

Welcome to the GSA figshare portal!

The GSA Journals are now partnered with **figshare**, an online data repository that will archive the supplemental material and/or data files associated with your *GENETICS* or *G3: Genes|Genomes|Genetics* manuscript.

When a manuscript is accepted at *GENETICS* or *G3*, related data uploaded to **figshare** will be published and assigned a DOI, which will be linked from the published article. **Figshare** complies with funder mandates around making data openly accessible and stored in perpetuity. Everything that is published to **figshare** after a manuscript is accepted is indexed with Google Scholar.

Uploading to the GSA portal is distinct from the workflow associated with an individual **figshare** account. Once you upload your files to the GSA portal, you will no longer have access to directly edit them. If you have additions/changes that need to be made to your files, or if you have any difficulty completing your upload, please contact Editorial Staff at genetics-gsa@thegsajournals.org or g3-gsa@thegsajournals.org.


Note: We strongly suggest that you upload supplemental material prior to submitting the manuscript in eJournal Press. This will prevent delays in the editorial process as Editorial Staff will not assign a manuscript to an editor until indicated uploaded materials are processed.

If you are submitting a revision or resubmission, please upload all supplemental and/or data files again if any changes have been made. If there have been no changes to the files, please notify Editorial Staff at genetics-gsa@thegsajournals.org or g3-gsa@thegsajournals.org.

If you originally submitted to *GENETICS* and your manuscript is transferred to *G3*, please contact genetics-gsa@thegsajournals.org to arrange for an update to the **figshare** record.

To Upload your Files to Figshare

1. Collect all previously prepared supplemental material. Name files so that they are clearly identified. We suggest Figure S1, Table S1, File S1, etc. as naming conventions. **All files must be uploaded at the same time, and individual file titles cannot be changed after upload.**
2. Navigate to the submission portal at <https://gsajournals.figshare.com/submit>.



Add files to your GSA Journals submission

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When you publish in the GSA Journals, you help to catalyze scientific advances by sharing your experimental reagents, results and interpretations. You should provide online access to data that is not represented fully within the tables and figures of the manuscript but that is necessary for confirming the conclusions presented in your manuscript. Specifically, the data that were used in the final analyses should be made publicly available.

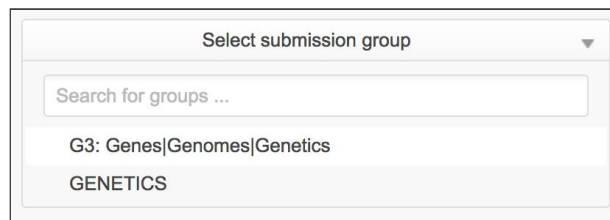
Journal Data Policy
GENETICS: <http://www.genetics.org/content/scope-and-publication-policies#data-reagent>
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Questions?
Email genetics-gsa@thegsajournals.org or g3-gsa@thegsajournals.org

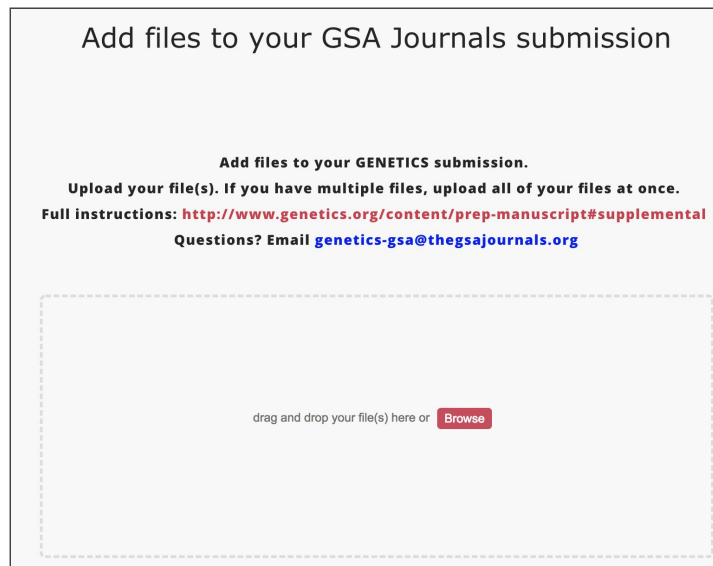
Please select the destination for your submission

