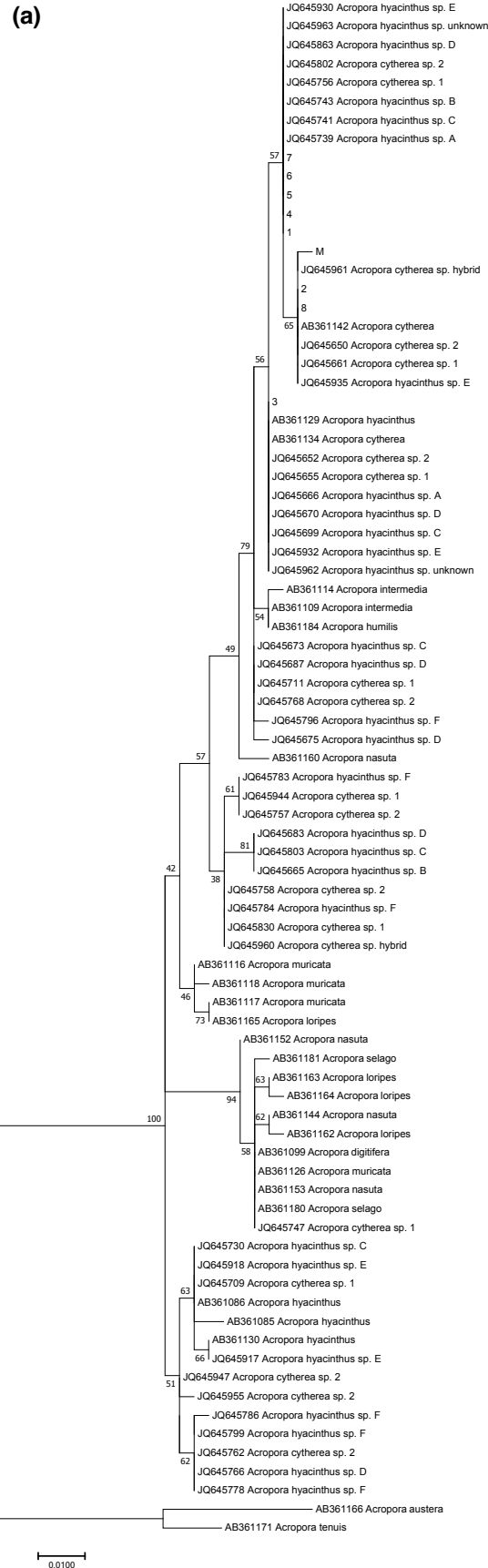
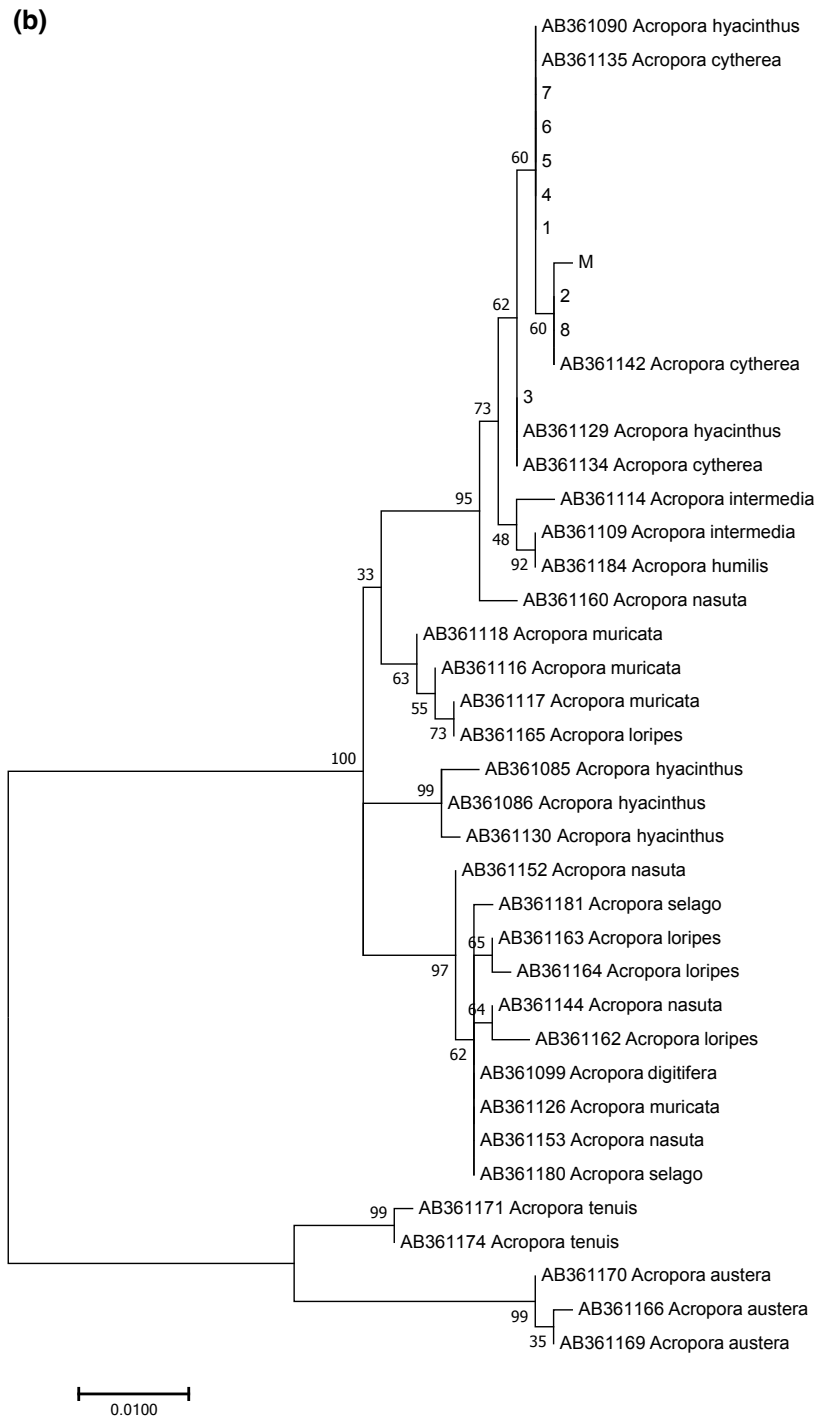


