Supplemental Materials

		Correlation C.
Maldi A	Maldi B	-0.267
	Maldi C	-0.168
	Maldi D	-0.126
	Maldi E	-0.031
	Maldi F	0.131
Maldi B	Maldi C	-0.117
	Maldi D	0.040
	Maldi E	-0.082
	Maldi F	-0.288
Maldi C	Maldi D	0.392
	Maldi E	-0.132
	Maldi F	-0.137
Maldi D	Maldi E	-0.188
	Maldi F	-0.259
Maldi E	Maldi F	0.198

Supplemental Table 1. Pearson’s correlation coefficients for all marker combinations (n=150).

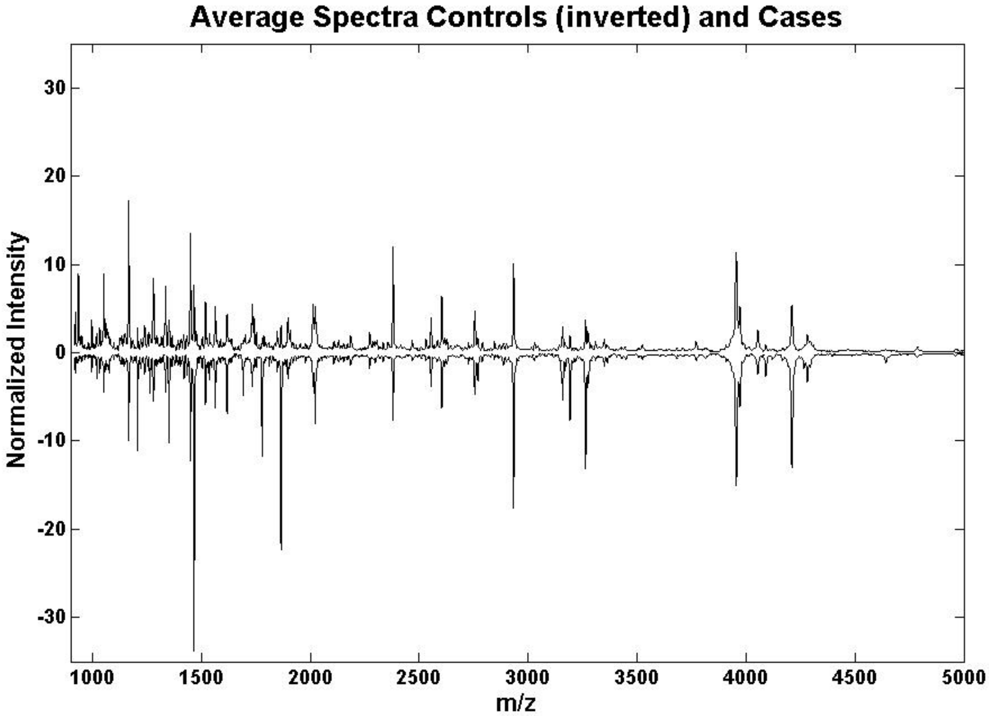
Among controls	**OR**	**CI**		**p**
Maldi A	1.0	0.98	1.03	0.7085
Maldi B	1.0	0.71	1.29	0.7687
Maldi C	0.5	0.16	1.80	0.3111
Maldi D	1.1	0.87	1.42	0.4080
Maldi E	1.0	0.51	1.91	0.9745
Maldi F	1.0	0.76	1.36	0.9293
Among cases	**OR**	**CI**		**p**
Maldi A	1.1	0.85	1.31	0.6221
Maldi B	1.0	0.94	1.01	0.1228
Maldi C	1.5	0.82	2.82	0.1838
Maldi D	0.9	0.85	1.05	0.2973
Maldi E	0.4	0.14	1.23	0.1125
Maldi F	0.9	0.60	1.48	0.7935

Supplemental Table 2. Association of marker candidates with HCV RNA status. Univariate logistic regression controlled for age and gender conducted separately among controls (N=72, 16 HCV RNA+, 56 HCV RNA-) and cases (N=78, 62 HCV RNA+, 16 HCV RNA-).

