

# Glyphosate primes mammary cells for tumorigenesis by reprogramming the epigenome in a TET3-dependent manner.

Manon Duforestel<sup>1-2-3-4-5</sup>, Arulraj Nadaradjane<sup>1-2-3-4-5</sup>, Gwenola Bougras-Cartron<sup>1-2-3-4-5</sup>, Joséphine Briand<sup>1-2-3-4-5</sup>, Christophe Olivier<sup>1-2-6</sup>, Jean-Sébastien Frenel<sup>1-2-3-4-5</sup>, François M Vallette<sup>1-2-3-4-5</sup>, Sophie A. Lelièvre<sup>7,8</sup> and Pierre-François Cartron<sup>1-2-3-4-5</sup>

<sup>1</sup> CRCINA, INSERM, Université de Nantes, Nantes, France.

<sup>2</sup> Equipe Apoptose et Progression tumorale, LaBCT, Institut de Cancérologie de l'Ouest, Saint Herblain, France.

<sup>3</sup> Cancéropole Grand-Ouest, réseau Epigénétique (RepiCGO).

<sup>4</sup> EpiSAVMEN Consortium (Région Pays de la Loire).

<sup>5</sup> LabEX IGO, Université de Nantes, France.

<sup>6</sup> Service de toxicologie, Faculté de pharmacie de Nantes. Nantes, France

<sup>7</sup> Department of Basic Medical Sciences, Purdue University, West Lafayette, IN United States of America

<sup>8</sup> Purdue University Center for Cancer Research, West Lafayette, IN, United States of America

\* Correspondence: [pierre-francois.cartron@inserm.fr](mailto:pierre-francois.cartron@inserm.fr), CRCINA, INSERM U1232, Equipe Apoptose et Progression tumorale, LaBCT, Institut de Cancérologie de l'Ouest, Boulevard du Pr Jacques Monod, Saint Herblain, 44805, France.

**Running title:** Glyphosate-mediated breast cancer risk

**Keywords:** DNA methylation, TET, breast cancer, hypomethylation, epigenetic mark.

**Supplementary File 1: Kaplan-Meier illustrated the potential outcome of TET3 expression in panel of cancer according to KM plotter website.** KM plotter website ([www.kmplot.com](http://www.kmplot.com)); In the meantime, please kindly cite our paper to support further development: Nagy Á, Lánckzy A, Menyhárt O, Gyórfy B: Validation of miRNA prognostic power in hepatocellular carcinoma using expression data of independent datasets, Scientific Reports, 2018;8:9277 | DOI:10.1038/s41598-018-27521-y) is a database having the ability to assess the effect of 54k genes on survival in a large number of cancer types (n=21).

# Kaplan- Meier Plotter

## Pan-cancer RNA-seq

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The desired RNAseq ID is valid: TET3 (-),

<b>RNAseq ID:</b>	TET3	=
<b>Survival:</b>	OS	
<b>Auto select best cutoff:</b>	checked	
<b>Follow up threshold:</b>	all	
<b>Censore at threshold:</b>	checked	
<b>Compute median over entire database:</b>	false	
<b>Cutoff value used in analysis:</b>	1483	
<b>Expression range of the probe:</b>	131 - 5949	
<b>Invert HR values below 1:</b>	not checked	

