

Aging-induced pseudouridine synthase 10 impairs hematopoietic stem cells

Yuqian Wang,^{1*} Zhenzhen Zhang,^{2*} Hanqing He,¹ Jinghui Song,³ Yang Cui,¹ Yunan Chen,⁴ Yuan Zhuang,⁵ Xiaoting Zhang,⁵ Mo Li,⁶ Xinxiang Zhang,⁴ Michael Q. Zhang,^{2,7,8} Minglei Shi,² Chengqi Yi,⁵ and Jianwei Wang¹

¹School of Pharmaceutical Sciences, Tsinghua University, Beijing, China; ²School of Medicine, Tsinghua University, Beijing, China; ³Department of Bioengineering, University of California San Diego, La Jolla, CA, USA; ⁴Beijing National Laboratory for Molecular Sciences, Key Laboratory of Bioorganic Chemistry and Molecular Engineering of Ministry of Education, College of Chemistry and Molecular Engineering, Peking University, Beijing, China; ⁵Department of Basic Medical Sciences, School of Medicine, Institute for Immunology, Beijing Key Laboratory for Immunological Research on Chronic Diseases, THU-PKU Center for Life Sciences, Tsinghua University, Beijing, China; ⁶Center for Reproductive Medicine, Department of Obstetrics and Gynecology, Peking University Third Hospital, Beijing, China; ⁷MOE Key Laboratory of Bioinformatics; Division and Center for Synthetic & Systems Biology, BNRist, Department of Automation, Tsinghua University, Beijing, China and ⁸Department of Biological Sciences, Center for Systems Biology, the University of Texas, Richardson, TX, USA

**YW and ZZ contributed equally as first authors.*

Correspondence:

M.Q. Zhang
michael.zhang@utdallas.edu

M. Shi
shiml79@tsinghua.edu.cn

C. Yi
chengqi.yi@pku.edu.cn

J. Wang
jianweiwang@mail.tsinghua.edu.cn;
wangjianwei@ihcams.ac.cn

Received: October 4, 2022.

Accepted: May 4, 2023.

Early view: May 11, 2023.

<https://doi.org/10.3324/haematol.2022.282211>

©2023 Ferrata Storti Foundation

Published under a CC BY-NC license



Supplemental Methods

Lentivirus Production and Transduction

The mouse cDNA (*Pus10* or *Pus10^{D342A}*) was cloned into the pRRL-PPT-SF-newMCS-IRES2-EGFP vector. The *Ddb1*-shRNA sequence was cloned into SF-LV-miRE-EGFP vector. Lentivirus was produced in HEK293T cells and concentrated by ultracentrifugation at 25000 rpm for 2.5 h. For lentiviral transduction, LSK (cKit⁺ Sca1⁺ Lineage⁻) cells were sorted and cultured in 96-well plate ($\sim 1 \times 10^5$ cells per well) with 100ul SFEM medium (Stem Cell Technology, 09650) containing 20 ng/ml mSCF, 20 ng/ml mTPO and 1 % penicillin/streptomycin. Lentivirus was added to LSK cells. 72 h later, 2×10^4 GFP⁺ cells were sorted and injected into lethally irradiated recipients.

Flow Cytometric Analysis and Cell Sorting

Bone marrow cells were harvested from femurs, tibias and pelvis. Viable cells were counted by Vi-CELL XR Cell Viability Analyzer (Beckman Coulter). Bone marrow cells were applied for hematopoietic cell and lineage cell analysis. Hematopoietic cells (antibodies containing CD117, Sca1, Lineage cocktail, CD34, CD150, CD127, CD135 and CD16/32) and lineage cells (antibodies containing CD3, B220 and CD11b) were stained with fluorochrome labeled antibodies and identified by BD LSRFortessa flow cytometer. For Chimerism analysis, red cells in peripheral blood were lysed by ACK buffer (150 mM NH₄Cl, 10 mM KHCO₃, 0.1 mM Na₂EDTA, pH7.2-7.4). Lineage cells stained with fluorochrome labeled antibodies (antibodies containing CD3, B220, CD11b, CD45.1 and CD45.2) and analyzed by flow cytometer. Data were analyzed using FlowJo software. For hematopoietic stem and progenitor cells sorting, cKit⁺ cells were enriched, then stained with antibodies. LSK cells, HSPCs and HSCs were sorted by BD Influx. The antibodies were listed in Table S1.

Transplantations and peripheral blood analysis

2×10^4 GFP⁺ LSK cells (CD45.2) and 2×10^5 competitor cells (CD45.1) were injected into lethally irradiated (10 Gy) recipient mice (CD45.2). 20 or 150 HSCs (CD45.2) and 3×10^5 competitor cells (CD45.1) were injected into lethally irradiated (10 Gy) recipient mice (CD45.1/2). Peripheral blood of recipients was collected to analyze donor-derived

chimerism (myeloid, B, and T cells) every 4 weeks until the 12th or 16th week.

HSPCs in vitro cultures

50 HSPCs (CD48⁻ LSK) were sorted into 96-well plate by BD Influx and cultured in SFEM medium containing 20 ng/ml mSCF, 20 ng/ml mTPO and 1 % penicillin/streptomycin for 7 days. Then, the clones were photographed and the cell numbers of these clones were analyzed by BD LSRFortessa flow cytometer and FlowJo software.

Quantification of Ψ by liquid chromatography-tandem mass spectrometry

RNA was extracted and purified using miRNeasy Mini Kit (Qiagen). The RNA was digested into single nucleosides by Nucleoside Digestion Mix (NEB). These nucleosides were detected by a label-free quantitation method. Finally, the Ψ /U ratio was analyzed.

Real-time PCR

Total RNA was isolated using TRIzol reagent (Invitrogen) according to the manufacturer's instruction. Total RNA was reverse transcribed by PrimeScript RT reagent Kit (Takara), followed by RT-PCR using PowerUpTM SYBRTM Green mix (Applied Biosystems) with indicated primers on a QuantStudio-3 Real-time PCR System (Applied Biosystems). The primers were listed in Table S3.

Western Blot

Freshly isolated HSPCs or 32D cells were lysed in sodium dodecyl sulfate (SDS) loading buffer, sonicated for 5 cycles using Bioruptor (Diagenode) and denatured by boiling at 100°C for 5 min. Samples were resolved on 10% SDS-PAGE, and the separated proteins were transferred onto a PVDF membrane. Membranes were blocked with 5% skimmed milk in Tris-buffered saline with Tween-20 (TBST) buffer for 1 h at room temperature and then probed with primary antibodies overnight at 4 °C.

32D cells were harvested and lysed with NETN buffer (20 mM Tris-HCl, pH 8.0, 100 mM NaCl, 1 mM EDTA, 0.5% Nonidet P-40, containing protease and phosphatase inhibitors cocktail) on ice for 30 minutes followed by centrifugation at 12000 rpm for 5 min. The supernatant was mixed with 2× protein loading buffer and denatured by boiling at 100 °C for 5 min. Samples were loaded onto 10% SDS-PAGE gel, and the

separated proteins were transferred onto a PVDF membrane. Membranes were blocked with 5% skimmed milk in Tris-buffered saline with Tween-20 (TBST) buffer for 1 h at room temperature and then probed with primary antibodies overnight at 4 °C.

Affinity Purification and Mass Spectrometry

HEK293T cells stably expressing Flag-tagged PUS10 were lysed in NETN buffer on ice for 30 min followed by centrifugation at 12000 rpm for 5 min. The supernatant was transferred to a fresh microcentrifuge tube and incubated with anti-Flag beads at 4 °C for 4 hr. Beads were washed with NETN buffer 3 times and boiled in 30 µL 2 x protein loading buffer. Samples were loaded onto 10% SDS-PAGE gel and analyzed by mass spectrometry.

Co-Immunoprecipitations

Plasmids encoding SFB-tagged PUS10 or Myc-tagged DDB1, DCAF1, CUL4B were co-transfected into HEK293T cells. 24 hr later, the transfected HEK293T cells were harvested and lysed with NETN buffer on ice for 30 minutes followed by centrifugation at 12000 rpm for 5 min. The supernatant was transferred to a fresh microcentrifuge tube and incubated with 20 µL S-protein beads at 4 °C for 2 hr. Beads were washed with NETN buffer 3 times, mixed with 2x protein loading buffer and denatured by boiling. Samples were loaded onto 10% SDS-PAGE gel, and the separated proteins were transferred onto a PVDF membrane. Membranes were blocked and then probed with anti-Flag, anti-Myc antibodies.

Ubiquitination assay

Plasmids encoding SFB-tagged PUS10, Myc-tagged DDB1, DCAF1, CUL4B and HA-tagged Ub-WT, Ub-K48R were co-transfected into HEK293T cells. 24 hr later, the transfected HEK293T cells were harvested and lysed with 100 µL denaturing TS buffer (50 mM Tris-HCl, pH 7.5, 1% SDS, 5 mM N-ethylmaleimide). The lysates were boiled at 100 °C for 10 min and sonicated for 5 cycles using Bioruptor (Diagenode). The lysates were diluted with 900 µL TNN buffer (0.5% Nonidet P-40, 50 mM Tris-HCl, pH 7.5, 250 mM NaCl, 5 mM N-ethylmaleimide) followed by centrifugation at 12000 rpm for 10 min. The supernatant was transferred to a fresh microcentrifuge tube and incubated with 20 µL S-protein beads at 4 °C for 2 hr. Beads were washed with NETN

buffer 3 times, mixed with 2× protein loading buffer and denatured by boiling. Samples were loaded onto 10% SDS-PAGE gel, and the separated proteins were transferred onto a PVDF membrane. Membranes were blocked and then probed with anti-HA, anti-Flag, anti-Myc antibodies.

Blood Cell Counts

Peripheral blood was collected from mice and analyzed using an Auto Hematology Analyzer BC-5000 (MINDRAY).

Statistical analysis

Data are shown as mean ± SD. Student's t test (Two-tailed unpaired) was used for comparisons between the groups using GraphPad Prism 6.0 software.

Supporting Tables

Table S1 Key resources table

| REAGENT or RESOURCE | SOURCE | IDENTIFIER |
|----------------------------|---------------------------|-------------------|
| Antibodies | | |
| Ter-119-Biotin | BioLegend | TER-119 |
| Gr-1-Biotin | BioLegend | RB6-8C5 |
| CD11b-Biotin | BioLegend | M1/70 |
| CD11b-PerCP-Cy5.5 | BioLegend | M1/70 |
| CD3e-Biotin | BioLegend | 145-2C11 |
| CD3e-APC | BioLegend | 145-2C11 |
| CD4-Biotin | BioLegend | GK1.5 |
| CD8a-Biotin | BioLegend | 53-6.7 |
| B220-Biotin | BioLegend | RA3-6B2 |
| B220-V500 | BioLegend | RA3-6B2 |
| B220-Pacific Blue | BioLegend | RA3-6B2 |
| Sca-1-PE-Cy7 | BD Biosciences | D7 |
| CD117-APC | BD Biosciences | 2B8 |
| CD150-PE | BioLegend | TC15-12F12.2 |
| CD48-FITC | BioLegend | HM48-1 |
| CD48-PerCP-Cy5.5 | BioLegend | HM48-1 |
| CD34-AlexaFlour700 | eBioscience | RAM34 |
| CD34-FITC | eBioscience | RAM34 |
| CD135-CF594 | BD Biosciences | A2F10.1 |
| CD135-PE | BD Biosciences | A2F10.1 |
| CD16/32-FITC | BD Biosciences | 2.4G2 |
| CD127-BV421 | BD Biosciences | A7R34 |
| CD45.1-FITC | BD Biosciences | A20 |
| CD45.1-PE | BD Biosciences | A20 |
| CD45.1-AlexaFluor700 | BD Biosciences | A20 |
| CD45.2-FITC | BD Biosciences | 104 |
| CD45.2-PE | BD Biosciences | 104 |
| CD45.2- PerCP-Cy5.5 | BD Biosciences | 104 |
| Streptavidin-APC-Cy7 | BioLegend | |
| PUS10 | Abcam | ab185078 |
| Myc | Biodragon | B1002 |
| Flag | Cell Signaling Technology | 2368S |
| HA | Cell Signaling Technology | 3724S |
| CUL4B | Abclonal | A12696 |
| DDB1 | Abcam | Ab109027 |
| H3 | Cell Signaling Technology | 4499 |
| H4 | Cell Signaling Technology | 13919 |
| GAPDH | Biodragon | B1034 |

| | | |
|--|---------------------------|-------------|
| Actin | Cell Signaling Technology | 4970 |
| Rabbit anti-mouse IgG (HRP conjugate) | Cell Signaling Technology | 58802 |
| Mouse anti-rabbit IgG (HRP conjugate) | Cell Signaling Technology | 93702 |
| Chemicals, Peptides, and Recombinant Proteins | | |
| SCF | Peprotech | #250-03 |
| TPO | Peprotech | #315-14 |
| DMSO | Sigma-Aldrich | D2650 |
| Fetal Bovine Serum | GEMINI | 900-108 |
| DMEM | Gibco | C11995500BT |
| StemSpan serum-free medium | Stem Cell Technologies | 09650 |
| DAPI | Sigma-Aldrich | D8417 |
| Penicillin-streptomycin | Gibco | 15140122 |
| D-Hanks | Solarbio | H1045 |
| Hepes | Solarbio | H1095 |
| PBS | Solarbio | P1022 |
| TRIZOL | Invitrogen | 15596018 |
| Critical Commercial Assays | | |
| PrimeScript RT Reagent Kit | Takara | RR047A |
| PowerUp SYBR Green mix | Applied Biosystems | A25780 |
| miRNeasy Mini Kit | Qiagen | 217004 |
| RNeasy MinElute Cleanup Kit | Qiagen | 74204 |
| RNase-Free DNase Set | Sangon Biotech | B618253 |
| Deposited Data | | |
| Small RNA DM-Ψ-seq data | | |
| Experimental Models: Cell Lines | | |
| HEK293T | ATCC | |
| Experimental Models: Organisms/Strains | | |
| Mouse: <i>Pus10</i> ^{-/-} mice | Mo Li Laboratory | N/A |
| Mouse: C57BL/6 (CD45.2) | Jackson Laboratory | N/A |
| Mouse: C57BL/6-SJL (CD45.1) | Jackson Laboratory | N/A |
| Oligonucleotides | | |
| Primers for mouse genotyping and qRT-PCR, see Table S3 | This paper | N/A |
| Recombinant DNA | | |
| pRRL-PPT-SF-newMCS-IRES2-EGFP (Vector) | This paper | N/A |
| pRRL- <i>mPus10</i> | This paper | N/A |
| SF-LV-miRE-EGFP (Vector) | This paper | N/A |
| miRE- <i>Ddb1</i> -shRNA1 | This paper | N/A |
| miRE- <i>Ddb1</i> -shRNA2 | This paper | N/A |

| | | |
|--------------------------------|-------------------------------|-----|
| SFB- <i>hPus10</i> | This paper | N/A |
| HA-Ub-WT | Yuancai Liu Lab | N/A |
| HA-Ub-K48R | Yuancai Liu Lab | N/A |
| <i>Myc-hDdb1</i> | Yeguang Chen Lab | N/A |
| <i>Myc-hDcaf1</i> | This paper | N/A |
| <i>Myc-hCul4b</i> | Qiang Ding Lab | N/A |
| Software and Algorithms | | |
| FlowJo Software | Becton, Dickinson and Company | N/A |
| GraphPad Prism 6 | GraphPad Software | N/A |
| Adobe Illustrator CS6 | Adobe | N/A |
| Adobe Photoshop CS5 | Adobe | N/A |

Table S2 The sequence of *Pus10*-gRNA and *Ddb1*-shRNA

| Gene | Sequence | Application |
|-----------------------|---------------------------|----------------------------------|
| <i>Pus10</i> -gRNA A1 | TAGGTGCTTGTTCCTCAGTCAG | <i>Pus10</i> ^{-/-} mice |
| <i>Pus10</i> -gRNA A2 | AAACCTGACTGAGGAGAACAAGCA | <i>Pus10</i> ^{-/-} mice |
| <i>Pus10</i> -gRNA B1 | TAGGGCACAGCTGTTGTTTCAGTTC | <i>Pus10</i> ^{-/-} mice |
| <i>Pus10</i> -gRNA B2 | AAACGAACTGAACAACAGCTGTGC | <i>Pus10</i> ^{-/-} mice |
| <i>Ddb1</i> -shRNA1 | TAGCATGAGAACTCTTGTCTGG | Knockdown DDB1 |
| <i>Ddb1</i> -shRNA2 | TAGGTCTCTAGTGAAGTGGTTT | Knockdown DDB1 |

Table S3 Primers for genotyping and RT-PCR

| Gene | Forward | Reverse | Application |
|--------------|-----------------------------|-----------------------------|-------------|
| <i>Pus10</i> | CAGCACGTAGCTGT AGAATACTG | GTTTGTAAGGTGCG GGAAGA | Genotyping |
| <i>Pus10</i> | TATTACGAAGGTGT GCCAAAAGG | GGACTACATCATTTC TTCCCAGG | RT-PCR |
| <i>Actin</i> | GTGACGTTGACATC CGTAAAGA | GCCGGACTCATCGT ACTCC | RT-qPCR |

Supplemental Figure Legends

Supplemental figure 1. Aging-activated PUS10 impairs the reconstitution capacity of HSPCs independently on its enzymatic activity.

(A) Representative western blot shows the efficient overexpression of PUS10 in lineage⁻ cells with lentivirus carrying cDNA of *Pus10*. (B) This histogram depicts the protein level of PUS10 in lineage⁻ cells with lentivirus carrying cDNA of *Pus10* from quantitative western blot data (n = 5). (C) The gating strategies for the frequency of indicated donor-derived GFP⁺ cells. (D) The gating strategies for quantifying lineage distribution of the test donor-derived GFP⁺ cells (B, T, myeloid cells).

