

Tool	Peak Calling	Normalization	Statistical Test	Sharp Signal	Broad Signal	Biological Replicates	Significance Measure	PMID
<u>SICER</u>	Window based approach, merging of eligible clusters in proximity closer than defined gap size	Library size	Poisson distribution, ChIP norm. counts in possible island against Control norm. counts	n	y	n	FDR	19505939
<u>MACS2</u>	Not required	Library size	Computation of log10 likelihood ratios and setting a pre-defined cutoff for following comparisons: Cond1 > Cond2 and Cond1 > Control1 Cond1 < Cond2 and Cond2 > Control2	y	y	n	log10 likelihood ratio	18798982
<u>ODIN</u>	Not required	- SES normalization (ChIP / input) combined with input subtraction - Library size normalization (Cond1 / Cond2)	Hidden Markov Model (HMM) with a three state topology Emissions are calculated with a Binomial or a mixture of Poisson distribution	y	y	n	p-value	25371479
<u>RSEG</u>	Not required	-	Hidden Markov Model (HMM) with a three state topology NBDiff distribution is used to model read count differences between both conditions	n	y	n	-	21325299
<u>MAnorm</u>	Requires peak calling e.g. with MACS	Genome-wide MA plot combined with LOWESS Regression	Bayesian model approach	y	y	n	p-value	22424423
<u>HOMER</u>	Window based approach; Peak calling done by HOMER	Library size normalization	Fold-change thresholding combined with a Poisson distribution based enrichment analysis	y	y	n	FDR or p-value	20513432
<u>QChIPat</u>	Peak calling possible with BELT, MACS, SISSRs or FindPeaks	1) Nonparametric empirical Bayes correction normalization 2) Quantile normalization 3) Linear normalization	1) Wilcoxon rank sum test 2) Wilcoxon signed rank test	y	y	n	p-value	24564479
<u>diffReps</u>	Sliding window approach	Linear normalization	- Without replicates: G-test or Chi-square test - Replicates: exact negative binomial test	n	y	y/n	p-value	23762400
<u>DBChIP</u>	Requires peak calling e.g. with MACS	median ratio strategy (DESeq)	Generalized linear model with negative Binomial distribution	y	n	y/n	FDR	22057161
<u>ChIPComp</u>	Requires peak calling e.g. with MACS	Normalization with a Poisson distribution based model	Wald's test followed by probability calculation Using a Bayesian approach	y	n	y	Posterior probability	25682068
<u>MultiGPS</u>	Expectation maximization learning scheme	edgeR		y	n	y	p-value	24675637
<u>MMDiff</u>	Requires peak calling e.g. with MACS	DESeq	Kernel-based non-parametric test	y	n	y	p-value	24267901
<u>DiffBind</u>	Requires peak calling e.g. with MACS	Differential peak analysis can be performed with: 1) DESeq 2) DESeq2 3) edgeR		y	y	y	p-value or FDR	22217937
<u>PePr</u>	Window based approach	Trimmed Mean of M values (TMM) approach (edgeR)	Binomial distribution	y	y	y	p-value	24894502