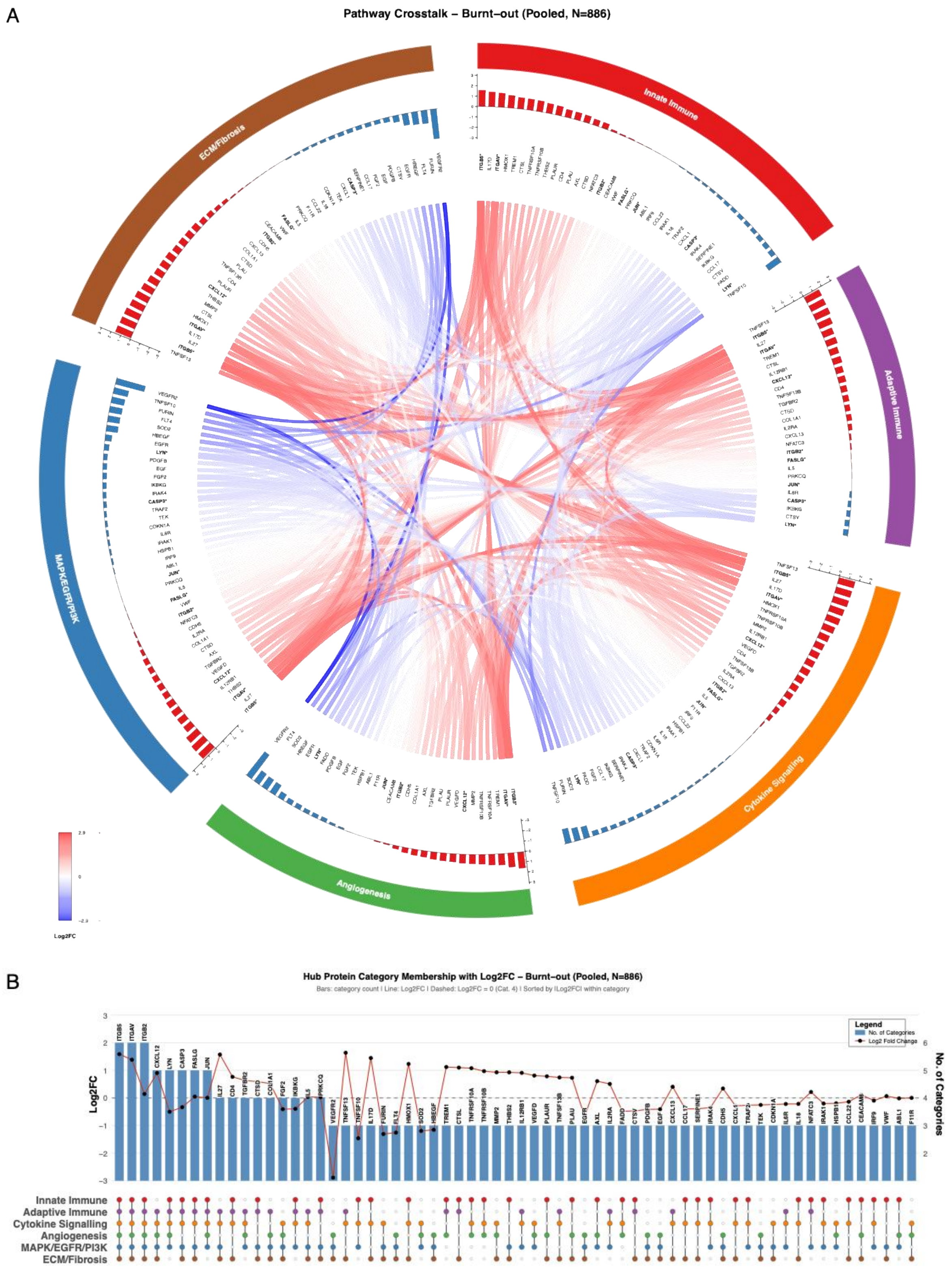
Supplementary Figure 2: Network graph showing shared proteins between significant pathways in liver fibrosis (LiverRisk) (KEGG, Reactome, WP)



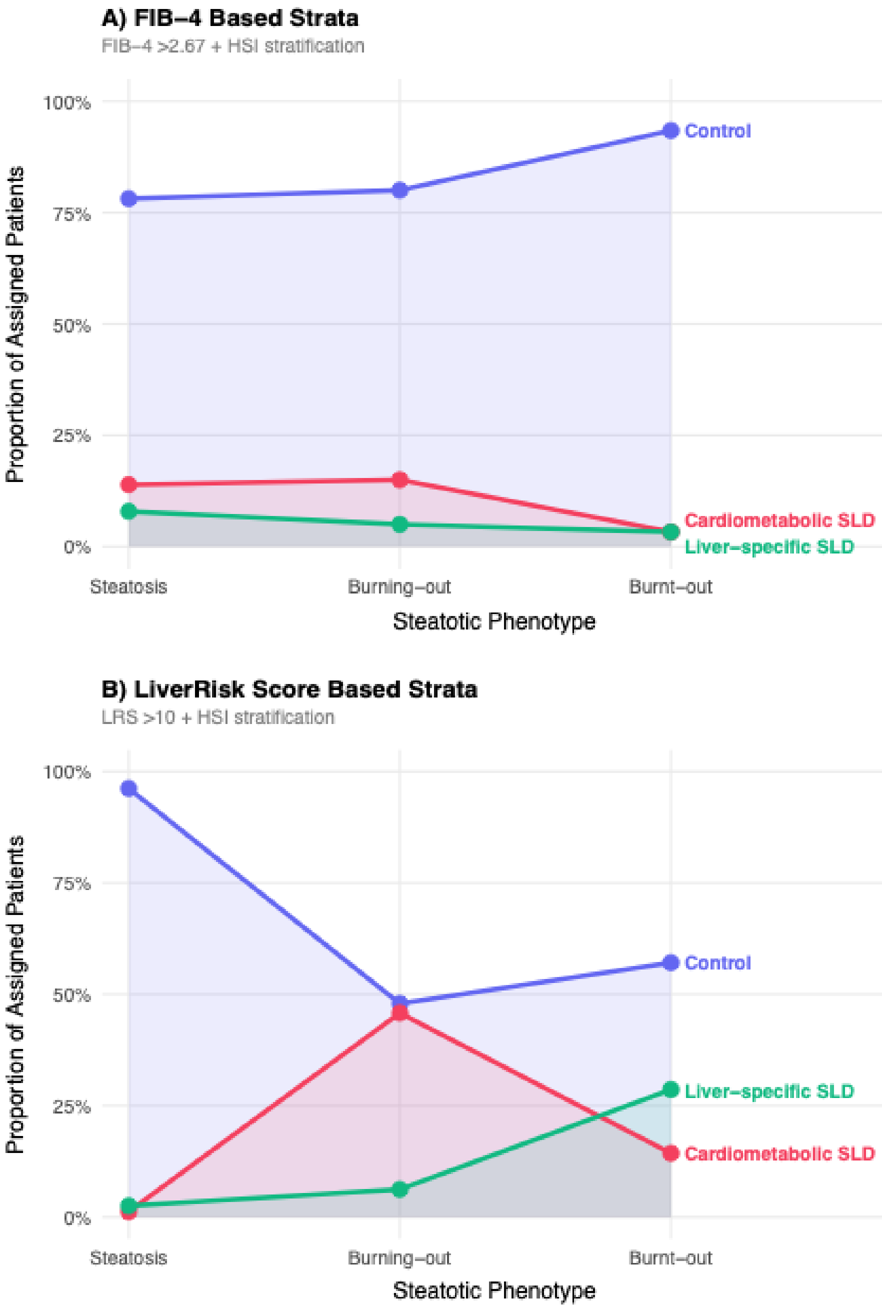
Supplementary Figure 3: (A) Chord diagram of biomarkers contributing to pathways in three or more biological categories with Log2 FC plotted on concentric bar plot. (B) UpSet plot showing number of different categories each biomarker contributes to with Log2 FC



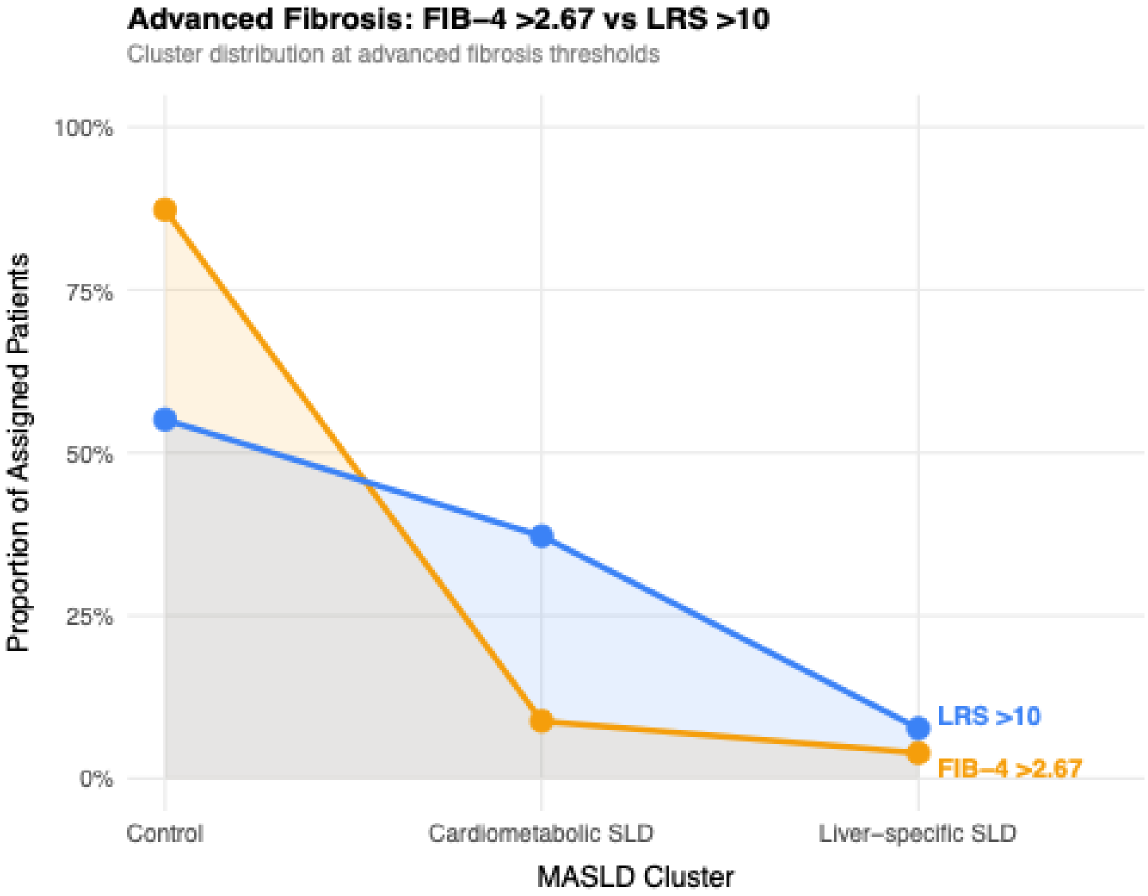
Supplementary Figure 4: (A) Chord diagram of biomarkers contributing to pathways in three or more biological categories relating to steatotic fibrosis with Log2 FC plotted on concentric bar plot. (B) UpSet plot showing number of different categories each biomarker contributes to with Log2 FC



