Table S5. Coordinate level per strain Jaccard distances for each SV type in *A. thaliana*

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Strain | Caller1 | BND2 | DEL2 | DUP2 | DUP:I2,3 | INS2 | INV2 | Total2 |
| 1254 | pbsv | 0.012±0.004 | 0.001±0.000 | 0.053±0.008 | NA | 0.012±0.001 | 0.000±0.000 | 0.007±0.001 |
| 1254 | sniffles | 0.000±0.000 | 0.000±0.000 | 0.000±0.000 | NA | 0.014±0.001 | 0.000±0.000 | 0.007±0.001 |
| 1254 | svim | 0.000±0.000 | 0.003±0.000 | 0.013±0.007 | 0.000±0.000 | 0.005±0.000 | 0.000±0.000 | 0.005±0.000 |
| 6021 | pbsv | 0.017±0.011 | 0.002±0.000 | 0.050±0.009 | NA | 0.010±0.001 | 0.000±0.000 | 0.007±0.001 |
| 6021 | sniffles | 0.000±0.000 | 0.000±0.000 | 0.000±0.000 | NA | 0.008±0.001 | 0.000±0.000 | 0.004±0.001 |
| 6021 | svim | 0.000±0.000 | 0.002±0.000 | 0.003±0.002 | 0.000±0.000 | 0.003±0.000 | 0.000±0.000 | 0.003±0.000 |
| 6024 | pbsv | 0.000±0.000 | 0.001±0.000 | 0.058±0.013 | NA | 0.014±0.001 | 0.000±0.000 | 0.008±0.000 |
| 6024 | sniffles | 0.000±0.000 | 0.000±0.000 | 0.000±0.000 | NA | 0.013±0.001 | 0.000±0.000 | 0.006±0.001 |
| 6024 | svim | 0.000±0.000 | 0.001±0.000 | 0.029±0.006 | 0.000±0.000 | 0.005±0.000 | 0.000±0.000 | 0.004±0.000 |
| 9470 | pbsv | 0.000±0.000 | 0.001±0.000 | 0.045±0.005 | NA | 0.013±0.001 | 0.000±0.000 | 0.007±0.001 |
| 9470 | sniffles | 0.000±0.000 | 0.000±0.000 | 0.000±0.000 | NA | 0.012±0.001 | 0.000±0.000 | 0.005±0.001 |
| 9470 | svim | 0.000±0.000 | 0.003±0.000 | 0.023±0.007 | 0.000±0.000 | 0.004±0.000 | 0.000±0.000 | 0.004±0.000 |

1. SV call sets were generated from Minimap2 aligned BAM files and SAMtools sorted BAM files (20X depth).
2. Values represent the Jaccard distances (mean and standard deviation) between the original and randomized FASTQ files for each ecotype.
3. The identification of interspersed duplications was only supported by SVIM.