

revive & restore

GENETIC RESCUE OF ENDANGERED AND EXTINCT SPECIES

REVIVE & RESTORE SCIENCE REPORT
Q3 2026

This quarter marks an exciting milestone for Revive & Restore: all 10 projects in our inaugural Climate Resilience cohort have officially kicked off. These projects represent a significant expansion of our efforts to advance biotechnologies that help vulnerable species and ecosystems withstand a changing climate.

Meanwhile, progress continues across our broader portfolio. In this report, we highlight breakthroughs in avian reproductive biotechnology, new approaches to coral reef resilience, advances in stem cell science, and findings from completed Wild Genomes projects that are informing conservation decisions in the field.

Beyond these scientific milestones this quarter, our team connected with researchers and shared ideas at gatherings including Sci Foo in Cambridge, UK, the Telomere-to-Telomere meeting in Santa Cruz, California, and conferences spanning evolutionary biology, ecology, genetic biocontrol, and wildlife reproductive biotechnology in the U.S., Denmark, and Brazil.

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Detail of *Understory, 2007* by Isabella Kirkland

FEATURED PROJECT
FIELD GENOMICS: TAKING GENETIC TOOLS INTO THE FIELD

Much of conservation genetics depends on a slow and costly journey. Samples are collected in the field, permitted across borders under CITES, and analyzed in well-equipped laboratories thousands of kilometers from where managers make decisions. When Dr. Mrinalini Watsa joined San Diego Zoo Wildlife Alliance, her brief was to reverse that model: to "take labs to samples instead of bringing samples to labs."

With support from Revive & Restore's Catalyst Science Fund, Mrinalini set out to build genetic fingerprinting panels for large, rare, and cryptic species, using DNA extracted from hair and scat. These animals are difficult to count or observe, and camera traps alone don't capture them well. Several separate proposals were consolidated into a single cross-species program covering Andean bears, giraffes, and African leopards, with exploratory work on Indian leopards.



Preparing sample collection kits in June 2025 for the Twiga Walinzi team at the Mpala Research Station in Kenya.

A new approach

Whole-genome sequencing produces millions of markers. However, genotyping thousands of them requires expensive infrastructure that many countries cannot afford. Mrinalini's approach was to go the other way and distill each panel to the smallest set of markers that can identify individuals and distinguish siblings. The panels combine microsatellites with flanking SNPs and are run on portable, low-cost Nanopore sequencers.

It was a genuine gamble. No one had ever attempted short-read genotyping on a platform marketed for long reads. "The question of whether we could actually run this on a portable sequencer was completely wide open," Mrinalini recalls. "Nobody knew; no one had ever tried." It worked, and it offered an unexpected advantage. Because Nanopore sequencing happens in real time, field teams can pause a run, fix a problem, and resume, making the most of reagents flown in at considerable cost.

From tool to transfer

Mrinalini convened the Andean Bear Genomics Network, bringing scientists from Colombia, Bolivia, Ecuador, and Peru to a solar-powered laboratory in the Peruvian Amazon. Participants generated whole-genome data sets, ran the full genotyping pipeline, and returned home equipped to analyze their own samples in-country. To protect irreplaceable samples, the team adapted a wildlife forensics practice. They built a synthetic "artificial Andean bear" proficiency standard so that new laboratories can validate the pipeline before running precious field material.

In Kenya, the Twiga Walinzi giraffe team was trained in scat collection and preservation. They collected more than 300 samples in a single month, and the program now targets 1,000 samples a year. For populations confined to fragmented protected areas, this offers something previously unavailable: evidence on relatedness, genetic diversity, and inbreeding risk to inform translocation decisions.

Leopards posed a different challenge. Their scat is rarely found, but they rub against almost everything, so hair is the more reliable sample. The solution came from an airport duty-free counter: a bottle of Chanel No. 5, purchased on grant funds and carried into the field triple-bagged, because "nobody wants to smell like Chanel in the field." The perfume's musky notes are irresistible to cats. Field teams spray it on hair snares, and leopards have obliged by rubbing against them.

Mrinalini is now presenting recommendations to management at the Kenya Wildlife Service.

