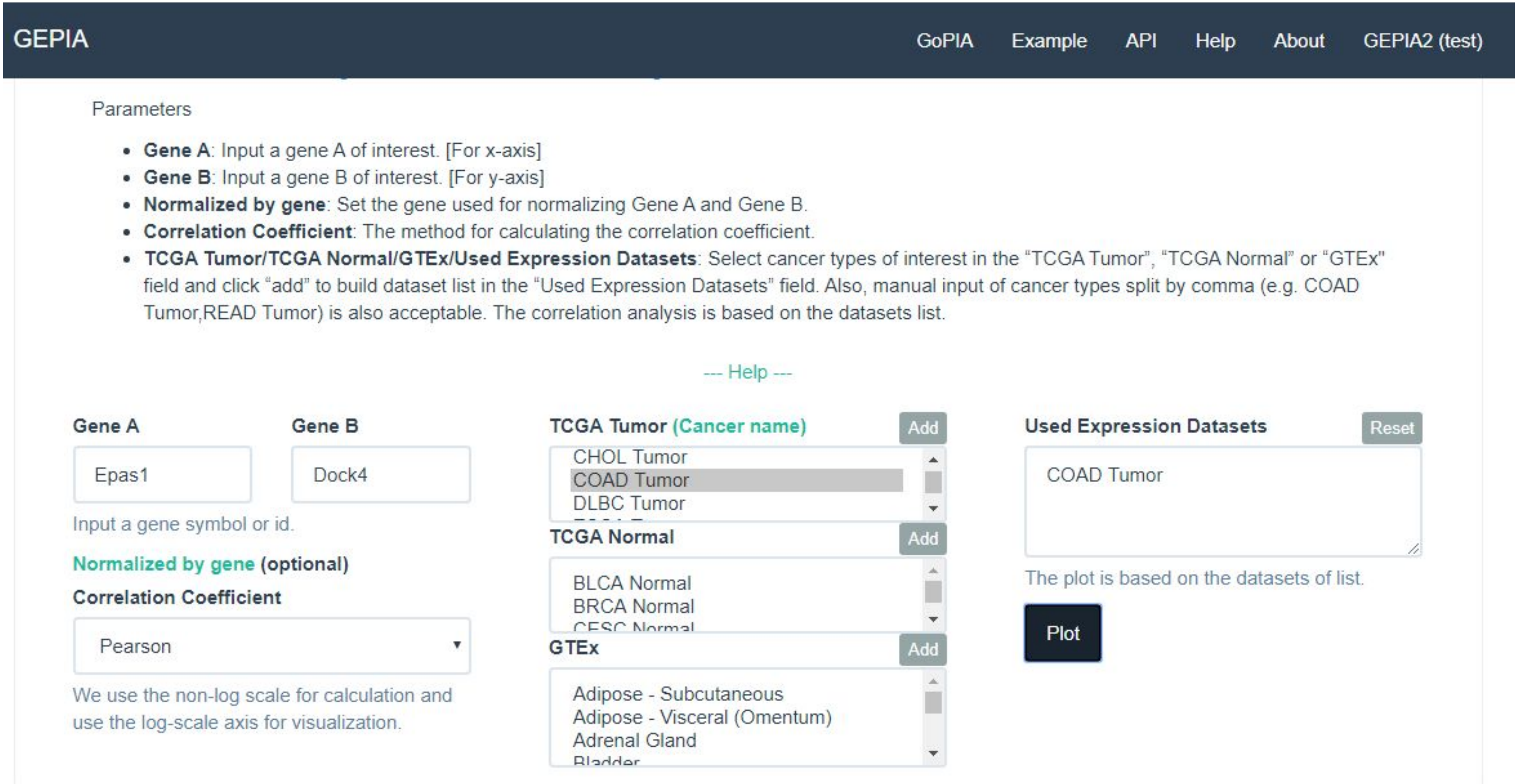


Parameters

- **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.

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)

CHOL Tumor
COAD Tumor
DLBC Tumor

TCGA Normal

BLCA Normal
BRCA Normal

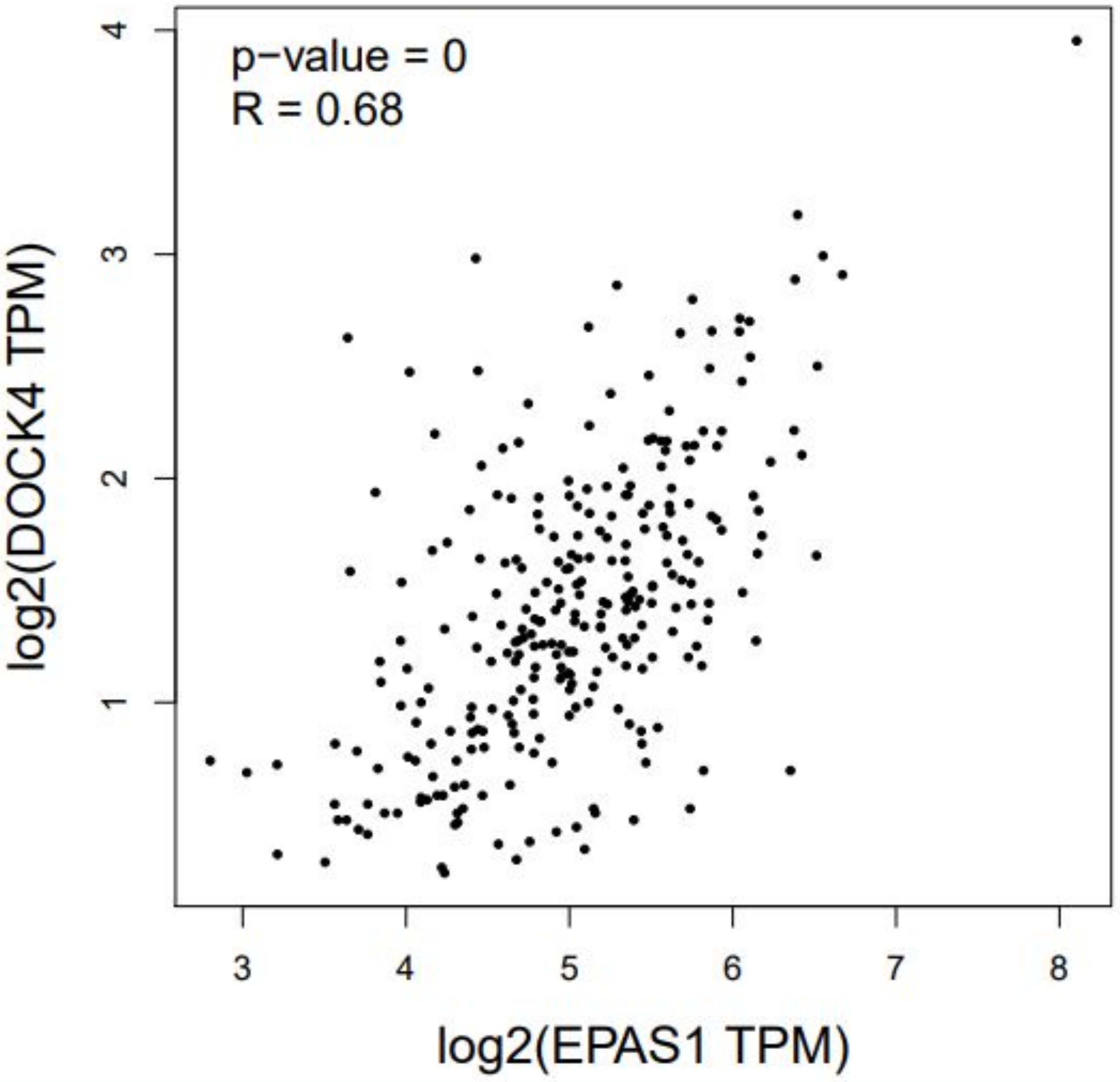
GTEx

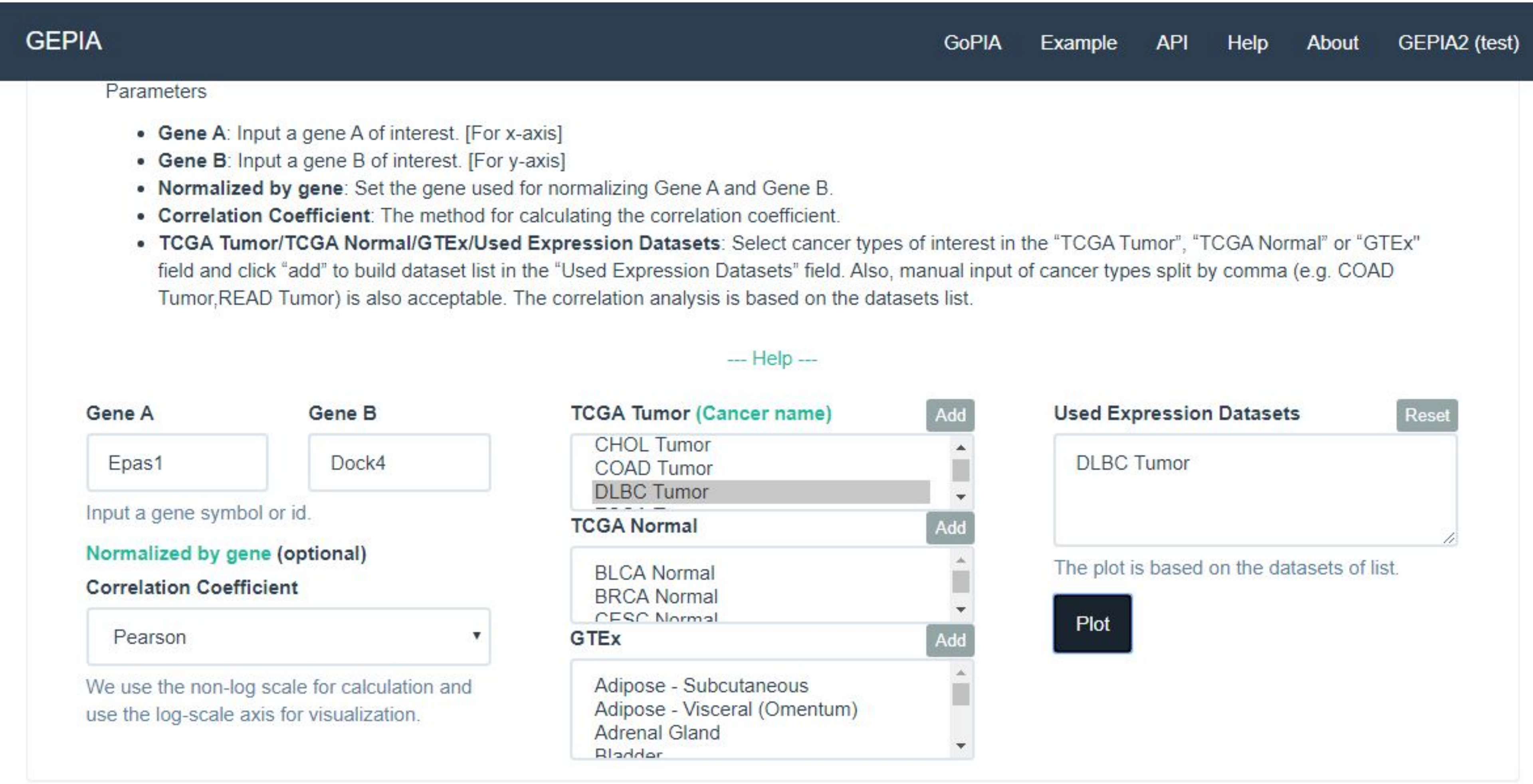
Adipose - Subcutaneous
Adipose - Visceral (Omentum)
Adrenal Gland

Used Expression Datasets

COAD Tumor

The plot is based on the datasets of list.


p−value = 0
R = 0.68
log2(DOCK4 TPM)
1
2
3
4
3
4
5
6
7
8
log2(EPAS1 TPM)



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: 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.

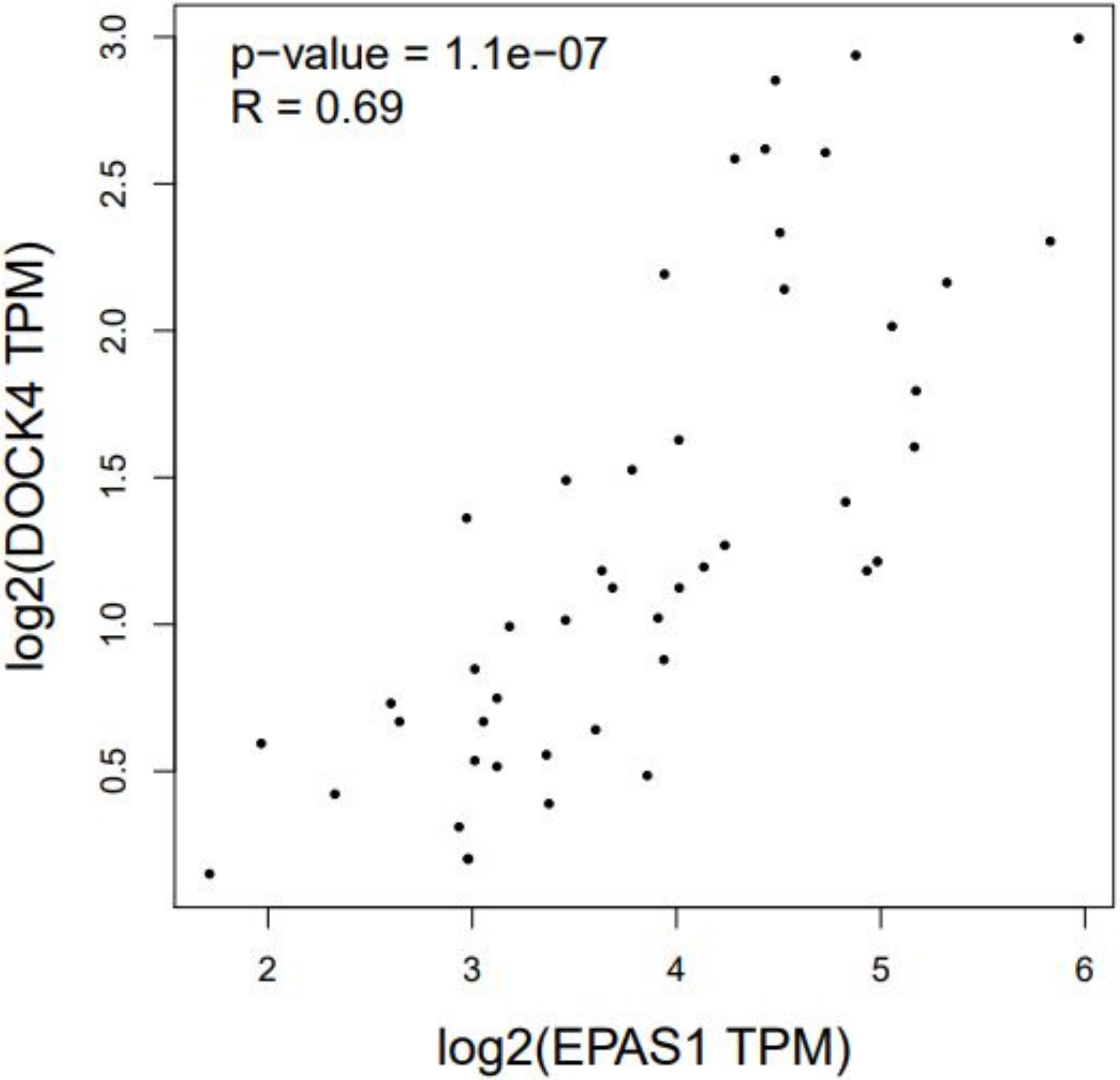
TCGA Tumor (Cancer name)

