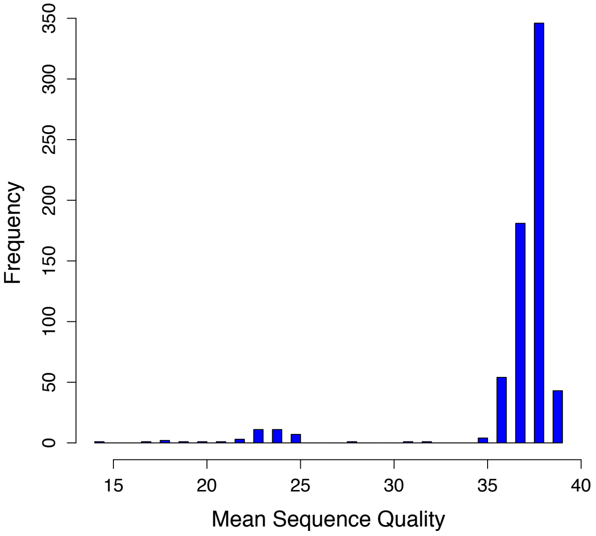
Tara Oceans Update 1/21/15

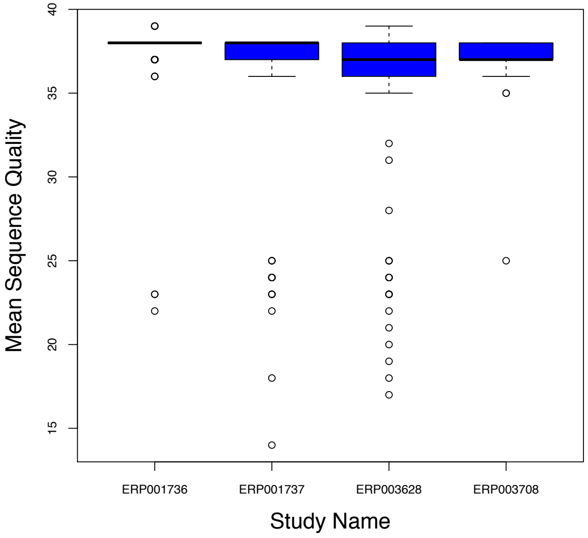
So, when was the data actually submitted…

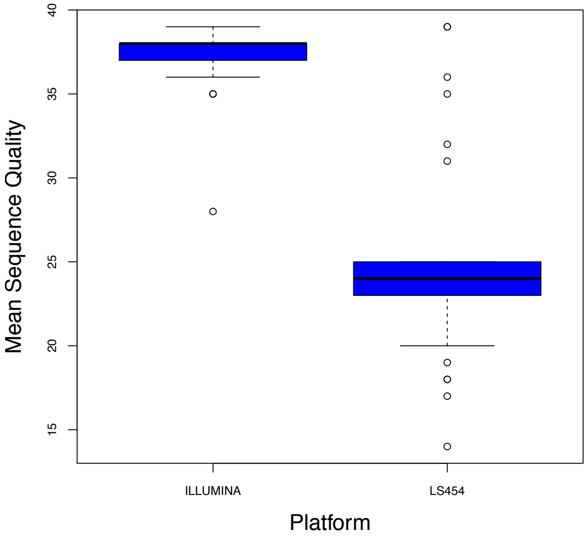
submission accession	count runs	submission date
ERA357871	235	1-Sep-14
ERA357903	104	10-Sep-14
ERA356217	66	1-Sep-14
ERA356219	64	1-Sep-14
ERA357908	48	
ERA242243	36	
ERA242028	30	
ERA357902	29	
ERA241291	23	
ERA320049	19	
ERA155563	17	
ERA242034	6	
ERA242244	4	
ERA155562	3	
ERA242033	2	
ERA245027	2	
ERA320050	1	
ERA352812	1	
ERA361805	1	

http://www.ebi.ac.uk/ena/data/view/ERA356219

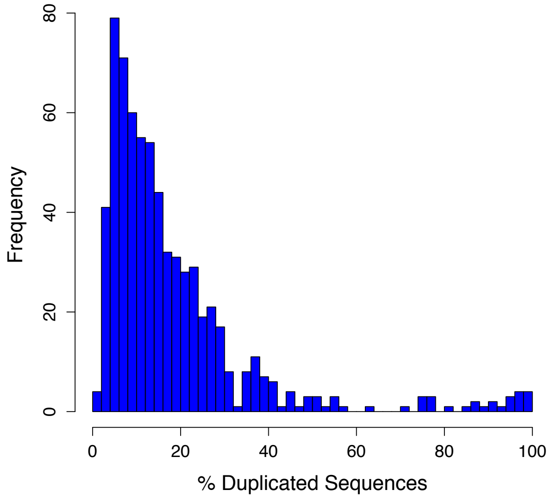
Distribution of Average Read Quality Across Runs