Translation and training

The pipeline has since expanded to elephants, with two panels now in operation. It has also been applied to tiger identification in Vietnam, timber barcoding in Peru, and ivory forensics with TRACE. One effort uses a nuclear marker to distinguish forest from savanna elephants, a distinction with direct consequences for trafficking prosecutions. "If this funding hadn't come for the bears," Mrinalini notes, "it would have taken me three years to work out all the kinks in those protocols again." Training remains central to the work. "I always tell people, if you can cook, you can do genomics," she says. "You just need to follow a recipe."



The Twiga Walinzi collection team collecting giraffe scat, later genotyped at the Mpala Research Center.

A career catalyzed

When Mrinalini applied, she was a postdoctoral researcher with six months of funding remaining. She now holds an endowed permanent position at the zoo.

Her advice to future applicants is direct. Communicate early when things go sideways, and do not wait for a perfect CV. "Sometimes you're uniquely positioned to actually get something done, and that's a good reason to be supported."

Or, in her own words: "I describe you guys as the people who fund the mad ideas."



Dr. Mrinalini Watsa (center) training the Twiga Walinzi collection team on using the collection survey that directly updates the database with each sample collected.

PRIMORDIAL GERM CELL TRANSMISSION IN THE ZEBRA FINCH

A major avian biotech milestone

Scientists at The Rockefeller University, led by Dr. Erich Jarvis and Dr. Matthew Biegler, funded by Revive & Restore's Biotechnology for Bird Conservation Program, have achieved an important milestone for bird conservation: demonstrating that reproductive cells collected from zebra finch embryos can be transferred into surrogate birds and successfully passed to the next generation. Previously, this achievement had been demonstrated almost exclusively in domestic chickens. The work was originally published in 2025 as a preprint and is now in Stem Cell Reports, with new data from an exceptional surrogate bird: a germline chimera that produced 100% donor-derived offspring, a level of transmission previously achieved only with sterilized surrogates in chicken studies. This milestone in a songbird (order Passeriformes) marks a major advance for the field.

This 100% donor transmission likely resulted from injecting more donor primordial germ cells (PGCs) into the surrogate male than into other surrogates, allowing the donor cells to outcompete the surrogate's endogenous PGCs. For comparison, the other successful germline chimeric male produces an average of 9% donor-derived offspring, a rate more typical of similar studies in chickens.

To achieve efficient germline transmission, PGCs must be cultured long enough to produce enough cells from a single donor bird to transplant into multiple surrogate hosts. Long-term culture is also necessary to induce complex gene edits, such as those that could provide disease resistance or restore diversity to endangered birds. The team at Rockefeller is still working on a stable long-term culture and has made significant progress, with putative PGCs growing in culture for several months, but those cells have not yet been tested in surrogates to produce offspring. To achieve this first proof of concept in germline transmission in the zebra finch, the team pooled cells from multiple donors to obtain enough cells to transfer to surrogates.



Zebra Finches (*Taeniopygia guttata*) left to right: donor-derived son (gray), mother (white), surrogate (chimeric) father (white), host-derived son (white)
Photo credit: Matt Biegler, Rockefeller University

Significance to avian conservation

While this short-term culture and pooling method won't enable certain types of gene editing, it is a major validation that conservationists can begin cryopreserving embryonic gonads of endangered songbirds with confidence that those preserved reproductive tissues can be reconstituted to produce offspring for genetic rescue one day, whether a long-term culture or sterile surrogates exist or not. Because songbirds, like the zebra finch, account for 60% of all birds, this is a major step forward for the avian genetic rescue toolkit.

The need for PGCs in songbird conservation

Songbirds pose an important limitation to avian biotechnologies: their germ cells contain an extra chromosome, likely vital to reproduction, that is absent from all other body cells. This means that cell cultures from skin or feathers are missing an important chromosome for reproduction - and therefore the majority of biobanked materials of songbirds to date may not be a genetic rescue resource in the future. It may be possible to turn feather cells into germ cells in non-passerine birds, but passerines require primary germ cells.

In all bird studies to date, the only donor PGCs proven reproductively competent come from embryos. This means that the gold standard of avian biobanking requires collecting embryonic gonads (ovaries and testes) to ensure future genetic rescue. To date, most conservationists have been hesitant to collect precious embryos for biobanking; these findings could change how conservationists view embryonic biobanking as insurance against future extinction. Biobanking the right tissues is imperative to prevent extinctions and rescue genetic diversity for endangered birds.