### Restrictions

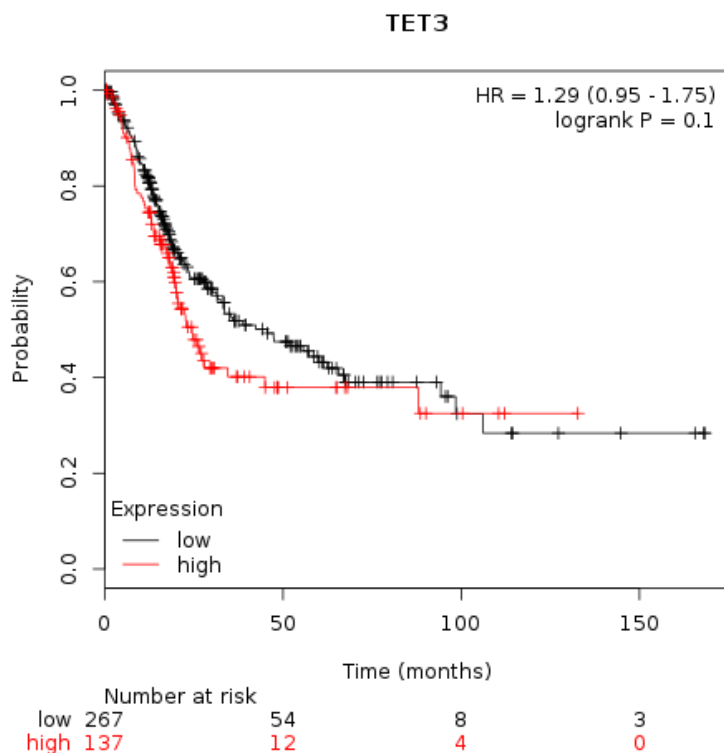
Tumor type: Bladder Carcinoma

### Restrictions

Stage: all  
Gender: all  
Race: all  
Grade: all  
Mutation burden: all

### Results

**P value:** 0.0999  
**FDR:** 100%



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**RNAseq ID:** TET3 =

**Survival:** OS

**Auto select best cutoff:** checked

**Follow up threshold:** all

**Censore at threshold:** checked

**Compute median over entire database:** false

**Cutoff value used in analysis:** 781

**Expression range of the probe:** 97 - 5141

**Invert HR values below 1:** not checked

## Restrictions

Tumor type: Breast cancer

## Restrictions

Stage: all

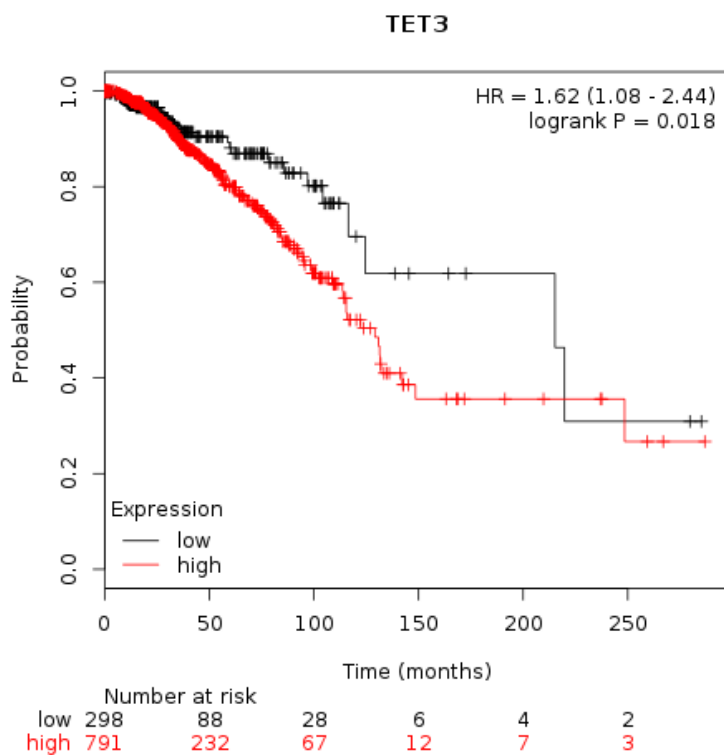
Gender: all

Race: all

Grade: all

Mutation burden: all

## Results

**P value:** 0.0177**FDR:** over 50%[Download plot as a PDF](#)[Download p values vs. cutoff table](#)

<b>RNAseq ID:</b>	TET3	=
<b>Survival:</b>	OS	
<b>Auto select best cutoff:</b>	checked	
<b>Follow up threshold:</b>	all	
<b>Censore at threshold:</b>	checked	
<b>Compute median over entire database:</b>	false	
<b>Cutoff value used in analysis:</b>	870	
<b>Expression range of the probe:</b>	90 - 4627	
<b>Invert HR values below 1:</b>	not checked	

## Restrictions

Tumor type: Cervical squamous cell carcinoma

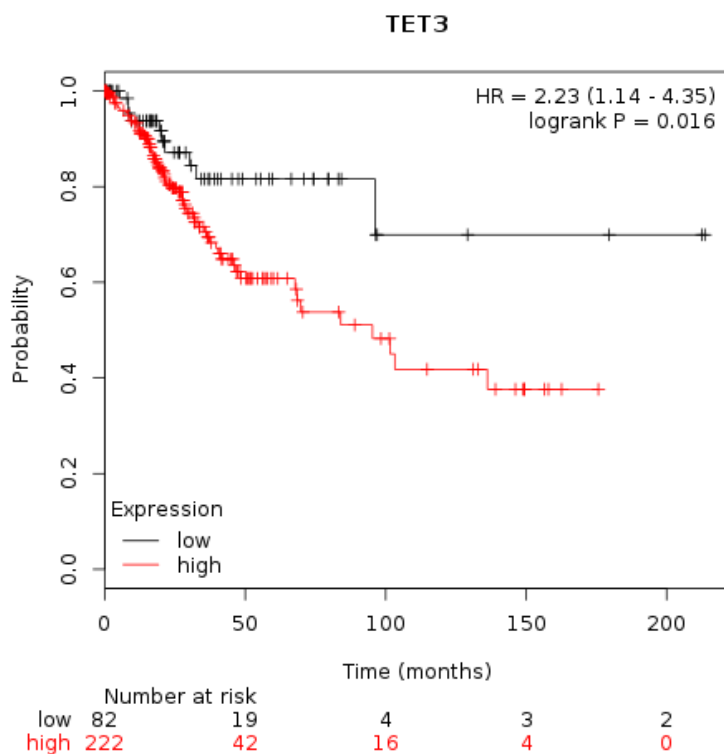
## Restrictions

Stage:	all
Gender:	all
Race:	all
Grade:	all
Mutation burden:	all

## Results

**P value:** 0.016

**FDR:** over 50%



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<b>RNAseq ID:</b>	TET3	=
<b>Survival:</b>	OS	
<b>Auto select best cutoff:</b>	checked	
<b>Follow up threshold:</b>	all	
<b>Censore at threshold:</b>	checked	
<b>Compute median over entire database:</b>	false	
<b>Cutoff value used in analysis:</b>	2318	
<b>Expression range of the probe:</b>	621 - 7710	
<b>Invert HR values below 1:</b>	not checked	

