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

**Automation & Integration**
- Fully automated analysis after Illumina sequencing run
- Export genotyping results in the standard Histocompatibility and Immunogenetics 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

**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

**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
![Fragment Size Chart]

Allele Balance
![Allele Balance Chart]

Coverage Plot
![Coverage Plot Chart]

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

<table>
<thead>
<tr>
<th></th>
<th>Desktop</th>
<th>Server</th>
<th>Client</th>
</tr>
</thead>
<tbody>
<tr>
<td>CPU</td>
<td>64 bit multi-core</td>
<td>64 bit multi-core</td>
<td>64 bit multi-core</td>
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<tr>
<td>Memory (minimum)</td>
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<td>24GB</td>
<td>6GB</td>
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<tr>
<td>Operating System</td>
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<td>64 bit Windows or Linux (OS X not supported)</td>
<td>64 bit Windows / Linux or OS X</td>
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</tbody>
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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 ESI accredited in Europe
- 253 samples in ASHI validation study at CHOP


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