



Figure S1. Genome coverage distributions of the 21 *Acropora cervicornis* samples. The one called “Acerv” is sequenced to an average depth of over 150. The 20 low-coverage samples, 5 each from Florida (FL), the Virgin Islands (VI), Belize (BE) and Curacao (CU), have coverage around 5 to 10. More precisely height of the curve indicates the proportion of the 1,692,739 SNVs described in the main paper where the sample has the number of sequencing reads indicated on the horizontal axis. For example, roughly 1% of the SNVs had exactly 150 reads in the high-coverage sample while nearly 2% had 170 reads.