



Functional genomic analysis of chromosomal aberrations in a compendium of 8000 cancer genomes

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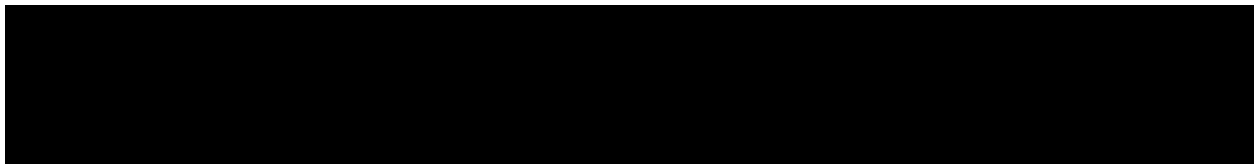
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