A Big Earth Data Platform for Three Poles

**Hi-C sequencing data of cyanine genome**

1、Description

Based on the high-quality genomic sequence analysis, the high-quality genome sequences can be obtained. Therefore, through this technology, the project team divides the sequences in the genome sequence sketch into groups that are consistent with the chromosome number of the species, and determines the order and orientation of all sequences in each group. After that, we can combine the reference vines genome, transcriptome assembly sequence (EST sequence), related species and genetic map data The accuracy of grouping and the sequence and direction between sequences were evaluated.

2、Keywords

Theme：Biological Resources  
Discipline：Terrestrial Surface,Human-nature Relationship  
Places：Qinghai-Tibet Plateau  
Time：2020

3、Data details

1.Scale：None

2.Projection：

3.Filesize：395.0MB

4.Data format：None

4、Space scope

|  |  |  |
| --- | --- | --- |
| - | north：32.0 | - |
| west：95.0 | - | east：97.0 |
| - | south：31.0 | - |

5、Time frame:2018-05-31 16:00:00+00:00--2018-11-06 03:59:59+00:00

6、Reference method

References to data:

DUAN Yuanwen. Hi-C sequencing data of cyanine genome. A Big Earth Data Platform for Three Poles, doi:10.11888/Ecolo.tpdc.2710692020

References to articles:

段元文，杨云强.蔓菁基因组Hi-C测序数据

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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