

LIFE-HNG. Genes whose expression is associated with survival in all patients (HPV-pos and neg). Overall survival

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Included are primary tumor patients with sample from the original tumor (not from the lymph node metastasis):

```
table(ds$ART_PROBE, ds$PRIMUM)
```

```
##
##      primary relapse
## FaDu      0      0
## HN5       0      0
## N         1      2
## T        253     17
```

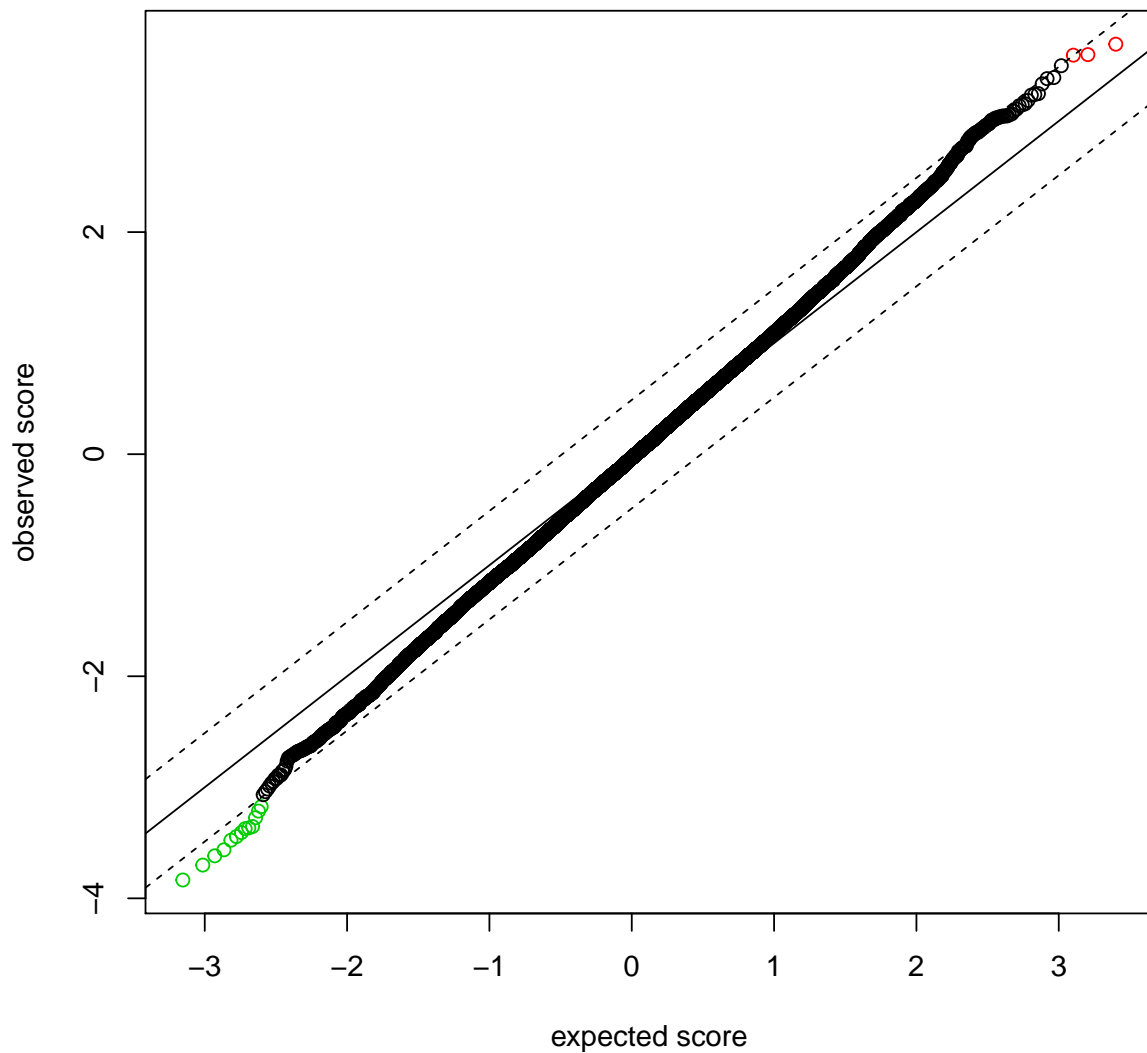
Number of analyzed patients:

```
## [1] 253
```

False discovery rate (FDR) threshold:

```
## [1] 0.1
```

1 Results of the Significance Analysis for Microarrays (SAM; Tusher, Tibshirani and Chu (2001))



```
siggenes.table
```

