



Linking transcriptional and genetic tumor heterogeneity through allele analysis of single-cell RNA-seq data

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Genome Res. 2018 28: 1217-1227 originally published online June 13, 2018

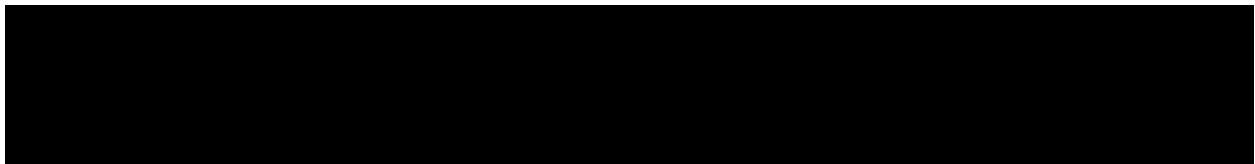
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