

# Analysis of CLIP data using iMaps

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## CLIP (cross-linking and immunoprecipitation)

is an established method to study protein-RNA interactions. Until now, the tools for data analysis and quality assessment have been neither standardized nor commoditized to enable adoption of CLIP among the broader research community. Thus: iMaps.

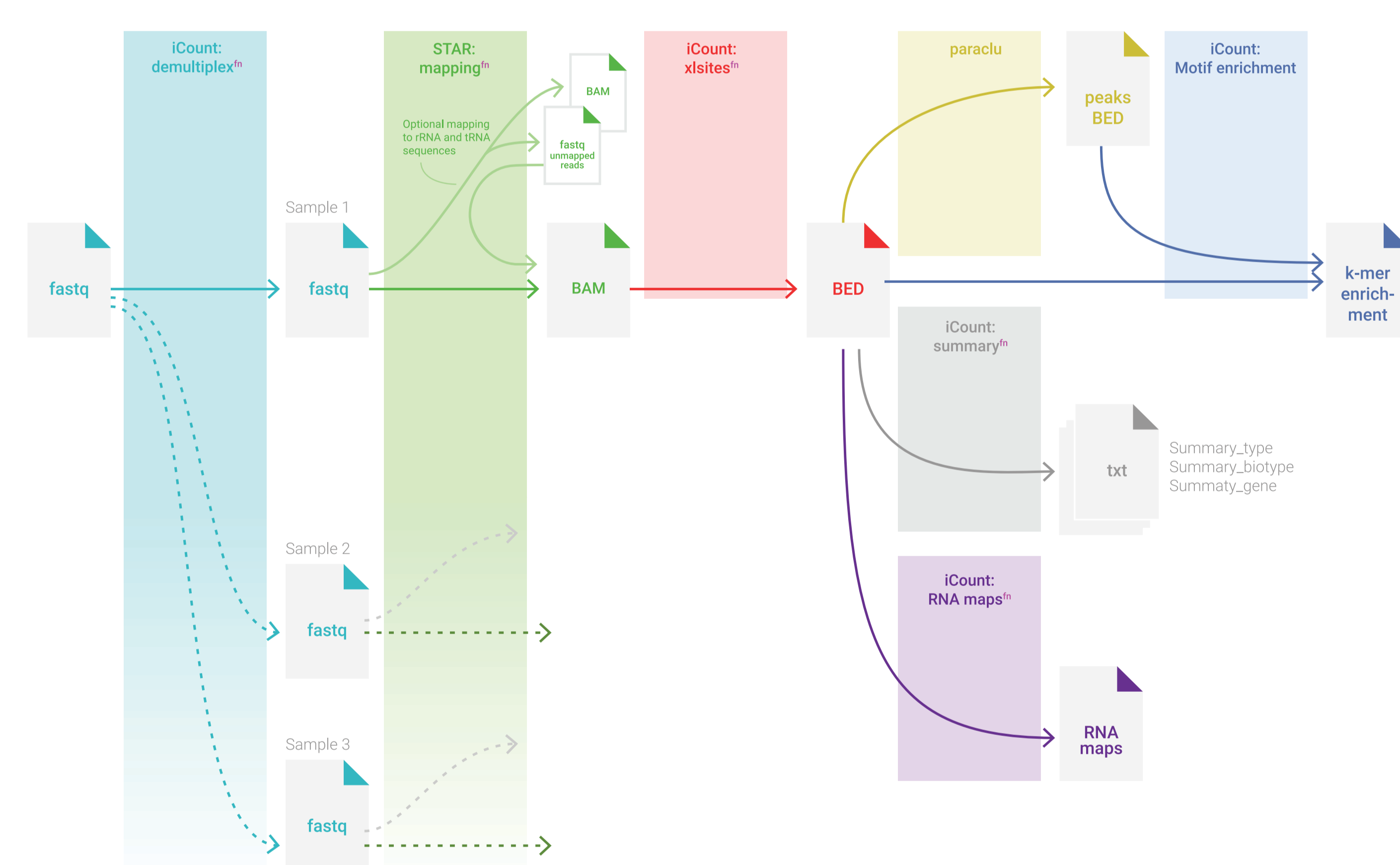
Use iMaps to browse a growing collection of consistently processed and annotated public CLIP data. Or analyse your own data using our recommended and thoroughly validated analysis pipelines.



