

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

Progression-free survival

Inhaltsverzeichnis

1	Results of the Significance Analysis for Microarrays (SAM; Tusher, Tibshirani and Chu (2001))	1
1.1	Higher expression = poorer survival	3
1.1.1	VAT1 ILMN_1700690	5
1.2	Higher expression = better survival	5
1.2.1	ATP1A1 ILMN_1775566	7
1.2.2	ATP1A1 ILMN_1731783	8
1.2.3	ZWINT ILMN_2362549	9
1.2.4	RBBP8 ILMN_2363621	10
1.2.5	ATP1A1 ILMN_2415189	11
1.2.6	TOM1L1 ILMN_1802642	12
1.2.7	NA ILMN_1738554	13
1.2.8	ZWINT ILMN_2362545	14
1.2.9	PCNA ILMN_1694177	15

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
```

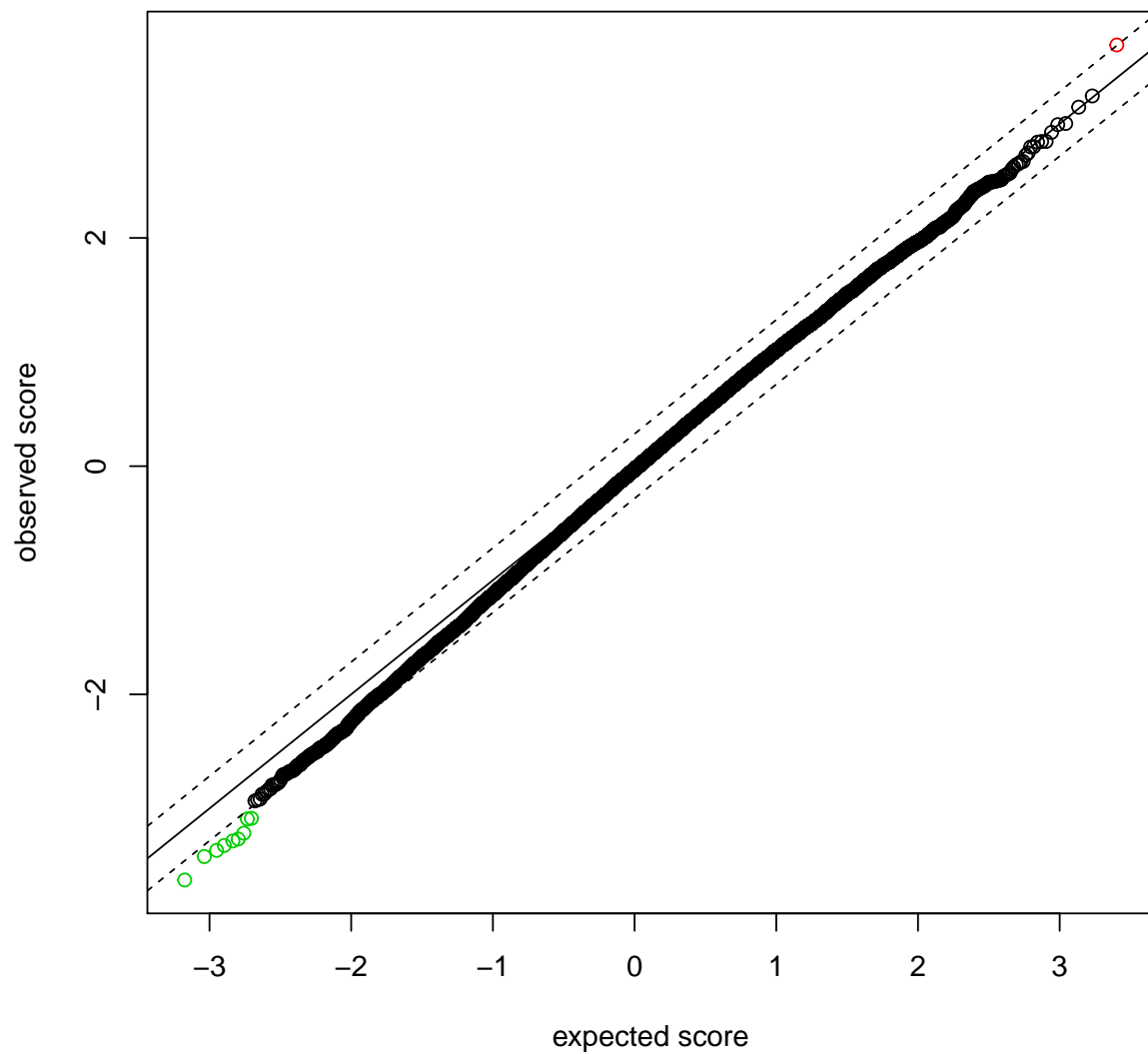
Number of analyzed patients:

```
## [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,] "29921" "VAT1"  "ILMN_1700690" "3.69107512047938" "15.8714423849835"
##      Denominator(s+s0)  q-value(%)
## [1,] "4.29995106220493" "9.38716884774976"
##
```

```

## $genes.lo
##      Row      Gene ID Gene Name      Score(d)
## [1,] "1502"  "ATP1A1" "ILMN_1775566" "-3.62700835436415"
## [2,] "1500"  "ATP1A1" "ILMN_1731783" "-3.42135642271465"
## [3,] "31319" "ZWINT"  "ILMN_2362549" "-3.36733046519887"
## [4,] "24446" "RBBP8"  "ILMN_2363621" "-3.32444890467644"
## [5,] "1501"  "ATP1A1" "ILMN_2415189" "-3.28440368428397"
## [6,] "28860" "TOM1L1" "ILMN_1802642" "-3.26790309831087"
## [7,] "17281" NA      "ILMN_1738554" "-3.21674346987759"
## [8,] "31318" "ZWINT"  "ILMN_2362545" "-3.09169180142681"
## [9,] "22413" "PCNA"   "ILMN_1694177" "-3.08663682526069"
##      Numerator(r)      Denominator(s+s0)  q-value(%)
## [1,] "-20.1023387578596" "5.54240211045329" "0"
## [2,] "-17.3026507595813" "5.05724882818629" "0"
## [3,] "-14.6055587608626" "4.33742957865586" "0"
## [4,] "-19.463427433305"  "5.85463275008564" "0"
## [5,] "-14.2227170563121" "4.33038031359194" "0"
## [6,] "-11.0195025992951" "3.37204080653153" "0"
## [7,] "-15.0202576552617" "4.66939866231648" "0"
## [8,] "-11.7627771874615" "3.80464093543638" "10.4301876086108"
## [9,] "-17.4530996335949" "5.65440659904033" "10.4301876086108"
##
## $color.ind.for.multi
## NULL
##
## $ngenes.up
## [1] 1
##
## $ngenes.lo
## [1] 9

```

1.1 Higher expression = poorer survival

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

