

Parameters

- **Gene A:** Input a gene A of interest. [For x-axis]
- **Gene B:** Input a gene B of interest. [For y-axis]
- **Normalized by gene:** Set the gene used for normalizing Gene A and Gene B.
- **Correlation Coefficient:** The method for calculating the correlation coefficient.
- **TCGA Tumor/TCGA Normal/GTEx/Used Expression Datasets:** Select cancer types of interest in the "TCGA Tumor", "TCGA Normal" or "GTEx" field and click "add" to build dataset list in the "Used Expression Datasets" field. Also, manual input of cancer types split by comma (e.g. COAD Tumor,READ Tumor) is also acceptable. The correlation analysis is based on the datasets list.

[--- Help ---](#)

Gene A

Gene B

Input a gene symbol or id.

Normalized by gene (optional)

Correlation Coefficient

We use the non-log scale for calculation and use the log-scale axis for visualization.

TCGA Tumor (Cancer name)

CHOL Tumor
COAD Tumor
DLBC Tumor

[Add](#)

TCGA Normal

BLCA Normal
BRCA Normal
CESC Normal

[Add](#)

GTEx

Adipose - Subcutaneous
Adipose - Visceral (Omentum)
Adrenal Gland
Bladder

[Add](#)

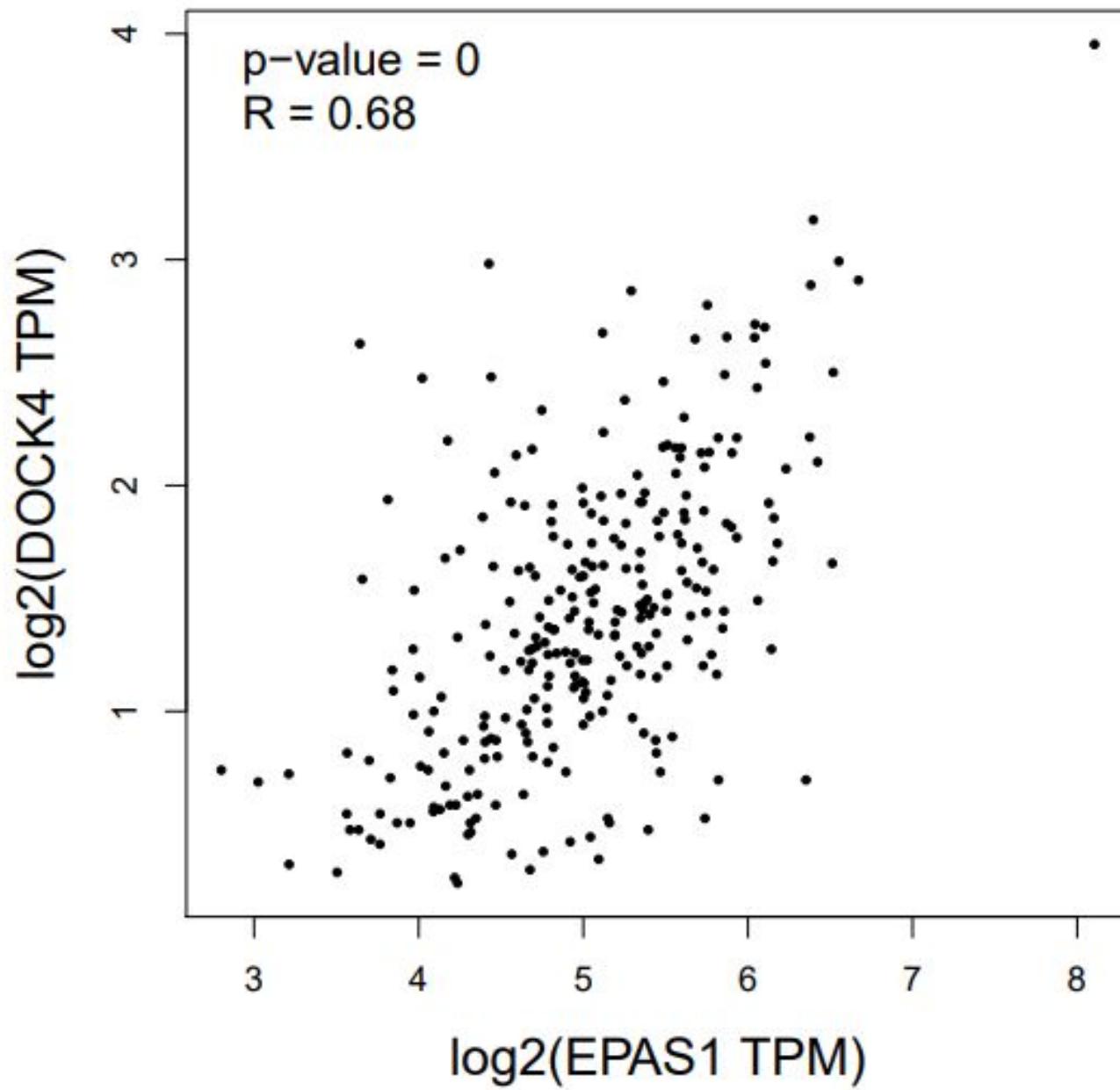
Used Expression Datasets

COAD Tumor

[Reset](#)

The plot is based on the datasets of list.

[Plot](#)



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Gene A

Gene B

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Normalized by gene (optional)

Correlation Coefficient

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TCGA Tumor (Cancer name)

- CHOL Tumor
- COAD Tumor
- DLBC Tumor**

[Add](#)

TCGA Normal

- BLCA Normal
- BRCA Normal
- CESC Normal

[Add](#)

GTEx

- Adipose - Subcutaneous
- Adipose - Visceral (Omentum)
- Adrenal Gland
- Bladder

