**Supplementary Table 1**. Description genomic files used as input in *RepeatExplorer* pipeline, the total number of 100bp *Illumina* reads used for each species and the respective genome coverage and assembly releases used in the present study.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Species | 1.688 satDNA | Genome Size (Mb)1 | Total reads analyzed | Genome Coverage | NCBI/SRA Files | NCBI/SRA Files Sequencing  Technology | Assembly release ID |
| *D. ananassae* | - | 196.6 | 5072230 | 2,5878 | SRX144727 | Illumina HiSeq 2000 | dana\_caf1 |
| *D. biarmipes* | + | 200 | 6693021 | 3,3465 | SRX097584 | Illumina Genome Analyzer IIx | Dbia\_2.0 |
| *D. bipectinata* | - | 204.6 | 1666248 | 0,8167 | SRX097590 | Illumina Genome Analyzer IIx | Dbip\_2.0 |
| *D. elegans* | + | 192.2 | 2408863 | 1,2546 | SRX097588 | Illumina Genome Analyzer IIx | Dele\_2.0 |
| *D. erecta* | + | 158.9 | 5045489 | 3,1732 | SRX997779 | Illumina HiSeq 2000 | dere\_caf1 |
| *D. eugracilis* | + | 228.9 | 2392509 | 1,0493 | SRX097591 | Illumina Genome Analyzer IIx | Deug\_2.0 |
| *D. ficusphila* | + | 190.8 | 4884243 | 2,5571 | SRX097589 | Illumina Genome Analyzer IIx | Dfic\_2.0 |
| *D. kikkawai* | - | 210.2 | 1801891 | 0,85804 | SRX097585 | Illumina Genome Analyzer IIx | Dkik\_2.0 |
| *D. leontia* | - | N/A | 2227008 | - | SRX883299 | Illumina HiSeq 2000 | UCB\_Dleo\_1.0 |
| *D. mauritiana* | + | 157.9 | 2243821 | 1,4201 | SRX183513 | Illumina Genome Analyzer IIx | ASM438214v1 |
| *D. melanogaster* | + | 174.5 | 4974307 | 2,8587 | SRX1961048 | Illumina HiSeq 2000 | BDGP Release 6 |
| *D. orena* | + | 280.7 | 3959570 | 1,4141 | SRX997798 | Illumina HiSeq 2000 | DoreRS1 |
| *D. rhopaloa* | + | 193.9 | 1628575 | 0,8438 | SRX097586 | Illumina Genome Analyzer IIx | Drho\_2.0 |
| *D. santomea* | + | 171.5 | 3189067 | 1,8649 | SRX752500 | Illumina Genome Analyzer IIx | N/A |
| *D. sechellia* | + | 166.7 | 6918830 | 4,1679 | SRX287396 | Illumina Genome Analyzer IIx | dsec\_caf1 |
| *D. simulans* | + | 159.6 | 1260769 | 0,7899 | SRX1799314 | Illumina HiSeq 2500 | ASM75419v2 |
| *D. takahashii* | + | 207.3 | 2049860 | 0,9902 | SRX097587 | Illumina Genome Analyzer IIx | Dtak\_2.0 |
| *D. teissieri* | + | 166.3 | 3929041 | 2,36689 | SRX854063 | Illumina HiSeq 2500 | N/A |
| *D. yakuba* | + | 170.7 | 3829418 | 2,2525 | SRX494771 | Illumina HiSeq 2500 | dyak\_caf1 |

1Genome sizes were accessed in the Animal Genome Size database (www.genomesize.com).