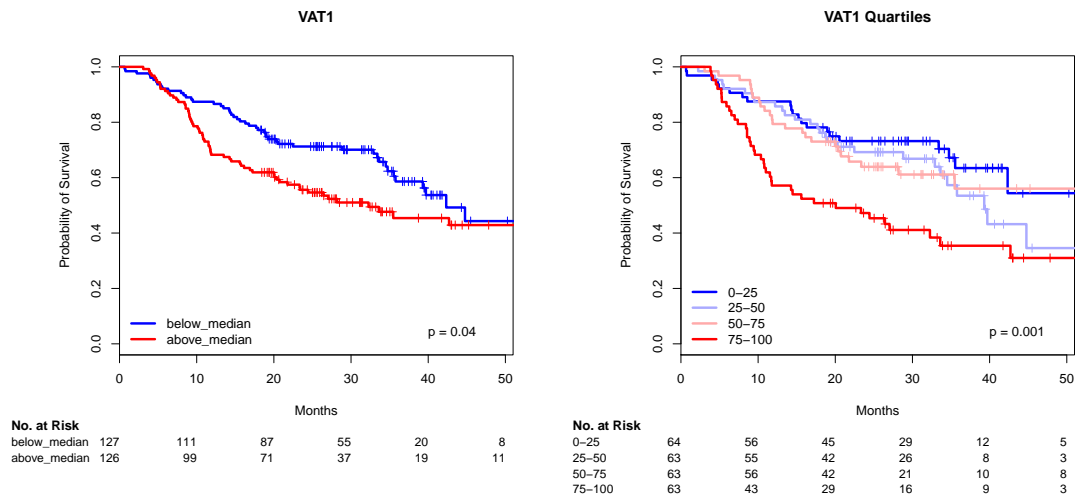
VAT1_ILMN_1700690

1

VAT1_ILMN_1700690

1.1.1 VAT1 ILMN_1700690

Gene symbol from a different, less reliable annotation table: VAT1



	coef	HR = exp(coef)	95% CI	p-value
splitabove_medial	0.39	1.48	[1.02, 2.15]	0.04

Tabelle 1: Cox regression model, $n = 253$, number of events = 117. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	0.38	1.46	[0.83, 2.56]	0.19
split50-75	0.23	1.25	[0.70, 2.24]	0.44
split75-100	0.93	2.54	[1.49, 4.31]	0.00058

Tabelle 2: Cox regression model, $n = 253$, number of events = 117. Model for the figure on the right. Patients split into quartiles

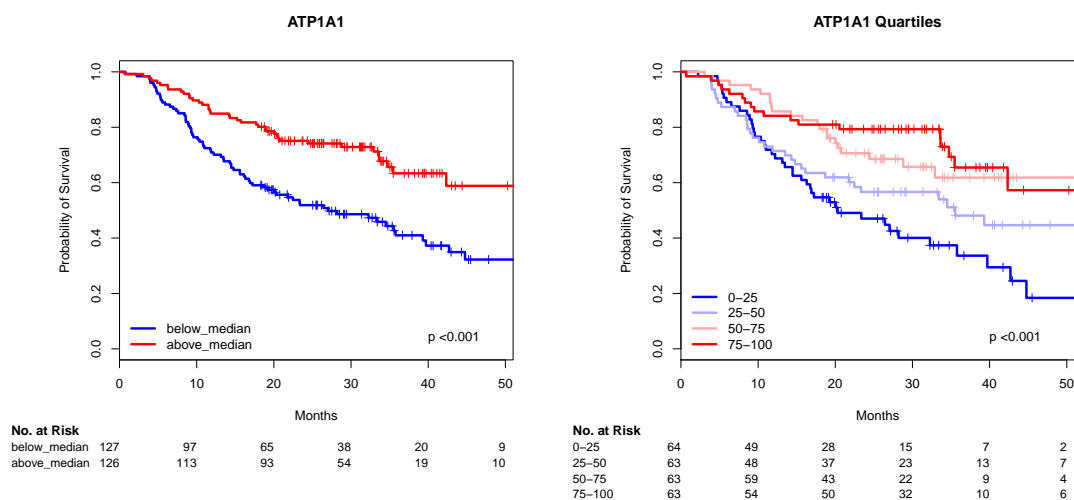
1.2 Higher expression = better survival

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

PCNA_ILMN_1694177	0.14	0.1	0.63	0.49	0.14	0.23	0.37	0.61	1
ZWINT_ILMN_2362545	0.22	0.22	0.92	0.44	0.22	0.23	0.36	1	0.61
NA_ILMN_1738554	0.12	0.06	0.33	0.36	0.11	0.36	1	0.36	0.37
TOM1L1_ILMN_1802642	0.35	0.23	0.24	0.35	0.21	1	0.36	0.23	0.23
ATP1A1_ILMN_2415189	0.87	0.92	0.2	0.27	1	0.21	0.11	0.22	0.14
RBBP8_ILMN_2363621	0.27	0.27	0.46	1	0.27	0.35	0.36	0.44	0.49
