Table 2 Salmon quantitative analysis of gut microbiota samples from three populations of *Viridovipera stejnegeri* (average values)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Population | Length (bp) | Effective Length (bp) | TPM | Num Reads |
| Anhui | 439.22 | 225.69 | 9.94 | 86.29 |
| Guizhou | 530.26 | 277.60 | 10.26 | 101.29 |
| Hunan | 634.17 | 399.12 | 9.60 | 106.09 |

Notes: Length (bp): actual length of original FASTQ sequence; Effective length (bp): FASTQ sequence effective length; TPM value (transcripts per kilobase of exon model per million mapped reads): transcripts per thousand base transcripts per million mapped reads, summarizing length, expression, and number of genes, used to estimate sample expression; Num reads: estimated number of reads matched to each sample.