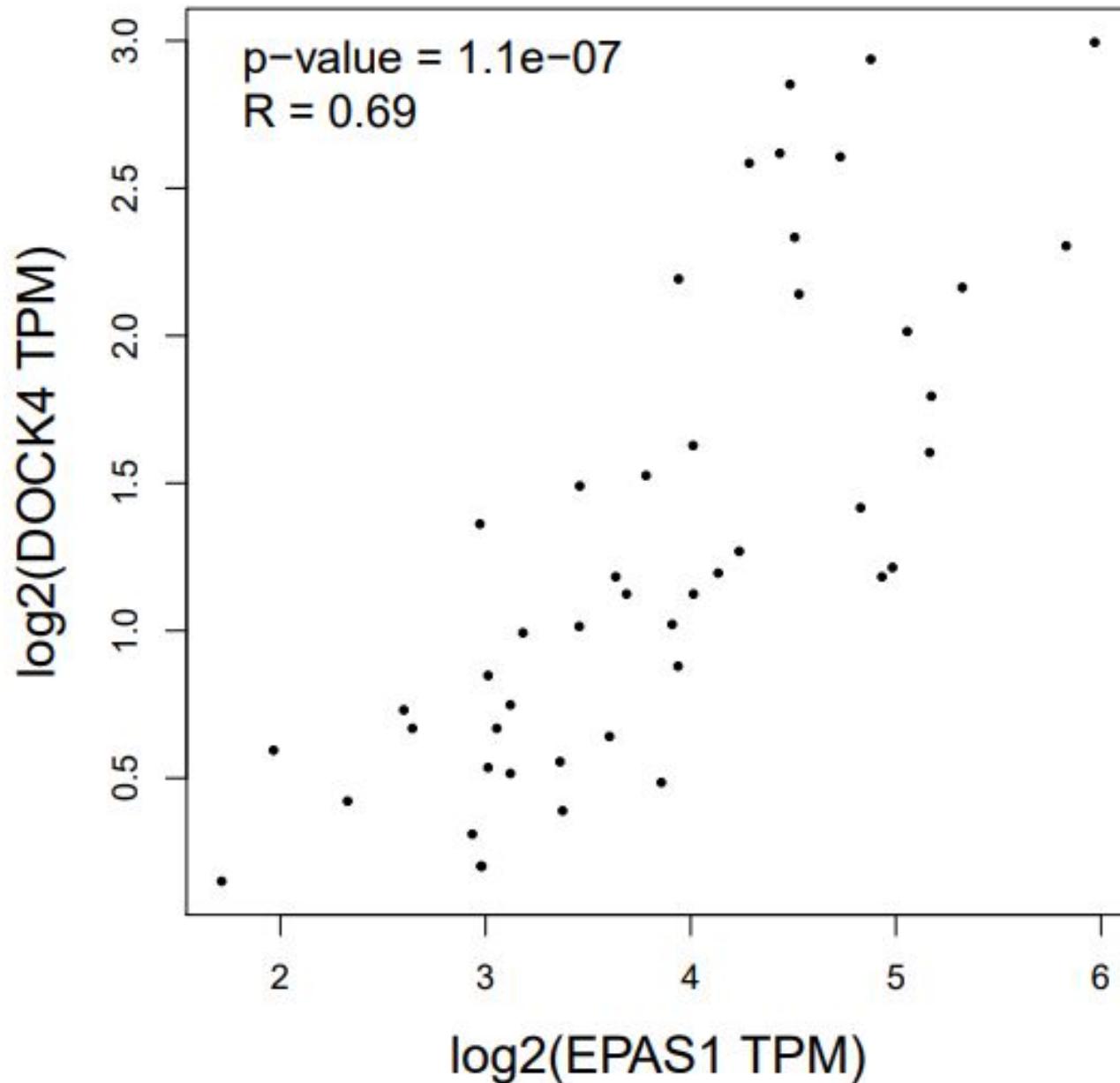
Used Expression Datasets

- DLBC Tumor

[Reset](#)

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[Plot](#)



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--- Help ---

Gene A

Input a gene symbol or id.

Normalized by gene (optional)

Correlation Coefficient

TCGA Tumor (Cancer name)

Add

↑

↓

TCGA Normal

Add

↑

↓

GTEx

Add

↑

↓

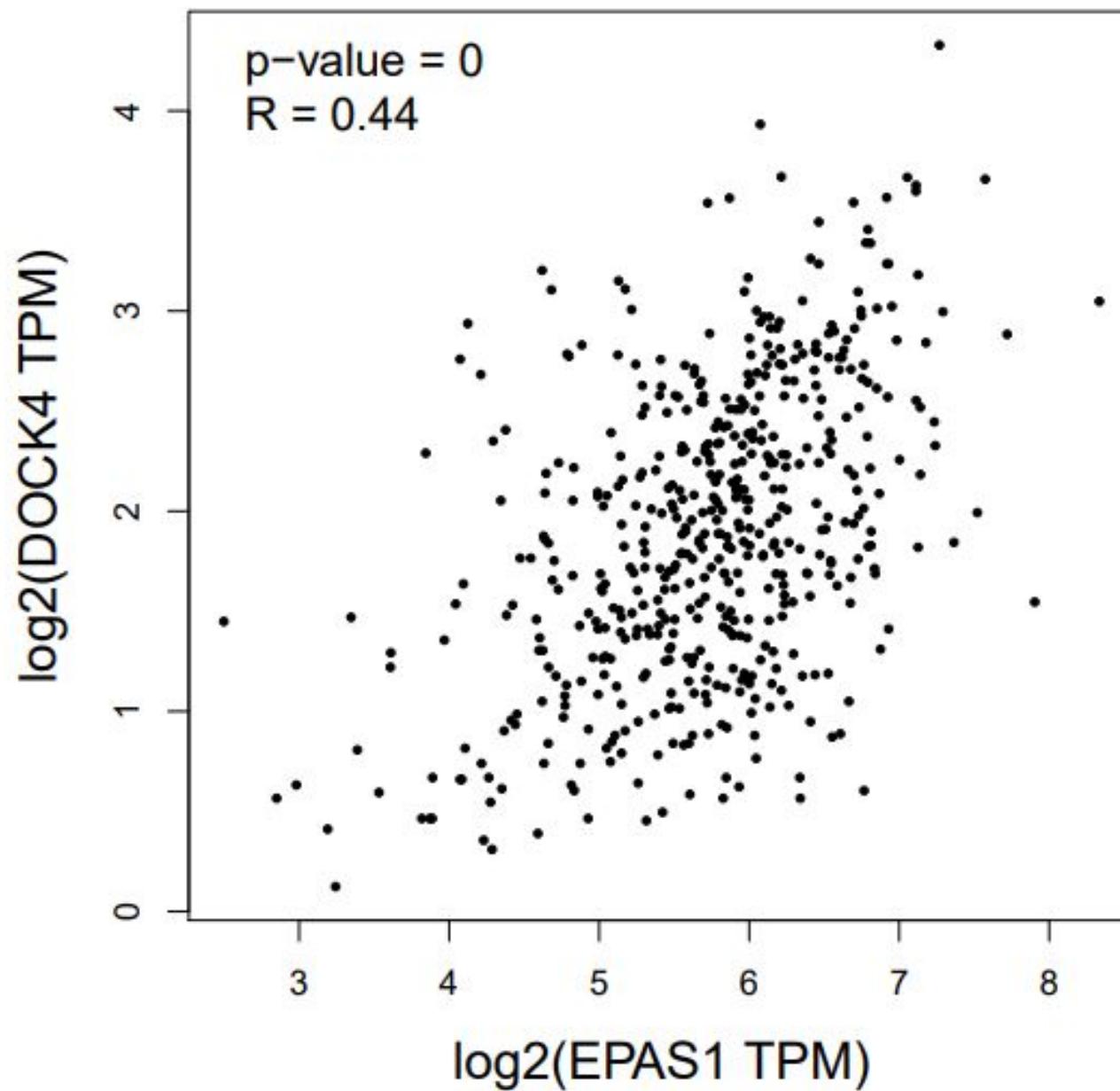
↓

Used Expression Datasets

Reset

The plot is based on the datasets of list.

Plot



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--- Help ---

Gene A	Gene B		
<input type="text" value="Epas1"/>	<input type="text" value="Dock4"/>		
Input a gene symbol or id.			
Normalized by gene (optional)			
Correlation Coefficient			
<input type="button" value="Pearson"/>			
We use the non-log scale for calculation and use the log-scale axis for visualization.			

TCGA Tumor (Cancer name)

- GBM Tumor
- HNSC Tumor
- KICH Tumor
- KIRC Tumor

TCGA Normal

- BLCA Normal
- BRCA Normal
- CESC Normal

GTEx

- Adipose - Subcutaneous
- Adipose - Visceral (Omentum)
- Adrenal Gland
- Bladder

