

LIFE-HNG. Genes whose expression is associated with survival in HPV-neg patients. Progression-free survival

Inhaltsverzeichnis

1	Results of the Significance Analysis for Microarrays (SAM; Tusher, Tibs-	1
	hirani and Chu (2001))	
1.1	Higher expression = poorer survival	3
1.2	Higher expression = better survival	3
1.2.1	CDH1 ILMN_1770940	5
1.2.2	FAM89A ILMN_2285817	6
1.2.3	FUT2 ILMN_1794659	7
1.2.4	ATP1A1 ILMN_1775566	8
1.2.5	DSC3 ILMN_1765363	9
1.2.6	ATP1B3 ILMN_1654322	10
1.2.7	FAM89A ILMN_1652677	11
1.2.8	BRD7 ILMN_1696420	12
1.2.9	MAPK6 ILMN_1757287	13
1.2.10	DSC3 ILMN_2359159	14
1.2.11	DST ILMN_1703913	15
1.2.12	NA ILMN_1699253	16

Included are primary tumors.

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

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

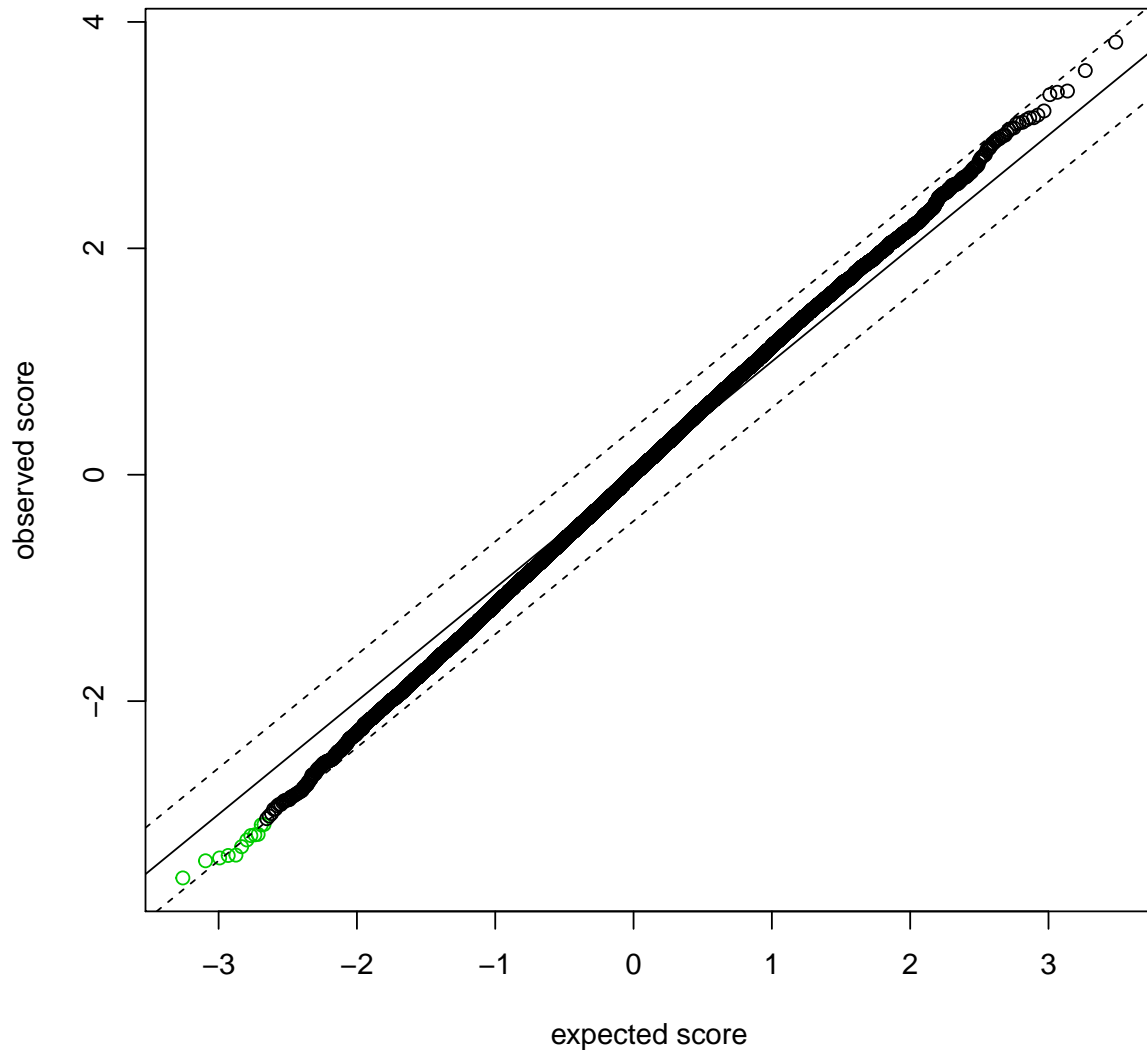
Number of analyzed patients:

```
## [1] 179
```