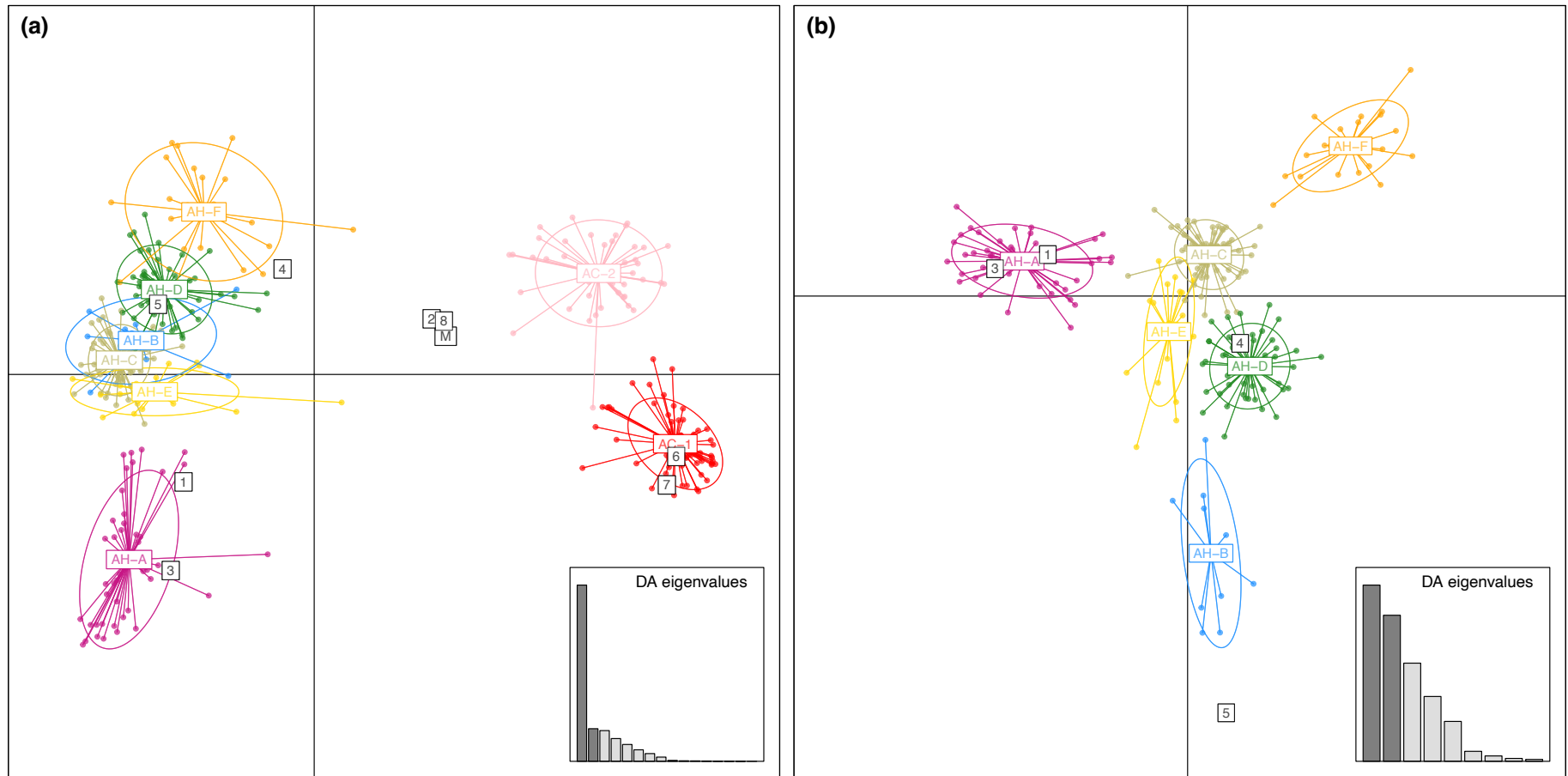
**Fig. S1.** Pictures of the main colony were automatically captured every day from 18 October 2015 to 14 April 2016 with a digital camera protected by a waterproof housing. We could not take pictures of the main colony on some days (dates in red font). We could not obtain any pictures at all on 25 and 26 January and from 28 January to 13 February because of errors