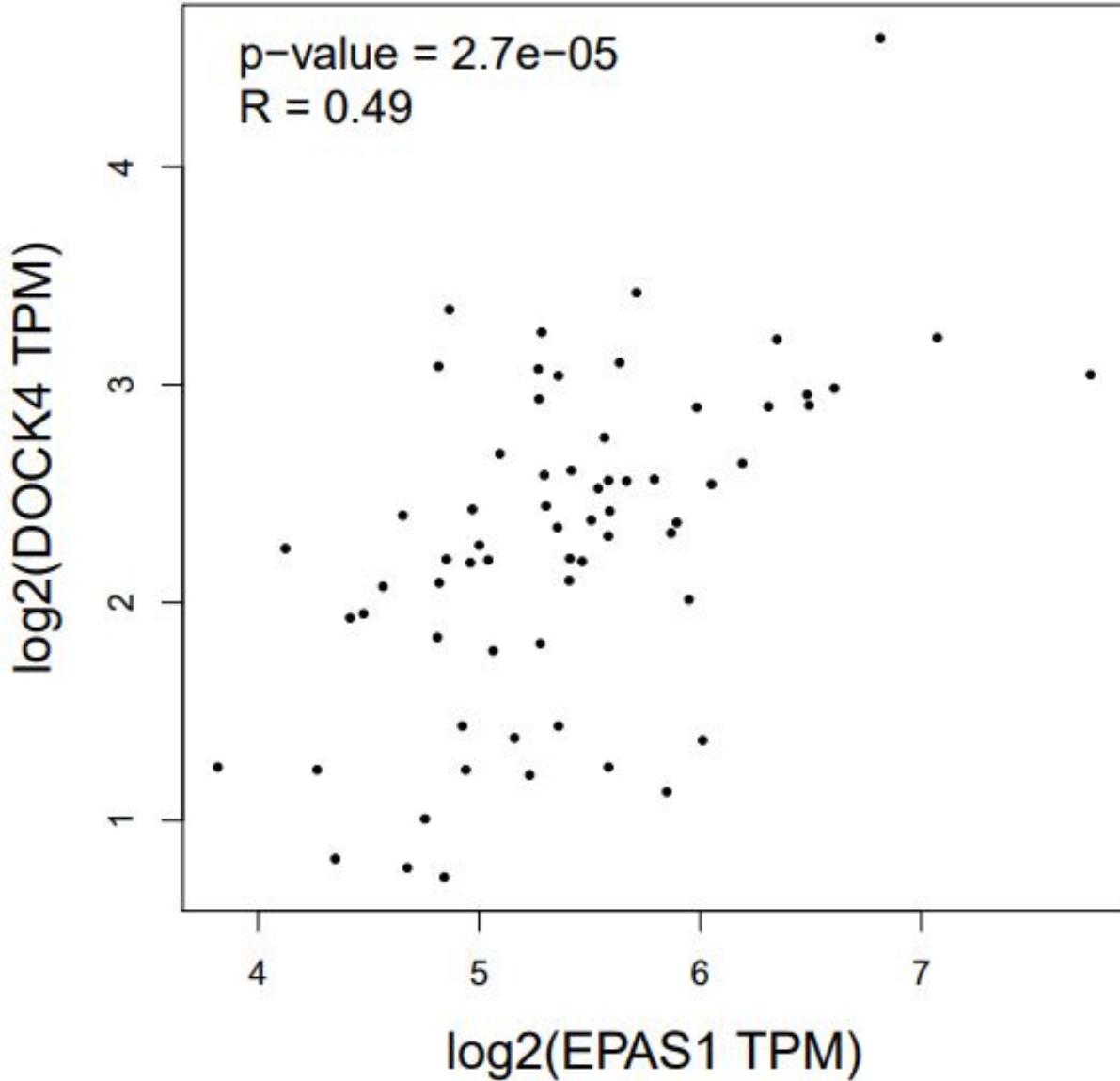
Used Expression Datasets

- KICH Tumor

Plot

Reset

The plot is based on the datasets of list.



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--- Help ---

Gene A

Input a gene symbol or id.

Normalized by gene (optional)

Correlation Coefficient

Pearson

We use the non-log scale for calculation and use the log-scale axis for visualization.

TCGA Tumor (Cancer name)

KIRC Tumor
KIRP Tumor
LAML Tumor

TCGA Normal

BLCA Normal
BRCA Normal
CESC Normal

GTEx

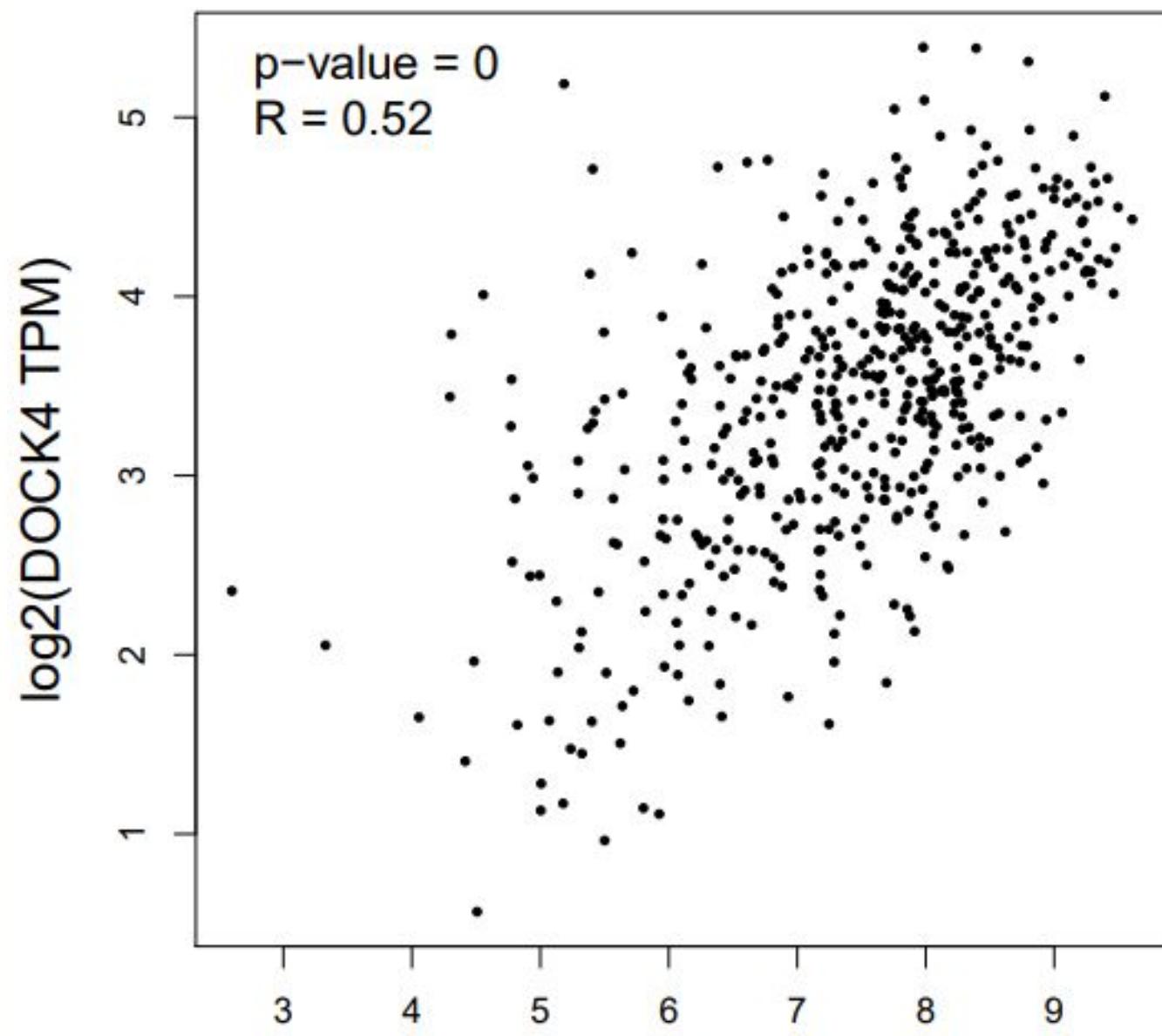
Adipose - Subcutaneous
Adipose - Visceral (Omentum)
Adrenal Gland
Bladder

Used Expression Datasets

KIRC Tumor

The plot is based on the datasets of list.

Plot



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--- Help ---

Gene A

Epas1

Gene B

Dock4

Input a gene symbol or id.

Normalized by gene (optional)

Correlation Coefficient

Pearson

We use the non-log scale for calculation and use the log-scale axis for visualization.

