

LIFE-HNG. Genes whose expression is associated with survival in HPV DNA+ RNA+ patients.

Progression-free 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
```

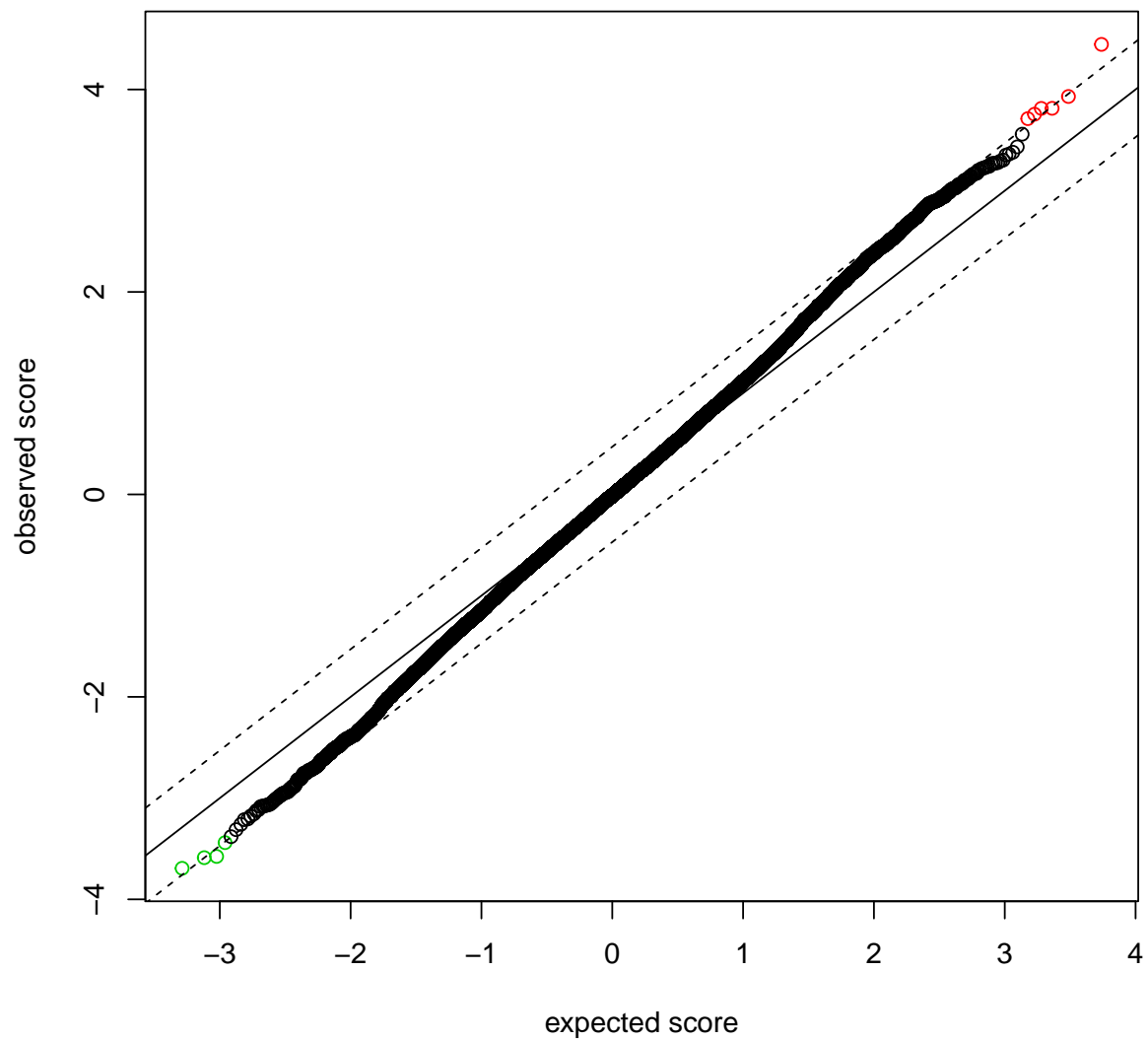
Number of analyzed patients:

```
## [1] 35
```

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)
## [1,] "20748" "MXD1"    "ILMN_2214678" "4.44552737782175"
## [2,] "5604"  "CYP51A1" "ILMN_1664718" "3.93087354756469"
## [3,] "6562"  "ECM1"     "ILMN_1658333" "3.8140065513434"
## [4,] "7015"  "ER01L"    "ILMN_1744963" "3.8130160741787"
```

```

## [5,] "21515" "NPEPPS" "ILMN_2116127" "3.75576042513679"
## [6,] "14211" NA      "ILMN_3176146" "3.71212649624232"
##      Numerator(r)      Denominator(s+s0)      q-value(%)
## [1,] "7.66725913744589" "1.7247130623235" "0"
## [2,] "4.74464730347593" "1.20702109749" "10.1521438450899"
## [3,] "6.86503974376114" "1.799954890309" "10.1521438450899"
## [4,] "7.76493648812707" "2.03642899402138" "10.1521438450899"
## [5,] "3.19886741157372" "0.851722966716443" "10.1521438450899"
## [6,] "6.3527564311179" "1.71135235761729" "10.1521438450899"
##
## $genes.lo
##      Row      Gene ID      Gene Name      Score(d)
## [1,] "12354" "ICOS"      "ILMN_1669927" "-3.69350904060638"
## [2,] "1053"  "APOBEC3G" "ILMN_2232478" "-3.58837641444214"
## [3,] "1052"  "APOBEC3G" "ILMN_1802106" "-3.57623669881428"
## [4,] "10939" NA      "ILMN_1916256" "-3.43976555664"
##      Numerator(r)      Denominator(s+s0)      q-value(%)
## [1,] "-4.59812516179654" "1.24492051088676" "0"
## [2,] "-3.501140734753" "0.975689373239092" "0"
## [3,] "-3.8796708329832" "1.08484732967186" "0"
## [4,] "-3.58576992647059" "1.04244602355203" "9.13692946058091"
##
## $color.ind.for.multi
## NULL
##
## $ngenes.up
## [1] 6
##
## $ngenes.lo
## [1] 4

```

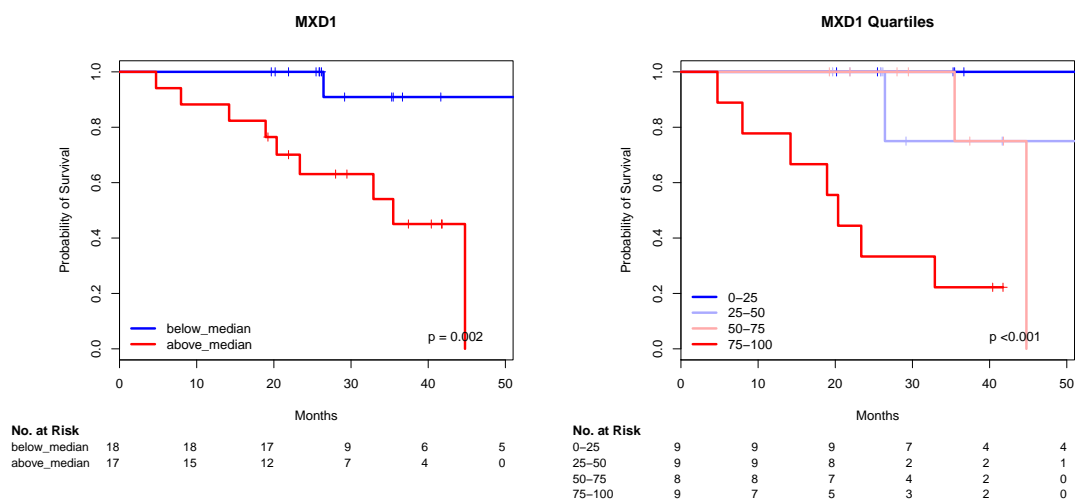
1.1 Higher expression = poorer survival

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

NA_ILMN_3176146	0.69	0.33	0.52	0.62	0.52	1
NPEPPS_ILMN_2116127	0.53	0.17	0.36	0.56	1	0.52
ERO1L_ILMN_1744963	0.57	0.34	0.51	1	0.56	0.62
ECM1_ILMN_1658333	0.54	0.12	1	0.51	0.36	0.52
CYP51A1_ILMN_1664718	0.22	1	0.12	0.34	0.17	0.33
MXD1_ILMN_2214678	1	0.22	0.54	0.57	0.53	0.69
	MXD1_ILMN_2214678	CYP51A1_ILMN_1664718	ECM1_ILMN_1658333	ERO1L_ILMN_1744963	NPEPPS_ILMN_2116127	NA_ILMN_3176146

