Supplement to

Two auxinic herbicides affect *Brassica napus* hormone levels and molecular changes in transcription

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Supplementary Methods for RNAseq

The following text was directly taken without changes from the methods supplied by Novogene.

RNA quantification and qualification

RNA degradation and contamination was monitored on 1% agarose gels. RNA purity was checked using the NanoPhotometer® spectrophotometer (IMPLEN, CA, USA). RNA integrity and quantitation were assessed using the RNA Nano 6000 Assay Kit of the Bioanalyzer 2100 system (Agilent Technologies, CA, USA).

Library preparation for transcriptome sequencing

A total amount of 1 μg RNA per sample was used as input material for the RNA sample preparations. Sequencing libraries were generated using NEBNext® UltraTM RNA Library Prep Kit for Illumina® (NEB, USA) following manufacturer's recommendations and index codes were added to attribute sequences to each sample. Briefly, mRNA was purified from total RNA using poly-T oligo-attached magnetic beads. Fragmentation was carried out using divalent cations under elevated temperature in NEBNext First Strand Synthesis Reaction Buffer (5X). First strand cDNA was synthesized using random hexamer primer and M-MuLV Reverse Transcriptase (RNase H-). Second strand cDNA synthesis was subsequently performed using DNA Polymerase I and RNase H. Remaining overhangs were converted into blunt ends via exonuclease/polymerase activities. After adenylation of 3' ends of DNA fragments, NEBNext Adaptor with hairpin loop structure were ligated to prepare for hybridization. In order to select cDNA fragments of preferentially 150~200 bp in length, the library fragments were purified with AMPure XP system (Beckman Coulter, Beverly, USA). Then 3 μl USER Enzyme (NEB, USA) was used with size-selected, adaptor ligated cDNA at 37 °C for 15 min followed by 5 min at 95 °C before PCR. Then PCR was performed with Phusion High-Fidelity DNA polymerase, Universal PCR primers and Index (X) Primer. At last, PCR products were purified (AMPure XP system) and library quality was assessed on the Agilent Bioanalyzer 2100 system.

Clustering and sequencing

The clustering of the index-coded samples was performed on a cBot Cluster Generation System using PE Cluster Kit cBot-HS (Illumina) according to the manufacturer's instructions. After cluster generation, the library preparations were sequenced on an Illumina platform and paired-end reads were generated.

Data Analysis

Quality control

Raw data (raw reads) of FASTQ format were firstly processed through fastp. In this step, clean data (clean reads) were obtained by removing reads containing adapter and poly-N sequences and reads with low quality from raw data. At the same time, Q20, Q30 and GC content of the clean data were calculated. All the downstream analyses were based on the clean data with high quality.

Mapping to reference genome

Reference genome and gene model annotation files were downloaded from genome website browser (NCBI/UCSC/Ensembl) directly. Paired-end clean reads were mapped to the reference genome using HISAT2 software. HISAT2 uses a large set of small GFM indexes that collectively cover the whole genome. These small indexes (called local indexes), combined with several alignment strategies, enable rapid and accurate alignment of sequencing reads.

Novel gene prediction

Because transcriptome annotations are still incomplete, most RNA-seq studies will reveal novel genes and transcripts. The Stringtie was used to assemble the set of transcript isoforms of each bam file obtained in the mapping step. gffcompare can compare Stringtie assemblies to reference annotation files and help sort out new genes from known ones.

Quantification

Feature counts was used to count the read numbers mapped of each gene, including known and novel genes. And then RPKM of each gene was calculated based on the length of the gene and reads count mapped to this gene. RPKM, Reads Per Kilobase of exon model per Million mapped reads, considers the effect of sequencing depth and gene length for the reads count at the same time, and is currently the most commonly used method for estimating gene expression levels.

Differential expression analysis

(For DESeq2 with biological replicates) Differential expression analysis between two conditions/groups (three biological replicates per condition) was performed using DESeq2 R package. DESeq2 provides statistical routines for determining differential expression in digital gene expression data using a model based on the negative binomial distribution. The resulting P values were adjusted using the Benjamini and Hochberg's approach for controlling the False Discovery Rate (FDR). Genes with an adjusted P value < 0.05 found by DESeq2 were assigned as differentially expressed. (For edgeR without biological replicates) Prior to differential gene expression analysis, for each sequenced library, the read counts were adjusted by Trimmed Mean of Mvalues (TMM) through one scaling normalized factor. Differential expression analysis of two conditions was performed using the edgeR R package. The P values were adjusted using the Benjamini and Hochberg methods. Corrected pvalue of 0.005 and |log2 (Fold Change)| of 1 were set as the threshold for significantly differential expression.

Enrichment analysis

A common way for searching shared functions among genes is to incorporate the biological knowledge provided by biological ontologies. Gene Ontology (GO) annotates genes to biological processes, molecular functions, and cellular components in a directed acyclic graph structure, and Kyoto Encyclopedia of Genes and Genomes (KEGG) annotates genes to pathway.

GO enrichment analysis: Gene Ontology (GO) enrichment analysis of differentially expressed genes was implemented by the clusterProfiler R package, in which gene length bias was corrected. GO terms with corrected Pvalue less than 0.05 were considered significantly enriched by differential expressed genes.

KEGG Pathway enrichment analysis: KEGG is a database resource for understanding high-level functions and utilities of the biological system, such as the cell, the organism and the ecosystem, from molecular level information, especially large-scale molecular datasets generated by genome sequencing and other high-through put experimental technologies (http://www.genome.jp/kegg/). We used clusterProfiler R package to test the statistical enrichment of differential expression genes in KEGG pathways.

Alternative splicing analysis

Alternative splicing analysis was performed by the software rMATS, a statistical method for robust and flexible detection of differential AS from replicate RNA-Seq data. It identifies

alternative splicing events corresponding to all major types of alternative splicing patterns and calculates the P value and FDR for differential splicing. These types include exon skipping (SE), alternative 5¢ splice sites (A5SS), alternative 3¢ splice sites (A3SS), mutually exclusive exons (MXE), and retained introns (RI).

Mutation analysis

Firstly, Picard tools and Samtools were used to sort, mark duplicated reads and reorder the bam alignment results of each sample. Then the tool HaplotypeCaller in GATK software was used to perform variant discovery. Raw VCF files were filtered with GATK standard filter method and other parameters (cluster: 3; WindowSize: 35; QD < 2.0 or FS > 30.0). Finally, ANNOVAR was used to functionally annotate genetic variants detected from diverse genomes with user-specified versions of genome builds.