TCGA Tumor (Cancer name)

LAML Tumor
LGG Tumor
LIHC Tumor

Add

TCGA Normal

BLCA Normal
BRCA Normal
CESC Normal

Add

GTEx

Adipose - Subcutaneous
Adipose - Visceral (Omentum)
Adrenal Gland
Bladder

Add

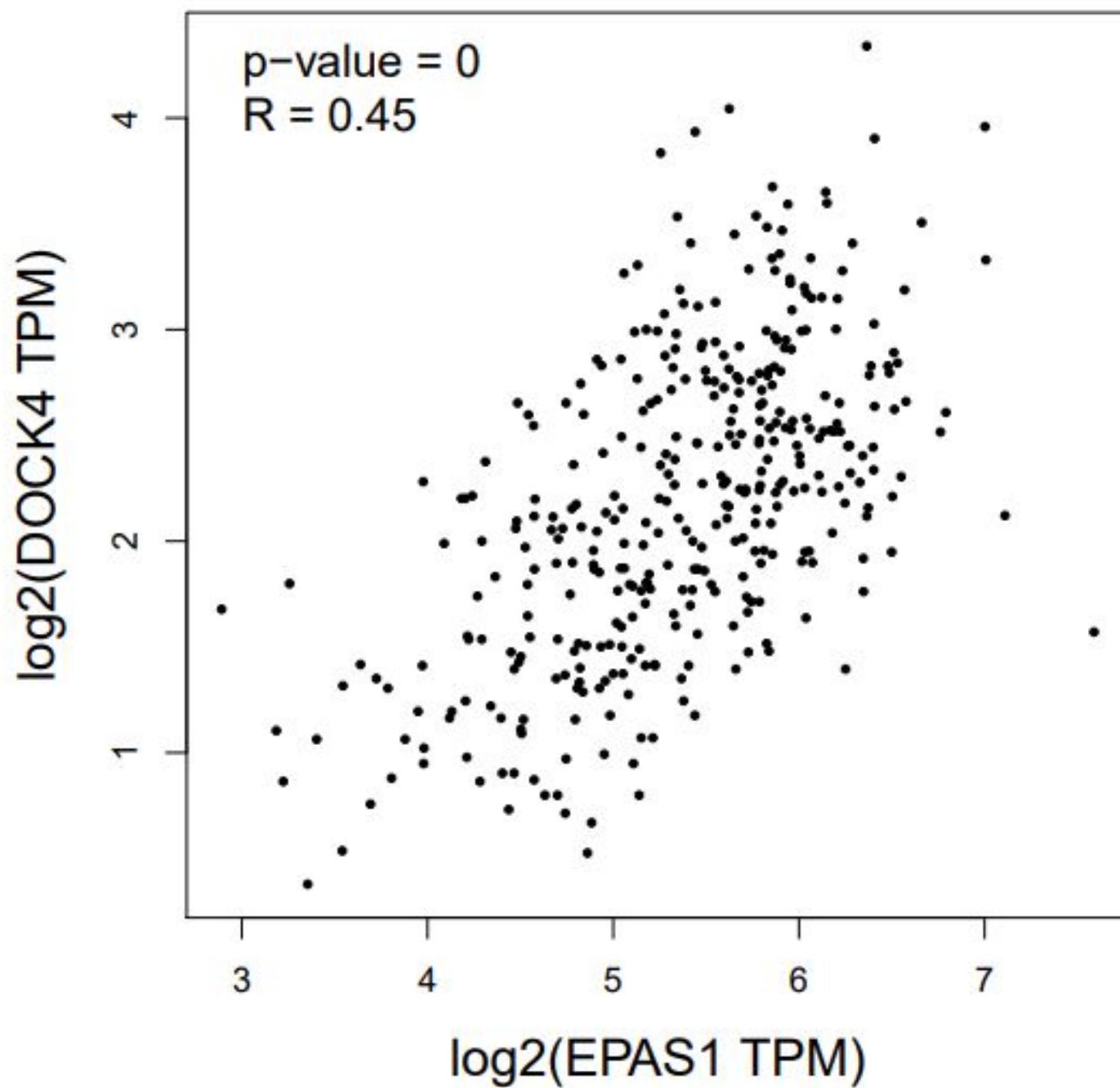
Used Expression Datasets

LIHC Tumor

Reset

The plot is based on the datasets of list.

Plot



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--- Help ---

Gene A

Gene B

Epas1

Dock4

Input a gene symbol or id.

Normalized by gene (optional)

Correlation Coefficient

Pearson

We use the non-log scale for calculation and use the log-scale axis for visualization.

TCGA Tumor (Cancer name)

ESOC Tumor
MESO Tumor
OV Tumor
PAAD Tumor

Add

TCGA Normal

BLCA Normal
BRCA Normal
CESC Normal

Add

GTEX

Adipose - Subcutaneous
Adipose - Visceral (Omentum)
Adrenal Gland
Bladder

Add

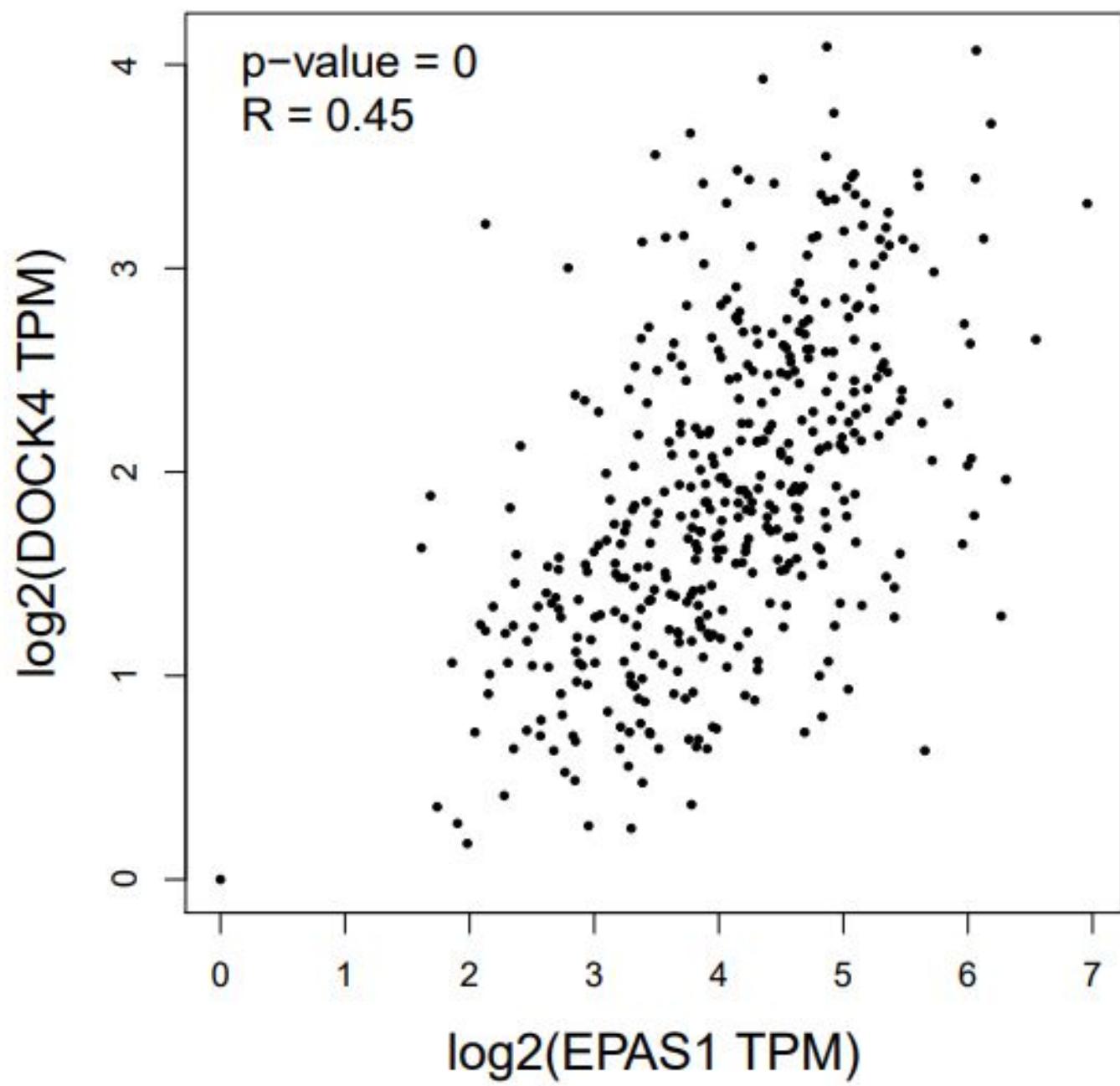
Used Expression Datasets

OV Tumor

Res

The plot is based on the datasets of list.

