

# **Development of a genetic and clinical data-based (GC) risk score for predicting survival of hepatocellular carcinoma patients after tumor resection**

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## **Supplementary information**

Number of tables: 10

<b>Table S1. Set of primers used for genes analyses</b>		
Primers for expression study		
Name	Sequence (5'-3')	Annealing temperature(°C)
CPT1A F	TCCAGTTGGCTTATCGTGGTG	60
CPT1A R	TCCAGAGTCCGATTGATTTTGC	60
PPAR $\alpha$ F	ATGGTGGACACGGAAAGCC	60
PPAR $\alpha$ R	CGATGGATTGCGAAATCTCTTGG	60
GAPDH F	GGAGCGAGATCCCTCCAAAAT	60
GAPDH R	GGCTGTTGTCATACTTCTCATGG	60

**Table S2. Correlation analysis between PPAR $\alpha$ /CPT1A expression and clinical factors in liver cancer patients**

	PPAR $\alpha$ expression(continuous)		CPT1A expression( continuous)	
Variable	r	P value(2-tailed)	r	P value(2-tailed)
Tumor or non-tumor	0.499	<b>&lt;0.001</b>	0.753	<b>&lt;0.001</b>
Gender	0.010	0.938	-0.021	0.865
Tumor size( $\geq 5$ cm or $< 5$ cm)	0.037	0.766	-0.372	<b>0.002</b>
Age	0.039	0.755	0.056	0.657
HBsAg	-0.295	<b>0.016</b>	-0.173	0.166
HBeAg	0.071	0.572	-0.038	0.759
Histological grade	-0.130	0.299	-0.443	<b>&lt;0.001</b>
AFP	0.016	0.898	-0.099	0.428
Intrahepatic metastasis	-0.169	0.175	-0.361	<b>0.003</b>
TNM stage	-0.269	<b>0.029</b>	-0.553	<b>&lt;0.001</b>
Lesion location	0.025	0.842	0.151	0.227
Hepatic cirrhosis	-0.199	0.110	0.039	0.755
DFST	0.244	<b>0.048</b>	0.596	<b>&lt;0.001</b>
OAST	0.320	<b>0.009</b>	0.558	<b>&lt;0.001</b>
r: Spearman rank correlation coefficient HBsAg: hepatitis B surface antigen; HBeAg: hepatitis B e antigen AFP: alpha fetoprotein Histological grade: according to the three-tier grading scheme DFST: Disease-free survival time OAST: Overall survival time				

Table S3. Correlation analysis between tumor size and other factors in liver cancer patients		
	Tumor size (continuous)	
Variable	r	P value(2-tailed)
Gender	0.096	0.445
PPAR $\alpha$ expression	0.097	0.439
CPT1A expression	-0.290	0.023
Age	-0.132	0.291
HBsAg	-0.120	0.338
HBeAg	-0.036	0.774
Histological grade	0.344	0.005
AFP	-0.139	0.267
Intrahepatic metastasis	0.383	0.002
TNM stage	0.284	<b>0.031</b>
Lesion location	0.093	0.459
Hepatic cirrhosis	-0.154	0.216
DFST	-0.268	0.042
OAST	-0.335	0.008
r: Spearman rank correlation coefficient HBsAg: hepatitis B surface antigen; HBeAg: hepatitis B e antigen AFP: alpha fetoprotein Histological grade: according to the three-tier grading scheme DFST: Disease-free survival time OAST: Overall survival time		

<b>Table S4. Patients were categorized into two groups to evaluate prognosis(groups depended on the optimal cutoff values of genes expression levels)</b>				
	Disease-free survival		Overall survival	
Gene	High expression	Low expression	High expression	Low expression
CPT1A	≥0.854	<0.854	≥0.873	<0.873
PPARα	≥1.330	<1.330	≥1.029	<1.029

## **Algorithm for score system (based on the Sullivan's scoring system)**

### **Estimate the parameters of the multivariable model**

Consider the model  $f(Y) = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \dots + \beta_p X_p$ , where  $Y$  is the dependent or outcome variable (e.g.  $Y = 1$  indicates the presence of a particular event and  $Y = 0$  indicates the absence of the event, or  $Y$  is a continuous outcome score),  $f(Y)$  is a function of  $Y$  that can be represented as a combination of the risk factors  $X_i$ , and  $X_1, \dots, X_p$  are the candidate risk factors ( $X_i$ ,  $i = 1, \dots, p$ , can be continuous or indicator/dummy variables reflecting dichotomous risk factors or categories of risk factors), and  $\beta_0, \beta_1, \dots, \beta_p$  are the estimates of the regression coefficients based on the appropriate regression model (e.g. Cox proportional hazards regression).