Supplementary figures

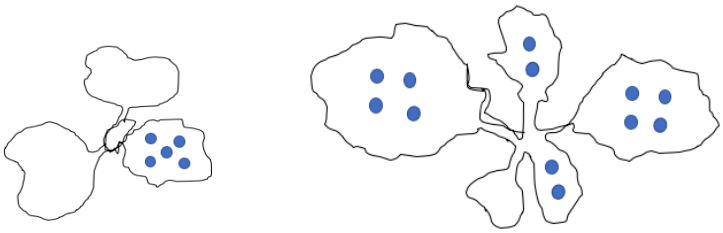


Figure S1. The two different growth stages BBCH11 (left) and BBCH14 (right) and the respective application points for auxinic herbicides (Halauxifen-methyl tech: 0,5 µg ai/plant; Picloram tech: 2,4 µg ai/plant; Controls were treated with the solvent only).

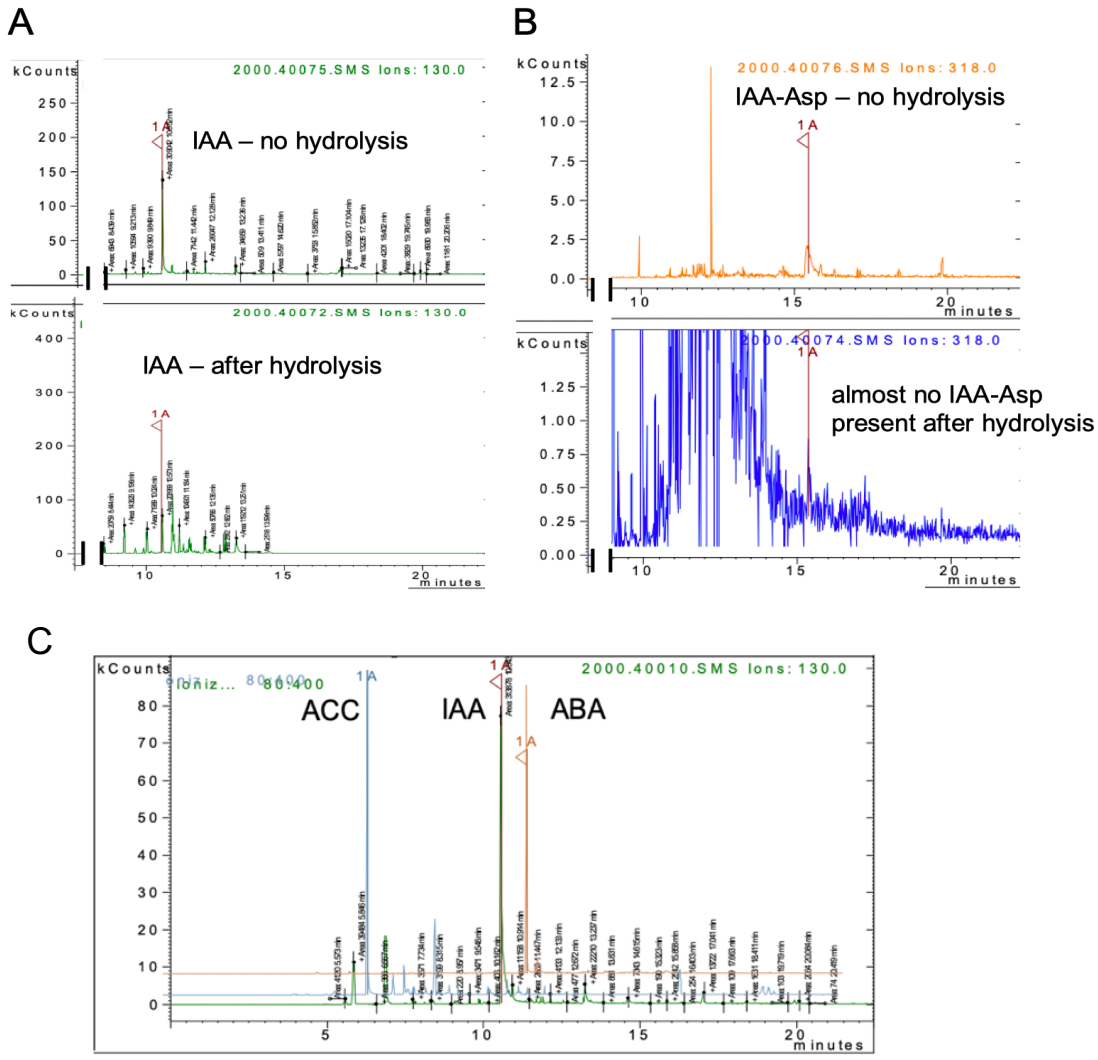
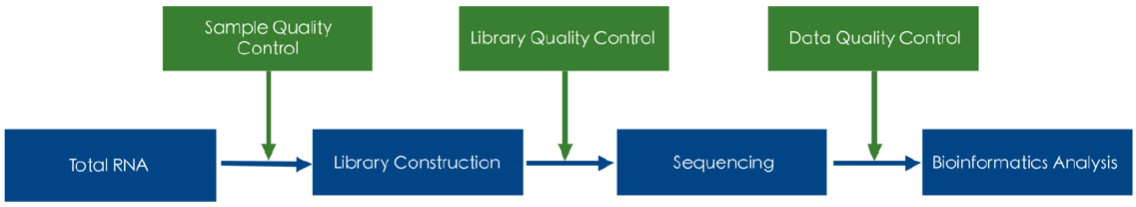
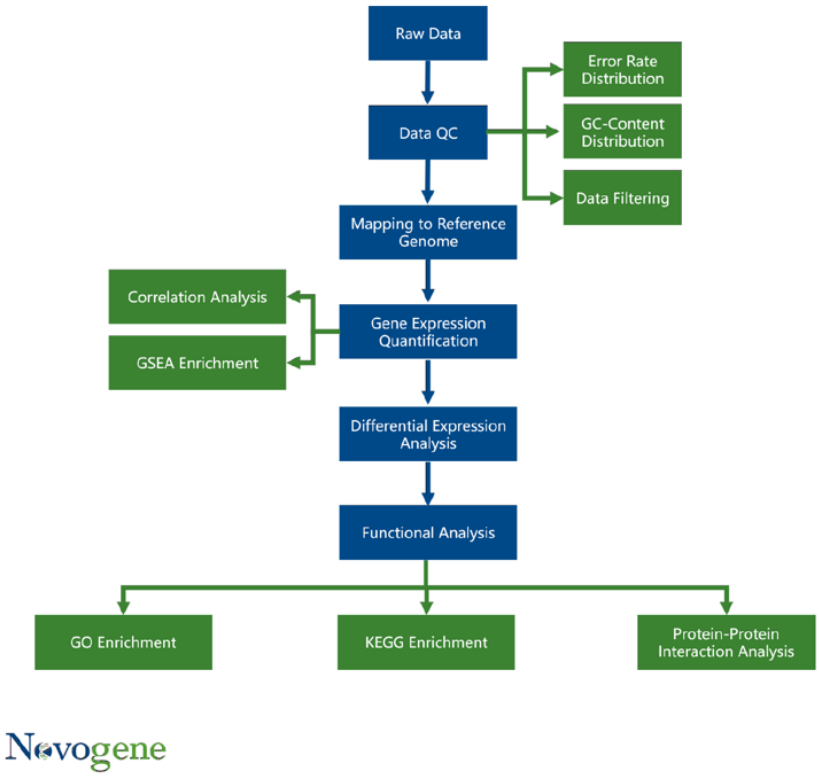


