

Геномика диатомовых водорослей

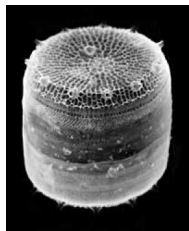
Содержание

- OUC (ornithine-urea cycle) in diatoms
- Methylome of *Phaeodactylum tricornutum*
- Small RNA transcriptome of *Thalassiosira pseudonana*
- Nuclear genome sequence of *Synedra acus*

Диатомовые водоросли: СИСТЕМАТИКА

centric diatoms:

*Thalassiosira
pseudonana*



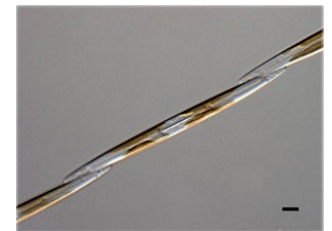
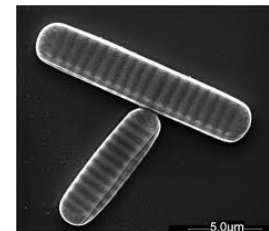
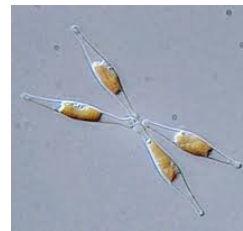
araphid pennates:

Synedra acus



raphid pennates:

Phaeodactylum tricornutum
Fragilariopsis sp.
Pseudo-nitzschia multiseries

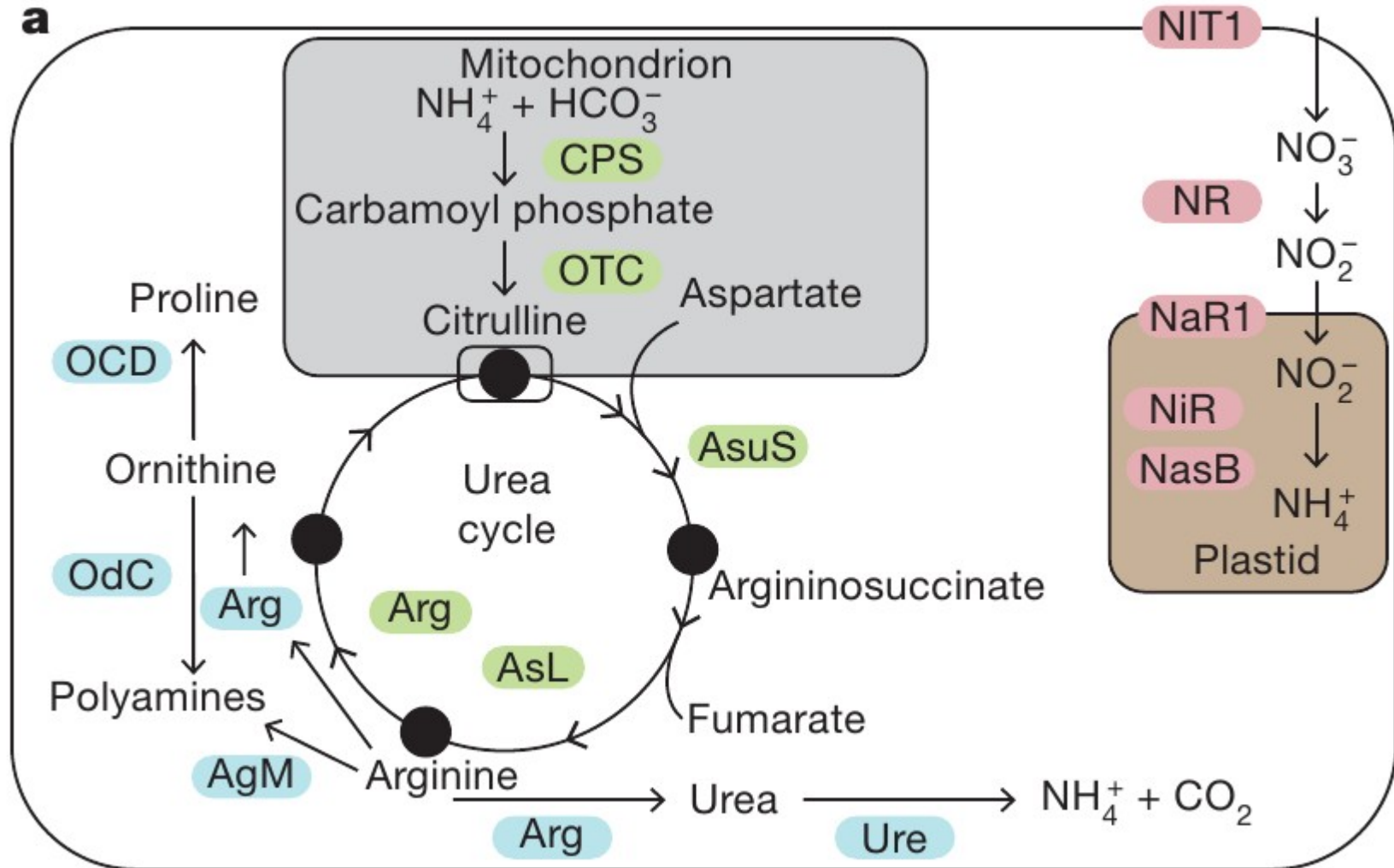


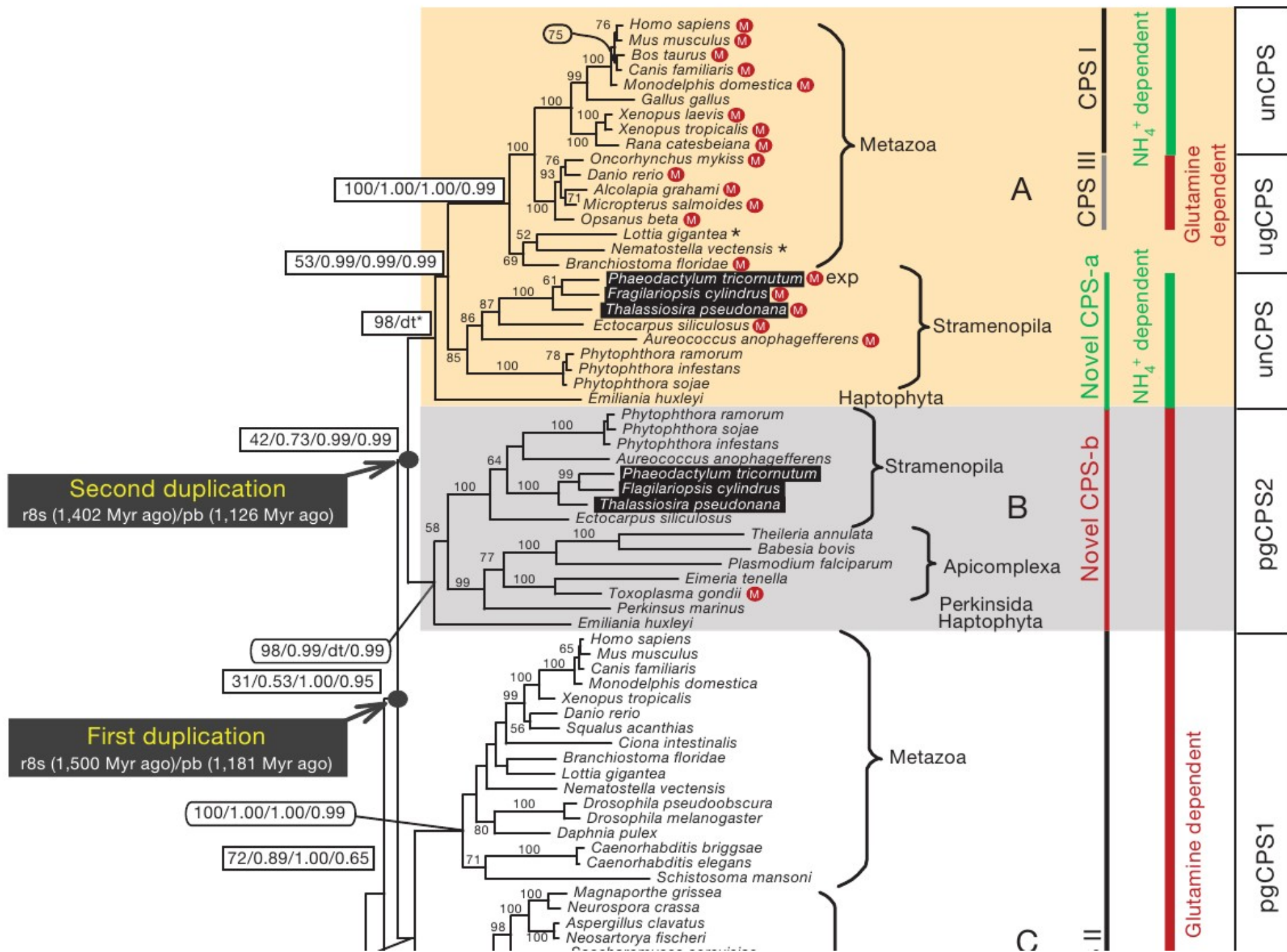
LETTER

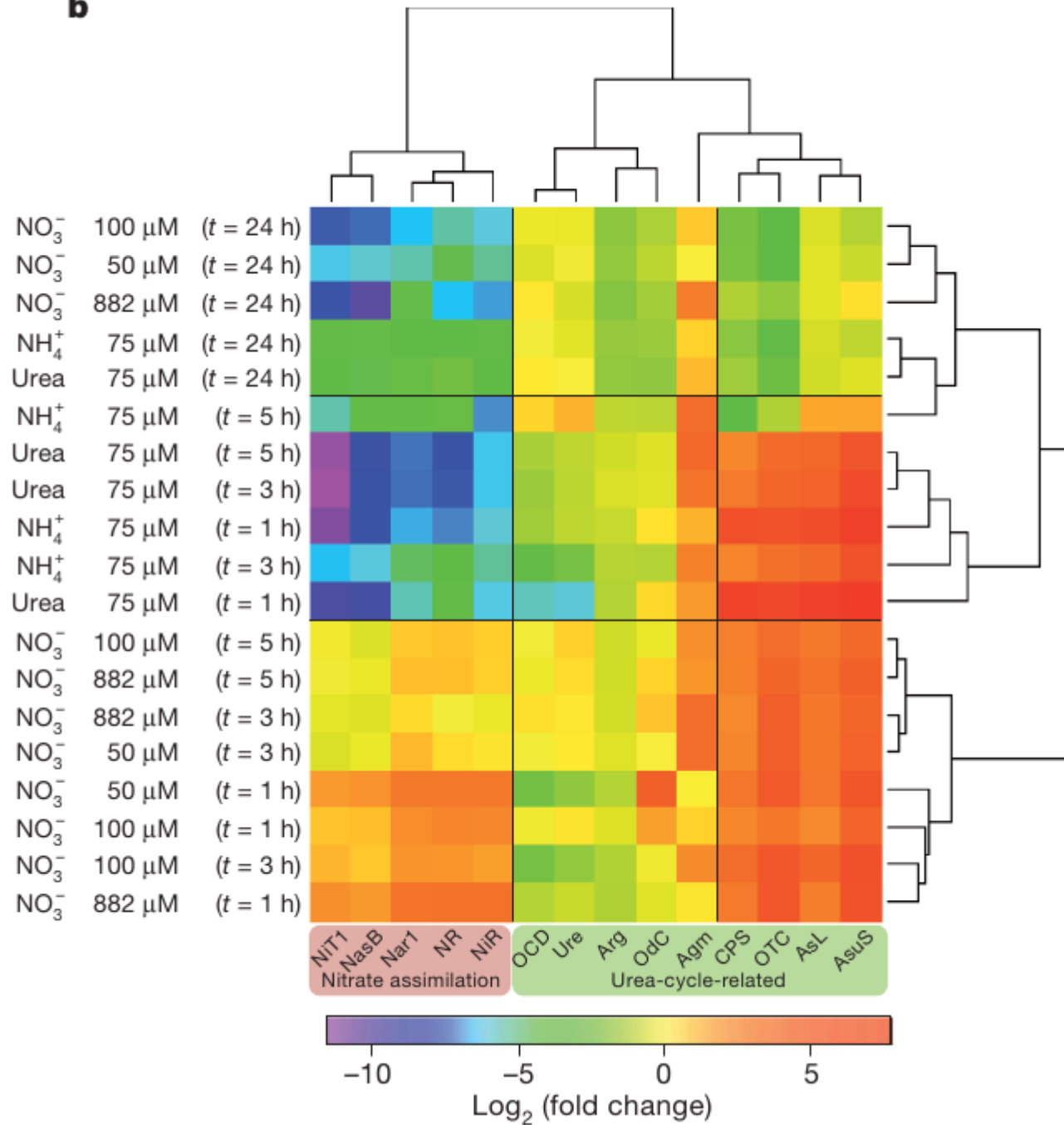
doi:10.1038/nature10074

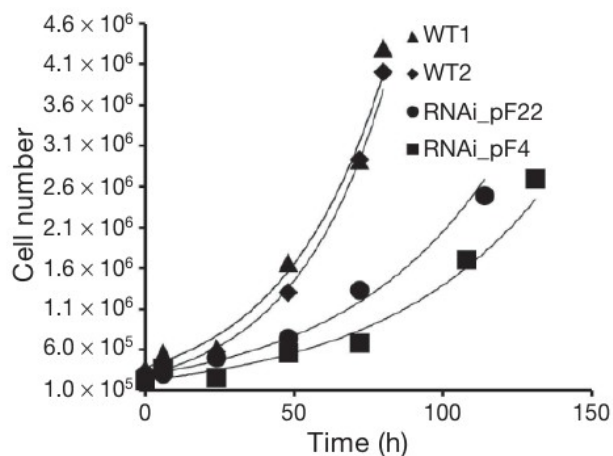
Evolution and metabolic significance of the urea cycle in photosynthetic diatoms

Andrew E. Allen^{1,2}, Christopher L. Dupont¹, Miroslav Oborník³, Aleš Horák³, Adriano Nunes-Nesi⁴†, John P. McCrow¹, Hong Zheng¹, Daniel A. Johnson¹, Hanhua Hu²†, Alisdair R. Fernie⁴ & Chris Bowler²