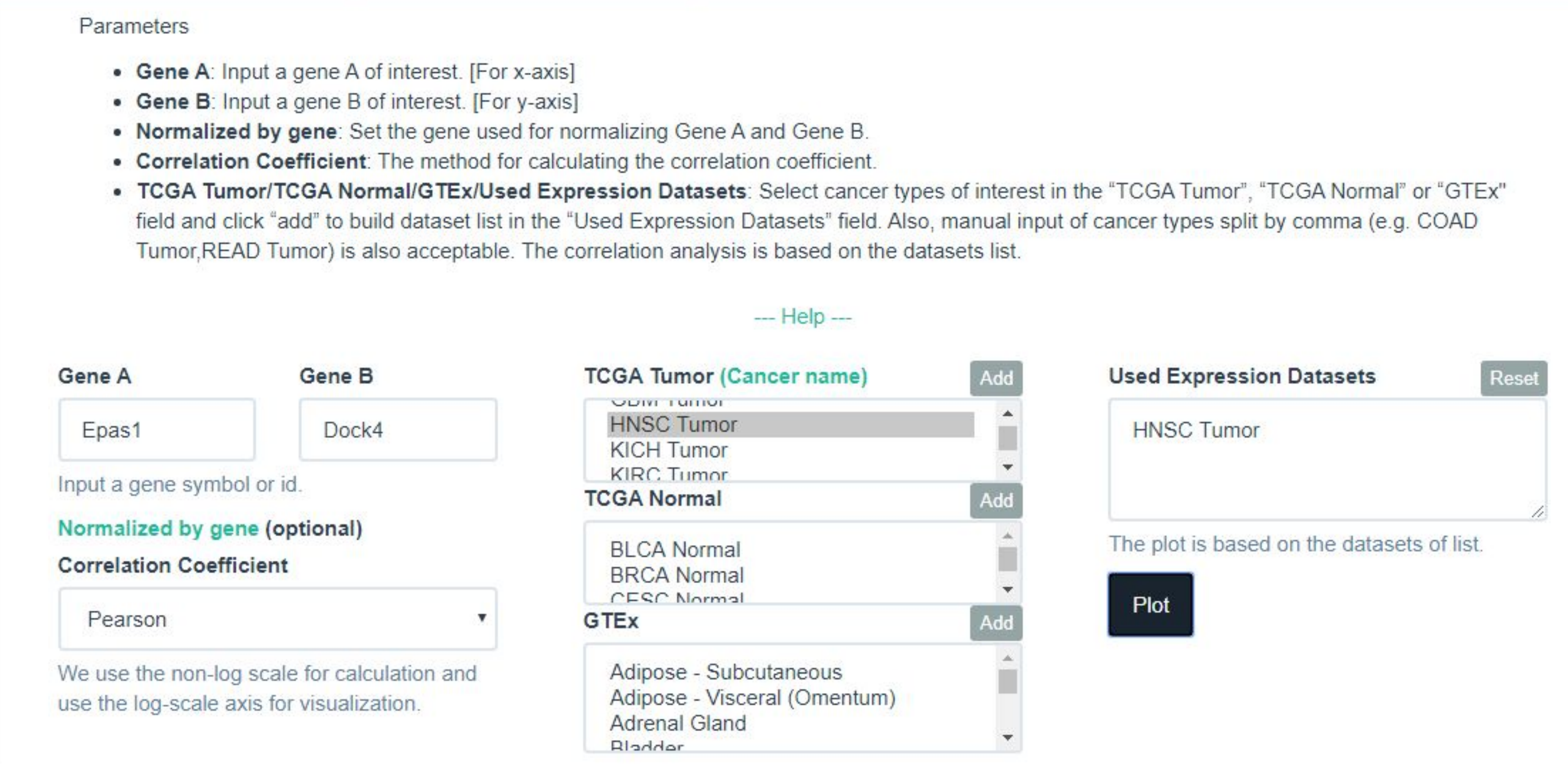
TCGA Normal

GTEx

Used Expression Datasets: DLBC Tumor

The plot is based on the datasets of list.


p−value = 1.1e−07
R = 0.69
log2(DOCK4 TPM)
3.0
2.5
2.0
1.5
1.0
0.5
2
3
4
5
6
log2(EPAS1 TPM)



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: 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.

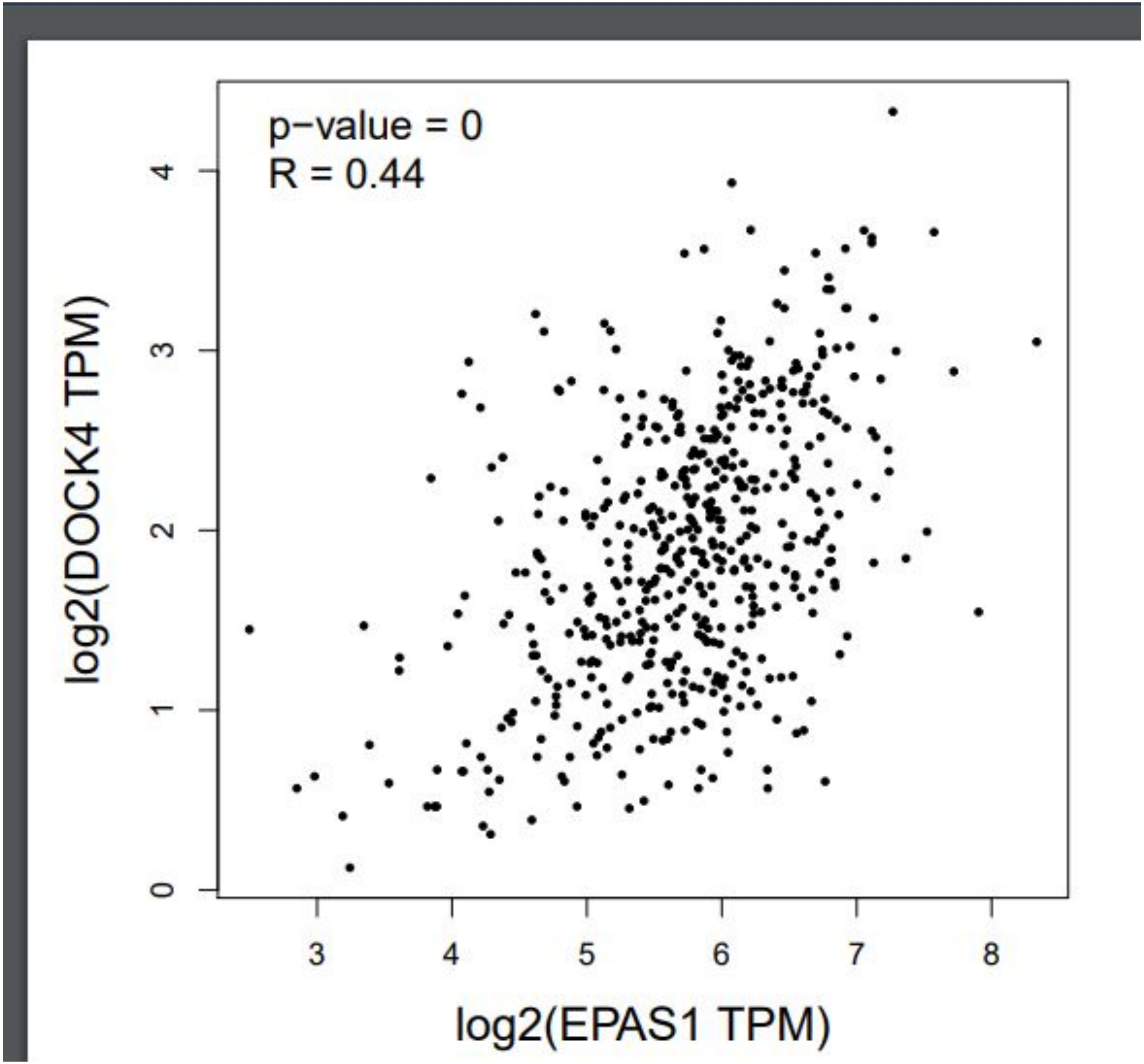
TCGA Tumor (Cancer name)

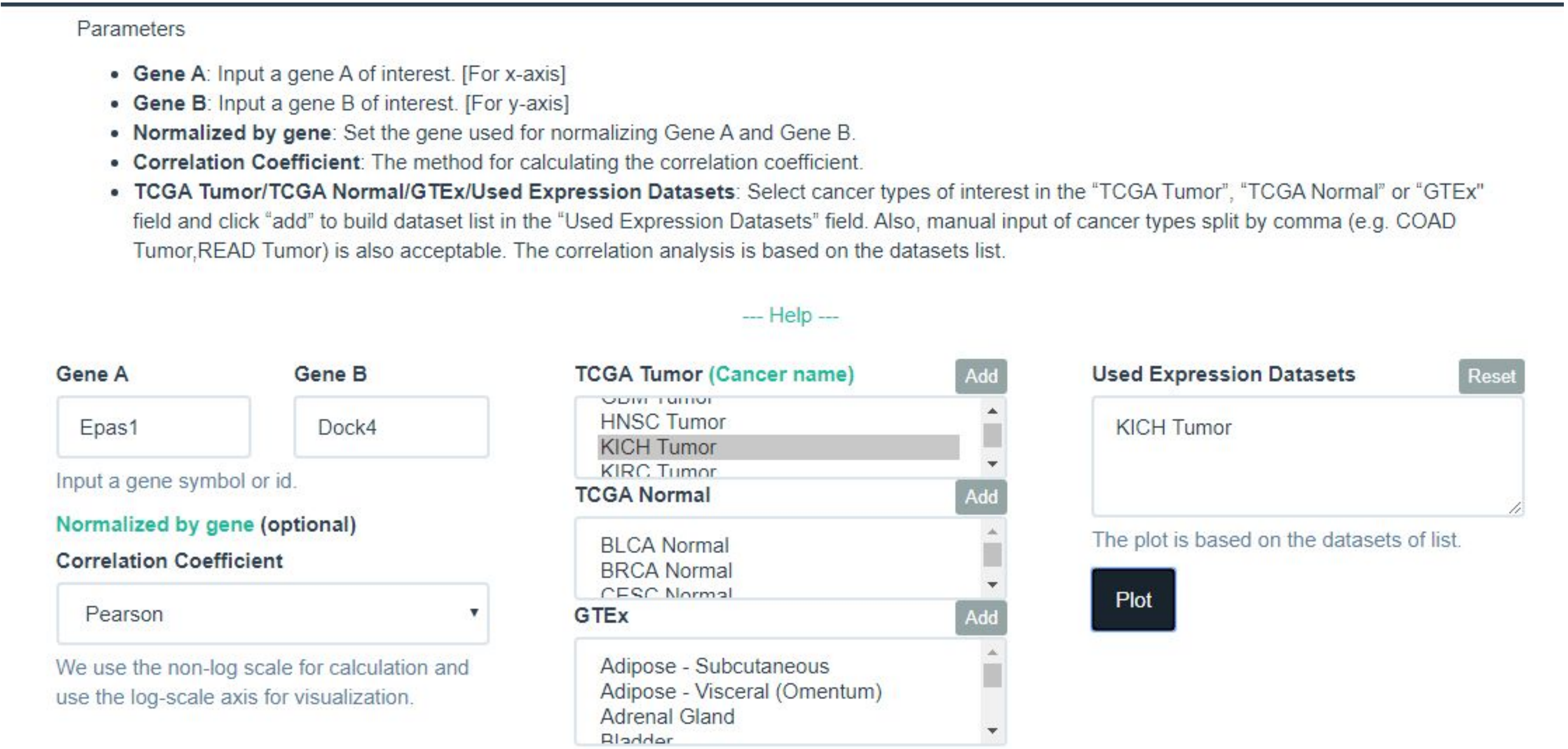
TCGA Normal

GTEx

Used Expression Datasets: HNSC Tumor

The plot is based on the datasets of list.


p−value = 0
R = 0.44
log2(DOCK4 TPM)
0
1
2
3
4
log2(EPAS1 TPM)
3
4
5
6
7
8



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: Epas1

Gene B: Dock4

Input a gene symbol or id.

