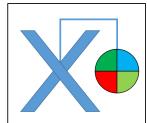


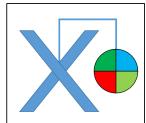
Analysis for LCL_ChIP_H3K27AC

Date: 19-October-2023



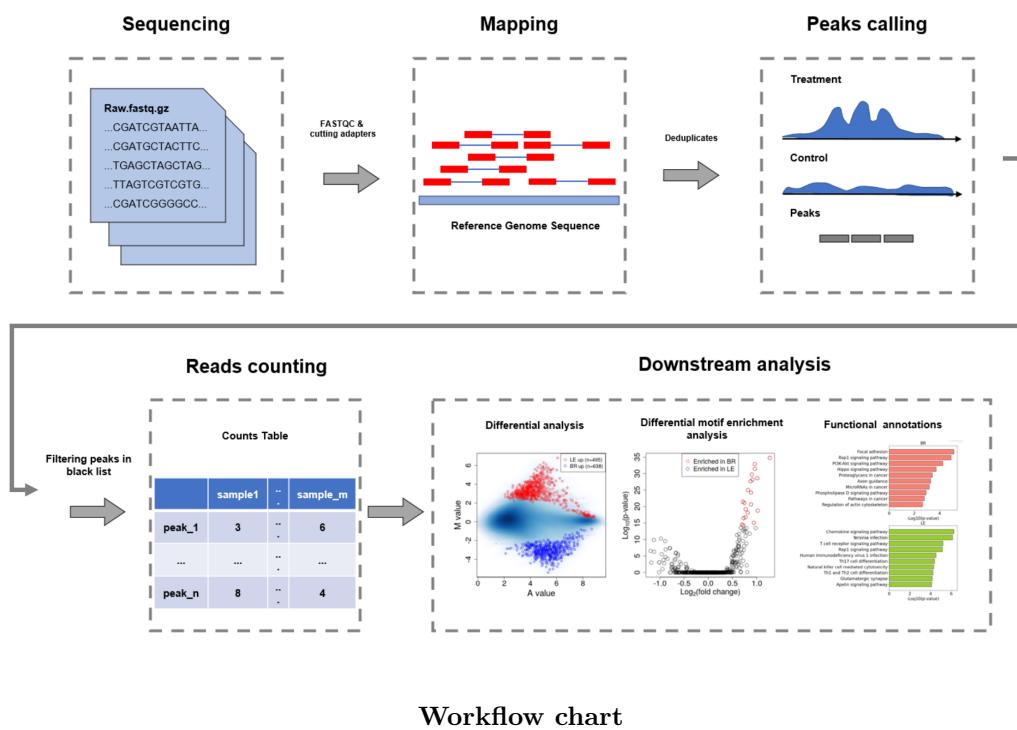
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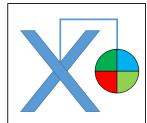


1 Introduction

In this analysis, we used FastQC for reads bases quality control and Trim-galore for cutting adapters and low quality bases in reads. Resulting ChIP/ATAC-seq reads were aligned to the user specified reference genome by using Bowtie. Then PCR duplicates were removed based on the genomic position. The remaining reads were used for peaks calling by using MACS. Finally, the count table was generated by using MAnorm2-utils. Downstream analyses were performed based on this count table (e.g. differential analysis, differential TF motif enrichment analysis and differential functional annotation). Users can further perform interactive analysis and customize their analysis by selecting an appropriate parameter (e.g. adjusted p-value cutoff, number of clusters) based on their context and requirements (Tools implemented in EAP).



Workflow chart



2 Quality control for bases

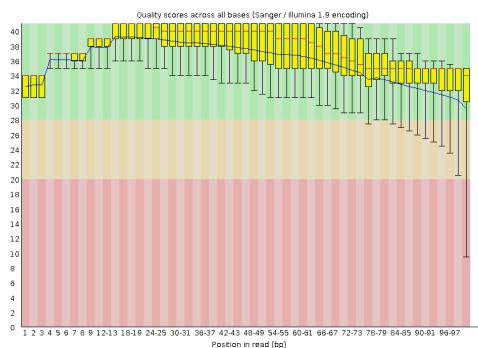
Here we showed the bases quality before and after trimming. Each plot shows the Q-scores in different positions on sequencing reads. Q-score represents base call quality, defined by the following equation: $Q\text{-score} = -10\log_{10}(e)$ where e is the estimated probability of the base call being wrong. Good quality (Illumina) is generally $Q\text{-score} > 28$. Concerning quality (Illumina) is $Q\text{-score} < 20$.

2.1 The figures below show the quality control of bases before and after trimming.

SRR1658122

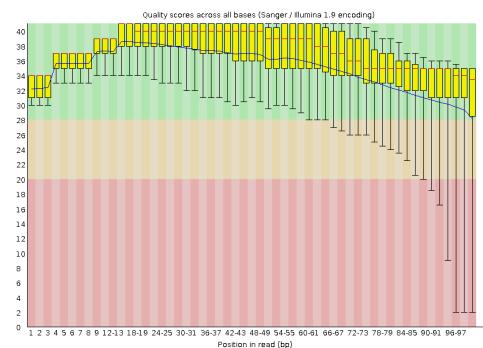
R1

Before trimming

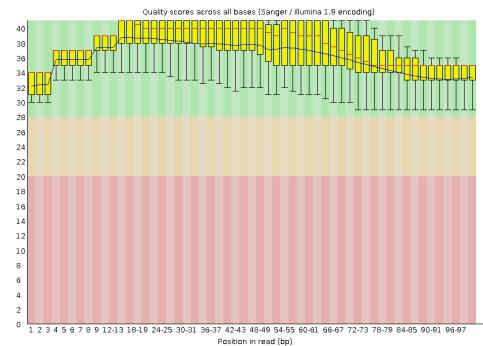
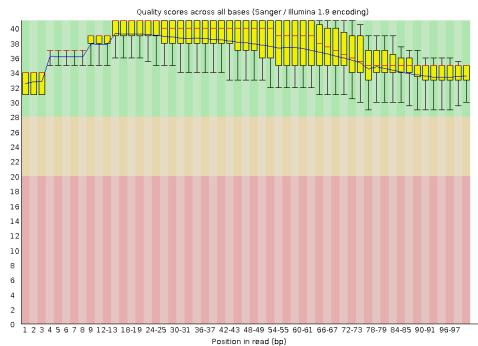


R2

Before trimming



After trimming

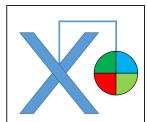


SRR1658320

R1

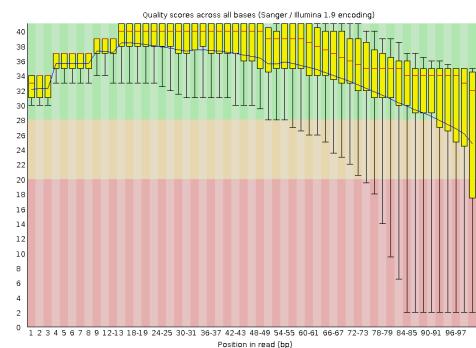
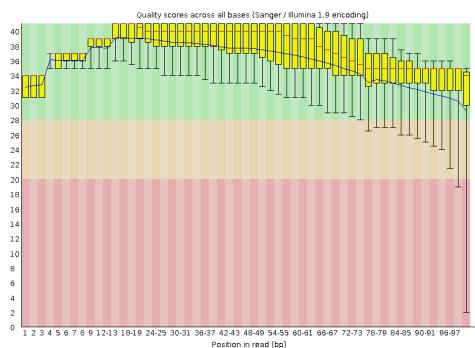
Before trimming

R2

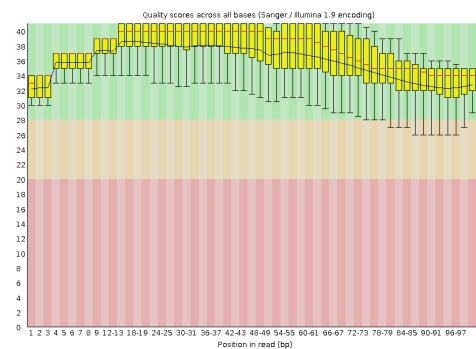
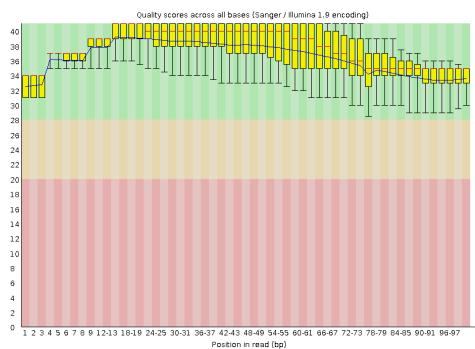


Epigenome Analysis Platform

Report



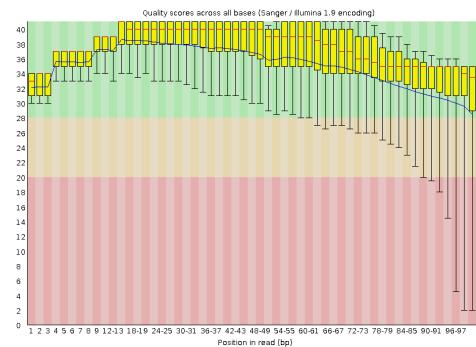
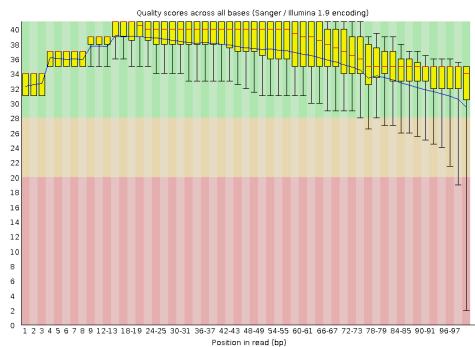
After trimming



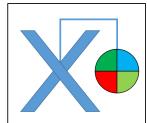
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R1

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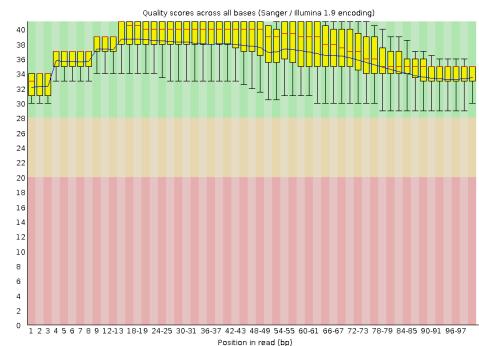
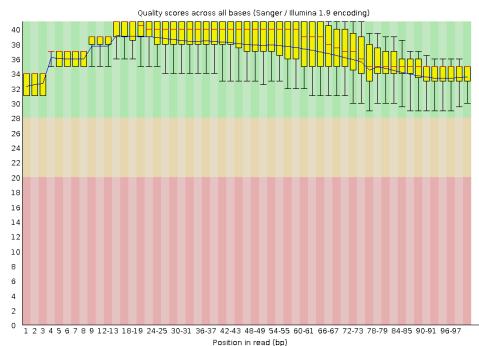


After trimming



Epigenome Analysis Platform

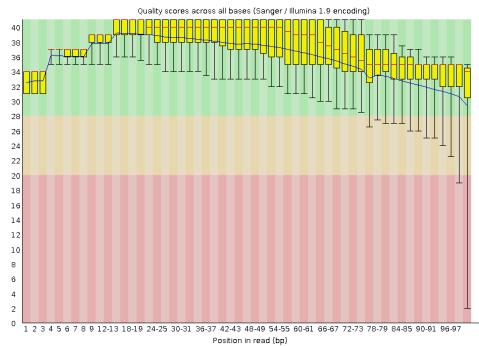
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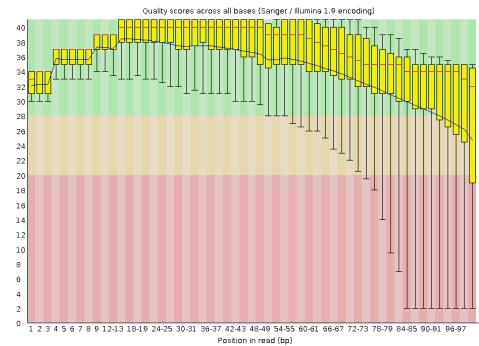
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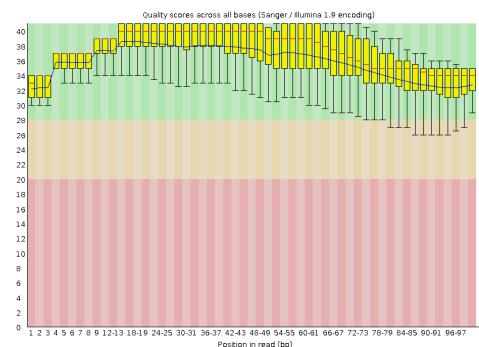
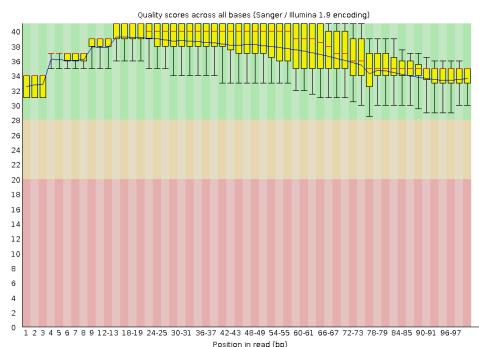
Before trimming



R2



After trimming

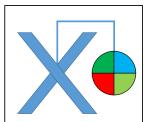


SRR1658311

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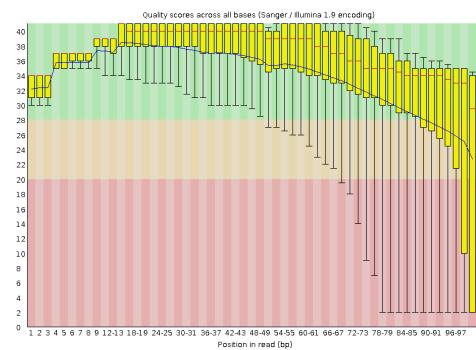
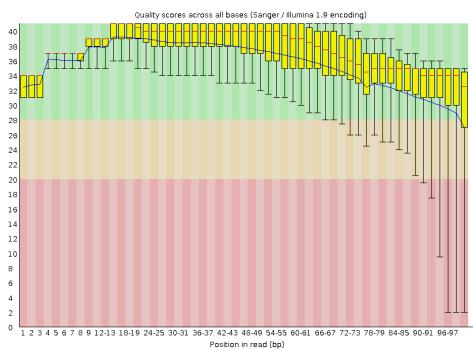
Before trimming

R2

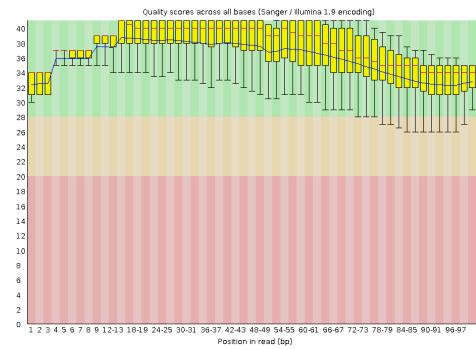
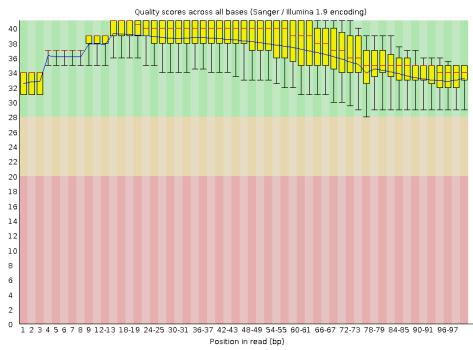


Epigenome Analysis Platform

Report



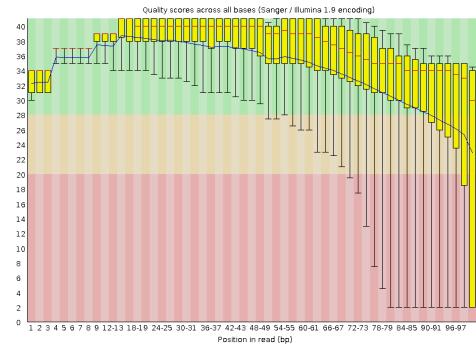
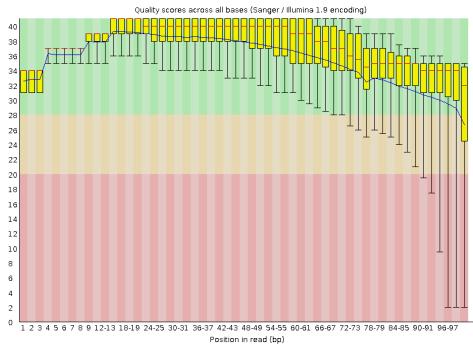
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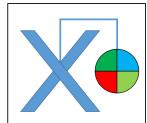
SRR1658328

R1

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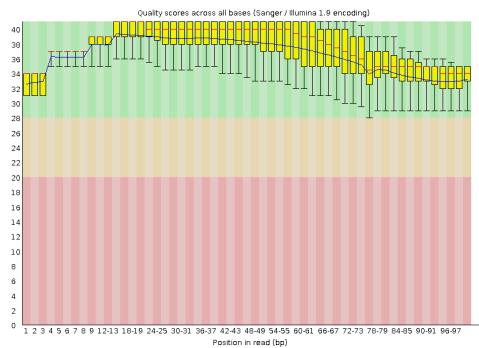


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Epigenome Analysis Platform

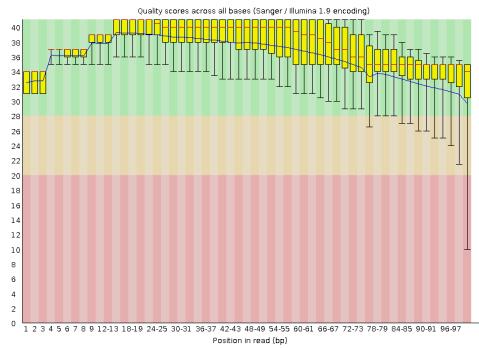
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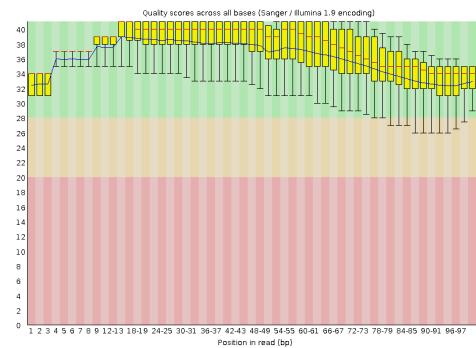
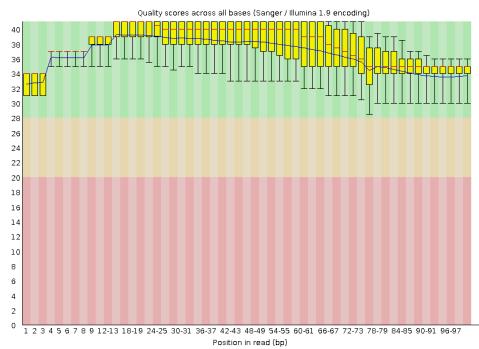
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R1

Before trimming



After trimming

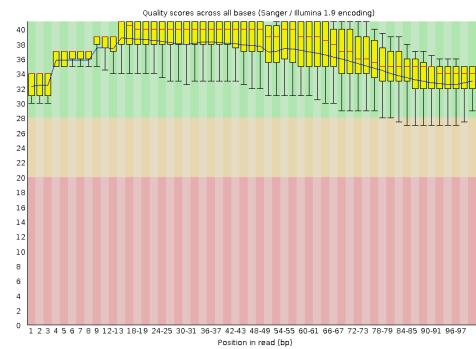


R2

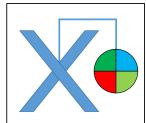
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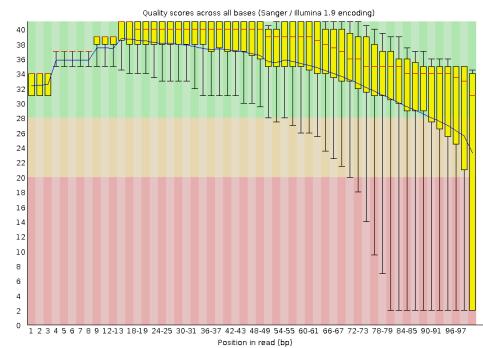
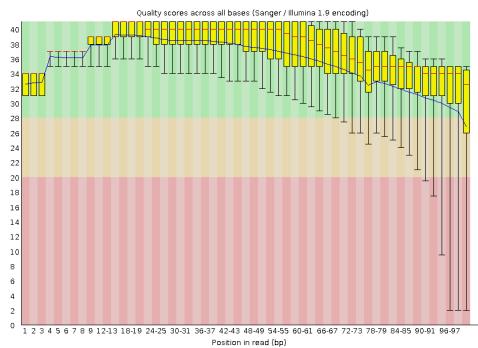


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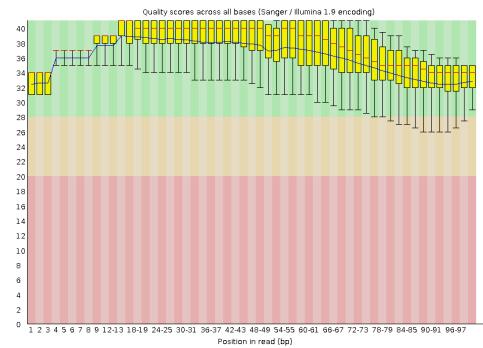
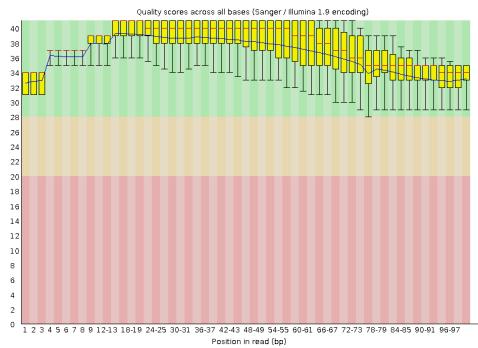


Epigenome Analysis Platform

Report



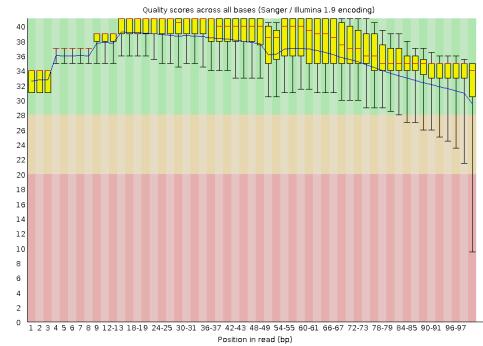
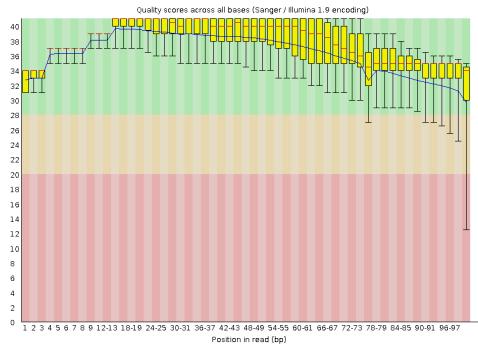
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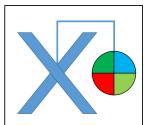
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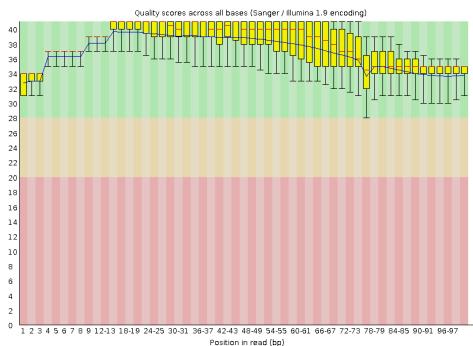


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Epigenome Analysis Platform

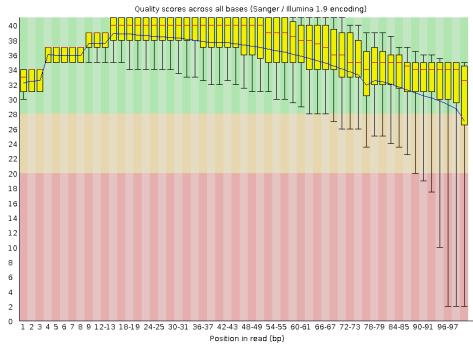
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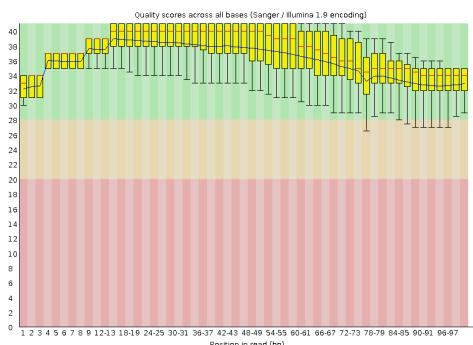
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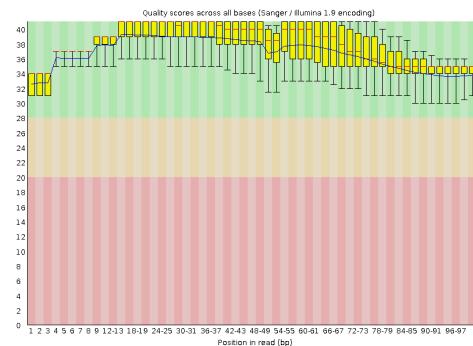
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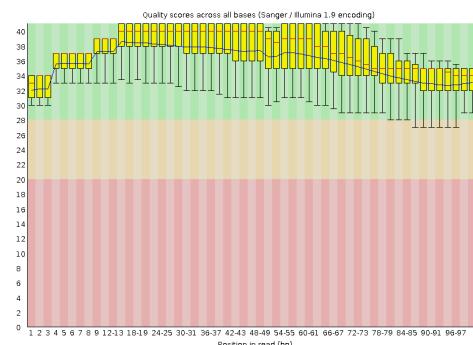
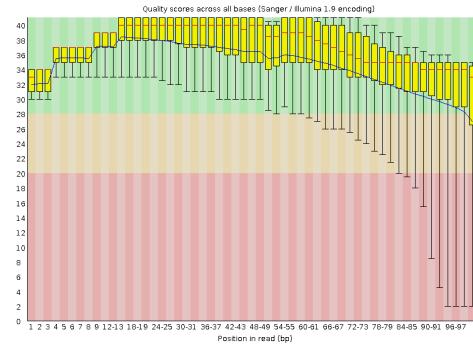
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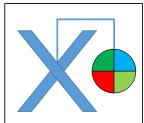
R1

Before trimming



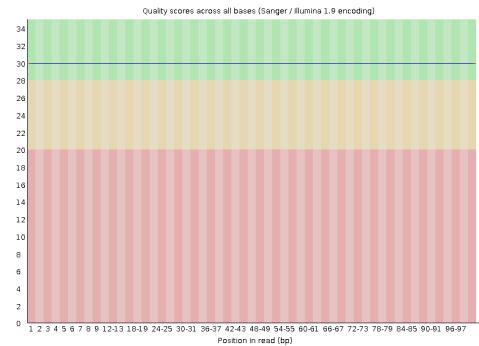
R2



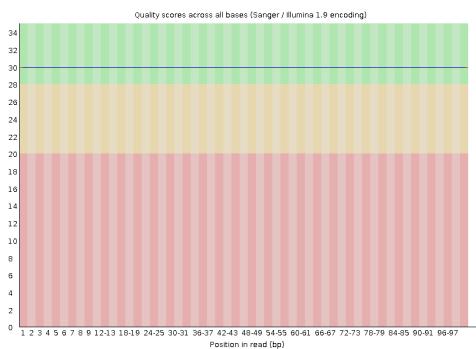


Epigenome Analysis Platform

Report



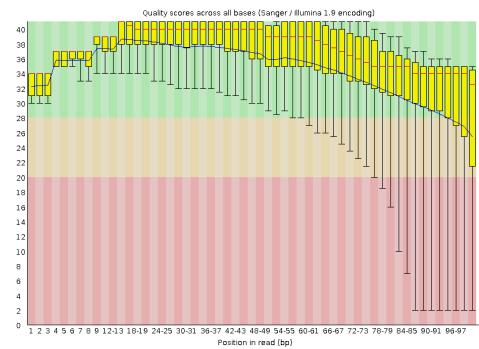
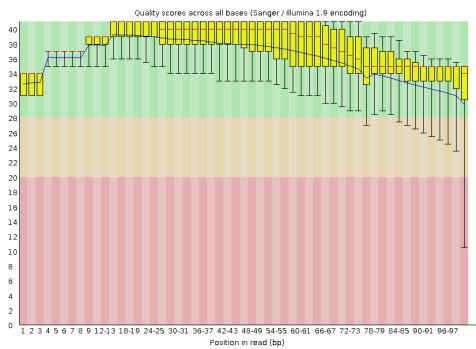
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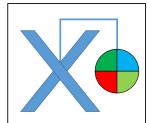
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R1

Before trimming

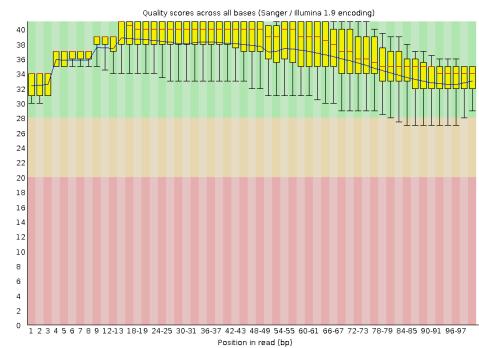
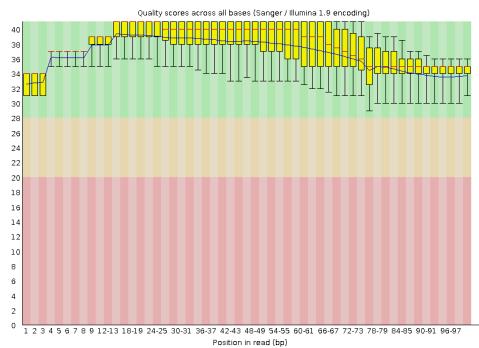


After trimming



Epigenome Analysis Platform

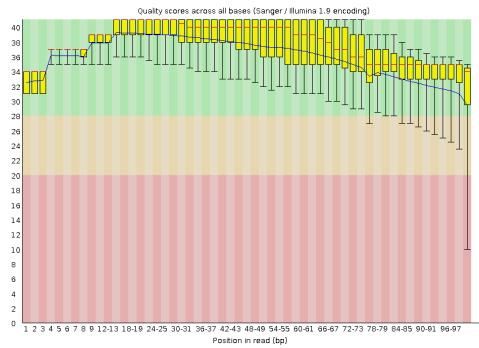
Report



SRR1658324

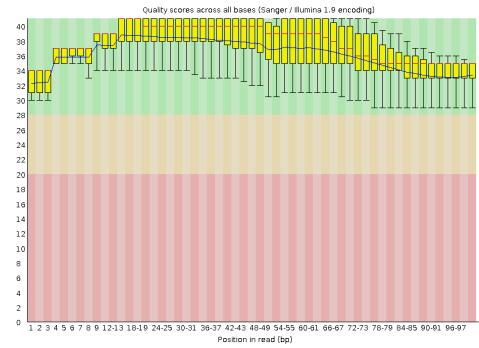
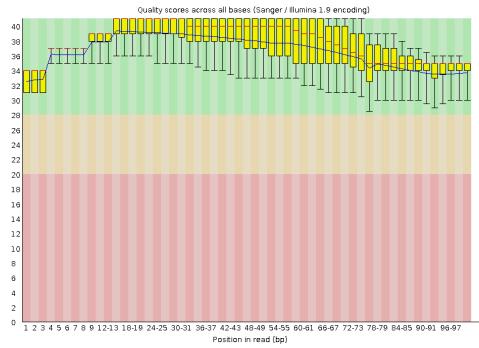
R1

Before trimming



R2

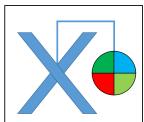
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SRR1658243

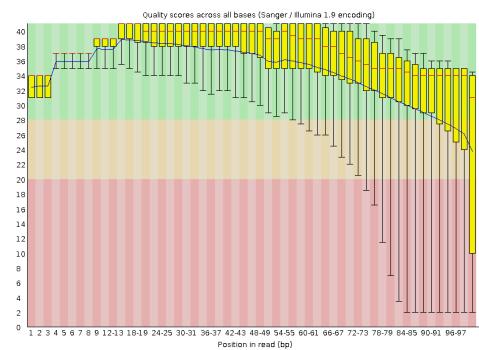
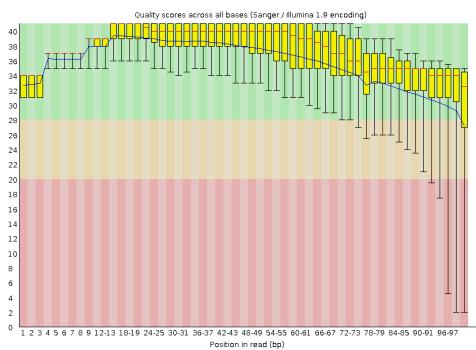
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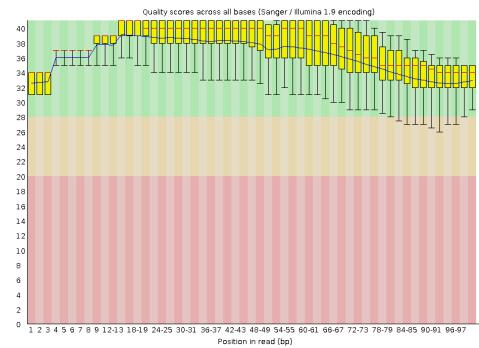
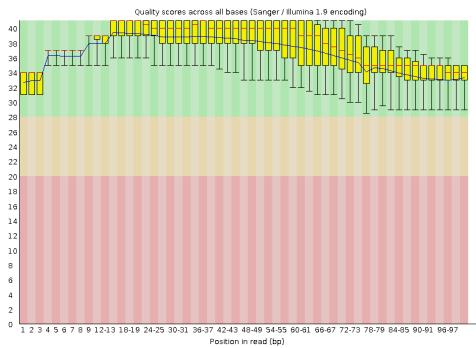


Epigenome Analysis Platform

Report



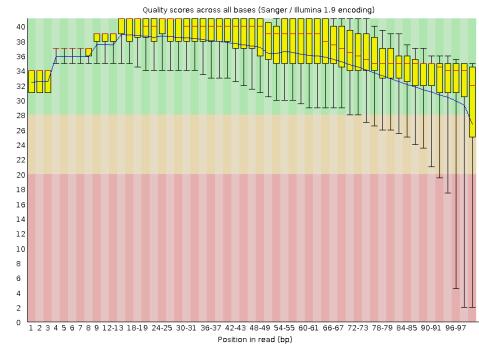
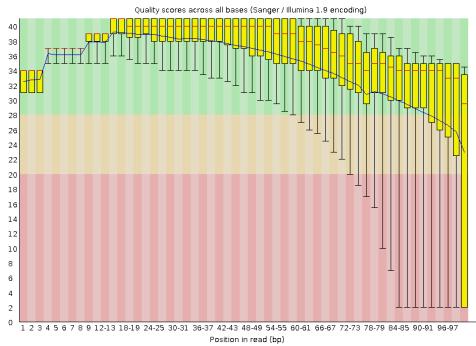
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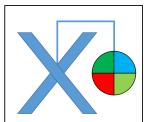
SRR1658306

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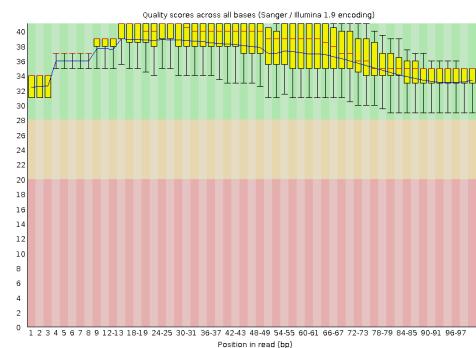
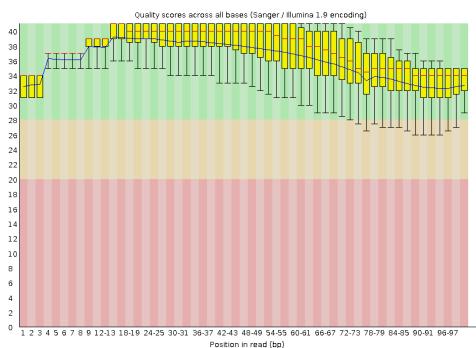


After trimming



Epigenome Analysis Platform

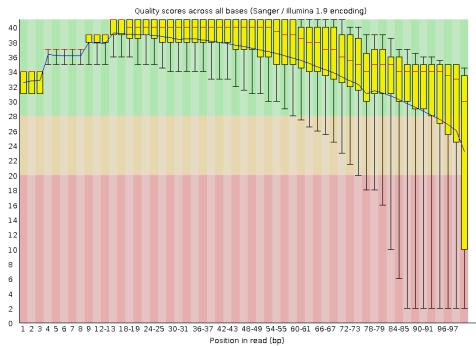
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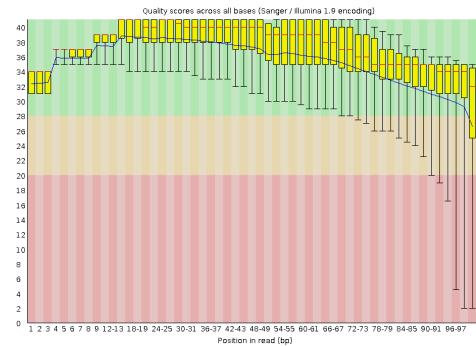
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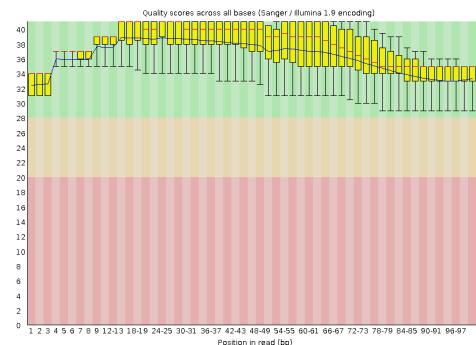
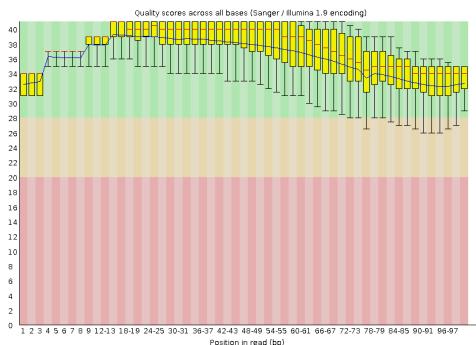
Before trimming



