

Supplementary Materials

BIQ: A method for searching circular RNAs in transcriptome databases by indexing backsplice junctions

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Fig. 1. Cumulative count of distinct BSJ k -mers in all SRA files from the (a) Drosophila and (b) ENCODE datasets.

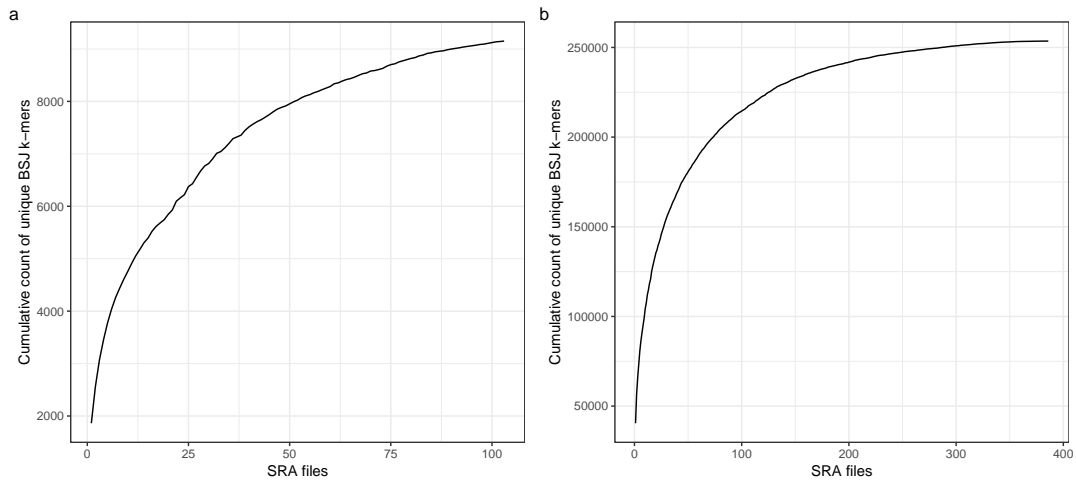


Fig. 2. Abundance of BSJ k -mers across all SRA files from the (a) Drosophila and (b) ENCODE datasets.

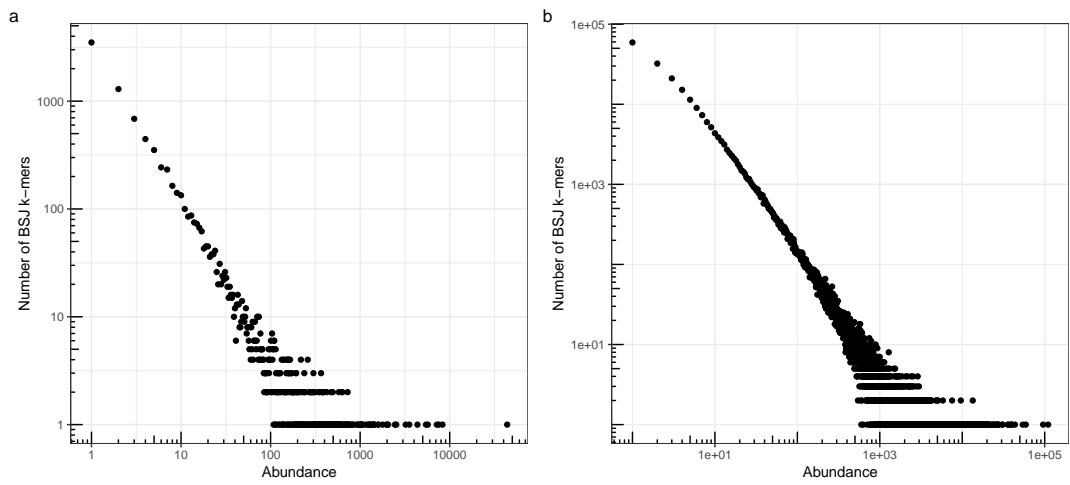


Fig. 3. Number of samples in which BSJ k -mers occur in (a) Drosophila and (b) ENCODE datasets.