Figure S2. Method for auxin hydrolysis (A, B) after the hormone extraction based on [25,26] and confirmation of standard chromatograms (C). The alkaline hydrolysis (7N NaOH, 3 h at 90°C under N_2) of samples with IAA (A) and IAA-Asp (B) added.

A



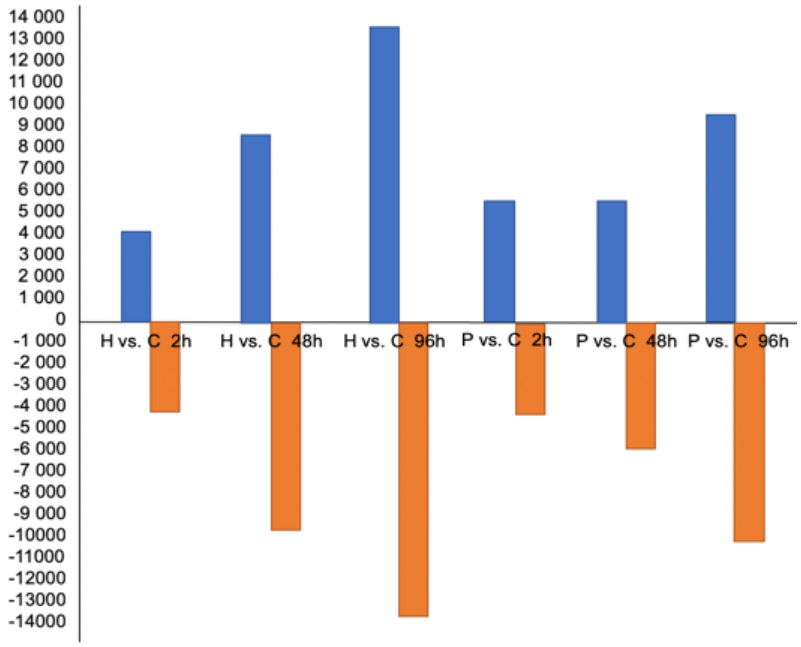
B



Novogene

Figure S3 Workflow for gene expression analysis done by Novogene on the dataset. (A) protocol for sequencing. (B) Bioinformatics analysis.

A



B

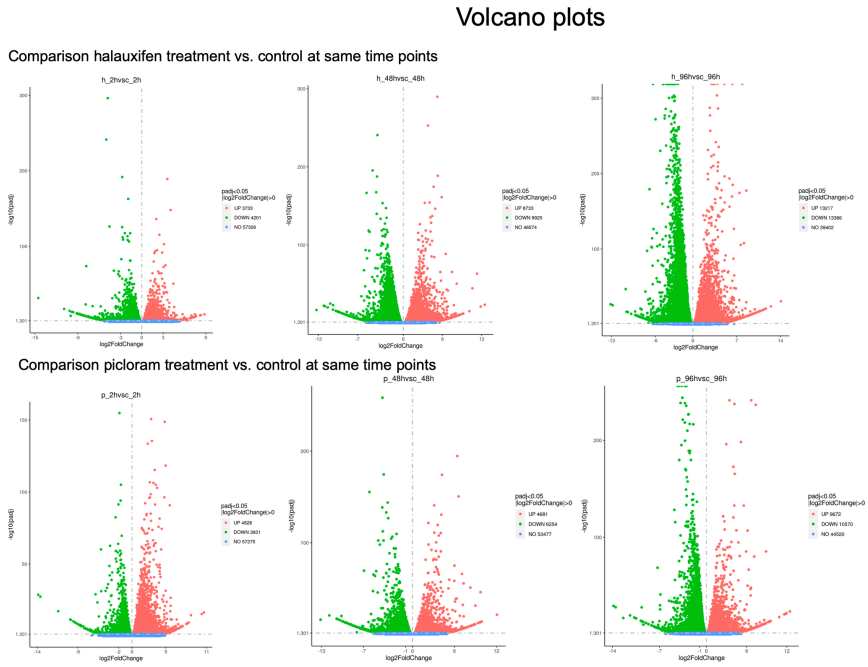


Figure S4. (A) The number of differentially regulated genes after treatment with halauxifen (h/H) and picloram (p/P) over time (2h, 48h, 96h). Both, up- and down-regulated genes increase over time. (B) Volcano plots where the x-axis shows how strong the genes are differentially regulated and the y-axis shows the significance of their regulation, the higher up a dot, the higher is the statistical significance.

