**Additional file3: Table S3:**

**Basic information of high-throughput sequencing based on bacteria 16S rRNA in the *Leptocybe invasa***

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Sample | Number ofPE Reads | Number ofRaw Tags | Number ofClean Tags | Number ofEffect Tags | Effective Proportion (%) |
| Female | 169818 | 162586 | 147688 | 147402 | 86.80 |
| Male | 382629 | 370680 | 355543 | 328833 | 85.94 |