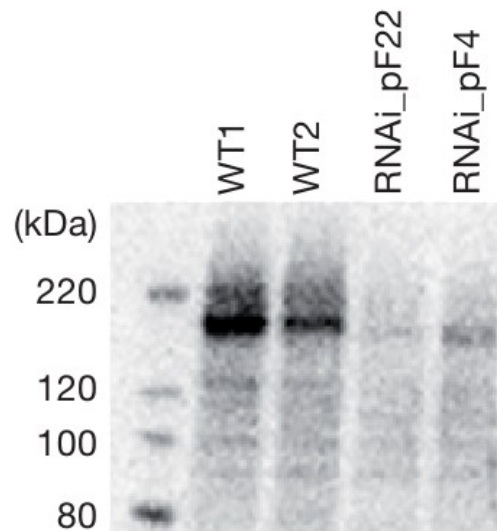
a



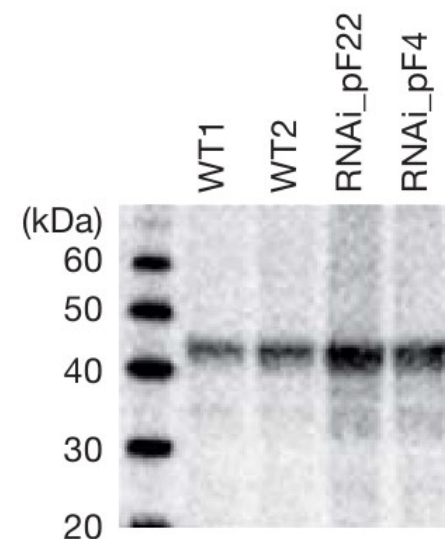
b



Growth curves

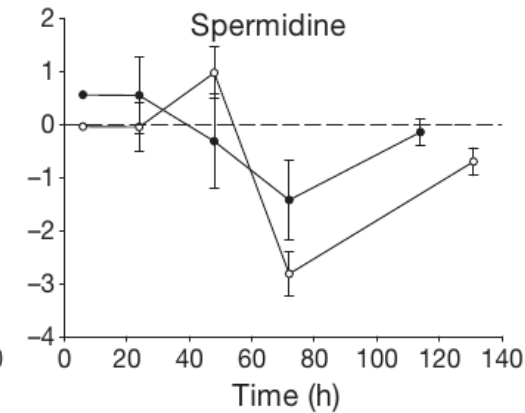
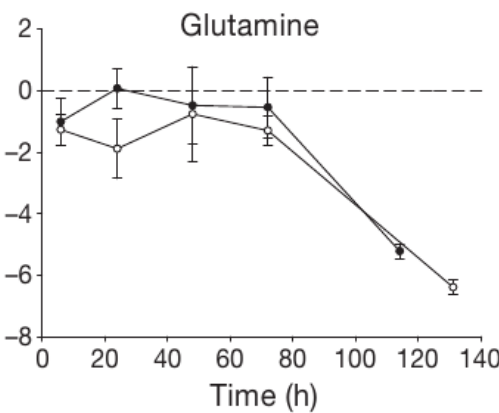
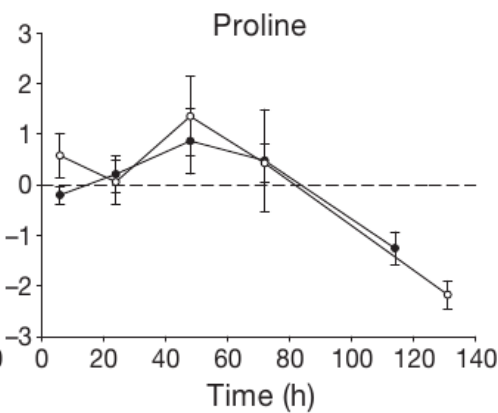
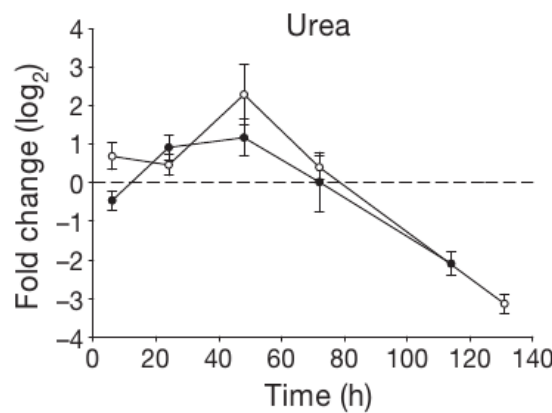
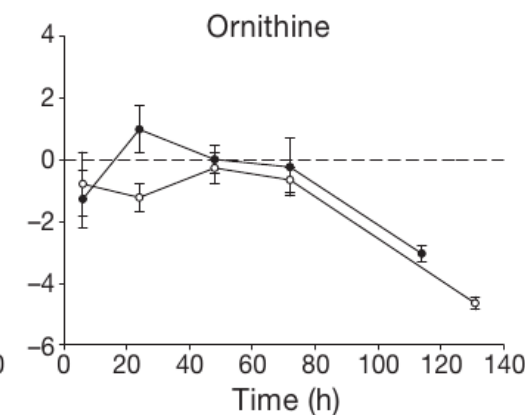
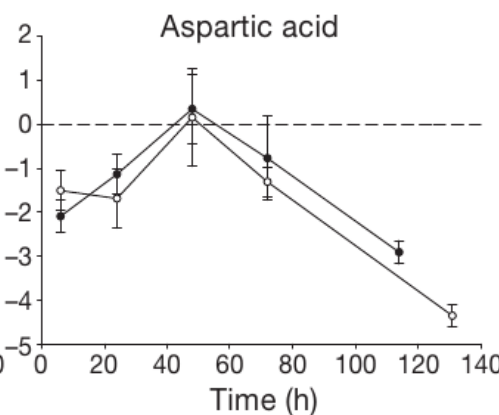
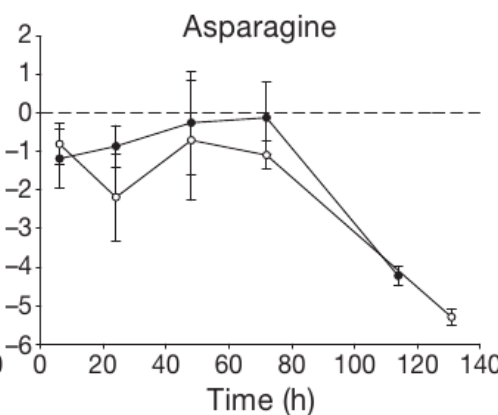
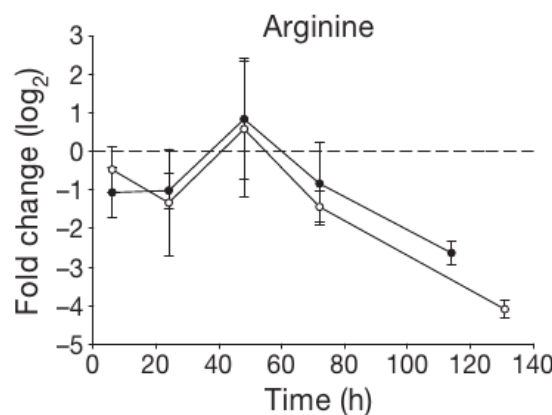


