

Group work report on ABC ——

Small Modification, Big Influence

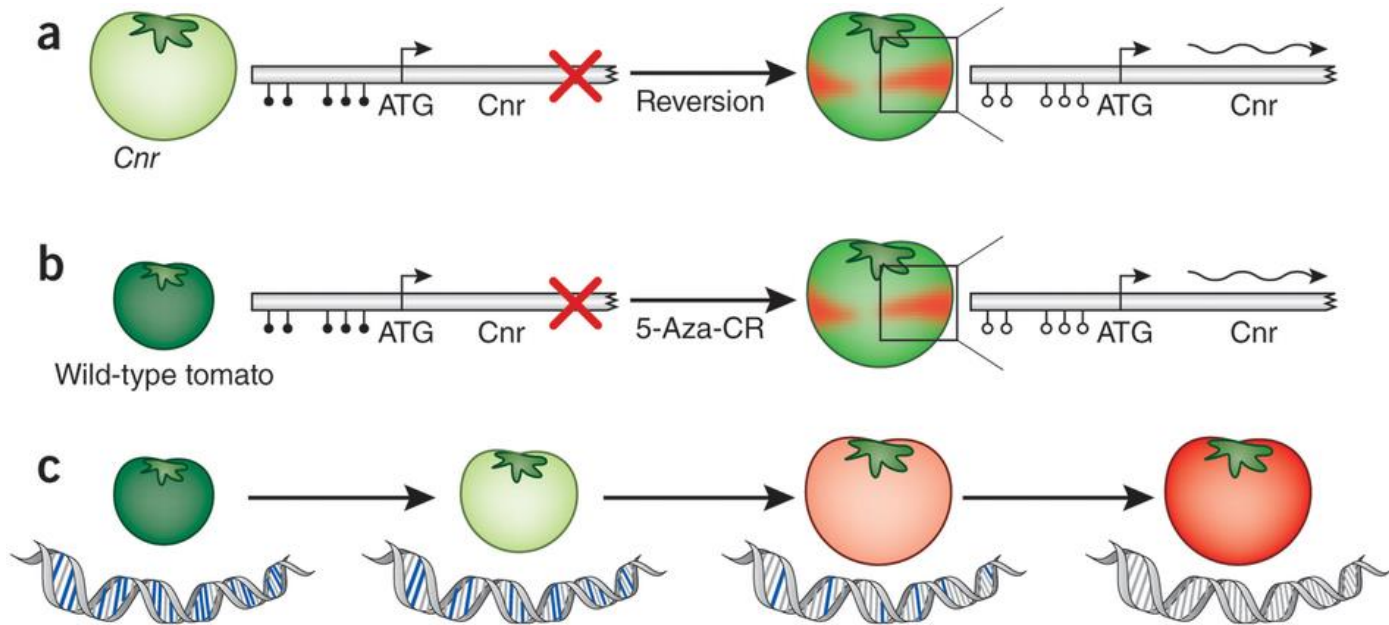
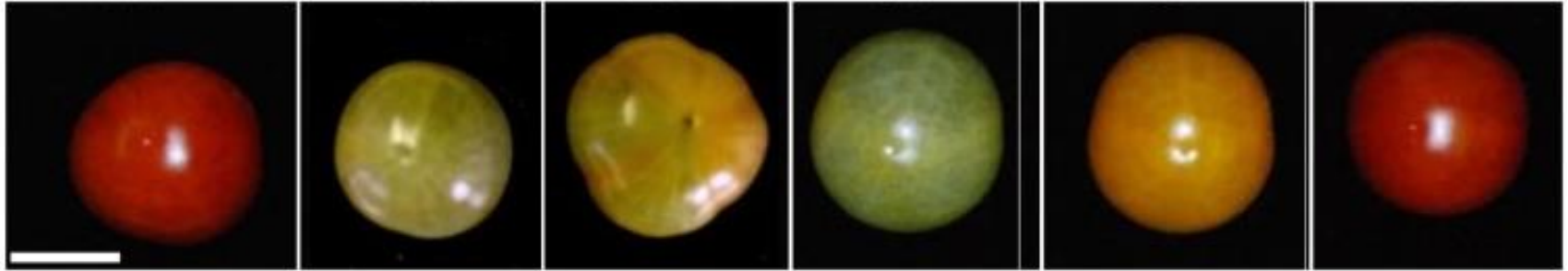
G13 Members: 贺博 汪菡
马良 涂晶波

2017/01/14

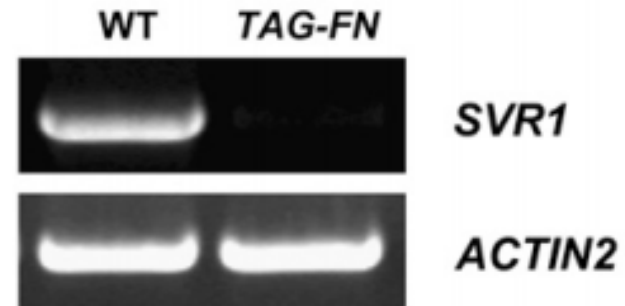
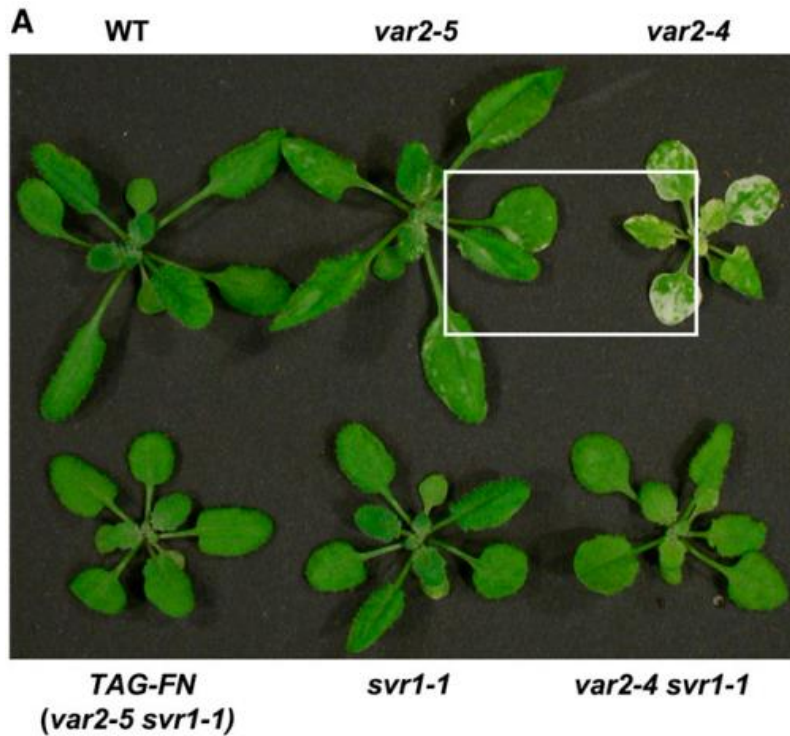
Outline

- Background
- Pseudouridine synthase（假尿嘧啶合成酶） in Arabidopsis
- Future Plan
- Acknowledgements

The factors influencing tomato's ripening?



