Sample ID:-	**886**
Sample Type:-	Whole Blood
Patient's Name:-	***HLA-demo***
Patient's DOB:-	2018-08-15
Patient's gender:-	Female

Data uploaded on:	**2024-06-06**	**Report Generated on:**	**2024-06-06**

HLA results:-

Sample HLA typing table		
HLA class	**Allele 1**	**Allele 2**
A	A*02:11	A*24:02
B	B*44:03	B*44:03
C	C*07:06	C*07:06
DPB1	DPB1*04:01	DPB1*04:01
DQB1	DQB1*02:02	DQB1*02:02
DRB1	DRB1*07:01	DRB1*07:01

Note:

• The human leukocyte antigen (HLA), the human major histocompatibility complex, is located on the short arm of chromosome 6 and is an important part of the human immune system. Different complexes bind to various exogenous or endogenous antigen fragments through their binding slots, and then interact with different T cells to activate downstream immune responses. Therefore, the functions undertaken by HLA require its own diversity: HLA coding genes are one of the most polymorphic coding regions on the human genome. HLA antigen polymorphism is associated with many diseases, vaccine and drug targeting population screening, tissue and organ transplantation and so on. The degree of HLA matching is a key factor in the success of organ, bone marrow and stem cell transplantation. In addition, the HLA genotype of the tumor patient and the systemic mutations in the tumor may affect the efficacy of immunotherapy. Therefore, accurate typing of HLA genes is particularly important.

Description:

The Genes2Me HLA Typing NGS panel was used for sequencing that screens 11 clinically relevant genes (coding regions of the genome) for diseases associated with genetic mutations.
The target size is 70 kb with hybridization-based target capture technique.

Explanation of the limitations of the results:-

1. Interpretation of this result requires clinical correlation with the patient's phenotype, family history, and other relevant clinical information, and should ideally be performed in consultation with a genetics professional or medical geneticist for accurate diagnosis and management recommendations.

2. This test specifically identifies variants within designated genes and does not assess DNA methylation, RNA, or protein levels.

3. The analysis and interpretation of this test rely on published literature and databases. It's important to note that interpretations of variations may evolve with new developments in the field.

4. In case there is a negative result and variant is not detected, the possibility of variation below the lower limit cannot be ruled out or The clinical sensitivity and specificity of NGS tests depend on various factors, including test design, detection algorithms, and interpretation criteria, and may not be 100% accurate for all variants or conditions.

5. Genetic variation can vary across populations, and NGS-based tests may have limitations in detecting rare or population-specific variants, particularly in underrepresented populations, which may affect the accuracy of risk assessment or diagnosis.

6. NGS data may contain technical artifacts, such as sequencing errors, PCR amplification bias, or alignment artifacts, which can affect the accuracy of variant calling and interpretation.

References:-

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Appendix: Gene list

A	B	C	DPA1	DPB1	DQA1	DQB1
DRB1	DRB3	DRB4	DRB5			