Plot



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--- Help ---

Gene A

Gene B

Input a gene symbol or id.

Normalized by gene (optional)

Correlation Coefficient

Pearson

We use the non-log scale for calculation and use the log-scale axis for visualization.

TCGA Tumor (Cancer name)

PAAD Tumor
PCPG Tumor
PRAD Tumor

TCGA Normal

BLCA Normal
BRCA Normal
CESC Normal

GTEx

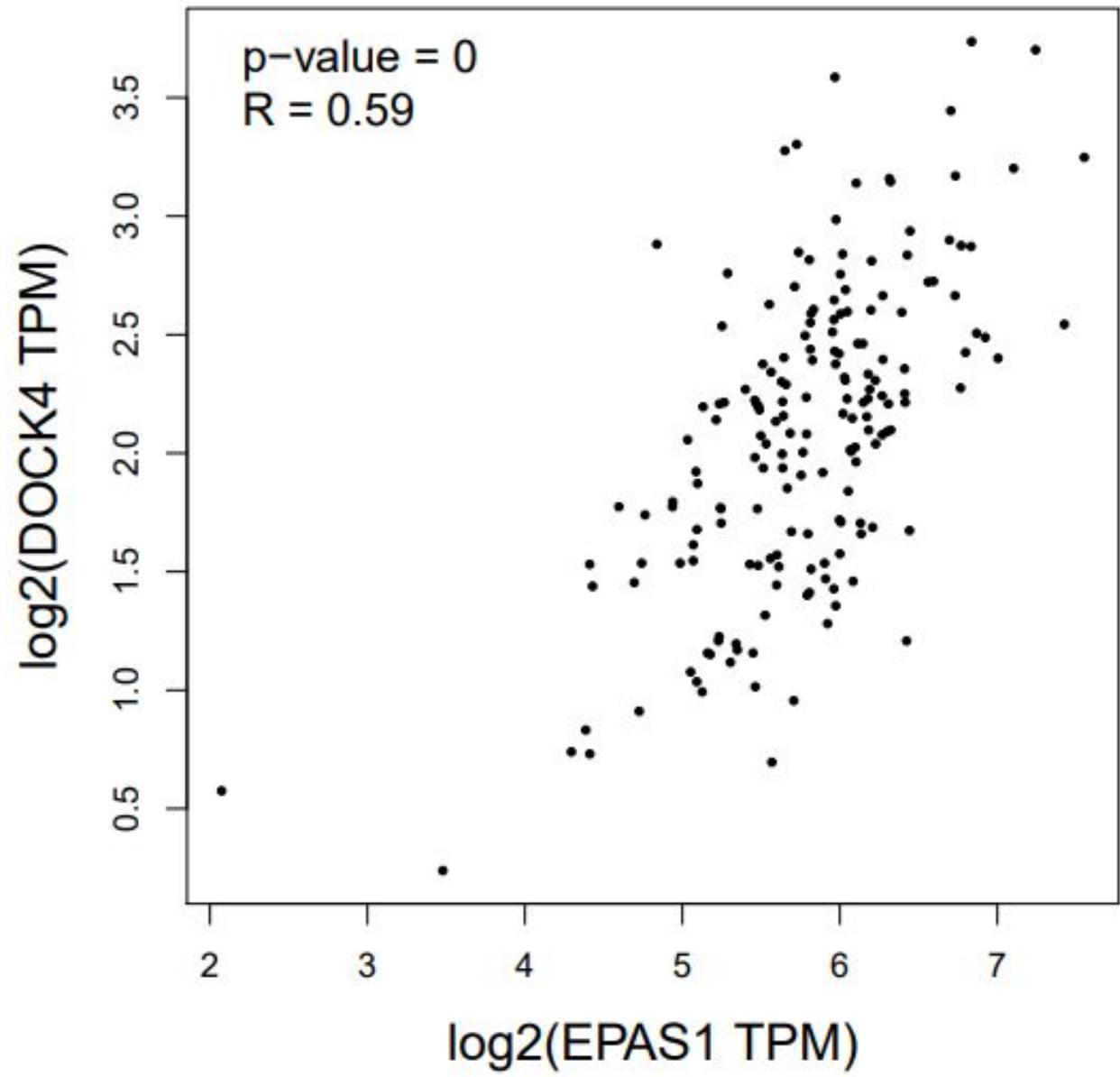
Adipose - Subcutaneous
Adipose - Visceral (Omentum)
Adrenal Gland
Bladder

Used Expression Datasets

PAAD Tumor

The plot is based on the datasets of list.