Work by Rockefeller University and the other funded Biotech for Bird Conservation teams continues to establish the long-term PGC and stem cell cultures needed to enable a full suite of genetic rescue tools for birds. In the meantime, we at Revive & Restore plan to use this achievement to further advocate and mobilize avian biobanking work worldwide through our continued facilitation of the International Avian Genetic Rescue Consortium, a community of over 60 avian biotechnologists and conservationists from 10 nations, and our biobanking MOU with the Association of Zoos and Aquariums.

ADVANCED CORAL TOOLKIT | HIGHLIGHTS

Our Advanced Coral Toolkit continues to grow, and this quarter's new projects push the portfolio in strategic new directions. We're expanding beyond the coral animal to target its algal symbionts, a promising space for intervention because this partnership shapes both bleaching susceptibility and heat tolerance. We're also moving beyond coral biology to tackle ecosystem-level barriers to recovery, like the macroalgae overgrowing degraded reefs and hindering restoration. With this macroalgae barrier, we're also testing approaches where commercial value and community ownership help scale tools, complementing restoration already underway. As the portfolio branches into new territory, we're keeping it connected, linking teams across technologies, geographies, and applications so each new direction strengthens the whole.

- Dr. Liv Liberman, Director of Ocean and Climate and ACT Program Director



Dr. Liv Liberman
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Macroalgae-Based Bioproducts for Reef Restoration NEW PROJECT

Project Vision

Based at UC Berkeley, a team led by coral reef ecologist Dr. Adrienne Correa and blue bioeconomist Dr. Thiago Correa is turning nuisance seaweed harvested from degraded reefs into bioethanol and agricultural biostimulants. Working with community partners in French Polynesia, they aim to create economic incentives that sustain the macroalgae removal efforts that aid reef recovery.



Macroalgae-based bioproducts

The Challenge

On stressed and degraded coral reefs, fast-growing brown macroalgae increasingly crowd out corals, blocking coral larvae from settling and harming both wild colonies and restored outplants. To help reefs recover, restoration groups are removing this excess algae, but the effort generates truckloads of biomass that must be hauled away, dried, and disposed of, often in landfills where it decomposes into potent greenhouse gases. Disposal logistics and economics can limit how much removal actually happens. Without a useful, valuable purpose for the harvested algae, removal campaigns are hard to sustain at the scale reefs need.

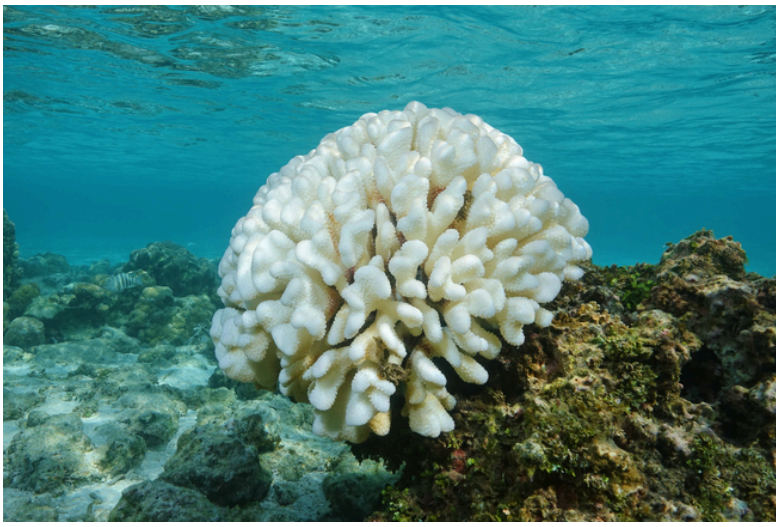
The Science

The team will use engineered strains of *Escherichia coli* and yeast that directly ferment the natural sugars in brown algae, without requiring conventional biomass pretreatment. The work has four parts:

1. **Fuel:** Starting with the nuisance seaweed *Turbinaria ornata*, the researchers are setting the first benchmarks for converting tropical macroalgae to ethanol.
2. **Fertilizer:** The team will process leftover biomass into plant biostimulants and test them on tomato crops. Sequencing will identify the microbial communities that drive the most promising formulations.
3. **Removal logistics:** Alongside local partners, the team will document community-led removal campaigns and measure removal rates, costs, and biomass yields.
4. **Reef response:** The team will track coral recruitment and benthic cover at removal sites and compare them with untouched reference reefs.