The factors influencing Arabidopsis leaves' color?



Plant cell, 2008

SVR1 GO Terms

GO Biological Process	involved in	enzyme-directed rRNA pseudouridine synthesis, maturation of LSU-rRNA from tetracistronic rRNA transcript (SSU-rRNA, LSU-rRNA, 4.5S-rRNA, 5S-rRNA), maturation of SSU-rRNA from tetracistronic rRNA transcript (SSU-rRNA, LSU-rRNA, 4.5S-rRNA, 5S-rRNA), plastid translation
GO Cellular Component	located in	amyloplast, chloroplast, plastid
GO Cellular Component	not located in	cytosol
GO Molecular Function	functions in	RNA binding
GO Molecular Function	has	RNA binding, pseudouridine synthase activity

Examples in Mammals

ARTICLE

doi:10.1038/nature20568

m⁶A modulates neuronal functions and sex determination in *Drosophila*

Tina Lence¹, Junaid Akhtar¹, Marc Bayer¹, Katharina Schmid², Laura Spindler³, Cheuk Hei Ho⁴, Nastasja Kreim¹, Miguel A. Andrade-Navarro^{1,5}, Burkhard Poeck³, Mark Helm² & Jean-Yves Roignant¹

Cancer Cell. 2016 Dec 13. pii: S1535-6108(16)30560-8. doi: 10.1016/j.ccell.2016.11.017. [Epub ahead of print]

FTO Plays an Oncogenic Role in Acute Myeloid Leukemia as a N6-Methyladenosine RNA Demethylase.

Li Z¹, Weng H², Su R³, Weng X⁴, Zuo Z⁵, Li C⁶, Huang H³, Nachtergaele S⁷, Dong L³, Hu C⁸, Qin X³, Tang L⁹, Wang Y⁸, Hong GM¹⁰, Huang H¹⁰, Wang X⁷, Chen P¹⁰, Gurbuxani S¹¹, Arnovitz S¹⁰, Li Y¹⁰, Li S¹⁰, Strong J³, Neilly MB¹⁰, Larson RA¹⁰, Jiang X², Zhang P⁹, Jin J¹², He C¹³, Chen J¹⁴.

⊕ Author information

Nature. 2016 Sep 15;537(7620):369-373. doi: 10.1038/nature19342. Epub 2016 Sep 7.

m6A RNA methylation promotes XIST-mediated transcriptional repression.

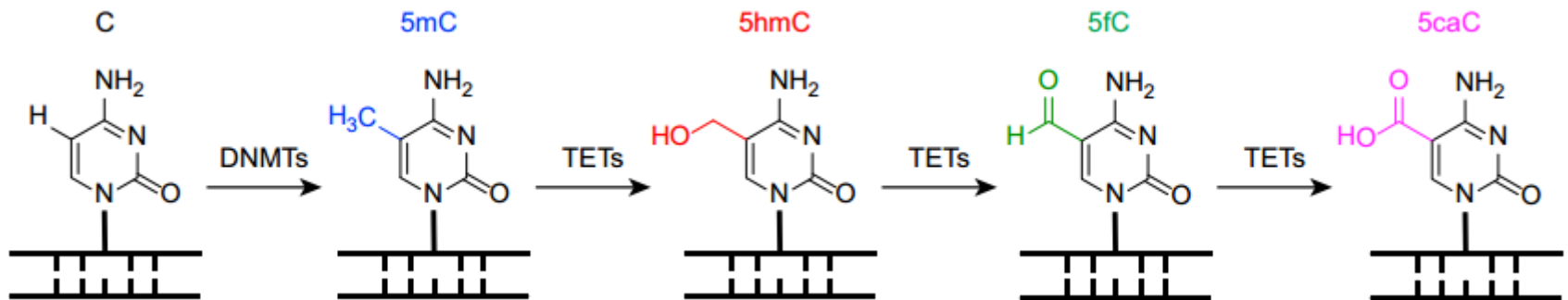
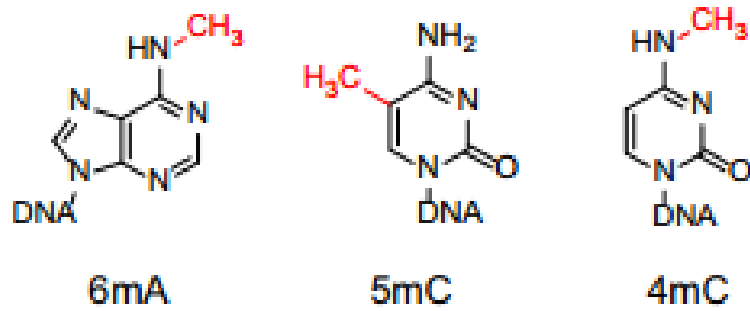
Patil DP¹, Chen CK², Pickering BF¹, Chow A², Jackson C², Guttman M², Jaffrey SR¹.

⊕ Author information

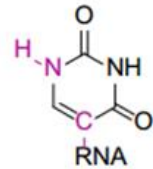
Epigenetics

- DNA modification
 - RNA modification
- } Nucleic Acid Modification
- Histone modification
 - Regulatory non-coding RNAs
 - Chromatin structure
 -