ZWINT_ILMN_2362549	0.21	0.18	1	0.46	0.2	0.24	0.33	0.92	0.63
ATP1A1_ILMN_1731783	0.9	1	0.18	0.27	0.92	0.23	0.06	0.22	0.1
ATP1A1_ILMN_1775566	1	0.9	0.21	0.27	0.87	0.35	0.12	0.22	0.14
	ATP1A1_ILMN_1775566	ATP1A1_ILMN_1731783	ZWINT_ILMN_2362549	RBBP8_ILMN_2363621	ATP1A1_ILMN_2415189	TOM1L1_ILMN_1802642	NA_ILMN_1738554	ZWINT_ILMN_2362545	PCNA_ILMN_1694177

1.2.1 ATP1A1 ILMN_1775566

Gene symbol from a different, less reliable annotation table: ATP1A1



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.78	0.46	[0.31, 0.67]	< 0.0001

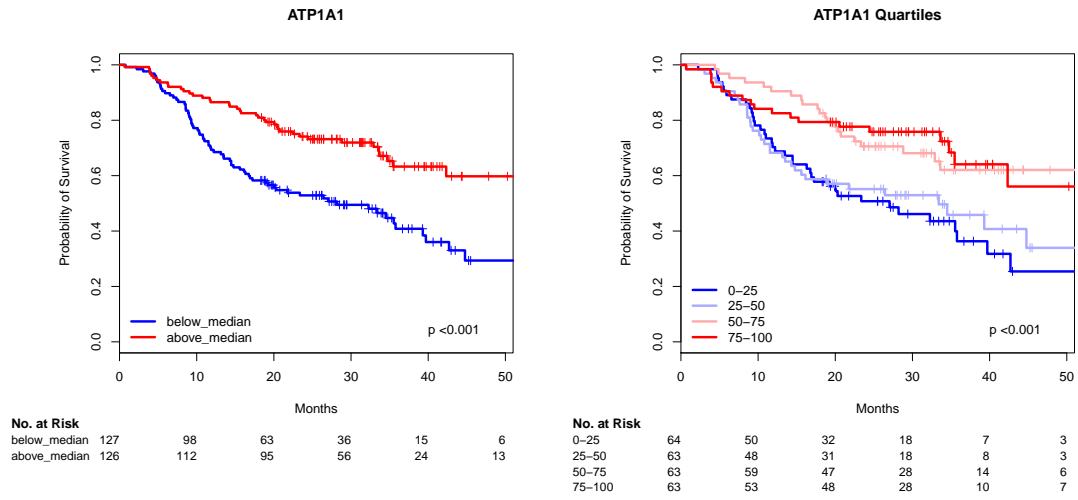
Tabelle 3: Cox regression model, $n = 253$, number of events = 117. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.46	0.63	[0.40, 1.01]	0.05
split50-75	-0.86	0.42	[0.25, 0.71]	0.00099
split75-100	-1.16	0.31	[0.18, 0.55]	< 0.0001

Tabelle 4: Cox regression model, $n = 253$, number of events = 117. Model for the figure on the right. Patients split into quartiles

1.2.2 ATP1A1 ILMN_1731783

Gene symbol from a different, less reliable annotation table: ATP1A1



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.83	0.44	[0.30, 0.64]	< 0.0001