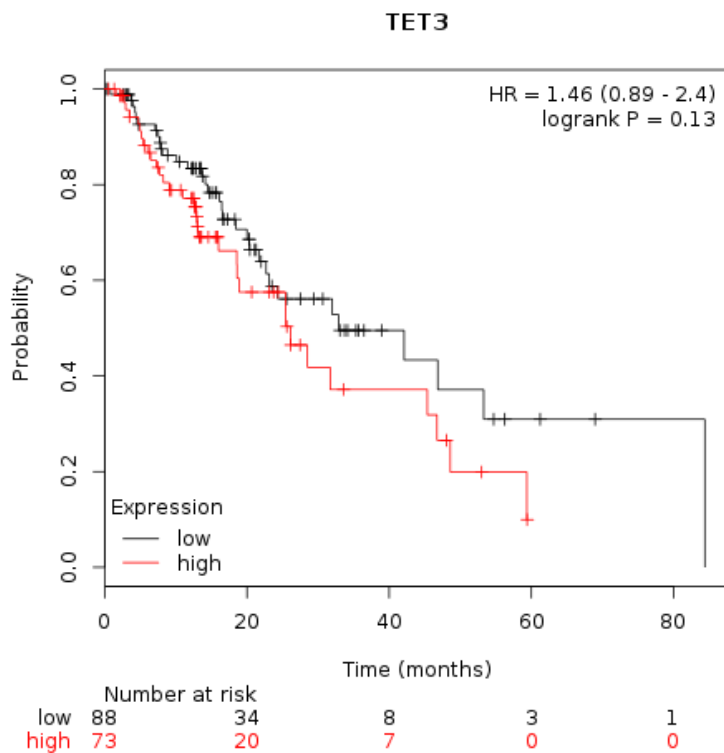
## Restrictions

Tumor type: Esophageal carcinoma

## Restrictions

Stage:	all
Gender:	all
Race:	all
Grade:	all

Mutation burden: all

**Results****P value:** 0.1295**FDR:** 100%[Download plot as a PDF](#)[Download p values vs. cutoff table](#)

**RNAseq ID:** TET3 =

**Survival:** OS

**Auto select best cutoff:** checked

**Follow up threshold:** all

**Censore at threshold:** checked

**Compute median over entire database:** false

**Cutoff value used in analysis:** 1245

**Expression range of the probe:** 95 - 7114

**Invert HR values below 1:** not checked

**Restrictions**

Tumor type: Head-neck squamous cell carcinoma

**Restrictions**

Stage: all

Gender: all

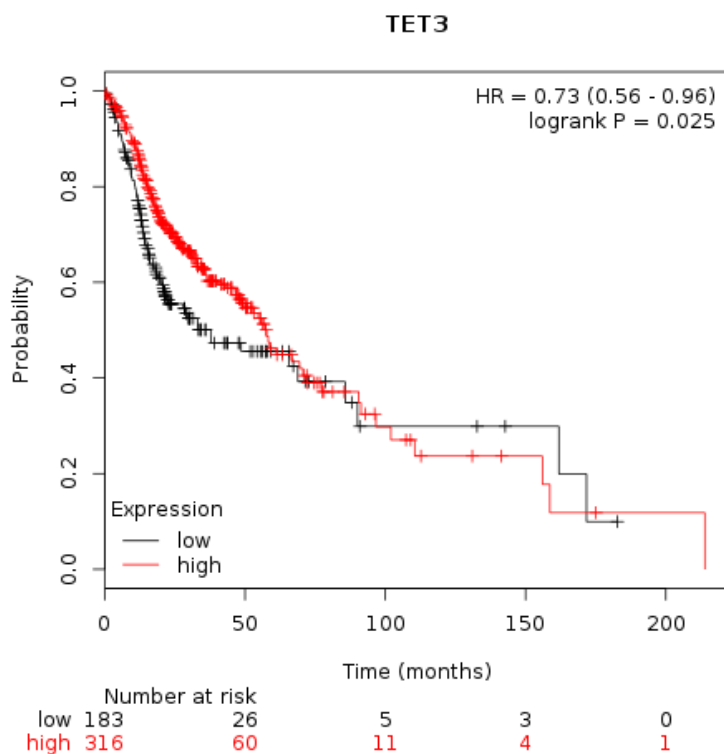
Race: all

Grade: all  
Mutation burden: all

## Results

**P value:** 0.0253

**FDR:** over 50%



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<b>RNAseq ID:</b>	TET3	=
<b>Survival:</b>	OS	
<b>Auto select best cutoff:</b>	checked	
<b>Follow up threshold:</b>	all	
<b>Censore at threshold:</b>	checked	
<b>Compute median over entire database:</b>	false	
<b>Cutoff value used in analysis:</b>	465	
<b>Expression range of the probe:</b>	11 - 2270	
<b>Invert HR values below 1:</b>	not checked	

## Restrictions

Tumor type: Kidney renal clear cell carcinoma

## Restrictions

Stage: all

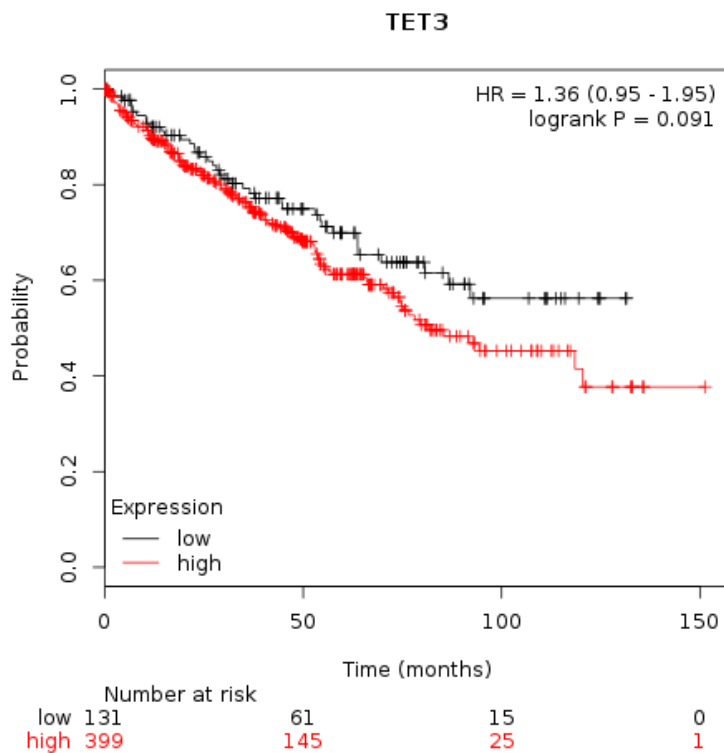


Gender: all  
 Race: all  
 Grade: all  
 Mutation burden: all

## Results

**P value:** 0.0905

**FDR:** 100%



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**RNAseq ID:** TET3 =  
**Survival:** OS  
**Auto select best cutoff:** checked  
**Follow up threshold:** all  
**Censore at threshold:** checked  
**Compute median over entire database:** false  
**Cutoff value used in analysis:** 600  
**Expression range of the probe:** 66 - 3118  
**Invert HR values below 1:** not checked