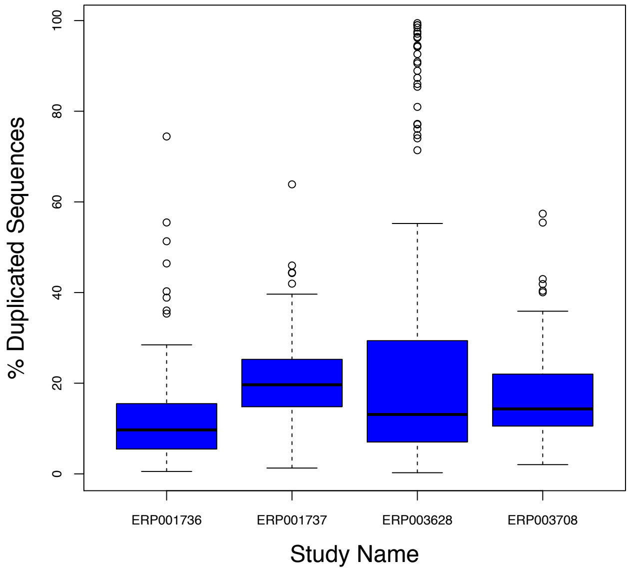


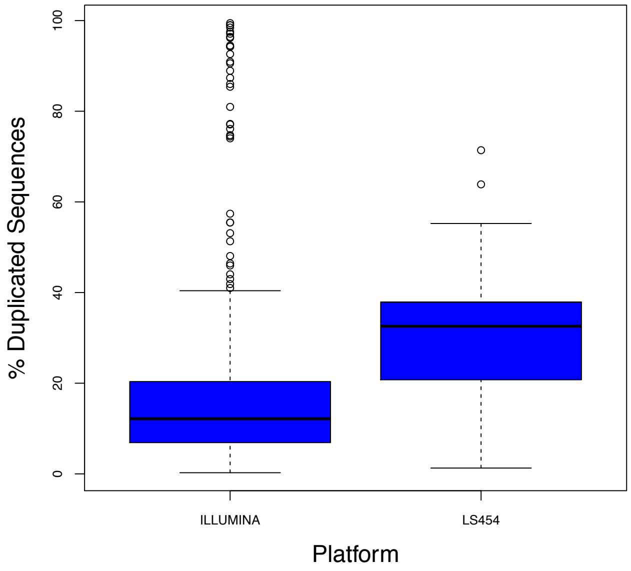




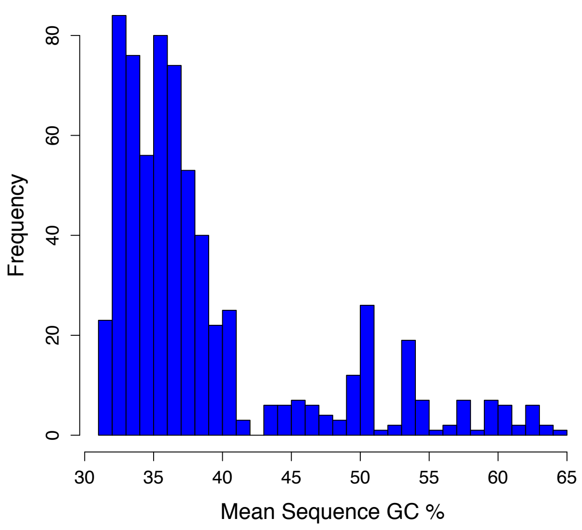
Distribution of % Duplicated Across Runs

