

HLA TWIN™ NGS software

HLA Twin™ is the dual-algorithm genotyping software component of Holotype HLA™. It has been co-developed with the Holotype HLA NGS Assay, to deliver the most accurate, high throughput HLA genotyping available.

Product Highlights



Confidence

- Two independent algorithms - Consensus Genotyping and Statistical Genotyping
- Consensus Genotyping:
 - De novo assembly: optimal for fully phased consensus sequences
 - Reference alignment: added analytical confidence, novel allele detection and null allele resolution
- Analyze data against any version of the IMGT/HLA Database
- DRB, DQ Linkage Disequilibrium checks

Quality

- 23 Quality Control metrics for confident assignment and detailed troubleshooting
- Traffic Light System for easy interpretation of genotyping results
- Whole Gene Consensus sequences for unambiguous allele assignment
- Complete Novel and Null allele detection

Automation & Integration

- Fully automated analysis after Illumina sequencing run
- Export genotyping results in the standard Histoimmunogenetics Markup Language format (HML 1.0.1) or detailed summary reports in PDF
- Integration with LIMS, such as Histotrac
- Simple assignment and approval workflows
- Simple and customizable allele assignment for ease of use
- Multi-layer clinical approval workflow

Flexibility & Scalability

- Platform independent (available for Windows, Linux and OS X)
- Desktop and Client-Server versions
- Customizable analysis and visualization

Quality Control



Traffic Light #1 - Algorithm Concordance Check

Evaluates the concordance between the results of the two algorithms.

Traffic Light #2 - Quality Check

Evaluates 23 different Quality Control metrics such as read length, read quality, noise ratio, fragment size, consensus coverage depth, allele balance, phasing and more at every locus for every sample.

Two green lights allow an analyst to have complete confidence in the genotyping call, with no manual inspection required.

Traffic Light System

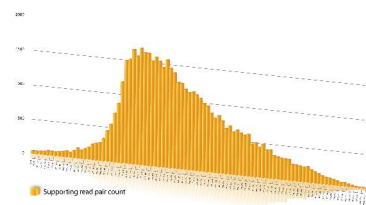
The Traffic Light System is one of Omixon's most significant time saving innovations to simplify interpretation of HLA genotyping results.

- Two orthogonal algorithms determine the genotype at every locus and are checked for concordance against one another.
- 23 locus-level Quality Control metrics provide confidence in the assignment and detailed troubleshooting for complex cases.

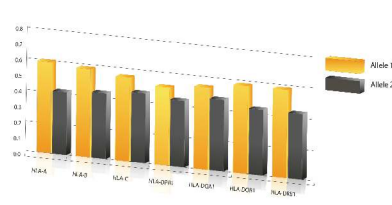
Data Visualization & Statistics

There are detailed visualization and data statistics, including graphical representations to help troubleshoot any potential quality issues.

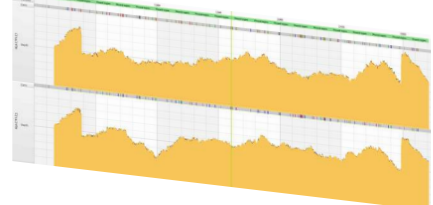
Fragment Size



Allele Balance



Coverage Plot



“It's disappointing sometimes how easily HLA Twin deals with challenging samples like rare alleles. The data is there - you're just convinced!”
Alexandre Walencik, Biologiste Médical, Laboratoire HLA - Nantes

HLA TWIN™ Technical Requirements

	Desktop	Server		Client
		Typing Server	Reporting Server	
CPU	64 bit multi-core	64 bit multi-core		64 bit multi-core
Memory (minimum)	16GB	24GB	6GB	4GB
Operating System	64 bit Windows / Linux or OS X	64 bit Windows or Linux (OS X not supported)		64 bit Windows / Linux or OS X

Believe the data

- 110+ HLA labs trained onsite worldwide
- 45+ HLA labs in clinical routine worldwide
- 20+ customers using CE-IVD products in Europe
- 12 labs ASHI or CAP accredited in North America
- 6 labs EFI accredited in Europe
- 253 samples in ASHI validation study at CHOP

All Omixon activities covered by an ISO 13485:2003 & EN ISO 13485:2012 Quality Management System (QMS)

