1. What is the method used to collect the data (GBS, array) platform, protocol?

Multiplexed GBS libraries were constructed by Plateforme d’Analyses Génomiques of the Institut de Biologie Intégrativeet des Systèmes (IBIS), Université Laval (Quebec City, Canada), based on the PstI–MspI method described by Huang et al. (2014). Complexity reductions were multiplexed using barcode adapters, with 96 samples per pooled library. Sequencing of each pooled library was performed on a single lane of a HiSeq 2500 platform (Illumina, San Diego, CA, USA) using standard Illumina protocols and kits, producing high-output paired-end 150 bp reads at the Genome Quebec sequencing centre (Montreal, Canada).

1. What software was used to call the genotypes

Raw sequence files in FASTQ format were processed using initial steps of the UNEAK-GBS pipeline within TASSEL 3.0 bioinformatics analysis package (Lu et al. 2013) to trim the reads, de-convolute the barcodes, and produce a single tag count file for each sample. These files were then used by the Haplotag production pipeline (Tinker et al. 2016) to call marker genotypes (including both tag-level haplotypes and GBS SNPs).

1. What reference was used for alignment

It was based on pre-determined genetic loci identified previously in a set of 4,657 A. sativa accessions reported by Bekele et al. (2018).

1. Any filtering of the data

Data matrix was filtered using in-house software, to remove all markers with lower than 80% completeness, less than 5% minor allele frequency, or greater than 10% heterozygosity from the data matrix.

1. Which accession / germplasm was used?

A collection of 709 accessions of white and red Avena sativa L. was assembled, containing a majority of landraces from the Mediterranean area.

1. If the accessions are not already in T3/Oat we need any passport information you can supply to identify the accessions

See information in the excel file attached

References

Huang Y-F, Poland JA, Wight CP, Jackson EW, Tinker NA. 2014. Using Genotyping-By-Sequencing (GBS) for Genomic Discovery in Cultivated Oat. Plos One, 9.

Lu F, Lipka AE, Glaubitz J, Elshire R, Cherney JH, Casler MD, Buckler ES, Costich DE (2013) Switchgrass genomic diversity, ploidy, and evolution: Novel insights from a network-based SNP discovery Protocol. Plos Genetics 9

Tinker NA, Bekele WA, Hattori J (2016) Haplotag: Software for haplotype-based genotyping-by-sequencing analysis. G3-Genes Genomes Genetics 6:857-863

Bekele WA, Wight CP, Chao S, Howarth CJ, Tinker NA (2018) Haplotype-based genotyping-by-sequencing in oat genome research. Plant Biotechnology Journal 16:1452-1463