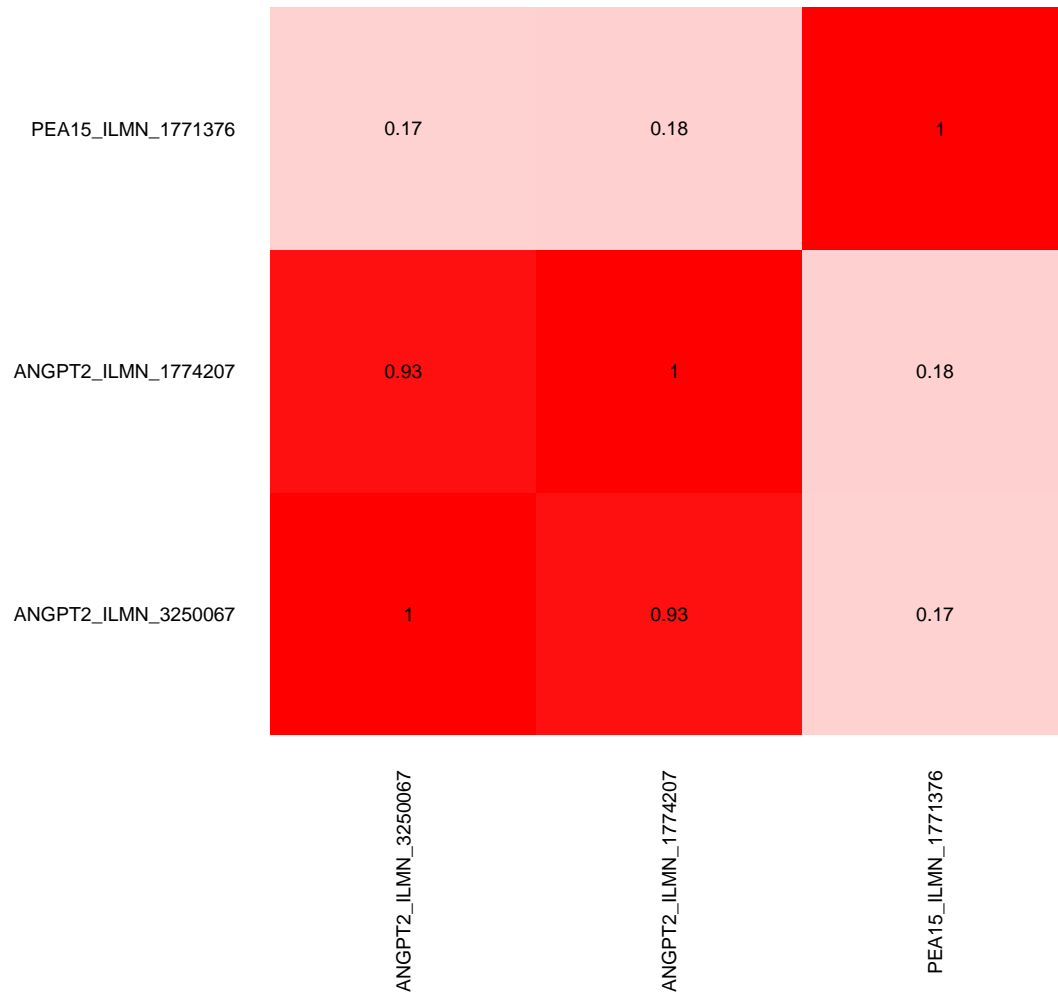
```

## $genes.up
##      Row      Gene ID Gene Name      Score(d)      Numerator(r)
## [1,] "799"      "ANGPT2" "ILMN_3250067" "3.69238693192867" "15.7218633391929"
## [2,] "801"      "ANGPT2" "ILMN_1774207" "3.59831052299979" "16.2692754290383"
## [3,] "22575"    "PEA15"  "ILMN_1771376" "3.59348577737597" "12.0256614815345"
##      Denominator(s+s0)  q-value(%)
## [1,] "4.25791327643464" "5.60165975103734"
## [2,] "4.52136504758215" "5.60165975103734"
## [3,] "3.346517066311"   "5.60165975103734"
##
## $genes.lo
##      Row      Gene ID Gene Name      Score(d)
## [1,] "4563"    "CIDEB"  "ILMN_1668910" "-3.83475571676021"
## [2,] "5591"    "CYP4F12" "ILMN_1809384" "-3.70037548465067"
## [3,] "13306"   NA      "ILMN_1772821" "-3.61729638198016"
## [4,] "8748"    "GGT6"   "ILMN_1788942" "-3.5630468095503"
## [5,] "12352"   "ICK"    "ILMN_1709882" "-3.47663327358822"
## [6,] "6964"    "ERBB2"  "ILMN_2352131" "-3.44367159098347"
## [7,] "25605"   "SCNN1A" "ILMN_1713995" "-3.4076536513479"
## [8,] "4988"    "COQ2"   "ILMN_1756572" "-3.37233495793515"
## [9,] "9756"    "HLF"    "ILMN_1722829" "-3.36603211064109"
## [10,] "23089"  "PLLP"   "ILMN_2082865" "-3.35315723124953"
## [11,] "28238"  "THAP9"  "ILMN_1809054" "-3.27387768484342"
## [12,] "23090"  "PLLP"   "ILMN_1787673" "-3.21428872117429"
## [13,] "394"    "ADI1"   "ILMN_1813975" "-3.1741451650553"
##      Numerator(r)      Denominator(s+s0)  q-value(%)
## [1,] "-12.3882378855673" "3.23051552708382" "0"
## [2,] "-23.0830915281029" "6.23804033505591" "0"
## [3,] "-16.6590694967215" "4.60539246374999" "0"
## [4,] "-14.7715975415787" "4.14577700803291" "0"
## [5,] "-16.2796470243661" "4.68258966168264" "0"
## [6,] "-18.5970369675494" "5.40035147841677" "0"
## [7,] "-31.0133564935913" "9.1010882169096"  "0"
## [8,] "-12.2467344645165" "3.63152967225268" "0"
## [9,] "-13.7235514710416" "4.07707087156333" "0"
## [10,] "-16.044148631911" "4.78478864110176" "0"
## [11,] "-4.53448039851955" "1.38504881215085" "0"
## [12,] "-10.1999504465673" "3.17331494814845" "0"
## [13,] "-10.2323891732272" "3.2236676777979"  "0"
##
## $color.ind.for.multi
## NULL
##
## $ngenes.up
## [1] 3
##
## $ngenes.lo
## [1] 13

```

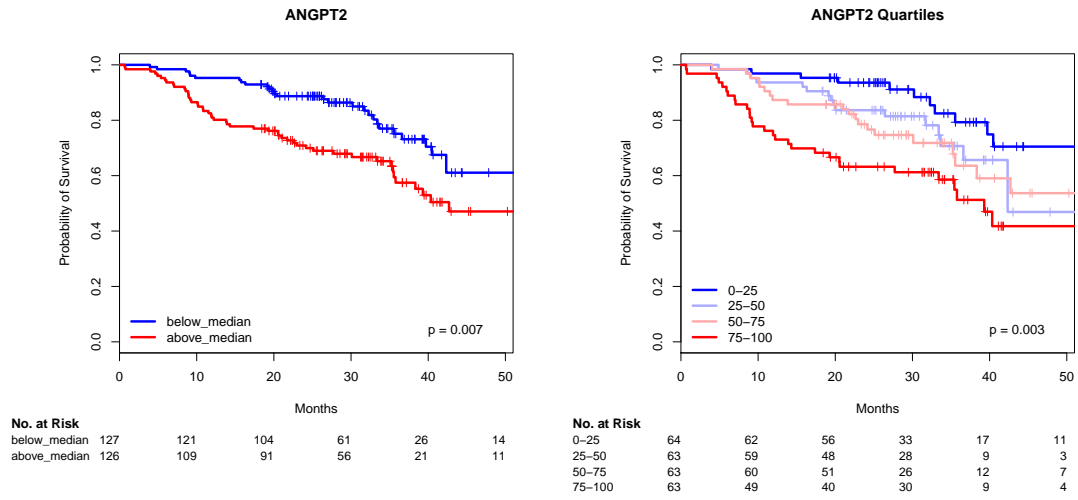
1.1 Higher expression = poorer survival

Correlation matrix of the genes whose higher expression is associated with poorer survival:



