

# LIFE-HNG. Genes whose expression is associated with survival in HPV-neg patients. Overall survival

## Inhaltsverzeichnis

<b>1</b>	<b>Results of the Significance Analysis for Microarrays (SAM; Tusher, Tibshirani and Chu (2001))</b>	<b>1</b>
1.1	Higher expression = poorer survival . . . . .	4
1.1.1	ANGPT2 ILMN_1774207 . . . . .	6
1.1.2	ANGPT2 ILMN_3250067 . . . . .	7
1.1.3	ESM1 ILMN_1773262 . . . . .	8
1.1.4	CARS ILMN_2367469 . . . . .	9
1.1.5	ESM1 ILMN_2212878 . . . . .	10
1.1.6	TMEM200A ILMN_1725387 . . . . .	11
1.1.7	LINC00152 ILMN_2143795 . . . . .	12
1.1.8	NA ILMN_1906423 . . . . .	13
1.1.9	TAGLN ILMN_1778668 . . . . .	14
1.1.10	COL4A1 ILMN_1653028 . . . . .	15
1.1.11	COL4A2 ILMN_1724994 . . . . .	16
1.1.12	SDSL ILMN_1750674 . . . . .	17
1.1.13	PEA15 ILMN_1771376 . . . . .	18
1.1.14	TNFAIP6 ILMN_1785732 . . . . .	19
1.1.15	DENND5A ILMN_3245413 . . . . .	20
1.1.16	DENND5A ILMN_1785356 . . . . .	21
1.1.17	NA ILMN_1677402 . . . . .	22
1.1.18	IGFBP7 ILMN_2062468 . . . . .	23
1.1.19	SUSD2 ILMN_1693270 . . . . .	24
1.1.20	TAGLN ILMN_2400935 . . . . .	25
1.2	Higher expression = better survival . . . . .	25
1.2.1	ABLIM1 ILMN_2396672 . . . . .	27
1.2.2	ABLIM1 ILMN_1785424 . . . . .	28
1.2.3	GSTA4 ILMN_1771964 . . . . .	29
1.2.4	CDH1 ILMN_1770940 . . . . .	30
1.2.5	BNIP1 ILMN_1699989 . . . . .	31
1.2.6	CIDEB ILMN_1668910 . . . . .	32
1.2.7	TACC2 ILMN_2315780 . . . . .	33
1.2.8	GLTP ILMN_1764380 . . . . .	34
1.2.9	RAB25 ILMN_1791826 . . . . .	35
1.2.10	CDS1 ILMN_1801476 . . . . .	36
1.2.11	C10orf99 ILMN_1802192 . . . . .	37

Included are primary tumors.

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

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

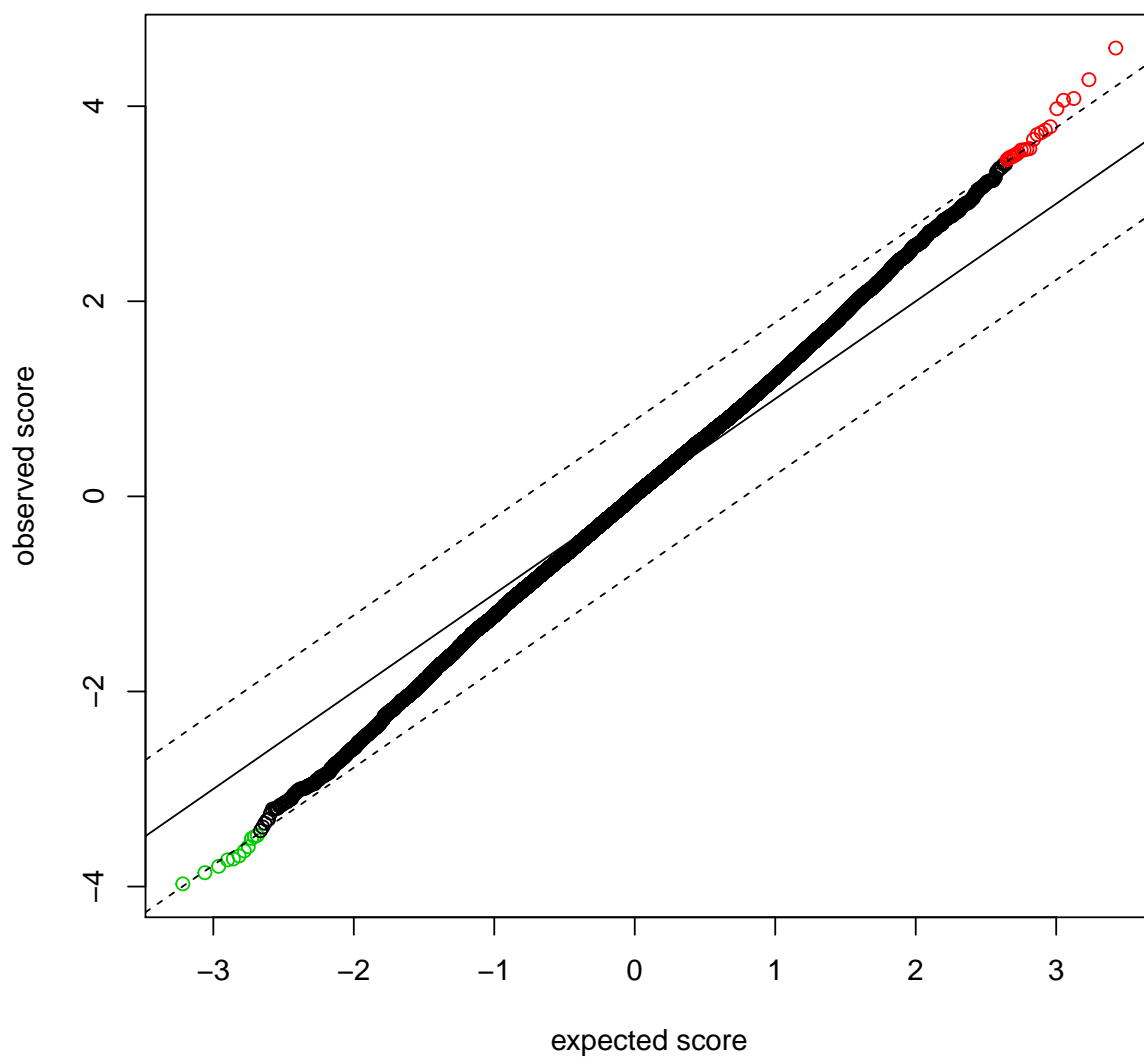
Number of analyzed patients:

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

False discovery rate (FDR) threshold:

```
## [1] 0.01
```

## 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)
## [1,] "801"    "ANGPT2"    "ILMN_1774207"  "4.59602259850781"
## [2,] "799"    "ANGPT2"    "ILMN_3250067"  "4.27198482581957"
## [3,] "7033"   "ESM1"     "ILMN_1773262"  "4.07882341961105"
## [4,] "3603"   "CARS"     "ILMN_2367469"  "4.06047207852355"
## [5,] "7032"   "ESM1"     "ILMN_2212878"  "3.97395600035549"
## [6,] "28592"  "TMEM200A" "ILMN_1725387"  "3.789541038037"
## [7,] "20036"  "LINC00152" "ILMN_2143795"  "3.7556477183385"
## [8,] "10614"  NA         "ILMN_1906423"  "3.72984815433105"
## [9,] "27867"  "TAGLN"    "ILMN_1778668"  "3.71012685499141"
## [10,] "4914"  "COL4A1"   "ILMN_1653028"  "3.66007683001535"
## [11,] "4915"  "COL4A2"   "ILMN_1724994"  "3.56560701118908"
## [12,] "25697" "SDSL"     "ILMN_1750674"  "3.55907855562277"
```

```

