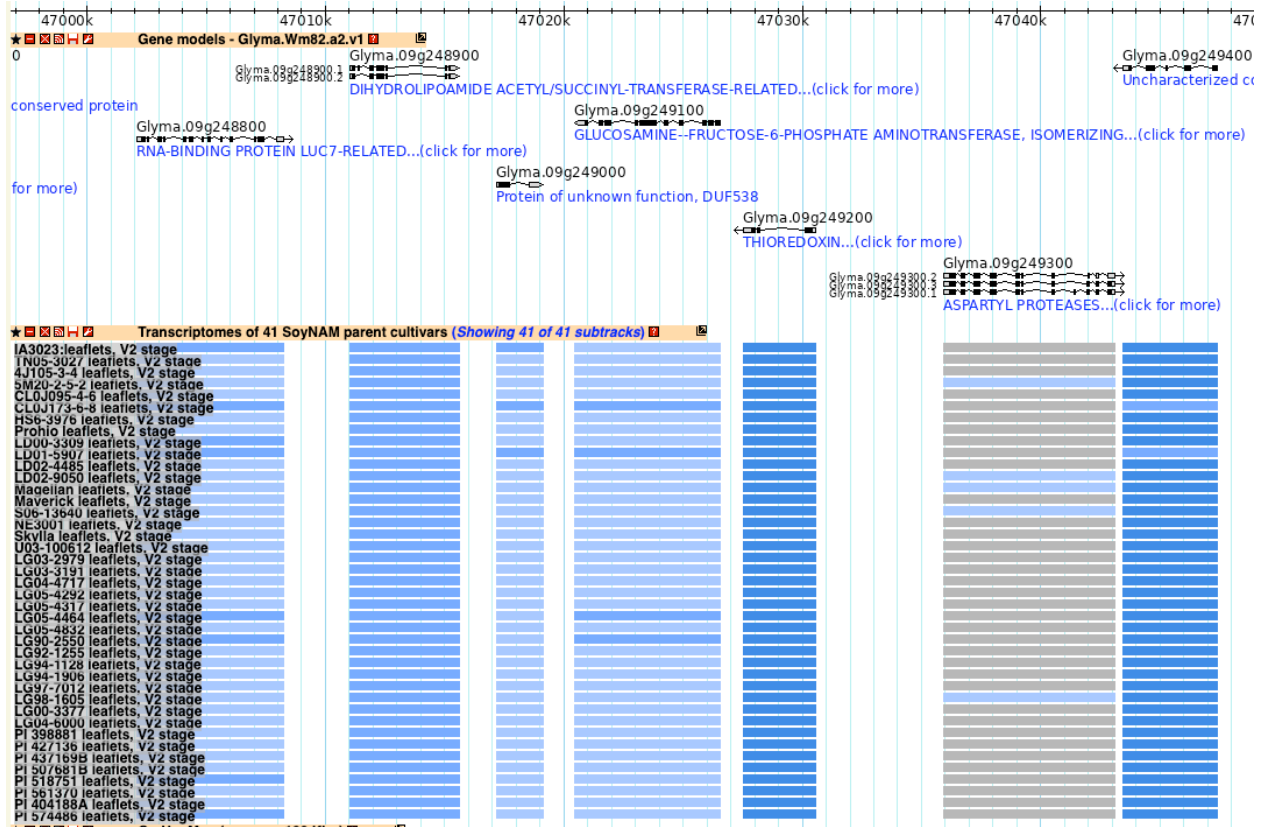


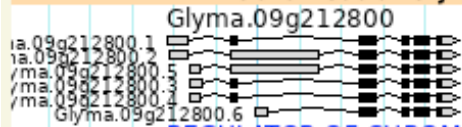
SUPPLEMENTAL FIGURES



Supplemental Figure 1. Gene Expression Display

Gene expression is displayed graphically as blocks of varying shades of blue. Expression values for each sample is processed by determining the range of values for each gene and dividing the range into 5 ranges. Each range is color coded from gray to dark blue. The darker blue the higher the expression. Gray indicates an expression value of zero.