R2



After trimming

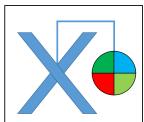


SRR1658270

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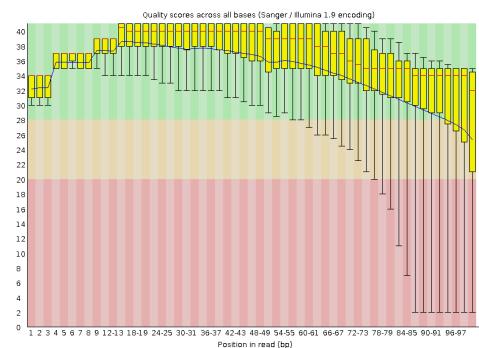
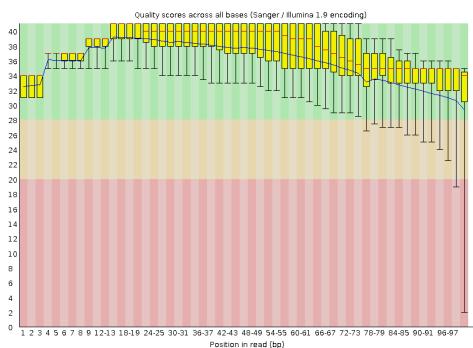
Before trimming

R2

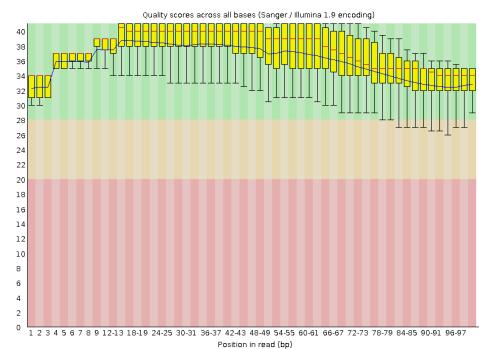
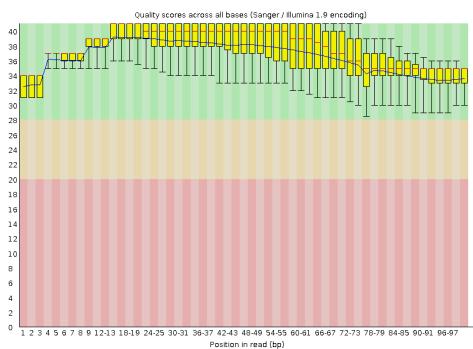


Epigenome Analysis Platform

Report



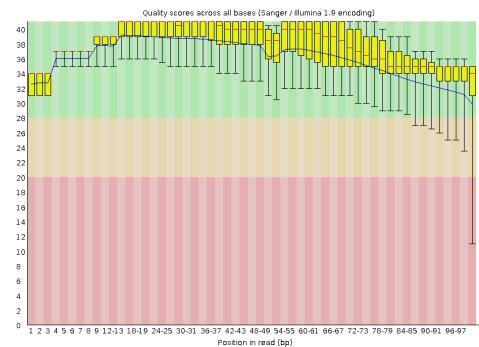
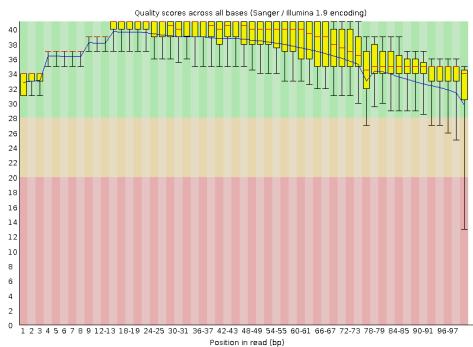
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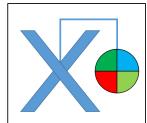
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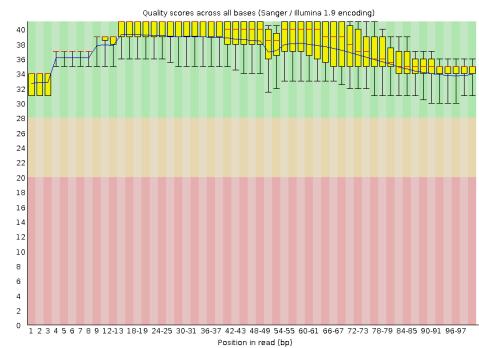
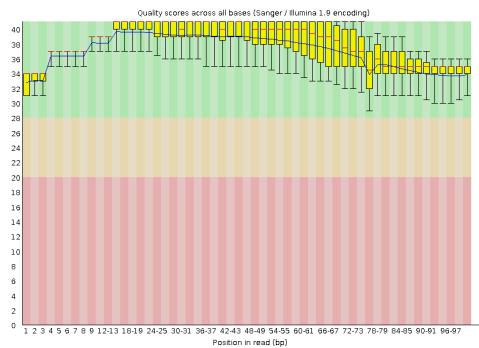


After trimming



Epigenome Analysis Platform

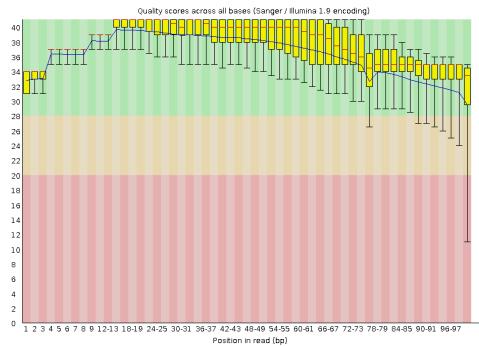
Report



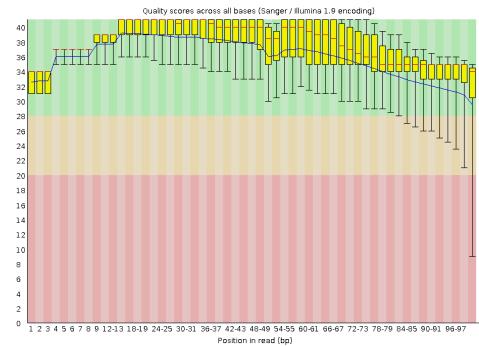
SRR1658296

R1

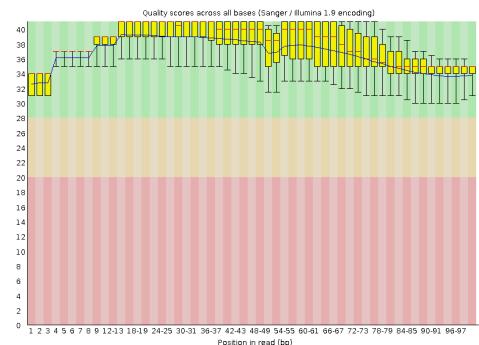
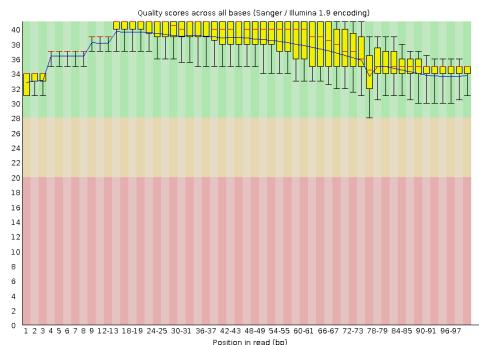
Before trimming



R2



After trimming

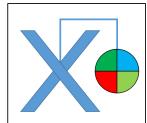


SRR1658197

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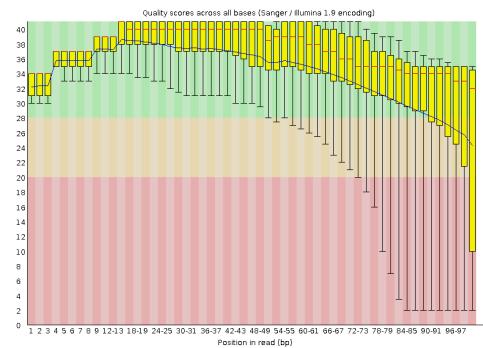
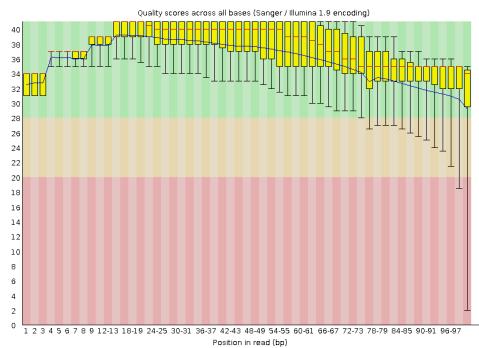
Before trimming

R2

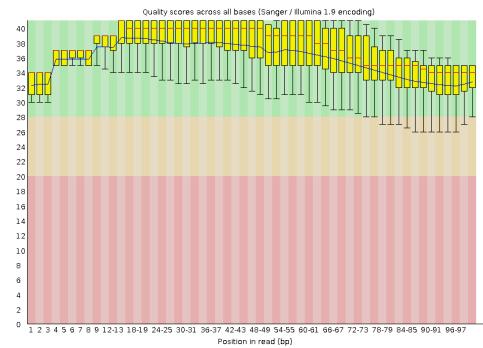
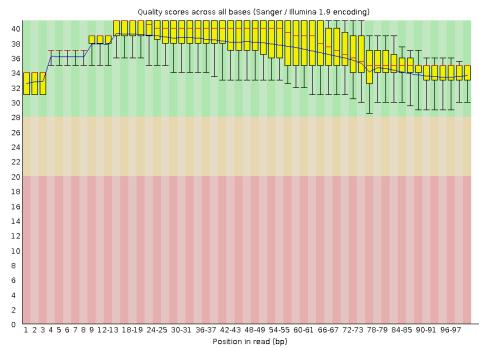


Epigenome Analysis Platform

Report



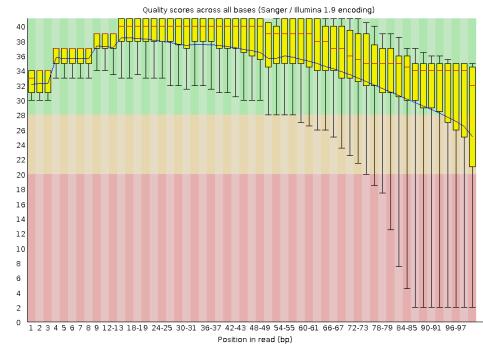
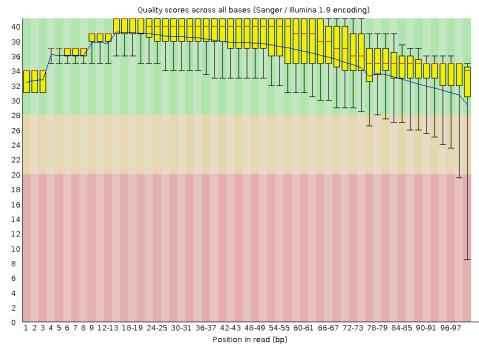
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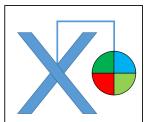
SRR1658278

R1

Before trimming

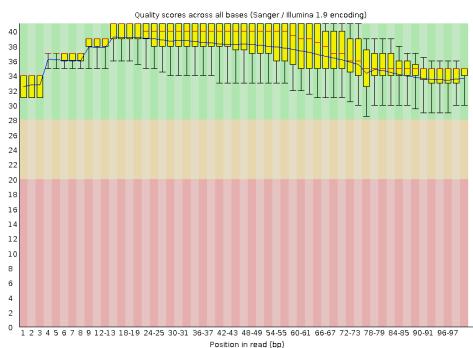


After trimming



Epigenome Analysis Platform

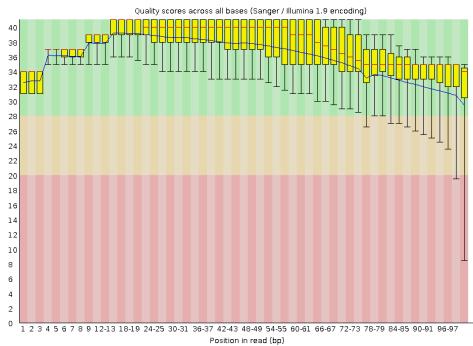
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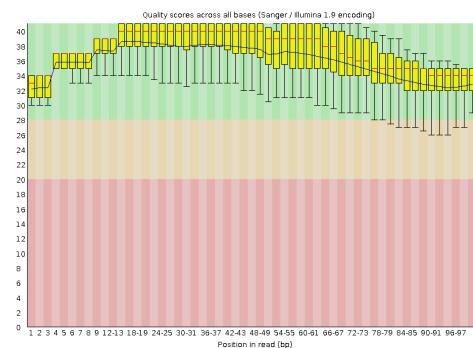
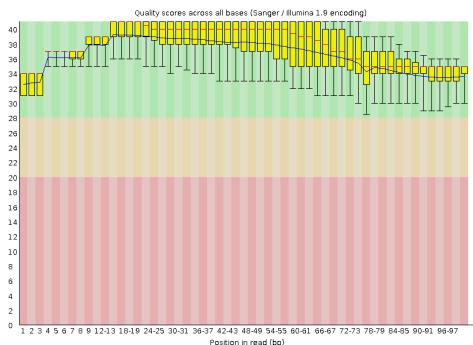
SRR1658205

R1

Before trimming



After trimming

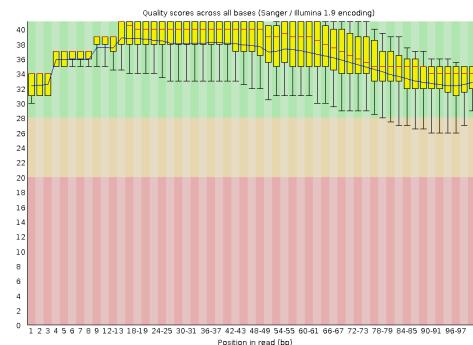
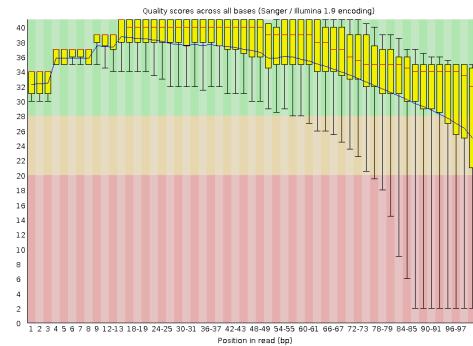


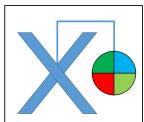
R2

SRR1658142

R1

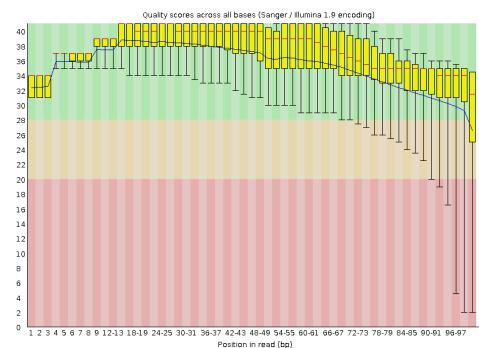
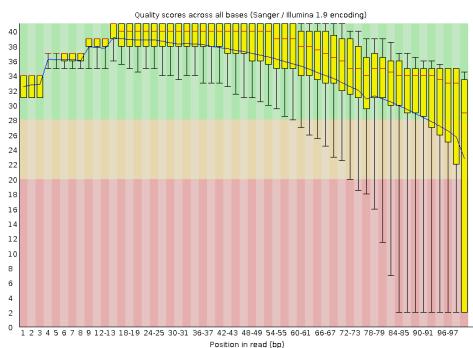
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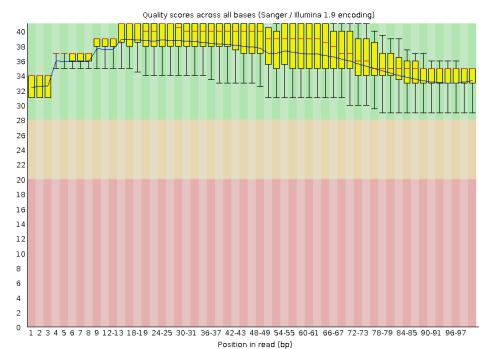
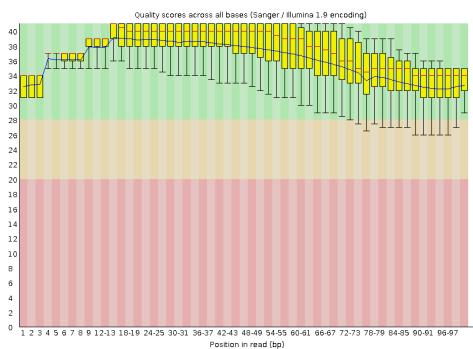


Epigenome Analysis Platform

Report



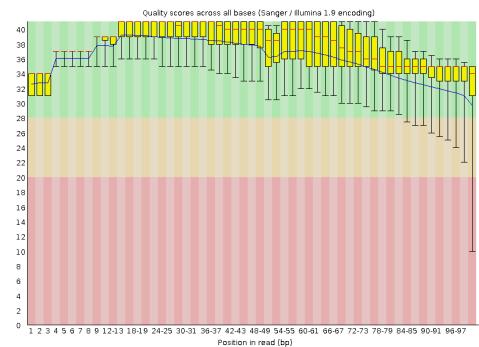
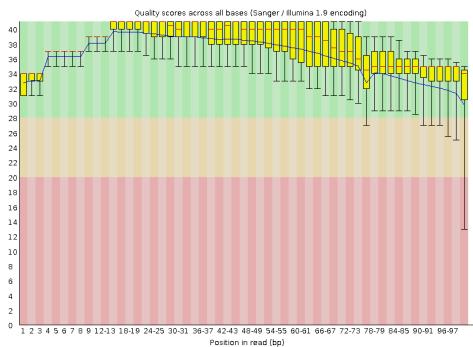
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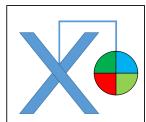
SRR1658340

R1

Before trimming

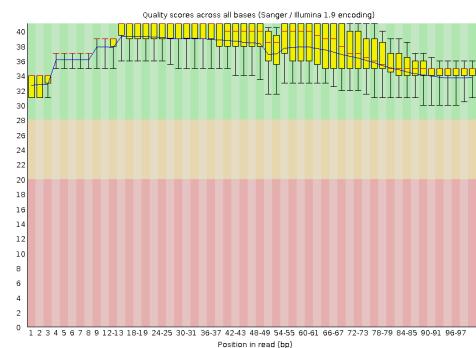
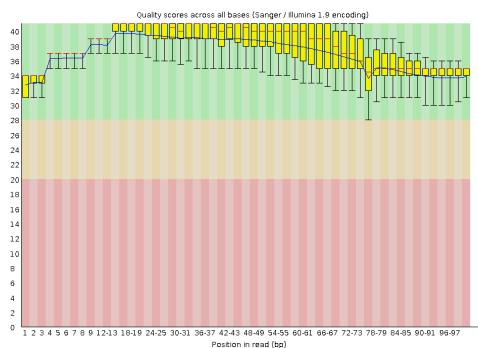


After trimming



Epigenome Analysis Platform

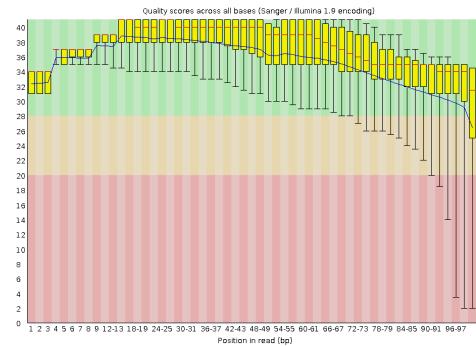
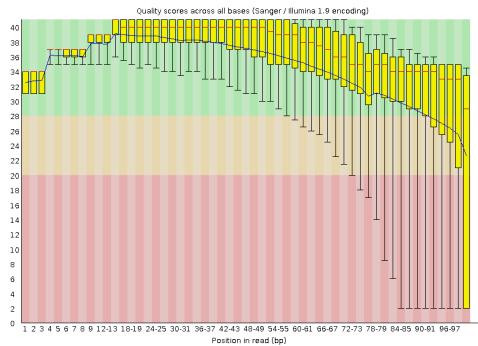
Report



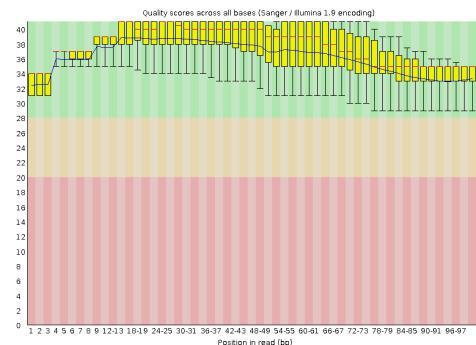
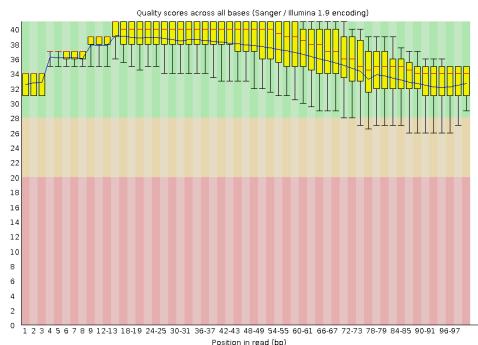
SRR1658133

R1

Before trimming



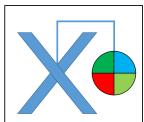
After trimming



SRR1658214

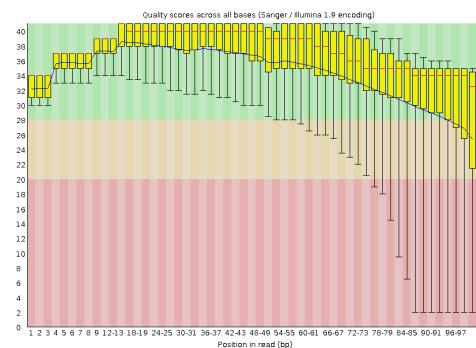
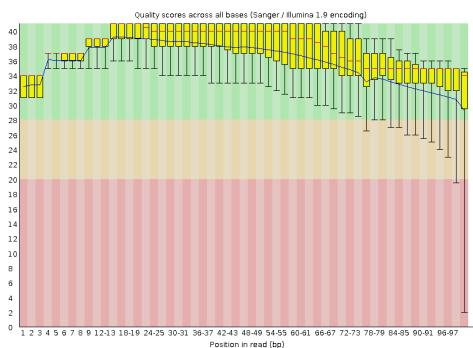
R1

Before trimming

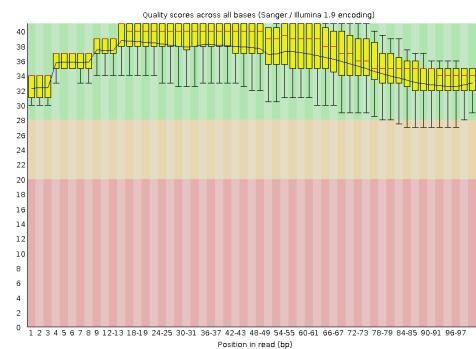
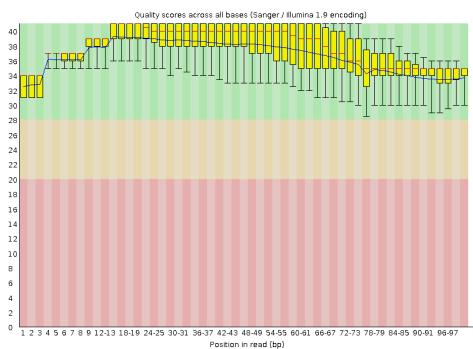


Epigenome Analysis Platform

Report



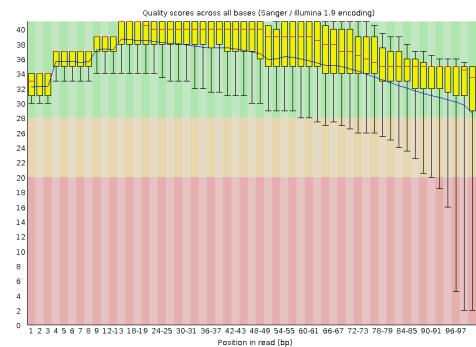
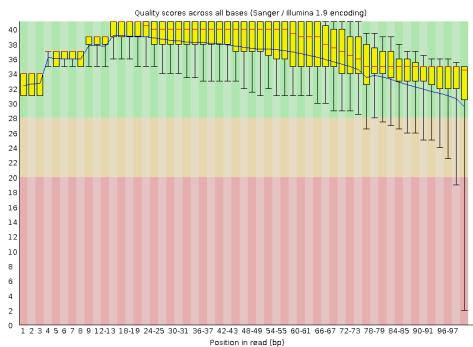
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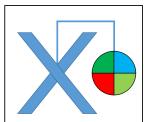
SRR1658232

R1

Before trimming

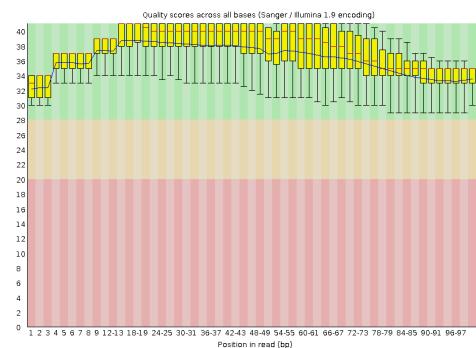
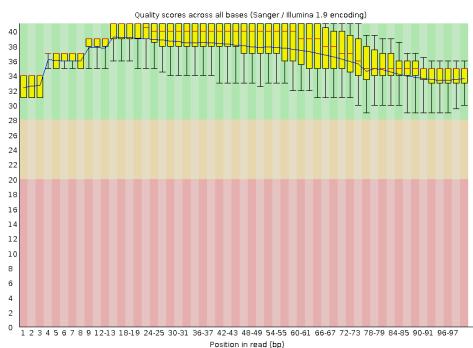


After trimming



Epigenome Analysis Platform

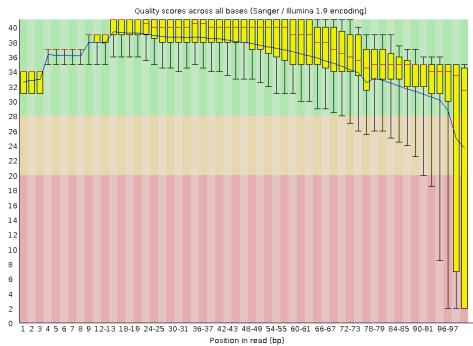
Report



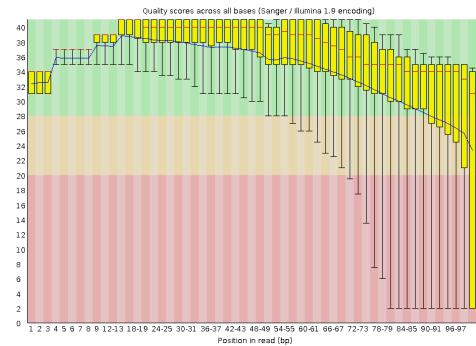
SRR1658168

R1

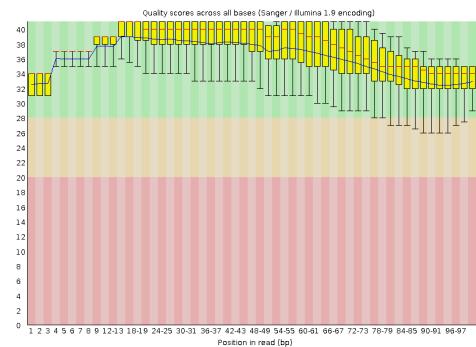
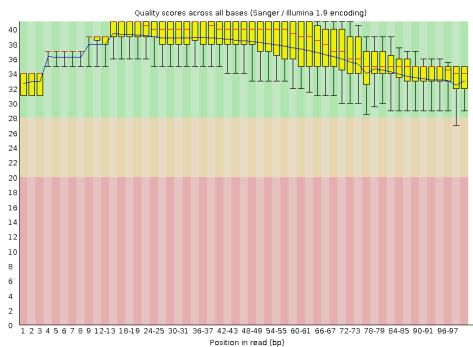
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R2



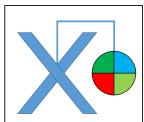
After trimming



SRR1658267

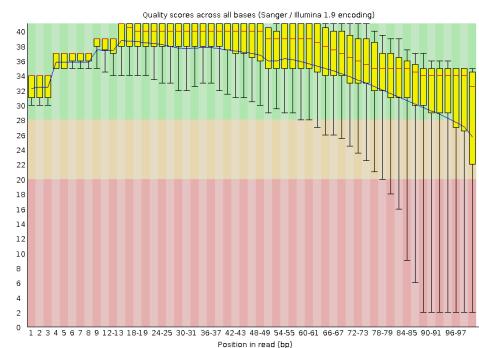
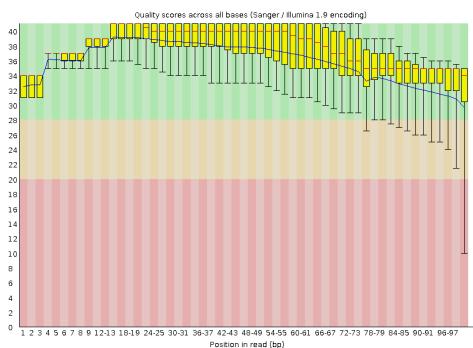
R1

Before trimming

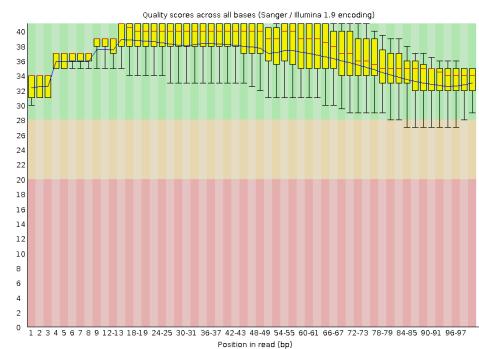
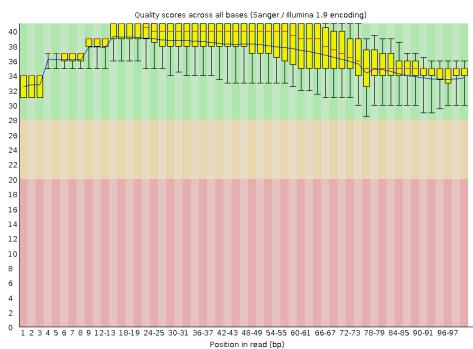


Epigenome Analysis Platform

Report



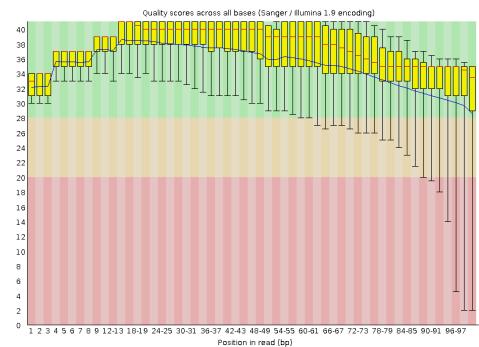
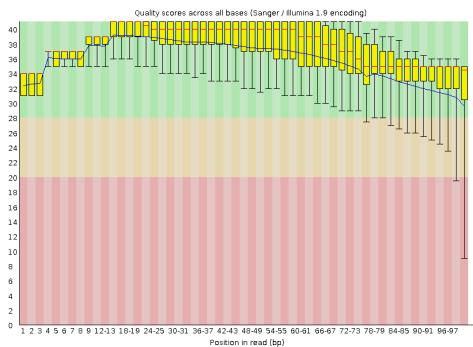
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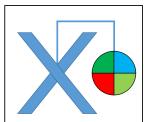
SRR1658177

R1

Before trimming

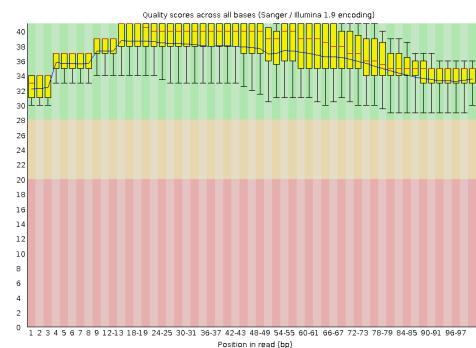
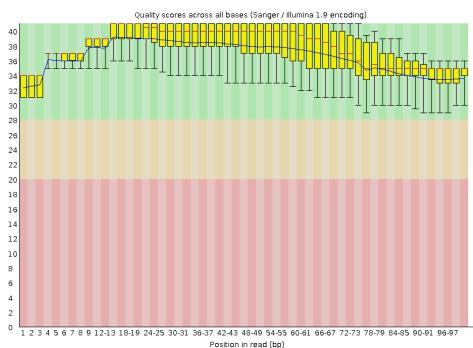


After trimming



Epigenome Analysis Platform

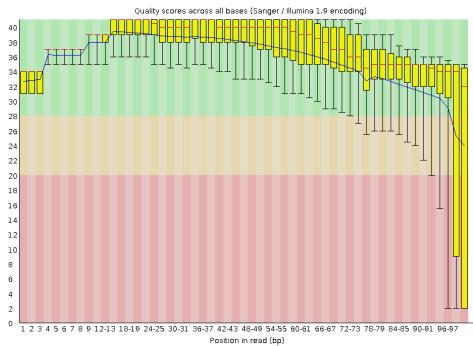
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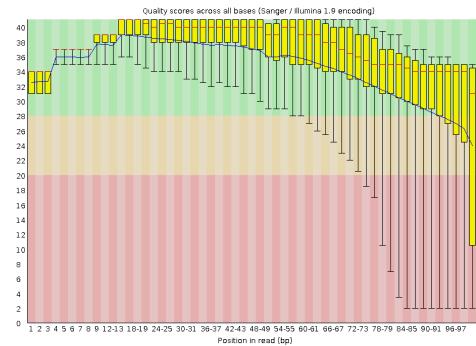
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R1

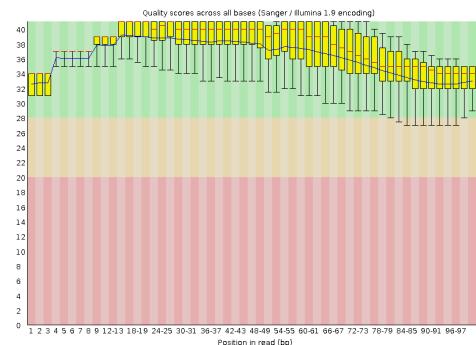
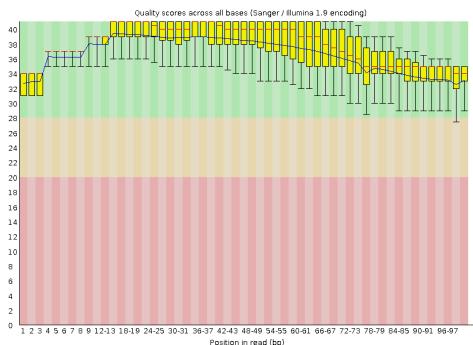
Before trimming



R2



After trimming

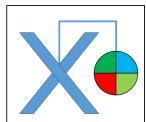


SRR1658276

R1

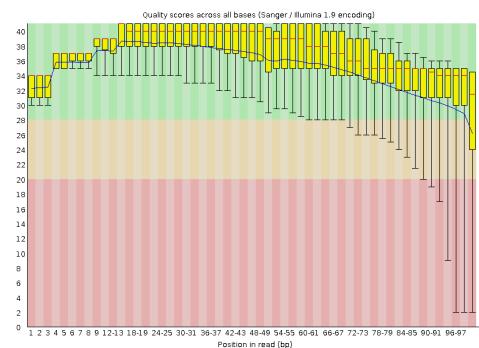
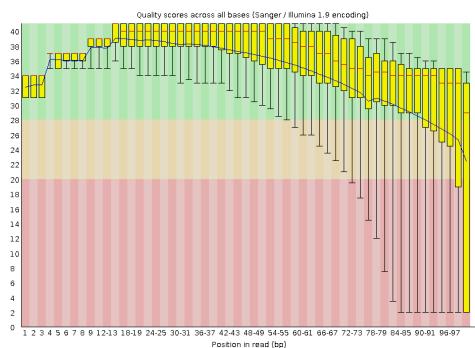
Before trimming

R2

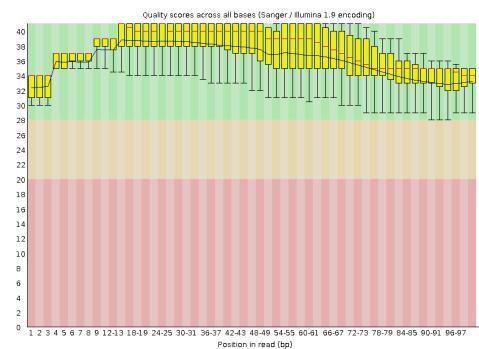
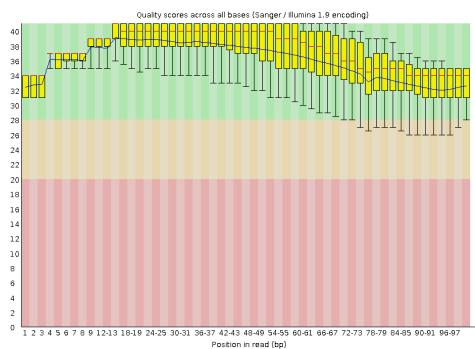


Epigenome Analysis Platform

Report



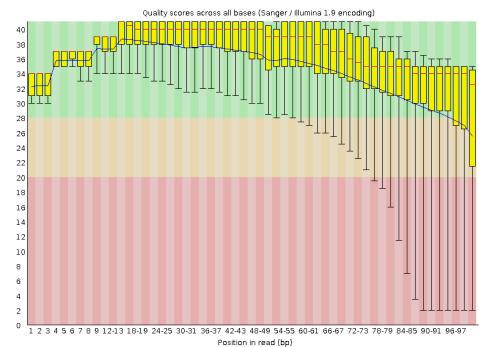
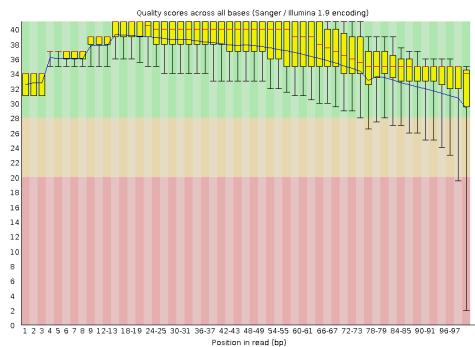
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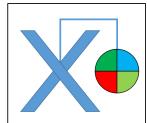
SRR1658128