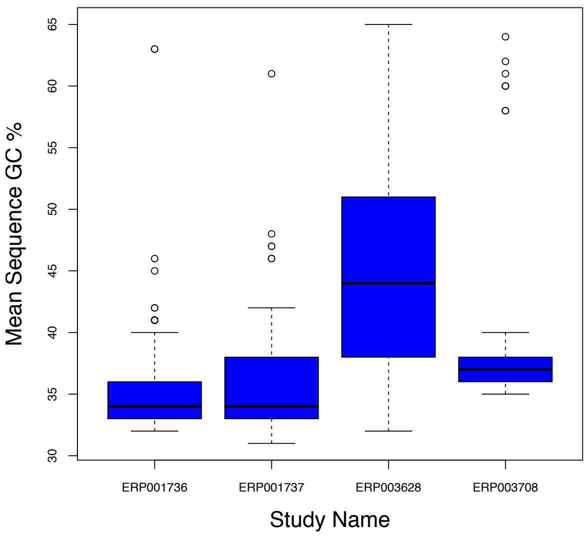


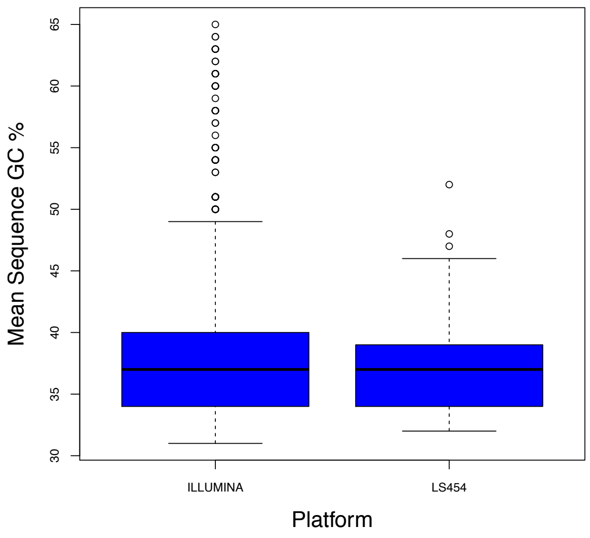




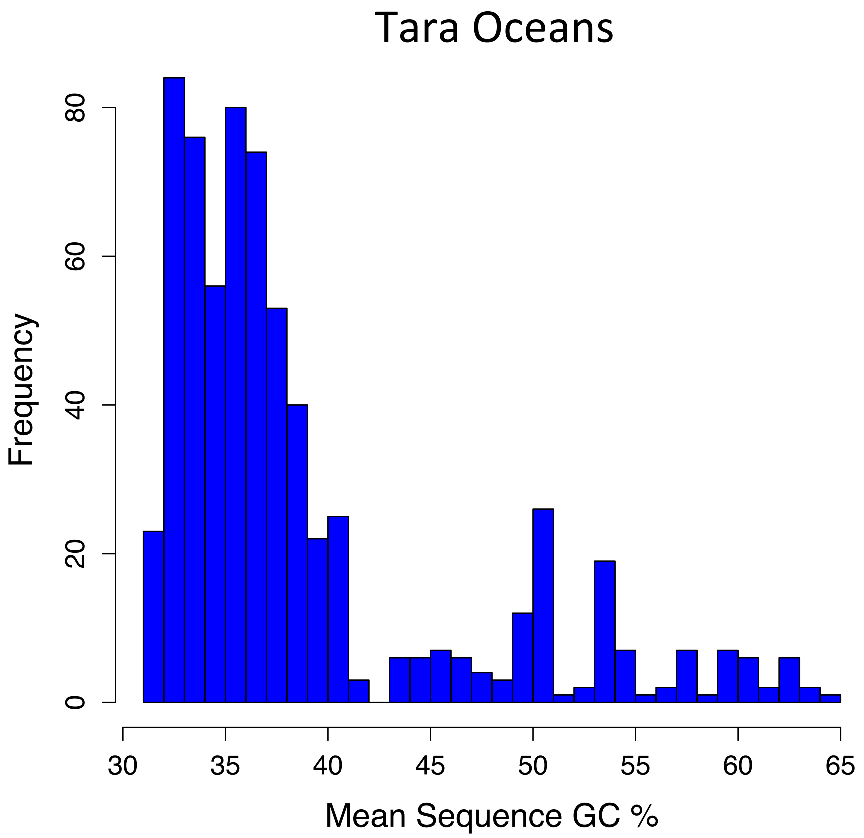
Distribution of Average % GC Across Runs