Western-Blot, ugCPS

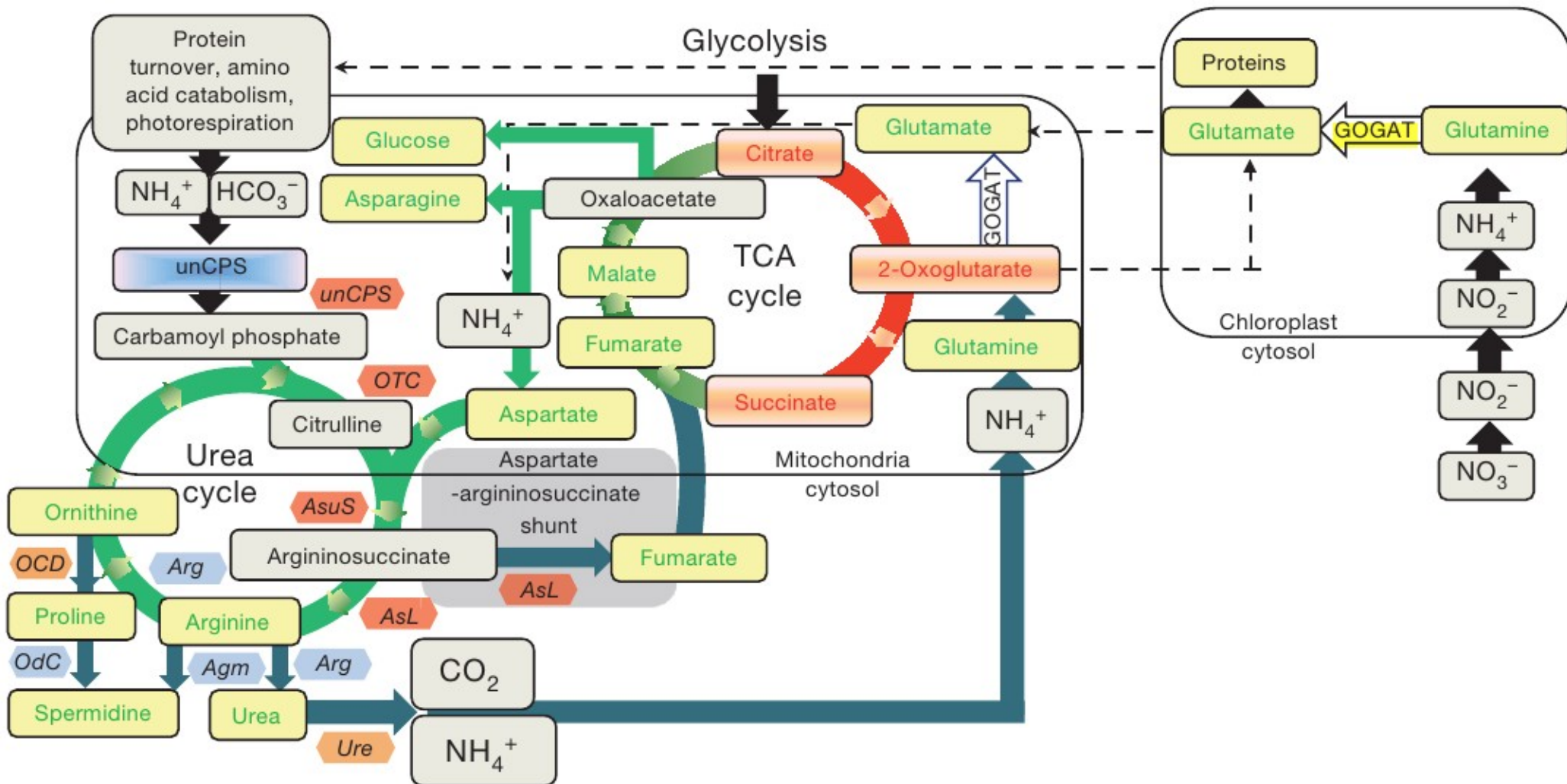


Western-Blot, AO

Urea-cycle-related



Overview of the roles of unCPS and the diatom urea cycle



ARTICLE

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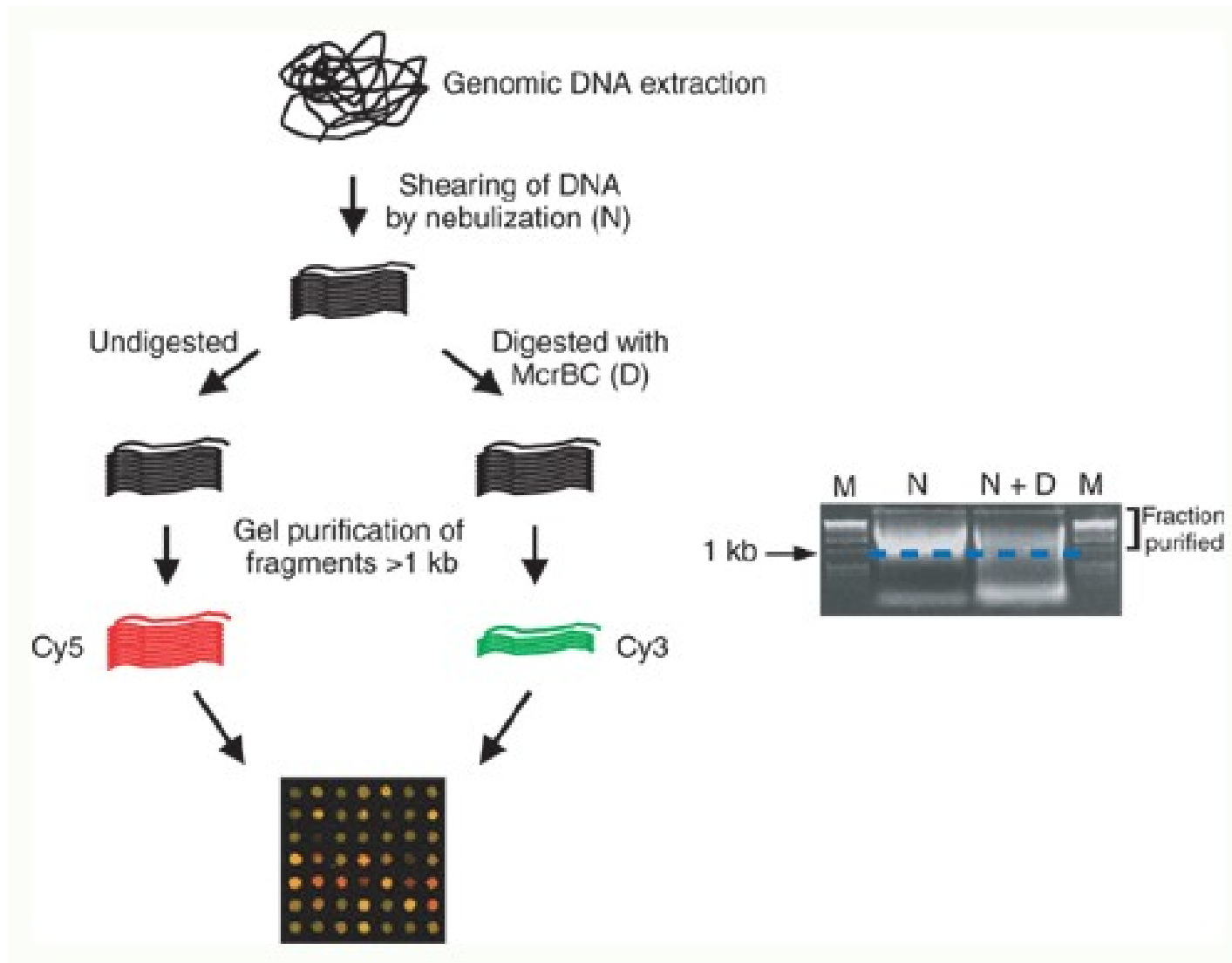
DOI: 10.1038/ncomms3091

OPEN

Insights into the role of DNA methylation in diatoms by genome-wide profiling in *Phaeodactylum tricornutum*

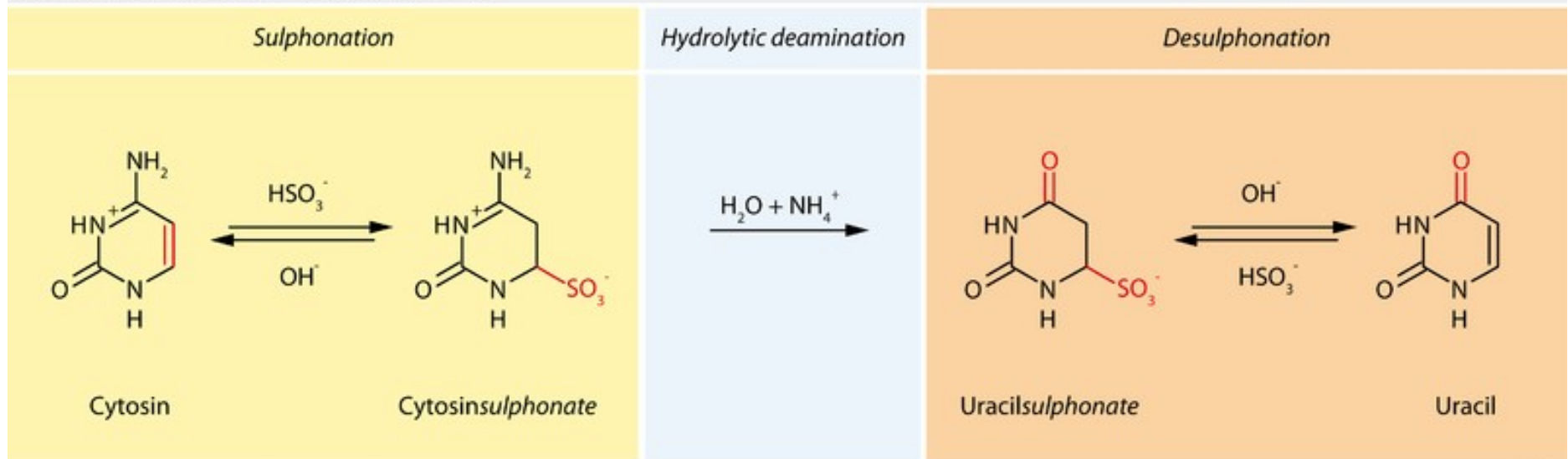
Alaguraj Veluchamy^{1,*}, Xin Lin^{1,*†}, Florian Maumus^{1,†}, Maximo Rivarola^{2,†}, Jaysheel Bhavsar², Todd Creasy², Kimberly O'Brien², Naomi A. Sengamalay², Luke J. Tallon², Andrew D. Smith³, Edda Rayko¹, Ikhlak Ahmed¹, Stéphane Le Crom⁴, Gregory K. Farrant¹, Jean-Yves Sgro⁵, Sue A. Olson⁶, Sandra Splinter Bondurant⁵, Andrew Allen⁷, Pablo D. Rabinowicz², Michael R. Sussman⁸, Chris Bowler¹ & Leïla Tirichine¹

McrBC and Tiling Array profiling



Bisulfite conversion and sequencing

Bisulfite-mediated conversion of cytosine to uracil



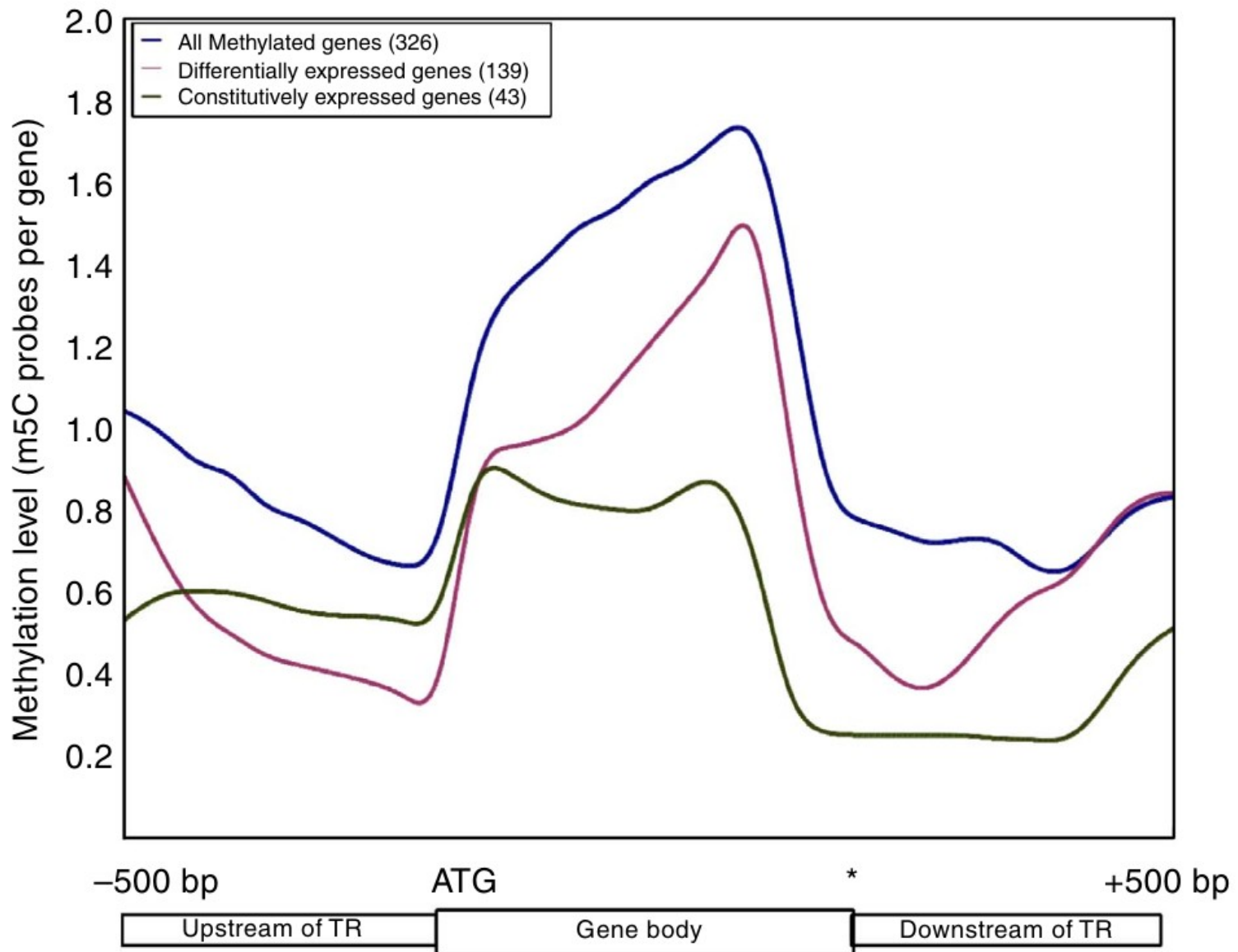
Tollefsbol T (ed.): *Handbook of Epigenetics: The New Molecular and Medical Genetics*. 1st edition. London, San Diego: Academic Press, 2011.