Supplementary Figure 5: (A) Chord diagram of biomarkers contributing to pathways in three or more biological categories relating to burnt-out fibrosis with Log2 FC plotted on concentric bar plot. (B) UpSet plot showing number of different categories each biomarker contributes to with Log2 FC



Supplementary Figure 6. Proportion of patients who were assigned to each SLD cluster according to online calculator by Raverdy *et al* for each stage of burnt-out progression. (A) Liver fibrosis assessed by FIB-4 (B) Liver fibrosis assessed by LRS



Supplementary Figure 7. Proportion of patients with liver fibrosis assessed by FIB-4 and LRS who were assigned to each SLD cluster according to online calculator by Raverdy *et al*

The vast majority of patients with liver fibrosis assessed by FIB-4 were assigned to the "control" cluster. While 55.1% of patients with LRS > 10 were also assigned to the "control" cluster, liver fibrosis assessed by LRS identified a higher proportion of patients with a "cardiometabolic SLD" profile. The proportion of patients with liver-specific SLD was low across all groups, except in patients with burnt-out fibrosis assessed by LRS (28.6%).

Supplementary Table 8: Pathways associated with liver fibrosis (FIB-4)

REAC:R-HSA-3781865	Diseases of glycosylation	Reactome	12	2.45	4.0e-15	3.14	5.1e-27
REAC:R-HSA-5668914	Diseases of metabolism	Reactome	15	2.36	2.3e-14	3.11	7.1e-27
WP:WP322	Osteoblast signaling	WikiPathways	6	0.46	2.5e-13	2.20	2.2e-18
REAC:R-HSA-3906995	Diseases associated with O-glycosylation of proteins	Reactome	8	2.16	6.1e-13	2.51	3.8e-22
WP:WP2877	Vitamin D receptor pathway	WikiPathways	13	0.48	6.1e-13	2.43	1.9e-21
KEGG:04148	Efferocytosis	KEGG	10	0.48	2.3e-12	2.50	5.0e-21
WP:WP5373	Osteoarthritic chondrocyte hypertrophy	WikiPathways	5	0.52	2.0e-11	2.00	2.6e-16
REAC:R-HSA-2980736	Peptide hormone metabolism	Reactome	7	0.51	4.4e-11	2.45	2.2e-21
WP:WP4331	Neovascularization processes	WikiPathways	8	0.52	7.4e-11	1.63	1.2e-08
REAC:R-HSA-9694614	Attachment and Entry	Reactome	6	1.96	7.7e-11	2.41	1.4e-20
REAC:R-HSA-9772572	Early SARS-CoV-2 Infection Events	Reactome	6	1.96	7.7e-11	2.41	1.4e-20
REAC:R-HSA-381426	Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	Reactome	13	0.53	9.9e-11	2.60	7.3e-23
KEGG:04145	Phagosome	KEGG	10	1.95	1.3e-10	2.50	2.2e-21
REAC:R-HSA-9615017	FOXO-mediated transcription of oxidative stress, metabolic and neuronal genes	Reactome	5	0.53	2.2e-10	2.02	2.3e-16
REAC:R-HSA-8957275	Post-translational protein phosphorylation	Reactome	9	0.55	7.0e-10	2.33	4.5e-20

REAC:R-HSA-1474228	Degradation of the extracellular matrix	Reactome	14	0.54	8.3e-10	2.62	1.9e-22
REAC:R-HSA-2022377	Metabolism of Angiotensinogen to Angiotensins	Reactome	5	1.83	8.3e-10	0.47	9.5e-18
REAC:R-HSA-5083635	Defective B3GALTL causes PpS	Reactome	5	1.87	1.0e-09	2.06	5.5e-16
REAC:R-HSA-5173214	O-glycosylation of TSR domain-containing proteins	Reactome	5	1.87	1.0e-09	2.06	5.5e-16
WP:WP1539	Angiogenesis	WikiPathways	6	0.55	1.2e-09	1.50	8.9e-07
KEGG:04672	Intestinal immune network for IgA production	KEGG	8	1.82	1.4e-09	2.45	3.0e-21
WP:WP3931	Embryonic stem cell pluripotency pathways	WikiPathways	9	0.56	3.8e-09	0.64	1.3e-07
KEGG:04380	Osteoclast differentiation	KEGG	11	1.77	4.0e-09	2.08	5.5e-17
KEGG:04512	ECM-receptor interaction	KEGG	8	1.79	4.1e-09	2.07	3.1e-16
KEGG:04658	Th1 and Th2 cell differentiation	KEGG	10	0.57	4.6e-09	0.47	2.2e-17
WP:WP5038	Mitochondrial immune response to SARS CoV 2	WikiPathways	5	1.77	5.1e-09	0.45	1.1e-18
KEGG:04659	Th17 cell differentiation	KEGG	10	0.58	7.9e-09	2.00	5.8e-16
WP:WP5236	Markers of kidney cell lineage	WikiPathways	7	1.75	9.0e-09	0.32	1.8e-26
REAC:R-HSA-3000178	ECM proteoglycans	Reactome	7	1.76	1.1e-08	0.46	2.3e-17
WP:WP5473	Cytokine cytokine receptor interaction	WikiPathways	43	0.58	1.1e-08	0.46	2.3e-18
REAC:R-HSA-5669034	TNFs bind their physiological receptors	Reactome	11	0.58	1.1e-08	0.46	5.7e-18
WP:WP129	Matrix metalloproteinases	WikiPathways	5	0.57	1.4e-08	2.01	3.9e-15
REAC:R-HSA-1442490	Collagen degradation	Reactome	8	0.57	1.6e-08	2.52	7.6e-21
REAC:R-HSA-5668541	TNFR2 non-canonical NF-kB pathway	Reactome	15	1.70	2.2e-08	2.10	1.7e-17
KEGG:04060	Cytokine-cytokine receptor interaction	KEGG	50	0.59	3.0e-08	0.46	2.5e-18

WP:WP4217	Ebola virus infection in host	WikiPathways	11	0.59	3.1e-08	2.14	6.3e-18
WP:WP5218	Extrafollicular and follicular B cell activation by SARS CoV 2	WikiPathways	8	0.59	4.7e-08	0.42	5.9e-20
KEGG:05205	Proteoglycans in cancer	KEGG	20	1.67	1.2e-07	0.44	4.3e-19
REAC:R-HSA-5673001	RAF/MAP kinase cascade	Reactome	15	0.60	1.2e-07	1.38	8.9e-05
WP:WP2848	Pluripotent stem cell differentiation pathway	WikiPathways	7	0.60	1.3e-07	1.38	7.7e-05
REAC:R-HSA-5684996	MAPK1/MAPK3 signaling	Reactome	16	0.60	1.7e-07	1.37	1.1e-04
WP:WP5130	Th17 cell differentiation pathway	WikiPathways	6	0.61	1.8e-07	1.93	1.1e-14
WP:WP5283	Chronic hyperglycemia impairment of neuron function	WikiPathways	6	0.61	1.9e-07	2.36	9.8e-20
REAC:R-HSA-2173782	Binding and Uptake of Ligands by Scavenger Receptors	Reactome	7	1.64	2.2e-07	1.83	1.5e-12
REAC:R-HSA-198933	Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	Reactome	15	0.62	2.6e-07	0.53	2.7e-14
WP:WP5390	Pancreatic cancer subtypes	WikiPathways	5	0.62	2.6e-07	1.70	4.4e-11
REAC:R-HSA-2219530	Constitutive Signaling by Aberrant PI3K in Cancer	Reactome	9	0.61	2.7e-07	1.39	7.6e-05
KEGG:01522	Endocrine resistance	KEGG	9	1.62	4.0e-07	0.44	2.1e-18
REAC:R-HSA-5683057	MAPK family signaling cascades	Reactome	18	0.62	4.0e-07	1.30	8.8e-04
REAC:R-HSA-182971	EGFR downregulation	Reactome	5	0.61	4.7e-07	1.40	5.6e-05
REAC:R-HSA-177929	Signaling by EGFR	Reactome	5	0.61	4.7e-07	1.40	5.6e-05
WP:WP5095	Overview of proinflammatory and profibrotic mediators	WikiPathways	19	0.62	5.1e-07	2.07	2.4e-16
KEGG:05219	Bladder cancer	KEGG	6	0.61	5.4e-07	1.43	2.2e-05
WP:WP2828	Bladder cancer	WikiPathways	6	0.61	5.4e-07	1.43	2.2e-05

KEGG:04514	Cell adhesion molecules	KEGG	11	0.62	5.7e-07	0.50	2.7e-15
KEGG:05214	Glioma	KEGG	7	0.63	6.4e-07	1.30	9.9e-04
REAC:R-HSA-2219528	PI3K/AKT Signaling in Cancer	Reactome	10	0.62	8.9e-07	1.34	3.6e-04
KEGG:05120	Epithelial cell signaling in Helicobacter pylori infection	KEGG	8	0.63	1.2e-06	1.24	7.1e-03
REAC:R-HSA-9820960	Respiratory syncytial virus (RSV) attachment and entry	Reactome	5	0.63	1.2e-06	2.17	5.7e-18
KEGG:05218	Melanoma	KEGG	9	0.63	1.3e-06	1.36	1.8e-04
REAC:R-HSA-9006931	Signaling by Nuclear Receptors	Reactome	14	0.64	1.4e-06	1.92	1.3e-14
REAC:R-HSA-1592389	Activation of Matrix Metalloproteinases	Reactome	6	0.63	1.6e-06	1.97	6.0e-15
REAC:R-HSA-216083	Integrin cell surface interactions	Reactome	9	0.64	1.6e-06	0.51	1.1e-14
KEGG:05223	Non-small cell lung cancer	KEGG	7	0.64	1.8e-06	1.45	5.2e-06
REAC:R-HSA-1280218	Adaptive Immune System	Reactome	35	0.64	1.8e-06	0.51	2.6e-15
WP:WP382	MAPK signaling	WikiPathways	17	0.64	1.9e-06	1.37	9.4e-05
REAC:R-HSA-8939211	ESR-mediated signaling	Reactome	13	0.64	2.0e-06	1.87	1.0e-13
WP:WP4255	Non small cell lung cancer	WikiPathways	7	0.64	2.0e-06	1.47	3.6e-06
REAC:R-HSA-6811558	PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling	Reactome	12	0.64	2.3e-06	1.27	2.9e-03
REAC:R-HSA-199418	Negative regulation of the PI3K/AKT network	Reactome	12	0.64	2.3e-06	1.27	2.9e-03
WP:WP3624	Lung fibrosis	WikiPathways	10	0.64	2.4e-06	1.39	5.8e-05
REAC:R-HSA-5676594	TNF receptor superfamily (TNFSF) members mediating non-canonical NF-kB pathway	Reactome	5	0.65	2.6e-06	1.88	4.3e-14
REAC:R-HSA-202733	Cell surface interactions at the vascular wall	Reactome	21	1.54	3.2e-06	0.49	2.9e-16