## Restrictions

Tumor type: Kidney renal papillary cell carcinoma

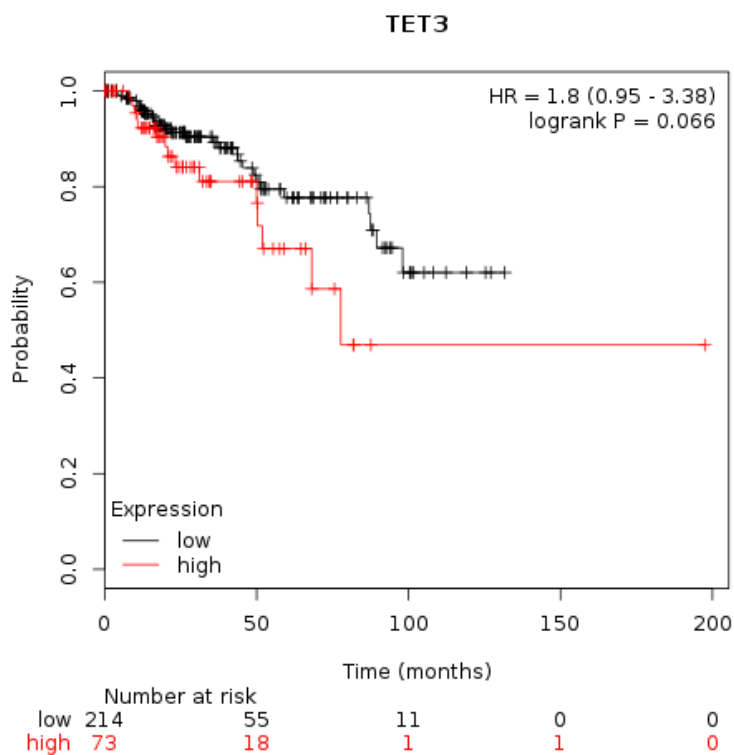
## Restrictions

Stage: all  
 Gender: all  
 Race: all  
 Grade: all  
 Mutation burden: all

## Results

**P value:** 0.0655

**FDR:** 100%



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<b>RNAseq ID:</b>	TET3	=
<b>Survival:</b>	OS	
<b>Auto select best cutoff:</b>	checked	
<b>Follow up threshold:</b>	all	
<b>Censore at threshold:</b>	checked	
<b>Compute median over entire database:</b>	false	
<b>Cutoff value used in analysis:</b>	359	
<b>Expression range of the probe:</b>	28 - 2145	
<b>Invert HR values below 1:</b>	not checked	

## Restrictions

Tumor type: Liver hepatocellular carcinoma

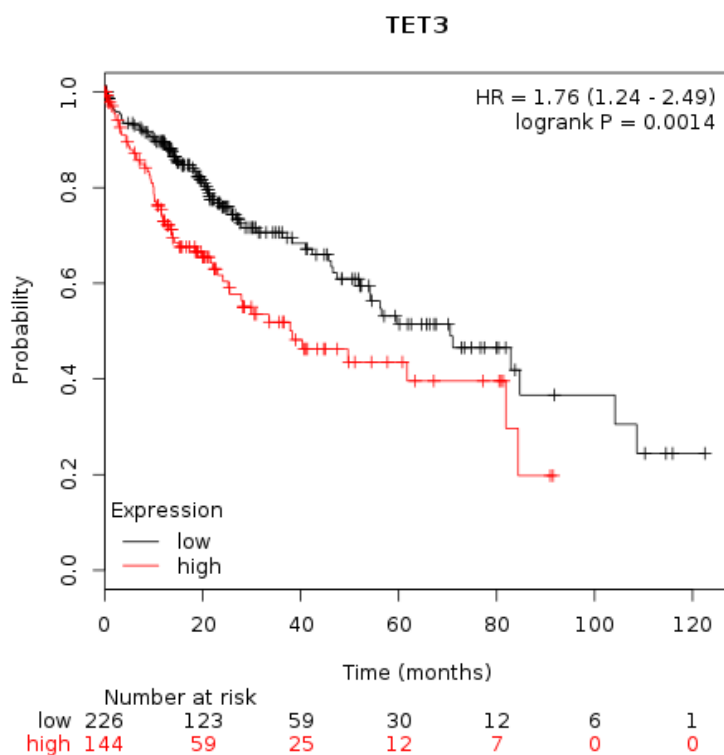
## Restrictions

Stage: all  
 Gender: all  
 Race: all  
 Grade: all  
 Mutation burden: all

## Results

**P value:** 0.0014

**FDR:** 20%



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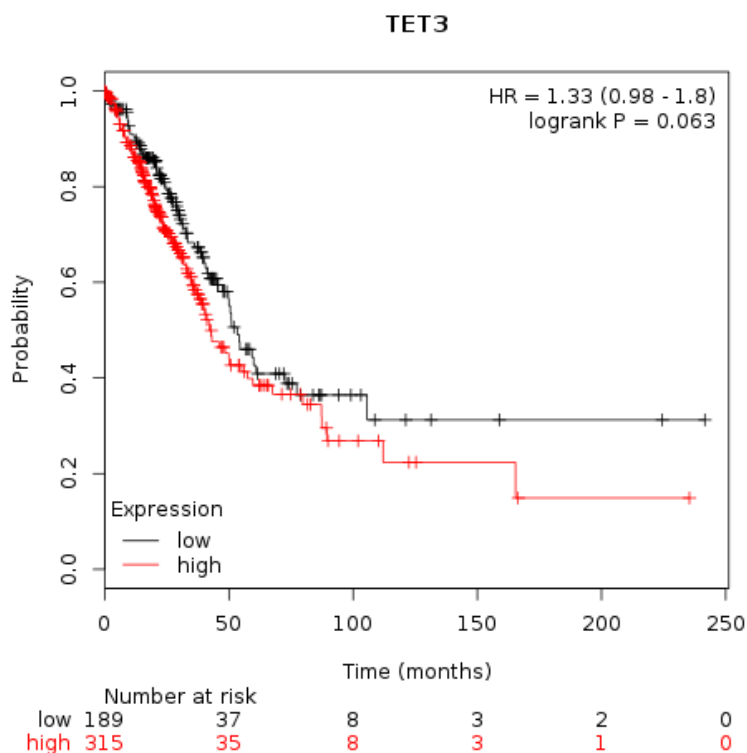
**RNAseq ID:** TET3 =  
**Survival:** OS  
**Auto select best cutoff:** checked  
**Follow up threshold:** all  
**Censore at threshold:** checked  
**Compute median over entire database:** false  
**Cutoff value used in analysis:** 777  
**Expression range of the probe:** 130 - 4045  
**Invert HR values below 1:** not checked

## Restrictions

Tumor type: Lung adenocarcinoma

**Restrictions**

Stage: all  
 Gender: all  
 Race: all  
 Grade: all  
 Mutation burden: all

**Results****P value:** 0.0627**FDR:** 100%[Download plot as a PDF](#)[Download p values vs. cutoff table](#)

**RNAseq ID:** TET3 =  
**Survival:** OS  
**Auto select best cutoff:** checked  
**Follow up threshold:** all  
**Censore at threshold:** checked  
**Compute median over entire database:** false  
**Cutoff value used in analysis:** 2587  
**Expression range of the probe:** 146 - 6967  
**Invert HR values below 1:** not checked