Supplemental figure 2. No difference of pseudouridine modification profile between young and aged HSPCs.

Schematic of identified pseudouridine sites are marked in individual tRNA. Pseudouridine sites (red arrows) and levels of individual tRNA are identified in young and aged HSPCs. The x axis represents nucleotide position. The y axis represents pseudouridine levels.

Supplemental figure 3. Aging-declined CRL4^{DCAF1}-mediated ubiquitination degradation signaling leads to the increase of PUS10.

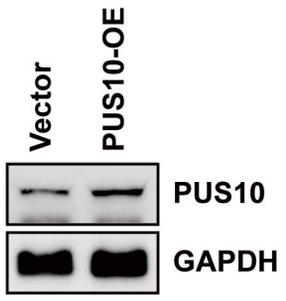
The expression of *Pus10* between young and old HSCs in the GSE27686, GSE39553, GSE4332 and GSE6503 datasets.

Supplemental figure 4. Young *Pus10*^{-/-} mice exhibit no influence on hematopoietic homeostasis and HSC function.

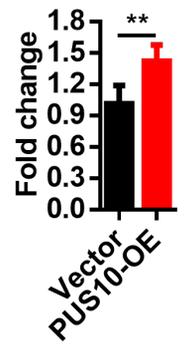
(A) The gating strategies for the frequency of B, T, myeloid cells in PB and BM of WT and *Pus10*^{-/-} mice. (B) The gating strategies for quantifying the progenitors and HSCs in WT and *Pus10*^{-/-} mice. (C) The gating strategies for the frequency of indicated donor-derived CD45.2⁺ cells. (D) The gating strategies for quantifying lineage distribution of the test donor-derived CD45.2⁺ cells (B, T, myeloid cells).

Supplemental figure 1

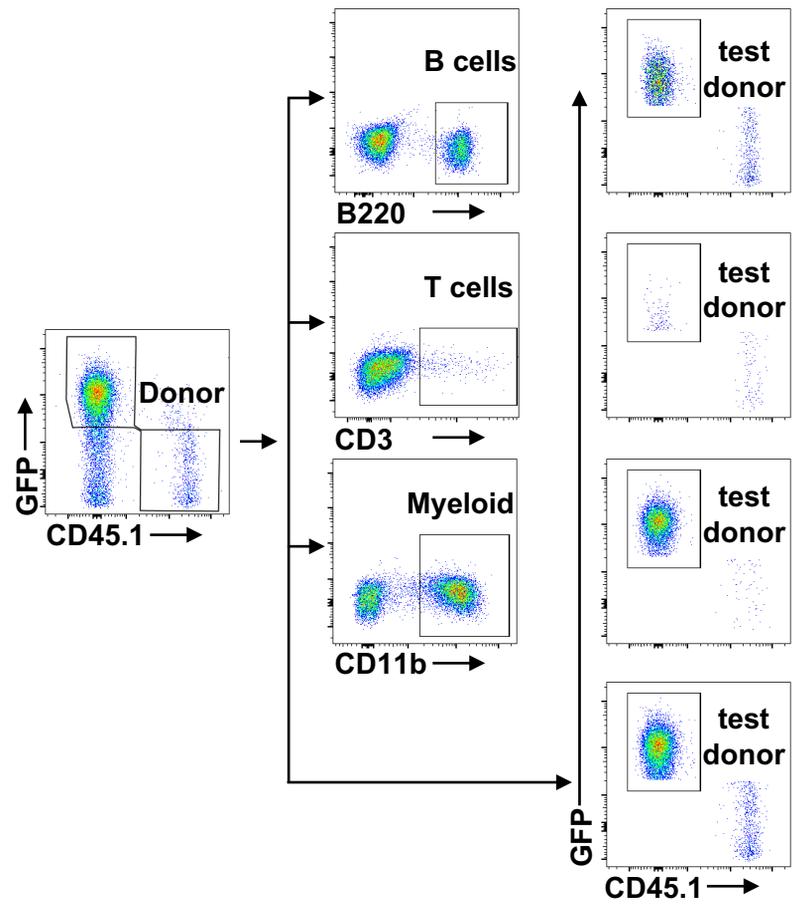
A



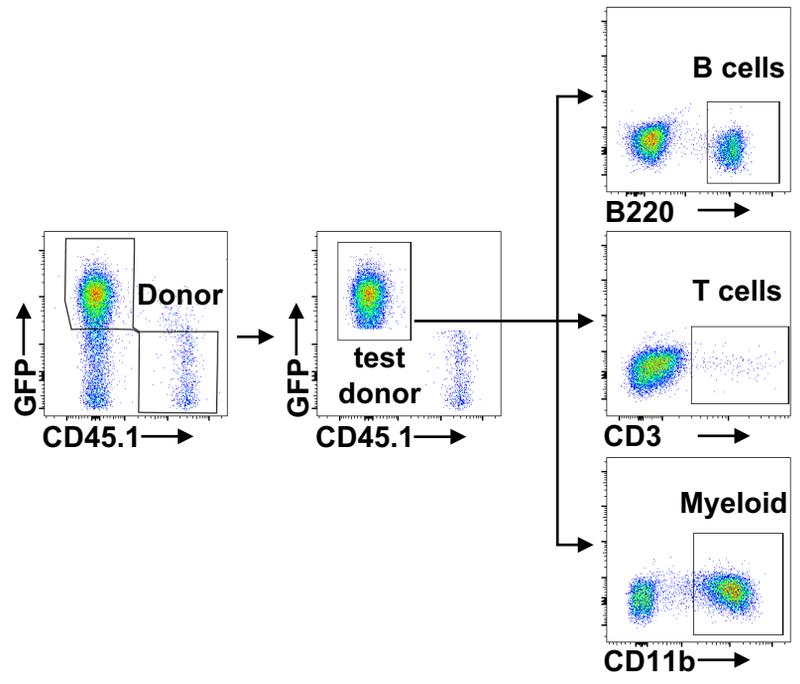
B



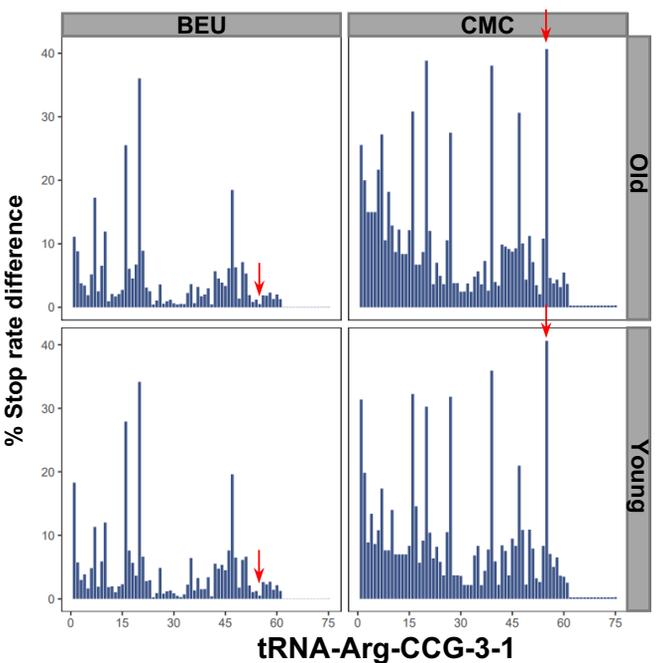
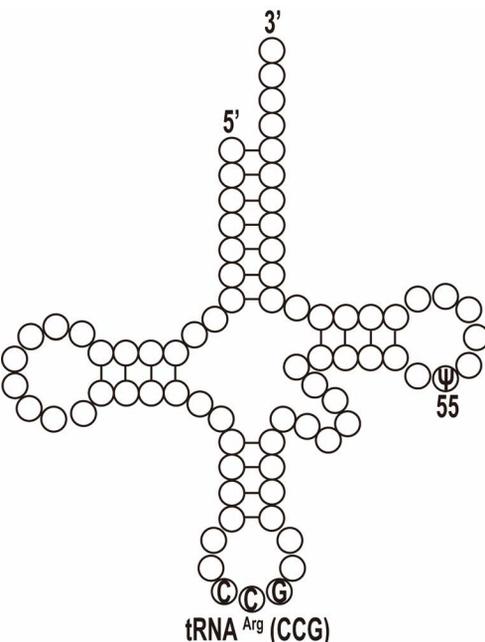
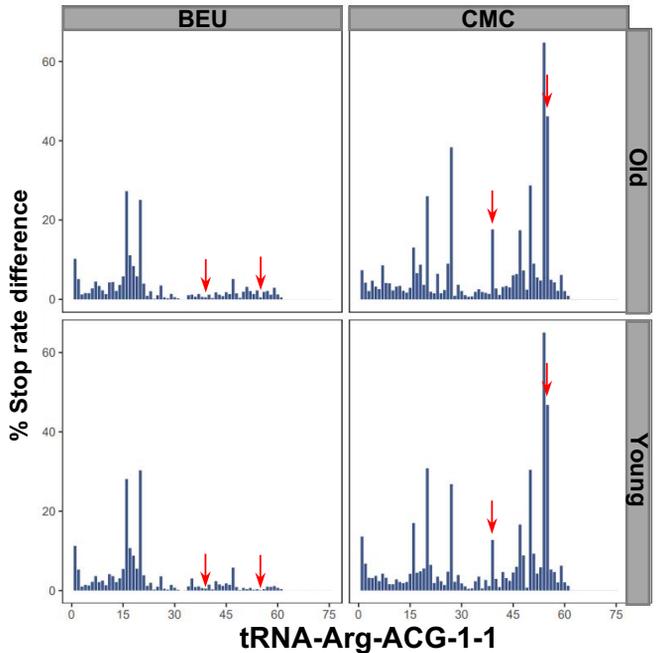
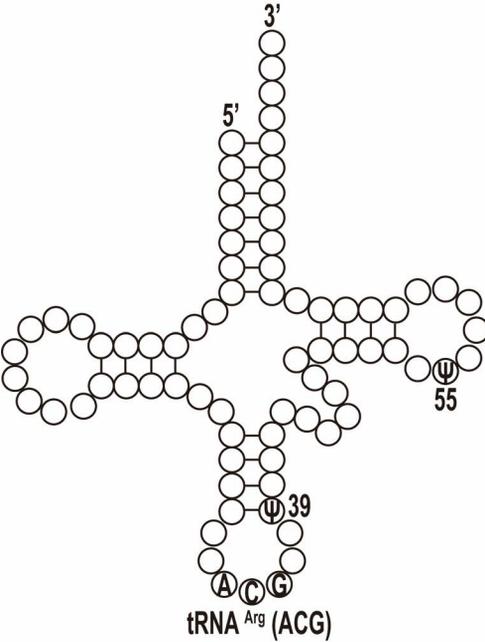
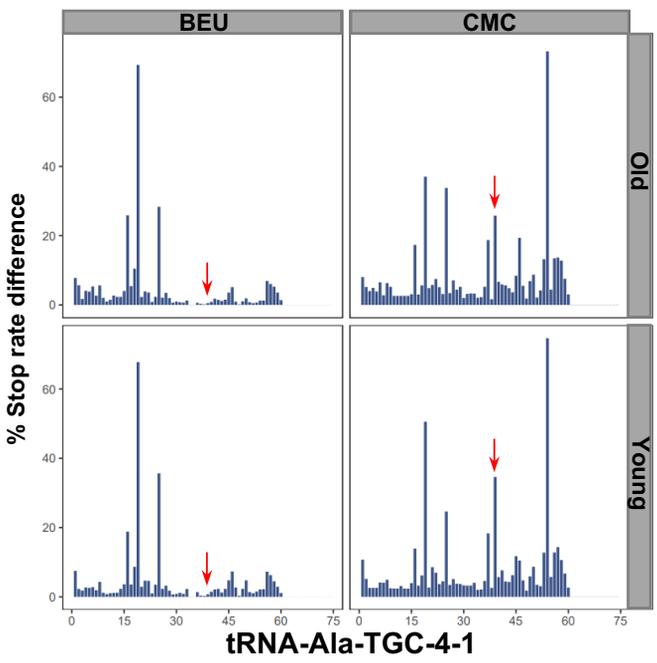
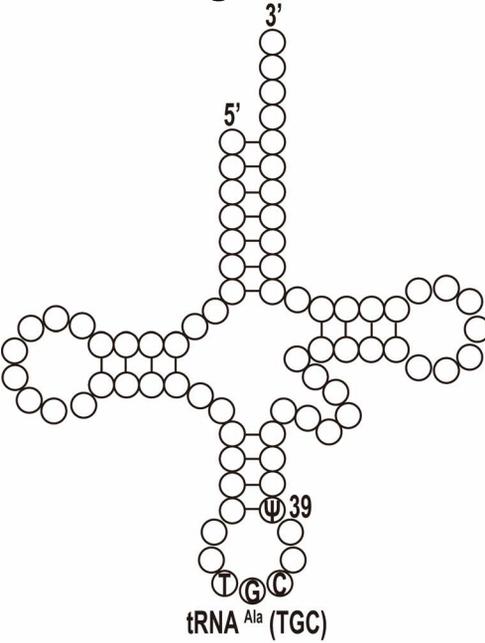
C

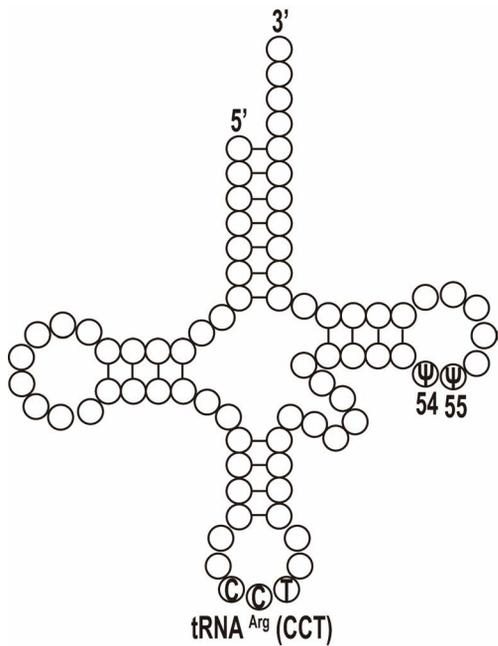


D

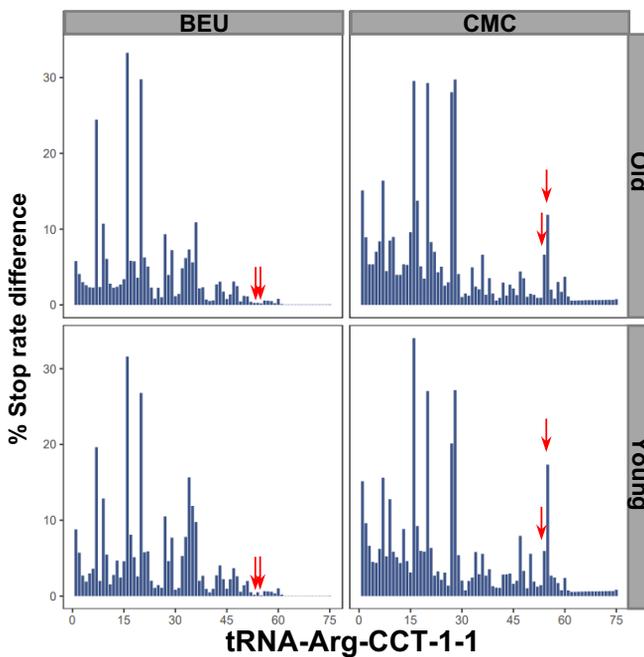


Supplemental figure 2

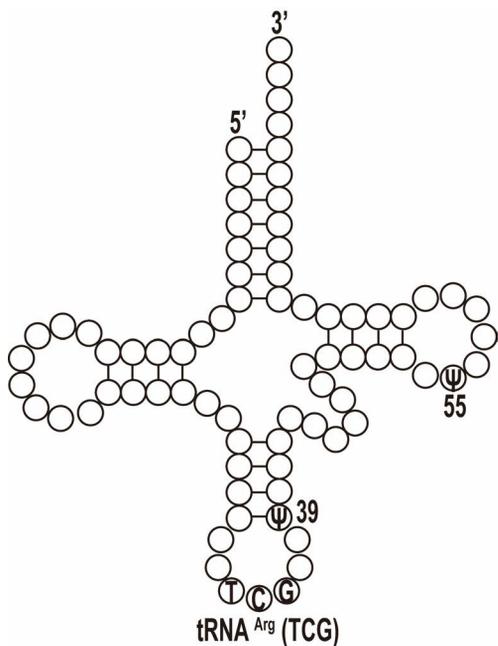




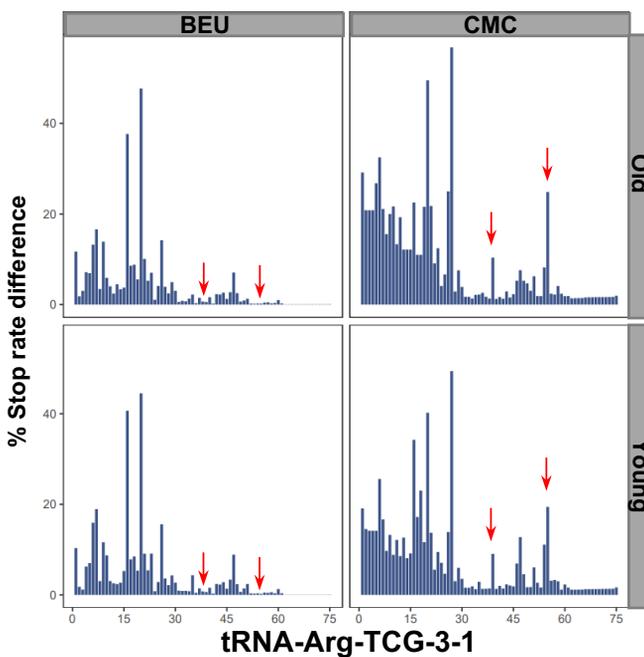
tRNA^{Arg} (CCT)



