*Cliona* microsatellite file description.

Sample ID is coded by site with a random collection number. For example, BE is a sample from Belize, BH, is from the Bahamas, and so forth.

Genotypes are listed in base pairs. Missing data are blank and cells are highlighted in pink. Alleles are listed in separate columns. So, for example, the A-1 column is the first allele and A-2 is the second allele at locus A. The following table can be used to match the loci in the spreadsheet to loci in the manuscript.

|  |  |
| --- | --- |
| Locus in spreadsheet | Locus in manuscript |
| A | Cd23 |
| B | Cd14 |
| C | Cd106 |
| D | Cd41 |
| E | Cd137 |
| F | Cd141 |
| G | Cd114 |
| H | Cd81 |
| I | Cd63 |
| J | Cd39 |  |

Geographic information: Location is collection site, specific areas are sites within collection sites (and the corresponding coordinates are listed in the next two columns).

Depth (in meters) is the depth at each specific area.