Supplementary table 6. Results from RepeatMasker analysis.

Total length: 2,551,871,755 bp (2551871755 bp excl N/X-runs)

GC level: 33.26 %

Bases masked: 1,311,902,262 bp (51.41 %)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  | Number of elements | Length occupied (bp) | % of sequence |
| SINEs: |  | 124,489 | 24,071,223 | 0.94 |
|  | ALUs | 0 | 0 | 0 |
|  | MIRs | 0 | 0 | 0 |
|  |  |  |  |  |
| LINEs: |  | 157,703 | 86,510,215 | 3.39 |
|  | LINE1 | 4,894 | 838,426 | 0.03 |
|  | LINE2 | 6,363 | 1,779,545 | 0.07 |
|  | L3/CR1 | 4,115 | 2,448,717 | 0.10 |
|  |  |  |  |  |
| LTR elements: |  | 177,900 | 180,395,521 | 7.07 |
|  | ERVL | 0 | 0 | 0 |
|  | ERVL-MaLRs | 0 | 0 | 0 |
|  | ERV\_classI | 0 | 0 | 0 |
|  | ERV\_classII | 0 | 0 | 0 |
|  |  |  |  |  |
| DNA elements: |  | 970,955 | 379,349,343 | 14.87 |
|  | hAT-Charlie | 107,132 | 38,932,939 | 1.53 |
|  | TcMar-Tigger | 120,876 | 47,180,712 | 1.85 |
|  |  |  |  |  |
| Unclassified: |  | 1,966,014 | 611,428,873 | 23.96 |
|  |  |  |  |  |
| Total interspersed repeats: |  |  | 1,281,755,175 | 50.23 |
|  |  |  |  |  |
| Small RNA: |  |  | 0 | 0 |
|  |  |  |  |  |
| Satellites: |  |  | 653,946 | 0.03 |
| Simple repeats: |  |  | 13,826,439 | 0.54 |
| Low complexity: |  |  | 18,487,267 | 0.72 |