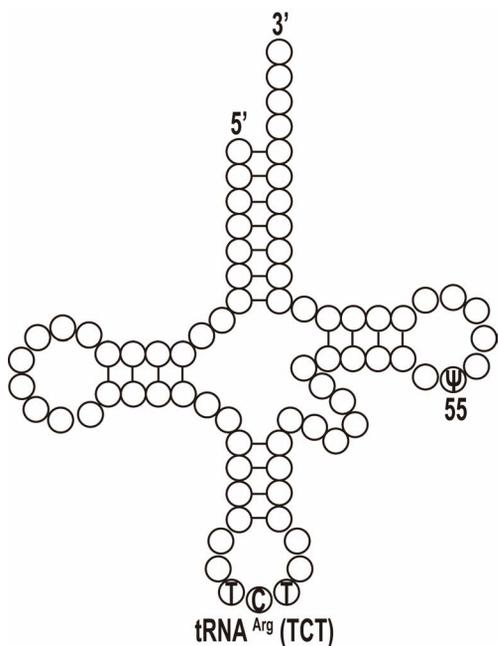
tRNA-Arg-CCT-1-1



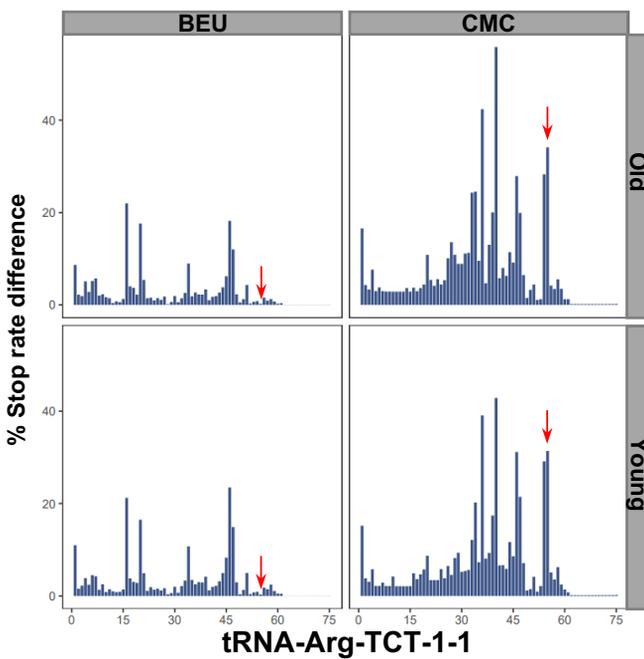
tRNA^{Arg} (TCG)



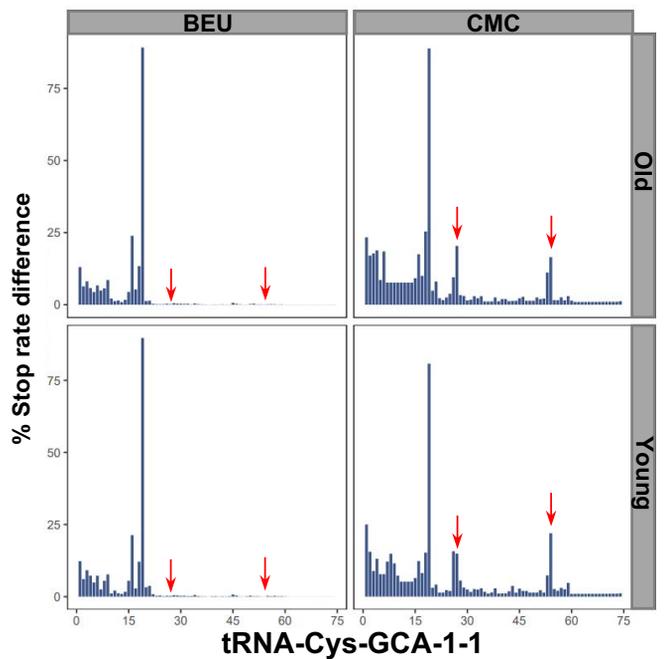
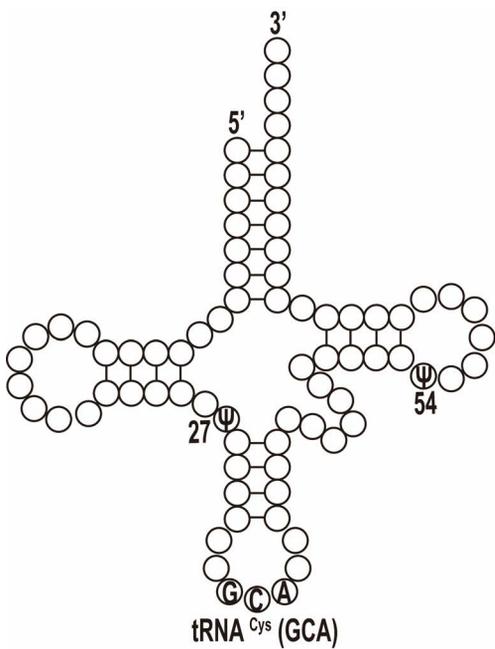
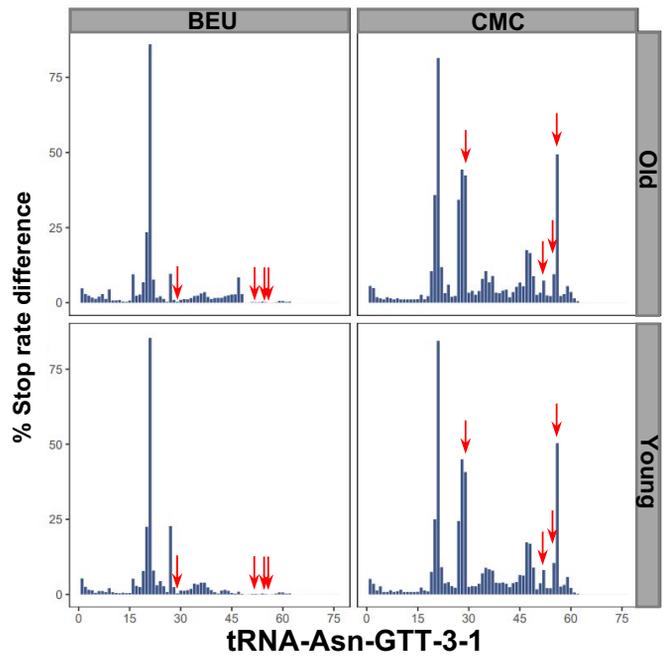
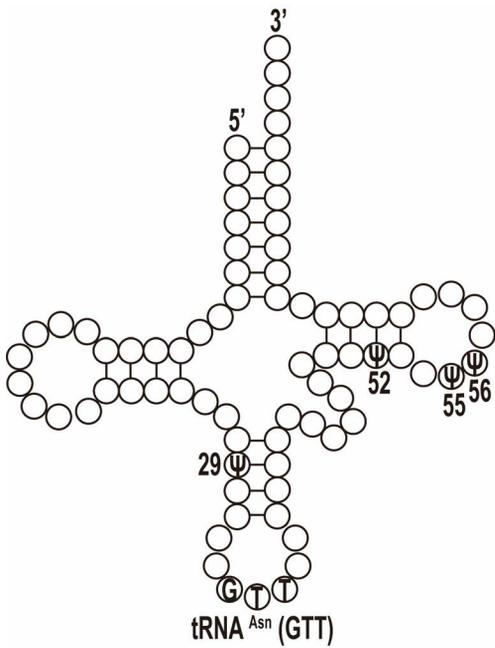
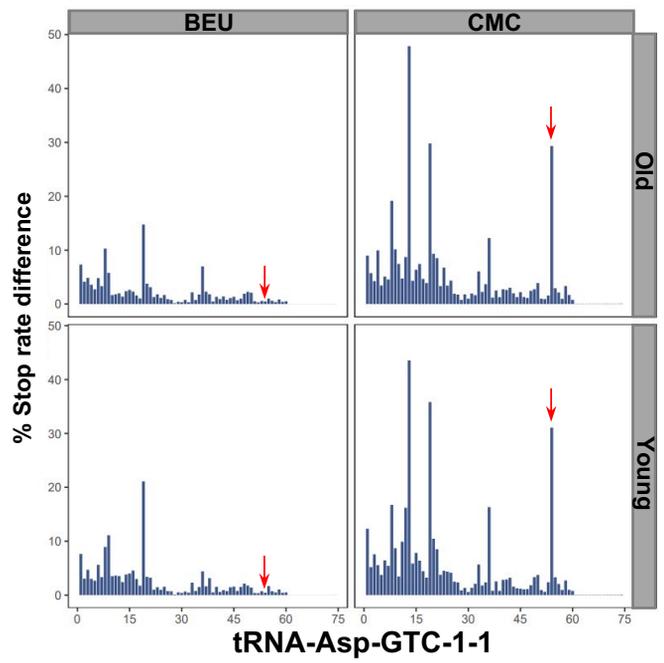
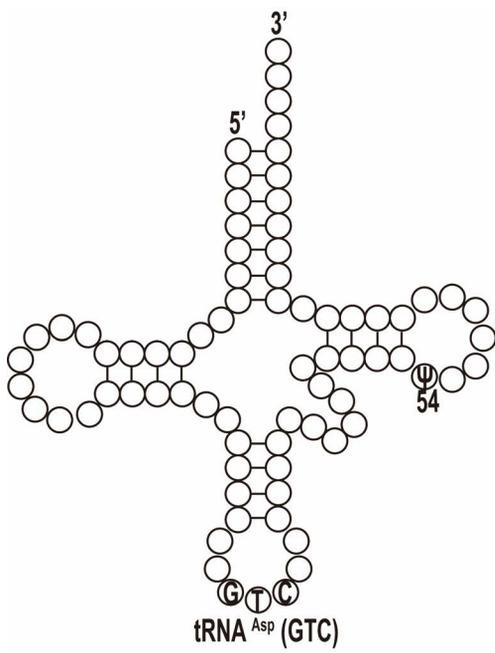
tRNA-Arg-TCG-3-1

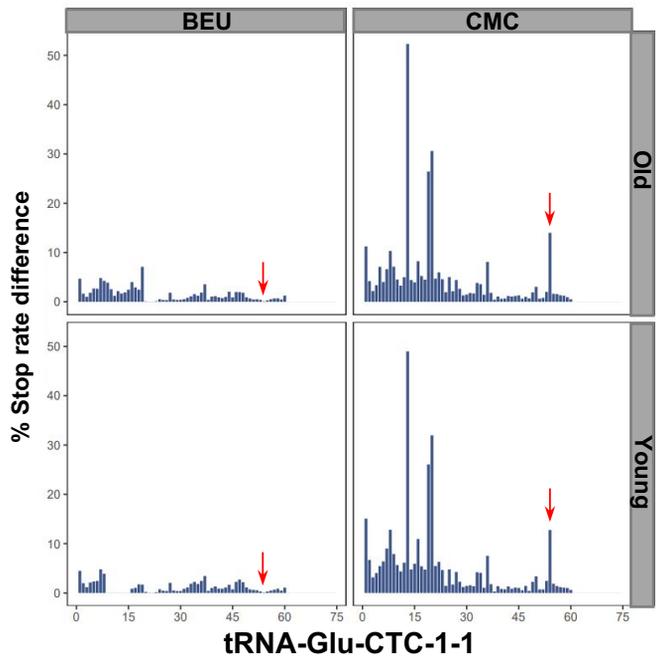
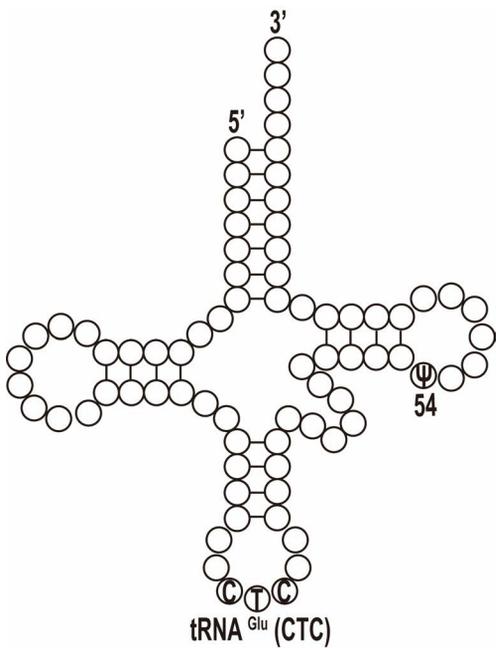
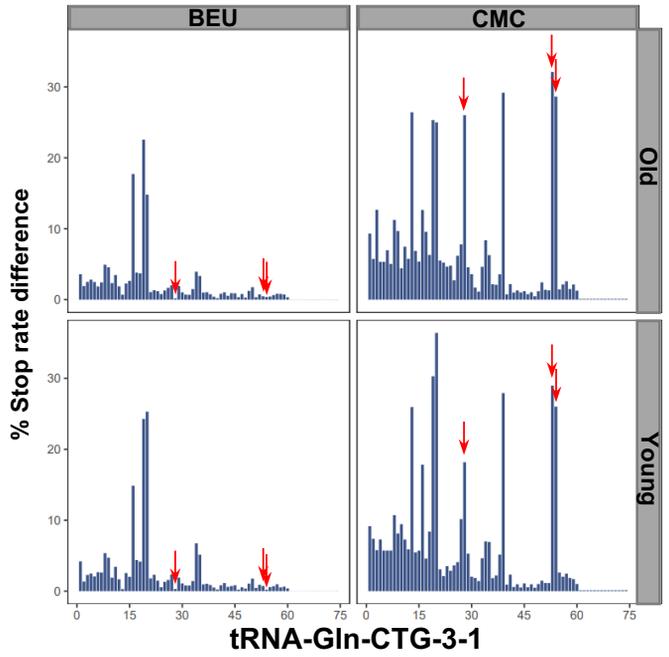
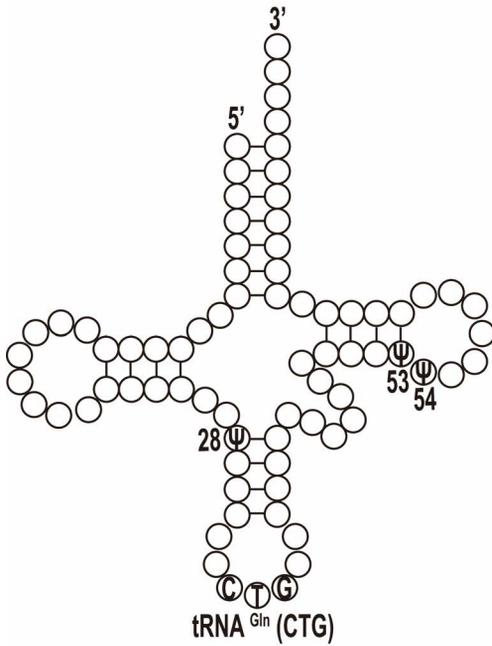
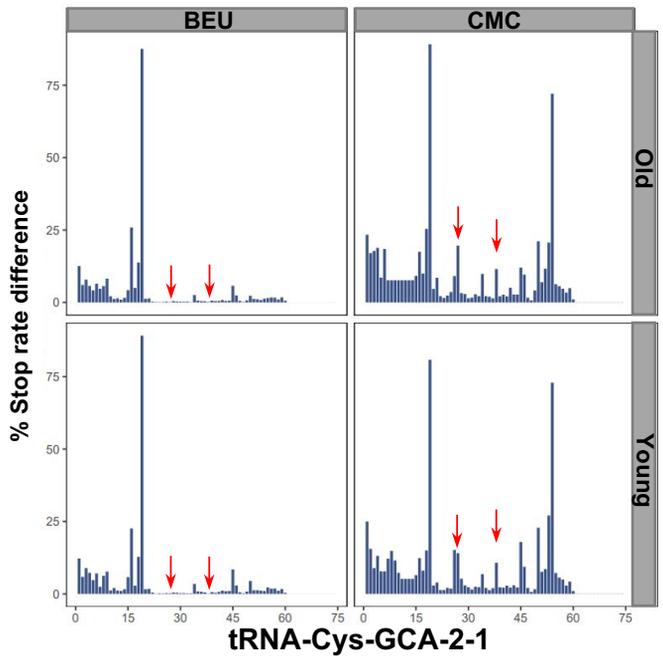
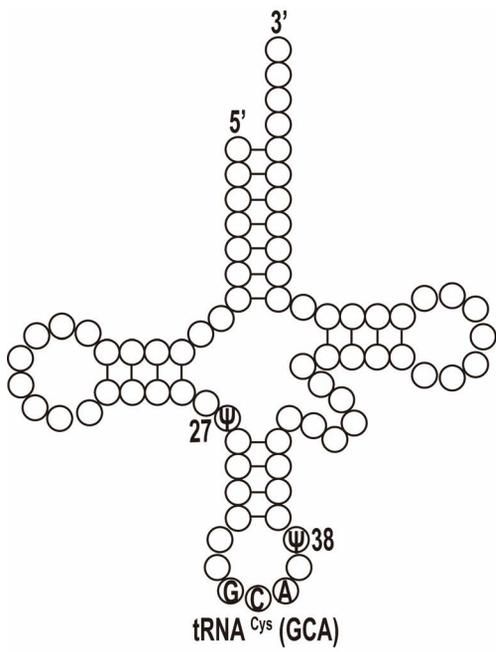


