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1. **113699262** SSR MOLECULAR MARKER PRIMER AND METHOD FOR IDENTIFYING SCUTELLARIA BAICALENSIS IN INNER MONGOLIA REGION — CN - 26.11.2021

Int.Class C12Q 1/6895 **Appl.No** 202011051978.2 **Applicant** CHINA NATIONAL TRADITIONAL CHINESE MEDICINE CO., LTD **Inventor** WANG JIYONG

The invention provides an SSR molecular marker primer and a method for identifying scutellaria baicalensis in the Inner Mongolia region, and the method comprises the following steps: taking total DNA of a to-be-identified scutellaria baicalensis sample as a template, and performing PCR amplification by using an SSR molecular marker to obtain an amplification product; performing capillary electrophoresis sequencing typing on the amplification product to obtain a typing result of the amplification product; carrying out peak map interpretation on the typing result of the amplification product by using GeneMarker 4.0 to obtain an allele matrix; calculating genetic diversity data of scutellaria baicalensis through GenALEx according to the allele matrix; and carrying out UPGMA clustering analysis through MEGA on the basis of genetic diversity data obtained by GenALEx calculation, and constructing a clustering tree. The technical problems that existing scutellaria baicalensis producing area identification mostly adopts character identification, microscopic identification and other methods, depends on personal experience and subjective judgment, and is low in accuracy and technology generalizability are solved.

2. **113684292** SSR MOLECULAR MARKER PRIMERS AND METHOD FOR IDENTIFYING WILD BUCKWHEAT RHIZOME IN GUIZHOU REGION — CN - 23.11.2021

Int.Class C12Q 1/6895 **Appl.No** 202011048796.X **Applicant** CHINA NATIONAL TRADITIONAL CHINESE MEDICINE CO., LTD **Inventor** WANG JIYONG

The invention provides SSR molecular marker primers and a method for identifying wild buckwheatrhizome in Guizhou region, and the method comprises the following steps: taking total DNA of a wild buckwheat rhizome sample to be identified as a template, and carrying out PCR amplification by using an SSR molecular marker to obtain an amplification product; performing capillary electrophoresis sequencing typing on the amplification product to obtain a typing result of the amplification product; carrying out peak map interpretation on the typing result of the amplification product by using GeneMarker 4.0 to obtain an allele matrix; according to the allele matrix, carrying outGenALEx calculation to obtain genetic diversity data of the wild buckwheat rhizome; and on the basis of genetic diversity data obtained by GenALEx calculation, carrying out UPGMA clustering analysis through MEGA to construct a clustering tree. The technical problems that existing wild buckwheat rhizome production area identification mostly adopts character identification, microscopic identification and other methods, depends on personal experience and subjective judgment, and is low in accuracy and technology generalizability are solved.

3. **113684293** SSR MOLECULAR MARKER PRIMERS AND METHOD FOR IDENTIFYING SCUTELLARIA BAICALENSIS IN SHANXI AND SHAANXI REGIONS — CN - 23.11.2021

Int.Class C12Q 1/6895 **Appl.No** 202011049479.X **Applicant** CHINA NATIONAL TRADITIONAL CHINESE MEDICINE CO., LTD **Inventor** WANG JIYONG

The invention provides SSR molecular marker primers and a method for identifying scutellaria baicalensis in Shanxi and Shaanxi regions, and the method comprises the following steps: taking total DNA of a to-be-identified scutellaria baicalensis sample as a template, and carrying out PCR amplification by using an SSR molecular marker to obtain an amplification product; performing capillary electrophoresis sequencing typing on the amplification product to obtain a typing result of the amplification product; carrying out peak map interpretation on the typing result of the amplification product by using GeneMarker 4.0 to obtain an allele matrix; according to the allele matrix, carrying out GenALEx calculation to obtain genetic diversity data of the scutellaria baicalensis; and on the basis of genetic diversity data obtained by GenALEx calculation, carrying out UPGMA clustering analysis through MEGA to construct a clustering tree. The technical problems that existing scutellaria baicalensis producing area identification mostly adopts character identification, microscopic identification and other methods, depends on personal experience and subjective judgment, and is low in accuracy and technology generalizability are solved.

