

Supplementary Materials of canvasDesigner2

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Web URLs of tools and online user guide

Google Chrome (<https://www.google.com/chrome>) is recommended for optimal use of the web-based tools.

canvasDesigner2: <https://baohongz.github.io/canvasDesigner2>

canvasDesigner2 source code: <https://github.com/baohongz/canvasDesigner2>

Example SVG files: <https://github.com/baohongz/canvasDesigner2/tree/gh-pages/SVG>

Inkscape: Tool to edit SVG files, convert image files from other formats to SVG format.
<https://inkscape.org>

pdf2svg: A simple PDF to SVG converter using the Poppler and Cairo libraries.
<https://github.com/dawbarton/pdf2svg>

SVGOMG: SVG Optimizer tool for optimizing SVG files. <https://jakearchibald.github.io/svgomg>

Coral: Clear and customizable visualization of human kinome data. <http://phanstiel-lab.med.unc.edu/CORAL/>

ComplexHeatmap: Complex heatmaps are efficient to visualize associations between different sources of data sets and reveal potential patterns.
<https://www.bioconductor.org/packages/release/bioc/html/ComplexHeatmap.html>

Wikimedia Commons: media file collection of 59.4 million freely usable media files to which anyone can contribute. https://commons.wikimedia.org/wiki/Main_Page

WikiPathways: a database of biological pathways maintained by and for the scientific community.
<https://www.wikipathways.org/index.php/WikiPathways>

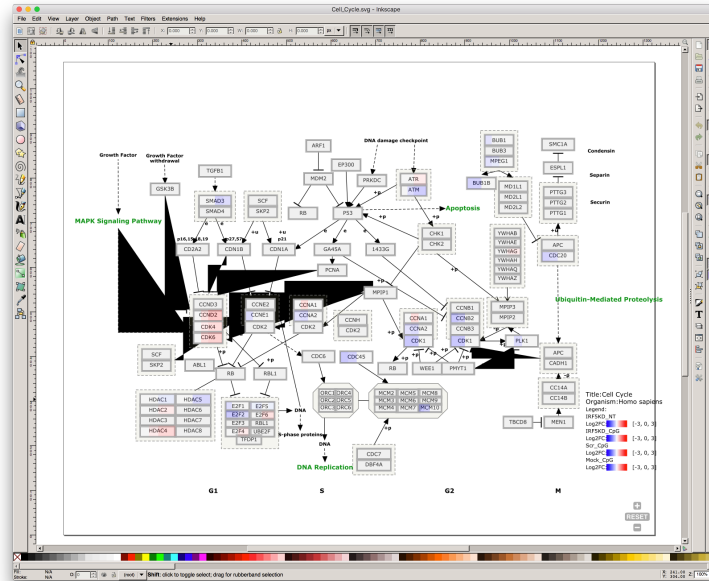
Reactome: a free, open-source, curated and peer-reviewed pathway database. Our goal is to provide intuitive bioinformatics tools for the visualization, interpretation and analysis of pathway knowledge to support basic research, genome analysis, modeling, systems biology and education.
<https://reactome.org/>

PyMOL: a user-sponsored molecular visualization system on an open-source foundation, maintained and distributed by Schrödinger. <https://pymol.org/>

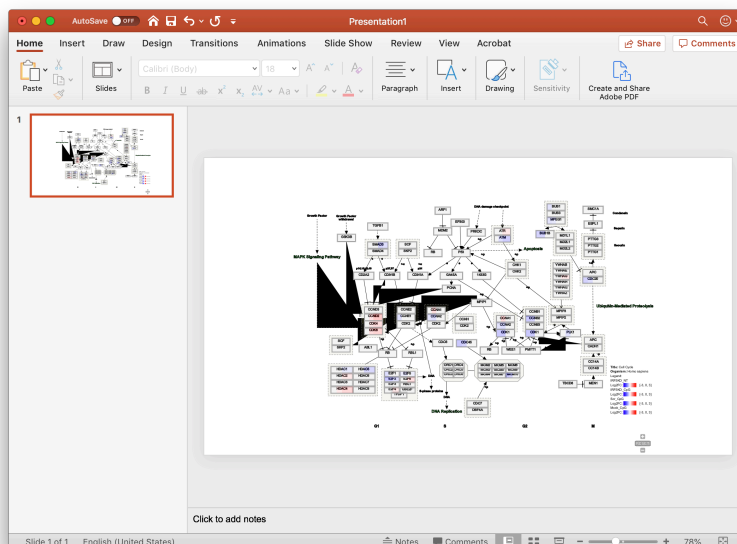
Limitation of SVG rendering by other popular tools (Fig. s2)

