

Aurelia aurita: ПОИСК НОВЫХ ГЕНОВ

Анна Гончар,

Кафедра зоологии беспозвоночных СПбГУ

anya.gonchar@gmail.com

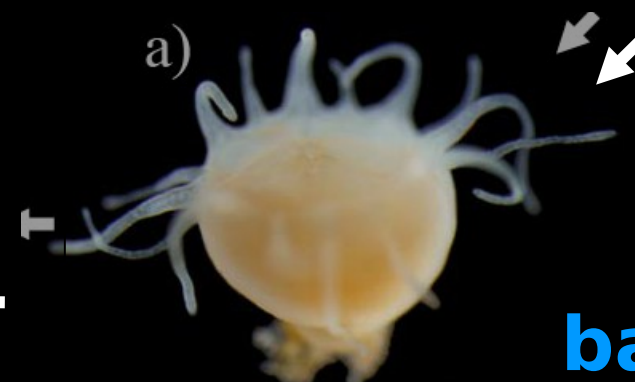
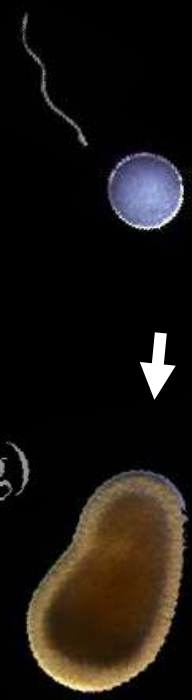
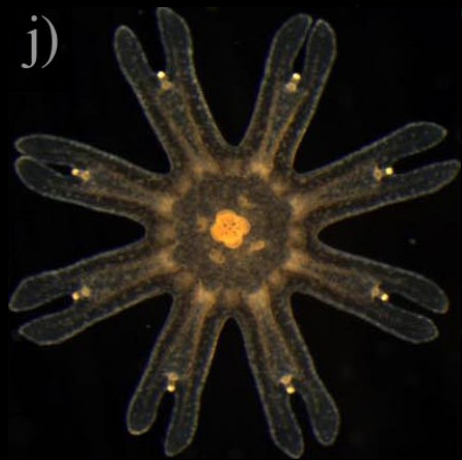
Научный руководитель: Павел Добрынин,

Центр геномной биоинформатики им. Т. Г. Добржанского



Transcriptome: metamorphosis regulation

(Submitted: Current Biology)



background

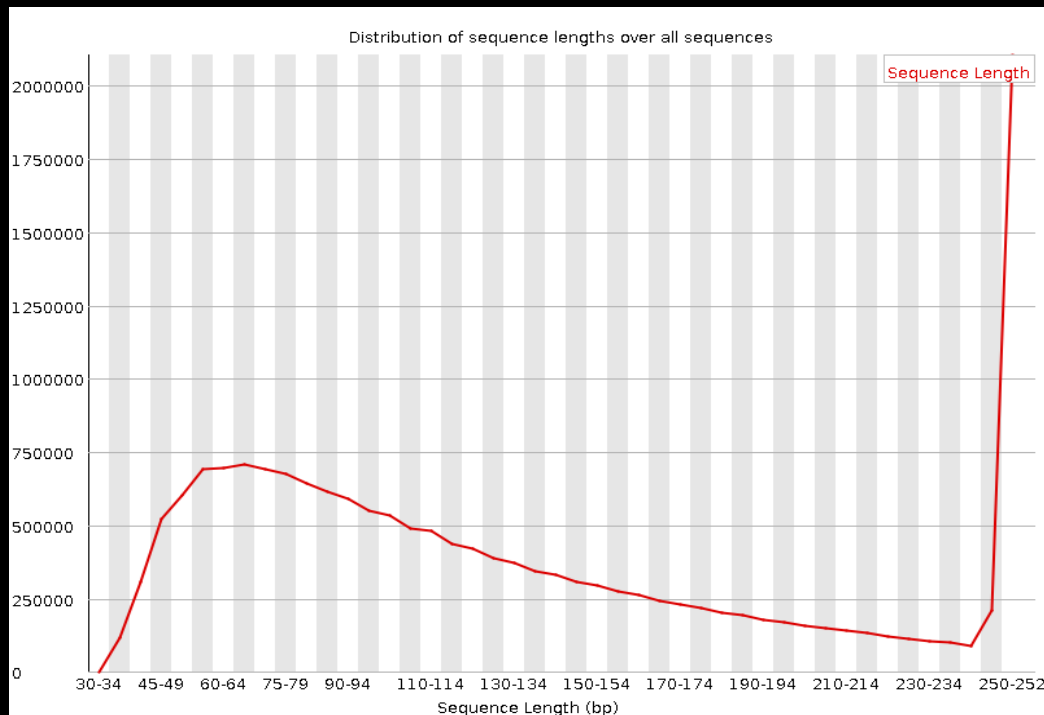
Aurelia aurita expected genome size: 713 Mb
DNA samples: *A. aurita* (Baltic sea)