## [13,] "22575" "PEA15" "ILMN_1771376" "3.55248191214064"
## [14,] "28763" "TNFAIP6" "ILMN_1785732" "3.55046617498477"
## [15,] "5884" "DENND5A" "ILMN_3245413" "3.52106821461104"
## [16,] "5885" "DENND5A" "ILMN_1785356" "3.5055883560348"
## [17,] "15541" NA "ILMN_1677402" "3.4966387443647"
## [18,] "12466" "IGFBP7" "ILMN_2062468" "3.48088717368527"
## [19,] "27704" "SUSD2" "ILMN_1693270" "3.47890923401265"
## [20,] "27868" "TAGLN" "ILMN_2400935" "3.46579709548066"
## [21,] "1666" "AXL" "ILMN_1701877" "3.45218850079406"
##      Numerator(r)      Denominator(s+s0)      q-value(%)
## [1,] "16.9019855305525" "3.6775244612679" "0"
## [2,] "14.7410845365058" "3.45064065944516" "0"
## [3,] "11.9850843167907" "2.93836802524136" "0"
## [4,] "12.930699007097" "3.18453095035166" "0"
## [5,] "12.4785829705465" "3.14009087403842" "0"
## [6,] "12.3183044676079" "3.25060590292192" "0"
## [7,] "15.9845603429625" "4.25613943099915" "0"
## [8,] "7.56149295590071" "2.0272924373933" "0"
## [9,] "23.6892604804749" "6.38502709108306" "0"
## [10,] "20.855747642981" "5.69817209080104" "0"
## [11,] "14.8337162942867" "4.16022187743563" "0"
## [12,] "10.4044077609972" "2.92334310647904" "0"
## [13,] "10.3041211743523" "2.90054148879347" "0"
## [14,] "21.2005302010851" "5.97119621937422" "0"
## [15,] "9.52117613680153" "2.70405898337681" "0"
## [16,] "11.5848487850284" "3.30468030140655" "0"
## [17,] "22.5508005450398" "6.4492794920217" "0"
## [18,] "19.7309644185797" "5.6683722953566" "0"
## [19,] "13.524917086397" "3.88768897853569" "0"
## [20,] "15.1854029629325" "4.38150374779122" "0"
## [21,] "14.4999475146121" "4.2002189368503" "0"
##
## $genes.lo
##      Row      Gene ID      Gene Name      Score(d)
## [1,] "148" "ABLIM1" "ILMN_2396672" "-3.97231436495946"
## [2,] "145" "ABLIM1" "ILMN_1785424" "-3.85792890149952"
## [3,] "9266" "GSTA4" "ILMN_1771964" "-3.79269403189259"
## [4,] "4188" "CDH1" "ILMN_1770940" "-3.72633717974112"
## [5,] "2002" "BNIPL" "ILMN_1699989" "-3.71679811099004"
## [6,] "4563" "CIDEB" "ILMN_1668910" "-3.68567840434606"
## [7,] "27811" "TACC2" "ILMN_2315780" "-3.63493461977242"
## [8,] "8852" "GLTP" "ILMN_1764380" "-3.59078382710775"
## [9,] "24184" "RAB25" "ILMN_1791826" "-3.50699699046813"
## [10,] "4273" "CDS1" "ILMN_1801476" "-3.48956711731648"
## [11,] "2229" "C10orf99" "ILMN_1802192" "-3.47592499260657"
##      Numerator(r)      Denominator(s+s0)      q-value(%)
## [1,] "-21.8893169008652" "5.51046943664756" "0"
## [2,] "-21.7143312639307" "5.62849441198635" "0"

```

```
## [3,] "-26.0575442587029" "6.87045779058006" "0"
## [4,] "-17.3641077521199" "4.65983267604523" "0"
## [5,] "-27.2742438501424" "7.33810205334974" "0"
## [6,] "-9.8840115325302" "2.68173466270829" "0"
## [7,] "-16.4996903338616" "4.53919865411351" "0"
## [8,] "-19.4582286932509" "5.41893626298407" "0"
## [9,] "-20.6032355233028" "5.87489398459751" "0"
## [10,] "-14.1372018825714" "4.05127667910943" "0"
## [11,] "-35.2250456867382" "10.1340062750673" "0"
##
## $color.ind.for.multi
## NULL
##
## $ngenes.up
## [1] 21
##
## $ngenes.lo
## [1] 11
```

## 1.1 Higher expression = poorer survival

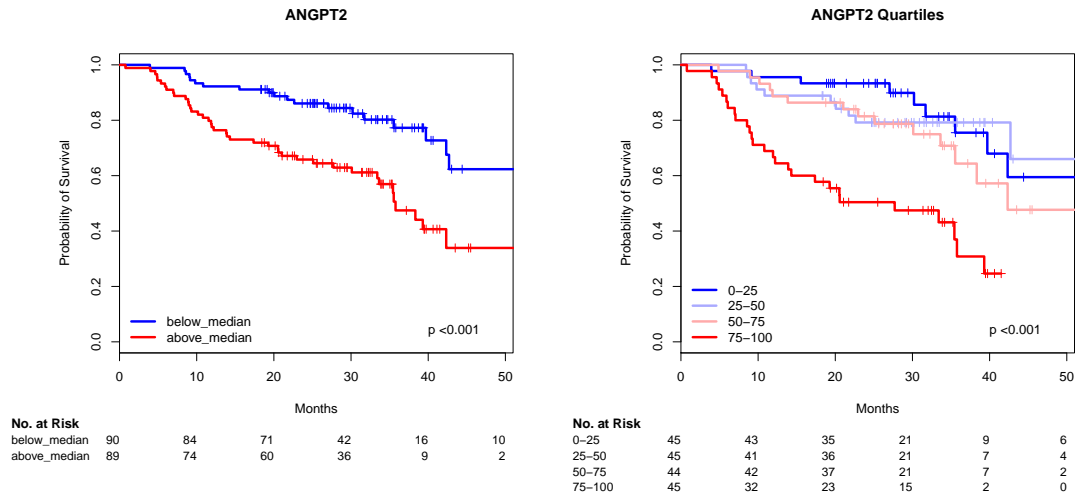
Correlation matrix of the genes whose higher expression is associated with poorer survival:

AXL_ILMN_1701877	0.260.28	0.2	0.350.18	0.4	0.61	0.5	0.550.360.440.62	0.5	0.51	0.3	0.320.420.470.460.49	1