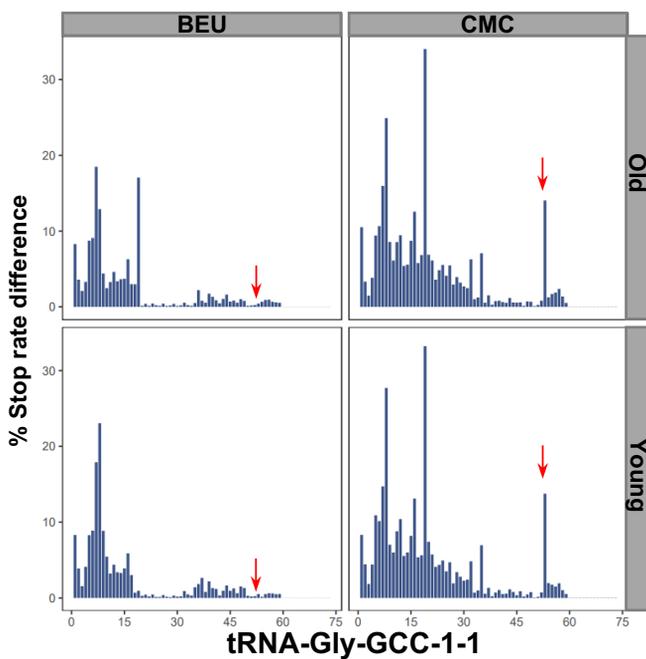
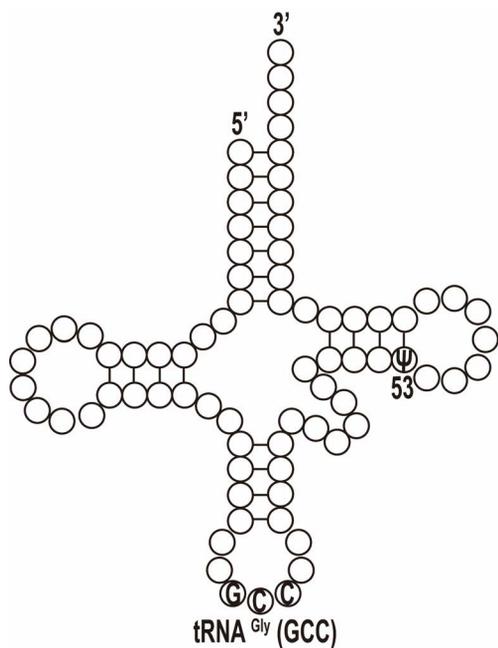
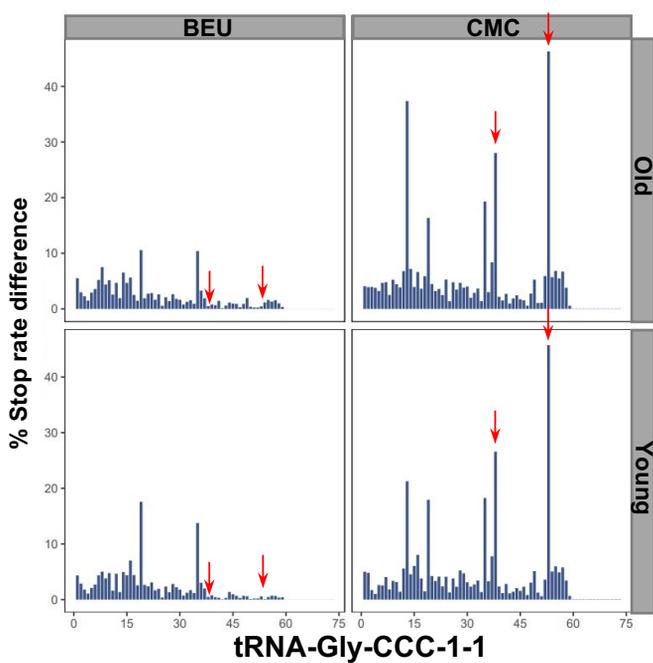
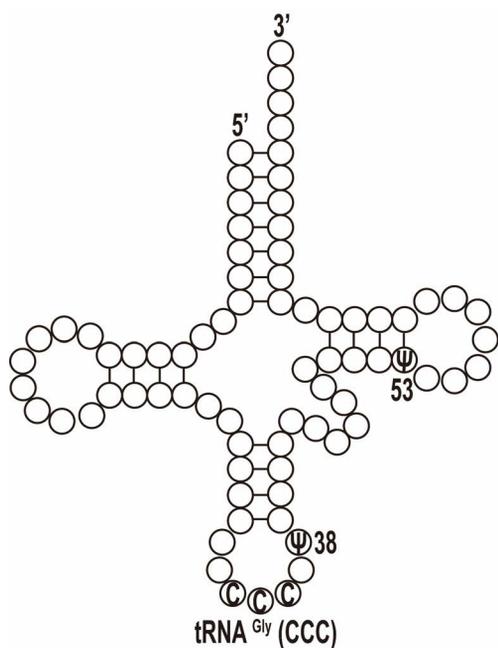
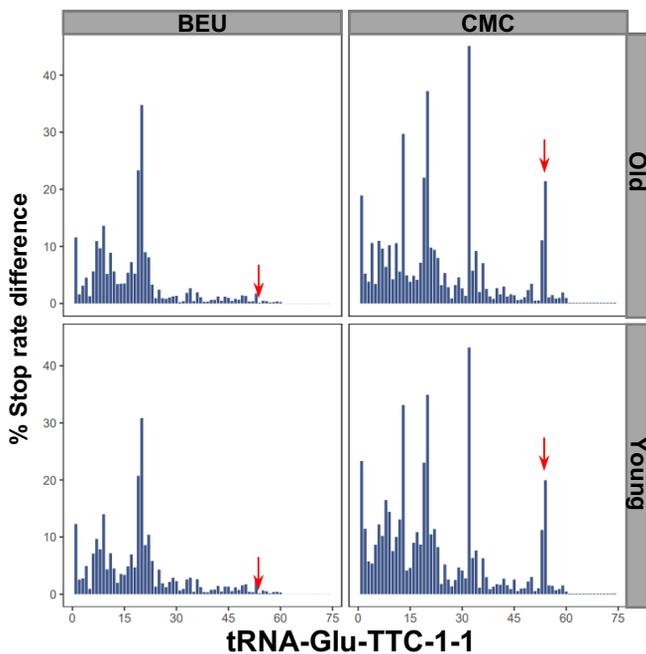
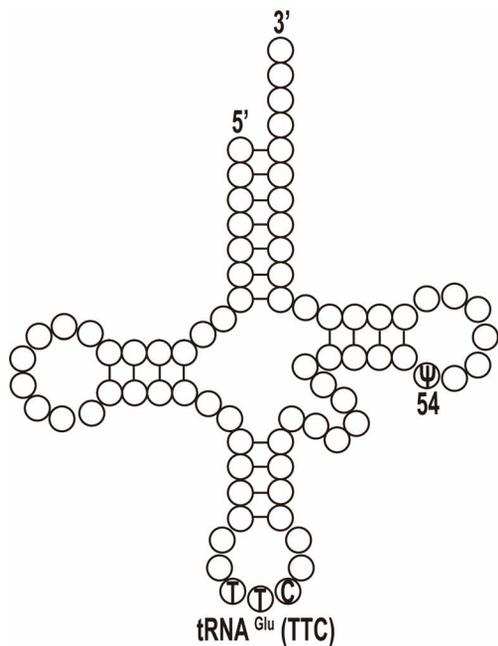
tRNA^{Arg} (TCT)

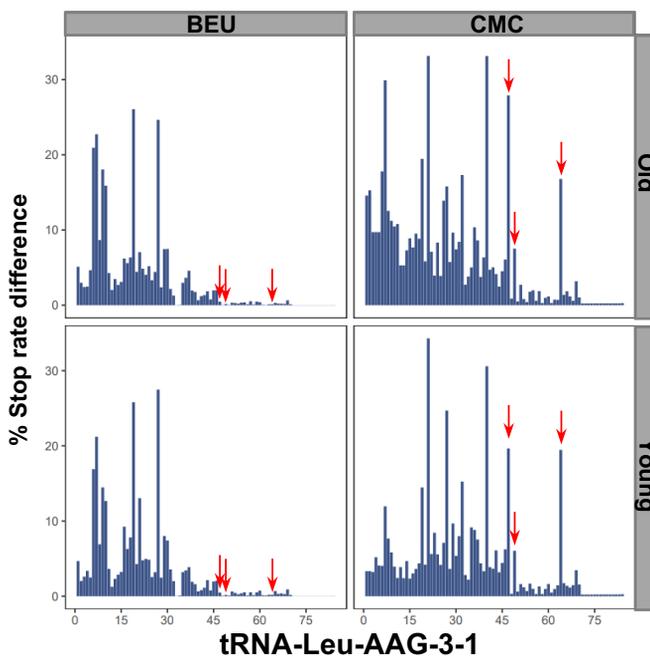
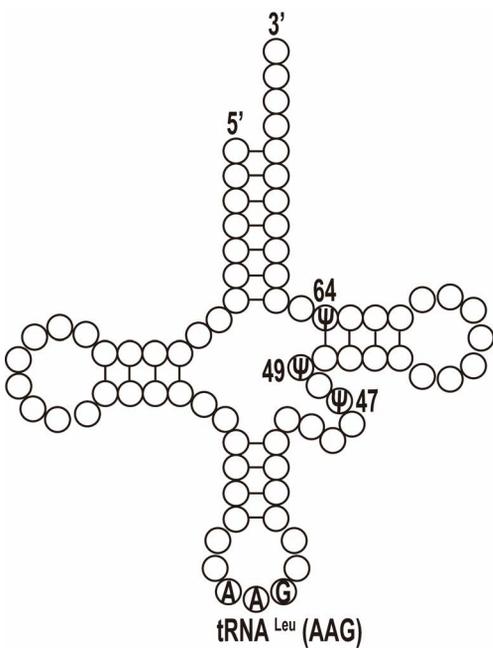
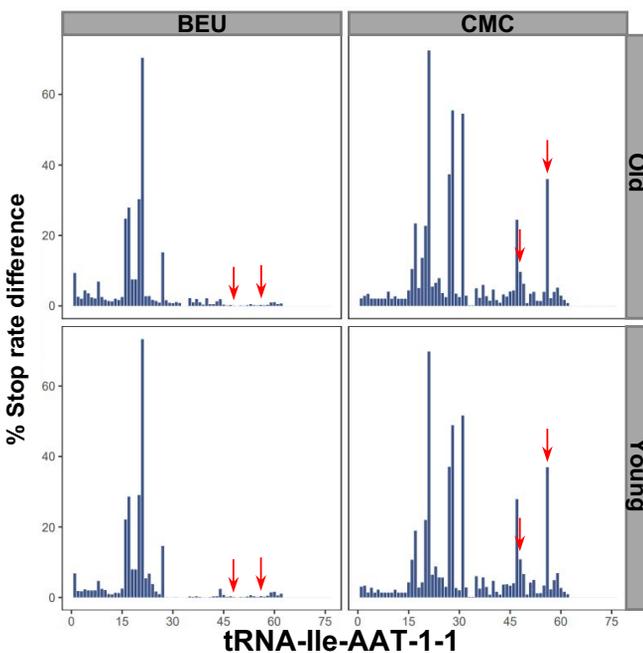
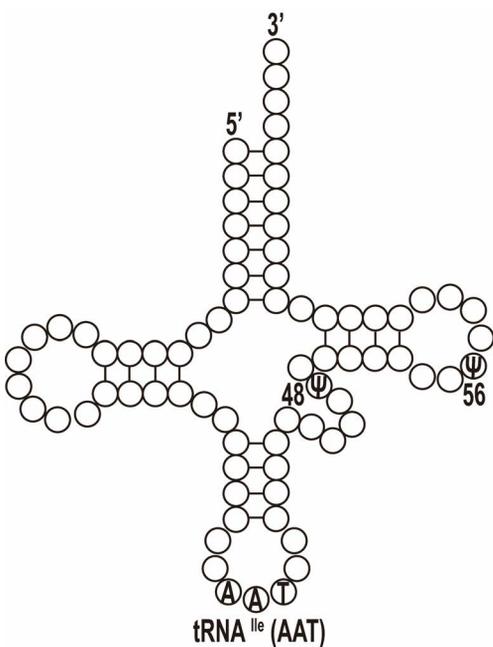
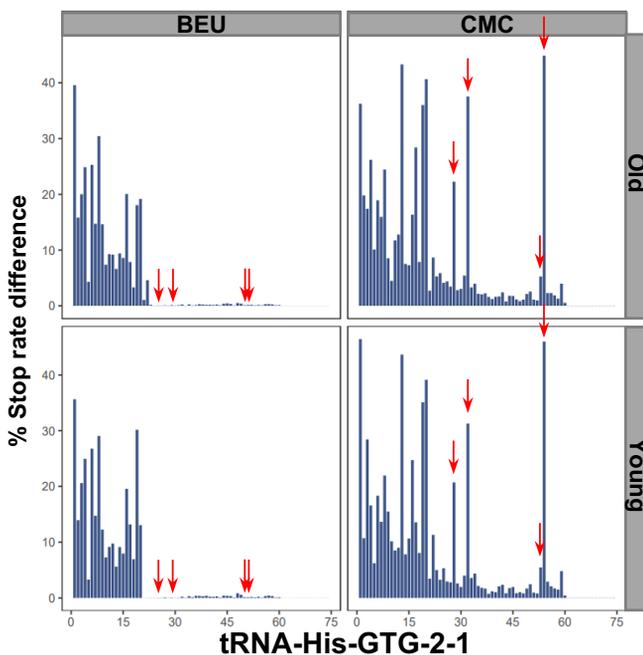
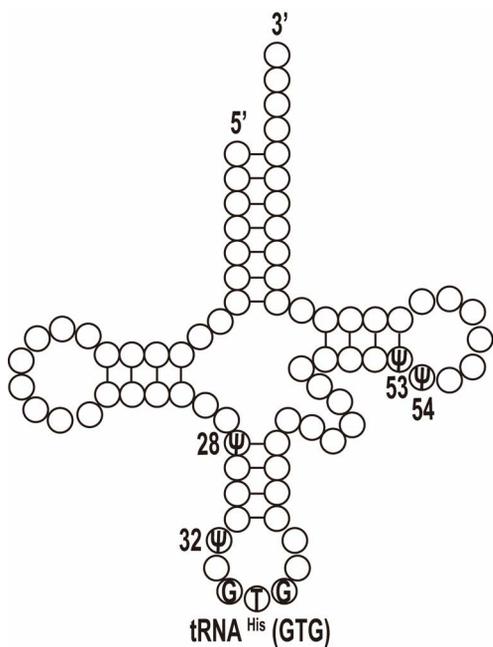