1.1.1 ANGPT2 ILMN_3250067

Gene symbol from a different, less reliable annotation table: ANGPT2



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	0.60	1.82	[1.17, 2.82]	0.0076

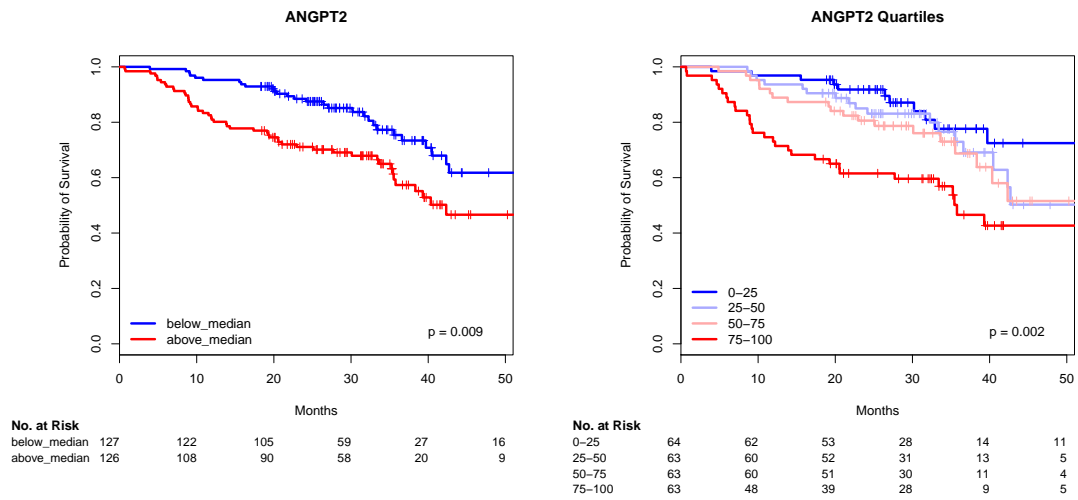
Tabelle 1: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	0.67	1.95	[0.97, 3.94]	0.06
split50-75	0.70	2.01	[1.00, 4.02]	0.05
split75-100	1.18	3.24	[1.68, 6.23]	0.00043

Tabelle 2: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the right. Patients split into quartiles

1.1.2 ANGPT2 ILMN_1774207

Gene symbol from a different, less reliable annotation table: ANGPT2



	coef	HR = exp(coef)	95% CI	p-value
splitabove__median	0.57	1.77	[1.14, 2.75]	0.01

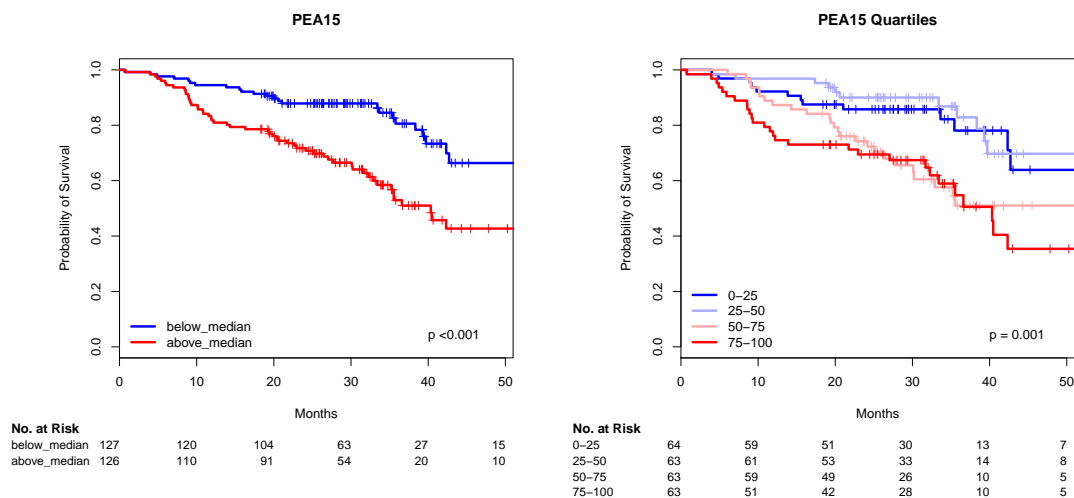
Tabelle 3: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	0.41	1.51	[0.76, 2.99]	0.24
split50-75	0.44	1.56	[0.78, 3.12]	0.21
split75-100	1.09	2.99	[1.58, 5.64]	0.00074

Tabelle 4: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the right. Patients split into quartiles

1.1.3 PEA15 ILMN_1771376

Gene symbol from a different, less reliable annotation table: PEA15



	coef	HR = exp(coef)	95% CI	p-value
splitabove_medial	0.87	2.39	[1.52, 3.77]	0.00018

Tabelle 5: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.16	0.85	[0.41, 1.79]	0.68
split50-75	0.68	1.98	[1.05, 3.72]	0.03
split75-100	0.91	2.49	[1.33, 4.65]	0.0043

Tabelle 6: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the right. Patients split into quartiles

