NEW GEO tracks on JBrowse

Xenbase developed standardized pipelines to process **NextGen *Xenopus* Sequence data from GEO/SRA** (Sequence Read Archive at NCBI). The goal was to wrangle diverse NGS data to make it organized, consistent and accessible, so you can compare data from different sources, all **aligned against latest genomes.** We built new tool to search and select experiments and load them into JBrowse and two complementary navigation/selection systems to view processed GEO data on JBrowse: a **faceted browser** and a **hierarchically organized browser**.

Xenbase is the first model organism database to have done this data wrangling for NGS !!!

Highlights:

- Xenbase processed **54% of the GSMs in GEO** (964/1547 data sets).
- **648 tracks on JBrowse**: 525 RNA-Seq and 123 ChIP-Seq tracks, more to come!
- Details of each GEO series (called a GSE) are summarized on **GSE pa**ge (click for an example)
- Search all the GEO data on Xenbase here. **Simple Search and Advanced Search options.**
- When you find data you want to compare, **check box and click Load to JBrowse**.
- Differential Expressed Genes (DEG) list can be filtered (fold change, FDR, TPM) and downloaded.
- Processed GEO data files are available to download from Xenbase FTP.

3 ways to get to GEO tools.

1. "GEO data @ Xenbase" link under Expression menu.
2. Quick search mini-bar, select "GEO data sets".
3. Genomes Menu or Genome Browser tile, select either *X. laevis* 'J-Strain 9.2' or *X. tropicalis* 'Nigerian 9.1 on JBrowse', then select the tracks from the left menu, or click on the floating box in the upper left called "GEO tracks" to open the faceted list view.

Coming Soon:

- *Webinar on 'How to Navigate GEO data on Xenbase', live and recorded.*
- *Differentially Expressed Genes (DEG) displayed in heatmaps and other interactive data displays.*
- *GEO Processing Pipeline will soon be available on GitHub.*

Interested in a **Xenbase GEO Workshop** at the October 11-14 XERT meeting in Woods Hole?
Please let us know if you, your students or postdocs can attend an afternoon workshop on 11/10/19.
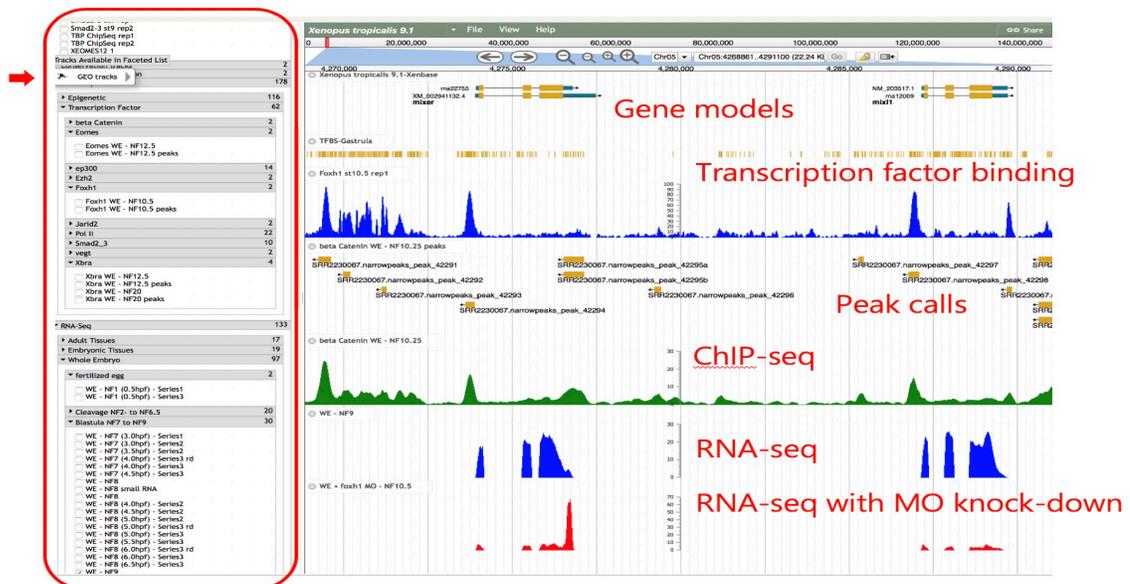Email your interest and potential numbers to Xenbase@ucalgary.ca with subject line 'GEO Workshop'.