★ Gene models - Glyma.Wm82.a2.v1



Glyma.09g212800

Glyma.09g2:
Glyma.09g2:

[REGULATOR OF CHROMOSOME CONDENSATION...\(click for more\)](#)

Glyma.09g212900

[MITOGEN-ACTIVATED PROTEIN KINASE...\(click for more\)](#)

Glyma.09g213000



★ Genome Wide Association QTL (Showing 4 of 4 subtracks)

seed_composition_and_yield

disease_and_stress

plant_architecture

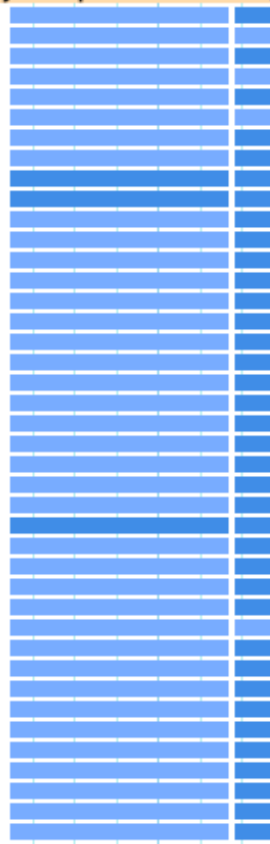
other

Plant height 6-g5

Plant height 1-g5

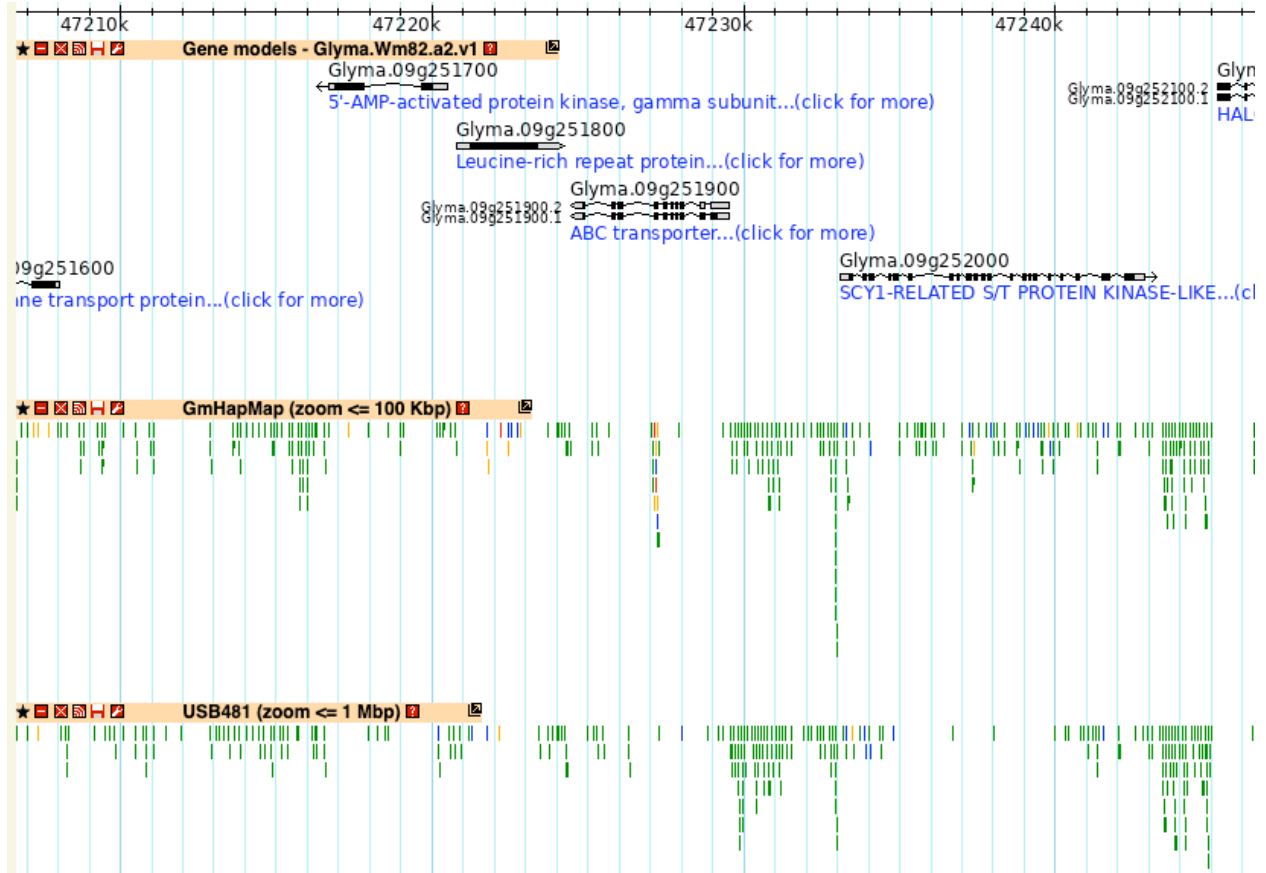
★ Transcriptomes of 41 SoyNAM parent cultivars (Showing 41 of 41 subtracks)