DNA modification

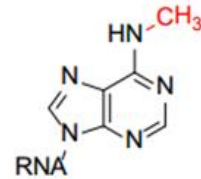


RNA modification



Pseudouridine
ψ

tRNA, rRNA, mRNA, snRNA



*N*⁶-methyladenosine
m⁶A

tRNA, rRNA, mRNA



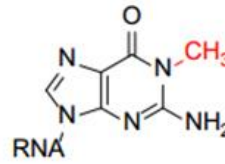
5-methylcytidine
m⁵C

tRNA, rRNA, mRNA



*N*¹-methyladenosine
m¹A

tRNA, rRNA



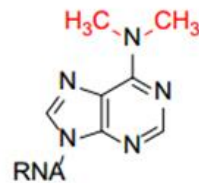
*N*¹-methylguanosine
m¹G

tRNA, rRNA



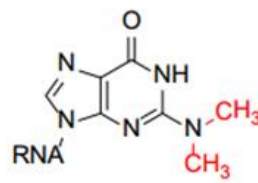
*N*⁷-methylguanosine
m⁷G

tRNA, rRNA, mRNA



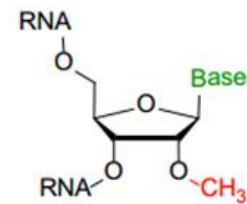
*N*⁶,*N*⁶-dimethyladenosine
m²₂A

rRNA



*N*²,*N*²-dimethylguanosine
m²₂G

tRNA, rRNA



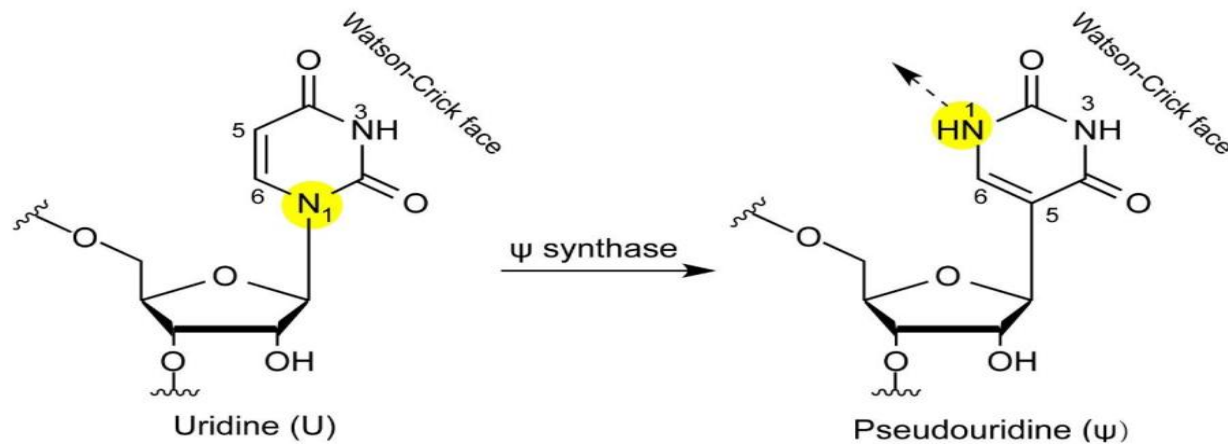
2'-*O*-methyl
Nm

tRNA, rRNA, mRNA, snRNA

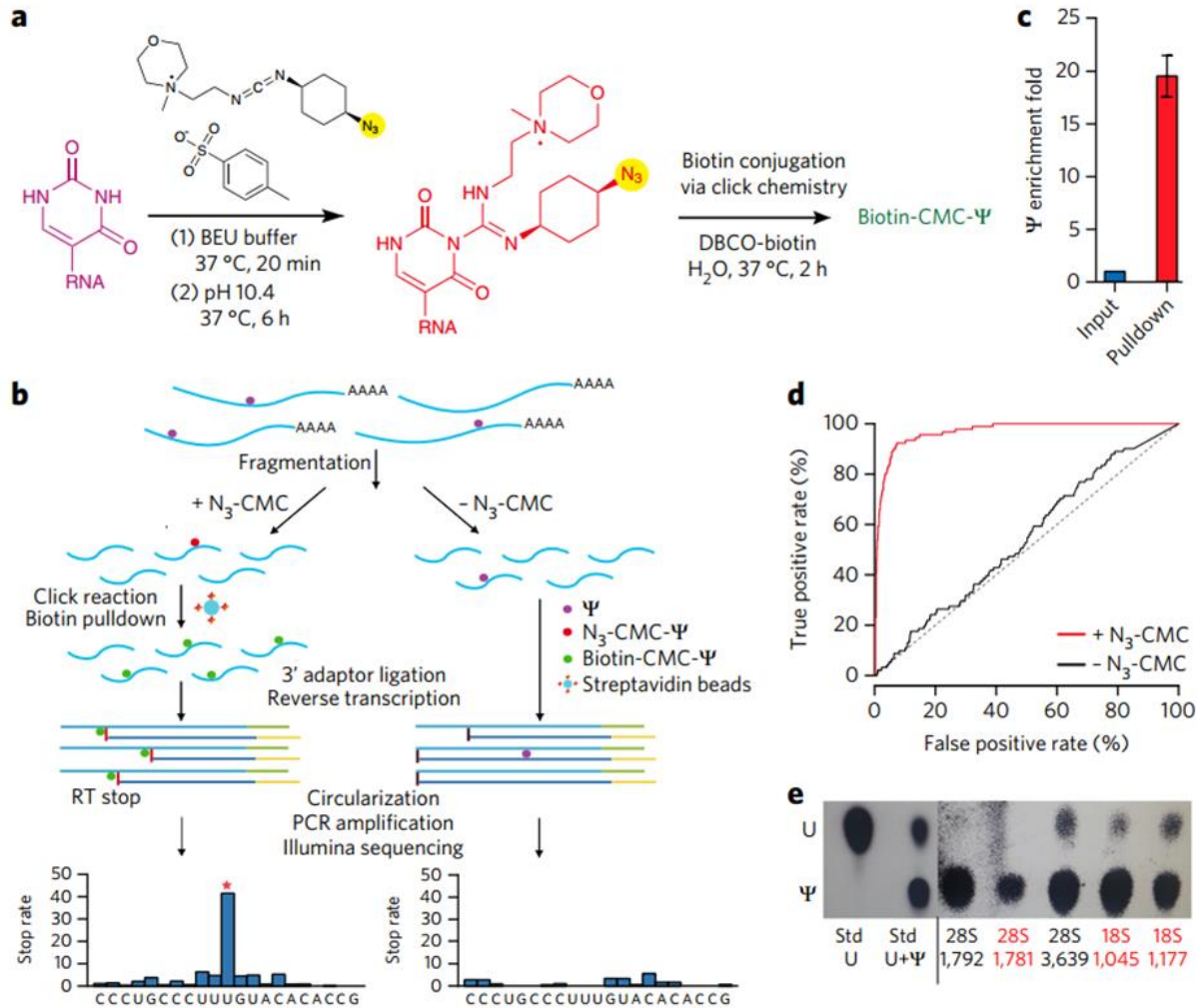
Cell chemical biology, 2016

Pseudouridine (假尿嘧啶) modification

- The earliest discovered RNA modification (1951)
- The most abundant modification in RNA (7%-9%)
- Widely distributed in tRNA, rRNA, snRNA
- Maintaining tRNA structure
- Involved in Translation



