Our informatics analysis was conducted using a pipeline starting with quality control using fastqc[1] tool and trim-galore[2] tools to remove low quality reads and trim adaptor sequences. The trimmed sequencing reads were then indexed and aligned to the B73 reference genome (AGPv4.38) for B73 samples; and to a FR697 denovo transcriptome assembly for FR697 samples, using HISAT2[3]. Once aligned the expression level for genes were quantified in terms of raw counts using htseq-count[4]. The raw counts served as input for EdgeR[5], in which the counts were normalized for batch effects using the TMM normalization method[6] and expression levels were reported in terms of actual normalized count of reads aligned to gene models and also as counts of per million(CPM) . GLM models[7] were used to calculate differential expression levels between the various conditions and treatments. The thresholds were set to 2-fold change and q-value <= 0.05 before calling genes to be differentially expressed. All results have been deposited in the KBCommons[8] maize specific database.

[1] Simon Andrews, “Babraham Bioinformatics - FastQC A Quality Control tool for High Throughput Sequence Data,” *2010*. [Online]. Available: http://www.bioinformatics.babraham.ac.uk/projects/fastqc/. [Accessed: 10-Feb-2017].

[2] ct Felix Krueger, “Babraham Bioinformatics - Trim Galore!,” 2012. [Online]. Available: http://www.bioinformatics.babraham.ac.uk/projects/trim\_galore/. [Accessed: 10-Feb-2017].

[3] D. Kim, B. Langmead, and S. L. Salzberg, “HISAT: a fast spliced aligner with low memory requirements.,” *Nat. Methods*, vol. 12, no. 4, pp. 357–60, Apr. 2015.

[4] S. Anders, P. T. Pyl, and W. Huber, “HTSeq--a Python framework to work with high-throughput sequencing data,” *Bioinformatics*, vol. 31, no. 2, pp. 166–169, Jan. 2015.

[5] M. D. Robinson, D. J. McCarthy, and G. K. Smyth, “edgeR: a Bioconductor package for differential expression analysis of digital gene expression data,” *Bioinformatics*, vol. 26, no. 1, pp. 139–140, Jan. 2010.

[6] M. D. Robinson and A. Oshlack, “A scaling normalization method for differential expression analysis of RNA-seq data,” *Genome Biol.*, vol. 11, no. 3, pp. 1–9, Mar. 2010.

[7] D. J. McCarthy, Y. Chen, and G. K. Smyth, “Differential expression analysis of multifactor RNA-Seq experiments with respect to biological variation.,” *Nucleic Acids Res.*, vol. 40, no. 10, pp. 4288–97, May 2012.

[8] S. Zeng, Z. Lyu, S. R. K. Narisetti, D. Xu, and T. Joshi, “Knowledge Base Commons (KBCommons) v1.0: A multi OMICS’ web-based data integration framework for biological discoveries,” in *2018 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, 2018, pp. 589–594.