## Restrictions

Tumor type: Lung squamous cell carcinoma

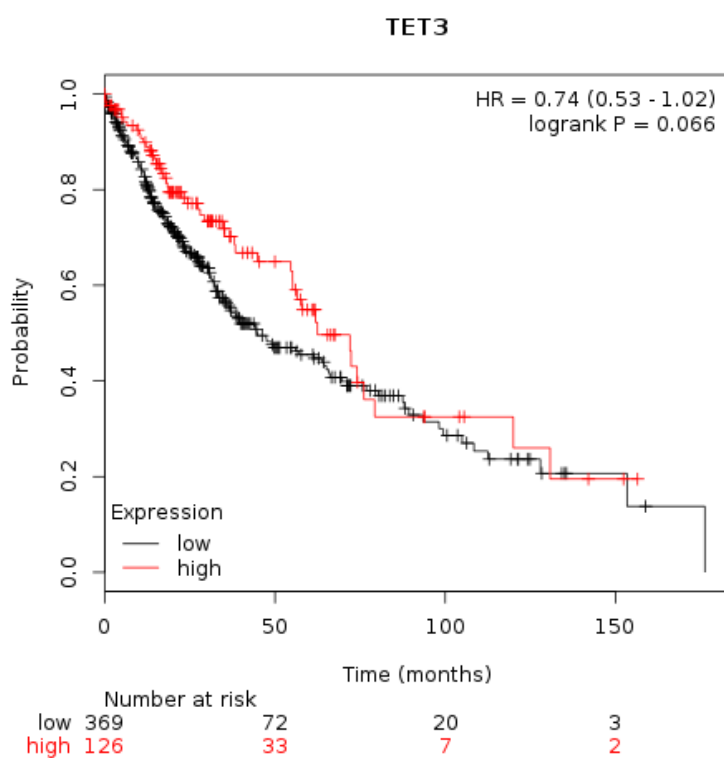
## Restrictions

Stage: all  
 Gender: all  
 Race: all  
 Grade: all  
 Mutation burden: all

## Results

**P value:** 0.0659

**FDR:** 100%



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<b>RNAseq ID:</b>	TET3	=
<b>Survival:</b>	OS	
<b>Auto select best cutoff:</b>	checked	
<b>Follow up threshold:</b>	all	
<b>Censore at threshold:</b>	checked	
<b>Compute median over entire database:</b>	false	
<b>Cutoff value used in analysis:</b>	791	
<b>Expression range of the probe:</b>	137 - 4458	

**Invert HR values below 1:** not checked

## Restrictions

Tumor type: Ovarian cancer

## Restrictions

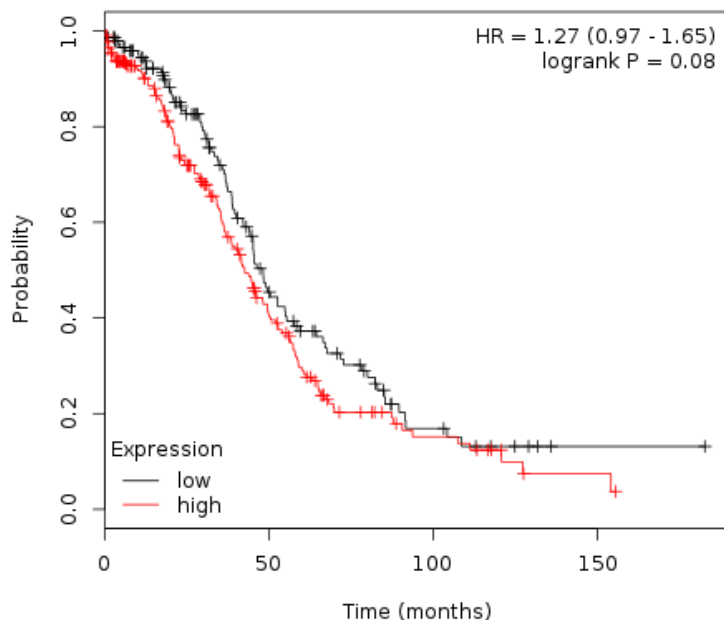
Stage: all  
 Gender: all  
 Race: all  
 Grade: all  
 Mutation burden: all

## Results

**P value:** 0.0801

**FDR:** 100%

### TET3



	0	50	100	150
low	149	46	10	1
high	224	60	11	2

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**RNAseq ID:** TET3 =  
**Survival:** OS  
**Auto select best cutoff:** checked  
**Follow up threshold:** all  
**Censore at threshold:** checked  
**Compute median over entire database:** false  
**Cutoff value used in analysis:** 849

**Expression range of the probe:** 74 - 1303  
**Invert HR values below 1:** not checked

## Restrictions

Tumor type: Pancreatic ductal adenocarcinoma

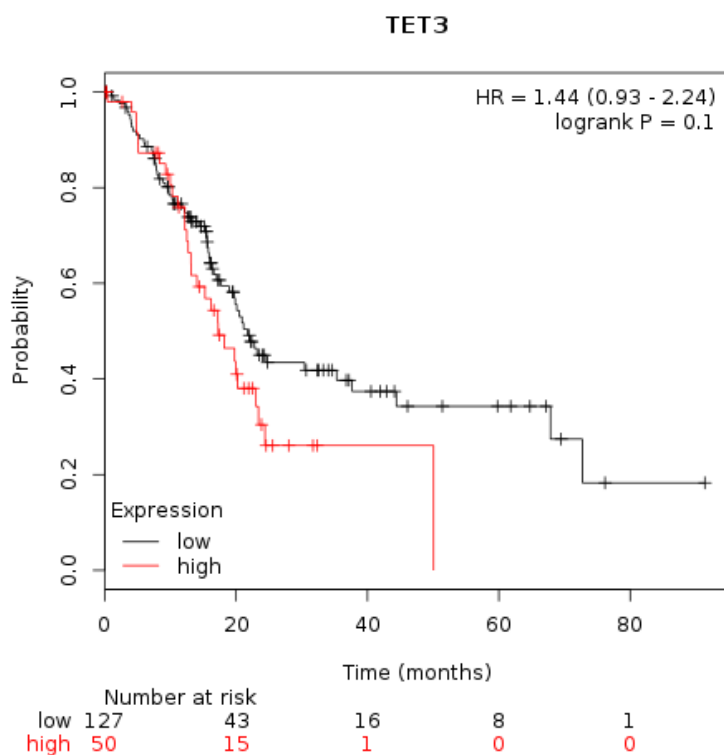
## Restrictions

Stage: all  
 Gender: all  
 Race: all  
 Grade: all  
 Mutation burden: all

## Results

**P value:** 0.1045

**FDR:** 100%



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**RNAseq ID:** TET3 =  
**Survival:** OS  
**Auto select best cutoff:** checked  
**Follow up threshold:** all  
**Censore at threshold:** checked