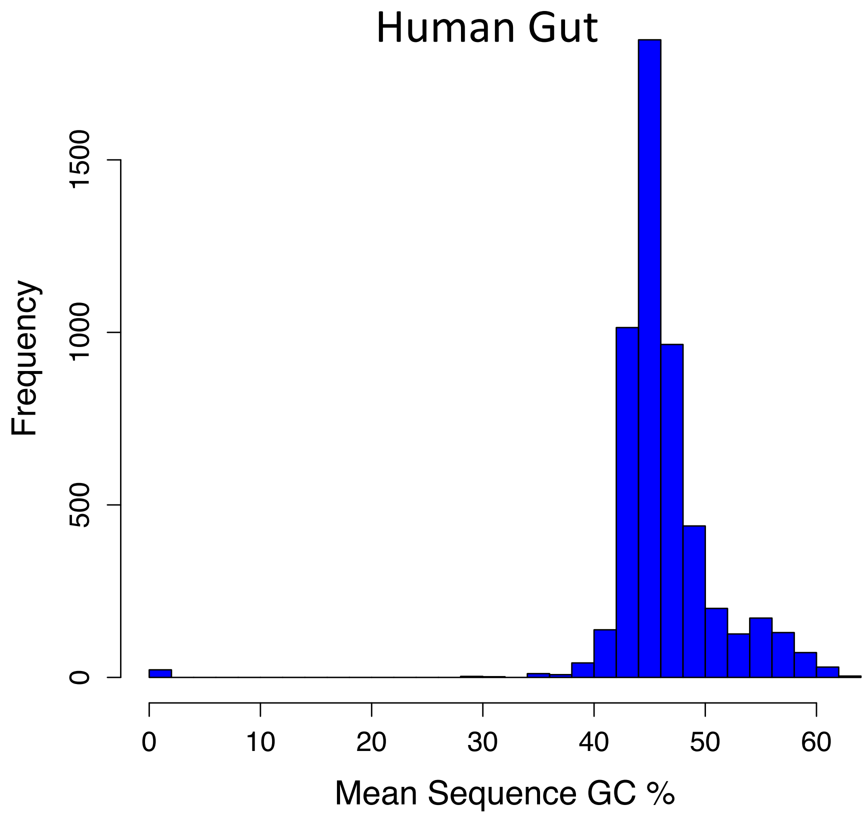






Different %GC Between Marine and Human Gut


Tara Oceans


Human Gut

Fraction of runs which failed FastQC checks

study_accession	ERP001736	ERP001737	ERP003628	ERP003708
count_runs	248	85	223	114
Basic Statistics	0.00	0.00	0.00	0.00
Per base sequence quality	0.01	0.25	0.19	0.02
Per sequence quality scores	0.00	0.02	0.02	0.00
Per base sequence content	0.25	0.41	0.10	0.04
Per base GC content	0.02	0.00	0.12	0.04
Per sequence GC content	0.64	0.41	0.26	0.50
Per base N content	0.00	0.01	0.01	0.00
Sequence Length Distribution	0.00	0.00	0.00	0.00
Sequence Duplication Levels	0.01	0.01	0.13	0.02
Overrepresented sequences	0.00	0.00	0.03	0.00
Kmer Content	0.00	0.14	0.16	0.02

Tara Oceans Update 1/12/15

Summary of Available Tara Oceans Data

study title	data type	size fraction	study accession	reads_1e6	bases_1e9	runs	experiments	samples
Shotgun Sequencing of size fractions for prokaryotes and large DNA viruses	Metagenome	prokaryotes	ERP001736	24,764	4,892	248	248	135
Shotgun Sequencing of size fractions for prokaryotes and large DNA viruses	Metagenome	prokaryotes	ERP001737	8,972	1,801	85	85	75
Shotgun Sequencing of size fractions for protist	Metagenome	protists	ERP003628	23,518	4,660	243	243	159
Shotgun Sequencing of size fractions for DNA viruses	Metagenome	DNA viruses	ERP003708	4,489	863	115	114	92
Metatranscriptome sequencing of size fractions for protists.	Metatranscriptome	protists	ERP006152	284	52	27	27	22
Metatranscriptome sequencing of size fractions for protists.	Metatranscriptome	protists	ERP006156	1	0	29	29	24
MAST4 Single Cell Whole Genome Amplification	Single-cell		ERP003711	125	12	4	4	2
16S Sequencing of size fractions for prokaryotes	16S	prokaryotes	ERP003634	0	0	6	6	6
Amplicon sequencing of size fractions for large DNA viruses.	16S	DNA viruses	ERP006153	2	1	35	35	19
Amplicon sequencing of size fractions for protists.	16S	protists	ERP006157	993	293	370	370	334
Amplicon sequencing of size fractions for protists.	16S	protists	ERP007024	24	6	20	20	14

