

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 normalization	yes	yes	yes website not reachable	Galaxy & python	yes	<a href="http://deeptools.ie-freiburg.mpg.de">http://deeptools.ie-freiburg.mpg.de</a>
seqminer	no	–	no	yes	no	no	yes	yes	yes	Java	yes	<a href="http://bips.u-strasbg.fr/seqminer/">http://bips.u-strasbg.fr/seqminer/</a>
spark	yes	no	no	yes	no	no	no	yes	yes	Java	yes	<a href="http://www.sparkinsight.org/">http://www.sparkinsight.org/</a>
CISTROME	yes	no	yes	no	no	no	limited	yes	Galaxy page	Galaxy, R, python	difficult	<a href="http://genomebiology.com/2011/12/8/r83">http://genomebiology.com/2011/12/8/r83</a>
HOMER	no	–	no	no	yes	yes	no	yes	yes	perl	yes	<a href="http://homer.salk.edu/homer/chipseq/">http://homer.salk.edu/homer/chipseq/</a>
NGS plot	no	–	yes	--	no	no	limited	images	no	R, python, perl	yes	<a href="https://code.google.com/p/ngsplot/">https://code.google.com/p/ngsplot/</a>
GeneProf	yes	not for analysis	no	--	no	yes	yes	yes	yes	Java, R, LaTeX	no	<a href="http://www.geneprof.org/">http://www.geneprof.org/</a>

Supplementary table 2. Performance details of the deeptools Galaxy server.

Hardware	
processors	16
RAM	141 GB
storage (directly attached)	2 TB
Galaxy Performance Settings	
concurrent users	unlimited
CPU cores per job	6
concurrent jobs per user	1
concurrent jobs	2
queueing system	Galaxy built-in
Exemplary run time	
BAM file	170 M reads
BED file	10000 regions
bamCoverage	10 minutes
computeMatrix	1 minute