### **Organize the risk factors into categories and determine reference values**

If a risk factor is continuous—set up contiguous classes and determine reference values for each.

If a risk factor is modelled by a set of dummy variables (each coded as 0 = absent or 1 = present) reflecting distinct categories of the risk factor, then the reference value is simply 0 or 1.

If a risk factor is dichotomous and modelled as an indicator variable (e.g. 0 = absent, 1 = present), the reference value is again either 0 or 1 and nothing more needs to be performed at this step.

Let  $W_{ij}$  denote the reference value (e.g. mid-points for continuous risk factors organized into categories, or values 0 or 1 for risk factors modelled by a set of dummy variables or a single indicator) for the  $j^{\text{th}}$  category of the  $i^{\text{th}}$  risk factor, where  $i = 1, \dots, p$ , and  $j = 1, \dots, c_i$ , where  $c_i$  = the total number of categories for risk factor  $i$ .

### **Determine the referent risk factor profile**

Next we determine the appropriate category for each risk factor to serve as the base category. The base category for each risk factor is the category assigned 0 points in the scoring system. Categories reflecting worse (less healthy) states of the risk factor will be assigned positive points, while categories reflecting healthier states will be assigned negative points. The reference value of the base category is denoted  $W_{i\text{REF}}$ , for each of the  $i$  risk factors,  $i = 1, \dots, p$ .

### **Determine how far each category is from the base category in regression units**

For each risk factor, we next determine how far each category is from the base category  $W_{i\text{REF}}$ , in terms of regression units. Specifically, we determine the following for each category  $j$  of each risk factor  $i$ :  $\beta_i(W_{ij} - W_{i\text{REF}})$ ,  $i = 1, \dots, p$  and  $j = 1, \dots, c_i$ .

### **Set the constant B**

The constant  $B$  is the smallest absolute value of regression coefficient of risk factors in the final score system.

### **Determine the score for each of the categories of each risk factor**

The points for each category of each risk factor are determined by the following:

$$\text{Score}_{ij} = \beta_i(W_{ij} - W_{i\text{REF}}) / B$$

Note that the base category of each risk factor is assigned 0 points using this formula.  $\text{Score}_{ij}$  is rounded to nearest integer.

<b>Table S5. Components of the disease-free survival prediction score</b>					
Risk factor	Categories	$W_{ij}$	$\beta_i$	$\beta_i(W_{ij} - W_{i\text{REF}})$	$\text{Score}_{ij} = \beta_i(W_{ij} - W_{i\text{REF}}) / B$
CPT1A expression			1.647		
	High expression	0 ( $W_{i\text{REF}}$ )		0	0
	Low expression	1		1.647	1
Tumor size			1.588		
	<5cm	0( $W_{i\text{REF}}$ )		0	0
	≥5cm	1		1.588	1
Intrahepatic metastasis			1.422		
	No	0( $W_{i\text{REF}}$ )		0	0
	Yes	1		1.422	1
TNM stage			1.814		
	Stage I or II	0( $W_{i\text{REF}}$ )		0	0
	Stage III or IV	1		1.814	1
Histological grade			1.707		
	Grade 1 or 2	0( $W_{i\text{REF}}$ )		0	0
	Grade 3	1		1.707	1
B=1.422, the smallest absolute value of regression coefficient among the risk factors					

<b>Table S6. Components of the overall survival prediction score</b>					
Risk factor	Categories	$W_{ij}$	$\beta_i$	$\beta_i(W_{ij} - W_{iREF})$	$Score_{ij} = \beta_i(W_{ij} - W_{iREF}) / B$
CPT1A expression			1.761		
	High expression	0 ( $W_{iREF}$ )		0	0
	Low expression	1		1.761	2
Tumor size			1.261		
	<5cm	0( $W_{iREF}$ )		0	0
	≥5cm	1		1.261	1
Intrahepatic metastasis			1.315		
	No	0( $W_{iREF}$ )		0	0
	Yes	1		1.315	1
TNM stage			2.267		
	Stage I or II	0( $W_{iREF}$ )		0	0
	Stage III or IV	1		2.267	2
Histological grade			1.089		
	Grade 1 or 2	0( $W_{iREF}$ )		0	0
	Grade 3	1		1.089	1
B=1.089, the smallest absolute value of regression coefficient among the risk factors					