For island nations that depend on imported fuel and synthetic fertilizers, this circular model links reef recovery to local economic benefit. Brown macroalgae like *Turbinaria* and *Sargassum* are increasingly overwhelming reefs across the Pacific and Caribbean. A working model in Mo'orea could therefore transfer widely, giving reef communities everywhere a reason to keep removal efforts going.

Biohybrid Algae to Mitigate Bleaching NEW PROJECT



Biohybrid algae

Project Vision

Led by Dr. Daniel Wangpraseurt (Scripps Institution of Oceanography) and Dr. Virginia Weis (Oregon State University), this team aims to equip native coral symbionts with temporary, biodegradable coatings that boost their uptake and buffer heat stress. Working with Kewalo Marine Lab in Hawai'i and the Coral Gardeners nursery network, they aim to deliver a practical, non-GMO intervention to help corals withstand intensifying bleaching events.

The Challenge

Reef-building corals depend on a partnership with single-celled algae that supply most of the energy corals need to grow and build reefs. Rising ocean temperatures break down this partnership, causing corals to expel their algae and bleach. As marine heatwaves grow more frequent and severe, mass bleaching is pushing reefs toward collapse, with consequences for ecosystems, livelihoods, and coastal communities worldwide. Most restoration efforts today focus on growing and outplanting corals, but even these will be lost if they cannot withstand repeated heat stress. What's missing is a scalable tool that helps corals hold onto their algal partners and recover faster when bleaching strikes.

The Science

Using biodegradable nanoparticles, the team will develop a coating for native algal symbionts that does two jobs at once:

1. **Boosting uptake:** The particles display sugar-based signals that mimic the molecular "handshake" corals use to recognize compatible algae.
2. **Buffering stress:** They also carry antioxidants that neutralize reactive oxygen species that drive bleaching.

The coating will break down within weeks and will involve no genetic modification. Once the stress passes, both the algae and the coral return to their natural state.

This work will advance in stages:

1. Screening a library of coating formulations under reef-relevant conditions.
2. Testing uptake in the anemone model *Aiptasia*.
3. Running controlled heat-stress trials in corals to identify the best treatment timing.
4. Testing locally isolated symbionts on wild corals during forecasted bleaching periods, alongside opportunistic nursery pilots with restoration partners.

From the start, the team is also building an Ethical, Legal, and Social Implications (ELSI) framework, paired with an ecological safety and biosecurity assessment, to guide responsible use of the technology and lay the groundwork for regulatory engagement and eventual in-water approvals.

If successful, this would be the first technology to target the recognition system that governs how corals take up their symbionts. Near-term use would focus on nurseries and mesocosms. The longer-term vision is to grow coated algae in bioreactors and deliver them as sprays or gels over priority reefs ahead of forecast bleaching events. The platform could also be adapted to deliver heat-tolerant symbiont strains, support coral early life stages, or help other symbiotic reef animals such as giant clams.

STEM CELLS | HIGHLIGHT

Stem cells, including induced pluripotent stem cells, embryonic stem cells, and primordial germ cells, have the capacity to become other cell types, including sperm, eggs, and embryos. But they also provide the resources needed to confer resilience to some of the 21st-century threats species are facing in today's biodiversity crisis.

- Dr. Ashlee Hutchinson, Director of Stem Cell and Reproductive Technologies



Dr. Ashlee Hutchinson
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Safeguarding Tortoises: Diapause and Biobanking for Conservation NEW PROJECT

Project Vision

Led by PI Lukas Kratochvíl at Charles University, with Co-PI Boris Tezak at Wesleyan University, this cross-continental team is taking Revive & Restore's stem cell portfolio beyond the mammalian model and into non-avian reptiles. The project focuses on two endangered species, the Burmese star tortoise and the radiated tortoise. Working with Revive & Restore's Biotechnology for Bird Conservation PI, Dr. Guojun Sheng, the team will isolate and culture tortoise primordial germ cells, the germline stem cells that give rise to eggs and sperm. These cells will be used to develop in vitro models of reproductive biology and advance tools that could help conservationists manage offspring sex ratios as temperatures rise.