1.1.1 MXD1 ILMN_2214678

Gene symbol from a different, less reliable annotation table: MXD1



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	2.65	14.10	[1.72, 115.21]	0.01

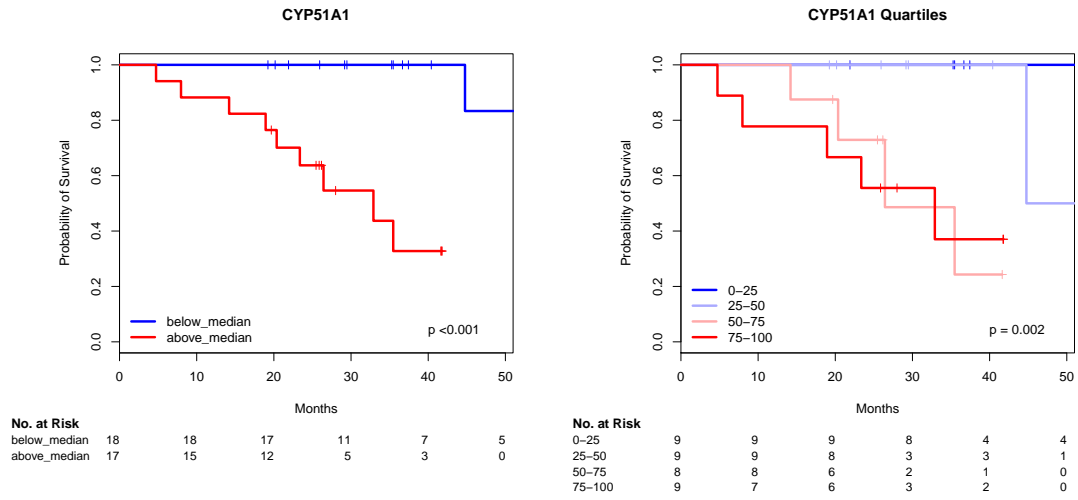
Tabelle 1: Cox regression model, $n = 35$, number of events = 11. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	1.09	2.98	[0.18, 50.04]	0.45
split50-75	2.27	9.70	[0.52, 181.25]	0.13
split75-100	4.19	66.11	[3.64, 1201.02]	0.0046

Tabelle 2: Cox regression model, $n = 35$, number of events = 11. Model for the figure on the right. Patients split into quartiles

1.1.2 CYP51A1 ILMN_1664718

Gene symbol from a different, less reliable annotation table: CYP51A1



	coef	HR = exp(coef)	95% CI	p-value
splitabove__median	20.71	984504326.67	[0.00, Inf]	1.00

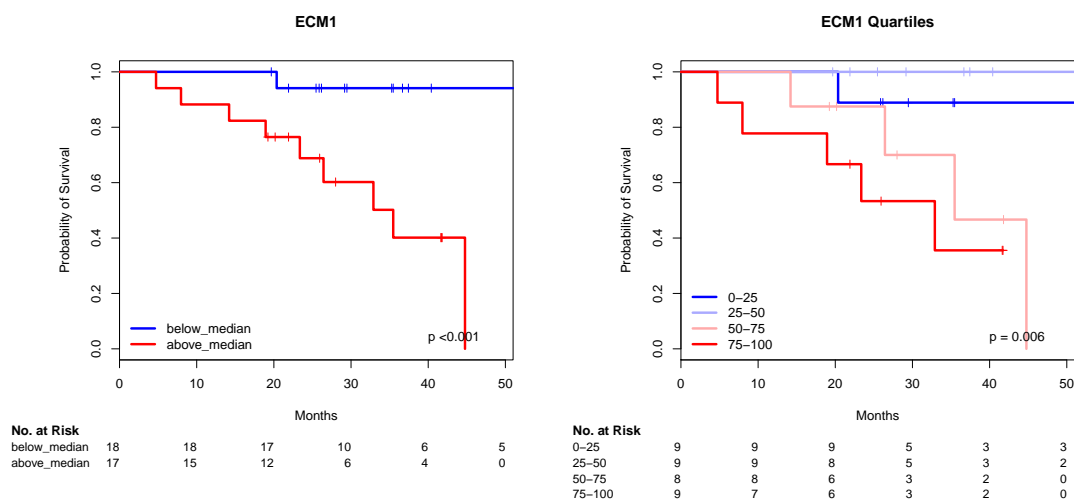
Tabelle 3: Cox regression model, $n = 35$, number of events = 11. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	20.59	875757560.39	[0.00, Inf]	1.00
split50-75	41.00	6.393e+17	[0.00, Inf]	1.00
split75-100	41.13	7.274e+17	[0.00, Inf]	1.00

