

Precision estimation for the novel predicted candidate disease genes

The procedures for precision estimation of the novel predicted disease genes are provided in Methods section of the main manuscript. Below we provide the plot of precision versus rank cutoff for the top 100 predicted candidate disease genes for each of the 110 diseases. The X axis denotes the rank cutoff; The Y axis denotes the prediction precision, which is calculated as the fraction of the known (seed) disease genes among all the predicted genes above a particular rank cutoff. The 110 diseases are arranged in the alphabetical order.





