Rendering of some complex SVG files is flawed in many other tools, such as popular tools like open-source Inkscape and MS Power Point. Here is an example of pathway diagram (https://baohongz.github.io/canvasDesigner2/SVG/Cell_Cycle.svg) from Wikipathways rendered by Inkscape or MS Power Point. Please note unexpected black triangles generated by both tools. The same SVG file is rendered perfectly by canvasDesigner2 as shown in Figure 1D.

Inkscape

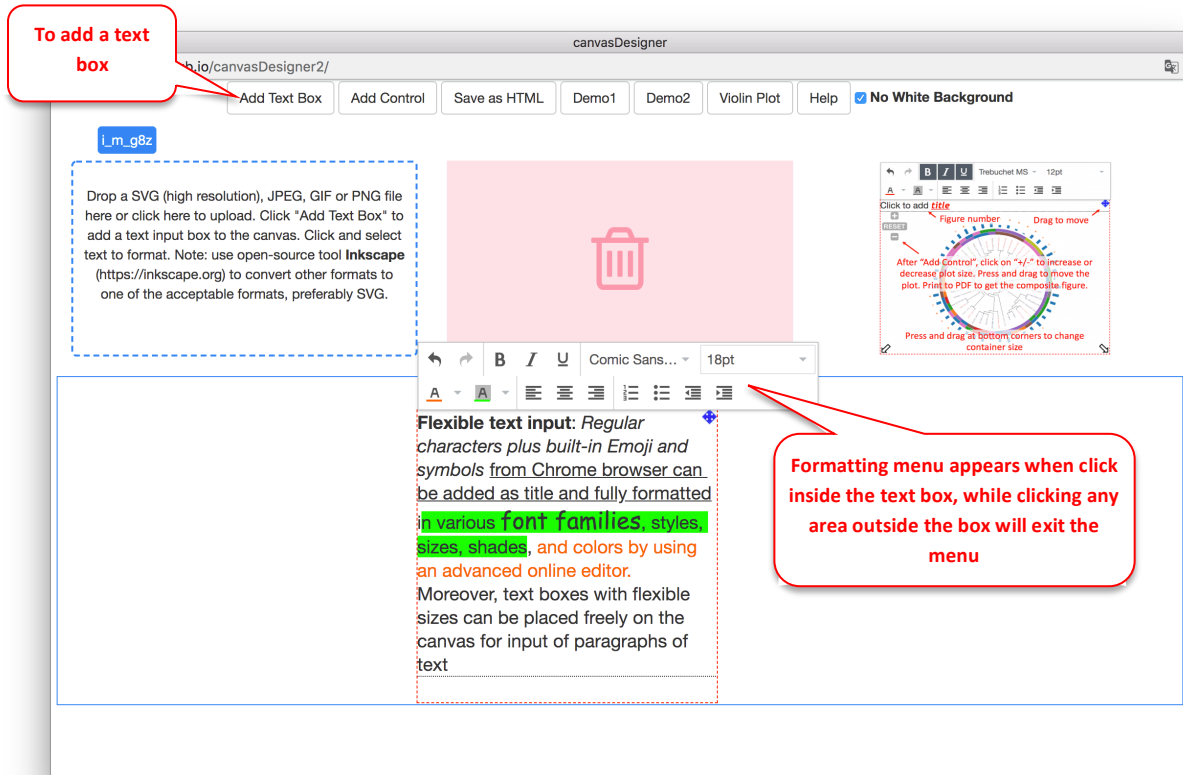


MS Power Point



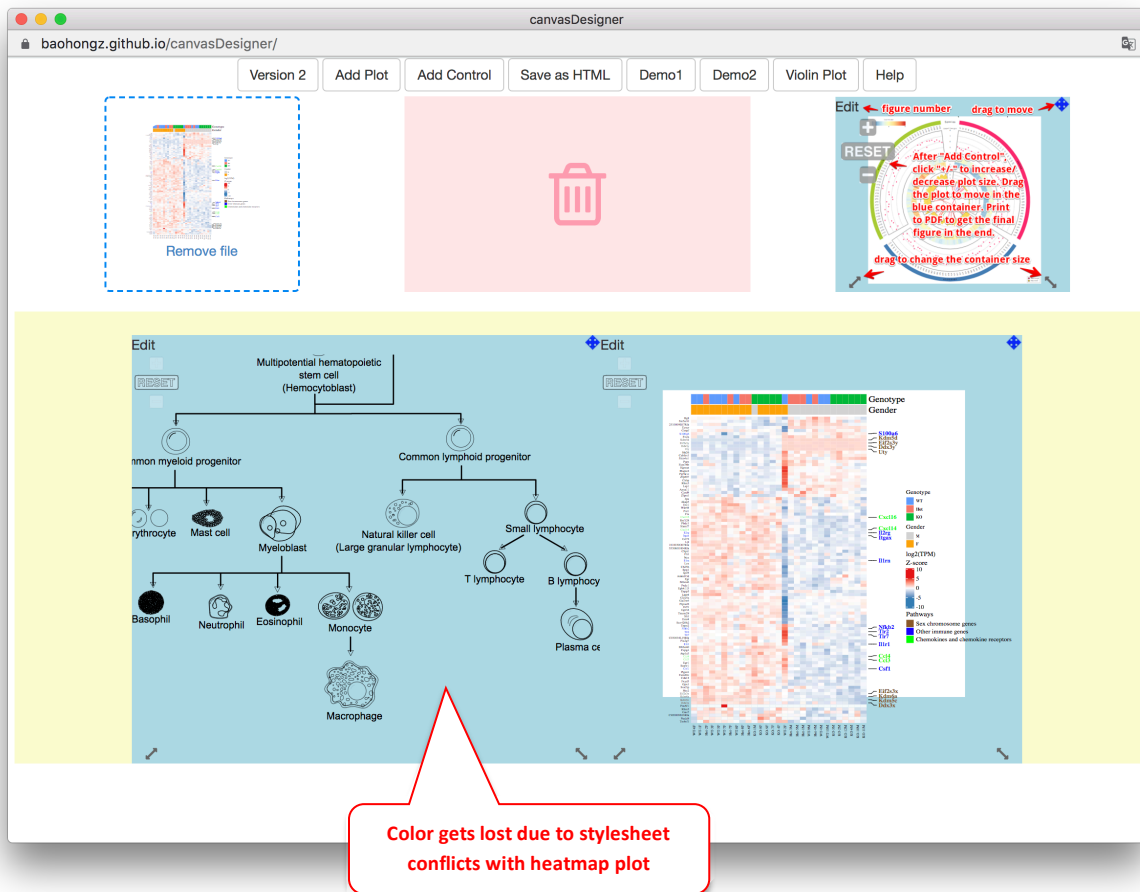
Flexible text input (Fig. s3)

Click on “Add Text Box” to add a box to the canvas. Selecting any text will fire up the formatting menu while clicking any area outside the box will exit the menu.