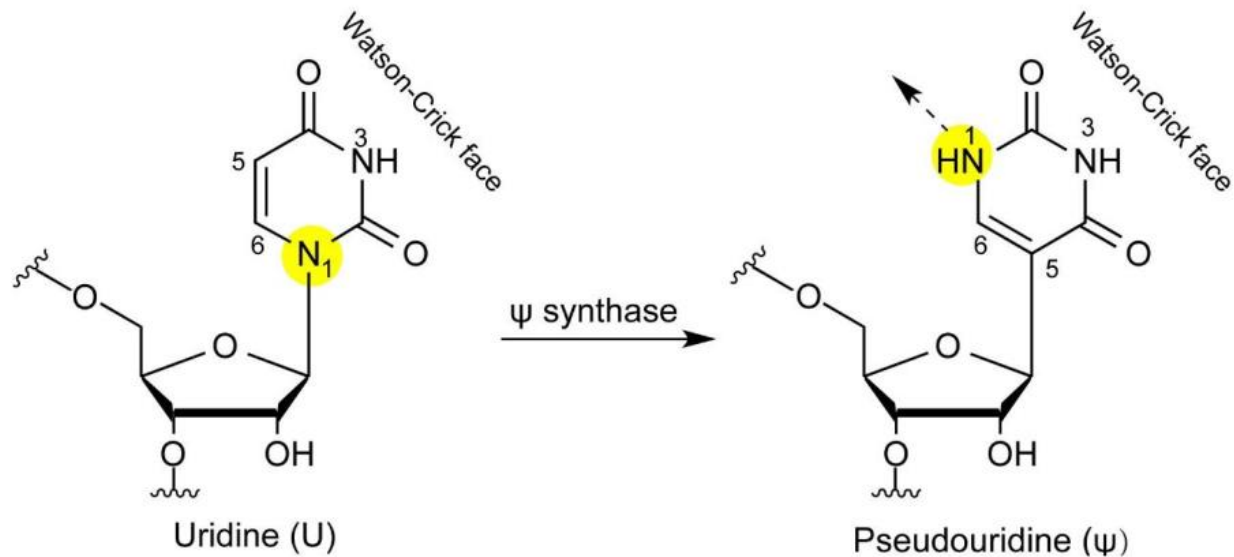
Pseudouridine detection



Nature chemical biology, 2015

Pseudouridine Formation

- pseudouridine synthases (13 PUSs in Human)
- H/ACA ribonucleoproteins

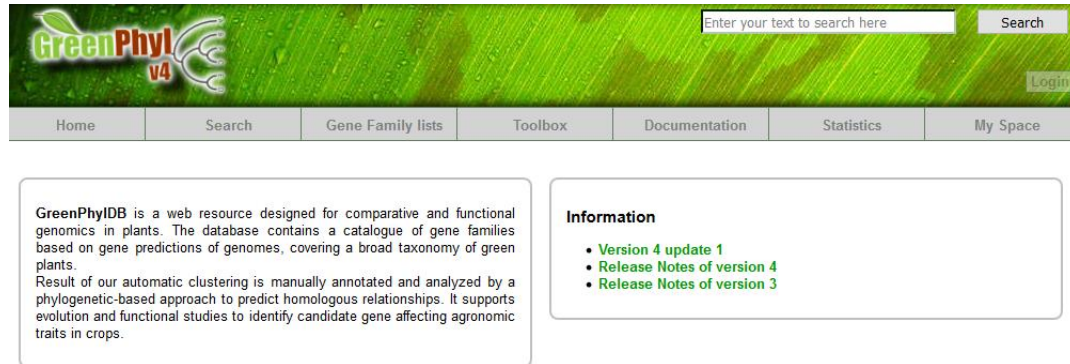


Pseudouridine synthases family

	Pseudouridine synthase in human	family
uridine-to-pseudouridine isomerization in tRNAs —— Tru Family	PUS1	TruA
	PUS3	TruA
	PUS7	TruD
uridine-to-pseudouridine isomerization in 50S rRNAs —— Rlu Family	PUS10	Pus10
	PUS7L	TruD
	DKC1	TruB
uridine-to-pseudouridine isomerization in 30S rRNAs —— Rsu Family	PUSL1	TruA
	RPUSD1	TruA
	RPUSD2	TruA
	RPUSD3	TruA
	RPUSD4	TruA

Pseudouridine synthase protein in Arabidopsis

- GreenPhylDB



GreenPhylDB is a web resource designed for comparative and functional genomics in plants. The database contains a catalogue of gene families based on gene predictions of genomes, covering a broad taxonomy of green plants. Result of our automatic clustering is manually annotated and analyzed by a phylogenetic-based approach to predict homologous relationships. It supports evolution and functional studies to identify candidate gene affecting agronomic traits in crops.

Information

- [Version 4 update 1](#)
- [Release Notes of version 4](#)
- [Release Notes of version 3](#)

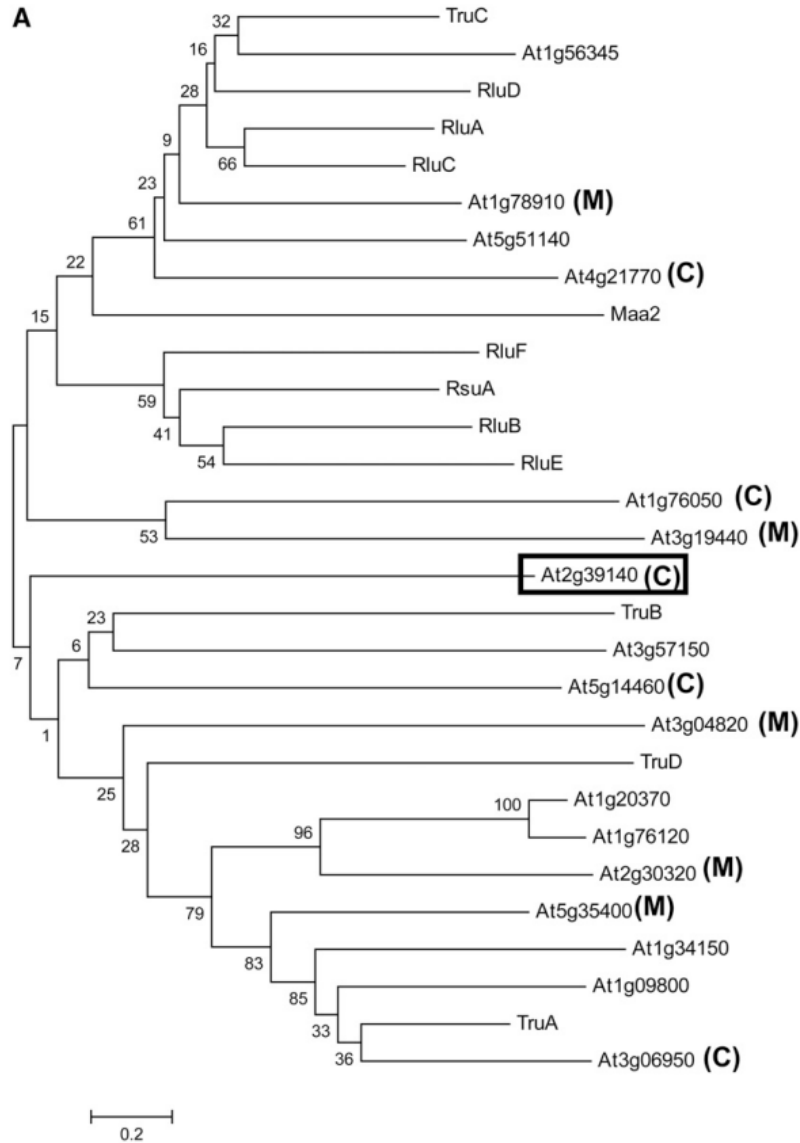
Species	Gene numbers	Transcripts numbers
Oryza sativa	14	23
Arabidopsis thaliana	23	29
Ricinus communis	10	10
Musa acuminata	10	10
Solanum lycopersicum	21	21
Musa balbisiana	14	14