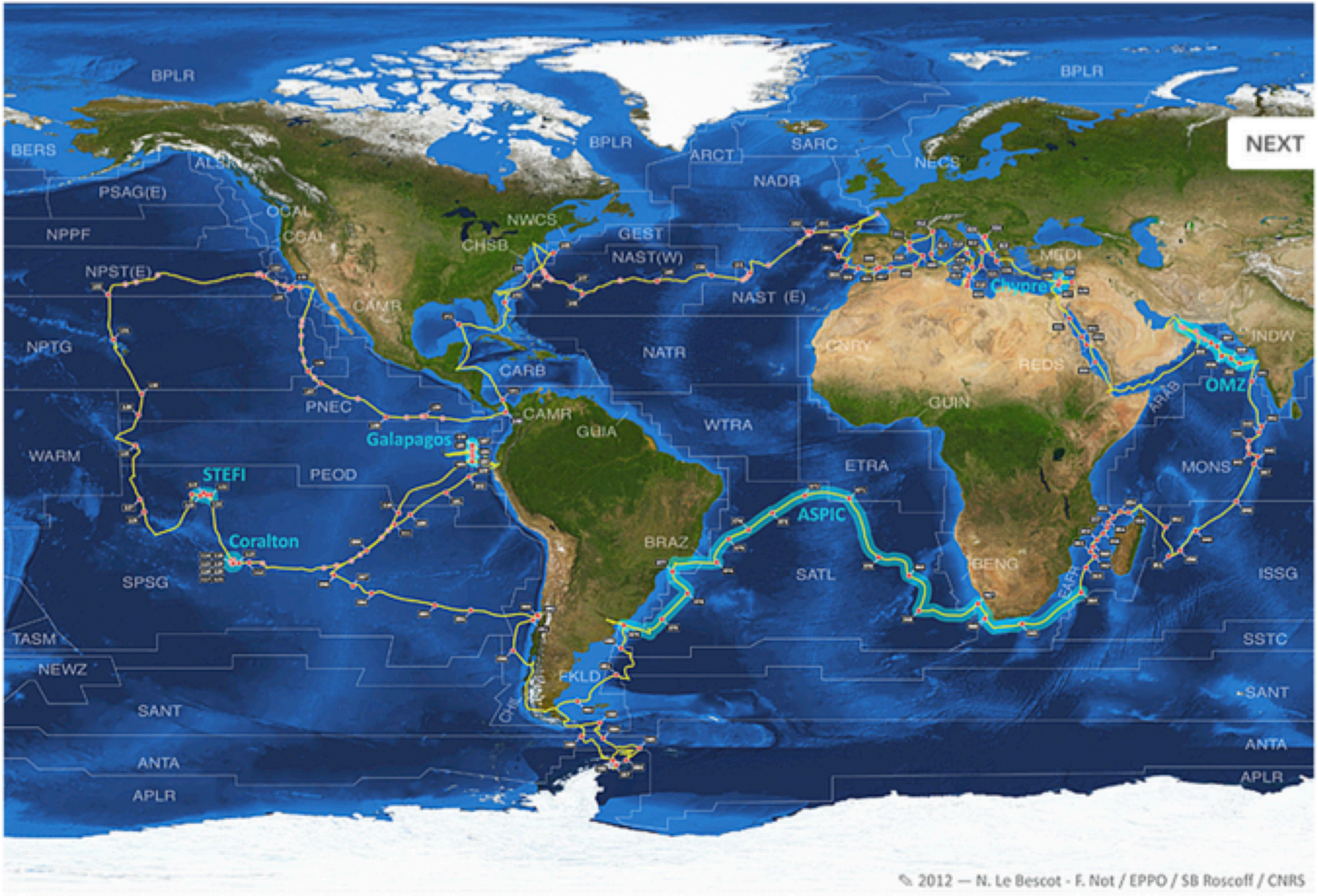
“This project will rely on samples collected during the scientific expedition Tara-Oceans (2009-2012). By March 2012, the schooner Tara, equipped with innovative systems for sampling of 11 organismal size-ranges covering entire planktonic communities from viruses to animals, has collected standardized genetic (total DNA/RNA), morphological, and physico-chemical (contextual) samples from 153 sites across the world oceans, locations carefully selected with input from near-real-time remote sensing and in-situ hydrographic criteria. Overall, a total of ~50,000 biological samples and ~13,000 contextual measures from 3 depths will be analysed. The metagenomics component of the project consists of size fractionated plankton samples that are submitted to barcoding and shotgun sequencing, as well as isolated single-cell amplified protists and single-organisms isolated metazoans that are sequenced as reference genomes.”

Data release policy

(http://www.embl.de/tara-oceans/start/facts_figures/Tara-Oceans-Data-Release-Policy.pdf)

The Tara Oceans Consortium has established a policy for pre-publication data usage with the aim to make quickly and broadly available the global data generated during the project for advancing science, while maintaining a priority for analyses by the laboratories that participate in the data production effort. **During one year after release in a public database, the data will be considered usable with the following restriction**: specifically, intended analyses may not compete with those reserved for the Tara Oceans Consortium, including global analyses at the genome and community level, and comparisons between samples. Therefore, **before starting any study on these reserved data sets, investigators are required to contact the Tara Oceans Consortium to obtain an agreement**. This restriction will be lifted after the publication of analyses on the considered data sets by the Tara Oceans Consortium, or automatically one year after the release of the data. If a publication is made from the released data sets, it is expected that the Tara Oceans Consortium is cited in the acknowledgment section. Raw data sets have the same limits for use than the advanced data sets derived from them. Download of data from the Tara Oceans project implies a full acceptance of the policy usage described in this paragraph.