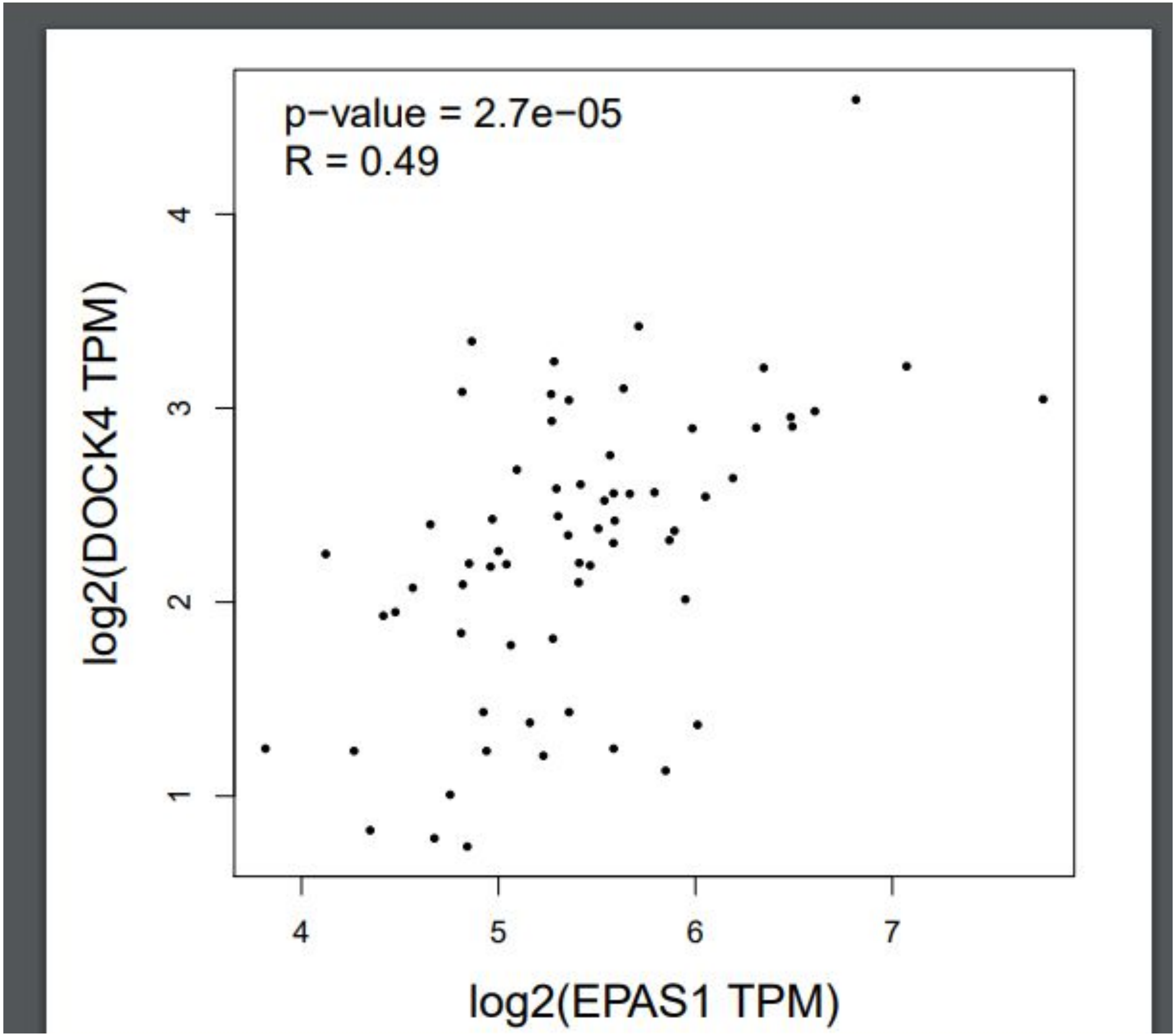
Normalized by gene (optional)

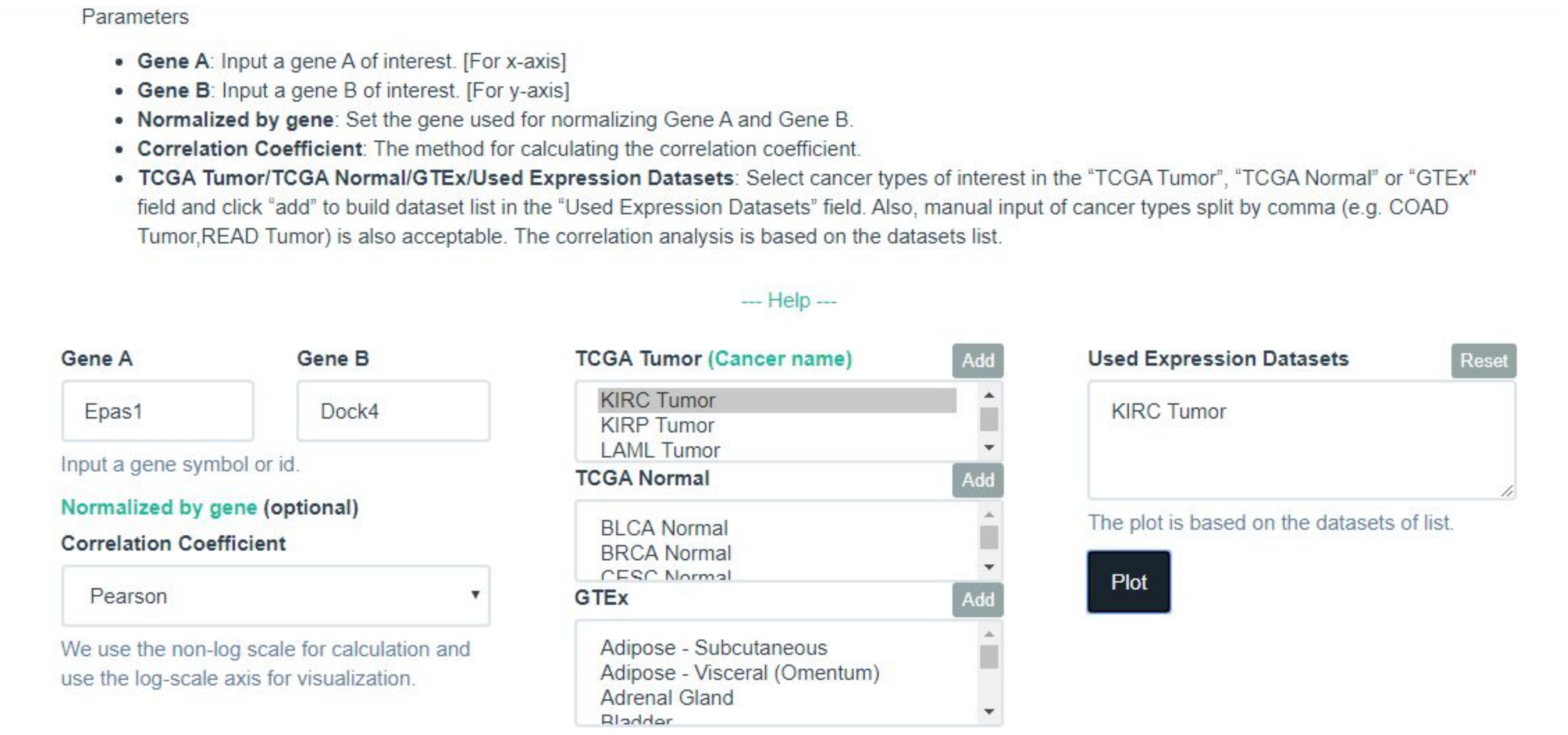
Correlation Coefficient: Pearson

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

Used Expression Datasets: KICH Tumor

The plot is based on the datasets of list.


p−value = 2.7e−05
R = 0.49
log2(DOCK4 TPM)
1
2
3
4
log2(EPAS1 TPM)
4
5
6
7



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: Epas1

Gene B: Dock4

Input a gene symbol or id.

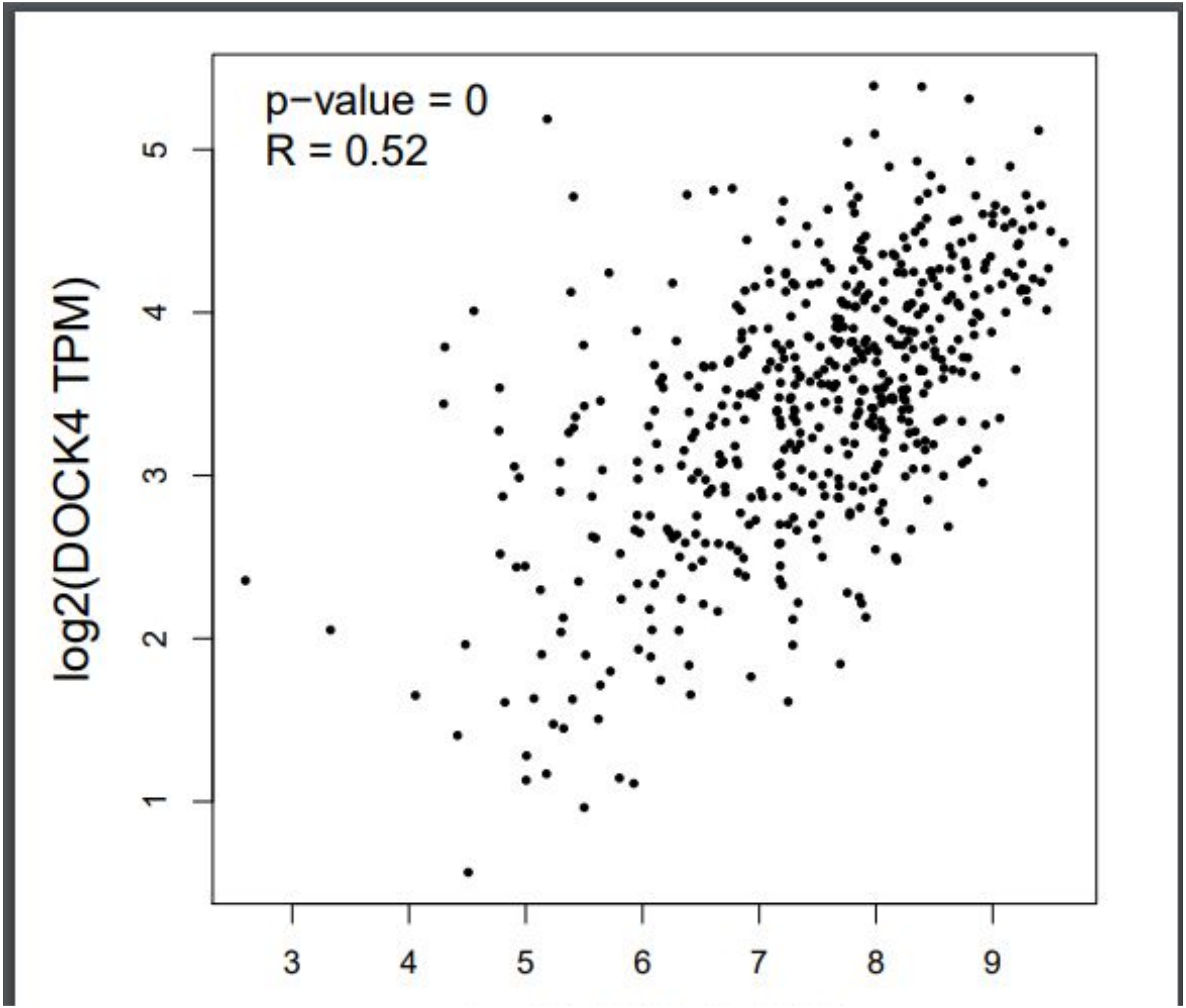
Normalized by gene (optional)

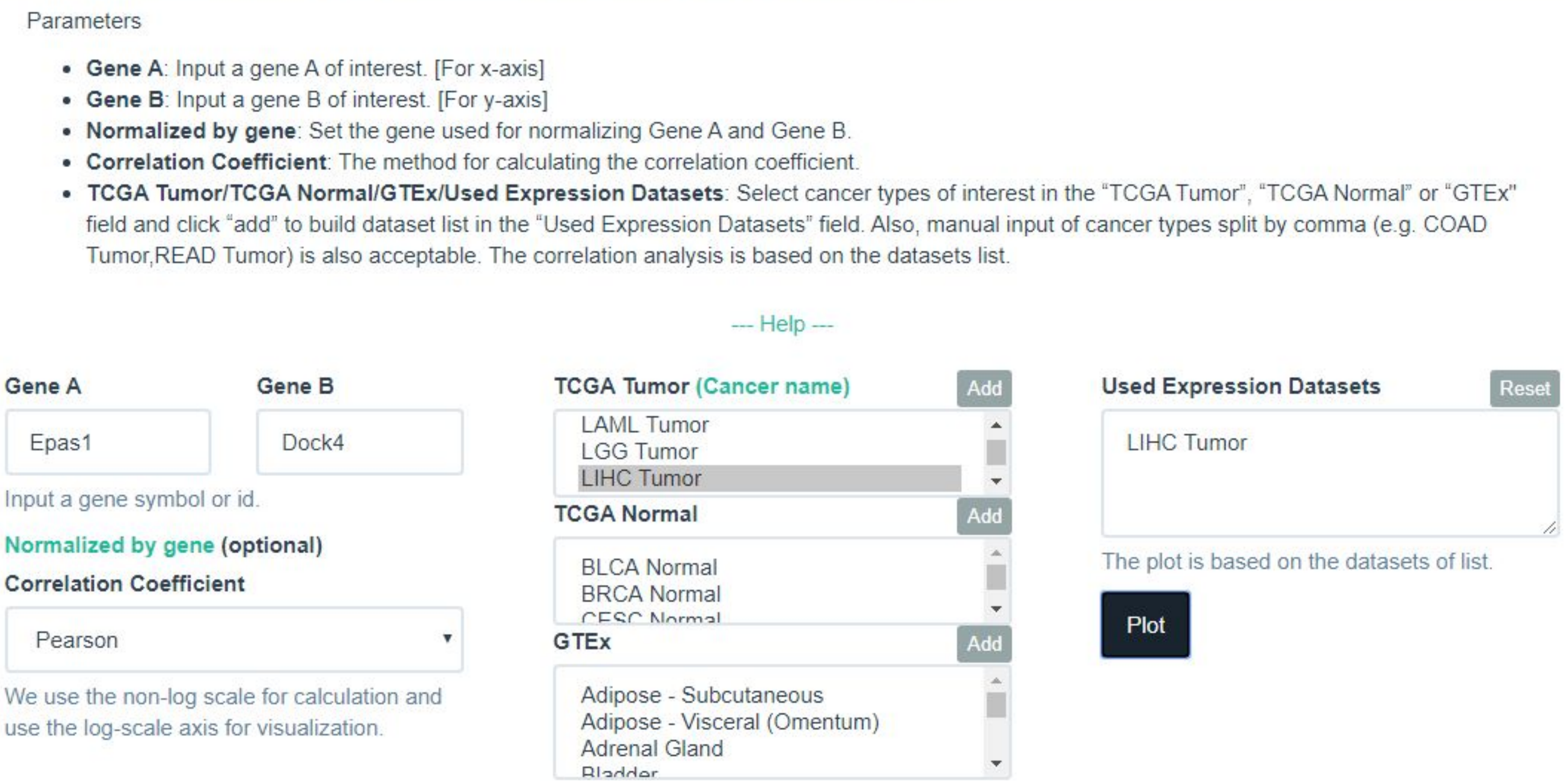
Correlation Coefficient: Pearson

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

Used Expression Datasets: KIRC Tumor

The plot is based on the datasets of list.