Conflicting Stylesheets (Fig. s4)

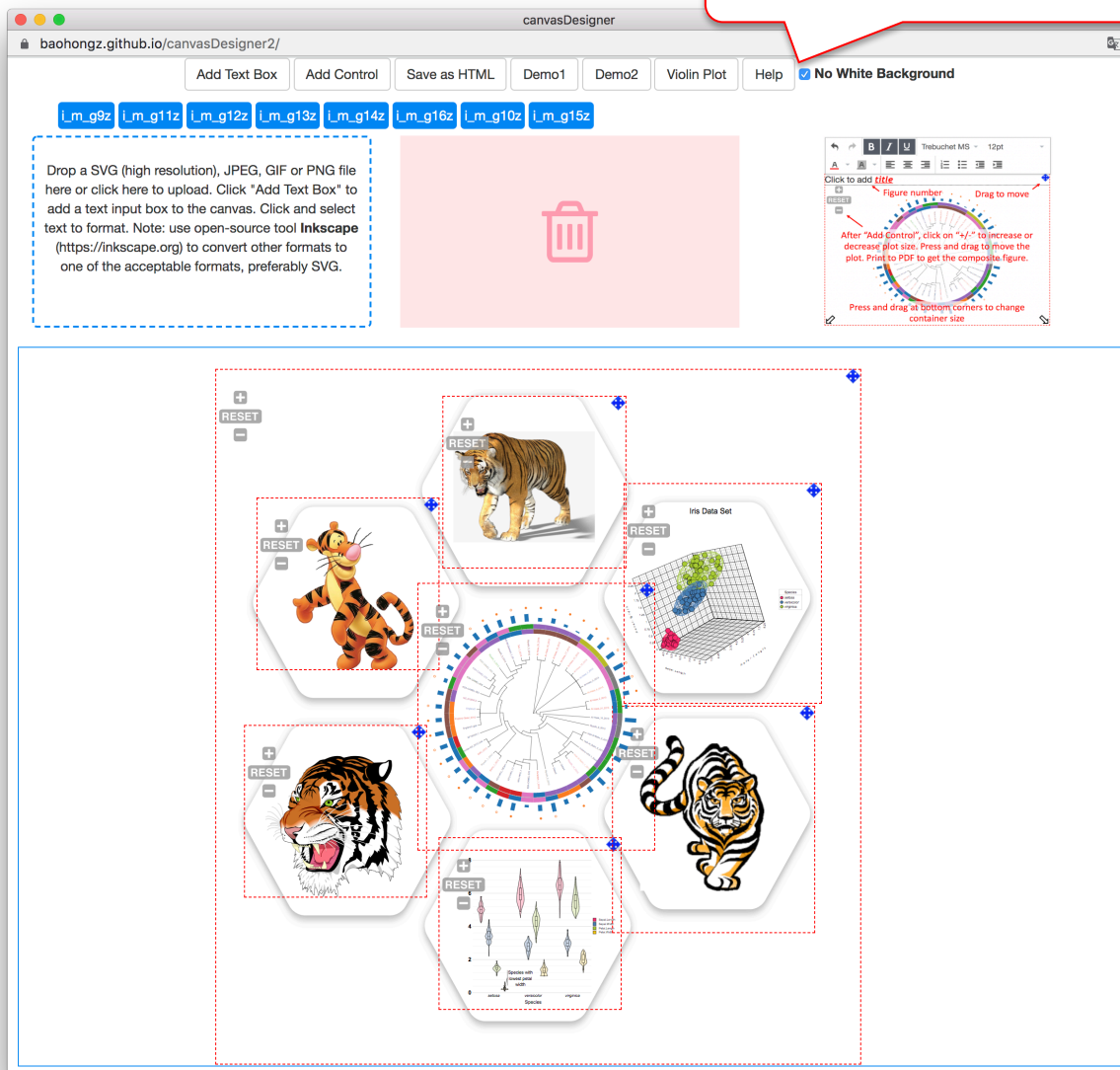
Human blood cell lineage plot loses all of its colors due to the conflict of the stylesheet defined in heatmap plot in the older version (version 1) of canvasDesigner. Localization of stylesheets in new version solves the issue as shown in Fig. s1.



Optionally removing white background (Fig. s5)

Overlaying plots onto each other to create more complex design is possible by optionally checking “No White Background” on the top menu. Moreover, images, tigers as example, in jpg, png, gif and svg formats can be loaded to the canvas directly for arrangement. The saved final HTML file is available at <https://baohongz.github.io/canvasDesigner2/figure/Fig.s5.html> .