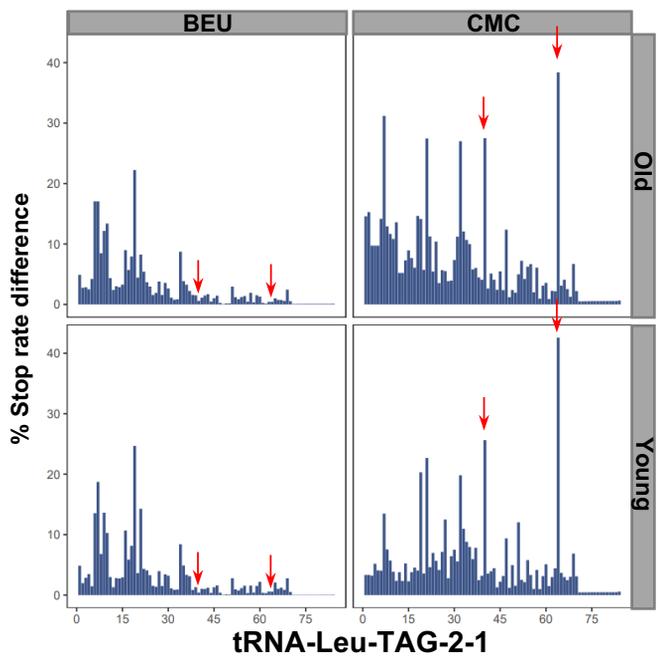
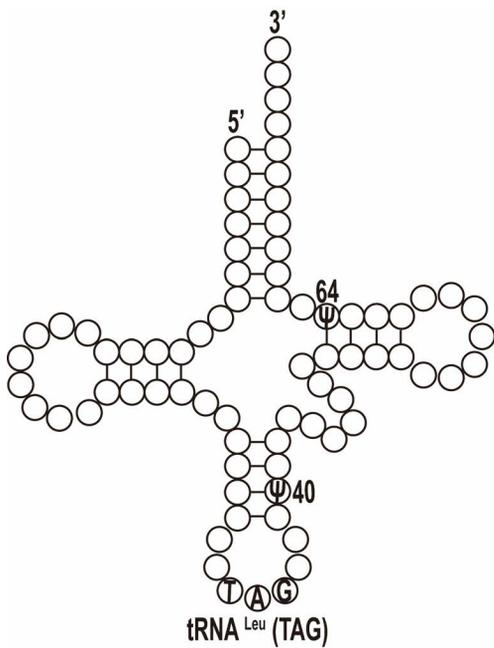
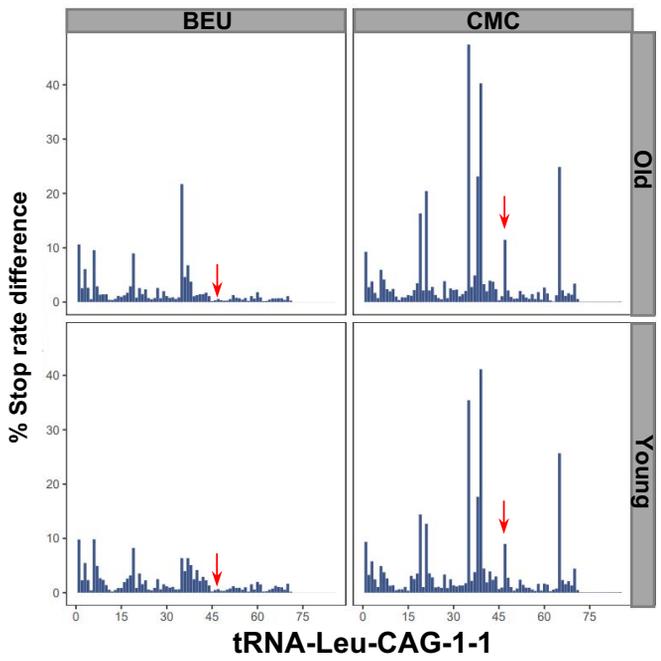
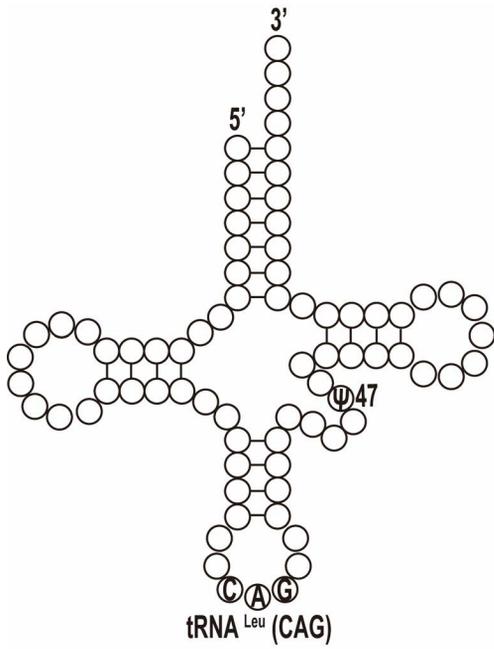
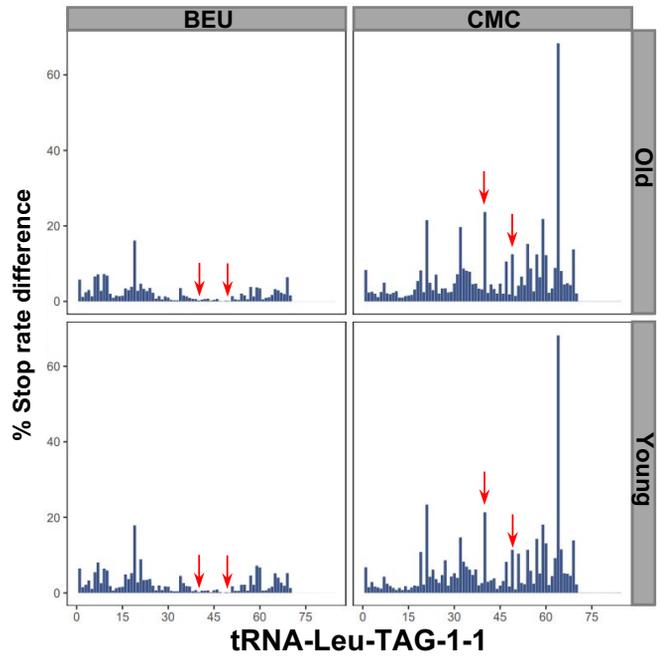
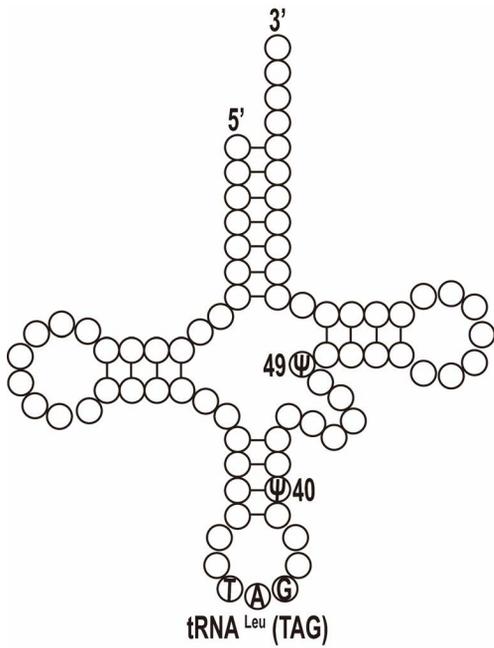
tRNA-Arg-TCT-1-1

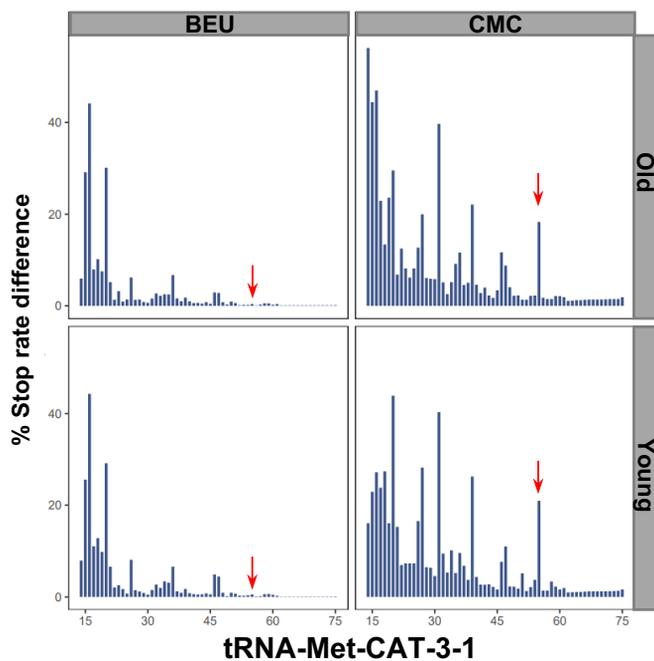
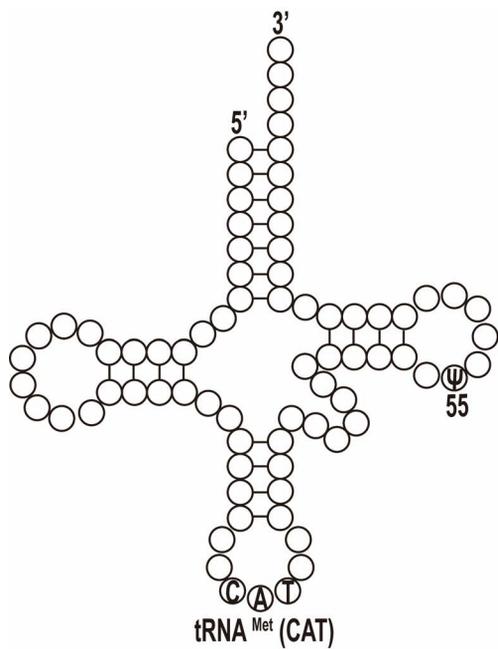
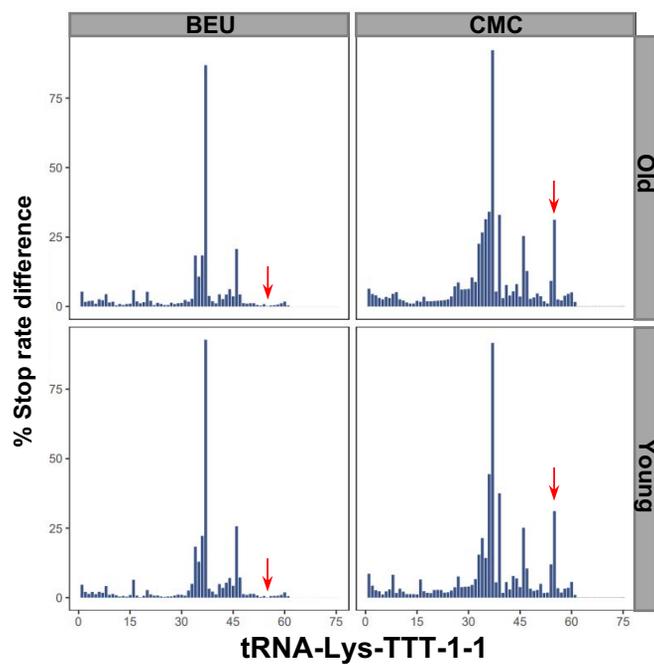
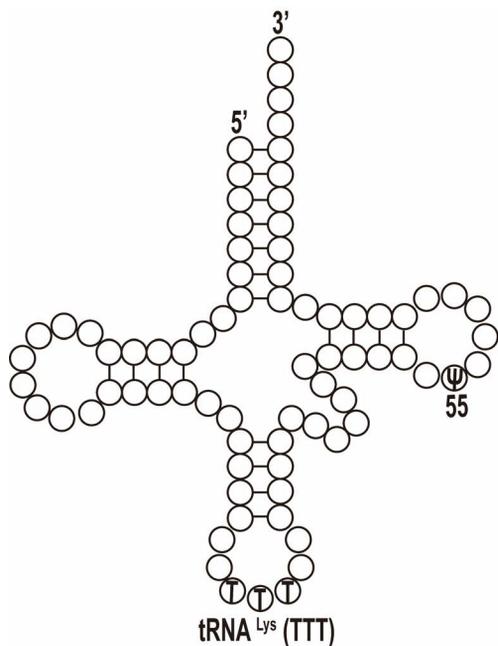
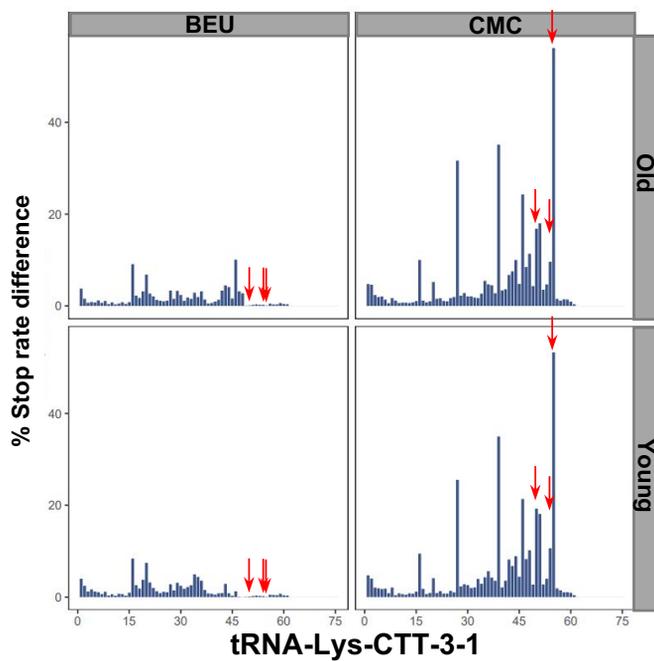
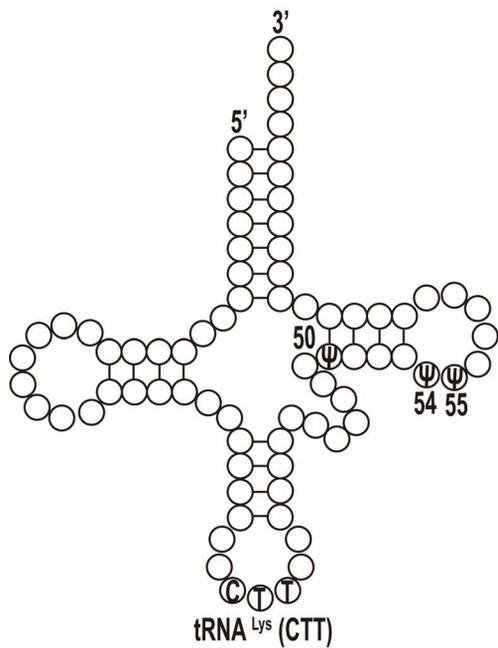


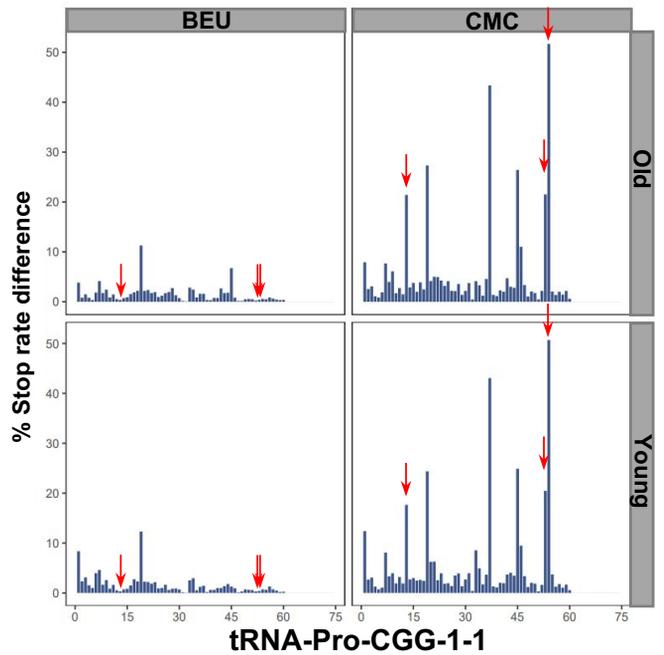
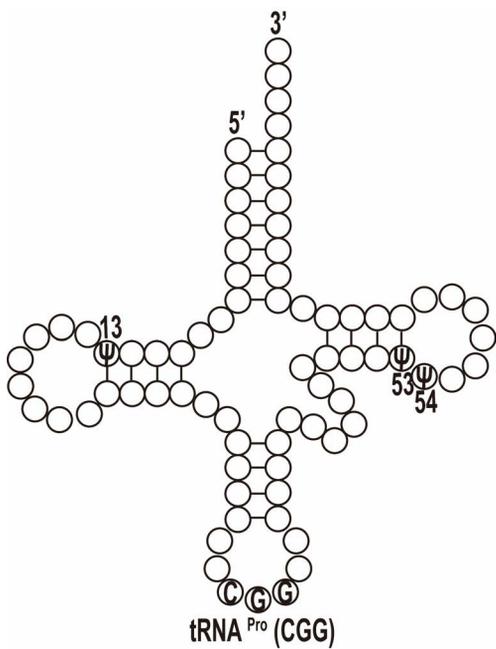
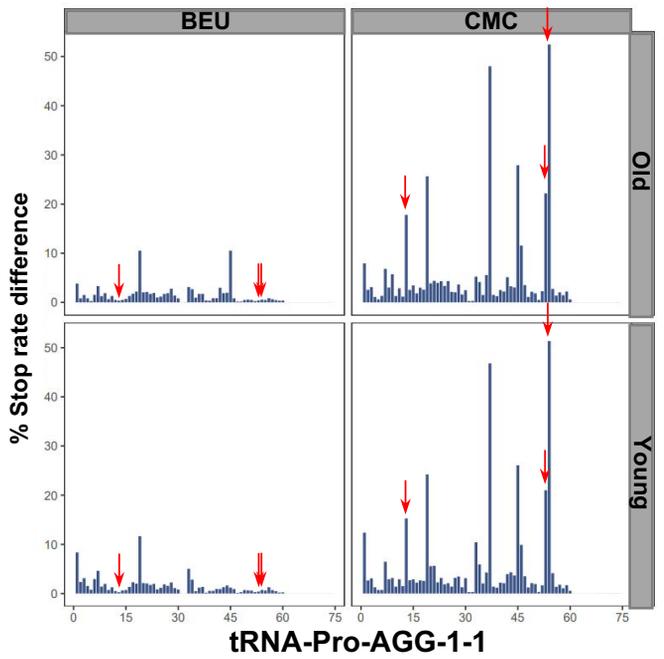
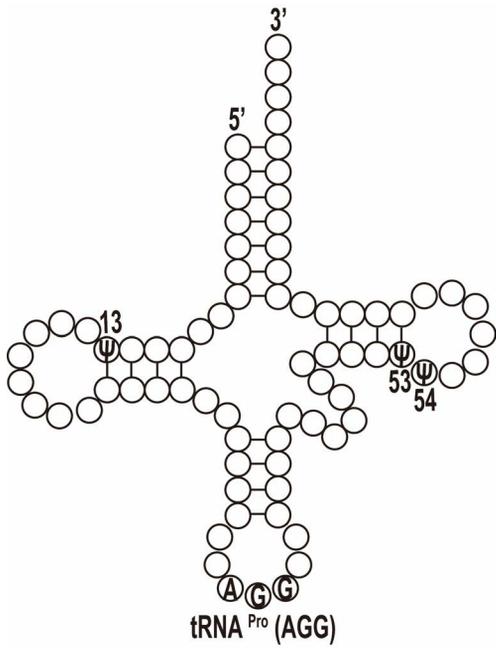
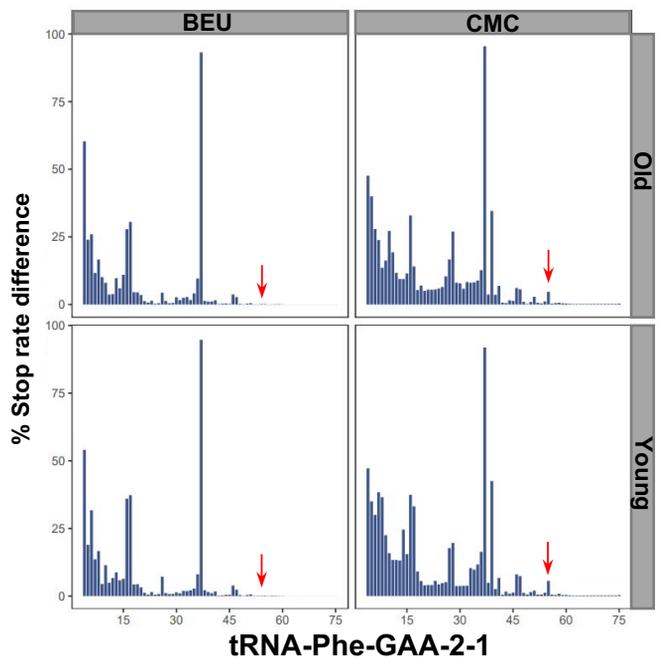
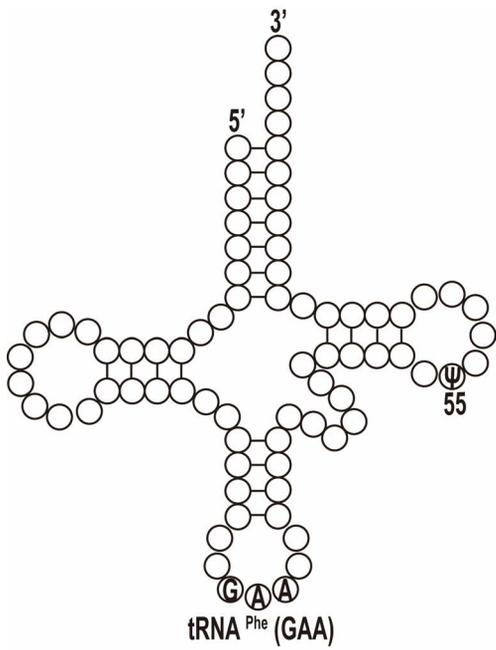