FD

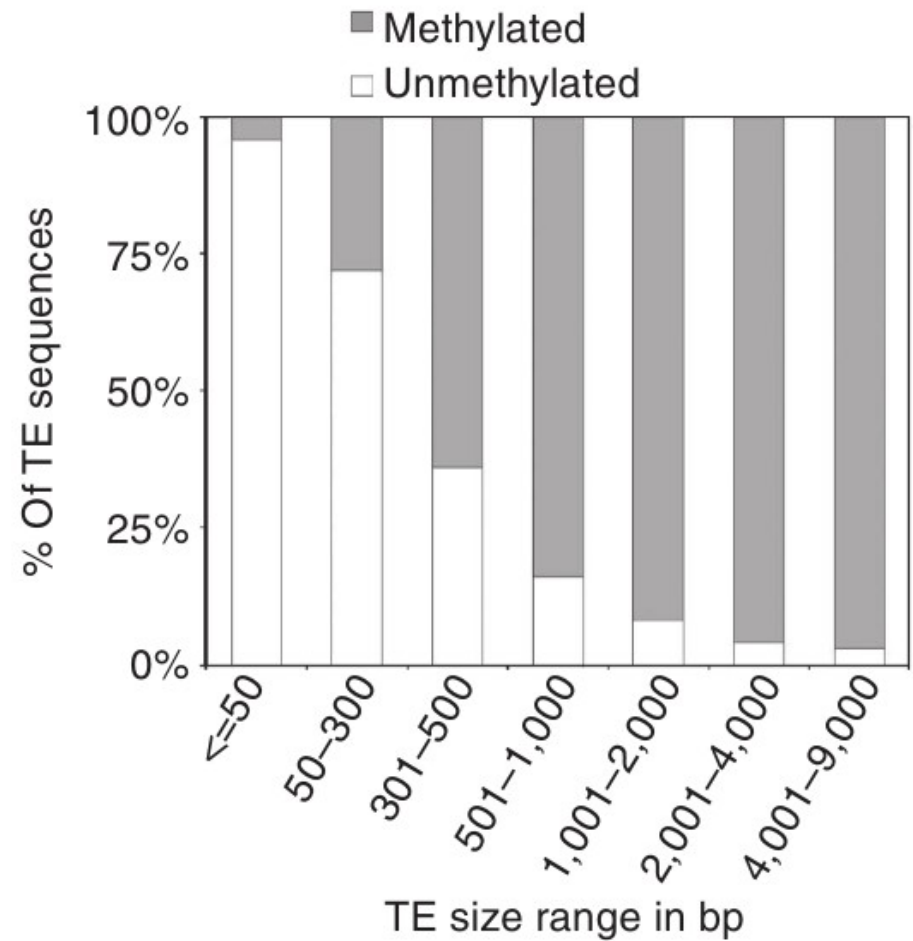
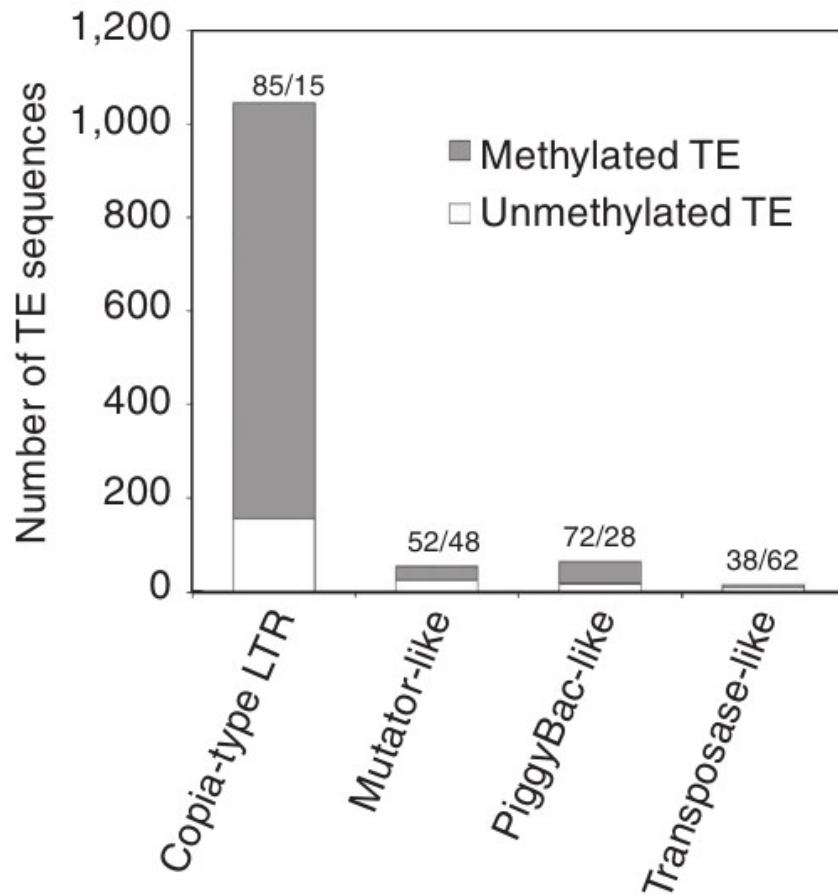
Overall statistics

- Обнаружено 3 887 HMRs (~1.4Mb, 5% генома)
- 39% HMRs картируются на TEs
- Значительная часть HMRs картируется на неповторяющиеся области генома:
 - 587 HMRs – межгенные области
 - 505 HMRs – области генов
 - 604 HMRs – области генов, перекрывающихся с TEs

