**Supplement table 1: The raw sequence of high-throughput sequencing of samples**

| Sample | Clean reads | Clean bases | Clean read pairs | Clean reads % | Clean bases % | Q20 %     | Q30 %     |
|--------|-------------|-------------|------------------|---------------|---------------|-----------|-----------|
| L1     | 163963156   | 23569788720 | 81981578         | 0.9825        | 0.9416        | 0.9709    | 0.9215    |
| L2     | 64399990    | 9317316027  | 32199995         | 0.9812        | 0.9464        | 0.9691    | 0.917     |
| L3     | 112921240   | 16312265626 | 56460620         | 0.9815        | 0.9452        | 0.97      | 0.9205    |
| N1     | 115600450   | 16771036134 | 57800225         | 0.98          | 0.9479        | 0.9691    | 0.9185    |
| N2     | 111324446   | 16060916799 | 55662223         | 0.9817        | 0.9442        | 0.9707    | 0.9219    |
| N3     | 109590462   | 15892948791 | 54795231         | 0.9781        | 0.9456        | 0.9677    | 0.9153    |

Q20: the percentage of bases with quality value more than 20;  
Q30: the percentage of bases with quality value more than 30  
L1, L2, L3: PAH+LPS  
N1, N2, N3: PAH
Supplement table 2: The mapped ratio of all samples

| Sample | Total reads | Total mapped | Mapped ratio(%) | Unique mapped | Unique mapped ratio(%) |
|--------|-------------|--------------|-----------------|---------------|------------------------|
| L1     | 163861670   | 148455160    | 90.6            | 137240519     | 83.8                   |
| L2     | 64391720    | 59904805     | 93.0            | 55155645      | 85.7                   |
| L3     | 112909718   | 102640921    | 90.9            | 95503501      | 84.6                   |
| N1     | 115593862   | 107520522    | 93.0            | 100825271     | 87.2                   |
| N2     | 111319630   | 101893976    | 91.5            | 94876644      | 85.2                   |
| N3     | 109550672   | 102353825    | 93.4            | 93566123      | 85.4                   |

L1,L2,L3: PAH+LPS

N1,N2,N3: PAH