R1

Before trimming

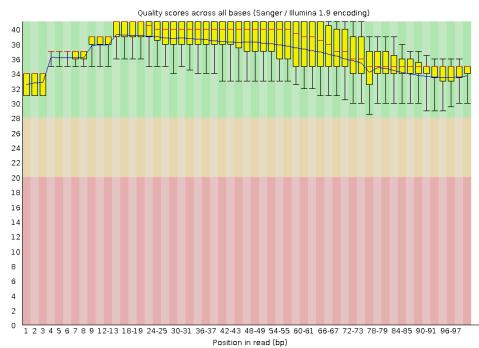


After trimming



Epigenome Analysis Platform

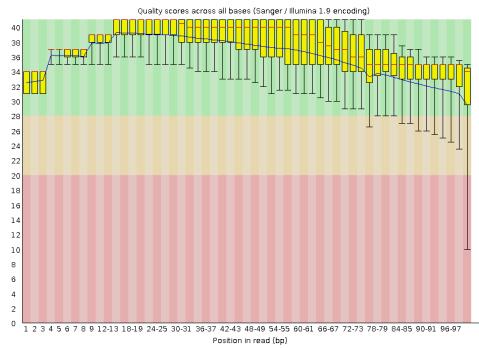
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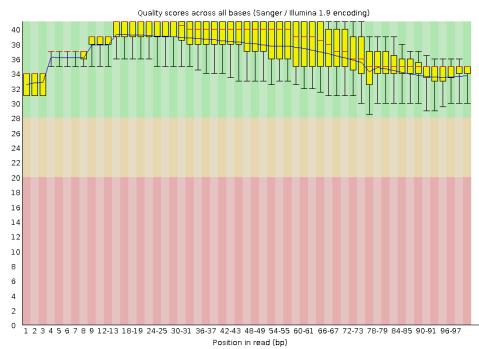
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R1

Before trimming



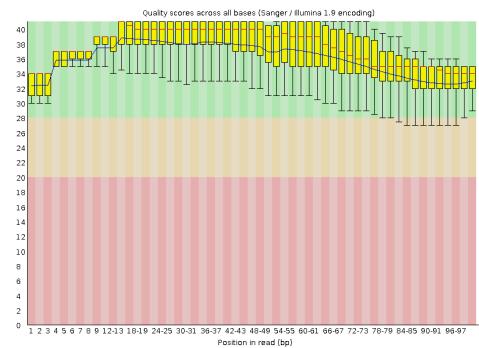
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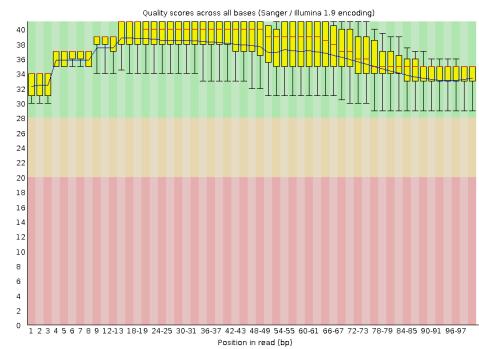
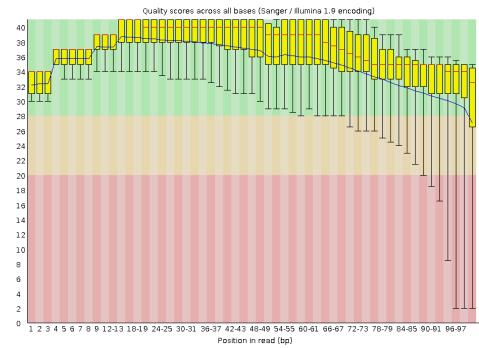
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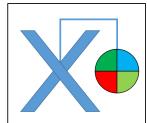
R1

Before trimming



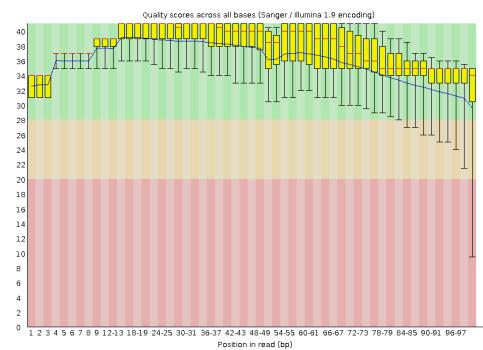
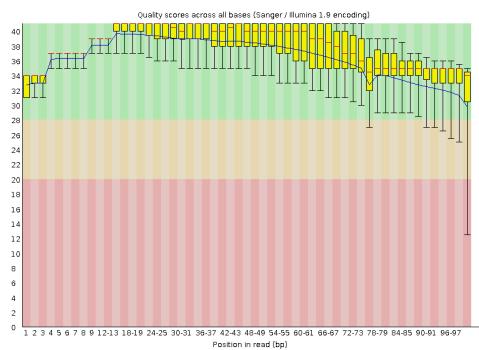
R2



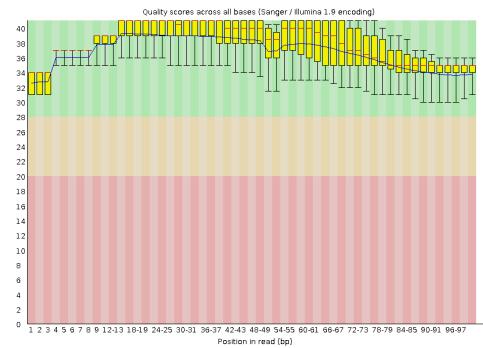
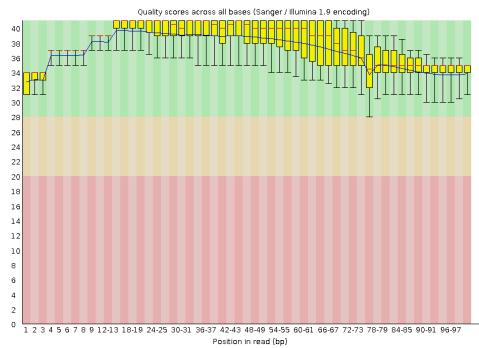


Epigenome Analysis Platform

Report



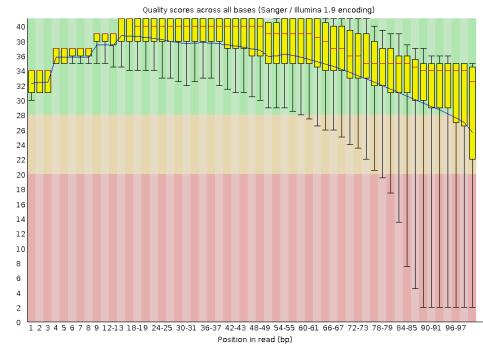
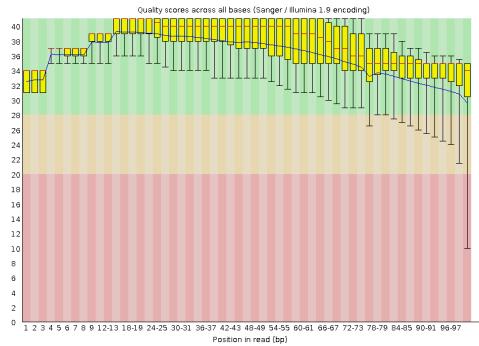
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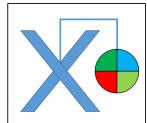
SRR1658182

R1

Before trimming

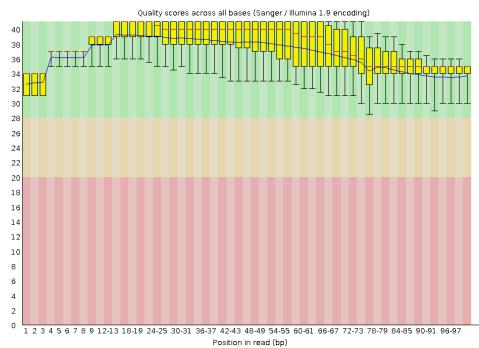


After trimming



Epigenome Analysis Platform

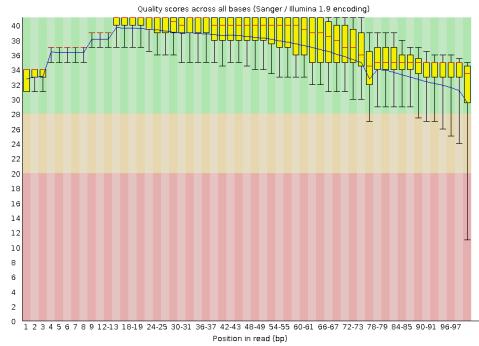
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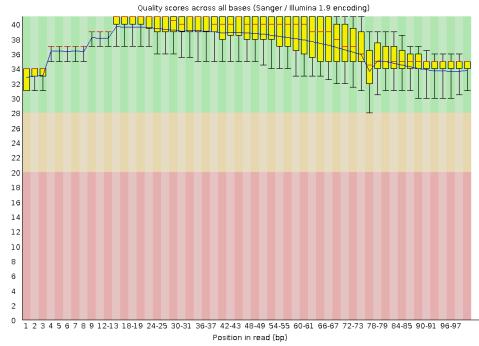
SRR1658263

R1

Before trimming



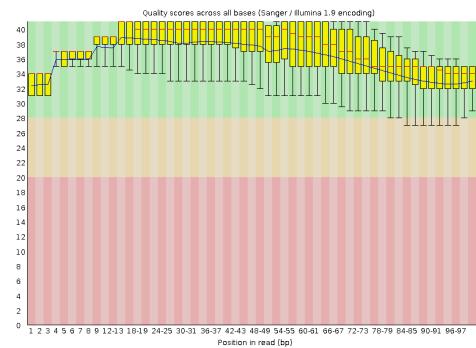
After trimming



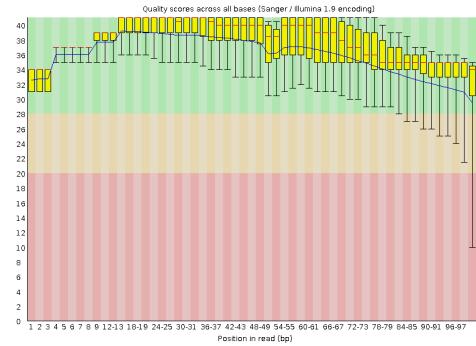
SRR1658173

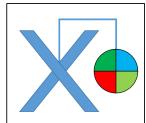
R1

Before trimming



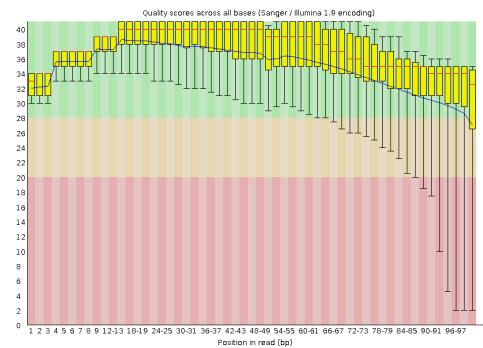
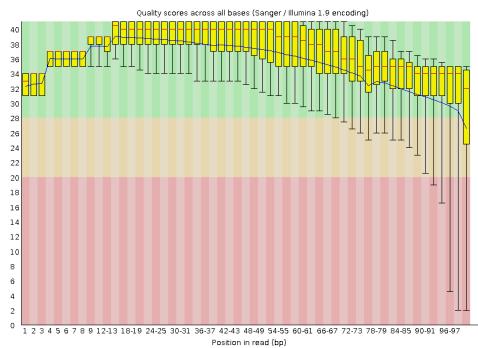
R2



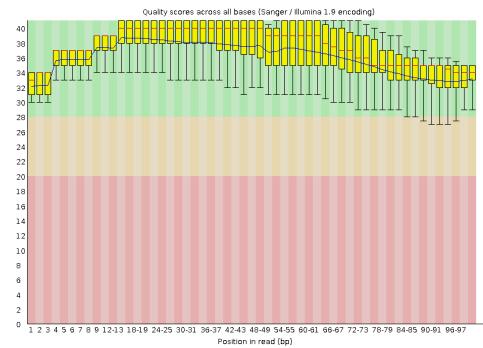
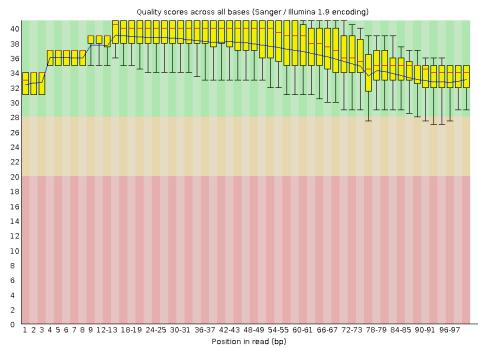


Epigenome Analysis Platform

Report



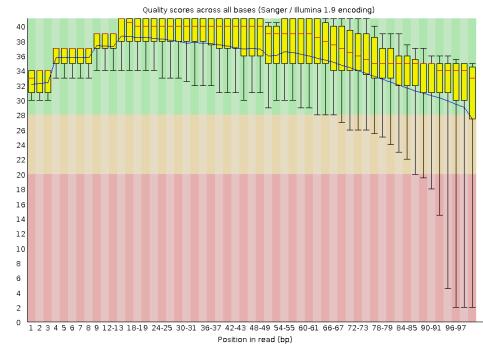
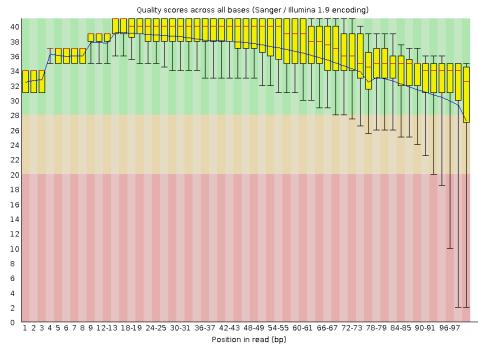
After trimming



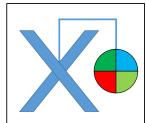
SRR1658155

R1

Before trimming

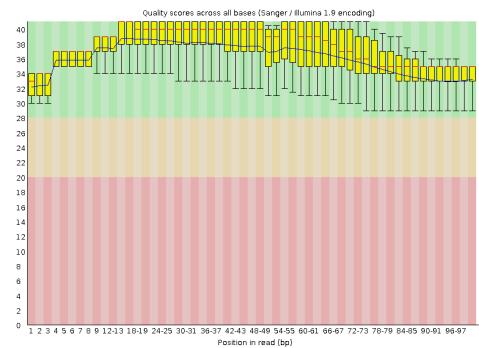
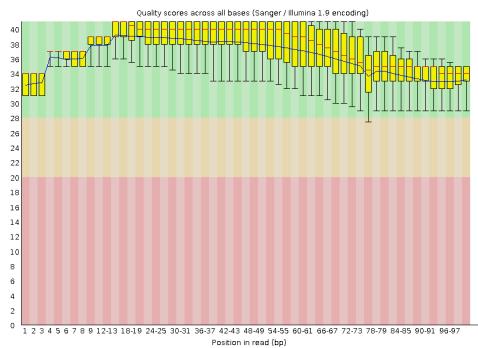


After trimming



Epigenome Analysis Platform

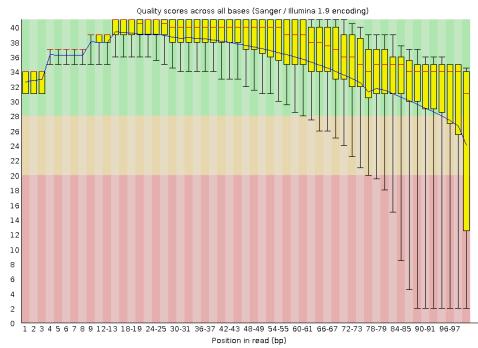
Report



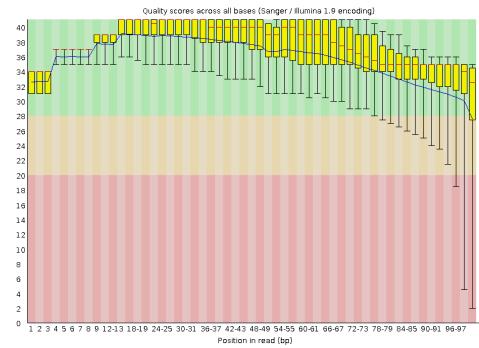
SRR1658317

R1

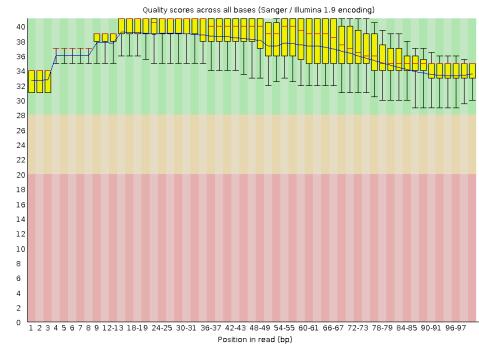
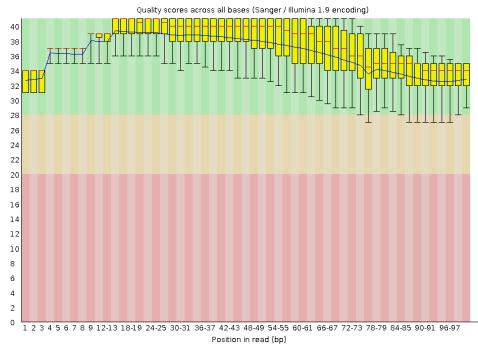
Before trimming



R2



After trimming

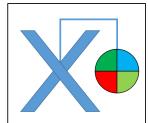


SRR1658191

R1

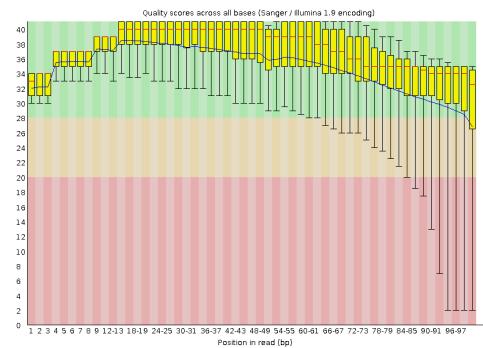
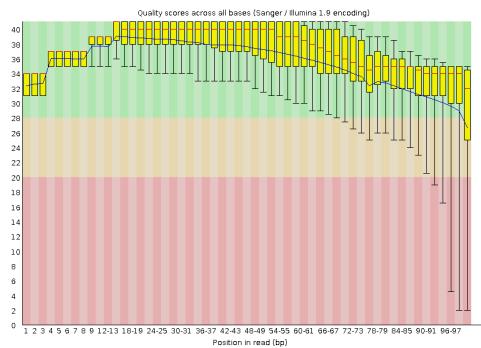
Before trimming

R2

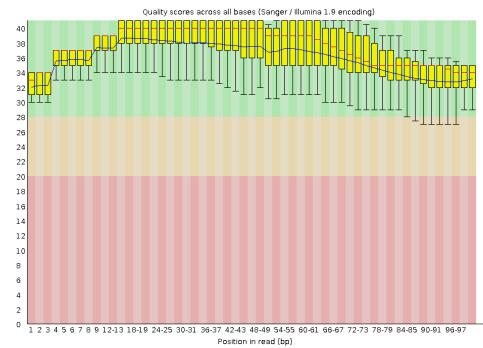
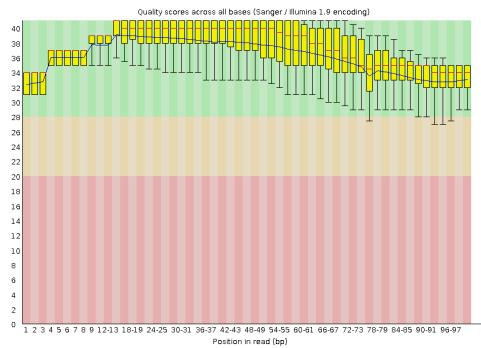


Epigenome Analysis Platform

Report



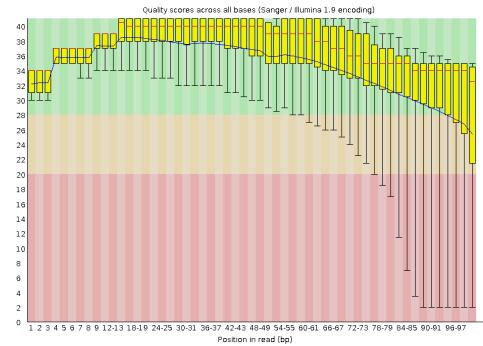
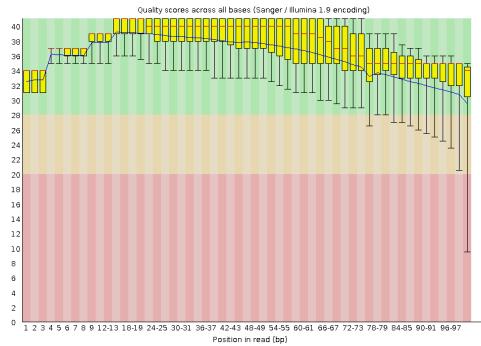
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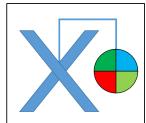
SRR1658210

R1

Before trimming

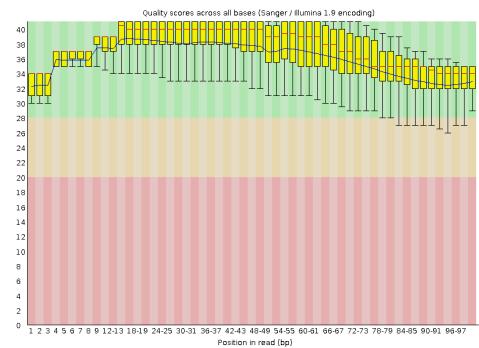
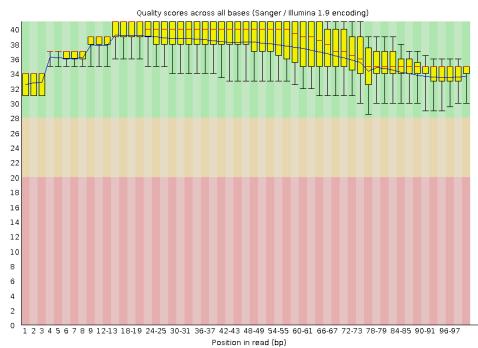


After trimming



Epigenome Analysis Platform

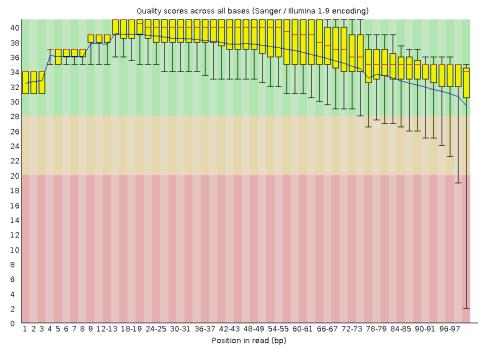
Report



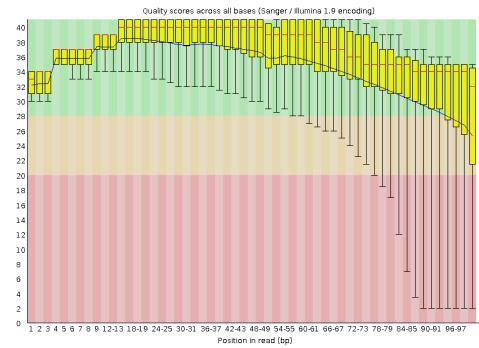
SRR1658111

R1

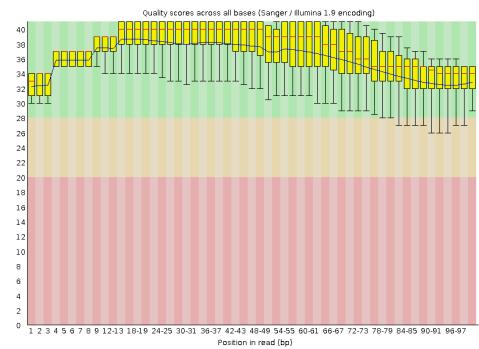
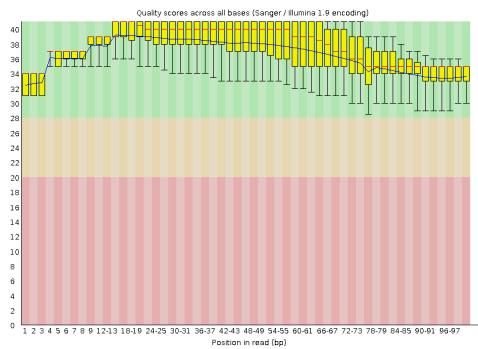
Before trimming



R2



After trimming

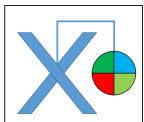


SRR1658201

R1

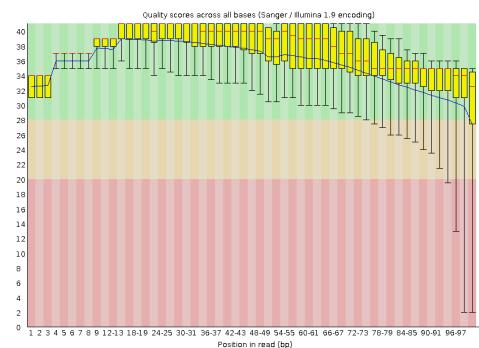
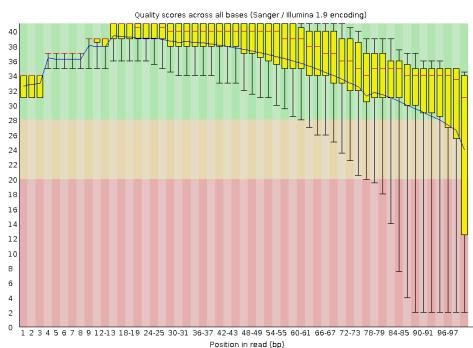
Before trimming

R2

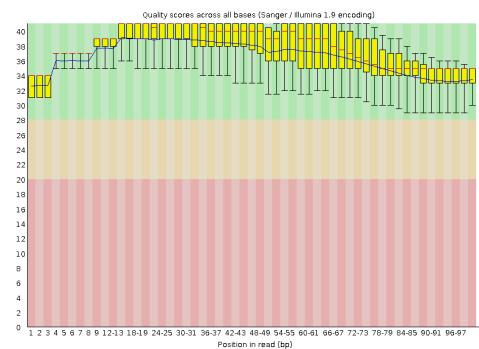
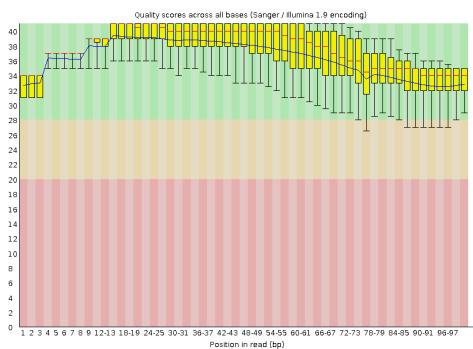


Epigenome Analysis Platform

Report



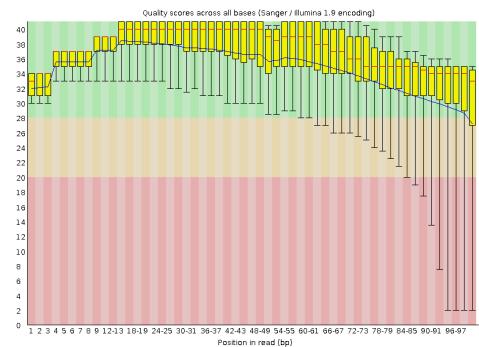
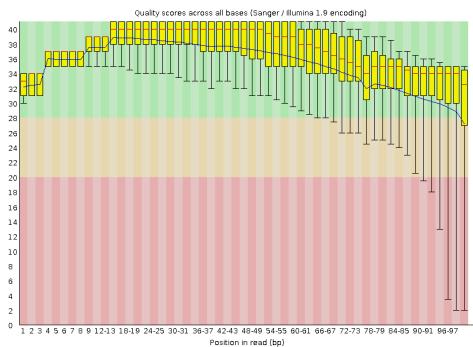
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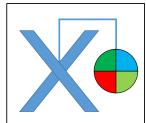
SRR1658240

R1

Before trimming

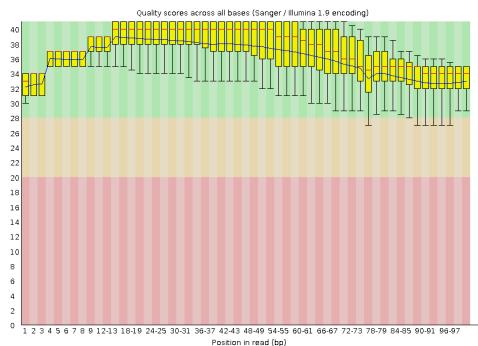


After trimming



Epigenome Analysis Platform

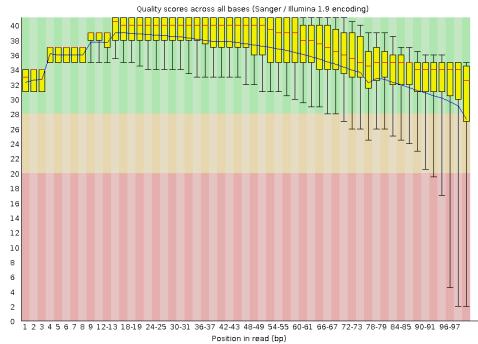
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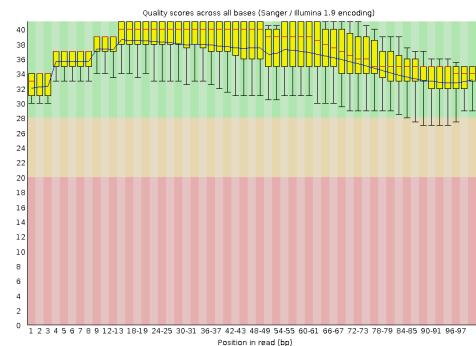
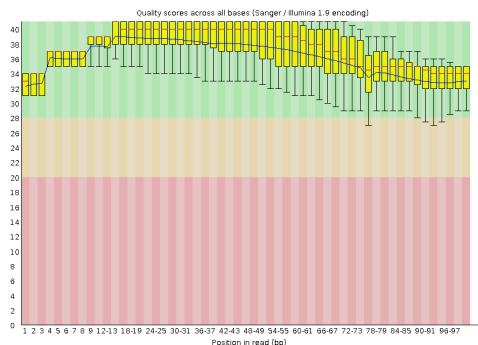
SRR1658141

R1

Before trimming



After trimming

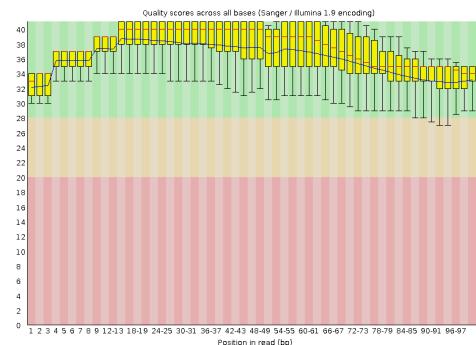


R2

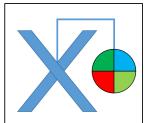
SRR1658303

R1

Before trimming



R2



Epigenome Analysis Platform

Report



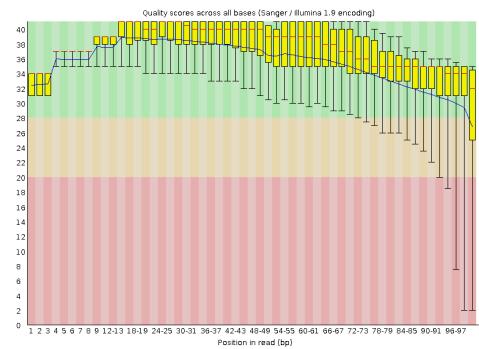
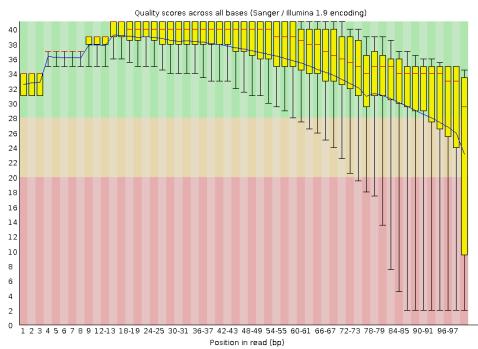
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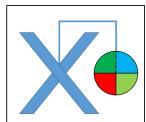
SRR1658312

R1

Before trimming

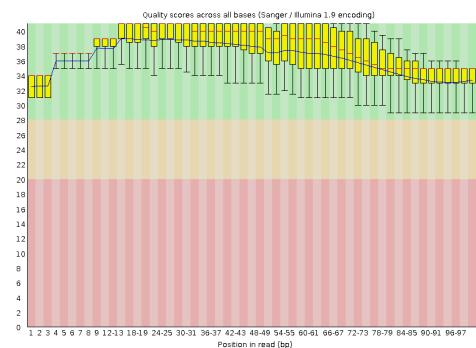
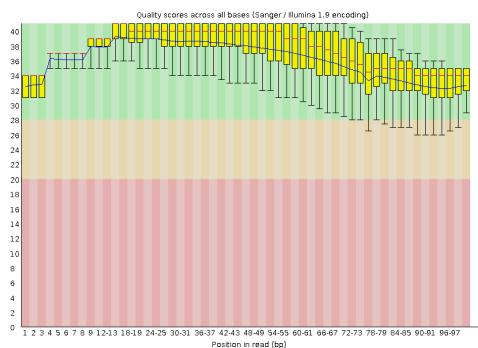


After trimming



Epigenome Analysis Platform

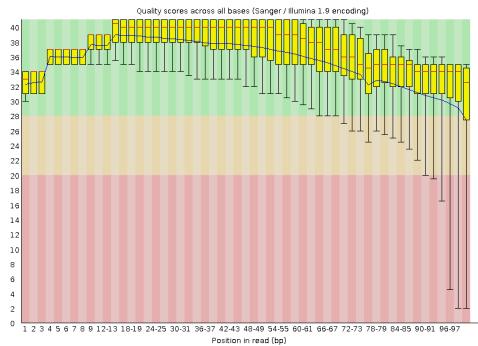
Report



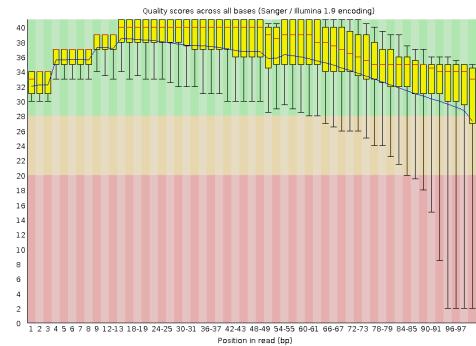
SRR1658114

R1

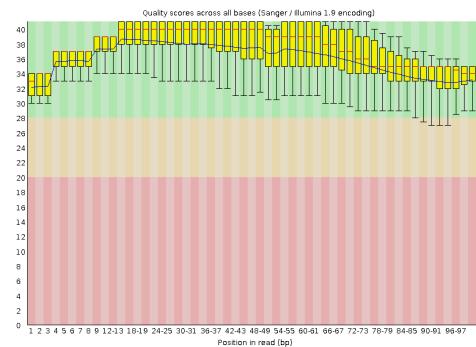
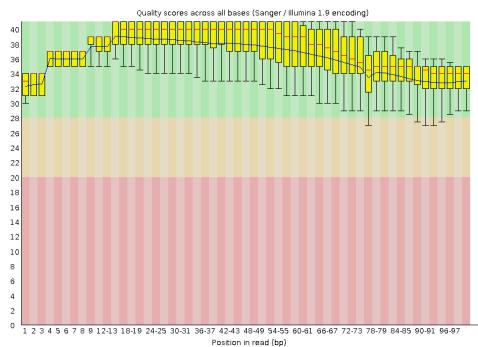
Before trimming



R2



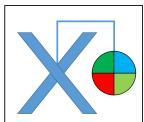
After trimming



SRR1658149

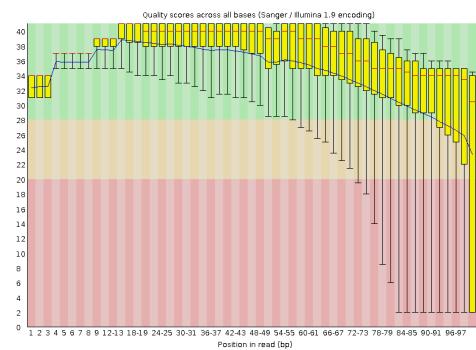
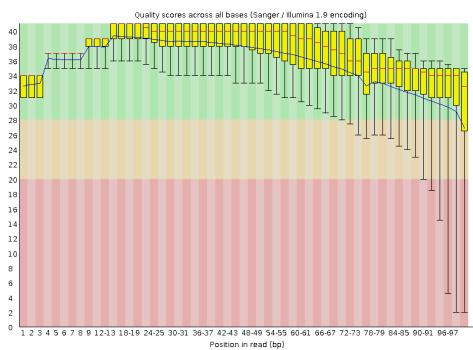
R1

Before trimming

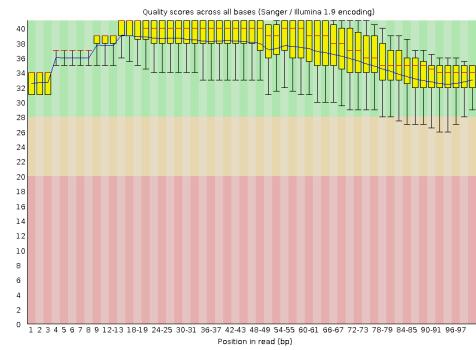
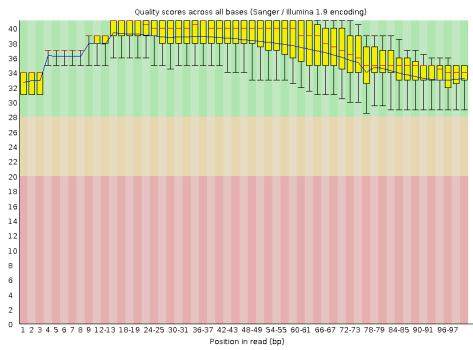


Epigenome Analysis Platform

Report



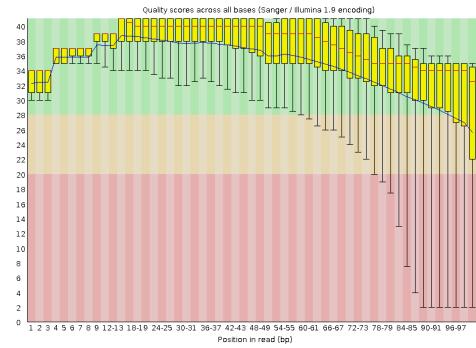
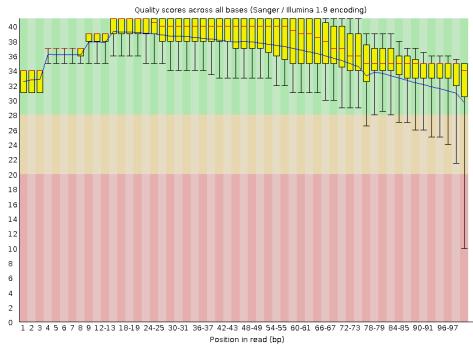
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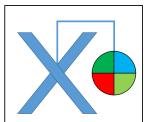
SRR1658176

