October 24, 2017

We're looking for more lovely people to join our team!!!

We are looking for a highly motivated person willing to be part of the upcoming personalized medicine revolution. The successful candidate will join our industry-leading team and be trained to perform routine clinical interpretation of NGS data, and reporting tasks, as well as contribute to the improvement of existing pipelines and procedures. We need someone that is able to understand not only science but also have an eye on the market and business, so apart from delivering excellent work, you'll be challenged for continuous improvement as well as detecting and addressing market needs and providing optimal and profitable solutions from all perspectives.

The right candidate must hold a PhD in biomedical sciences and have experience in a genetics laboratory routines; a decent bioinformatics background, or the other way around, a PhD in bioinformatics and solid background in molecular genetics. Previous experience in other public hospitals, public research institutions, or other health sector companies (pharma, clinical laboratories or biotech companies) is desirable but not required.

Will you be our next labmate?

You have a solid background in human genetics AND and have acquired decent skills in bioinformatics over time. You are competent in genomics and are experienced in state-of-the-art technologies and applications. You understand NGS wet and dry-lab procedures enough to question established protocols and procedures. You have previous experience in dealing with clinical laboratory routines or in genetic counseling ... so you are not afraid of reading papers, communicating with others and have sufficient knowledge and judgement to choose among different available molecular genetic tools to find the right answer for each case. You feel comfortable working hard and under pressure. You know about and understand the plethora of existing tools and algorithms to deal with NGS data in research and medical environments.

You are capable of doing 'soft' shell programming, you have some experience using programming languages like Perl, Python or Ruby, and have made some insights into R statistical language. You have used main databases and datasets in the human

genetics field (such as HGMD, OMIM, ClinVar, GnomAD, or Cosmic). You are familiar with existing algorithms for variant interpretation like Polyphen, snpEff, and SIFT, but you also bear in mind the complexities of drawing conclusions and reporting in a medical environment.

You have a structured mind and are committed to accomplish team goals rigorously, and are willing to get involved, no matter what it takes, in the growth of a young and dynamic company. You have successfully worked with large teams and are willing to take additional responsibilities and leadership.

What do we offer?

The successful candidate will initially be employed full-time on a 6+6 month renewable contract, with an attractive remuneration package dependent on experience. After this initial period and subject to satisfactory performance and outputs, a permanent position will be offered. We offer an dynamic and excellent working environment, a challenging position, an exceptional bunch of committed fellows, and working for a company that understands that only serving people we will construct a sustainable and long-lasting business.

If you have appetite for sunshine, nice fellows, hard working and making a difference in a young company, make sure your CV and motivation letter reaches us. Apply now: **click here** or scan the following QR code.

Who we are?

qGenomics is a young biotech company based in Esplugues del Llobregat (Barcelona), that operates in the diagnostics and R&D fields. We spun off from two of the most important biomedical research institutions in Barcelona (UPF and CRG), with whom we still collaborate in different R&D projects. We are devoted to the development of excellent services and products based in -omic technologies, that help solving everyday questions of researchers and clinicians trying to elucidate the genetic basis of human disease. We work with our collaborators from the very beginning, trying to understand their needs and use the most effective molecular tools to solve their questions.