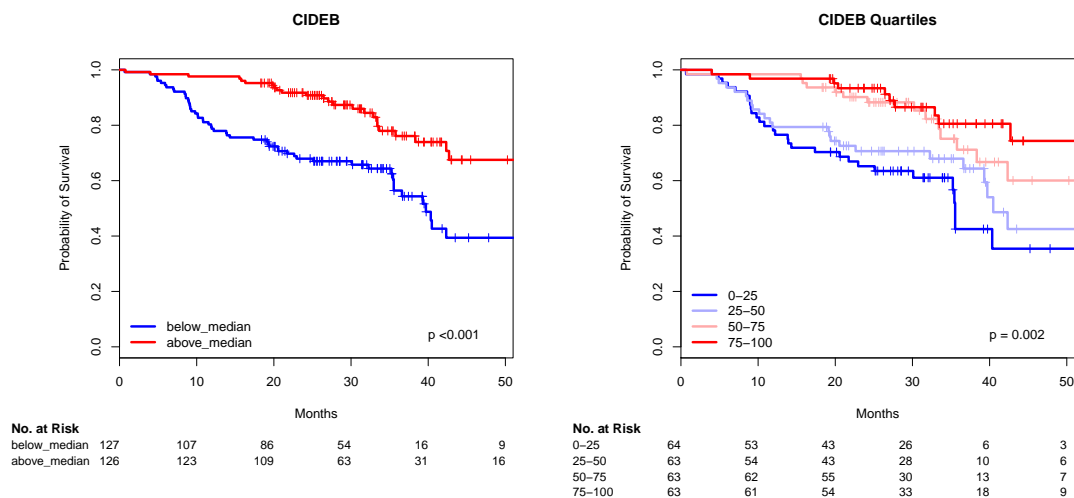
1.2 Higher expression = better survival

Correlation matrix of the genes whose higher expression is associated with better survival:

ADI1_ILMN_1813975	0.2	0.14	0.3	0.24	0.28	0.29	0.33	0.34	0.21	0.36	0.25	0.33	1
PLLP_ILMN_1787673	0.24	0.3	0.36	0.37	0.47	0.33	0.42	0.41	0.47	0.96	0.27	1	0.33
THAP9_ILMN_1809054	0.0036	0.077	0.3	0.046	0.49	0.032	0.069	0.33	0.29	0.25	1	0.27	0.25
PLLP_ILMN_2082865	0.3	0.36	0.37	0.42	0.44	0.38	0.47	0.39	0.48	1	0.25	0.96	0.36
HLF_ILMN_1722829	0.43	0.67	0.46	0.49	0.44	0.36	0.43	0.34	1	0.48	0.29	0.47	0.21
COQ2_ILMN_1756572	0.23	0.24	0.27	0.3	0.32	0.12	0.29	1	0.34	0.39	0.33	0.41	0.34
SCNN1A_ILMN_1713995	0.3	0.4	0.42	0.66	0.33	0.51	1	0.29	0.43	0.47	0.069	0.42	0.33
ERBB2_ILMN_2352131	0.32	0.45	0.37	0.51	0.24	1	0.51	0.12	0.36	0.38	0.032	0.33	0.29
ICK_ILMN_1709882	0.07	0.29	0.5	0.19	1	0.24	0.33	0.32	0.44	0.44	0.49	0.47	0.28
GGT6_ILMN_1788942	0.43	0.52	0.45	1	0.19	0.51	0.66	0.3	0.49	0.42	0.046	0.37	0.24
NA_ILMN_1772821	0.25	0.43	1	0.45	0.5	0.37	0.42	0.27	0.46	0.37	0.3	0.36	0.3
CYP4F12_ILMN_1809384	0.46	1	0.43	0.52	0.29	0.45	0.4	0.24	0.67	0.36	0.077	0.3	0.14
CIDEB_ILMN_1668910	1	0.46	0.25	0.43	0.07	0.32	0.3	0.23	0.43	0.3	0.0036	0.24	0.2
CIDEB_ILMN_1668910													
CYP4F12_ILMN_1809384													
NA_ILMN_1772821													
GGT6_ILMN_1788942													
ICK_ILMN_1709882													
ERBB2_ILMN_2352131													
SCNN1A_ILMN_1713995													
COQ2_ILMN_1756572													
HLF_ILMN_1722829													
PLLP_ILMN_2082865													
THAP9_ILMN_1809054													
PLLP_ILMN_1787673													
ADI1_ILMN_1813975													

1.2.1 CIDEB ILMN_1668910

Gene symbol from a different, less reliable annotation table: CIDEB



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.80	0.45	[0.29, 0.71]	0.0005

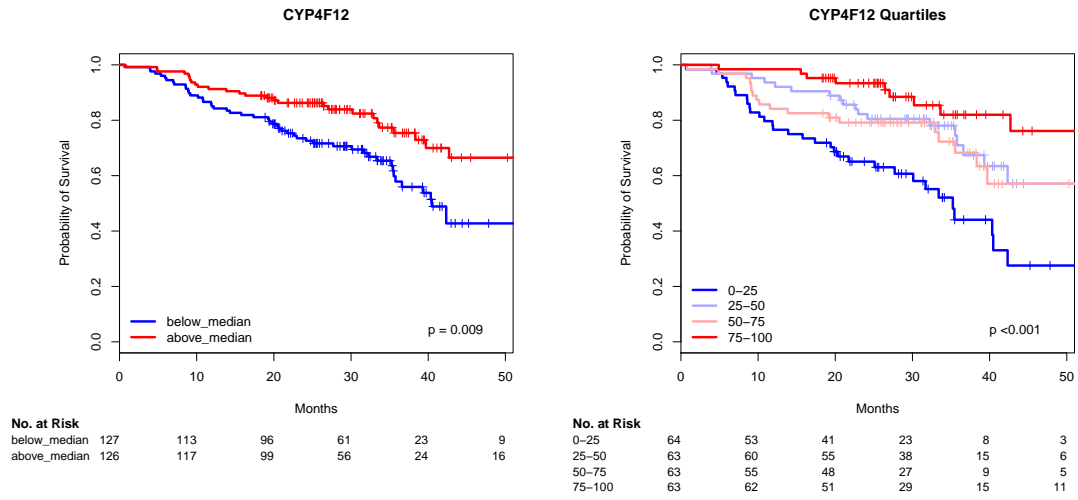
Tabelle 7: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.26	0.77	[0.45, 1.32]	0.34
split50-75	-0.71	0.49	[0.27, 0.88]	0.02
split75-100	-1.18	0.31	[0.16, 0.60]	0.00061

Tabelle 8: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the right. Patients split into quartiles

1.2.2 CYP4F12 ILMN_1809384

Gene symbol from a different, less reliable annotation table: CYP4F12



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.59	0.55	[0.35, 0.87]	0.0096