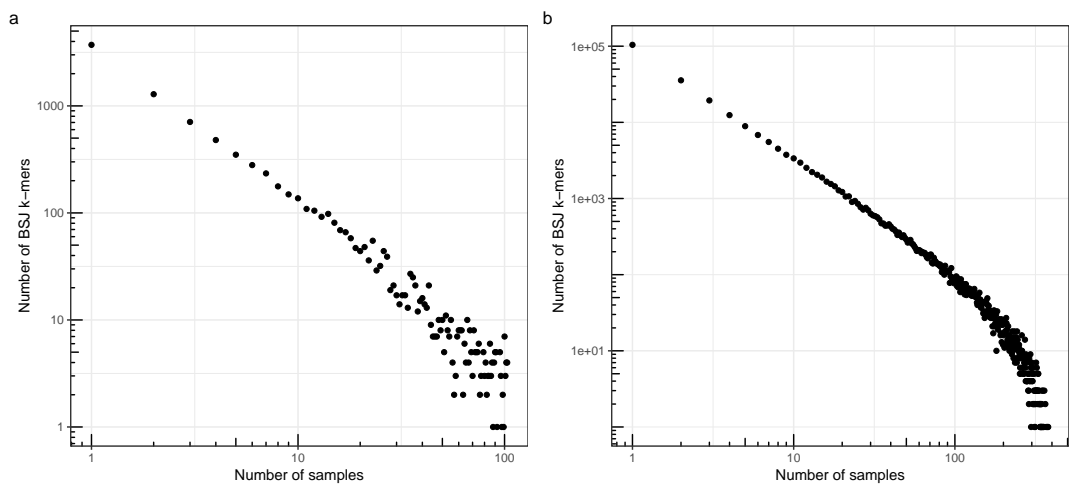


Fig. 4. Number of distinct observed BSJ *k*-mers (points) from *D. melanogaster* developmental transcriptomes and cumulative count of distinct BSJ *k*-mers (line)

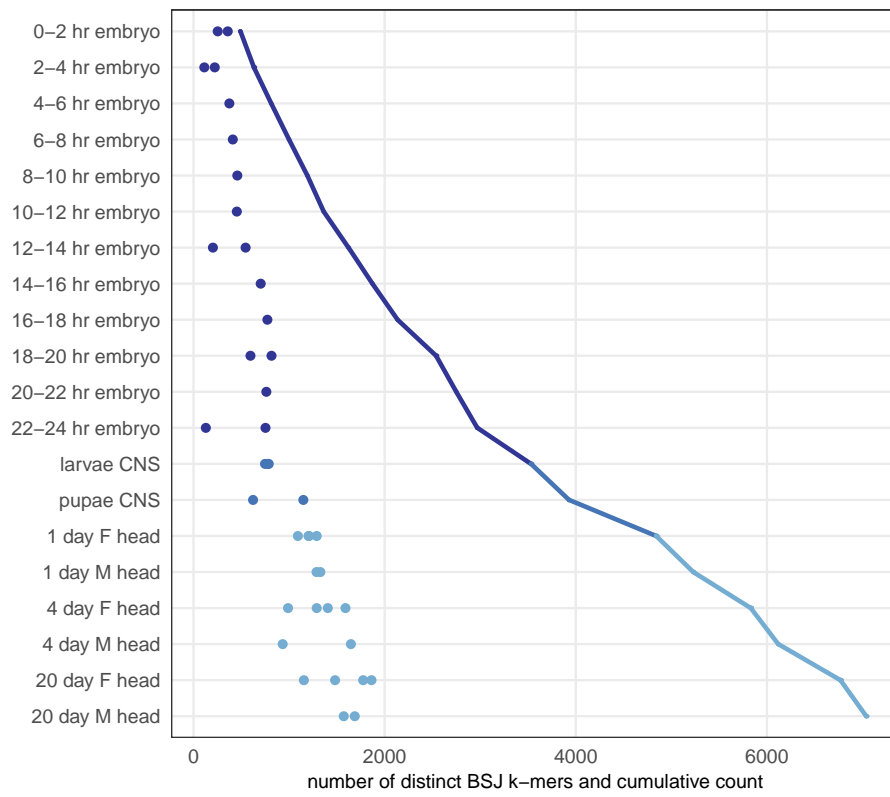


Fig. 5. Two-dimensional embedding of BSJ profiles of all ENCODE transcriptome datasets.

