

# User guide

## 1.数据库简介

The Poly(A) Length & Composition Database 是一个专注于收集和分析 poly(A)尾特征的综合数据库。PALC-DB 提供人和小鼠卵母细胞、早期胚胎、组织以及细胞系的 poly(A)尾长度以及内部非 A 残基组成的详细信息，通过整合 RNA-seq、Ribo-seq 以及 poly(A)尾提取分析技术为科研人员提供一个以表观修饰之一的 poly(A)尾的角度去理解不同物种、组织、时期基因的表达和翻译变化，帮助科研人员理解 poly(A)尾修饰在健康和疾病中重要作用。

## 2 用户指南

### ① 数据库结构

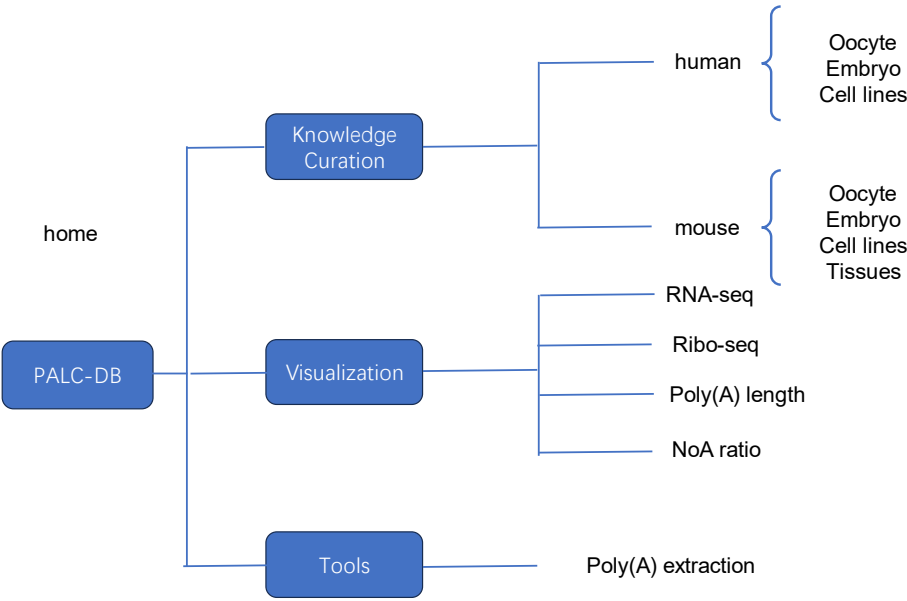
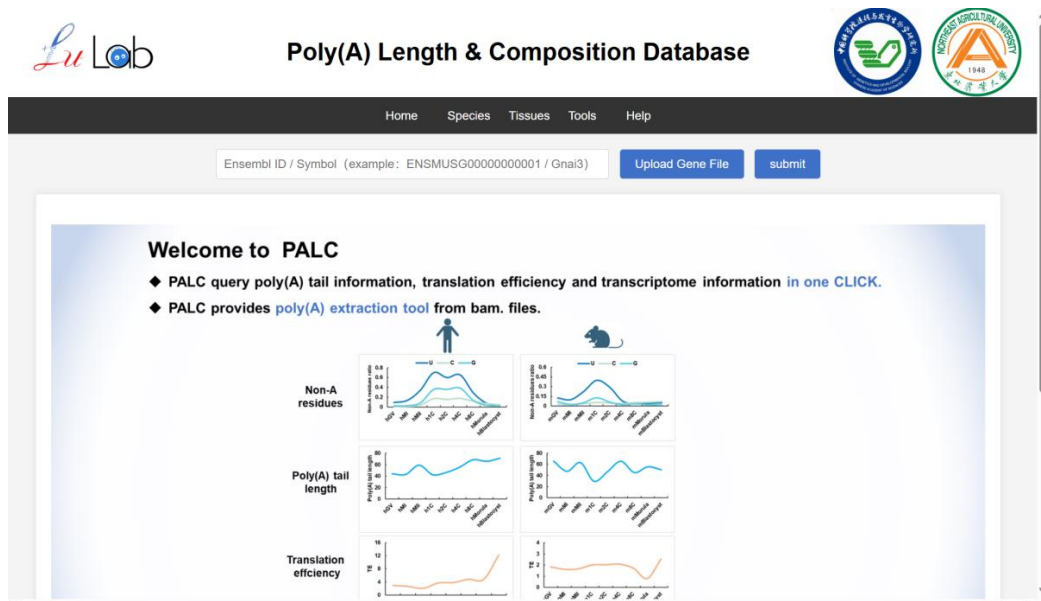
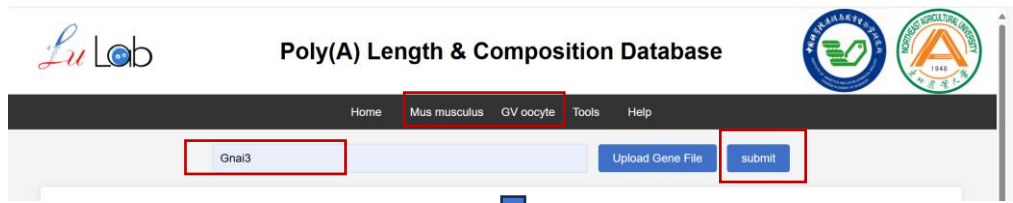


