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# Interactive web tool to manage sequencing data for the detection of viral insertion sites in gene therapy experiments

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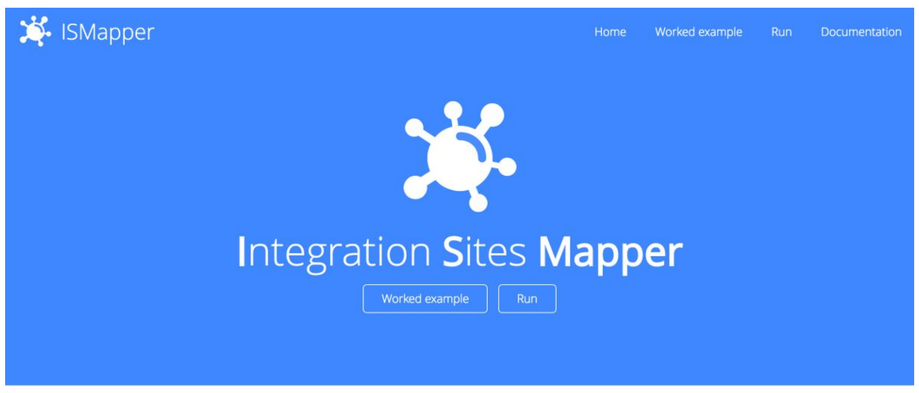
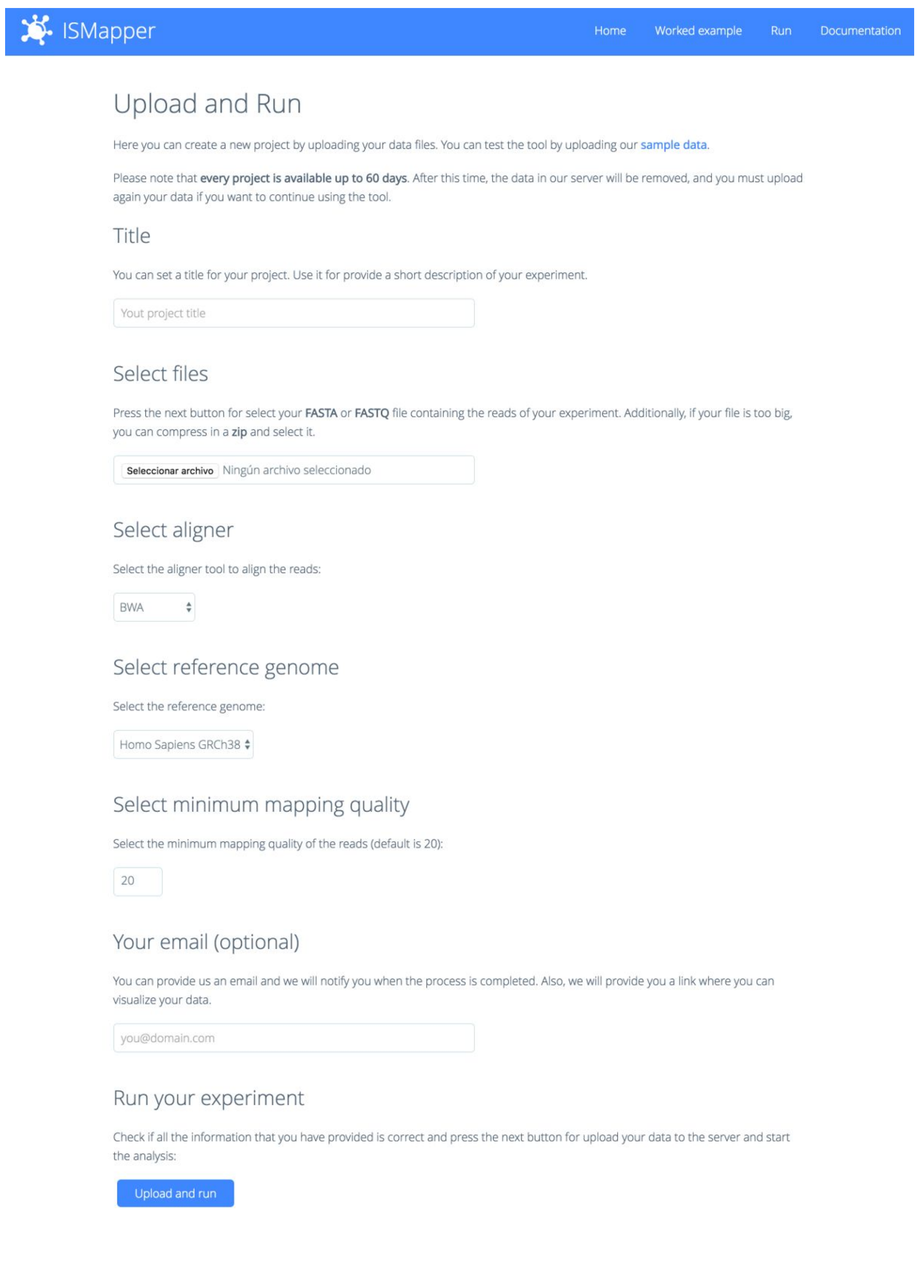
## INTRODUCTION

