Configure ChIP-Seq Analysis Data

UGENE integrates the Cistrome workflow for analysis of ChIP-Seq data. The workflow requires reference data to be present in the UGENE data folder. Reference data for human can be installed via the Online Installer. To configure them manually download the data from the web page http://ugene.net/download-all.html and unpack to the "cistrome" folder inside the UGENE data folder.

Note that RScript external tool should also be provided.