R1

Before trimming

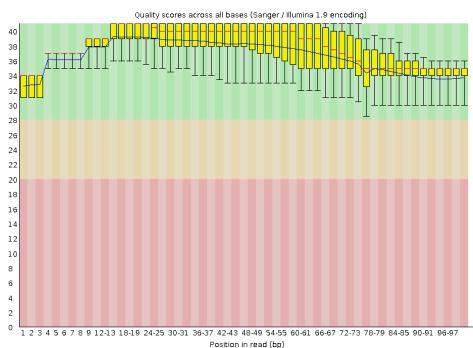


After trimming



Epigenome Analysis Platform

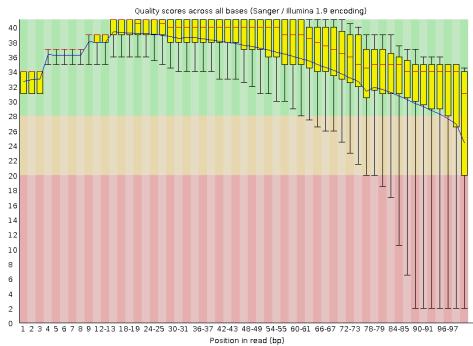
Report



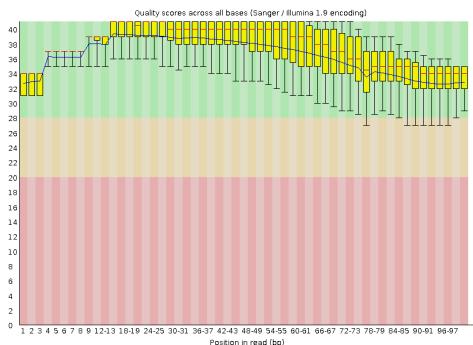
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R1

Before trimming



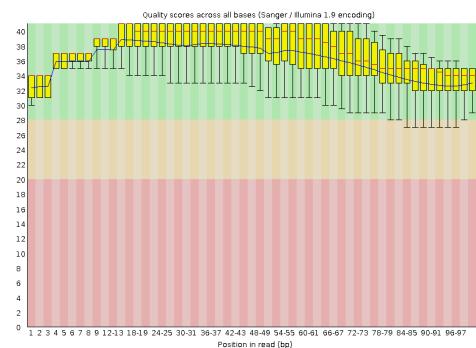
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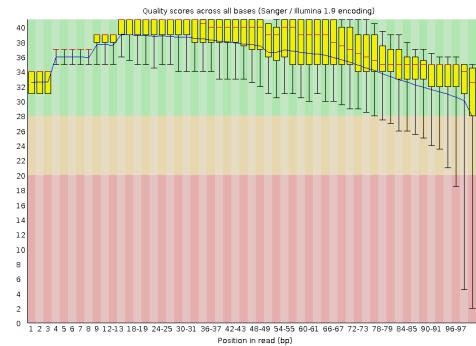
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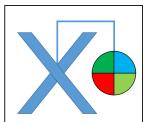
R1

Before trimming



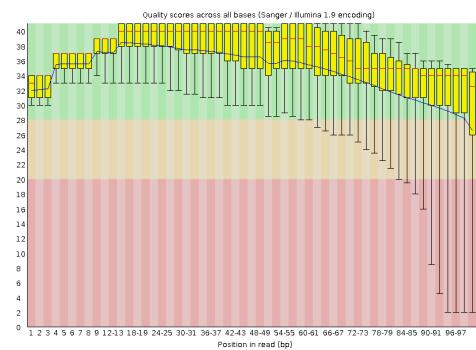
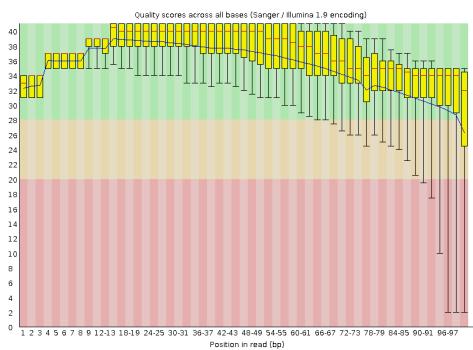
R2



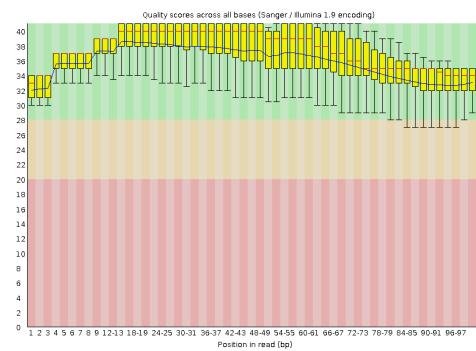
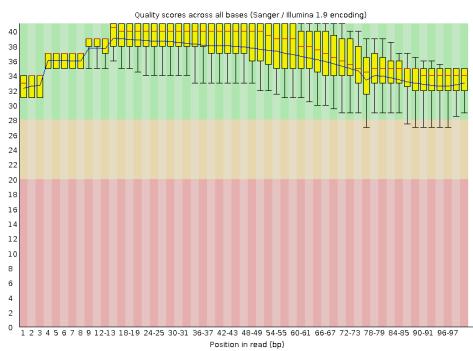


Epigenome Analysis Platform

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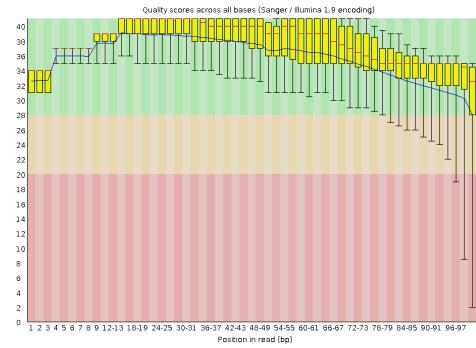
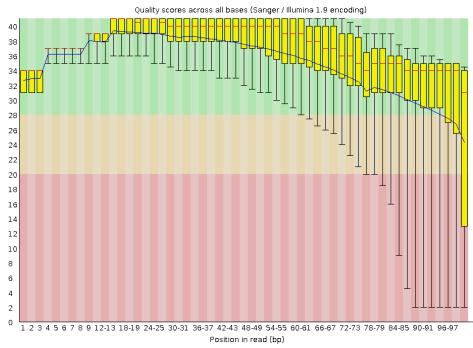
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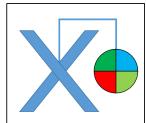
SRR1658325

R1

Before trimming

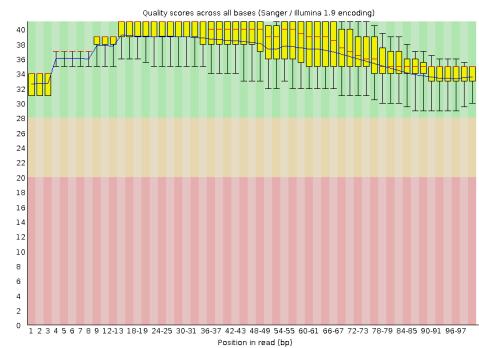
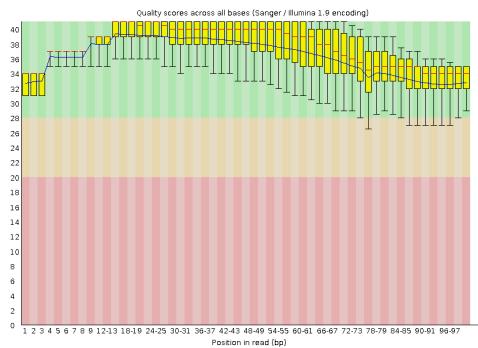


After trimming



Epigenome Analysis Platform

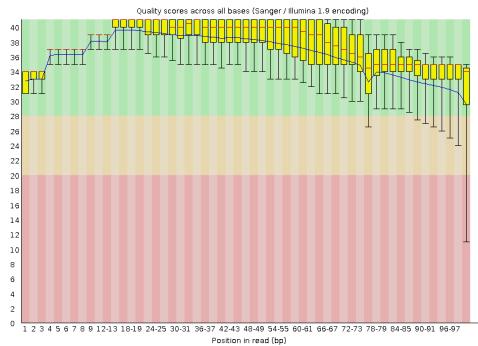
Report



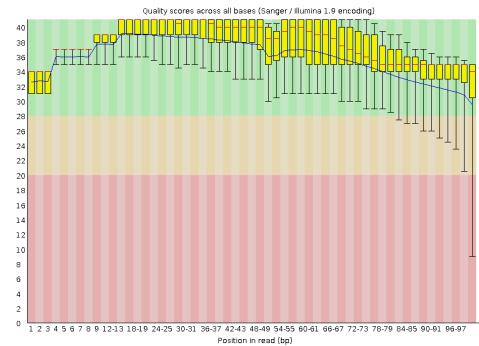
SRR1658244

R1

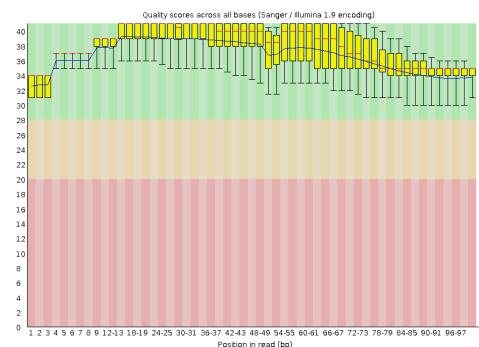
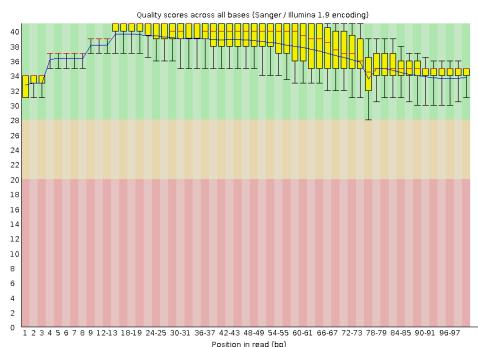
Before trimming



R2



After trimming

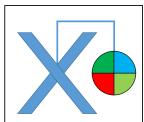


SRR1658181

R1

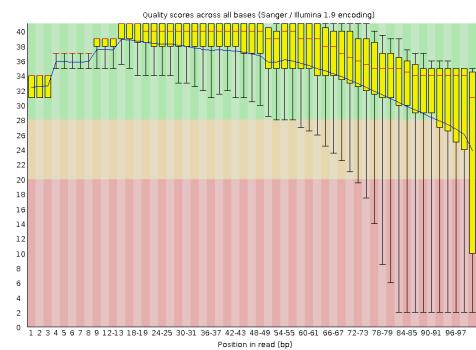
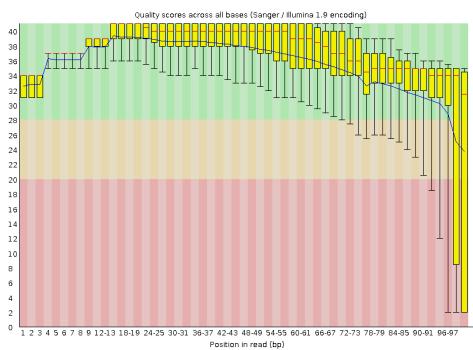
Before trimming

R2

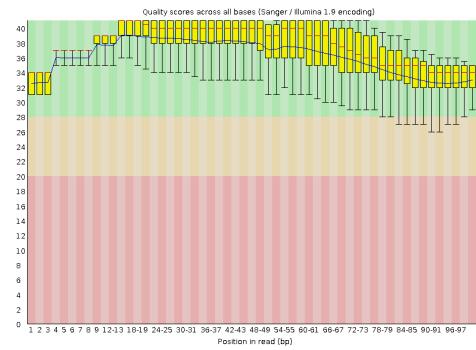
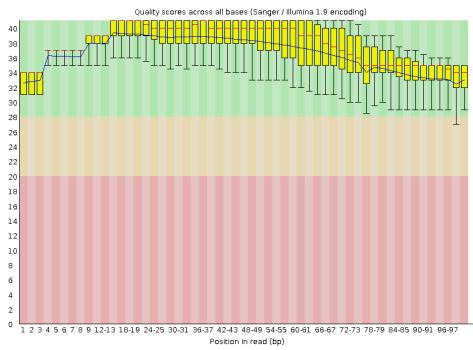


Epigenome Analysis Platform

Report



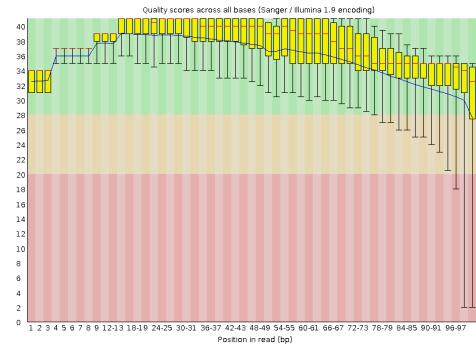
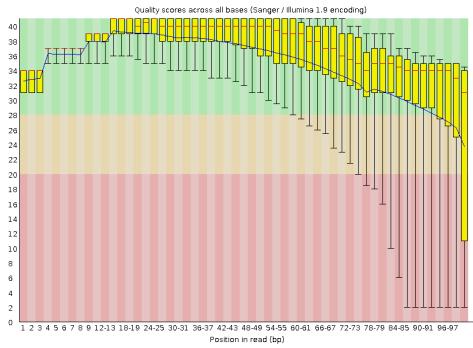
After trimming



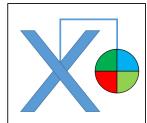
SRR1658288

R1

Before trimming

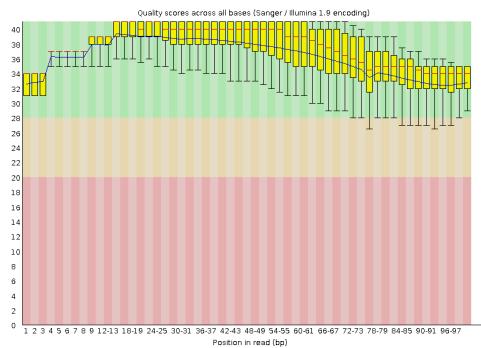


After trimming



Epigenome Analysis Platform

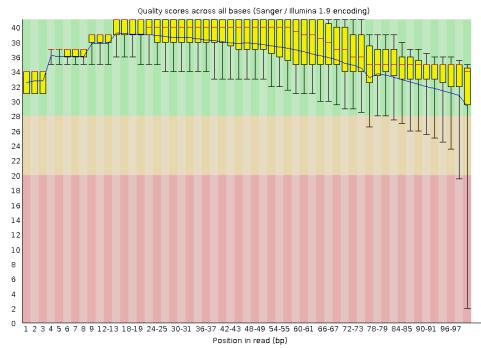
Report



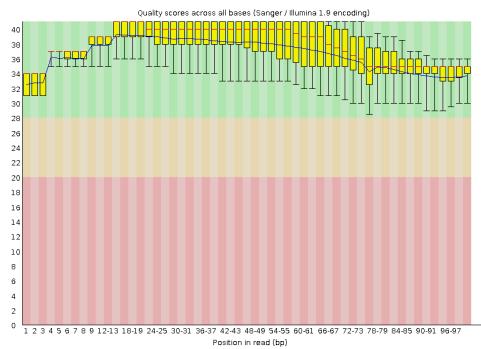
SRR1658110

R1

Before trimming



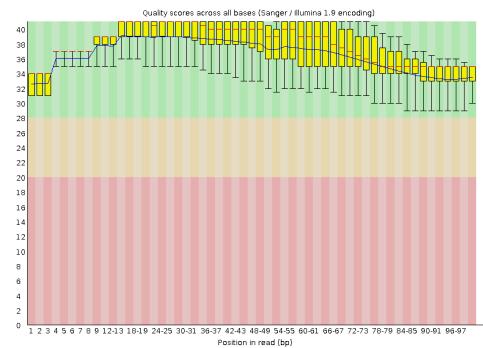
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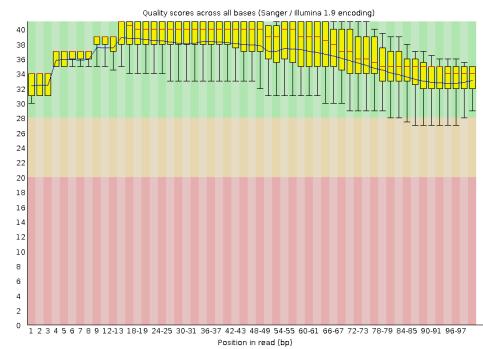
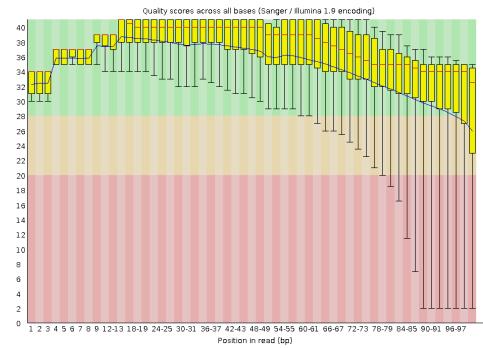
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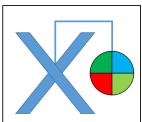
R1

Before trimming



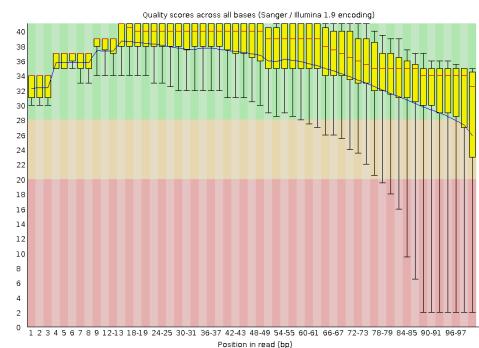
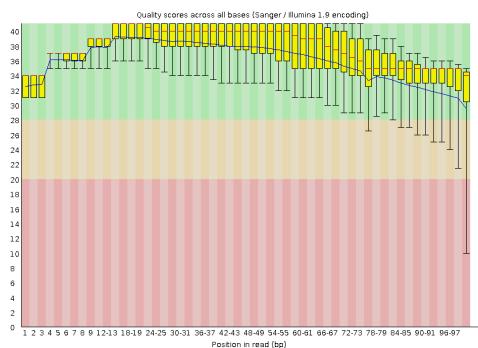
R2



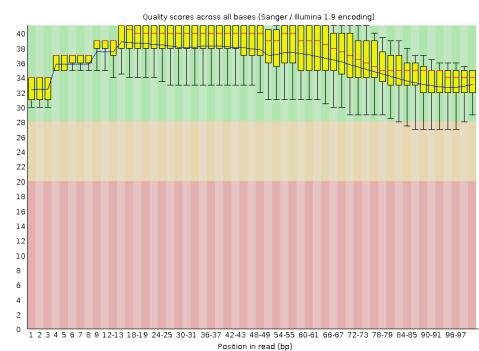
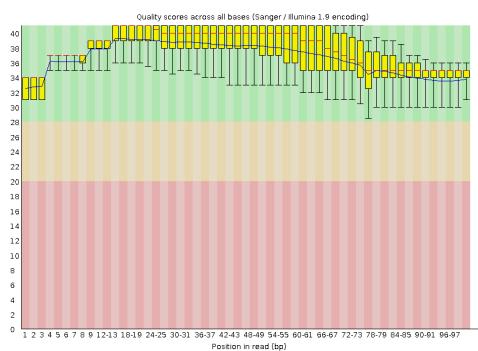


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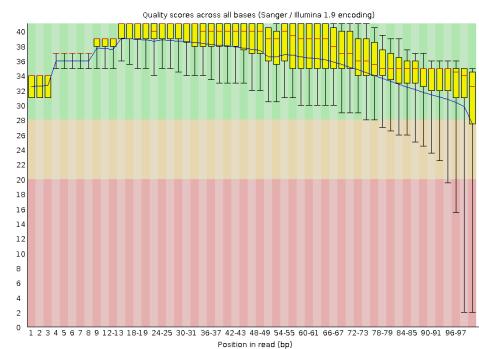
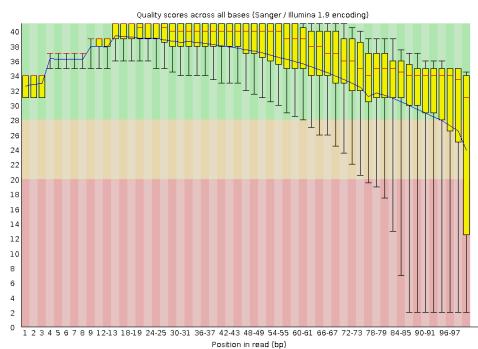
After trimming



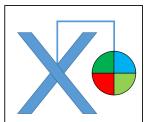
SRR1658323

R1

Before trimming

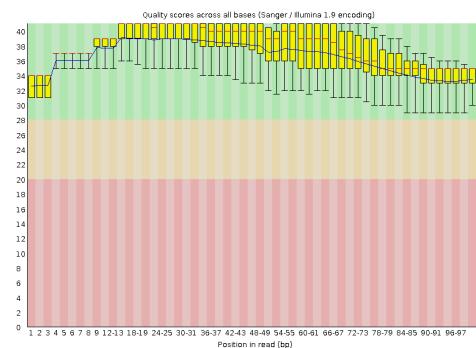
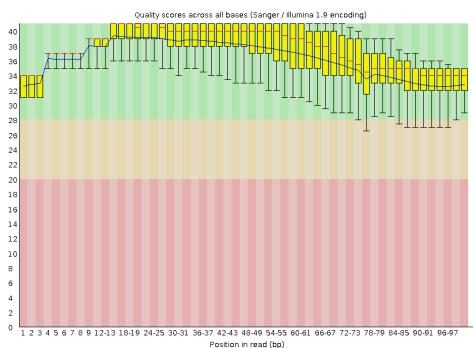


After trimming



Epigenome Analysis Platform

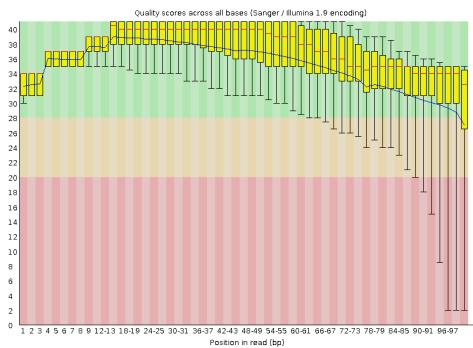
Report



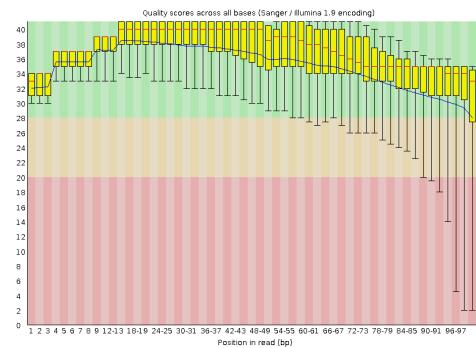
SRR1658242

R1

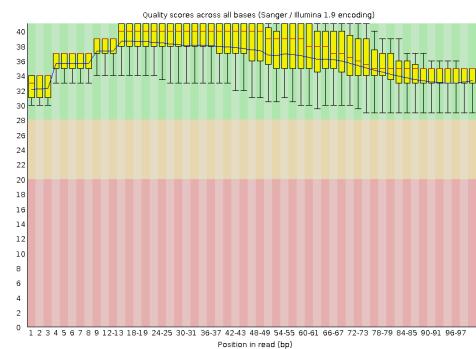
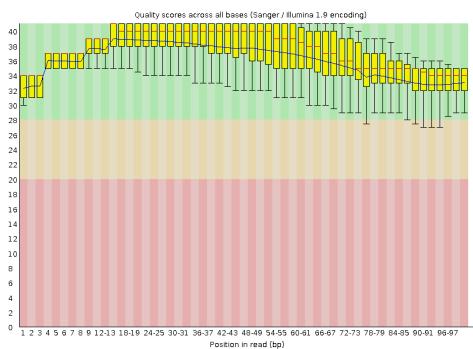
Before trimming



R2



After trimming

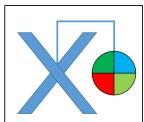


SRR1658224

R1

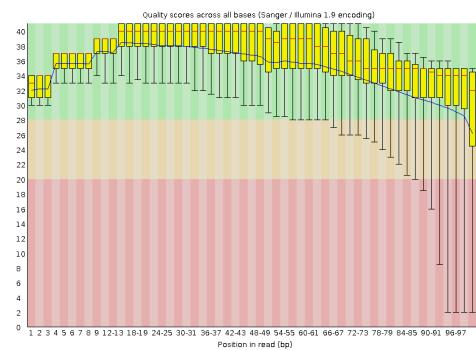
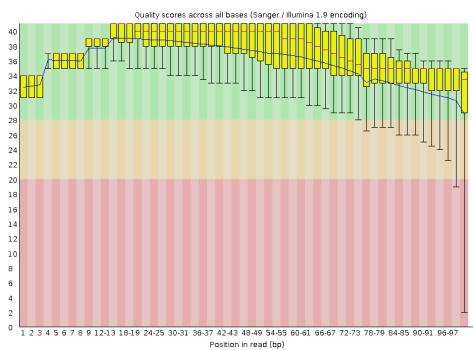
Before trimming

R2

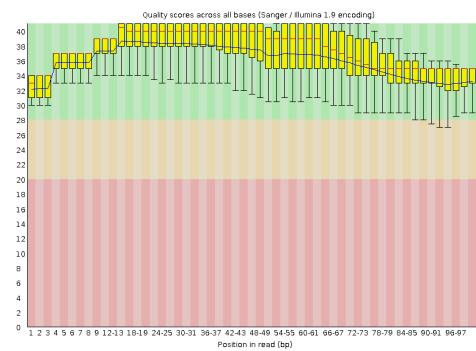
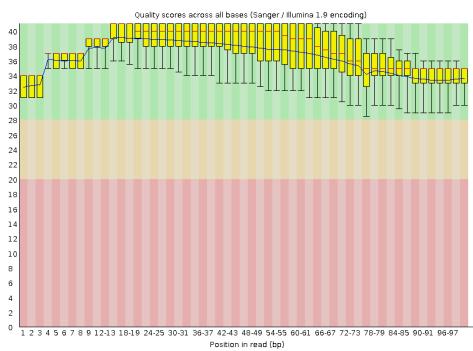


Epigenome Analysis Platform

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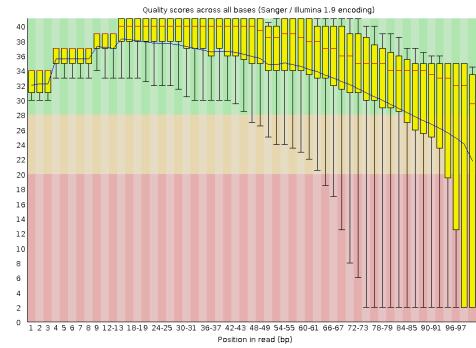
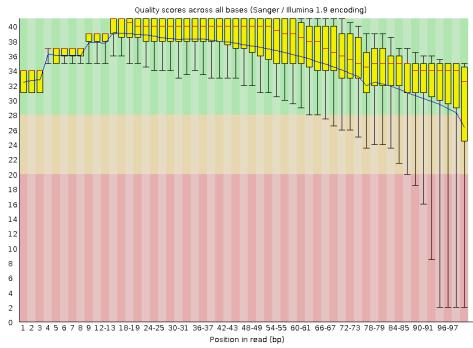
After trimming



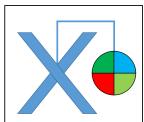
SRR1658341

R1

Before trimming

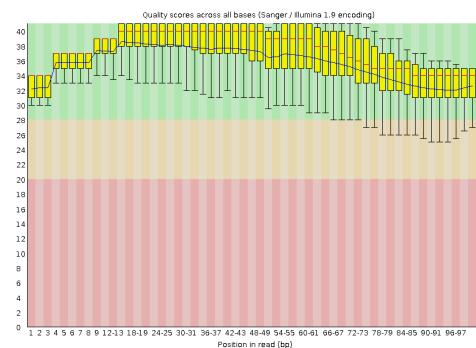
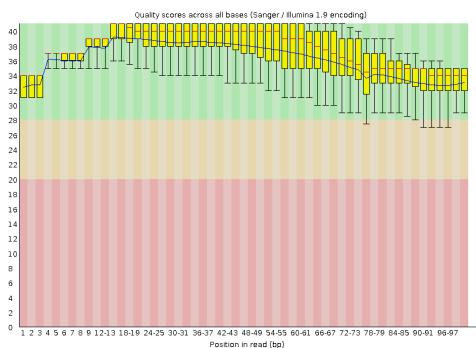


After trimming



Epigenome Analysis Platform

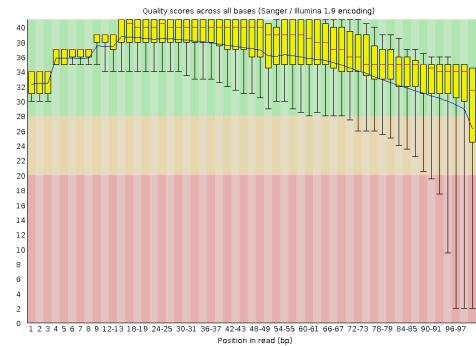
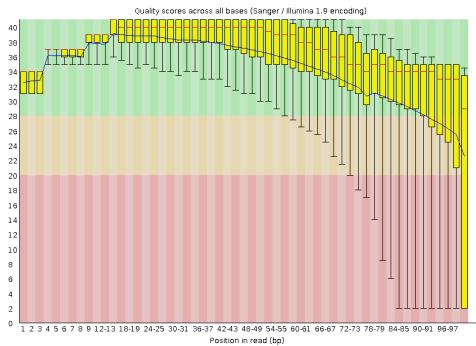
Report



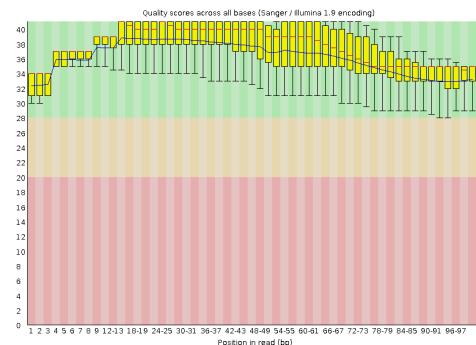
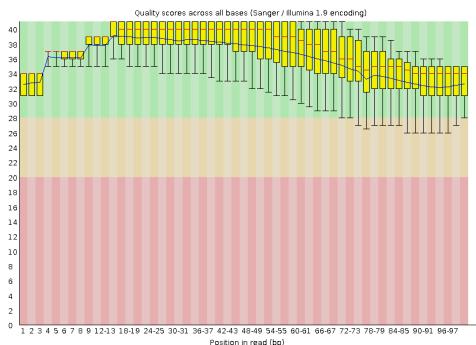
SRR1658215

R1

Before trimming



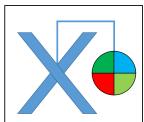
After trimming



SRR1658170

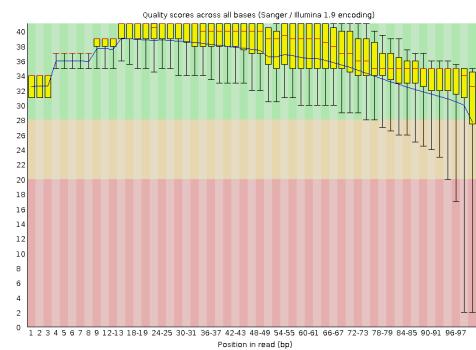
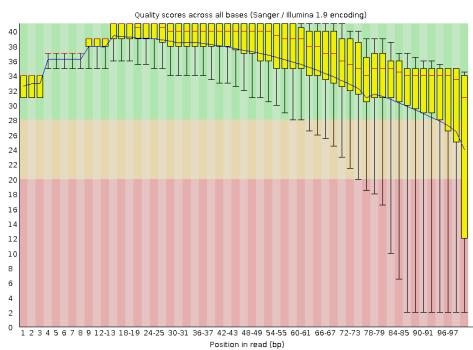
R1

Before trimming

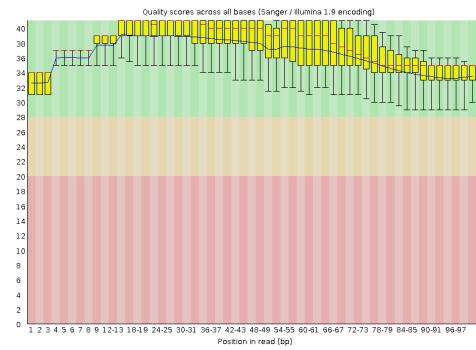
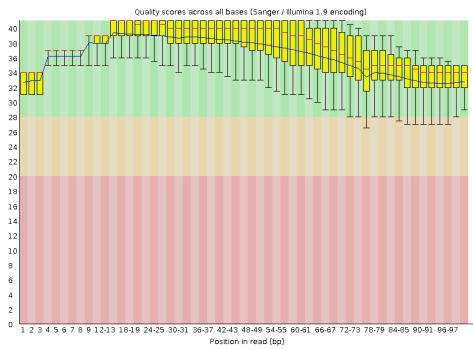


Epigenome Analysis Platform

Report



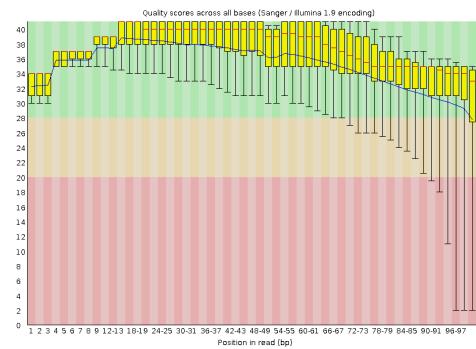
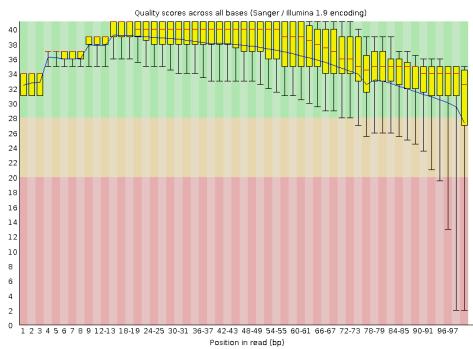
After trimming



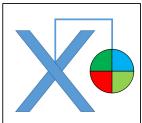
SRR1658152

R1

Before trimming

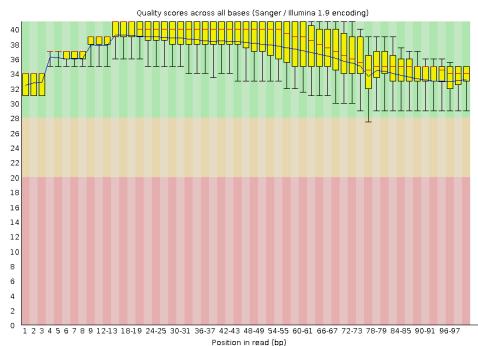


After trimming



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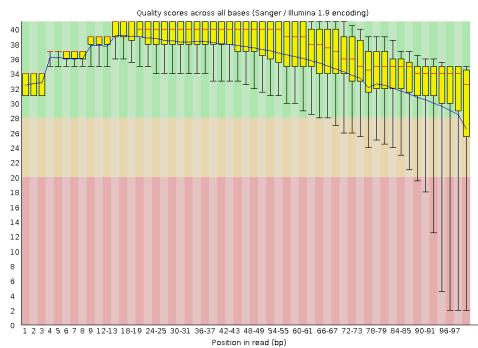
Report



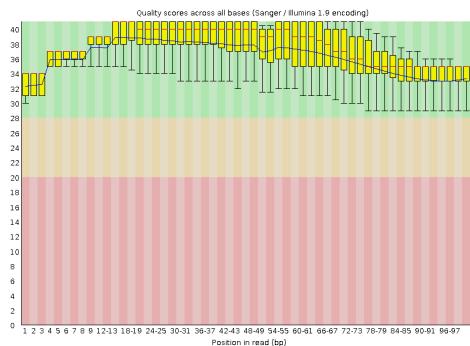
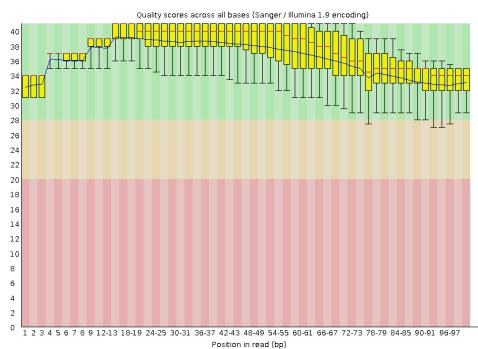
SRR1658295

R1

Before trimming



After trimming

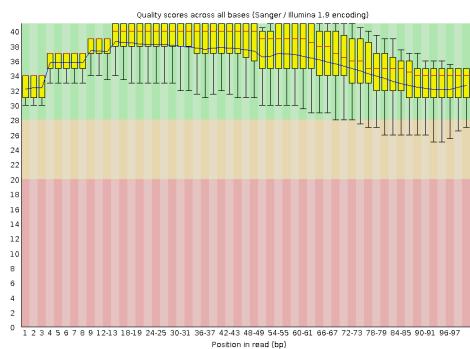


R2

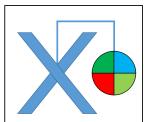
SRR1658277

R1

Before trimming

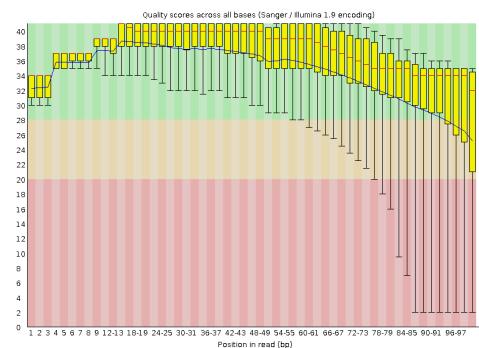
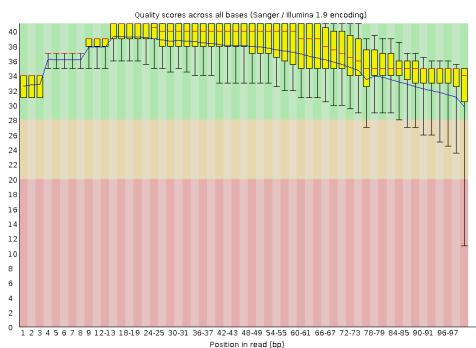


R2

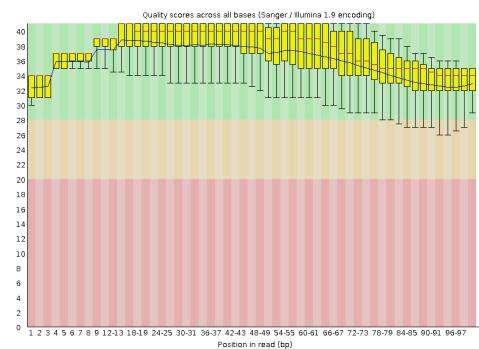
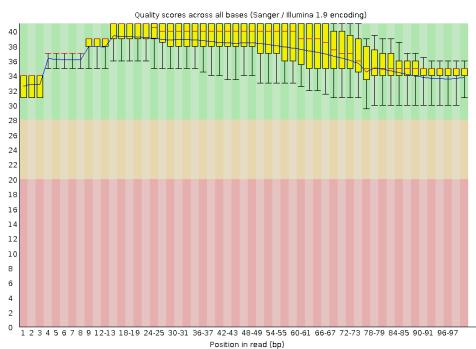