4. **113684291** SSR MOLECULAR MARKER PRIMERS AND METHOD FOR IDENTIFYING SCUTELLARIA BAICALENSIS IN NORTHEAST REGION — CN - 23.11.2021

Int.Class C12Q 1/6895 **Appl.No** 202011048452.9 **Applicant** CHINA NATIONAL TRADITIONAL CHINESE MEDICINE CO., LTD **Inventor** WANG JIYONG

The invention provides SSR (simple sequence repeat) molecular marker primers and method for identifying scutellaria baicalensis in the northeast region, and the method comprises the following steps: taking total DNA (deoxyribonucleic acid) of a scutellaria baicalensis sample to be identified as a template, and performing PCR (polymerase chain reaction) amplification by using the SSR molecular marker primers to obtain an amplification product; performing capillary electrophoresis sequencing typing on the amplification product to obtain a typing result of the amplification product; carrying out peak map interpretation on the typing result of the amplification product by using GeneMarker 4.0 to obtain an allele matrix; according to the allele matrix, carrying out GenALEx calculation to obtain genetic diversity data of the scutellaria baicalensis; and on the basis of genetic diversity data obtained by GenALEx calculation, carrying out UPGMA clustering analysis through MEGA to construct a clustering tree. A genome technology and an SSR molecular marker technology are applied, the SSR primers are designed by utilizing the scutellaria baicalensis genome, the SSR primers are screened through scutellaria baicalensis samples in Hebei, Shanxi, Shandong, Shaanxi, Inner Mongolia, Liaoning, Jilin and the like, and the primers are used for specifically identifying scutellaria baicalensis samples in the northeast region, are high in accuracy and stability and are easy to popularize and apply in a large scale.

5. **113684294** SSR MOLECULAR MARKER PRIMERS AND METHOD FOR IDENTIFYING WILD BUCKWHEAT RHIZOME IN SICHUAN REGION — CN - 23.11.2021

Int.Class C12Q 1/6895 **Appl.No** 202011049953.9 **Applicant** BGI TECH SOLUTIONS CO., LTD. **Inventor** GAO QIANG

The invention provides SSR (simple sequence repeat) molecular marker primers and a method for identifying wild buckwheat in Sichuan region, and the method comprises the following steps: taking total DNA (deoxyribonucleic acid) of a wild buckwheat rhizome as a template, and performing PCR (polymerase

chain reaction) amplification by using an SSR molecular marker to obtain an amplification product; performing capillary electrophoresis sequencing typing on the amplification product to obtain a typing result of the amplification product; carrying out peak map interpretation on the typing result of the amplification product by using GeneMarker 4.0 to obtain an allele matrix; according to the allele matrix, carrying out GenALExcalculation to obtain genetic diversity data of the wild buckwheat rhizome; and on the basis of genetic diversity data obtained by GenALEx calculation, carrying out UPGMA clustering analysis to construct a clustering tree. The technical problems that existing wild buckwheat rhizome production area identification mostly adopts character identification, microscopic identification and other methods, depends on personal experience and subjective judgment, and is low in accuracy and technology generalizability are solved.

6. **113528655** MARKER FOR BREAST CANCER DOCETAXEL CHEMOTHERAPY RESISTANCE AND DETECTION KIT CN - 22.10.2021

Int.Class C12Q 1/6886 **Appl.No** 202010296136.7 **Applicant** BGI TECH SOLUTIONS CO., LTD. **Inventor** HUANG PEIDE

The invention discloses a marker for breast cancer docetaxel chemotherapy resistance and a detection kit. The marker for the breast cancer docetaxel chemotherapy drug resistance is circular RNA (Ribonucleic Acid) for controlling ABCB1 gene expression, and the circular RNA has a sequence shown as Seq ID (Identity) No. 1. According to the application, a novel marker for breast cancer docetaxel chemotherapy drug resistance is found through research, namely, the annular RNA for controlling ABCB1 gene expression with the sequence shown as Seq ID No.1. Through the detection of the marker, namely the detection of the expression quantity of the circular RNA molecule CircABCB1, the drug resistance of the breast cancer to paclitaxel can be predicted, the drug resistance risk can be found as early as possible, the selection process of chemotherapy drugs is optimized, the treatment time is saved, the mental pain and economic burden of a patient are reduced, and a foundation is laid for customizing an individualized breast cancer chemotherapy regimen.