Tabelle 4: Cox regression model, $n = 35$, number of events = 11. Model for the figure on the right. Patients split into quartiles

1.1.3 ECM1 ILMN_1658333

Gene symbol from a different, less reliable annotation table: ECM1



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	2.73	15.36	[1.89, 124.88]	0.01

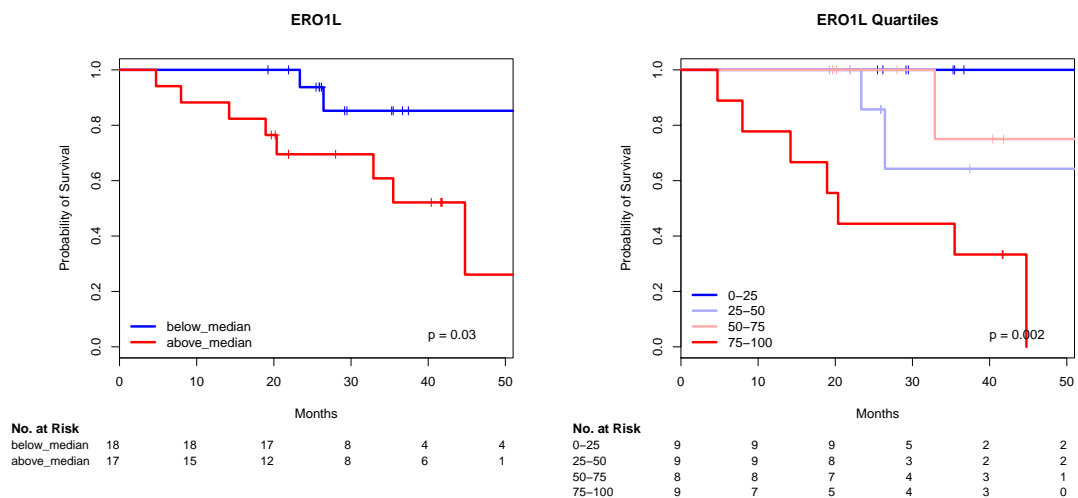
Tabelle 5: Cox regression model, $n = 35$, number of events = 11. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-18.70	0.000000008	[0.00, Inf]	1.00
split50-75	1.88	6.53	[0.71, 59.82]	0.10
split75-100	2.37	10.73	[1.12, 102.97]	0.04

Tabelle 6: Cox regression model, $n = 35$, number of events = 11. Model for the figure on the right. Patients split into quartiles

1.1.4 ERO1L ILMN_1744963

Gene symbol from a different, less reliable annotation table: ERO1L



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	1.37	3.92	[1.01, 15.14]	0.05

