A Big Earth Data Platform for Three Poles

**Equine genome sequencing data (2022)**

1、Description

In order to study the population evolution history and local adaptive genetic mechanism of the main domesticated equine animals in the Qinghai Tibet Plateau and its surrounding areas, and to establish the corresponding germplasm genetic resource bank. We sequenced the equine samples collected in Qinghai Province, Tibet Autonomous Region and Xinjiang Autonomous Region from the Qinghai Tibet Plateau and surrounding areas, including Tibetan donkey, plain donkey and other breeds. Sequencing includes denove and resequencing data, which provides data for tracing the historical events of domestication, migration, expansion and other groups of the main equine domesticated animals in the region, and further exploring the adaptation mechanism of equine animals to the harsh environment such as hypoxia, cold, and dryness. At the same time, all tissues of domestic donkeys were sequenced, including hifi genome data and HIC genome data, to prepare for the assembly of complete donkey genome and facilitate subsequent analysis.

2、Keywords

Theme：Biological Resources,Domestic animal,Animal resources  
Discipline：Human-nature Relationship  
Places：Tibetan Plateau  
Time：2020-2022

3、Data details

1.Scale：None

2.Projection：

3.Filesize：1000000.0MB

4.Data format：None

4、Space scope

|  |  |  |
| --- | --- | --- |
| - | north：30.0 | - |
| west：94.0 | - | east：100.0 |
| - | south：28.0 | - |

5、Time frame:2021-12-31 16:00:00+00:00--2022-09-30 03:59:59+00:00

6、Reference method

References to data:

LI Yan. Equine genome sequencing data (2022). A Big Earth Data Platform for Three Poles, doi:10.11888/HumanNat.tpdc.2727532022

References to articles:

7、Supporting project information

Pan-Third Pole Environment Study for a Green Silk Road-A CAS Strategic Priority A Program

8、Data resource provider

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