

Supplementary table 1. Comparison of available software similar to deepTools

Tool suite	web-server	if there is a webserver, can it be used without login?	Galaxy implementation	Parallelization	QC of BAM files (beyond FASTQC)	processing and normalization of BAM files	generates customizable images	allows for export of data	tutorial	Software	stand alone local installation	url
deepTools	yes	yes	yes	yes	yes	yes just	yes	yes	yes website not reachable	Galaxy & python	yes	http://deeptools.ie-freiburg.mpg.de
seqminer	no	--	no	yes	no	normalization	yes	yes	yes	Java	yes	http://bips.u-strasbg.fr/seqminer/
spark	yes	no	no	yes	no	no	no	yes	yes	Java	yes	http://www.sparkinsight.org/
CISTROME	yes	no	yes	no	no	no	limited	yes	Galaxy page	Galaxy, R, python	difficult	http://genomebiology.com/2011/12/8/r83
HOMER	no	--	no	no	yes	yes	no	yes	yes	perl	yes	http://homer.salk.edu/homer/chipseq/
NGS plot	no	--	yes	--	no	no	limited	images	no	R, python, perl	yes	https://code.google.com/p/ngsplot/
GeneProf	yes	not for analysis	no	--	no	yes	yes	yes	yes	Java, R, LaTeX	no	http://www.geneprof.org/