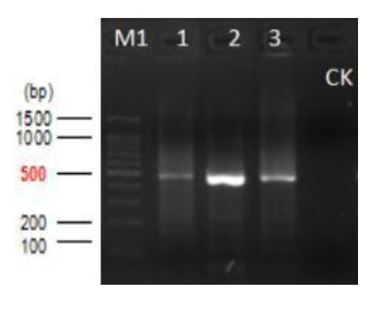
**Table S1. Raw read count of honey bee at three different migratory site and the number of reads that have passed through different analysis process**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Sample Name** | **Raw paired end read** | **Raw tag merged using FLASH** | **Clean tags after specific filtering** | **Effective tags after removing the chimera sequence** | **Effective %** | **Average Length  (nucleotides)** | **Number of bases in the Effective tag** | **Per cent GC** | **Read Phred quality score distribution (%)** | |
| **Q20** | **Q30** |
| KKL | 1,67,676 | 1,50,654 | 1,48,162 | 1,40,723 | 83.93 | 426 | 6,00,04,015 | 53.49 | 98.50 | 94.76 |
| CDM | 1,55,799 | 1,44,629 | 1,42,033 | 1,31,266 | 84.25 | 418 | 5,48,97,723 | 52.35 | 98.34 | 94.37 |
| PY | 1,55,622 | 1,14,893 | 1,12,776 | 1,02,377 | 65.79 | 418 | 4,27,94,358 | 50.95 | 98.18 | 93.95 |



**Figure S1. DNA extraction - DNeasy Blood and Tissue Kit**

**Figure** **S2. Agarose gel showing amplification of 500 bp gene corresponding to V3-V4 region of 16srDNA gene of *Apis cerana indica,* M-100bp ladder, CK- Water control**