

# **OncotRF: an online resource for exploration of tRNA-derived fragments in human cancers**

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## **Supplementary Data**

### Search Results for keyword 'bladder cancer':

- tRF expression in BLCA, click the link of each tRF type for details:

[3'U-tRF](#)

[3'-tRF](#)

[5'-tRF](#)

[i-tRF](#)

- Differential expression analysis, click the link of each tRF type for details:

[3'U-tRF](#)

[3'-tRF](#)

[5'-tRF](#)

[i-tRF](#)

- Survival analysis, click the link of each tRF type for details:

[3'U-tRF](#)

[3'-tRF](#)

[5'-tRF](#)

[i-tRF](#)

**Figure S1. Search results for keyword “bladder cancer”.**

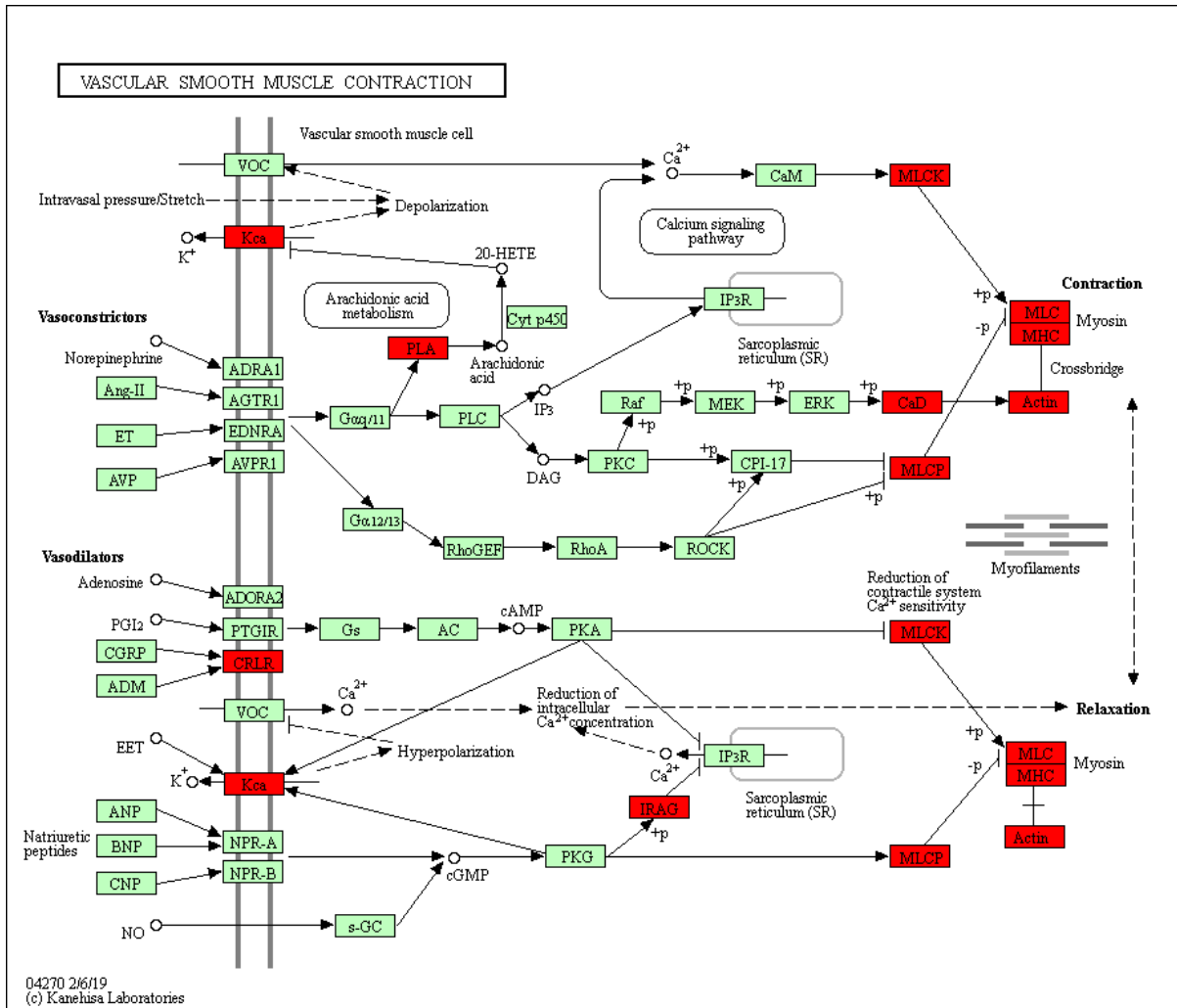
**There is a gene for keyword 'CALD1'.**

