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| **STEP** | **PARAMETER DESCRIPTION** | **PARAMETER(S)** |
| **PREPROCESSING** | Minimum length threshold | 350 |
|  | Number of ambiguities tolerated | 0 |
|  | Detection of proximal primer sequence | Complete and perfect |
|  | Detection of distal primer sequence | Incomplete, with a maximum of two mismatches |
| **CLUSTERING** | Chosen level of similarity (%) | 95 |
|  | Ignoring differences in homopolymer lengths | Yes |
| **FILTERING** | Chosen clustering similarity threshold | 95 |
|  | Used taxonomic database | SILVA (r114) |
|  | Chosen taxonomic level | Phylum |
|  | Similarity or confidence threshold (%) | 90 |
| **HOMOGENIZATION** | High-quality reads kept for each sample | 10,000 |
| **GLOBAL ANALYSIS** | Chosen level of similarity (%) | 95 |
|  | Ignoring differences in homopolymer lengths | Yes |