**Supplementary tables**

**Table T1**. Number of reads generated from the multiplexed samples on Illumina MiSeq. Number of fastq reads represents the raw reads and number of fasta reads represents the reads after adapter/primer cutting and quality filtering process

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Sample number | Sample name | Forward reads (R1) | | Reverse reads (R2) | |
| Number of fastq reads | Number of fasta reads | Number of fastq reads | Number of fasta reads |
| 1 | GR2\_150303 | 1 278 402 | 1 262 993 | 1 278 402 | 1 210 674 |
| 2 | GR2\_150414 | 1 825 726 | 1 803 465 | 1 825 726 | 1 727 875 |
| 3 | GR2\_150519 | 1 237 967 | 1 223 698 | 1 237 967 | 1 174 589 |
| 4 | GR2\_150709 | 1 129 891 | 1 116 172 | 1 129 891 | 1 075 076 |
| 5 | GR2\_151117 | 1 107 818 | 1 093 554 | 1 107 818 | 1 048 223 |