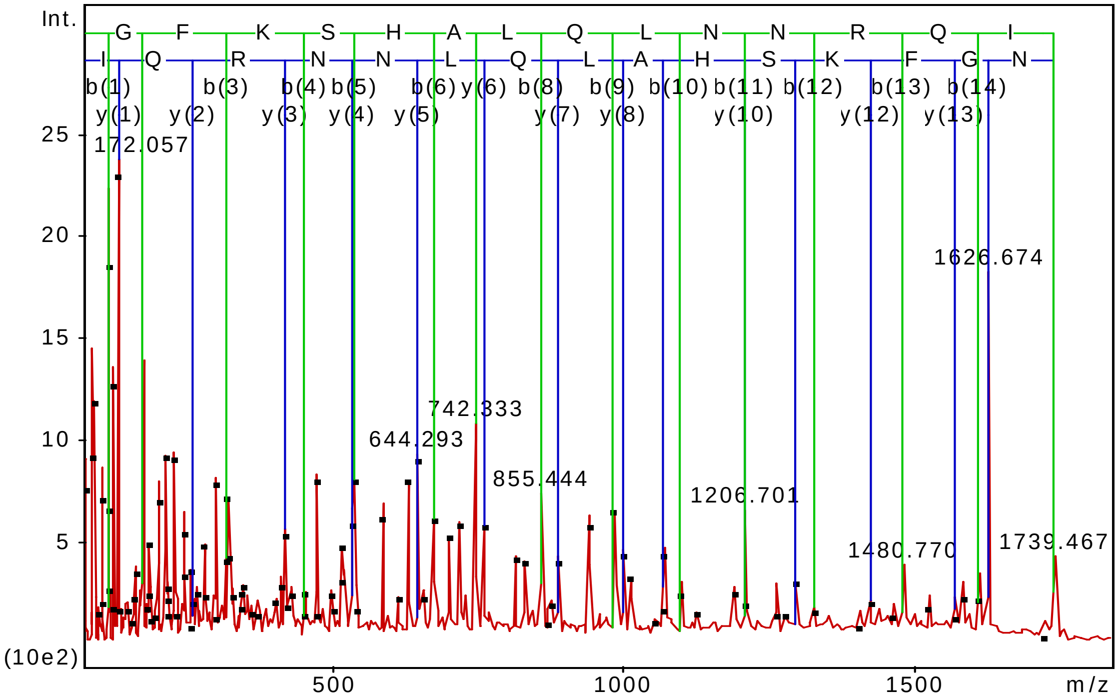
	p-value	OR	95% CI	
Maldi A	0.003	0.6	0.47	0.85
Maldi B	0.003	1.5	1.14	1.85
Maldi C	0.010	3.5	1.34	8.87
Maldi D	0.007	1.4	1.09	1.70
Maldi E	0.113	0.5	0.19	1.20
Maldi F	0.001	0.2	0.11	0.56

Supplemental Table 3. Association of MALDI biomarkers with HCC

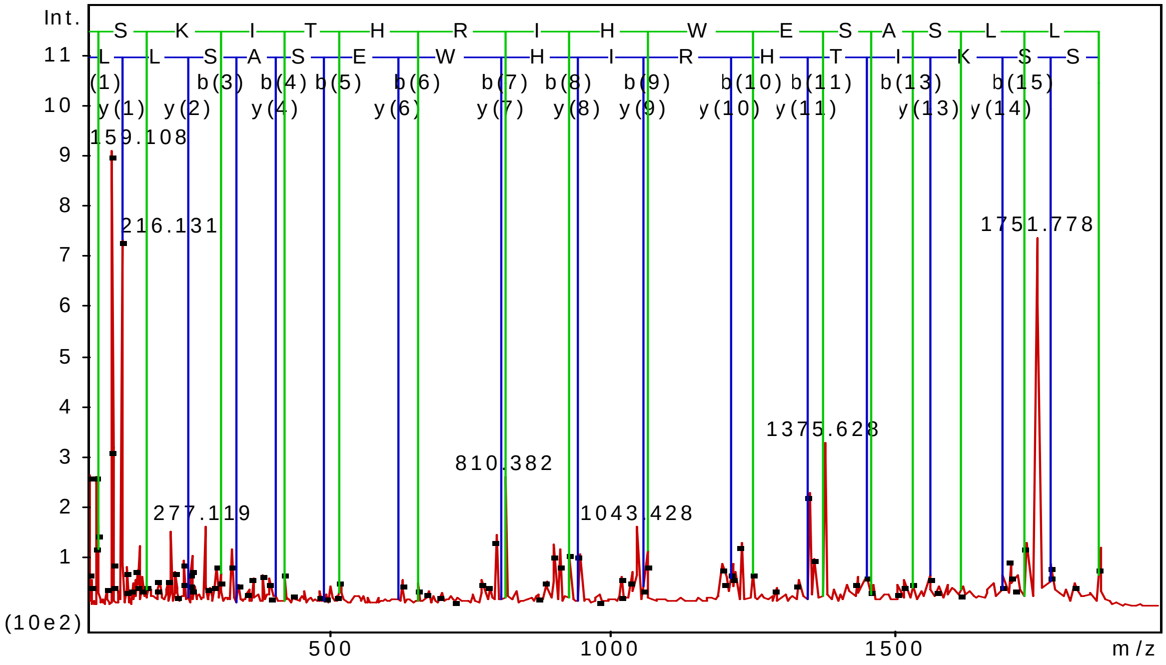
HCC samples collected between January and April 2002 (21 cases; 72 controls); analysis controlled for HCV-RNA, anti-HBC, residency, age, and gender.



Supplemental Figure 1. Comparison of average spectra in HCC cases (n=78) and controls (n=72) in the full mass range from 900 to 5,000 Da. The average spectrum in controls is inverted to facilitate the comparison.



Supplemental Figure 2A.



Supplemental Figure 2B.

