

## Omixon HLA Twin™

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.

**Confidence** – HLA Twin uses two orthogonal algorithms to make two independent genotyping calls on every locus of every sample.

**Quality** – With a quality metric for every ASHI NGS standard, and more of our own, the Traffic Light System in HLA Twin will guide and facilitate the interpretation of your data.

**Automation** – When correctly configured, HLA Twin can be configured to run without user intervention, to process data immediately after the completion of an Illumina MiSeq run.

**High Throughput** – HLA Twin can process 96 samples of Holotype X2 with 7 loci in under 6 hours on an 8-core server with 16 GB of RAM.

### Features

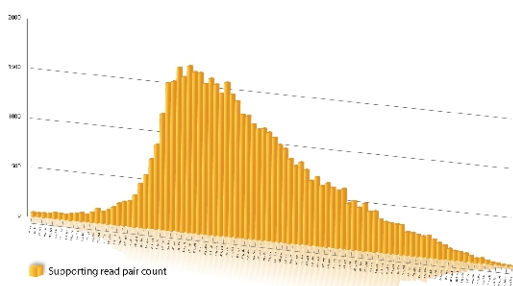
- Two independent algorithms: Consensus Genotyping and Statistical Genotyping (see below for details)
- Full-length consensus sequences
- Novel allele and Null allele detection
- Traffic Light System (TLS) for easy interpretation of genotyping results
- Dual-algorithm concordance check with Traffic Light #1
- 15 locus related quality metrics checked with Traffic Light #2
- Analyze data against any version of the IMGT/HLA Database
- Ability to analyze more reads for phase resolution, if required
- Export genotyping results in NMDP standard, HML 0.9.7 format

Paired result	Mismatch overview	Alignment statistics	Quality control	Data statistics
Measure				HLA-A
<b>Overall</b>				<b>PASSED</b>
Fragment size				403
Read length				222
Crossmapping (intergenic ambiguity)				4.798%
Read quality				36.2
Noise level				0.13%
Contamination ratio				0.056%
PCR crossover artifact ratio				1.32%
Allele imbalance				56.135% : 43.865%
Exon mismatch count				0

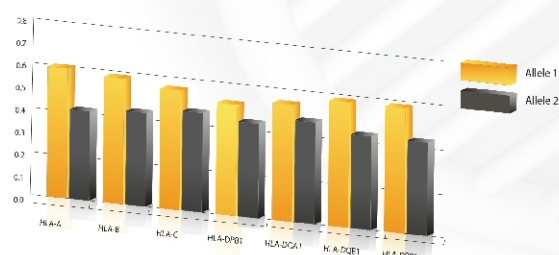
### Quality Metrics, Alignment & Data Statistics

15 independent locus-related quality control metrics (see screenshot above) are used at every locus for every sample – for example, read length and quality, noise ratio, consensus coverage, and allele imbalance, phasing and more. In addition, there are detailed alignment and data statistics, including graphical representations, to help troubleshoot any potential quality issues (see figures below).