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
```

```
## NULL
```

```
##
```

```
## $genes.lo
```

```
##      Row      Gene ID  Gene Name      Score(d)
##  [1,] "4188"  "CDH1"    "ILMN_1770940" "-3.56199678510814"
##  [2,] "7542"  "FAM89A"  "ILMN_2285817" "-3.41043905410131"
##  [3,] "8409"  "FUT2"    "ILMN_1794659" "-3.3853905200457"
##  [4,] "1502"  "ATP1A1"  "ILMN_1775566" "-3.36376183042406"
##  [5,] "6370"  "DSC3"    "ILMN_1765363" "-3.36016129932756"
```

```

## [6,] "1510" "ATP1B3" "ILMN_1654322" "-3.28601468230565"
## [7,] "7540" "FAM89A" "ILMN_1652677" "-3.2265142343366"
## [8,] "2042" "BRD7" "ILMN_1696420" "-3.18736519522593"
## [9,] "19587" "MAPK6" "ILMN_1757287" "-3.18102199700609"
## [10,] "6371" "DSC3" "ILMN_2359159" "-3.17737052542725"
## [11,] "6395" "DST" "ILMN_1703913" "-3.09367041581074"
## [12,] "18667" NA "ILMN_1699253" "-3.08996346278443"
##      Numerator(r)      Denominator(s+s0)  q-value(%)
## [1,] "-18.6530934228822" "5.23669574909959" "0"
## [2,] "-20.4565058548892" "5.99820302617305" "0"
## [3,] "-15.5919021295101" "4.60564358445112" "0"
## [4,] "-15.6261032848486" "4.64542499516938" "0"
## [5,] "-25.7853080903185" "7.67383044840099" "0"
## [6,] "-19.8095891960781" "6.028454255773" "0"
## [7,] "-16.1919687957427" "5.01840922424193" "8.81583147143313"
## [8,] "-9.98734985745462" "3.13341874737598" "8.81583147143313"
## [9,] "-17.5019167902231" "5.50197917735104" "8.81583147143313"
## [10,] "-18.8365848268279" "5.92835638024778" "8.81583147143313"
## [11,] "-23.187494957806" "7.49514067151505" "8.81583147143313"
## [12,] "-10.3191802176661" "3.33958001185143" "8.81583147143313"
##
## $color.ind.for.multi
## NULL
##
## $ngenes.up
## [1] 0
##
## $ngenes.lo
## [1] 12

```

1.1 Higher expression = poorer survival

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

