

# Whole Genome Sequencing

“

**Great quality data, highly competitive pricing with excellent alignment and variant calling included. These data have helped us make confident genetic diagnoses in families with severe and complex developmental disorders.**

Professor David FitzPatrick  
The University of Edinburgh

**Edinburgh Genomics Clinical (EGC) Division** specialises in providing Whole Genome Sequencing (WGS) by means of a fully automated workflow. EGC, which is based at the renowned Roslin Institute, has the capacity to deliver the equivalent of 9,000 human genomes at 30X coverage per year.

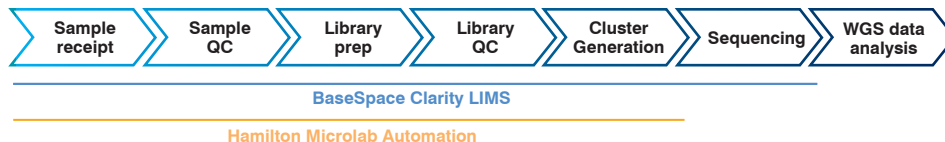
EGC's compute infrastructure includes a large cluster with 2,000 processor cores and 6 Pb (Petabytes) of data storage capacity. All securely housed within the University of Edinburgh's Advanced Compute Facility with technical support from the Edinburgh Parallel Computer Centre (EPCC). Deliverables are sent across our free high speed transfer server.

## Edinburgh Genomics Clinical WGS:

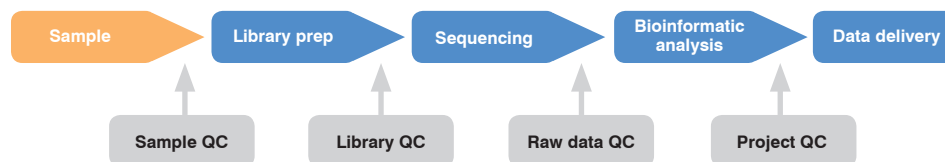
- Sequencing coverage of 15X, 30X, 60X and higher are available for any species
- Deliverables included as standard: FastQ, BAM and gVCF files\*
- Library insert size of 450 bp and sequencing with paired reads of 150 bp
- Guaranteed quality of 75% of bases above Q30
- Storage of data for 3 months free of charge
- Submission of samples either in 96 well plates (frozen) or tubes (ambient)

## Illumina SeqLab

Edinburgh Genomics Clinical provides a fully automated end-to-end solution for whole genome sequencing by implementing Illumina's SeqLab. This provides full traceability for samples along the entire workflow, from sample receipt to data analysis.



## Project workflow overview:



\* For all human and well annotated mammalian genomes



THE UNIVERSITY  
of EDINBURGH

edinburgh  
genomics.

To contact us regarding your WGS project please see:

[genomics.ed.ac.uk/contact/project-enquiry](https://genomics.ed.ac.uk/contact/project-enquiry)