

Genomic technologies are constantly evolving. Today, we produce a large amount of data and bioinformatics has become crucial for biology and medicine. Several free solutions already exist to process genomic data, but most of them are not-so-user-friendly command-line applications and require advanced computer skills. To help non-experts to analyze their data, several commercial companies are already on the move and are seducing people with nice graphical user interfaces. Labsquare would like to be an alternative: a non-profit organization which produces simple and accessible open source genomic GUI software for everyone.

# Technology

**We favour Qt framework - a GPL C++ framework which allows us to develop modern cross-platform applications. It is an alternative to Java for building modern user interface with advantage and power of C++.**

# Community

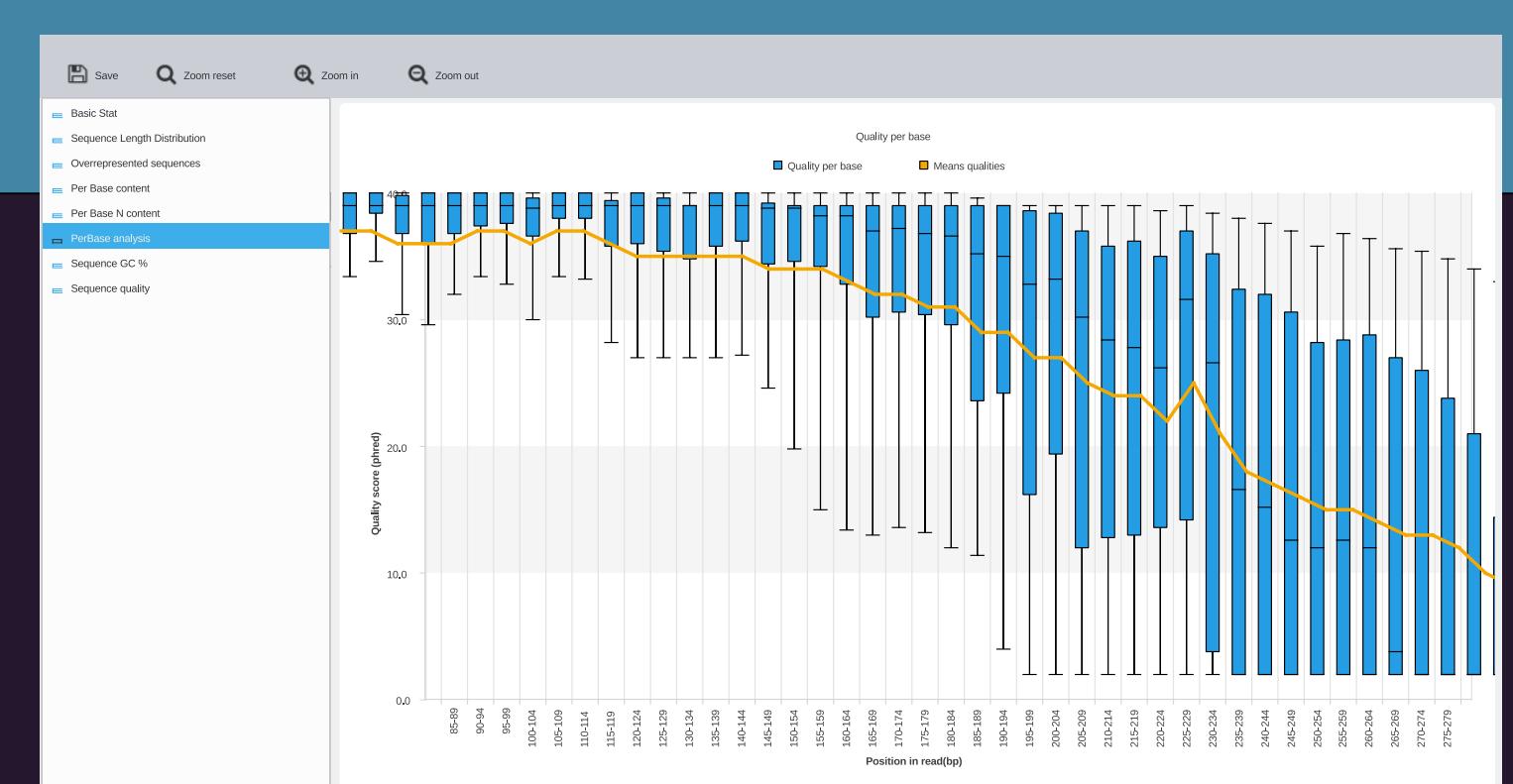
**So far we are just a small team, but all skills are present. We are bioinformaticians, geneticists, physicians, developers, and designers. Our open source projects are available on GitHub and we are talking on #Gitter.**

