

Supplementary

Table S1. OTU statistics for gut microbiome samples of adult honeybee workers of *A.m.carnica*(C1-C5)

| Sample name | No. tags | No. OTUs |
|-------------|----------|----------|
| C1 | 61242 | 55 |
| C2 | 59904 | 49 |
| C3 | 62694 | 61 |
| C4 | 62913 | 54 |
| C5 | 69815 | 154 |
| J1 | 54270 | 47 |
| J2 | 59215 | 52 |
| J3 | 55643 | 45 |
| J4 | 56287 | 46 |
| J5 | 59502 | 51 |
| Total | 601485 | 117 |

and *A.m.jemenitica* (J1-J5).

Table S3. Statistical analysis (t test) at phylum level between gut microbiome of adult honeybee workers of *A.m.carnica*(A.M.C) and *A.m.jemenitica*(A.M.J).

| Phylum | Average relative abundance(A.M.C) | Average relative abundance(A.M.J) | P-value |
|----------------|-----------------------------------|-----------------------------------|----------|
| Actinobacteria | 9.9462362 | 6.4824688 | 0.208133 |
| Bacteroidetes | 1.3256144 | 0.4242898 | 0.420635 |
| Cyanobacteria | 0.0348738 | 0.0046542 | 0.031746 |
| Firmicutes | 57.278132 | 48.569838 | 0.06698 |
| Proteobacteria | 31.402252 | 44.518749 | 0.037724 |
| TM7 | 0.0060158 | 0 | - |
| Tenericutes | 0.000573 | 0 | - |
| Thermi | 0.0063024 | 0 | - |

Table S4. Statistical analysis (t test) at species level between gut microbiome of adult honeybee workers of *A.m.carnica*(A.M.C) and *A.m.jemenitica*(A.M.J).

| species | Average relative abundance(A.M.C) | Average relative abundance(A.M.J) | P-value |
|-----------------------------------|-----------------------------------|-----------------------------------|-----------|
| <i>Bacteroides_fragilis</i> | 0.1568376 | 0.0016822 | 0.655836 |
| <i>Bacteroides_ovatus</i> | 0.2062484 | 0.00101 | 0.372748 |
| <i>Blautia_producta</i> | 0.1177438 | 0.0024168 | 0.517904 |
| <i>Commensalibacter_intestini</i> | 0.0034778 | 3.1556746 | 0.066955 |
| <i>Melissococcus_plutonius</i> | 3.3557112 | 0.000674 | 0.034454* |
| <i>Ruminococcus_gnavus</i> | 0.1689268 | 0 | - |
| <i>Saccharibacter_floricola</i> | 0.4808742 | 0 | - |
| <i>Snodgrassella_alvi</i> | 1.3992314 | 17.900698 | 0.008948* |