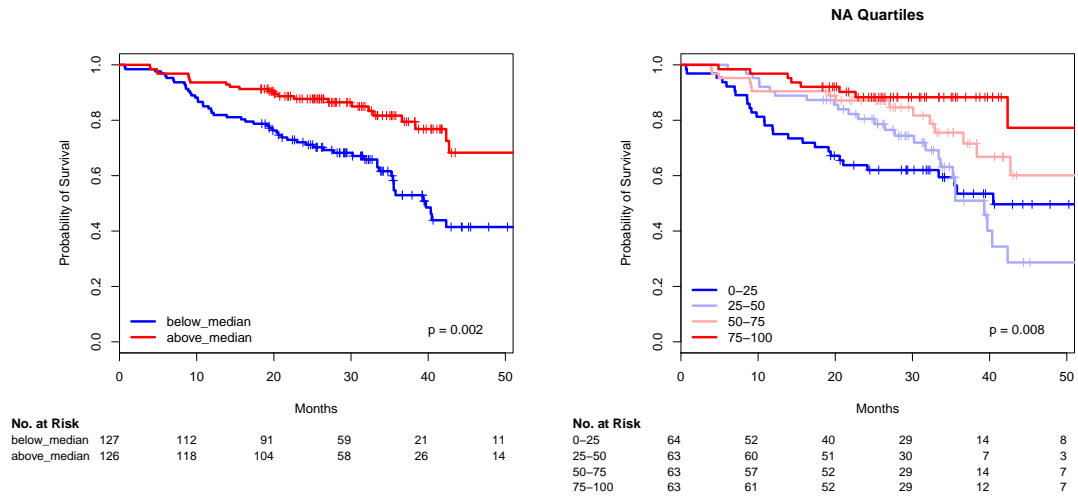
Tabelle 9: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.70	0.50	[0.28, 0.86]	0.01
split50-75	-0.62	0.54	[0.30, 0.95]	0.03
split75-100	-1.29	0.28	[0.14, 0.54]	0.00016

Tabelle 10: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the right. Patients split into quartiles

1.2.3 NA ILMN_1772821

Gene symbol from a different, less reliable annotation table: KIAA1671



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.72	0.49	[0.31, 0.77]	0.0019

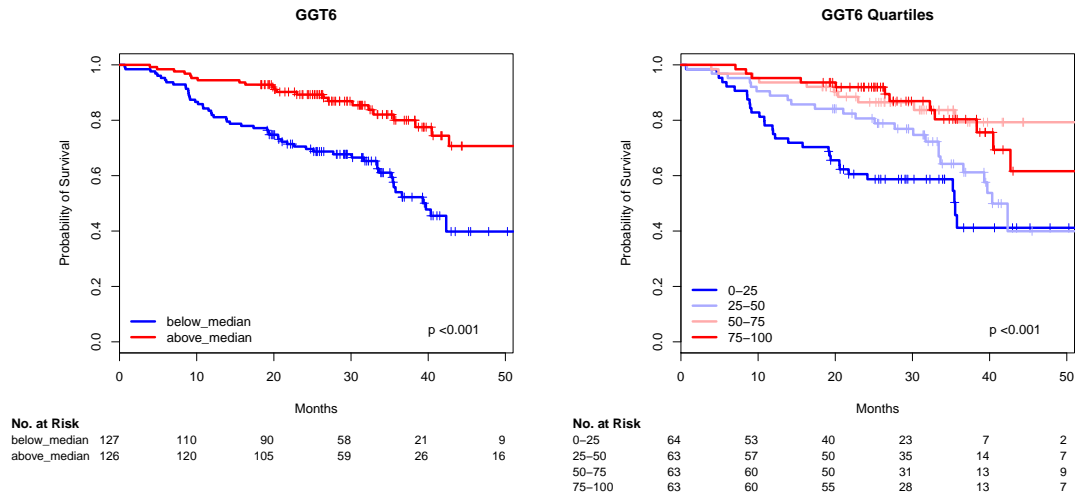
Tabelle 11: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.12	0.88	[0.52, 1.50]	0.65
split50-75	-0.52	0.59	[0.33, 1.07]	0.08
split75-100	-1.13	0.32	[0.16, 0.66]	0.0021

Tabelle 12: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the right. Patients split into quartiles

1.2.4 GGT6 ILMN_1788942

Gene symbol from a different, less reliable annotation table: GGT6



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.84	0.43	[0.27, 0.68]	0.00034

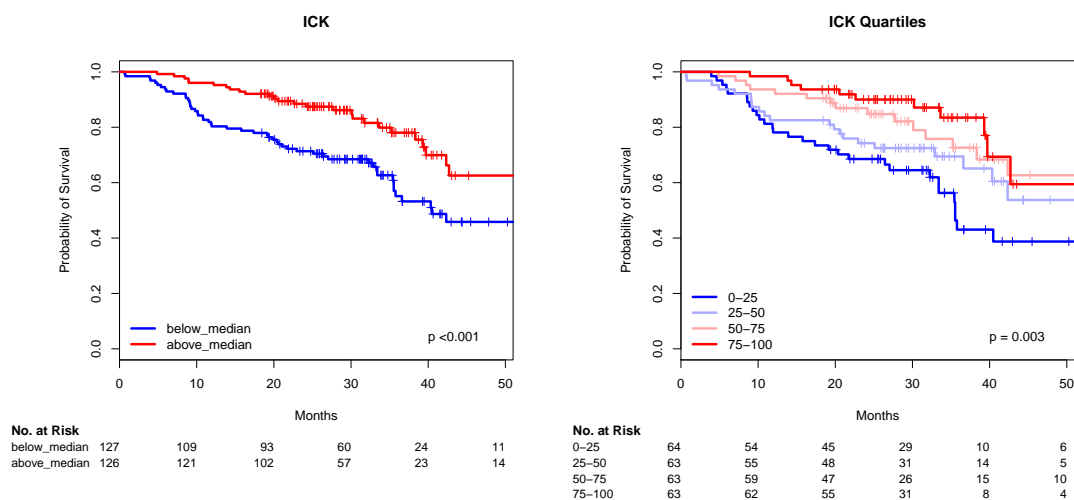
Tabelle 13: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.60	0.55	[0.32, 0.94]	0.03
split50-75	-1.19	0.30	[0.16, 0.58]	0.00034
split75-100	-1.12	0.33	[0.17, 0.62]	0.00056

