Epigenomics

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Supplementary Tables

A specific criteria is used for enclosure of tools in Epigenomics. Softwares which are included are due to these specific reasons:

- Publication Date
- Freeware License
- Linux Based
- Offline

Table 1. Epigenomics Selection Criteria.

Sr No.	Software Tools Names	Post Date (2014)	Free	Linux	Offline	Installed		
	DNA-Protein interactions							
		4C-seq analysis						
1	4C-ker [1]	✓	√	✓	✓	✓		
2	Basic4Cseq [2]	✓	\checkmark	✓	✓	✓		
3	FourCSeq [3]	✓	\checkmark	✓	✓	✓		
4	fourSig [4]	✓	\checkmark	✓	✓	✓		
5	HTSstation [5]	✓	\checkmark	✓	✓	✓		
6	w4CSeq [6]	✓	\checkmark					
		5C-seq analysis						
7	HiFive [7]	✓	√	✓	✓	✓		
8	MCMC5C [8]		✓	✓	✓			
9	ShRec3D [9]	✓	✓	✓	✓	✓		
10	Sushi.R [10]	✓	✓	✓	✓	✓		
	3C-seq analysis							
11	chromoHBM [11]	✓	✓	√	√	√		
12	InfMod3DGen [12]	✓	✓	✓	✓	✓		
13	r3Cseq [13]		✓	✓	✓			

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Sr No.	Software Tools Names	Post Date (2014)	Free	Linux	Offline	Installed			
ChIP-on-chip analysis									
14	GeneNetworkBuilder [14]		✓	√	✓				
15	kmerHMM [15]		✓	✓	✓				
	ChIA-PET analysis								
16	Mango [16]	✓	✓	✓	√	✓			
17	3D-GNOME [17]	\checkmark	✓						
18	diffloop [18]	√	√	√	√	√			
19	ChiaSig [19]	√	 	√	√	✓			
20	Delta [20]	√ / / / / / / / / / / / / / / / / / / /	√						
		ChIP-exo analysis							
21	ChIP-nexus [21]	√	√	√	√	√			
22	PeakXus [22]	√	√	√	√	 			
23	CexoR [23]	√	√	√	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	√			
24	Q-nexus [24]		 	√	✓	√			
		otein interaction an							
		matin-state detection							
25	chromstaR [25]	\checkmark	✓	✓	✓	✓			
26	hiHMM [26]	\checkmark	✓	✓	✓	✓			
27	EpiCSeg [27]	\checkmark	✓	✓	✓	✓			
28	GenoSTAN [28]	√	✓ .	√	√	√			
29	Deopen [29]	√	√	✓		✓			
Histone modification prediction									
30	DeepChrome [30]	✓	✓						
31	Mutalisk [31]	√	✓						
32	DeepDiff [32]		√	√		√			
		Unclassified Tools							
33	TRX-LOGOS [33]	✓	✓	✓	✓	✓			
		tein interaction Dat							
		matin-state databas	ses						
34	Cistrome DB [34]	✓	✓						
	Histone	e modification predic	ction						
35	EpiFactors [35]	✓	✓						
36	dbHiMo [36]	\checkmark	✓						
37	WERAM [37]	✓	✓						
		tine interaction data	bases						
38	TFmapper [38]	✓	✓ _						
39	Multicontactchromatin [39]	\checkmark	✓						
40	3DGD [40]	√	√ .						
41	4DGenome [41]	√	 						
		leosome positioning	_						
		cleosome positioning			,				
42	nuMAP [42]	√	√						
43	iNuc-PseKNC [43]	√	√						
44	LeNup [44]	√	✓	✓	✓	✓			