Check out the documentation and request a free trial at [imaps.genialis.com](https://imaps.genialis.com).

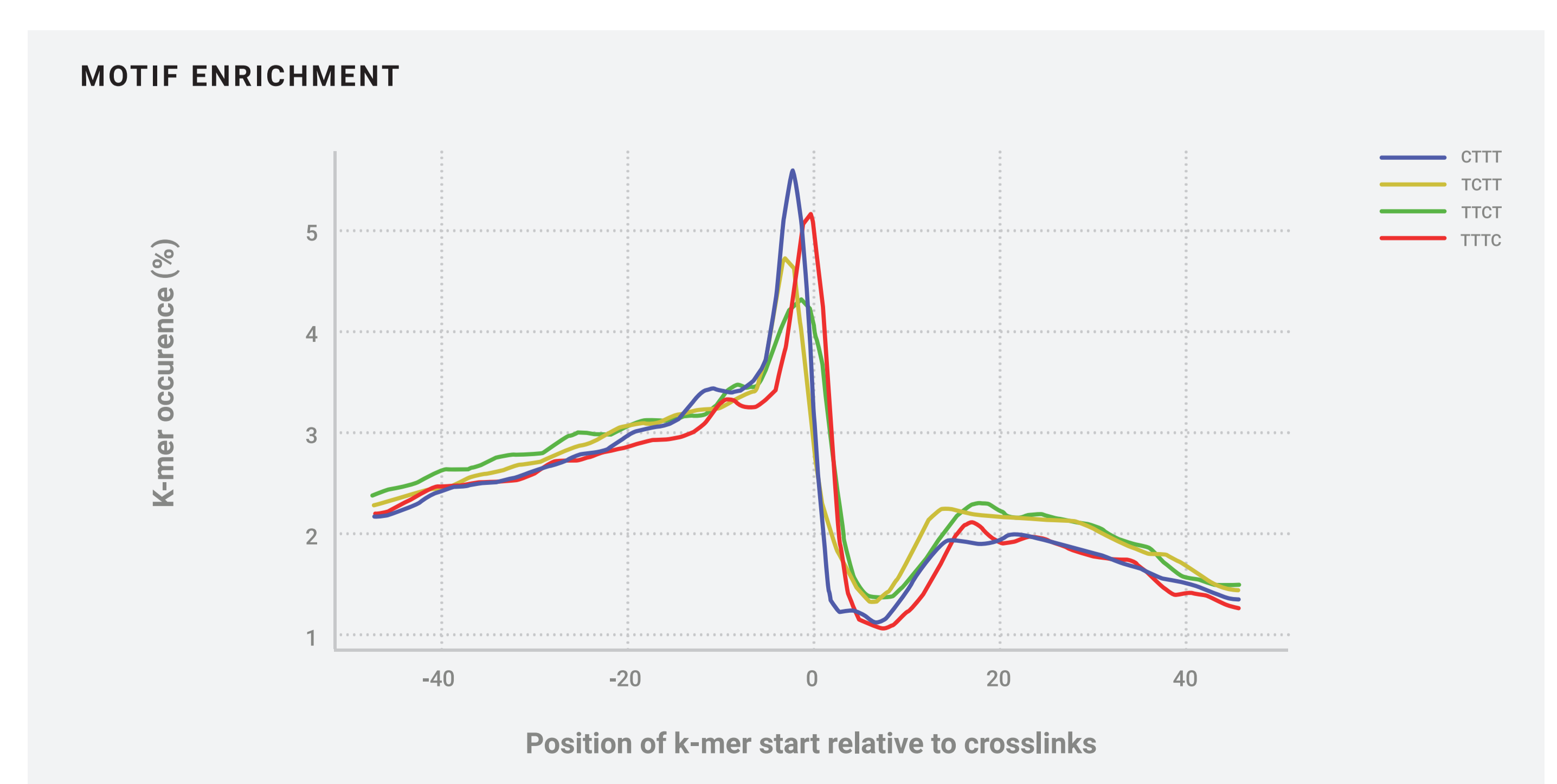
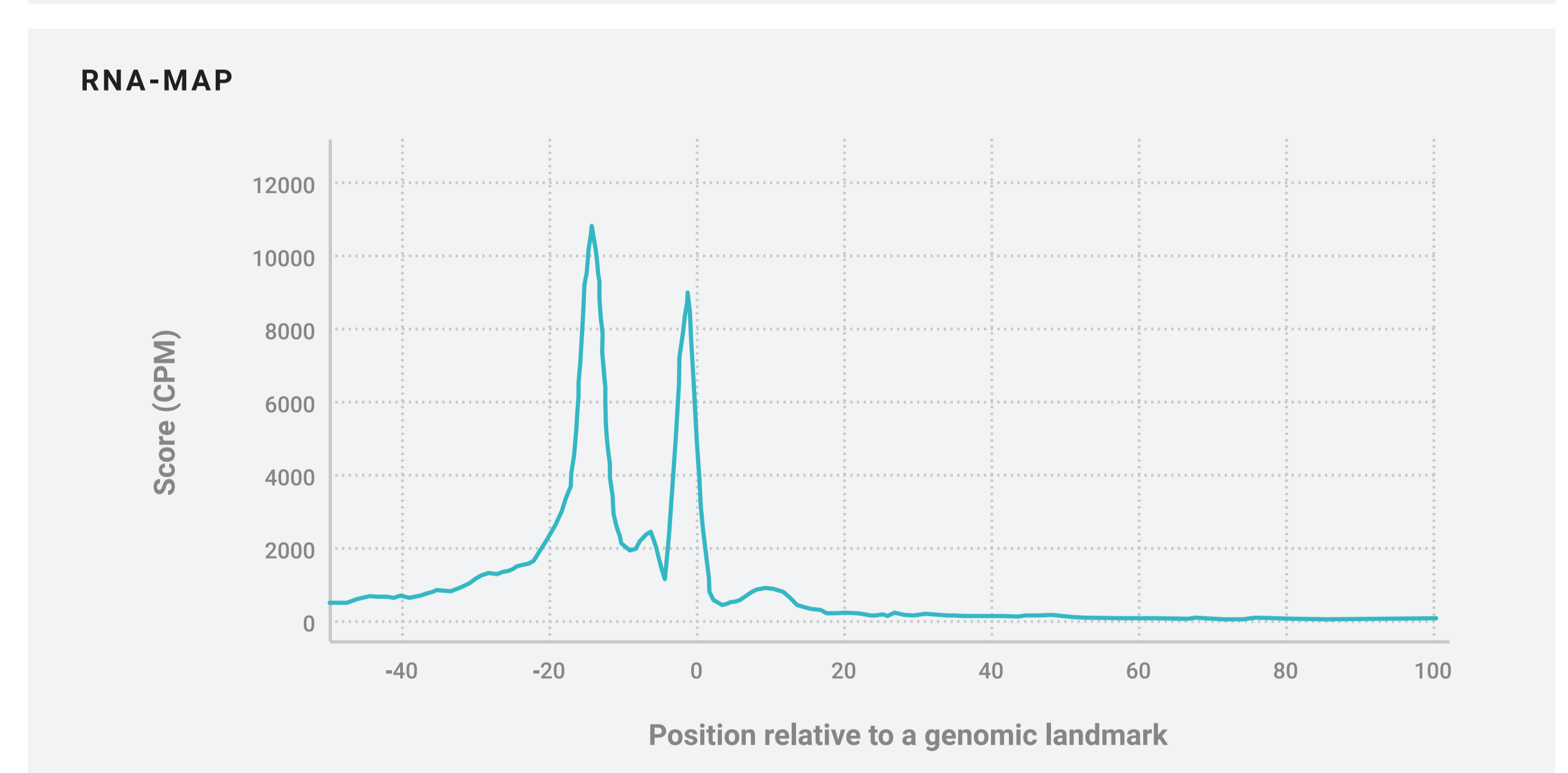
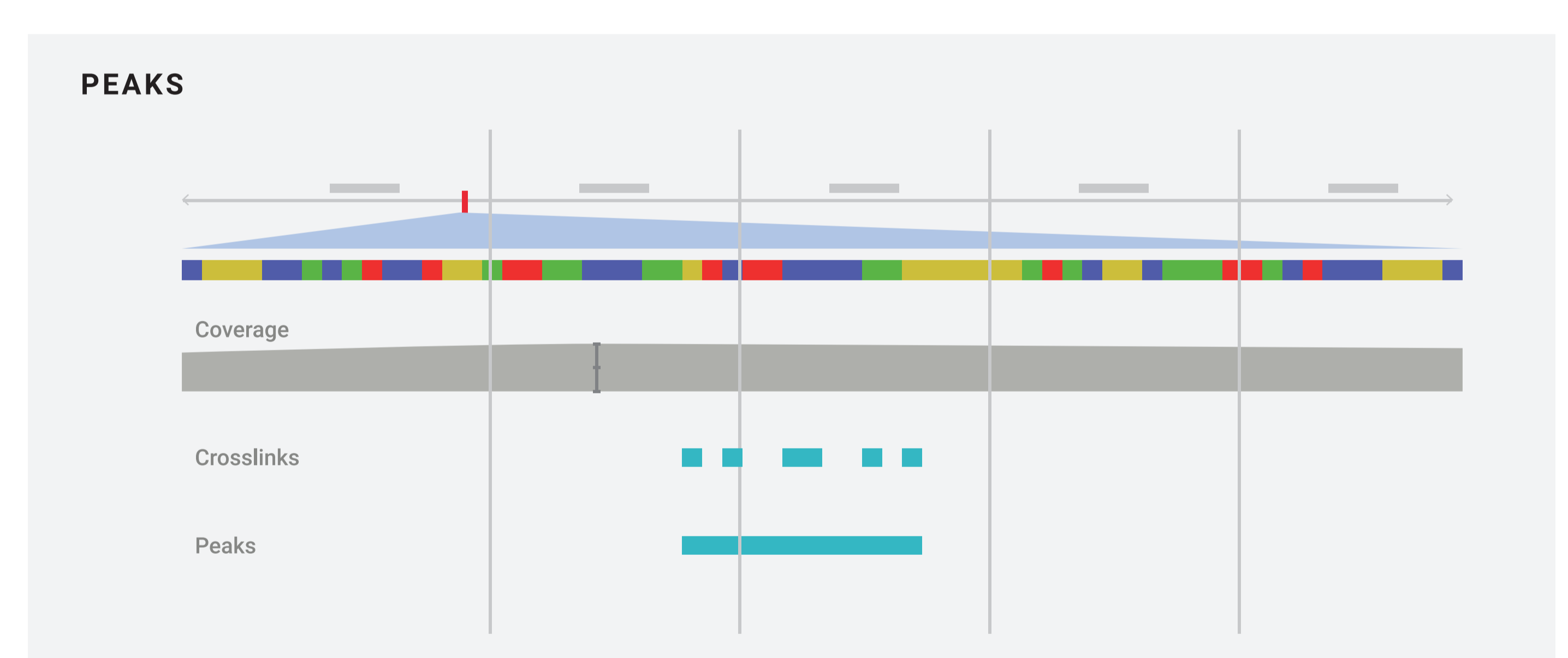
## iMaps

The basic pipeline starts with multiplexed raw reads and ends up with crosslink sites for individual samples as well as several downstream results such as peaks and RNA maps.



## Results

Results include protein binding sites (peaks), oligonucleotide motif ...



iMaps is a web application that allows users to reproducibly analyse CLIP data, build and utilise data repositories, and manage data according to the FAIR principles.