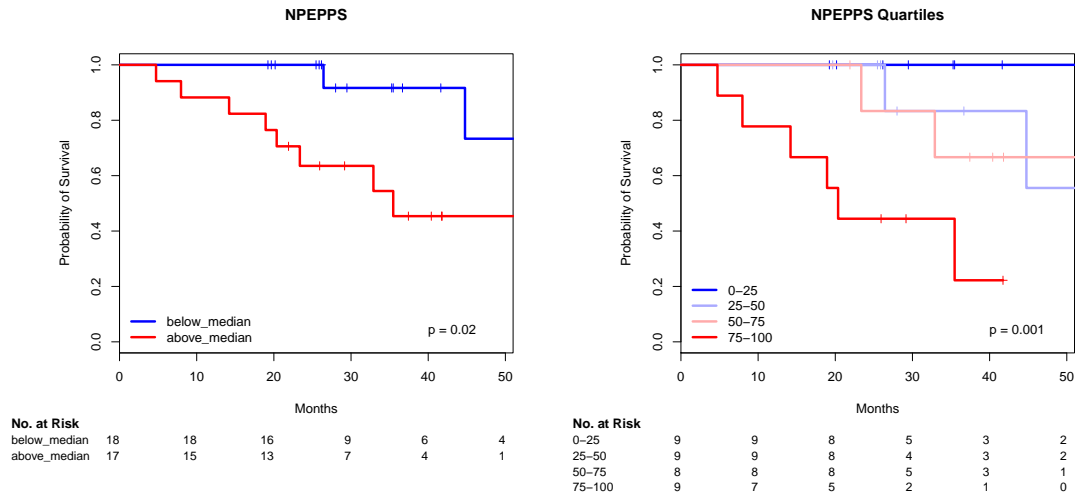
Tabelle 7: Cox regression model, $n = 35$, number of events = 11. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	0.81	2.25	[0.20, 24.93]	0.51
split50-75	0.40	1.49	[0.09, 23.91]	0.78
split75-100	2.62	13.71	[1.55, 120.99]	0.02

Tabelle 8: Cox regression model, $n = 35$, number of events = 11. Model for the figure on the right. Patients split into quartiles

1.1.5 NPEPPS ILMN_2116127

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



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	1.49	4.45	[1.13, 17.48]	0.03

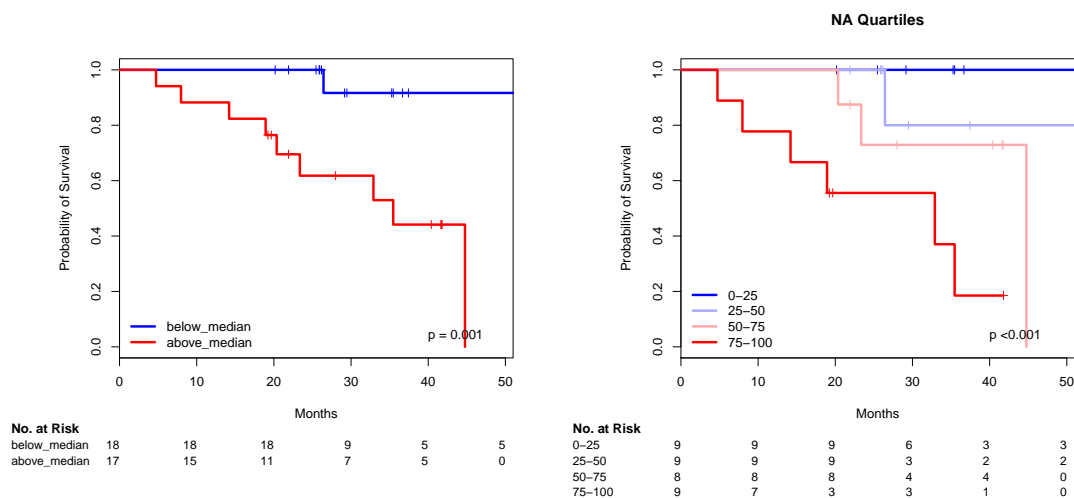
Tabelle 9: Cox regression model, $n = 35$, number of events = 11. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	19.51	297867916.41	[0.00, Inf]	1.00
split50-75	19.48	289830455.95	[0.00, Inf]	1.00
split75-100	21.31	1.795e+09	[0.00, Inf]	1.00

Tabelle 10: Cox regression model, $n = 35$, number of events = 11. Model for the figure on the right. Patients split into quartiles

1.1.6 NA ILMN_3176146

Gene symbol from a different, less reliable annotation table: LOC100128918



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	2.70	14.82	[1.82, 120.76]	0.01