<b>Table S7. Prediction score for disease-free survival</b>						
Sample	Score1	Score2	Score3	Score4	Score5	Total score
1	0	1	1	1	0	3
2	1	1	1	1	1	5
3	0	1	1	1	0	3
4	1	1	1	1	1	5
5	0	1	1	1	0	3
6	0	1	0	1	0	2
7	1	1	1	1	1	5
8	0	1	0	0	0	1
9	0	1	1	0	0	2
10	1	1	1	1	0	4
11	0	1	0	0	0	1
12	1	1	1	1	1	5
13	1	1	1	1	1	5
14	0	1	0	0	0	1
15	0	1	1	1	1	4
16	0	0	0	0	0	0
17	1	1	1	1	0	4
18	1	1	1	1	1	5
19	0	0	0	0	0	0
20	1	1	1	1	0	4
21	0	1	1	1	0	3
22	1	1	1	1	1	5
23	1	1	1	1	1	5
24	1	0	0	0	0	1
25	1	1	1	1	1	5
26	1	1	1	1	1	5
27	0	1	1	1	1	4
28	0	1	1	0	0	2
29	1	1	1	1	1	5
30	0	1	1	1	0	3
31	1	0	0	1	1	3
32	1	1	1	1	0	4
33	1	1	1	1	1	5
34	1	1	1	1	0	4
35	0	0	0	0	0	0
36	1	1	0	0	0	2
37	1	1	1	1	1	5
38	1	0	0	1	0	2
39	1	1	0	0	0	2
40	0	1	0	0	0	1

41	1	1	0	0	0	2
42	1	0	0	0	0	1
43	1	1	1	1	1	5
44	1	1	0	0	0	2
45	1	1	1	1	0	4
46	1	1	1	1	1	5
47	1	1	1	1	1	5
48	0	0	0	0	0	0
49	0	0	0	0	0	0
50	0	1	1	1	0	3
51	0	1	0	0	0	1
52	0	1	1	1	1	4
53	1	1	1	1	0	4
54	0	0	0	0	0	0
55	0	1	0	0	1	2
56	0	0	0	0	0	0
57	1	1	1	1	0	4
58	1	1	1	1	0	4
59	0	0	0	0	0	0
60	0	1	1	0	0	2
61	0	0	0	0	0	0
62	1	0	0	1	0	2
63	1	0	0	1	0	2
64	0	1	0	0	0	1
65	0	0	0	0	0	0
66	0	0	0	0	0	0
Score1:score of CPT1A expression; Score2:score of tumor size; Score3:score of intrahepatic metastasis; Score4: score of TNM stage; Score5:score of histological grade; Total score=Score1+Score2+Score3+Score4+Score5						

Table S8. Prediction score for overall survival						
Sample	Score1	Score2	Score3	Score4	Score5	Total score
1	0	1	1	2	0	4
2	2	1	1	2	1	7
3	0	1	1	2	0	4
4	2	1	1	2	1	7
5	2	1	1	2	0	6
6	0	1	0	2	0	3
7	2	1	1	2	1	7
8	0	1	0	0	0	1
9	0	1	1	0	0	2
10	2	1	1	2	0	6
11	0	1	0	0	0	1
12	2	1	1	2	1	7
13	2	1	1	2	1	7
14	0	1	0	0	0	1
15	0	1	1	2	1	5
16	0	0	0	0	0	0
17	2	1	1	2	0	6
18	2	1	1	2	1	7
19	0	0	0	0	0	0
20	2	1	1	2	0	6
21	0	1	1	2	0	4
22	2	1	1	2	1	7
23	2	1	1	2	1	7
24	2	0	0	0	0	2
25	2	1	1	2	1	7
26	2	1	1	2	1	7
27	0	1	1	2	1	5
28	0	1	1	0	0	2
29	2	1	1	2	1	7
30	0	1	1	2	0	4
31	2	0	0	2	1	5
32	2	1	1	2	0	6
33	2	1	1	2	1	7
34	2	1	1	2	0	6
35	0	0	0	0	0	0
36	2	1	0	0	0	3
37	2	1	1	2	1	7
38	2	0	0	2	0	4
39	2	1	0	0	0	3
40	0	1	0	0	0	1
41	2	1	0	0	0	3