# Labsquare

is a community of dedicated individuals focusing on development of simple and usable genomic software

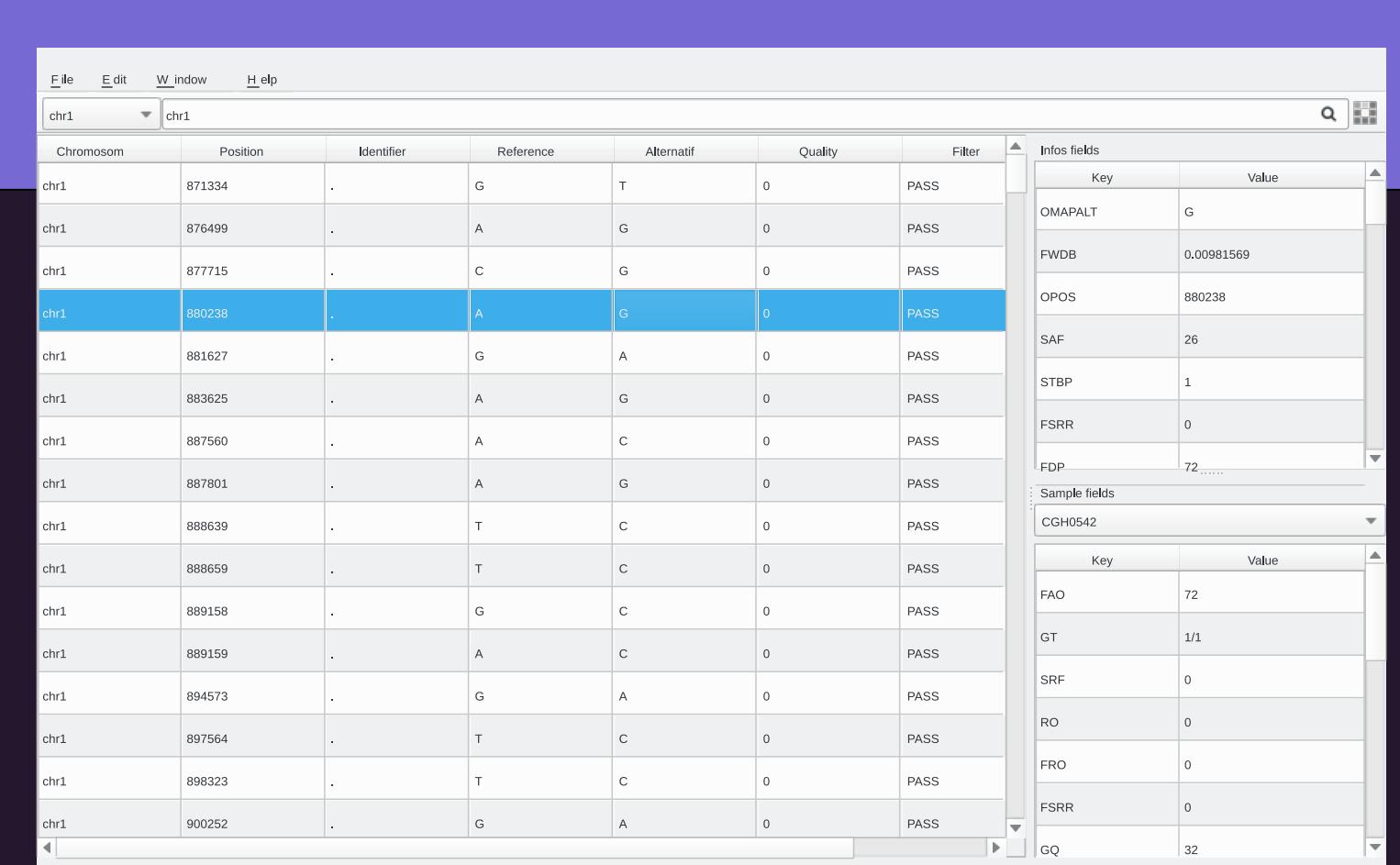
# Fastot

**FastQt is a fast, clean and intuitive tool designed to process FASTQ files. We developed it from ground up and it's taking a lot of inspiration by the famous FastQC app.**