Pseudouridine synthase protein in Arabidopsis

TAIR ID	Exon numbers	Length	TAIR ID	Exon numbers	Length
AT1G09800	10	372	AT3G04820	20	715
AT1G56345	2	322	AT3G06950	6	323
AT1G34150	14	446	AT3G19440	10	477
AT1G20370	2	549	AT3G43340	3	74
AT1G76050	7	430	AT3G52260	13	417
AT1G20410	15	504	AT3G57150	1	565
AT1G76120	2	463	AT4G21770	9	472
AT1G78910	9	478	AT5G14460	9	540
AT2G39140	9	410	AT5G35400	10	471
AT2G30320	7	510	AT5G51140	13	410

Combination information from TAIR, NCBI, GreenPhylDB

Phylogenetic analysis of *Arabidopsis* pseudouridine synthases



Plant Cell, 2008

Arabidopsis Pseudouridine synthase protein structure

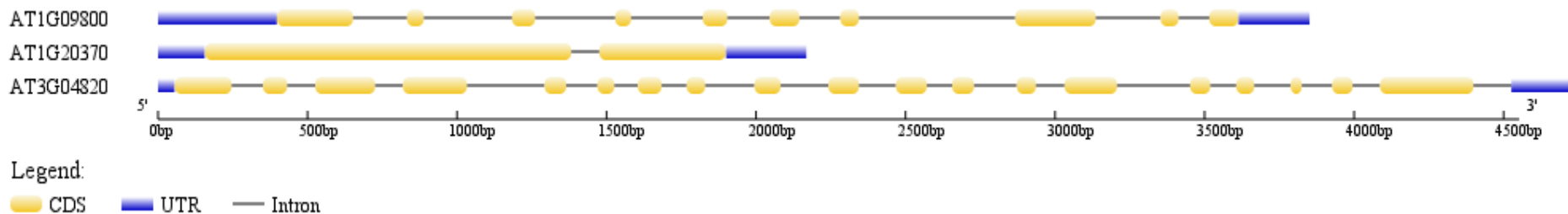
GSDS_{2.0} Gene Structure Display Server

Home | Help |

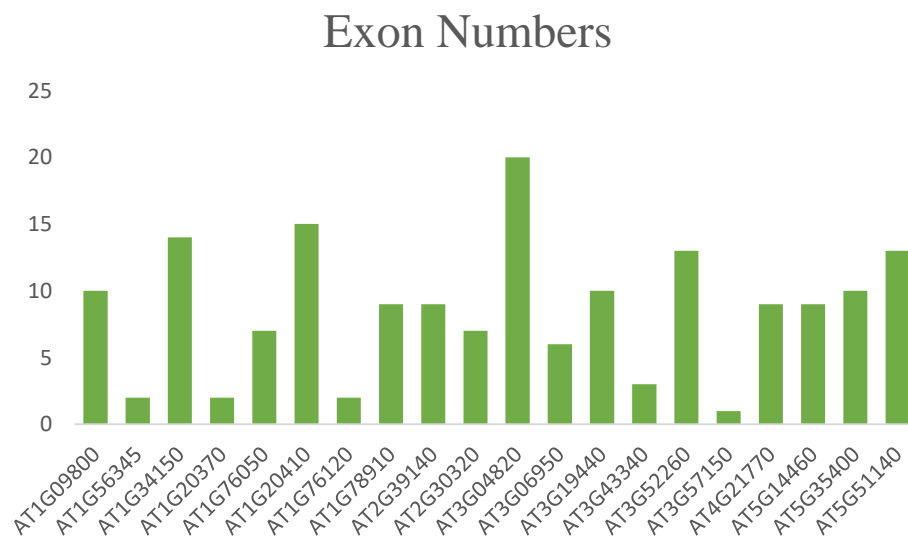
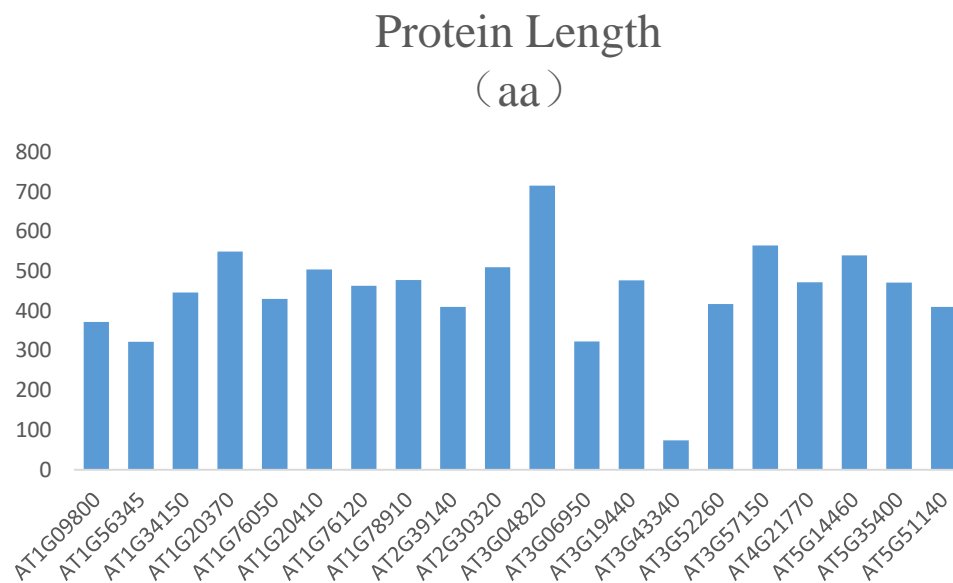
Contents