Epigenome Analysis Platform

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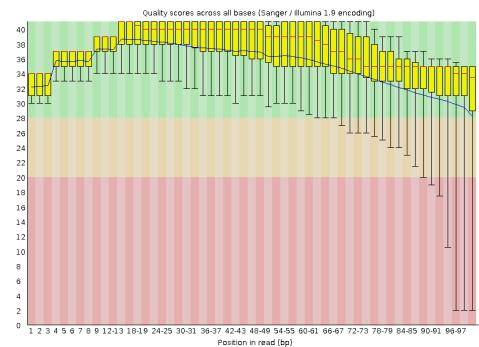
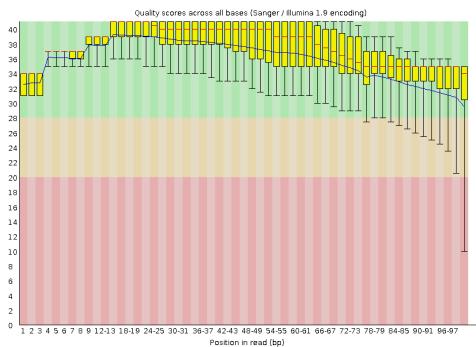
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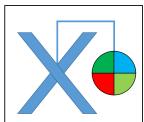
SRR1658246

R1

Before trimming

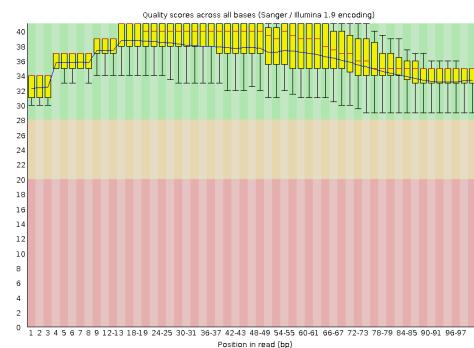
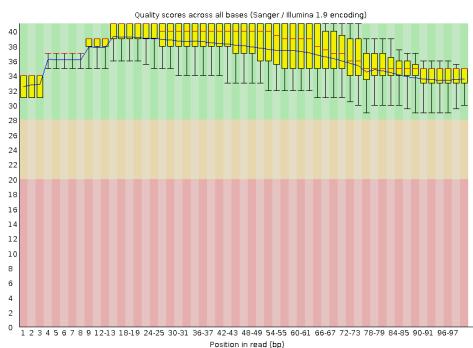


After trimming



Epigenome Analysis Platform

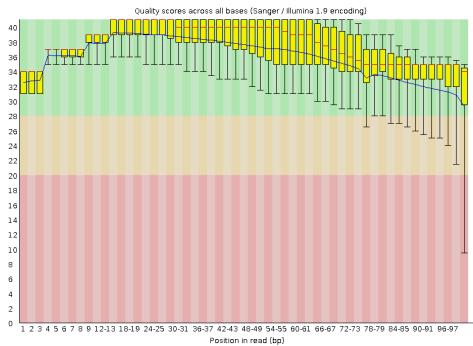
Report



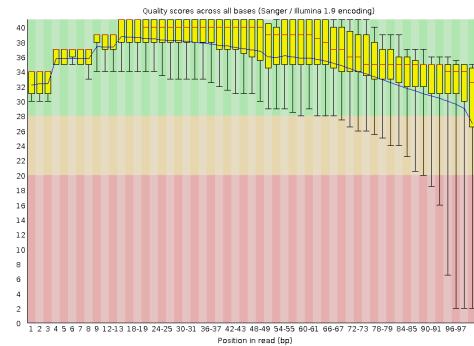
SRR1658309

R1

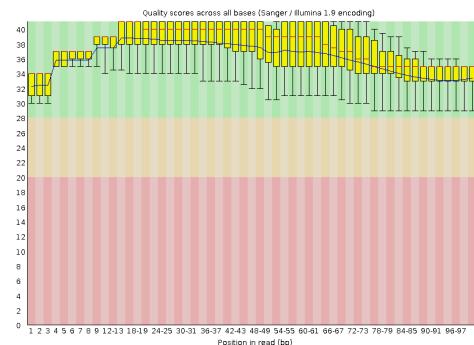
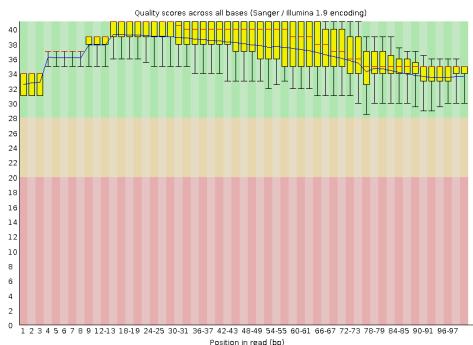
Before trimming



R2



After trimming

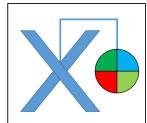


SRR1658228

R1

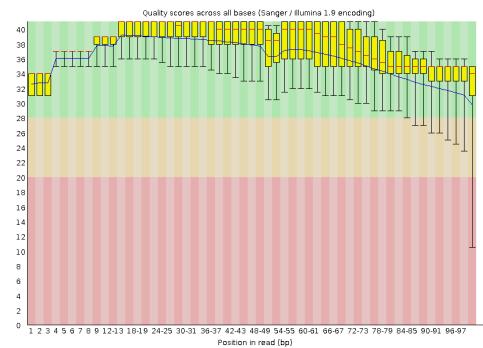
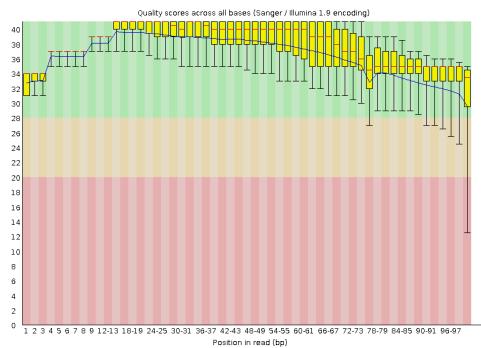
Before trimming

R2

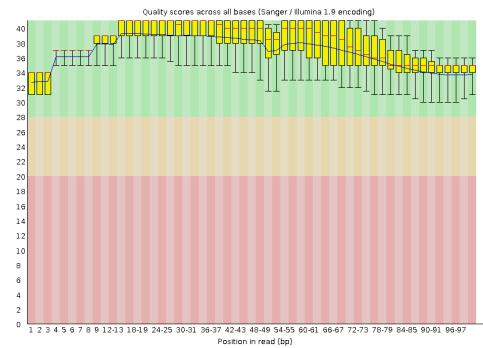
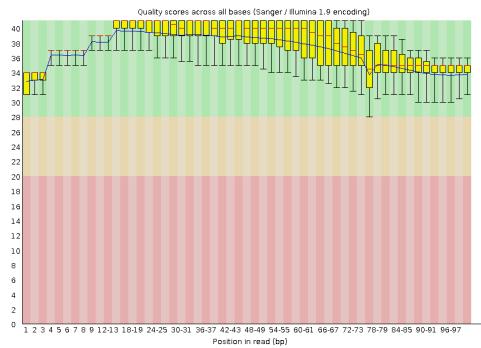


Epigenome Analysis Platform

Report



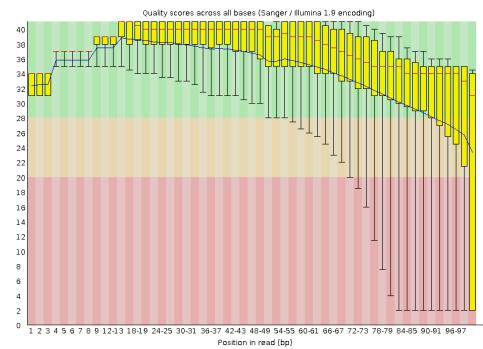
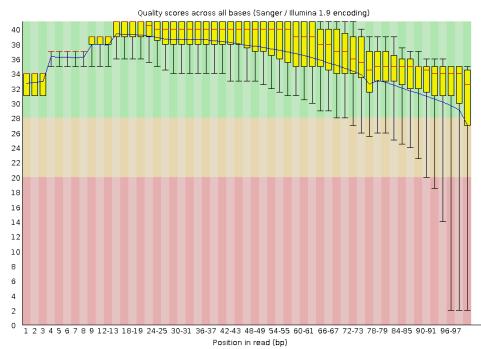
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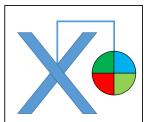
SRR1658183

R1

Before trimming

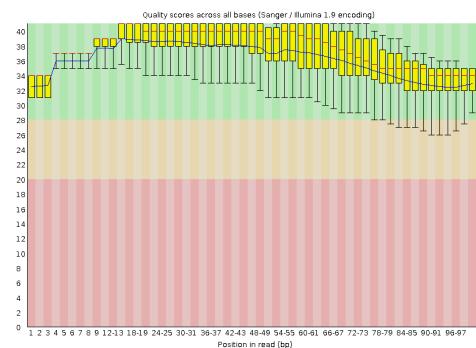
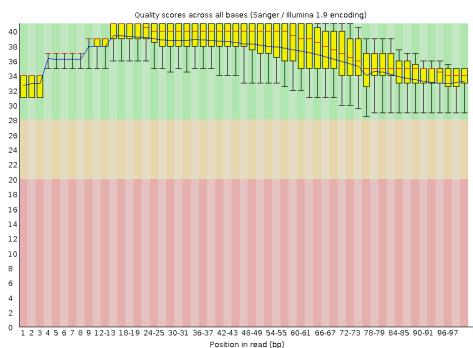


After trimming



Epigenome Analysis Platform

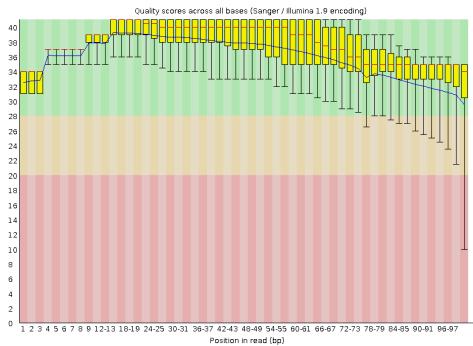
Report



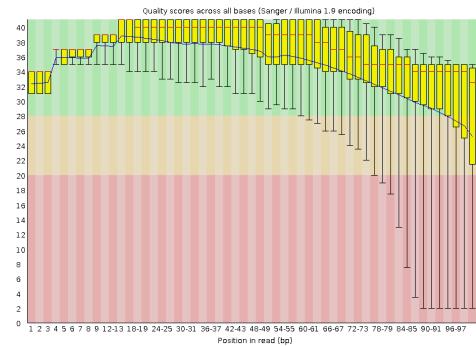
SRR1658264

R1

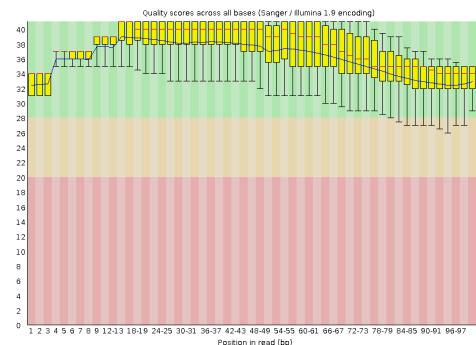
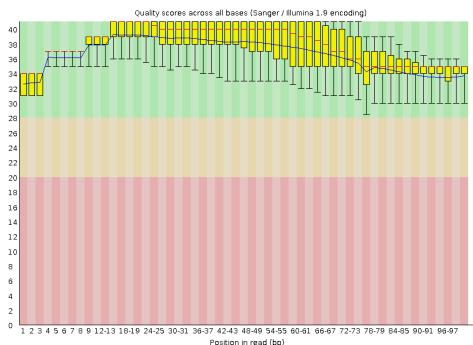
Before trimming



R2



After trimming

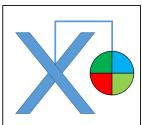


SRR1658318

R1

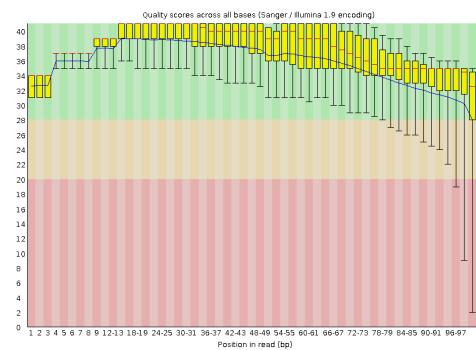
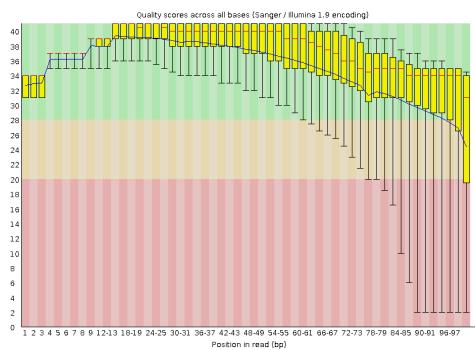
Before trimming

R2

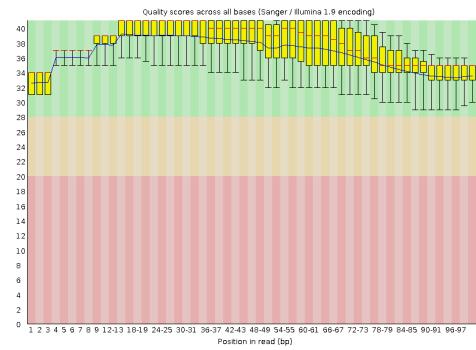
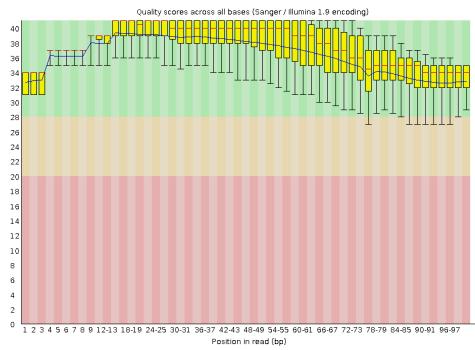


Epigenome Analysis Platform

Report



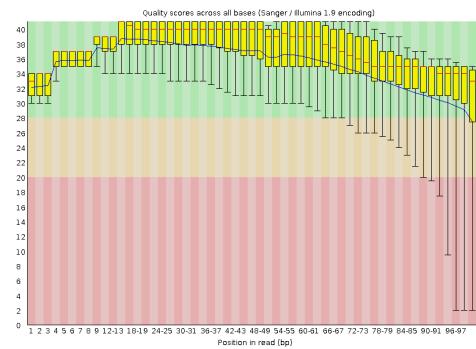
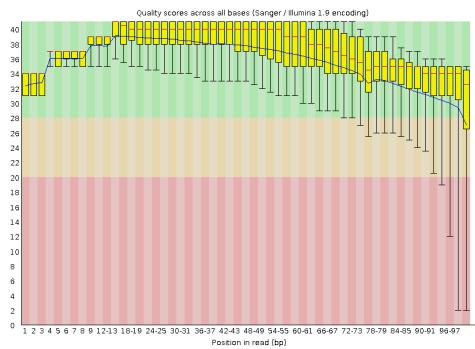
After trimming



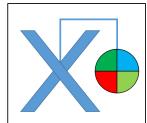
SRR1658192

R1

Before trimming

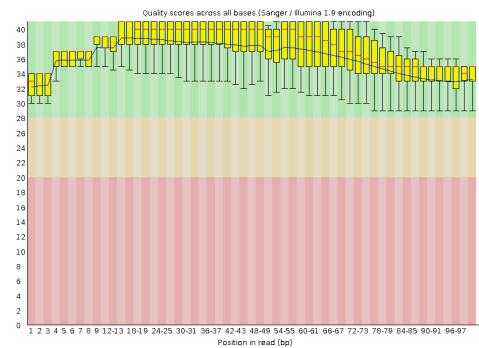
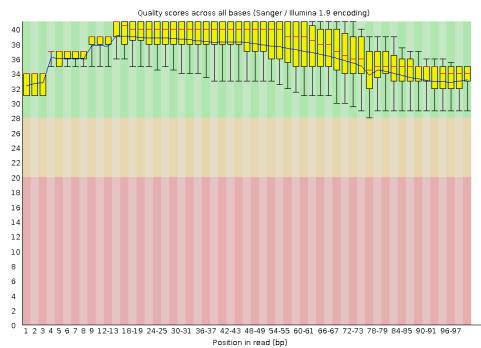


After trimming



Epigenome Analysis Platform

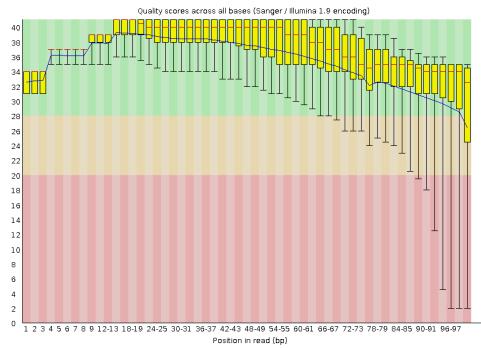
Report



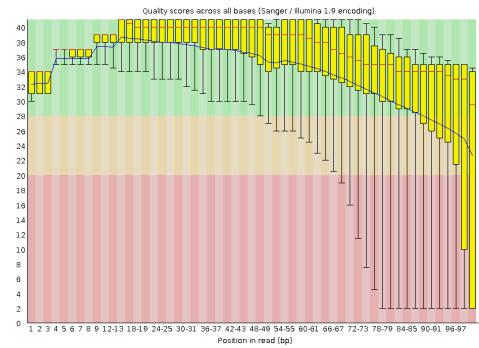
SRR1658130

R1

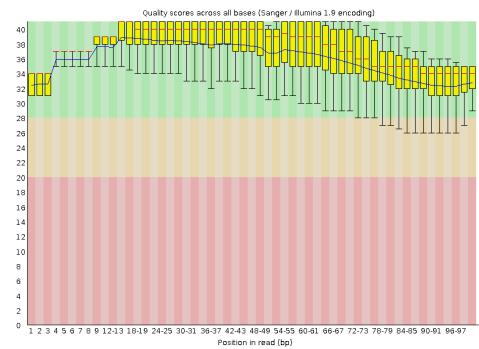
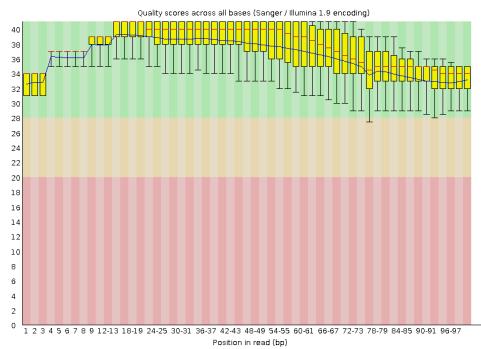
Before trimming



R2



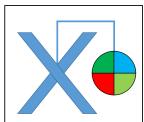
After trimming



SRR1658310

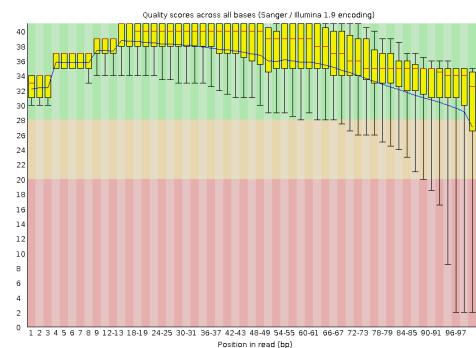
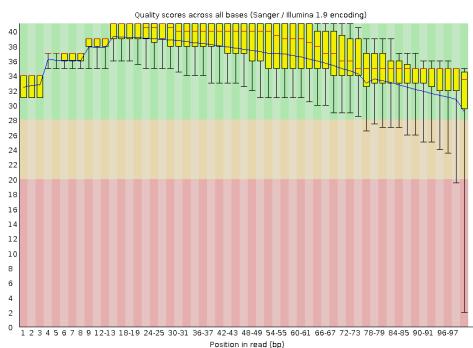
R1

Before trimming

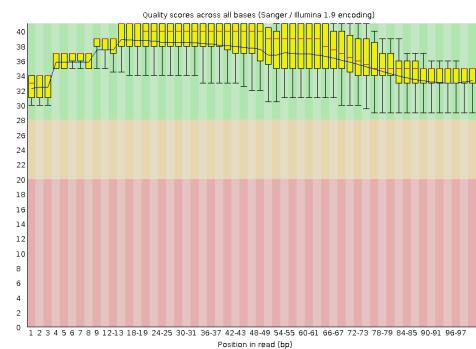
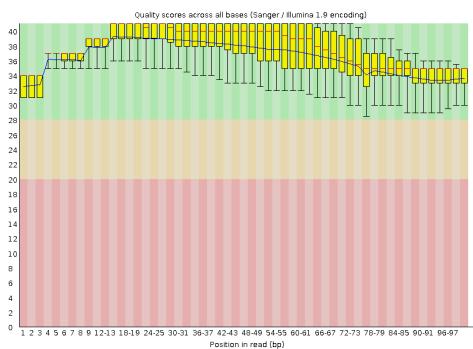


Epigenome Analysis Platform

Report



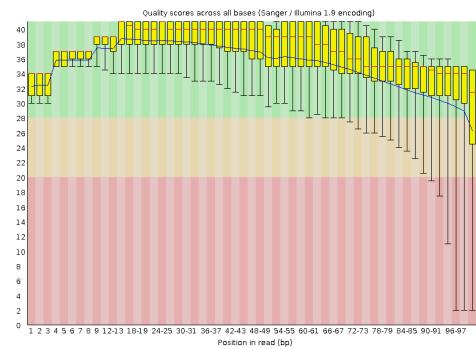
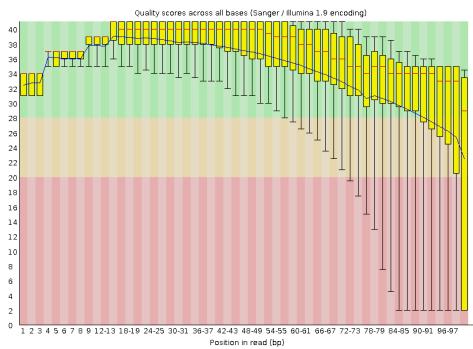
After trimming



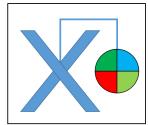
SRR1658202

R1

Before trimming

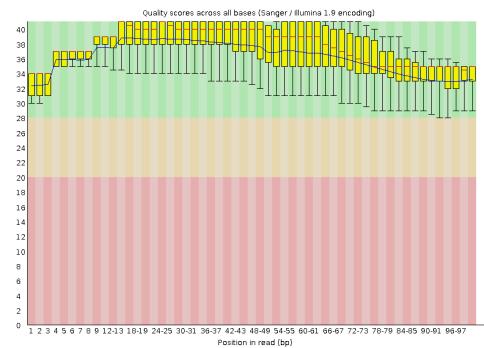
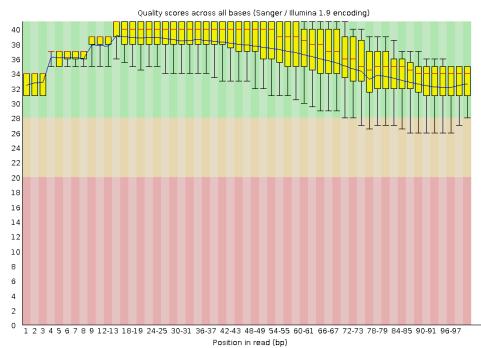


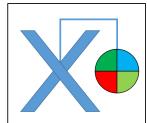
After trimming



Epigenome Analysis Platform

Report



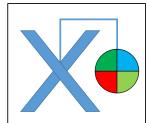


3 Quality control for reads mapping

Here we showed the mapping statistics in this analysis. Subsection 3.1 showed total number of reads (pairs), number of uniquely mapped reads (pairs) (i.e. a read that maps to a single position in reference genome) and number of deduplicated reads (pairs) (only keep at most one read at each genomic position). Subsection 3.2 showed the reads distribution across gene body (from TSS-2kb to TES+2kb). This coverage is calculated as the number of reads in each bin (normalized by Reads Per Kilobase per Million mapped reads, RPKM), where bins are a list of consecutive windows for counting reads.

3.1 The table below shows the number of reads kepted after reads mapping and removing PCR duplicates.

Sample_ID	Total number of reads (pairs)	Number of uniquely mapped reads (pairs)	Number of deduplicated reads (pairs)
SRR1658122	28572278	24447779 (85.56%)	24090945 (84.32%)
SRR1658320	29031887	24947510 (85.93%)	23114762 (79.62%)
SRR1658140	30032905	25601900 (85.25%)	23980667 (79.85%)
SRR1658131	30300271	25952653 (85.65%)	23448025 (77.39%)
SRR1658311	30991556	26827902 (86.57%)	26130947 (84.32%)
SRR1658328	27581572	23855102 (86.49%)	21619876 (78.39%)
SRR1658247	26399484	22684745 (85.93%)	21824999 (82.67%)
SRR1658229	30821041	26804802 (86.97%)	26175446 (84.93%)
SRR1658184	28164566	24649203 (87.52%)	20984856 (74.51%)
SRR1658265	29353036	25054536 (85.36%)	24731521 (84.26%)
SRR1658319	31841172	15420882 (48.43%)	14694460 (46.15%)
SRR1658126	28174620	24274507 (86.16%)	22607285 (80.24%)
SRR1658324	27639523	23648640 (85.56%)	22227569 (80.42%)
SRR1658243	29863186	26031219 (87.17%)	25314093 (84.77%)
SRR1658306	31983916	27695616 (86.59%)	25579253 (79.98%)
SRR1658342	24781567	21420564 (86.44%)	20237856 (81.66%)
SRR1658270	32295708	27884721 (86.34%)	25915977 (80.25%)
SRR1658269	28977040	25415961 (87.71%)	19384950 (66.90%)
SRR1658296	33689018	29573302 (87.78%)	24660170 (73.20%)
SRR1658197	28307781	24453955 (86.39%)	22682492 (80.13%)
SRR1658278	30487532	26141949 (85.75%)	24161395 (79.25%)
SRR1658205	27250149	23517709 (86.30%)	21750208 (79.82%)
SRR1658142	27825928	24019741 (86.32%)	22730117 (81.69%)
SRR1658340	32292176	28267774 (87.54%)	24284186 (75.20%)



Epigenome Analysis Platform

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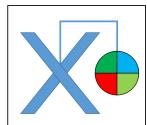
SRR1658133	31731530	27500911 (86.67%)	25538064 (80.48%)
SRR1658214	28124638	24247166 (86.21%)	23294904 (82.83%)
SRR1658232	30670240	26264618 (85.64%)	20255948 (66.04%)
SRR1658168	29417034	25579260 (86.95%)	25097138 (85.31%)
SRR1658267	29126977	25183990 (86.46%)	24103732 (82.75%)
SRR1658177	28322701	24144558 (85.25%)	16766878 (59.20%)
SRR1658339	29344736	25621569 (87.31%)	24372707 (83.06%)
SRR1658276	25443425	21948703 (86.26%)	20856018 (81.97%)
SRR1658128	33000326	28575177 (86.59%)	27258322 (82.60%)
SRR1658245	26007726	22394932 (86.11%)	20971694 (80.64%)
SRR1658227	29981408	26220367 (87.46%)	22960929 (76.58%)
SRR1658182	34399945	29857976 (86.80%)	28748662 (83.57%)
SRR1658263	29446081	25762146 (87.49%)	21177755 (71.92%)
SRR1658173	30490591	26155231 (85.78%)	25692675 (84.26%)
SRR1658155	28544289	24570742 (86.08%)	24275262 (85.04%)
SRR1658317	27936123	24419377 (87.41%)	23441486 (83.91%)
SRR1658191	26853023	22991490 (85.62%)	22550060 (83.98%)
SRR1658210	33474555	28759847 (85.92%)	25927456 (77.45%)
SRR1658111	28166725	24140041 (85.70%)	21464754 (76.21%)
SRR1658201	23892051	20775861 (86.96%)	19245039 (80.55%)
SRR1658240	33473723	28545767 (85.28%)	28149771 (84.10%)
SRR1658141	34051588	29079920 (85.40%)	28610565 (84.02%)
SRR1658303	20616870	10255772 (49.74%)	10167562 (49.32%)
SRR1658312	31798012	27718396 (87.17%)	25773956 (81.06%)
SRR1658114	31378079	26608279 (84.80%)	26221575 (83.57%)
SRR1658149	30430464	26324462 (86.51%)	20830926 (68.45%)
SRR1658176	31777892	27406687 (86.24%)	25989663 (81.79%)
SRR1658127	25534938	22298118 (87.32%)	21258477 (83.25%)
SRR1658208	31687349	27185958 (85.79%)	26705788 (84.28%)
SRR1658325	29490870	25704698 (87.16%)	24289408 (82.36%)
SRR1658244	29807745	25990444 (87.19%)	22499833 (75.48%)
SRR1658181	30296170	26338384 (86.94%)	25527200 (84.26%)
SRR1658288	26939663	23491755 (87.20%)	22329340 (82.89%)
SRR1658110	27901939	23938665 (85.80%)	22718774 (81.42%)



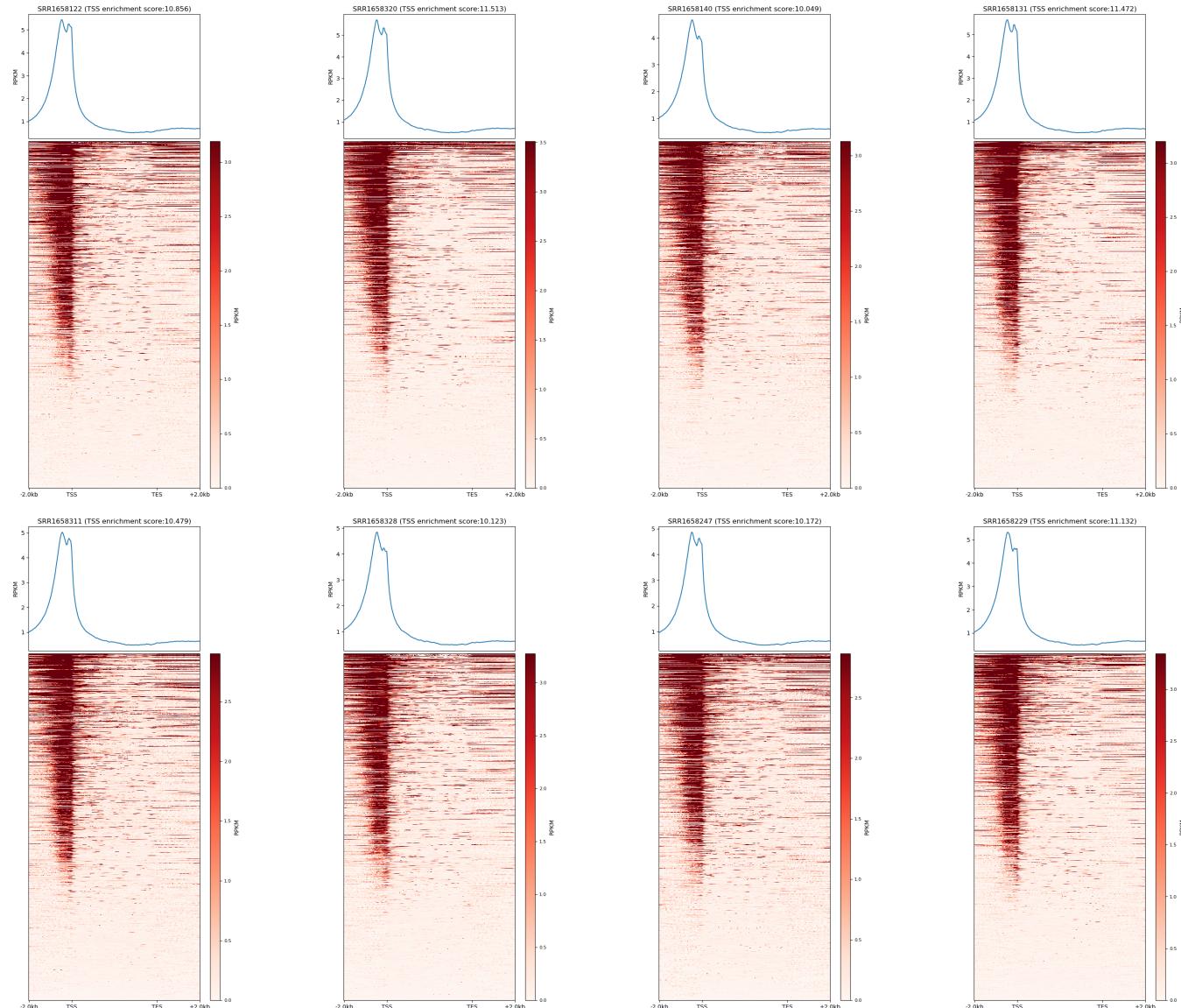
Epigenome Analysis Platform

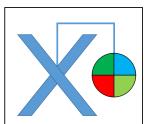
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SRR1658161	30350425	26162533 (86.20%)	24804268 (81.73%)
SRR1658323	24449561	21339559 (87.28%)	20494692 (83.82%)
SRR1658242	32614987	27851121 (85.39%)	27471686 (84.23%)
SRR1658224	36396881	31204272 (85.73%)	28859638 (79.29%)
SRR1658341	28076581	24097731 (85.83%)	23507033 (83.72%)
SRR1658215	29081233	25163820 (86.53%)	23664757 (81.37%)
SRR1658170	25009938	21752487 (86.98%)	20979298 (83.88%)
SRR1658152	18603368	16068393 (86.37%)	15913338 (85.54%)
SRR1658295	24559751	21019283 (85.58%)	19802582 (80.63%)
SRR1658277	28095374	24239211 (86.27%)	22240998 (79.16%)
SRR1658246	27252005	23338699 (85.64%)	22969896 (84.29%)
SRR1658309	30430477	26192123 (86.07%)	24250050 (79.69%)
SRR1658228	30010689	26165781 (87.19%)	18603550 (61.99%)
SRR1658183	29702979	25795030 (86.84%)	25285265 (85.13%)
SRR1658264	34511424	29978644 (86.87%)	28345775 (82.13%)
SRR1658318	30322265	26467240 (87.29%)	25087576 (82.74%)
SRR1658192	31796207	27313028 (85.90%)	26855550 (84.46%)
SRR1658130	27628771	23849398 (86.32%)	23126768 (83.71%)
SRR1658310	28590396	24621528 (86.12%)	23346993 (81.66%)
SRR1658202	29228342	25233763 (86.33%)	23663521 (80.96%)



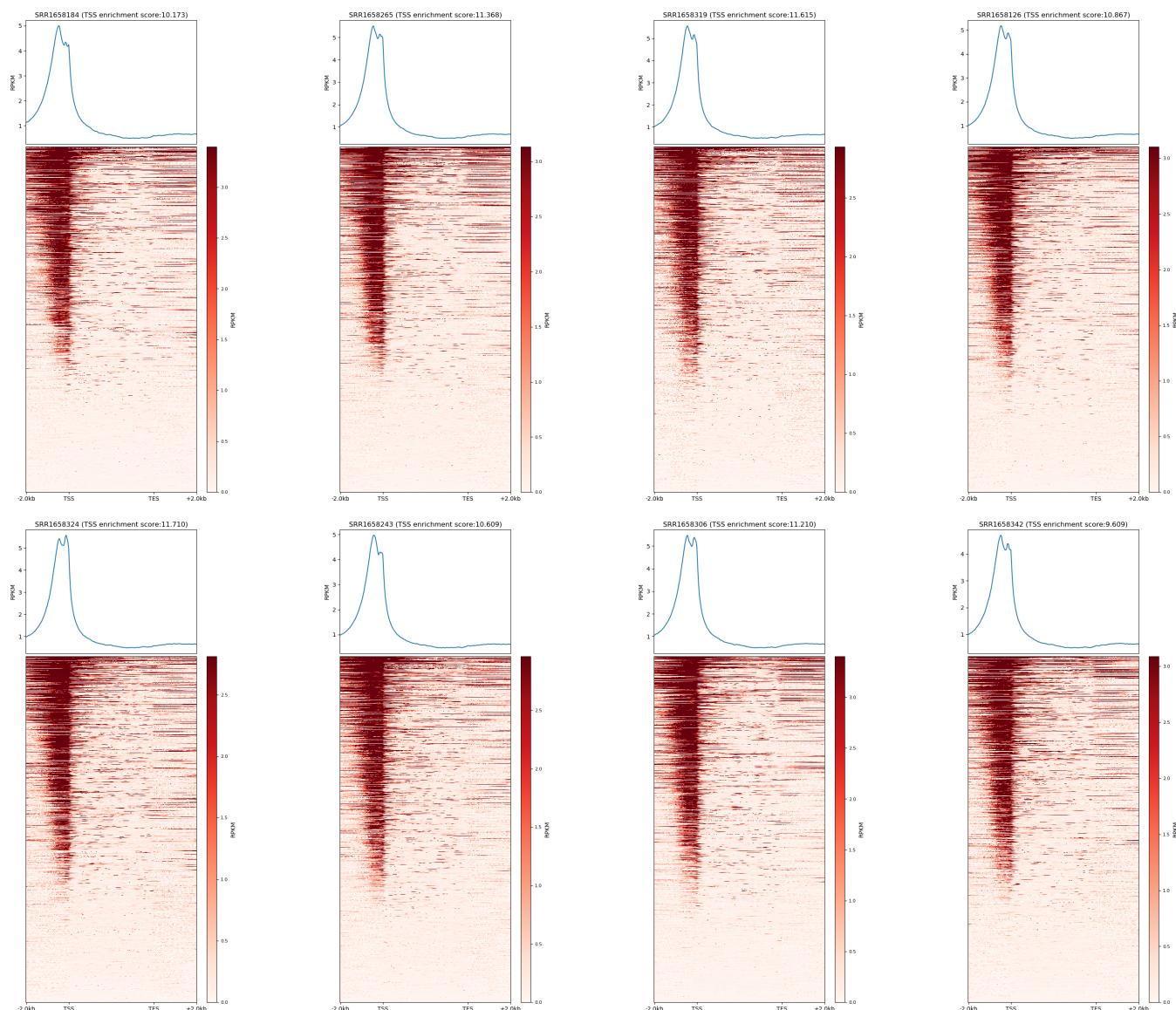
3.2 The figures below show the reads distribution across gene body.