REAC:R-HSA-1257604	PIP3 activates AKT signaling	Reactome	14	0.65	6.7e-06	1.25	5.4e-03
KEGG:04015	Rap1 signaling pathway	KEGG	15	0.66	6.7e-06	1.37	9.7e-05
KEGG:04650	Natural killer cell mediated cytotoxicity	KEGG	11	0.66	6.9e-06	0.53	7.4e-14
KEGG:05210	Colorectal cancer	KEGG	7	0.66	7.8e-06	1.18	3.5e-02
REAC:R-HSA-6798695	Neutrophil degranulation	Reactome	27	1.51	8.3e-06	0.57	9.0e-12
KEGG:04630	JAK-STAT signaling pathway	KEGG	15	0.66	9.1e-06	1.22	1.2e-02
KEGG:04933	AGE-RAGE signaling pathway in diabetic complications	KEGG	9	0.67	1.4e-05	2.34	9.8e-20
KEGG:05167	Kaposi sarcoma-associated herpesvirus infection	KEGG	14	0.68	3.2e-05	1.24	7.1e-03
KEGG:05323	Rheumatoid arthritis	KEGG	12	1.46	3.9e-05	0.46	3.3e-18
WP:WP5144	NRP1 triggered signaling in pancreatic cancer	WikiPathways	8	0.69	5.9e-05	1.59	2.5e-08
KEGG:04061	Viral protein interaction with cytokine and cytokine receptor	KEGG	19	0.69	6.4e-05	0.58	3.1e-11
WP:WP2572	Primary focal segmental glomerulosclerosis FSGS	WikiPathways	7	1.44	7.3e-05	0.53	1.4e-14
KEGG:04014	Ras signaling pathway	KEGG	19	0.71	1.4e-04	1.17	4.0e-02
KEGG:04010	MAPK signaling pathway	KEGG	29	0.71	2.1e-04	1.19	2.5e-02
KEGG:01521	EGFR tyrosine kinase inhibitor resistance	KEGG	11	0.72	2.1e-04	1.31	8.9e-04
KEGG:05418	Fluid shear stress and atherosclerosis	KEGG	14	1.40	2.1e-04	0.56	8.1e-12
WP:WP4806	EGFR tyrosine kinase inhibitor resistance	WikiPathways	11	0.72	2.1e-04	1.31	8.9e-04
KEGG:05160	Hepatitis C	KEGG	12	0.71	2.5e-04	1.19	3.0e-02
WP:WP474	Endochondral ossification	WikiPathways	7	0.72	3.4e-04	1.93	4.0e-15
WP:WP4808	Endochondral ossification with skeletal dysplasias	WikiPathways	7	0.72	3.4e-04	1.93	4.0e-15
KEGG:01524	Platinum drug resistance	KEGG	6	0.72	3.6e-04	1.22	1.4e-02
KEGG:04610	Complement and coagulation cascades	KEGG	8	0.72	4.7e-04	1.75	2.3e-11

REAC:R-HSA-168256	Immune System	Reactome	119	0.73	4.8e-04	0.56	8.0e-13
WP:WP2328	Allograft rejection	WikiPathways	8	0.74	5.8e-04	1.69	7.5e-11
KEGG:04020	Calcium signaling pathway	KEGG	15	0.74	6.1e-04	1.18	3.5e-02
KEGG:04662	B cell receptor signaling pathway	KEGG	8	1.36	7.1e-04	0.79	2.6e-03
KEGG:04068	FoxO signaling pathway	KEGG	9	0.74	8.5e-04	1.24	6.2e-03
WP:WP2586	Aryl hydrocarbon receptor pathway	WikiPathways	6	1.34	1.2e-03	0.67	3.7e-07
WP:WP558	Complement and coagulation cascades	WikiPathways	7	0.75	1.4e-03	1.70	7.3e-11
WP:WP3896	Dengue 2 interactions with complement and coagulation cascades	WikiPathways	7	0.75	1.4e-03	1.70	7.3e-11
WP:WP2817	Mammary gland development pregnancy and lactation stage 3 of 4	WikiPathways	6	1.31	3.0e-03	1.87	1.9e-12
WP:WP4541	Hippo Merlin signaling dysregulation	WikiPathways	11	0.77	3.3e-03	0.61	2.6e-09
REAC:R-HSA-6785807	Interleukin-4 and Interleukin-13 signaling	Reactome	13	0.79	7.4e-03	0.57	6.6e-12
WP:WP5285	Immune infiltration in pancreatic cancer	WikiPathways	8	1.27	8.0e-03	0.60	4.9e-10
REAC:R-HSA-168249	Innate Immune System	Reactome	55	1.26	8.2e-03	0.60	2.1e-10
WP:WP3680	Physico chemical features and toxicity associated pathways	WikiPathways	6	0.79	1.0e-02	0.60	3.9e-09
REAC:R-HSA-170834	Signaling by TGF-beta Receptor Complex	Reactome	7	1.25	1.3e-02	0.59	1.5e-10
WP:WP615	Senescence and autophagy in cancer	WikiPathways	11	1.24	1.5e-02	0.65	8.6e-08
REAC:R-HSA-9009391	Extra-nuclear estrogen signaling	Reactome	9	0.81	1.8e-02	1.36	7.7e-05
REAC:R-HSA-194138	Signaling by VEGF	Reactome	8	0.82	3.0e-02	1.75	4.0e-11
KEGG:05224	Breast cancer	KEGG	12	0.83	3.1e-02	0.68	8.7e-07

KEGG:04210	Apoptosis	KEGG	16	1.20	4.1e-02	0.72	1.1e-05
WP:WP3888	VEGFA VEGFR2 signaling	WikiPathways	23	0.84	4.5e-02	1.68	9.2e-11
WP:WP5078	T cell modulation and desmoplasia in pancreatic cancer	WikiPathways	14	0.84	4.7e-02	1.71	7.5e-11

Supplementary Table 9: Log-fold change of all proteins, liver fibrosis assessed by FIB-4

UniProt_ID	Gene_Symbol	Gene_Name	Log2FC_Index (95% CI)	P_Index	Log2FC_Validation (95% CI)	P_Validation
Q9BUD6	SPON2	spondin 2	2.37 (1.54, 3.21)	<0.001	3.53 (2.65, 4.42)	<0.001
P51888	PRELP	proline and arginine rich end leucine rich repeat protein	2.15 (1.61, 2.68)	<0.001	3.59 (2.95, 4.24)	<0.001
P07585	DCN	decorin	2.11 (1.63, 2.59)	<0.001	3.24 (2.70, 3.79)	<0.001
P35968	KDR	kinase insert domain receptor	-1.85 (-2.36, -1.35)	<0.001	-2.23 (-2.83, -1.62)	<0.001
Q14956	GPNMB	glycoprotein nmb	1.82 (1.17, 2.47)	<0.001	3.25 (2.52, 3.98)	<0.001
P06756	ITGAV	integrin subunit alpha V	1.68 (1.15, 2.20)	<0.001	2.12 (1.59, 2.64)	<0.001
P09326	CD48	CD48 molecule	1.68 (1.20, 2.15)	<0.001	2.22 (1.72, 2.73)	<0.001
P15260	IFNGR1	interferon gamma receptor 1	1.59 (1.19, 1.99)	<0.001	1.93 (1.52, 2.34)	<0.001
P04179	SOD2	superoxide dismutase 2	-1.58 (-2.75, -0.41)	0.008	0.25 (-0.97, 1.47)	0.692
P18084	ITGB5	integrin subunit beta 5	1.57 (1.15, 1.99)	<0.001	2.03 (1.57, 2.50)	<0.001
P01833	PIGR	polymeric immunoglobulin receptor	1.48 (0.27, 2.69)	0.017	1.33 (0.24, 2.42)	0.017
Q14242	SELPLG	selectin P ligand	-1.46 (-2.03, -0.88)	<0.001	-0.47 (-0.99, 0.05)	0.075
Q8NEV9	IL27	interleukin 27	1.31 (0.95, 1.66)	<0.001	1.48 (1.17, 1.80)	<0.001

Q8IYS5	OSCAR	osteoclast associated Ig-like receptor	1.24 (0.68, 1.80)	<0.001	2.58 (1.91, 3.25)	<0.001
O75888	TNFSF13	TNF superfamily member 13	1.23 (0.89, 1.56)	<0.001	1.61 (1.25, 1.97)	<0.001
P13726	F3	coagulation factor III, tissue factor	1.22 (0.83, 1.60)	<0.001	1.77 (1.35, 2.19)	<0.001
P18627	LAG3	lymphocyte activating 3	1.21 (0.90, 1.52)	<0.001	1.52 (1.23, 1.82)	<0.001
P24394	IL4R	interleukin 4 receptor	1.18 (0.88, 1.47)	<0.001	1.36 (1.09, 1.64)	<0.001
Q9UM47	NOTCH3	notch receptor 3	1.16 (0.91, 1.42)	<0.001	1.56 (1.26, 1.86)	<0.001
Q9BYH1	SEZ6L	seizure related 6 homolog like	1.12 (0.65, 1.58)	<0.001	2.05 (1.54, 2.56)	<0.001
P35442	THBS2	thrombospondin 2	1.10 (0.51, 1.68)	<0.001	1.47 (0.88, 2.06)	<0.001
Q7Z6M3	MILR1	mast cell immunoglobulin like receptor 1	1.10 (0.82, 1.37)	<0.001	1.34 (1.07, 1.61)	<0.001
P09486	SPARC	secreted protein acidic and cysteine rich	-1.08 (-1.61, -0.55)	<0.001	-0.26 (-0.72, 0.19)	0.252
O00300	TNFRSF11B	TNF receptor superfamily member 11b	1.06 (0.81, 1.32)	<0.001	1.42 (1.11, 1.72)	<0.001
P09601	HMOX1	heme oxygenase 1	1.04 (0.70, 1.38)	<0.001	1.35 (1.02, 1.68)	<0.001
Q9BQ51	PDCD1LG2	programmed cell death 1 ligand 2	1.04 (0.69, 1.39)	<0.001	1.73 (1.33, 2.12)	<0.001
P50591	TNFSF10	TNF superfamily member 10	-1.03 (-1.37, -0.68)	<0.001	-1.25 (-1.62, -0.88)	<0.001
Q8TAD2	IL17D	interleukin 17D	1.03 (0.61, 1.44)	<0.001	1.35 (0.94, 1.76)	<0.001