TAGLN_ILMN_2400935	0.350.330.280.190.250.360.52	0.3	0.9	0.560.590.310.480.650.450.680.650.51	1	0.49						
SUSD2_ILMN_1693270	0.270.260.180.280.130.25	0.4	0.4	0.570.340.370.370.420.430.350.390.460.45	1	0.510.46						
IGFBP7_ILMN_2062468	0.6	0.550.440.110.470.440.420.270.620.690.660.220.380.630.510.540.67	1	0.450.650.47								
NA_ILMN_1677402	0.5	0.470.340.110.330.330.550.350.670.620.610.220.47	0.7	0.450.46	1	0.670.460.680.42						
DENND5A_ILMN_1785356	0.320.290.260.310.250.460.270.330.42	0.4	0.39	0.2	0.270.480.95	1	0.460.540.390.450.32					
DENND5A_ILMN_3245413	0.34	0.3	0.280.320.270.430.27	0.3	0.390.420.420.190.250.46	1	0.950.450.510.350.45	0.3				
TNFAIP6_ILMN_1785732	0.5	0.490.480.250.430.330.570.460.610.74	0.7	0.320.45	1	0.460.48	0.7	0.630.430.650.51				
PEA15_ILMN_1771376	0.180.170.090.210.060.330.430.460.520.270.320.45	1	0.450.250.270.470.380.420.48	0.5								
SDSL_ILMN_1750674	0.050.060.010.330.020.230.410.470.380.110.13	1	0.450.320.19	0.2	0.220.220.370.310.62							
COL4A2_ILMN_1724994	0.64	0.6	0.540.180.560.310.470.230.53	0.9	1	0.130.32	0.7	0.420.390.610.660.370.590.44				
COL4A1_ILMN_1653028	0.690.690.620.120.620.280.450.190.52	1	0.9	0.110.270.740.42	0.4	0.620.690.340.560.36						
TAGLN_ILMN_1778668	0.3	0.320.260.24	0.2	0.360.570.36	1	0.520.530.380.520.610.390.420.670.620.57	0.9	0.55				
NA_ILMN_1906423	0.260.240.14	0.40.070.37	0.5	1	0.360.190.230.470.460.46	0.3	0.330.350.27	0.4	0.3	0.5		
LINC00152_ILMN_2143795	0.370.390.270.260.240.24	1	0.5	0.570.450.470.410.430.570.270.270.550.42	0.4	0.520.61						
TMEM200A_ILMN_1725387	0.230.230.180.270.19	1	0.240.370.360.280.310.230.330.330.430.460.330.440.250.36	0.4								
ESM1_ILMN_2212878	0.720.690.930.11	1	0.190.240.0730.2	0.620.560.020.060.430.270.250.330.470.130.250.18								
CARS_ILMN_2367469	0.260.240.15	1	0.110.270.26	0.4	0.240.120.180.330.210.250.320.310.110.110.280.190.35							
ESM1_ILMN_1773262	0.680.68	1	0.150.930.180.270.140.260.620.540.010.090.480.280.260.340.440.180.28	0.2								
ANGPT2_ILMN_3250067	0.93	1	0.680.240.690.230.390.240.320.69	0.60.060.170.49	0.3	0.290.470.550.260.330.28						
ANGPT2_ILMN_1774207	1	0.930.680.260.720.230.370.26	0.3	0.690.640.050.18	0.5	0.340.32	0.5	0.6	0.270.350.26			

ANGPT2\_ILMN\_1774207  
 ANGPT2\_ILMN\_3250067  
 ESM1\_ILMN\_1773262  
 CARS\_ILMN\_2367469  
 ESM1\_ILMN\_2212878  
 TMEM200A\_ILMN\_1725387  
 LINC00152\_ILMN\_2143795  
 NA\_ILMN\_1906423  
 TAGLN\_ILMN\_1778668  
 COL4A1\_ILMN\_1653028  
 COL4A2\_ILMN\_1724994  
 SDSL\_ILMN\_1750674  
 PEA15\_ILMN\_1771376  
 TNFAIP6\_ILMN\_1785732  
 DENND5A\_ILMN\_3245413  
 DENND5A\_ILMN\_1785356  
 NA\_ILMN\_1677402  
 IGFBP7\_ILMN\_2062468  
 SUSD2\_ILMN\_1693270  
 TAGLN\_ILMN\_2400935  
 AXL\_ILMN\_1701877

### 1.1.1 ANGPT2 ILMN\_1774207

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



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	0.89	2.45	[1.45, 4.13]	0.00082

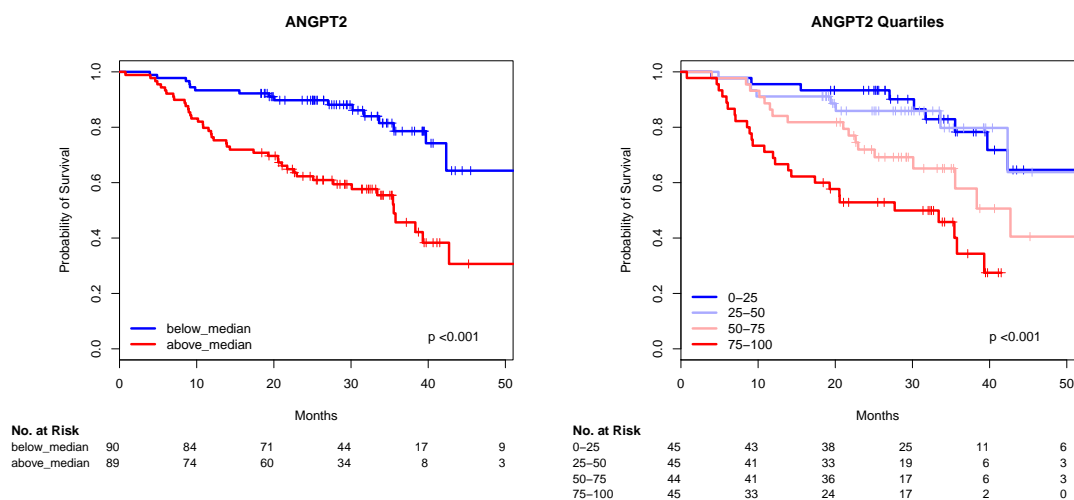
Tabelle 1: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	0.25	1.29	[0.56, 2.98]	0.56
split50-75	0.46	1.58	[0.70, 3.58]	0.27
split75-100	1.59	4.90	[2.32, 10.36]	< 0.0001