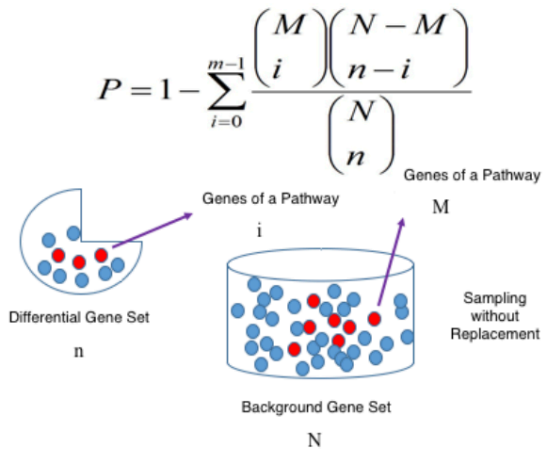
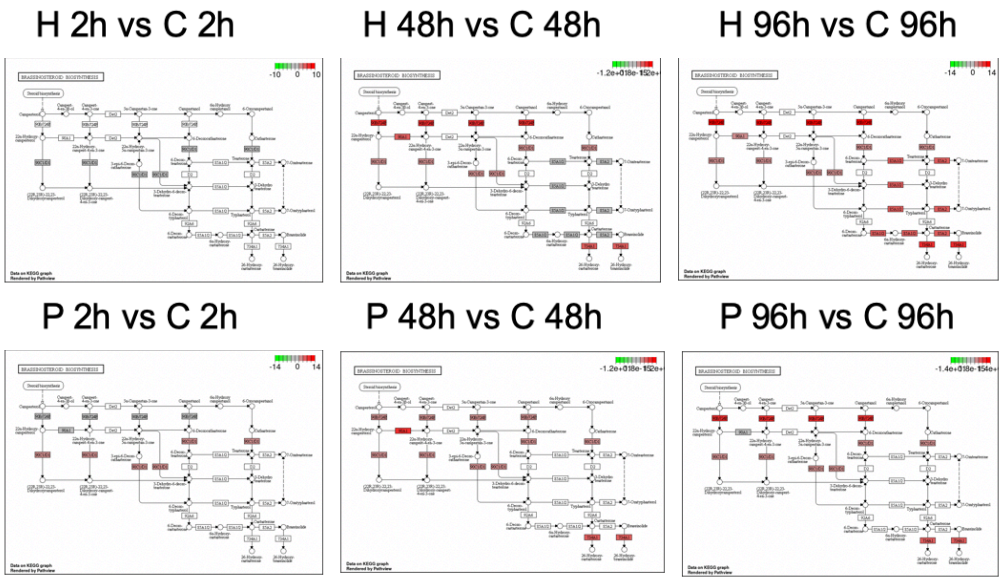
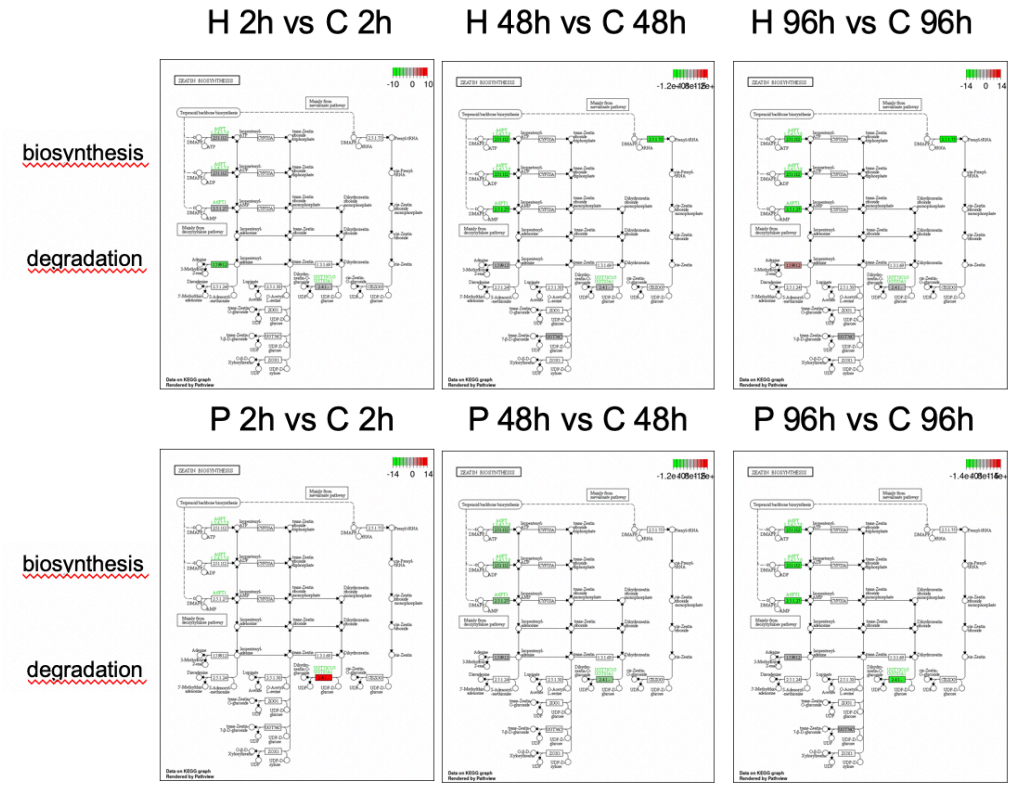


Figure S5. The interactions of multiple genes may be involved in certain biological functions. KEGG (Kyoto Encyclopedia of Genes and Genomes, http://www.kegg.jp/) is a collection of manually curated databases containing resources on genomic, biological-pathway and disease information. Here, N is the number of all genes with a KEGG annotation, n is the number of DEGs (Differentially Expressed Genes) in N, M is the number of all genes annotated to specific pathways, and m is number of DEGs in M. Pathway enrichment analysis identifies significantly enriched metabolic pathways or signal transduction pathways associated with differentially expressed genes, comparing the whole genome background. KEGG terms with padj < 0.05 are significant enrichment.

A. Brassinosteroid

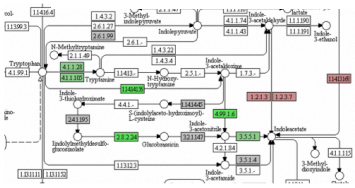


B. Zeatin

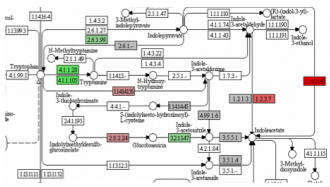


C. IAA

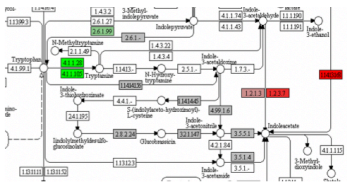
H 2h vs C 2h



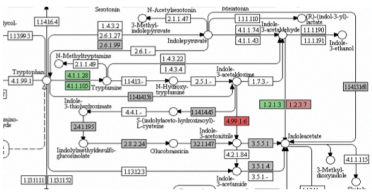
H 48h vs C 48h



H 96h vs C 96h



P 2h vs C 2h



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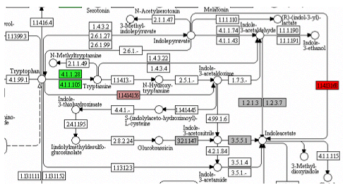
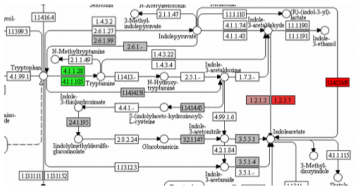
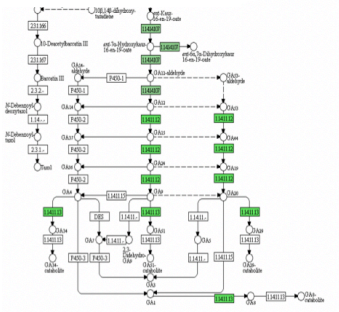