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Sr No.	Software Tools Names	Post Date (2014)	Free	Linux	Offline	Installed
		ATAC-seq analysis	s			
45	SUSHI [45]	√	✓	✓	√	√
46	ATACseqQC [46]	✓	✓	✓	✓	✓
	Chromat	in accessibility and	ΓF Act	ivity		
47	I-ATAC [47]	√	√	√		
48	HMMRATAC [48]	✓	✓	✓	✓	✓
49	MMARGE [49]	✓	\checkmark	✓	✓	✓
50	DAStk [50]	✓	✓		✓	
51	DeepATAC [51]	✓	✓	✓	✓	✓
	sing	gle cell ATAC-seq ar	alysis			
52	chromVAR [52]	✓	✓	✓	✓	✓
53	cisTopic [53]	✓	✓	✓	✓	✓
54	plate-scATAC-seq [54]	✓	\checkmark	✓	✓	✓
	E	Bioinformatics workfl	ows			
55	atacR [55]	_	√	√	√	√
56	ATAC-pipe [56]	✓	✓	✓	✓	✓
57	esATAC [57]	✓	✓	✓	✓	✓
		Bioinformatics to	ols			1
	Epi_{i}	genome Data Visual	ization			
	Tag	density plot visuali	zation			
58	ngs.plot [58]	√		√	√	
59	ChIPseeker [59]	✓	✓	✓	_	✓
60	SeqPlots [60]	✓	✓	✓		
61	metaseq [61]	✓	✓	✓	✓	✓
62	iTagPlot [62]	✓	✓	✓	✓	✓
		Venn diagram creati	on.			
63	gplots [63]	√	√	√	√	√
64	eulerAPE [64]	√	✓	✓		
65	jvenn [65]	✓	✓			
66	Vennerable [66]		✓	✓	_	
67	OrthoVenn [67]	✓	✓			
68	GeneVenn [68]		✓			
69	venneuler [69]		✓	/	_	
70	Anduril [70]		✓	✓	_	
71	VennMaster [71]		√	/	_	
72	VENNTURE [72]		✓			
73	CanvasXpress [73]	√	✓	✓	_	✓
74	VennBLAST [74]		✓			
75	canvasDesigner [75]		✓			
76	BioVenn [76]		✓			
77	AnyExpress [77]		✓	✓		
78	DrawVenn [78]		<i>\</i>	\ \ \		
79	NeuVenn [79]	√	<i>\</i>			
		A methylation visual	-	<u> </u>	<u> </u>	<u> </u>
80	EpiExplorer [80]		\square \square \q			
81	CpGviewer [81]		√			
01	Charlemer [91]			1		

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Sr No.	Software Tools Names	Post Date (2014)	Free	Linux	Offline	Installed
82	VizHub [82]	✓	✓			
83	methyAnalysis [83]		✓	✓	✓	
84	MethylViewer [84]		✓	✓	✓	
85	methVisual [85]		✓	✓	✓	
86	Epiviz [86]	✓	✓			
87	MethPat [87]	_	/		_	
88	TABSAT [88]	_	/			
89	Epigenomics in JBrowse [89]	_	/	/	✓	√
90	iMethy [90]		/	/	_	
91	Methylyzer [91]		/			
92	BSviewer [92]	_		/	_	
93	MeViz [93]		/			_
94	chroGPS [94]	·	/			·
95	MassArray [95]		/			
96	MethTools [96]		/	\ \ \		
97	Methylmapper [97]		/	\ \ \ \ \	\ \ \ \	
31	V 11 L J	Genome Viewers				
98	EMBOSS [98]	Cononio Flowers				
99	GBrowse [99]		/		_	
100	JBrowse [100]		\ \ \		V	
100	rtracklayer [101]		\ \ \ \			
102	ZENBU [102]		\ \ \ \			
102	ggbio [103]	V	\ \ \ \		/	
103	ggblo [103] Apollo [104]		\ \ \ \		√	
104	GenePlotter [105]		\ \ \ \	\ \frac{1}{3}	√ √	
105					V	
	Fastbreak [106]	,	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \			
107	Microreact [107]	√	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \			
108	GenomeView [108]		\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \		
109	gaggle [109]		√	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	,	
110	GenomeGraphs [110]	,	√	√	√	
111	GenVisR [111]	√	√	√		
112	GenomeJack [112]		√	√		
113	GenPlay [113]		√	√	,	
114	SynTView [114]		√	✓	✓	
115	FriPan [115]		✓			
116	IGV [116]	,	<			
117	Circleator [117]	✓	/	√	✓	√
118	GenePalette [118]			√		
119	VisSR [119]		✓	/		
120	3D Genome Browser [120]	✓	✓			
121	TASUKE [121]		✓	✓		
122	Gff2ps [122]		✓	✓	✓	
123	CisGenome Browser [123]			✓		
124	Trackster [124]		✓			
125	Genewindow [125]		✓			
126	IRscope [126]	✓	✓			
127	WiggleTools [127]		✓	✓		
128	Biodalliance [128]	✓	✓			
129	DensityMap [129]		✓			