Checking “No White Background” allows transparent background and more complex design



Vertical stacking (Fig. s6)

Each plot will get a button handle when it is loaded onto the canvas. A plot and the linked handle will be highlighted in yellow when hovering mouse over the handle. Dragging the handle and dropping it at desired position among these buttons will change the relative vertical stacking, also known as z-index of the plot. The rightmost horizontal position represents the top layer of the stack of plots on the canvas.

Drag the handle to position #1 or #2 to arrange the order of the plot in terms of vertical stacking

Bottom

1

2

Top

Drop a SVG (high resolution), JPEG, GIF or PNG file here or click here to upload. Click "Add Text Box" to add a text input box to the canvas. Click and select text to format. Note: use open-source tool [inkscape](https://inkscape.org) (<https://inkscape.org>) to convert other formats to one of the acceptable formats, preferably SVG.

canvasDesigner

baohongz.github.io canvasDesigner2/

Add Text Box Add Control Save as HTML Demo1 Demo2 Violin Plot Help No White Background

i_m_g4z i_m_g1z i_m_g2z

Click to add title

Figure number Drag to move

After "Add Control", click on "+/-" to increase or decrease plot size. Press and drag to move the plot. Print to PDF to get the composite figure.

Press and drag at bottom corners to change container size

B

C

A

RESET

RESET

RESET

Multipotential hematopoietic stem cell (hematocytoblast)

Common myeloid progenitor

Common lymphoid progenitor

Granulocyte

Monocyte

Macrophage

Myeloid stem cell (L116 progenitor lymphocyte)