Tabelle 2: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.1.2 ANGPT2 ILMN\_3250067

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



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	1.11	3.04	[1.77, 5.23]	< 0.0001

Tabelle 3: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

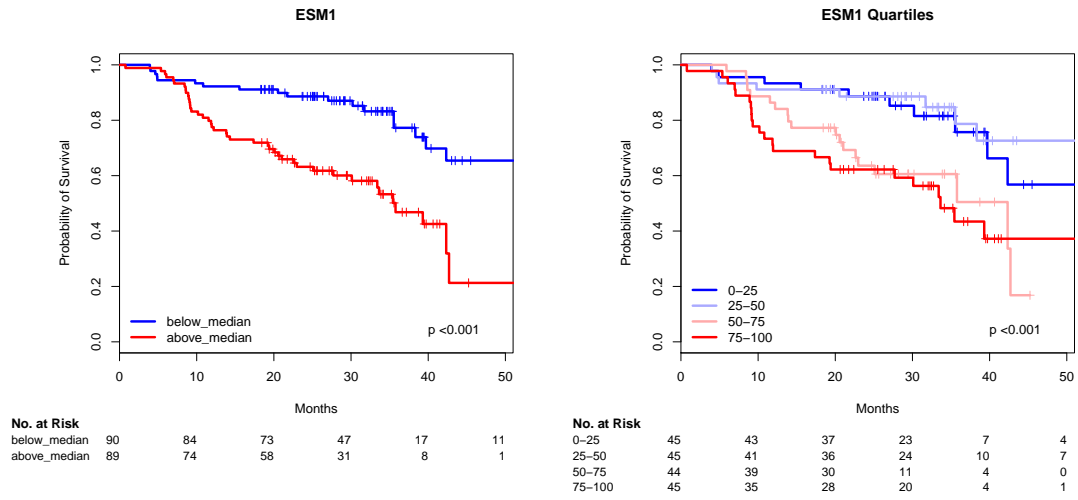
	coef	HR = exp(coef)	95% CI	p-value
split25-50	0.37	1.45	[0.58, 3.57]	0.42
split50-75	0.93	2.53	[1.13, 5.65]	0.02
split75-100	1.68	5.37	[2.46, 11.71]	< 0.0001

Tabelle 4: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles



### 1.1.3 ESM1 ILMN\_1773262

Gene symbol from a different, less reliable annotation table: ESM1



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	1.13	3.11	[1.79, 5.41]	< 0.0001

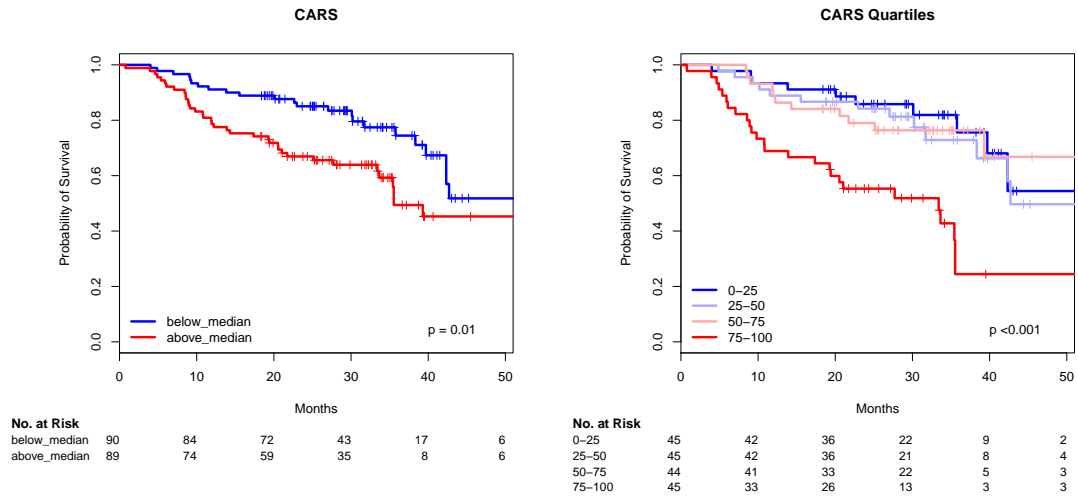
Tabelle 5: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.07	0.93	[0.39, 2.20]	0.87
split50-75	1.01	2.75	[1.27, 5.95]	0.01
split75-100	1.17	3.23	[1.53, 6.83]	0.0021

Tabelle 6: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.1.4 CARS ILMN\_2367469

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



	coef	HR = exp(coef)	95% CI	p-value
splitabove__median	0.64	1.89	[1.13, 3.16]	0.02

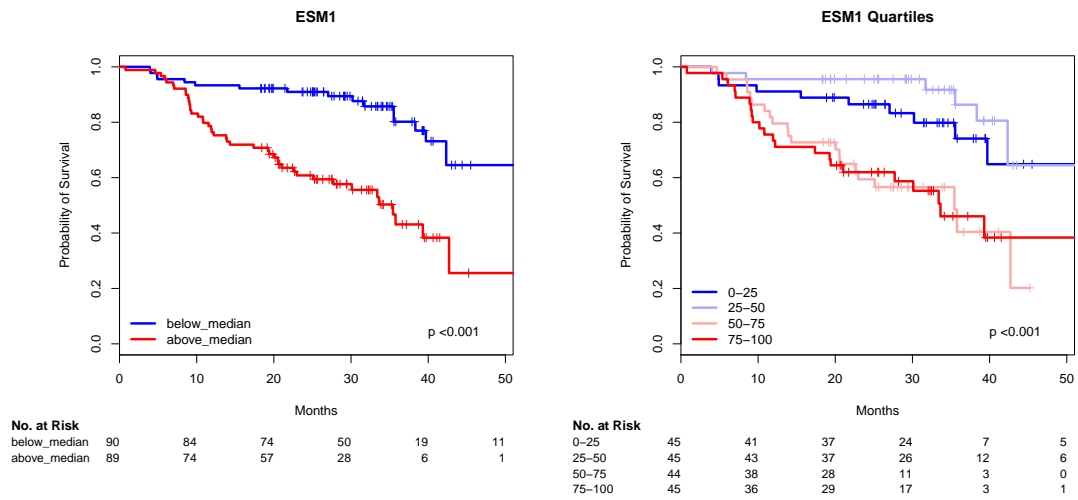
Tabelle 7: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	0.30	1.35	[0.60, 3.05]	0.47
split50-75	0.22	1.24	[0.53, 2.88]	0.62
split75-100	1.26	3.54	[1.70, 7.38]	0.00075

Tabelle 8: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.1.5 ESM1 ILMN\_2212878

Gene symbol from a different, less reliable annotation table: ESM1



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	1.30	3.67	[2.09, 6.47]	< 0.0001

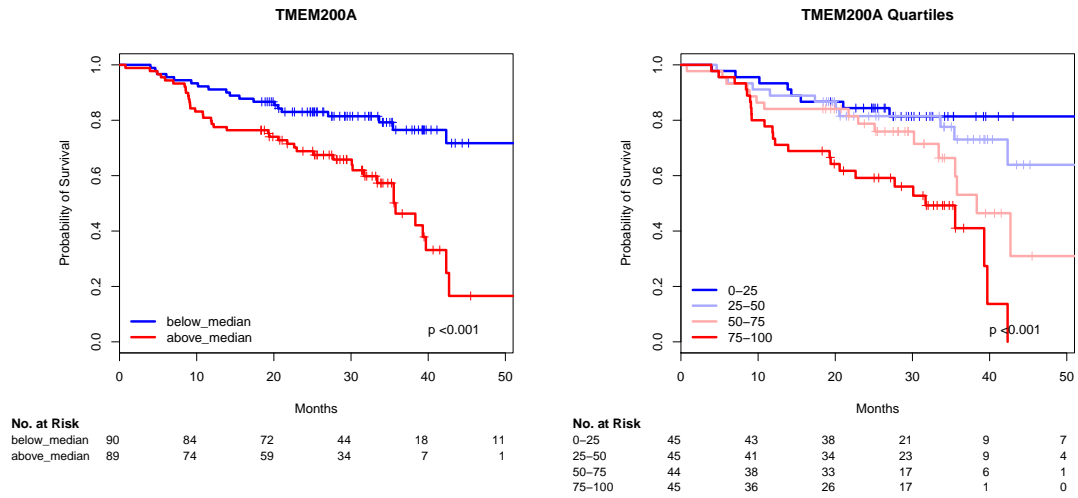
Tabelle 9: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.23	0.79	[0.33, 1.93]	0.61
split50-75	1.18	3.27	[1.52, 7.03]	0.0024
split75-100	1.19	3.28	[1.54, 7.00]	0.0021

Tabelle 10: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.1.6 TMEM200A ILMN\_1725387

Gene symbol from a different, less reliable annotation table: TMEM200A



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	1.06	2.87	[1.65, 4.99]	0.00018

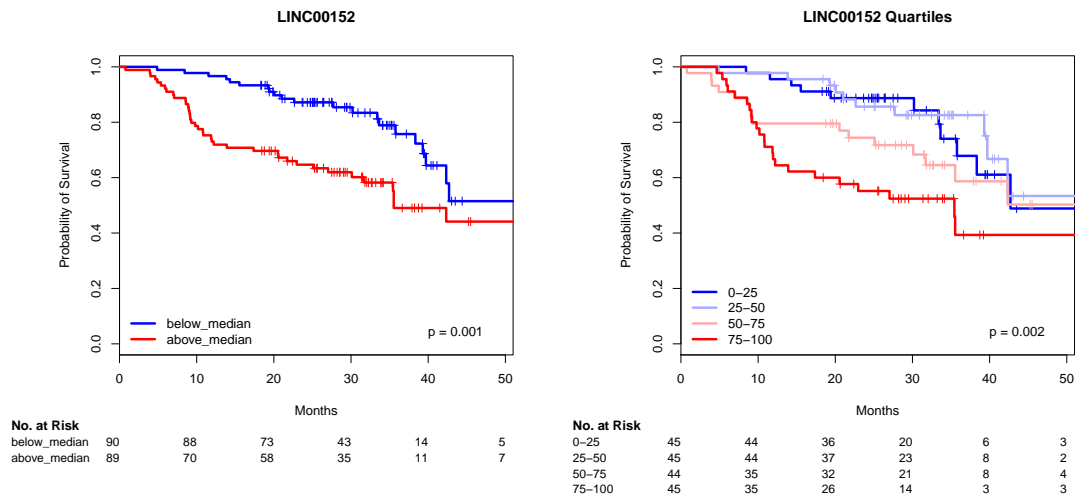
Tabelle 11: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	0.32	1.37	[0.58, 3.22]	0.47
split50-75	0.90	2.45	[1.07, 5.63]	0.03
split75-100	1.54	4.65	[2.12, 10.23]	0.00013

Tabelle 12: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.1.7 LINC00152 ILMN\_2143795

Gene symbol from a different, less reliable annotation table: MGC4677



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	0.85	2.35	[1.38, 3.99]	0.0016

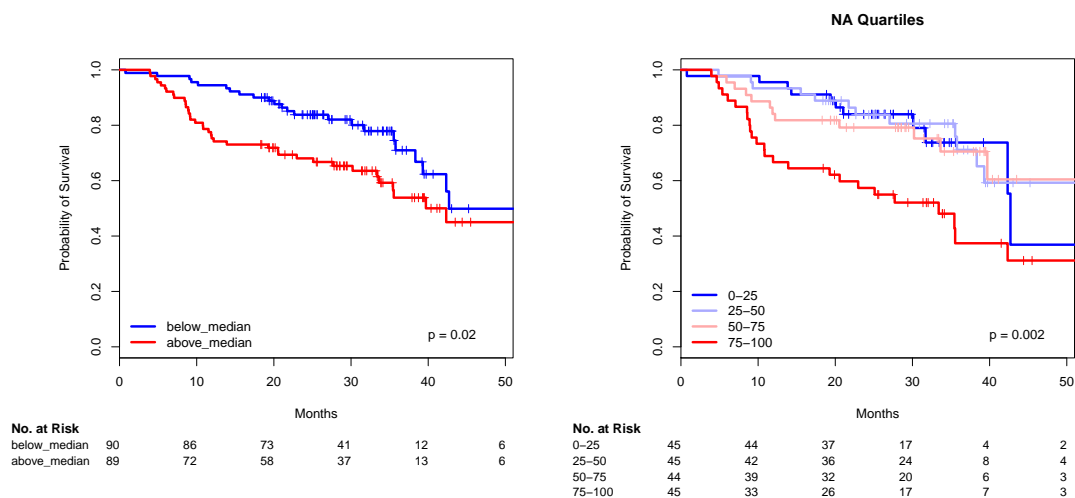
Tabelle 13: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.12	0.88	[0.37, 2.08]	0.78
split50-75	0.50	1.65	[0.77, 3.54]	0.20
split75-100	1.06	2.89	[1.41, 5.91]	0.0037

Tabelle 14: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.1.8 NA ILMN\_1906423

Gene symbol from a different, less reliable annotation table:



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	0.59	1.80	[1.08, 3.00]	0.02

