Initial cCRE filtering. We developed a machine learning model, called MatchedFilter, that predicts cis-regulatory elements by considering multiple types of histone marks and integrating information about the distribution of each histone mark signal [74]. For example, a ‘peak-valley-peak’ shape of H3K27ac signal is often observed at enhancer regions [75]. This model is based on a support vector machine (SVM) algorithm that has been tested thoroughly and has high accuracy for identifying functional cis-regulatory elements in human (**Figure 8**). We will use MatchedFilter to identify high-confidence human cCREs.