- 1 Work Flow of GSDS 2.0
- 2 Supported Gene Features and Formats
 - 2.1 Input Main Features
 - 2.1.1 BED Format
 - 2.1.2 GTF/GFF3 Format
 - 2.1.3 GenBank Accession Number/GI
 - 2.1.4 FASTA Sequences
 - 2.2 Add Other Features
- 3 Adding Phylogenetic Tree/Output Order
- 4 Modifying the Generated Figure
- 5 Installing a Local Version

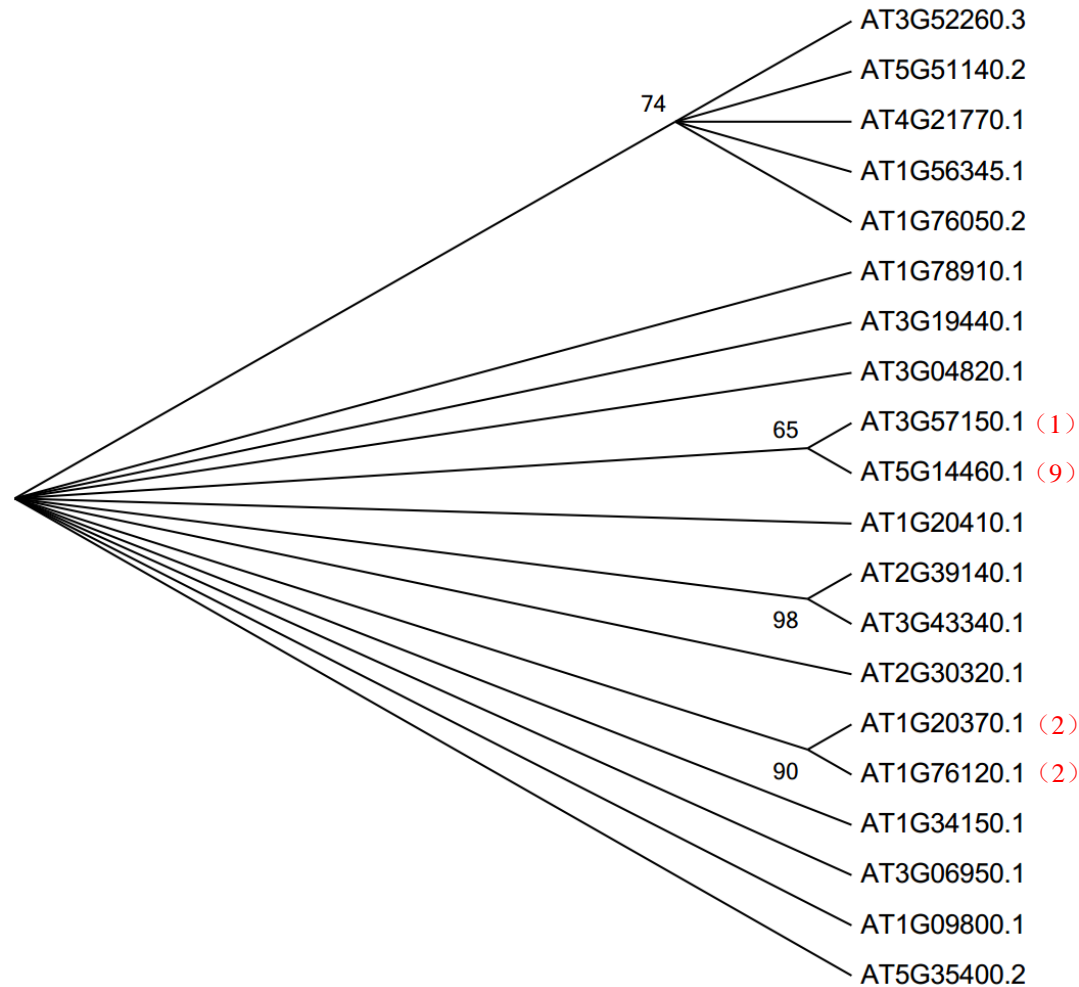
<http://gsds1.cbi.pku.edu.cn/>



Arabidopsis Pseudouridine synthase protein structure

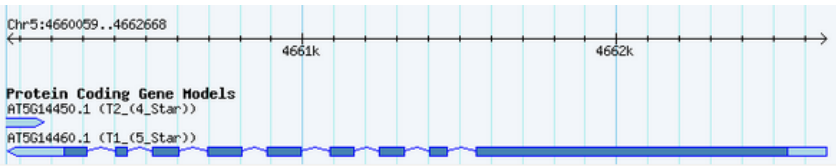


Arabidopsis pseudouridine synthase protein tree



Maximum Likelihood Method
Bootstrapping

AT3G57150 & AT5G14460



AT5G14460



AT3G57150

Pairwise Alignment Result

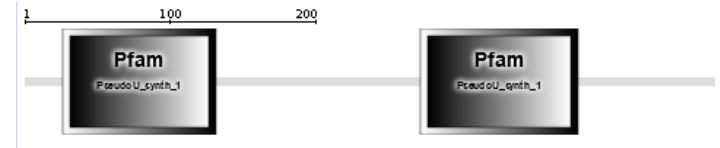
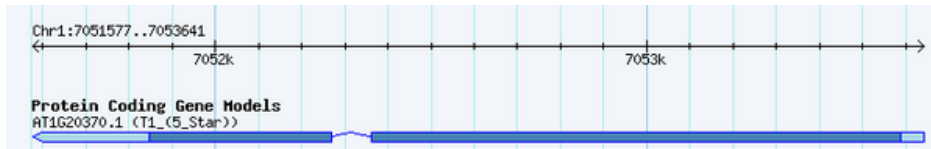
LENGTH	SCORE	IDENTITY	SIMILARITY	GAPS
202	265.5	67/202 (33.2%)	102/202 (50.5%)	34/202 (16.8%)

```

82 VINLDKPANPSSHEVWAWIKRILRVEKTGHSGTLDPKVITGNLIVCIDRAT 131
|:>::|:|...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
323 VLLVNKPKGWTSTFTVCGKLRRLVVKVKGHAGTLDPMATGLLIVCVGKAT 372
132 RLVKSQQGAGKEYVCVARLHSAV-----PDVAK-----VARAL 164
::|...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
373 KVVDRYQGMIKGYSGVFRLGEATSTLDADSPVIQRESWEHIKDDDIKKAL 422
165 ESLTGAVFQRPLISAVK-----RQLRIRIYES---KLEVDADR 202
-|...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
423 TSFLGEIQVPPMFSAIKVGGEKMYEKARRGETVELSPRRISIFQFDIER 472
203 HL-----VVFVWSCAAGTYIRIMCVHLGLLLGVGGHMQELRRVRSGLIGE 247
-|...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
473 SLDDRQNLIFRVICSKGTIIR-QLCADLAKALGSCAHLTALRRDSIGEYSA 522
248 NN      249
   |:
523 ND      524
    
```

