

Predicting treatment response using shallow whole genome sequencing of cell-free DNA using in patients with metastatic Her2+ve breast cancer.

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28 May, 2019

`## 'select()' returned 1:many mapping between keys and columns`

Abstract

Introduction

Methods

Results

Discussion

Conclusion

Tables

Measure	value	N
Age at primary diagnosis	(0,40]	4
	(40,50]	10
	(50,60]	17
	(60,70]	9
	(70,120]	8
Race	White	47
	Unknown	1
Primary receptor status	ER Negative, HER2 Positive	8
	ER Positive, HER2 Positive	36
	Indeterminate	3
Grade at primary diagnosis	I	1
	II	17
	III	27
	Unknown	3
Vital status	Alive	13
	Deceased	35

Measure Comparison

Time Dependent Cox Model

Progression Free Survival

ichorCNA.default

0.860***

1.370***

(0.210)

(0.437)

t.Mad

0.503***

-0.645

(0.161)

(1.240)

ichorCNA.low

0.383***

0.366

(0.126)

(0.517)

z.OR

0.444***

-0.358

(0.162)

(0.730)

absolute
 0.432***
 0.122
 (0.165)
 (0.258)
 AIC
 135.1
 143.9
 145
 145.7
 146.1
 140.6
 Concordance
 0.809
 0.767
 0.798
 0.704
 0.607
 0.772
 R2
 0.092
 0.043
 0.036
 0.032
 0.030
 0.106
 Log Likelihood
 -66.600
 -71.000
 -71.500
 -71.800
 -72.000
 -65.300
 Wald Test
 16.800***
 9.750***

9.180***

7.490***

6.830***

19.700***

LR Test

16.000***

7.220***

6.160**

5.480**

5.060**

18.600***

Score (Logrank) Test

30.200***

15.800***

15.400***

9.590***

8.240***

31.200***

Note:

$p < 0.1$; $p < \mathbf{0.05}$; $p < 0.01$

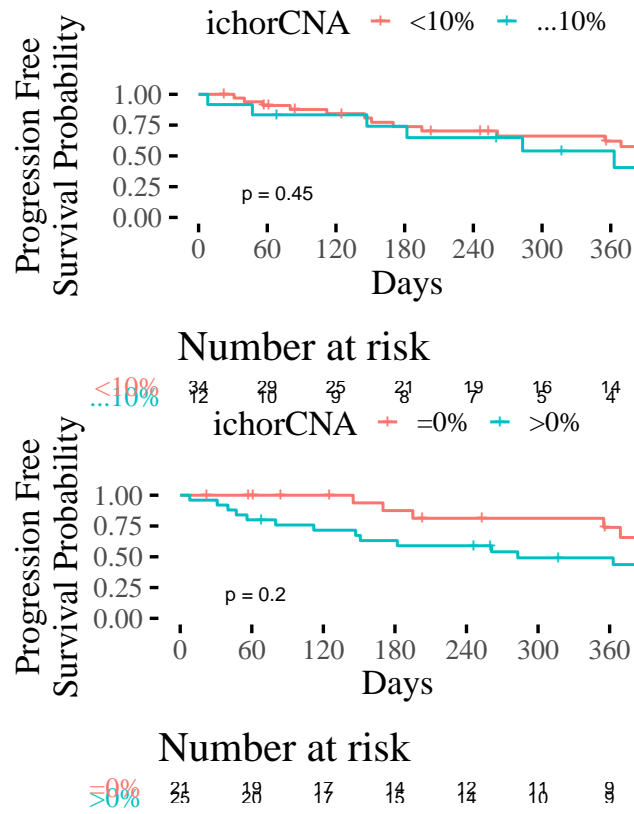


Figure 1: Cox propotional hazard models based on ichorCNA as a predictor
 (#fig:survival.cox.ichor.cut.plot)