Show  entries Search:

Gene	Cancer	tRF	Correlation	Pvalue	Qvalue
CALD1	BLCA	3'U-mito-tRNA-Val-TAC_L22	-0.606	8.564e-33	9.697e-29
CALD1	BLCA	3'U-mito-tRNA-Val-TAC_L21	-0.597	1.276e-31	9.790e-28
CALD1	BLCA	3'U-mito-tRNA-Val-TAC_L23	-0.574	7.481e-29	2.481e-25
CALD1	BLCA	3'U-mito-tRNA-Ile-GAT_L21	-0.539	5.408e-25	6.845e-22
CALD1	BLCA	i-mito-tRNA-Gln-TTG_L21_pos49	-0.539	5.408e-25	2.633e-20
CALD1	BLCA	3'U-mito-tRNA-Cys-GCA_L23	-0.507	6.875e-22	4.667e-19
CALD1	BLCA	3'U-mito-tRNA-Val-TAC_L24	-0.507	7.484e-22	5.025e-19
CALD1	BLCA	5'-M-tRNA-Tyr-GTA-chr21-2_L30	-0.468	1.771e-18	2.770e-15
CALD1	BLCA	3'U-mito-tRNA-Trp-TCA_L21	-0.467	2.183e-18	7.169e-16
CALD1	BLCA	5'-mito-tRNA-Lys-TT_L23	-0.464	4.095e-18	5.727e-15

Showing 1 to 10 of 42 entries Previous | 2 3 4 5 Next

**Figure S2. Search results for keyword “CALD1”.**



**Figure S3. The KEGG pathway “Vascular smooth muscle contraction”.** Genes with red background were significantly dysregulated in BLCA and had a strong correlation with differentially expressed tRFs in BLCA.

**Browse Analysis**

- Differential Expression Analysis
- Survival Analysis
  - tRF
    - 3U-IRF
      - 3U-M-mito-tRNA-Tyr-GTA\_L20
      - 3U-M-mito-tRNA-Tyr-GTA\_L22
      - 3U-M-tRNA-Gly-GCC-4-1\_L16
      - 3U-M-tRNA-Gly-GCC-4-1\_L17
      - 3U-M-tRNA-Gly-TCC-2-5\_L15
      - 3U-M-tRNA-His-GTG-1-4\_L23
      - 3U-M-tRNA-His-GTG-1-4\_L24
      - 3U-M-tRNA-His-GTG-1-4\_L25
      - 3U-M-tRNA-His-GTG-1-4\_L30
      - 3U-mito-tRNA-Asp-GTC\_L20
      - 3U-mito-tRNA-Asp-GTC\_L21
      - 3U-mito-tRNA-Asp-GTC\_L23
      - 3U-mito-tRNA-Asp-GTC\_L28
      - 3U-mito-tRNA-Cys-GCA\_L15
      - 3U-mito-tRNA-Cys-GCA\_L16
      - 3U-mito-tRNA-Cys-GCA\_L17
      - 3U-mito-tRNA-Cys-GCA\_L18
      - 3U-mito-tRNA-Cys-GCA\_L20
      - 3U-mito-tRNA-Cys-GCA\_L21
      - 3U-mito-tRNA-Cys-GCA\_L23
      - 3U-mito-tRNA-Cys-GCA\_L25
      - 3U-mito-tRNA-Cys-GCA\_L26
      - 3U-mito-tRNA-Cys-GCA\_L29
      - 3U-mito-tRNA-Ile-GAT\_L15
      - 3U-mito-tRNA-Ile-GAT\_L17
      - 3U-mito-tRNA-Ile-GAT\_L18
      - 3U-mito-tRNA-Ile-GAT\_L19
      - 3U-mito-tRNA-Ile-GAT\_L20