图 1 数据库结构

② 单基因检索



Search



Result

基因转录本水平，翻译水平，TE 水平，poly(A)长度及非 A 碱基组成表格

**results (total results: 1)**

species: **Mus musculus**

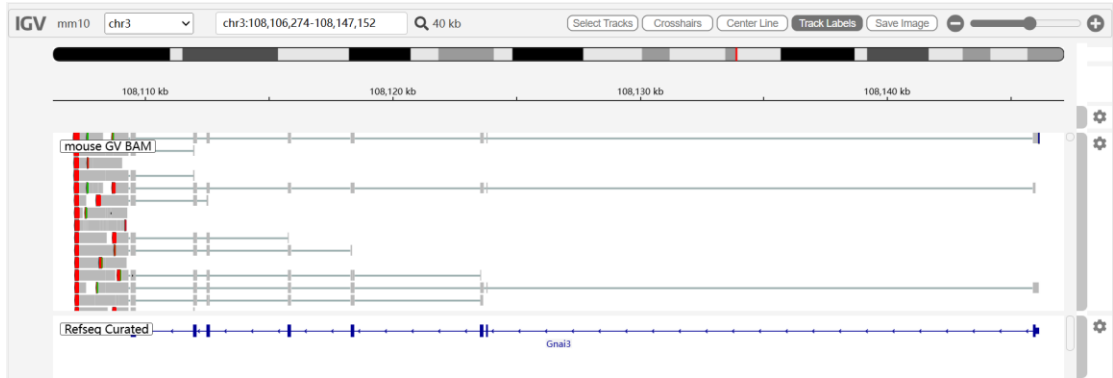
tissues: **GV oocyte**

Source Data: RNA-seq: [GSE165782](#) | Ribo-seq: [GSE165782](#) | PAL: [PRJCA006144](#)

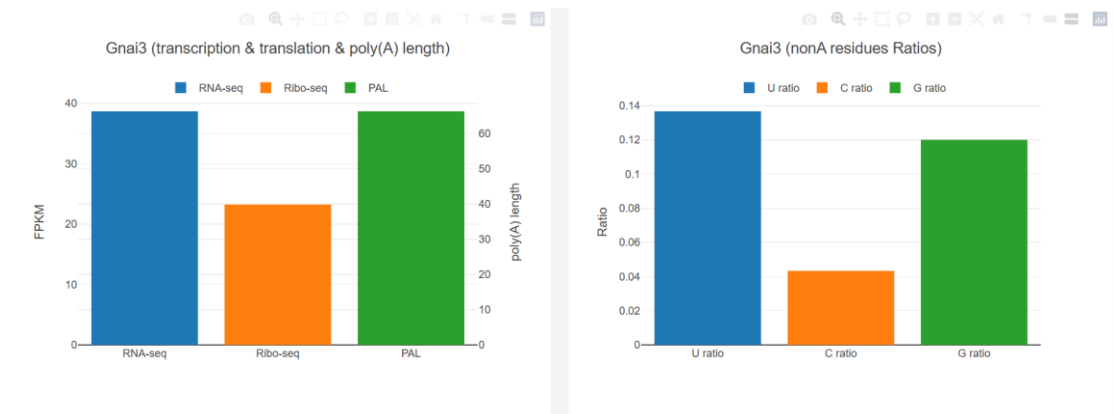
Ensembl ID	Symbol	Gene Type	RNAseq FPKM	Riboseq FPKM	TE	PAL	Uratio	Cratio	Gratio
ENSMUSG00000000001.4	<a href="#">Gnai3</a>	protein_coding	38.6468	23.2272	0.611076	66.2755	0.136667	0.0433333	0.12

download output (total: 1)