The endangered Burmese star Tortoise

The Challenge

Tortoises lack sex chromosomes. Instead, the incubation temperature determines whether the hatchling is male or female. As climate change shifts environmental temperatures, tortoise sex ratios are becoming increasingly imbalanced, which puts these ancient lineages at risk. Captive breeding programs face a parallel problem, because incubation protocols that are not optimized can reduce hatch success and skew the sex ratios of the next generation.

The Science

Tortoise embryos can enter diapause, a natural pause in development. The team will study how diapause works to learn how these species control reproductive timing with a view toward a natural mechanism for biobanking. Germline stem cell cultures will give the team in vitro models of both diapause and temperature-dependent sex determination (TSD). In partnership with Prague Zoo, Plzeň Zoo and Turtle Island, the team will turn these findings into optimized, standardized incubation protocols that support balanced sex ratios and healthy hatchlings in captive breeding programs.

Learn more about the project

WILD GENOMES | HIGHLIGHTS

As Wild Genomes projects reach completion, we're seeing how foundational genomic research can reveal critical conservation insights. This quarter's highlights demonstrate the value of looking beneath the surface by identifying genetic differences that could help restore kelp forests threatened by warming oceans and uncovering distinct sea cucumber populations with important implications for fisheries management and species recovery. Together, these projects illustrate how genomic discoveries can inform more precise, effective conservation strategies.

- Program Directors Ben Novak, Liv Liberman, and Ashlee Hutchinson

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Kelp Gametos | COMPLETED PROJECT

Project Vision
Use a living biobank of kelp gametophytes to test how bull kelp (*Nereocystis luetkeana*) from different parts of its range responds to marine heatwaves, and identify the genetic basis of thermal tolerance. The goal is to give managers and restoration practitioners options for populations already in decline.

Q&A with Project PI, Dr. Filipe Alberto, at the University of Wisconsin–Milwaukee

What is a big-picture takeaway that you learned during your project?

Bull kelp populations don't handle heat equally well. Nash, a PhD student in my lab, exposed gametophytes from six California sites to a simulated heatwave. Across that latitudinal gradient, California kelp held up well: photosynthetic efficiency stayed within a healthy range at peak heat and fully recovered afterward. Washington gametophytes were tested in a companion study at a milder 18°C, compared with 21°C for California. They did not stay healthy or recover. Those are real differences in thermal tolerance, and they matter because Washington's kelp populations are disappearing now. It also points to the value of biobanking. Much of the species' genetic diversity sits in its southern range, which is the part most threatened by climate change, so preserving it now keeps options open while science and policy catch up.



Dr. Filipe Alberto
Professor, Biological Sciences
University of Wisconsin, Milwaukee

Has anything surprised you along the way?

The results were broadly what you would hypothesize, but it was satisfying to see them borne out. What struck us was the scale of the underlying biology. About 9,000 genes were differentially expressed. Some differences between central and northern California appear constitutive rather than simply stress-triggered. The real challenge now is separating the genes that drive adaptation from those that merely react to heat. A second finding came from maintaining individual, single-genotype cultures over roughly eight years. The older a culture gets, the harder it becomes to cross that genotype on demand. Most labs keep mixed cultures and would never notice this, but it is critical once a specific genotype is selected for breeding or restoration.

Did you encounter any barriers or challenges?

Permitting, what the field calls "green tape," was the biggest obstacle. We planned a reciprocal transplant with the Puget Sound Restoration Fund, which is the gold standard for testing local adaptation. Permitting took a long time and ultimately didn't go forward. At one point, shipments of kelp crosses to Washington were blocked over concerns about an oyster virus found north of Humboldt. There was no evidence that our cultures carried it, or that it can grow on kelp at all. We were able to send a copy of the gametophyte biobank, but not live experimental crosses. The broader risk is that species can go extinct faster than permits allow the research needed to make hard decisions. The project itself ran smoothly, and Revive & Restore made a no-cost extension straightforward.

What's coming up for this work that you're excited about?

Our next step is to run California and Washington populations in a single combined experiment, which will confirm the differences directly. We will also keep narrowing thousands of candidate genes down to the ones that are causal. From there, two paths open up. One is classical breeding to bring heat-tolerant California backgrounds into Washington populations. The other is CRISPR, which I think the field is close to applying in kelp. Meanwhile, the Puget Sound Restoration Fund is testing gametophyte-based restoration using a copy of our biobank. Because gametophytes can be kept in a vegetative state year-round, restoration no longer has to wait for wild spore release.