- IA3023:leaflets, V2 stage
- IN05-3027 leaflets, V2 stage
- 4J105-3-4 leaflets, V2 stage
- 5M20-2-5-2 leaflets, V2 stage
- CL0J095-4-6 leaflets, V2 stage
- CL0J173-6-8 leaflets, V2 stage
- HS6-3976 leaflets, V2 stage
- Pronio leaflets, V2 stage
- LD00-3309 leaflets, V2 stage
- LD01-5907 leaflets, V2 stage
- LD02-4485 leaflets, V2 stage
- LD02-9050 leaflets, V2 stage
- Magellan leaflets, V2 stage
- Maverick leaflets, V2 stage
- S06-13640 leaflets, V2 stage
- NE3001 leaflets, V2 stage
- Skylla leaflets, V2 stage
- U03-100612 leaflets, V2 stage
- LG03-2979 leaflets, V2 stage
- LG03-3191 leaflets, V2 stage
- LG04-4717 leaflets, V2 stage
- LG05-4292 leaflets, V2 stage
- LG05-4317 leaflets, V2 stage
- LG05-4464 leaflets, V2 stage
- LG05-4832 leaflets, V2 stage
- LG90-2550 leaflets, V2 stage
- LG92-1255 leaflets, V2 stage
- LG94-1128 leaflets, V2 stage
- LG94-1906 leaflets, V2 stage
- LG97-7012 leaflets, V2 stage
- LG98-1605 leaflets, V2 stage
- LG00-3377 leaflets, V2 stage
- LG04-6000 leaflets, V2 stage
- PI 398881 leaflets, V2 stage
- PI 427136 leaflets, V2 stage
- PI 437169B leaflets, V2 stage
- PI 507681B leaflets, V2 stage
- PI 518751 leaflets, V2 stage
- PI 561370 leaflets, V2 stage
- PI 404188A leaflets, V2 stage
- PI 574486 leaflets, V2 stage



Supplemental Figure 2. Utilization of the Genome Browser to Identify Candidate Genes

Using the Genome Wide Association QTL track, the user is able to display the QTL in the context of gene models and expression values. In this display the Plant height 6-g5 and 1-g5 SNP appear to be associated either Glyma.09g212900 or Glyma.09g213000. The 41 SoyNAM parental cultivars are displayed. It may be possible to correlate strains with tall or short stature to the expression of these two gene models



Supplemental Figure 3. Sequence Diversity in Soybean

SoyBase Genome Browser with GmHapMap and USB481 diversity tracks. Soybean gene models (Glyma.Wm82.a2.v1) in relation to SNPs identified in the two diversity experiments. The effect of each SNP is color coded to identify SNPs that might impact gene function. Modifier SNPs are green, low effect in blue, moderate effect in orange and high effect in red.