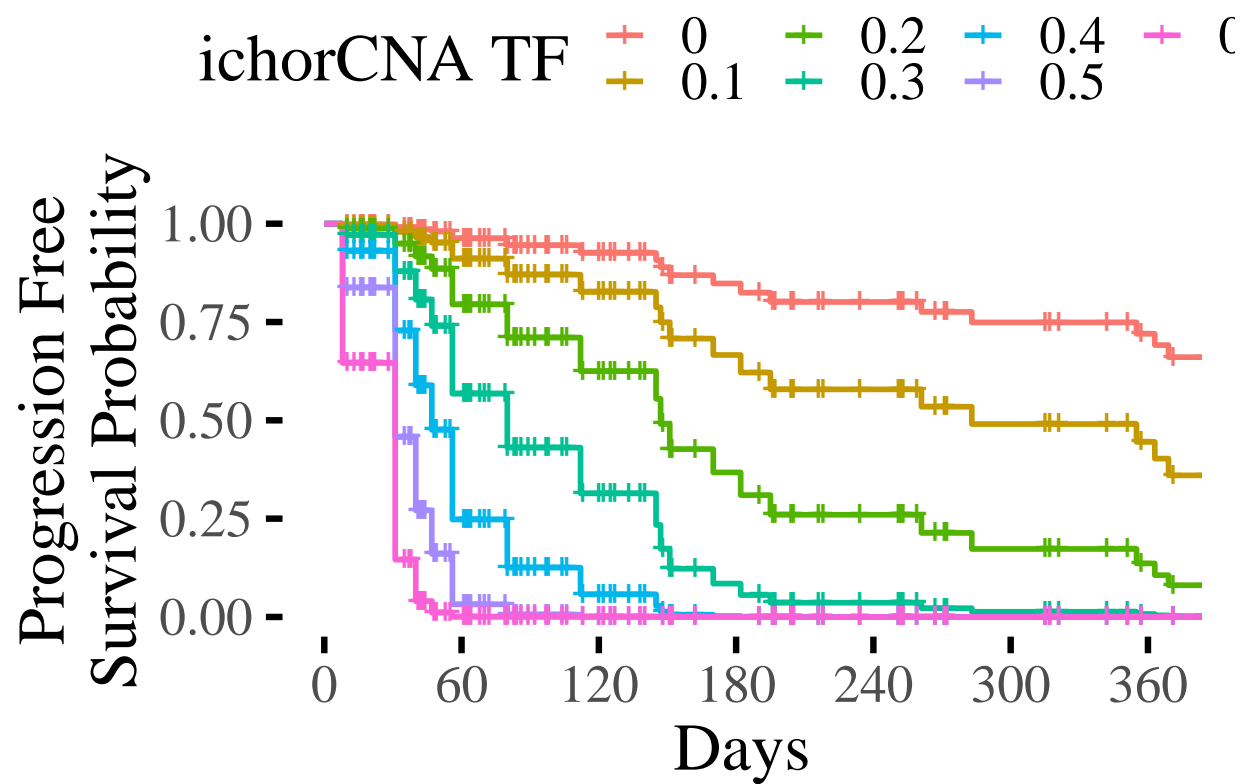


Figure 2: Time-dependent Cox regression using ichorCNA as a predictor
 (#fig:survival.AG.ichor.cont.plot)