Tabelle 14: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the right. Patients split into quartiles

1.2.5 ICK ILMN_1709882

Gene symbol from a different, less reliable annotation table: ICK



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.74	0.48	[0.30, 0.75]	0.0013

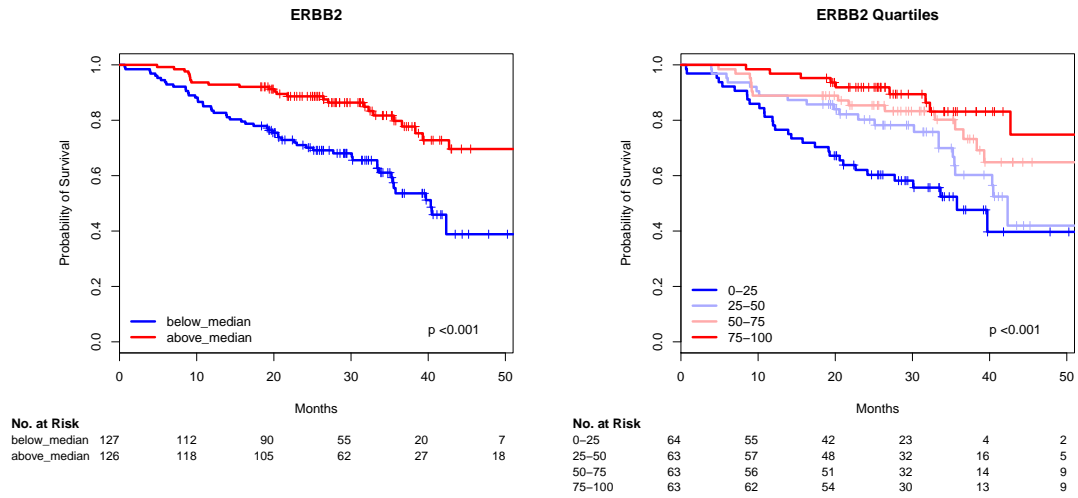
Tabelle 15: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.41	0.67	[0.39, 1.15]	0.14
split50-75	-0.81	0.45	[0.25, 0.81]	0.0076
split75-100	-1.10	0.33	[0.17, 0.65]	0.0013

Tabelle 16: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the right. Patients split into quartiles

1.2.6 ERBB2 ILMN_2352131

Gene symbol from a different, less reliable annotation table: ERBB2



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.79	0.45	[0.29, 0.71]	0.00052

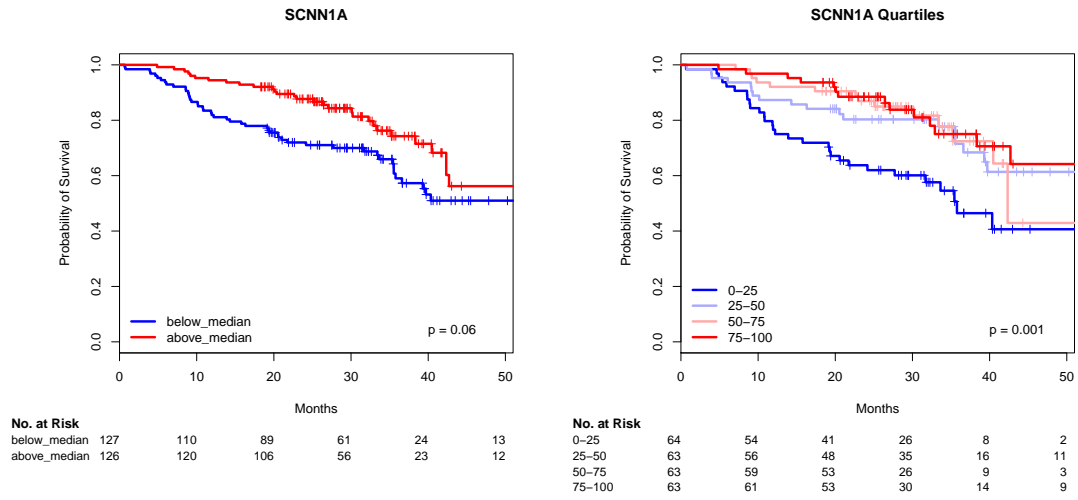
Tabelle 17: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.51	0.60	[0.35, 1.03]	0.06
split50-75	-0.96	0.38	[0.21, 0.70]	0.002
split75-100	-1.18	0.31	[0.16, 0.59]	0.00041

Tabelle 18: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the right. Patients split into quartiles

1.2.7 SCNN1A ILMN_1713995

Gene symbol from a different, less reliable annotation table: SCNN1A



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.41	0.67	[0.43, 1.03]	0.07

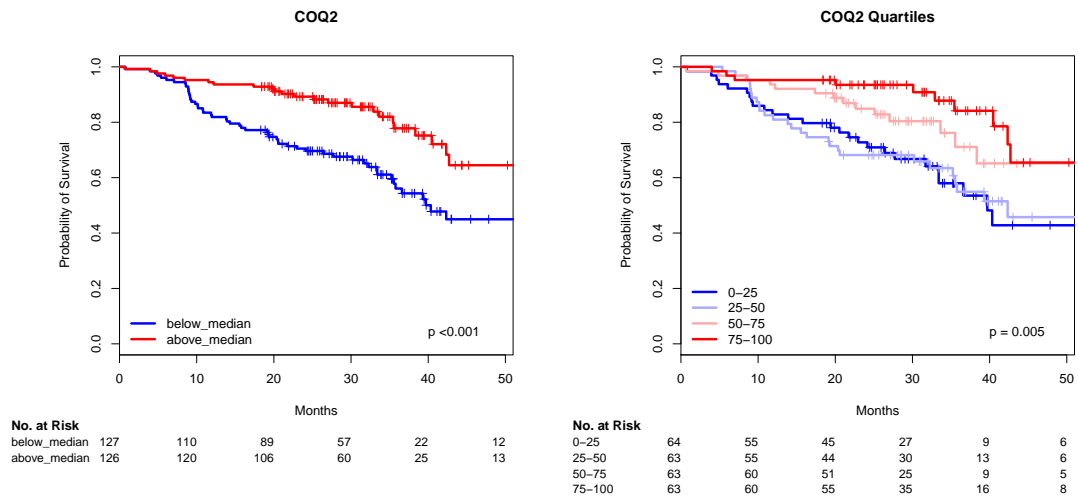
Tabelle 19: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.96	0.38	[0.21, 0.70]	0.0017
split50-75	-0.86	0.42	[0.23, 0.77]	0.0054
split75-100	-0.88	0.42	[0.23, 0.75]	0.0032