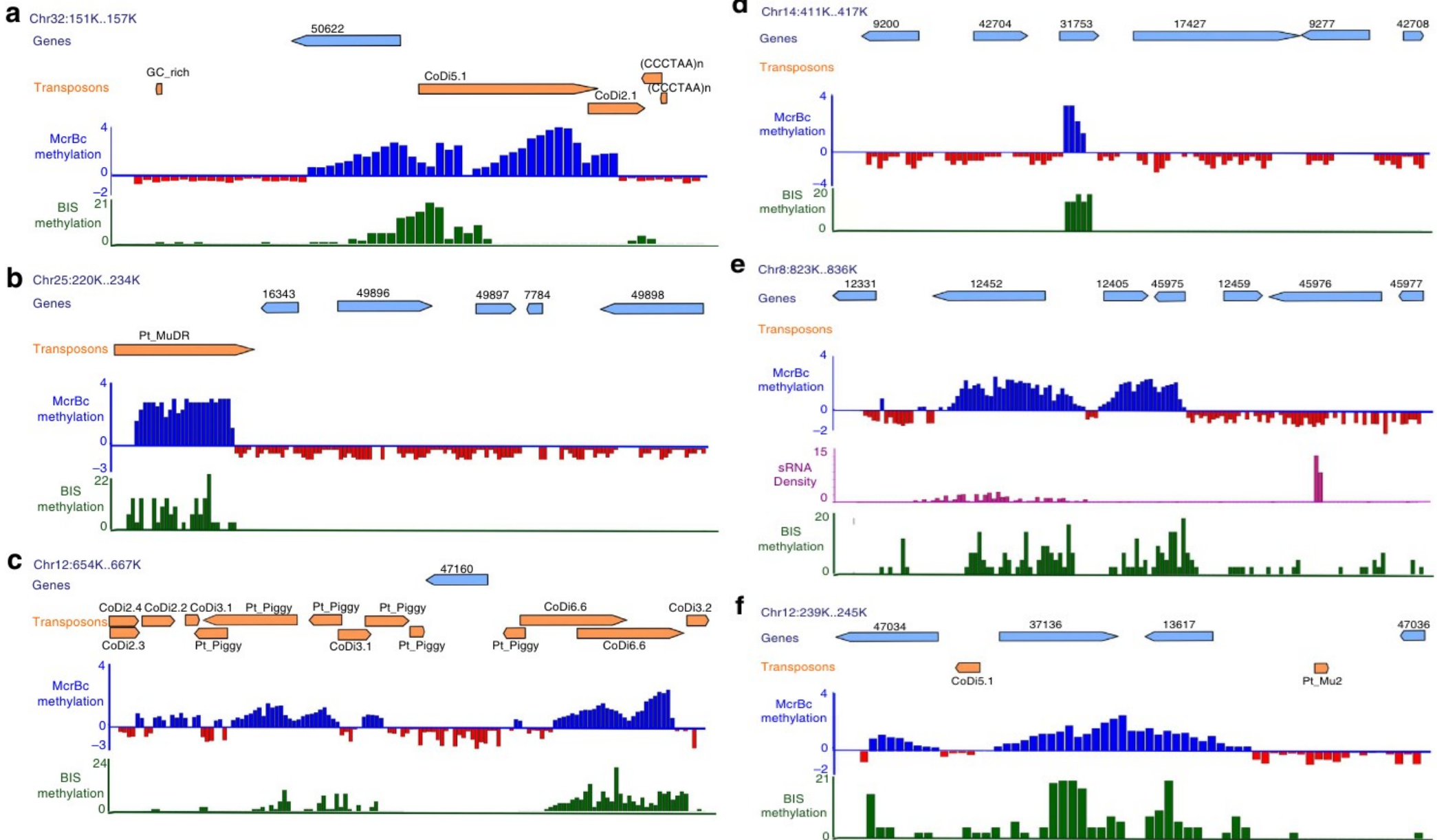
Methylation profiles of genes



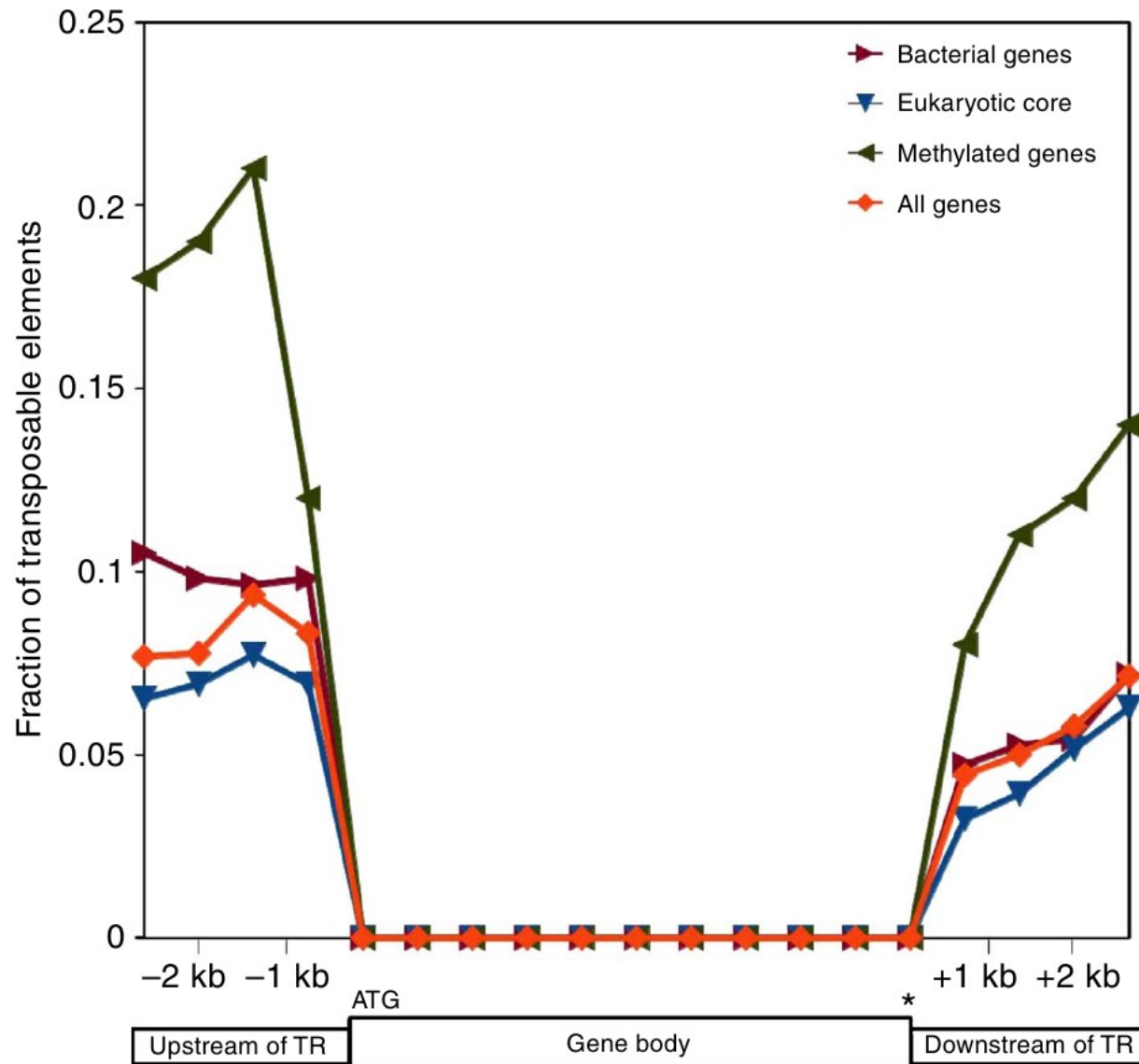
DNA methylation in TEs



Methylation patterns of selected genes



Distribution of TEs around genes

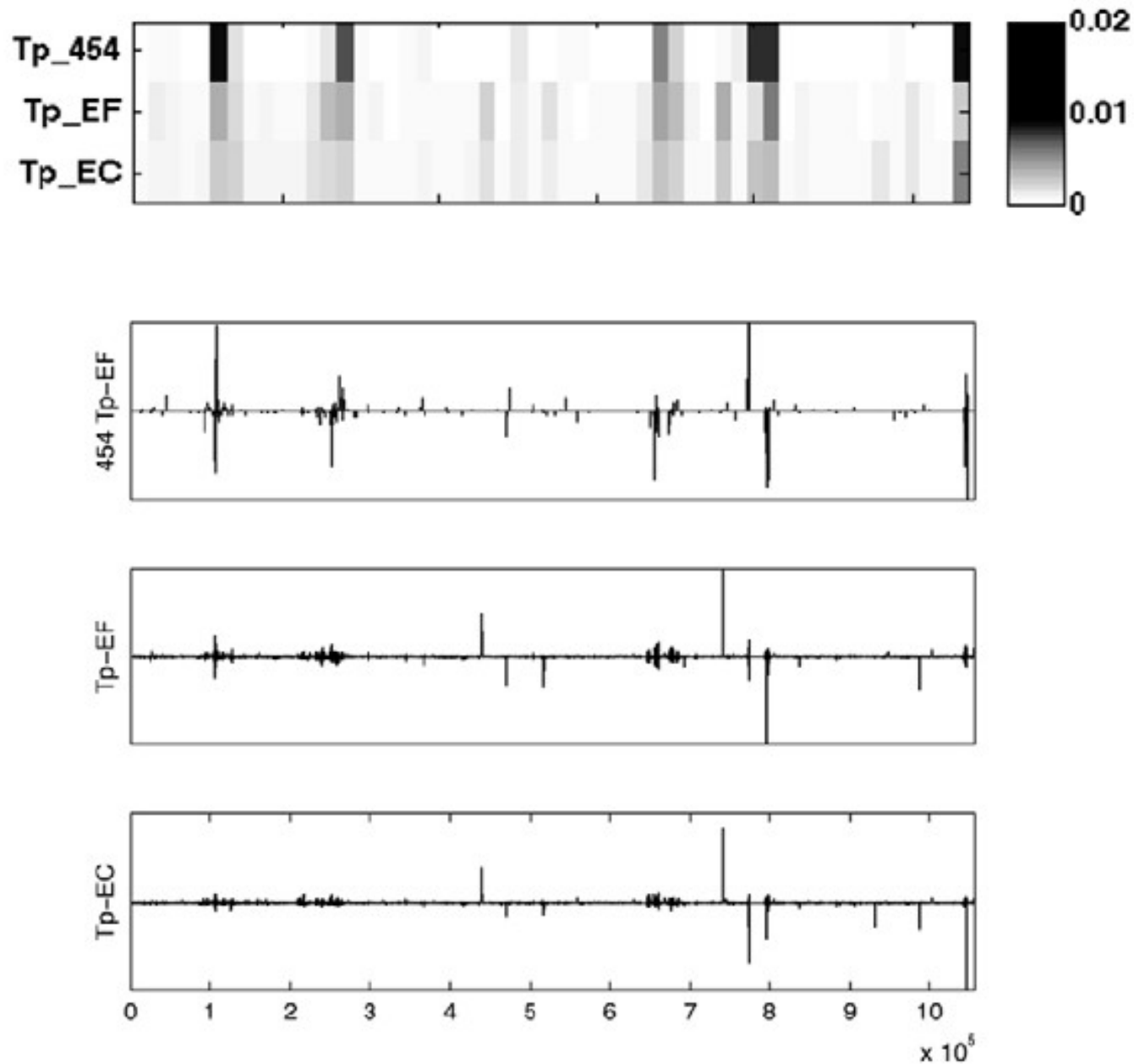


Characterization of the Small RNA Transcriptome of the Diatom, *Thalassiosira pseudonana*