Library preparation: Nextera kit
Illumina MiSeq: 2 runs

Sequences: coverage 4x,

FastQC: poor quality

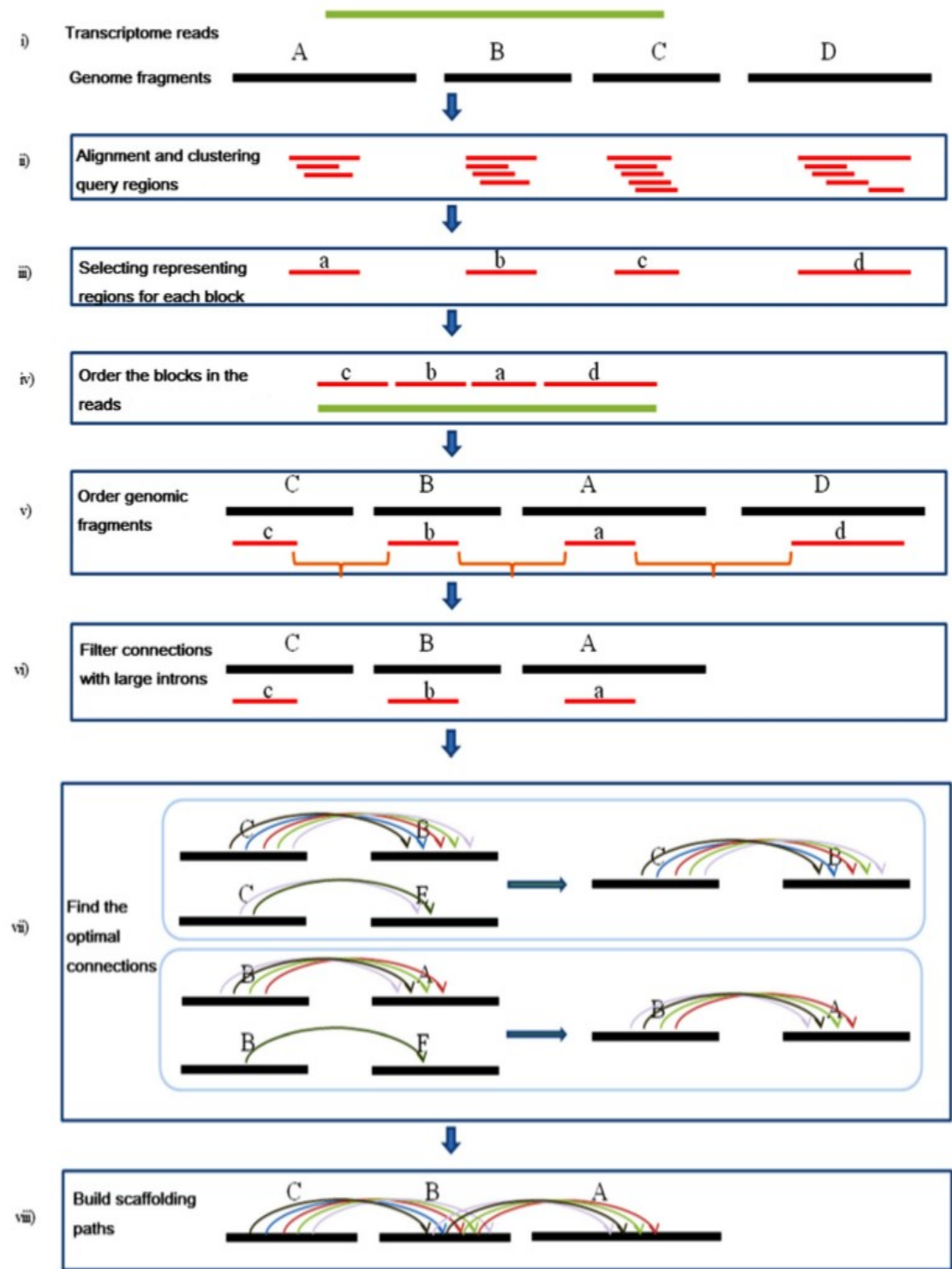
Assembly: SPADES (no normalization)
Assembly: IDBA (with normalization)