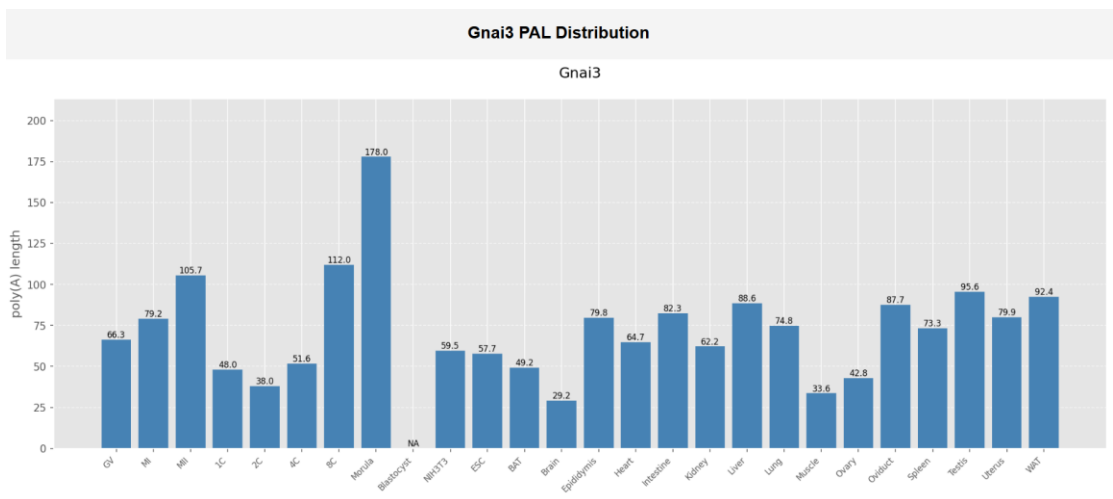
基因 poly(A)尾 IGV



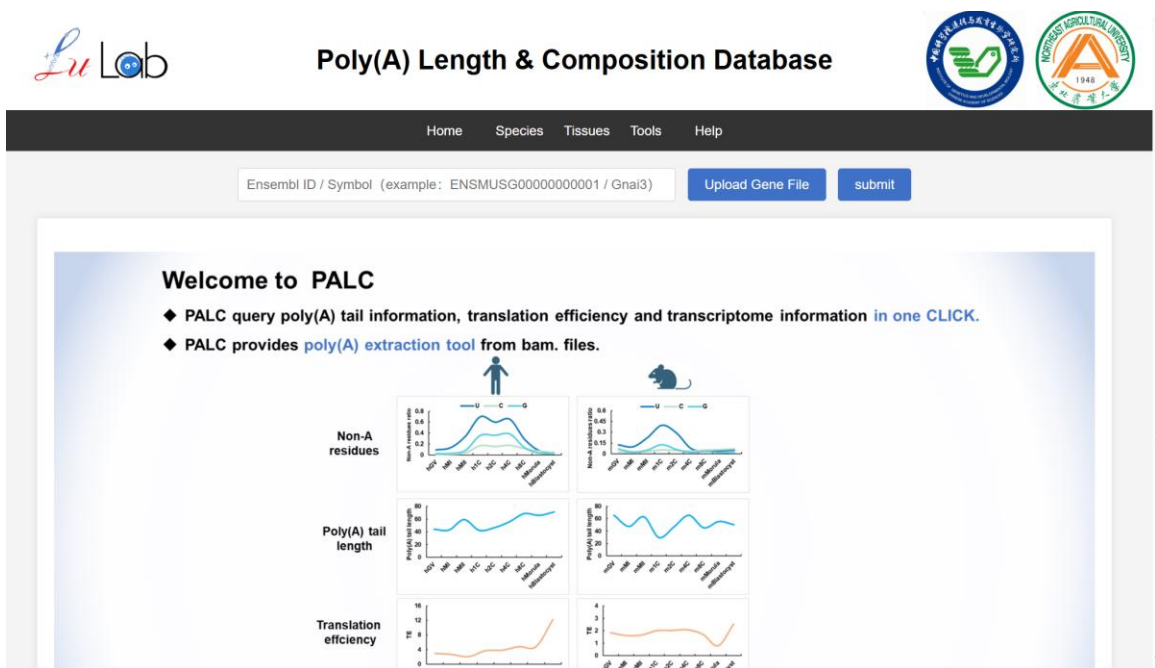
基因转录本水平，翻译水平，TE 水平，poly(A)长度及非 A 碱基组成柱状图