P 96h vs C 96h

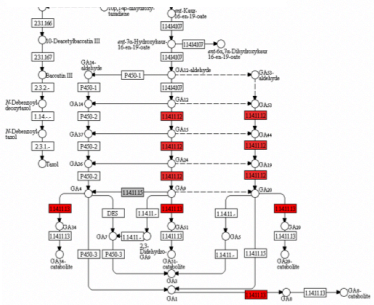


D. Gibberellin

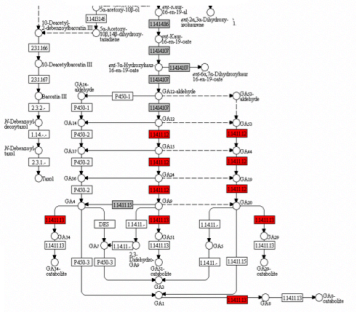
H 2h vs C 2h



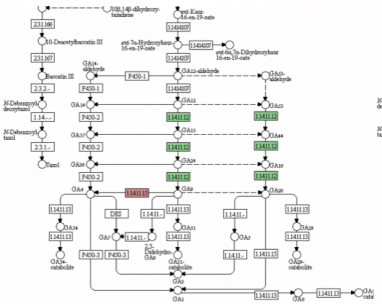
H 48h vs C 48h



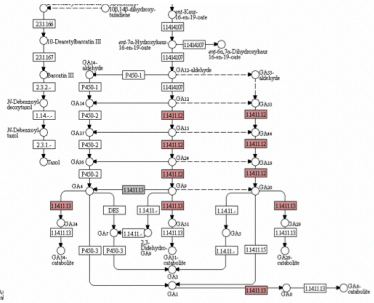
H 96h vs C 96h



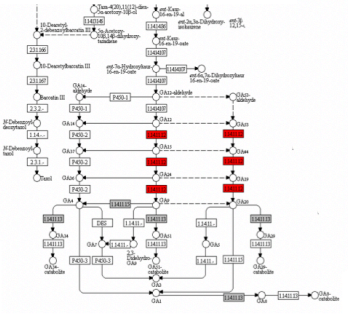
P 2h vs C 2h



P 48h vs C 48h

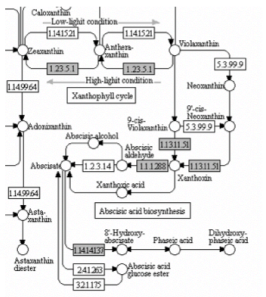


P 96h vs C 96h

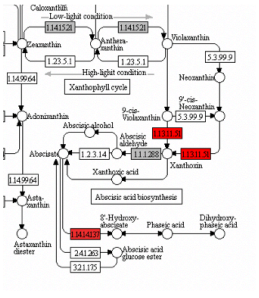


E. ABA

H 2h vs C 2h



H 48h vs C 48h



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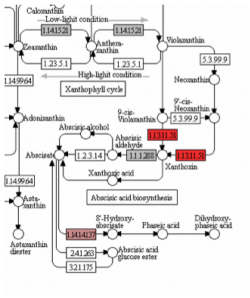

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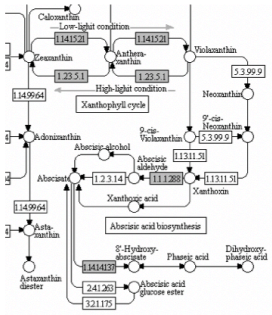

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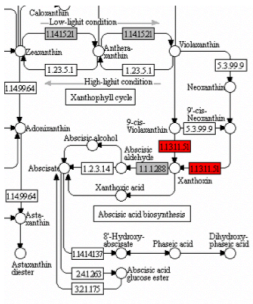

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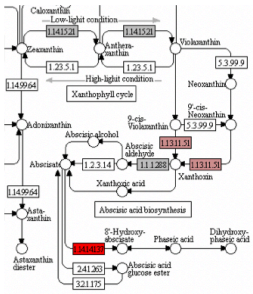
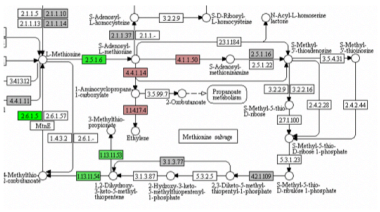


F. Ethylene

H 2h vs C 2h



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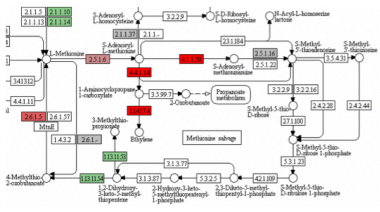

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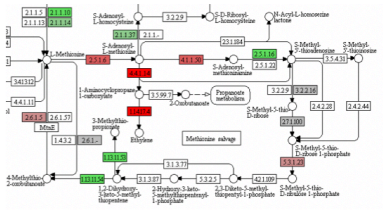
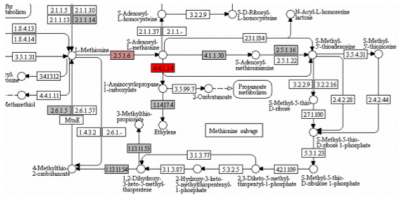


P 2h vs C 2h



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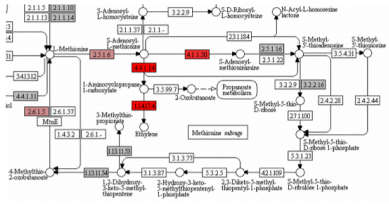

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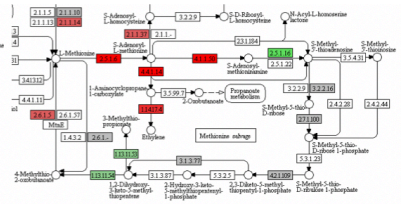

