

Supplementary Table 2. miRNA 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	20,602,815	16,812,961	377,421,323	99.87	99.51	44.36
N2	22,727,522	20,734,859	465,420,146	99.83	99.35	44.74
N3	22,748,552	20,582,359	461,812,858	99.66	98.88	44.74
C1	22,729,802	20,742,210	466,871,047	99.75	99.17	43.61
C2	22,150,180	18,354,613	419,632,428	99.77	99.21	43.93
C3	20,686,274	19,211,731	431,076,550	99.63	98.81	43.25
C4	20,841,939	19,403,461	435,164,686	99.66	98.90	43.60
C5	18,848,171	17,295,282	400,237,795	99.58	98.59	44.14
EA1	18,299,038	16,575,668	392,659,262	99.66	98.78	44.41
EA2	22,075,844	18,428,421	430,949,517	99.74	99.14	44.61
EA3	18,517,079	16,376,516	380,947,950	99.61	98.63	44.14
EA4	22,998,863	20,797,725	488,440,076	99.79	99.26	44.19
EA5	19,253,414	16,829,851	397,464,526	99.76	99.20	44.54

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.