Q14508	WFDC2	WAP four-disulfide core domain 2	1.02 (0.68, 1.36)	<0.001	1.26 (0.91, 1.61)	<0.001
Q9HBG7	LY9	lymphocyte antigen 9	1.01 (0.65, 1.36)	<0.001	1.65 (1.26, 2.03)	<0.001
P07711	CTSL	cathepsin L	1.00 (0.66, 1.33)	<0.001	1.24 (0.95, 1.53)	<0.001
P52823	STC1	stanniocalcin 1	0.99 (0.65, 1.32)	<0.001	1.28 (0.83, 1.74)	<0.001
P29317	EPHA2	EPH receptor A2	0.98 (0.68, 1.29)	<0.001	1.28 (0.98, 1.57)	<0.001
O00182	LGALS9	galectin 9	0.96 (0.56, 1.36)	<0.001	1.24 (0.83, 1.65)	<0.001
P08069	IGF1R	insulin like growth factor 1 receptor	0.94 (0.59, 1.29)	<0.001	1.64 (1.26, 2.02)	<0.001
O00548	DLL1	delta like canonical Notch ligand 1	0.94 (0.58, 1.30)	<0.001	1.41 (1.02, 1.80)	<0.001
Q76LX8	ADAMTS13	ADAM metallopeptidase with thrombospondin type 1 motif 13	-0.93 (-1.55, -0.31)	0.003	-0.41 (-1.11, 0.29)	0.246
Q99075	HBEGF	heparin binding EGF like growth factor	-0.92 (-1.21, -0.64)	<0.001	-0.59 (-0.97, -0.21)	0.002
Q9HCB6	SPON1	spondin 1	0.92 (0.65, 1.18)	<0.001	1.12 (0.85, 1.40)	<0.001
O43736	ITM2A	integral membrane protein 2A	0.92 (0.65, 1.18)	<0.001	0.63 (0.41, 0.86)	<0.001
Q9BYF1	ACE2	angiotensin converting enzyme 2	0.91 (0.68, 1.15)	<0.001	0.76 (0.56, 0.95)	<0.001
P35052	GPC1	glypican 1	0.91 (0.57, 1.26)	<0.001	1.52 (1.14, 1.90)	<0.001
Q96PD2	DCBLD2	discoidin, CUB and LCCL domain containing 2	0.91 (0.49, 1.33)	<0.001	1.00 (0.59, 1.41)	<0.001

P21860	ERBB3	erb-b2 receptor tyrosine kinase 3	-0.89 (-1.38, -0.41)	<0.001	-1.10 (-1.70, -0.51)	<0.001
P42701	IL12RB1	interleukin 12 receptor subunit beta 1	0.89 (0.57, 1.21)	<0.001	1.08 (0.76, 1.41)	<0.001
Q9UMR7	CLEC4A	C-type lectin domain family 4 member A	-0.87 (-1.22, -0.51)	<0.001	0.05 (-0.29, 0.40)	0.758
P16870	CPE	carboxypeptidase E	0.86 (0.52, 1.20)	<0.001	1.90 (1.48, 2.31)	<0.001
P35916	FLT4	fms related receptor tyrosine kinase 4	-0.85 (-1.35, -0.35)	<0.001	-0.16 (-0.72, 0.40)	0.572
Q8NHJ6	LILRB4	leukocyte immunoglobulin like receptor B4	0.85 (0.61, 1.08)	<0.001	0.75 (0.53, 0.97)	<0.001
P78310	CXADR	CXADR Ig-like cell adhesion molecule	0.83 (0.60, 1.06)	<0.001	1.01 (0.78, 1.24)	<0.001
O00220	TNFRSF10A	TNF receptor superfamily member 10a	0.82 (0.53, 1.12)	<0.001	1.10 (0.81, 1.38)	<0.001
Q9UBX7	KLK11	kallikrein related peptidase 11	0.82 (0.55, 1.09)	<0.001	1.06 (0.80, 1.33)	<0.001
O95388	CCN4	cellular communication network factor 4	0.82 (0.58, 1.05)	<0.001	1.12 (0.88, 1.37)	<0.001
Q9NQ30	ESM1	endothelial cell specific molecule 1	0.80 (0.57, 1.03)	<0.001	1.31 (1.06, 1.57)	<0.001
Q8N608	DPP10	dipeptidyl peptidase like 10	0.80 (0.56, 1.04)	<0.001	1.11 (0.84, 1.37)	<0.001
P06858	LPL	lipoprotein lipase	0.79 (0.49, 1.10)	<0.001	0.49 (0.17, 0.81)	0.002
P18564	ITGB6	integrin subunit beta 6	0.79 (0.43, 1.15)	<0.001	1.47 (1.11, 1.83)	<0.001
P37173	TGFBR2	transforming growth factor beta receptor 2	0.79 (0.50, 1.07)	<0.001	1.01 (0.71, 1.30)	<0.001

O14763	TNFRSF10B	TNF receptor superfamily member 10b	0.78 (0.54, 1.02)	<0.001	0.93 (0.70, 1.15)	<0.001
O95998	IL18BP	interleukin 18 binding protein	0.77 (0.55, 1.00)	<0.001	1.03 (0.77, 1.29)	<0.001
P54760	EPHB4	EPH receptor B4	0.76 (0.49, 1.03)	<0.001	1.05 (0.74, 1.36)	<0.001
P10747	CD28	CD28 molecule	0.75 (0.44, 1.07)	<0.001	1.16 (0.83, 1.49)	<0.001
Q86VB7	CD163	CD163 molecule	0.74 (0.53, 0.96)	<0.001	0.87 (0.63, 1.12)	<0.001
Q9BWV1	BOC	BOC cell adhesion associated, oncogene regulated	0.73 (0.34, 1.12)	<0.001	1.80 (1.36, 2.24)	<0.001
Q16790	CA9	carbonic anhydrase 9	0.73 (0.53, 0.92)	<0.001	0.91 (0.71, 1.12)	<0.001
P14778	IL1R1	interleukin 1 receptor type 1	0.73 (0.49, 0.97)	<0.001	1.02 (0.71, 1.32)	<0.001
P30530	AXL	AXL receptor tyrosine kinase	0.73 (0.49, 0.96)	<0.001	0.96 (0.68, 1.25)	<0.001
P07949	RET	ret proto-oncogene	-0.72 (-0.97, -0.47)	<0.001	-0.74 (-0.98, -0.49)	<0.001
Q99988	GDF15	growth differentiation factor 15	0.71 (0.54, 0.88)	<0.001	0.85 (0.67, 1.03)	<0.001
P18065	IGFBP2	insulin like growth factor binding protein 2	0.71 (0.52, 0.89)	<0.001	0.71 (0.52, 0.90)	<0.001
O00592	PODXL	podocalyxin like	0.70 (0.12, 1.28)	0.019	1.16 (0.48, 1.83)	<0.001
Q12866	MERTK	MER proto-oncogene, tyrosine kinase	0.70 (0.41, 0.98)	<0.001	1.29 (0.96, 1.62)	<0.001
Q16270	IGFBP7	insulin like growth factor binding protein 7	0.69 (0.50, 0.89)	<0.001	1.12 (0.89, 1.35)	<0.001

Q6EIG7	CLEC6A	C-type lectin domain containing 6A	0.68 (0.41, 0.96)	<0.001	0.81 (0.56, 1.07)	<0.001
Q99727	TIMP4	TIMP metallopeptidase inhibitor 4	0.68 (0.47, 0.89)	<0.001	0.60 (0.36, 0.83)	<0.001
Q9NP99	TREM1	triggering receptor expressed on myeloid cells 1	0.68 (0.41, 0.95)	<0.001	0.93 (0.67, 1.19)	<0.001
P98160	HSPG2	heparan sulfate proteoglycan 2	0.68 (0.46, 0.90)	<0.001	1.00 (0.73, 1.28)	<0.001
P01135	TGFA	transforming growth factor alpha	0.67 (0.39, 0.95)	<0.001	1.11 (0.79, 1.43)	<0.001
Q03405	PLAUR	plasminogen activator, urokinase receptor	0.66 (0.45, 0.88)	<0.001	0.82 (0.58, 1.06)	<0.001
O95407	TNFRSF6B	TNF receptor superfamily member 6b	0.66 (0.47, 0.85)	<0.001	0.76 (0.58, 0.94)	<0.001
P78324	SIRPA	signal regulatory protein alpha	0.66 (0.42, 0.89)	<0.001	0.62 (0.39, 0.86)	<0.001
O60449	LY75	lymphocyte antigen 75	0.65 (0.33, 0.98)	<0.001	1.33 (0.96, 1.71)	<0.001
P26842	CD27	CD27 molecule	0.65 (0.37, 0.93)	<0.001	0.92 (0.64, 1.21)	<0.001
P10451	SPP1	secreted phosphoprotein 1	0.65 (0.47, 0.83)	<0.001	0.79 (0.58, 0.99)	<0.001
Q9Y3P8	SIT1	signaling threshold regulating transmembrane adaptor 1	-0.65 (-0.94, -0.36)	<0.001	-0.52 (-0.79, -0.26)	<0.001
P08253	MMP2	matrix metallopeptidase 2	0.65 (0.44, 0.86)	<0.001	1.02 (0.77, 1.28)	<0.001
Q13740	ALCAM	activated leukocyte cell adhesion molecule	0.65 (0.38, 0.91)	<0.001	1.12 (0.78, 1.45)	<0.001
P15514	AREG	amphiregulin	0.65 (0.40, 0.89)	<0.001	0.84 (0.63, 1.06)	<0.001

