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Nomenclature for sequence-based STR alleles

序列多态STR等位基因命名规则

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Foreword

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Introduction

STR genetic markers are widely used in forensic science, forensic identification, medicine and anthropology research.

It is necessary to formulate a universal naming rule for sequence polymorphic STR alleles, which is unified, unique, coordinated, and extensible, so as to improve the Application value.

Nomenclature of sequence polymorphic STR alleles

1 Scope

This document specifies the general requirements and specific rules for naming sequence polymorphic STR alleles.

This document is applicable to laboratories and enterprises engaged in STR sequencing, scientific research, production, testing, etc., for human STR alleles name.

2 Normative references

GB/T 41009

3 Terms and definitions

The following terms and definitions apply to this document.

3.1 short tandem repeat; STR

Widely present in eukaryotic genomes, the repeating unit is usually composed of 2 to 6 bases, and the number of repetitions is usually 5 to 60 times. DNA fragments.

3.2 STR allele

Fragments of DNA that differ in sequence and/or length at the STR locus.

3.3 length polymorphism

The polymorphism is caused by the difference in DNA length between alleles at the same locus.

3.4 sequence polymorphism

The polymorphism is caused by the difference in DNA sequence between alleles at the same locus.

3.5 repeat region sequence repeatregionsequence

sequence.

3.6

The DNA sequences on both sides of the STR repeat region.

Note. refers to the sequence between the PCR primer binding position and the STR repeat region in the amplified fragment of STR.

The binding position may vary, and the range of positions at which flanking sequences are detected and reported may vary.

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