Table S1 The repetitive sequences of *M. dispar* GS01

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Type | Number | Total length (bp) | In Genome (%) | Average length (bp) |
| Interspersed nuclear elements | LTR | 29 | 2,183 | 0.2048 | 75 |
| DNA | 20 | 1,083 | 0.1016 | 54 |
| LINE | 12 | 859 | 0.0806 | 72 |
| SINE | 2 | 104 | 0.0098 | 52 |
| RC | 0 | 0 | 0 | 0 |
| Total | 63 | 4,229 | 0.3968 | 67 |
| Type | Number | Total length (bp) | In Genome (%) | Repeat Size (bp) |
| Tandem repeat | TR | 106 | 34,633 | 3.2495 | 2~1,921 |
| Minisatellite DNA | 72 | 3,585 | 0.3364 | 11~57 |
| Microsatellite DNA | 12 | 363 | 0.0341 | 2~6 |

Note that the LTR means long terminal repeat, DNA means DNA transposons, RC represents rolling circle, LINE represents long interspersed nuclear elements, SINE represents short interspersed nuclear elements, and TR means tandem repeat.