Tabelle 20: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the right. Patients split into quartiles

1.2.8 COQ2 ILMN_1756572

Gene symbol from a different, less reliable annotation table: COQ2



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.78	0.46	[0.29, 0.72]	0.00085

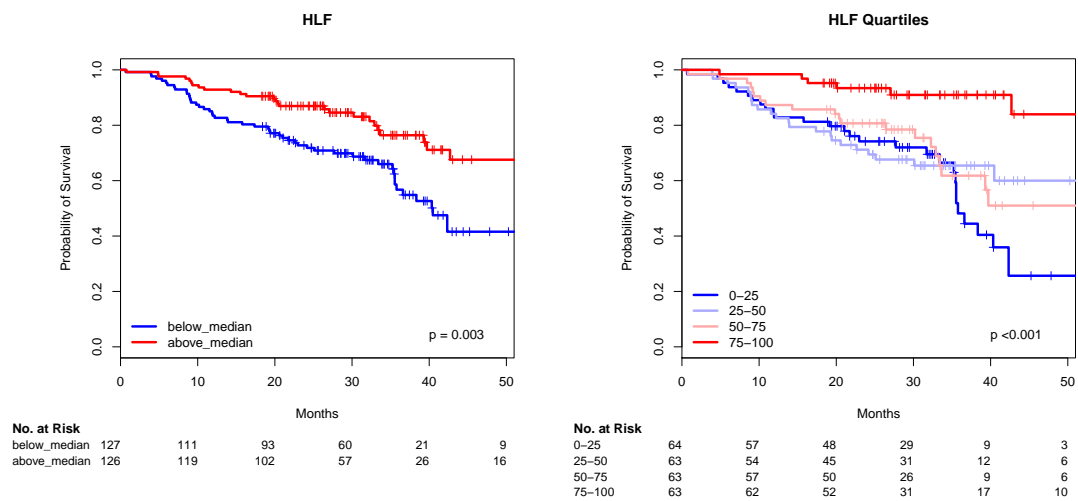
Tabelle 21: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	0.004	1.00	[0.59, 1.71]	0.99
split50-75	-0.52	0.60	[0.32, 1.11]	0.10
split75-100	-1.07	0.34	[0.17, 0.69]	0.0027

Tabelle 22: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the right. Patients split into quartiles

1.2.9 HLF ILMN_1722829

Gene symbol from a different, less reliable annotation table: HLF



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.68	0.51	[0.33, 0.80]	0.0031

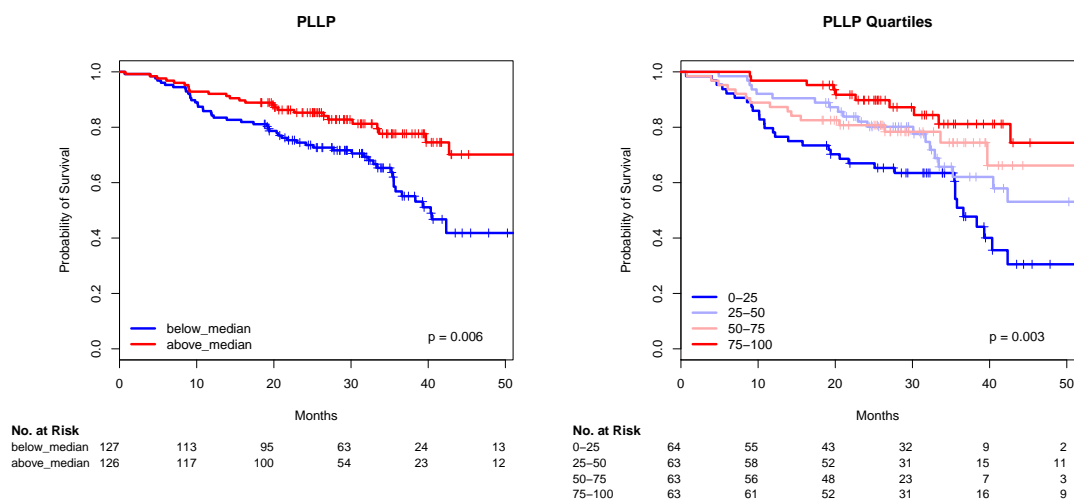
Tabelle 23: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.23	0.79	[0.46, 1.36]	0.39
split50-75	-0.31	0.73	[0.42, 1.27]	0.27
split75-100	-1.50	0.22	[0.10, 0.49]	0.00017

Tabelle 24: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the right. Patients split into quartiles

1.2.10 PLLP ILMN_2082865

Gene symbol from a different, less reliable annotation table: PLLP



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.62	0.54	[0.34, 0.84]	0.0067