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Sr No.	Software Tools Names	Post Date (2014)	Free	Linux	Offline	Installed
130	BasePlayer [130]	✓	✓	✓		
131	ColoWeb [131]	✓	✓			
132	GenomicInteractions [132]		✓	✓	✓	
133	PlasmaDNA [133]		✓			
134	EPIC-CoGe [134]	✓	✓			
135	OmicBrowse [135]		✓		✓	
136	Cosmoss [136]		✓			
137	Pairoscope [137]		✓	✓	✓	
138	BugView [138]		✓	✓		
139	HiCBrowser [139]	✓	✓	✓	✓	✓
140	GenomePlot [140]			✓	✓	
141	chromPlot [141]	✓		✓	✓	
142	caOmicsV [142]	✓	✓	✓	✓	✓
143	karyoploteR [143]	✓	✓	✓	✓	✓
144	VisualRepbase [144]		✓	✓		
145	PopFly [145]		✓			
146	PBrowse [146]	✓	✓			
147	myGenomeBrowser [147]	✓	✓			
148	GUPPY [148]			✓	✓	
149	tracktables [149]	✓	✓	✓	✓	✓
150	gFACs [150]		✓	✓	✓	
151	Scribl [151]		✓	✓	✓	
152	Idiogram [152]		✓	✓	✓	
153	gtrellis [153]	✓	✓	✓	✓	✓
154	GeneViTo [154]			✓		
155	epiTAD [155]	✓	✓			
156	Skittle [156]		✓			
157	ERGO [157]			✓		
158	Blobsplorer [158]		✓	✓	✓	
159	SeqBox [159]	✓			✓	
160	ZMap [160]		✓	✓	✓	
161	CrossBrowse [161]	✓	✓	✓		
162	GenomeHubs [162]	✓	✓	✓	✓	✓
163	AncestryView [163]	✓	✓	✓	✓	✓
164	SeqGenome Browser [164]		✓	✓		
165	PopHuman [165]	✓	✓	✓		
166	Savant [166]		✓	✓		
167	D3GB [167]	✓	✓	✓		
168	PoGo [168]		✓	✓	✓	
169	chromoMap [169]	✓	✓	✓	✓	✓
170	Squiggle [170]	✓	✓	✓	✓	✓
171	MitoZ [171]	✓	✓	✓	✓	✓
172	Artemis [172]		✓	✓		
173	ASCIIGenome [173]	✓	✓	✓	✓	✓
174	kmerPyramid [174]	✓	✓	✓	✓	✓
175	Paplot [175]	√	✓	✓	✓	✓
176	bulkVis [176]	✓	✓	✓	✓	✓
177	FluentDNA [177]		✓	√	√	
178	genomeview [178]	✓	✓	✓	✓	✓

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Sr No.	Software Tools Names	Post Date (2014)	Free	Linux	Offline	Installed
179	GC-Profile [179]		√			
180	GeneTrack [180]		✓	✓	√	
181	Genome2D [181]		✓	✓		
182	GenomeComp [182]		√			
183	HiView [183]		<i>\</i>	ľ		
184	my5C [184]	•	\ \ \			
185	ViewGene [185]		ľ	_		
186	chromoWIZ [186]		/	v	•	
187	MetaLook [187]	V	\ \ \	_		
188	LocusView [188]		\ \ \	· ·	√	
189	ABrowse [189]		\ \ \	✓	V	
190	GraphDNA [190]		\ \ \	\ \ \		
190		igan ama data anniah		V		
		notype enrichment a				
101		/		/	/	/
191	PrediXcan [191]	√	√	✓	✓	✓
192	MamPhEA [192]	,	√	,	,	,
193	PhenoNet [193]	√	√	✓	\checkmark	√
194	POEAS [194]	√	√	,	,	,
195	Phenopredict [195]	√	√	✓	✓	✓
196	DroPhEA [196]		✓.			
197	modPhEA [197]	✓	✓			
198	PhenotypeSeeker [198]	✓	✓	✓	✓	✓
	M	lotif enrichment ana	lysis			
199	MEME-ChIP [199]		✓			
200	CentriMo [200]	✓	✓			
201	BaMM!motif [201]	✓	✓	✓	✓	✓
202	Clover [202]		✓	✓	✓	
203	PASTAA [203]		✓	✓	✓	
204	CENTDIST [204]		✓			
205	GOMo [205]			✓	\checkmark	
206	i-cisTarget [206]		✓			
207	PWMEnrich [207]		√	_	✓	
208	RTFBSDB [208]	√	✓	✓	✓	✓
209	hiddenDomains [209]	_	✓	✓	✓	✓
210	GANN [210]	·	1			·
211	Regmex [211]		<i>\</i>	√	√	1
212	POIMs [212]	_	\ \ \			•
213	GenFam [213]	./	✓ ✓		v	
213	LocaMo Finder [214]	V	✓ ✓			
1	1	/		/	/	/
215	chequeR [215]	√	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	√	√	√
216	winflat [216]	,	√	√	√	
217	JFreq [217]	√	√	√	,	
218	GenometriCorr [218]		√	✓	✓	
219	PscanChIP [219]	,	√		,	,
220	LOLA [220]	√	√	√	✓	✓
221	DRIMust [221]		✓.			
222	genomation [222]	√	✓	✓	✓	✓
223	EDD [223]	✓	✓			