```

## Error: Länge von 'dimnames' [1] ungleich der Arrayausdehnung
## Error: increasing 'x' and 'y' values expected

```

no significant genes

1.2 Higher expression = better survival

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

NA_ILMN_1699253	0.45	0.36	0.35	0.42	0.54	0.51	0.37	0.35	0.53	0.51	0.32	1
DST_ILMN_1703913	0.25	0.35	0.13	0.37	0.49	0.39	0.35	0.23	0.49	0.45	1	0.32
DSC3_ILMN_2359159	0.57	0.5	0.4	0.49	0.96	0.62	0.51	0.33	0.65	1	0.45	0.51
MAPK6_ILMN_1757287	0.53	0.6	0.4	0.4	0.69	0.68	0.59	0.44	1	0.65	0.49	0.53
BRD7_ILMN_1696420	0.57	0.33	0.22	0.34	0.35	0.44	0.32	1	0.44	0.33	0.23	0.35
FAM89A_ILMN_1652677	0.38	0.98	0.3	0.38	0.53	0.57	1	0.32	0.59	0.51	0.35	0.37
ATP1B3_ILMN_1654322	0.47	0.56	0.28	0.56	0.65	1	0.57	0.44	0.68	0.62	0.39	0.51
DSC3_ILMN_1765363	0.61	0.52	0.42	0.5	1	0.65	0.53	0.35	0.69	0.96	0.49	0.54
ATP1A1_ILMN_1775566	0.4	0.38	0.22	1	0.5	0.56	0.38	0.34	0.4	0.49	0.37	0.42
FUT2_ILMN_1794659	0.51	0.3	1	0.22	0.42	0.28	0.3	0.22	0.4	0.4	0.13	0.35
FAM89A_ILMN_2285817	0.39	1	0.3	0.38	0.52	0.56	0.98	0.33	0.6	0.5	0.35	0.36
CDH1_ILMN_1770940	1	0.39	0.51	0.4	0.61	0.47	0.38	0.57	0.53	0.57	0.25	0.45

CDH1_ILMN_1770940

FAM89A_ILMN_2285817

FUT2_ILMN_1794659

ATP1A1_ILMN_1775566

DSC3_ILMN_1765363