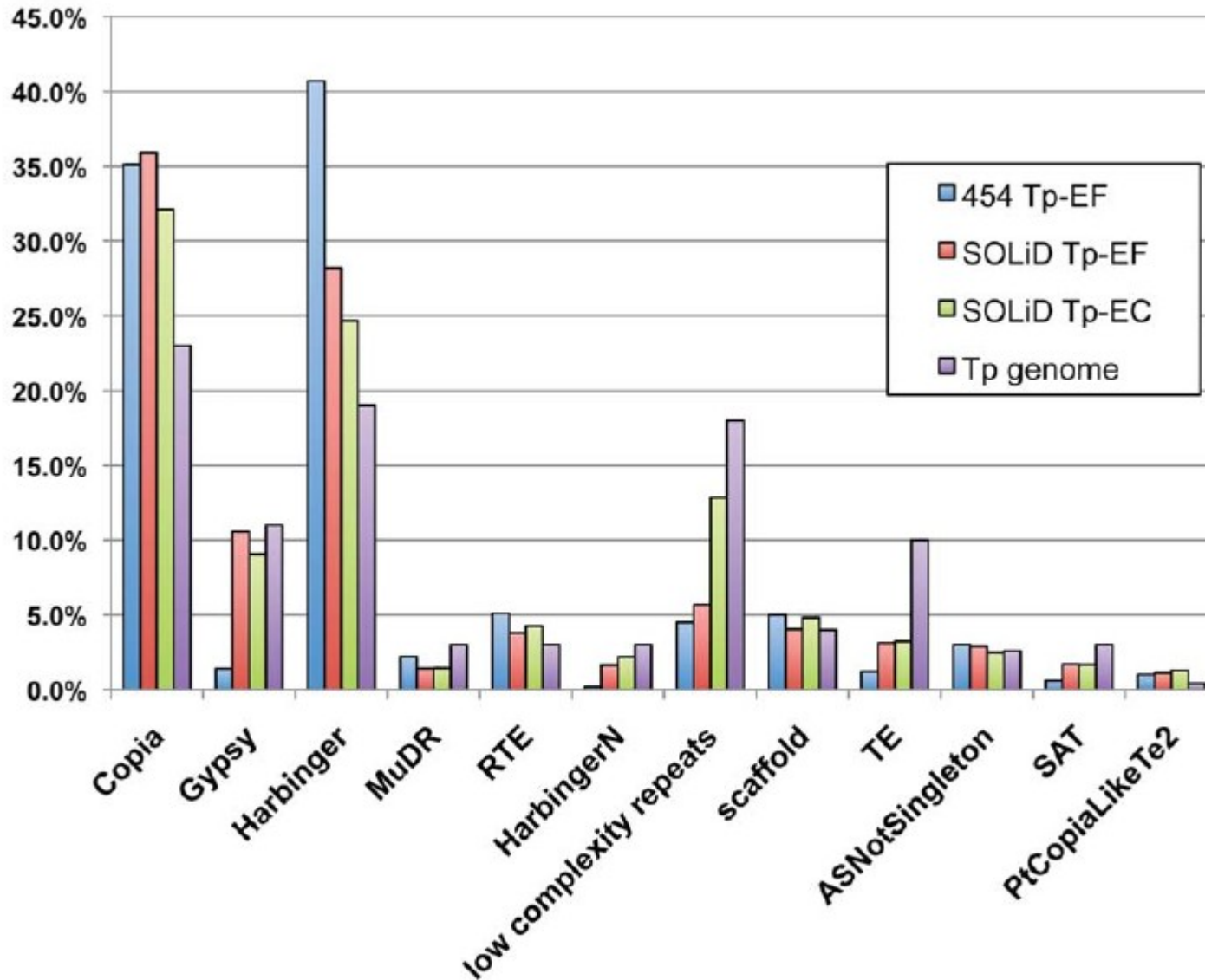
Trina M. Norden-Krichmar^{1,2}, Andrew E. Allen^{2*}, Terry Gaasterland¹, Mark Hildebrand¹

1 Scripps Institution of Oceanography, University of California San Diego, La Jolla, California, United States of America, **2** J. Craig Venter Institute, San Diego, California, United States of America

