NewGene
Next Generation Diagnostics

NewGene Research Services

NewGene is a leading provider of R&D support to the NHS, academic community and industry. Its technology platforms, combined with the expertise and flexibility of its team, offer exciting opportunities for clients with specific research DNA sequencing and genotyping projects.

NewGene core services

- Next generation sequencing
- Roche 454 GS-FLX+ technology
- Illumina MiSeq
- Genotyping on the Sequenom platform

Optional services

- Extraction of DNA
- Real time PCR
- Bioinformatics analysis

Next Generation Sequencing Technologies

NewGene operates two complementary next generation sequencing platforms.

The ***Roche 454 GS FLX+*** system combines long read lengths, accuracy and high-throughput sequencing. The technique is based upon emulsion PCR and pyrosequencing and enables full DNA sequencing of clonally amplified targets. The use of multiplex identifier tags (MIDs) enables efficient use of sequencing runs.

The ***Illumina MiSeq*** is an integrated and automated sequencing system that generates highly accurate data with good read depths and accuracy, especially within homopolymer regions. The compact system incorporates cluster generation, pair end fluidics and analysis allowing rapid generation of results.

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	Roche GS FLX+		Illumina MiSeq	
	XL+	XLR70	Single reads	Paired reads
Read length	Up to 1000 bp	Up to 600 bp	300 bp	2 x 300 bp
Mode read length	700 bp	450 bp		
Throughput	700 bp	450 bp	13.2 – 15 Gb	13.2 – 15 Gb
Reads per run	1 million	1 million	22 – 25 million	44 – 50 million

Based on Roche and Illumina data. Results are dependent upon a range of variables such as sequencing strategy and sample type.

Genotyping Services

The ***Sequenom MassARRAY 4*** is a highly accurate, MALDI-TOF mass spectrometry based platform providing specificity and sensitivity for studies of genetic variation including somatic mutation detection in heterogeneous samples. The technology is able to identify SNPs and other stretches of DNA sequence that differ by one, or a small number of bases via an extension reaction. From this the genotype is determined. Variant detection can be carried out in multiplex, with up to 30 sites targeted in a single assay.

Bioinformatics

Bioinformatics expertise is required to maximise the value from the large amount of data generated by high throughput sequencing techniques. NewGene works closely with the Newcastle University Bioinformatics Support Unit to provide services for data analysis, experimental design, pipeline building, database design and software tutorials.

Commonly used software packages include:

- BWA, Bowtie and other aligners for all next generation sequencing platforms and applications
- Mira and Velvet for de novo assembly
- Tophat, Cufflinks, DESeq and Trinity (among others) for RNA-Seq analysis
- GATK for variant calling
- MACS, SISSRs and other peak callers for ChIP-Seq analysis
- DMuDB, LOVD, and Alamut software for clinical work.

For more information visit our website:
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The Newcastle upon Tyne Hospitals NHS
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