A

Descriptive

Development

Early maturation-stage seed

- Gene expression profiles of tissues in soybean **seeds** at the early-maturation stage [NGS]
- Early maturation-stage **seed** compartments [GeneChip]

Globular-stage seed

- Gene expression profiles of tissues in soybean **seeds** at the globular stage [NGS]
- Globular-stage **seed** compartments [GeneChip]

Heart-stage seed

- Gene expression profiles of tissues in soybean **seeds** at the heart stage [NGS]
- Heart-stage **seed** compartments [GeneChip]

Cotyledon-stage seed

- Gene expression profiles of tissues in soybean **seeds** at the **cotyledon** stage [NGS]
- Cotyledon-stage **seed** compartments [GeneChip]

B

<p>Seedling</p> <p>Comparative</p> <ul style="list-style-type: none"><input type="checkbox"/> Seedling<input type="checkbox"/> Seedling Cotyledon	<p>Leaflet</p> <p>Comparative</p> <ul style="list-style-type: none"><input type="checkbox"/> Leaflet<input type="checkbox"/> Leaflet (RNAi Stunted)<input type="checkbox"/> Leaflet (RNAi Varigated) <hr/> <p>Descriptive</p> <ul style="list-style-type: none"><input type="checkbox"/> Leaflet<input type="checkbox"/> Leaflet Palisade Mesophyll Parenchyma<input type="checkbox"/> Leaflet Paraveinal Mesophyll	<p>Root</p> <p>Comparative</p> <ul style="list-style-type: none"><input type="checkbox"/> Root<input type="checkbox"/> Root Hair<input type="checkbox"/> Root Nodules <hr/> <p>Descriptive</p> <ul style="list-style-type: none"><input type="checkbox"/> Root Apical Meristem
<p>Shoot</p> <p>Comparative</p> <ul style="list-style-type: none"><input type="checkbox"/> Shoot<input type="checkbox"/> Shoot Apical Meristem <hr/> <p>Descriptive</p> <ul style="list-style-type: none"><input type="checkbox"/> Shoot Apical Meristem	<p>Embryo</p> <p>Descriptive</p> <ul style="list-style-type: none"><input type="checkbox"/> Embryo<input type="checkbox"/> Embryo Axis Epidermis<input type="checkbox"/> Embryo Axis Root Apical Meristem<input type="checkbox"/> Embryo Axis Shoot Apical Meristem<input type="checkbox"/> Embryo Axis Vascular Bundle<input type="checkbox"/> Embryo Endothelium<input type="checkbox"/> Embryo Epidermis<input type="checkbox"/> Embryo Parenchyma<input type="checkbox"/> Embryo Plumule	<p>Seed</p> <p>Descriptive</p> <ul style="list-style-type: none"><input type="checkbox"/> Seed<input type="checkbox"/> Seed Coat<input type="checkbox"/> Seed Coat Aleurone Layer<input type="checkbox"/> Seed Coat Hilum<input type="checkbox"/> Seed Coat Hourglass<input type="checkbox"/> Seed Coat Inner Integument<input type="checkbox"/> Seed Coat Outer Integument<input type="checkbox"/> Seed Coat Palisade<input type="checkbox"/> Seed Coat Parenchyma<input type="checkbox"/> Seed Cotyledon Abaxial Epidermis<input type="checkbox"/> Seed Cotyledon Abaxial Parenchyma<input type="checkbox"/> Seed Cotyledon Adaxial Epidermis<input type="checkbox"/> Seed Cotyledon Vascular Bundle<input type="checkbox"/> Seed Endosperm<input type="checkbox"/> Seed Suspensor
<p>Hypocotyl</p> <p>Comparative</p> <ul style="list-style-type: none"><input type="checkbox"/> Hypocotyl<input type="checkbox"/> Hypocotyl Root	<p>Multiple Tissues</p> <p>Descriptive</p> <ul style="list-style-type: none"><input type="checkbox"/> Root, Stem, Leaflet	<p>Axillary Meristem</p> <p>Descriptive</p> <ul style="list-style-type: none"><input type="checkbox"/> Axillary Meristem

Supplemental Figure 4. Gene Expression Explorer Tool

The Gene Expression Explorer Tool allows the user to choose GEO expression experiments to visualize in the genome browser. The tool allows the user to select expression tracks to view in two different ways. Experiments can be shown as a unified group by choosing the experiment names (A) or by tissue or treatments (B). This way the user could choose to view all tracks of gene expression from leaflets or seedlings.