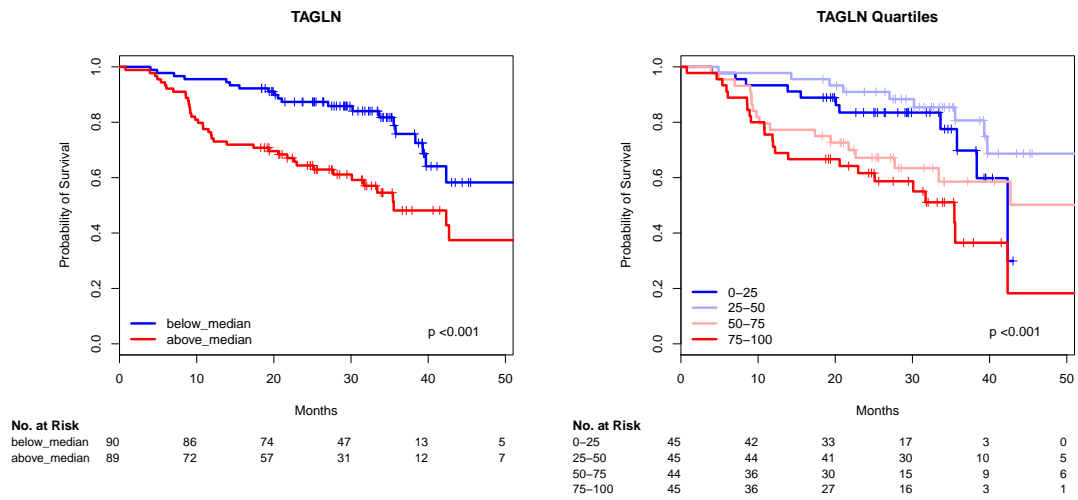
Tabelle 15: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	0.02	1.02	[0.45, 2.28]	0.97
split50-75	0.09	1.10	[0.49, 2.46]	0.83
split75-100	0.98	2.68	[1.32, 5.44]	0.0065

Tabelle 16: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.1.9 TAGLN ILMN\_1778668

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



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	0.96	2.61	[1.53, 4.46]	0.00046

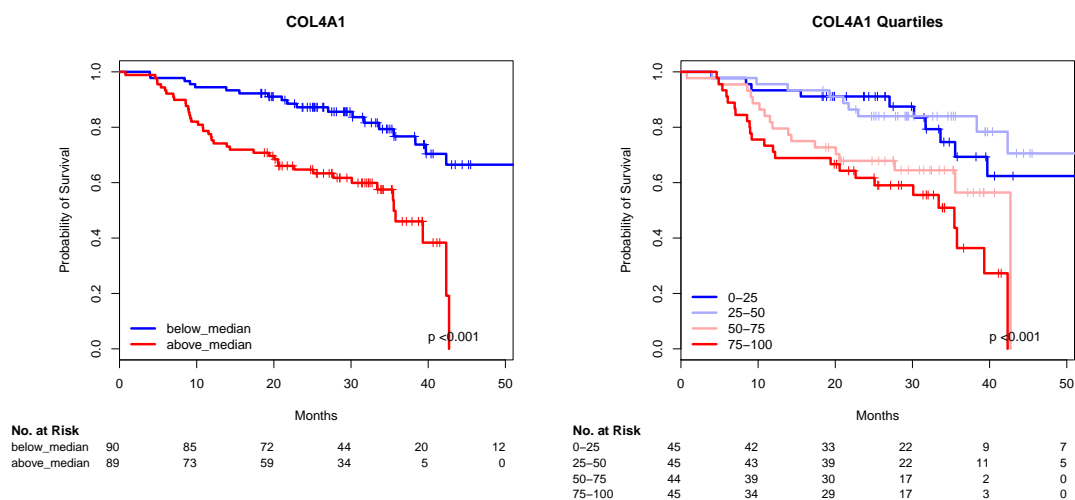
Tabelle 17: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.53	0.59	[0.24, 1.43]	0.24
split50-75	0.39	1.48	[0.69, 3.18]	0.32
split75-100	0.97	2.64	[1.29, 5.39]	0.0079

Tabelle 18: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.1.10 COL4A1 ILMN\_1653028

Gene symbol from a different, less reliable annotation table: COL4A1



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	1.18	3.27	[1.86, 5.75]	< 0.0001

Tabelle 19: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

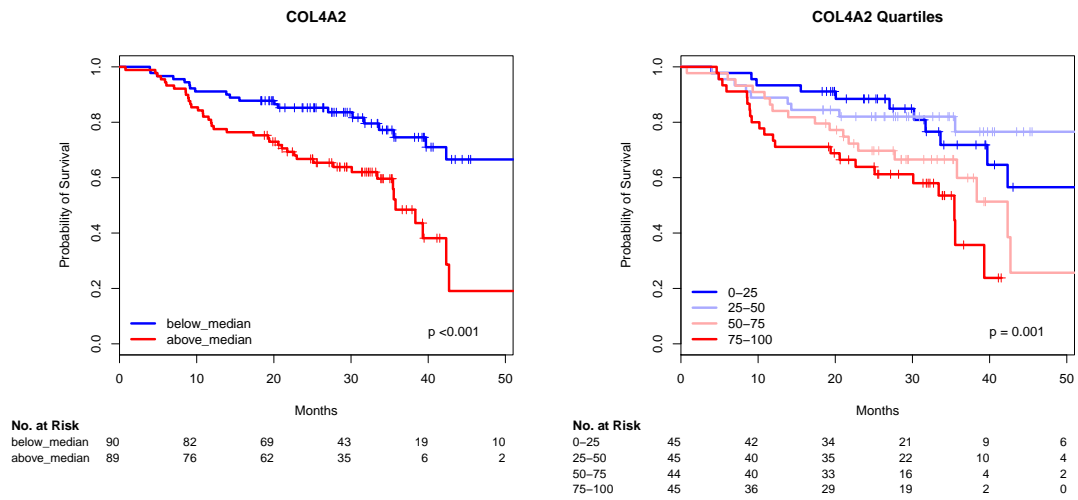
	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.18	0.84	[0.36, 1.97]	0.69
split50-75	0.88	2.41	[1.10, 5.28]	0.03
split75-100	1.29	3.63	[1.72, 7.63]	0.00069

Tabelle 20: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles



### 1.1.11 COL4A2 ILMN\_1724994

Gene symbol from a different, less reliable annotation table: COL4A2



	coef	HR = exp(coef)	95% CI	p-value
splitabove_medial	0.95	2.58	[1.52, 4.39]	0.00046

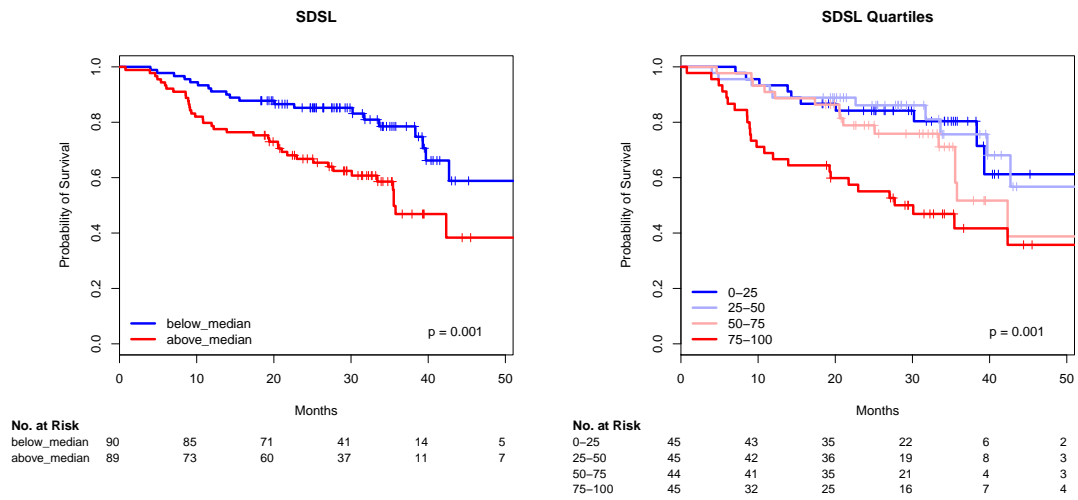
Tabelle 21: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.31	0.73	[0.31, 1.72]	0.47
split50-75	0.63	1.88	[0.92, 3.83]	0.08
split75-100	1.02	2.76	[1.36, 5.63]	0.0051

Tabelle 22: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.1.12 SDSL ILMN\_1750674

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



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	0.85	2.34	[1.37, 4.00]	0.0018

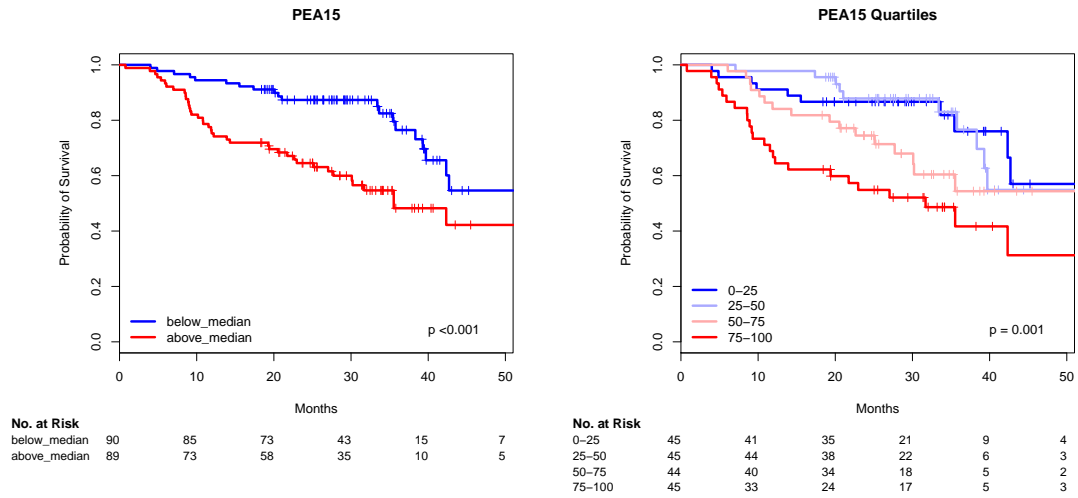
Tabelle 23: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.03	0.97	[0.40, 2.34]	0.95
split50-75	0.50	1.65	[0.75, 3.64]	0.21
split75-100	1.12	3.06	[1.47, 6.36]	0.0028

Tabelle 24: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.1.13 PEA15 ILMN\_1771376

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



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	0.85	2.35	[1.40, 3.96]	0.0013

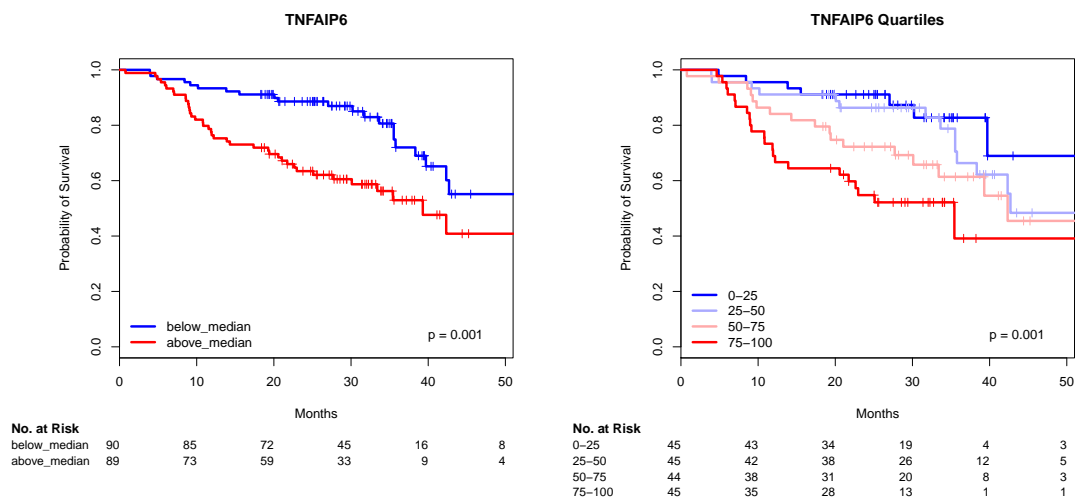
Tabelle 25: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	0.009	1.01	[0.44, 2.33]	0.98
split50-75	0.55	1.73	[0.80, 3.73]	0.17
split75-100	1.13	3.09	[1.52, 6.31]	0.0019

Tabelle 26: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.1.14 TNFAIP6 ILMN\_1785732

Gene symbol from a different, less reliable annotation table: TNFAIP6



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	0.84	2.32	[1.38, 3.89]	0.0015

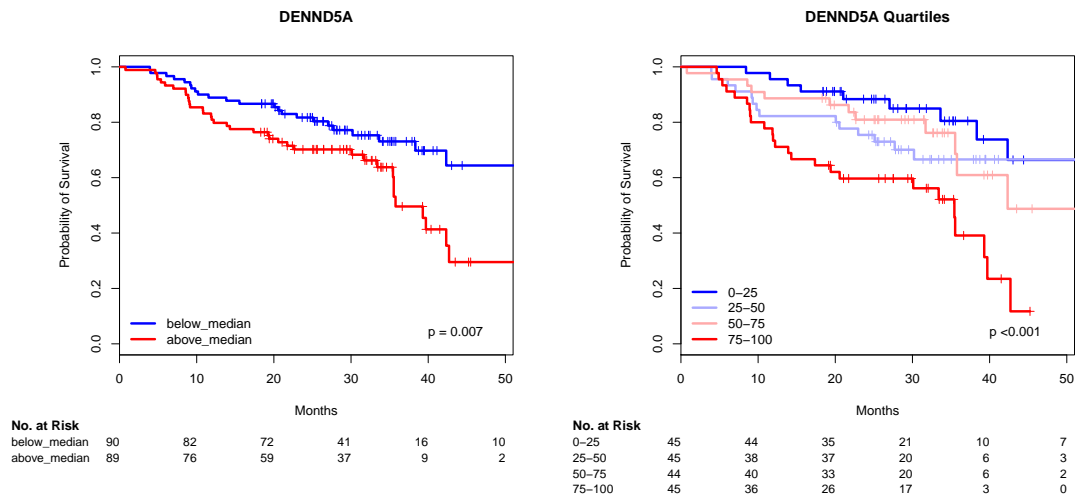
Tabelle 27: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	0.28	1.32	[0.57, 3.06]	0.52
split50-75	0.73	2.07	[0.93, 4.62]	0.08
split75-100	1.32	3.76	[1.71, 8.27]	0.001

