Reads were first trimmed for the and quality using Cutadapt v1.9.dev1 [1] using the following parameters: --quality-base=64 --trim-n --max-n 0.1 -m 30 -q 20,20 -e 0.1 -O 3. An assessment of read quality using FastQC v0.11.4 [2] after trimming revealed an unexpected base-pair composition at the 5’ end indicating the presence of some adaptor or primer sequence contamination remaining. An second round of trimming to remove the first base of each read, trailing Ns, and ensure a minimum length of 30 bps was performed using PRINSEQ v0.20.3 [3] with the following parameters: -trim\_left 1 -trim\_ns\_right 1 -min\_len 30 -out\_format 3. Reads were then mapped to the *B. oleracea* v2 genome using Tophat2 v2.0.14 [4] supplied with v2.1.31 annotations and the following arguments: -F 0.1 --phred64-quals --no-coverage-search --b2-sensitive --no-mixed --read-realign-edit-dist 0 -i 30 -M -I 10000 -p 10 --library-type fr-unstranded .

Uniquely mapped reads mapping to exons were counted using HTSeq-count v0.6.1p1 [5] using the union mode. Differential expression was called using DESeq2 v1.14.1 [6]. Gene count data was first normalized for size factors and then dispersions estimated using fitType = “parametric”. Genes were tested for differential expression using the Wald test. As three different pair-wise comparisons were made between genotypes, all comparisons were combined into a single table and corrected for multiple testing using the Benjamini–Hochberg procedure [7]. Genes with a q-value <= 0.05 and a fold change greater than 2 were considered differentially expressed. All figures were made in R using ggplot2 [8].

*B. oleracea* proteins were BLAST [9] against the Angiosperm sequences in the NCBI Non-Redundant (nr) protein sequence database downloaded on March 24, 2017. BLAST2GO [10] was then used to annotated *B. oleracea* genes with Gene Ontology (GO) terms [11]. Differentially expressed genes were tested for GO term enrichment using topGO [12] using the parentCHILD algorithm [13], a minimum node size of 5, and Fisher’s Exact Test. GO terms were considered enriched after multiple testing correction by the Benjamini–Hochberg procedure if they had a q-value of <= 5.

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