TruB Family

AT1G20370 & AT1G76120



AT1G20370

AT1G76120

Pairwise Alignment Result

LENGTH	SCORE	IDENTITY	SIMILARITY	GAPS
492	1531.0	314/492 (63.8%)	371/492 (75.4%)	38/492 (7.7%)

```

 4 TTTDEEIDLSC--DGG--VTE-----PQKVAIIFAFCGVGYQGMQKNP      42
   :|:|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|. 78
29 STTGQETDSSAVTIGGSNVAERRAPKYRRRKVAIVFAFCGVGYQGMQKNP
   43 GAKTIEGELEELFHAGAVPE$IRGKPKLYDFARSARIDKGV$AVGQVVS      92
   |||:|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|. 128
79 GAKTIEGELEELFHAGAVPDADR$NKP$RNY$EWR$ARSARIDKGV$AVGQVVS
   93 GRFIVDPLGFV$NRLNSNLPNQIRIFGYKHVTP$FSS$KKFCDRRRYVYLLP     142
   |||.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|. 178
129 GRFYVDP$PF$VERLNSKLPDQIRVFGYKR$VAP$FSS$KKFCDRRRYVYLLP
   143 VFALDPISHRDREIVMASLGPGE$EYVKCFEC$ER$RKIP$PGLV$GK$W$KGTN  192
   |||:|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|. 224
179 VFALD$P$CVHGEA$EMV$RTDL--GYE$YVK$VECS$EKGYKIP$LV$MG--KDT
   193 -FGIKSLDFQS$DISS$N$SALR$SDIKIEAL$SNL-----AG            227
   ..|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|. 274
225 CCDTRK$LEIQ$DISS$TCD$AIGAD$VKCETL$SSV$P$AEN$NLNS$EVL$DGAD
   228 LCSVDVEVGRIQEDS--CKLNIN$SE---TKVK$KFCYGEK$EKER$FSRI     271
   :.:.:.:.:.:.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|. 324
275 VSAL$SSKAE$GME$SNTLAKVEMNNGEGEDMTK$E$KFCYGEK$EKER$FNRI

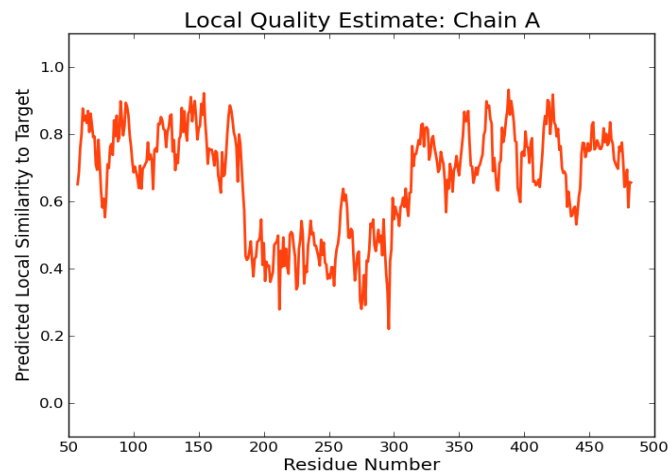
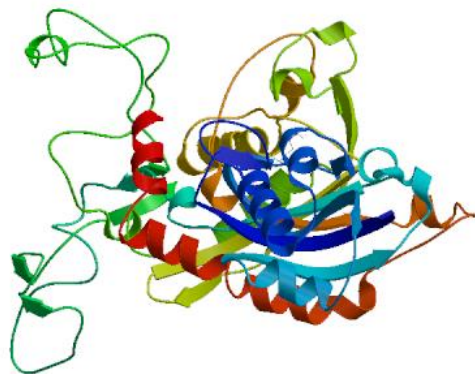
```

AT1G20370 & AT1G76120

- homologous modeling using Swiss-model
- Using AT1G20370's full length protein to search database

hPus1p's X-RAY DIFFRACTION structure

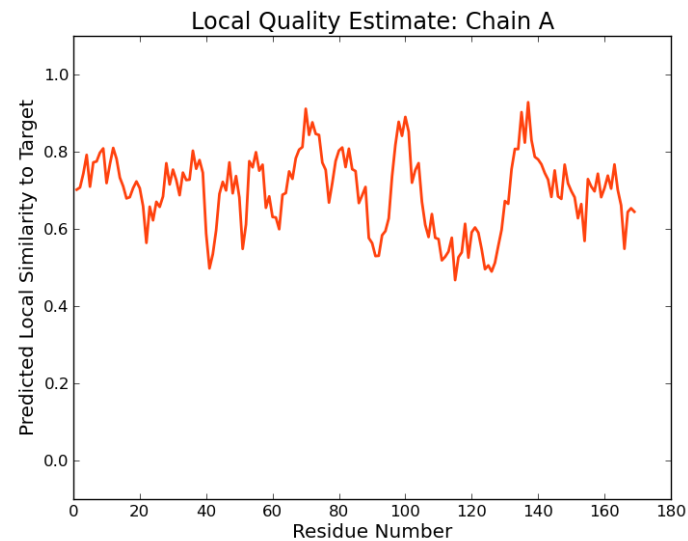
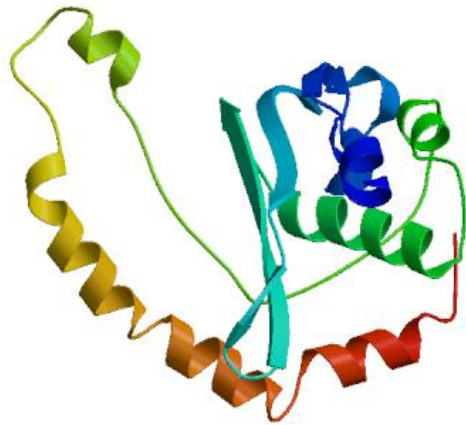
Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
4nz6.1.A	41.37	monomer	HHblits	X-ray	2.00Å	0.40	57 - 482	0.56	tRNA pseudouridine synthase A, mitochondrial



