



Welcome to the 3rd issue of the CottonGen newsletter in 2024. This newsletter is issued to inform users about **new or updated data and tools in CottonGen**. In addition to new and updated data, each issue will provide more information on data or tools in **the featured tools/data** section.

## What's New in CottonGen?

### Short video tutorial

- [Search and Download Protein Sequences](#). (1:26mins)
- [How to use the Ortholog/Paralog search](#). (2:01mins)

### New data and Tools

- Four maps with 50 QTLs from *Li et al.* [QTL mapping of agronomic and economic traits for four F2 populations of upland cotton](#)
- One map with 148 QTLs from *Abdelraheem et al.* [QTL analysis of agronomic, fiber quality, and abiotic stress tolerance traits in a recombinant inbred population of pima cotton](#).
- Three gene annotation data from *MicroPub Biol publications* ([Hernandez et al.](#) or [Graffam et al.](#), or [Zirkel et al.](#))
- **CottonGen Team** aligned markers on two *G.hirsutum* genomes: [Gossypium hirsutum \(AD1\) 'TM-1' genome NAU-NBI v1.1](#) and [Gossypium hirsutum \(AD1\) 'TM-1' genome UTX v2.1](#). New JBrowse tracks were added to the two genomes for the aligned marker locations and identified QTLs and GWAS locations (**See Page 2 for detailed information**).

### New Genome Assemblies and Functional Annotations

Three *G. hirsutum* cultivar genomes obtained from [DOE-JGI](#):

- [Gossypium hirsutum \(AD1\) 'UA48' genome HGS v1.1](#)
- [Gossypium hirsutum \(AD1\) 'UGA230' genome HGS v1.1](#)
- [Gossypium hirsutum \(AD1\) 'CSX8308' genome HGS v1.1](#)

Three *Kokia* genomes from ([Kayal et al., 2024](#)):

- [Kokia cookei 'WAI 16c69' genome ISU v1](#)
- [Kokia drynarioides genome ISU v1](#)
- [K et al.\)okia kauaiensis 'WAI 19s9' genome ISU v1](#)

Functional annotations (InterProScan, Protein, Homologies, and Synteny Analysis) were added to these genomes, too.

Gene annotations added from [Zirkel et al.](#)

Gohir.A02G039501.1

- Transcript Overview
- Alignments
- Analyses
- Contact
- Cross References
- Homology
- Orthologs
- Publications
- Relationships
- Sequences

#### Cross References

External references for this mRNA

Database	Accession
NCBI Protein	XP_016732548
DB:uniprot	ADA1U8MC48

Gossypium hirsutum gene of unknown function, Gohir.A02G039501.1, encodes a potential DNA-binding ALOG protein involved in gene regulation.

#### Publication Overview

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<b>Title</b>	Gossypium hirsutum gene of unknown function, Gohir.A02G039501.1, encodes a potential DNA-binding ALOG protein involved in gene regulation.
<b>Authors</b>	Zirkel J, Hulse-Kemp AM, Storm AR
<b>Type</b>	Journal Article
<b>Journal Name</b>	microPublication biology
<b>Volume</b>	2023
<b>Year</b>	2023



## Aligned marker Primers and new JBrowse tracks

We are looking for ways to take existing data and make it more useful for researchers. For this purpose, we aligned all marker sequences using BLAT to genomes to make the genome comparable with genetic maps. Recently, we aligned PCR-based marker primer sequences using BLAST to genomes. We then mapped QTLs which are associated with both marker-sequence and marker-primers aligned markers to genomes. We have also added three new JBrowse tracks for the new marker-primer aligned positions, and tracts for QTL and GWAS positions, which were identified based on both marker-sequences and marker primers alignments.

The screenshot displays the JBrowse genome browser interface. On the left, the 'Available Tracks' panel is expanded to show 'CottonGen Marker Alignments' and 'CottonGen Primer & QTL Alignments'. The main browser area shows a genomic region with various tracks including 'Reference sequence', 'Gene', and 'Aligned GWAS from CottonGen'. A red arrow points to a track labeled 'fiber uniformity'. A callout box 'Click to get details' points to this track. Another callout box 'Click to get details' points to the 'Dbxref' field in the 'match fiber uniformity' pop-up window, which shows details for the marker qFU.Y7-RIL\_ch15.bb09-12. A third callout box 'Click to get details' points to the 'QTL Overview' section of the pop-up window, which lists QTL statistics and parent information.

**Tracks for marker sequence alignment**

**New tracks for recent marker primer alignment, QTL and GWAS identified based on both marker-sequence and marker-primer aligned positions**

**match fiber uniformity**

**Primary Data**

Name	fiber uniformity
Type	match
Position	A01:45168742..45168936
Length	195 bp

**Attributes**

Dbxref	4787080
Id	qFU.Y7-RIL_ch15.bb09-12
Seq_id	A01
Source	CottonGen

**Region sequence**

```
>A01 A01:45168742..45168936 class=ma
TCATAACGGAAGCATTTTATTCAAAAATCAAGTT
GGTATCATAAATACATACATACATATATATA
AGCCAAACAGCCCTTCATTTAATGCTTGAGAA
CAA
```

**fiber uniformity, qFU.Y7-RIL\_ch15.bb09-12 (QTL) Gossypium hirsutum**

**QTL Overview**

QTL Label	qFU.Y7-RIL_ch15.bb09-12
Published Symbol	qFU15.1.09-12
Trait Name	fiber uniformity
Trait Alias	N/A
Trait Study	Y7-RIL-2015
Population	Yumian-1 x 7235, RIL
Female Parent	Yumian-1
Male Parent	7235
Colocalizing Marker	NAU3384
Neighboring Marker	N/A
Environment	N/A
LOD	2.1
Additivity Dominance Ratio	N/A
R2	5.3
Comments	N/A

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