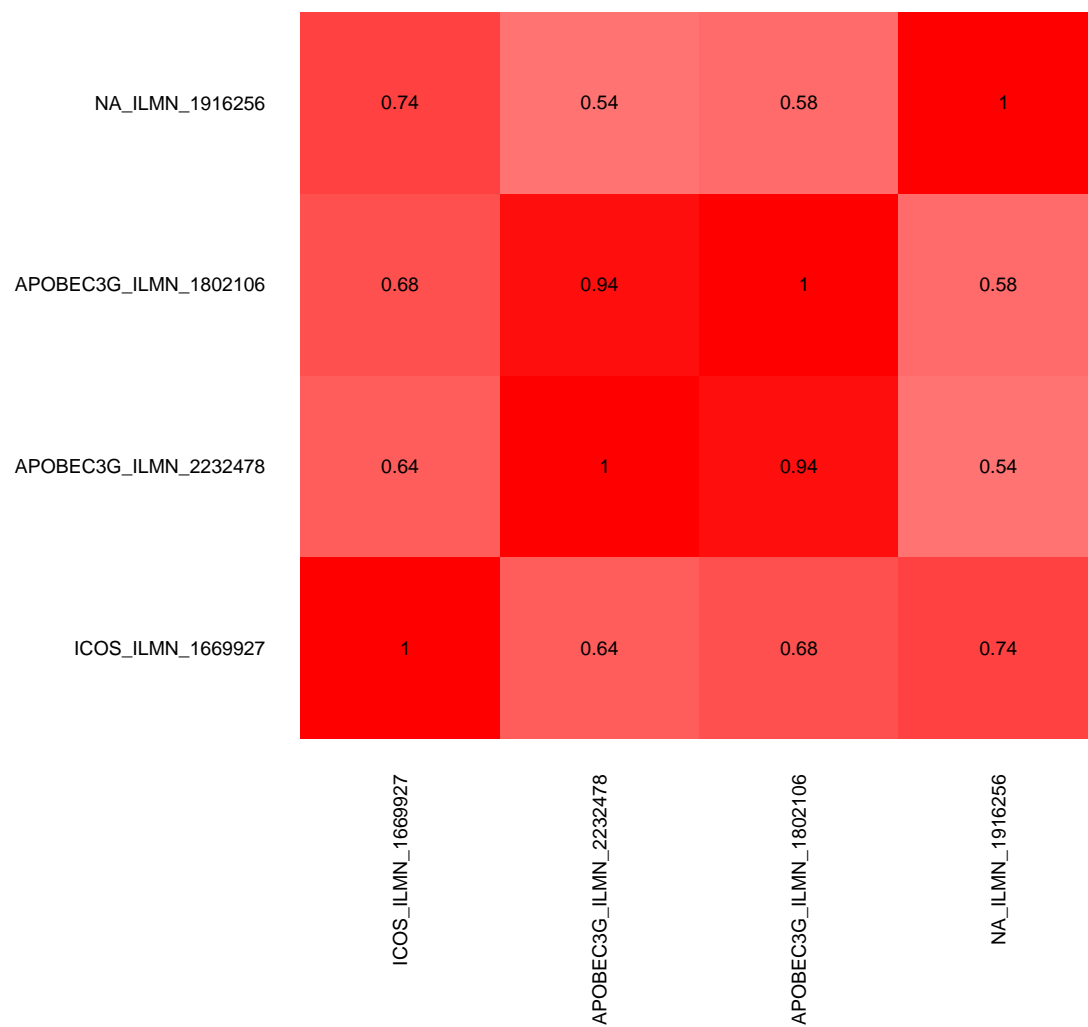
Tabelle 11: Cox regression model, $n = 35$, number of events = 11. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	0.33	1.38	[0.09, 22.22]	0.82
split50-75	2.30	9.98	[0.66, 150.33]	0.10
split75-100	3.64	37.91	[2.51, 573.25]	0.0087

Tabelle 12: Cox regression model, $n = 35$, number of events = 11. Model for the figure on the right. Patients split into quartiles