Abundance of small RNAs mapped along chromosome 22

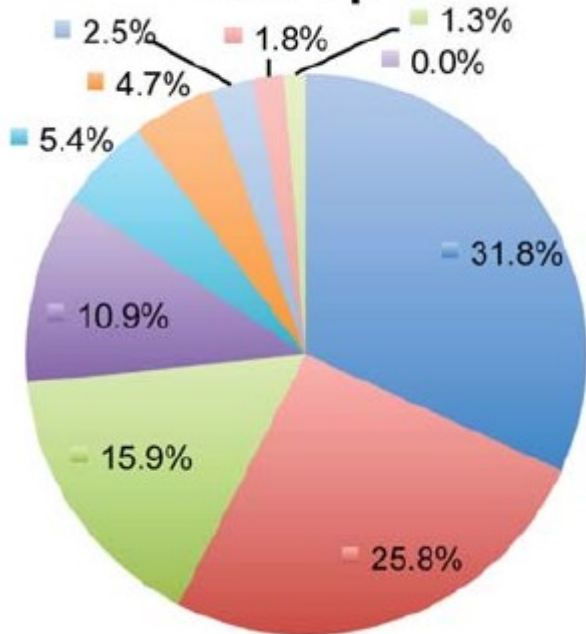


Percentage of small RNA sequences

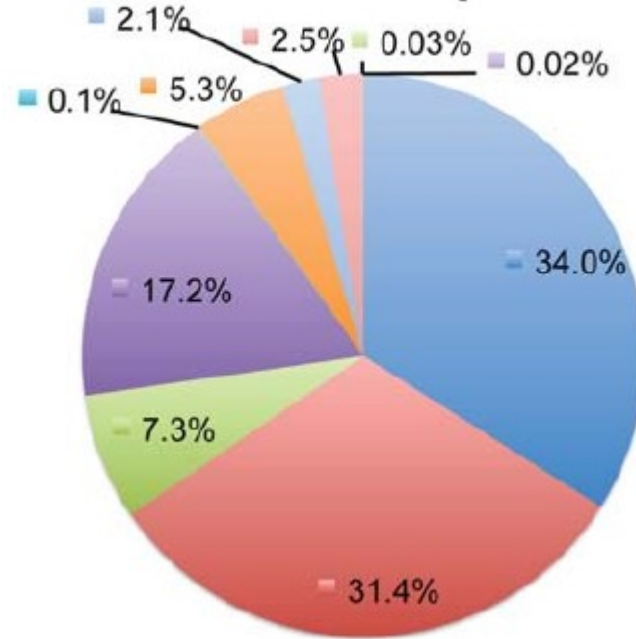


Small RNA distribution by genic features

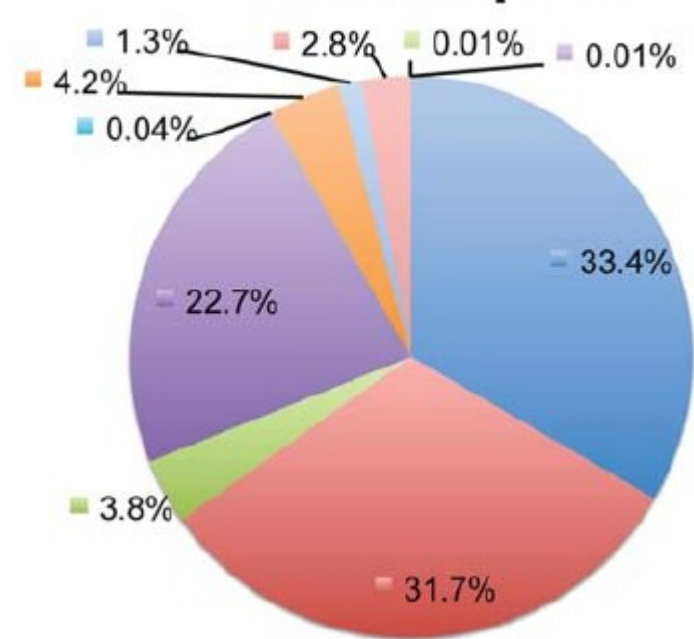
454 Tp-EF



SOLiD Tp-EF



SOLiD Tp-EC

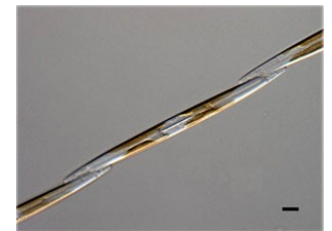
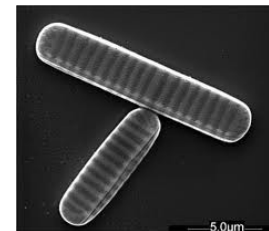
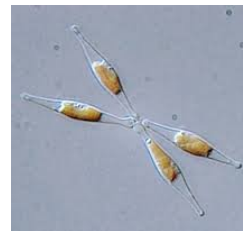
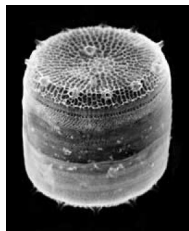
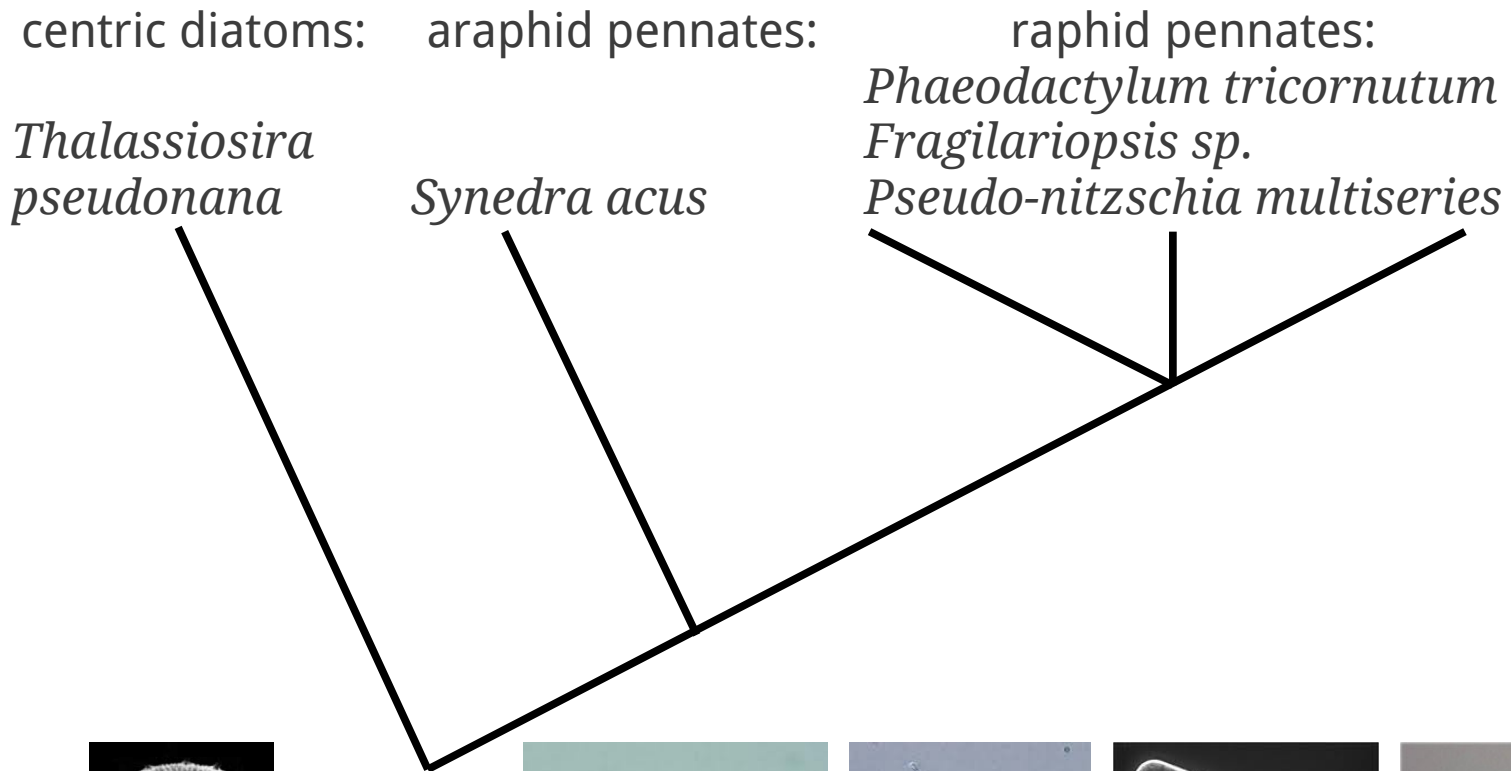


- Sense to exons
- Intergenic only
- Repeat-associated
- Antisense to exons
- mitochondria
- Sense to introns
- Intergenic and intron/exon
- Antisense to introns
- chloroplast
- miRNA candidates

Актуальность получения последовательности ядерного генома *S. acus*

- Диатомовые водоросли:
 - важнейший компонент глобальной экосистемы
 - перспективный биотехнологический объект
 - группа организмов со сложной эволюционной историей
- Только один вид Bacillariophyta является модельным организмом
- Известны последовательности ядерных геномов четырех видов диатомей (2 опубликованы)

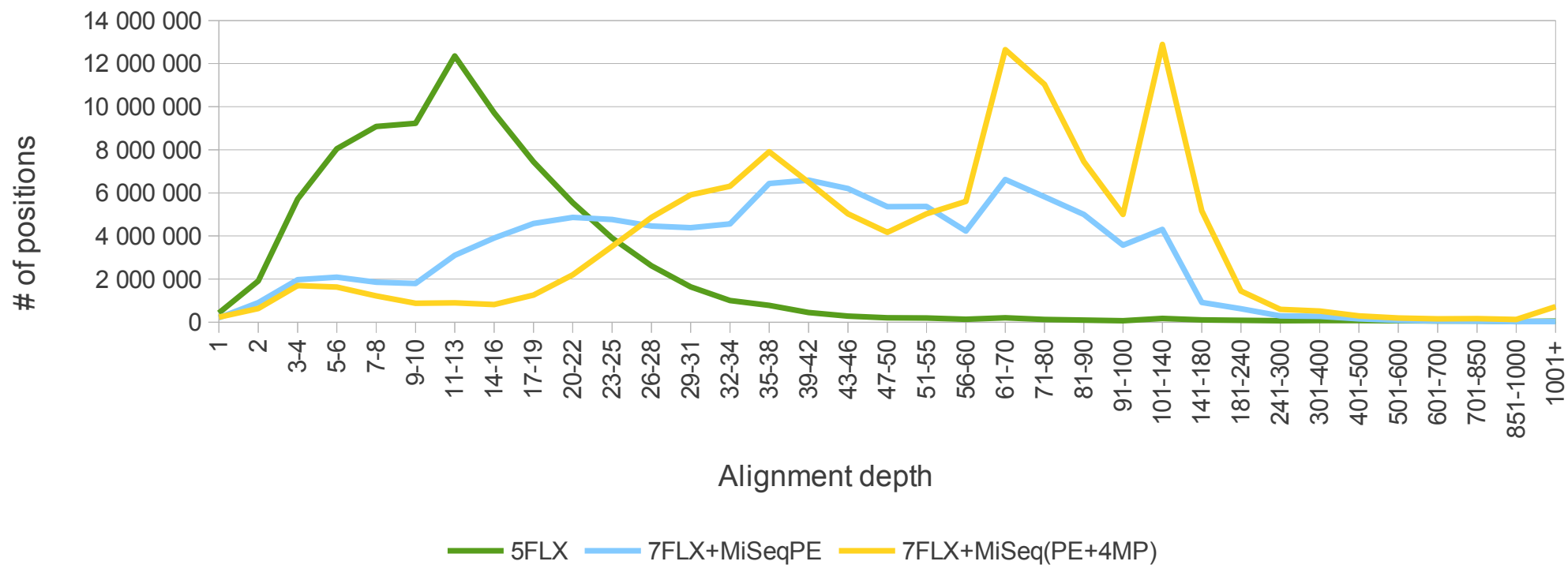
Актуальность получения последовательности ядерного генома *S. acus* (продолжение)



Статистика сборки ядерного генома *S. acus*

Assembly	5FLX	7FLX+MiSeq(PE)	7FLX+2MiSeq(PE+4MP)		
Alignment statistics					
peakDeth	9	40	<i>PE Reads</i>	33	<i>PE Reads</i>
estimatedGenomeSize	149,60	146,50		271,1	
numAlignedReads	3.7M	4.5M	11M	4.5M	30.8M
numAlignedBases	1 240M	3 004M	2 241M	3 004M	5 337M
<i>Contigs</i>					
numberOfContigs	34K	37K	9.8K	40.8K	3.9K
numberOfBases	67M	81M	73M	96M	98M
N50ContigSize	3.0K	3.4K	10.5K	3.8K	100.1K

Покры́тие сборки ядерного генома *S. acis*



Представленность ультраконсервативных CEGs (Conserved Eukaryotic Genes) в геномах диатомовых водорослей

	Proteins	Completeness, %*	Total	Average
<i>T. pseudonana</i>	223	90	276	1.24
<i>P. tricornutum</i>	223	90	274	1.24
<i>F. cylindrus</i>	219	88	401	1.83
<i>S. acus</i>	217	88	359	1.65

* out of 248 highly-conserved CEGs

Вопросы?