L_RNA_Scaffolder

BLAT genome
transcriptome

input .psl
output .fasta

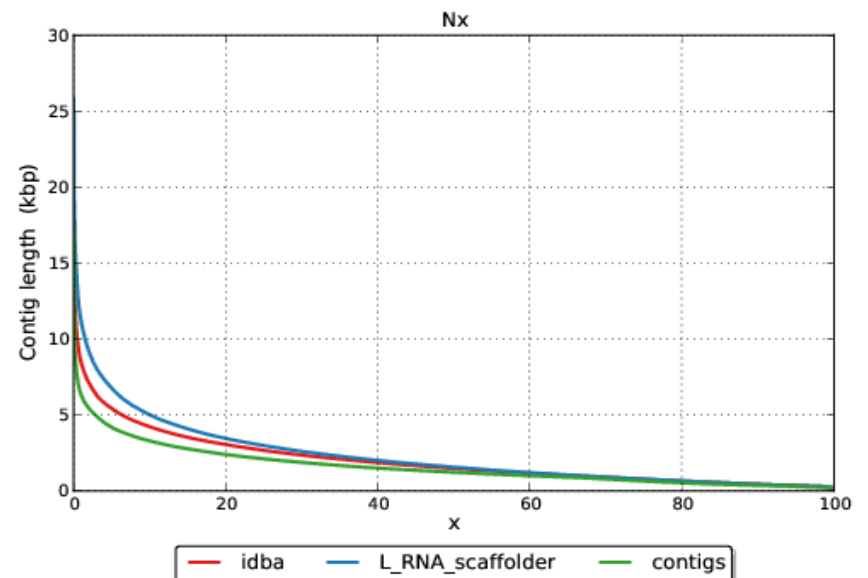
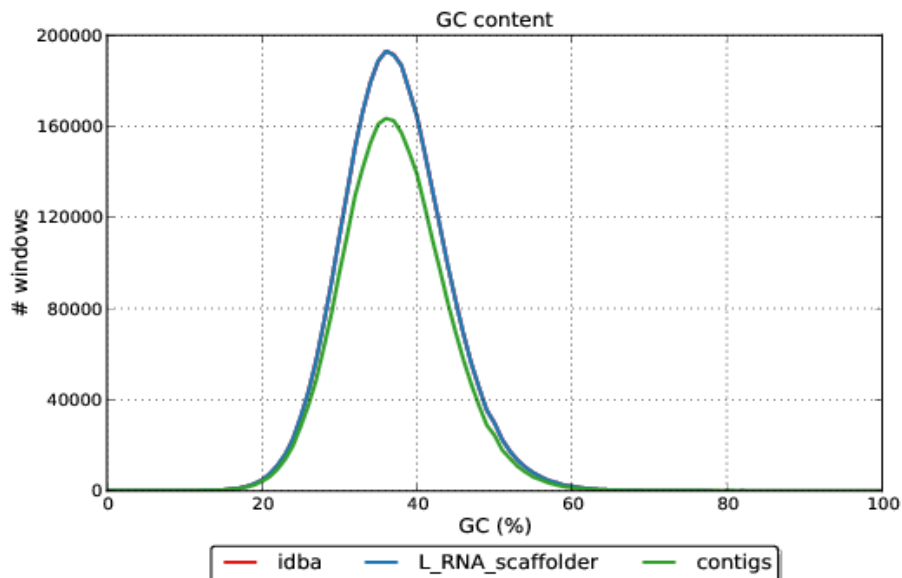
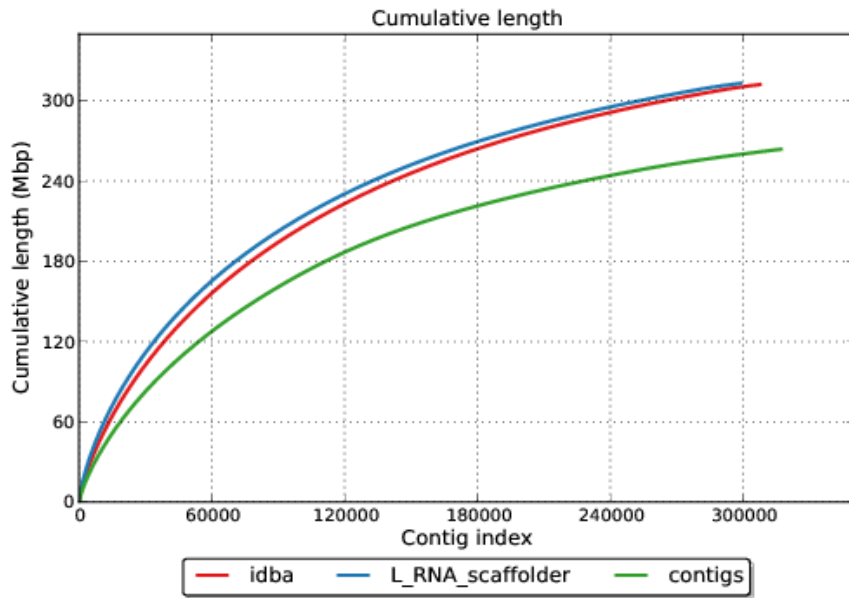