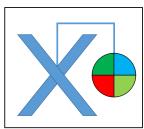




Epigenome Analysis Platform

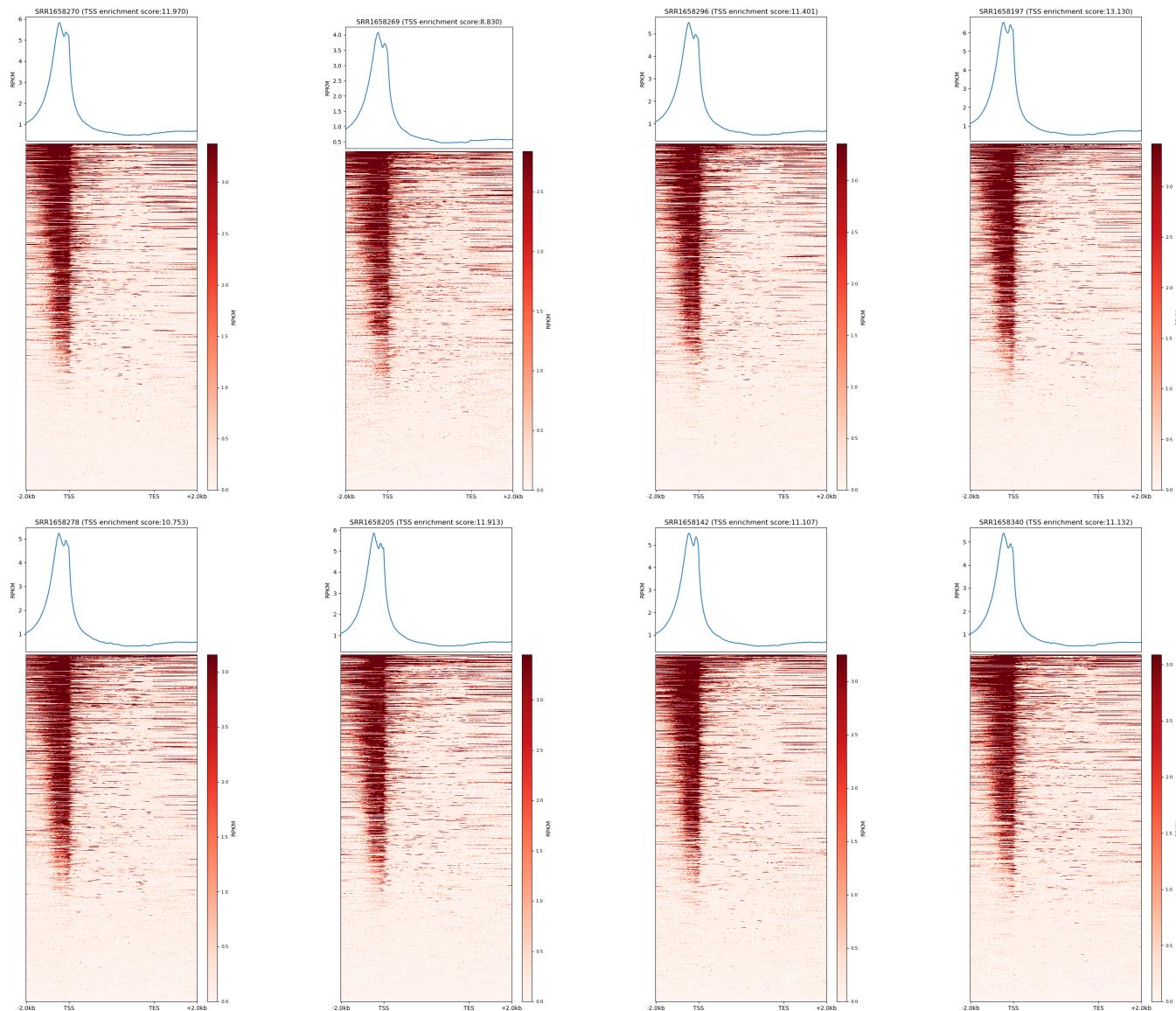
Report

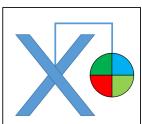




Epigenome Analysis Platform

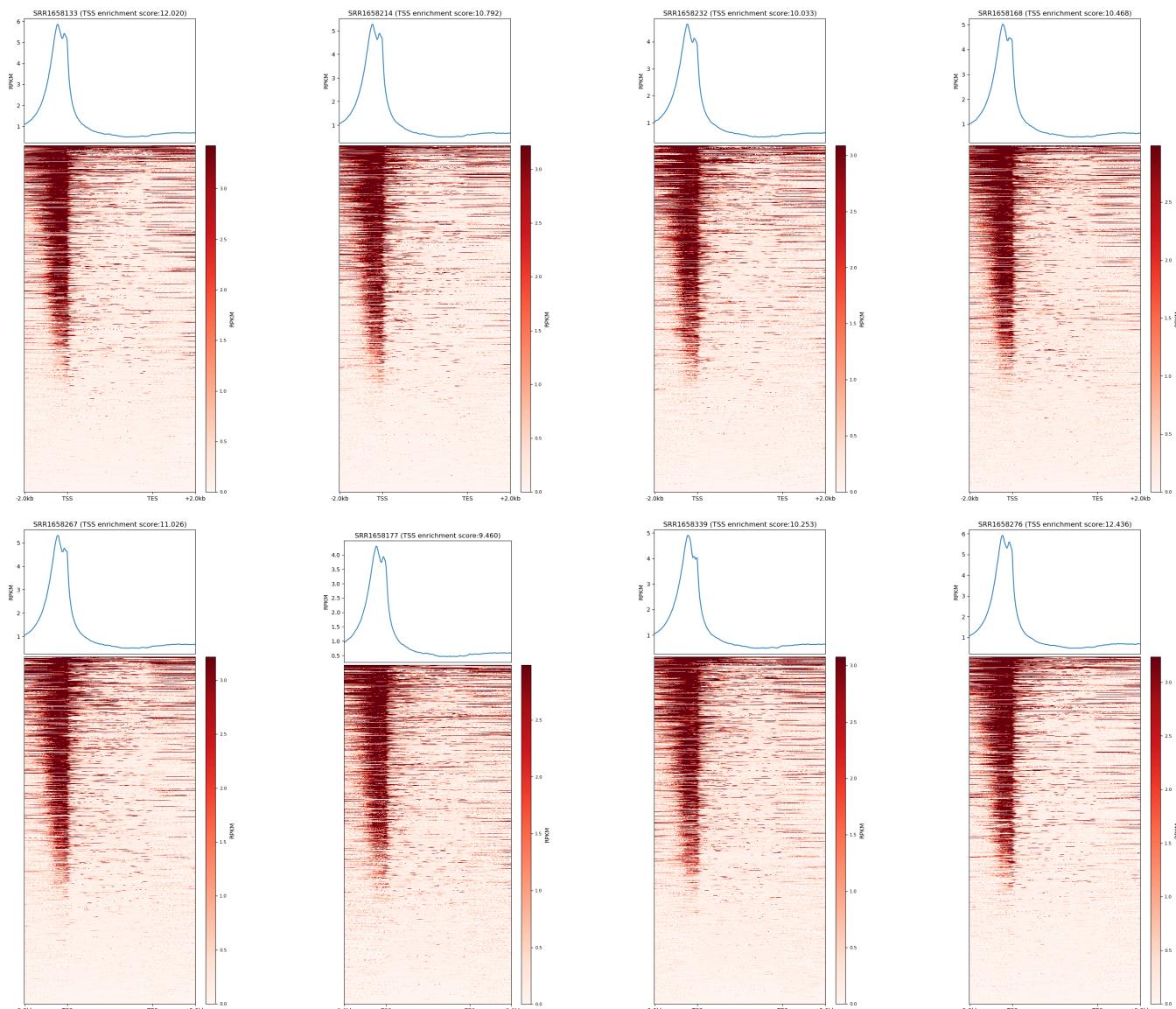
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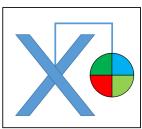




Epigenome Analysis Platform

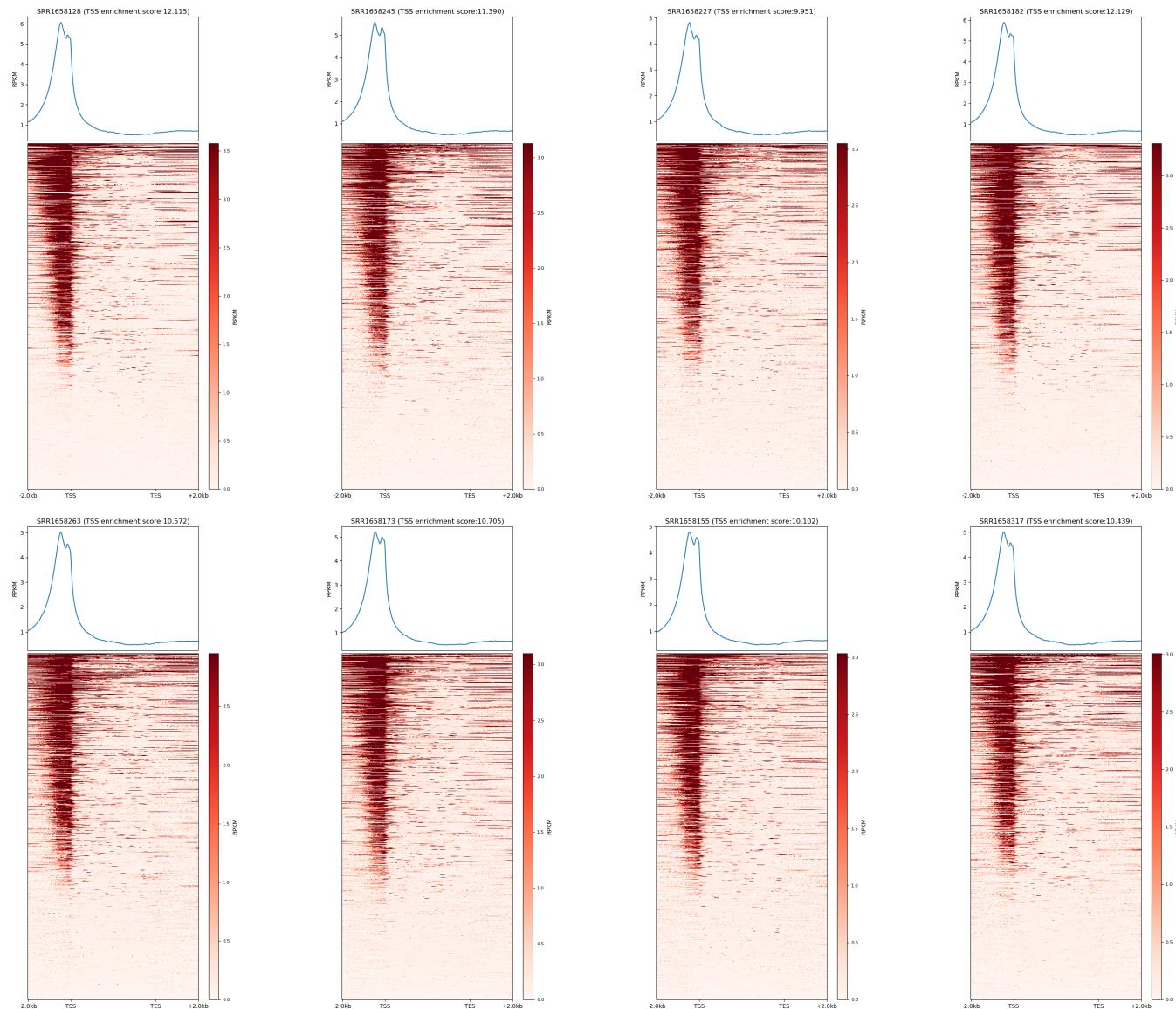
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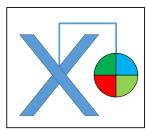




Epigenome Analysis Platform

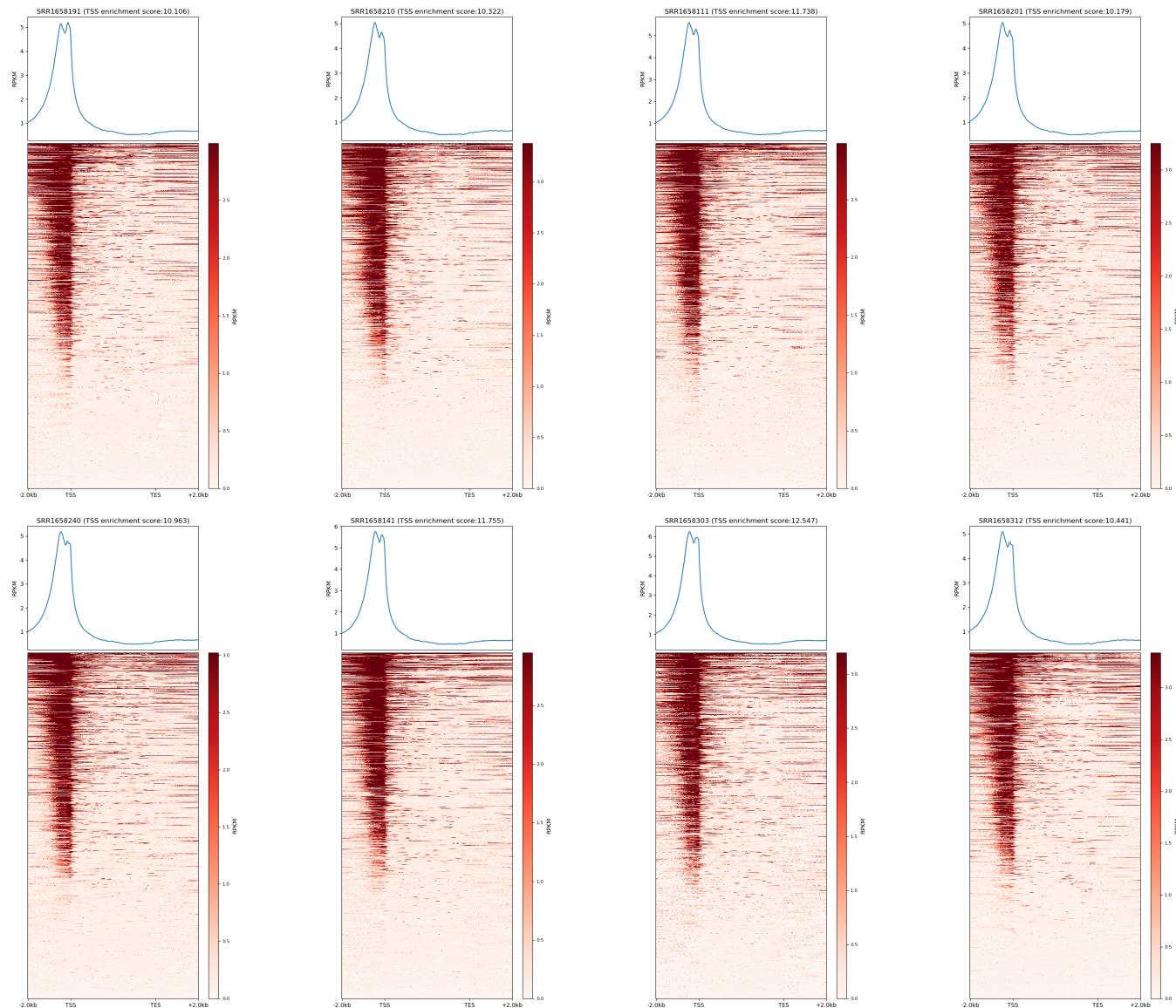
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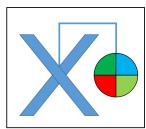




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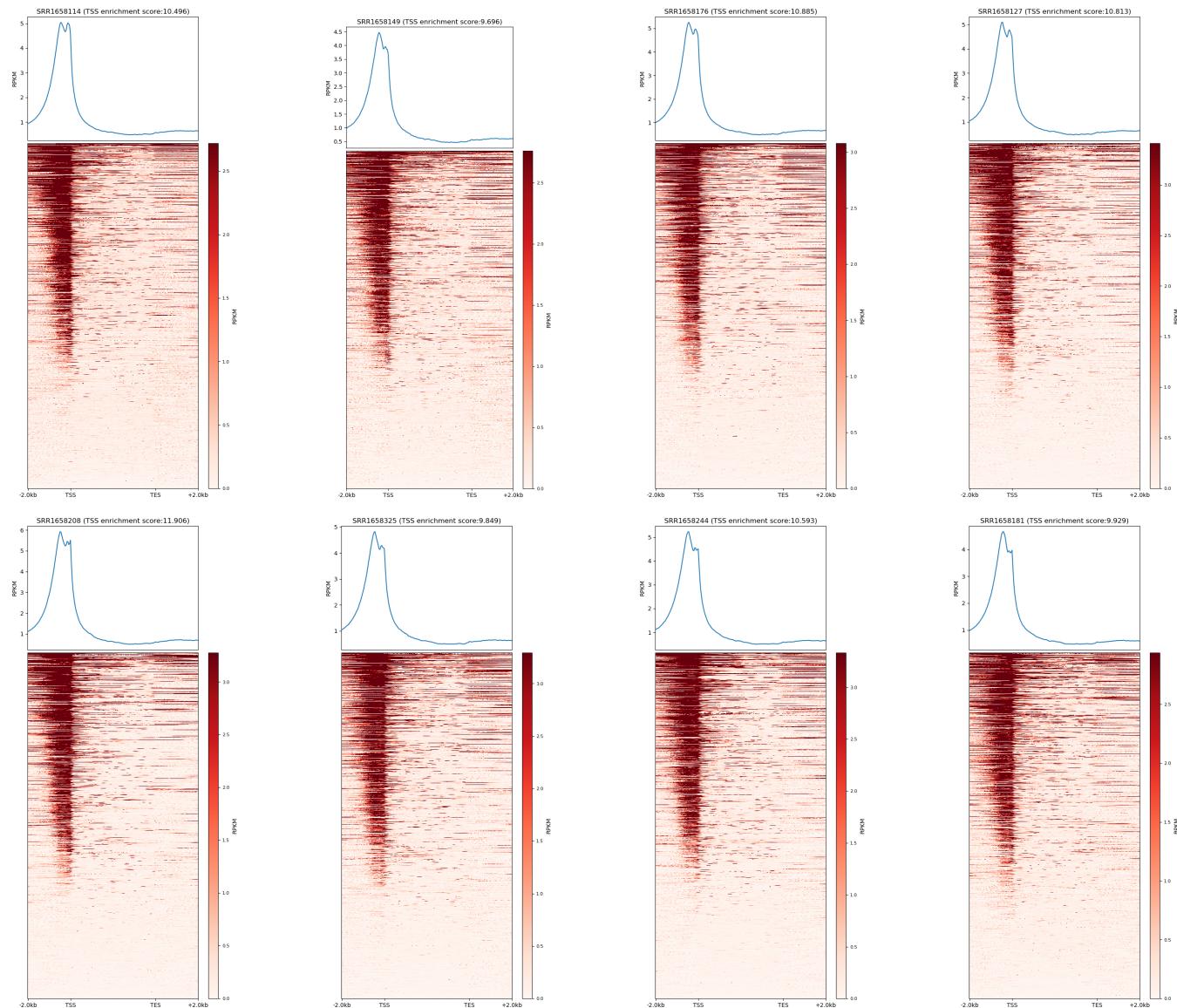
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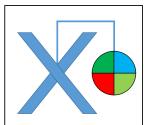




Epigenome Analysis Platform

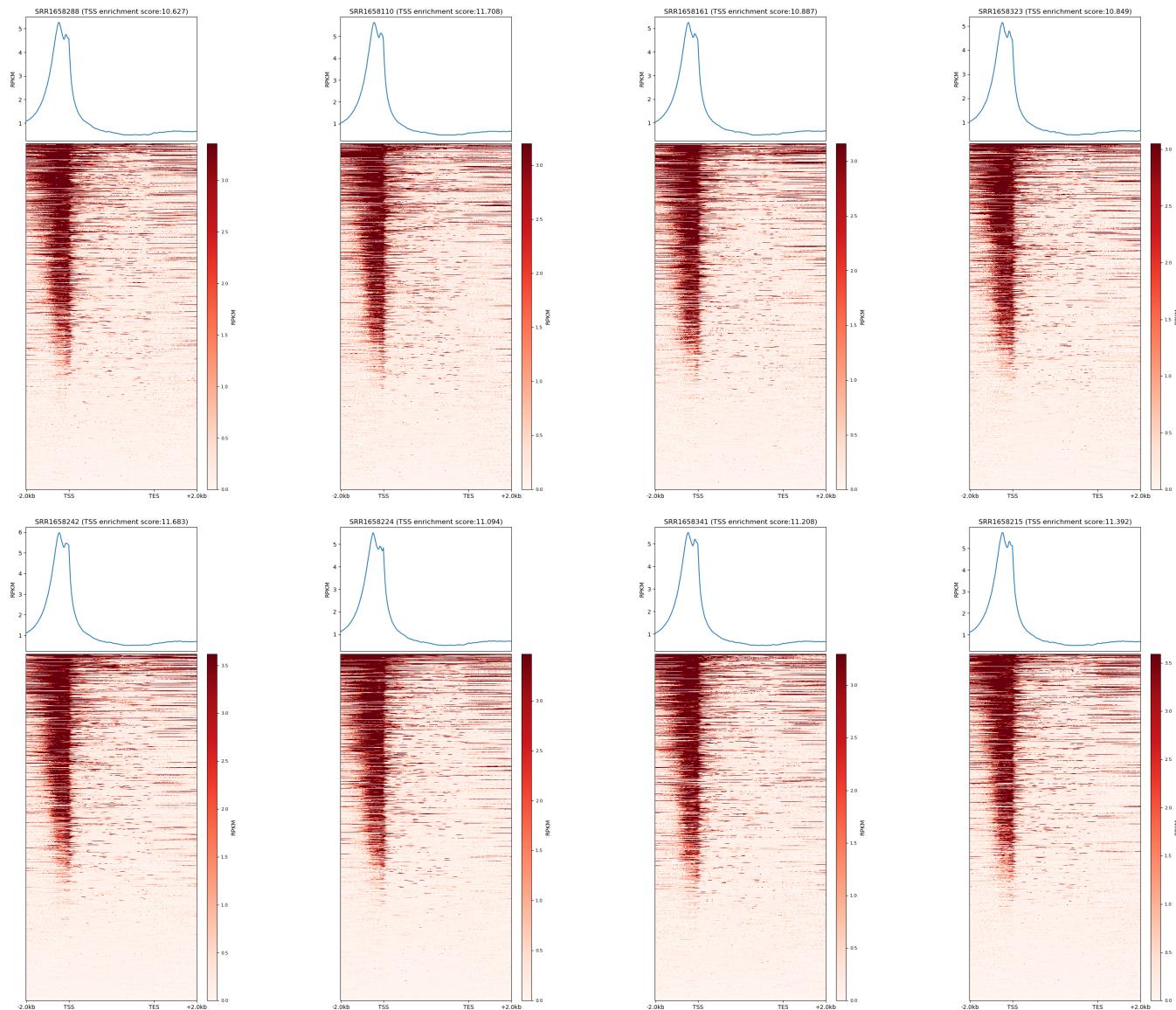
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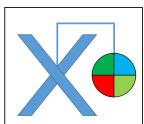




Epigenome Analysis Platform

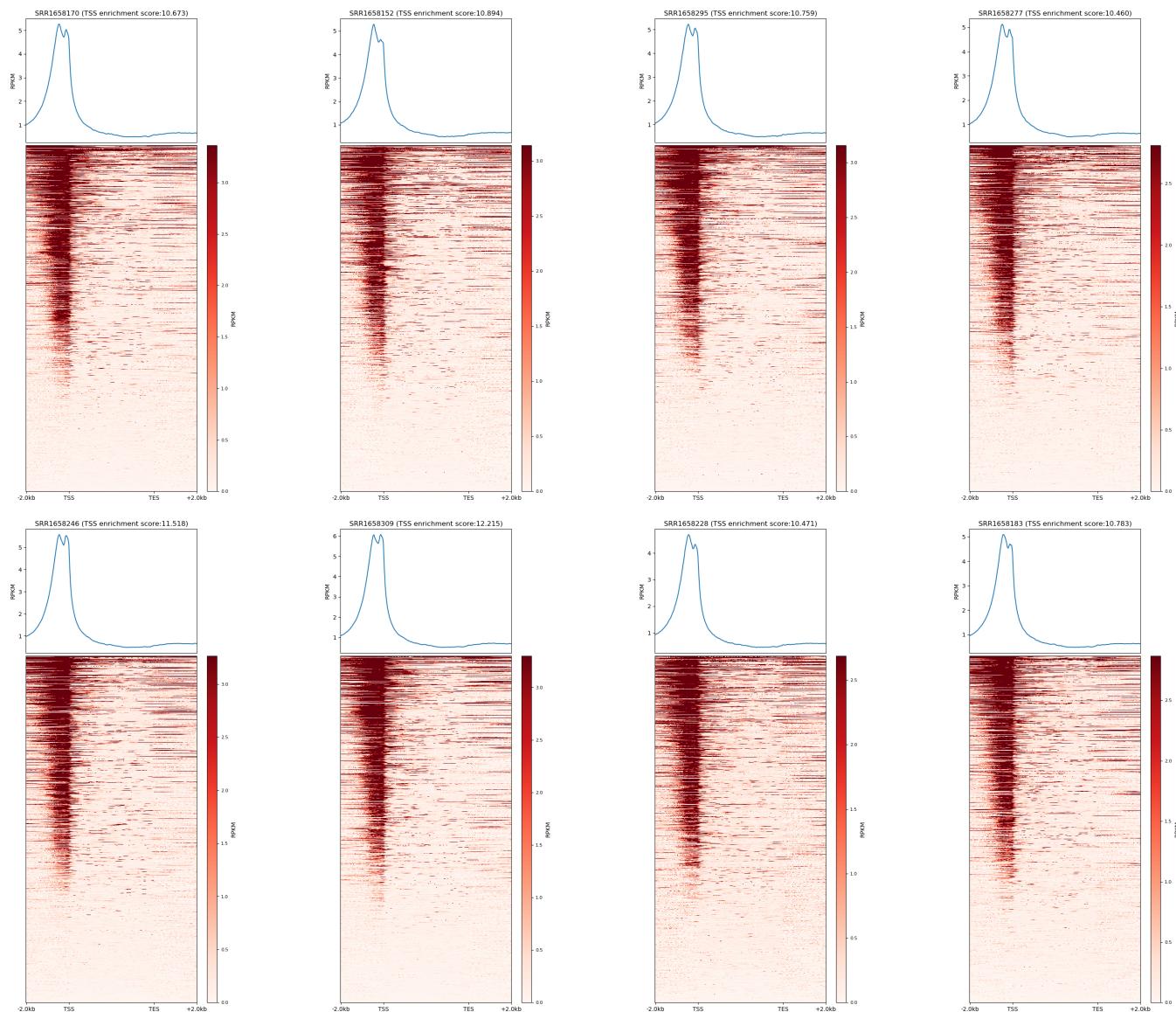
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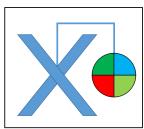




Epigenome Analysis Platform

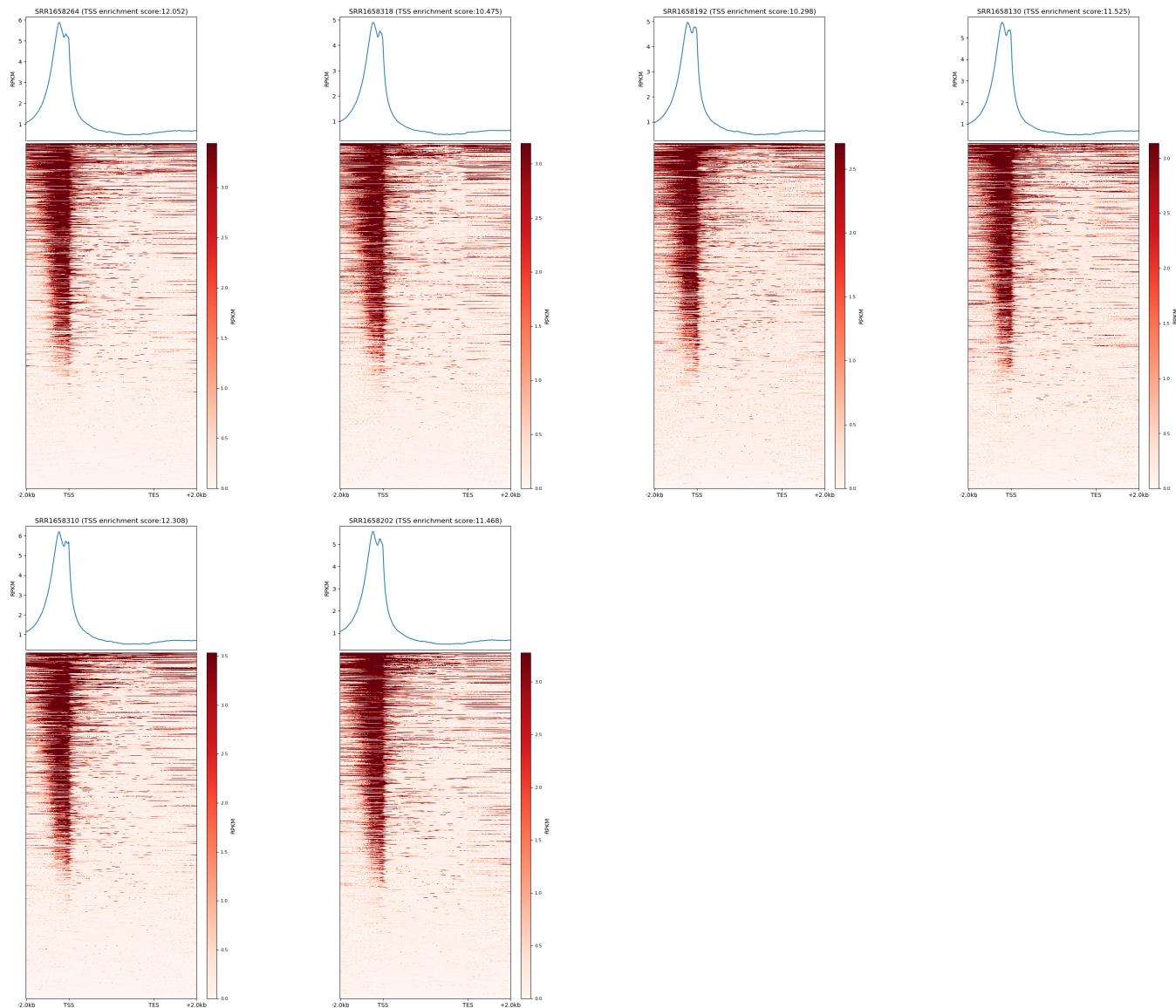
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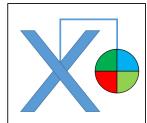




Epigenome Analysis Platform

Report



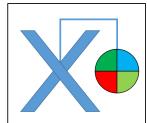


4 Quality control for peaks calling

In this section, we showed the statistics of peaks calling analysis. The table showed number of peaks (i.e. number of peaks identified by MACS), Number of peaks after filtering (i.e. number of peaks after removing those in blacklisted regions), Number of peaks after merging (i.e. number of peaks after merging peaks from each sample), Number of reads after filtering (i.e. number of reads after removing those overlapped with blacklisted regions), Number of reads within peaks (i.e. number of reads that fall into a peak) and Reads within peaks ratio (defined as the fraction of reads that fall into a peak and is often used as a measure of ChIP/ATAC-seq quality.).

4.1 The table below shows the number of peaks and reads within peaks ratio in each sample.

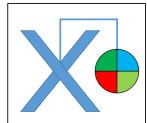
Sample_ID	Number of peaks	Number of peaks after filtering	Number of peaks after merging	Number of reads after filtering	Number of reads within peaks	Reads within peaks ratio
SRR1658122	488066	488066	78026	48181890	28266418	58.70%
SRR1658320	512373	512373	83677	46229524	28723602	62.10%
SRR1658140	503847	503847	90414	47961334	26563415	55.40%
SRR1658131	509748	509748	78501	46896050	29012982	61.90%
SRR1658311	515228	515228	81307	52261894	29699869	56.80%
SRR1658328	472643	472643	88731	43239752	25375086	58.70%
SRR1658247	463644	463644	79272	43649998	25070570	57.40%
SRR1658229	547964	547964	83200	52350892	31139834	59.50%
SRR1658184	492067	492067	88033	41969712	25346835	60.40%
SRR1658265	522193	522193	76162	49463042	29621389	59.90%
SRR1658319	354575	354575	70678	29388920	17311749	58.90%
SRR1658126	494053	494053	79110	45214570	26471141	58.50%
SRR1658324	460990	460990	72063	44455138	25297982	56.90%
SRR1658243	524511	524511	85333	50628186	27941039	55.20%
SRR1658306	533208	533208	86536	51158506	30566541	59.70%
SRR1658342	447704	447704	85515	40475712	22734969	56.20%
SRR1658270	563926	563926	79781	51831954	32698921	63.10%
SRR1658269	419398	419398	93108	38769900	20690051	53.40%
SRR1658296	561636	561636	83796	49320340	30417892	61.70%
SRR1658197	505547	505547	68288	45364984	29759207	65.60%
SRR1658278	514895	514895	81499	48322790	29010362	60.00%
SRR1658205	502748	502748	77677	43500416	27529842	63.30%
SRR1658142	478943	478943	75357	45460234	26265226	57.80%
SRR1658340	557728	557728	84970	48568372	29110081	59.90%



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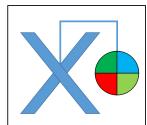
SRR1658133	552748	552748	79536	51076128	31636624	61.90%
SRR1658214	500244	500244	84013	46589808	28577246	61.30%
SRR1658232	459918	459918	88665	40511896	22964934	56.70%
SRR1658168	487944	487944	81052	50194276	27593149	55.00%
SRR1658267	540834	540834	84131	48207464	29171822	60.50%
SRR1658177	353605	353605	83368	33533756	17880429	53.30%
SRR1658339	505977	505977	82312	48745414	26670132	54.70%
SRR1658276	487929	487929	74327	41712036	26878687	64.40%
SRR1658128	599148	599148	83113	54516644	36048768	66.10%
SRR1658245	465986	465986	75521	41943388	26461828	63.10%
SRR1658227	512342	512342	83746	45921858	26541145	57.80%
SRR1658182	599093	599093	80679	57497324	36799577	64.00%
SRR1658263	494708	494708	83079	42355510	25418590	60.00%
SRR1658173	519744	519744	80334	51385350	29325086	57.10%
SRR1658155	484970	484970	80800	48550524	27211795	56.00%
SRR1658317	502996	502996	81906	46882972	27750542	59.20%
SRR1658191	455855	455855	72350	45100120	26519925	58.80%
SRR1658210	519591	519591	87533	51854912	29607515	57.10%
SRR1658111	467549	467549	71748	42929508	25410600	59.20%
SRR1658201	438907	438907	80006	38490078	22876224	59.40%
SRR1658240	541181	541181	77710	56299542	31730105	56.40%
SRR1658141	512292	512292	69636	57221130	32624389	57.00%
SRR1658303	331413	331413	80646	20335124	11802932	58.00%
SRR1658312	562092	562092	88581	51547912	30956886	60.10%
SRR1658114	459745	459745	70494	52443150	26928823	51.30%
SRR1658149	421084	421084	79541	41661852	21984557	52.80%
SRR1658176	529682	529682	78818	51979326	29749794	57.20%
SRR1658127	484424	484424	88689	42516954	24686390	58.10%
SRR1658208	535424	535424	74083	53411576	35102404	65.70%
SRR1658325	504888	504888	88785	48578816	27643757	56.90%
SRR1658244	511665	511665	84435	44999666	27002256	60.00%
SRR1658181	497608	497608	87778	51054400	27996760	54.80%
SRR1658288	471097	471097	83454	44658680	25511010	57.10%
SRR1658110	483847	483847	77759	45437548	26245382	57.80%



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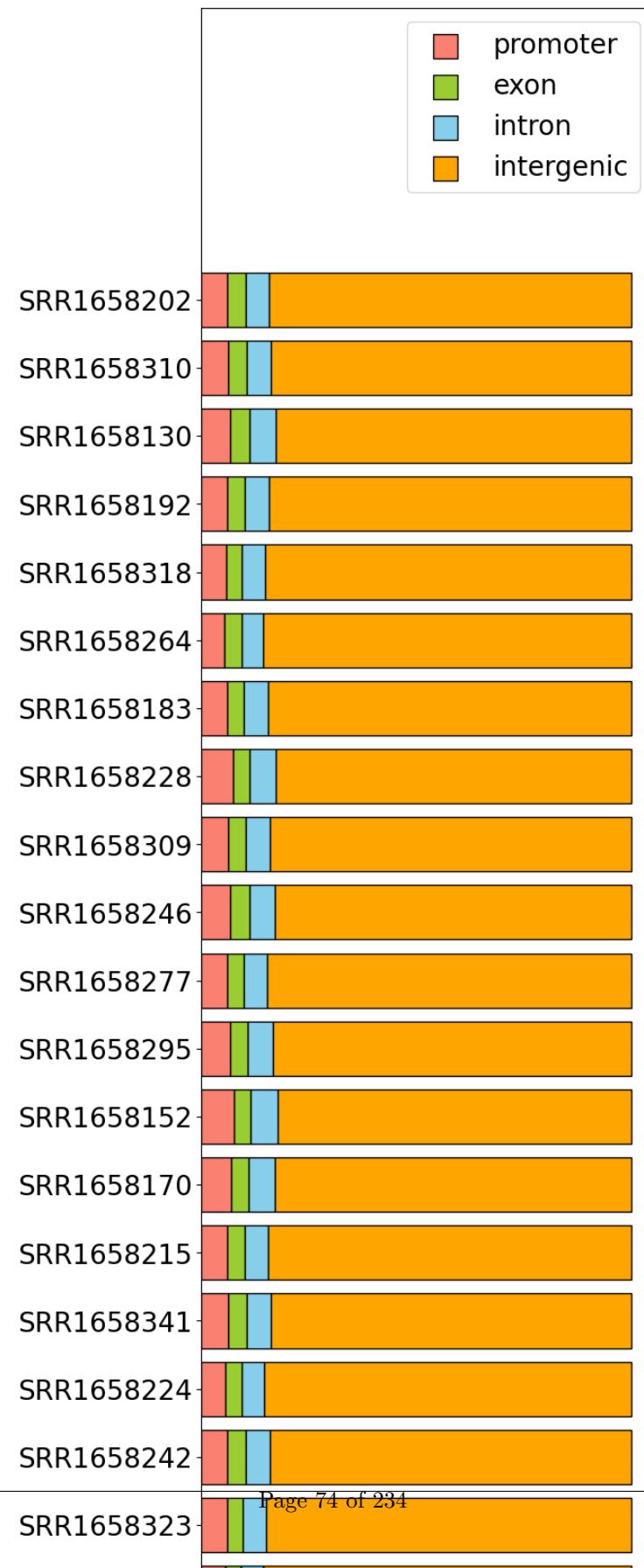
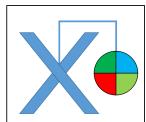
SRR1658161	565014	565014	84705	49608536	30066702	60.60%
SRR1658323	485304	485304	78982	40989384	25472214	62.10%
SRR1658242	535542	535542	78779	54943372	34150335	62.20%
SRR1658224	581631	581631	85404	57719276	35611221	61.70%
SRR1658341	503669	503669	80031	47014066	28256486	60.10%
SRR1658215	534259	534259	81014	47329514	29883716	63.10%
SRR1658170	450363	450363	82360	41958596	23806157	56.70%
SRR1658152	355364	355364	69851	31826676	19011582	59.70%
SRR1658295	435041	435041	75472	39605164	23850914	60.20%
SRR1658277	490649	490649	79450	44481996	26286097	59.10%
SRR1658246	470485	470485	74936	45939792	26207082	57.00%
SRR1658309	516236	516236	78212	48500100	30423466	62.70%
SRR1658228	383281	383281	77194	37207100	19114419	51.40%
SRR1658183	498844	498844	80350	50570530	28401796	56.20%
SRR1658264	602792	602792	85222	56691550	35920930	63.40%
SRR1658318	541451	541451	89896	50175152	28263293	56.30%
SRR1658192	499462	499462	72931	53711100	29932281	55.70%
SRR1658130	464437	464437	71706	46253536	25981040	56.20%
SRR1658310	509298	509298	73058	46693986	29672592	63.50%
SRR1658202	516250	516250	79443	47327042	29187562	61.70%

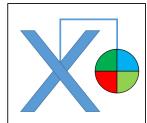


5 Genomic annotations of peaks

In this section, peaks were annotated by relative location relationship with genomic features (Priority: promoter > exon > intron > intergenic).