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Sr No.	Software Tools Names	Post Date (2014)	Free	Linux	Offline	Installed
224	ChIP-Part [224]		✓			
225	LONUT [225]		✓	✓	_	
226	MUSIC [226]	_	√	✓	_	
227	MSR [227]		√	√	_	
228	GREAT [228]		√	-		-
229	RECAP [229]		√	✓	_	
230	Bedsect [230]	, 	√		·	
		er-representation an				
231	DAVID [231]	-	√			
232	Blast2GO [232]			✓		
233	BiNGO [233]		✓	✓		
234	WEGO [234]		✓			
235	WebGestalt [235]		✓			
236	GOseq [236]		✓	✓	_	
237	ClueGO [237]			✓		
238	GOstats [238]		✓	✓	_	
239	GenMAPP [239]		✓	✓		
240	GOstat [240]		√	-		
241	Babelomics [241]	_	√	√	_	
242	GoMiner [242]	·	√	<i></i>		
243	GOEAST [243]		√ ·		·	
244	FuncAssociate [244]		√ ·			
245	ArrayTrack [245]		<i>\</i>			
246	FunSpec [246]		\ \ \			
247	GO-Elite [247]		\ \ \	✓	_	
248	GOAtools [248]	_	\ \ \	√	\ \ \ \	
249	PageMan [249]	V	\ \ \	<i></i>	'	·
250	STEM [250]			√	√	
251	ErmineJ [251]		/	\ \ \ \	\ \ \ \	
251 252	CARMAweb [252]		\ \ \		'	
252 253	Onto-Tools [253]		\ \ \			
253 254	EasyGO [254]		√			
$\begin{array}{ c c c }\hline 254 \\ 255 \\ \end{array}$	CisFinder [255]		√	✓	_	
$\frac{255}{256}$	GOFFA [256]		✓ ✓	✓ ✓	√	
257	GOFFA [250] GOHyperGAll [257]		✓ ✓	✓ ✓	\ \ \ \ \	
257 258	BayGO [258]		✓ ✓			
258 259	MET [259]		✓ ✓			
$\frac{259}{260}$	ME1 [239] Categorizer [260]	√ √	✓ ✓	✓	_	_
260	goCluster [261]	<u> </u>	✓ ✓	✓ ✓		
261	goCluster [261] myTAI [262]	\		✓ ✓		,
		√	✓ ✓	✓ ✓	√ √	
263	MOTVIS [263]	/				
264	RegulatorTrail [264]	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	√	,		
265	GOexpress [265]	√	√	√	√	
266	REA [266]		\	√		
267	GOTM [267]		\			
268	ProbCD [268]		√	,	,	,
269	mvGST [269]	√	√	✓	√	
270	OE2GO [270]		√		✓	