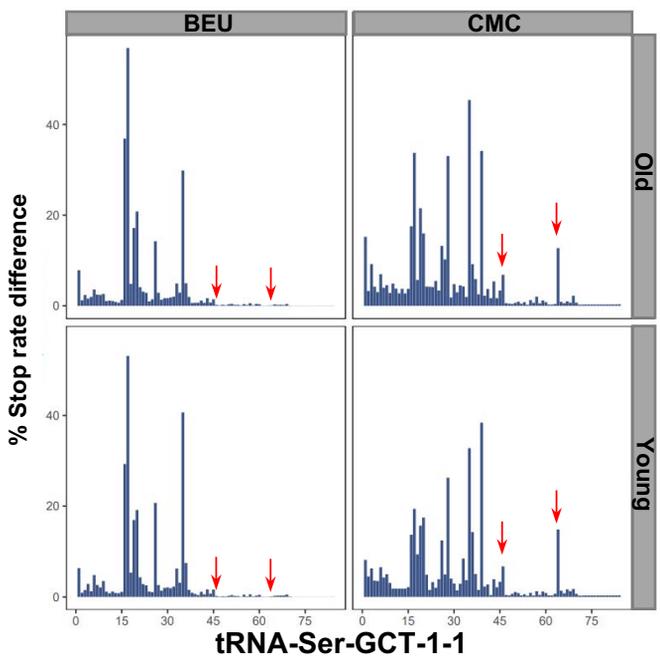
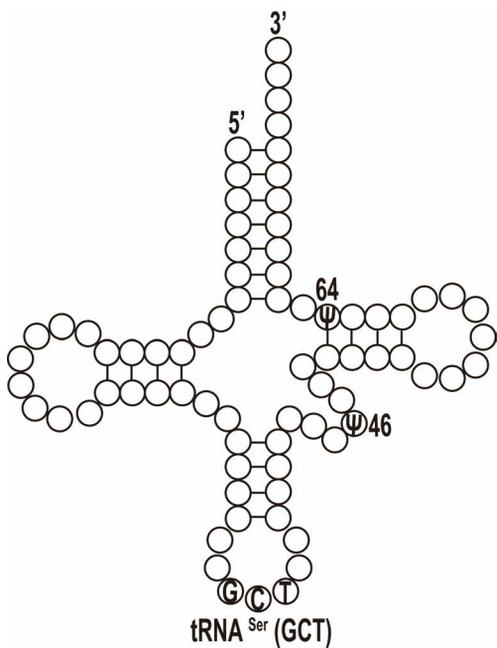
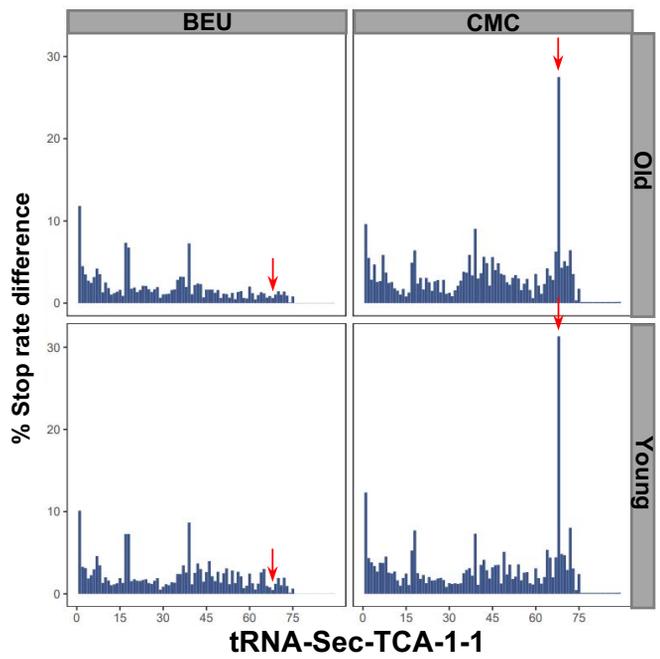
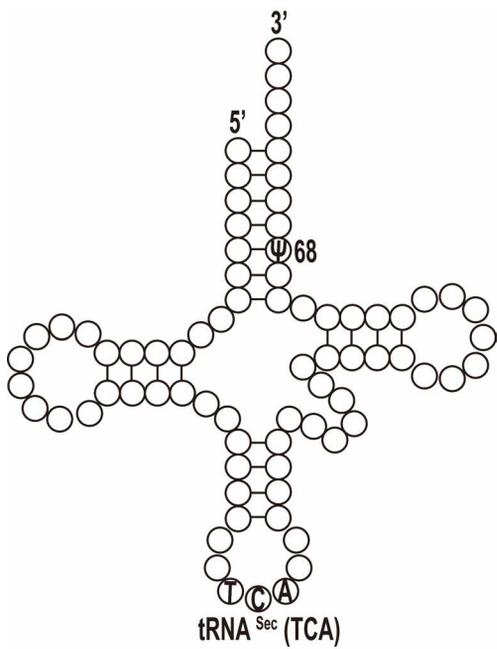
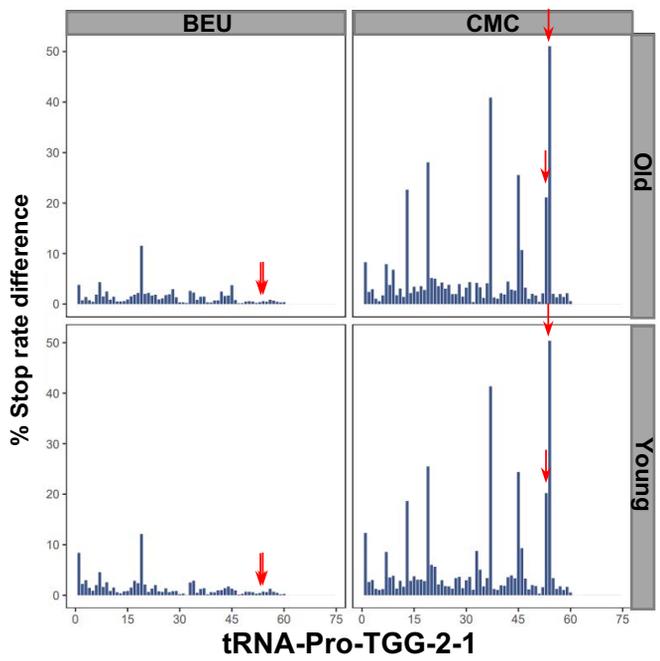
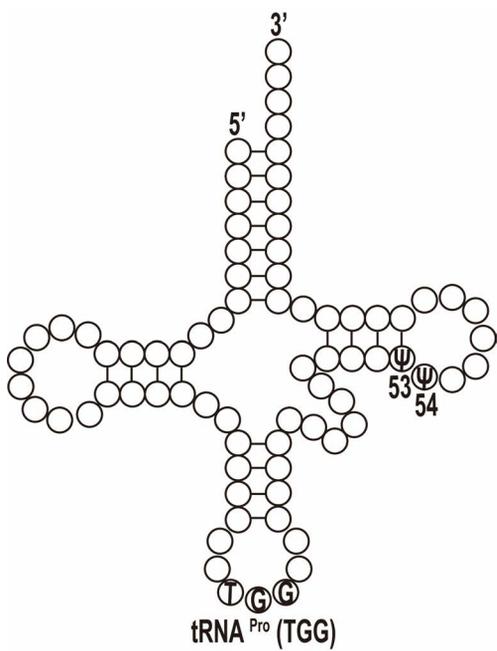


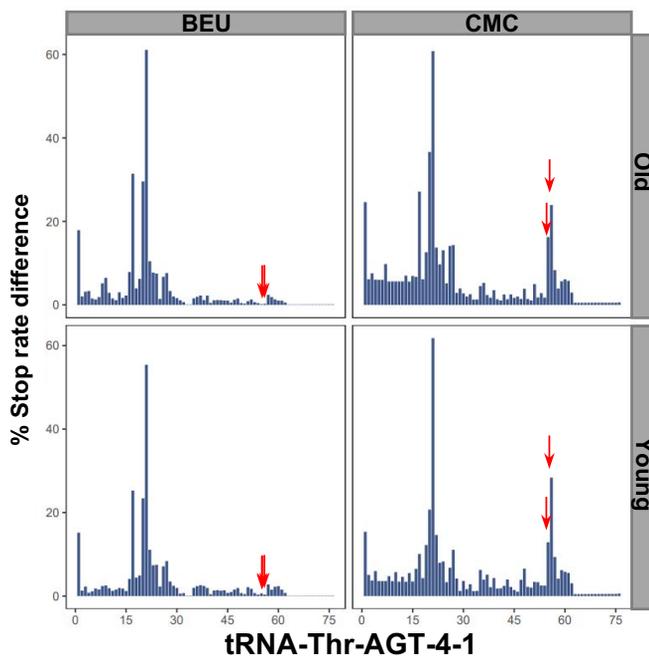
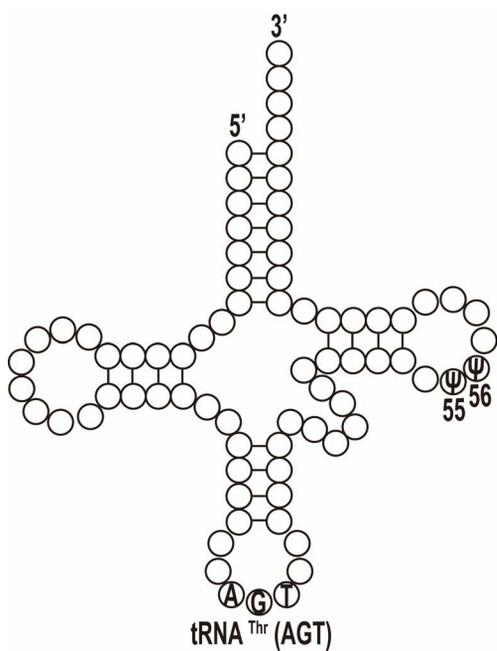
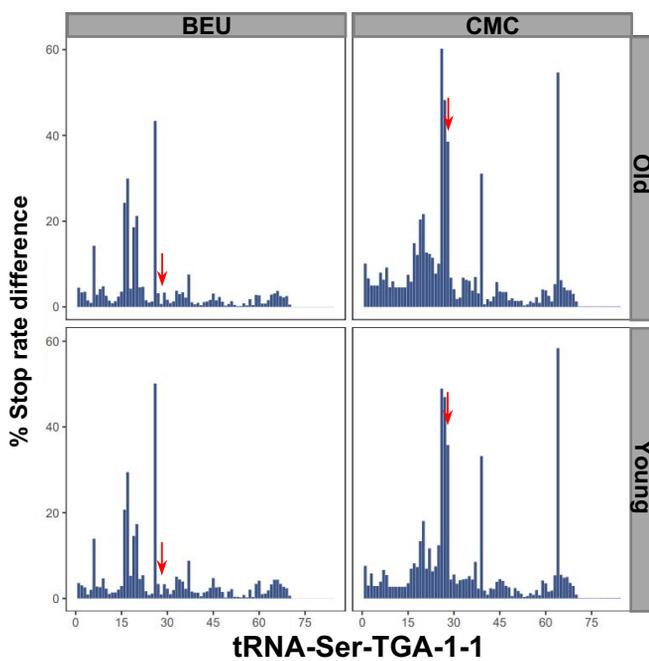
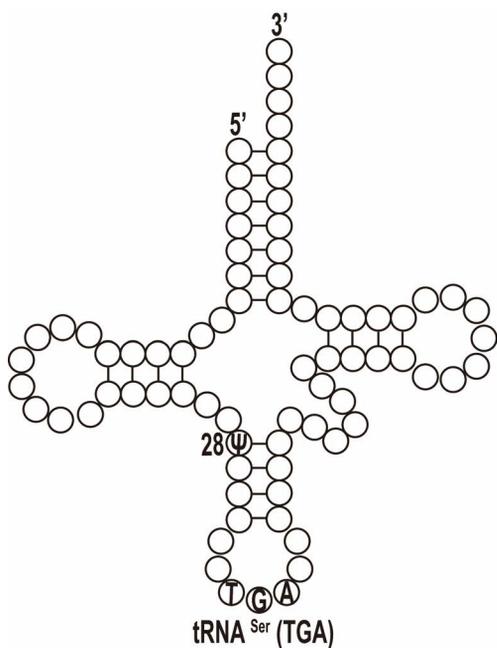
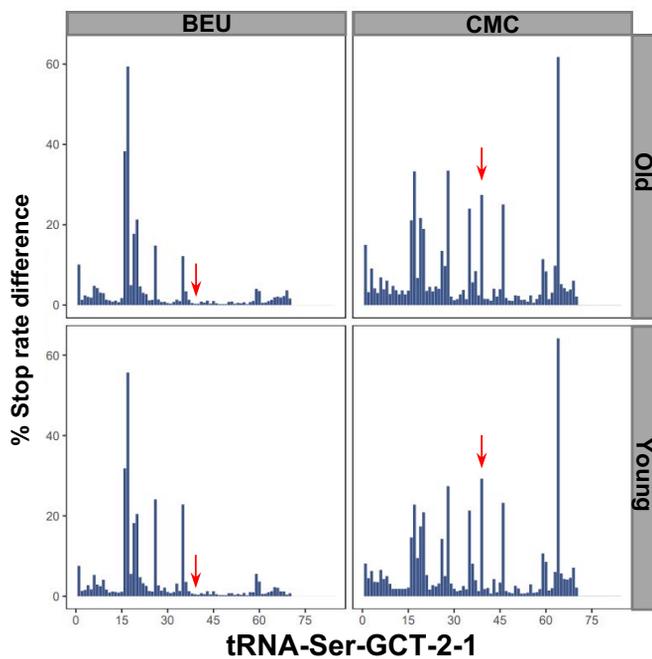
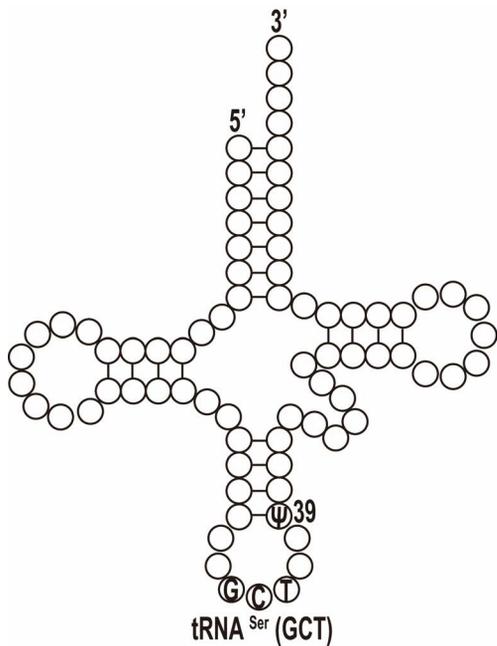