ATP1B3_ILMN_1654322

FAM89A_ILMN_1652677

BRD7_ILMN_1696420

MAPK6_ILMN_1757287

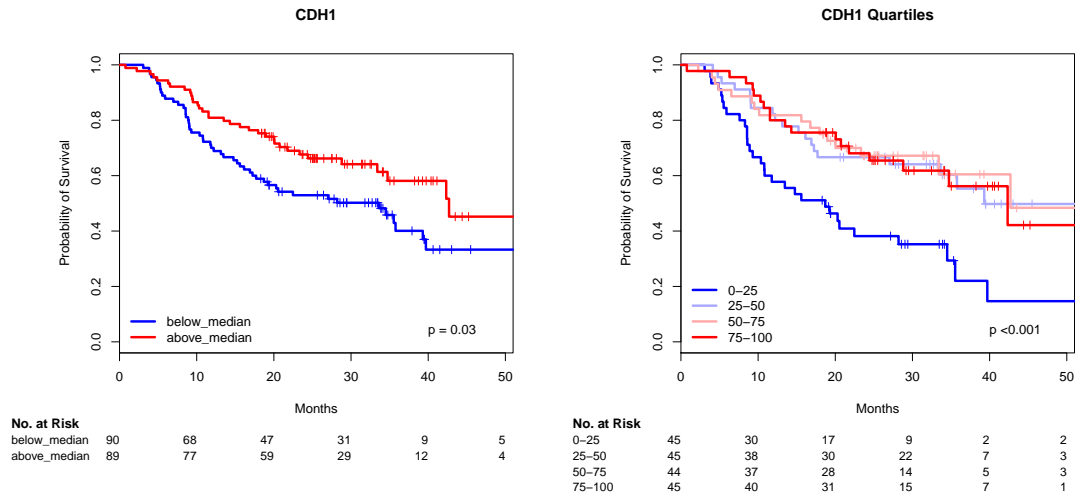
DSC3_ILMN_2359159

DST_ILMN_1703913

NA_ILMN_1699253

1.2.1 CDH1 ILMN_1770940

Gene symbol from a different, less reliable annotation table: CDH1



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.47	0.62	[0.41, 0.96]	0.03

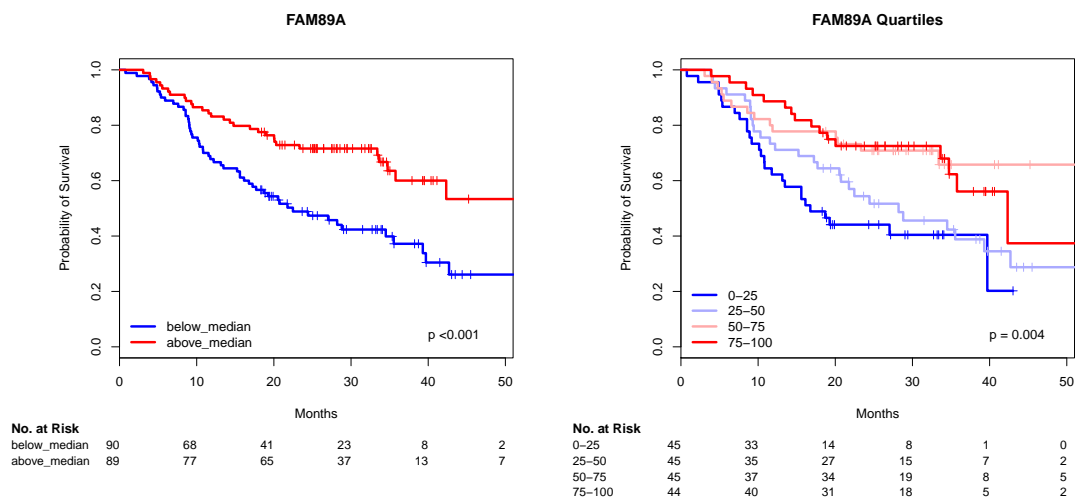
Tabelle 1: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.88	0.41	[0.23, 0.73]	0.0025
split50-75	-0.96	0.38	[0.21, 0.70]	0.0017
split75-100	-0.83	0.44	[0.25, 0.77]	0.0043

Tabelle 2: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the right. Patients split into quartiles

1.2.2 FAM89A ILMN_2285817

Gene symbol from a different, less reliable annotation table: FAM89A



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.74	0.48	[0.31, 0.74]	0.00093

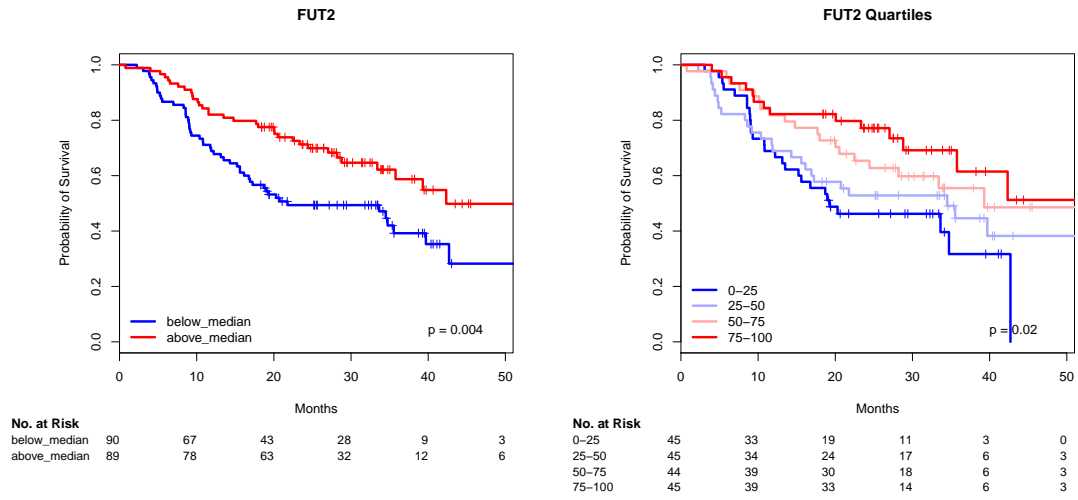
Tabelle 3: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.34	0.71	[0.42, 1.23]	0.22
split50-75	-0.94	0.39	[0.21, 0.73]	0.0032
split75-100	-0.91	0.40	[0.22, 0.75]	0.0041

Tabelle 4: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the right. Patients split into quartiles

1.2.3 FUT2 ILMN_1794659