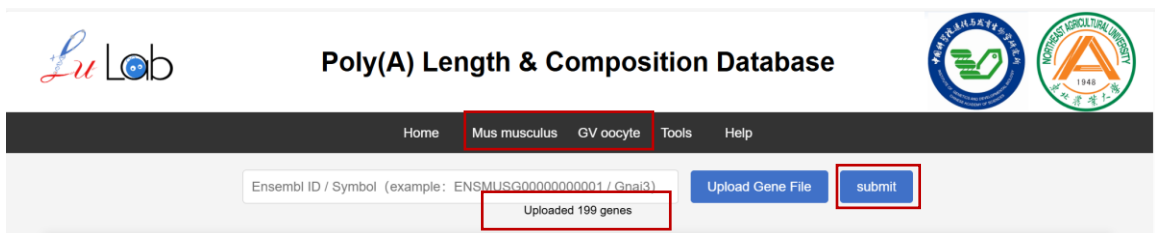
基因在数据库所有组织中的 poly(A)尾长度分布



③ 多基因检索



Search



result

基因转录本水平，翻译水平，TE 水平，poly(A)长度及非 A 碱基组成表格

results (total results: 194)

species: Mus musculus

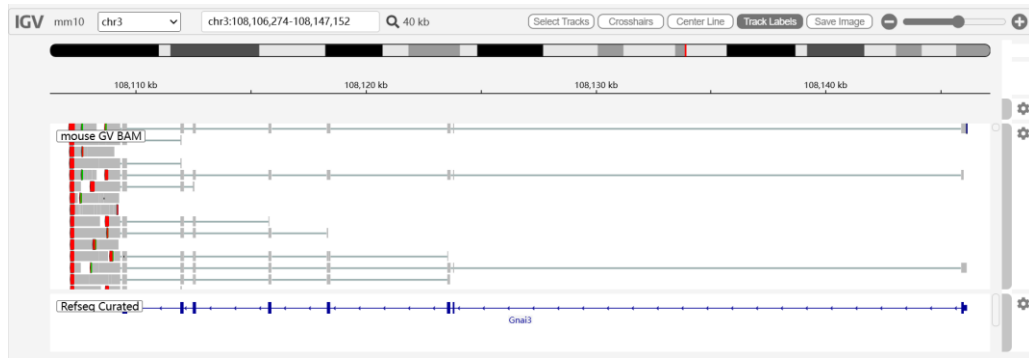
tissues: GV oocyte

Source Data: RNA-seq: [GSE165782](#) | Ribo-seq: [GSE165782](#) | PAL: [PRJCA006144](#)