p−value = 0
R = 0.52
log2(DOCK4 TPM)
1
2
3
4
5
3
4
5
6
7
8
9



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: 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

TCGA Normal

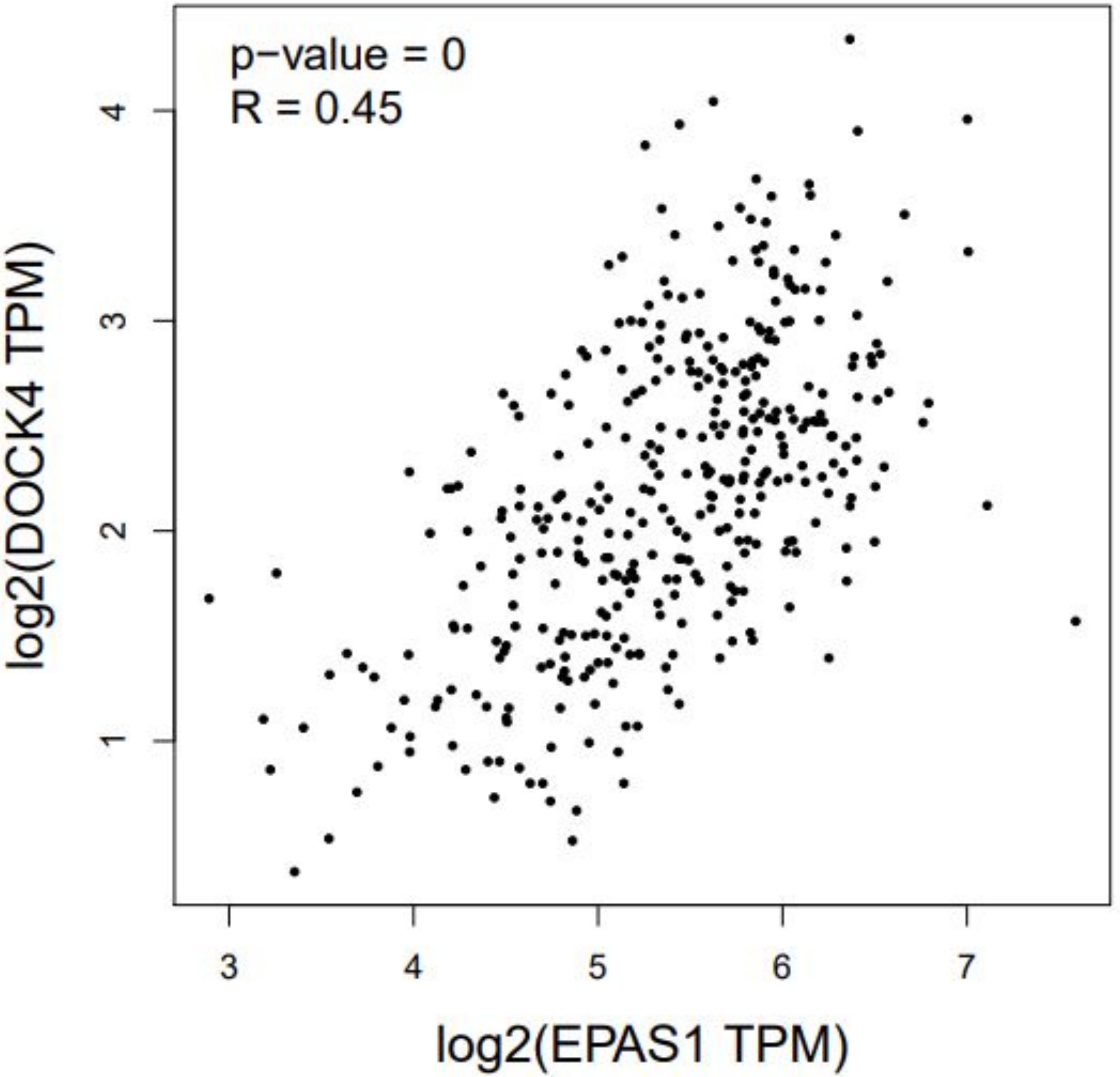
BLCA Normal
BRCA Normal
CESC Normal

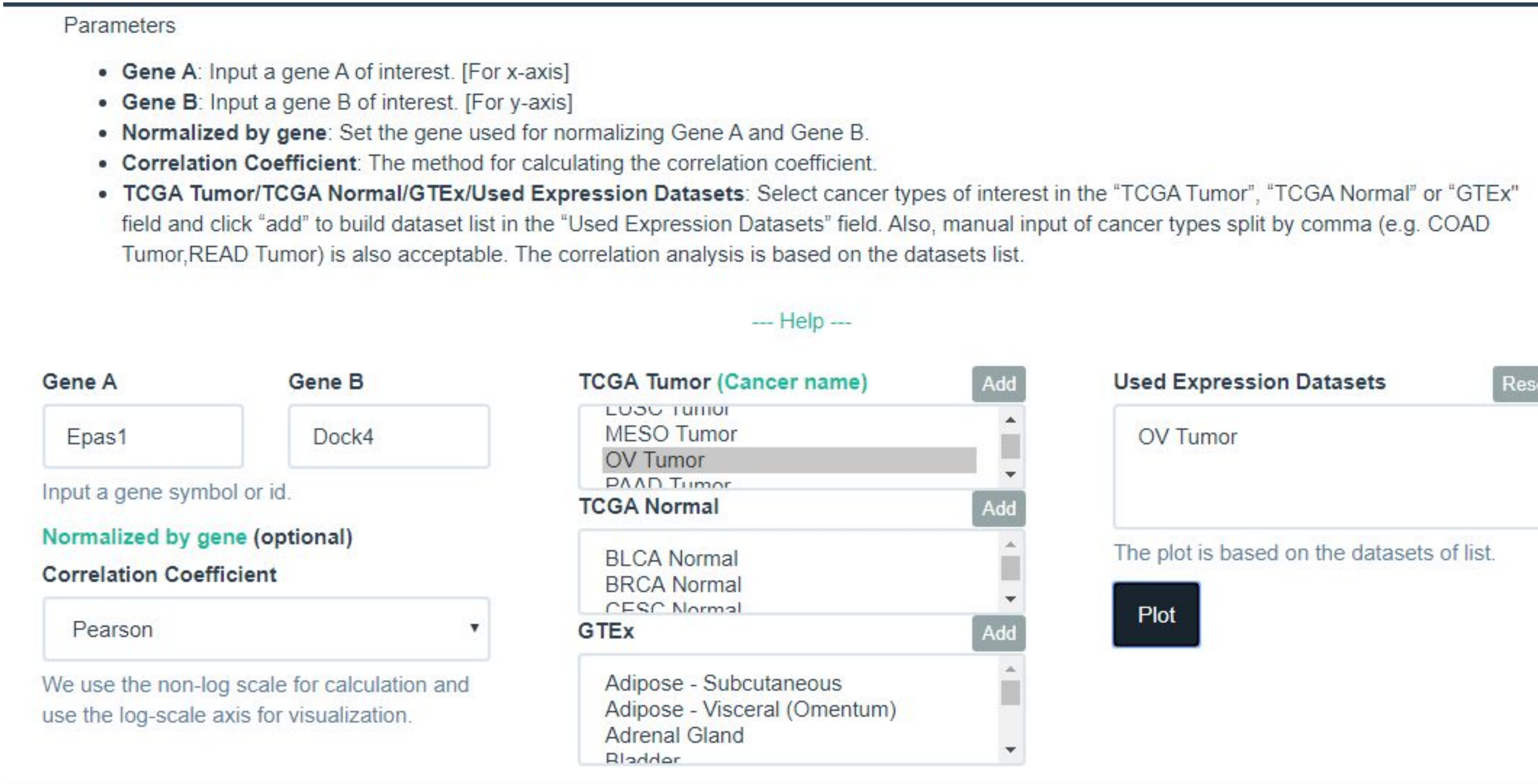
GTEx

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

Used Expression Datasets: LIHC Tumor

The plot is based on the datasets of list.


p−value = 0
R = 0.45
log2(DOCK4 TPM)
1
2
3
4
log2(EPAS1 TPM)
3
4
5
6
7



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: 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) Add

LUSC Tumor
MESO Tumor
OV Tumor
PAAD Tumor

TCGA Normal Add

BLCA Normal
BRCA Normal
CESC Normal

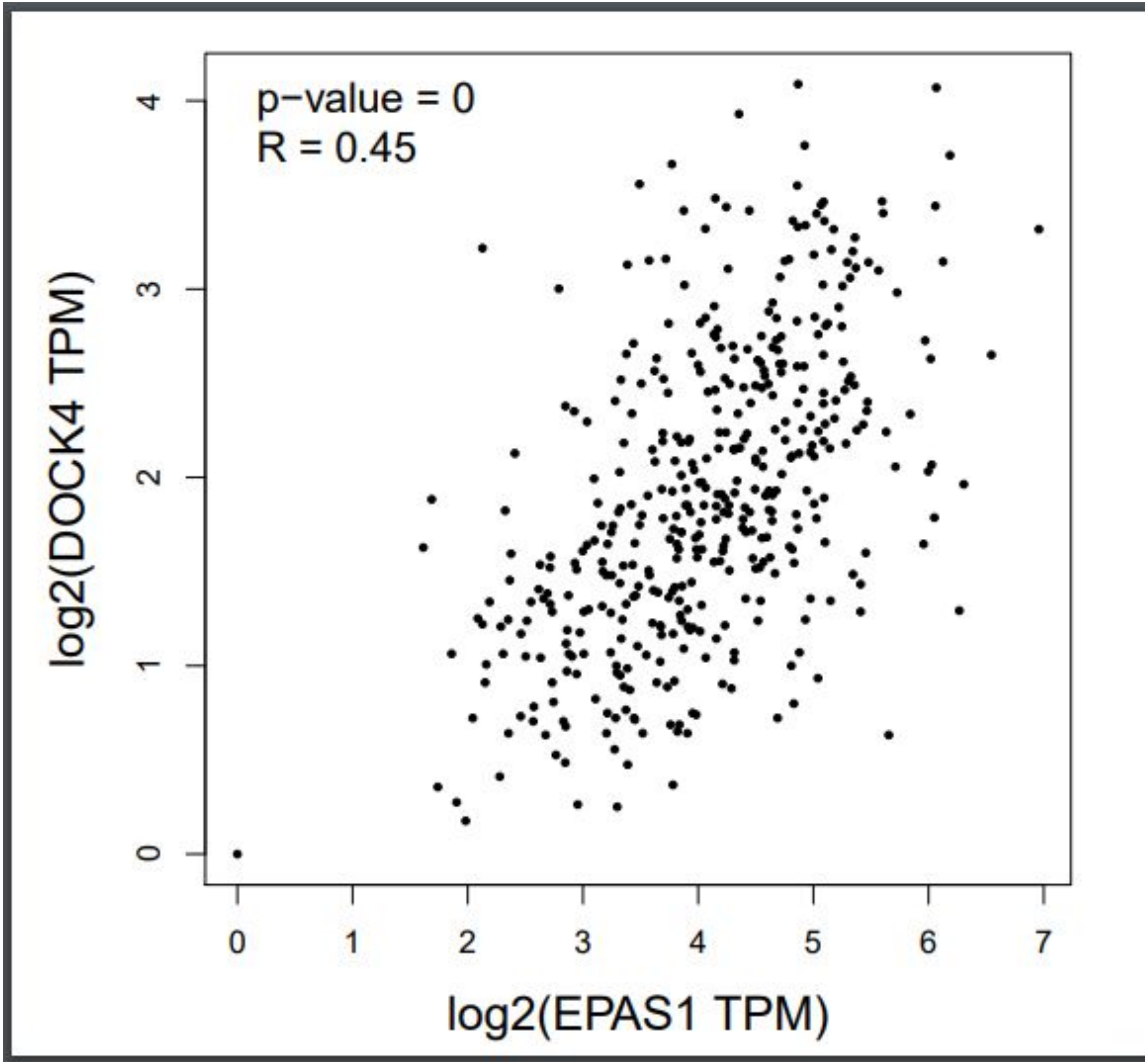
GTEx Add

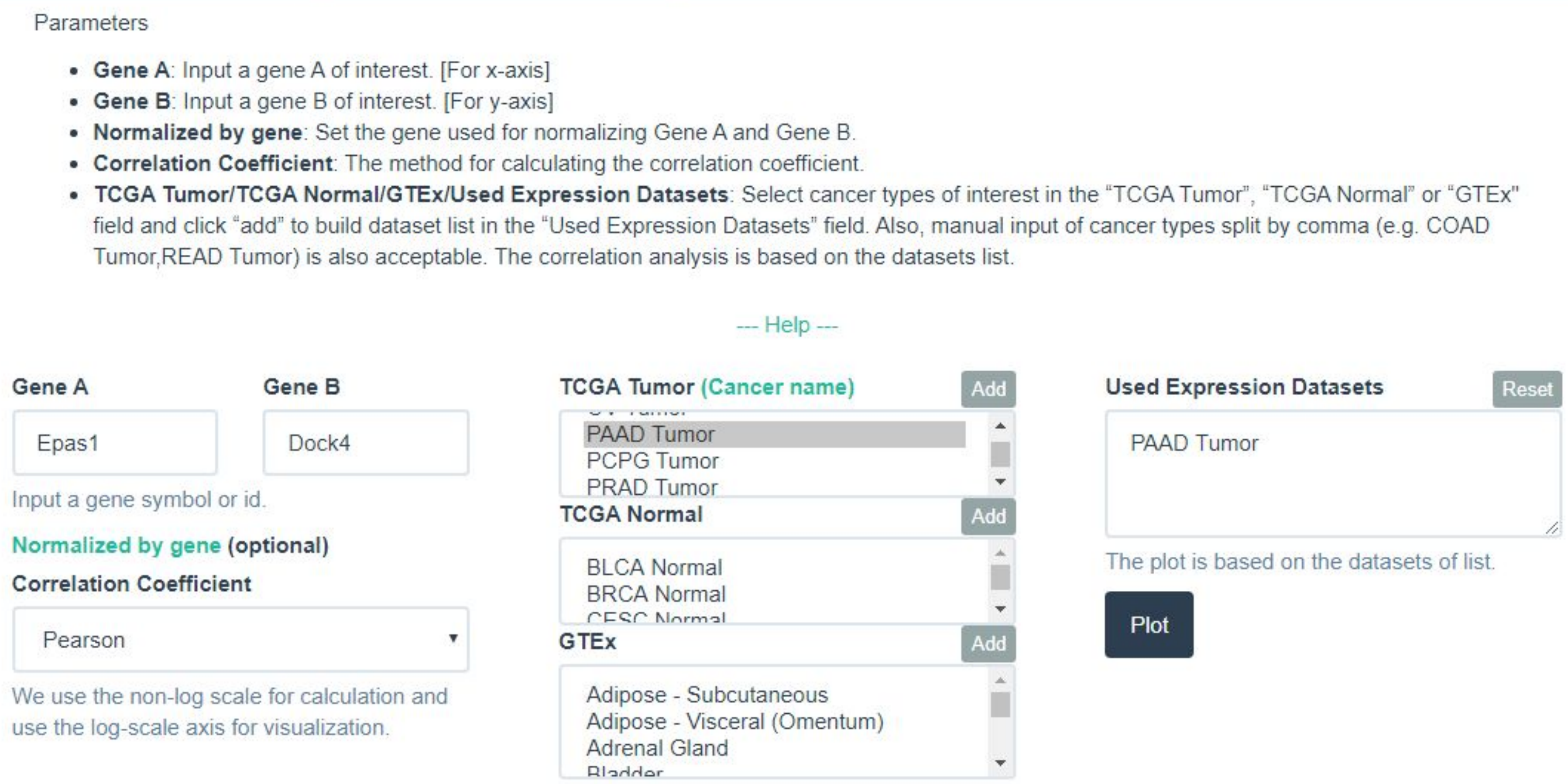
Adipose - Subcutaneous
Adipose - Visceral (Omentum)
Adrenal Gland
Bladder