Plot

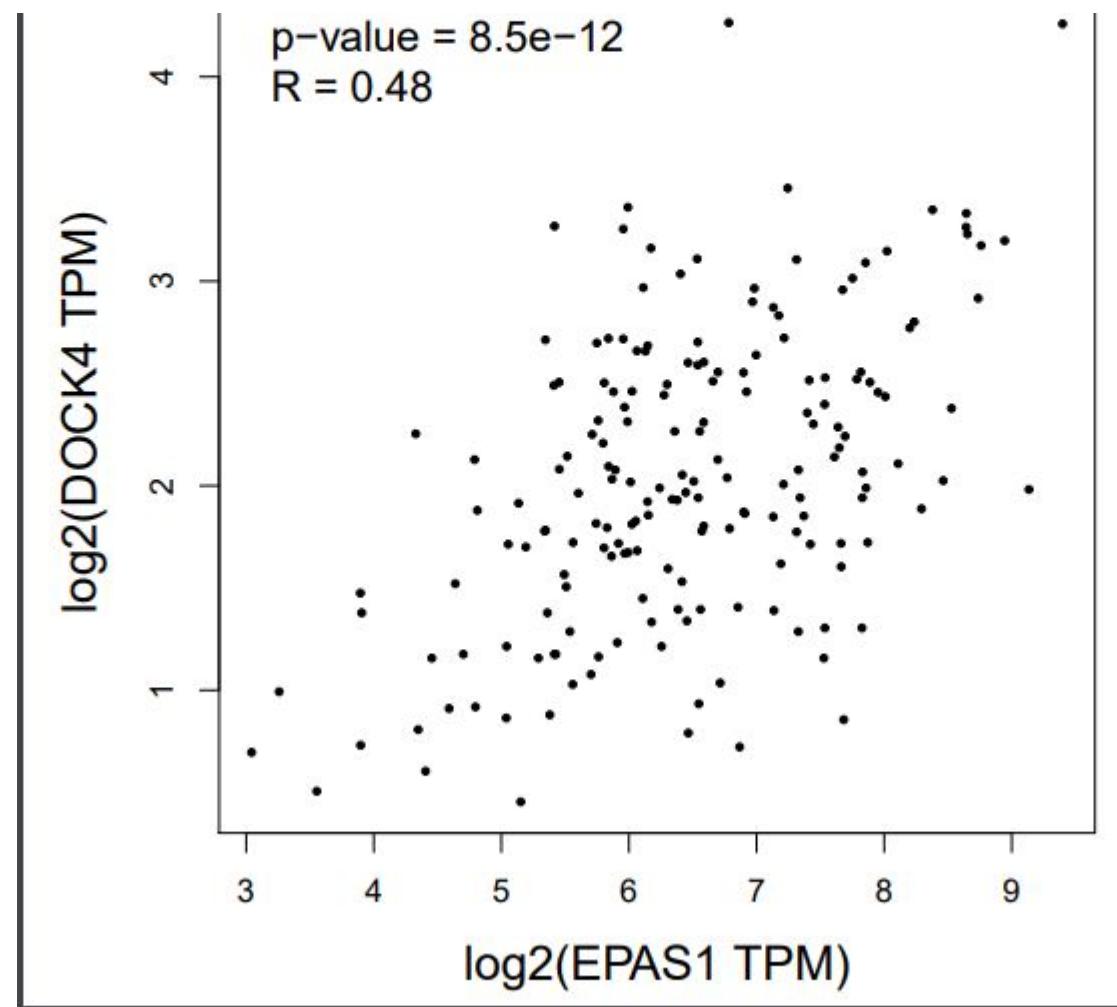


Parameters

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--- Help ---

Gene A <input type="text" value="Epas1"/>	Gene B <input type="text" value="Dock4"/> Input a gene symbol or id.	TCGA Tumor (Cancer name) <input type="text" value="PAAD Tumor"/> <input type="text" value="PCPG Tumor"/> Add <input type="text" value="PRAD Tumor"/>	Used Expression Datasets <input type="text" value="PCPG Tumor"/> Reset
Normalized by gene (optional)			The plot is based on the datasets of list.
Correlation Coefficient <input type="text" value="Pearson"/>		TCGA Normal <input type="text" value="BLCA Normal"/> <input type="text" value="BRCA Normal"/> <input type="text" value="CESC Normal"/> Add	Plot
We use the non-log scale for calculation and use the log-scale axis for visualization.		GTEx <input type="text" value="Adipose - Subcutaneous"/> <input type="text" value="Adipose - Visceral (Omentum)"/> <input type="text" value="Adrenal Gland"/> <input type="text" value="Bladder"/> Add	



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--- Help ---

Gene A Gene B

Epas1 Dock4

Input a gene symbol or id.

Normalized by gene (optional)

Correlation Coefficient

Pearson

We use the non-log scale for calculation and use the log-scale axis for visualization.

TCGA Tumor (Cancer name)

PRAD Tumor
READ Tumor
SARC Tumor

Add

TCGA Normal

BLCA Normal
BRCA Normal
CESC Normal

Add

GTEx

Adipose - Subcutaneous
Adipose - Visceral (Omentum)
Adrenal Gland
Bladder

Add

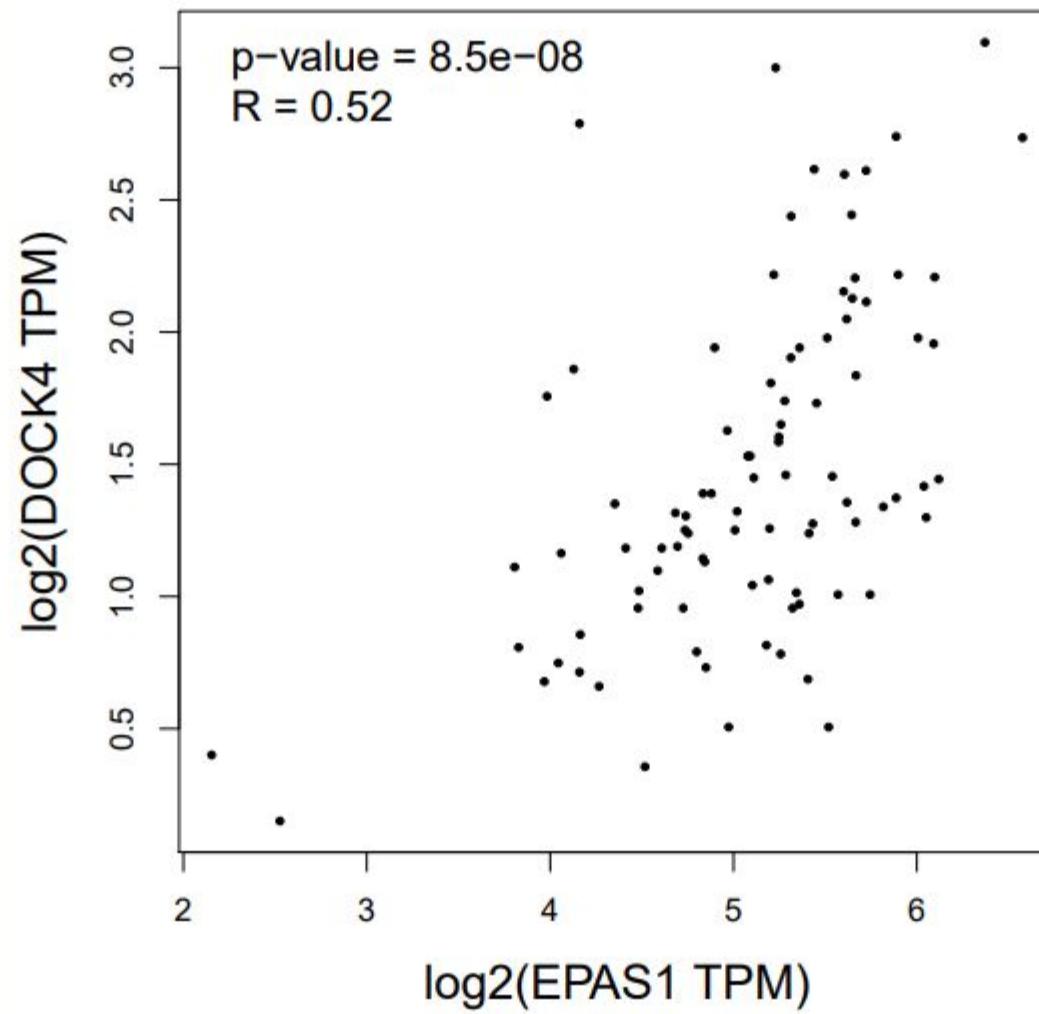
Used Expression Datasets

READ Tumor

Reset

The plot is based on the datasets of list.