**Compute median over entire database:** false  
**Cutoff value used in analysis:** 302  
**Expression range of the probe:** 42 - 1229  
**Invert HR values below 1:** not checked

## Restrictions

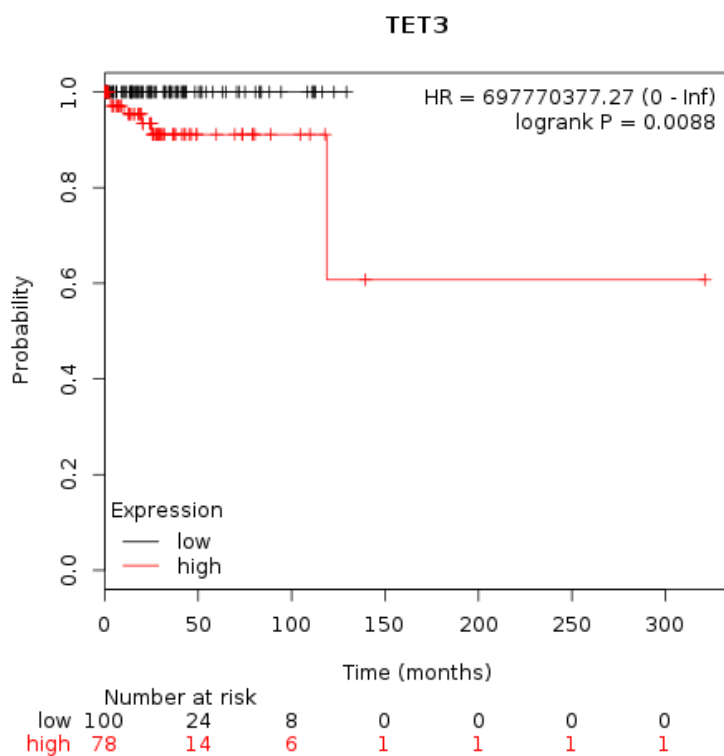
Tumor type: Pheochromocytoma and Paraganglioma

## Restrictions

Stage: all  
 Gender: all  
 Race: all  
 Grade: all  
 Mutation burden: all

## Results

**P value:** 0.0088  
**FDR:** over 50%



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**RNAseq ID:** TET3 =  
**Survival:** OS  
**Auto select best cutoff:** checked  
**Follow up threshold:** all



**Censore at threshold:** checked  
**Compute median over entire database:** false  
**Cutoff value used in analysis:** 1286  
**Expression range of the probe:** 150 - 2312  
**Invert HR values below 1:** not checked

## Restrictions

Tumor type: Rectum adenocarcinoma

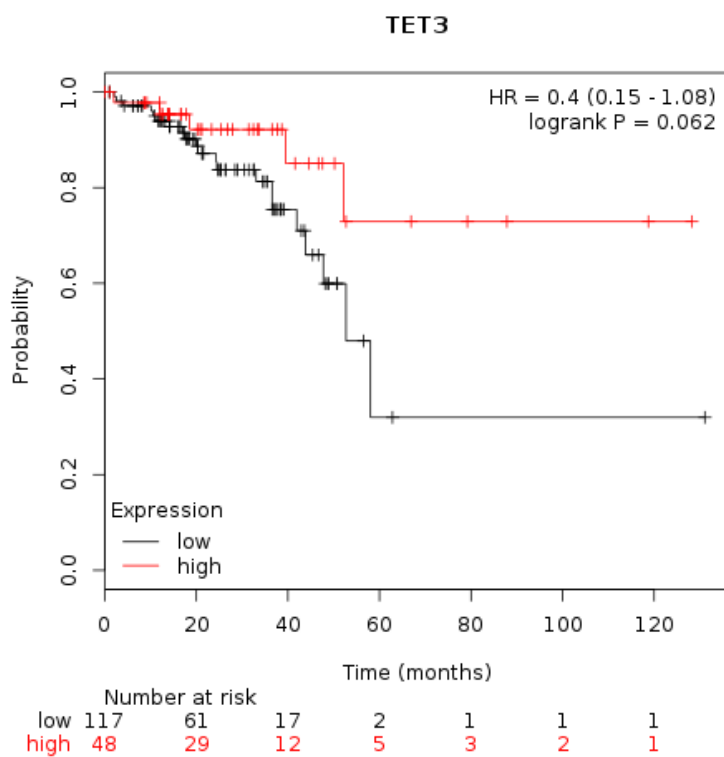
## Restrictions

Stage: all  
 Gender: all  
 Race: all  
 Grade: all  
 Mutation burden: all

## Results

**P value:** 0.062

**FDR:** 100%



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**RNAseq ID:** TET3 =  
**Survival:** OS

**Auto select best cutoff:** checked  
**Follow up threshold:** all  
**Censore at threshold:** checked  
**Compute median over entire database:** false  
**Cutoff value used in analysis:** 450  
**Expression range of the probe:** 45 - 3781  
**Invert HR values below 1:** not checked

### Restrictions

Tumor type: Sarcoma

### Restrictions

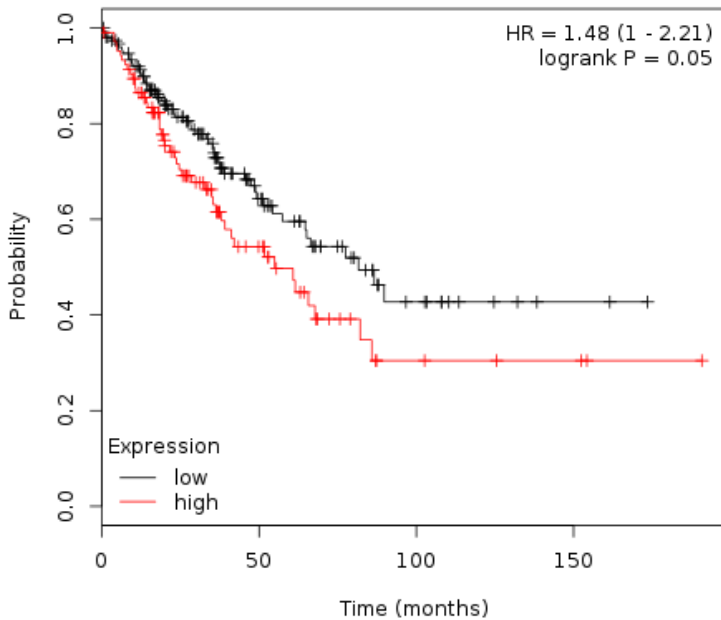
Stage: all  
 Gender: all  
 Race: all  
 Grade: all  
 Mutation burden: all