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Sr No.	Software Tools Names	Post Date (2014)	Free	Linux	Offline	Installed		
	Topology enrichment analysis							
271	ChIPseeqer [271]		√	√	√			
272	HOMER [272]		✓	✓	✓			
273	TopGO [273]		✓		✓			
274	GeneCodis [274]		✓					
275	CHRONOS [275]	✓	✓	✓	✓	✓		
276	Ontologizer [276]		✓	✓	✓			
277	SPIA [277]		✓	✓	✓			
278	GOSim [278]		✓	✓	✓			
279	EnrichNet [279]		✓					
280	SubpathwayMiner [280]		✓	✓	✓			
281	ProfCom [281]		✓					
282	NOA [282]		✓	✓				
283	PathNet [283]	✓	✓	✓	✓	✓		
284	BrainCell [284]	✓	✓	✓	✓	✓		
285	NetGSA [285]	✓	✓	_	✓	✓		
286	sLDA [286]		√	_	✓			
287	DEGraph [287]		/	_	✓			
288	GANPA [288]		/		√			
289	EnrichmentBrowser [289]	_	/			 		
290	TEAK [290]	, v	\ \ \		·	•		
291	ToPASeq [291]		\ \ \		✓	√		
292	topologyGSA [292]		\ \ \		\ \ \			
293	CePa [293]	V	\ \ \	\ \ \ \	\ \ \	'		
294	timeClip [294]	√	\ \ \	\ \frac{\sqrt{1}}{\sqrt{1}}	./	./		
295	PI [295]	√	\ \ \			·		
296	ICoVeR [296]		\ \ \		√			
297	AMBIENT [297]	V	\ \ \ \		/	·		
298	AMDIENT [297] ADGO [298]		✓ ✓		V			
					/			
299	ACST [299]	,	√	√	√			
300	MORPH [300]	√	√	√				
		ial motif enrichment	analys	is				
301	MultiGPS [301]	✓	✓	✓	✓	✓		
302	SANEFALCON [302]	✓		✓	✓			
303	MuSERA [303]	✓						
304	DChIPRep [304]	✓	✓	✓	✓	✓		
305	SignalSpider [305]	✓	✓	✓	✓	✓		
306	Jmosaics [306]		✓	✓	✓			
307	ChIPdig [307]	✓	✓	✓				
	Gene	set enrichment ana	lysis					
308	limma [308]		√	✓	✓			
309	edgeR [309]		✓	✓	✓			
310	DESeq2 [310]	✓	✓	✓	✓	 		
311	GSEA [311]		✓	_	✓			
312	xCell [312]	✓	✓					
313	KOBAS [313]		√					
314	KAAS [314]		/					
315	BaseSpace [315]	_		_	_			
	F []	l	L		l			

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Sr No.	Software Tools Names	Post Date (2014)	Free	Linux	Offline	Installed
316	Strand NGS [316]	✓		√		
317	GSVA [317]		✓	✓	✓	
318	Pathview [318]		✓	✓	✓	
319	Gitools [319]		✓			
320	piano [320]		✓	✓	✓	
	DN	A Modifications			1	
	DNA	$Modification \ Analys$	is			
321	AltAnalyze [321]	✓	√	√	√	✓
322	scLVM [322]	✓	✓	✓	✓	✓
323	Repliscan [323]	✓	✓	✓	✓	✓
	DNA A	Modification Databas	ses			
324	GEO [324]	√	✓			
325	DevMouse [325]	✓	✓			
326	ViralEpi [326]	✓	✓			
327	dBEM [327]	✓	✓			
328	BLUEPRINT [328]		✓			
329	MethHC [329]	✓	✓			
330	iMETHYL [330]	✓	✓			
331	START [331]	✓	✓			
332	MethyCancer [332]		✓			
333	DNAmod [333]		✓			
334	BCaPE [334]	✓	✓			
335	EWASdb [335]	✓	✓			
336	MetaImprint [336]	✓	✓			
337	Geneimprint [337]		✓			
338	EICO [338]		✓			
339	FACER [339]	✓	✓			
	DNA me	ethylation array ana	lysis			
340	Marmal-aid [340]		✓	✓	√	
341	SCANN [341]		✓	✓	✓	
342	COHCAP [342]		✓	✓	✓	
343	MultiDataSet [343]	✓	✓	✓	✓	✓
344	MMCOP [344]	✓	✓			
345	ACES [345]		✓	✓	✓	
346	Clustrophile [346]		✓	✓	✓	
347	WFMM [347]		✓	✓	✓	
348	CpGassoc [348]		✓	✓	✓	
349	IMA [349]		✓	✓	✓	
		BS-seq analysis				
350	QUMA [350]		√			
351	RnBeads [351]	✓	✓	✓	✓	✓
352	BDPC [352]		✓ ·			
353	MethPipe [353]		✓ ·	_	✓	
354	SAAP-RRBS [354]		✓	_	_	
355	Genomic HyperBrowser [355]		✓ ·			
356	OTP [356]	✓	✓ ·			
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Sr No.	Software Tools Names	Post Date (2014)	Free	Linux	Offline	Installed			
	MeDIP-seq analysis								
357	MEDME [357]		✓	√	√				
358	RepiTools [358]		✓	✓	✓				
359	MeDUSA [359]		✓	✓	✓				
360	MeQA [360]		✓	✓	✓				
361	DISMISS [361]	✓	✓	✓	✓	✓			
	ox	BS/TAB/fCAB/CA	B-seq						
362	MOABS [362]	√	√	√	√	✓			
363	MLML [363]		✓	✓	✓				
	$Methyl Cap\text{-}seq\ analysis$								
364	Methylpy [364]		✓	✓	√				
365	MethylAction [365]	✓	✓	✓	✓	✓			

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