Plot

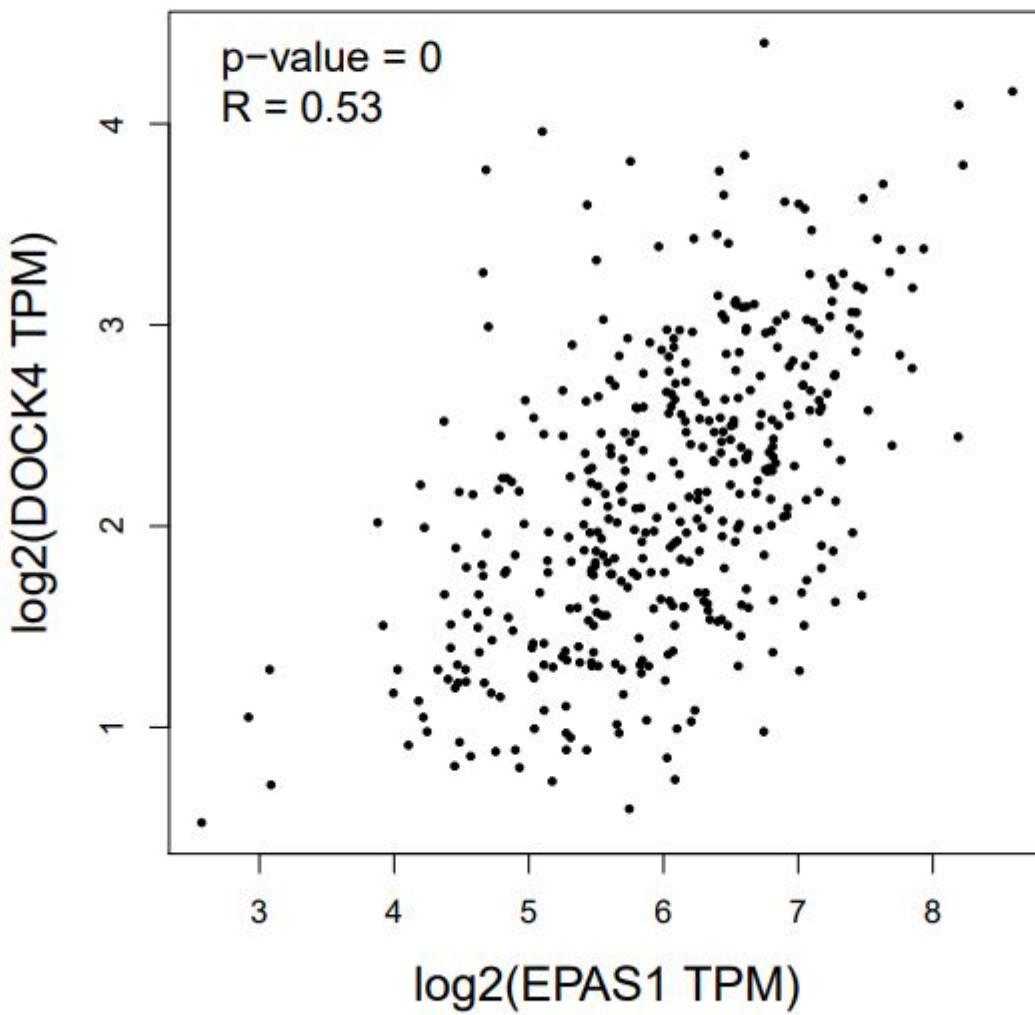


- **Gene B:** Input a gene B of interest. [!-or y-axis]
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- **Correlation Coefficient:** The method for calculating the correlation coefficient.
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--- Help ---

Gene A	Gene B	TCGA Tumor (Cancer name)	Used Expression Datasets
Epas1	Dock4	SARC Tumor SKCM Tumor STAD Tumor TCCT Tumor	STAD Tumor
Input a gene symbol or id.		TCGA Normal	Reset
Normalized by gene (optional)		BLCA Normal BRCA Normal CESC Normal	
Correlation Coefficient		GTEx	
Pearson		Adipose - Subcutaneous Adipose - Visceral (Omentum) Adrenal Gland Bladder	Plot
We use the non-log scale for calculation and use the log-scale axis for visualization.			

The plot is based on the datasets of list.



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--- Help ---

Gene A	Gene B
Epas1	Dock4

Input a gene symbol or id.

Normalized by gene (optional)

Correlation Coefficient

Pearson	▼
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We use the non-log scale for calculation and use the log-scale axis for visualization.

TCGA Tumor (Cancer name)

STAD Tumor
TGCT Tumor
THCA Tumor
THYM Tumor

TCGA Normal

BLCA Normal
BRCA Normal
CESC Normal

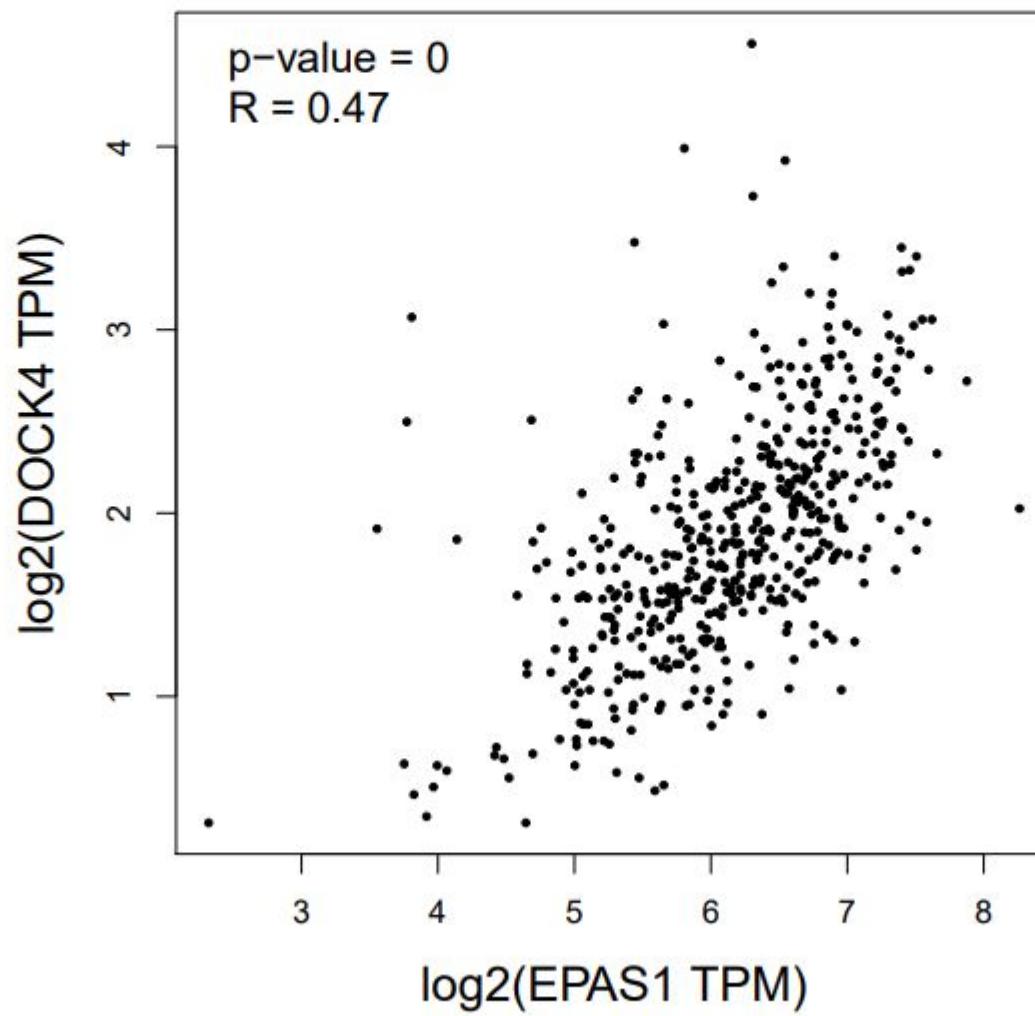
GTEx

Adipose - Subcutaneous
Adipose - Visceral (Omentum)
Adrenal Gland
Bladder

Used Expression Datasets

THCA Tumor

The plot is based on the datasets of list.



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- **Normalized by gene:** Set the gene used for normalizing Gene A and Gene B.
- **Correlation Coefficient:** The method for calculating the correlation coefficient.
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--- Help ---

Gene A

Input a gene symbol or id.

Normalized by gene (optional)

Correlation Coefficient

Pearson

▼

We use the non-log scale for calculation and use the log-scale axis for visualization.

