

# RNA sequence accession numbers for coral colonies that displayed a strong bleaching phenotype at Ofu Island, American Samoa between 2015 and 2016.

Website: <https://www.bco-dmo.org/dataset/762511>

Data Type: Other Field Results

Version: 2

Version Date: 2019-03-18

## Project

» [Ecological, evolutionary and physiological responses of corals to a mass bleaching event in American Samoa](#) (Bleaching American Samoa)

Contributors	Affiliation	Role
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## Abstract

RNA sequence accession numbers for coral colonies that displayed a strong bleaching phenotype at Ofu Island, American Samoa between 2015 and 2016. This dataset includes accession numbers for 36 RNAseq libraries housed at The National Center for Biotechnology Information (NCBI).

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## Coverage

**Spatial Extent:** Lat:-14.1799 Lon:-169.65448

**Temporal Extent:** 2015-04 - 2016-04

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## Dataset Description

This dataset includes accession numbers for 36 RNAseq libraries housed at The National Center for Biotechnology Information (NCBI). Coral colonies that displayed a strong bleaching phenotype at Ofu Island, American Samoa were sampled between 2015 and 2016.

The genetic accessions at NCBI referenced in this dataset will not be publicly accessible until 2019-05-01. This includes accession numbers and links to the accession page.

These data were published in Thomas & Palumbi (2017).

## Acquisition Description

Colonies that displayed a strong bleaching phenotype in April 2015 were selected for transcriptome-wide gene expression analyses. These colonies were subsequently sampled in August 2015, December 2015 and April 2016. For these 36 field-collected tissue samples (five colonies of *A. gemmifera* and four colonies of *A. hyacinthus* across four sample dates), total RNA was extracted Qiagen's RNeasy Plus Kit. In total 36 cDNA libraries were generated using the Illumina TruSeq RNA Library Prep Kit v2 with ProtoScript II Reverse Transcriptase. We carried out multiplexed Illumina sequencing at the University of Utah Microarray and Genomic Analysis Core Facility. Fastq files were mapped to a reference transcriptome (Barshis et al., 2013) using HISAT2 (Langmead & Salzberg, 2012) with a minimum mapping quality of 10. We used SAMtools (Li et al., 2009) to generate counts for each contig in our reference transcriptome. Counts matrices were normalized in DESeq2.0 (Love, Huber, & Anders, 2014).

Approximate coordinates for this dataset are "Pool 400", back reef lagoon, Ofu, American Samoa (-14.17990, -169.65448)

## Processing Description

BCO-DMO Data Manager Processing Notes:

- \* added a conventional header with dataset name, PI name, version date
- \* modified parameter names to conform with BCO-DMO naming conventions
- \* added column of links to genetic accessions at NCBI
- \* Added separate year and month columns from parsing the Date column (format yyyy\_mm )

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## Related Publications

Thomas, L., & Palumbi, S. R. (2017). The genomics of recovery from coral bleaching. *Proceedings of the Royal Society B: Biological Sciences*, 284(1865), 20171790.  
doi:[10.1098/rspb.2017.1790](https://doi.org/10.1098/rspb.2017.1790)

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## Parameters

Parameter	Description	Units
sample	Sample identifier	unitless
colony	Colony identifier	unitless
species	Coral species	unitless
date	Month and year of sampling in format yyyy_mm	unitless
year	Year of sampling	unitless
month	Month of sampling	unitless
bleaching_status	Bleaching status	percent
Accession	Genetic accession number at NCBI	unitless
Accession_link	Link to genetic accession at NCBI	unitless

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## Instruments

<b>Dataset-specific Instrument Name</b>	Illumina HiSeq 2500
<b>Generic Instrument Name</b>	Automated DNA Sequencer
<b>Generic Instrument Description</b>	General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step.

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## Deployments

### Palumbi\_AmSamoa\_2013-2015

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/676237">https://www.bco-dmo.org/deployment/676237</a>
<b>Platform</b>	American_Samoa
<b>Start Date</b>	2013-01-04
<b>End Date</b>	2015-08-21
<b>Description</b>	Coral colony samples, temperature, DNA/RNA, bleaching metrics.

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## Project Information

## **Ecological, evolutionary and physiological responses of corals to a mass bleaching event in American Samoa (Bleaching American Samoa)**

**Coverage:** American Samoa

Description from NSF award abstract: The strongest coral bleaching event in nearly 20 years began in American Samoa in January 2015. Coral bleaching occurs when ocean water temperatures exceed a coral's normal heat tolerance. But bleaching events usually show an unexplained pattern - colonies next to one another can show very different levels of bleaching - from pure white to the normal tan color of a healthy coral. The investigators have observed this pattern among 280 corals on reefs in American Samoa that have been studied for years. This system will be used to test four major hypotheses about what causes some corals to bleach and some not: differences in 1) species, 2) the temperature the corals experienced, 3) the symbiont they harbor, and 4) the genotype of the coral host. In addition, the investigators will return to American Samoa at regular intervals to measure the rate of recovery of each coral colony and conduct the same tests as above for recovery rate. The stark-white reefs left behind by bleaching events are one of the most common signals of increased ocean warming. This work will take advantage of years of prior study and the advent of a coral bleaching event to understand the rules for survival on reefs. The reefs of American Samoa began showing a major bleaching event starting in January 2015, including 62 corals that have been intensively studied for coral thermal resistance, field temperatures, and symbiont type. In April 2015 the investigators monitored bleaching status of these and additional corals, totaling 280 corals from four species, and uncovered marked variation in bleaching extent within and between species and within and between reef regions. The team will test the relative importance of microclimate to bleaching state by examining records of approximately 50 temperature loggers in place since before the bleaching event. They will test the influence of symbiont type and host gene expression profiles by examining samples of 60 colonies taken at four time points after bleaching. The investigators will also examine the full suite of 280 corals for genetic variation to estimate the relationship between bleaching state, recovery rate and genetic polymorphism. These data will be used to test micro-climate, symbiont, and coral genetics as determinants of bleaching and bleaching recovery. Because the investigators have samples from these 280 colonies before bleaching mortality, this study will provide the first estimate for the evolutionary impact of a bleaching event on coral populations.

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## Funding

Funding Source	Award
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1547921</a>

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