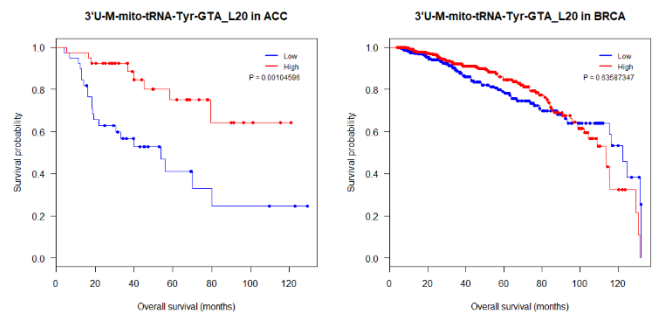
### 3'U-M-mito-tRNA-Tyr-GTA\_L20 Survival Analysis

**Overall Survival Analysis**

Show 10 entries

Cancer	Logtest Pvalue	Logtest Qvalue	HR	Lower	Upper
ACC	1.593e-3	0.015	0.335	0.148	0.757
BRCA	0.132	0.422	0.875	0.734	1.044
KIRC	0.683	0.788	0.964	0.805	1.153
KIRP	0.142	0.259	0.716	0.441	1.163
LHCC	0.123	0.523	0.820	0.630	1.068
LIUAD	0.083	0.815	0.853	0.725	1.028
LUSC	0.512	0.690	1.041	0.924	1.173
STAD	0.909	0.937	0.988	0.893	1.216
THCA	0.105	0.322	1.546	0.938	2.549
UCEC	3.902e-3	0.078	0.738	0.592	0.919

Showing 1 to 10 of 10 entries



**Figure S4. Survival analysis results and Kaplan-Meier curves of 3'U-M-mito-tRNA-Tyr-GTA\_L20 among cancers.**

**Browse Analysis**

- Differential Expression Analysis
- Survival Analysis
  - IRF
    - Cancer Type
      - ACC
        - 3'-IRF
          - 3'-IRF
          - 5'-IRF
          - I-IRF
      - BLCA
      - BRCA
      - CESC
      - CHOL
      - COAD
      - DLBC
      - ESCA
      - HNSC
      - KICH
      - KIRC
      - KIRP
      - LGG
      - LIHC
      - LUAD
      - LUSC
      - MESO
      - OV
      - PAAD
      - PCPG
      - PRAD
      - READ

### 3'-tRF Survival Analysis in ACC

**Overall Survival Analysis**

Show 10 entries Search:

tRF ID	Logtest Pvalue	Logtest Qvalue	HR	Lower	Upper
3'U-mito-tRNA-Val-TAC_L22	1.060e-6	1.071e-4	0.417	0.275	0.632
3'U-mito-tRNA-Val-TAC_L24	2.620e-6	1.323e-4	0.436	0.295	0.645
3'U-mito-tRNA-Val-TAC_L23	1.212e-5	4.079e-4	0.525	0.388	0.711
3'U-mito-tRNA-Val-TAC_L21	2.913e-5	7.355e-4	0.493	0.331	0.734
3'U-mito-tRNA-Cys-GCA_L15	4.891e-5	9.881e-4	0.387	0.222	0.673
3'U-mito-tRNA-Ile-GAT_L28	2.938e-4	4.945e-3	0.245	0.091	0.657
3'U-tRNA-His-GTG-1-7_L25	3.902e-4	5.630e-3	2.635	1.621	4.283
3'U-mito-tRNA-Cys-GCA_L23	4.702e-4	5.937e-3	0.632	0.481	0.831
3'U-mito-tRNA-Ile-GAT_L29	8.729e-4	9.796e-3	0.636	0.463	0.874
3'U-mito-tRNA-Ile-GAT_L22	9.724e-4	9.821e-3	0.550	0.367	0.825