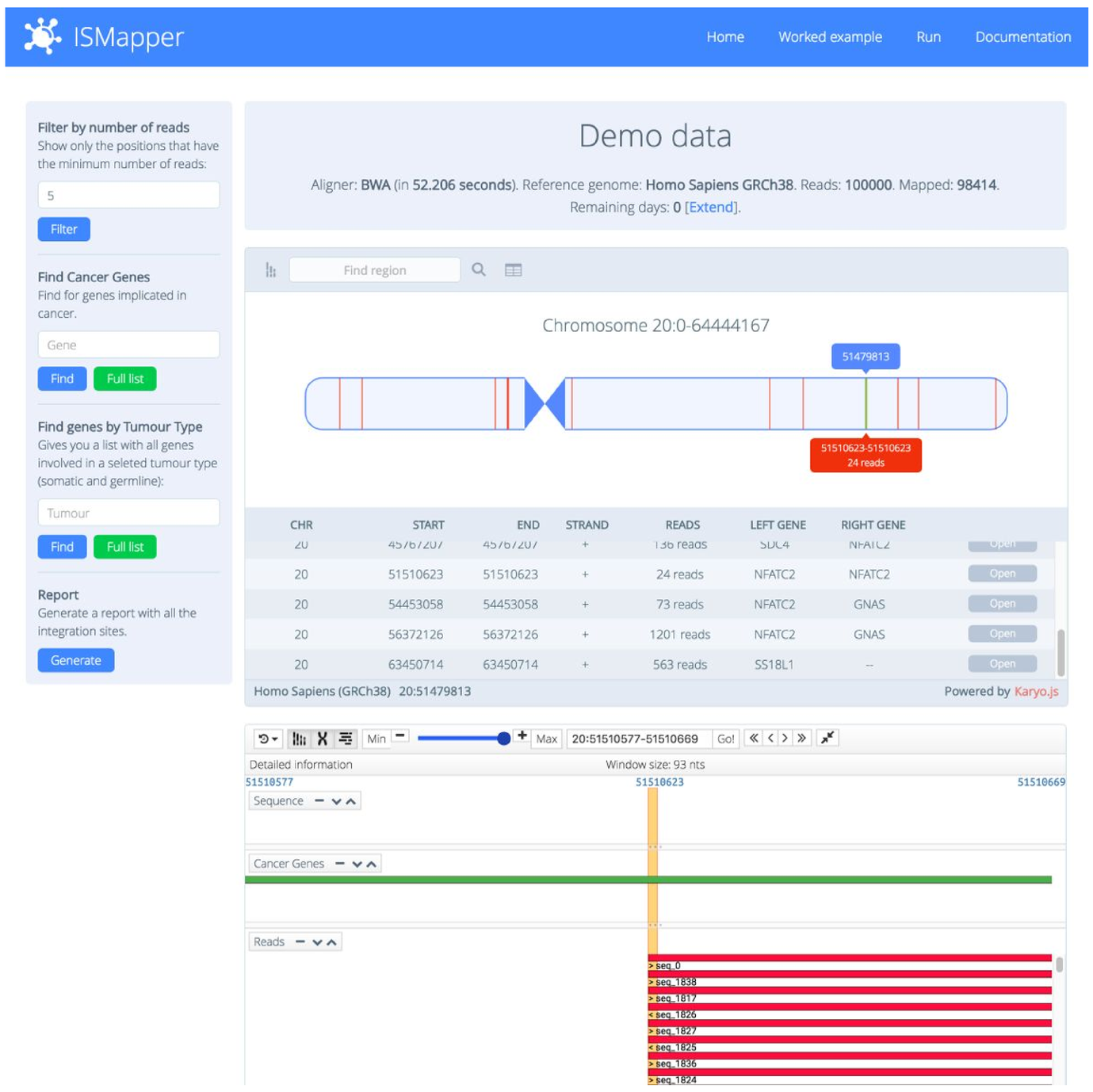
The possibility of integrating viral vectors to become a persistent part of the host genome makes them a crucial element of clinical gene therapy. However, viral integration has associated risks, such as the unintentional activation of oncogenes that can derive in cancers. Therefore, the analysis of integration sites of retroviral vectors is a crucial step in developing safer vectors for therapeutic use. Here we present **ISMapper**, a vector integration site analysis web server to analyse next-generation sequencing data for retroviral vector integration sites. Because it uses novel mapping algorithms, **ISMapper** is remarkably faster than previous available options and provides a useful interactive graphical interface to analyse the integration sites found in the genomic context.

## WEB APPLICATION http://ismapper.babelomics.org/




**ISMapper** reads standard FASTQ or FASTA files containing reads corresponding to the insertion sites of the virus. These reads are mapped onto the reference human genome using BWA [1] or HPG-Align [2]. The results are presented using a graphical environment with a kariotype viewer (that provides a general perspective of the insertion sites) and a genome viewer implemented with GenomeMaps [3] (that provides a more detailed information about the insertion sites).




## REFERENCES

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