42	2	0	0	0	0	2
43	2	1	1	2	1	7
44	2	1	0	0	0	3
45	2	1	1	2	0	6
46	2	1	1	2	1	7
47	2	1	1	2	1	7
48	0	0	0	0	0	0
49	0	0	0	0	0	0
50	0	1	1	2	0	4
51	0	1	0	0	0	1
52	2	1	1	2	1	7
53	2	1	1	2	0	6
54	0	0	0	0	0	0
55	0	1	0	0	1	2
56	0	0	0	0	0	0
57	2	1	1	2	0	6
58	2	1	1	2	0	6
59	0	0	0	0	0	0
60	0	1	1	0	0	2
61	0	0	0	0	0	0
62	2	0	0	2	0	4
63	2	0	0	2	0	4
64	0	1	0	0	0	1
65	0	0	0	0	0	0
66	0	0	0	0	0	0
Score1:score of CPT1A expression; Score2:score of tumor size; Score3:score of intrahepatic metastasis; Score4: score of TNM stage; Score5:score of histological grade; Total score=Score1+Score2+Score3+Score4+Score5						

Table S9. Probabilities list of discriminant analysis for HCC recurrence										
Case	Actual Group	Highest Group					Second Highest Group			Discriminant Scores
		Predicted Group	P(D>d   G=g)		P(G=g   D=d)	Squared Distance	Group	P(G=g   D=d)	Squared Distance	Function 1
			p	df						
1	0	0	0.967	1	0.903	0.002	1	0.097	4.467	-1.004
2	1	1	0.287	1	0.990	1.134	0	0.010	10.366	2.175
3	0	0	0.967	1	0.903	0.002	1	0.097	4.467	-1.004
4	1	1	0.287	1	0.990	1.134	0	0.010	10.366	2.175
5	0	0	0.967	1	0.903	0.002	1	0.097	4.467	-1.004
6	0	0	0.507	1	0.977	0.440	1	0.023	7.942	-1.708
7	1	1	0.287	1	0.990	1.134	0	0.010	10.366	2.175
8	0	0	0.639	1	0.965	0.219	1	0.035	6.882	-1.513
9	0	0	0.813	1	0.860	0.056	1	0.140	3.682	-0.809
10	0	1**	0.440	1	0.659	0.596	0	0.341	1.913	0.338
11	0	0	0.639	1	0.965	0.219	1	0.035	6.882	-1.513
12	1	1	0.287	1	0.990	1.134	0	0.010	10.366	2.175
13	1	1	0.287	1	0.990	1.134	0	0.010	10.366	2.175
14	0	0	0.639	1	0.965	0.219	1	0.035	6.882	-1.513
15	1	1	0.782	1	0.849	0.077	0	0.151	3.526	0.833
16	0	0	0.477	1	0.979	0.506	1	0.021	8.214	-1.756
17	0	1**	0.440	1	0.659	0.596	0	0.341	1.913	0.338
18	1	1	0.287	1	0.990	1.134	0	0.010	10.366	2.175
19	0	0	0.477	1	0.979	0.506	1	0.021	8.214	-1.756
20	1	1	0.440	1	0.659	0.596	0	0.341	1.913	0.338
21	0	0	0.967	1	0.903	0.002	1	0.097	4.467	-1.004
22	1	1	0.287	1	0.990	1.134	0	0.010	10.366	2.175
23	1	1	0.287	1	0.990	1.134	0	0.010	10.366	2.175
24	0	0	0.528	1	0.724	0.398	1	0.276	2.323	-0.414
25	1	1	0.287	1	0.990	1.134	0	0.010	10.366	2.175
26	1	1	0.287	1	0.990	1.134	0	0.010	10.366	2.175
27	1	1	0.782	1	0.849	0.077	0	0.151	3.526	0.833
28	1	0**	0.813	1	0.860	0.056	1	0.140	3.682	-0.809
29	1	1	0.287	1	0.990	1.134	0	0.010	10.366	2.175
30	0	0	0.967	1	0.903	0.002	1	0.097	4.467	-1.004
31	1	1	0.906	1	0.929	0.014	0	0.071	5.164	1.228
32	1	1	0.440	1	0.659	0.596	0	0.341	1.913	0.338
33	1	1	0.287	1	0.990	1.134	0	0.010	10.366	2.175
34	1	1	0.440	1	0.659	0.596	0	0.341	1.913	0.338
35	0	0	0.477	1	0.979	0.506	1	0.021	8.214	-1.756
36	1	0**	0.382	1	0.608	0.763	1	0.392	1.642	-0.171