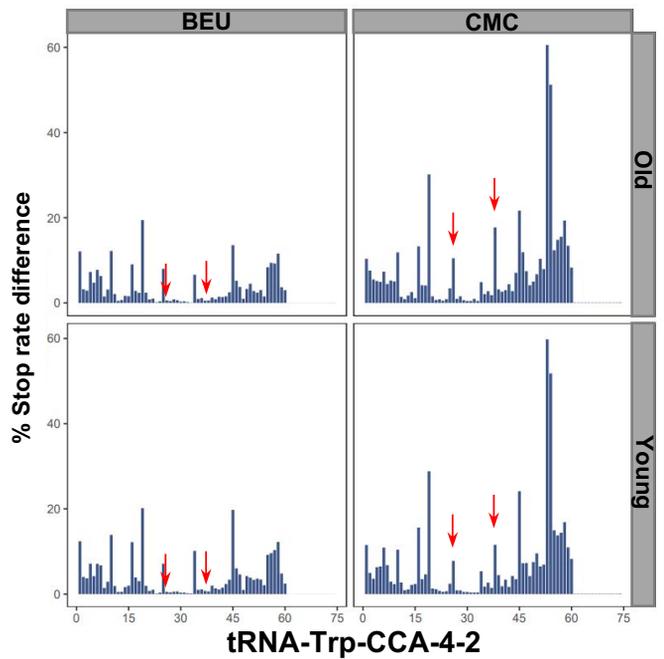
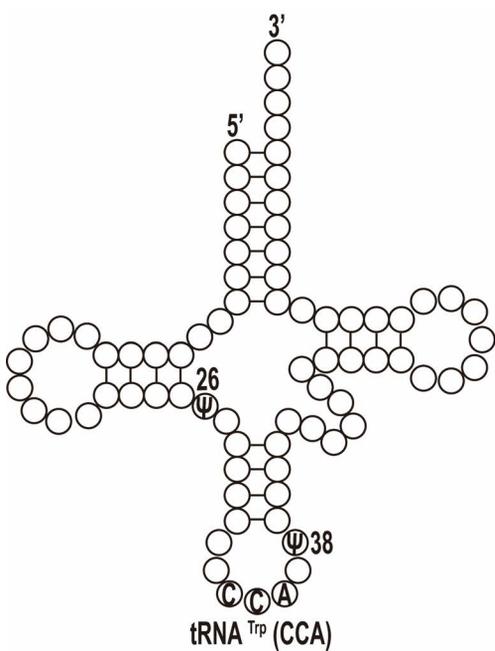
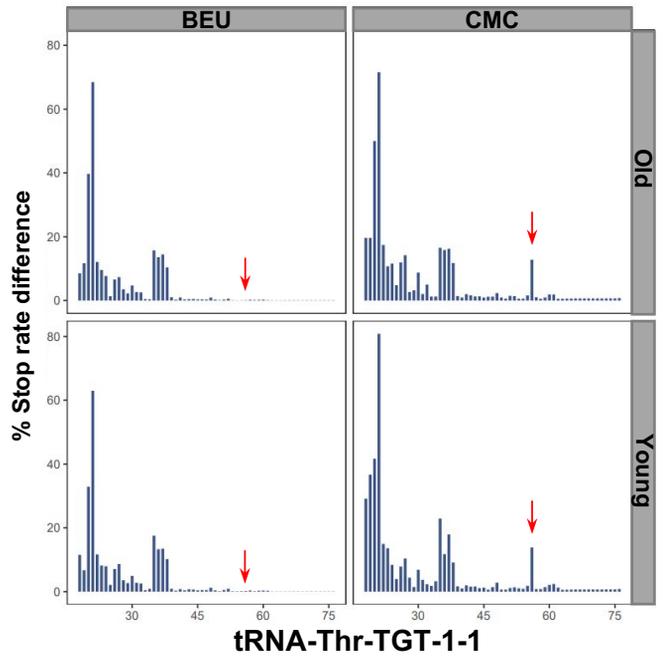
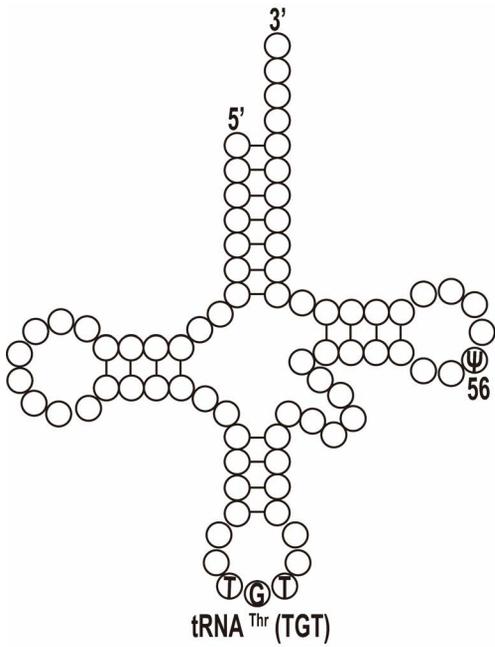
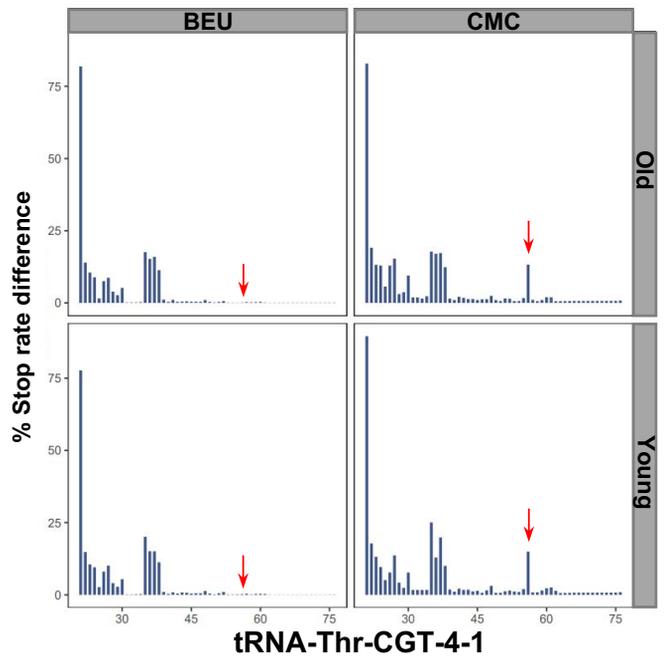
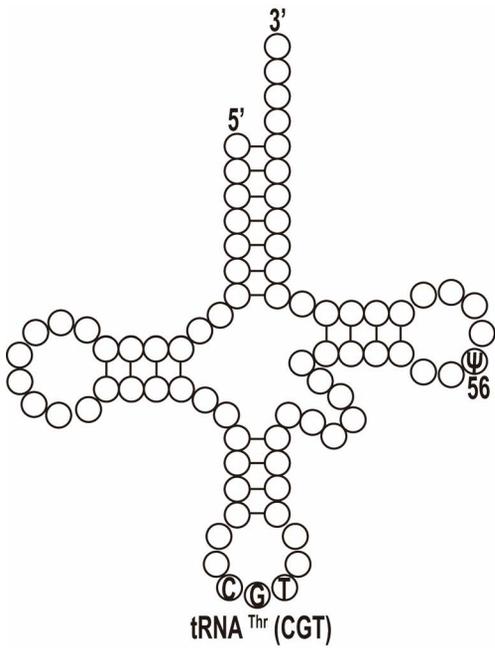


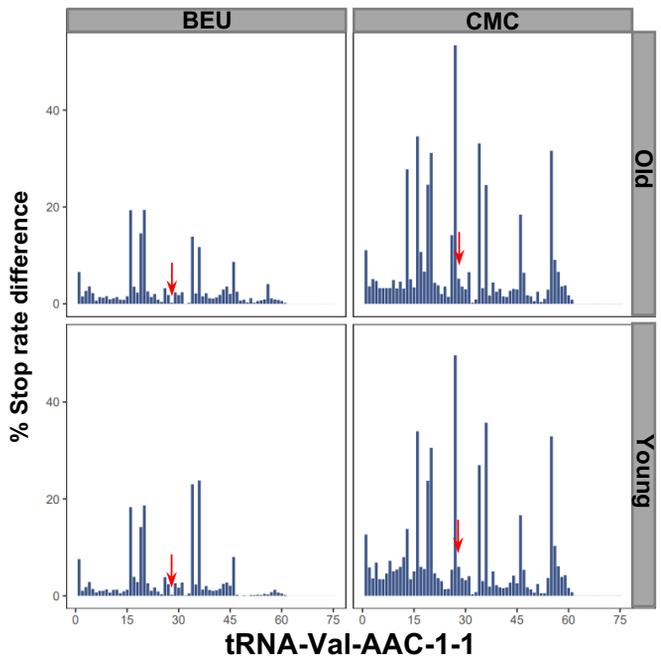
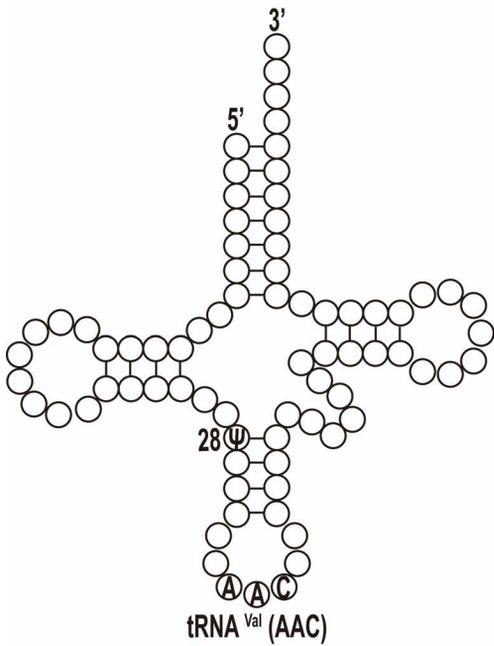
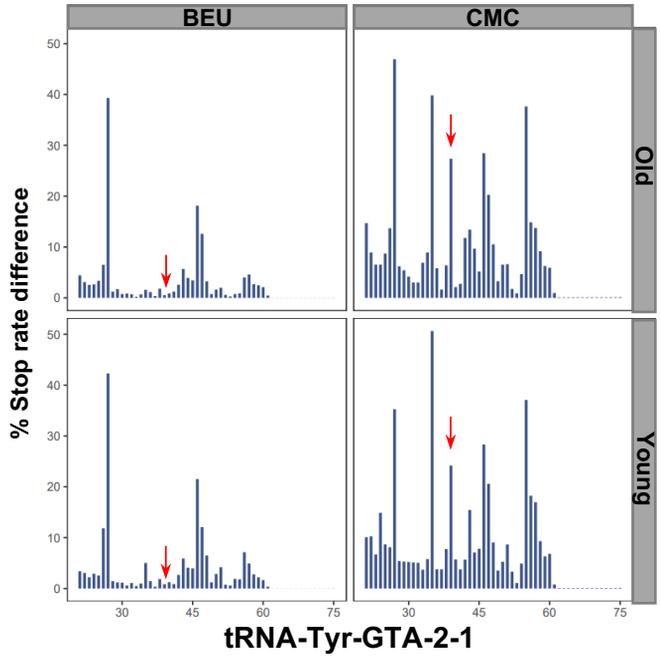
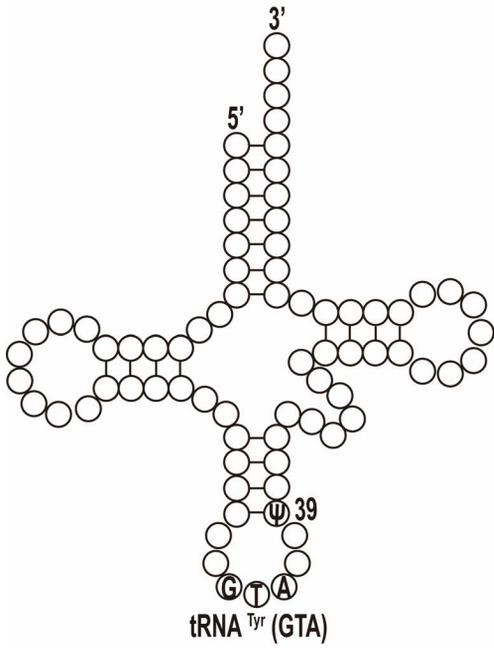
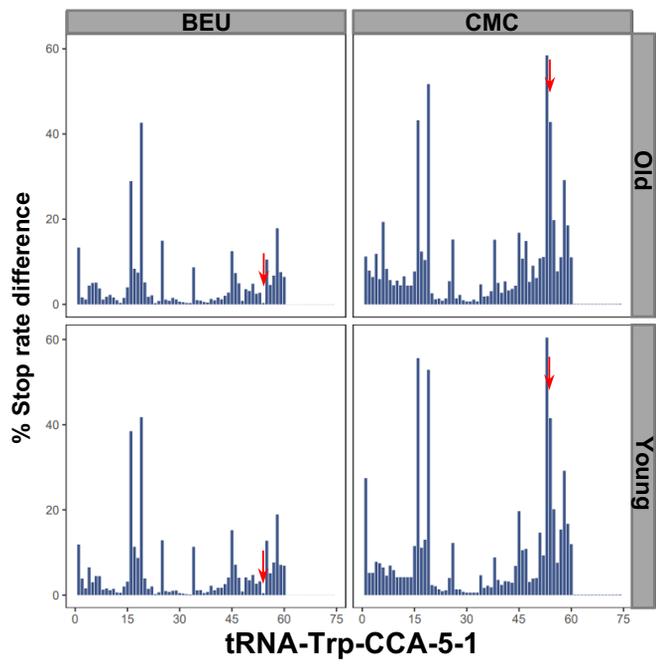
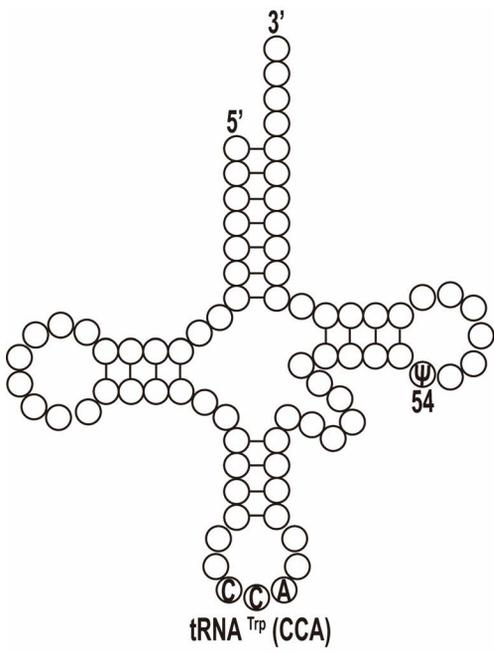


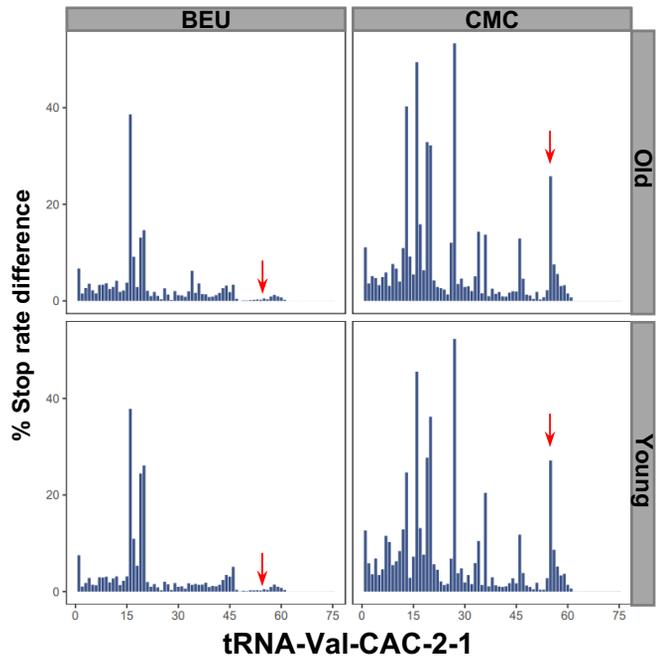
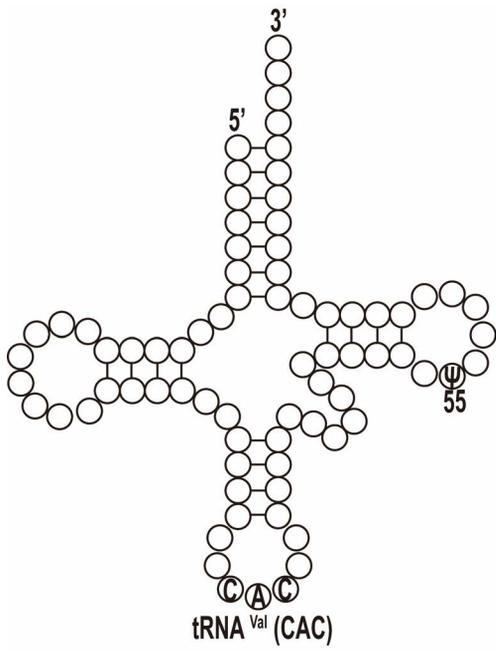
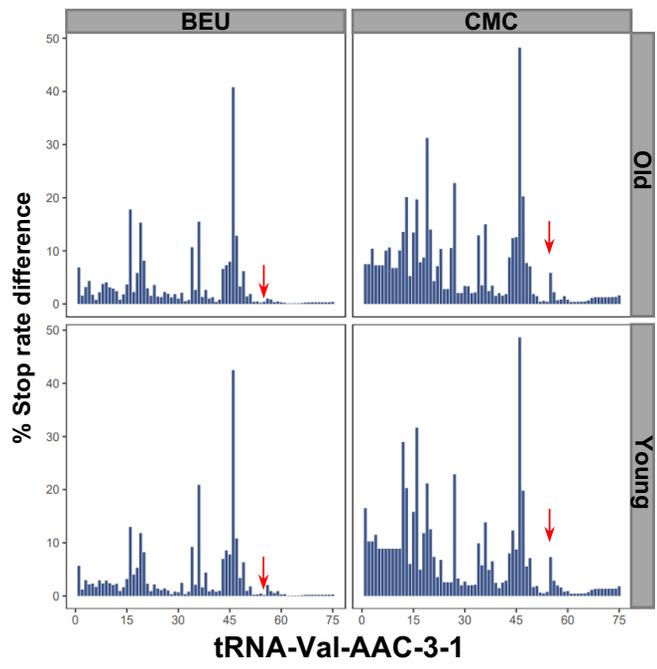
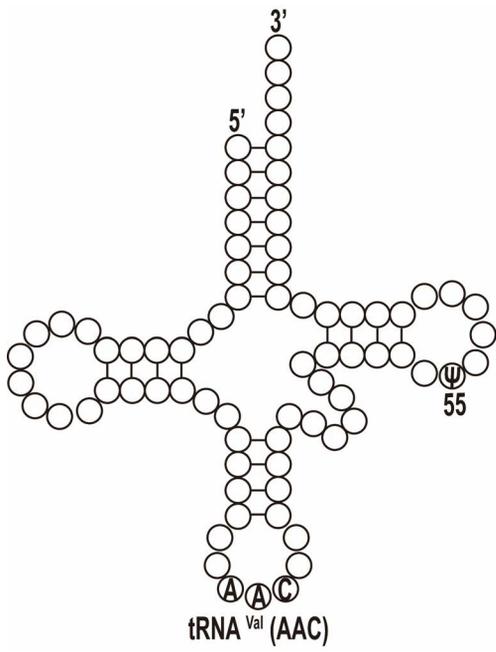