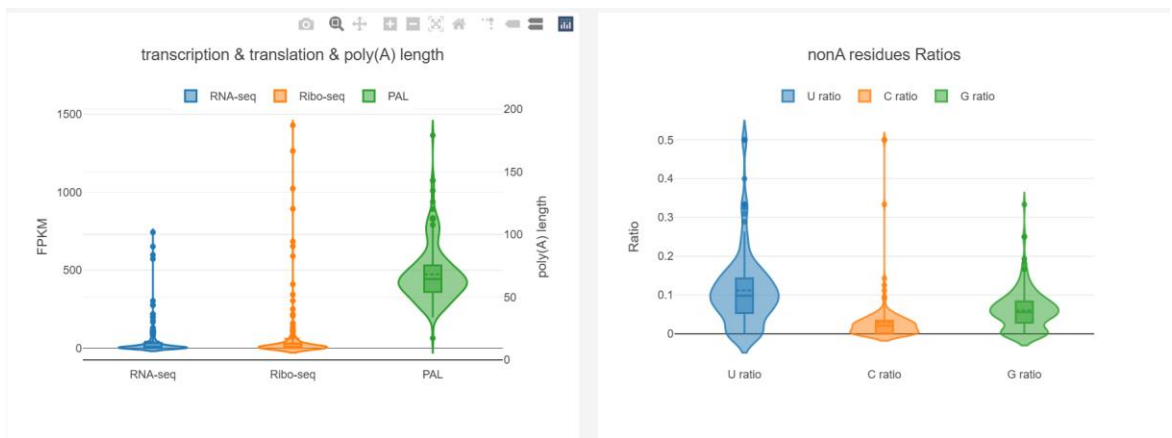
Ensembl ID	Symbol	Gene Type	RNAseq FPKM	Riboseq FPKM	TE	PAL	Uratio	Cratio	Gratio
ENSMUSG000000000001.4	Gnai3	protein_coding	38.6468	23.2272	0.611076	66.2755	0.136667	0.0433333	0.12
ENSMUSG000000000002.15	Cdc45	protein_coding	48.841	3.78097	0.0959244	48.9078	0.0875	0.009375	0.071875
ENSMUSG000000000003.17	Scml2	protein_coding	62.3624	1.91768	0.0460475	42.332	0.178451	0.030303	0.040404
ENSMUSG000000000005.7	Narf	protein_coding	5.90423	57.0232	8.40401	105.846	0.08	0.0533333	0.0933333
ENSMUSG000000000007.8	Klf6	protein_coding	0.824941	0.623529	0.889634	46.2351	0.166667	0	0.333333
ENSMUSG000000000008.16	Scmh1	protein_coding	26.5152	36.9145	1.37795	64.575	0.105528	0.0150754	0.0904523
ENSMUSG000000000008.7	Cox5a	protein_coding	572.647	218.392	0.382451	65.6078	0.0989399	0.00353357	0.0424028
ENSMUSG000000000009.12	Tbx4	protein_coding	19.8654	8.1677	0.439373	52.451	0.15	0.0166667	0.0333333
ENSMUSG0000000000126.11	Wnt9a	protein_coding	0.125559	0.273093	1.13108	40.232	0	0	0

download output (total: 194)

## 基因 poly(A)尾 IGV



## 基因转录本水平,翻译水平,TE 水平,poly(A)长度及非 A 碱基组成小提琴图



## ④ 提取 poly(A)尾

**LuLob Poly(A) Length & Composition Database**

Home Species Tissues Tools Help

Ensembl ID / Symbol (example: ENSMUSG00000000001 / Gna13)

**Welcome to PALC**

- ◆ PALC query poly(A) tail information, translation efficiency and transcriptome information in one CLICK.
- ◆ PALC provides poly(A) extraction tool from bam. files.

Non-A residues

Poly(A) tail length

Translation efficiency

Search

result

[illegible]

The figure is a line plot titled 'test.sort' showing the 'Fraction of CCS reads' on the y-axis (ranging from 0.00 to 0.12) against 'Poly(A) tail length (nt)' on the x-axis (ranging from 0 to 240). The plot displays a series of vertical steps, indicating the fraction of reads for each integer length of the poly(A) tail. The highest fraction is at 0 nt (approx. 0.12). There are smaller peaks at various lengths, including 5 nt (approx. 0.05), 10 nt (approx. 0.05), 30 nt (approx. 0.02), 40 nt (approx. 0.02), 50 nt (approx. 0.03), 60 nt (approx. 0.01), 70 nt (approx. 0.03), 80 nt (approx. 0.02), 90 nt (approx. 0.03), 100 nt (approx. 0.01), 110 nt (approx. 0.02), 120 nt (approx. 0.01), 130 nt (approx. 0.02), 140 nt (approx. 0.02), 150 nt (approx. 0.01), 160 nt (approx. 0.01), 170 nt (approx. 0.01), 180 nt (approx. 0.01), 190 nt (approx. 0.01), 200 nt (approx. 0.01), 210 nt (approx. 0.01), and 220 nt (approx. 0.01). The fraction of reads generally decreases as the tail length increases, with some fluctuations.

3.cite

4.contact

如果有任何问题请联系: [ywzhang12345@163.com](mailto:ywzhang12345@163.com)