Table S5. General statistics of amplicon survey quality control.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Raw data | Nucleotide sequences after quality processing | | | Number of sequences after frameshift and stop-codon correction | Low-quality sequences discarded |
| Number of sequences | Mean sequence length ± SD (bp) | Percentage of GC (%) |
| SCD0-A | 230,221 | 39,297 | 343.7 ± 14.7 | 38.93 | 31,696 | 198,525 (86.2%) |
| SCDE-A | 168,403 | 55,519 | 346.9 ± 10.2 | 38.57 | 42,508 | 125,895 (74.8%) |
| SCD0-E | 115,970 | 12,653 | 377.9 ± 12.0 | 41.24 | 8,273 | 107,697 (92.9%) |