Tabelle 28: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.1.15 DENND5A ILMN\_3245413

Gene symbol from a different, less reliable annotation table: DENND5A



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	0.71	2.04	[1.21, 3.44]	0.0077

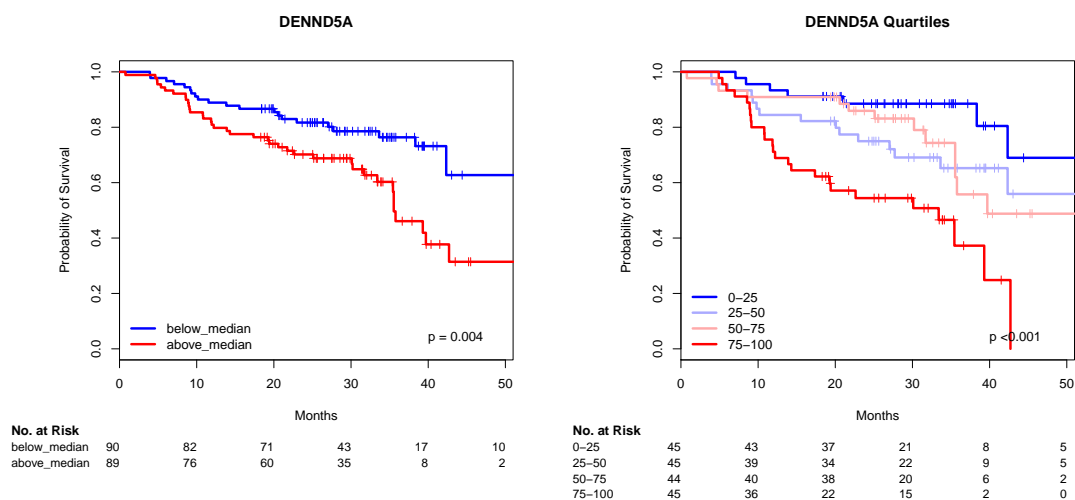
Tabelle 29: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	0.40	1.49	[0.67, 3.31]	0.33
split50-75	0.45	1.57	[0.70, 3.56]	0.28
split75-100	1.30	3.65	[1.76, 7.59]	0.00052

Tabelle 30: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.1.16 DENND5A ILMN\_1785356

Gene symbol from a different, less reliable annotation table: DENND5A



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	0.75	2.11	[1.25, 3.56]	0.0054

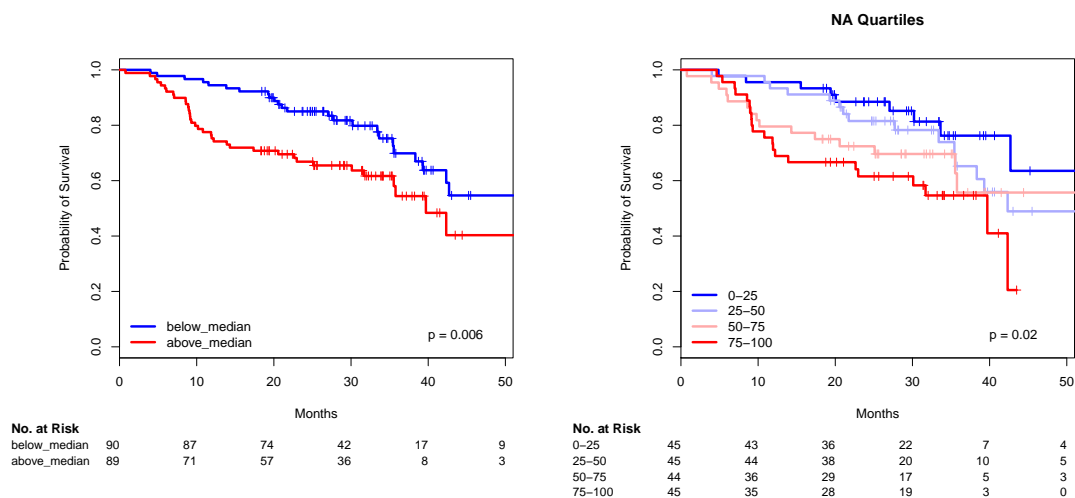
Tabelle 31: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	0.56	1.74	[0.77, 3.95]	0.18
split50-75	0.54	1.71	[0.73, 4.04]	0.22
split75-100	1.53	4.62	[2.12, 10.06]	0.00012

Tabelle 32: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.1.17 NA ILMN\_1677402

Gene symbol from a different, less reliable annotation table: LOC387763



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	0.71	2.04	[1.22, 3.43]	0.0069

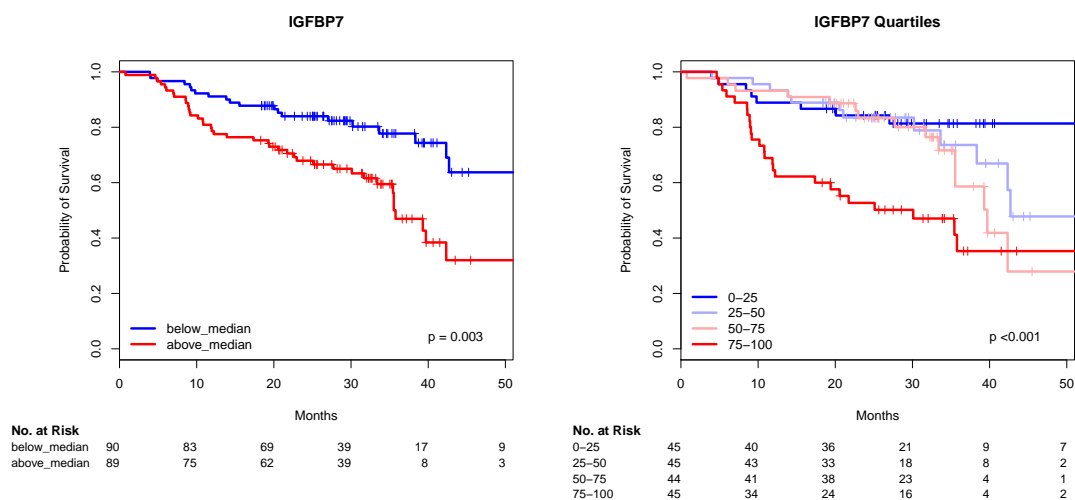
Tabelle 33: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	0.30	1.35	[0.61, 3.02]	0.46
split50-75	0.69	2.00	[0.90, 4.41]	0.09
split75-100	1.06	2.89	[1.35, 6.17]	0.0062

Tabelle 34: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.1.18 IGFBP7 ILMN\_2062468

Gene symbol from a different, less reliable annotation table: IGFBP7



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	0.76	2.13	[1.27, 3.58]	0.0042

Tabelle 35: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

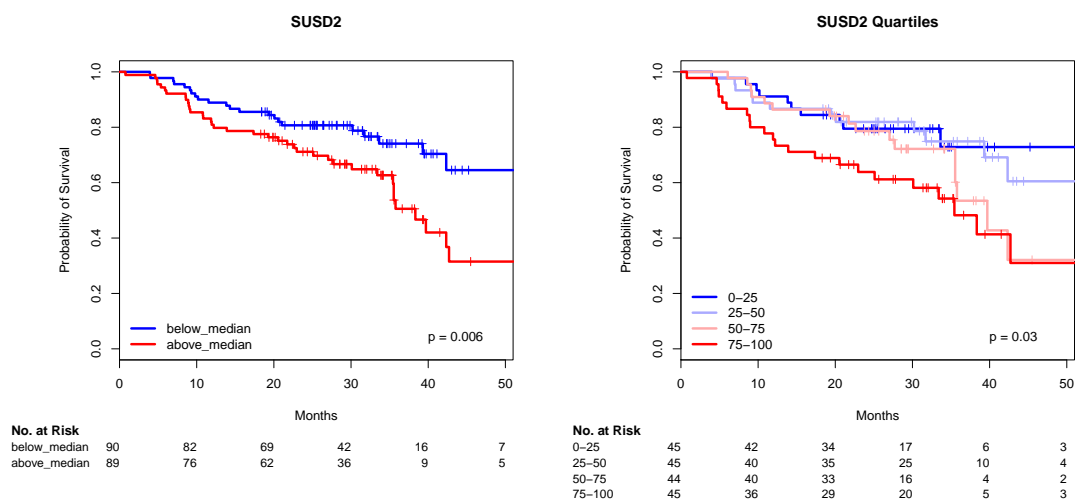
	coef	HR = exp(coef)	95% CI	p-value
split25-50	0.34	1.40	[0.61, 3.21]	0.42
split50-75	0.54	1.72	[0.77, 3.86]	0.19
split75-100	1.28	3.59	[1.71, 7.53]	0.00072

Tabelle 36: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles



### 1.1.19 SUS D2 ILMN\_1693270

Gene symbol from a different, less reliable annotation table: SUS D2



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	0.71	2.03	[1.22, 3.40]	0.0068

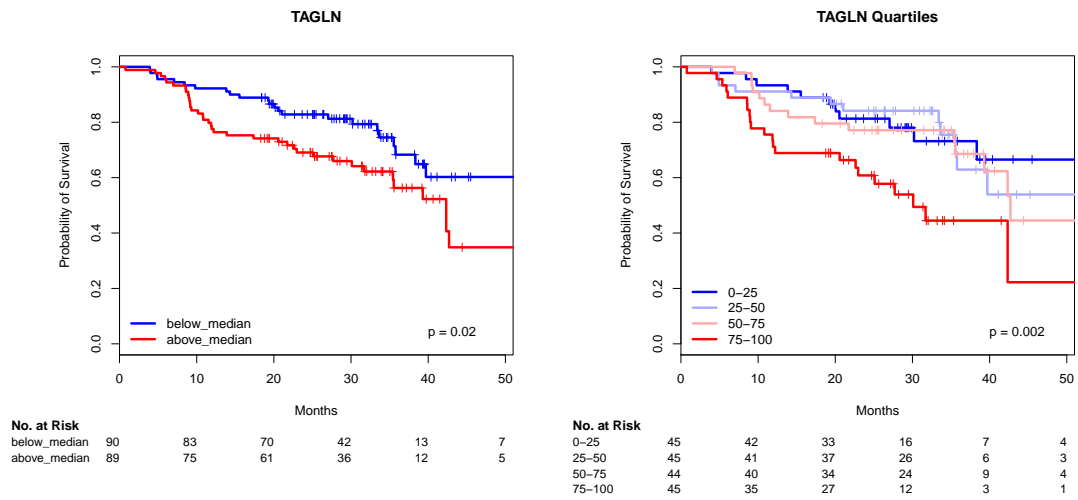
Tabelle 37: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	0.08	1.08	[0.47, 2.48]	0.85
split50-75	0.57	1.77	[0.81, 3.88]	0.15
split75-100	0.91	2.48	[1.18, 5.22]	0.02

Tabelle 38: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.1.20 TAGLN ILMN\_2400935

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



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	0.60	1.83	[1.10, 3.05]	0.02

Tabelle 39: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	0.03	1.03	[0.46, 2.30]	0.95
split50-75	0.19	1.21	[0.57, 2.57]	0.61
split75-100	1.07	2.93	[1.44, 5.95]	0.003

Tabelle 40: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

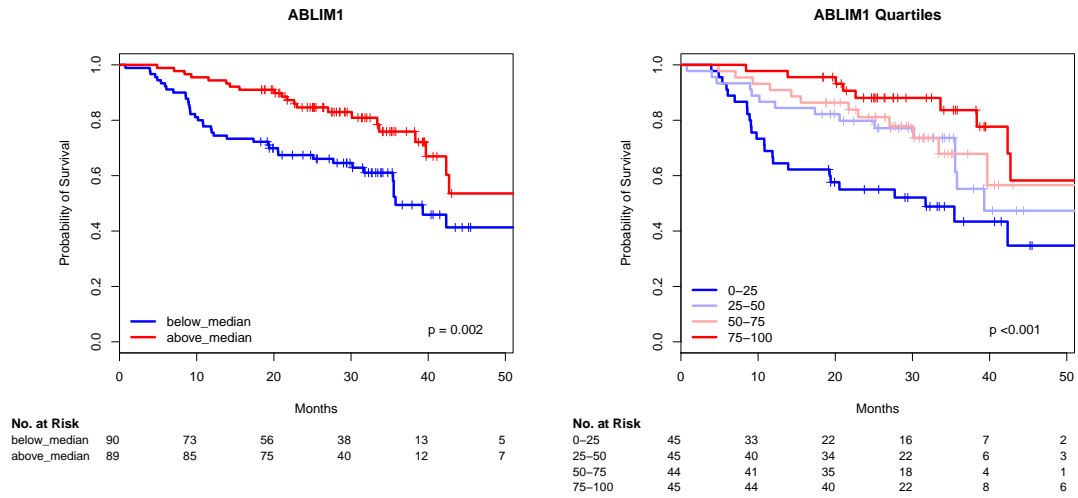
## 1.2 Higher expression = better survival

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

C10orf99_ILMN_1802192	0.65	0.63	0.45	0.47	0.72	0.23	0.54	0.7	0.63	0.55	1