Used Expression Datasets Res

OV Tumor

The plot is based on the datasets of list.


p−value = 0
R = 0.45
log2(DOCK4 TPM)
0
1
2
3
4
log2(EPAS1 TPM)
0
1
2
3
4
5
6
7



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: Epas1

Gene B: Dock4

Input a gene symbol or id.

Normalized by gene (optional)

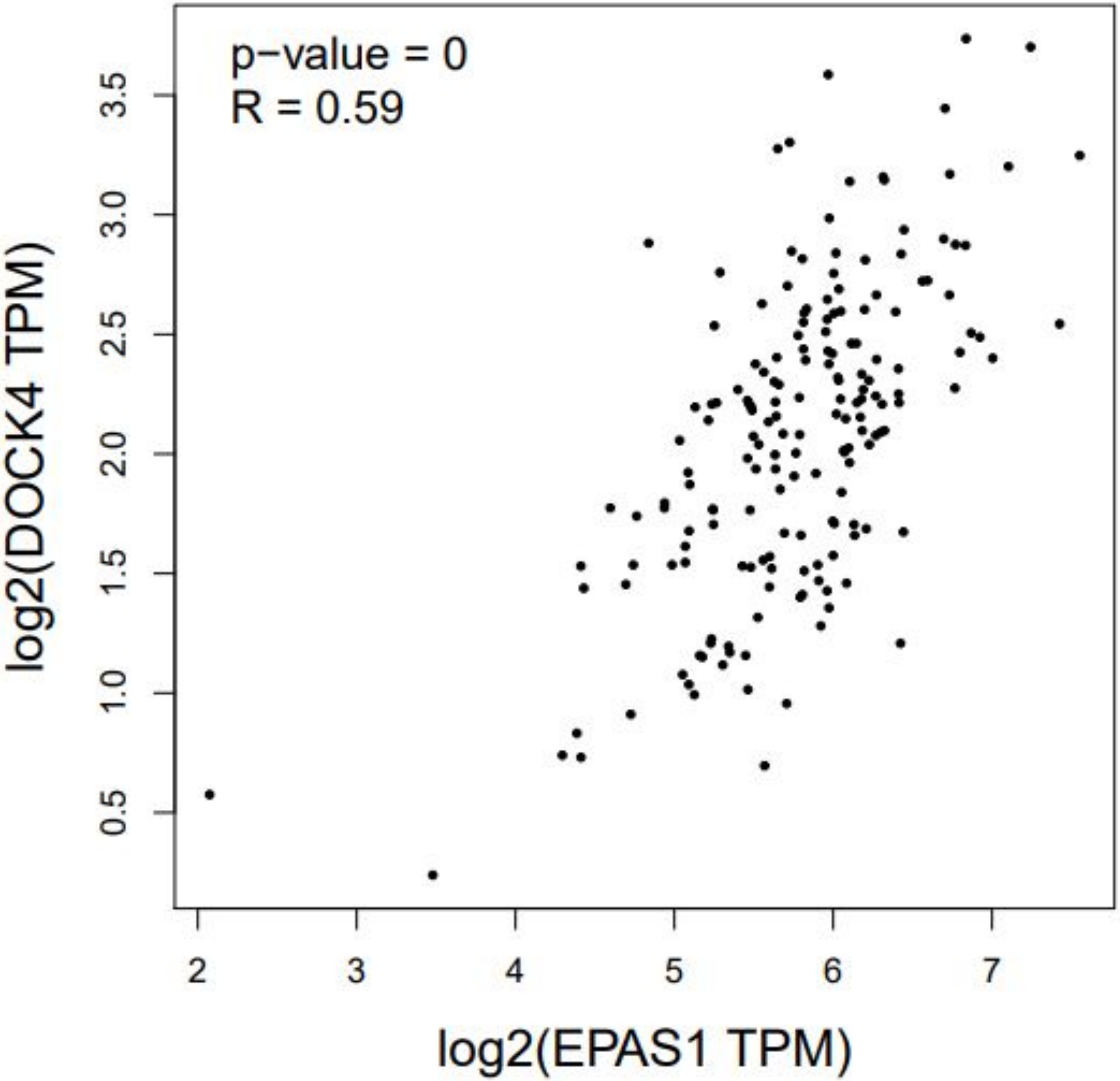
Correlation Coefficient: Pearson

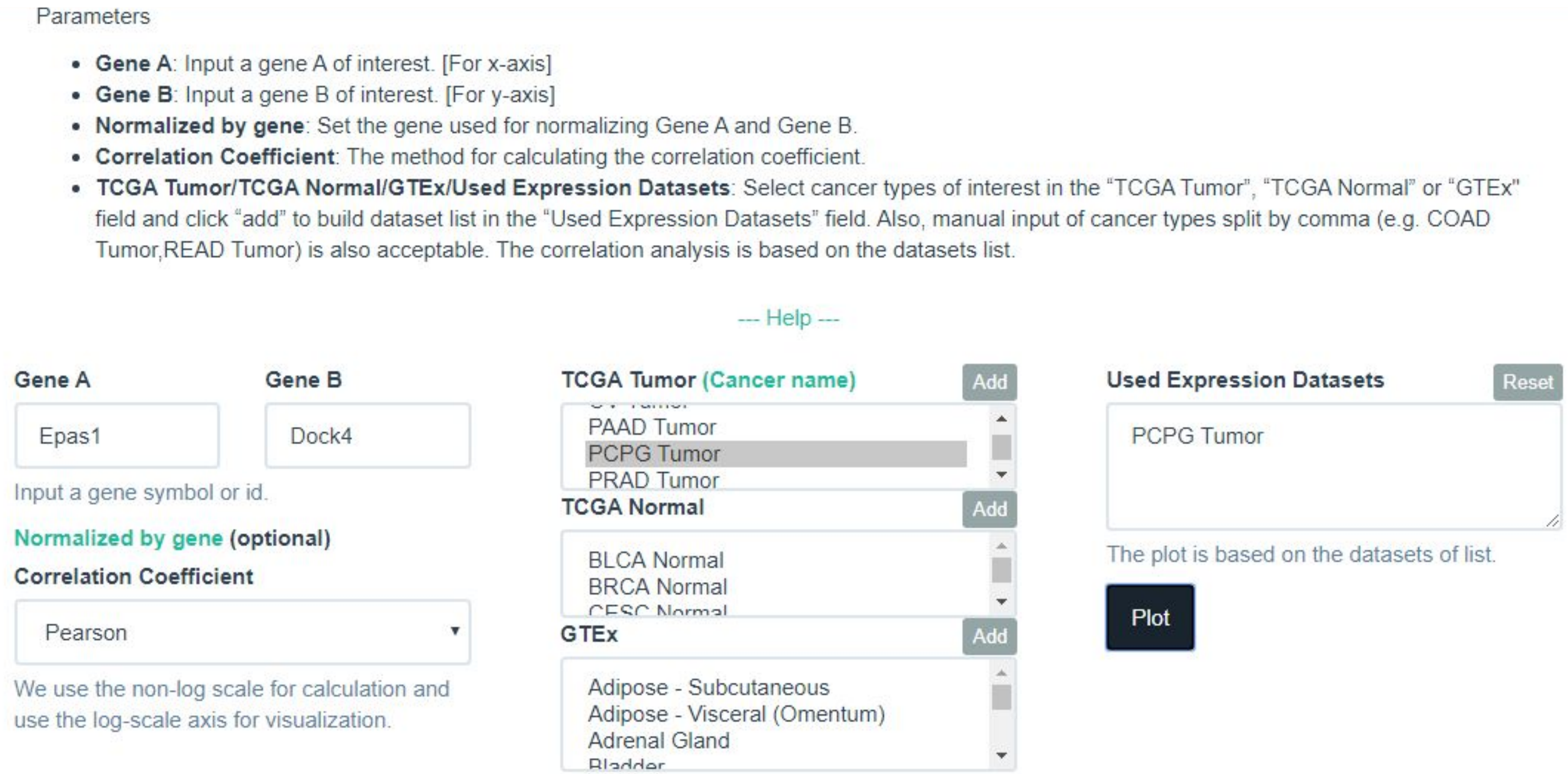
We use the non-log scale for calculation and use the log-scale axis for visualization.

TCGA Tumor (Cancer name): PAAD Tumor

Used Expression Datasets: PAAD Tumor

The plot is based on the datasets of list.


p−value = 0
R = 0.59
log2(DOCK4 TPM)
0.5
1.0
1.5
2.0
2.5
3.0
3.5
log2(EPAS1 TPM)
2
3
4
5
6
7



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: 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)

