|  |  |
| --- | --- |
| **Pipeline step** | **Sequences output** |
| Total read number | 28438 |
| Quality trimming | 28438 (100%) |
| Filtering by 5’ sequence | 27876 (98%) |
| Filtering by 5’ sequence #2 | 27708 (97%) |
| Filtering by 3’ sequence | 26777 (94%) |
| Filtering by 3’ sequence #2 | 26206\* (92%) |
| Unique sequences | 1185 |

**Supplementary Table 1: Analysis by next generation sequencing of recovered compatible origins.** Total read number obtained and the impact of the analysis pipeline are shown. \*Number of sequences used in downstream analysis.