Table of Contents

Daytime soybean transcriptome fluctuations during water deficit stress

Select All Samples Across All Selected Experiments

Clear All Selected Samples

Daytime soybean transcriptome fluctuations during water deficit stress

ID:

GSE69469

Group:

Comparison:drought

Platform:

GPL15008

Type:

Expression_NGS

Class:

comparative

Description:

BR16 plants were grown in watered (control) and drought conditions. Samples were taken throughout the day to document changes in gene expression over time and treatments. Time points were sampled in triplicate (biological reps). Six time points were examined, 4 am, 6 am, 12 am, 4 pm, 8 pm and 12 pm.

↓ Select Experiment Samples

Clear Experiment Samples

	Tissue(s)	Cultivar	Treatment
<input checked="" type="checkbox"/>	leaflet	BR16	BR16 drought 8 am
<input checked="" type="checkbox"/>	leaflet	BR16	BR16 control 8 am
<input checked="" type="checkbox"/>	leaflet	BR16	BR16 drought 12 am
<input checked="" type="checkbox"/>	leaflet	BR16	BR16 control 12 am
<input checked="" type="checkbox"/>	leaflet	BR16	BR16 drought 4 pm
<input checked="" type="checkbox"/>	leaflet	BR16	BR16 control 4 pm
<input checked="" type="checkbox"/>	leaflet	BR16	BR16 drought 8 pm
<input checked="" type="checkbox"/>	leaflet	BR16	BR16 control 8 pm
<input checked="" type="checkbox"/>	leaflet	BR16	BR16 drought 12 pm
<input checked="" type="checkbox"/>	leaflet	BR16	BR16 control 12 pm
<input checked="" type="checkbox"/>	leaflet	BR16	BR16 drought 4 am
<input checked="" type="checkbox"/>	leaflet	BR16	BR16 control 4 am

Supplemental Figure 5. Expression Track Selector Panel

Once expression experiments or tissue/treatments have been chosen, the user has the option to drill down into the available tracks and activate/inactivate tracks that are more germane to the users' query. Going on to the next step, the user will be taken to the Genome Browser with the selected tracks displayed.

GSE42871

Williams 43 100-200 mg seed cotyledon	Williams 43 400-500 mg seed cotyledon	Williams 43 5-6 mg seed cotyledon	Williams 43 5-6 mg seed seed coat	Williams 43 5-6 mg whole seed	Williams 43 dry seed	Williams 43 whole seed 12-14 DAF	Williams 43 whole seed 22-24 DAF	Williams 43 whole seed 4 DAF
0.28, 0.33	0.05, 0.05	1.73	78.55	66.82, 154.98	0.04, 0.05	180.64, 180.98	269.35, 252.58	227.89, 213.62

[Graph this experiment](#)**GSE46096**

Williams 82 Early Maturation Stage Axis Parenchyma	Williams 82 Early Maturation Stage Axis Vasculature	Williams 82 Early Maturation Stage Cotyledon Abaxial Epidermis	Williams 82 Early Maturation Stage Cotyledon Vasculature	Williams 82 Early Maturation Stage Endosperm	Williams 82 Early Maturation Stage Endosperm	Williams 82 Early Maturation Stage Root Tip	Williams 82 Early Maturation Stage Seed Coat Hilum	Williams 82 Early Maturation Stage Seed Coat Hourglass Cells	Williams 82 Early Maturation Stage Seed Coat Palisade	Williams 82 Early Maturation Stage Seed Coat Parenchyma
4, 3, 6	5, 3, 4	0, 0, 0	40, 43	0, 1	1	1, 2	3, 3, 3	256, 234, 114	10, 10, 12	921, 1095, 739

[Graph this experiment](#)**Supplemental Figure 6. Tabular Display of GEO Gene Expression**

Tabular display of GEO experiments for a specified gene. Expression values are expressed as intensity units for chip experiments and RPKM or FPKM counts for resequencing experiments.