P01730	CD4	CD4 molecule	0.64 (0.32, 0.97)	<0.001	1.48 (1.08, 1.88)	<0.001
Q15303	ERBB4	erb-b2 receptor tyrosine kinase 4	0.64 (0.23, 1.05)	0.002	1.52 (1.04, 1.99)	<0.001
P36941	LTBR	lymphotoxin beta receptor	0.64 (0.42, 0.86)	<0.001	0.88 (0.63, 1.13)	<0.001
Q6UXB4	CLEC4G	C-type lectin domain family 4 member G	-0.64 (-0.98, -0.30)	<0.001	-0.27 (-0.61, 0.07)	0.123
P20333	TNFRSF1B	TNF receptor superfamily member 1B	0.63 (0.44, 0.81)	<0.001	0.86 (0.65, 1.07)	<0.001
P00749	PLAU	plasminogen activator, urokinase	0.61 (0.37, 0.85)	<0.001	1.08 (0.76, 1.39)	<0.001
P09958	FURIN	furin, paired basic amino acid cleaving enzyme	-0.61 (-0.93, -0.30)	<0.001	-0.69 (-1.04, -0.35)	<0.001
Q13219	PAPPA	pappalysin 1	0.61 (0.39, 0.83)	<0.001	1.01 (0.78, 1.23)	<0.001
P78410	BTN3A2	butyrophilin subfamily 3 member A2	0.60 (0.33, 0.88)	<0.001	0.76 (0.49, 1.03)	<0.001
Q07065	CKAP4	cytoskeleton associated protein 4	0.60 (0.36, 0.83)	<0.001	0.96 (0.72, 1.20)	<0.001
P49763	PGF	placental growth factor	0.59 (0.33, 0.86)	<0.001	1.24 (0.94, 1.54)	<0.001
O00622	CCN1	cellular communication network factor 1	0.59 (0.35, 0.84)	<0.001	1.27 (0.99, 1.55)	<0.001
P40225	THPO	thrombopoietin	-0.59 (-0.92, -0.26)	<0.001	-0.12 (-0.46, 0.22)	0.493
P47992	XCL1	X-C motif chemokine ligand 1	0.59 (0.35, 0.83)	<0.001	0.83 (0.59, 1.06)	<0.001
Q01638	IL1RL1	interleukin 1 receptor like 1	0.59 (0.44, 0.74)	<0.001	0.77 (0.60, 0.94)	<0.001

P07339	CTSD	cathepsin D	0.59 (0.37, 0.81)	<0.001	0.88 (0.62, 1.13)	<0.001
O60911	CTSV	cathepsin V	-0.59 (-0.88, -0.29)	<0.001	-0.17 (-0.42, 0.08)	0.193
Q6BAA4	FCRLB	Fc receptor like B	0.58 (0.38, 0.78)	<0.001	0.56 (0.37, 0.75)	<0.001
Q96P31	FCRL3	Fc receptor like 3	0.58 (0.21, 0.95)	0.002	0.89 (0.55, 1.22)	<0.001
P48061	CXCL12	C-X-C motif chemokine ligand 12	0.58 (-0.07, 1.23)	0.08	1.81 (1.11, 2.52)	<0.001
Q9UHC6	CNTNAP2	contactin associated protein 2	0.56 (0.26, 0.86)	<0.001	0.96 (0.66, 1.27)	<0.001
O76036	NCR1	natural cytotoxicity triggering receptor 1	0.56 (0.33, 0.79)	<0.001	0.59 (0.35, 0.83)	<0.001
P19883	FST	follistatin	0.56 (0.31, 0.81)	<0.001	1.41 (1.11, 1.71)	<0.001
P48740	MASP1	MBL associated serine protease 1	0.56 (0.14, 0.98)	0.01	1.44 (0.98, 1.91)	<0.001
Q9UBR2	CTSZ	cathepsin Z	0.56 (0.32, 0.80)	<0.001	0.72 (0.43, 1.00)	<0.001
P58499	FAM3B	FAM3 metabolism regulating signaling molecule B	0.55 (0.28, 0.82)	<0.001	0.71 (0.41, 1.01)	<0.001
Q14435	GALNT3	polypeptide N-acetylgalactosaminyltransferase 3	0.54 (0.25, 0.83)	<0.001	1.04 (0.74, 1.35)	<0.001
Q9Y5W5	WIF1	WNT inhibitory factor 1	0.54 (0.25, 0.83)	<0.001	1.27 (0.97, 1.58)	<0.001
P15144	ANPEP	alanyl aminopeptidase, membrane	0.53 (0.31, 0.76)	<0.001	0.62 (0.36, 0.88)	<0.001
O00253	AGRP	agouti related neuropeptide	0.52 (0.28, 0.77)	<0.001	1.00 (0.73, 1.28)	<0.001

P36222	CHI3L1	chitinase 3 like 1	0.52 (0.38, 0.66)	<0.001	0.50 (0.36, 0.64)	<0.001
P19438	TNFRSF1A	TNF receptor superfamily member 1A	0.52 (0.32, 0.71)	<0.001	0.81 (0.60, 1.02)	<0.001
P50135	HNMT	histamine N-methyltransferase	0.51 (0.31, 0.72)	<0.001	1.10 (0.85, 1.35)	<0.001
P26022	PTX3	pentraxin 3	0.51 (0.28, 0.75)	<0.001	0.96 (0.71, 1.22)	<0.001
Q9NQ25	SLAMF7	SLAM family member 7	0.51 (0.31, 0.71)	<0.001	0.65 (0.46, 0.85)	<0.001
Q9UNE0	EDAR	ectodysplasin A receptor	-0.51 (-0.76, -0.26)	<0.001	-0.09 (-0.38, 0.20)	0.548
P33151	CDH5	cadherin 5	0.51 (0.28, 0.74)	<0.001	0.76 (0.49, 1.04)	<0.001
P08833	IGFBP1	insulin like growth factor binding protein 1	0.51 (0.38, 0.64)	<0.001	0.55 (0.43, 0.66)	<0.001
Q9NS68	TNFRSF19	TNF receptor superfamily member 19	0.50 (0.31, 0.69)	<0.001	0.78 (0.58, 0.97)	<0.001
P22004	BMP6	bone morphogenetic protein 6	0.50 (0.33, 0.67)	<0.001	1.22 (0.91, 1.53)	<0.001
P13500	CCL2	C-C motif chemokine ligand 2	0.50 (0.25, 0.75)	<0.001	0.86 (0.56, 1.15)	<0.001
Q05084	ICA1	islet cell autoantigen 1	-0.50 (-0.76, -0.23)	<0.001	-0.30 (-0.64, 0.04)	0.082
Q13490	BIRC2	baculoviral IAP repeat containing 2	-0.50 (-0.88, -0.12)	0.011	0.08 (-0.31, 0.48)	0.679
Q8WTT0	CLEC4C	C-type lectin domain family 4 member C	-0.50 (-0.74, -0.25)	<0.001	-0.22 (-0.43, -0.01)	0.041
P02452	COL1A1	collagen type I alpha 1 chain	0.49 (0.26, 0.72)	<0.001	0.66 (0.41, 0.91)	<0.001

P31949	S100A11	S100 calcium binding protein A11	0.49 (0.08, 0.90)	0.018	1.63 (1.14, 2.13)	<0.001
P08727	KRT19	keratin 19	0.49 (0.29, 0.68)	<0.001	0.43 (0.27, 0.59)	<0.001
Q9BXY4	RSPO3	R-spondin 3	0.48 (0.33, 0.64)	<0.001	0.78 (0.60, 0.96)	<0.001
P15328	FOLR1	folate receptor alpha	0.48 (0.23, 0.73)	<0.001	0.84 (0.59, 1.09)	<0.001
P04085	PDGFA	platelet derived growth factor subunit A	-0.48 (-0.62, -0.33)	<0.001	-0.29 (-0.46, -0.13)	<0.001
Q9Y6Q6	TNFRSF11A	TNF receptor superfamily member 11a	0.48 (0.28, 0.67)	<0.001	0.73 (0.52, 0.93)	<0.001
Q9BXN2	CLEC7A	C-type lectin domain containing 7A	0.47 (0.27, 0.67)	<0.001	0.53 (0.34, 0.73)	<0.001
P35475	IDUA	alpha-L-iduronidase	-0.47 (-0.76, -0.19)	0.001	0.00 (-0.29, 0.29)	0.998
Q15517	CDSN	corneodesmosin	0.47 (0.23, 0.71)	<0.001	0.60 (0.39, 0.82)	<0.001
Q96DB9	FXYD5	FXYD domain containing ion transport regulator 5	-0.47 (-0.81, -0.13)	0.007	-0.16 (-0.55, 0.23)	0.416
Q99717	SMAD5	SMAD family member 5	-0.47 (-1.20, 0.27)	0.213	-0.89 (-1.72, -0.06)	0.036
Q96PL1	SCGB3A2	secretoglobin family 3A member 2	0.46 (0.30, 0.62)	<0.001	0.36 (0.24, 0.48)	<0.001
Q13574	DGKZ	diacylglycerol kinase zeta	-0.46 (-1.10, 0.18)	0.157	0.02 (-0.54, 0.59)	0.932
P28799	GRN	granulin precursor	0.46 (0.21, 0.71)	<0.001	0.85 (0.53, 1.18)	<0.001
P35318	ADM	adrenomedullin	0.45 (0.26, 0.65)	<0.001	1.09 (0.78, 1.40)	<0.001

O14836	TNFRSF13B	TNF receptor superfamily member 13B	0.45 (0.20, 0.71)	<0.001	1.06 (0.78, 1.35)	<0.001
P80370	DLK1	delta like non-canonical Notch ligand 1	0.45 (0.28, 0.62)	<0.001	0.53 (0.34, 0.71)	<0.001
P07204	THBD	thrombomodulin	0.45 (0.16, 0.74)	0.002	1.14 (0.78, 1.49)	<0.001
P78325	ADAM8	ADAM metallopeptidase domain 8	0.45 (0.13, 0.76)	0.006	0.82 (0.48, 1.16)	<0.001
P21583	KITLG	KIT ligand	-0.44 (-0.66, -0.23)	<0.001	-0.32 (-0.53, -0.10)	0.004
P08670	VIM	vimentin	0.44 (0.21, 0.67)	<0.001	0.95 (0.74, 1.16)	<0.001
P13598	ICAM2	intercellular adhesion molecule 2	0.43 (0.22, 0.65)	<0.001	0.52 (0.26, 0.78)	<0.001
P25445	FAS	Fas cell surface death receptor	0.43 (0.20, 0.66)	<0.001	0.81 (0.52, 1.09)	<0.001
Q12860	CNTN1	contactin 1	0.43 (0.19, 0.67)	<0.001	0.65 (0.38, 0.93)	<0.001
Q9Y275	TNFSF13B	TNF superfamily member 13b	0.43 (0.22, 0.63)	<0.001	0.60 (0.39, 0.82)	<0.001
Q07654	TFF3	trefoil factor 3	0.43 (0.26, 0.59)	<0.001	0.52 (0.34, 0.70)	<0.001
P05107	ITGB2	integrin subunit beta 2	0.42 (0.20, 0.64)	<0.001	0.59 (0.34, 0.85)	<0.001
Q15389	ANGPT1	angiopoietin 1	-0.42 (-0.56, -0.29)	<0.001	-0.27 (-0.40, -0.14)	<0.001
P01589	IL2RA	interleukin 2 receptor subunit alpha	0.42 (0.23, 0.62)	<0.001	0.42 (0.21, 0.63)	<0.001
P56470	LGALS4	galectin 4	0.42 (0.23, 0.62)	<0.001	0.40 (0.20, 0.59)	<0.001

