Table: Analysis of raw sequence data before accounting Primer ID for downstream analysis.

|  |  |  |
| --- | --- | --- |
|  | Run1 | Run2 |
| Total raw reads | 125865 | 40544 |
| Total read discarded for no primer | 2962 | 751 |
| Total reads discarded for no MID | 7557 | 1105 |
| Total reads discarded for short length | 32 | 14 |
| Total reads discarded for ambiguous base in Primer ID | 257 | 37 |
| Total reads after demultiplexing | 115057 | 38637 |

Table: Analysis of demultiplexed sequence reads with Primer ID into generation of consensus sequences

|  |  |  |
| --- | --- | --- |
|  | Run1 | Run2 |
| Total reads discarded because their Primer ID had less than 3 representative sequences | 18011 | 7397 |
| Total reads after discarding Primer ID with less than 3 representative sequences | 97046 | 31240 |
| Total reads after quality trimming | 94096 | 31323 |
| Total reads after filtering by sequence length and Primer ID with less than 3 representative sequences | 93731 | 31321 |
| Total consensus sequence generated | 4704 | 2751 |