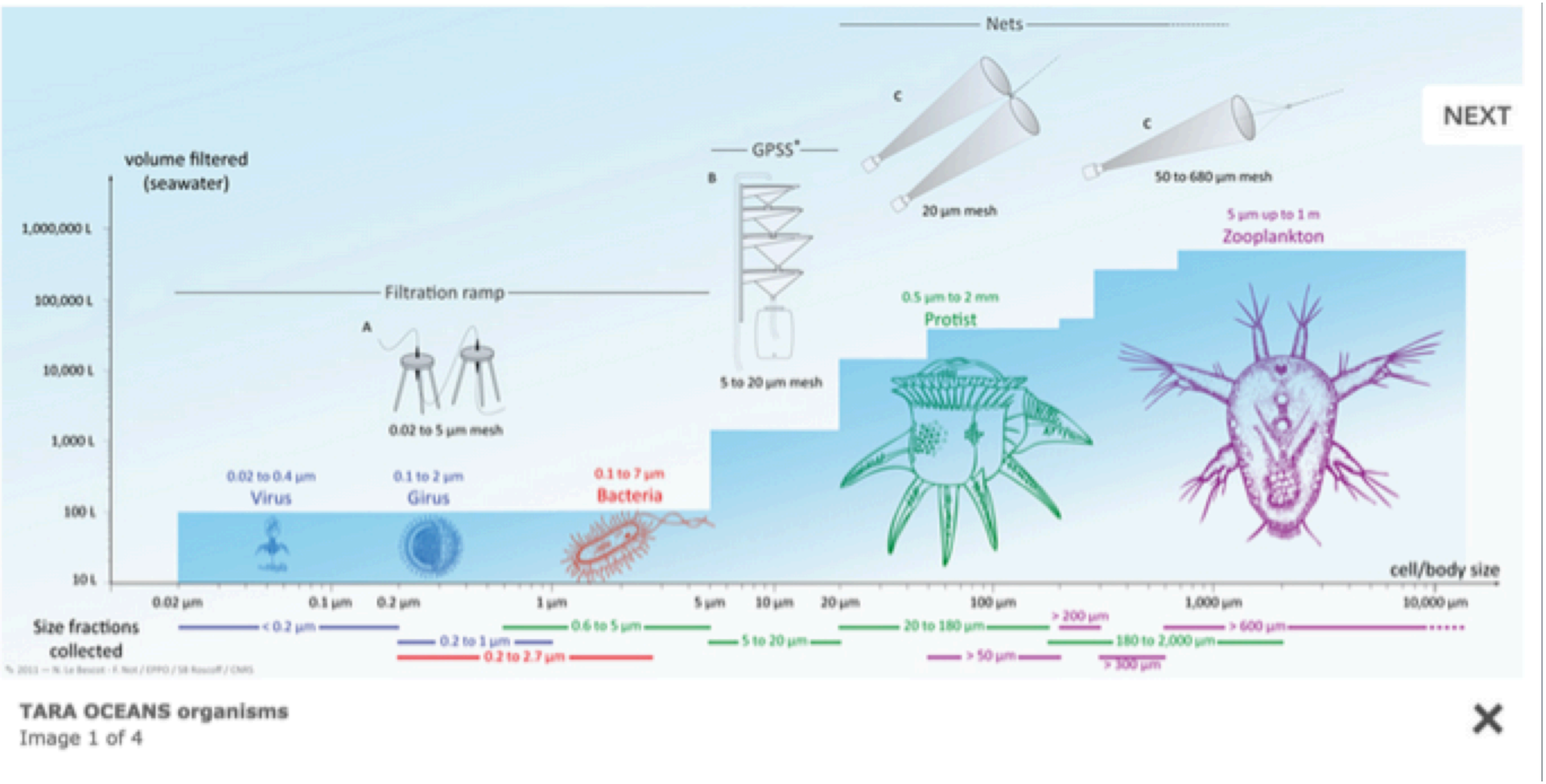
- All runs in the SRA were updated at some point in 2014
- Run dates range from 3/19/2010 to 11/20/2013 (one in 2014)



✎ 2012 — N. Le Bescot - F. Not / EPPO / SB Roscoff / CNRS

Voyage of the schooner TARA during the TARA Oceans expedition, showing station numbers (red dots) and specific experiments (in blue and named)

Image 1 of 4



© 2011 — N. Le Bescot - F. Not / EPPO / SB Roscoff / CNRS

TARA OCEANS organisms

Image 1 of 4

http://www.embl.de/tara-oceans/start/publications/index.html

Karsenti, E. et al. A Holistic Approach to Marine Eco-Systems Biology. Plos Biol 9, doi:ARTN e1001177 DOI 10.1371/journal.pbio.1001177 (2011).