5.1 The figure below show the proportion of peaks assigned to different genomic features in each sample.





6 Motif enrichment

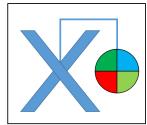
In this section, we showed the motif enrichment results in each sample, including Known motif enrichment and de novo motif enrichment. Two motif enrichment analysis were both used to detecting motifs that are more enriched in ChIP/ATAC-seq peaks than random genomic regions.

6.1 Known motif enrichment

The table below shows the known motif enrichment result using Homer.

SRR1658122

Motif	Rank	Name	P-value	log P-pvalue	q-value	# Tar- (Benjamini)	% of Tar- gets	# Tar- sequences	% of Back-ground	# Back-sequences	% of Back-ground
						Se-jamini)	Se-gets	Se-sequences	Se-sequences	Se-sequences	Se-sequences
						Se-	Se-	Se-	Se-	Se-	Se-
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3702	-8.526e+03	0.0000	88211.0	18.07%	55478.6	11.66%		
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3294	-7.585e+03	0.0000	97303.0	19.94%	64474.9	13.55%		
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3261	-7.509e+03	0.0000	88419.0	18.12%	57305.6	12.05%		
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3177	-7.317e+03	0.0000	69778.0	14.30%	42665.5	8.97%		
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3044	-7.010e+03	0.0000	75381.0	15.44%	47589.8	10.00%		
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2803	-6.454e+03	0.0000	73065.0	14.97%	46641.7	9.80%		
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2774	-6.389e+03	0.0000	103718.0	21.25%	72148.6	15.17%		
	8	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2593	-5.972e+03	0.0000	65216.0	13.36%	41151.6	8.65%		



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	9	Elk1(ETS)/Hela- Elk1-ChIP- Seq(GSE31477)/Homer	1e- 2509	- 5.779e+03	0.0000	53041.0	10.87%	31877.7	6.70%
	10	IRF8(IRF)/BMDM- IRF8-ChIP- Seq(GSE77884)/Homer	1e- 2492	- 5.738e+03	0.0000	29634.0	6.07%	14659.2	3.08%



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SRR1658320

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Background Sequences	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3768	-8.677e+03	0.0000	89909.0	17.55%	56764.2	11.31%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3364	-7.746e+03	0.0000	100303.0	19.58%	66854.0	13.32%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3314	-7.631e+03	0.0000	89478.0	17.46%	58128.3	11.59%
	4	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3176	-7.315e+03	0.0000	78026.0	15.23%	49370.0	9.84%
	5	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3174	-7.309e+03	0.0000	71184.0	13.89%	43922.9	8.75%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2963	-6.824e+03	0.0000	76262.0	14.88%	48752.4	9.72%
	7	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2886	-6.646e+03	0.0000	32499.0	6.34%	15823.6	3.15%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2863	-6.593e+03	0.0000	108199.0	21.12%	75743.8	15.10%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2705	-6.231e+03	0.0000	67867.0	13.25%	42984.6	8.57%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2518	-5.799e+03	0.0000	52567.0	10.26%	31593.1	6.30%



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SRR1658140

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets with Motif	# Sequences with Motif	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3699	-8.518e+03	0.0000	83986.0	16.67%	52607.0	10.60%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3304	-7.608e+03	0.0000	95094.0	18.87%	63205.5	12.73%
	3	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3158	-7.272e+03	0.0000	74648.0	14.82%	47041.3	9.48%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3143	-7.237e+03	0.0000	67058.0	13.31%	41047.3	8.27%
	5	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3108	-7.158e+03	0.0000	81283.0	16.13%	52602.3	10.60%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3044	-7.011e+03	0.0000	73910.0	14.67%	46864.5	9.44%
	7	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2830	-6.518e+03	0.0000	33541.0	6.66%	16773.0	3.38%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2754	-6.342e+03	0.0000	104735.0	20.79%	73807.9	14.87%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2645	-6.092e+03	0.0000	65746.0	13.05%	41787.4	8.42%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2471	-5.692e+03	0.0000	46624.0	9.25%	27356.0	5.51%



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SRR1658131

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Background Sequences	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3875	-8.923e+03	0.0000	90065.0	17.67%	56393.5	11.32%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3509	-8.080e+03	0.0000	100389.0	19.69%	66197.1	13.29%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3408	-7.848e+03	0.0000	89774.0	17.61%	57888.8	11.62%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3391	-7.809e+03	0.0000	71809.0	14.09%	43580.8	8.75%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3248	-7.481e+03	0.0000	78113.0	15.32%	49074.2	9.85%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3234	-7.449e+03	0.0000	77028.0	15.11%	48258.2	9.69%
	7	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3025	-6.966e+03	0.0000	32617.0	6.40%	15576.7	3.13%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2977	-6.856e+03	0.0000	107818.0	21.15%	74731.0	15.00%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2769	-6.378e+03	0.0000	67745.0	13.29%	42561.0	8.54%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2601	-5.990e+03	0.0000	53274.0	10.45%	31798.7	6.38%



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SRR1658311

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Background Sequences	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3981	-9.168e+03	0.0000	89696.0	17.41%	56029.5	11.06%
	2	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3880	-8.934e+03	0.0000	36466.0	7.08%	16561.9	3.27%
	3	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3774	-8.690e+03	0.0000	100965.0	19.60%	65980.2	13.03%
	4	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3556	-8.189e+03	0.0000	79054.0	15.34%	48999.3	9.68%
	5	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3519	-8.104e+03	0.0000	88621.0	17.20%	56841.2	11.22%
	6	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3507	-8.076e+03	0.0000	71612.0	13.90%	43280.1	8.55%
	7	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-3479	-8.013e+03	0.0000	16723.0	3.25%	5171.0	1.02%
	8	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3406	-7.844e+03	0.0000	77508.0	15.04%	48293.4	9.54%
	9	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-3361	-7.741e+03	0.0000	110227.0	21.39%	75438.6	14.90%
	10	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	1e-3177	-7.316e+03	0.0000	34941.0	6.78%	16936.4	3.34%



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SRR1658328

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
						Sequences	Sequences	Sequences	Background
						with Motif	with Motif	with Motif	ground Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-2891	-6.659e+03	0.0000	76080.0	16.10%	49260.2	10.59%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-2656	-6.117e+03	0.0000	86839.0	18.37%	59153.1	12.71%
	3	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2549	-5.870e+03	0.0000	60915.0	12.89%	38305.1	8.23%
	4	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2512	-5.786e+03	0.0000	74395.0	15.74%	49408.3	10.62%
	5	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2477	-5.705e+03	0.0000	67103.0	14.20%	43573.5	9.37%
	6	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2467	-5.683e+03	0.0000	30385.0	6.43%	15393.4	3.31%
	7	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2443	-5.626e+03	0.0000	67388.0	14.26%	43943.2	9.44%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2112	-4.864e+03	0.0000	95355.0	20.17%	69087.5	14.85%
	9	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2076	-4.782e+03	0.0000	42820.0	9.06%	25721.4	5.53%
	10	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2041	-4.701e+03	0.0000	59020.0	12.49%	38760.8	8.33%



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Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Sequences with Motif	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3747	-8.628e+03	0.0000	81844.0	17.65%	50824.6	11.14%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3476	-8.004e+03	0.0000	91791.0	19.80%	59917.4	13.13%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3365	-7.749e+03	0.0000	81369.0	17.55%	51799.1	11.35%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3337	-7.684e+03	0.0000	65545.0	14.14%	39274.3	8.61%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3297	-7.594e+03	0.0000	71812.0	15.49%	44352.5	9.72%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3129	-7.205e+03	0.0000	70631.0	15.23%	43999.5	9.64%
	7	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3083	-7.100e+03	0.0000	30976.0	6.68%	14482.8	3.17%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2866	-6.601e+03	0.0000	98975.0	21.35%	68507.2	15.01%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2767	-6.372e+03	0.0000	62546.0	13.49%	38833.6	8.51%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2499	-5.755e+03	0.0000	47708.0	10.29%	28121.0	6.16%



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SRR1658229

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets with Motif	# Sequences with Motif	% of Background with Motif	# Targets with Motif	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3590	-8.268e+03	0.0000	92221.0	16.83%	59287.4	11.02%		
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3386	-7.797e+03	0.0000	104143.0	19.01%	69939.2	13.01%		
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3195	-7.358e+03	0.0000	91336.0	16.67%	60124.8	11.18%		
	4	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3169	-7.299e+03	0.0000	81237.0	14.83%	51991.2	9.67%		
	5	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3169	-7.298e+03	0.0000	73681.0	13.45%	45933.1	8.54%		
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3003	-6.916e+03	0.0000	79881.0	14.58%	51537.3	9.58%		
	7	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2978	-6.859e+03	0.0000	35100.0	6.41%	17435.6	3.24%		
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2846	-6.555e+03	0.0000	113549.0	20.72%	80381.3	14.95%		
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2689	-6.192e+03	0.0000	70960.0	12.95%	45555.0	8.47%		
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2356	-5.426e+03	0.0000	52839.0	9.64%	32388.1	6.02%		



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Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Targets	% of Targets	# Sequences with Motif	% of Background
						Sequences	Sequences	Sequences	Background
						with Motif	with Motif	with Motif	ground Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3277	-7.547e+03	0.0000	80697.0	16.40%	51538.3	10.63%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-2923	-6.733e+03	0.0000	91427.0	18.58%	61816.2	12.75%
	3	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2822	-6.499e+03	0.0000	64209.0	13.05%	39946.9	8.24%
	4	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2761	-6.358e+03	0.0000	78662.0	15.99%	51892.2	10.70%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2755	-6.344e+03	0.0000	71406.0	14.51%	45982.0	9.48%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2700	-6.219e+03	0.0000	70565.0	14.34%	45510.6	9.38%
	7	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2524	-5.812e+03	0.0000	31216.0	6.34%	15855.6	3.27%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2421	-5.576e+03	0.0000	100569.0	20.44%	71960.2	14.84%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2374	-5.468e+03	0.0000	63045.0	12.81%	40688.3	8.39%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2168	-4.993e+03	0.0000	44990.0	9.14%	27105.3	5.59%



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SRR1658265

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Background Sequences	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3691	-8.500e+03	0.0000	91856.0	17.59%	58305.5	11.46%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3373	-7.768e+03	0.0000	102280.0	19.59%	68088.9	13.38%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3286	-7.567e+03	0.0000	92077.0	17.63%	60045.3	11.80%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3225	-7.428e+03	0.0000	72989.0	13.98%	44932.8	8.83%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3172	-7.304e+03	0.0000	79402.0	15.21%	50226.6	9.87%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2967	-6.834e+03	0.0000	77667.0	14.87%	49608.2	9.75%
	7	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2967	-6.833e+03	0.0000	32902.0	6.30%	15845.8	3.11%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2926	-6.739e+03	0.0000	110224.0	21.11%	76750.0	15.08%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2801	-6.450e+03	0.0000	69232.0	13.26%	43491.1	8.55%
	10	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-2548	-5.868e+03	0.0000	14503.0	2.78%	4960.0	0.97%



SRR1658319

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
						Sequences	Sequences	Sequences	Background
						with Motif	with Motif	with Motif	ground Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3376	-7.774e+03	0.0000	65969.0	18.61%	39625.1	11.43%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3002	-6.913e+03	0.0000	73051.0	20.60%	46582.1	13.43%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2929	-6.746e+03	0.0000	65012.0	18.34%	40341.1	11.63%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2837	-6.534e+03	0.0000	52389.0	14.78%	30707.6	8.85%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2819	-6.493e+03	0.0000	57234.0	16.14%	34538.5	9.96%
	6	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2668	-6.144e+03	0.0000	24766.0	6.98%	11129.5	3.21%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2642	-6.086e+03	0.0000	56056.0	15.81%	34197.8	9.86%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2485	-5.722e+03	0.0000	78352.0	22.10%	53019.7	15.29%
	9	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2294	-5.283e+03	0.0000	39011.0	11.00%	22129.4	6.38%
	10	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2264	-5.214e+03	0.0000	49336.0	13.91%	30185.6	8.70%



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Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets with Motif	# Sequences with Motif	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-4384	-1.010e+04	0.0000	88677.0	17.95%	53902.5	11.11%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-4028	-9.275e+03	0.0000	99378.0	20.11%	63774.6	13.14%
	3	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3858	-8.885e+03	0.0000	71178.0	14.41%	41846.5	8.62%
	4	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3856	-8.879e+03	0.0000	78087.0	15.81%	47253.4	9.74%
	5	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3820	-8.797e+03	0.0000	87579.0	17.73%	54940.7	11.32%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3690	-8.498e+03	0.0000	76770.0	15.54%	46761.5	9.64%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-3429	-7.897e+03	0.0000	107334.0	21.73%	72772.7	15.00%
	8	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3413	-7.859e+03	0.0000	33638.0	6.81%	15572.3	3.21%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-3385	-7.796e+03	0.0000	68243.0	13.81%	41064.2	8.46%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2863	-6.594e+03	0.0000	51533.0	10.43%	29812.2	6.14%



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Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Background sequences	% of Background
						Sequences with Motif	Sequences with Motif	Sequences with Motif	Sequences with Motif
	1	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3966	-9.134e+03	0.0000	33093.0	7.18%	14175.0	3.14%
	2	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-3400	-7.829e+03	0.0000	15201.0	3.30%	4447.6	0.99%
	3	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	1e-3382	-7.789e+03	0.0000	31815.0	6.90%	14384.2	3.19%
	4	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3284	-7.564e+03	0.0000	80910.0	17.55%	51440.4	11.40%
	5	IRF1(IRF)/PBMC-IRF1-ChIP-Seq(GSE43036)/Homer	1e-3257	-7.502e+03	0.0000	18217.0	3.95%	6210.3	1.38%
	6	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-2846	-6.554e+03	0.0000	89500.0	19.41%	60255.8	13.36%
	7	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2819	-6.493e+03	0.0000	80393.0	17.44%	52821.8	11.71%
	8	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2761	-6.358e+03	0.0000	63973.0	13.88%	39771.0	8.82%
	9	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2639	-6.078e+03	0.0000	69222.0	15.02%	44429.8	9.85%
	10	ISRE(IRF)/ThioMac-LPS-Expression(GSE23622)/Homer	1e-2555	-5.885e+03	0.0000	10244.0	2.22%	2749.1	0.61%



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Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Tar- get Se- quences	% of Tar- gets Se- quences with Mo- tif	# Back- ground Se- quences with Mo- tif	% of Back- ground Se- quences with Mo- tif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-4053	-9.333e+03	0.0000	90624.0	17.28%	56601.1	10.96%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3818	-8.793e+03	0.0000	102623.0	19.57%	67264.6	13.02%
	3	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3746	-8.627e+03	0.0000	80675.0	15.38%	49704.3	9.62%
	4	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3644	-8.392e+03	0.0000	79616.0	15.18%	49211.2	9.53%
	5	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3622	-8.342e+03	0.0000	72712.0	13.86%	43829.0	8.48%
	6	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3536	-8.143e+03	0.0000	89309.0	17.03%	57417.6	11.11%
	7	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3384	-7.794e+03	0.0000	35233.0	6.72%	16731.9	3.24%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-3371	-7.763e+03	0.0000	112500.0	21.45%	77423.7	14.99%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-3208	-7.387e+03	0.0000	70668.0	13.47%	43616.0	8.44%
	10	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-2886	-6.647e+03	0.0000	15553.0	2.97%	5195.4	1.01%



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Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
						Sequences	Sequences	Sequences	Background
						with Motif	with Motif	with Motif	ground Motif
	1	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-4408	-1.015e+04	0.0000	38314.0	7.19%	16754.9	3.21%
	2	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-3843	-8.851e+03	0.0000	17782.0	3.33%	5340.4	1.02%
	3	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	1e-3773	-8.690e+03	0.0000	37286.0	6.99%	17251.2	3.30%
	4	IRF1(IRF)/PBMC-IRF1-ChIP-Seq(GSE43036)/Homer	1e-3578	-8.240e+03	0.0000	21349.0	4.00%	7583.4	1.45%
	5	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3469	-7.989e+03	0.0000	89879.0	16.86%	57823.4	11.06%
	6	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3039	-6.998e+03	0.0000	100449.0	18.84%	68334.0	13.08%
	7	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2960	-6.817e+03	0.0000	88713.0	16.64%	58909.2	11.27%
	8	ISRE(IRF)/ThioMac-LPS-Expression(GSE23622)/Homer	1e-2959	-6.815e+03	0.0000	12012.0	2.25%	3260.3	0.62%
	9	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2883	-6.640e+03	0.0000	78085.0	14.64%	50523.4	9.67%
	10	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2882	-6.637e+03	0.0000	71005.0	13.32%	44824.4	8.58%

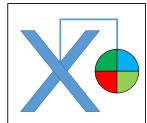


Epigenome Analysis Platform

Report

SRR1658342

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3177	-7.316e+03	0.0000	76817.0	17.16%	48954.1	11.09%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-2906	-6.692e+03	0.0000	86730.0	19.37%	58199.8	13.18%
	3	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2741	-6.314e+03	0.0000	61372.0	13.71%	38100.6	8.63%
	4	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2711	-6.243e+03	0.0000	67513.0	15.08%	43144.8	9.77%
	5	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2705	-6.229e+03	0.0000	75845.0	16.94%	49982.6	11.32%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2526	-5.818e+03	0.0000	66101.0	14.76%	42706.9	9.67%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2516	-5.794e+03	0.0000	94722.0	21.16%	66733.0	15.12%
	8	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2449	-5.639e+03	0.0000	28745.0	6.42%	14326.2	3.25%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2307	-5.312e+03	0.0000	59182.0	13.22%	37946.4	8.60%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2091	-4.815e+03	0.0000	43798.0	9.78%	26505.5	6.00%

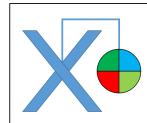


Epigenome Analysis Platform

Report

SRR1658270

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
						Sequences	Targets	Sequences	Background
						with Motif	with Motif	with Motif	with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3801	-8.754e+03	0.0000	96840.0	17.17%	61657.3	11.24%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3581	-8.247e+03	0.0000	108707.0	19.28%	72227.3	13.16%
	3	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3498	-8.055e+03	0.0000	36475.0	6.47%	17115.5	3.12%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3406	-7.844e+03	0.0000	77284.0	13.70%	47507.7	8.66%
	5	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3404	-7.839e+03	0.0000	96469.0	17.11%	62903.9	11.46%
	6	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3328	-7.665e+03	0.0000	84412.0	14.97%	53449.5	9.74%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3272	-7.534e+03	0.0000	83119.0	14.74%	52628.6	9.59%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-3071	-7.073e+03	0.0000	117655.0	20.86%	82010.6	14.94%
	9	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-2806	-6.462e+03	0.0000	15922.0	2.82%	5426.9	0.99%
	10	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2800	-6.447e+03	0.0000	73581.0	13.05%	46802.7	8.53%



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Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Background Sequences	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-4098	-9.437e+03	0.0000	72001.0	17.17%	42235.5	10.20%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3793	-8.734e+03	0.0000	82708.0	19.72%	51738.2	12.49%
	3	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3717	-8.559e+03	0.0000	65956.0	15.73%	38669.3	9.34%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3628	-8.356e+03	0.0000	58430.0	13.93%	33134.4	8.00%
	5	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3609	-8.312e+03	0.0000	69559.0	16.59%	41825.2	10.10%
	6	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-3440	-7.922e+03	0.0000	92709.0	22.11%	61274.1	14.80%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3363	-7.744e+03	0.0000	64545.0	15.39%	38662.5	9.34%
	8	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-3242	-7.465e+03	0.0000	58878.0	14.04%	34616.1	8.36%
	9	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3066	-7.061e+03	0.0000	30493.0	7.27%	14264.5	3.44%
	10	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-2830	-6.518e+03	0.0000	13968.0	3.33%	4420.5	1.07%



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Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets	# Sequences with Motif	% of Background
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3974	-9.152e+03	0.0000	95029.0	16.92%	60133.3	10.90%
	2	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3776	-8.696e+03	0.0000	38211.0	6.80%	17889.2	3.24%
	3	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3692	-8.502e+03	0.0000	107618.0	19.16%	71548.5	12.97%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3495	-8.048e+03	0.0000	76339.0	13.59%	46900.3	8.50%
	5	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3494	-8.048e+03	0.0000	93887.0	16.72%	61022.0	11.06%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3424	-7.885e+03	0.0000	83102.0	14.80%	52544.9	9.52%
	7	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3392	-7.810e+03	0.0000	83782.0	14.92%	53212.4	9.65%
	8	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-3191	-7.349e+03	0.0000	16877.0	3.00%	5556.9	1.01%
	9	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-3127	-7.201e+03	0.0000	117321.0	20.89%	82241.8	14.91%
	10	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	1e-3071	-7.071e+03	0.0000	36746.0	6.54%	18382.7	3.33%



SRR1658197

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Sequences with Motif	% of Back-ground Sequences
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3582	-8.248e+03	0.0000	90312.0	17.86%	56972.4	11.68%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3165	-7.290e+03	0.0000	99584.0	19.70%	66158.0	13.56%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3076	-7.084e+03	0.0000	90791.0	17.96%	59325.9	12.16%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3001	-6.912e+03	0.0000	71318.0	14.11%	44017.0	9.02%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2904	-6.688e+03	0.0000	76718.0	15.18%	48655.8	9.97%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2768	-6.374e+03	0.0000	75065.0	14.85%	47862.5	9.81%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2643	-6.087e+03	0.0000	105756.0	20.92%	73686.6	15.10%
	8	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2539	-5.849e+03	0.0000	30218.0	5.98%	14799.6	3.03%
	9	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2465	-5.678e+03	0.0000	55164.0	10.91%	33320.0	6.83%
	10	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2395	-5.516e+03	0.0000	65852.0	13.03%	41970.7	8.60%



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Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Sequences with Motif	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3861	-8.892e+03	0.0000	89694.0	17.42%	56334.8	11.16%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3412	-7.858e+03	0.0000	100161.0	19.45%	66627.4	13.19%
	3	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3343	-7.699e+03	0.0000	71501.0	13.89%	43651.6	8.64%
	4	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3326	-7.659e+03	0.0000	88984.0	17.28%	57759.9	11.44%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3259	-7.505e+03	0.0000	78111.0	15.17%	49203.6	9.74%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3139	-7.230e+03	0.0000	76891.0	14.93%	48665.0	9.64%
	7	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3097	-7.133e+03	0.0000	33688.0	6.54%	16211.4	3.21%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2937	-6.763e+03	0.0000	108644.0	21.10%	75877.8	15.02%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2820	-6.494e+03	0.0000	68211.0	13.25%	42894.3	8.49%
	10	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	1e-2593	-5.973e+03	0.0000	32407.0	6.29%	16441.4	3.26%



SRR1658205

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Targets	% of Targets	# Sequences with Motif	% of Background
						Sequences	Sequences	Sequences	Background
						with Motif	with Motif	with Motif	ground Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3346	-7.707e+03	0.0000	86251.0	17.16%	55471.0	11.25%
	2	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3109	-7.159e+03	0.0000	32963.0	6.56%	15694.0	3.18%
	3	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3037	-6.995e+03	0.0000	96604.0	19.22%	65276.7	13.24%
	4	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2946	-6.785e+03	0.0000	85931.0	17.09%	56797.8	11.52%
	5	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2925	-6.737e+03	0.0000	68719.0	13.67%	42922.8	8.71%
	6	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2785	-6.413e+03	0.0000	74708.0	14.86%	48268.5	9.79%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2661	-6.128e+03	0.0000	73572.0	14.63%	47837.8	9.71%
	8	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-2596	-5.979e+03	0.0000	14503.0	2.88%	4932.3	1.00%
	9	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2545	-5.862e+03	0.0000	104284.0	20.74%	74091.8	15.03%
	10	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	1e-2525	-5.816e+03	0.0000	31386.0	6.24%	15882.9	3.22%



Epigenome Analysis Platform

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SRR1658142

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Background Sequences	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3505	-8.071e+03	0.0000	84615.0	17.67%	53562.5	11.43%
	2	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3180	-7.324e+03	0.0000	32153.0	6.71%	14991.4	3.20%
	3	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3107	-7.156e+03	0.0000	94154.0	19.66%	62948.0	13.43%
	4	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3079	-7.091e+03	0.0000	84336.0	17.61%	54955.9	11.72%
	5	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2993	-6.893e+03	0.0000	67358.0	14.06%	41593.8	8.87%
	6	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2823	-6.502e+03	0.0000	72627.0	15.16%	46429.3	9.90%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2807	-6.465e+03	0.0000	71742.0	14.98%	45776.4	9.76%
	8	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	1e-2634	-6.067e+03	0.0000	30615.0	6.39%	15086.8	3.22%
	9	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2564	-5.905e+03	0.0000	100651.0	21.02%	70898.9	15.12%
	10	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-2500	-5.758e+03	0.0000	13990.0	2.92%	4756.6	1.01%



Epigenome Analysis Platform

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SRR1658340

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Background Sequences	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-4537	-1.045e+04	0.0000	96885.0	17.37%	59649.5	10.89%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-4024	-9.267e+03	0.0000	108761.0	19.50%	71162.9	12.99%
	3	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3900	-8.982e+03	0.0000	77484.0	13.89%	46443.5	8.48%
	4	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3866	-8.903e+03	0.0000	85208.0	15.28%	52646.7	9.61%
	5	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3862	-8.893e+03	0.0000	38555.0	6.91%	17949.1	3.28%
	6	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3824	-8.805e+03	0.0000	94900.0	17.02%	60586.5	11.06%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3682	-8.479e+03	0.0000	83795.0	15.02%	52166.3	9.52%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-3523	-8.114e+03	0.0000	118909.0	21.32%	81757.0	14.93%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-3372	-7.766e+03	0.0000	75018.0	13.45%	46280.7	8.45%
	10	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-3245	-7.473e+03	0.0000	17047.0	3.06%	5587.7	1.02%



Epigenome Analysis Platform

Report

SRR1658133

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
						Sequences	Targets	Sequences	Background
						with Motif	with Motif	with Motif	with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3957	-9.112e+03	0.0000	95814.0	17.33%	60463.1	11.21%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3579	-8.243e+03	0.0000	107175.0	19.39%	71215.3	13.20%
	3	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3487	-8.031e+03	0.0000	36269.0	6.56%	17051.0	3.16%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3429	-7.896e+03	0.0000	76394.0	13.82%	46883.5	8.69%
	5	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3415	-7.865e+03	0.0000	95173.0	17.22%	62011.0	11.50%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3377	-7.777e+03	0.0000	82509.0	14.93%	51920.5	9.63%
	7	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3336	-7.683e+03	0.0000	83510.0	15.11%	52874.0	9.80%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-3025	-6.967e+03	0.0000	115926.0	20.97%	81046.4	15.03%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2817	-6.488e+03	0.0000	72580.0	13.13%	46084.0	8.54%
	10	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	1e-2746	-6.323e+03	0.0000	34401.0	6.22%	17377.2	3.22%



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SRR1658214

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Sequences with Motif	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3279	-7.551e+03	0.0000	85153.0	17.02%	54960.9	11.18%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-2911	-6.704e+03	0.0000	95192.0	19.03%	64794.9	13.18%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2809	-6.470e+03	0.0000	84249.0	16.84%	56108.7	11.42%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2698	-6.213e+03	0.0000	66998.0	13.39%	42482.1	8.64%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2691	-6.197e+03	0.0000	73773.0	14.75%	47989.8	9.76%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2539	-5.846e+03	0.0000	72272.0	14.45%	47380.3	9.64%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2363	-5.442e+03	0.0000	102824.0	20.55%	73941.5	15.05%
	8	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2219	-5.111e+03	0.0000	63961.0	12.79%	41913.8	8.53%
	9	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2192	-5.047e+03	0.0000	49314.0	9.86%	30298.3	6.17%
	10	Elk4(ETS)/Hela-Elk4-ChIP-Seq(GSE31477)/Homer	1e-2135	-4.918e+03	0.0000	49327.0	9.86%	30509.4	6.21%



Epigenome Analysis Platform

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SRR1658232

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3592	-8.273e+03	0.0000	77660.0	16.89%	48107.4	10.61%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3308	-7.617e+03	0.0000	88497.0	19.24%	57977.9	12.78%
	3	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3193	-7.352e+03	0.0000	62547.0	13.60%	37475.4	8.26%
	4	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3131	-7.211e+03	0.0000	75928.0	16.51%	48352.4	10.66%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3082	-7.097e+03	0.0000	69155.0	15.04%	43076.3	9.50%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3001	-6.912e+03	0.0000	68479.0	14.89%	42820.6	9.44%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2822	-6.498e+03	0.0000	97173.0	21.13%	67322.2	14.85%
	8	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2763	-6.363e+03	0.0000	30653.0	6.66%	14952.2	3.30%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2599	-5.986e+03	0.0000	60984.0	13.26%	38269.5	8.44%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2338	-5.384e+03	0.0000	43192.0	9.39%	25220.8	5.56%



Epigenome Analysis Platform

Report

SRR1658168

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target	% of Targets	# Background	% of Background
						Sequences with Motif	Sequences with Motif	Sequences with Motif	Sequences with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3042	-7.005e+03	0.0000	82929.0	17.00%	54112.8	11.29%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-2808	-6.466e+03	0.0000	93291.0	19.12%	63710.1	13.29%
	3	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2665	-6.137e+03	0.0000	66045.0	13.54%	41867.7	8.73%
	4	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2619	-6.031e+03	0.0000	72372.0	14.83%	47167.6	9.84%
	5	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2595	-5.976e+03	0.0000	82089.0	16.82%	55277.9	11.53%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2564	-5.904e+03	0.0000	71413.0	14.64%	46607.4	9.72%
	7	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2461	-5.668e+03	0.0000	30192.0	6.19%	15233.1	3.18%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2287	-5.267e+03	0.0000	100814.0	20.66%	72663.2	15.16%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2189	-5.042e+03	0.0000	62921.0	12.90%	41214.7	8.60%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2004	-4.615e+03	0.0000	48057.0	9.85%	30001.1	6.26%



Epigenome Analysis Platform

Report

SRR1658267

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
						Sequences	Sequences	Sequences	Background
						with Motif	with Motif	with Motif	ground Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-4138	-9.528e+03	0.0000	93480.0	17.28%	58418.6	10.99%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3811	-8.777e+03	0.0000	105379.0	19.48%	69352.9	13.05%
	3	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3609	-8.312e+03	0.0000	82353.0	15.23%	51366.9	9.66%
	4	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3584	-8.254e+03	0.0000	92304.0	17.07%	59496.9	11.19%
	5	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3583	-8.252e+03	0.0000	74691.0	13.81%	45381.1	8.54%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3412	-7.858e+03	0.0000	80769.0	14.93%	50806.8	9.56%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-3357	-7.732e+03	0.0000	115370.0	21.33%	79669.8	14.99%
	8	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-3182	-7.329e+03	0.0000	72507.0	13.41%	45037.8	8.47%
	9	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3054	-7.034e+03	0.0000	34819.0	6.44%	17102.2	3.22%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2601	-5.989e+03	0.0000	53237.0	9.84%	31917.9	6.00%



Epigenome Analysis Platform

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SRR1658177

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3524	-8.117e+03	0.0000	62345.0	17.63%	36616.9	10.51%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3181	-7.325e+03	0.0000	70727.0	20.00%	44406.9	12.74%
	3	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3064	-7.056e+03	0.0000	50273.0	14.22%	28641.8	8.22%
	4	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3060	-7.047e+03	0.0000	55878.0	15.80%	32976.2	9.46%
	5	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3020	-6.954e+03	0.0000	55486.0	15.69%	32795.9	9.41%
	6	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3003	-6.917e+03	0.0000	60307.0	17.05%	36639.6	10.51%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2852	-6.568e+03	0.0000	78374.0	22.16%	51933.4	14.90%
	8	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2774	-6.388e+03	0.0000	49853.0	14.10%	29173.0	8.37%
	9	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2585	-5.954e+03	0.0000	25402.0	7.18%	11797.6	3.39%
	10	ELF1(ETS)/Jurkat-ELF1-ChIP-Seq(SRA014231)/Homer	1e-2163	-4.982e+03	0.0000	31868.0	9.01%	17326.4	4.97%



Epigenome Analysis Platform

Report

SRR1658339

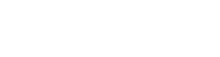
Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Background Sequences	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3267	-7.523e+03	0.0000	84272.0	16.66%	54413.3	10.92%
	2	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3037	-6.995e+03	0.0000	33227.0	6.57%	16096.7	3.23%
	3	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3019	-6.952e+03	0.0000	95984.0	18.97%	65133.7	13.07%
	4	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2849	-6.562e+03	0.0000	74592.0	14.74%	48142.3	9.66%
	5	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2813	-6.479e+03	0.0000	67265.0	13.29%	42365.9	8.50%
	6	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2802	-6.454e+03	0.0000	83096.0	16.42%	55310.8	11.10%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2784	-6.411e+03	0.0000	73952.0	14.62%	47877.1	9.61%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2603	-5.995e+03	0.0000	105493.0	20.85%	75177.2	15.08%
	9	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-2564	-5.905e+03	0.0000	14619.0	2.89%	5059.4	1.02%
	10	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	1e-2481	-5.714e+03	0.0000	31961.0	6.32%	16468.9	3.30%



Epigenome Analysis Platform

Report

SRR1658276

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Background Sequences	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3822	-8.802e+03	0.0000	86129.0	17.65%	53744.8	11.22%
	2	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3468	-7.986e+03	0.0000	33356.0	6.84%	15267.1	3.19%
	3	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3368	-7.755e+03	0.0000	96069.0	19.69%	63578.4	13.28%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3303	-7.606e+03	0.0000	68953.0	14.13%	41872.2	8.75%
	5	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3300	-7.599e+03	0.0000	85752.0	17.57%	55354.2	11.56%
	6	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3181	-7.325e+03	0.0000	74662.0	15.30%	46828.5	9.78%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3179	-7.322e+03	0.0000	74256.0	15.22%	46508.9	9.71%
	8	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-3009	-6.930e+03	0.0000	14893.0	3.05%	4688.1	0.98%
	9	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	1e-2911	-6.703e+03	0.0000	31979.0	6.55%	15459.1	3.23%
	10	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2816	-6.486e+03	0.0000	103146.0	21.14%	71944.6	15.03%



Epigenome Analysis Platform

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Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
						Sequences	Sequences	Sequences	Background
						with Motif	with Motif	with Motif	ground Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-4236	-9.756e+03	0.0000	102305	0.01708%	64469.8	11.03%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3891	-8.962e+03	0.0000	115068	0.01921%	76216.0	13.04%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3755	-8.648e+03	0.0000	101582	0.01695%	65704.7	11.24%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3751	-8.639e+03	0.0000	81724.0	0.1364%	49837.0	8.53%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3711	-8.546e+03	0.0000	89865.0	0.1500%	56425.9	9.65%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3604	-8.299e+03	0.0000	88475.0	0.1477%	55710.9	9.53%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-3409	-7.850e+03	0.0000	125475	0.02094%	87059.9	14.89%
	8	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3318	-7.642e+03	0.0000	37793.0	0.631%	18411.1	3.15%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-3175	-7.313e+03	0.0000	78534.0	0.1311%	49372.0	8.45%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2788	-6.420e+03	0.0000	58971.0	0.984%	35402.3	6.06%



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Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Tar- get Se- quen- ces with Mo- tif	% of Tar- gets Se- quen- ces with Mo- tif	# Back- ground Se- quen- ces with Mo- tif	% of Back- ground Se- quen- ces with Mo- tif
	1	Fli1(ETS)/CD8-FLI-ChIP-Sq(GSE20898)/Homer	1e-3528	-8.126e+03	0.0000	81423.0	17.47%	51071.8	11.17%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Sq(GSE22441)/Homer	1e-3199	-7.367e+03	0.0000	90950.0	19.52%	60107.1	13.15%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Sq(ENCODE)/Homer	1e-3121	-7.188e+03	0.0000	80762.0	17.33%	52038.0	11.38%
	4	IRF8(IRF)/BMDM-IRF8-ChIP-Sq(GSE77884)/Homer	1e-3090	-7.117e+03	0.0000	31414.0	6.74%	14713.4	3.22%
	5	GABPA(ETS)/Jurkat-GABPa-ChIP-Sq(GSE17954)/Homer	1e-3081	-7.095e+03	0.0000	64914.0	13.93%	39486.1	8.64%
	6	ETS1(ETS)/Jurkat-ETS1-ChIP-Sq(GSE17954)/Homer	1e-2903	-6.686e+03	0.0000	70614.0	15.15%	44646.0	9.77%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Sq(GSE88699)/Homer	1e-2763	-6.362e+03	0.0000	69106.0	14.83%	43956.3	9.62%
	8	IRF3(IRF)/BMDM-Irf3-ChIP-Sq(GSE67343)/Homer	1e-2642	-6.085e+03	0.0000	30499.0	6.55%	15028.2	3.29%
	9	ERG(ETS)/VCaP-ERG-ChIP-Sq(GSE14097)/Homer	1e-2599	-5.985e+03	0.0000	97716.0	20.97%	68444.4	14.97%
	10	IRF2(IRF)/Erythroblas-IRF2-ChIP-Sq(GSE36985)/Homer	1e-2548	-5.869e+03	0.0000	13864.0	2.98%	4641.0	1.02%



Epigenome Analysis Platform

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Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
						Sequences	Targets	Sequences	Background
						with Motif	with Motif	with Motif	ground Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3745	-8.625e+03	0.0000	85778.0	16.74%	53860.8	10.67%
	2	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3433	-7.907e+03	0.0000	35119.0	6.85%	16570.0	3.28%
	3	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3337	-7.685e+03	0.0000	97334.0	19.00%	64902.5	12.86%
	4	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3204	-7.379e+03	0.0000	76103.0	14.85%	48024.3	9.51%
	5	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3168	-7.296e+03	0.0000	68570.0	13.38%	42142.2	8.35%
	6	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3158	-7.274e+03	0.0000	83830.0	16.36%	54468.8	10.79%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3097	-7.131e+03	0.0000	75071.0	14.65%	47589.9	9.43%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2788	-6.422e+03	0.0000	106774.0	20.84%	75355.8	14.93%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2670	-6.149e+03	0.0000	66972.0	13.07%	42667.3	8.45%
	10	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-2633	-6.064e+03	0.0000	14969.0	2.92%	5174.0	1.02%