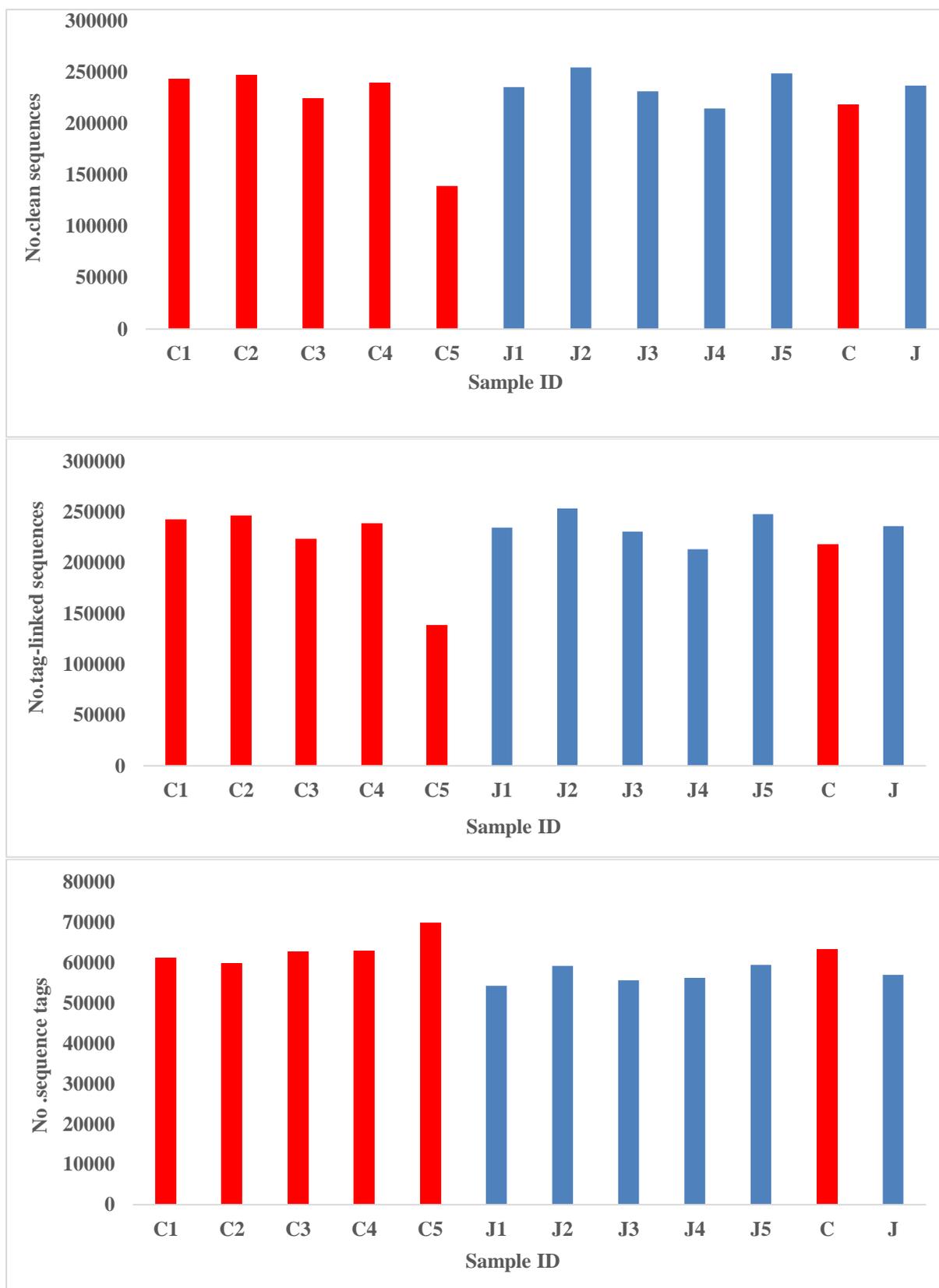


Figure S1. Comparison among numbers of clean sequences, tagged sequences, and recovered sequence tags at the sample and group levels for gut microbiome of adult honeybee workers of *A.m.carnica* (C1-C5, red) and *A.m.jemenitica* (J1-J5, blue).