37	0	1**	0.287	1	0.990	1.134	0	0.010	10.366	2.175
38	0	0	0.663	1	0.799	0.190	1	0.201	2.954	-0.609
39	1	0**	0.382	1	0.608	0.763	1	0.392	1.642	-0.171
40	0	0	0.639	1	0.965	0.219	1	0.035	6.882	-1.513
41	0	0	0.382	1	0.608	0.763	1	0.392	1.642	-0.171
42	0	0	0.528	1	0.724	0.398	1	0.276	2.323	-0.414
43	1	1	0.287	1	0.990	1.134	0	0.010	10.366	2.175
44	0	0	0.382	1	0.608	0.763	1	0.392	1.642	-0.171
45	1	1	0.440	1	0.659	0.596	0	0.341	1.913	0.338
46	1	1	0.287	1	0.990	1.134	0	0.010	10.366	2.175
47	1	1	0.287	1	0.990	1.134	0	0.010	10.366	2.175
48	0	0	0.477	1	0.979	0.506	1	0.021	8.214	-1.756
49	0	0	0.477	1	0.979	0.506	1	0.021	8.214	-1.756
50	0	0	0.967	1	0.903	0.002	1	0.097	4.467	-1.004
51	0	0	0.639	1	0.965	0.219	1	0.035	6.882	-1.513
52	1	1	0.782	1	0.849	0.077	0	0.151	3.526	0.833
53	1	1	0.440	1	0.659	0.596	0	0.341	1.913	0.338
54	0	0	0.477	1	0.979	0.506	1	0.021	8.214	-1.756
55	1	1	0.431	1	0.652	0.619	0	0.348	1.871	0.323
56	0	0	0.477	1	0.979	0.506	1	0.021	8.214	-1.756
57	1	1	0.440	1	0.659	0.596	0	0.341	1.913	0.338
58	0	1**	0.440	1	0.659	0.596	0	0.341	1.913	0.338
59	0	0	0.477	1	0.979	0.506	1	0.021	8.214	-1.756
60	1	0**	0.813	1	0.860	0.056	1	0.140	3.682	-0.809
61	0	0	0.477	1	0.979	0.506	1	0.021	8.214	-1.756
62	1	0**	0.663	1	0.799	0.190	1	0.201	2.954	-0.609
63	1	0**	0.663	1	0.799	0.190	1	0.201	2.954	-0.609
64	0	0	0.639	1	0.965	0.219	1	0.035	6.882	-1.513
65	0	0	0.477	1	0.979	0.506	1	0.021	8.214	-1.756
66	0	0	0.477	1	0.979	0.506	1	0.021	8.214	-1.756

\*\* . Misclassified case      0=non recurrence, 1=recurrence

The classification table lists the two highest groups amongst the classification functions for each of the 66 observations used to fit the model, as well as for any new observations. P (G | D) in the discriminant analysis was identified as posterior probability.

**Table S10. Probabilities list of discriminant analysis for the death of HCC patients**

Case	Actual Group	Highest Group					Second Highest Group			Discriminant Scores
		Predicted Group	P(D>d   G=g)		P(G=g   D=d)	Squared Distance	Group	P(G=g   D=d)	Squared Distance	Function 1
			p	df						
1	1	0**	0.199	1	0.672	1.646	1	0.328	3.080	-0.558
2	1	1	0.360	1	0.999	0.840	0	0.001	15.637	2.113
3	0	0	0.199	1	0.672	1.646	1	0.328	3.080	-0.558
4	1	1	0.360	1	0.999	0.840	0	0.001	15.637	2.113
5	1	1	0.868	1	0.994	0.028	0	0.006	10.268	1.363
6	0	0	0.500	1	0.929	0.454	1	0.071	5.589	-1.167
7	1	1	0.360	1	0.999	0.840	0	0.001	15.637	2.113
8	0	0	0.604	1	0.998	0.269	1	0.002	12.652	-2.360
9	0	0	0.928	1	0.987	0.008	1	0.013	8.690	-1.751
10	1	1	0.868	1	0.994	0.028	0	0.006	10.268	1.363
11	0	0	0.604	1	0.998	0.269	1	0.002	12.652	-2.360
12	1	1	0.360	1	0.999	0.840	0	0.001	15.637	2.113
13	1	1	0.360	1	0.999	0.840	0	0.001	15.637	2.113
14	0	0	0.604	1	0.998	0.269	1	0.002	12.652	-2.360
15	1	1	0.315	1	0.827	1.010	0	0.173	4.133	0.192
16	0	0	0.599	1	0.998	0.277	1	0.002	12.705	-2.368
17	1	1	0.868	1	0.994	0.028	0	0.006	10.268	1.363
18	1	1	0.360	1	0.999	0.840	0	0.001	15.637	2.113
19	0	0	0.599	1	0.998	0.277	1	0.002	12.705	-2.368
20	1	1	0.868	1	0.994	0.028	0	0.006	10.268	1.363
21	0	0	0.199	1	0.672	1.646	1	0.328	3.080	-0.558
22	1	1	0.360	1	0.999	0.840	0	0.001	15.637	2.113
23	1	1	0.360	1	0.999	0.840	0	0.001	15.637	2.113
24	1	0**	0.163	1	0.593	1.946	1	0.407	2.700	-0.446
25	1	1	0.360	1	0.999	0.840	0	0.001	15.637	2.113
26	1	1	0.360	1	0.999	0.840	0	0.001	15.637	2.113
27	1	1	0.315	1	0.827	1.010	0	0.173	4.133	0.192
28	0	0	0.928	1	0.987	0.008	1	0.013	8.690	-1.751
29	1	1	0.360	1	0.999	0.840	0	0.001	15.637	2.113
30	1	0**	0.199	1	0.672	1.646	1	0.328	3.080	-0.558
31	1	1	0.764	1	0.996	0.090	0	0.004	11.141	1.497
32	1	1	0.868	1	0.994	0.028	0	0.006	10.268	1.363
33	1	1	0.360	1	0.999	0.840	0	0.001	15.637	2.113
34	1	1	0.868	1	0.994	0.028	0	0.006	10.268	1.363
35	0	0	0.599	1	0.998	0.277	1	0.002	12.705	-2.368
36	1	0**	0.161	1	0.588	1.967	1	0.412	2.675	-0.439

