Table 3 Important parameters for each peak calling algorithm

Algorithm	Important parameters
CCAT	Minimum score: minimum score of normalized difference
	Minimum count: minimum number of read counts at the peak
	Moving Step: step of window sliding
	SlidingWinSize: size of sliding window
	Bootstrap pass: number of passes in the bootstrapping process
MACS	NoLambda: if True, MACS will use fixed background lambda as local lambda for every peak region
	NoModel: whether or not to build the shifting model
	MFold: regions within MFOLD range of high-confidence enrichment ratio against background to build model
	PValue: *p*-value cutoff for peak detection
SICER	WindowSize: size of the windows to scan the genome width
	GapSize: allowed gap in base pairs between islands
	FDR: false discovery rate controlling significance
ZINBA	Selectmodel: Specifying select model = FALSE skips the model selection process altogether and may save a significant amount of time
	extension: average fragment library length (size selected)
	winSize: Selecting a larger window size increases speed of analysis but decreases resolution and sensitivity to detect enrichment
	offset: Smaller non-zero offset distances increase sensitivity but also increase computational builden
	FDR: FDR = TRUE specifies the model to use the FDR threshold rather than posterior probabilities. This typically results in more liberal peak calls. If false, then uses posterior probability to threshold peaks using 1-threshold.
F-seq	FeatureLength: feature length
	Threshold: standard deviations