A Big Earth Data Platform for Three Poles

**Transcriptome sequencing data of main domestic animals in the Tibetan Plateau (2019)**

1、Description

In order to describe the distribution pattern of the genetic diversity of the main domesticated animals in the Qinghai Tibet Plateau and its surrounding areas, and to clarify the related genetic background. In 2019, we selected two breeds of pigs in Yunnan Province as low altitude reference, collected RNA tissue samples from the brain of two breeds of pigs, extracted total RNA, built a database and sequenced the transcriptome. Sequencing produced a batch of 322g transcriptome sequencing raw data. To provide basic data for the study of the adaptation of domestic animals to the extreme environment of the Qinghai Tibet Plateau, to explore the historical events of domestication, migration and expansion of the main domesticated animals in the region, and to further explore the adaptation mechanism of domesticated animals to the poor environment such as hypoxia, high cold and dry.

2、Keywords

Theme：Forest
Discipline：Terrestrial Surface
Places：Pan-Third Pole
Time：2019

3、Data details

1.Scale：None

2.Projection：

3.Filesize：322000.0MB

4.Data format：None

4、Space scope

|  |  |  |
| --- | --- | --- |
| - | north：25.143489 | - |
| west：102.746654 | - | east：102.746654 |
| - | south：25.143489 | - |

5、Time frame:2019-01-09 08:00:00+00:00--2020-01-08 19:59:59+00:00

6、Reference method

References to data:

PENG Minsheng. Transcriptome sequencing data of main domestic animals in the Tibetan Plateau (2019). A Big Earth Data Platform for Three Poles, doi:10.11888/Ecolo.tpdc.2704332020

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

name: PENG Minsheng
unit: Kunming Institute of Zoology, Chinese Academy of Sciences
email: pengminsheng@mail.kiz.ac.cn