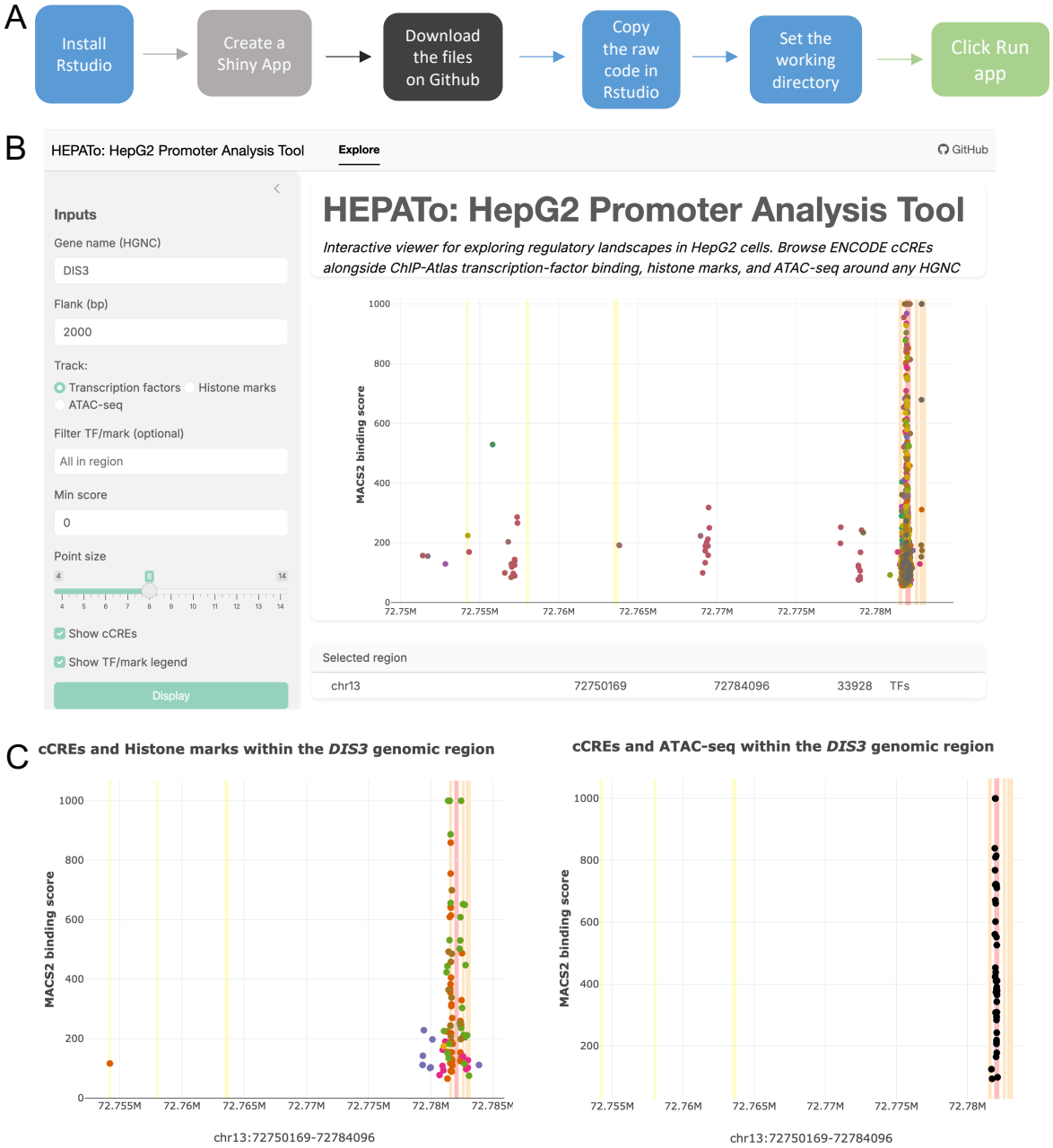

Supplemental Figure S2. HEPATo user interface. (A) To run HEPATo, which is implemented as an R Shiny app, on your computer you need to install RStudio (https://cran.r-project.org). Next, go to https://github.com/JulianPrim/HEPATo and download the four files in the Releases link. Save them in a folder with the App.R script, set R on this folder (session>set working directory), copy and paste the rawCodeV1.0 into the App.R window of RStudio and click the Run App button. Please refer to the brief GitHub web page for more detailed information concerning the setup and query processes. (B) The HEPATo user interface enables users to query the viewer with gene names (in capital letters) from the HUGO Gene Nomenclature Committee (HGNC; https://www.genenames.org), define the size of flanking up- and downstream sequences to be included in the output, select ChIP-Seq TFs/marks or ATAC-Seq experiments and specific TFs. To limit the output, users can select individual TFs/marks and set a minimal MACS binding score. To refine the graphs, it is possible to alter the point size and choose whether to include legends. Click the Display button to execute the code that creates the graph (this may take some time depending on the computing power available). The graph shown is for DIS3 and TFs. The chromosome number, genome coordinates, gene length in bases and the data type (TFs, marks or ATAC-Seq) are given at the bottom. In the viewer, scroll down to see the list of TFs. (C) The two other data types are displayed as indicated.