### Results

**P value:** 0.0505

**FDR:** 100%

#### TET3



	0	50	100	150
low	154	46	11	2
high	105	27	5	3

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**RNAseq ID:** TET3 -

**Survival:** OS  
**Auto select best cutoff:** checked  
**Follow up threshold:** all  
**Censore at threshold:** checked  
**Compute median over entire database:** false  
**Cutoff value used in analysis:** 1012  
**Expression range of the probe:** 273 - 4358  
**Invert HR values below 1:** not checked

## Restrictions

Tumor type: Stomach adenocarcinoma

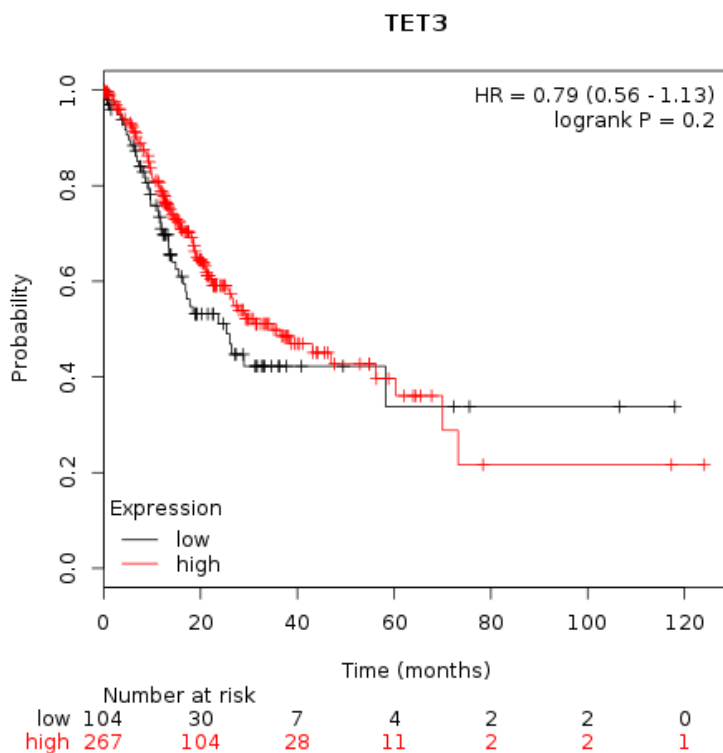
## Restrictions

Stage: all  
 Gender: all  
 Race: all  
 Grade: all  
 Mutation burden: all

## Results

**P value:** 0.199

**FDR:** 100%



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**RNAseq ID:** TET3 =  
**Survival:** OS  
**Auto select best cutoff:** checked  
**Follow up threshold:** all  
**Censore at threshold:** checked  
**Compute median over entire database:** false  
**Cutoff value used in analysis:** 579  
**Expression range of the probe:** 101 - 3565  
**Invert HR values below 1:** not checked

## Restrictions

Tumor type: Testicular Germ Cell Tumor

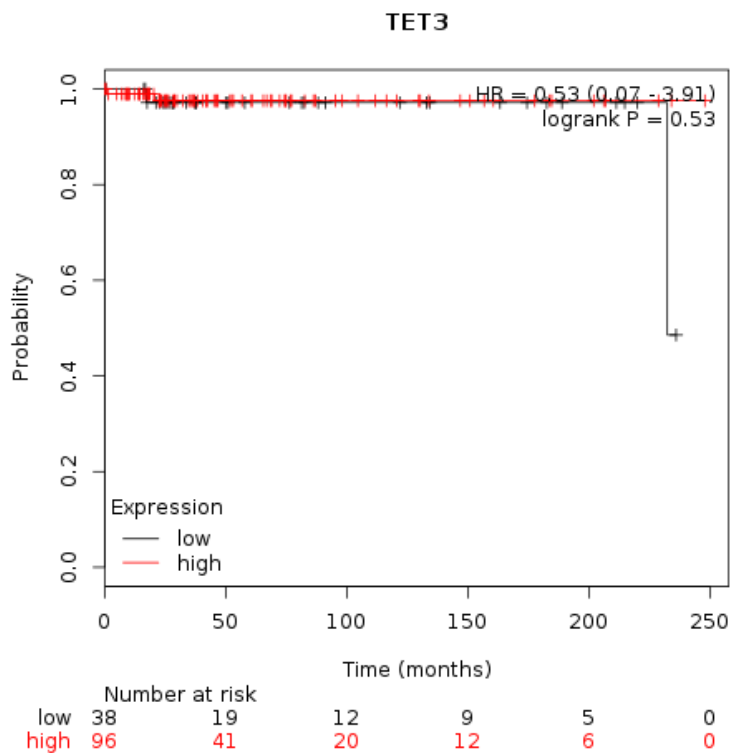
## Restrictions

Stage: all  
 Gender: all  
 Race: all  
 Grade: all  
 Mutation burden: all

## Results

**P value:** 0.5297

**FDR:** 100%



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**RNAseq ID:** TET3 =  
**Survival:** OS  
**Auto select best cutoff:** checked  
**Follow up threshold:** all  
**Censore at threshold:** checked  
**Compute median over entire database:** false  
**Cutoff value used in analysis:** 786  
**Expression range of the probe:** 49 - 1907  
**Invert HR values below 1:** not checked