Gene symbol from a different, less reliable annotation table: FUT2



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.63	0.53	[0.34, 0.82]	0.0044

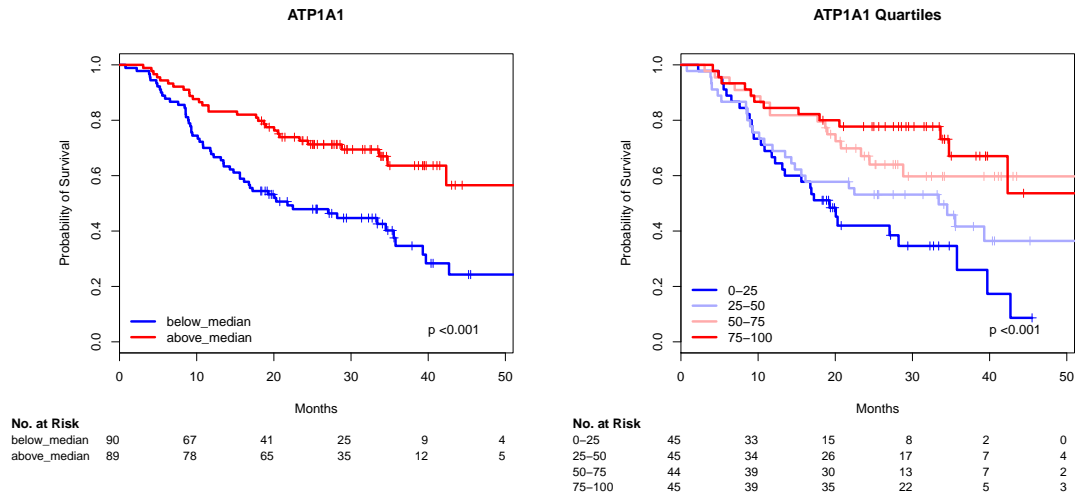
Tabelle 5: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.24	0.79	[0.45, 1.37]	0.40
split50-75	-0.57	0.57	[0.32, 1.02]	0.06
split75-100	-0.97	0.38	[0.20, 0.72]	0.0033

Tabelle 6: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the right. Patients split into quartiles

1.2.4 ATP1A1 ILMN_1775566

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



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.83	0.44	[0.28, 0.68]	0.00025

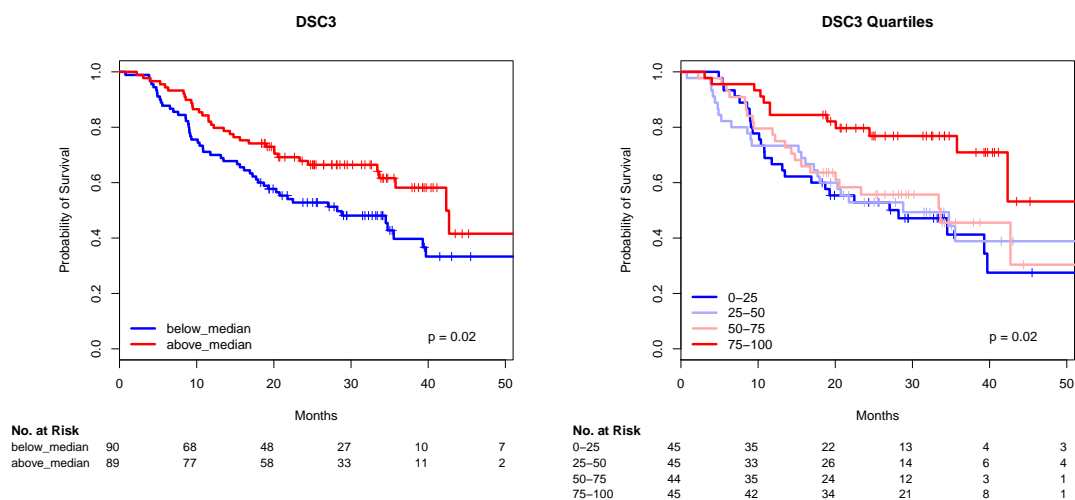
Tabelle 7: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.39	0.67	[0.40, 1.15]	0.15
split50-75	-0.86	0.43	[0.23, 0.77]	0.0051
split75-100	-1.23	0.29	[0.15, 0.56]	0.00024

Tabelle 8: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the right. Patients split into quartiles

1.2.5 DSC3 ILMN_1765363

Gene symbol from a different, less reliable annotation table: DSC3



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.51	0.60	[0.39, 0.93]	0.02

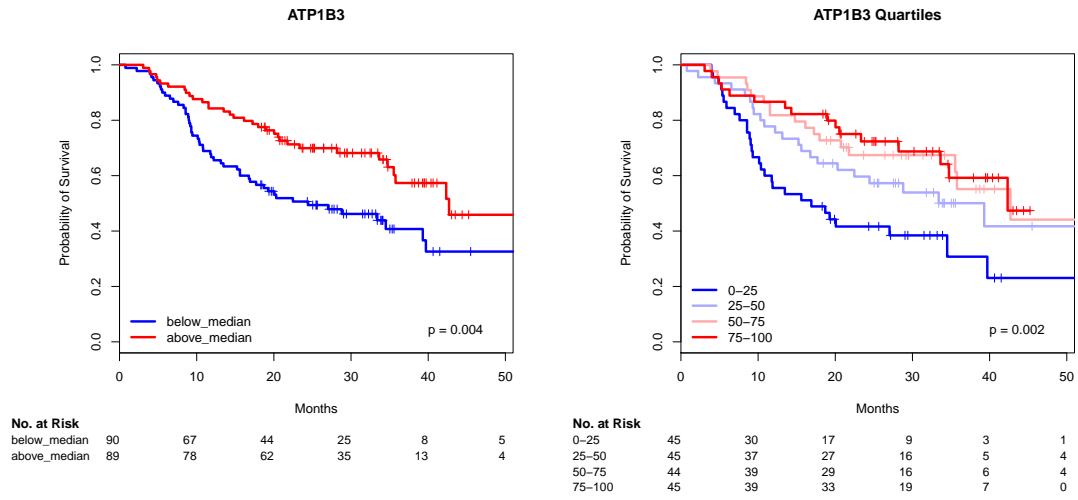
Tabelle 9: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.08	0.92	[0.53, 1.59]	0.76
