

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

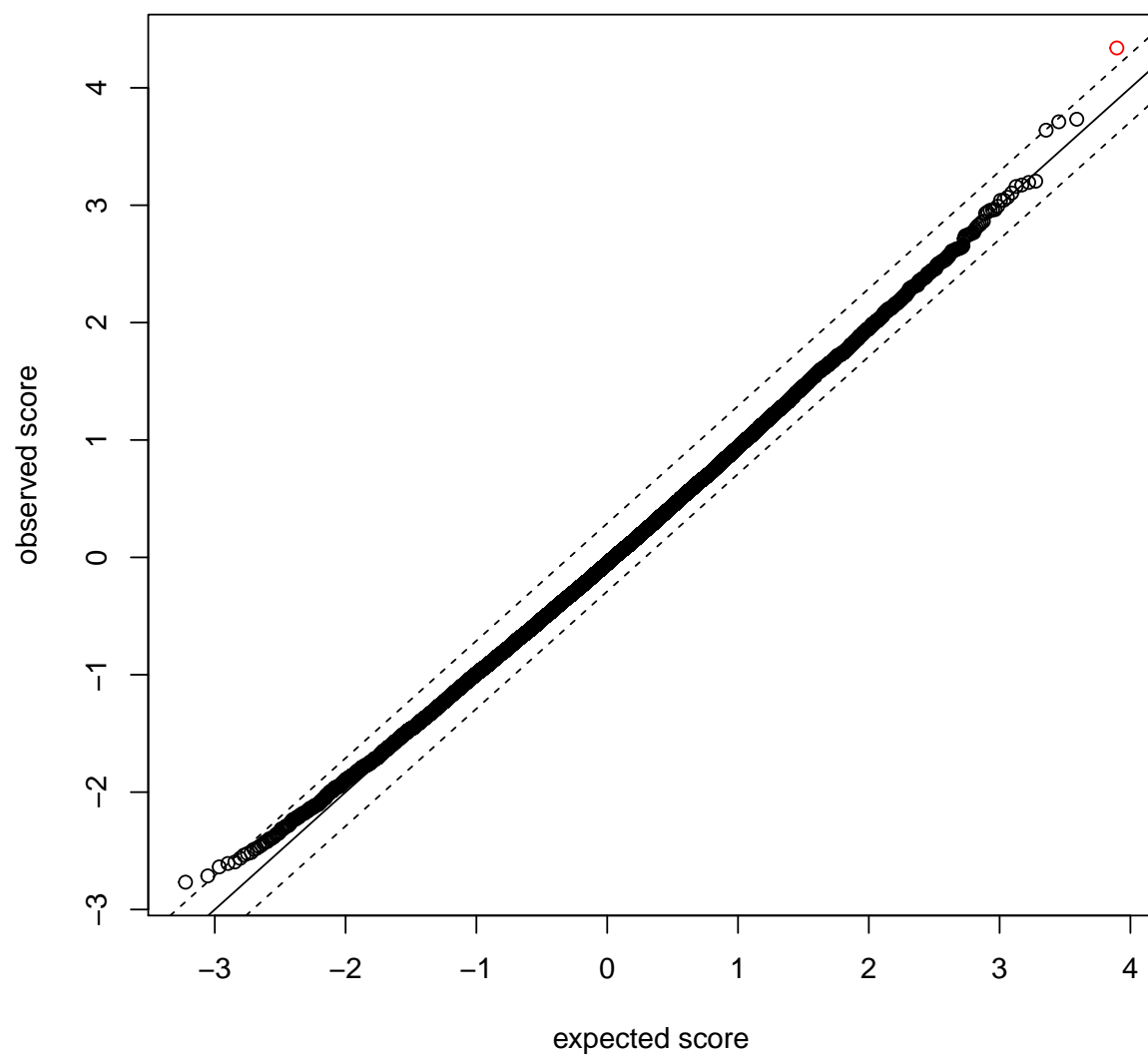
Number of analyzed patients:

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

False discovery rate (FDR) threshold:

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

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



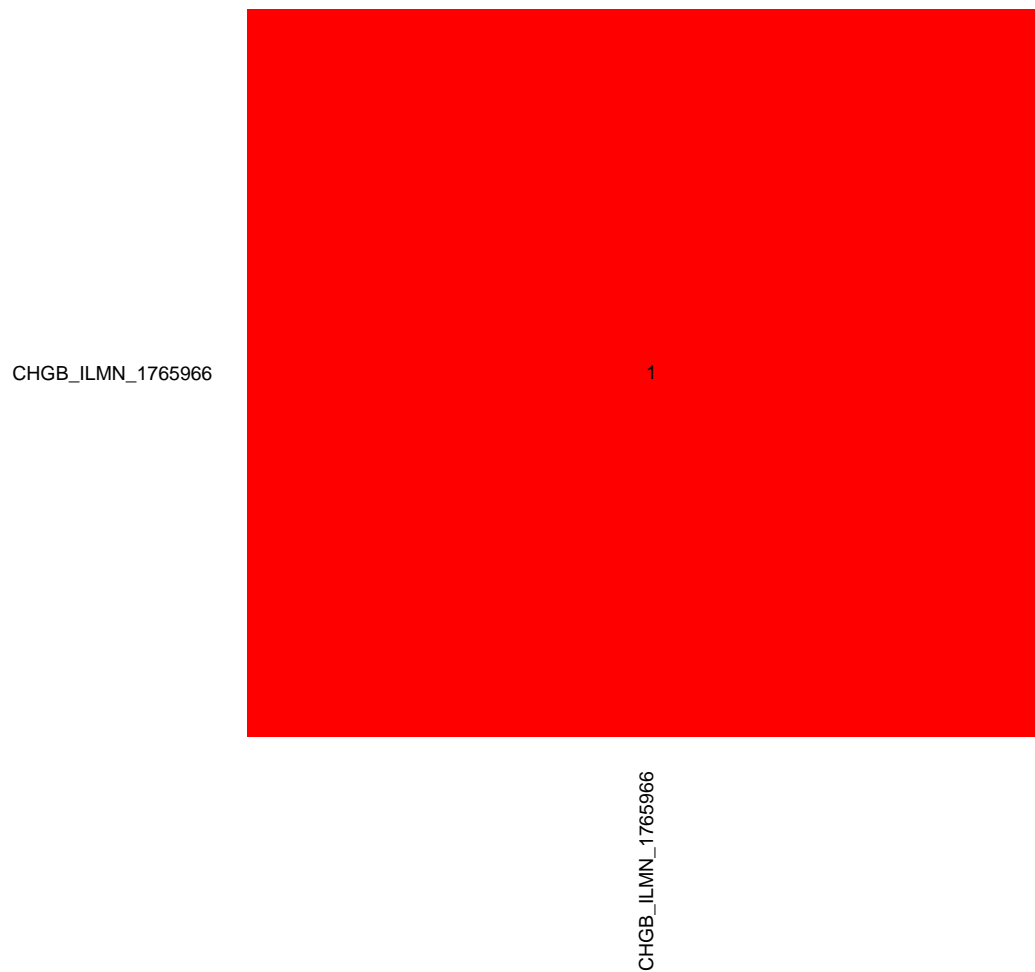
```
siggenes.table
```

```
## $genes.up
##      Row   Gene ID Gene Name      Score(d)      Numerator(r)
## [1,] "4466" "CHGB"  "ILMN_1765966" "4.3396573230577" "2.36593380328997"
##      Denominator(s+s0)  q-value(%)
## [1,] "0.545189084566462" "0"
##
## $genes.lo
## NULL
##
## $color.ind.for.multi
## NULL
##
## $ngenes.up
## [1] 1
```

```
##  
## $ngenes.lo  
## [1] 0
```

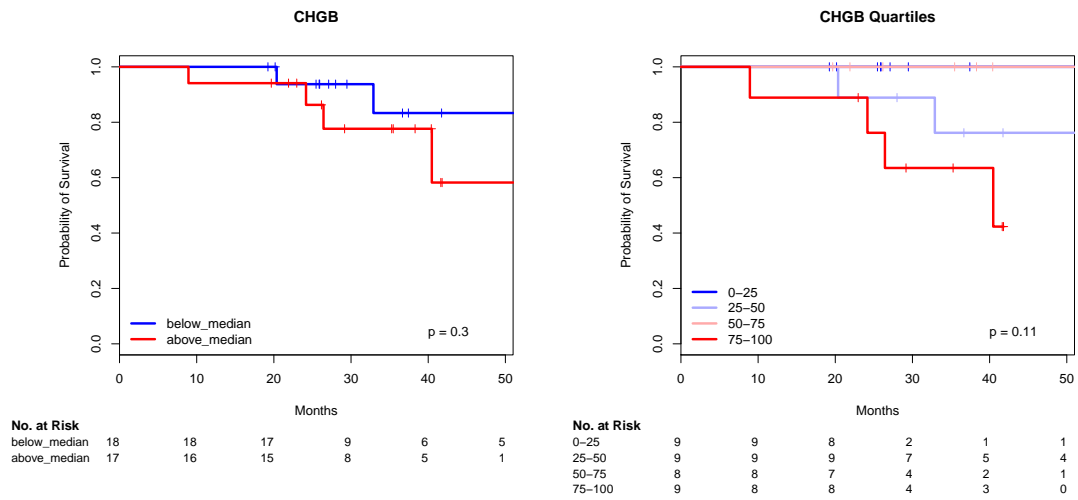
1.1 Higher expression = poorer survival

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



1.1.1 CHGB ILMN_1765966

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



	coef	HR = exp(coef)	95% CI	p-value
splitabove_median	0.87	2.39	[0.44, 13.07]	0.32

Tabelle 1: Cox regression model, $n = 35$, number of events = 6. Model for the figure on the left. Patients split by median.

	coef	HR = exp(coef)	95% CI	p-value
split25-50	19.65	340301009.70	[0.00, Inf]	1.00
split50-75	0.01	1.01	[0.00, Inf]	1.00
split75-100	20.61	896250341.72	[0.00, Inf]	1.00

Tabelle 2: Cox regression model, $n = 35$, number of events = 6. 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:

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

no significant genes