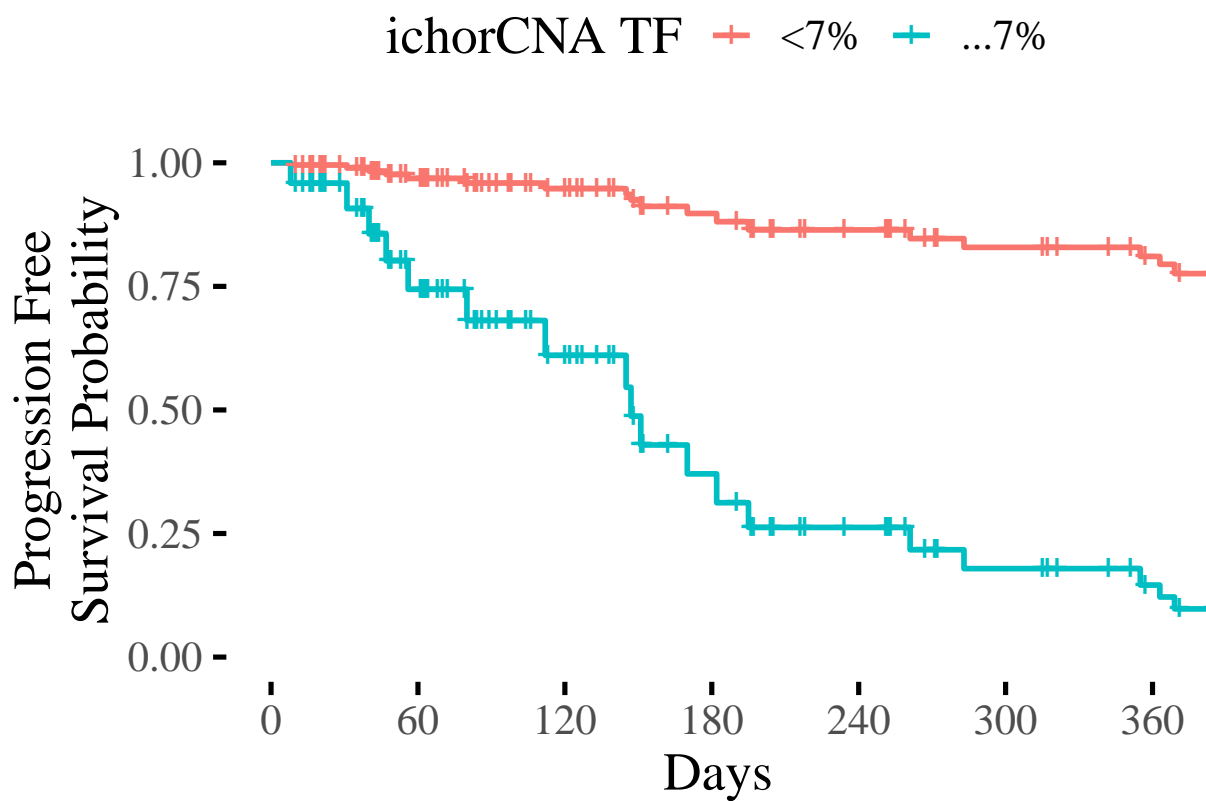
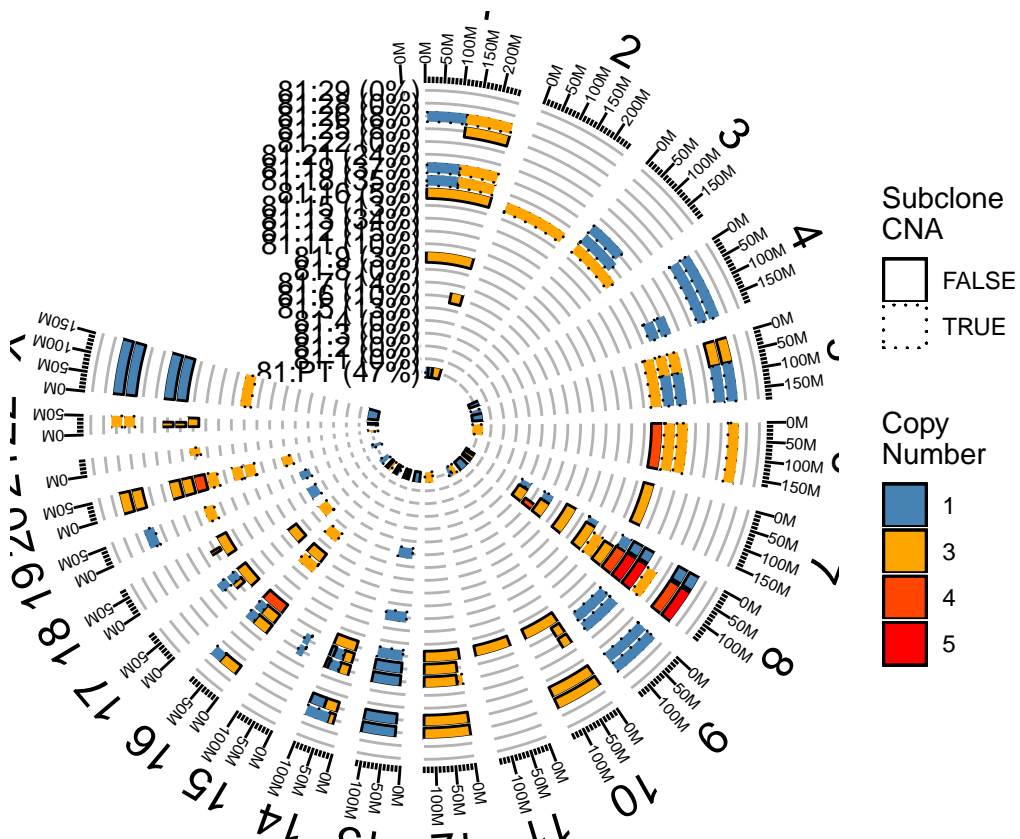
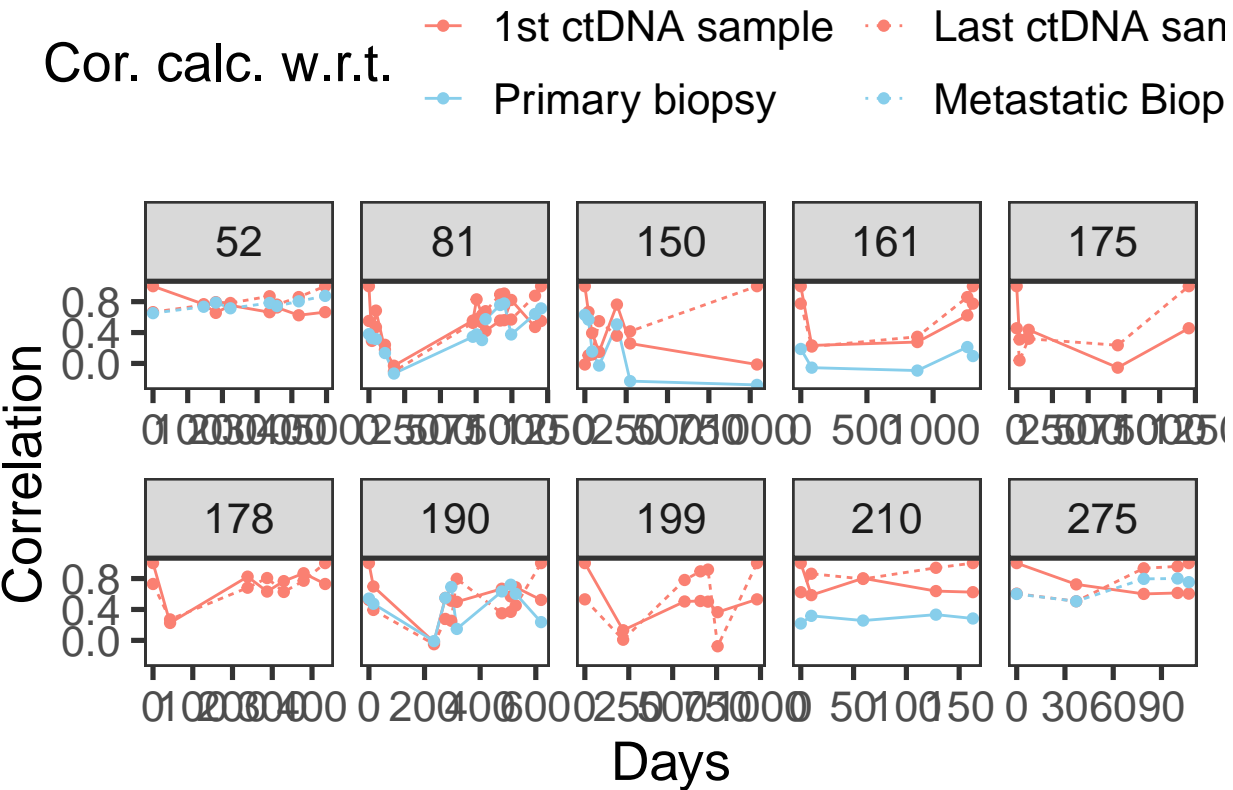


Figure 3: Optimal thresholding of a time-dependent Cox regression using ichorCNA as a predictor
 (#fig:survival.AG.ichor.cut.plot)

Figures



Patient: 81