Corse, E. et al. Phylogenetic Analysis of Thecosomata Blainville, 1824 (Holoplanktonic Opisthobranchia) Using Morphological and Molecular Data. Plos One 8, doi:ARTN e59439 DOI 10.1371/journal.pone.0059439 (2013).

Hingamp, P. et al. Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. Isme J 7, 1678-1695, doi:DOI 10.1038/ismej.2013.59 (2013).

Brum, J. R. et al. Global morphological analysis of marine viruses shows minimal regional variation and dominance of non-tailed viruses. Isme J 7, 1738-1751, doi:DOI 10.1038/ismej.2013.67 (2013).

Solonenko, S. A. et al. Sequencing platform and library preparation choices impact viral metagenomes. Bmc Genomics 14, doi:Artn 320 Doi 10.1186/1471-2164-14-320 (2013).

Swan, B. K. et al. Prevalent genome streamlining and latitudinal divergence of planktonic bacteria in the surface ocean. P Natl Acad Sci USA 110, 11463-11468, doi:DOI 10.1073/pnas.1304246110 (2013).

Benzoni, F. Echinophyllia tarae sp n. (Cnidaria, Anthozoa, Scleractinia), a new reef coral species from the Gambier Islands, French Polynesia. Zookeys, 59-79, doi:DOI 10.3897/zookeys.318.5351 (2013).

Logares, R. et al. Metagenomic 16S rDNA Illumina tags are a powerful alternative to amplicon sequencing to explore diversity and structure of microbial communities. Environmental Microbiology, n/a-n/a, doi:10.1111/1462-2920.12250 (2013).

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Boss, E. et al. The characteristics of particulate absorption, scattering and attenuation coefficients in the surface ocean; Contribution of the Tara Oceans expedition. Methods in Oceanography 7, 52-62, doi:http://dx.doi.org/10.1016/j.mio.2013.11.002 (2013).

Chase, A. et al. Decomposition of in situ particulate absorption spectra. Methods in Oceanography 7, 110-124, doi:http://dx.doi.org/10.1016/j.mio.2014.02.002 (2013).

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Benzoni, F. et al. Phylogenetic relationships and revision of the genus Blastomussa (Cnidaria: Anthozoa: Scleractinia) with description of a new species. RAFFLES BULLETIN OF ZOOLOGY, 358–378 (2014).

Cunningham, B. R. et al.

Acinas, S. G. et al. Validation of a new catalysed reporter deposition-fluorescence in situ hybridization probe for the accurate quantification of marine Bacteroidetes populations. Environ Microbiol, doi:10.1111/1462-2920.12517 (2014).

Arrigoni, R. et al. A phylogeny reconstruction of the Dendrophylliidae (Cnidaria, Scleractinia) based on molecular and micromorphological criteria, and its ecological implications. Zoologica Scripta, n/a-n/a, doi:10.1111/zsc.12072 (2014).

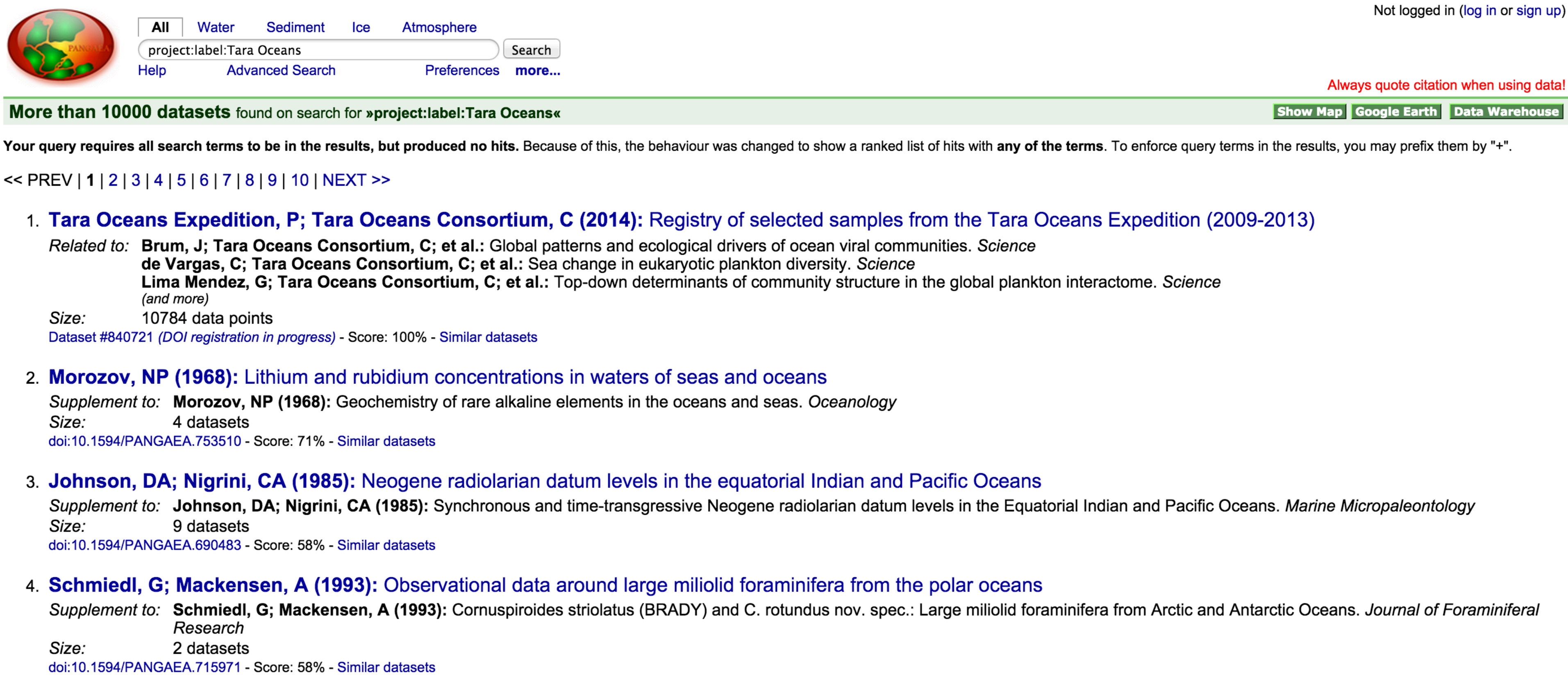
Arrigoni, R. et al. Phylogenetic relationships and taxonomy of the coral genera Australomussa and Parascolymia (Scleractinia, Lobophylliidae). Contributions to Zoology (2014).