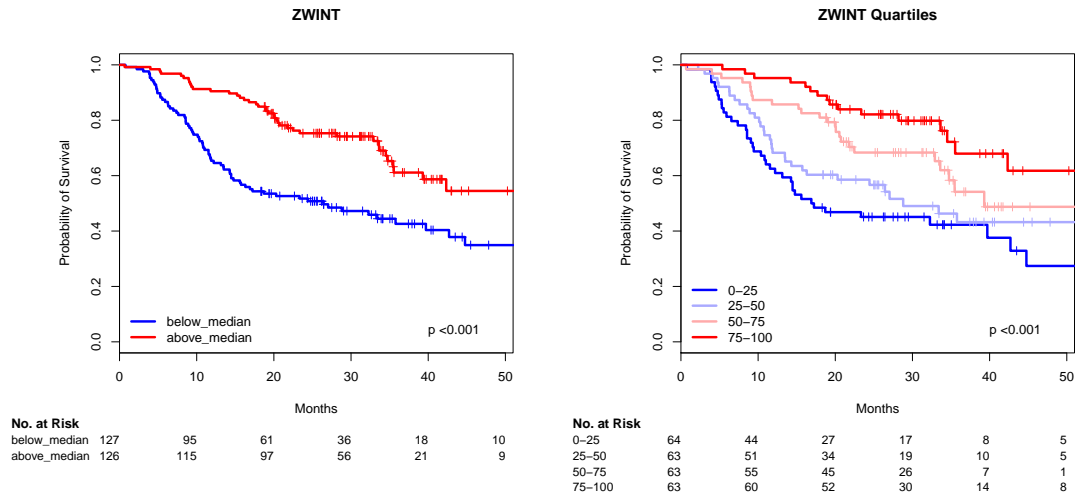
Tabelle 5: Cox regression model, $n = 253$, number of events = 117. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.15	0.86	[0.54, 1.36]	0.51
split50-75	-0.87	0.42	[0.25, 0.70]	0.0011
split75-100	-0.94	0.39	[0.23, 0.67]	0.00072

Tabelle 6: Cox regression model, $n = 253$, number of events = 117. Model for the figure on the right. Patients split into quartiles

1.2.3 ZWINT ILMN_2362549

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



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.77	0.46	[0.31, 0.68]	< 0.0001

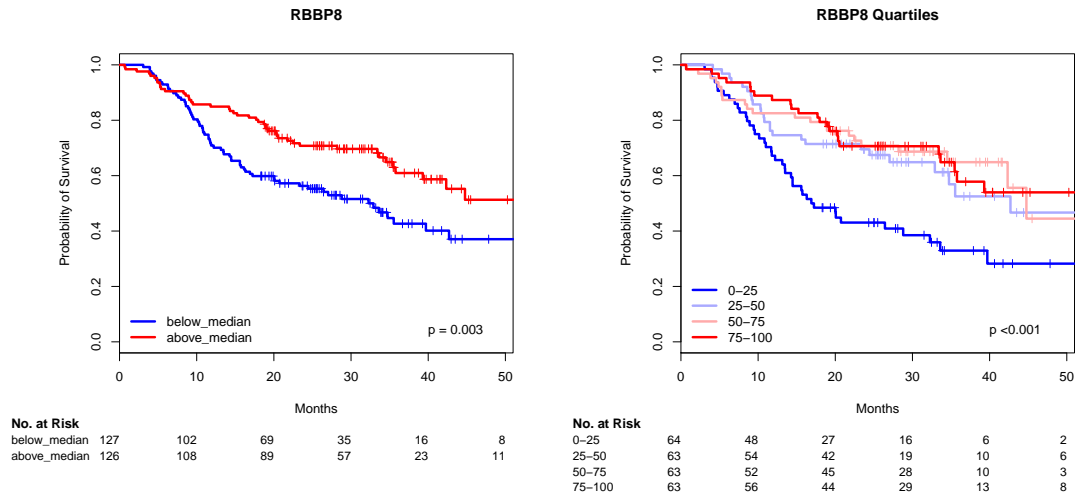
Tabelle 7: Cox regression model, $n = 253$, number of events = 117. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.32	0.72	[0.46, 1.15]	0.17
split50-75	-0.72	0.49	[0.29, 0.81]	0.0057
split75-100	-1.16	0.31	[0.18, 0.55]	< 0.0001

Tabelle 8: Cox regression model, $n = 253$, number of events = 117. Model for the figure on the right. Patients split into quartiles

1.2.4 RBBP8 ILMN_2363621

Gene symbol from a different, less reliable annotation table: RBBP8