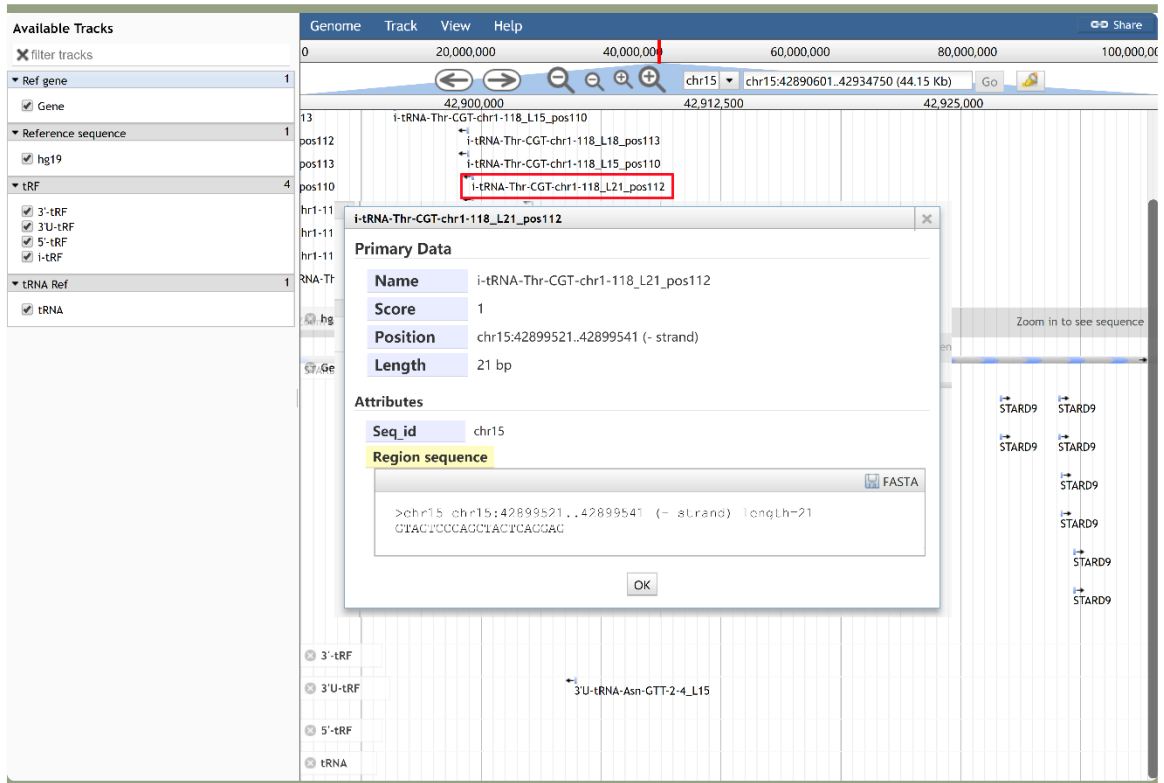
Showing 1 to 10 of 101 entries Previous 1 2 3 4 5 11 Next

**Disease-free Survival Analysis**

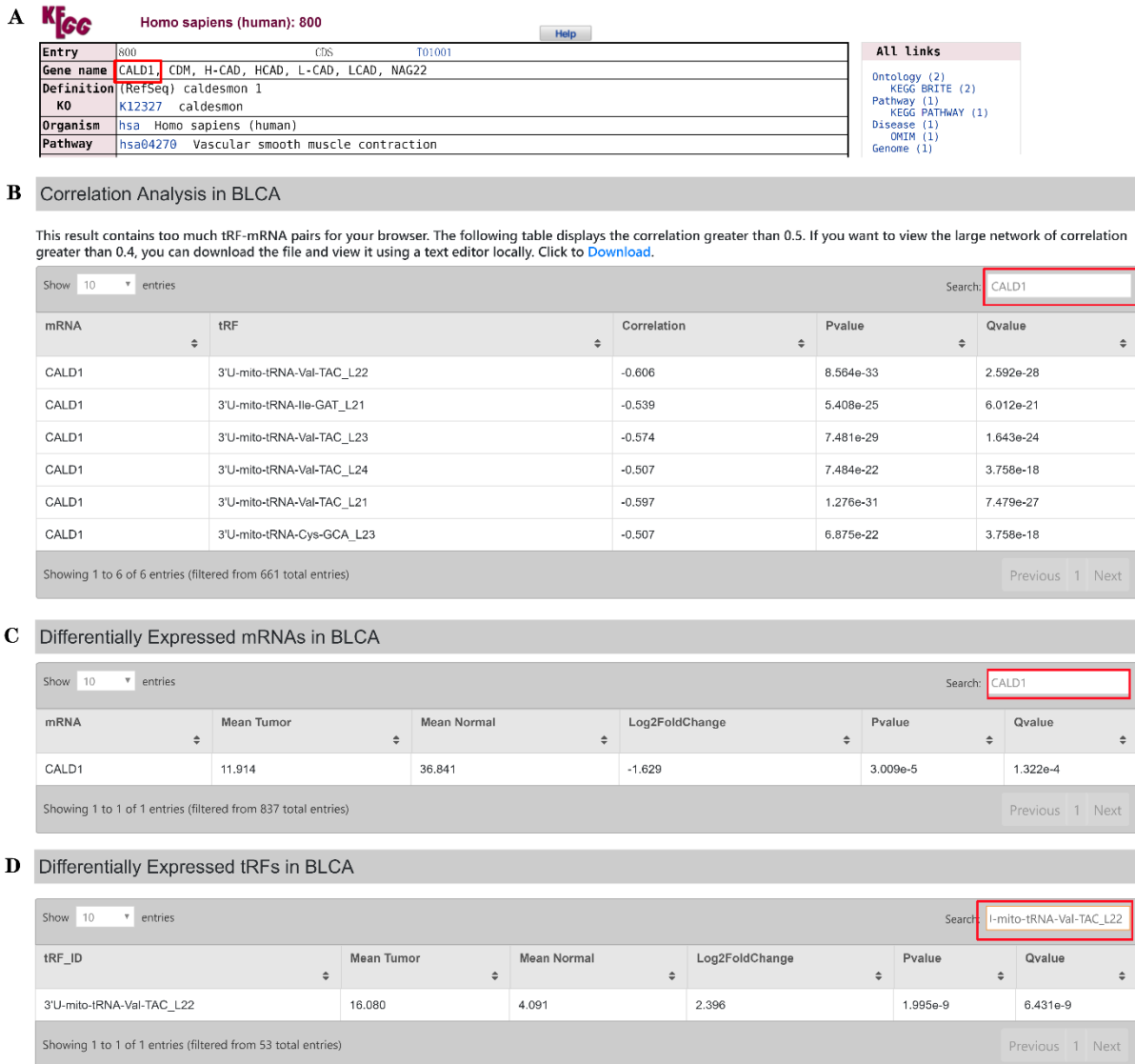
Show 10 entries Search:

tRF ID	Logtest Pvalue	Logtest Qvalue	HR	Lower	Upper
3'U-mito-tRNA-Val-TAC_L22	2.352e-9	2.376e-7	0.364	0.246	0.539
3'U-mito-tRNA-Val-TAC_L21	1.484e-8	7.494e-7	0.385	0.257	0.577
3'U-mito-tRNA-Val-TAC_L23	4.366e-7	1.470e-5	0.469	0.342	0.643
3'U-mito-tRNA-Val-TAC_L24	9.935e-7	2.509e-5	0.455	0.320	0.646
3'U-mito-tRNA-Cys-GCA_L15	2.342e-5	4.731e-4	0.439	0.278	0.693

**Figure S5. Survival analysis results of 3'-tRFs in ACC.**



**Figure S6. Example feature tracks of “i-tRNA-Thr-CGT-chr-118\_L21\_pos112” in JBrowse.**



**Figure S7. A case study in BLCA. (A)** General information of gene “CALD1”. **(B)** tRFs correlated with gene “CALD1” in BLCA. **(C)** Differential expression of “CALD1” between tumor and normal tissues in BLCA. **(D)** Differential expression of 3'U-mito-tRNA-Val-TAC\_L22 between tumor and normal tissues in BLCA.



	Single source tRNA	Multiple source tRNA
<b>3'U-tRF</b>	3'U-mito-tRNA-Val-TAC_L22	3'U-M-tRNA-Gln-CTG-3-2_L23
<b>3'-tRF</b>	3'-tRNA-Ala-AGC-1-1_L19	3'-M-tRNA-Gly-GCC-2-6_L22
<b>5'-tRF</b>	5'-tRNA-Ala-AGC-11-1_L19	5'-M-tRNA-Ala-TGC-7-1_L26
<b>i-tRF</b>	i-tRNA-Ala-AGC-1-1_L21_pos54	i-M-tRNA-Ala-AGC-1-1_L17_pos58

**Figure S8. Nomenclature of tRFs.** First line: 3'U-tRFs. Second line: 3'-tRFs. Third line: 5'-tRFs. Fourth line: i-tRFs. Red font (i.e., 3'U-, 3'-, 5'- and i-) represents a tRF class identifier. Green font (i.e., "M") indicates that the tRF was derived from multiple tRNA genes. Purple font represents a tRNA gene identifier. Black font represents the length of the tRF sequence. Golden font represents start position of an i-tRF on its source tRNA.