Fully Phased, Allele-Specific HLA Sequencing with the PacBio® RS II
**SMRT® Sequencing Solution for HLA Typing**

**Advantages of Single Molecule, Real-Time Sequencing**

The PacBio® RS II, with its industry leading read lengths, accuracy, and fast turn-around time, is the only system available that can sequence full-length HLA gene alleles and reliably provide directly phased HLA types without imputation.

- **Longest read lengths:** Average read lengths > 10 kb (maximum > 40 kb)
- **Highest accuracy:** Achieves ≥ 99.999 (QV50)
- **Multiplexing of amplicons supported by DNA barcoding**
- **Fastest turn-around time**
- **Flexible, low-cost run designs**

**Generate Full-Length Allele Sequence**

- Phase entire length of amplicon, including SNP-poor regions
- Allele-level segregation without imputation
- Direct evidence for new alleles
Flexible Primer Design

Use your own primers & assays...

- Open platform for customized assays of all insert sizes (250 bp to 40 kb)
- Use your well-established primer designs and assays for obtaining high-resolution sequences for complete HLA genes or simply amplify partial genes to phase between exons

Or use the GenDx NGSgo®-AmpX Reagent Kit

- NGSgo®-AmpX kits include ready-to-use amplification primers designed for full-length HLA-A, B, C, and contiguous amplicons covering the relevant exons and introns for DRB1, DQB1, DPA1, DPB1, DQA1, DRB3/4/5
- Currently available as single-sample amplification assays
- Coming soon: Integration of DNA Barcode sequences for multiplexing full-length class I genes

Compatible With Third-Party HLA Typing Software

Sequence files generated by SMRT Analysis Software are compatible with industry-standard NGS typing software to generate HLA genotypes for comparison with the IMGT/HLA database.

- The Assign™ MPS HLA Sequence Analysis Software
- NGSengine® Software

Emerging Immunogenomic Research Applications

Haplotyping KIR and the MHC region

- PacBio’s long read lengths and unbiased coverage generate highly accurate de novo assemblies of complex and repetitive genomic regions.
- A specialized 40 kb fosmid-based target enrichment strategy combined with these ultra-long read lengths can provide simultaneous genotyping and haplotype-level characterization of highly complex and difficult-to-assemble repetitive regions.