A lack of evidence for extensive horizontal gene transfer in the genome of the tardigrade *Hypsibius dujardini*

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Supplemental File 5: Library insert sizes

We estimated library insert sizes by mapping read pairs to the initial single-end CLC assembly. This works well for short insert libraries, but less well for mate-pairs, where many read pairs do not map to the same contig. This failure to map to the same contig means that the mate pair reads are under-counted.

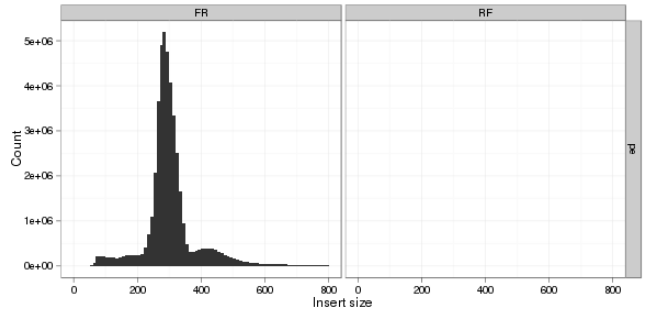
The insert size distribution of the "300 base" standard library on the preliminary SE assembly had a median of 292 bases (Standard Deviation (SD) 96 bases) (Figure S4A). The insert size distribution of the 4000 base mate pair library has a median of 1133 bases (1460 bases SD) (Figure S4B). There were many mate-pair fragments with very small virtual inserts in this library.

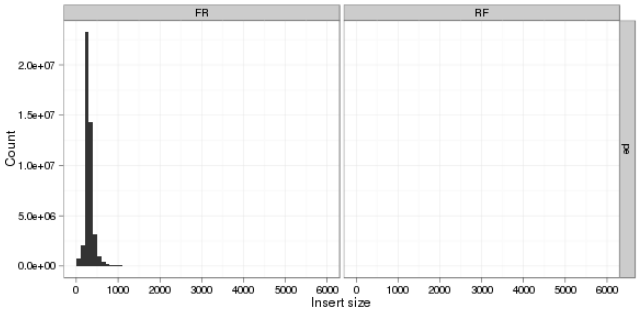
Figure S5 Insert size estimation for Illumina libraries

A Insert size distribution for the short-insert library. Left panel, left graph: read pairs mapping in the expected F-R orientation. Left panel, right graph: read pairs mapping in the unexpected R-F (mate) orientation. The right panel shows the same data with an expanded X-axis.

B Insert size distribution for the mate-pair library. Left panel, left graph: read pairs mapping in the unexpected F-R orientation. Left panel, right graph: read pairs mapping in the expected R-F (mate) orientation. The right panel shows the same data with an expanded X-axis.

A


FR
RF
pe
Count
Insert size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RF
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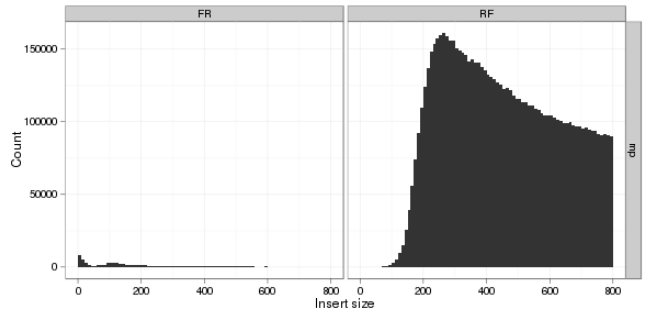
Count
Insert size

B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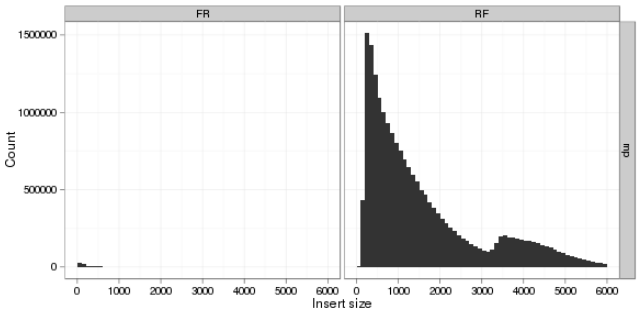
Count
Insert size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RF
mp
Count
Insert size