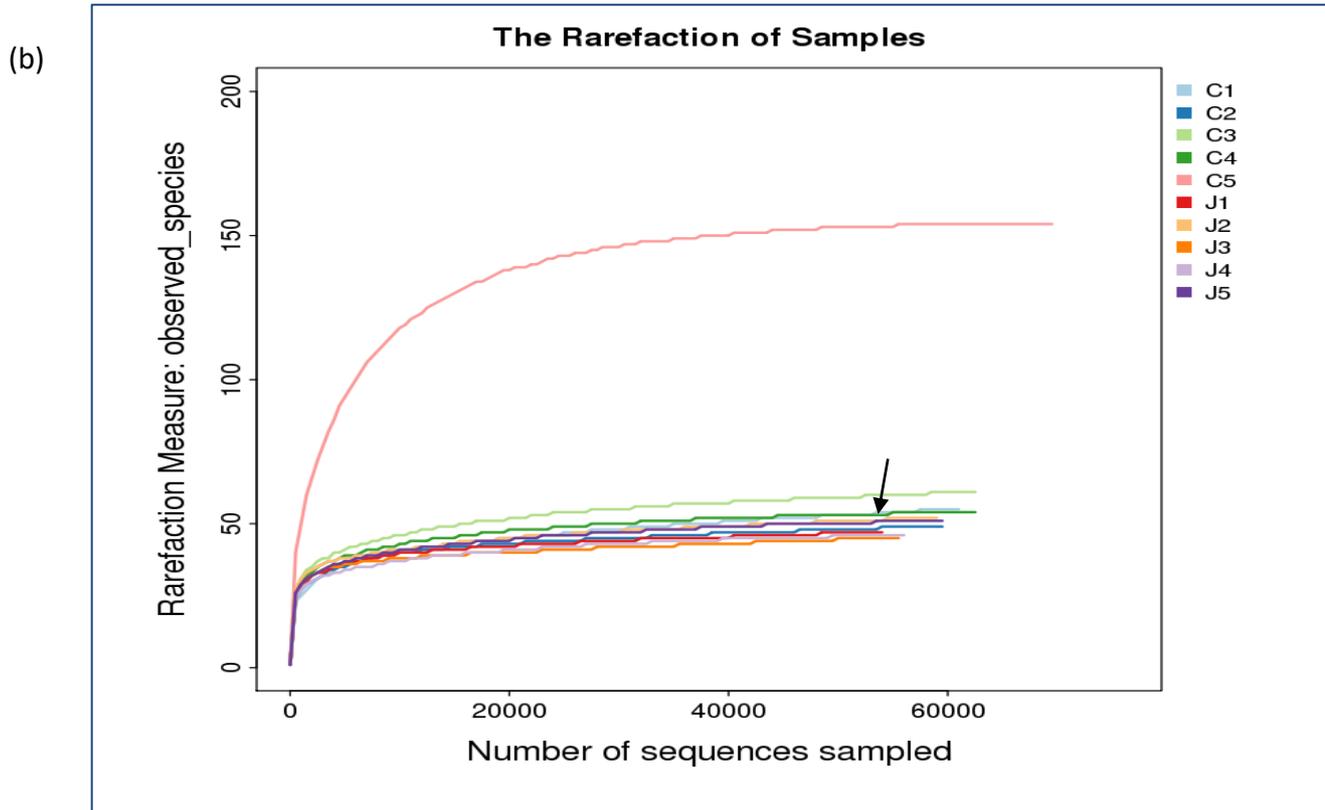
