Table S1: Overall Jaccard distances for each SV type in *C. elegans* and *A. thaliana*.

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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Species | Caller1 | BND2 | DEL2 | DUP2 | DUP:I2,3 | INS2 | INV2 | Total2 |
| *C. elegans* | pbsv | 0.077 (0.004) | 0.019 (0.003) | 0.040 (0.022) | NA | 0.021 (0.012) | 0.011 (0.000) | 0.022 (0.009) |
| sniffles | 0.000 (0.000) | 0.000 (0.000) | 0.000 (0.000) | NA | 0.007 (0.007) | 0.000 (0.000) | 0.004 (0.004) |
| svim | 0.000 (0.000) | 0.002 (0.001) | 0.000 (0.000) | 0.000 (0.000) | 0.002 (0.002) | 0.000 (0.000) | 0.002 (0.002) |
| *A. thaliana* | pbsv | 0.105 (0.007) | 0.008 (0.001) | 0.075 (0.051) | NA | 0.021 (0.012) | 0.107 (0.000) | 0.017 (0.007) |
| sniffles | 0.000 (0.000) | 0.000 (0.000) | 0.000 (0.000) | NA | 0.012 (0.012) | 0.000 (0.000) | 0.006 (0.006) |
| svim | 0.000 (0.000) | 0.005 (0.002) | 0.019 (0.017) | 0.000 (0.000) | 0.005 (0.004) | 0.003 (0.000) | 0.005 (0.004) |

1. SV call sets were generated from Minimap2 aligned and SAMtools sorted BAM files (20X depth).
2. Values represent the global mean of the Jaccard distances between the original and randomized FASTQ files for each strain or ecotype. Values outside parentheses describe the VCF level differences. Values inside parentheses describe the coordinate level differences.
3. The identification of interspersed duplications was only supported by SVIM.