37	1	1	0.360	1	0.999	0.840	0	0.001	15.637	2.113
38	1	1	0.653	1	0.963	0.203	0	0.037	6.697	0.747
39	1	0**	0.161	1	0.588	1.967	1	0.412	2.675	-0.439
40	0	0	0.604	1	0.998	0.269	1	0.002	12.652	-2.360
41	0	0	0.161	1	0.588	1.967	1	0.412	2.675	-0.439
42	0	0	0.163	1	0.593	1.946	1	0.407	2.700	-0.446
43	1	1	0.360	1	0.999	0.840	0	0.001	15.637	2.113
44	0	0	0.161	1	0.588	1.967	1	0.412	2.675	-0.439
45	1	1	0.868	1	0.994	0.028	0	0.006	10.268	1.363
46	1	1	0.360	1	0.999	0.840	0	0.001	15.637	2.113
47	1	1	0.360	1	0.999	0.840	0	0.001	15.637	2.113
48	0	0	0.599	1	0.998	0.277	1	0.002	12.705	-2.368
49	0	0	0.599	1	0.998	0.277	1	0.002	12.705	-2.368
50	0	0	0.199	1	0.672	1.646	1	0.328	3.080	-0.558
51	0	0	0.604	1	0.998	0.269	1	0.002	12.652	-2.360
52	1	1	0.360	1	0.999	0.840	0	0.001	15.637	2.113
53	1	1	0.868	1	0.994	0.028	0	0.006	10.268	1.363
54	0	0	0.599	1	0.998	0.277	1	0.002	12.705	-2.368
55	1	0**	0.817	1	0.980	0.053	1	0.020	7.879	-1.610
56	0	0	0.599	1	0.998	0.277	1	0.002	12.705	-2.368
57	1	1	0.868	1	0.994	0.028	0	0.006	10.268	1.363
58	1	1	0.868	1	0.994	0.028	0	0.006	10.268	1.363
59	0	0	0.599	1	0.998	0.277	1	0.002	12.705	-2.368
60	1	0**	0.928	1	0.987	0.008	1	0.013	8.690	-1.751
61	0	0	0.599	1	0.998	0.277	1	0.002	12.705	-2.368
62	1	1	0.653	1	0.963	0.203	0	0.037	6.697	0.747
63	1	1	0.653	1	0.963	0.203	0	0.037	6.697	0.747
64	0	0	0.604	1	0.998	0.269	1	0.002	12.652	-2.360
65	0	0	0.599	1	0.998	0.277	1	0.002	12.705	-2.368
66	0	0	0.599	1	0.998	0.277	1	0.002	12.705	-2.368

\*\* . Misclassified case      0=non death, 1=death

The classification table lists the two highest groups amongst the classification functions for each of the 66 observations used to fit the model, as well as for any new observations. P (G | D) in the discriminant analysis was identified as posterior probability.