split50-75	-0.16	0.85	[0.48, 1.49]	0.57
split75-100	-1.01	0.36	[0.18, 0.72]	0.0038

Tabelle 10: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the right. Patients split into quartiles

1.2.6 ATP1B3 ILMN_1654322

Gene symbol from a different, less reliable annotation table: ATP1B3



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.63	0.53	[0.35, 0.82]	0.0046

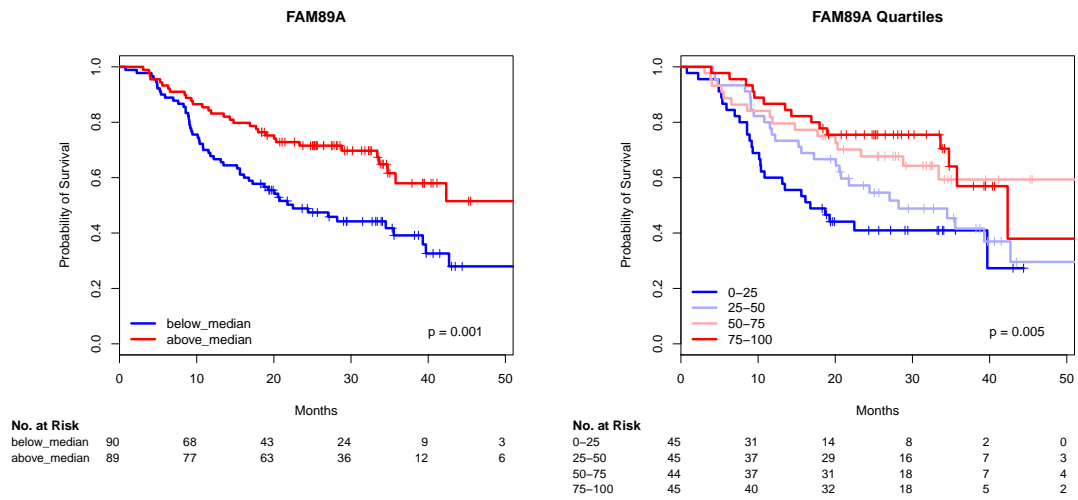
Tabelle 11: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.59	0.55	[0.32, 0.96]	0.04
split50-75	-0.86	0.42	[0.23, 0.76]	0.0041
split75-100	-0.99	0.37	[0.20, 0.68]	0.0015

Tabelle 12: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the right. Patients split into quartiles

1.2.7 FAM89A ILMN_1652677

Gene symbol from a different, less reliable annotation table: FAM89A



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.71	0.49	[0.32, 0.76]	0.0015

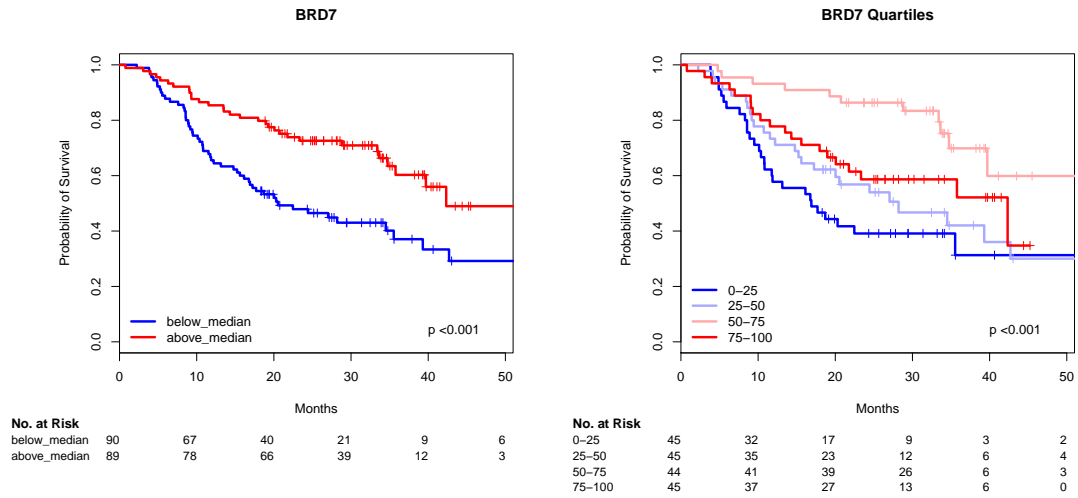
Tabelle 13: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.36	0.70	[0.41, 1.20]	0.19
split50-75	-0.84	0.43	[0.23, 0.80]	0.0075
split75-100	-0.99	0.37	[0.20, 0.70]	0.0023

Tabelle 14: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the right. Patients split into quartiles

1.2.8 BRD7 ILMN_1696420

