Predicting Distal Regulatory Regions For A Gene:
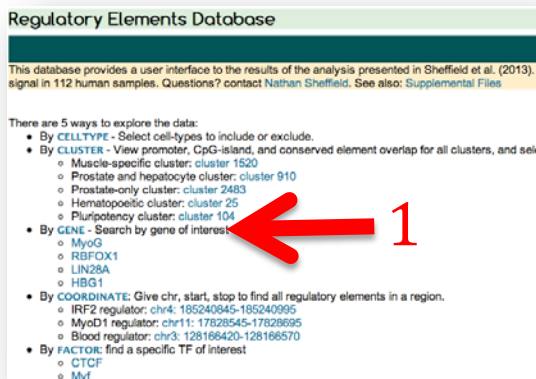
(Updated 24 October 2013, Mike Pazin)

The Regulatory Elements Database is an ENCODE-funded tool described in a recent publication that can be used to make predictions about the linkage between regulatory regions and genes, based on the statistical association of DNase I Hypersensitive Sties (DHS) and gene expression across more than 100 samples consisting of over 70 diverse cell types.

From the Regulatory Elements Database site, click on the "By GENE" link (Arrow 1).

In the new screen, enter a gene name (such as IL10) in the box, and click the "Submit" button.

A list of the 10 DHS that are best correlated with the gene of interest is displayed at the right (near Arrow 2), and the expression profile of the gene across cell types is also shown (Arrow 3). For each DHS, the display indicates the genomic coordinate, p value (green for positive correlation with expression, red for negative correlation with expression), and the cluster number (hyperlink to DHS with a similar signal profile across cell types). The list can be downloaded as a BED file (which can be opened in excel); the complete list can also be displayed. To display details of any paritcular DHS, click on the location, which is also a hyperlink (eg., Arrow 2).
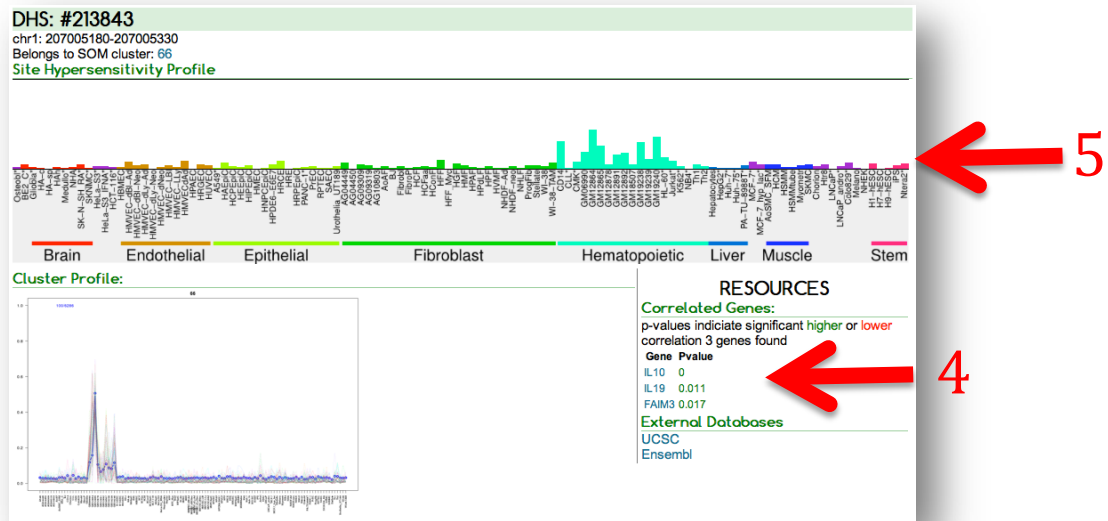
The new display indicates the genes that are predicted to be regulated by this DHS at the right (arrow 4), and the DHS signal profile across individual cell types (arrow 5).