Figure 1. GEO data on Xenbase: Tracks on JBrowse, track selector (red box) and faceted browser (red arrow).

JBrowse Video-Tutorials
JBrowse is the genome browser on Xenbase where you can interrogate the latest genome builds for *X. tropicalis* and *X. laevis*, transcription factor binding sites, and, as described above, NGS data. Learn how to navigate JBrowse via our helpful video tutorials:

- Introduction to JBrowse. How to select tracks, species, genome version and find genes.
- JBrowse 1: How to view all aspects of a gene sequence (e.g., UTR, intron, CDS).
- JBrowse 2: How to save track data for a particular region.
- JBrowse 3: How to add custom tracks from your computer.

Coming soon: JBrowse 4: How to view JBrowse tracks for ChIP-Seq and RNA-Seq data from GEO.

NEW Gene Expression Ribbon
Each Gene Page now has a ribbon that summarizes *in situ* and RNA-Seq data for embryonic stages, embryonic tissues and adult tissues of *X. laevis* and *X. tropicalis*.

- Green represents *in situ* data from the vast collection of curated gene expression in Xenbase. Mouse over to show number of records for expression in that stage or tissue.
- Click 'Xenbase Expression Details' to go to the full gene expression data.
- RNA-Seq data from Sessions *et al.* 2016 (adult tissues) are shown in color gradients of TPM values in top right half of NF stage and adult tissues ribbon. Mouse over to see the TPM value for a particular tissue/stage.

Single-cell RNA-Seq data from Briggs et al. 2018 for embryonic tissues are being processed. In the meantime, explore pre-loaded single cell data via the links to SPRING, a tool to uncover high-dimensional structure in single cell gene expression built by the Klein lab at Harvard.

This is the first iteration of the gene expression ribbon-please send us feedback: xenbase@ucalgary.ca
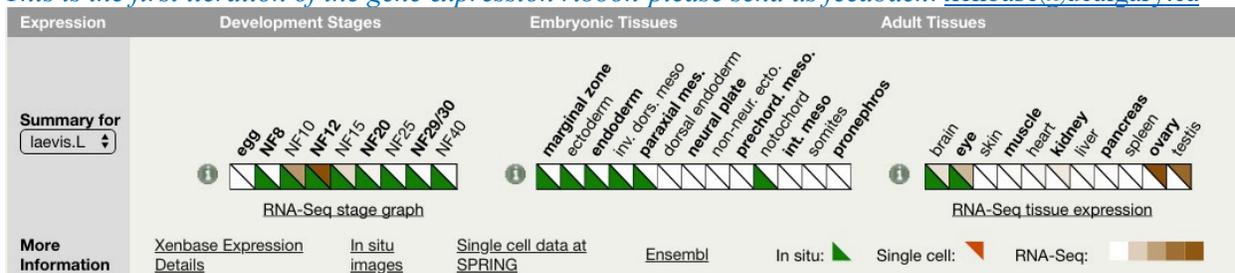

Figure 2. Gene Expression ribbon on gene pages*: in situ* and RNA-Seq data.

Updated Marker genes, anatomy tree and more images for XAO Anatomy Pages (see Fig 3. below left).
Each anatomical term we use to describe gene expression has its own XAO page. XAO pages are useful to find out more about a structure, at what time in development it is observed, and which genes are expressed. We're adding validated marker genes, exemplary gene expression images, and annotated diagrams as we curate new research articles and data from large screens. Let us know your favorite markers, and we'll share your insights! Email xenbase@ucalgary.ca.

***Xenopus* Stock Center frogs all catalogued on Xenbase**
Transgenic and mutant *Xenopus* lines and wildtypes strains supplied by the NXR (USA), the NBRP (Japan) and the EXRC (Europe) are catalogued and searchable on Xenbase. The stock centers hold over 130 different transgenic lines, and the NXR has developed 74 mutant lines. Many lines are shared between the centers, yet each line has a single entry on Xenbase, and carry unique RRIDs (identification numbers) depending on supplier. We encourage researchers to use the official standardized name and cite the RRID number in their papers.