	coef	HR = exp(coef)	95% CI	p-value
splitabove_medial	-0.56	0.57	[0.40, 0.83]	0.0034

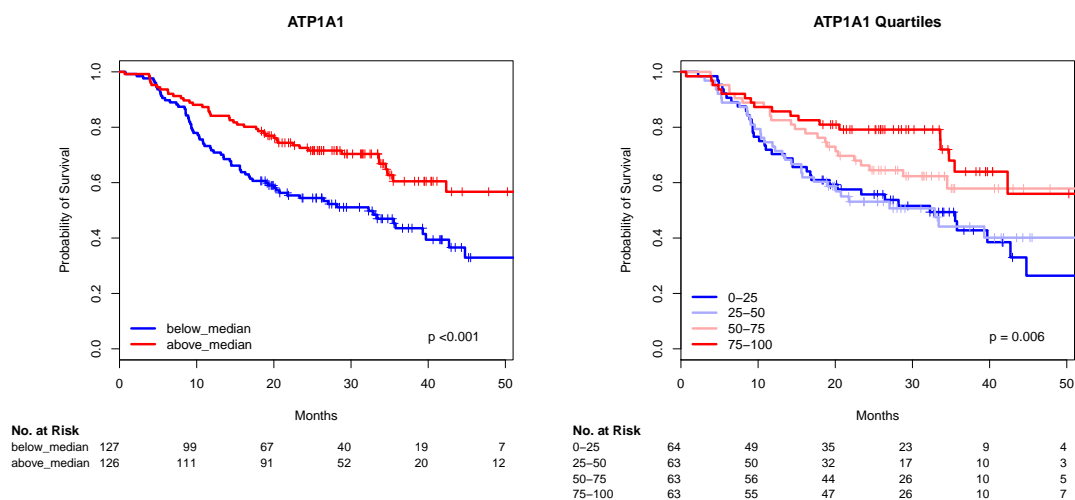
Tabelle 9: Cox regression model, $n = 253$, number of events = 117. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.68	0.51	[0.31, 0.83]	0.0063
split50-75	-0.90	0.41	[0.24, 0.68]	0.00064
split75-100	-0.86	0.42	[0.26, 0.70]	0.00072

Tabelle 10: Cox regression model, $n = 253$, number of events = 117. Model for the figure on the right. Patients split into quartiles

1.2.5 ATP1A1 ILMN_2415189

Gene symbol from a different, less reliable annotation table: ATP1A1



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.64	0.53	[0.36, 0.77]	0.00092

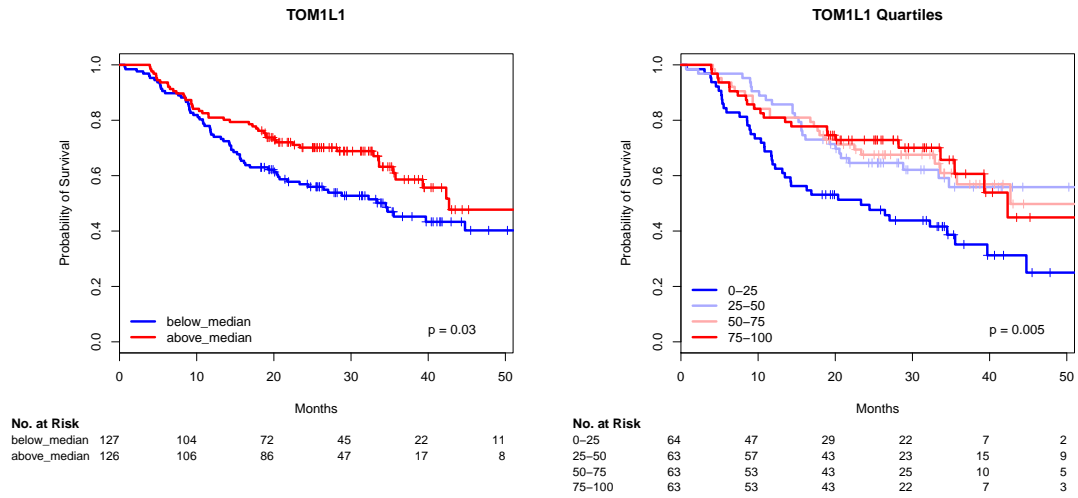
Tabelle 11: Cox regression model, $n = 253$, number of events = 117. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.07	0.93	[0.58, 1.48]	0.75
split50-75	-0.51	0.60	[0.36, 1.00]	0.05
split75-100	-0.85	0.43	[0.25, 0.74]	0.0025

Tabelle 12: Cox regression model, $n = 253$, number of events = 117. Model for the figure on the right. Patients split into quartiles

1.2.6 TOM1L1 ILMN_1802642