PAAD Tumor
PCPG Tumor
PRAD Tumor

TCGA Normal

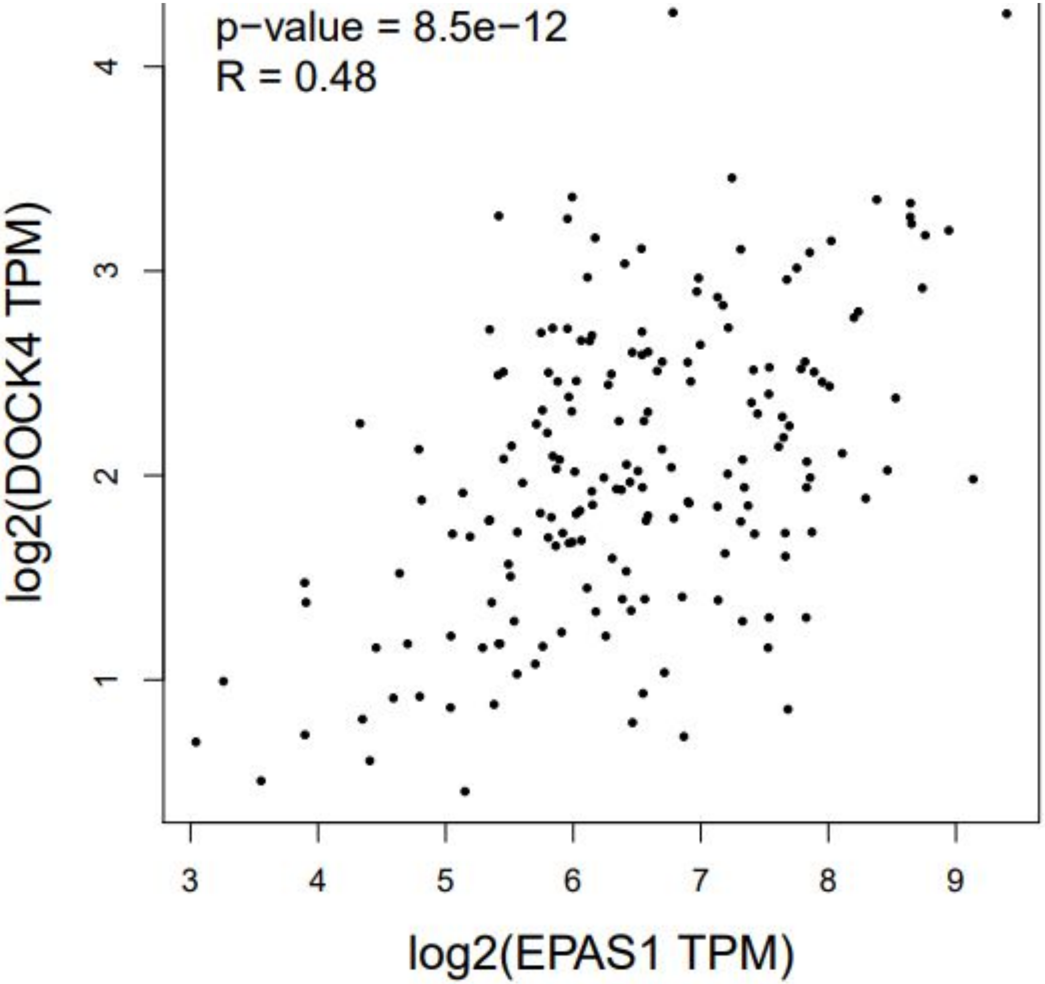
BLCA Normal
BRCA Normal
CESC Normal

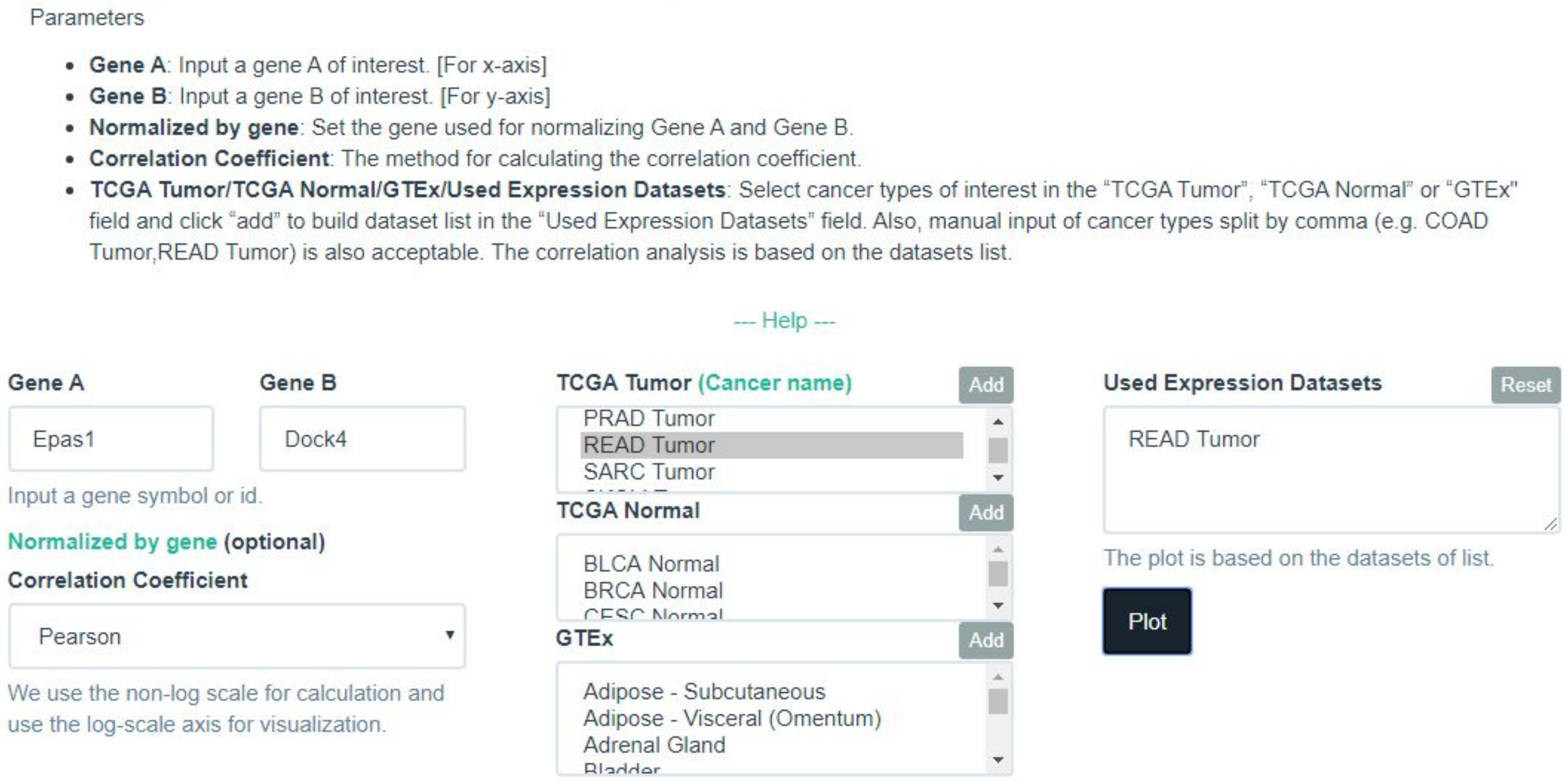
GTEx

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

Used Expression Datasets: PCPG Tumor

The plot is based on the datasets of list.


p−value = 8.5e−12
R = 0.48
log2(DOCK4 TPM)
1
2
3
4
3
4
5
6
7
8
9
log2(EPAS1 TPM)



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: Epas1

Gene B: Dock4

Input a gene symbol or id.

Normalized by gene (optional)

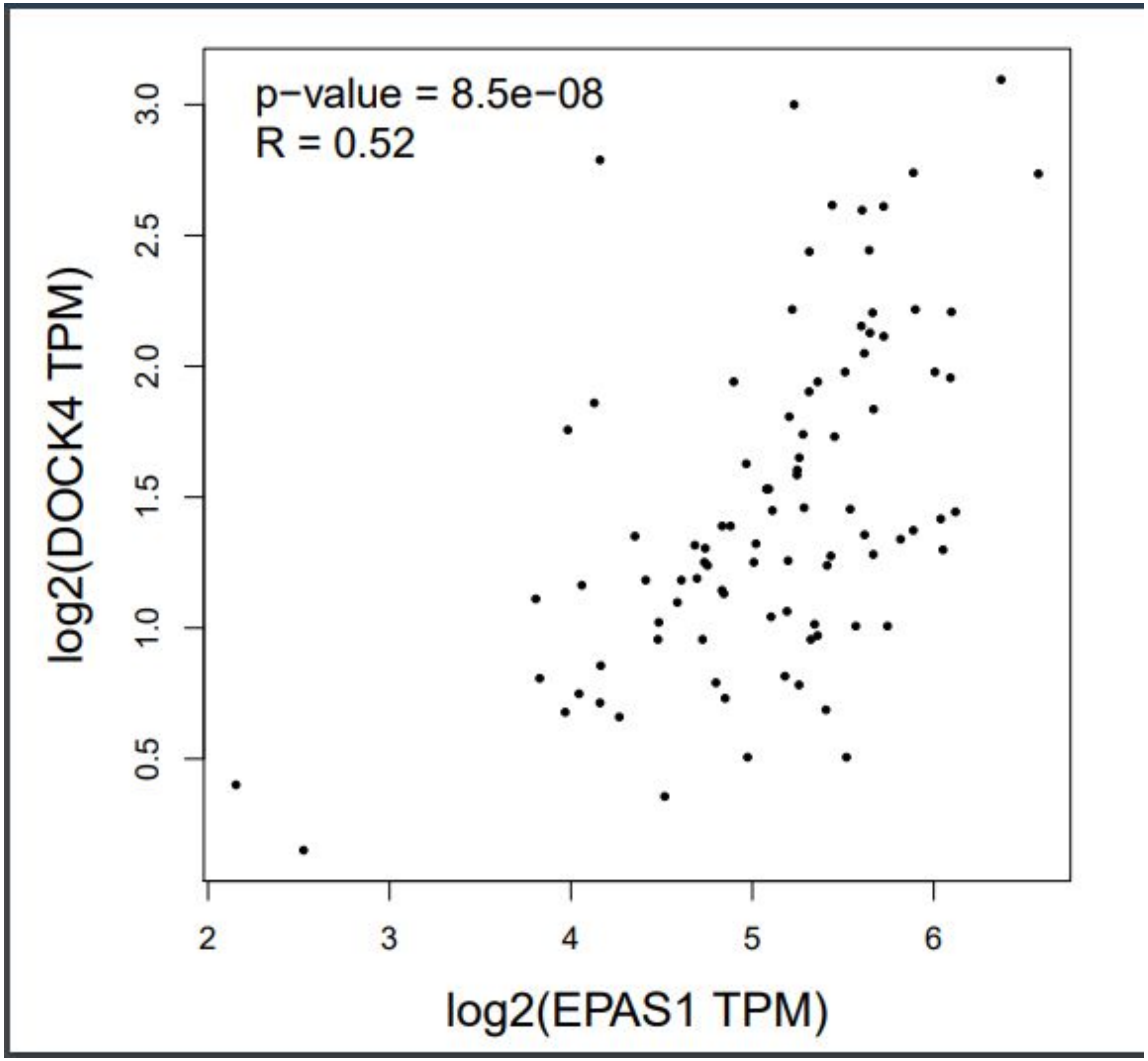
Correlation Coefficient: Pearson

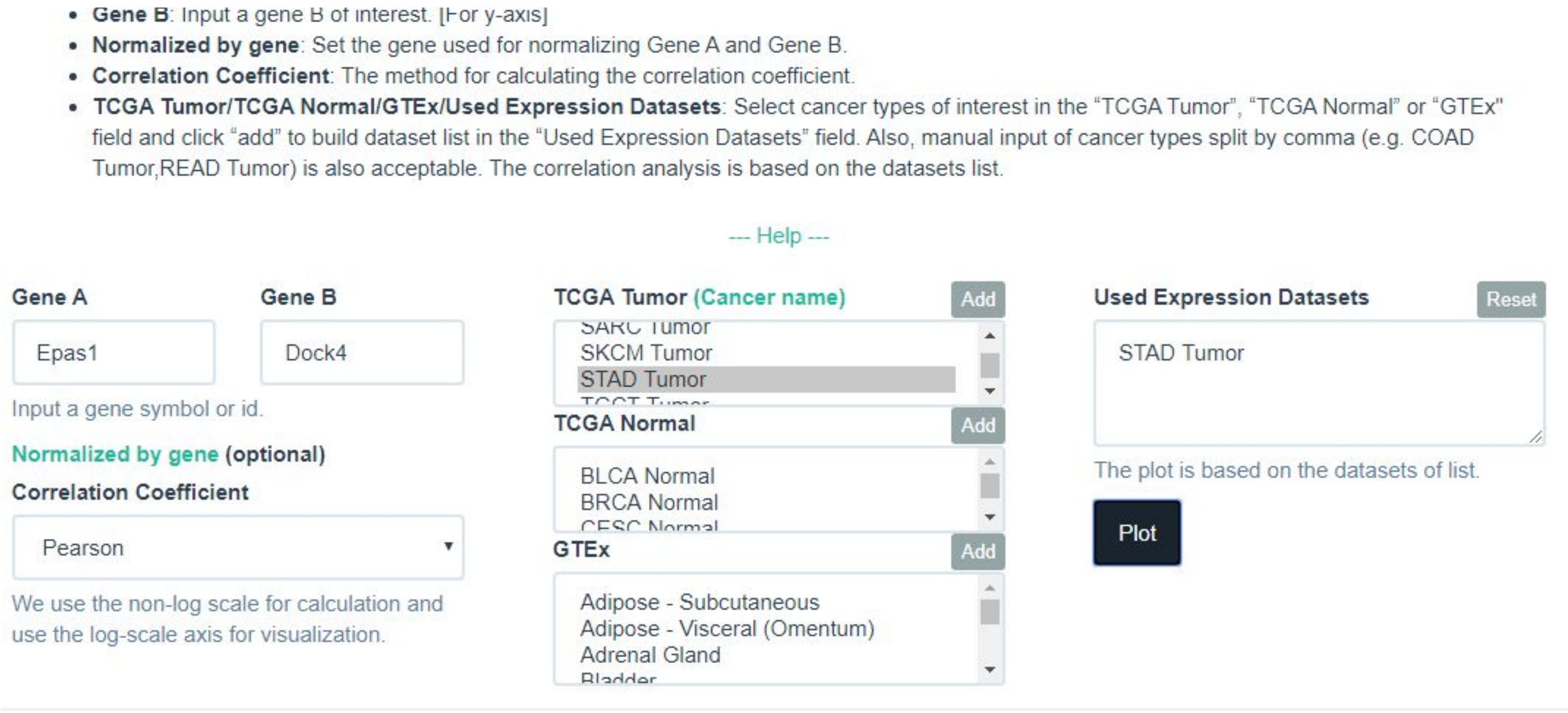
We use the non-log scale for calculation and use the log-scale axis for visualization.

TCGA Tumor (Cancer name): READ Tumor

Used Expression Datasets: READ Tumor

The plot is based on the datasets of list.


p−value = 8.5e−08
R = 0.52
log2(DOCK4 TPM)
0.5
1.0
1.5
2.0
2.5
3.0
2
3
4
5
6
log2(EPAS1 TPM)



- **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: Epas1

Gene B: Dock4

Input a gene symbol or id.

Normalized by gene (optional)