#### Fragment Size

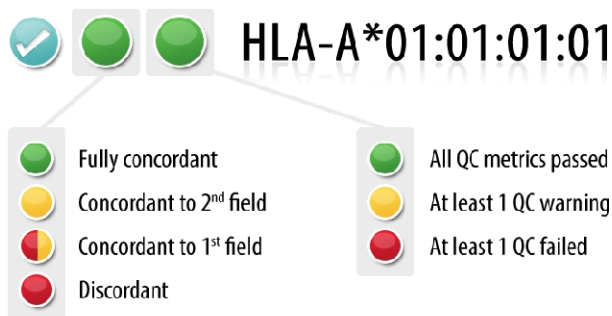


#### Allele Balance



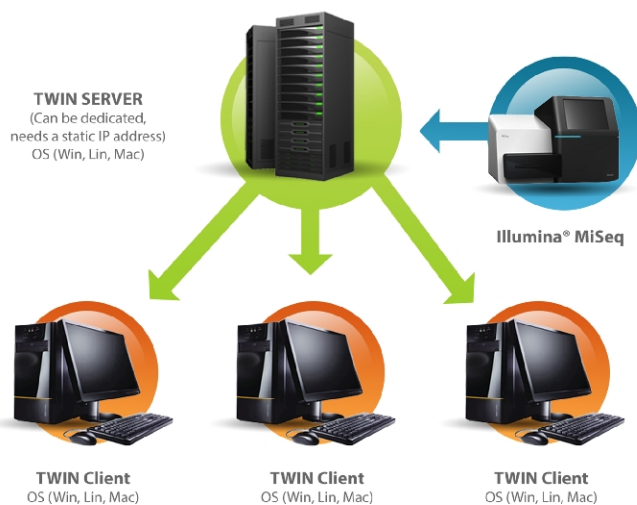
## Traffic Lights System (TLS)

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



Traffic Light #1 is the dual algorithm concordance check. A green light indicates the results are concordant to the 3<sup>rd</sup> field or higher.

Traffic Light #2 is the locus-related quality check. HLA Twin evaluates 15 different quality metrics at every locus for every sample. If there is a single QC warning the Yellow Traffic Light suggests a manual inspection of the data. Two green lights allow an analyst to have complete confidence in the genotyping call, with no manual inspection required.

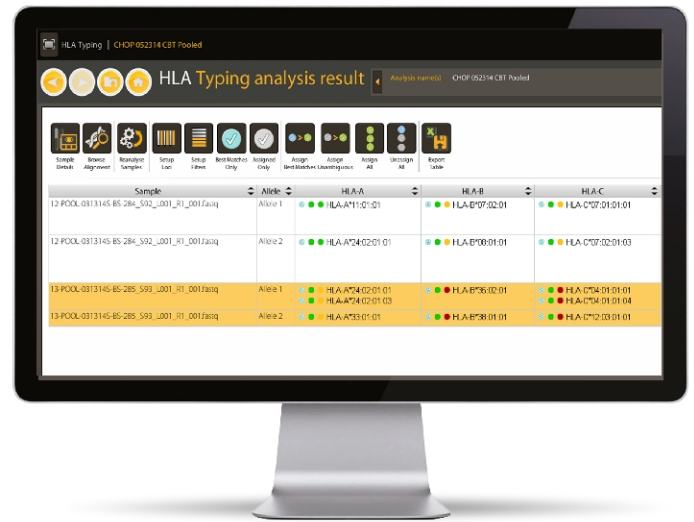


HLA Twin can be configured on a Server to run automatically after the completion of the MiSeq run.

When configured for automatic analysis, there is no hands-on time before the analysis is initiated – allowing for immediate focus on interpreting genotyping results with the Traffic Light System, at your convenience.

“ Together with Omixon, we have used next-generation sequencing tools to significantly advance HLA typing.

*Prof. Dimitri Monos, The Children's Hospital of Philadelphia*



## Believe the Data

1000+ routine clinical samples analyzed at CHOP since 2013

253 samples in ASHI validation study

Performance Evaluation Study on 200 carefully selected reference samples at 7 loci

25 Early Access Program labs, 1500+ samples

### Alpha Study (Monos et al.)

99.8% concordance

0.2% ambiguity

99.7% reproducibility

99.5% accuracy (Target HLA)

100% accuracy (HLA Twin reanalysis)



For more information:  
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## HLA Twin Server Technical Requirements

Minimum:

- » 4+ processing cores
- » 8+ GB of memory
- » 64 bit OS

Recommended:

- » 8+ processing cores
- » 16+ GB of memory
- » Storage space requirements depend on the size of data usually used for analysis.

If you would like us to specify the server requirements for your environment, contact [support@omixon.com](mailto:support@omixon.com)