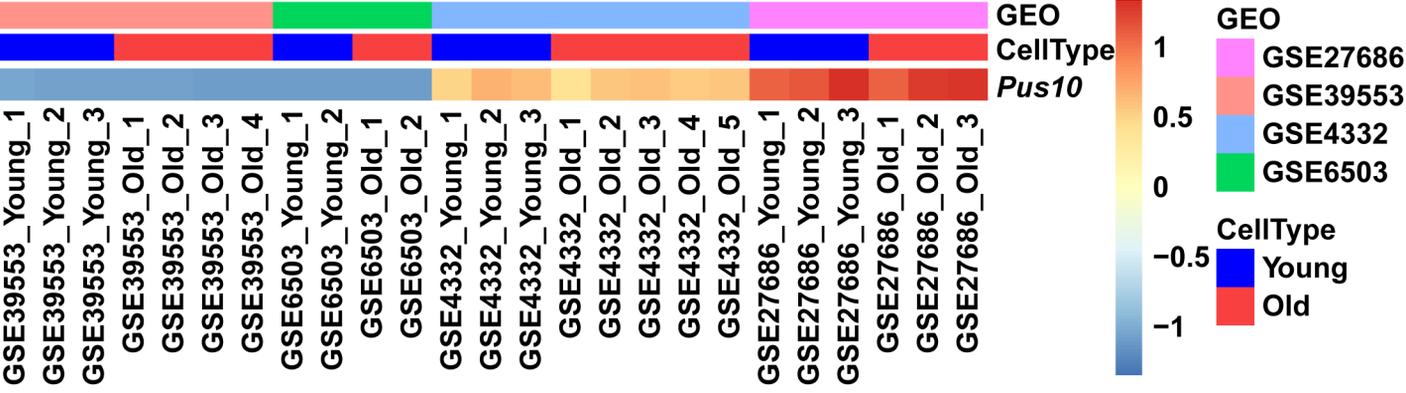






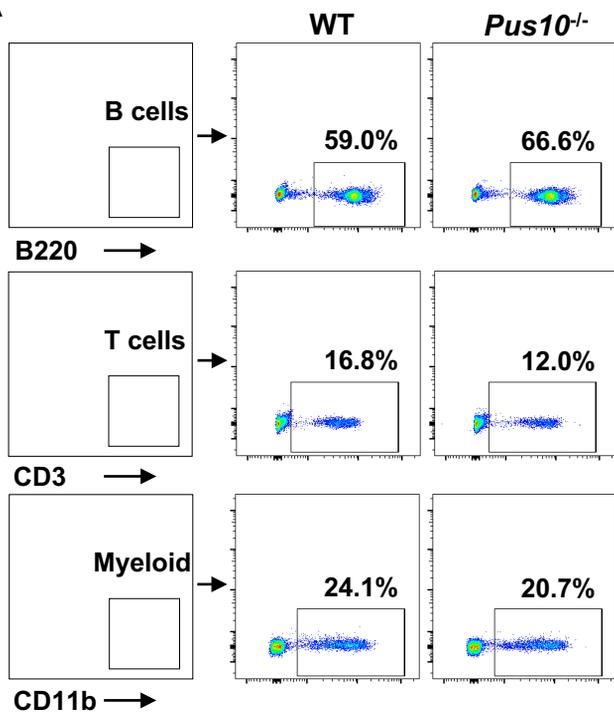


Supplemental figure 3

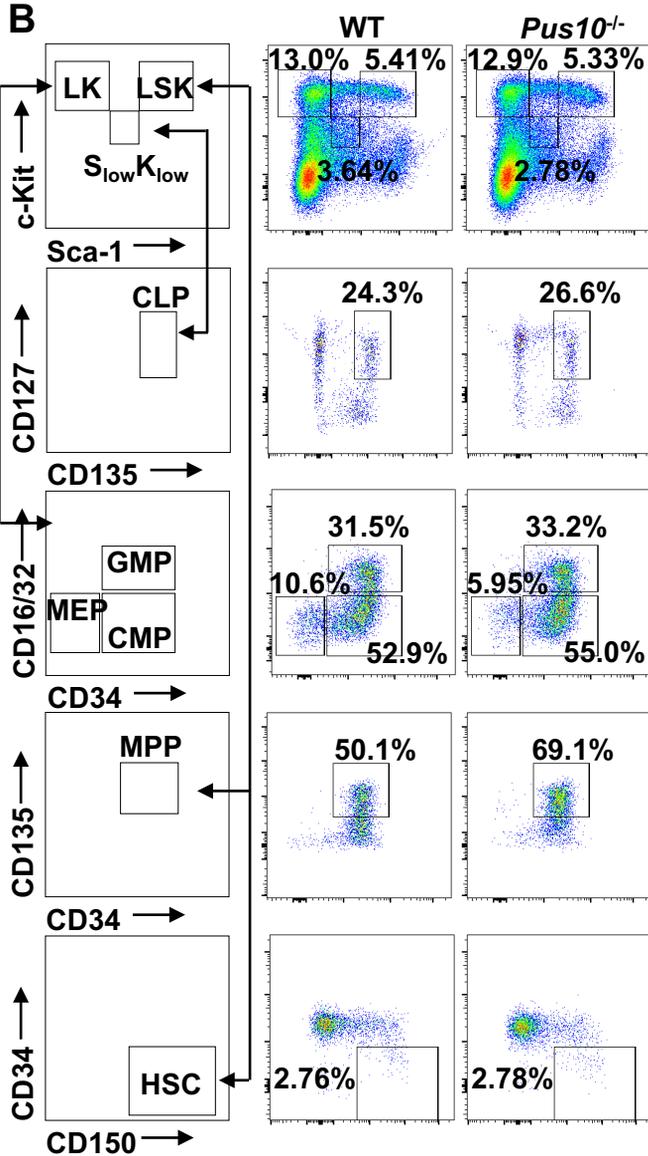


Supplemental figure 4

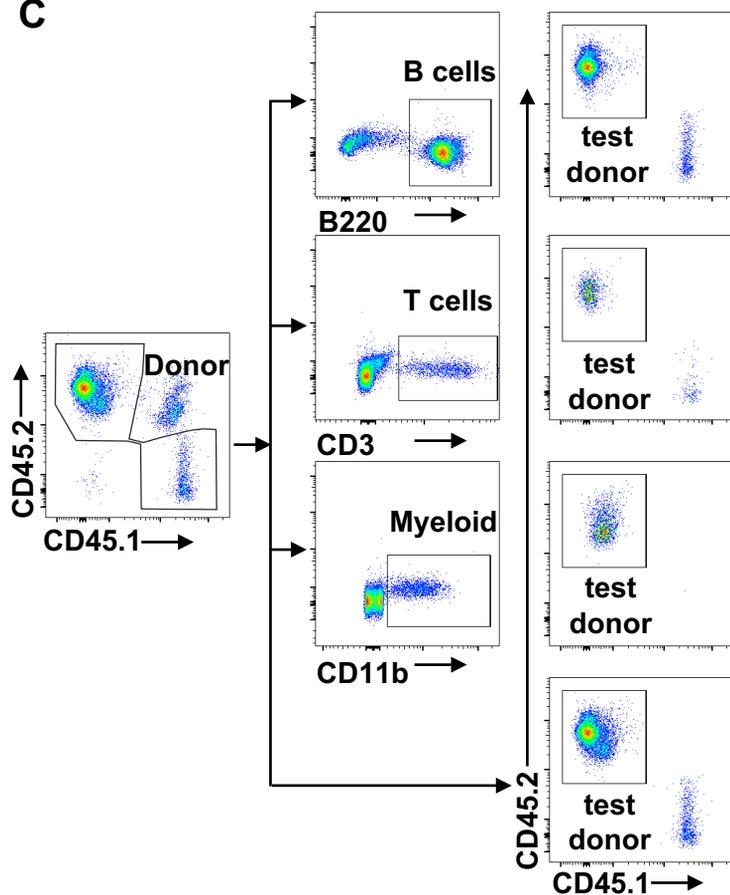
A



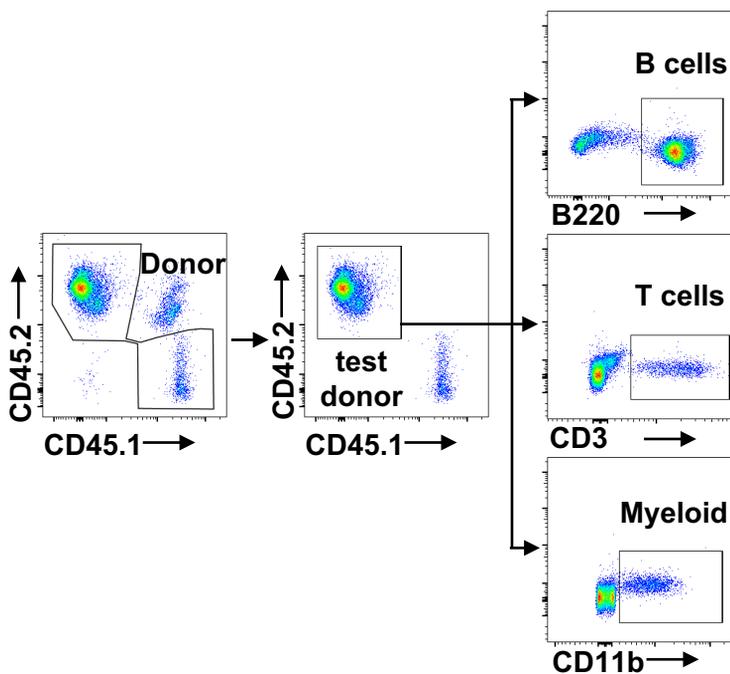
B



C

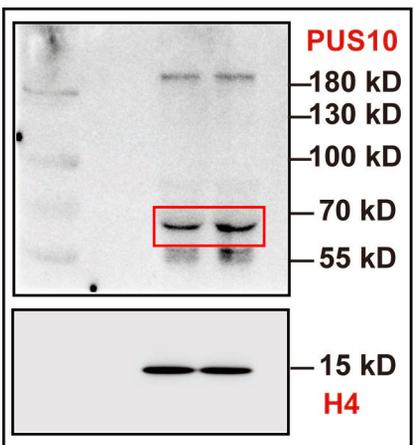


D

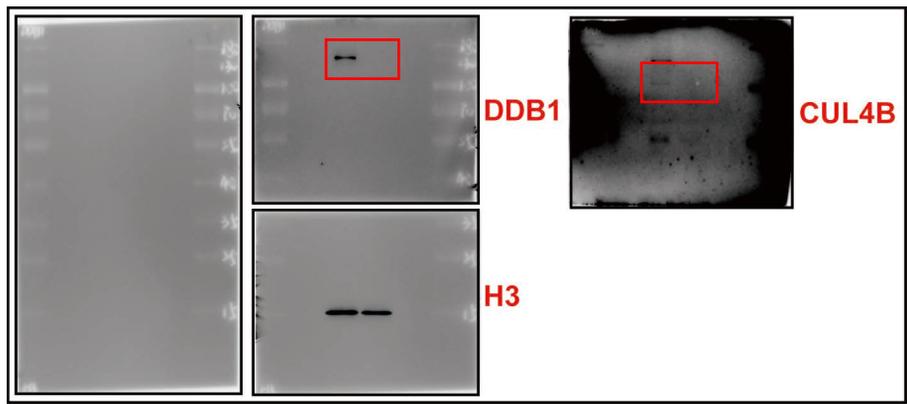


Uncropped blot Images for Fig.1A, Fig.3C,D,E,F and Fig.4B.

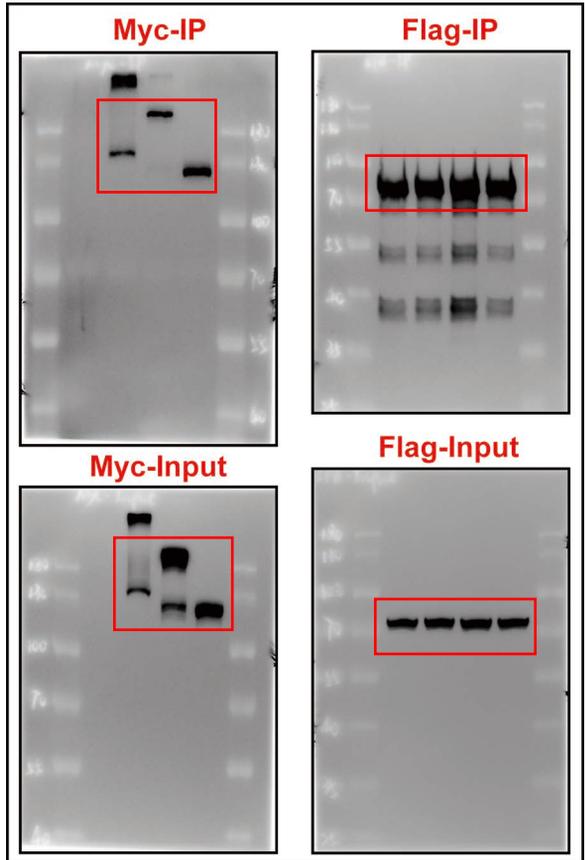
For Fig. 1A



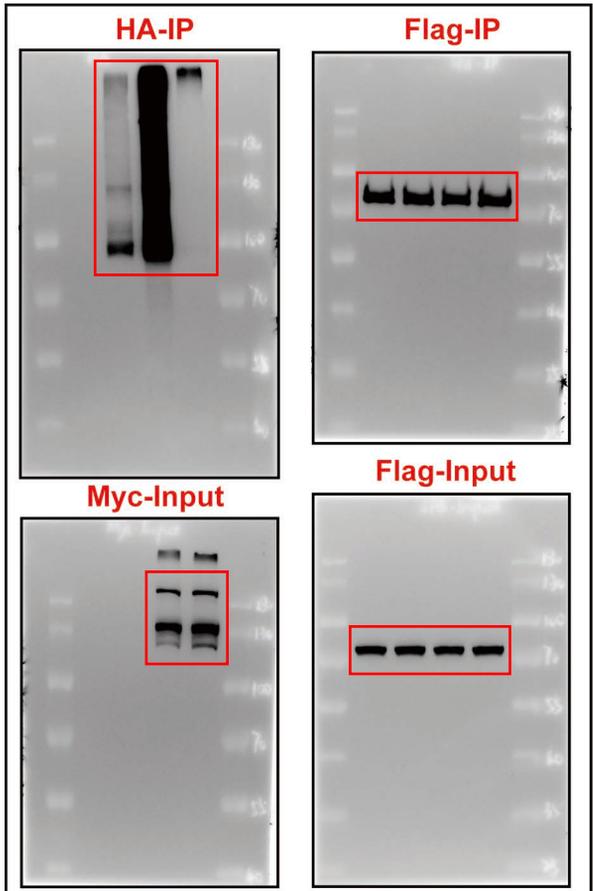
For Fig. 3E



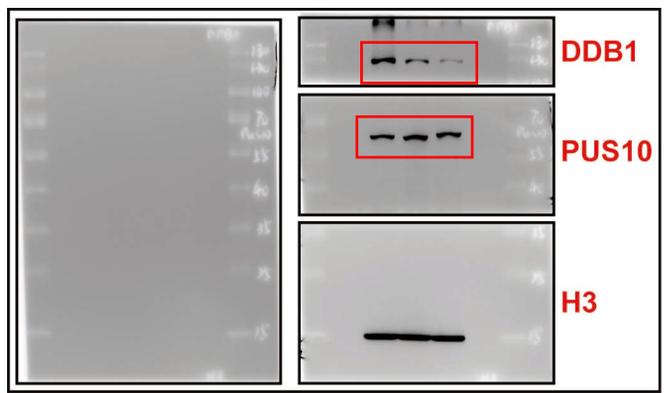
For Fig. 3C



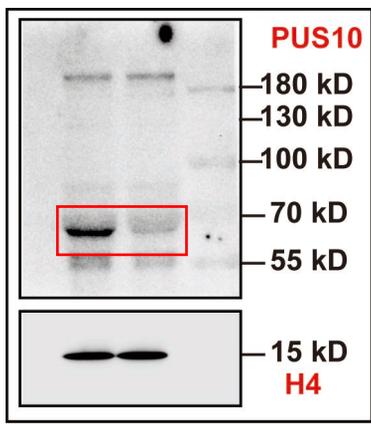
For Fig. 3D



For Fig. 3F



For Fig. 4B



Uncropped blot Images for Supplemental Fig.1A

For Supplemental. Fig. 1A