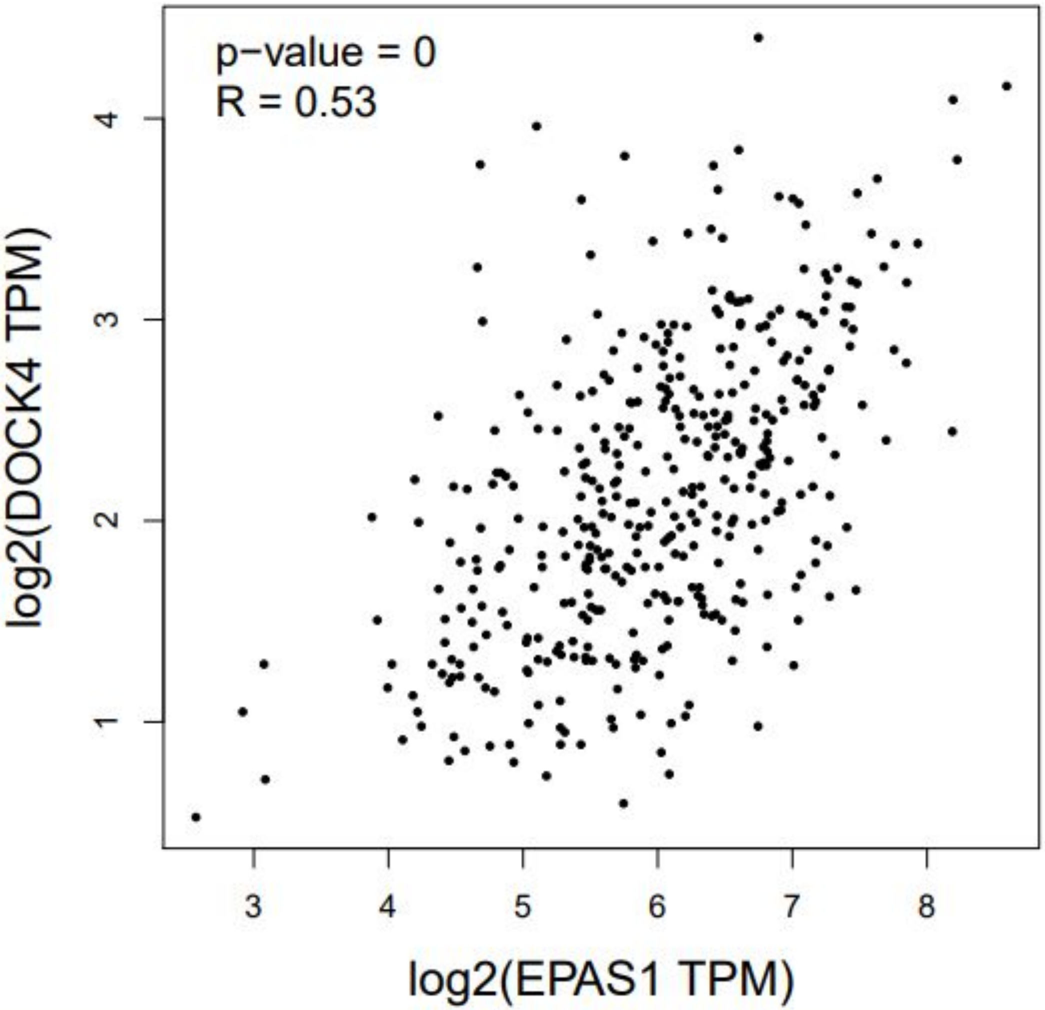
Correlation Coefficient: Pearson

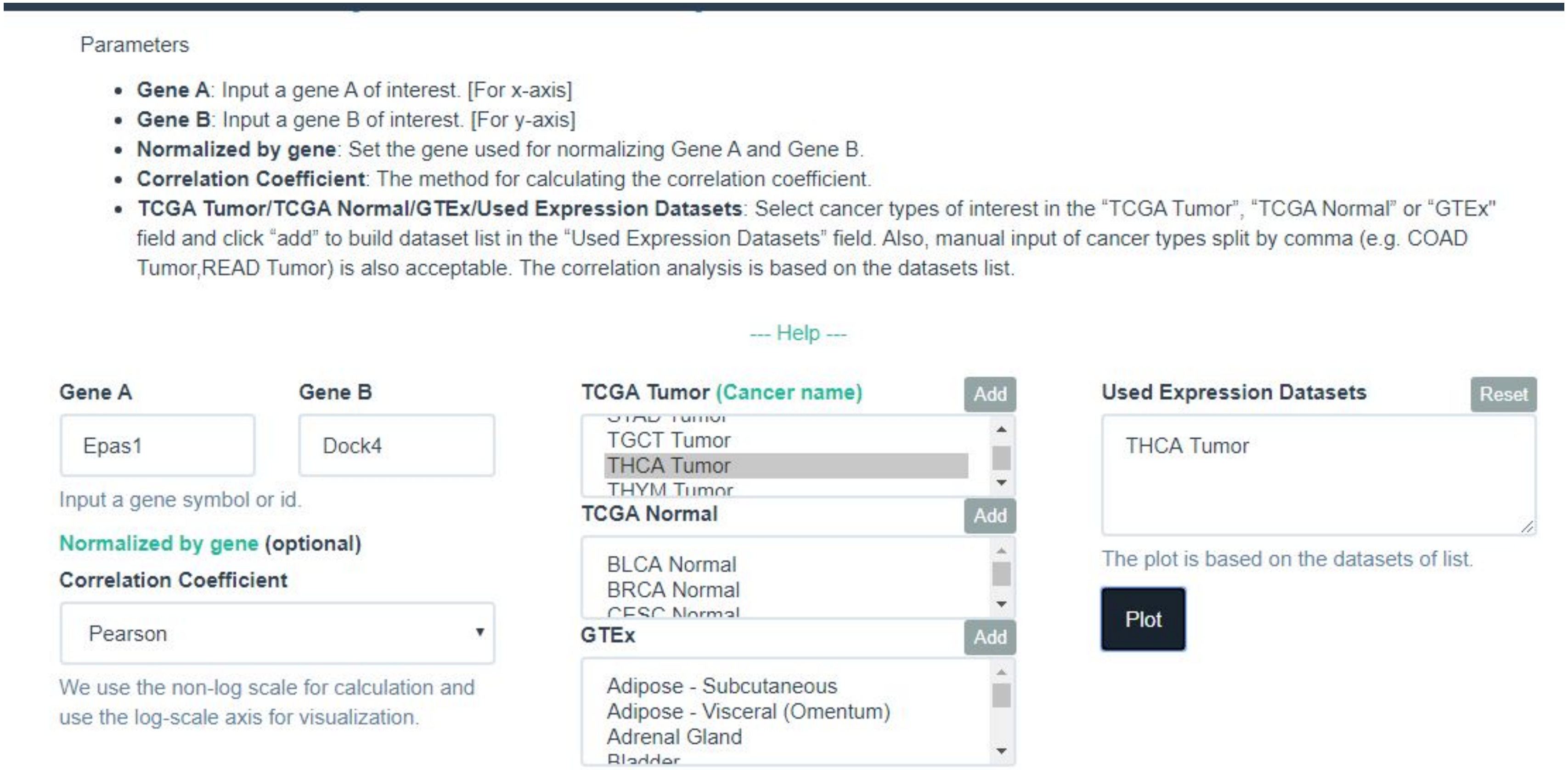
We use the non-log scale for calculation and use the log-scale axis for visualization.

TCGA Tumor (Cancer name): STAD Tumor

Used Expression Datasets: STAD Tumor

The plot is based on the datasets of list.


p−value = 0
R = 0.53
log2(DOCK4 TPM)
1
2
3
4
log2(EPAS1 TPM)
3
4
5
6
7
8



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: Epas1

Gene B: Dock4

Input a gene symbol or id.

Normalized by gene (optional)

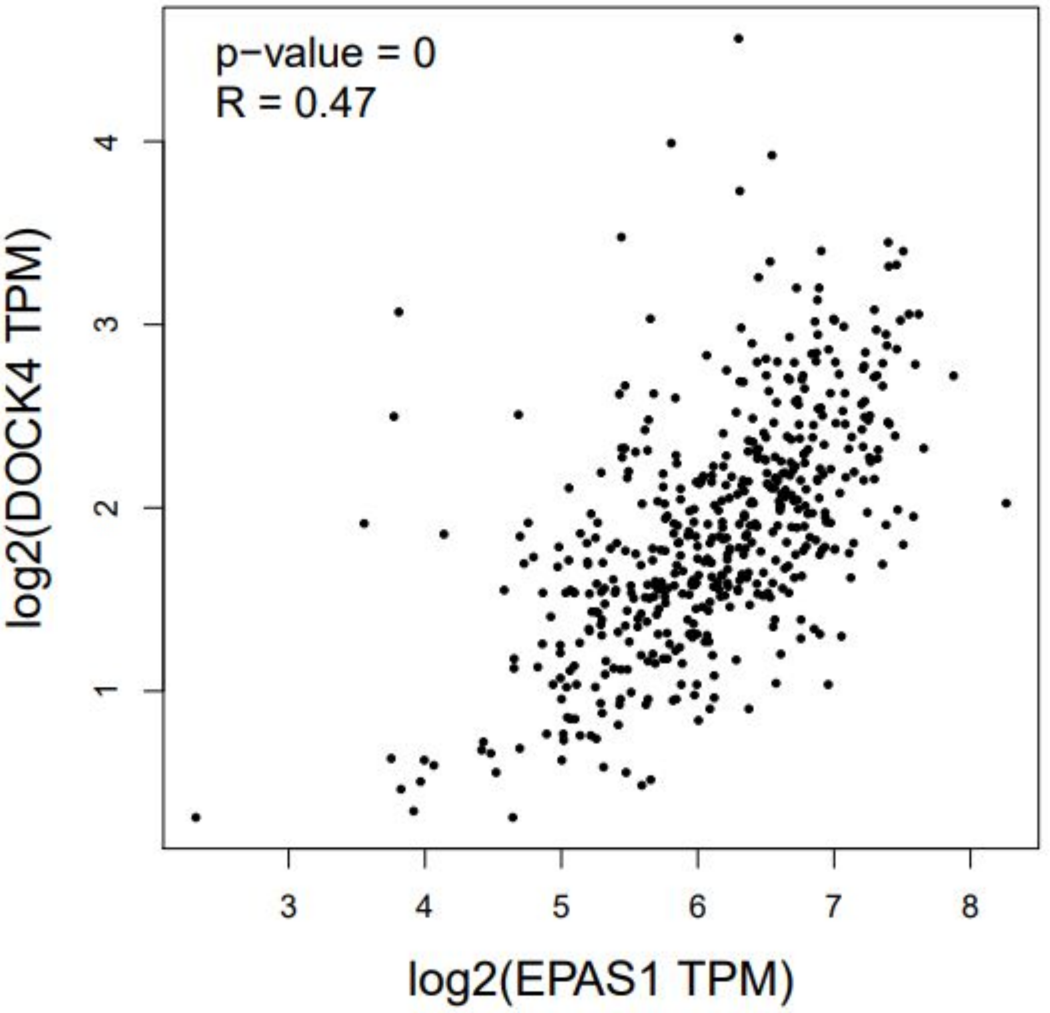
Correlation Coefficient: Pearson

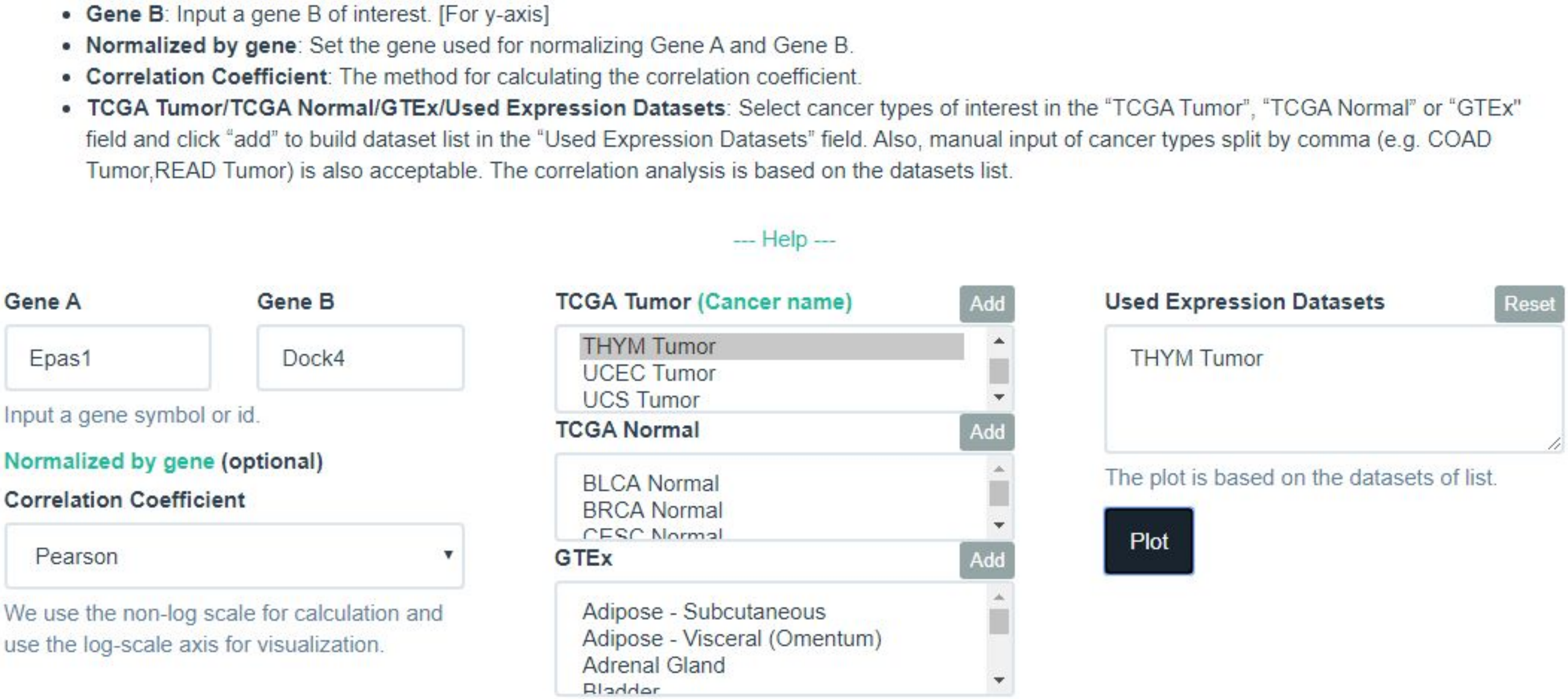
We use the non-log scale for calculation and use the log-scale axis for visualization.

TCGA Tumor (Cancer name): THCA Tumor

Used Expression Datasets: THCA Tumor

The plot is based on the datasets of list.


p−value = 0
R = 0.47
log2(DOCK4 TPM)
1
2
3
4
3
4
5
6
7
8
log2(EPAS1 TPM)



- **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: 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)