Gene symbol from a different, less reliable annotation table: BRD7



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.74	0.48	[0.31, 0.74]	0.00092

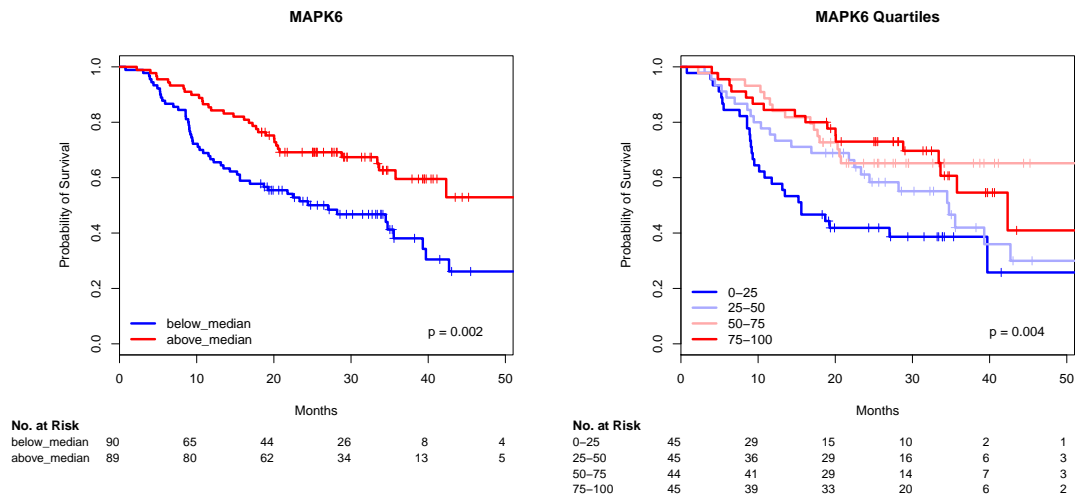
Tabelle 15: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.35	0.71	[0.41, 1.21]	0.21
split50-75	-1.32	0.27	[0.14, 0.53]	0.00014
split75-100	-0.58	0.56	[0.32, 1.00]	0.05

Tabelle 16: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the right. Patients split into quartiles

1.2.9 MAPK6 ILMN_1757287

Gene symbol from a different, less reliable annotation table: MAPK6



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.68	0.51	[0.33, 0.79]	0.0024

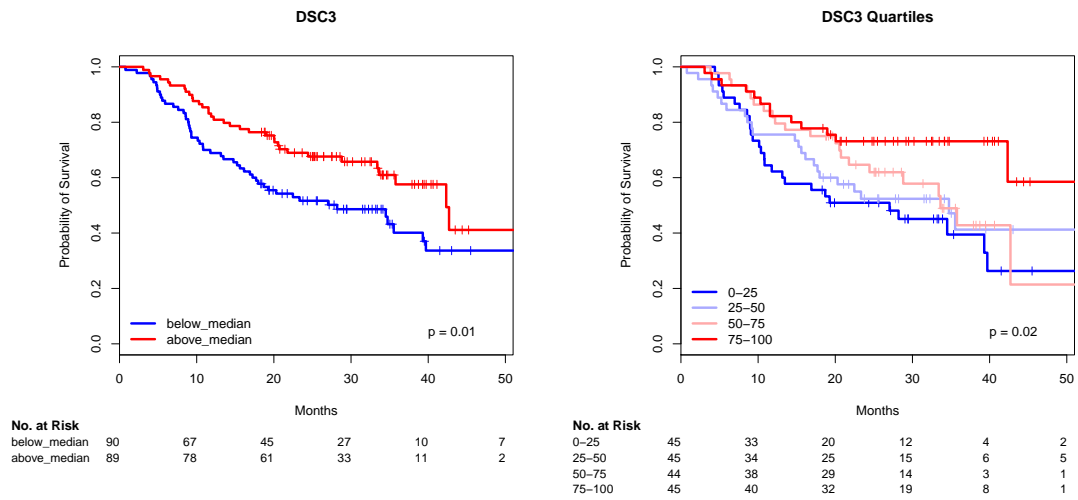
Tabelle 17: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.47	0.63	[0.36, 1.08]	0.09
split50-75	-1.00	0.37	[0.20, 0.69]	0.0019
split75-100	-0.85	0.43	[0.23, 0.77]	0.005

Tabelle 18: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the right. Patients split into quartiles

1.2.10 DSC3 ILMN_2359159

Gene symbol from a different, less reliable annotation table: DSC3



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.54	0.58	[0.38, 0.90]	0.02

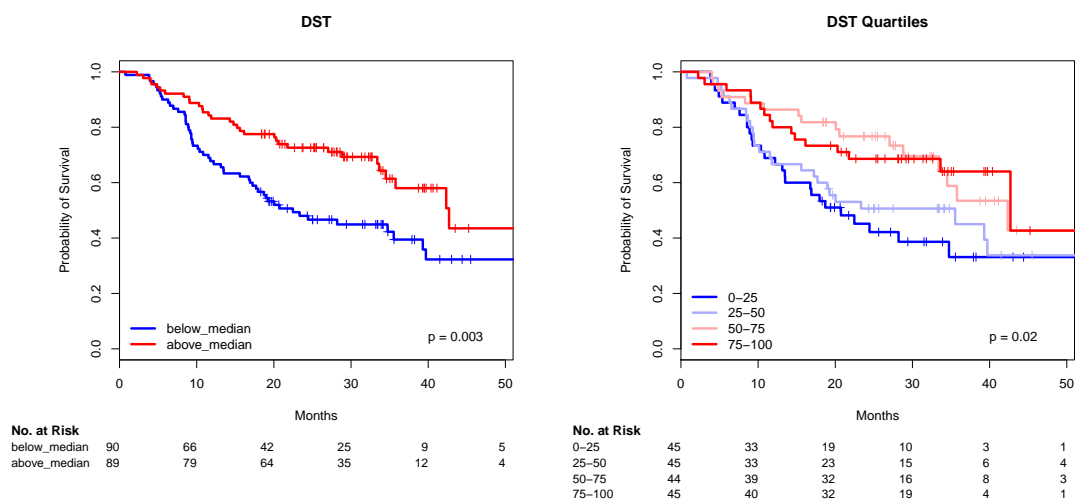