Any new developments in your field worth highlighting?

Genetic tools for brown algae are advancing quickly. The most advanced gene-editing work comes from Susana Coelho's group on *Ectocarpus*, a related brown alga. Breeding cycles are also getting faster: Mike Graham's work shows that bull kelp can complete two generations a year rather than one. That is essential for breeding, which otherwise takes a decade to produce ten generations. I think progress on these husbandry problems will track kelp aquaculture growth. If commercial farming and conservation breeding develop together, the economics could finally support solving problems that no single academic lab can tackle alone.



Kelp gametos

Galápagos Sea Cucumbers | COMPLETED PROJECT

Project Vision
Generate the first genomic resources for the endangered and overexploited brown sea cucumber (*Isostichopus fuscus*), revealing how populations across the Galápagos Marine Reserve are structured and connected, and giving managers the biological foundation they need before managed breeding or genetic rescue.



Researchers from Cornell University and their collaborators collecting and measuring brown sea cucumbers in the Galápagos
Photo credit: Wilson Rivadeneira

Q&A with Project PI, Dr. Nina Overgaard Therkildsen, at Cornell University

What is a big-picture takeaway that you learned during your project?

This project started with a student in my lab, Jaime Ortiz-Pachar, who grew up in the Galápagos. Fishermen in his family had watched the sea cucumber fishery become depleted, and he wanted to help. When we started, we knew almost nothing about how the species is genetically structured across the islands. Because they are broadcast spawners whose larvae drift for weeks before settling, we expected one big, well-connected population. Instead, we found that the Galápagos holds genetically distinct groups living side by side on the same reefs that rarely interbreed. That matters for management because it suggests we shouldn't treat these sea cucumbers as a single stock, and future recovery efforts, such as breeding programs, will need to account for which group an animal belongs to. Geography alone won't tell you which population a sea cucumber belongs to.

Has anything surprised you along the way?
The two lineages themselves were the main surprise, but how they differ was just as striking. In many marine species, recent studies find that differentiation is concentrated in a few large chromosomal inversions that hold co-adapted genes together despite gene flow. We found numerous inversions, but they don't explain the split. Instead, the differences are spread across all 23 chromosomes and across a wide range of metabolic, cellular, and neuroendocrine pathways. That points to a history of isolation followed by secondary contact, making this species a potentially important counterexample for understanding how reproductive barriers persist in the ocean. One hypothesis we're excited to test is timing. Because these animals broadcast spawn, even small differences in gamete release timing could keep lineages apart on the same reef. We also found two highly divergent individuals that may represent a third cryptic lineage, possibly even a separate species.

Did you encounter any barriers or challenges?

The project became an exercise in what was possible. Getting permits to collect samples and export them from Ecuador took much longer than expected, partly because *I. fuscus* is listed under CITES and shipping is complicated. In addition, many populations live in remote, hard-to-reach sites. We couldn't sample every part of the species' range as planned, so we made up for it by sampling much more widely within the Galápagos. Revive & Restore's flexibility with timelines was critical to getting it all done.

What's coming up for this work that you're excited about?

Our reference genome for *I. fuscus* has been published, and we're now preparing a manuscript describing our other findings. Next, we want to sample more of the species' range across mainland Central and South America to learn where these genetic groups originated. On the applied side, we're working toward a fast, practical way to tell the groups apart, suitable for use locally in the Galápagos. I'd most love to see protected areas that preserve enough spawning populations, with harvest managed so source populations aren't depleted. We're also excited to expand genomic work to other Galápagos species, such as mangroves.

Any new developments in your field worth highlighting?

My lab focuses on making whole-genome sequencing affordable enough to study entire populations, because you need large numbers of animals to answer these questions. This project yielded very detailed data, thanks in part to Illumina's donated sequencing capacity. But I think you can learn most of the same things from lighter, cheaper sequencing of many more animals. That's the direction I'm excited about: sequencing broadly across many species, which leaves room to discover things you didn't expect, just like we did here.



The brown sea cucumber, *Isostichopus fuscus*
Photo credit: Wilson Rivadeneira



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Detail of *Understory, 2007* by Isabella Kirkland