G. Jasmonate

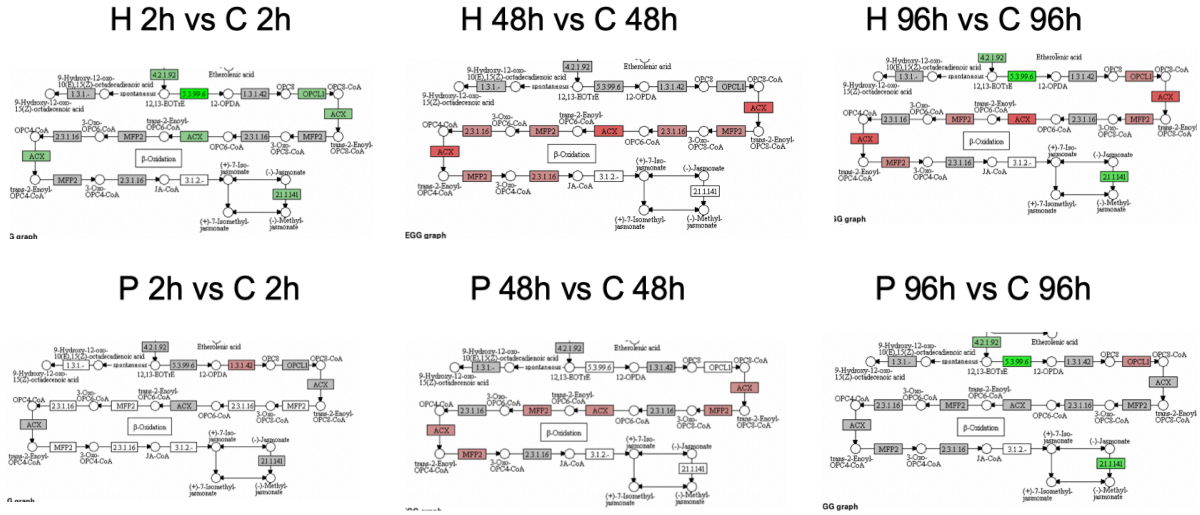

Figure S6 Differentially regulated KEGG pathways for halauxifen (H) and picloram (P) treatments after 2, 48 and 96 hours compared to controls with respect to hormonal pathways. Green=downregulated; red=upregulated genes. (A) Brassinosteroid, (B) Zeatin (biosynthesis and degradation), (C) IAA, (D) Gibberellin, (E) ABA, (F) Ethylene, (G) Jasmonate.

Supplementary tables

Table S1. Data quality summary as provided by Novogene. *

Sample name	Raw reads	Clean reads	Raw bases	Clean bases	Error rate(%)	Q20(%)	Q30(%)	GC content(%)
c_2h_1	21770371	21158844	6.5G	6.3G	0.03	96.57	91.09	48.41
c_2h_2	22438338	21776995	6.7G	6.5G	0.03	96.86	91.70	48.48
c_2h_3	21495992	20838347	6.4G	6.3G	0.03	97.03	92.08	48.51
p_2h_1	20630371	20065996	6.2G	6.0G	0.03	96.67	91.29	48.36
p_2h_2	22492311	21982411	6.7G	6.6G	0.03	96.79	91.59	48.47
p_2h_3	23296327	22667399	7.0G	6.8G	0.03	96.70	91.40	48.51
h_2h_1	20485897	19890296	6.1G	6.0G	0.03	96.71	91.39	48.46
h_2h_2	25411957	24585772	7.6G	7.4G	0.03	96.70	91.39	48.55
h_2h_3	22416492	21059179	6.7G	6.3G	0.03	96.61	91.30	47.77
c_48h_1	21546834	20987675	6.5G	6.3G	0.03	96.76	91.45	48.43
c_48h_2	21783855	21191730	6.5G	6.4G	0.03	96.74	91.42	49.25
c_48h_3	22843717	22184089	6.9G	6.7G	0.03	96.88	91.71	48.86
p_48h_1	22336908	21707238	6.7G	6.5G	0.03	96.94	91.92	48.97
p_48h_2	21165544	20505125	6.3G	6.2G	0.03	96.84	91.62	48.88
p_48h_3	22792731	22090439	6.8G	6.6G	0.03	96.60	91.14	49.01
h_48h_1	23102112	22498431	6.9G	6.7G	0.03	96.73	91.43	48.74
h_48h_2	21093614	20589249	6.3G	6.2G	0.03	96.86	91.67	48.90
h_48h_3	20486399	19916730	6.1G	6.0G	0.03	96.80	91.59	48.78
c_96h_1	21493128	20800672	6.4G	6.2G	0.03	96.87	91.72	48.84
c_96h_2	23955049	23158036	7.2G	6.9G	0.03	96.68	91.31	49.03
c_96h_3	22924070	22073579	6.9G	6.6G	0.03	96.78	91.55	49.03
p_96h_1	22235770	21521136	6.7G	6.5G	0.03	97.06	92.13	48.77
p_96h_2	21228373	20627934	6.4G	6.2G	0.03	96.77	91.47	48.62
p_96h_3	20086238	19465401	6.0G	5.8G	0.03	96.68	91.32	48.86
h_96h_1	22982783	22298469	6.9G	6.7G	0.03	96.88	91.72	48.34
h_96h_2	22882634	22225610	6.9G	6.7G	0.03	96.76	91.50	48.59
h_96h_3	21079449	20466724	6.3G	6.1G	0.03	96.73	91.44	48.31

*Sample name: c= control, hal=halauxifen-methyl, pic=picloram 2,48,96 hrs after treatment, 1-3 replicates. Raw reads: reads count from the raw data, four rows as a unit, with statistics of reads count for every sequencing. Clean reads: Clean data are reads count filtered from raw data. Statistics method is similar with raw reads. All the following analysis is based on clean data. Raw bases: Base number of raw data. (number of raw reads) * (sequence length), converting unit to G. Clean bases: Base number of raw data after filtering. (number of clean reads) * (sequence length), converting unit to G. Error rate(%): base error rate of whole

sequencing. Q20(%): The percentage of the bases whose Q Phred values is greater than 20. (Number of bases with Q Phred value > 20) / (Number of total bases) *100. Q30(%): The percentage of the bases whose Q Phred values is greater than 30. (Number of bases with Q Phred value > 30) / (Number of total bases) *100. GC content(%): The percentage of G&C base numbers of total bases.(G&C base number) / (Total base number)*100.

