**Supplementary Table 3. cirRNA of sequence assembly after Illumina sequencing**

| Sample | Total raw reads | Total clean reads | Total clean bases (G) | Clean reads Q20 (%) | Clean reads Q30 (%) | Clean reads GC (%) |
|--------|----------------|-------------------|-----------------------|---------------------|---------------------|-------------------|
| N1     | 86,513,462     | 86,111,490        | 12,765,377,103        | 97.75               | 94.01               | 46.05             |
| N2     | 87,686,226     | 87,318,658        | 12,951,267,527        | 97.89               | 94.20               | 46.12             |
| N3     | 87,117,818     | 86,747,888        | 12,851,118,144        | 97.90               | 94.22               | 46.32             |
| C1     | 86,365,144     | 85,961,488        | 12,762,351,542        | 97.72               | 93.83               | 46.79             |
| C2     | 84,021,294     | 83,638,776        | 12,418,027,143        | 97.74               | 93.88               | 46.68             |
| C3     | 87,917,400     | 87,522,794        | 12,991,272,724        | 97.79               | 93.97               | 46.44             |
| C4     | 86,401,168     | 86,050,726        | 12,777,420,665        | 97.88               | 94.20               | 46.30             |
| C5     | 87,564,628     | 87,172,452        | 12,931,472,941        | 97.79               | 94.07               | 46.82             |
| EA1    | 87,036,710     | 86,731,504        | 12,859,715,146        | 98.31               | 95.30               | 47.00             |
| EA2    | 87,240,660     | 86,922,730        | 12,902,054,859        | 97.97               | 94.50               | 46.42             |
| EA3    | 87,933,844     | 87,563,098        | 12,989,306,382        | 97.72               | 93.93               | 46.69             |
| EA4    | 86,232,240     | 85,855,694        | 12,733,206,431        | 97.83               | 94.16               | 47.20             |
| EA5    | 86,747,152     | 86,403,232        | 12,831,165,103        | 97.90               | 94.33               | 46.49             |

N1–N3: 3 samples of sham group; C1–C5: 5 samples of control group; EA1–EA5: 5 samples of GV-EA group.
GV-EA, governor vessel electroacupuncture.
Q20, the percentage of bases with a Phred value > 20; Q30, the percentage of bases with a Phred value > 30.