Q6UXB2	CXCL17	C-X-C motif chemokine ligand 17	0.42 (0.20, 0.64)	<0.001	0.50 (0.27, 0.72)	<0.001
Q16663	CCL15	C-C motif chemokine ligand 15	0.41 (0.21, 0.61)	<0.001	0.66 (0.43, 0.89)	<0.001
P10147	CCL3	C-C motif chemokine ligand 3	0.41 (0.19, 0.63)	<0.001	0.73 (0.52, 0.95)	<0.001
Q99969	RARRES2	retinoic acid receptor responder 2	-0.41 (-0.67, -0.15)	0.002	-0.82 (-1.17, -0.47)	<0.001
P14210	HGF	hepatocyte growth factor	0.41 (0.25, 0.57)	<0.001	1.00 (0.76, 1.23)	<0.001
Q9UEW3	MARCO	macrophage receptor with collagenous structure	0.40 (-0.16, 0.96)	0.161	0.99 (0.36, 1.62)	0.002
Q96IQ7	VSIG2	V-set and immunoglobulin domain containing 2	0.40 (0.19, 0.61)	<0.001	0.47 (0.28, 0.66)	<0.001
P32970	CD70	CD70 molecule	0.39 (0.14, 0.65)	0.003	0.77 (0.50, 1.04)	<0.001
P25116	F2R	coagulation factor II thrombin receptor	0.39 (0.11, 0.67)	0.006	0.90 (0.60, 1.21)	<0.001
Q15109	AGER	advanced glycosylation end-product specific receptor	0.39 (0.11, 0.67)	0.007	1.17 (0.87, 1.46)	<0.001
Q96NY8	NECTIN4	nectin cell adhesion molecule 4	0.39 (0.16, 0.63)	0.001	0.66 (0.43, 0.89)	<0.001
P01130	LDLR	low density lipoprotein receptor	-0.39 (-0.58, -0.20)	<0.001	-0.42 (-0.62, -0.22)	<0.001
P21589	NT5E	5'-nucleotidase ecto	0.39 (0.20, 0.58)	<0.001	0.46 (0.28, 0.65)	<0.001
Q16651	PRSS8	serine protease 8	0.39 (0.01, 0.77)	0.047	0.74 (0.31, 1.17)	<0.001
P18827	SDC1	syndecan 1	0.39 (0.18, 0.59)	<0.001	0.64 (0.43, 0.85)	<0.001

O95971	CD160	CD160 molecule	0.39 (0.18, 0.60)	<0.001	0.55 (0.33, 0.76)	<0.001
P04792	HSPB1	heat shock protein family B (small) member 1	-0.38 (-0.72, -0.04)	0.027	0.01 (-0.30, 0.32)	0.938
Q9H2A7	CXCL16	C-X-C motif chemokine ligand 16	0.38 (0.14, 0.62)	0.002	0.44 (0.16, 0.72)	0.002
Q9UIB8	CD84	CD84 molecule	-0.37 (-0.68, -0.07)	0.016	0.07 (-0.26, 0.40)	0.683
P01127	PDGFB	platelet derived growth factor subunit B	-0.37 (-0.48, -0.26)	<0.001	-0.28 (-0.38, -0.18)	<0.001
Q6DN72	FCRL6	Fc receptor like 6	0.36 (0.15, 0.57)	<0.001	0.53 (0.32, 0.74)	<0.001
O43927	CXCL13	C-X-C motif chemokine ligand 13	0.36 (0.17, 0.54)	<0.001	0.44 (0.28, 0.61)	<0.001
Q13158	FADD	Fas associated via death domain	-0.35 (-0.50, -0.20)	<0.001	-0.24 (-0.50, 0.02)	0.069
Q92876	KLK6	kallikrein related peptidase 6	0.35 (0.01, 0.69)	0.044	0.52 (0.25, 0.80)	<0.001
Q92956	TNFRSF14	TNF receptor superfamily member 14	0.35 (0.17, 0.53)	<0.001	0.70 (0.48, 0.91)	<0.001
Q01151	CD83	CD83 molecule	0.35 (0.07, 0.63)	0.015	0.79 (0.49, 1.09)	<0.001
P07948	LYN	LYN proto-oncogene, Src family tyrosine kinase	-0.33 (-0.49, -0.18)	<0.001	-0.46 (-0.67, -0.24)	<0.001
P48023	FASLG	Fas ligand	0.33 (0.07, 0.59)	0.012	0.50 (0.23, 0.77)	<0.001
P22301	IL10	interleukin 10	0.33 (0.12, 0.53)	0.002	0.22 (0.06, 0.37)	0.006
P26447	S100A4	S100 calcium binding protein A4	-0.33 (-0.59, -0.07)	0.014	0.55 (0.25, 0.86)	<0.001

P39900	MMP12	matrix metallopeptidase 12	0.32 (0.16, 0.49)	<0.001	0.41 (0.24, 0.57)	<0.001
Q96D42	HAVCR1	hepatitis A virus cellular receptor 1	0.32 (0.17, 0.47)	<0.001	0.30 (0.16, 0.44)	<0.001
P27930	IL1R2	interleukin 1 receptor type 2	0.32 (0.09, 0.55)	0.006	0.22 (-0.04, 0.49)	0.1
Q13421	MSLN	mesothelin	0.32 (0.12, 0.52)	0.001	0.34 (0.16, 0.52)	<0.001
P51161	FABP6	fatty acid binding protein 6	0.32 (0.09, 0.54)	0.005	0.41 (0.23, 0.59)	<0.001
P43489	TNFRSF4	TNF receptor superfamily member 4	0.32 (0.09, 0.54)	0.005	0.62 (0.40, 0.84)	<0.001
P04080	CSTB	cystatin B	0.32 (0.15, 0.48)	<0.001	0.53 (0.35, 0.71)	<0.001
P48307	TFPI2	tissue factor pathway inhibitor 2	0.31 (0.12, 0.50)	0.001	0.97 (0.72, 1.21)	<0.001
P12931	SRC	SRC proto-oncogene, non-receptor tyrosine kinase	-0.30 (-0.43, -0.18)	<0.001	-0.44 (-0.58, -0.30)	<0.001
P16278	GLB1	galactosidase beta 1	-0.30 (-0.55, -0.05)	0.017	0.41 (0.00, 0.81)	0.047
Q9HD89	RETN	resistin	0.30 (0.12, 0.49)	0.001	0.38 (0.17, 0.60)	<0.001
O75144	ICOSLG	inducible T cell costimulator ligand	0.30 (-0.09, 0.70)	0.136	1.69 (1.17, 2.21)	<0.001
P29965	CD40LG	CD40 ligand	-0.30 (-0.43, -0.17)	<0.001	-0.33 (-0.48, -0.19)	<0.001
P01133	EGF	epidermal growth factor	-0.30 (-0.40, -0.20)	<0.001	-0.37 (-0.48, -0.26)	<0.001
Q9UQV4	LAMP3	lysosomal associated membrane protein 3	0.30 (0.08, 0.52)	0.008	0.40 (0.18, 0.61)	<0.001

Q06830	PRDX1	peroxiredoxin 1	-0.30 (-0.47, -0.12)	<0.001	0.83 (0.52, 1.14)	<0.001
Q04760	GLO1	glyoxalase I	-0.30 (-0.49, -0.10)	0.003	0.31 (0.10, 0.52)	0.004
P15086	CPB1	carboxypeptidase B1	0.29 (0.15, 0.44)	<0.001	0.20 (0.05, 0.35)	0.008
P09038	FGF2	fibroblast growth factor 2	-0.29 (-0.46, -0.12)	<0.001	-0.49 (-0.74, -0.24)	<0.001
P01298	PPY	pancreatic polypeptide	0.29 (0.16, 0.42)	<0.001	0.22 (0.10, 0.34)	<0.001
Q9C035	TRIM5	tripartite motif containing 5	-0.29 (-0.52, -0.05)	0.016	0.30 (-0.01, 0.60)	0.054
P16109	SELP	selectin P	-0.28 (-0.42, -0.14)	<0.001	-0.27 (-0.47, -0.07)	0.008
P09341	CXCL1	C-X-C motif chemokine ligand 1	-0.28 (-0.41, -0.16)	<0.001	-0.06 (-0.20, 0.08)	0.402
Q9UK05	GDF2	growth differentiation factor 2	-0.28 (-0.49, -0.07)	0.01	-0.02 (-0.22, 0.18)	0.847
P50579	METAP2	methionyl aminopeptidase 2	-0.27 (-0.46, -0.08)	0.005	0.17 (-0.06, 0.40)	0.147
P31994	FCGR2B	Fc gamma receptor IIb	0.27 (0.12, 0.42)	<0.001	0.19 (0.03, 0.34)	0.016
Q9GZV9	FGF23	fibroblast growth factor 23	0.27 (0.18, 0.36)	<0.001	0.30 (0.21, 0.39)	<0.001
Q13043	STK4	serine/threonine kinase 4	-0.27 (-0.38, -0.16)	<0.001	-0.39 (-0.52, -0.26)	<0.001
P42574	CASP3	caspase 3	-0.27 (-0.37, -0.17)	<0.001	-0.33 (-0.47, -0.19)	<0.001
P63241	EIF5A	eukaryotic translation initiation factor 5A	0.27 (-0.14, 0.67)	0.194	0.34 (0.05, 0.63)	0.02