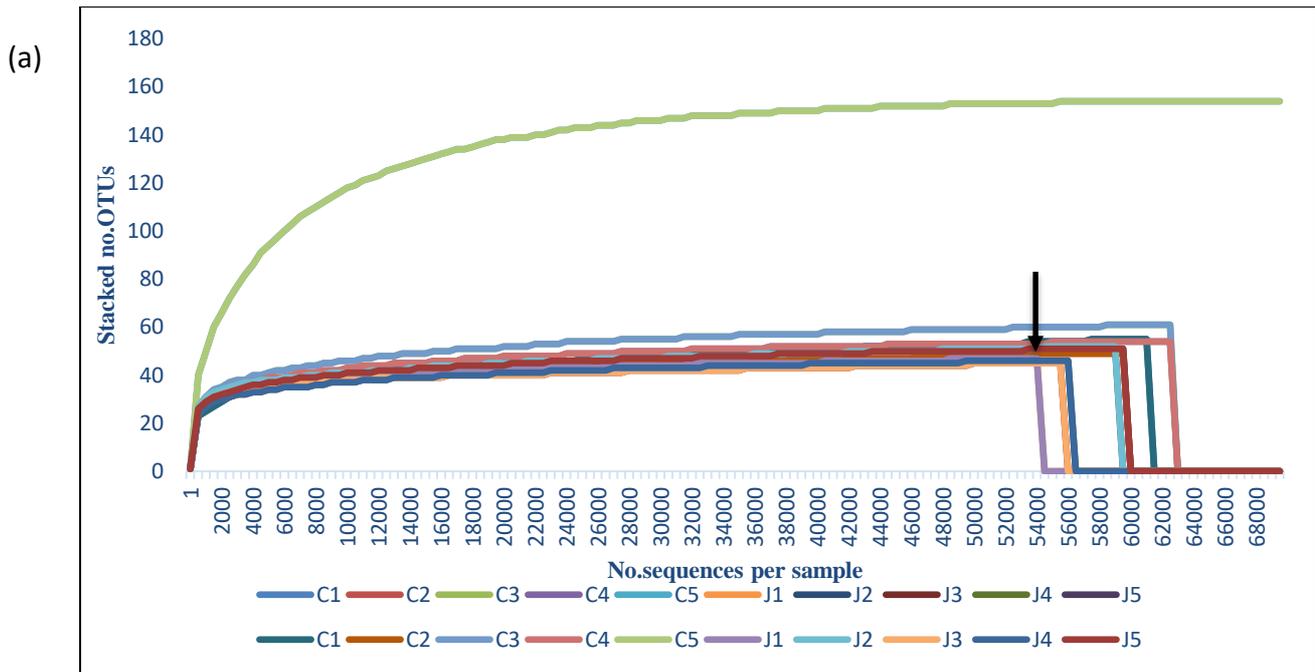