Tabelle 19: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.27	0.76	[0.44, 1.32]	0.33
split50-75	-0.41	0.67	[0.38, 1.18]	0.16
split75-100	-0.99	0.37	[0.19, 0.72]	0.0032

Tabelle 20: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the right. Patients split into quartiles

1.2.11 DST ILMN_1703913

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



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.65	0.52	[0.34, 0.81]	0.0036

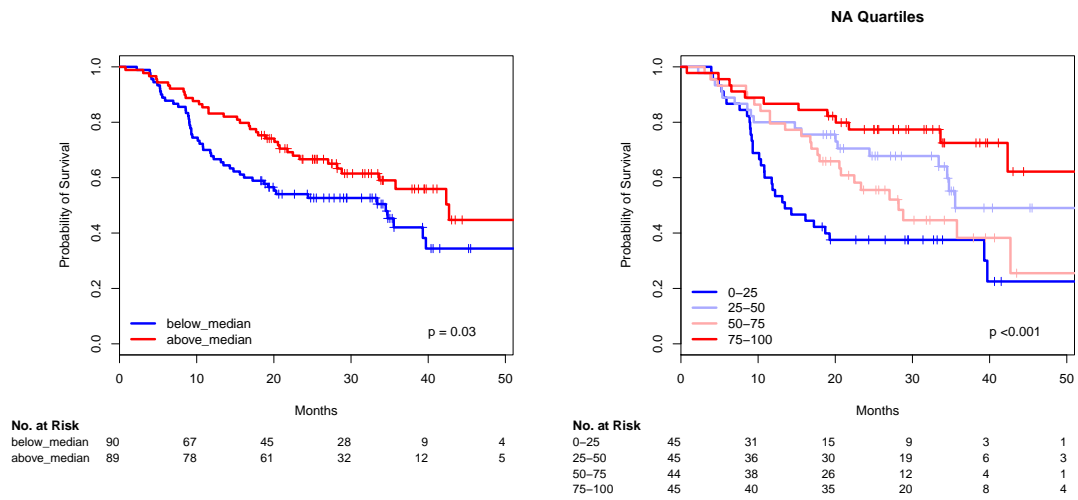
Tabelle 21: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.20	0.82	[0.48, 1.41]	0.47
split50-75	-0.75	0.47	[0.26, 0.87]	0.02
split75-100	-0.75	0.47	[0.25, 0.88]	0.02

Tabelle 22: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the right. Patients split into quartiles

1.2.12 NA ILMN_1699253

Gene symbol from a different, less reliable annotation table: LOC729317



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.49	0.62	[0.40, 0.95]	0.03

Tabelle 23: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.83	0.44	[0.24, 0.77]	0.0047
split50-75	-0.48	0.62	[0.36, 1.06]	0.08
split75-100	-1.41	0.24	[0.13, 0.48]	< 0.0001

Tabelle 24: Cox regression model, $n = 179$, number of events = 86. Model for the figure on the right. Patients split into quartiles