New Xenbase paper
Take a look! **Xenbase: Facilitating the use of Xenopus to Model Human Disease**. Nenni *et al*. (2019). Front. Physiol. doi: 10.3389/fphys.2019.00154. This review by Xenbase, which assessed 1000+ articles, describes the breadth of recent *Xenopus*-Human disease modeling and describes the integration of the Human Disease Ontology (DO) into Xenbase Disease Pages.

Disease Ontology Pages with interactive tree viewers. (see Fig 3. below right)
To further support human disease modeling in *Xenopus*, we have added dynamic tree viewers to the Disease Ontology (DO) Disease Pages. (Note: OMIM is not an ontology, so OMIM Disease Pages *do not* have ontology tree viewer).

- The DO tree viewer shows how diseases are related, e.g., 'diabetes mellitus' has five subtypes, 'gestational', 'neonatal', 'type 1' and 'type 2', and 'prediabetes syndrome'.
- To explore the ontology in tree-view, click the nodes.
- Solid blue nodes indicate more subtypes, e.g., type1 diabetes has 24 subtypes!
- Numbers in parenthesis show the number of *Xenopus* papers that refer to that disease.
- Literature tab lists all of the articles, and you can navigate back to the Article Page.
- Genes associated with the disease are also shown, and link back to the Xenbase Gene Pages.
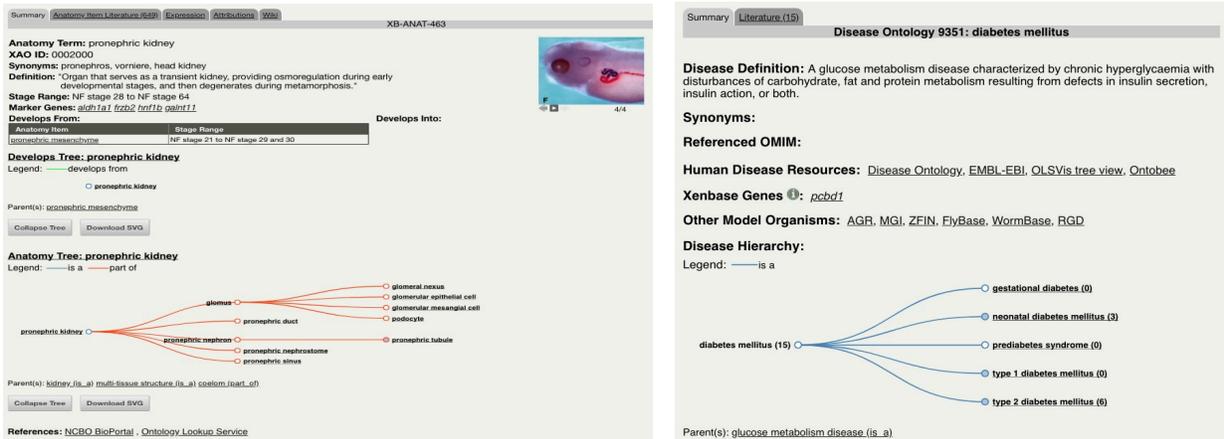

Fig 3. Anatomy Page with marker genes and interactive XAO tree viewer (left). Disease Page with associated gene(s) and DO tree viewer (no. articles).

Lastly…
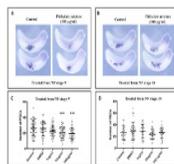**microPublication Biology (µP for short)** Call for papers!
µP is currently accepting single-experiment submissions of high-quality *Xenopus* research:

-**Expression patterns** (RT-PCR, WISH, IHC)   -**Phenotypic data** (e.g., toxicology, SEM, histology)
-**Sequence data** (SNPS, polymorphisms)   -**Genotypic data** (mutants or Tg lines)
-**Methods** (new or updated protocols)

Each **open-access** µP article is **peer-reviewed**, assigned a **DOI**, and published **online as HTML and PDF**. This is an especially accessible format to get undergraduate student research published quickly!
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