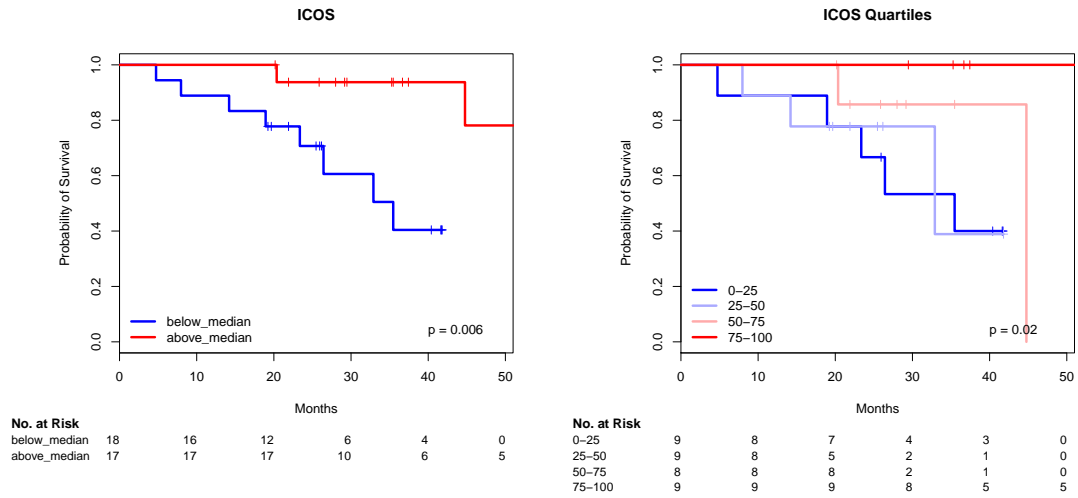
1.2 Higher expression = better survival

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



1.2.1 ICOS ILMN_1669927

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



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-2.37	0.09	[0.01, 0.75]	0.03

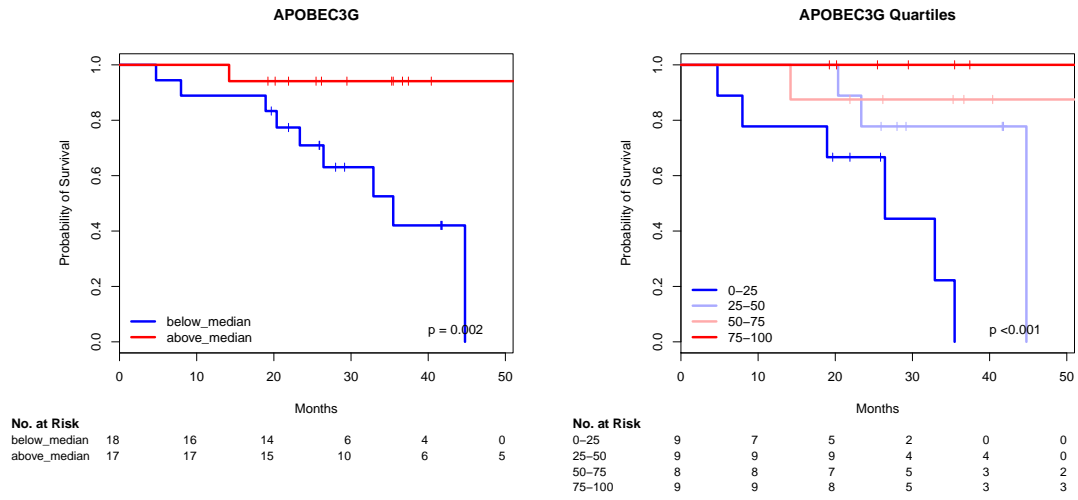
Tabelle 13: Cox regression model, $n = 35$, number of events = 11. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-0.11	0.90	[0.21, 3.88]	0.89
split50-75	-1.38	0.25	[0.03, 2.18]	0.21
split75-100	-21.33	0.0000000005	[0.00, Inf]	1.00

Tabelle 14: Cox regression model, $n = 35$, number of events = 11. Model for the figure on the right. Patients split into quartiles

1.2.2 APOBEC3G ILMN_2232478

Gene symbol from a different, less reliable annotation table: APOBEC3G



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-2.60	0.07	[0.01, 0.61]	0.02