**Restrictions**

Tumor type: Thymoma

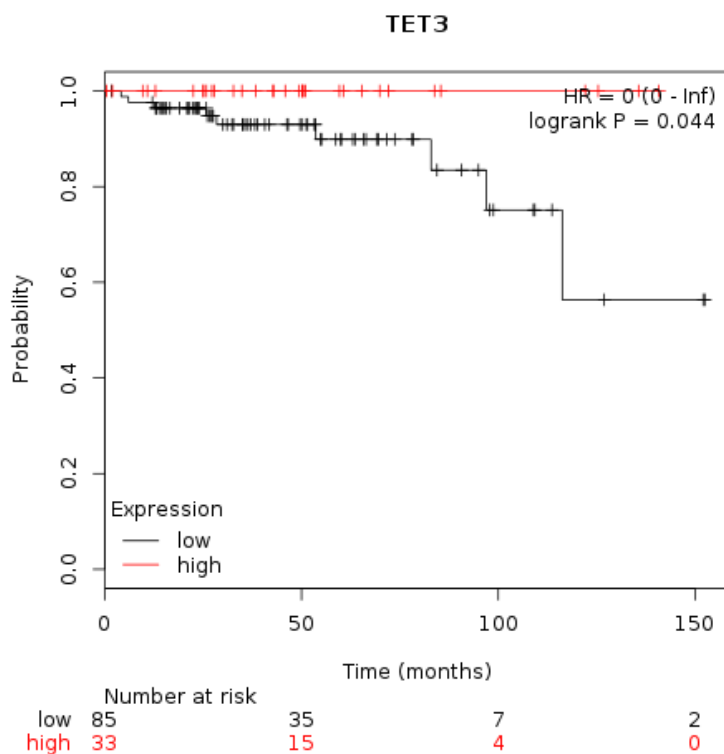
**Restrictions**

Stage: all  
 Gender: all  
 Race: all  
 Grade: all  
 Mutation burden: all

**Results**

**P value:** 0.0441

**FDR:** over 50%



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<b>RNAseq ID:</b>	TET3	=
<b>Survival:</b>	OS	
<b>Auto select best cutoff:</b>	checked	
<b>Follow up threshold:</b>	all	
<b>Censore at threshold:</b>	checked	
<b>Compute median over entire database:</b>	false	
<b>Cutoff value used in analysis:</b>	602	
<b>Expression range of the probe:</b>	109 - 1553	
<b>Invert HR values below 1:</b>	not checked	

### Restrictions

Tumor type: Thyroid carcinoma

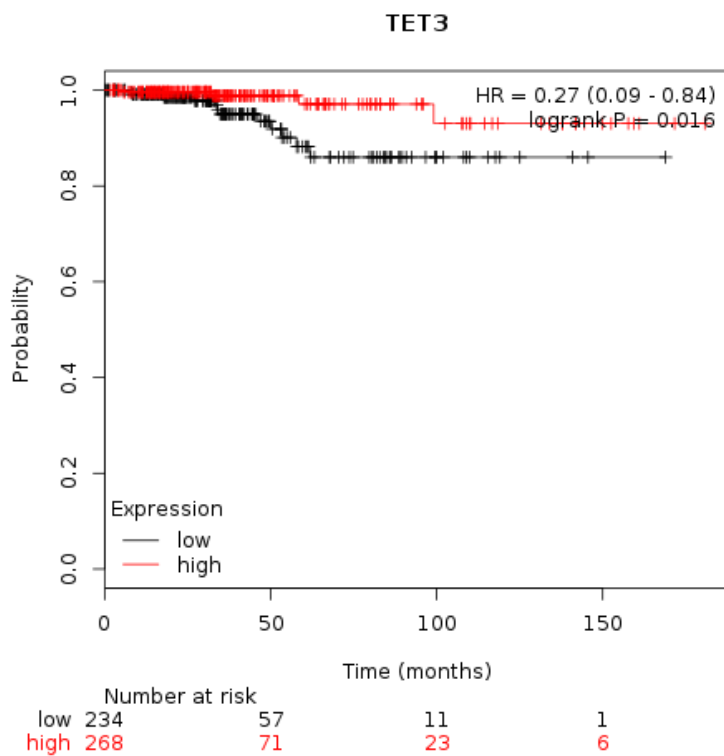
### Restrictions

Stage: all  
Gender: all  
Race: all  
Grade: all  
Mutation burden: all

### Results

**P value:** 0.0157

**FDR:** over 50%



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**RNAseq ID:** TET3 =  
**Survival:** OS  
**Auto select best cutoff:** checked  
**Follow up threshold:** all  
**Censore at threshold:** checked  
**Compute median over entire database:** false  
**Cutoff value used in analysis:** 1279  
**Expression range of the probe:** 77 - 4774  
**Invert HR values below 1:** not checked

## Restrictions

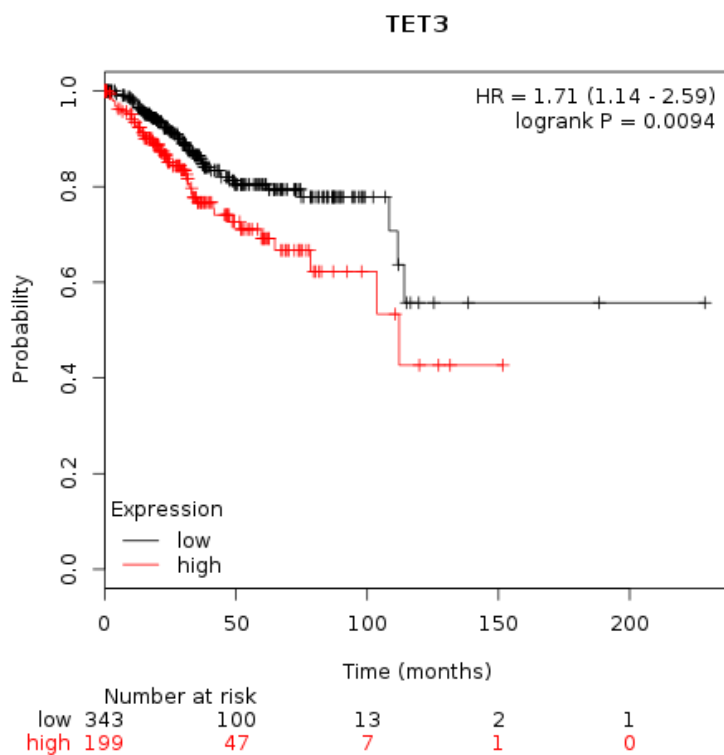
Tumor type: Uterine corpus endometrial carcinoma

## Restrictions

Stage: all  
 Gender: all  
 Race: all  
 Grade: all  
 Mutation burden: all

## Results

**P value:** 0.0094  
**FDR:** over 50%



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