CDS1_ILMN_1801476	0.54	0.54	0.36	0.54	0.62	0.22	0.58	0.59	0.59	1	0.55
RAB25_ILMN_1791826	0.61	0.63	0.52	0.52	0.8	0.37	0.44	0.72	1	0.59	0.63
GLTP_ILMN_1764380	0.74	0.71	0.56	0.59	0.75	0.24	0.55	1	0.72	0.59	0.7
TACC2_ILMN_2315780	0.65	0.63	0.39	0.6	0.56	0.1	1	0.55	0.44	0.58	0.54
CIDEB_ILMN_1668910	0.16	0.2	0.07	0.12	0.24	1	0.1	0.24	0.37	0.22	0.23
BNIP1_ILMN_1699989	0.69	0.68	0.56	0.57	1	0.24	0.56	0.75	0.8	0.62	0.72
CDH1_ILMN_1770940	0.59	0.51	0.42	1	0.57	0.12	0.6	0.59	0.52	0.54	0.47
GSTA4_ILMN_1771964	0.52	0.43	1	0.42	0.56	0.07	0.39	0.56	0.52	0.36	0.45
ABLIM1_ILMN_1785424	0.91	1	0.43	0.51	0.68	0.2	0.63	0.71	0.63	0.54	0.63
ABLIM1_ILMN_2396672	1	0.91	0.52	0.59	0.69	0.16	0.65	0.74	0.61	0.54	0.65
	ABLIM1_ILMN_2396672	ABLIM1_ILMN_1785424	GSTA4_ILMN_1771964	CDH1_ILMN_1770940	BNIP1_ILMN_1699989	CIDEB_ILMN_1668910	TACC2_ILMN_2315780	GLTP_ILMN_1764380	RAB25_ILMN_1791826	CDS1_ILMN_1801476	C10orf99_ILMN_1802192

### 1.2.1 ABLIM1 ILMN\_2396672

Gene symbol from a different, less reliable annotation table: ABLIM1



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.78	0.46	[0.27, 0.77]	0.0031

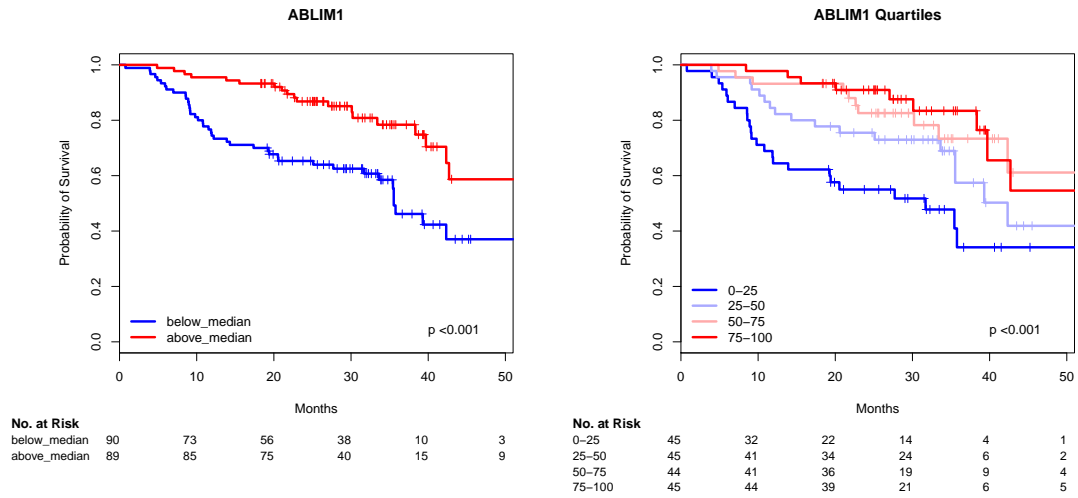
Tabelle 41: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.72	0.49	[0.26, 0.92]	0.03
split50-75	-0.88	0.41	[0.21, 0.82]	0.01
split75-100	-1.32	0.27	[0.13, 0.55]	0.00039

Tabelle 42: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

## 1.2.2 ABLIM1 ILMN\_1785424

Gene symbol from a different, less reliable annotation table: ABLIM1



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-1.01	0.36	[0.21, 0.63]	0.00026

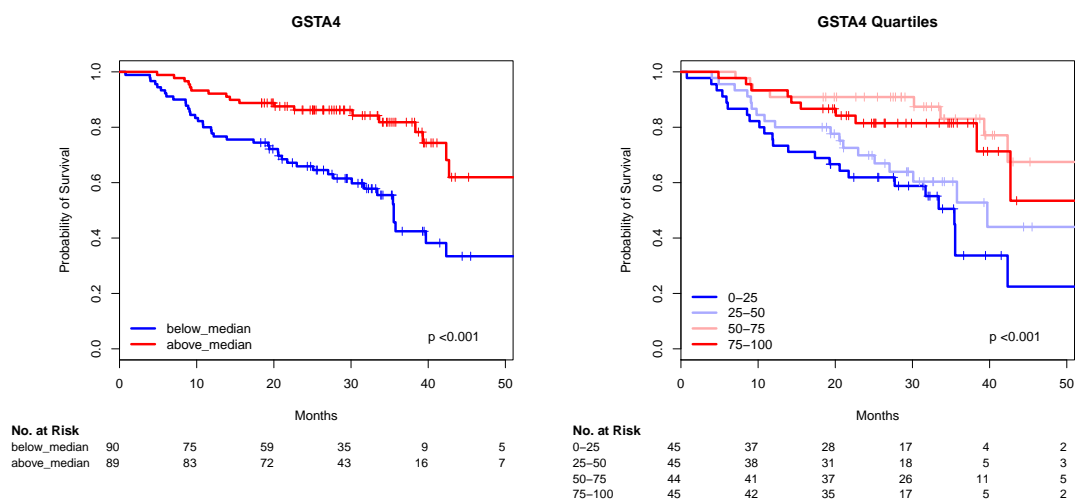
Tabelle 43: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.72	0.49	[0.26, 0.91]	0.02
split50-75	-1.28	0.28	[0.14, 0.58]	0.00055
split75-100	-1.46	0.23	[0.11, 0.49]	0.00014

Tabelle 44: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.2.3 GSTA4 ILMN\_1771964

Gene symbol from a different, less reliable annotation table: GSTA4



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.95	0.39	[0.23, 0.66]	0.0005

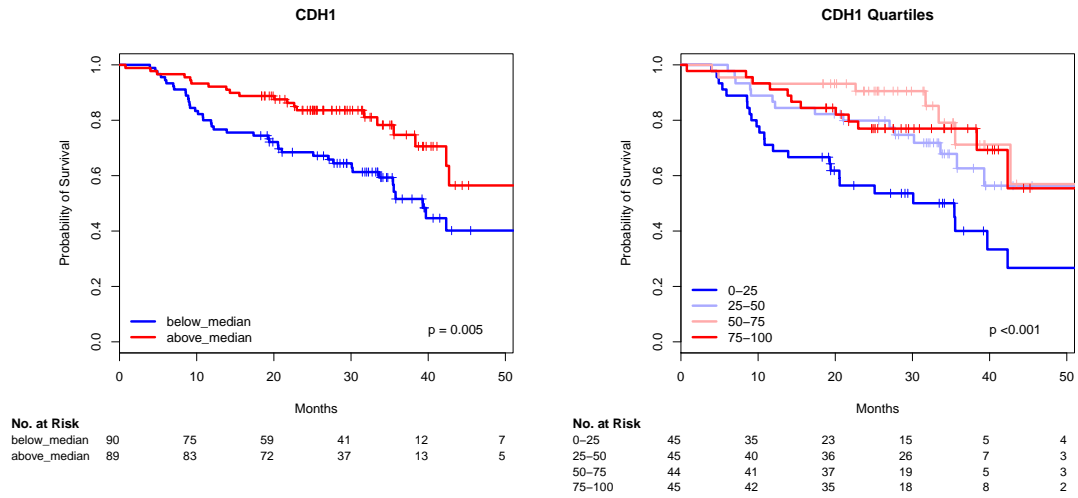
Tabelle 45: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.46	0.63	[0.34, 1.16]	0.14
split50-75	-1.26	0.28	[0.14, 0.59]	0.0008
split75-100	-1.06	0.35	[0.17, 0.72]	0.0048

Tabelle 46: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.2.4 CDH1 ILMN\_1770940

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



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.73	0.48	[0.28, 0.81]	0.0061

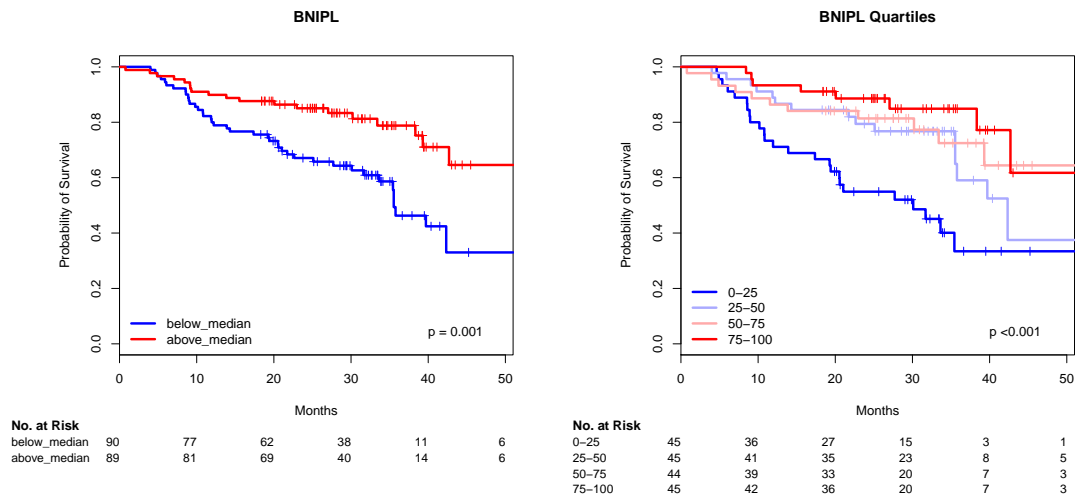
Tabelle 47: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.80	0.45	[0.24, 0.85]	0.01
split50-75	-1.38	0.25	[0.11, 0.56]	0.00063
split75-100	-0.88	0.42	[0.21, 0.81]	0.0098

Tabelle 48: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.2.5 BNIPL ILMN\_1699989

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



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.84	0.43	[0.26, 0.73]	0.0018

Tabelle 49: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

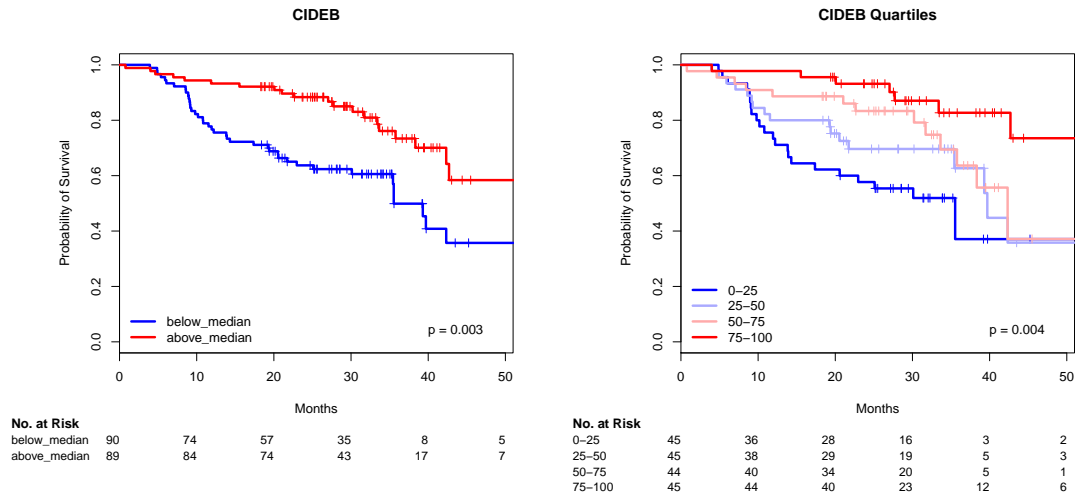
