



a) Construct architecture of the *AtCIPK16* transgene; b) the sequence in between the 35S promoter and the *AtCIPK16* exon 1; c) 35S promoter sequence that was used to bait the 5' UTR region of the transgene; d) NOS terminator sequence that was used to bait the 3' UTR region of the transgene; e) wild type *AtCIPK16* 5' UTR region; f) wild type *AtCIPK16* 3' UTR region; g) baiting results from the 3 hour time point; h) baiting results from the 51 hour time point; for g and h the columns from left to right represent the following: column1: name of the fastq file, column2: number of baits for the transgene 3' UTR region, column3: number of baits for the transgene 5' UTR region, column4: number of baits for the transgene 5' UTR region between exon1 and the 35S promoter, column5: number of baits for the wild type 3' UTR region, column6: number of baits for the transgene 5' UTR region, column7-9: experimental conditions of each sample. Rows of g and h are coloured for green shades to represent the shoot samples and brown shades to represent root samples.