**METHODS**

*Study Design and Location*

Colonies of *Montipora capitata* across Kāne’ohe Bay, O’ahu, Hawai’i, USA were tagged and sampled in order to analyze spatial variability of *Symbiodinium* clades. Corals were tagged on patch reefs and fringing reefs in the northern, central and southern regions of Kāne’ohe Bay (Figure \_). Five patch reefs and three fringing reefs were tagged in each region of the bay. At each patch reef, 30 colonies were tagged; 10 colonies each from windward slope, top and leeward slope of the patch reef. Along the windward and leeward slopes, colonies were tagged along a depth gradient. Given the lack of leeward slope on fringing reefs, 20 colonies were tagged at each site; 10 colonies each from the top and slope of the fringing reef. Tagging and sampling of colonies took place between 7 June 2016 and \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_. Fragments from each colony were frozen in liquid nitrogen and archived for future use in DNA extraction and collaborative efforts analyzing biogeochemistry and energetics in Kāne’ohe Bay. In total, 15 patch reefs and \_\_\_ fringing reefs were sampled across Kāne’ohe Bay resulting in a total sample size of n=\_\_\_\_\_\_\_ colonies.

*Colony Tagging and Sample Collection*

Ten weights with attached floats were randomly deployed at each area of the reef. The closest colony of *Montipora capitata* in proximity to each float was then tagged and a small branch fragment (~4-5cm) was removed. Photographs were taken of each colony for color morph and size analysis by visual assessment. Tissue biopsies were taken from each collected fragment and placed in 500μL DNA buffer (5M NaCl, 0.5M EDTA) with 1% sodium dodecyl sulfate (SDS) while the remaining fragment was frozen in liquid nitrogen to be stored at -80°C as an archive for future analyses. DNA was extracted from each sample biopsy following a modified CTAB-chloroform protocol (dx.doi.org/10.17504/protocols.io.dyq7vv).

*Symbiodinium Community Analysis*

Quantitative PCR was used to determine the symbiont community of clade C and D *Symbiodinium* in each collected sample. Based on internal transcribed spacer (ITS2), onlyclade C and D *Symbiodinium* were expected to result from existing clade-level primers.