Table S2. Mapping of reads. *

Sample name	c_2h_1	c_2h_2	c_2h_3	c_48h_1	c_48h_2	c_48h_3	c_96h_1	c_96h_2	c_96h_3	h_2h_1	h_2h_2	h_2h_3	h_48h_1	h_48h_2	h_48h_3	h_96h_1	h_96h_2	h_96h_3	p_2h_1	p_2h_2	p_2h_3	p_48h_1	p_48h_2	p_48h_3	p_96h_1	p_96h_2	p_96h_3
Total reads	42317688	43553990	41676694	41975350	42383460	44368178	41601344	46316072	44147158	39780592	49171544	42118358	44996862	41178498	39833460	44596938	44451220	40933448	40131992	43964822	45334798	43414476	41010250	44180878	43042272	41255868	38930802
Total mapped reads	39005049	40264669	38611528	38699314	39322224	41146621	38518226	42733734	40801699	36822496	45519785	38790722	41347999	37987491	36640287	40932487	40726179	37494873	37095087	40659695	41909824	40179034	37954033	40757313	39934645	38234301	36005529
Uniquely mapped reads	36960217	38116634	36599766	36525326	37172940	38932536	36360260	40317626	38485990	34989046	43191291	36711620	39094325	35978179	34665143	38833733	38628893	35670925	35124072	38527852	39766529	38085572	35903375	38567866	37879953	36345181	34216685
Multiple mapped reads	2044832	2148035	2011762	2173988	2149284	2214085	2157966	2416108	2315709	1833450	2328494	2079102	2253674	2009312	1975144	2098754	2097286	1823948	1971015	2131843	2143295	2093462	2050658	2189447	2054692	1889120	1788844
Total mapping rate	92.17%	92.45%	92.65%	92.20%	92.78%	92.74%	92.59%	92.27%	92.42%	92.56%	92.57%	92.10%	91.89%	92.25%	91.98%	91.78%	91.62%	91.60%	92.43%	92.48%	92.45%	92.55%	92.55%	92.25%	92.78%	92.68%	92.49%
Uniquely mapping rate	87.34%	87.52%	87.82%	87.02%	87.71%	87.75%	87.40%	87.05%	87.18%	87.96%	87.84%	87.16%	86.88%	87.37%	87.03%	87.08%	86.90%	87.14%	87.52%	87.63%	87.72%	87.73%	87.55%	87.30%	88.01%	88.10%	87.89%
Multiple mapping rate	4.83%	4.93%	4.83%	5.18%	5.07%	4.99%	5.19%	5.22%	5.25%	4.61%	4.74%	4.94%	5.01%	4.88%	4.96%	4.71%	4.72%	4.46%	4.91%	4.85%	4.73%	4.82%	5.00%	4.96%	4.77%	4.58%	4.59%

* Total reads: total clean reads used for analysis. Total mapped reads: numbers of reads being mapped on the genome, the ratio should higher than 70%. Uniquely mapped reads: numbers of reads being mapped on single position of the genome. Multiple mapped reads: numbers of reads being mapped on more than one position of the genome. Total mapping rate: (mapped reads)/(total reads)*100. Uniquely mapping rate: (uniquely mapped reads)/(total reads)*100. Multiple mapping rate: (multiple mapped reads)/(total reads)*100.

Table S3. GO is the abbreviation of Gene Ontology (http://www.geneontology.org/), which is a major bioinformatics classification system to unify the presentation of gene properties across all species. It includes three main branches: cellular component, molecular function and biological process. GO terms with padj < 0.05 are significant enrichment. The table shows a part of the complete analysis. *

Category	GOID	Description	GeneRatio	BgRatio	pvalue	padj
BP	GO:0009733	response to auxin	123|4509	398|28297	5.01184403174344e-14	6.91634476380595e-11
BP	GO:0015979	photosynthesis	92|4509	323|28297	7.56949568112022e-09	5.22295201997295e-06
BP	GO:0042737	drug catabolic process	101|4509	370|28297	1.63418769451362e-08	7.11849342371176e-06
BP	GO:0071555	cell wall organization	122|4509	474|28297	2.39561434158461e-08	7.11849342371176e-06

*Category: different class of GO id. CC, BP and MF are the abbreviation for Cellular_Component, Biological_Process and Molecular_Function respectively. GOID: unique identification id of Gene Ontology database. Description: function description of Gene Ontology. GeneRatio: ratio between the number of differentially expressed genes in each GO term and all differentially expressed genes that can be found in GO database. BgRatio: in background GO database, the ratio of all genes concerning this GO term to all genes. pvalue: statistics category term; abbreviation for probability value. padj: adjusted p-value. Generally, GO terms with Corrected_pValue < 0.05 are significant enrichment.

Table S4. Auxin-related GH3 genes and their expression as (A) ratio for the mean of three replicates. (B) For all genes the mean expression levels ± SD are shown for controls and treatments in all upregulated combinations. No GH3.4 annotation since it is similar to GH3.2 (in *Arabidopsis thaliana* presumably a gene duplication). BrnaA: A genome; BrnaC: C genome. The small letters denote duplications of the respective genes as found in the annotation by Wang et al. (2019). GH3.5 of *A. thaliana* also catalyzes the conjugation of salicylic acid (SA) to amino acids. In yellow the only gene that was slightly downregulated is marked.

A.

Gene ID	**Differential regulation**						**Description (uniport)**
	Halauxifen			**Picloram**			
	2	**48**	**96**	**2**	**48**	**96 hrs**	
BnaA09R.GH3-1.a	0	0	0	0	0	19	Catalyzes the synthesis of indole-3-acetic acid (IAA)-amino acid conjugates.
BnaCX.GH3-1.a	0	0	0	0	0	0	
BnaA01.GH3-2.a	12	3976	1457	27	421	226	Catalyzes the synthesis of indole-3-acetic acid (IAA)-amino acid conjugates. Strongly reactive with Glu, Gln, Trp, Asp, Ala, Leu, Phe, Gly, Tyr, Met, Ile and Val.
BnaC01.GH3-2.a	19	2565	2231	55	266	318	
BnaA09.GH3-3.a	11	3144	14574	28	974	3937	Catalyzes the synthesis of indole-3-acetic acid (IAA)-amino acid conjugates. Strongly reactive with Glu, Gln, Trp, Asp, Ala, Leu, Phe, Gly, Tyr, Met, Ile and Val.
BnaC08.GH3-3.a	31	1934	4783	119	590	2596	
BnaA01.GH3-5.a	0	19	65	0	0	14	Catalyzes the synthesis of indole-3-acetic acid (IAA)-amino acid conjugates. Strongly reactive with Glu, Gln, Trp, Asp, Ala, Leu, Phe, Gly, Tyr, Met, Ile and Val.
BnaA03.GH3-5.b	0	141	146	0	0	30	
BnaC01.GH3-5.a	0	17	22	0	0	0	
BnaC07.GH3-5.b	0	40	88	0	0	21	
BnaA03.GH3-6.a	3	7	11	0	4	8	Catalyzes the synthesis of indole-3-acetic acid (IAA)-amino acid conjugates. Strongly reactive with Glu, Gln, Trp, Asp,
BnaAX.GH3-6.b							

	0	8	9	4	0	0	Ala, Leu, Phe, Gly, Tyr, Met, Ile and Val. Involved in auxin signal transduction. Inhibits shoot and hypocotyl cell elongation, and lateral root cell differentiation in light.
BnaC03.GH3-6.a	0	11	125	0	5	89	
BnaCX.GH3-6.b	0	15	107	0	0	8	
BnaA03.GH3-15.a	0	2	0	0.78	2	3	Indole-3-acetic acid-amido (IAA) synthetase that catalyzes the conjugation of amino acids to auxin specifically using the auxin precursor indole-3-butyric acid (IBA) and glutamine and, possibly, cysteine as substrates. Displays high catalytic activity with the auxinic phenoxyalkanoic acid herbicides 4-(2,4-dichlorophenoxy)butyric acid (2,4-DB) and to some extent 2,4-dichlorophenoxylacetic acid (2,4-D) as substrates, thus conferring resistance to herbicides.
BnaC03.GH3-15.a	0	2	0	0	0	0	
BnaA07.GH3-17.a	0	31	21	0	0	0	Catalyzes the synthesis of indole-3-acetic acid (IAA)-amino acid conjugates. Strongly reactive with Glu, Gln, Trp, Asp, Ala, Leu, Phe, Gly, Tyr, Met, Ile and Val.
BnaA08.GH3-17.b	0	0	0	0	0	0	
BnaA09.GH3-17.c	0	33	40	0	0	0	
BnaC08.GH3-17.a	0	0	0	0	0	0	
BnaCX.GH3-17.b	0	24	48	0	0	0	
BnaCX.GH3-17.c	0	0	0	0	0	0	

B.

