**Supplemental Table S3. Sequence variants identified by read mapping relative to the reference *T. parva* Muguga genome assembly.**

|  |  |  |  |
| --- | --- | --- | --- |
|  | ***T. parva* Muguga genome with coverage that satisfies SNP calling filter** | **Sequence variants *vs*. reference *T. parva* Muguga genome1** | |
| **Isolate** | **Base pairs (%)** | **SNPs** | **INDELs** |
| BV115 | 99.50 | 107 | 18 |
| Marikebuni | 96.81 | 40,228 | 11 |
| Uganda | 97.48 | 40,835 | 7 |
| Buffalo\_3081 | 95.61 | 91,840 | 4 |

1Sequence variants, including single nucleotide polymorphisms (SNPs) and small insertions and deletions (INDELs) were identified using the Genome Analysis Toolkit.