TCGA Tumor (Cancer name)

THYM Tumor

Add

UCEC Tumor

Add

UCS Tumor

Add

TCGA Normal

BLCA Normal

Add

BRCA Normal

Add

CESC Normal

Add

GTEx

Adipose - Subcutaneous

Add

Adipose - Visceral (Omentum)

Add

Adrenal Gland

Add

Bladder

Add

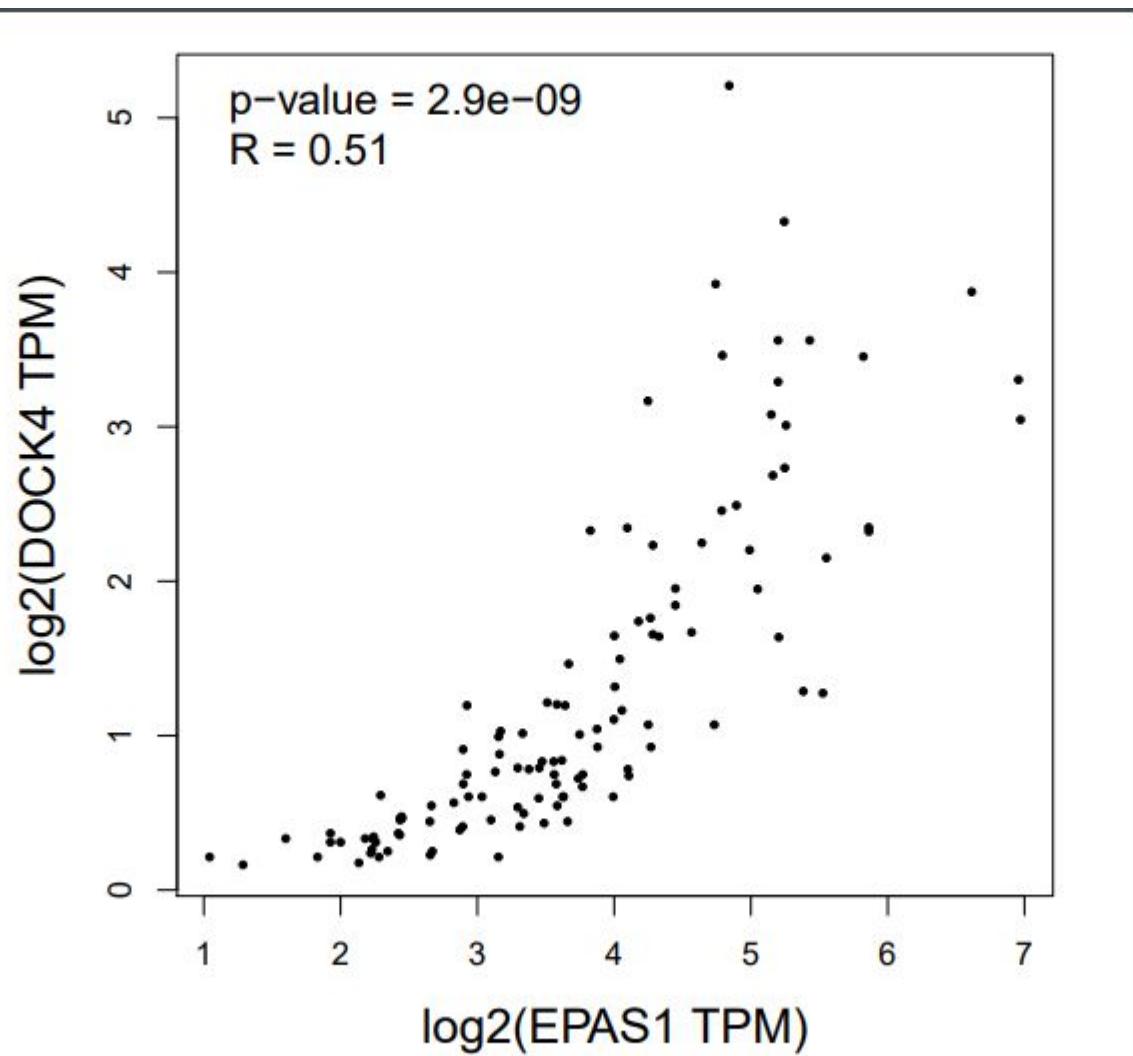
Used Expression Datasets

THYM Tumor

Reset

The plot is based on the datasets of list.

Plot



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--- Help ---

Gene A	Gene B
Epas1	Dock4

Input a gene symbol or id.

Normalized by gene (optional)

Correlation Coefficient

Pearson	▼
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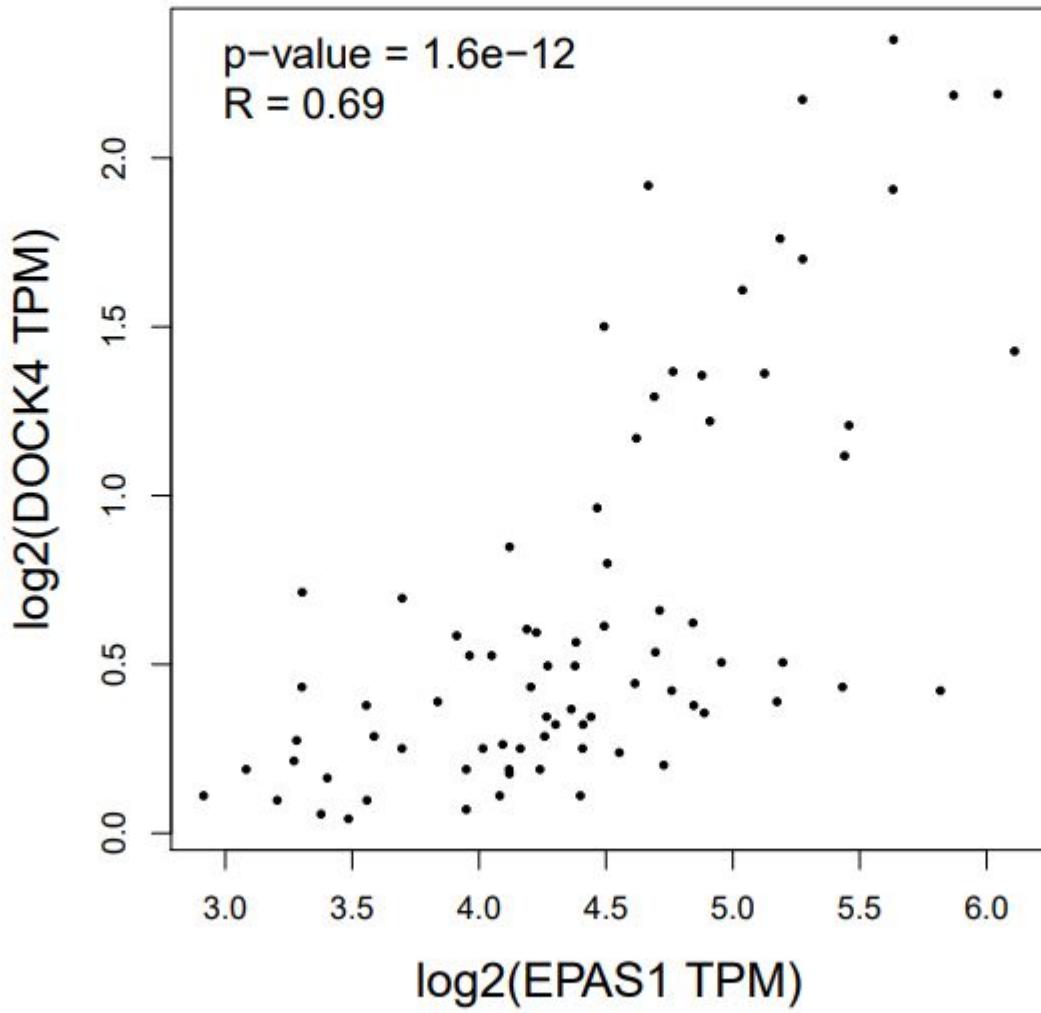
We use the non-log scale for calculation and use the log-scale axis for visualization.

TCGA Tumor (Cancer name)	Add
UCEC Tumor	▲
UCS Tumor	▼
UVM Tumor	■
TCGA Normal	Add
BLCA Normal	▲
BRCA Normal	▼
GESC Normal	■
GTEx	Add
Adipose - Subcutaneous	▲
Adipose - Visceral (Omentum)	▼
Adrenal Gland	■
Bladder	▼

Used Expression Datasets	Reset
UVM Tumor	▼

The plot is based on the datasets of list.

Plot



R

COAD	0.68
DLBC	0.69
HNSC	0.44
KICH	0.49
KIRC	0.52
LIHC	0.45
OV	0.45
PAAD	0.59
PCPG	0.48
READ	0.52
STAD	0.53
THCA	0.47
THYM	0.51
UVM	0.69
all	0.68

