

S5 Table. Statistics of genome assemblies.

| | <i>Meloidogyne incognita</i> | <i>Meloidogyne arenaria</i> | <i>Meloidogyne javanica</i> |
|-----------------------|------------------------------|-----------------------------|-----------------------------|
| Assembly software | Mira + Sspace | Mira + Sspace | Mira + Sspace |
| # of contigs | 13,148 | 28,641 | 33,008 |
| Cumulative size (bp) | 180,221,179 | 256,294,081 | 235,523,531 |
| Contig N50 bp (L50) | 32,388 (1,440) | 14,448 (5,017) | 9,986 (6,981) |
| # of scaffolds | 12,091 | 26,196 | 31,341 |
| Cumulative size (bp) | 183,531,997 | 258,067,405 | 235,798,407 |
| Scaffold N50 bp (L50) | 38,588 (1,209) | 16,462 (4,438) | 10,388 (6,741) |
| Number of N's | 3,319,814 (1.8%) | 1,803,958 (0.69%) | 312,237 (0.13%) |
| GC percent | 29.75% | 29.97% | 29.96% |
| Accession Numbers | PRJEB8714 (ERS1696677) | PRJEB8714 (ERS671129) | PRJEB8714 (ERS671128) |