	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.68	0.51	[0.27, 0.94]	0.03
split50-75	-0.99	0.37	[0.19, 0.75]	0.0055
split75-100	-1.38	0.25	[0.12, 0.54]	0.00041

Tabelle 50: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles



## 1.2.6 CIDEB ILMN\_1668910

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



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.77	0.46	[0.28, 0.77]	0.0033

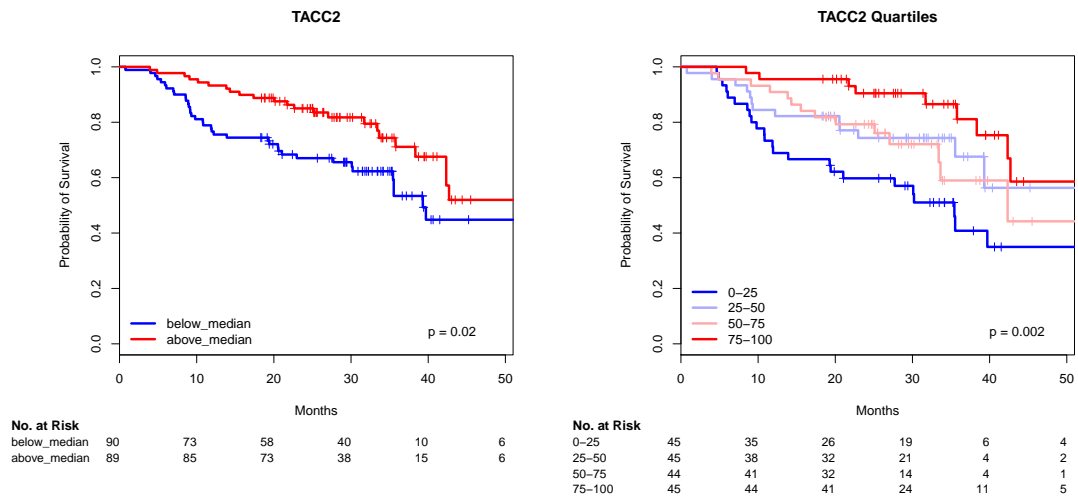
Tabelle 51: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.42	0.66	[0.35, 1.23]	0.19
split50-75	-0.62	0.54	[0.28, 1.05]	0.07
split75-100	-1.36	0.26	[0.12, 0.56]	0.00059

Tabelle 52: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.2.7 TACC2 ILMN\_2315780

Gene symbol from a different, less reliable annotation table: TACC2



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.62	0.54	[0.32, 0.90]	0.02

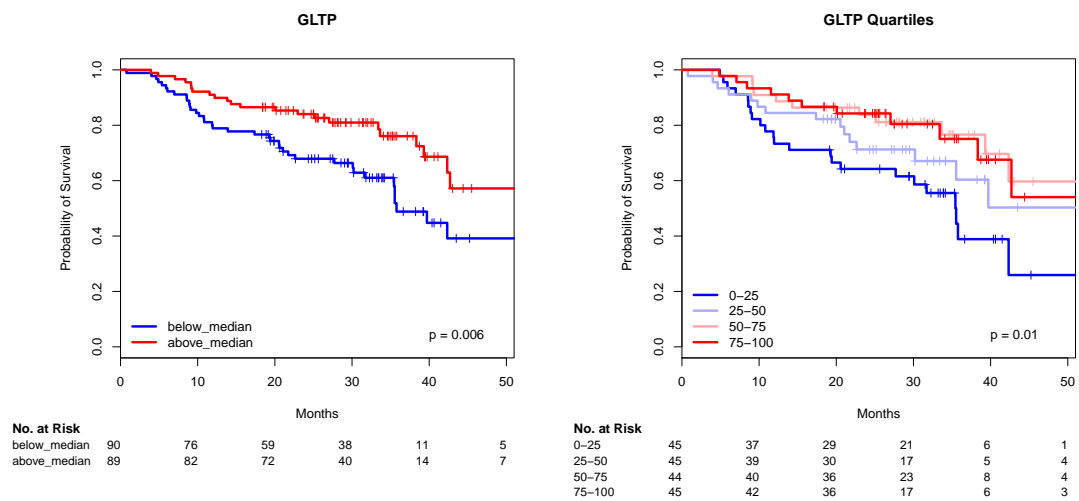
Tabelle 53: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.77	0.46	[0.24, 0.90]	0.02
split50-75	-0.60	0.55	[0.29, 1.06]	0.07
split75-100	-1.29	0.28	[0.13, 0.58]	0.00058

Tabelle 54: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

## 1.2.8 GLTP ILMN\_1764380

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



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.70	0.49	[0.30, 0.83]	0.0072

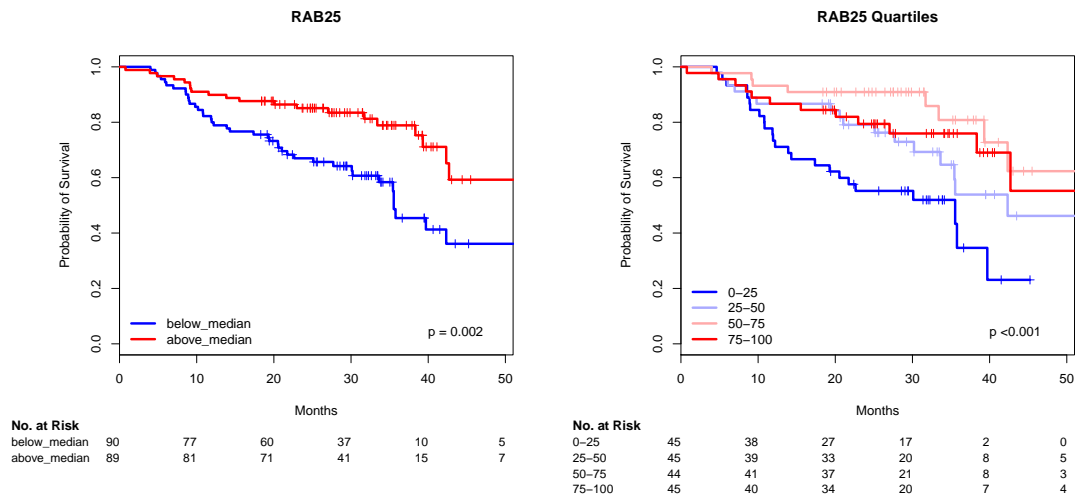
Tabelle 55: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.54	0.58	[0.31, 1.11]	0.10
split50-75	-0.98	0.38	[0.19, 0.76]	0.0064
split75-100	-0.94	0.39	[0.19, 0.80]	0.01

Tabelle 56: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.2.9 RAB25 ILMN\_1791826

Gene symbol from a different, less reliable annotation table: RAB25



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.78	0.46	[0.27, 0.77]	0.0032

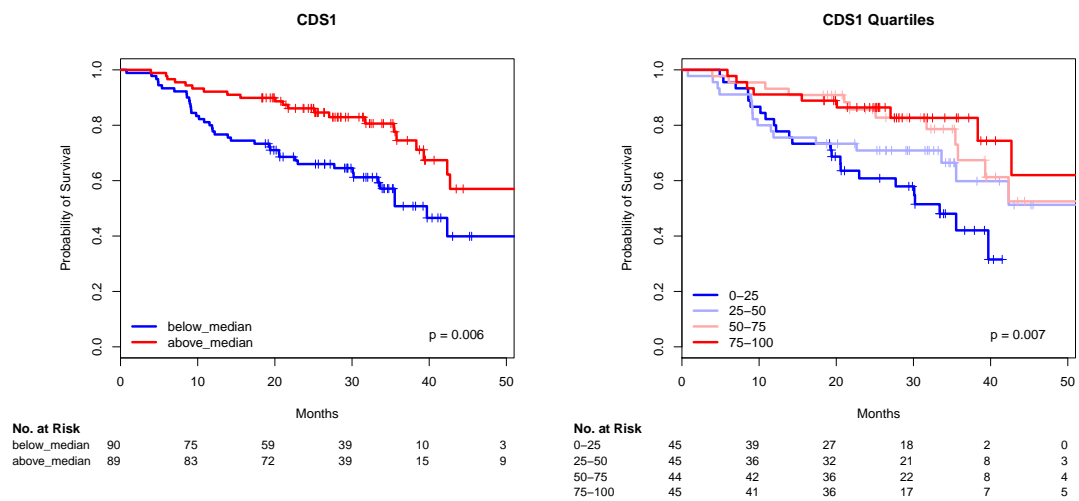
Tabelle 57: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.70	0.50	[0.26, 0.94]	0.03
split50-75	-1.38	0.25	[0.12, 0.55]	0.0005
split75-100	-0.93	0.39	[0.20, 0.78]	0.0075

Tabelle 58: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.2.10 CDS1 ILMN\_1801476

Gene symbol from a different, less reliable annotation table: CDS1



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-0.70	0.50	[0.30, 0.83]	0.0075

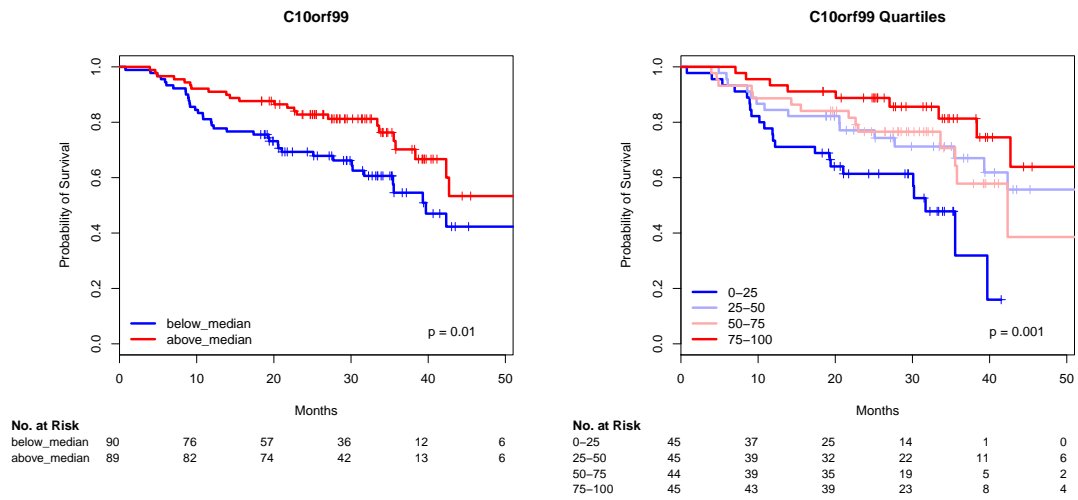
Tabelle 59: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.60	0.55	[0.29, 1.06]	0.07
split50-75	-0.88	0.41	[0.21, 0.82]	0.01
split75-100	-1.14	0.32	[0.15, 0.68]	0.003

Tabelle 60: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles

### 1.2.11 C10orf99 ILMN\_1802192

Gene symbol from a different, less reliable annotation table: C10orf99



	coef	HR = exp(coef)	95% CI	p-value
splitabove_medial	-0.66	0.52	[0.31, 0.86]	0.01

Tabelle 61: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.80	0.45	[0.23, 0.87]	0.02
split50-75	-0.78	0.46	[0.23, 0.91]	0.02
split75-100	-1.45	0.23	[0.11, 0.52]	0.00034

Tabelle 62: Cox regression model,  $n = 179$ , number of events = 63. Model for the figure on the right. Patients split into quartiles