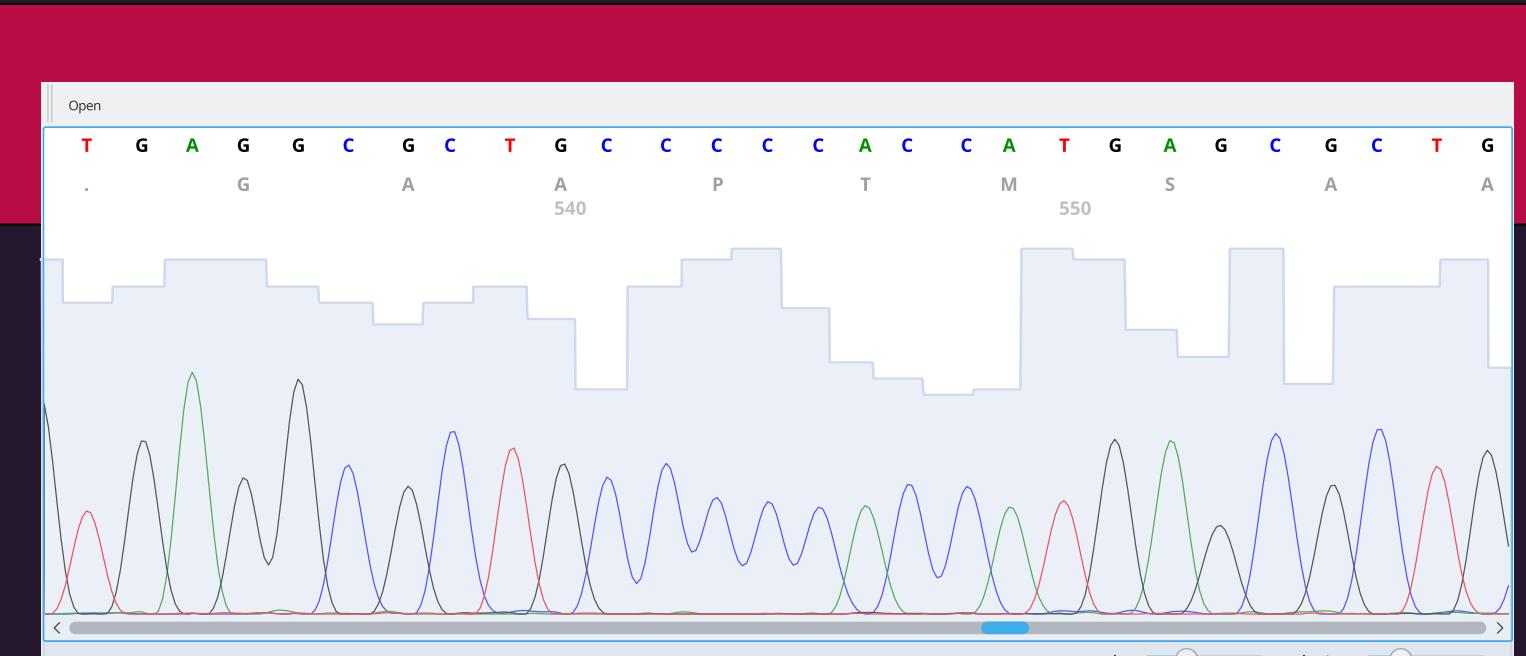
# CuteVCF

**CuteVCF is a simple and intuitive VCF viewer. We are also working on another similar app, inspired by Variant Tools.**



# Clif Peaks

**Cutepeaks allows to display Sanger trace data in a fashion way. It support AB1 and SCF trace file.**



And other apps are under development ( a genome browser, a fasta editor, a pipeline launcher, )