CeGaT

Research &
Pharma Solutions | HLA Typing

Bioinformatic Note

HLA Typing

The human leukocyte antigen (HLA) system is a group of genes that have an important function in the human immune system. The HLA region is highly polymorphic and contains six classical HLA genes: class I with *HLA-A*, *-B*, and *-C*, and class II with *HLA-DRB1*, *-DQB1* and, *-DPB1*. Furthermore, the HLA region is known to be associated with more than 100 multifactorial, complex diseases, mainly with inflammatory and autoimmune pathogenesis. Next-generation sequencing (NGS)-based HLA typing can be very helpful to learn more about the functions and complex interactions of the HLA system.

The application areas of HLA typing are diverse:

- supporting the characterization of an individual's response to drug therapy, including pharmacogenetics.
- providing important information for immunotherapy to fight cancer.
- matching HLA regions of a donor and a recipient for a transplantation.

Our HLA class I and II typing is based on Whole Exome Sequencing (WES). Only one level of bioinformatic analysis is available. However, additional to HLA typing, we can offer further bioinformatic analysis for the exome data, of course.

Table 1 | Excerpt of the alleles file of the HLA typing.

locus	allele_1	allele_2
A	A*01:01	A*29:02
B	B*08:01	B*44:03
C	C*07:01	C*16:01

Bioinformatic Analysis

The sequencing data are demultiplexed and trimmed. The trimmed reads are delivered in FASTQ format.

The additionally generated project report provides information for every sample about the laboratory protocol, including data about quality control of the starting material, library preparation, sequencing parameters, and the Q30 value of the sequencing. For the trimmed data, the number of sequenced fragments and bases is reported, and the sequence length, quality of the reads and the GC content are illustrated in bar plots for all samples.

HLA-typing is performed with a special algorithm. It allows typing of HLA class I (*A, B, C*) and HLA class II (*DPA1, DPB1, DQA1, DQB1, DRB1, DRB3, DRB4, DRB5*).

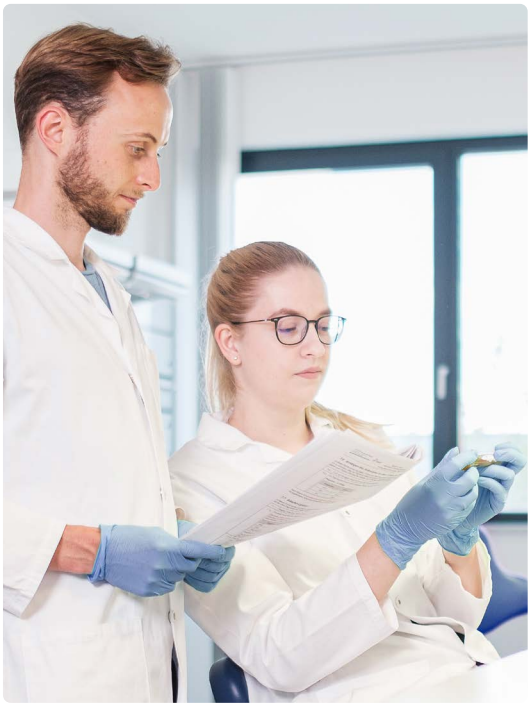
For each sample, you receive a file containing the alleles obtained during the HLA-typing as TSV file. An excerpt of this file is shown in table 1. For your convenience, the identified HLA types are also listed in the project report.

About Us

CeGaT was founded in 2009 in Tübingen, Germany. Our scientists are specialized in next-generation sequencing (NGS) for genetic diagnostics, and we also provide a variety of sequencing services for research purposes and pharma solutions. Our sequencing service portfolio is complemented by analyses suited for microbiome, immunology, and translational oncology studies.

Our dedicated project management team of scientists and bio-informaticians works closely with you to develop the best strategy to realize your project. Depending on its scope, we select the most suitable library preparation and conditions on our sequencing platforms.

We would be pleased to provide you with our excellent service.
Contact us today to start planning your next project.



For more details please visit
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