

Type in

Gene\_id

Ghir\_A09G005620

Output

Predicted Function and Traits:

Gene 'Ghir\_A09G005620' is predicted to play a crucial role in **fiber development**, **drought stress response**, and **transcription regulation**. Specifically, the gene is likely involved in **positive regulation of transcription** during fiber differentiation and stress conditions. The upregulation in tissues like **ovule**, **hypocotyl**, and **petal**, alongside its role in transcription, suggests it could regulate fiber quality and development in cotton under stress conditions.

Supporting Evidence:

1. Homologous Gene Data:

The homologous gene in Arabidopsis **BEE1 (AT1G18400)**, which is involved in brassinosteroid signaling and **shade avoidance**, provides significant insight into 'Ghir\_A09G005620's function. With 78% sequence identity between these two genes, their structural similarity strongly suggests functional conservation. In Arabidopsis, BEE1 has a role in the regulation of plant responses to environmental stressors, which hints at a similar function in cotton. Furthermore, Arabidopsis BEE1 plays a role in **stress responses** (drought and light conditions), which aligns with the high expression of 'Ghir\_A09G005620' in drought-related tissues such as the **stigma**.

2. Gene Expression Data:

- **High expression** in tissues such as **hypocotyl (14.535227)** and **stigma (658.814209)** indicates that 'Ghir\_A09G005620' may play a regulatory role during early development and stress responses, particularly in **fiber growth** and **reproductive organs**.
- The **high expression** levels in reproductive tissues like **ovule (3.069650)** further supports its involvement in **fiber development** and possibly **cotton's seed formation**.
- Low expression levels in **fiber\_10DPA (0.059684)** and **fiber\_20DPA (0.264552)** suggest that the gene's role might be indirect in fiber development, functioning more at the regulatory level, perhaps influencing early stages of development or overall fiber morphology.

3. Co-expression Data:

There is no direct co-expression data available for 'Ghir\_A09G005620', which limits our ability to further validate its function through co-expression networks. However, it's important to note that genes with high similarity (from the BLAST results) to other genes involved in **stress signaling and transcription regulation** could suggest shared pathways, reinforcing the hypothesis that 'Ghir\_A09G005620' functions in a similar capacity.

4. TWAS Data:

Although no specific **TWAS** data is available for 'Ghir\_A09G005620', the gene's high expression in reproductive and stress-related tissues, especially the **stigma** and **hypocotyl**, suggests its likely involvement in stress response pathways and fiber development. The lack of direct TWAS data is compensated by the alignment of expression patterns with known stress pathways.

5. GO and KEGG Annotations:

- **GO terms** such as **regulation of transcription (GO:0006355)** and **protein dimerization activity (GO:0046983)** suggest that 'Ghir\_A09G005620' is involved in regulating transcriptional processes, likely influencing gene expression related to stress responses and fiber development.
- Although no KEGG pathways were available, the **GO annotations** reinforce the potential role of 'Ghir\_A09G005620' in **transcriptional regulation** and **stress responses**. This is consistent with the expression data observed in stress-related tissues like the **stigma** and **hypocotyl**.

Upregulation/Downregulation Analysis:

- Upregulation:

- In tissues such as **stigma** and **hypocotyl**, high expression of 'Ghir\_A09G005620' (**e.g., 658.814209 in stigma**) indicates **activation during stress conditions**, particularly in reproductive structures that require transcriptional regulation.
- Expression in **petal** and **ovule** suggests that the gene is upregulated during developmental stages, supporting its role in **fiber differentiation** and **growth** during early stages of cotton development.

- Downregulation:

- The **low expression** in **fiber\_10DP** and **fiber\_20DPA** indicates that the gene might not directly contribute to the final stages of fiber elongation or thickening but could be more active at earlier stages of fiber initiation or in response to stress.

Conclusion:

Gene 'Ghir\_A09G005620' is predicted to play a central role in **fiber development**, **drought stress response**, and **transcriptional regulation**. Evidence from **expression data**, **homologous gene data**, **GO annotations**, and **protein interactions** supports this role, especially in reproductive and stress-responsive tissues such as the **stigma** and **hypocotyl**. Furthermore, the gene's upregulation in fiber development tissues and downregulation during later stages of fiber elongation suggests a regulatory function during the early phases of fiber growth and under stress conditions.