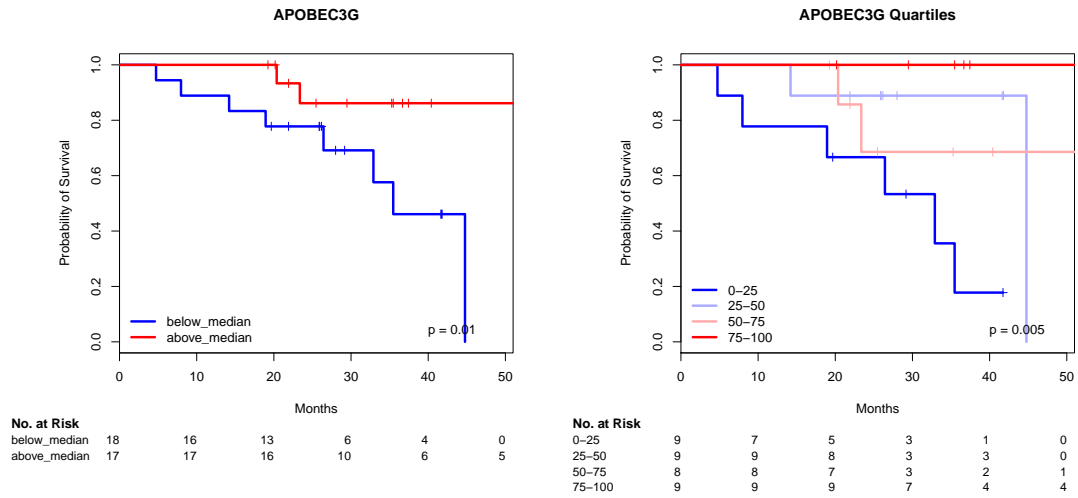
Tabelle 15: Cox regression model, $n = 35$, number of events = 11. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-1.47	0.23	[0.05, 1.02]	0.05
split50-75	-2.69	0.07	[0.01, 0.68]	0.02
split75-100	-22.09	0.0000000003	[0.00, Inf]	1.00

Tabelle 16: Cox regression model, $n = 35$, number of events = 11. Model for the figure on the right. Patients split into quartiles

1.2.3 APOBEC3G ILMN_1802106

Gene symbol from a different, less reliable annotation table: APOBEC3G



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-1.77	0.17	[0.03, 0.83]	0.03

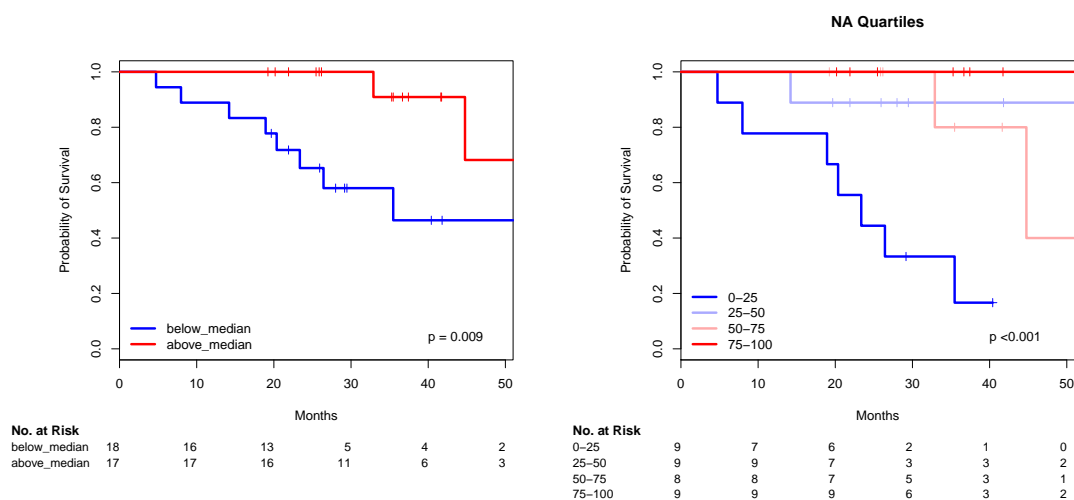
Tabelle 17: Cox regression model, $n = 35$, number of events = 11. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-1.51	0.22	[0.04, 1.18]	0.08
split50-75	-1.72	0.18	[0.03, 1.14]	0.07
split75-100	-3.42	0.03	[0.00, 0.40]	0.0076

Tabelle 18: Cox regression model, $n = 35$, number of events = 11. Model for the figure on the right. Patients split into quartiles

1.2.4 NA ILMN_1916256

Gene symbol from a different, less reliable annotation table:



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	-1.82	0.16	[0.03, 0.76]	0.02

Tabelle 19: Cox regression model, $n = 35$, number of events = 11. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	-2.27	0.10	[0.02, 0.71]	0.02
split50-75	-2.15	0.12	[0.02, 0.71]	0.02
split75-100	-21.54	0.0000000004	[0.00, Inf]	1.00

Tabelle 20: Cox regression model, $n = 35$, number of events = 11. Model for the figure on the right. Patients split into quartiles