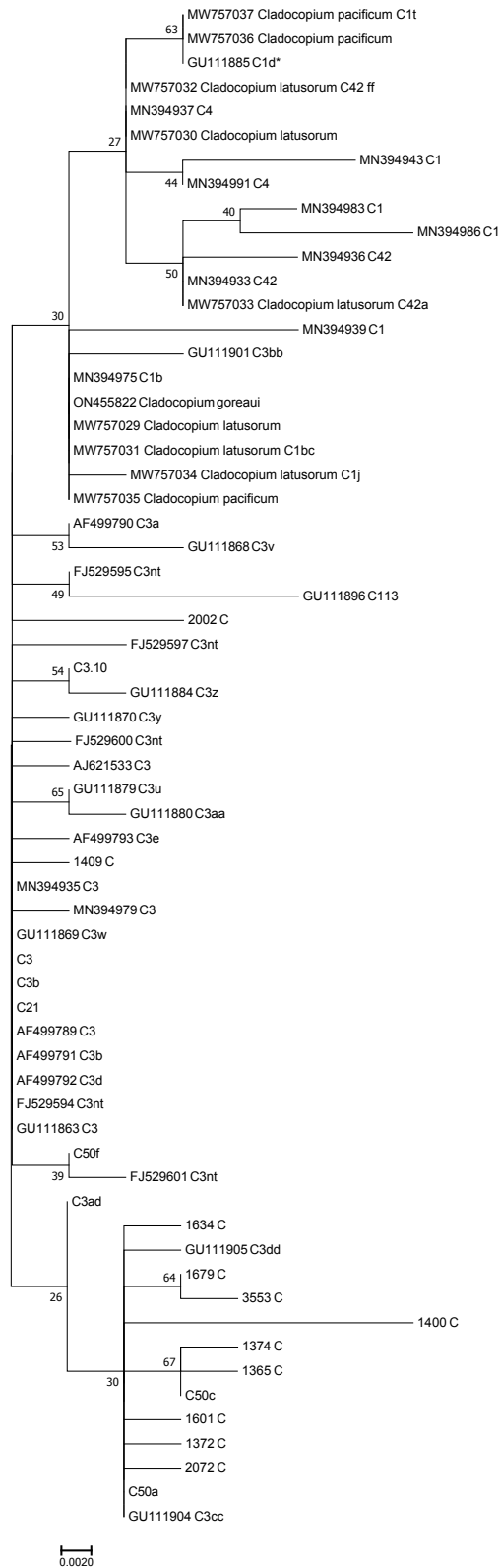


**Fig. S2.** Maximum-likelihood-based phylogenetic trees constructed by using (a) 331-bp-long and (b) 604-bp-long mtCR sequences of *Acropora* corals. The reference sequences were derived from studies by Ladner and Palumbi (2012) and Suzuki et al. (2016). The GenBank accession numbers of the reference sequences are listed in the phylogenetic trees. The reference sequences were selected to avoid duplication of sequences in the same region and to identify the morphological/genetic lineages





**Fig. S3.** Discriminant analysis of principal components (DAPC) clustering of the data obtained from the nine *Acropora* colonies and previous data from Ladner and Palumbi (2012). DAPC clusters of (a) all lineages and (b) lineages related to *Acropora hyacinthus*. The AC-1 and AC-2 genetic lineages are related to *Acropora cytherea*, and the AH-A to AH-F genetic lineages are related to *A. hyacinthus*. Each plot depicts the multilocus genotypes, including the nuclear loci and mtCR sequences, of the nine colonies. M: main colony; 1–8: nearby colonies



**Fig. S4.** Maximum-likelihood-based phylogenetic tree of the ITS2 sequences of the symbionts