GMQE: 0.42

AT1G20370 & AT1G76120

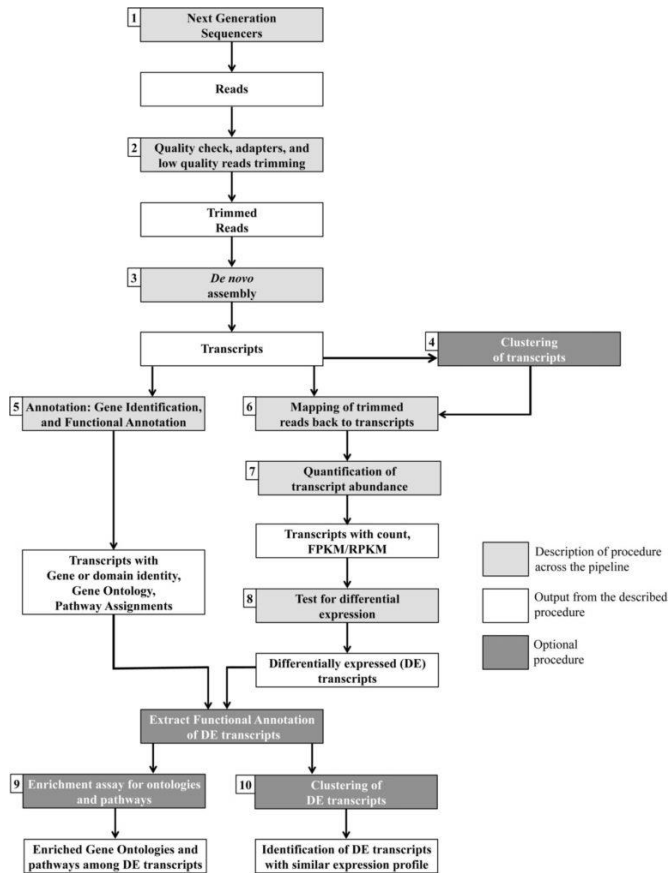
- homologous modeling using Swiss-model



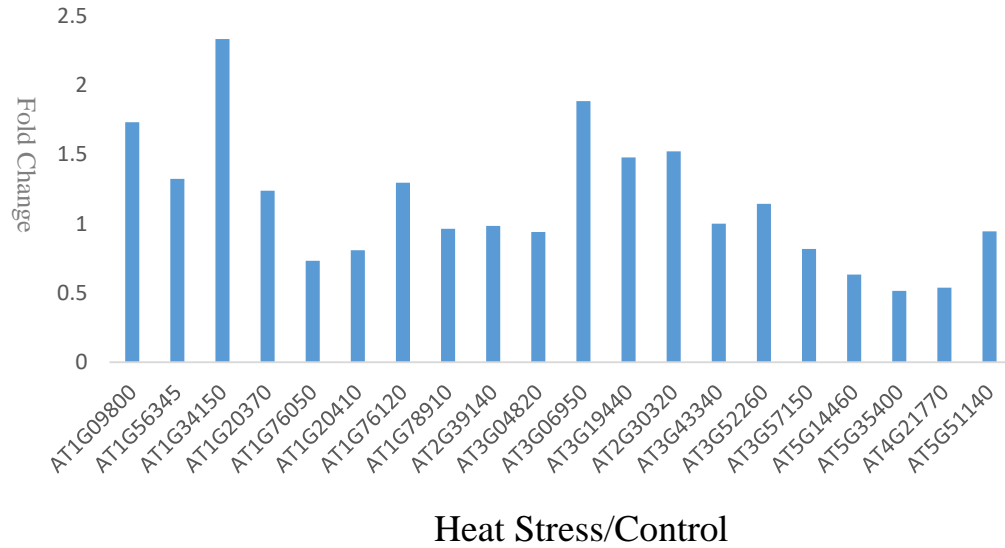
GMQE: 0.72

TruA Family

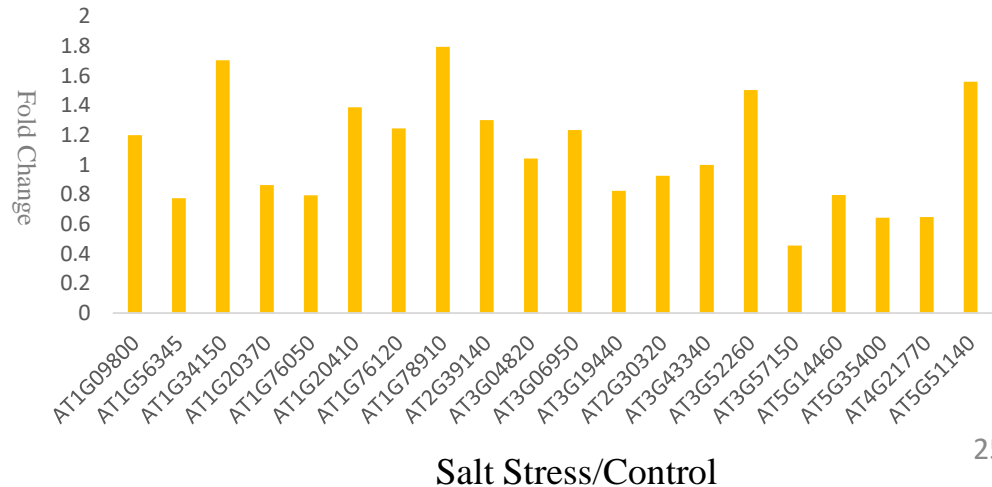
Arabidopsis pseudouridine synthase gene expression under stress



Heat Stress Induced Gene Expression Variation



Salt Stress Induced Gene Expression Variation



<http://www.rna-seqblog.com>

Acknowledgements

- Prof. Luo Jingchu
- PI Chengqi Yi
- PI Weiqiang Qian
- TA Lan Ke
- All the group members
- All the students in the class

A scenic view of a lake with autumn foliage and a pagoda in the background. The water is calm, reflecting the surrounding trees and the clear blue sky. The trees on the left bank are in various stages of autumn, with some showing vibrant orange and yellow leaves. In the distance, a tall, multi-tiered pagoda stands prominently against the sky. The overall atmosphere is peaceful and serene.

Thank you!