Gasmi, S. et al. Evolutionary history of Chaetognatha inferred from molecular and morphological data: a case study for body plan simplification. Frontiers in zoology 11, 84, doi:10.1186/s12983-014-0084-7 (2014).

Roullier, F. et al. Particle size distribution and estimated carbon flux across the Arabian Sea oxygen minimum zone. Biogeosciences 11, 4541-4557, doi:DOI 10.5194/bg-11-4541-2014 (2014).

Environmental data stored at Pangaea

http://www.pangaea.de/search?env=All&q=project%3Alabel%3ATara+Oceans



Not logged in (log in or sign up)

Always quote citation when using data!

More than 10000 datasets found on search for **»project:label:Tara Oceans«**

Your query requires all search terms to be in the results, but produced no hits. Because of this, the behaviour was changed to show a ranked list of hits with **any of the terms**. To enforce query terms in the results, you may prefix them by "+".

<< PREV | **1** | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | NEXT >>

1. **Tara Oceans Expedition, P; Tara Oceans Consortium, C (2014):** Registry of selected samples from the Tara Oceans Expedition (2009-2013)

   Related to: **Brum, J; Tara Oceans Consortium, C; et al.:** Global patterns and ecological drivers of ocean viral communities. *Science*
   de Vargas, C; Tara Oceans Consortium, C; et al.: Sea change in eukaryotic plankton diversity. *Science*
   Lima Mendez, G; Tara Oceans Consortium, C; et al.: Top-down determinants of community structure in the global plankton interactome. *Science*
   (and more)
   Size: 10784 data points
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2. **Morozov, NP (1968):** Lithium and rubidium concentrations in waters of seas and oceans

   Supplement to: **Morozov, NP (1968):** Geochemistry of rare alkaline elements in the oceans and seas. *Oceanology*
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   doi:10.1594/PANGAEA.753510 - Score: 71% - Similar datasets

3. **Johnson, DA; Nigrini, CA (1985):** Neogene radiolarian datum levels in the equatorial Indian and Pacific Oceans

   Supplement to: **Johnson, DA; Nigrini, CA (1985):** Synchronous and time-transgressive Neogene radiolarian datum levels in the Equatorial Indian and Pacific Oceans. *Marine Micropaleontology*
   Size: 9 datasets
   doi:10.1594/PANGAEA.690483 - Score: 58% - Similar datasets

4. **Schmiedl, G; Mackensen, A (1993):** Observational data around large miliolid foraminifera from the polar oceans

   Supplement to: **Schmiedl, G; Mackensen, A (1993):** Cornuspiroides striolatus (BRADY) and C. rotundus nov. spec.: Large miliolid foraminifera from Arctic and Antarctic Oceans. *Journal of Foraminiferal Research*
   Size: 2 datasets
   doi:10.1594/PANGAEA.715971 - Score: 58% - Similar datasets

Questions

- Data embargos?
- Which studies?
- What's already been done?
- Analysis plan?
- Data QC?