THYM Tumor
UCEC Tumor
UCS Tumor

TCGA Normal

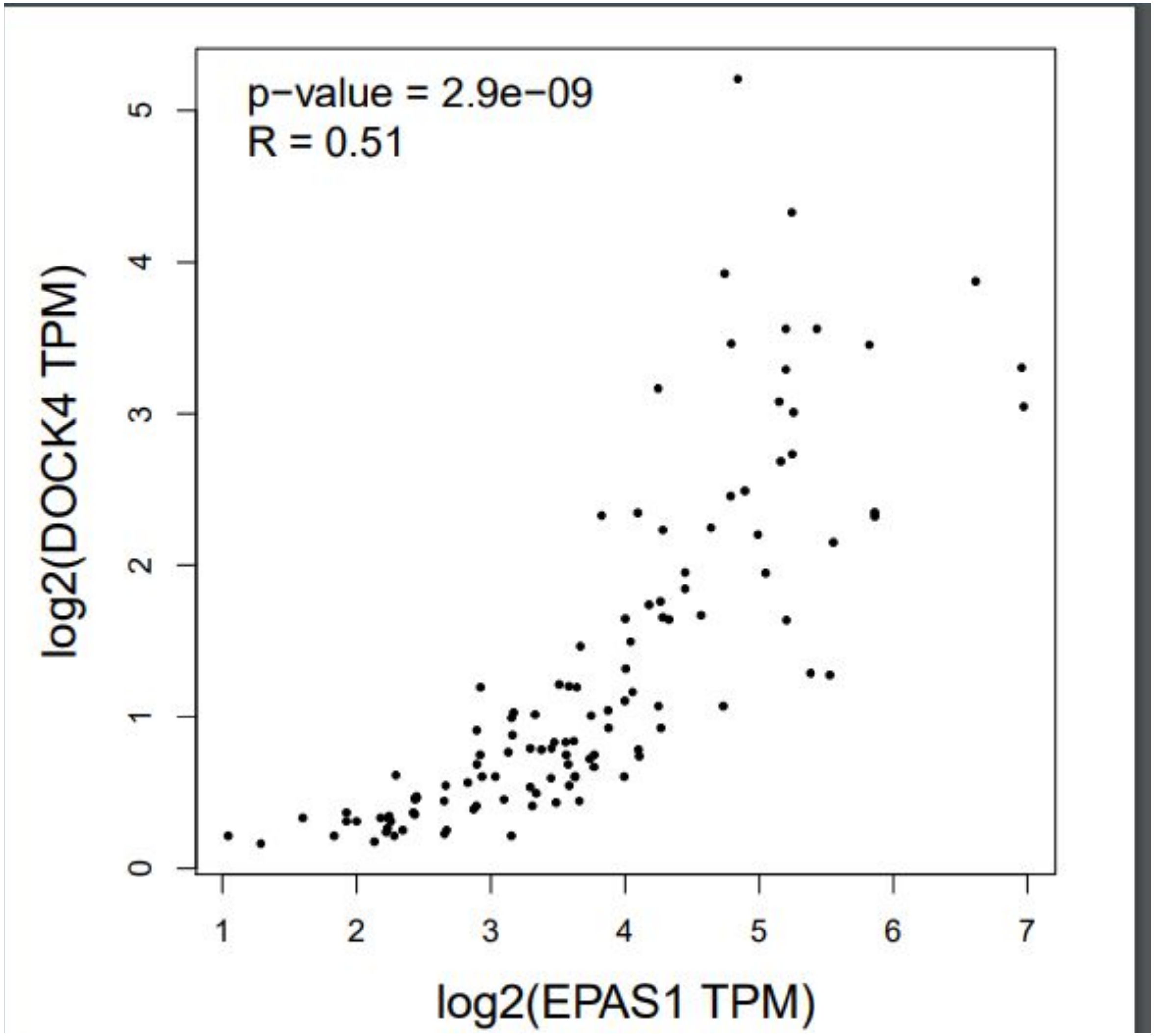
BLCA Normal
BRCA Normal
CESC Normal

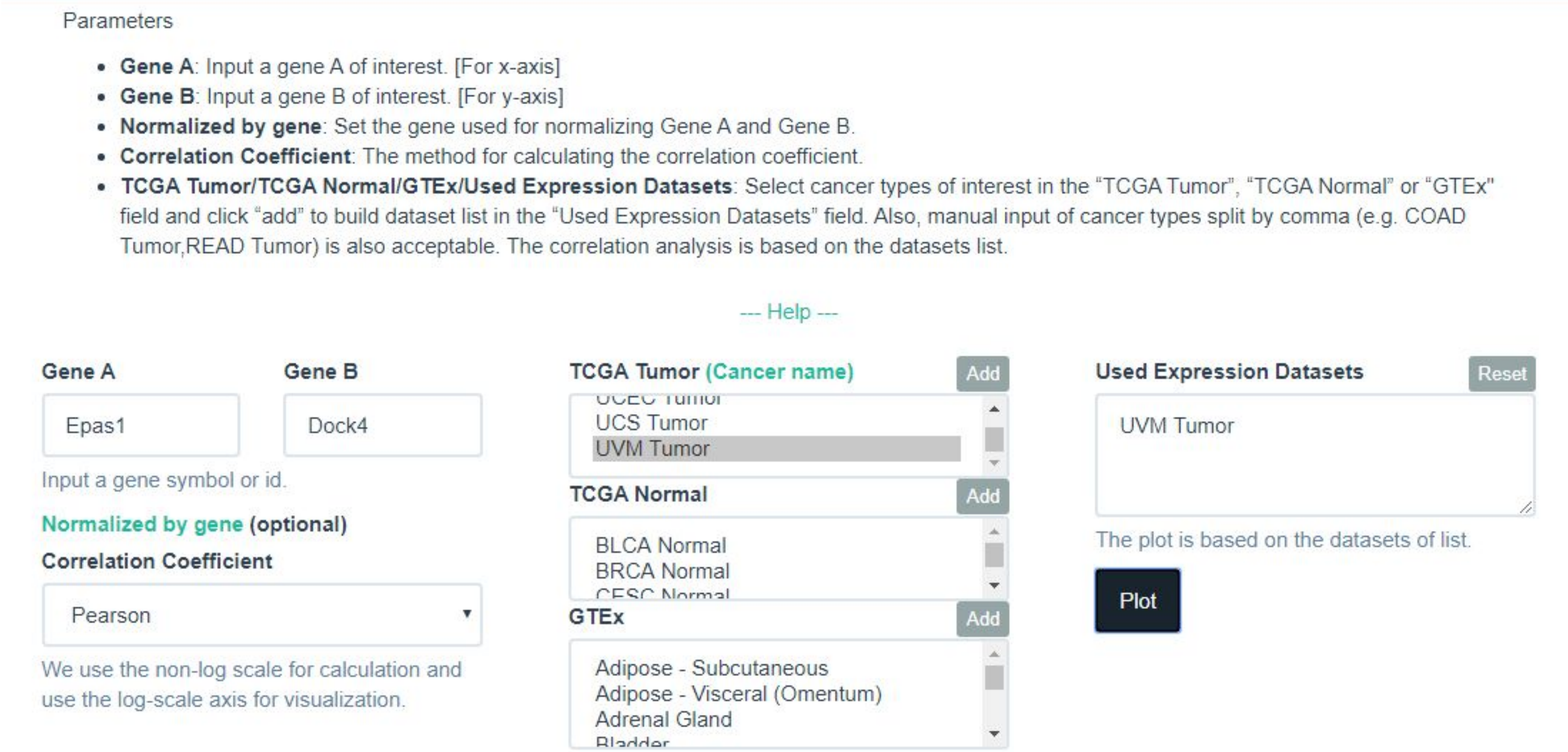
GTEx

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

Used Expression Datasets: THYM Tumor

The plot is based on the datasets of list.


p−value = 2.9e−09
R = 0.51
log2(DOCK4 TPM)
0
1
2
3
4
5
log2(EPAS1 TPM)
1
2
3
4
5
6
7



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

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)

UCS Tumor
UVM Tumor

TCGA Normal

BLCA Normal
BRCA Normal

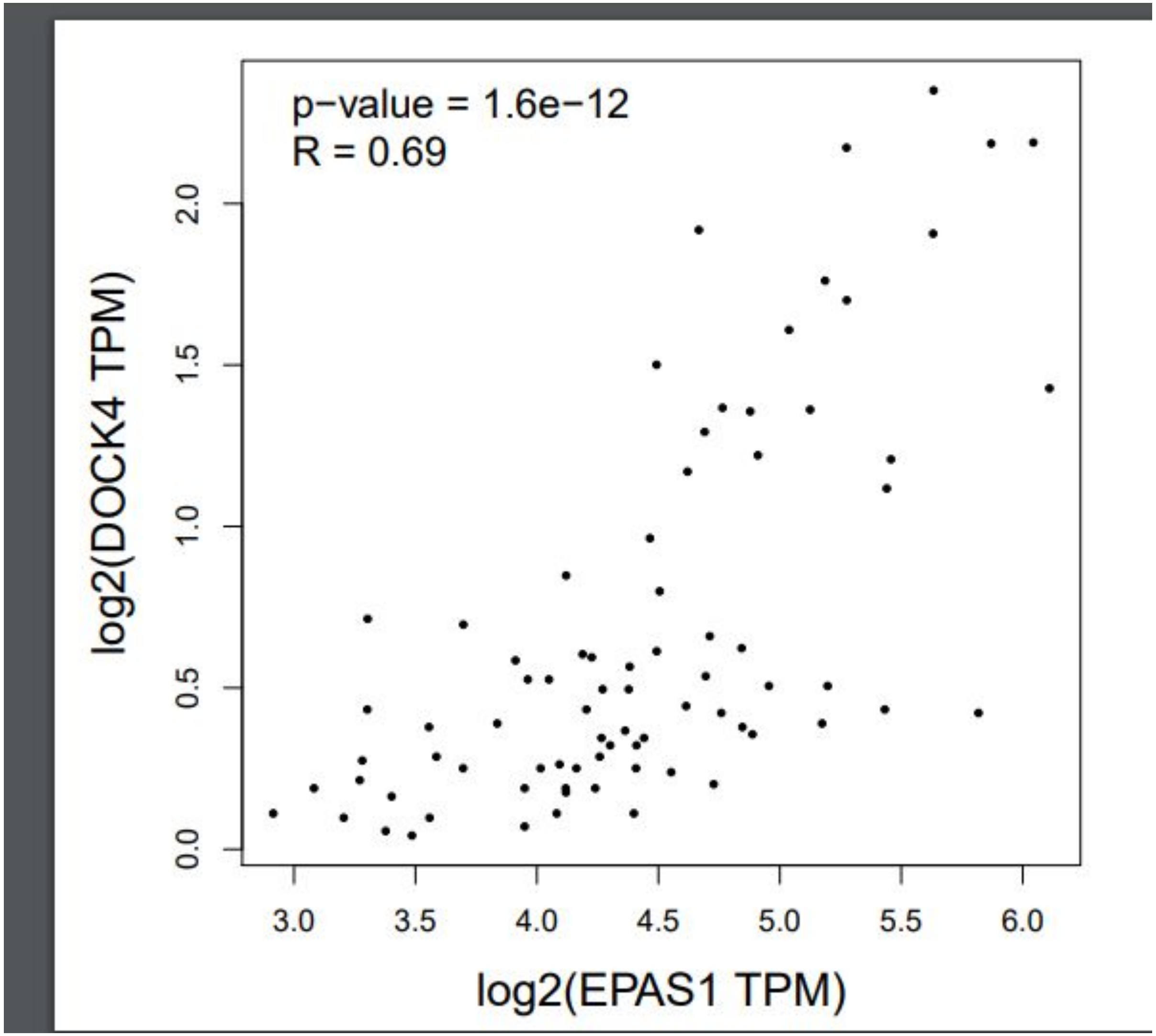
GTEx

Adipose - Subcutaneous
Adipose - Visceral (Omentum)
Adrenal Gland

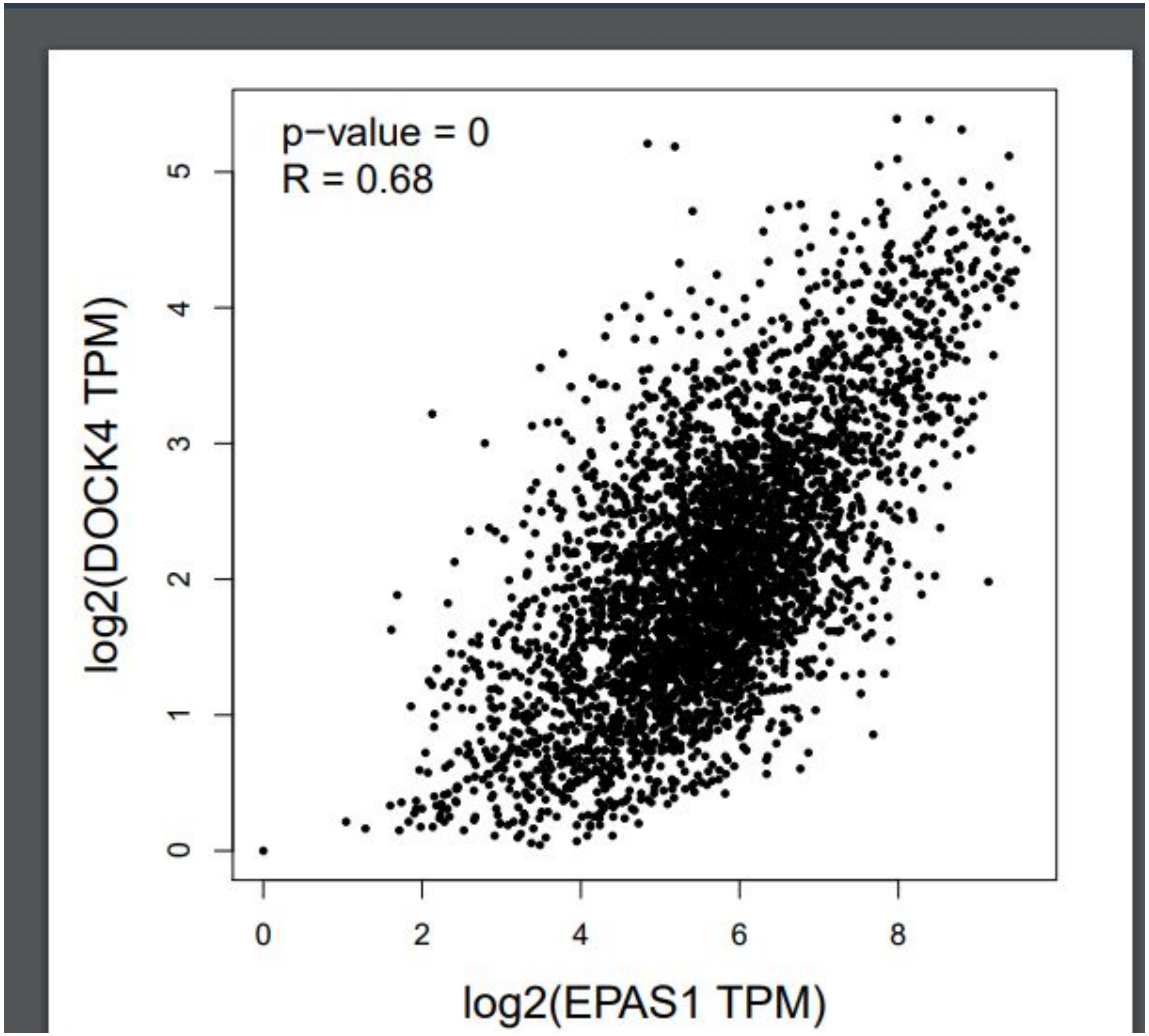
Used Expression Datasets

UVM Tumor

The plot is based on the datasets of list.


p−value = 1.6e−12
R = 0.69
log2(DOCK4 TPM)
0.0
0.5
1.0
1.5
2.0
log2(EPAS1 TPM)
3.0
3.5
4.0
4.5
5.0
5.5
6.0

	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**


p−value = 0
R = 0.68
log2(DOCK4 TPM)
0
1
2
3
4
5
0
2
4
6
8
log2(EPAS1 TPM)