Select submission group

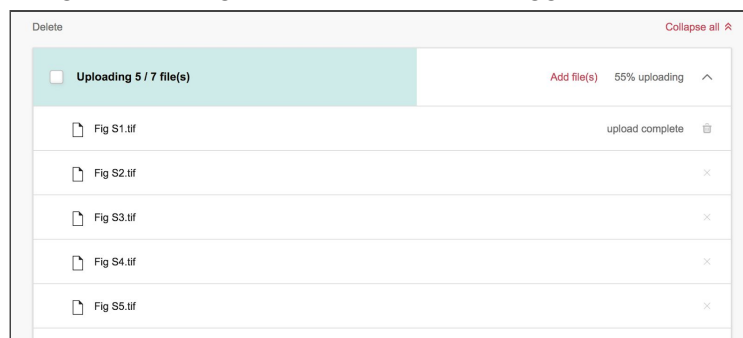
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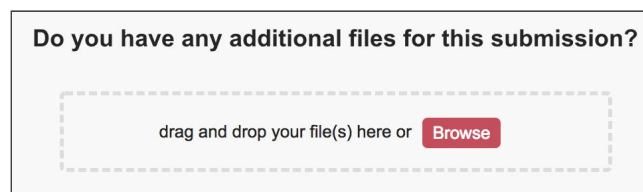
4. Add all of your supplemental material and/or data files either by drag-and-dropping or by using the “Browse” button.



5. Drag-and-dropping or selecting files via Browse will trigger immediate upload.



6. If necessary, add additional files by scrolling to the bottom of the page to the additional files box. This is located past your loaded files and information fields. Add all relevant files before moving on.



7. Once all files have been uploaded, fill out the information associated with your files on the screen that loads.

The screenshot shows a web form for entering metadata for an uploaded file. The fields are as follows:

- Title ***: Text input containing "Fig S1.tif".
- Item type (what's this?)**: Dropdown menu set to "Fileset".
- Authors ***: Text input with placeholder "Add co-authors by name, full email or ORCID. Hit enter after each".
- Description ***: Text area with placeholder "Describe your data as well as you can" and a rich text toolbar below it containing icons for Bold (B), Italic (I), Underline (U), Link (x), and Unlink (x²).
- Categories ***: Dropdown menu set to "Select categories".
- Keywords ***: Text input with placeholder "Add keywords for easy discovery. Hit enter after each".
- Licence (what's this?) ***: Dropdown menu set to "CC BY".
- Article title**: Text input containing "Article title".
- Manuscript #**: Text input containing "Manuscript #".
- Article DOI**: Text input containing "Article DOI".

- a. Insert a **Title**. By default, the title field will be the name of your first uploaded file. Edit it and **use the format “Supplemental Material for Author et al., year.”** If your manuscript has fewer than four authors, then list all last names.
 - i. *Example:* Supplemental Material for Smith et al., 2018
 - ii. *Example:* Supplemental Material for Smith, Jones, and Brown, 2018
- b. If you uploaded multiple types of file, your **Item type** will be Fileset by default. If you uploaded a single file or type of file, then please choose the correct type from the drop-down menu (Figure, Table, etc.).
- c. Add **Authors** by **typing each author’s name and pressing enter**. You can rearrange the order in which the authors appear.
- d. Select a **Category**. These are taken from the Australian Fields of Research classification system. You can choose more than one either by selecting from the drop-down menu or by searching for your subject area. If you can’t find exactly what you’re looking for, we recommend finding the best option and getting more specific in the Keywords section.
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- f. Write a **Description**. This should include a full description of each file uploaded.
 - i. *Example*: Figure S1 contains examples of spindle categories. Table S1 contains SNP ID numbers and locations. File S1 contains genotypes for each individual. Code used to generate the simulated data is provided in File S2.
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 - i. CC BY
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