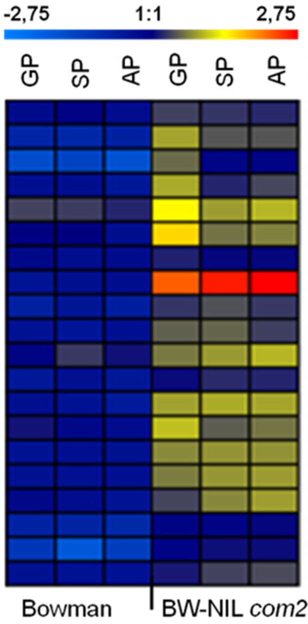
A



HarvEST-ID	**ATH_SEQ_DESC**	**FUNCAT**
35_4012	IAA8 (indoleacetic acid-induced protein 8); transcription factor	hormone metabolism,auxin,induced-regulated-responsive-activated
Contig10299_at	gibberellin 2-oxidase / GA2-oxidase (GA2OX2)	hormone metabolism,gibberelin,synthesis-degradation,GA2 oxidase
Contig602_at	sucrose synthase, putative / sucrose-UDP glucosyltransferase,	major CHO metabolism,degradation,sucrose,Susy
Contig481_at	sucrose synthase / sucrose-UDP glucosyltransferase (SUS1)	major CHO metabolism,degradation,sucrose,Susy
35_14480	sucrose synthase/ transferase, transferring glycosyl groups	major CHO metabolism,degradation,sucrose,Susy
Contig481_s_at	sucrose synthase, putative / sucrose-UDP glucosyltransferase,	major CHO metabolism,degradation,sucrose,Susy
HU05I05u_x_at	sucrose synthase type I	major CHO metabolism,degradation,sucrose,Susy
35_13498	no description	not assigned,unknown
35_49587	AGP9 (ARABINOGALACTAN PROTEIN 9)	not assigned,unknown
35_29657	F-box family protein (FBL10)	not assigned,unknown
35_35664	no description	not assigned,unknown
35_50591	zinc finger (MYND type) family protein / F-box family protein	not assigned,unknown
35_16272	BTB-POZ AND MATH DOMAIN 1; protein binding	protein,degradation,ubiquitin,E3,BTB/POZ Cullin3,BTB/POZ
35_4488	BRASSINOSTEROID-RESPONSIVE RING-H2; protein binding	protein,degradation,ubiquitin,E3,RING
Contig12668_s_at	E2F transcription factor-3 (E2F3)	RNA,regulation of transcription,E2F/DP transcription factor family
Contig12668_at	E2F transcription factor-3 (E2F3)	RNA,regulation of transcription,E2F/DP transcription factor family
35_20248	E2F3 (E2F TRANSCRIPTION FACTOR-3)	RNA,regulation of transcription,E2F/DP transcription factor family
Contig15953_at	F-box family protein / tubby family protein	RNA,regulation of transcription,TUB transcription factor family
35_15379	DNA-directed RNA polymerase II, putative	RNA,transcription
35_16422	DNA-directed RNA polymerase I, II, and III, putative	RNA,transcription

B

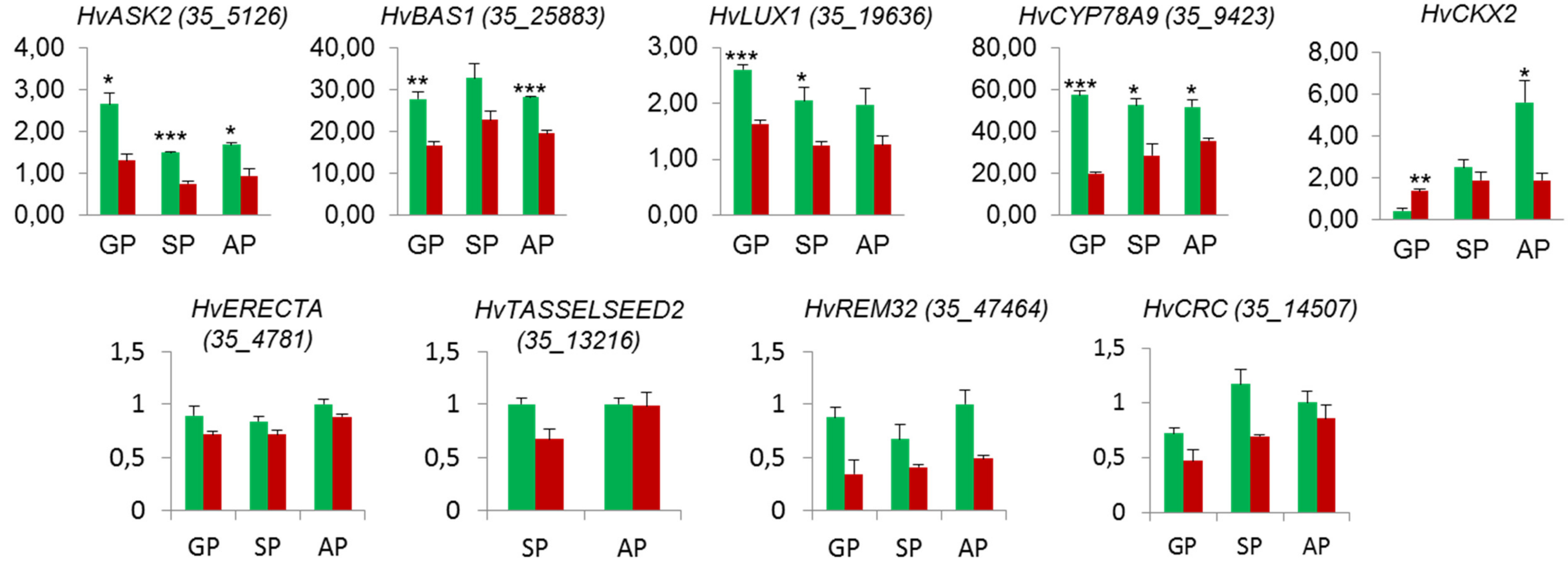


Figure S5 Transcriptome analysis of *com2.g* using microarray experiments and independent qRT PCR validations. (A) Heat map of genes conjointly up-regulated in the BW-NIL(*com2.g*) as compared to the corresponding wild type cv. Bowman. For down-regulated genes in the mutant; see Figure S5A. The scale bar at the top of the heat map indicates the transcript level of differentially regulated genes observed between wild type and mutant (blue color indicates down-regulation while red shows up-regulation). (**B**) qRT-PCR analysis performed for validation of down-regulated genes identified in the BW-NIL*com2.g* (red) as compared to the corresponding wild type cv. Bowman (green). Only highly relevant genes (9 genes) were picked up for qRT-PCR validation. Of these genes, five randomly selected genes were validated using three different biological replicates (B; upper panel) while the remaining four genes were validated using one biological, (with four technical replicates). The mean ± SE of three biological or technical replicates is shown. Expression values were log10 transformed. Asterisks show the significance level calculated by Student's t-test, (no asterisk corresponds to $p > 0.05$. While, single, double and triple asterisks stand for $p \leq 0.05$, $p \leq 0.01$ and $p \leq 0.001$, respectively). The Y-axis value shows the expression relative to *HvActin*. For the description of the genes; see Figure 4A and File S1. Corresponding unigene IDs or barley MLOC IDs are given in parentheses. Mean ± S.E of one biological replicate is shown. Y axis is the relative expression of the corresponding gene to *HvActin*. The developmental stages analyzed during microarray and qRT PCR experiments include TM: triple mound, GP: glume primordium, SP: stamen primordium and AP: awn primordium.