Comparing assemblies with QUAST

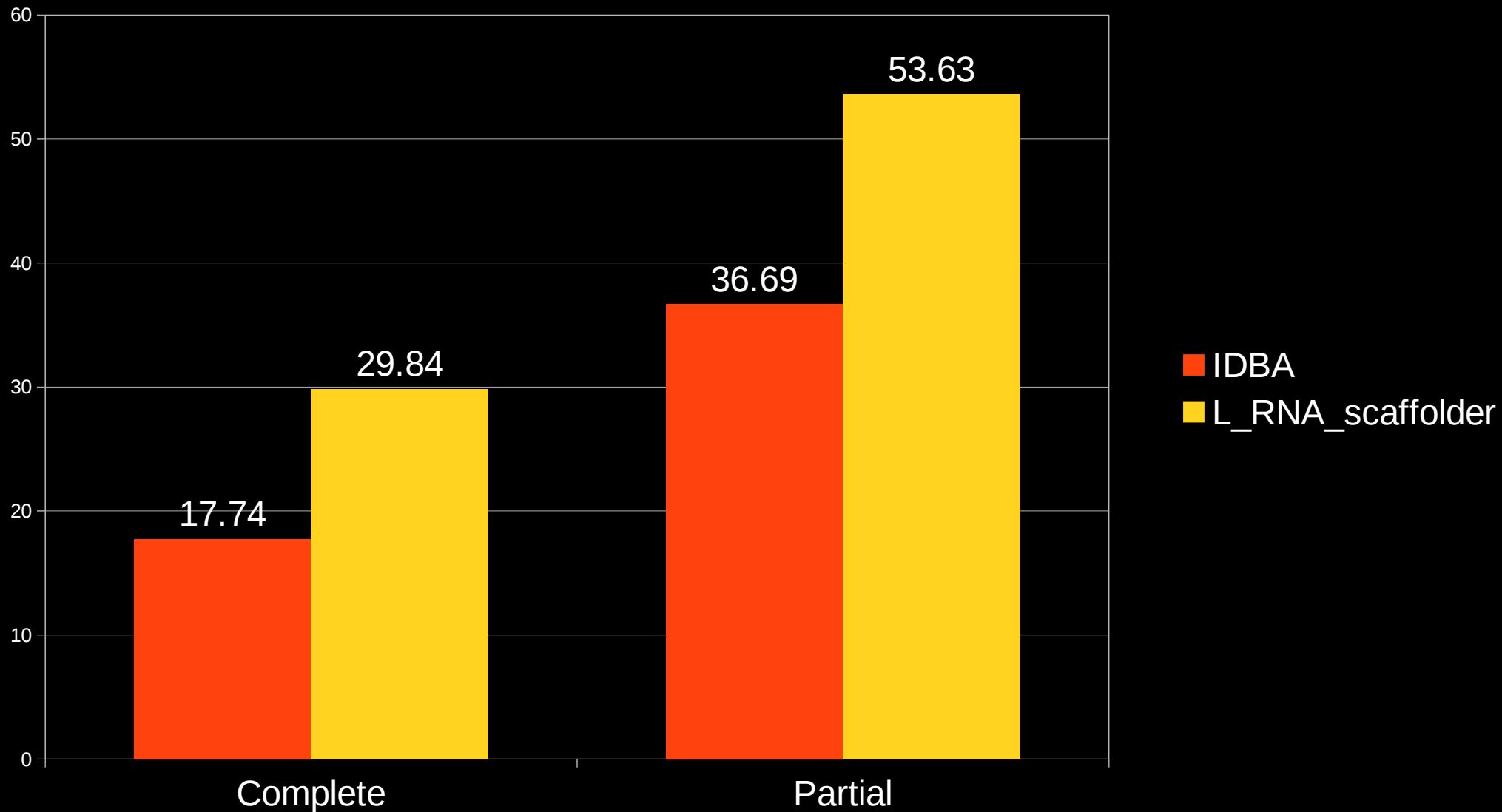
IDBA (with normalization)

L_RNA_scaffolder

SPADES (without normalization)



CEGMA: assembly assessment based on 458 core proteins present in a wide range of taxa (% completeness)



= An initial goal to search for genes has been postponed by a set of goals to obtain better assembly

Further steps:

- **Deeper sequencing**
- **Jumping libraries**
- **Optic maps**
- **Third generation DNA nanoball sequencing technology (Complete Genomics)**

A beginner's guide to eukaryotic genome annotation

Mark Yandell and Daniel Ence