Figure S2. (a) Stacked number of OTUs,(b) number of observed species as rarefaction measures. The arrows point at the suitable sample size (54,000 sequence reads) for analysing taxonomy abundance. (C1 -C5)=*A.m.carnica*, (J1 - J5)=*A.m.jemenitica*.

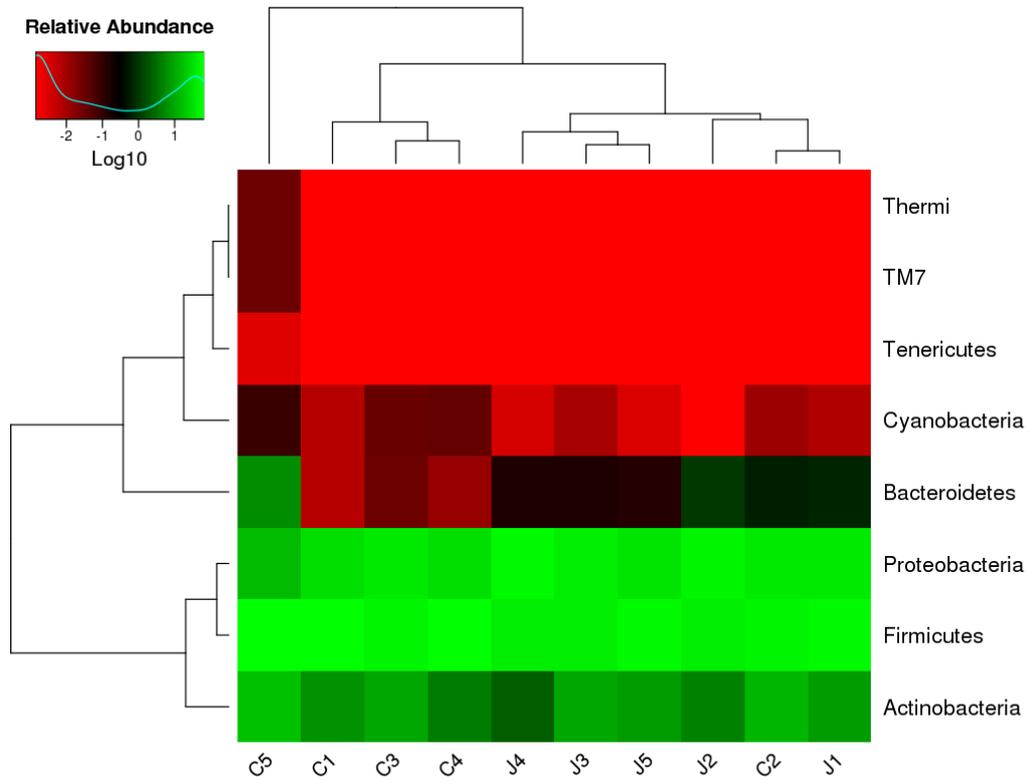


Figure S3. Heat map at the phylum level for gut microbiome of adult honeybee workers of *A.m.carnica*(C1-C5) and *A.m.jemenitica*(J1-J5).

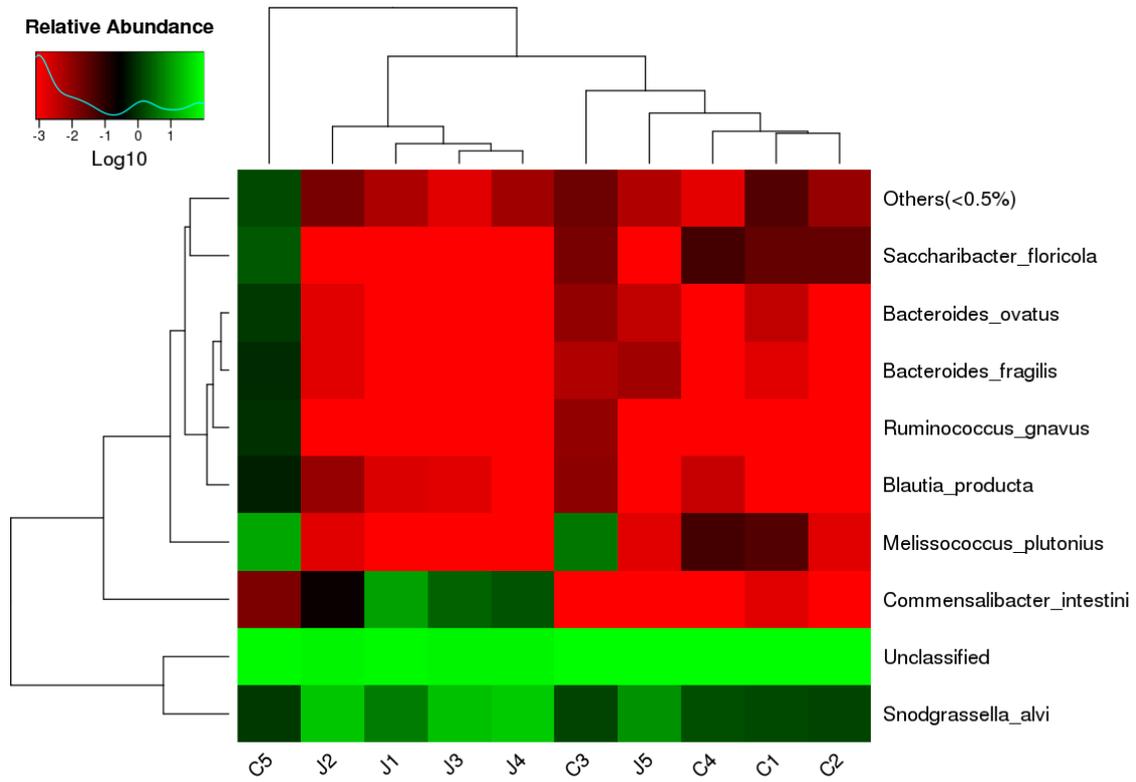


Figure S4. Heat map at the species level for gut microbiome of adult honeybee workers of *A.m.carnica*(C1-C5) and *A.m.jemenitica*(J1-J5).