7. **113496760** POLYPLOIDY GENOME ASSEMBLING METHOD AND DEVICE BASED ON THIRD-GENERATION SEQUENCING CN - 12.10.2021

Int.Class G16B 20/10 **Appl.No** 202010250558.0 **Applicant** BGI TECH SOLUTIONS CO., LTD. **Inventor** HE LIJUAN

The invention discloses a polyploidy genome assembly method and device based on third-generation sequencing. The method comprises the following steps: acquiring third-generation single molecule sequencing data of a polyploidy genome, and performing data error correction and assembly to obtain a first assembly result; comparing the sequencing data to a first assembly result, carrying out deep evaluation, and counting the coverage degree of the whole genome to obtain an assembled single-copy and multi-copy area; selecting the sequences of the areas assembled with the multiple copies for comparison between the sequences so as to remove repetition between the sequences covered in the areas of the multiple copies, and obtaining a first round of redundancy removal result; identifying and interrupting possible wrong connection, and then re-splicing the genome sequence to remove splicing problems on the genome to obtain a second assembly result; after it is determined that redundancy elimination succeeds, merging the partial sequence, not included in the second assembly result, in the first assembly result into the second assembly result, and then carrying out optimization and correction to obtain a third assembly result. According to the method and device, a single set of chromosome group can be effectively separated from the complex polyploidy.

8. **214315990** GENE DATA ANALYSIS ALL-IN-ONE MACHINE CN - 28.09.2021

Int.Class H05K 7/14 **Appl.No** 202120314687.1 **Applicant** BGI TECH SOLUTIONS CO., LTD. **Inventor** JIN XIANGQIAN

The utility model discloses a gene data analysis all-in-one machine which comprises a box body, a server, a switch and a front-end processor, the front-end processor comprises a display and a front-end processor host, the server, the switch and the front-end processor host are installed in the box body, and the display is movably connected to the upper end of the front face of the box body through a connecting piece. Due to the fact that the server, the switch and the front-end host are integrated in the box body, integrated integration of a plurality of devices is achieved, connecting lines among the devices can be stored in the box body, and the gene data analysis all-in-one machine is made to have smaller occupied space. Moreover, the display is movably connected to the upper end of the front surface of the box body, so that a user can conveniently watch at different angles or positions.

9. **214206176** GENE DATA ANALYSIS ALL-IN-ONE MACHINE CN - 14.09.2021

Int.Class H05K 7/14 **Appl.No** 202120314347.9 **Applicant** BGI TECH SOLUTIONS CO., LTD. **Inventor** JIN XIANGQIAN

The utility model discloses a gene data analysis all-in-one machine, which comprises a box body, a server, a switch and a front-end processor, the front-end processor comprises a display and a front-end processor host, the box body comprises a comprehensive layer and at least one server layer, the comprehensive layer and the at least one server layer are sequentially and detachably laminated and connected, and the comprehensive layer is positioned at the uppermost end. Due to the fact that the box body is arranged to be the detachable comprehensive layer and the detachable server layer, the gene data analysis all-in-one machine can expand the number of servers according to requirements so as to meet use in different scenes. Moreover, the server, the switch and the front-end processor host are integrated in the box body, so that integrated integration of a plurality of devices is realized, and connecting lines among the devices can be accommodated in the box body, so that the gene data analysis all-in-one machine has a smaller occupied space.

10. **113377765** MULTI-OMICS DATA ANALYSIS SYSTEM AND DATA CONVERSION METHOD THEREOF CN - 10.09.2021

Int.Class G06F 16/22 **Appl.No** 202110545036.8 **Applicant** BGI TECH SOLUTIONS CO., LTD. **Inventor** SHI MINGMING

The invention relates to a multi-omics data analysis system and a data conversion method thereof. The analysis system comprises an interaction module, a processing module and a plurality of omics databases, the interaction module is used for providing an interactive form for a user so as to collect data analysis demand information of the user on one or more omics databases; the processing module is used for extracting or converting associated data matched with the analysis demand information from one or more omics databases according to the data analysis demand information and returning the associated data to the interaction module; and the plurality of omics databases includes a genomics database, a transcriptomics database, an epimics database, and a proteomics database. Different data analysis requirements of the user for one or more omics are collected in a mode of interacting with the user, and different analysis and mining of multiple omics data are realized by utilizing a mutual mapping relation of different omics data.