

Supplementary Table 3. ciccRNA 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.