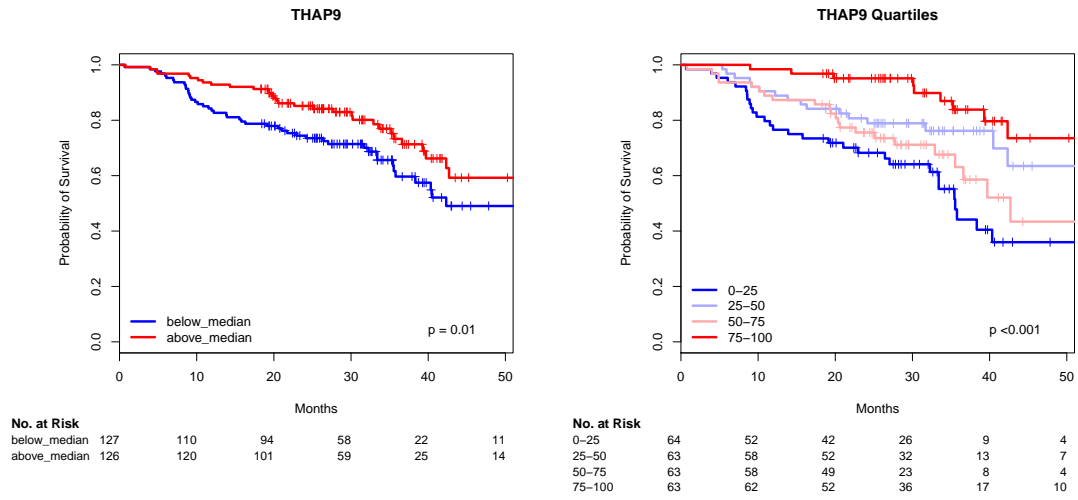
Tabelle 25: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.59	0.56	[0.32, 0.97]	0.04
split50-75	-0.69	0.50	[0.28, 0.91]	0.02
split75-100	-1.08	0.34	[0.18, 0.64]	0.00077

Tabelle 26: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the right. Patients split into quartiles

1.2.11 THAP9 ILMN_1809054

Gene symbol from a different, less reliable annotation table: THAP9



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.55	0.58	[0.37, 0.90]	0.01

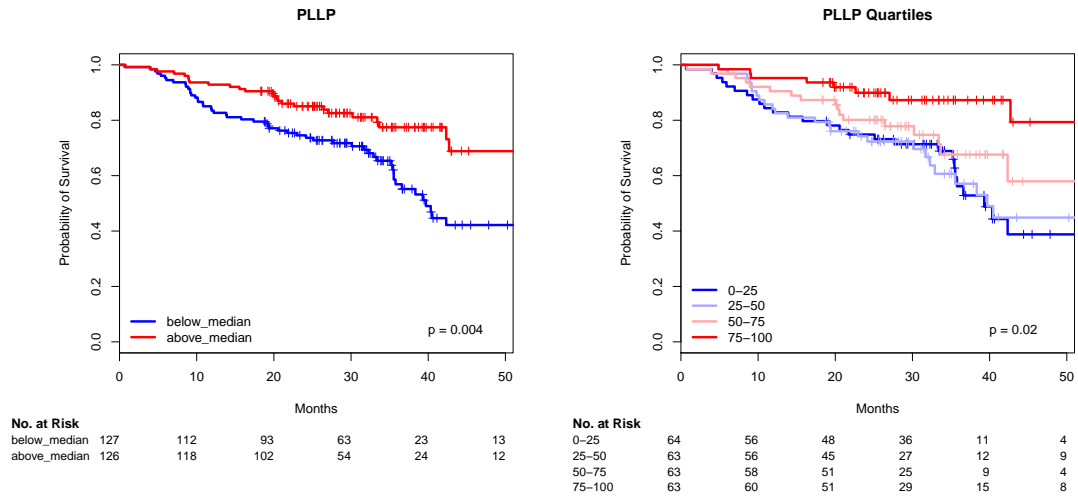
Tabelle 27: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.76	0.47	[0.26, 0.83]	0.0092
split50-75	-0.39	0.67	[0.39, 1.15]	0.15
split75-100	-1.57	0.21	[0.10, 0.43]	< 0.0001

Tabelle 28: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the right. Patients split into quartiles

1.2.12 PLLP ILMN_1787673

Gene symbol from a different, less reliable annotation table: PLLP



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.66	0.52	[0.33, 0.81]	0.0042

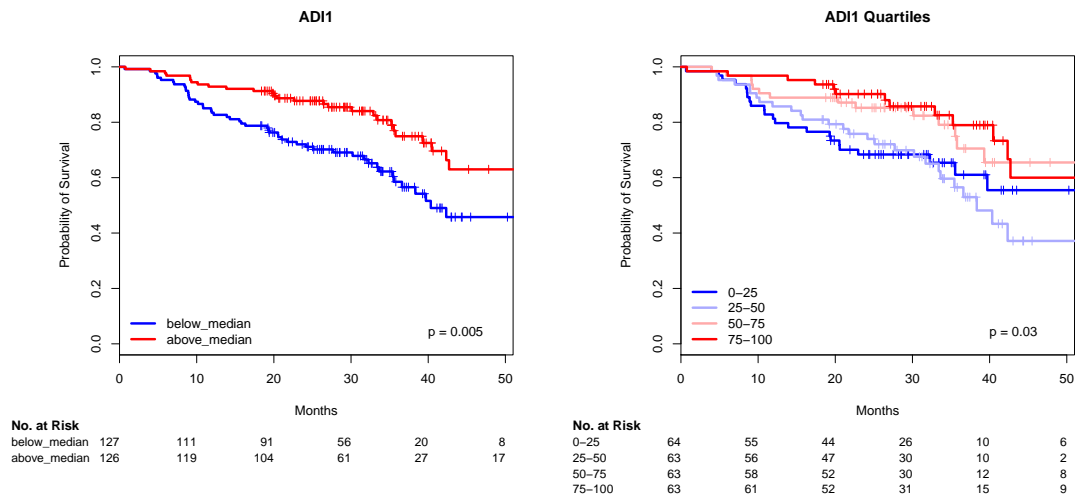
Tabelle 29: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.15	0.86	[0.50, 1.47]	0.58
split50-75	-0.51	0.60	[0.33, 1.10]	0.10
split75-100	-0.98	0.38	[0.19, 0.74]	0.0044

Tabelle 30: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the right. Patients split into quartiles

1.2.13 ADI1 ILMN_1813975

Gene symbol from a different, less reliable annotation table: ADI1



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.62	0.54	[0.34, 0.83]	0.0057

Tabelle 31: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	0.26	1.29	[0.74, 2.25]	0.37
split50-75	-0.42	0.66	[0.35, 1.23]	0.19
split75-100	-0.57	0.56	[0.29, 1.08]	0.08

Tabelle 32: Cox regression model, $n = 253$, number of events = 85. Model for the figure on the right. Patients split into quartiles