Neutrophil

Eosinophil

Basophil

T lymphocyte

B lymphocyte

Plasma cell

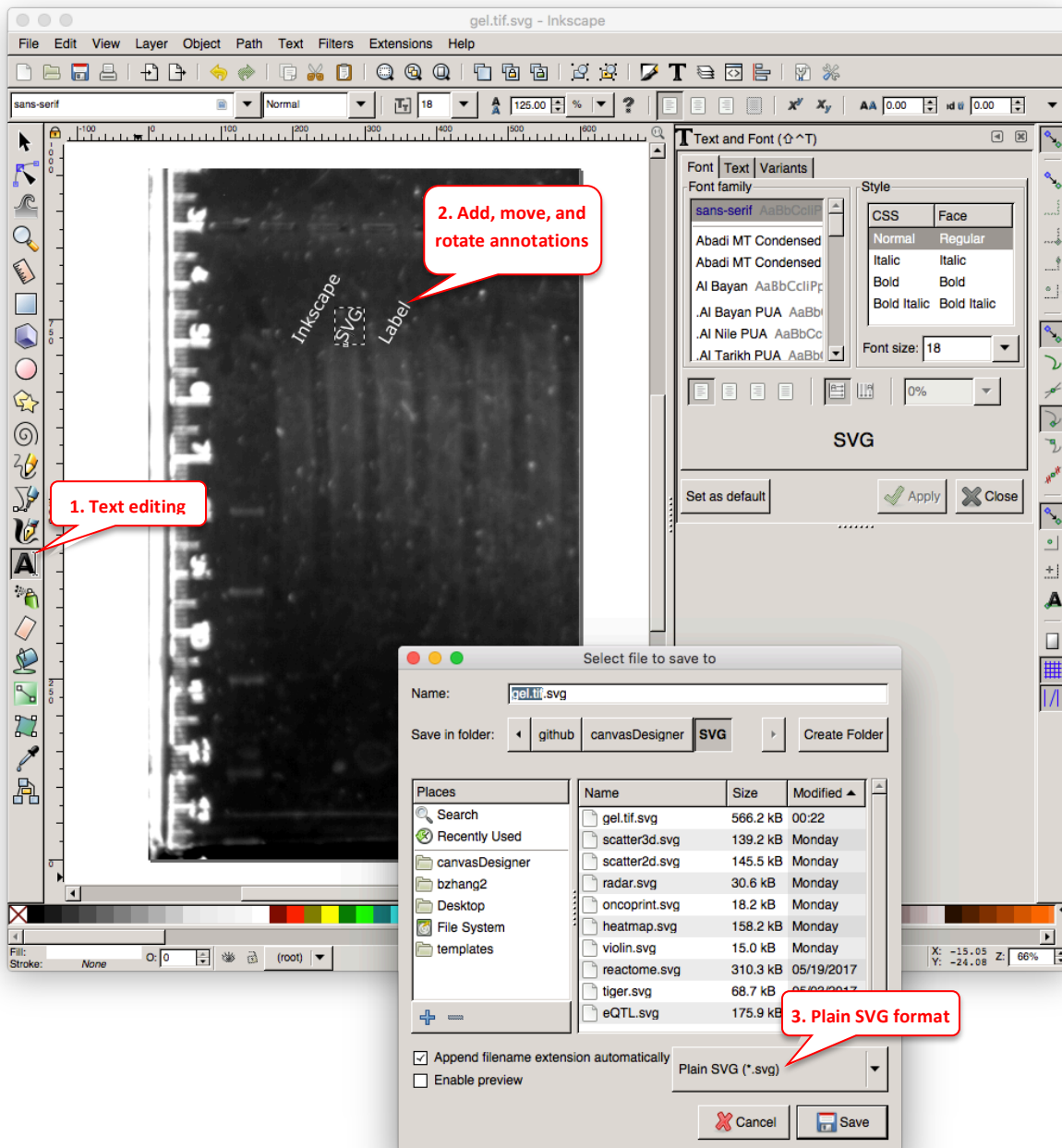
Megakaryocyte

Thrombocyte

Macrophage

Inkscape to annotate and convert images to SVG if needed

Inkscape (<https://inkscape.org>) is a powerful open-source vector graphics editor. You can add text annotations to an image in jpeg, png, gif, or tiff format and save it as “Plain SVG” file to be used in canvasDesigner2 tool. The example here is showing how to add annotations to a TIFF image and then save as SVG format.



Optimize SVG files by SVGOMG

SVG files, especially exported from various tools, usually contain a lot of redundant and useless information such as editor metadata, comments, hidden elements, default or non-optimal values and other stuff that can be safely removed or converted by the online tool SVGOMG (<https://jakearchibald.github.io/svgomg>) without affecting SVG rendering result.

The screenshot displays the SVGOMG web interface. At the top, there are tabs for 'IMAGE' and 'CODE'. The main area shows a box plot titled 'Gene expression of TUFM' for SNP rs7187776. The y-axis is labeled $\log_2(\text{CPM}+1)$ and ranges from 6.40 to 7.20. The x-axis shows 'High' and 'Low' expression levels for three SNP groups: AA (red), AG (blue), and GG (green). A legend on the right indicates the SNP groups. A red callout bubble points to the top of the plot area with the text '1. Drag-n-drop a SVG file'. A green callout bubble points to the 'Precision' slider on the right with the text '2. (Optional) Change optimization parameters'. At the bottom right, there are icons for 'Save', 'Copy', and 'Download'. A red callout bubble points to the 'Save' icon with the text '3. Save'. Below the 'Save' icon, a status bar shows '3.24k - 72.62% saving'. On the right side, there are 'Global settings' and 'Features' sections, each with a list of toggleable options.

Global settings

- Show original
- Compare gzipped
- Prettyfy code
- Multipass

Precision

Features

- Cleanup attribute whitespace
- Remove/tidy enable-background
- Clean IDs
- Round/rewrite number lists
- Round/rewrite numbers
- Collapse useless groups
- Minify colours
- Round/rewrite paths
- Shapes to (smaller) paths
- Style to attributes
- Round/rewrite transforms
- Merge paths
- Move attrs to parent group
- Move group attrs to elements
- Remove comments
- Remove <desc>

Gene expression of TUFM

$\log_2(\text{CPM}+1)$

rs7187776

SNP

- AA
- AG
- GG

High Low High Low High Low

3.24k - 72.62% saving

3. Save