1789

#	b	Seq.	y	y*	#
1	**115.0502**	**N**			**15**
2	**172.0717**	**G**	1625.8870	**1608.8605**	**14**
3	**319.1401**	**F**	1568.8656	1551.8390	**13**
4	**447.2350**	**K**	**1421.7972**	**1404.7706**	**12**
5	**534.2671**	**S**	**1293.7022**	**1276.6757**	**11**
6	**671.3260**	**H**	**1206.6702**	**1189.6436**	**10**
7	**742.3631**	**A**	**1069.6113**	**1052.5847**	**9**
8	**855.4472**	**L**	**998.5742**	981.5476	**8**
9	**983.5057**	**Q**	**885.4901**	**868.4635**	**7**
10	**1096.5898**	**L**	**757.4315**	740.4050	**6**
11	**1210.6327**	**N**	**644.3474**	**627.3209**	**5**
12	**1324.6757**	**N**	**530.3045**	**513.2780**	**4**
13	**1480.7768**	**R**	**416.2616**	**399.2350**	**3**
14	**1608.8353**	**Q**	260.1605	**243.1339**	**2**
15		**I**	132.1019		**1**

1864

#	b	b^0	Seq.	y	#
1	88.0393	**70.0287**	**S**		**16**
2	**175.0713**	157.0608	**S**	**1777.9708**	**15**
3	**303.1663**	**285.1557**	**K**	**1690.9388**	**14**
4	**416.2504**	**398.2398**	**I**	**1562.8438**	**13**
5	**517.2980**	499.2875	**T**	**1449.7597**	**12**
6	654.3569	636.3464	**H**	**1348.7120**	**11**
7	**810.4581**	792.4475	**R**	**1211.6531**	**10**
8	**923.5421**	905.5316	**I**	**1055.5520**	**9**
9	**1060.6010**	1042.5905	**H**	**942.4680**	**8**
10	**1246.6804**	1228.6698	**W**	805.4090	**7**
11	**1375.7229**	1357.7124	**E**	619.3297	**6**
12	**1462.7550**	1444.7444	**S**	490.2871	**5**
13	**1533.7921**	1515.7815	**A**	403.2551	**4**
14	**1620.8241**	1602.8135	**S**	332.2180	**3**
15	**1733.9082**	1715.8976	**L**	245.1860	**2**
16			**L**	132.1019	**1**

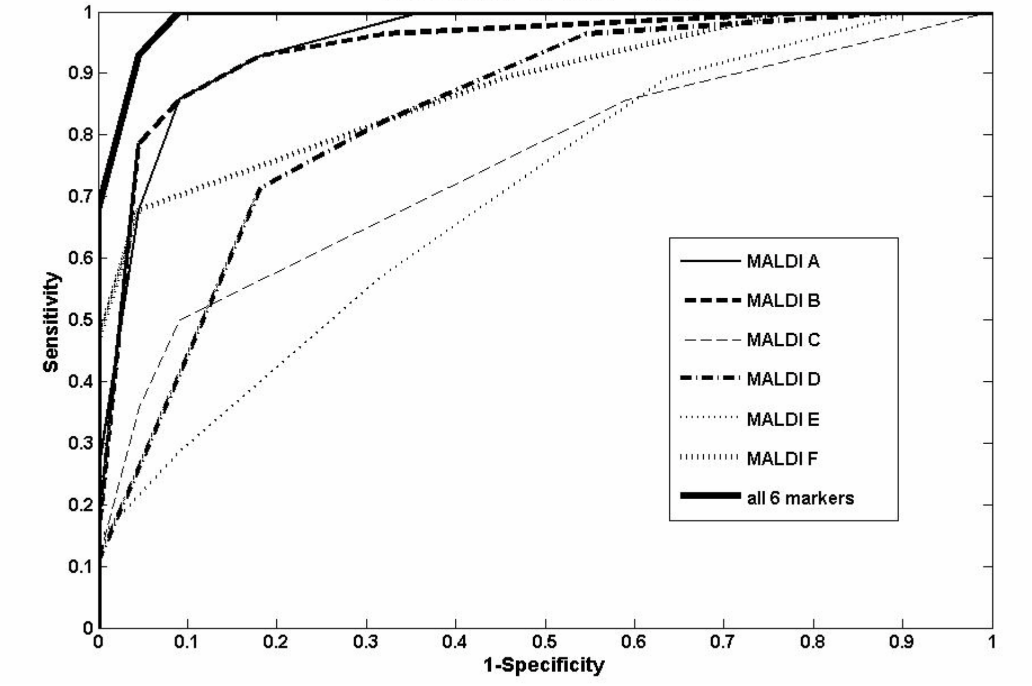
Supplemental Figure 2C.

Supplemental Figure 2. MS/MS spectra of two ions obtained by MALDI-TOF/TOF sequencing:

A. m/z 1739.842, NGFKSHALQLNNRQI, ions score 131, expect 5.9e-10. Found in CO4A_HUMAN, Complement C4-A precursor;

B. m/z 1864.9993, SSKITHRIHWESASLL, ions score 99, expect 3.5e-6. Found in CO3_Human, Complement C3 precursor

C. Tables of fragment ions for the 1739.84 and 1864.99 peptides matched by MASCOT



Supplemental Figure 3. ROC curve for six individual marker candidates and for a combined classifier consisting of all six markers. Each curve is based on 50 spectra from an independent test set of samples. Areas under the individual curves are listed in Table 5.