Gene ID	**Halauxifen 2**		**Control 2**	
	mean	SD	mean	SD
BnaA01.GH3-2.a	73	10.5356538	6.33333333	3.05505046
BnaC01.GH3-2.a	64	29.0516781	3.33333333	3.21455025
BnaA09.GH3-3.a	41.3333333	19.5533458	3.66666667	0.57735027
BnaC08.GH3-3.a	41.6666667	13.5030861	1.33333333	0.57735027
BnaA03.GH3-6.a	49.3333333	14.571662	16	7
	Halauxifen 48		**Control 48**	
	mean	SD	mean	SD
BnaA01.GH3-2.a	1325.333333	118.0056496	0.333333333	0.577350269
BnaC01.GH3-2.a	855	54.61684722	0.333333333	0.577350269
BnaA09.GH3-3.a	5239.333333	224.1346322	1.666666667	2.886751346
BnaC08.GH3-3.a	2578.666667	29.68725877	1.333333333	1.527525232
BnaA01.GH3-5.a	50	6	2.666666667	1.154700538
BnaA03.GH3-5.b	47	8.717797887	0.333333333	0.577350269
BnaC01.GH3-5.a	5.666666667	3.214550254	0.333333333	0.577350269
BnaC07.GH3-5.b	26.66666667	3.511884584	0.666666667	0.577350269
BnaA03.GH3-6.a	35.33333333	4.932882862	5.333333333	1.527525232
BnaAX.GH3-6.b	96.33333333	18.50225212	12.66666667	3.214550254
BnaC03.GH3-6.a	35	3	3.333333333	2.309401077
BnaCX.GH3-6.b	133.3333333	19.60442127	9	1
BnaA03.GH3-15.a	185	29.54657341	96	21
BnaC03.GH3-15.a	295.6666667	53.14445722	165	19.31320792
BnaA07.GH3-17.a	10.33333333	5.033222957	0.333333333	0.577350269
BnaA09.GH3-17.c	11	4.358898944	0.333333333	0.577350269
BnaCX.GH3-17.b	8	2.645751311	0.333333333	0.577350269
	Halauxifen 96		**Control 96**	
	mean	SD	mean	SD
BnaA01.GH3-2.a	971	117.145209	0.666666667	1.154700538
BnaC01.GH3-2.a	743.6666667	98.39884823	0.333333333	0.577350269
BnaA09.GH3-3.a	4858	485.0268034	0.333333333	0.577350269
BnaC08.GH3-3.a	1594.333333	284.3876462	0.333333333	0.577350269
BnaA01.GH3-5.a	43	13.52774926	0.666666667	1.154700538
BnaA03.GH3-5.b	48.66666667	4.041451884	0.333333333	0.577350269
BnaC01.GH3-5.a	7.333333333	2.516611478	0.333333333	0.577350269

BnaC07.GH3-5.b	29.33333333	14.571662	0.333333333	0.577350269
BnaA03.GH3-6.a	40.66666667	3.055050463	3.666666667	1.154700538
BnaAX.GH3-6.b	71.66666667	12.85820101	8	2.645751311
BnaC03.GH3-6.a	41.66666667	10.0166528	0.333333333	0.577350269
BnaCX.GH3-6.b	178.3333333	20.10804151	1.666666667	2.081665999
BnaA07.GH3-17.a	7	4	0.333333333	0.577350269
BnaA09.GH3-17.c	13.33333333	6.658328118	0.333333333	0.577350269
BnaCX.GH3-17.b	16	5	0.333333333	0.577350269
	Picloram 2		**Control 2**	
	mean	SD	mean	SD
BnaA01.GH3-2.a	168.666667	39.1450295	6.33333333	3.05505046
BnaC01.GH3-2.a	182	19.5192213	3.33333333	3.21455025
BnaA09.GH3-3.a	103.666667	19.0087699	3.66666667	0.57735027
BnaC08.GH3-3.a	79.3333333	7.3711148	0.66666667	1.15470054
BnaAX.GH3-6.b	24.6666667	19.7568554	6.33333333	1.52752523
	Picloram 48		**Control 48**	
	mean	SD	mean	SD
BnaA01.GH3-2.a	140.333333	11.2398102	0.33333333	0.57735027
BnaC01.GH3-2.a	88.6666667	14.4683563	0.33333333	0.57735027
BnaA09.GH3-3.a	1623.33333	134.183953	1.66666667	2.88675135
BnaC08.GH3-3.a	786.666667	77.3907833	1.33333333	1.52752523
BnaA03.GH3-6.a	20.6666667	7.63762616	5.33333333	1.52752523
BnaC03.GH3-6.a	16	3	3.33333333	2.30940108
BnaA03.GH3-15.a	215	47.0319041	96	21
	Picloram 96		**Control 96**	
	mean	SD	mean	SD
BnaA09R.GH3-1.a	6.33333333	3.51188458	0.33333333	0.57735027
BnaA01.GH3-2.a	150.333333	16.2583312	0.66666667	1.15470054
BnaC01.GH3-2.a	106	13.114877	0.33333333	0.57735027
BnaA09.GH3-3.a	1312.33333	96.6247035	0.33333333	0.57735027
BnaC08.GH3-3.a	865.333333	96.9346859	0.33333333	0.57735027
BnaA01.GH3-5.a	9.33333333	2.081666	0.66666667	1.15470054
BnaA03.GH3-5.b	10	2.64575131	0.33333333	0.57735027
BnaC07.GH3-5.b	7	2.64575131	0.33333333	0.57735027
BnaA03.GH3-6.a	29	7	3.66666667	1.15470054
BnaC03.GH3-6.a	29.6666667	3.21455025	0.33333333	0.57735027

BnaCX.GH3-6.b	14	5.56776436	1.66666667	2.081666
BnaA03.GH3-15.a	285.666667	32.3161466	108.666667	8.08290377