P35240	NF2	NF2, moesin-ezrin-radixin like (MERLIN) tumor suppressor	-0.27 (-0.39, -0.15)	<0.001	-0.32 (-0.50, -0.14)	<0.001
Q92583	CCL17	C-C motif chemokine ligand 17	-0.27 (-0.39, -0.14)	<0.001	-0.21 (-0.35, -0.07)	0.003
P30044	PRDX5	peroxiredoxin 5	-0.26 (-0.41, -0.12)	<0.001	-0.04 (-0.19, 0.12)	0.665
Q16674	MIA	MIA SH3 domain containing	-0.26 (-0.71, 0.18)	0.246	0.05 (-0.37, 0.46)	0.824
Q13241	KLRD1	killer cell lectin like receptor D1	0.26 (0.04, 0.48)	0.02	0.42 (0.21, 0.64)	<0.001
P05121	SERPINE1	serpin family E member 1	-0.26 (-0.40, -0.12)	<0.001	-0.12 (-0.24, 0.01)	0.06
P23229	ITGA6	integrin subunit alpha 6	-0.26 (-0.42, -0.10)	0.002	0.01 (-0.33, 0.34)	0.975
P15090	FABP4	fatty acid binding protein 4	0.26 (0.14, 0.37)	<0.001	0.12 (0.00, 0.25)	0.049
P08254	MMP3	matrix metallopeptidase 3	0.25 (0.11, 0.40)	<0.001	0.45 (0.28, 0.61)	<0.001
Q99523	SORT1	sortilin 1	-0.25 (-0.62, 0.11)	0.174	0.30 (-0.15, 0.76)	0.186
O43915	VEGFD	vascular endothelial growth factor D	0.25 (-0.09, 0.59)	0.145	1.04 (0.68, 1.39)	<0.001
P19957	PI3	peptidase inhibitor 3	0.25 (0.06, 0.44)	0.008	0.46 (0.29, 0.62)	<0.001
Q00978	IRF9	interferon regulatory factor 9	-0.25 (-0.48, -0.02)	0.035	0.22 (-0.05, 0.49)	0.112
Q12968	NFATC3	nuclear factor of activated T cells 3	0.24 (0.05, 0.44)	0.015	0.56 (0.36, 0.76)	<0.001
P01241	GH1	growth hormone 1	0.24 (0.14, 0.34)	<0.001	0.24 (0.15, 0.33)	<0.001

P51617	IRAK1	interleukin 1 receptor associated kinase 1	-0.24 (-0.45, -0.03)	0.024	0.21 (-0.09, 0.50)	0.169
P15692	VEGFA	vascular endothelial growth factor A	0.24 (-0.03, 0.51)	0.086	0.59 (0.30, 0.88)	<0.001
P14780	MMP9	matrix metallopeptidase 9	-0.23 (-0.38, -0.09)	0.002	-0.18 (-0.33, -0.03)	0.022
Q9Y6K9	IKBKG	inhibitor of nuclear factor kappa B kinase regulatory subunit gamma	-0.23 (-0.38, -0.08)	0.003	-0.21 (-0.40, -0.02)	0.028
O14798	TNFRSF10C	TNF receptor superfamily member 10c	0.23 (0.03, 0.43)	0.021	0.29 (0.05, 0.53)	0.017
Q6ZUJ8	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	-0.23 (-0.40, -0.06)	0.007	0.05 (-0.15, 0.26)	0.614
P15085	CPA1	carboxypeptidase A1	0.23 (0.09, 0.37)	0.001	0.14 (0.01, 0.28)	0.04
P04626	ERBB2	erb-b2 receptor tyrosine kinase 2	0.23 (-0.13, 0.58)	0.218	1.02 (0.60, 1.43)	<0.001
Q12933	TRAF2	TNF receptor associated factor 2	-0.22 (-0.45, 0.01)	0.058	0.50 (0.22, 0.79)	<0.001
Q9NWZ3	IRAK4	interleukin 1 receptor associated kinase 4	-0.22 (-0.33, -0.11)	<0.001	-0.32 (-0.46, -0.18)	<0.001
O00273	DFFA	DNA fragmentation factor subunit alpha	-0.22 (-0.39, -0.05)	0.012	0.31 (0.10, 0.52)	0.004
P14317	HCLS1	hematopoietic cell-specific Lyn substrate 1	-0.22 (-0.34, -0.09)	<0.001	-0.17 (-0.33, -0.01)	0.041
P02760	AMBP	alpha-1-microglobulin/bikunin precursor	-0.22 (-0.66, 0.23)	0.346	-0.46 (-0.94, 0.03)	0.067
Q9UKP3	ITGB1BP2	integrin subunit beta 1 binding protein 2	-0.21 (-0.32, -0.11)	<0.001	-0.28 (-0.41, -0.15)	<0.001
Q13231	CHIT1	chitinase 1	0.21 (0.10, 0.32)	<0.001	0.23 (0.12, 0.35)	<0.001

O94992	HEXIM1	HEXIM P-TEFb complex subunit 1	-0.21 (-0.35, -0.06)	0.005	-0.12 (-0.29, 0.06)	0.186
P16860	NPPB	natriuretic peptide B	0.21 (0.12, 0.30)	<0.001	0.29 (0.22, 0.37)	<0.001
Q15166	PON3	paraoxonase 3	-0.21 (-0.36, -0.05)	0.008	-0.26 (-0.42, -0.09)	0.002
P16581	SELE	selectin E	0.20 (-0.00, 0.40)	0.053	-0.02 (-0.22, 0.19)	0.885
P10144	GZMB	granzyme B	0.20 (-0.01, 0.41)	0.06	0.46 (0.23, 0.70)	<0.001
O15455	TLR3	toll like receptor 3	0.20 (-0.03, 0.42)	0.085	0.35 (0.14, 0.56)	0.001
Q92844	TANK	TRAF family member associated NFKB activator	-0.20 (-0.40, 0.01)	0.06	-0.33 (-0.58, -0.08)	0.009
Q9UQQ2	SH2B3	SH2B adaptor protein 3	-0.19 (-0.31, -0.08)	<0.001	-0.37 (-0.52, -0.23)	<0.001
Q05516	ZBTB16	zinc finger and BTB domain containing 16	-0.19 (-0.35, -0.03)	0.017	-0.24 (-0.43, -0.04)	0.016
Q14005	IL16	interleukin 16	0.19 (-0.03, 0.40)	0.091	0.79 (0.53, 1.06)	<0.001
P16455	MGMT	O-6-methylguanine-DNA methyltransferase	-0.18 (-0.30, -0.07)	0.001	-0.07 (-0.19, 0.05)	0.271
P38936	CDKN1A	cyclin dependent kinase inhibitor 1A	-0.18 (-0.30, -0.06)	0.003	-0.16 (-0.31, -0.01)	0.033
Q9HCM2	PLXNA4	plexin A4	-0.18 (-0.31, -0.05)	0.005	-0.43 (-0.58, -0.28)	<0.001
O00626	CCL22	C-C motif chemokine ligand 22	-0.18 (-0.34, -0.02)	0.031	-0.01 (-0.15, 0.12)	0.835
P56279	TCL1A	TCL1 family AKT coactivator A	-0.18 (-0.30, -0.06)	0.003	-0.16 (-0.28, -0.05)	0.005

P20718	GZMH	granzyme H	0.17 (0.03, 0.32)	0.017	0.63 (0.44, 0.81)	<0.001
P78362	SRPK2	SRSF protein kinase 2	-0.17 (-0.29, -0.05)	0.006	-0.04 (-0.21, 0.13)	0.63
Q9NQ76	MEPE	matrix extracellular phosphoglycoprotein	0.17 (-0.04, 0.39)	0.118	0.39 (0.16, 0.62)	0.001
Q9UKX5	ITGA11	integrin subunit alpha 11	0.17 (-0.12, 0.46)	0.257	0.75 (0.45, 1.05)	<0.001
Q13867	BLMH	bleomycin hydrolase	0.17 (-0.06, 0.40)	0.144	0.54 (0.27, 0.81)	<0.001
Q14116	IL18	interleukin 18	0.17 (-0.06, 0.39)	0.141	0.38 (0.14, 0.61)	0.002
P27540	ARNT	aryl hydrocarbon receptor nuclear translocator	0.16 (0.03, 0.30)	0.02	0.11 (-0.04, 0.27)	0.14
P40222	TXLNA	taxilin alpha	-0.16 (-0.30, -0.03)	0.016	-0.19 (-0.34, -0.04)	0.016
Q9HB29	IL1RL2	interleukin 1 receptor like 2	-0.16 (-0.45, 0.13)	0.272	0.24 (-0.08, 0.56)	0.137
P35247	SFTPD	surfactant protein D	0.16 (-0.03, 0.35)	0.107	0.20 (0.04, 0.37)	0.016
Q96F46	IL17RA	interleukin 17 receptor A	0.16 (-0.05, 0.37)	0.144	0.53 (0.28, 0.79)	<0.001
Q8WXI7	MUC16	mucin 16, cell surface associated	0.16 (0.06, 0.25)	<0.001	0.21 (0.13, 0.30)	<0.001
Q8TE58	ADAMTS15	ADAM metallopeptidase with thrombospondin type 1 motif 15	0.16 (-0.05, 0.37)	0.143	0.24 (-0.05, 0.53)	0.102
P13688	CEACAM1	CEA cell adhesion molecule 1	0.16 (-0.57, 0.88)	0.672	0.95 (0.10, 1.80)	0.028
Q9UN19	DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides 1	-0.15 (-0.22, -0.08)	<0.001	-0.29 (-0.39, -0.20)	<0.001

Q96SB3	PPP1R9B	protein phosphatase 1 regulatory subunit 9B	-0.15 (-0.26, -0.04)	0.009	-0.42 (-0.57, -0.26)	<0.001
Q04637	EIF4G1	eukaryotic translation initiation factor 4 gamma 1	-0.14 (-0.26, -0.03)	0.014	-0.14 (-0.28, -0.00)	0.049
P78380	OLR1	oxidized low density lipoprotein receptor 1	-0.14 (-0.34, 0.05)	0.147	0.39 (0.15, 0.63)	0.002
P41159	LEP	leptin	-0.14 (-0.25, -0.03)	0.014	-0.35 (-0.46, -0.25)	<0.001
P10646	TFPI	tissue factor pathway inhibitor	-0.14 (-0.35, 0.07)	0.19	0.02 (-0.26, 0.31)	0.877
P35218	CA5A	carbonic anhydrase 5A	0.13 (0.00, 0.26)	0.047	0.44 (0.31, 0.57)	<0.001
P05412	JUN	Jun proto-oncogene, AP-1 transcription factor subunit	0.13 (-0.14, 0.40)	0.336	0.20 (0.00, 0.39)	0.049
Q8IU57	IFNLR1	interferon lambda receptor 1	-0.13 (-0.50, 0.23)	0.48	0.32 (-0.05, 0.69)	0.088
O94907	DKK1	dickkopf WNT signaling pathway inhibitor 1	-0.13 (-0.31, 0.05)	0.153	0.48 (0.28, 0.67)	<0.001
P04083	ANXA1	annexin A1	-0.13 (-0.35, 0.09)	0.243	0.53 (0.27, 0.79)	<0.001
Q14512	FGFBP1	fibroblast growth factor binding protein 1	0.13 (0.00, 0.26)	0.049	0.46 (0.30, 0.62)	<0.001
O43597	SPRY2	sprouty RTK signaling antagonist 2	-0.13 (-0.24, -0.01)	0.031	-0.28 (-0.43, -0.12)	<0.001
Q9Y624	F11R	F11 receptor	-0.13 (-0.25, -0.00)	0.044	0.20 (0.02, 0.38)	0.031
Q16698	DECR1	2,4-dienoyl-CoA reductase 1	-0.13 (-0.24, -0.01)	0.028	-0.02 (-0.14, 0.10)	0.756
P21741	MDK	midkine	0.13 (-0.02, 0.27)	0.08	0.42 (0.26, 0.58)	<0.001

