A Big Earth Data Platform for Three Poles

**Sequence data of mice transcriptome (2019)**

1、Description

According to the genomic data obtained, most of the candidate genes are related to physiological development. In order to study the specific regulatory mechanism of the candidate genes, corresponding functional verification tests are carried out. Therefore, we obtained the corresponding transgenic mice and sequenced the corresponding tissues of homozygous and wild-type samples (22 tissue samples in total, including brain, bone marrow and muscle tissues). Then through the analysis of this batch of transcriptome data, we can improve the functional verification of candidate genes, in order to provide powerful data for understanding the adaptive genetic mechanism of species in different regions and physiological regulation in the process of growth and development.

2、Keywords

Theme：Biological Resources,Vertebrate
Discipline：Human-nature Relationship
Places：Tibetan Plateau
Time：2019

3、Data details

1.Scale：None

2.Projection：

3.Filesize：91000.0MB

4.Data format：None

4、Space scope

|  |  |  |
| --- | --- | --- |
| - | north：25.059195 | - |
| west：102.708843 | - | east：102.708843 |
| - | south：25.059195 | - |

5、Time frame:2021-12-08 00:00:00+00:00--2022-02-07 11:59:59+00:00

6、Reference method

References to data:

LI Yan. Sequence data of mice transcriptome (2019). A Big Earth Data Platform for Three Poles, doi:10.11888/Ecolo.tpdc.2708992020

References to articles:

7、Supporting project information

Pan-Third Pole Environment Study for a Green Silk Road-A CAS Strategic Priority A Program
Second Tibetan Plateau Scientific Expedition Program

8、Data resource provider

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