Genea BIOMEDX

Genie

Genie-A Solution

To detect CNV, ploidy, Sibling QC and ROH in preimplantation embryo biopsy samples

Comprehensive detection

A single solution to detect CNV, Ploidy, Sibling QC and ROH (Regions of Homozygosity)

Default SNP analysis

Genie-A uses Genome-wide SNP information to detect Ploidy, Sibling QC and ROH

High Resolution

≥4Mb CNVs (unknown), and ≥1 Mb inherited CNVs (known)

High throughput and Scalability

5M reads/sample, up to 96 samples/run, 1 x 100 bp reads.
Sequencers: Genie Sequencer and DNBSEQ-G400

Genie-A Fast: Fast workflow, combining WGA and library preparation to reduce cost and time.

Genie-A Advanced: Separate WGA (MDA) followed by a patented library preparation method to support wider genome coverage.

Two versions of Genie-A kits with different sample preparation methods for greater flexibility, but with the same outcome.

Genie-A Kits	Amplification method	Sequencers	Reporting content
Genie-A Fast	PicoPlex	Genie Sequencer DNBSEQ-G400*	• Aneuploidy, Triploidy,Haploidy • ≥4Mb CNVs in unknown regions • ≥1Mb known inherited CNVS • Mosaicism ≥30% C ≥10Mb • Whole chromosome level ROH • Sibling QC
Genie-A Advanced	MDA		

Competitive Pricing

Offering significant cost savings without compromising on quality

Accurate detection of CNVs

5M reads/sample combined with CBS algorithm provides accurate detection of CNVs

Supports Localised Deployment

Compatible with various devices and capable of quick report generation

End-to-end Support

Sample preparation

Genie-A Fast

Genie-A Advanced

Flexible Sample Preparation Methods

Sequencing

Genie Sequencer

High Throughput Sequencing Platform

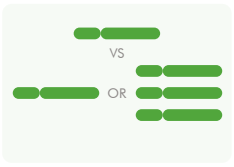
Data Analysis

Genie Analysis Software

Automated Data Analysis

Results & Reporting

Genie Software



CNV, Ploidy, ROH, Sibling QC

Genea BIOMEDX

Genie

Genie-Plus Solution

A single test for pre-implantation genetic testing of embryo biopsy samples

Comprehensive genetic testing

A single solution for the detection of CNV, Ploidy, Sibling QC, ROH, structural rearrangements and linkage analysis

Genome-wide coverage

WGA by MDA and a patented library preparation method for better whole-genome coverage

High Resolution

≥4Mb CNVs (unknown), and ≥1 Mb inherited CNVs (known)

High throughput and Scalability

20M paired-end reads/sample, up to 96 samples/run, 2x 100 bp reads:Genie Sequencer and DNBSEQ-G400

Genie Plus: A Single workflow for genetic testing of preimplantation embryo biopsies

Sample Prep	Sequencing	Software	Reads/samples	Results
			Genie-A Advanced	
Genie WGA + Genie-Plus Library prep	Genie Sequencer (500 M reads)	Genie Data Analysis Software	96 samples (5M each)	CNV, Ploidy, ROH and Sibling QC
			24 samples (40M each)	CNV, Ploidy, ROH, Sibling QC, SR and Linkage Analysis
			Genie Plus	
• MDA (Phi29) • Patented Library Preparation	• Sequencing by Synthesis (SBS)	• CBS algorithm • LLR • SNPs • Linkage Analysis		

Competitive Pricing

Offering significant cost savings without compromising on quality

Patented Library Prep

Better genome coverage, need only 1/10th of 30x WGS data

Supports Localised Deployment

Compatible with various devices and capable of quick report generation

End-to-end Support

Sample preparation

Genie-Plus

Single Workflow Patented Method

Sequencing

Genie Sequencer

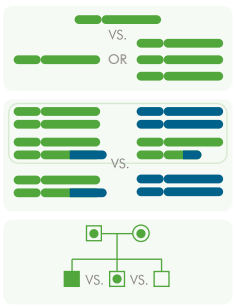
High Throughput Sequencing Platform

Data Analysis

Genie Analysis Software

Automated Data Analysis

Results & Reporting



Genetic testing of pre-implantation embryo biopsy samples