Table S1: Distribution of clean data (%) retrieved in each sample (C = control and G = Gongolase extract (PEF)).

| Sample | Seq. Strategy | Raw Data Size (bp) | Raw Read Number | Clean Data Size (bp) | Clean Read Number | Clean Data Rate (%) |
|--------|--------------|-------------------|-----------------|----------------------|-------------------|---------------------|
| C-HCT  | SE50         | 1,180,781,750     | 23,615,635      | 1,172,348,200        | 23,446,964        | 99.28               |
| C-MCF  | SE50         | 1,185,079,300     | 23,701,586      | 1,181,977,900        | 23,639,558        | 99.73               |
| G-HCT  | SE50         | 1,187,083,100     | 23,741,662      | 1,174,294,400        | 23,485,888        | 98.92               |
| G-MCF  | SE50         | 1,196,192,700     | 23,923,854      | 1,193,964,450        | 23,879,289        | 99.81               |

Table S2: Summary of the quality control analysis of whole genome RNA sequencing (C = control, G = Gongolase extract (PEF) and Y= yes passed the QC).

| Sample | Clean Read 1 Q20 (%) ≥ 90 | Clean Reads ≥ 20 (M) | Gene Unique Mapping Ratio (%) ≥ 80 | Genome Mapping Ratio (%) ≥ 50 |
|--------|---------------------------|----------------------|------------------------------------|-----------------------------|
| C-HCT  | 98.7 (Y)                  | 23.45 (Y)            | 91.37 (Y)                          | 96.31 (Y)                   |
| C-MCF  | 98.8 (Y)                  | 23.64 (Y)            | 90.38 (Y)                          | 96.53 (Y)                   |
| G-HCT  | 98.8 (Y)                  | 23.49 (Y)            | 90.34 (Y)                          | 96.28 (Y)                   |
| G-MCF  | 98.7 (Y)                  | 23.88 (Y)            | 86.45 (Y)                          | 95.23 (Y)                   |