February 4th, 2021

Dear Editors,

We are delighted to submit our manuscript, “**Oo-site: Dashboard to visualize gene expression in the Drosophila germarium reveals entry into meiosis is regulated post-transcriptionally** for consideration as a Research Article at *Development*.

The *Drosophila* ovary is a powerful and widely used model to study stem cell differentiation and meiosis. Numerous studies have applied sequencing techniques to monitor gene expression during differentiation of *Drosophila* germline stem cells including single cell mRNA sequencing. However, although a large amount op-0f data has been generated, it remains inaccessible to much of the scientific community as analyzing RNAseq data requires bioinformatic expertise. Here, we present a tool, Oo-site, which provides users access to mRNA, polysome and single cell sequencing data through an easy-to-use interface.

Oo-site provides three modules with which users can explore changes in gene expression at the mRNA level or translation efficiency (TE) of mRNAs. Users can examine this expression landscape at the level of a single gene using the ovary-map module, globally with the ovary-heatmap, or examine groups of genes either from a custom list or by GO-term using ovary-violin. Oo-site allows users to export reports of their visualizations to allow them to easily create publication-ready figures.

We demonstrated that observations from Oo-site are representative of meaningful changes in gene expression changes both at the mRNA and TE level by using previously published sequencing data as well as by FISH and usage of tagged reporters. Furthermore, we have demonstrated the utility of Oo-site in hypothesis generation and discovery by using it to find that Ord, a crucial regulator of proper meiosis, is controlled primarily post-transcriptionally during meiotic entry.

Furthermore, Oo-site has potential as a teaching and demonstration tool as it can provide a window in the world of genomics and development to those without bioinformatic training. Oo-site is not only useful to researchers in *Drosophila* oogenesis as it provides an easy way to examine gene expression of a highly conserved process and therefore will be useful to those interested in oogenesis and stem cell differentiation more generally.

Finally, as single cell sequencing becomes ubiquitous, we believe that Oo-site provides a model to be built upon to allow those without familiarity with a given developmental system to better appreciate the results of single cell sequencing. To facilitate this we provide the full source-code of Oo-site under an open source (GPL3) license so that other researchers can use the underlying code in their own work.

We are confident that Oo-site will be of broad interest to those studying development, stem cells, gene regulation, and disease.

We would like to propose the following experts as excellent candidates to serve as reviewers:

Best,

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