Gene symbol from a different, less reliable annotation table: TOM1L1



	coef	HR = exp(coef)	95% CI	p-value
splitabove_medial	-0.40	0.67	[0.46, 0.97]	0.03

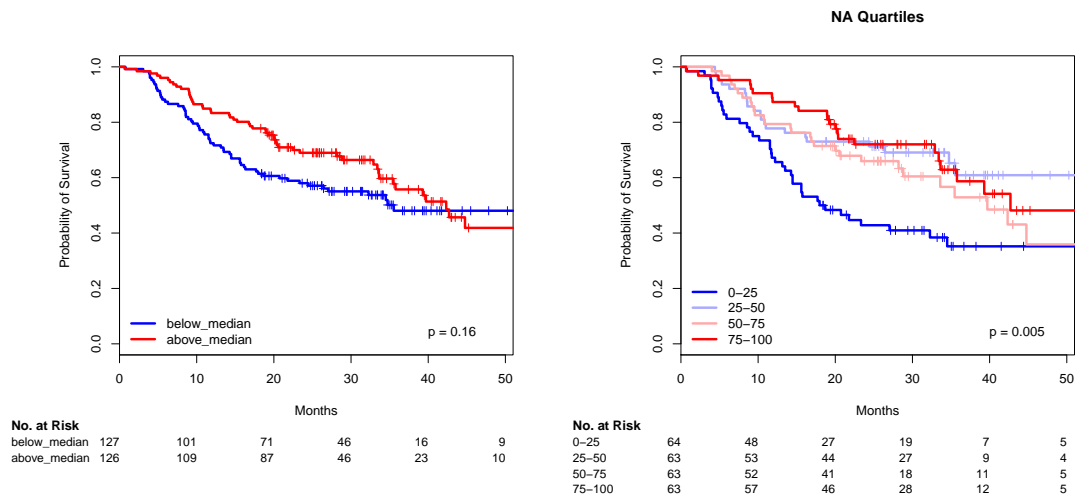
Tabelle 13: Cox regression model, $n = 253$, number of events = 117. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.64	0.53	[0.32, 0.86]	0.01
split50-75	-0.74	0.48	[0.29, 0.79]	0.0041
split75-100	-0.68	0.51	[0.31, 0.84]	0.0087

Tabelle 14: Cox regression model, $n = 253$, number of events = 117. Model for the figure on the right. Patients split into quartiles

1.2.7 NA ILMN_1738554

Gene symbol from a different, less reliable annotation table: LOC647346



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.26	0.77	[0.53, 1.11]	0.16

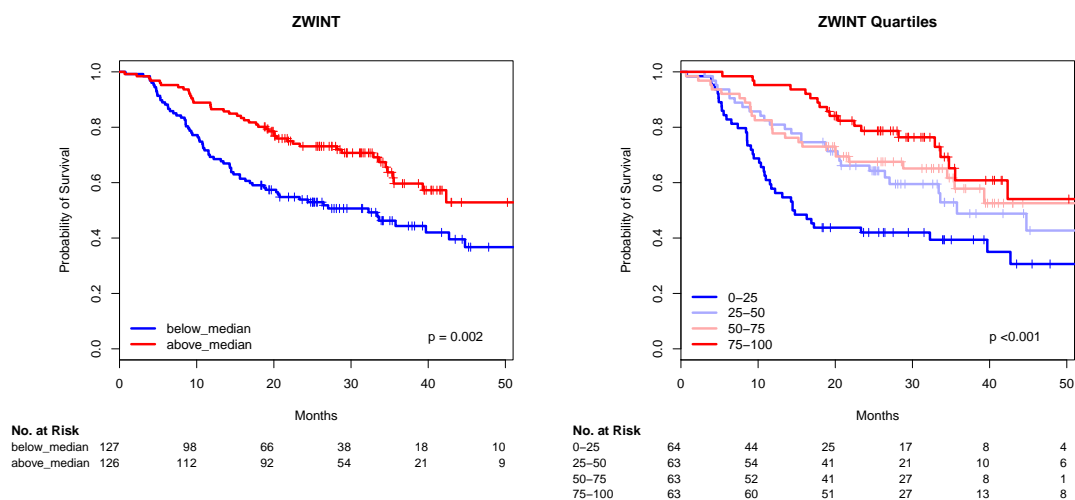
Tabelle 15: Cox regression model, $n = 253$, number of events = 117. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.78	0.46	[0.27, 0.78]	0.0035
split50-75	-0.48	0.62	[0.39, 1.00]	0.05
split75-100	-0.75	0.47	[0.28, 0.78]	0.0038

Tabelle 16: Cox regression model, $n = 253$, number of events = 117. Model for the figure on the right. Patients split into quartiles

