Manuscript Title: Mapping Freezing Tolerance QTL in Alfalfa: Based on Indoor Phenotyping

Data Title: Alfalfa genotyping-by-sequencing (GBS) data

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Description:

This Readme file explains about the dataset.

Data Availability:

The sequence FASTQ files were generated using genotyping-by-sequencing (GBS) of two alfalfa (*Medicag*o *sativa* L.) cultivars [3010 (♀) x CW 1010 (♂)] and their 184 F_1 progenies. The FASTQ files were deposited at the National Center for Biotechnology Information (NCBI) Sequence Read Archive (SRA) under the accession number SRP150116 and with the link https://www.ncbi.nlm.nih.gov/sra/?term=SRP150116. The barcode key file provided here is required to call single nucleotide polymorphisms (SNPs) using TASSEL UNEAK and GBS-SNP-CROP pipelines. We used only R1 reads (Forward reads) and did not use the R2 (Reverse reads) uploaded on NCBI SRA while running UNEAK pipeline. However, we used both R1 and R2 reads with the GBS-SNP-CROP pipeline.

Files:

1. SRA FASTQ files generated for alfalfa population which is available at NCBI SRA under the accession number SRP150116. The FASTQ files can be downloaded and used to identify SNPs.
2. Alfalfa GBS Barcode key file includes sample name, flowcell, barcodes, lane and necessary information required to demultiplex the FASTQ files.