A Big Earth Data Platform for Three Poles

**Genome Assembly of Alpine Species Salix Brachista on the Tibetan Plateau (2019)**

1、Description

This dataset is collected from the paper: Chen, J.\*#, Huang, Y.\*#, Brachi, B.\*#, Yun, Q.\*#, Zhang, W., Lu, W., Li, H., Li, W., Sun, X., Wang, G., He, J., Zhou, Z., Chen, K., Ji, Y., Shi, M., Sun, W., Yang, Y.\*, Zhang, R.#, Abbott, R. J.\*, & Sun, H.\* (2019). Genome-wide analysis of Cushion willow provides insights into alpine plant divergence in a biodiversity hotspot. Nature Communications, 10(1), 5230. doi:10.1038/s41467-019-13128-y.   
This data contains the genome assembly of alpine species Salix brachista on the Tibetan Plateau, it contains DNA, RNA, Protein files in Fasta format and the annotation file in gff format.  
Assembly Level: Draft genome in chromosome level  
Genome Representation: Full Genome  
Reference Genome: yes  
Assembly method: SMARTdenovo 1.0; CANU 1.3  
Sequencing & coverage: PacBio 125.0; Illumina Hiseq X Ten 43.0; Oxford Nanopore Technologies 74.0  
Statistics of Genome Assembly:  
Genome size (bp): 339,587,529  
GC content: 34.15%  
Chromosomes sequence No.: 19  
Organellas sequence No.: 2  
Genome sequence No.: 30  
Maximum genome sequence length (bp): 39,688,537  
Minimum genome sequence length (bp): 57,080  
Average genome sequence length (bp): 11,319,584  
Genome sequence N50 (bp): 17,922,059  
Genome sequence N90 (bp): 13,388,179  
Annotation of Whole Genome Assembly:  
Protein：30,209  
tRNA：784  
rRNA：118  
ncRNA：671  
Please see attachments for more details of annotation.  
The tables in the Supplementary Information of this article can also be found in this dataset. The table list is represented in attachments.  
The accession no. of genome assembly is GWHAAZH00000000 (https://bigd.big.ac.cn/gwh/Assembly/663/show).

2、Keywords

Theme：Vegetation,Genomics  
Discipline：Terrestrial Surface  
Places：the Qinghai-Tibet Pleatu  
Time：2019

3、Data details

1.Scale：None

2.Projection：

3.Filesize：136.93MB

4.Data format：None

4、Space scope

|  |  |  |
| --- | --- | --- |
| - | north：30.71 | - |
| west：95.69 | - | east：103.17 |
| - | south：26.15 | - |

5、Time frame:2019-01-16 08:00:00+00:00--2020-01-15 19:59:59+00:00

6、Reference method

References to data:

Richard John Abbott, YANG Yongping, CHEN Jiahui, SUN Hang. Genome Assembly of Alpine Species Salix Brachista on the Tibetan Plateau (2019). A Big Earth Data Platform for Three Poles, doi:10.11888/Ecolo.tpdc.2709082020

References to articles:

Chen, J., Huang, Y., Brachi, B., Yun, Q., Zhang, W., Lu, W., Li, H., Li, W., Sun, X., Wang, G., He, J., Zhou, Z., Chen, K., Ji, Y., Shi, M., Sun, W., Yang, Y., Zhang, R., Abbott, R. J., & Sun, H. (2019). Genome-wide analysis of Cushion willow provides insights into alpine plant divergence in a biodiversity hotspot. Nature Communications, 10(1), 5230. doi:10.1038/s41467-019-13128-y

7、Supporting project information

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

8、Data resource provider

name: SUN Hang  
unit: Kunming Institute of Botany, Chinese Academy of Sciences  
email: sunhang@mail.kib.ac.cn  
  
name: CHEN Jiahui  
unit:   
email: chenjh@mail.kib.ac.cn  
  
name: YANG Yongping  
unit:   
email: yangyp@mail.kib.ac.cn  
  
name: Richard John Abbott  
unit:   
email: rja@st-andrews.ac.uk