Q14203	DCTN1	dynactin subunit 1	-0.13 (-0.26, 0.01)	0.065	-0.03 (-0.23, 0.17)	0.758
O14867	BACH1	BTB domain and CNC homolog 1	-0.13 (-0.37, 0.12)	0.325	0.03 (-0.26, 0.32)	0.835
O75594	PGLYRP1	peptidoglycan recognition protein 1	0.12 (-0.06, 0.30)	0.18	0.17 (-0.05, 0.38)	0.126
Q8WXI8	CLEC4D	C-type lectin domain family 4 member D	0.12 (-0.07, 0.31)	0.206	0.27 (0.10, 0.45)	0.002
P09874	PARP1	poly(ADP-ribose) polymerase 1	-0.11 (-0.28, 0.05)	0.17	0.79 (0.53, 1.04)	<0.001
O60259	KLK8	kallikrein related peptidase 8	0.11 (-0.20, 0.43)	0.485	0.70 (0.40, 0.99)	<0.001
P00533	EGFR	epidermal growth factor receptor	-0.11 (-0.42, 0.19)	0.473	-0.36 (-0.72, -0.00)	0.049
P09382	LGALS1	galectin 1	-0.11 (-0.63, 0.41)	0.673	0.74 (0.14, 1.33)	0.015
P00797	REN	renin	0.11 (-0.04, 0.26)	0.159	0.00 (-0.15, 0.16)	0.963
P28845	HSD11B1	hydroxysteroid 11-beta dehydrogenase 1	0.11 (-0.22, 0.43)	0.509	0.53 (0.23, 0.83)	<0.001
P04275	VWF	von Willebrand factor	0.11 (-0.01, 0.22)	0.062	0.11 (-0.01, 0.23)	0.083
Q9NSA1	FGF21	fibroblast growth factor 21	0.11 (0.02, 0.20)	0.023	0.18 (0.10, 0.26)	<0.001
P27352	CBLIF	cobalamin binding intrinsic factor	-0.11 (-0.24, 0.03)	0.128	-0.03 (-0.14, 0.08)	0.535
P24158	PRTN3	proteinase 3	0.10 (-0.09, 0.29)	0.29	0.44 (0.22, 0.65)	<0.001
P09237	MMP7	matrix metallopeptidase 7	0.10 (-0.08, 0.29)	0.281	0.31 (0.01, 0.61)	0.043

P06731	CEACAM5	CEA cell adhesion molecule 5	0.10 (-0.09, 0.29)	0.297	0.17 (0.01, 0.33)	0.036
P16284	PECAM1	platelet and endothelial cell adhesion molecule 1	-0.10 (-0.25, 0.05)	0.206	0.15 (-0.09, 0.38)	0.222
O14828	SCAMP3	secretory carrier membrane protein 3	-0.10 (-0.22, 0.02)	0.118	-0.23 (-0.37, -0.09)	0.001
Q04759	PRKCQ	protein kinase C theta	-0.10 (-0.37, 0.18)	0.497	0.01 (-0.28, 0.31)	0.926
P20160	AZU1	azurocidin 1	-0.10 (-0.26, 0.07)	0.26	0.35 (0.13, 0.57)	0.002
P34130	NTF4	neurotrophin 4	0.10 (-0.24, 0.43)	0.572	0.73 (0.41, 1.05)	<0.001
P00750	PLAT	plasminogen activator, tissue type	0.10 (-0.01, 0.21)	0.09	0.29 (0.17, 0.41)	<0.001
P17931	LGALS3	galectin 3	0.09 (-0.13, 0.32)	0.41	0.03 (-0.25, 0.31)	0.841
P19474	TRIM21	tripartite motif containing 21	-0.09 (-0.27, 0.08)	0.296	0.52 (0.28, 0.75)	<0.001
Q9NPY3	CD93	CD93 molecule	0.09 (-0.13, 0.31)	0.417	0.19 (-0.07, 0.45)	0.15
P30048	PRDX3	peroxiredoxin 3	-0.09 (-0.27, 0.10)	0.352	0.30 (0.09, 0.51)	0.005
O15467	CCL16	C-C motif chemokine ligand 16	0.08 (-0.10, 0.27)	0.369	-0.10 (-0.31, 0.10)	0.314
Q03431	PTH1R	parathyroid hormone 1 receptor	-0.08 (-0.32, 0.17)	0.531	-0.28 (-0.60, 0.04)	0.092
O95786	RIGI	RNA sensor RIG-I	-0.08 (-0.25, 0.10)	0.391	0.42 (0.17, 0.67)	0.001
P18510	IL1RN	interleukin 1 receptor antagonist	-0.08 (-0.25, 0.10)	0.396	-0.10 (-0.27, 0.07)	0.261

P13686	ACP5	acid phosphatase 5, tartrate resistant	-0.07 (-0.29, 0.15)	0.532	-0.21 (-0.47, 0.05)	0.114
O75475	PSIP1	PC4 and SRSF1 interacting protein 1	-0.07 (-0.22, 0.08)	0.372	0.43 (0.24, 0.61)	<0.001
Q8NBP7	PCSK9	proprotein convertase subtilisin/kexin type 9	-0.07 (-0.34, 0.20)	0.619	-0.36 (-0.66, -0.05)	0.021
Q9UKR3	KLK13	kallikrein related peptidase 13	-0.07 (-0.40, 0.27)	0.69	0.12 (-0.13, 0.37)	0.348
P52294	KPNA1	karyopherin subunit alpha 1	0.06 (-0.11, 0.24)	0.474	0.10 (-0.02, 0.23)	0.109
Q9UBG3	CRNN	cornulin	0.06 (-0.11, 0.24)	0.475	-0.08 (-0.23, 0.06)	0.259
Q9P0G3	KLK14	kallikrein related peptidase 14	0.06 (-0.18, 0.31)	0.604	0.46 (0.23, 0.70)	<0.001
O60880	SH2D1A	SH2 domain containing 1A	-0.06 (-0.26, 0.13)	0.525	0.39 (0.14, 0.64)	0.002
Q29983	MICA	MHC class I polypeptide-related sequence A	-0.06 (-0.17, 0.05)	0.278	-0.06 (-0.17, 0.05)	0.301
P05113	IL5	interleukin 5	0.05 (-0.09, 0.20)	0.457	0.09 (-0.04, 0.21)	0.164
P00519	ABL1	ABL proto-oncogene 1, non-receptor tyrosine kinase	-0.05 (-0.21, 0.11)	0.515	0.33 (0.12, 0.54)	0.002
Q02763	TEK	TEK receptor tyrosine kinase	0.05 (-0.36, 0.46)	0.804	1.34 (0.81, 1.87)	<0.001
P12104	FABP2	fatty acid binding protein 2	0.05 (-0.11, 0.21)	0.551	0.09 (-0.06, 0.24)	0.225
P21980	TGM2	transglutaminase 2	-0.04 (-0.25, 0.16)	0.669	0.45 (0.22, 0.68)	<0.001
O00175	CCL24	C-C motif chemokine ligand 24	0.04 (-0.10, 0.18)	0.538	0.06 (-0.08, 0.20)	0.415

Q9UJM8	HAO1	hydroxyacid oxidase 1	0.04 (-0.05, 0.14)	0.369	0.19 (0.11, 0.28)	<0.001
Q5T2D2	TREML2	triggering receptor expressed on myeloid cells like 2	-0.04 (-0.24, 0.15)	0.673	-0.04 (-0.27, 0.20)	0.768
P31997	CEACAM8	CEA cell adhesion molecule 8	0.04 (-0.13, 0.21)	0.639	0.26 (0.06, 0.46)	0.012
Q99895	CTRC	chymotrypsin C	0.04 (-0.11, 0.19)	0.589	-0.00 (-0.14, 0.13)	0.96
Q8IW75	SERPINA12	serpin family A member 12	0.04 (-0.10, 0.19)	0.581	0.04 (-0.11, 0.19)	0.583
P16422	EPCAM	epithelial cell adhesion molecule	0.04 (-0.12, 0.20)	0.655	-0.02 (-0.17, 0.12)	0.746
Q9GZT9	EGLN1	egl-9 family hypoxia inducible factor 1	-0.04 (-0.32, 0.25)	0.805	0.87 (0.54, 1.19)	<0.001
Q9BQR3	PRSS27	serine protease 27	0.03 (-0.24, 0.30)	0.809	0.47 (0.21, 0.74)	<0.001
O43895	XPNPEP2	X-prolyl aminopeptidase 2	-0.03 (-0.21, 0.15)	0.754	0.10 (-0.06, 0.26)	0.214
Q15661	TPSAB1	tryptase alpha/beta 1	0.03 (-0.22, 0.28)	0.824	0.20 (-0.05, 0.45)	0.121
P08887	IL6R	interleukin 6 receptor	0.02 (-0.21, 0.26)	0.835	-0.06 (-0.34, 0.22)	0.686
Q9Y2J8	PADI2	peptidyl arginine deiminase 2	-0.02 (-0.27, 0.23)	0.849	0.33 (0.07, 0.59)	0.012
P41439	FOLR3	folate receptor gamma	-0.02 (-0.10, 0.07)	0.686	-0.01 (-0.10, 0.07)	0.761
O95274	LYPD3	LY6/PLAUR domain containing 3	0.01 (-0.33, 0.36)	0.934	0.35 (0.04, 0.65)	0.027
Q9UJ71	CD207	CD207 molecule	0.01 (-0.32, 0.34)	0.941	0.43 (0.16, 0.70)	0.002

P51671	CCL11	C-C motif chemokine ligand 11	0.00 (-0.27, 0.28)	0.99	0.45 (0.16, 0.74)	0.002

Supplementary