1.2.8 ZWINT ILMN_2362545

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



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.59	0.55	[0.38, 0.80]	0.002

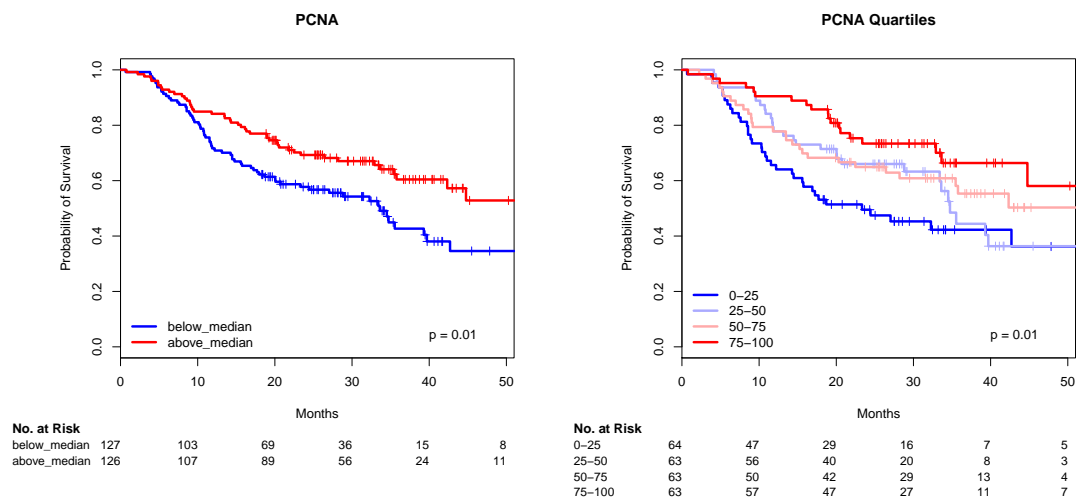
Tabelle 17: Cox regression model, $n = 253$, number of events = 117. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.56	0.57	[0.35, 0.92]	0.02
split50-75	-0.66	0.52	[0.31, 0.85]	0.0095
split75-100	-1.07	0.34	[0.20, 0.58]	< 0.0001

Tabelle 18: Cox regression model, $n = 253$, number of events = 117. Model for the figure on the right. Patients split into quartiles

1.2.9 PCNA ILMN_1694177

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



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.49	0.62	[0.42, 0.89]	0.01

Tabelle 19: Cox regression model, $n = 253$, number of events = 117. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.35	0.70	[0.44, 1.14]	0.15
split50-75	-0.47	0.62	[0.38, 1.02]	0.06
split75-100	-0.87	0.42	[0.24, 0.72]	0.0017

Tabelle 20: Cox regression model, $n = 253$, number of events = 117. Model for the figure on the right. Patients split into quartiles