Epigenome Analysis Platform

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SRR1658182

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
						Sequences	Targets	Sequences	Background
						with Motif	with Motif	with Motif	ground Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3802	-8.757e+03	0.0000	99670.0	16.64%	63770.0	10.94%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3480	-8.013e+03	0.0000	112137.0	18.72%	75299.4	12.92%
	3	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3309	-7.620e+03	0.0000	79218.0	13.22%	49270.1	8.46%
	4	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3304	-7.610e+03	0.0000	87551.0	14.61%	55930.7	9.60%
	5	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3279	-7.550e+03	0.0000	98708.0	16.48%	65086.1	11.17%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3132	-7.214e+03	0.0000	85634.0	14.29%	55061.3	9.45%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2999	-6.908e+03	0.0000	122181.0	20.39%	85978.4	14.76%
	8	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2981	-6.865e+03	0.0000	37097.0	6.19%	18629.5	3.20%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2825	-6.505e+03	0.0000	76249.0	12.73%	48739.2	8.36%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2492	-5.739e+03	0.0000	57705.0	9.63%	35338.7	6.07%



Epigenome Analysis Platform

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SRR1658263

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
						Sequences	Targets	Sequences	Background
						with Motif	with Motif	with Motif	with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-4076	-9.386e+03	0.0000	84588.0	17.10%	51889.3	10.63%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3626	-8.350e+03	0.0000	95686.0	19.34%	62528.4	12.81%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3523	-8.113e+03	0.0000	83133.0	16.80%	52645.3	10.79%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3489	-8.034e+03	0.0000	67820.0	13.71%	40571.8	8.31%
	5	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3443	-7.928e+03	0.0000	34397.0	6.95%	16091.6	3.30%
	6	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3419	-7.874e+03	0.0000	74648.0	15.09%	46195.8	9.47%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-3155	-7.266e+03	0.0000	105131.0	21.25%	72414.1	14.84%
	8	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3130	-7.208e+03	0.0000	73399.0	14.84%	46221.0	9.47%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2977	-6.856e+03	0.0000	66212.0	13.38%	41021.8	8.41%
	10	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-2811	-6.474e+03	0.0000	15164.0	3.07%	5078.6	1.04%



Epigenome Analysis Platform

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SRR1658173

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
						Sequences	Sequences	Sequences	Background
						with Motif	with Motif	with Motif	ground Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3768	-8.677e+03	0.0000	91077.0	17.52%	57607.4	11.33%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3430	-7.899e+03	0.0000	101639.0	19.56%	67568.8	13.29%
	3	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3309	-7.620e+03	0.0000	79539.0	15.30%	50012.7	9.84%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3274	-7.539e+03	0.0000	72382.0	13.93%	44447.3	8.74%
	5	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3258	-7.503e+03	0.0000	90551.0	17.42%	59127.2	11.63%
	6	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3160	-7.277e+03	0.0000	33592.0	6.46%	15967.3	3.14%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3031	-6.980e+03	0.0000	77469.0	14.91%	49385.5	9.72%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-3002	-6.914e+03	0.0000	110377.0	21.24%	76802.2	15.11%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2867	-6.603e+03	0.0000	69405.0	13.35%	43540.8	8.57%
	10	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	1e-2548	-5.867e+03	0.0000	32047.0	6.17%	16247.3	3.20%



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Report

SRR1658155

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Sequences with Motif	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3480	-8.014e+03	0.0000	84226.0	17.37%	53551.6	11.23%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3224	-7.425e+03	0.0000	94533.0	19.49%	63023.3	13.22%
	3	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3027	-6.972e+03	0.0000	67109.0	13.84%	41444.7	8.69%
	4	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2999	-6.907e+03	0.0000	83709.0	17.26%	54978.9	11.53%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2923	-6.733e+03	0.0000	73247.0	15.10%	46737.3	9.80%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2779	-6.400e+03	0.0000	71828.0	14.81%	46139.8	9.68%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2754	-6.342e+03	0.0000	102338.0	21.10%	71703.7	15.04%
	8	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2626	-6.047e+03	0.0000	30643.0	6.32%	15188.4	3.19%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2553	-5.880e+03	0.0000	63993.0	13.20%	40680.6	8.53%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2287	-5.268e+03	0.0000	49129.0	10.13%	29861.4	6.26%



Epigenome Analysis Platform

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SRR1658317

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Background Sequences	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-4247	-9.781e+03	0.0000	88172.0	17.53%	54064.8	10.91%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3935	-9.062e+03	0.0000	99486.0	19.78%	64341.8	12.99%
	3	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3782	-8.709e+03	0.0000	70859.0	14.09%	41930.5	8.46%
	4	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3741	-8.615e+03	0.0000	78102.0	15.53%	47749.4	9.64%
	5	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3687	-8.490e+03	0.0000	86578.0	17.21%	54728.1	11.05%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3605	-8.301e+03	0.0000	76851.0	15.28%	47217.1	9.53%
	7	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3409	-7.850e+03	0.0000	34696.0	6.90%	16332.6	3.30%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-3300	-7.600e+03	0.0000	108347.0	21.54%	74343.7	15.01%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-3076	-7.083e+03	0.0000	68455.0	13.61%	42375.5	8.55%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2852	-6.568e+03	0.0000	50225.0	9.99%	28923.8	5.84%



Epigenome Analysis Platform

Report

SRR1658191

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Background Sequences	% of Background with Motif
	1	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3149	-7.253e+03	0.0000	30519.0	6.69%	14056.3	3.13%
	2	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-2815	-6.484e+03	0.0000	76727.0	16.83%	50159.5	11.18%
	3	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-2795	-6.437e+03	0.0000	13910.0	3.05%	4410.7	0.98%
	4	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	1e-2742	-6.315e+03	0.0000	29963.0	6.57%	14503.2	3.23%
	5	IRF1(IRF)/PBMC-IRF1-ChIP-Seq(GSE43036)/Homer	1e-2585	-5.954e+03	0.0000	16818.0	3.69%	6304.6	1.40%
	6	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-2498	-5.752e+03	0.0000	85715.0	18.80%	59008.5	13.15%
	7	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2484	-5.721e+03	0.0000	76422.0	16.76%	51276.1	11.42%
	8	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2455	-5.653e+03	0.0000	60981.0	13.38%	38756.4	8.63%
	9	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2273	-5.235e+03	0.0000	66063.0	14.49%	43607.3	9.72%
	10	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2122	-4.887e+03	0.0000	64634.0	14.18%	43070.6	9.60%



Epigenome Analysis Platform

Report

SRR1658210

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Sequences with Motif	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3580	-8.244e+03	0.0000	88740.0	17.08%	56716.2	11.10%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3256	-7.499e+03	0.0000	99908.0	19.23%	67217.8	13.16%
	3	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3207	-7.385e+03	0.0000	34071.0	6.56%	16282.9	3.19%
	4	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3105	-7.152e+03	0.0000	87754.0	16.89%	57757.2	11.30%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3094	-7.125e+03	0.0000	77886.0	14.99%	49749.9	9.74%
	6	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3073	-7.076e+03	0.0000	70635.0	13.59%	44008.9	8.61%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2962	-6.822e+03	0.0000	76690.0	14.76%	49284.3	9.65%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2651	-6.105e+03	0.0000	108172.0	20.82%	77039.2	15.08%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2608	-6.006e+03	0.0000	68036.0	13.09%	43657.1	8.54%
	10	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	1e-2540	-5.851e+03	0.0000	32498.0	6.25%	16670.8	3.26%



Epigenome Analysis Platform

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SRR1658111

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Tar- get Se- quences	% of Tar- gets Se- quences with Mo- tif	# Back- ground Se- quences with Mo- tif	% of Back- ground Se- quences with Mo- tif
	1	Fli1(ETS)/CD8-FLI-ChIP-Sq(GSE20898)/Homer	1e-3998	-9.208e+03	0.0000	84613.0	18.10%	51974.2	11.34%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Sq(GSE22441)/Homer	1e-3723	-8.573e+03	0.0000	94291.0	20.17%	60784.8	13.26%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Sq(ENCODE)/Homer	1e-3570	-8.221e+03	0.0000	84087.0	17.98%	53042.6	11.57%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Sq(GSE17954)/Homer	1e-3546	-8.167e+03	0.0000	67650.0	14.47%	40088.3	8.74%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Sq(GSE17954)/Homer	1e-3434	-7.907e+03	0.0000	73318.0	15.68%	44903.9	9.79%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Sq(GSE88699)/Homer	1e-3417	-7.868e+03	0.0000	72583.0	15.52%	44379.4	9.68%
	7	IRF8(IRF)/BMDM-IRF8-ChIP-Sq(GSE77884)/Homer	1e-3224	-7.425e+03	0.0000	31667.0	6.77%	14612.1	3.19%
	8	ERG(ETS)/VCaP-ERG-ChIP-Sq(GSE14097)/Homer	1e-3094	-7.126e+03	0.0000	100992.0	21.60%	68915.5	15.03%
	9	Etv2(ETS)/ES-ER71-ChIP-Sq(GSE59402)/Homer	1e-2948	-6.789e+03	0.0000	63978.0	13.68%	39180.2	8.55%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Sq(GSE31477)/Homer	1e-2813	-6.479e+03	0.0000	50387.0	10.78%	29082.4	6.34%



Epigenome Analysis Platform

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SRR1658201

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Sequences with Motif	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3446	-7.936e+03	0.0000	76117.0	17.34%	47362.9	10.97%
	2	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3244	-7.471e+03	0.0000	31003.0	7.06%	14201.0	3.29%
	3	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3193	-7.353e+03	0.0000	85853.0	19.56%	56231.8	13.02%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3055	-7.036e+03	0.0000	60981.0	13.89%	36674.1	8.49%
	5	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2976	-6.853e+03	0.0000	74883.0	17.06%	48065.1	11.13%
	6	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2928	-6.743e+03	0.0000	66966.0	15.26%	41847.4	9.69%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2875	-6.621e+03	0.0000	66289.0	15.10%	41495.7	9.61%
	8	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	1e-2687	-6.188e+03	0.0000	30030.0	6.84%	14669.3	3.40%
	9	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-2674	-6.157e+03	0.0000	13697.0	3.12%	4426.2	1.02%
	10	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2637	-6.073e+03	0.0000	93607.0	21.33%	65119.2	15.08%



SRR1658240

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
						Sequences	Sequences	Sequences	Background
						with Motif	with Motif	with Motif	ground Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3873	-8.920e+03	0.0000	94470.0	17.46%	59658.0	11.31%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3472	-7.996e+03	0.0000	105372.0	19.47%	70138.5	13.30%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3344	-7.700e+03	0.0000	94300.0	17.42%	61552.2	11.67%
	4	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3294	-7.585e+03	0.0000	81745.0	15.10%	51587.1	9.78%
	5	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3284	-7.563e+03	0.0000	74886.0	13.84%	46171.4	8.75%
	6	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3178	-7.318e+03	0.0000	34298.0	6.34%	16340.2	3.10%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-3058	-7.042e+03	0.0000	113987.0	21.06%	79206.3	15.02%
	8	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3052	-7.029e+03	0.0000	79847.0	14.75%	50979.6	9.67%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2840	-6.541e+03	0.0000	71401.0	13.19%	45024.4	8.54%
	10	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-2683	-6.178e+03	0.0000	15240.0	2.82%	5205.6	0.99%



Epigenome Analysis Platform

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Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Background Sequences	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3854	-8.874e+03	0.0000	91109.0	17.78%	56742.3	11.45%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3492	-8.042e+03	0.0000	100681.0	19.65%	65848.0	13.28%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3384	-7.792e+03	0.0000	91178.0	17.80%	58543.4	11.81%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3333	-7.675e+03	0.0000	72156.0	14.08%	43617.2	8.80%
	5	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3182	-7.329e+03	0.0000	76669.0	14.97%	47686.4	9.62%
	6	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3155	-7.265e+03	0.0000	77802.0	15.19%	48686.9	9.82%
	7	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3108	-7.158e+03	0.0000	33036.0	6.45%	15534.5	3.13%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2915	-6.713e+03	0.0000	107082.0	20.90%	73662.7	14.86%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2840	-6.541e+03	0.0000	67665.0	13.21%	41822.7	8.44%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2712	-6.246e+03	0.0000	55297.0	10.79%	32668.3	6.59%



SRR1658303

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
						Sequences	Sequences	Sequences	Background
						with Motif	with Motif	with Motif	ground Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-2197	-5.059e+03	0.0000	59845.0	18.06%	38837.8	12.02%
	2	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-1870	-4.307e+03	0.0000	60387.0	18.22%	40636.4	12.57%
	3	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-1855	-4.273e+03	0.0000	65094.0	19.64%	44637.2	13.81%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-1772	-4.081e+03	0.0000	46918.0	14.16%	30021.2	9.29%
	5	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-1679	-3.867e+03	0.0000	49232.0	14.86%	32268.1	9.99%
	6	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-1670	-3.847e+03	0.0000	37909.0	11.44%	23244.3	7.19%
	7	Elk4(ETS)/Hela-Elk4-ChIP-Seq(GSE31477)/Homer	1e-1669	-3.844e+03	0.0000	38139.0	11.51%	23429.7	7.25%
	8	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-1653	-3.807e+03	0.0000	49923.0	15.06%	32941.5	10.19%
	9	ELF1(ETS)/Jurkat-ELF1-ChIP-Seq(SRA014231)/Homer	1e-1583	-3.647e+03	0.0000	34903.0	10.53%	21203.4	6.56%
	10	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-1453	-3.348e+03	0.0000	67973.0	20.51%	49091.3	15.19%



SRR1658312

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Tar- get Se- quences	% of Tar- gets Se- quences with Mo- tif	# Back- ground Se- quences with Mo- tif	% of Back- ground Se- quences with Mo- tif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3574	-8.230e+03	0.0000	94436.0	16.80%	61165.0	11.08%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3454	-7.954e+03	0.0000	107423.0	19.11%	72393.1	13.11%
	3	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3210	-7.392e+03	0.0000	75654.0	13.46%	47370.0	8.58%
	4	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3193	-7.353e+03	0.0000	83606.0	14.87%	53832.4	9.75%
	5	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3163	-7.283e+03	0.0000	82684.0	14.71%	53201.2	9.63%
	6	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3155	-7.267e+03	0.0000	93308.0	16.60%	61925.3	11.21%
	7	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3103	-7.146e+03	0.0000	36193.0	6.44%	17926.8	3.25%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2901	-6.680e+03	0.0000	117308.0	20.87%	83346.2	15.09%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2672	-6.153e+03	0.0000	73098.0	13.00%	47366.2	8.58%
	10	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-2534	-5.836e+03	0.0000	15614.0	2.78%	5644.6	1.02%



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Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Background Sequences	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3848	-8.862e+03	0.0000	84835.0	18.45%	52341.6	11.69%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3425	-7.886e+03	0.0000	93388.0	20.31%	60815.2	13.58%
	3	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3380	-7.783e+03	0.0000	67635.0	14.71%	40356.4	9.01%
	4	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3350	-7.714e+03	0.0000	84783.0	18.44%	54082.0	12.08%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3289	-7.575e+03	0.0000	72979.0	15.87%	44848.6	10.02%
	6	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3249	-7.482e+03	0.0000	30734.0	6.69%	13854.7	3.09%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3185	-7.334e+03	0.0000	71545.0	15.56%	44076.6	9.84%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2918	-6.720e+03	0.0000	99323.0	21.60%	67870.2	15.16%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2797	-6.441e+03	0.0000	63012.0	13.71%	38697.8	8.64%
	10	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	1e-2661	-6.129e+03	0.0000	28715.0	6.25%	13666.9	3.05%



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SRR1658149

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Background Sequences	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3450	-7.945e+03	0.0000	71719.0	17.03%	43958.5	10.60%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3189	-7.345e+03	0.0000	81791.0	19.42%	53051.0	12.79%
	3	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3143	-7.239e+03	0.0000	58056.0	13.79%	34203.3	8.24%
	4	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2994	-6.895e+03	0.0000	70013.0	16.63%	44172.5	10.65%
	5	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2980	-6.862e+03	0.0000	63940.0	15.18%	39356.7	9.49%
	6	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2961	-6.820e+03	0.0000	63962.0	15.19%	39437.5	9.51%
	7	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2931	-6.749e+03	0.0000	29469.0	7.00%	13809.5	3.33%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2625	-6.046e+03	0.0000	89405.0	21.23%	61771.9	14.89%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2521	-5.805e+03	0.0000	56336.0	13.38%	34905.4	8.41%
	10	ELF1(ETS)/Jurkat-ELF1-ChIP-Seq(SRA014231)/Homer	1e-2389	-5.502e+03	0.0000	37887.0	9.00%	21088.0	5.08%



SRR1658176

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
						Sequences	Sequences	Sequences	Background
						with Motif	with Motif	with Motif	ground Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-4485	-1.033e+04	0.0000	94635.0	17.87%	57890.8	11.18%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-4063	-9.356e+03	0.0000	105392.0	19.90%	68078.0	13.15%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3934	-9.060e+03	0.0000	94275.0	17.80%	59519.8	11.49%
	4	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3912	-9.008e+03	0.0000	82723.0	15.62%	50383.7	9.73%
	5	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3864	-8.898e+03	0.0000	75454.0	14.25%	44851.8	8.66%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3706	-8.534e+03	0.0000	80953.0	15.28%	49684.9	9.59%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-3518	-8.102e+03	0.0000	113690.0	21.46%	77186.7	14.90%
	8	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3445	-7.934e+03	0.0000	34905.0	6.59%	16264.6	3.14%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-3320	-7.646e+03	0.0000	71866.0	13.57%	43842.1	8.47%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-3004	-6.918e+03	0.0000	55941.0	10.56%	32545.6	6.28%



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SRR1658127

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Sequences with Motif	% of Background ground motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-4208	-9.690e+03	0.0000	86320.0	17.82%	52720.5	11.07%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3922	-9.033e+03	0.0000	97032.0	20.03%	62379.9	13.09%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3762	-8.663e+03	0.0000	84758.0	17.50%	52988.6	11.12%
	4	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3717	-8.561e+03	0.0000	76292.0	15.75%	46387.3	9.74%
	5	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3693	-8.505e+03	0.0000	69076.0	14.26%	40810.7	8.57%
	6	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3616	-8.328e+03	0.0000	34492.0	7.12%	15777.9	3.31%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-3478	-8.010e+03	0.0000	106412.0	21.97%	71943.1	15.10%
	8	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3421	-7.878e+03	0.0000	74636.0	15.41%	46075.2	9.67%
	9	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-3290	-7.577e+03	0.0000	15792.0	3.26%	4882.7	1.02%
	10	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-3237	-7.455e+03	0.0000	67320.0	13.90%	40909.1	8.59%



Epigenome Analysis Platform

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SRR1658208

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Background Sequences	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-2913	-6.708e+03	0.0000	89038.0	16.63%	58953.6	11.31%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-2677	-6.164e+03	0.0000	99803.0	18.64%	68963.0	13.23%
	3	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2582	-5.948e+03	0.0000	70721.0	13.21%	45425.2	8.72%
	4	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2566	-5.909e+03	0.0000	89291.0	16.68%	60691.5	11.65%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2524	-5.813e+03	0.0000	77178.0	14.41%	50895.6	9.77%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2523	-5.811e+03	0.0000	76150.0	14.22%	50060.7	9.61%
	7	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2290	-5.274e+03	0.0000	31483.0	5.88%	16385.0	3.14%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2222	-5.119e+03	0.0000	107485.0	20.07%	77836.9	14.94%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2109	-4.857e+03	0.0000	66818.0	12.48%	44237.6	8.49%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-1937	-4.462e+03	0.0000	52469.0	9.80%	33400.3	6.41%



Epigenome Analysis Platform

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SRR1658325

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Sequences with Motif	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3300	-7.601e+03	0.0000	83782.0	16.59%	53869.8	10.84%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-2820	-6.495e+03	0.0000	94354.0	18.69%	64623.8	13.00%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2810	-6.471e+03	0.0000	82518.0	16.34%	54786.4	11.02%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2638	-6.075e+03	0.0000	66076.0	13.09%	42055.3	8.46%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2622	-6.038e+03	0.0000	73156.0	14.49%	47861.1	9.63%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2423	-5.581e+03	0.0000	71865.0	14.23%	47624.1	9.58%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2369	-5.456e+03	0.0000	103288.0	20.46%	74457.1	14.98%
	8	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2366	-5.449e+03	0.0000	31345.0	6.21%	16304.2	3.28%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2269	-5.226e+03	0.0000	64371.0	12.75%	42129.4	8.47%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2240	-5.158e+03	0.0000	47570.0	9.42%	28830.7	5.80%



Epigenome Analysis Platform

Report

SRR1658244

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
						Sequences	Sequences	Sequences	Background
						with Motif	with Motif	with Motif	ground Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3077	-7.085e+03	0.0000	84244.0	16.46%	54998.2	10.94%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-2765	-6.368e+03	0.0000	95182.0	18.60%	65428.7	13.01%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2693	-6.203e+03	0.0000	82969.0	16.22%	55532.2	11.04%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2668	-6.144e+03	0.0000	66968.0	13.09%	42568.8	8.46%
	5	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2436	-5.609e+03	0.0000	72636.0	14.20%	48104.5	9.56%
	6	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2416	-5.565e+03	0.0000	73182.0	14.30%	48636.0	9.67%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2297	-5.289e+03	0.0000	104097.0	20.34%	75379.9	14.99%
	8	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2191	-5.046e+03	0.0000	64746.0	12.65%	42672.7	8.48%
	9	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2077	-4.783e+03	0.0000	47837.0	9.35%	29552.0	5.88%
	10	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2061	-4.746e+03	0.0000	30310.0	5.92%	16305.2	3.24%



Epigenome Analysis Platform

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SRR1658181

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Sequences with Motif	% of Background ground motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3172	-7.305e+03	0.0000	82444.0	16.57%	53324.5	10.88%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-2854	-6.573e+03	0.0000	93791.0	18.85%	64063.4	13.07%
	3	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2704	-6.228e+03	0.0000	65839.0	13.23%	41653.2	8.50%
	4	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2669	-6.147e+03	0.0000	72854.0	14.64%	47469.9	9.68%
	5	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2667	-6.142e+03	0.0000	80926.0	16.26%	54122.6	11.04%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2592	-5.970e+03	0.0000	72255.0	14.52%	47289.1	9.65%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2489	-5.732e+03	0.0000	103138.0	20.73%	73783.4	15.05%
	8	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2439	-5.618e+03	0.0000	31565.0	6.34%	16294.7	3.32%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2263	-5.212e+03	0.0000	64107.0	12.88%	41976.9	8.56%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2083	-4.798e+03	0.0000	46364.0	9.32%	28455.7	5.80%



Epigenome Analysis Platform

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SRR1658288

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Sequences with Motif	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3119	-7.184e+03	0.0000	80502.0	17.09%	51813.2	11.21%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-2782	-6.406e+03	0.0000	90005.0	19.11%	61052.3	13.21%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2708	-6.238e+03	0.0000	79717.0	16.92%	52808.6	11.43%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2620	-6.034e+03	0.0000	63565.0	13.49%	40028.7	8.66%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2488	-5.729e+03	0.0000	69475.0	14.75%	45312.9	9.81%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2465	-5.677e+03	0.0000	68743.0	14.59%	44807.2	9.70%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2272	-5.233e+03	0.0000	97304.0	20.65%	69691.2	15.08%
	8	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2206	-5.081e+03	0.0000	28857.0	6.13%	14882.1	3.22%
	9	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2148	-4.947e+03	0.0000	46825.0	9.94%	28496.8	6.17%
	10	Elk4(ETS)/Hela-Elk4-ChIP-Seq(GSE31477)/Homer	1e-2133	-4.913e+03	0.0000	47080.0	9.99%	28746.2	6.22%



Epigenome Analysis Platform

Report

SRR1658110

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Background Sequences	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3513	-8.091e+03	0.0000	84097.0	17.38%	53108.6	11.21%
	2	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2974	-6.849e+03	0.0000	83234.0	17.20%	54468.3	11.50%
	3	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-2955	-6.805e+03	0.0000	92952.0	19.21%	62588.6	13.21%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2924	-6.735e+03	0.0000	66527.0	13.75%	41177.9	8.69%
	5	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2839	-6.537e+03	0.0000	31349.0	6.48%	15149.5	3.20%
	6	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2772	-6.384e+03	0.0000	72221.0	14.93%	46297.4	9.77%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2678	-6.169e+03	0.0000	70861.0	14.65%	45560.3	9.62%
	8	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2448	-5.639e+03	0.0000	49998.0	10.33%	29871.6	6.31%
	9	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2434	-5.605e+03	0.0000	99992.0	20.67%	70976.6	14.98%
	10	Elk4(ETS)/Hela-Elk4-ChIP-Seq(GSE31477)/Homer	1e-2414	-5.560e+03	0.0000	50093.0	10.35%	30058.2	6.34%



Epigenome Analysis Platform

Report

SRR1658161

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Background Sequences	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-4424	-1.019e+04	0.0000	97267.0	17.21%	60396.5	10.87%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-4024	-9.266e+03	0.0000	109874.0	19.45%	72150.8	12.98%
	3	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3850	-8.865e+03	0.0000	86133.0	15.24%	53494.1	9.63%
	4	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3834	-8.829e+03	0.0000	95658.0	16.93%	61223.5	11.02%
	5	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3760	-8.658e+03	0.0000	77587.0	13.73%	47034.4	8.46%
	6	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3599	-8.288e+03	0.0000	38329.0	6.78%	18349.8	3.30%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3542	-8.157e+03	0.0000	84292.0	14.92%	53121.5	9.56%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-3516	-8.097e+03	0.0000	120375.0	21.30%	83111.6	14.96%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-3267	-7.525e+03	0.0000	75700.0	13.40%	47244.7	8.50%
	10	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-3098	-7.136e+03	0.0000	16963.0	3.00%	5716.3	1.03%



SRR1658323

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
						Sequences	Sequences	Sequences	Background
						with Motif	with Motif	with Motif	ground Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-4449	-1.024e+04	0.0000	85611.0	17.64%	51538.8	10.76%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-4259	-9.809e+03	0.0000	96954.0	19.98%	61285.3	12.80%
	3	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-4010	-9.235e+03	0.0000	69055.0	14.23%	39958.6	8.35%
	4	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-4008	-9.231e+03	0.0000	76310.0	15.72%	45602.9	9.52%
	5	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3899	-8.979e+03	0.0000	75211.0	15.50%	45086.4	9.42%
	6	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3832	-8.825e+03	0.0000	83628.0	17.23%	51996.4	10.86%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-3560	-8.199e+03	0.0000	105410.0	21.72%	70973.5	14.82%
	8	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3472	-7.997e+03	0.0000	33788.0	6.96%	15632.9	3.27%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-3391	-7.810e+03	0.0000	67033.0	13.81%	40301.6	8.42%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2904	-6.687e+03	0.0000	48432.0	9.98%	27483.1	5.74%



SRR1658242

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Sequences with Motif	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3071	-7.073e+03	0.0000	90074.0	16.82%	59139.2	11.35%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-2779	-6.401e+03	0.0000	100666.0	18.80%	69202.4	13.28%
	3	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2682	-6.176e+03	0.0000	32425.0	6.05%	16113.0	3.09%
	4	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2639	-6.077e+03	0.0000	89891.0	16.79%	60855.9	11.68%
	5	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2633	-6.065e+03	0.0000	71116.0	13.28%	45540.3	8.74%
	6	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2553	-5.880e+03	0.0000	77607.0	14.49%	51120.4	9.81%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2524	-5.813e+03	0.0000	76571.0	14.30%	50398.3	9.67%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2338	-5.386e+03	0.0000	108408.0	20.24%	77993.6	14.96%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2196	-5.058e+03	0.0000	67375.0	12.58%	44311.1	8.50%
	10	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	1e-2131	-4.909e+03	0.0000	30825.0	5.76%	16318.6	3.13%



Epigenome Analysis Platform

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SRR1658224

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
						Sequences	Targets	Sequences	Background
						with Motif	with Motif	with Motif	with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3369	-7.758e+03	0.0000	95502.0	16.42%	62463.6	10.99%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3089	-7.113e+03	0.0000	107608.0	18.50%	73705.5	12.97%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2921	-6.728e+03	0.0000	94736.0	16.29%	63722.7	11.21%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2914	-6.712e+03	0.0000	75807.0	13.03%	48309.4	8.50%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2831	-6.521e+03	0.0000	83177.0	14.30%	54603.3	9.61%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2767	-6.372e+03	0.0000	82079.0	14.11%	53977.3	9.50%
	7	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2724	-6.273e+03	0.0000	35109.0	6.04%	17940.8	3.16%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2582	-5.946e+03	0.0000	117123.0	20.14%	84311.9	14.83%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2497	-5.752e+03	0.0000	73130.0	12.57%	47820.4	8.41%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2194	-5.054e+03	0.0000	54850.0	9.43%	34383.3	6.05%

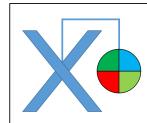


Epigenome Analysis Platform

Report

SRR1658341

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Sequences with Motif	% of Back-ground Sequences	# Targets with Motif	% of Back-ground Targets
	1	Fli1(ETS)/CD8-FLI-ChIP-Sq(GSE20898)/Homer	1e-3711	-8.546e+03	0.0000	89268.0	17.72%	56311.3	11.45%		
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Sq(GSE22441)/Homer	1e-3257	-7.500e+03	0.0000	98929.0	19.64%	65990.8	13.42%		
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Sq(ENCODE)/Homer	1e-3243	-7.469e+03	0.0000	89220.0	17.71%	58045.4	11.81%		
	4	ETS1(ETS)/Jurkat-ETS1-ChIP-Sq(GSE17954)/Homer	1e-3058	-7.042e+03	0.0000	76758.0	15.24%	48664.0	9.90%		
	5	GABPA(ETS)/Jurkat-GABPa-ChIP-Sq(GSE17954)/Homer	1e-3056	-7.039e+03	0.0000	70278.0	13.95%	43502.2	8.85%		
	6	ERG(ETS)/VCaP-ERG-ChIP-Sq(GSE14097)/Homer	1e-2843	-6.547e+03	0.0000	106691.0	21.18%	74365.4	15.13%		
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Sq(GSE88699)/Homer	1e-2777	-6.395e+03	0.0000	74617.0	14.81%	48017.7	9.77%		
	8	IRF8(IRF)/BMDM-IRF8-ChIP-Sq(GSE77884)/Homer	1e-2674	-6.158e+03	0.0000	31283.0	6.21%	15405.7	3.13%		
	9	Etv2(ETS)/ES-ER71-ChIP-Sq(GSE59402)/Homer	1e-2653	-6.110e+03	0.0000	66966.0	13.30%	42345.7	8.61%		
	10	Elk1(ETS)/Hela-Elk1-ChIP-Sq(GSE31477)/Homer	1e-2447	-5.636e+03	0.0000	52872.0	10.50%	31981.8	6.50%		



Epigenome Analysis Platform

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SRR1658215

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
	1	Fli1(ETS)/CD8-FLI-ChIP-Sq(GSE20898)/Homer	1e-3352	-7.719e+03	0.0000	90668.0	16.97%	58801.2	11.25%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Sq(GSE22441)/Homer	1e-3060	-7.047e+03	0.0000	101632.0	19.02%	69091.6	13.22%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Sq(ENCODE)/Homer	1e-2923	-6.732e+03	0.0000	90149.0	16.87%	60131.1	11.51%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Sq(GSE17954)/Homer	1e-2879	-6.629e+03	0.0000	71915.0	13.46%	45472.4	8.70%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Sq(GSE17954)/Homer	1e-2816	-6.485e+03	0.0000	78596.0	14.71%	51105.8	9.78%
	6	IRF8(IRF)/BMDM-IRF8-ChIP-Sq(GSE77884)/Homer	1e-2813	-6.479e+03	0.0000	33672.0	6.30%	16764.6	3.21%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Sq(GSE88699)/Homer	1e-2782	-6.407e+03	0.0000	77757.0	14.55%	50559.2	9.67%
	8	ERG(ETS)/VCaP-ERG-ChIP-Sq(GSE14097)/Homer	1e-2551	-5.874e+03	0.0000	110043.0	20.60%	78680.7	15.06%
	9	Etv2(ETS)/ES-ER71-ChIP-Sq(GSE59402)/Homer	1e-2391	-5.506e+03	0.0000	68423.0	12.81%	44575.3	8.53%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Sq(GSE31477)/Homer	1e-2294	-5.284e+03	0.0000	53092.0	9.94%	32714.8	6.26%



Epigenome Analysis Platform

Report

SRR1658170

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
						Sequences	Sequences	Sequences	Sequences
						with Motif	with Motif	with Motif	with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3354	-7.724e+03	0.0000	80028.0	17.77%	50625.4	11.46%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-2992	-6.891e+03	0.0000	88972.0	19.76%	59375.9	13.44%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2920	-6.724e+03	0.0000	79786.0	17.72%	52074.2	11.79%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2857	-6.580e+03	0.0000	63643.0	14.13%	39280.8	8.89%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2713	-6.249e+03	0.0000	68822.0	15.28%	43947.9	9.95%
	6	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2713	-6.247e+03	0.0000	29261.0	6.50%	14031.7	3.18%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2449	-5.641e+03	0.0000	66990.0	14.87%	43489.4	9.85%
	8	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2395	-5.516e+03	0.0000	47942.0	10.65%	28553.7	6.46%
	9	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2349	-5.411e+03	0.0000	95052.0	21.11%	67451.4	15.27%
	10	Elk4(ETS)/Hela-Elk4-ChIP-Seq(GSE31477)/Homer	1e-2292	-5.279e+03	0.0000	47820.0	10.62%	28800.0	6.52%



Epigenome Analysis Platform

Report

SRR1658152

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Background Sequences	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-2765	-6.368e+03	0.0000	61399.0	17.28%	38294.2	10.94%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-2506	-5.772e+03	0.0000	68792.0	19.36%	45297.8	12.94%
	3	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2354	-5.421e+03	0.0000	48807.0	13.73%	29678.1	8.48%
	4	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2339	-5.388e+03	0.0000	60261.0	16.96%	38928.5	11.12%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2328	-5.362e+03	0.0000	53686.0	15.11%	33645.5	9.61%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2197	-5.060e+03	0.0000	52446.0	14.76%	33125.4	9.46%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2029	-4.672e+03	0.0000	74120.0	20.86%	51857.7	14.81%
	8	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-1998	-4.603e+03	0.0000	46923.0	13.20%	29423.1	8.40%
	9	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-1940	-4.468e+03	0.0000	35686.0	10.04%	20823.5	5.95%
	10	Elk4(ETS)/Hela-Elk4-ChIP-Seq(GSE31477)/Homer	1e-1907	-4.393e+03	0.0000	35775.0	10.07%	20993.5	6.00%



Epigenome Analysis Platform

Report

SRR1658295

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Tar- get Se- quences	% of Tar- gets Se- quences with Mo- tif	# Back- ground Se- quences with Mo- tif	% of Back- ground Se- quences with Mo- tif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3708	-8.540e+03	0.0000	77468.0	17.81%	47469.4	11.11%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3415	-7.866e+03	0.0000	86664.0	19.92%	55948.6	13.10%
	3	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3305	-7.612e+03	0.0000	30879.0	7.10%	13975.6	3.27%
	4	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3291	-7.580e+03	0.0000	76308.0	17.54%	47978.1	11.23%
	5	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3221	-7.419e+03	0.0000	61784.0	14.20%	36701.6	8.59%
	6	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3051	-7.026e+03	0.0000	67097.0	15.42%	41447.0	9.70%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2881	-6.634e+03	0.0000	65887.0	15.15%	41079.8	9.62%
	8	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	1e-2770	-6.380e+03	0.0000	29926.0	6.88%	14393.3	3.37%
	9	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2765	-6.367e+03	0.0000	93100.0	21.40%	63994.1	14.98%
	10	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2619	-6.031e+03	0.0000	58684.0	13.49%	36274.8	8.49%



Epigenome Analysis Platform

Report

SRR1658277

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Tar- get Se- quen- ces with Mo- tif	% of Tar- gets Se- quen- ces with Mo- tif	# Back- ground Se- quen- ces with Mo- tif	% of Back- ground Se- quen- ces with Mo- tif
	1	Fli1(ETS)/CD8-FLI-ChIP-Sq(GSE20898)/Homer	1e-3213	-7.400e+03	0.0000	81391.0	16.59%	52151.2	10.83%
	2	ETV4(ETS)/HepG2-ETV4-ChIP-Sq(ENCODE)/Homer	1e-2843	-6.548e+03	0.0000	80313.0	16.37%	52723.5	10.94%
	3	ETV1(ETS)/GIST48-ETV1-ChIP-Sq(GSE22441)/Homer	1e-2814	-6.480e+03	0.0000	91002.0	18.55%	61713.2	12.81%
	4	IRF8(IRF)/BMDM-IRF8-ChIP-Sq(GSE77884)/Homer	1e-2783	-6.409e+03	0.0000	31937.0	6.51%	15713.2	3.26%
	5	GABPA(ETS)/Jurkat-GABPa-ChIP-Sq(GSE17954)/Homer	1e-2755	-6.346e+03	0.0000	64631.0	13.17%	40373.1	8.38%
	6	ETS1(ETS)/Jurkat-ETS1-ChIP-Sq(GSE17954)/Homer	1e-2662	-6.131e+03	0.0000	70909.0	14.45%	45771.1	9.50%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Sq(GSE88699)/Homer	1e-2403	-5.533e+03	0.0000	69074.0	14.08%	45321.6	9.41%
	8	IRF2(IRF)/Erythroblas-IRF2-ChIP-Sq(GSE36985)/Homer	1e-2401	-5.530e+03	0.0000	14210.0	2.90%	5014.8	1.04%
	9	Elk1(ETS)/Hela-Elk1-ChIP-Sq(GSE31477)/Homer	1e-2352	-5.418e+03	0.0000	47583.0	9.70%	28395.3	5.89%
	10	Elk4(ETS)/Hela-Elk4-ChIP-Sq(GSE31477)/Homer	1e-2348	-5.408e+03	0.0000	47953.0	9.77%	28695.7	5.96%



Epigenome Analysis Platform

Report

SRR1658246

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3496	-8.050e+03	0.0000	84879.0	18.04%	53410.6	11.69%
	2	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3295	-7.587e+03	0.0000	30873.0	6.56%	13812.7	3.02%
	3	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3087	-7.109e+03	0.0000	93383.0	19.85%	61930.6	13.56%
	4	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3006	-6.923e+03	0.0000	85105.0	18.09%	55461.4	12.14%
	5	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2987	-6.879e+03	0.0000	67177.0	14.28%	41159.9	9.01%
	6	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2825	-6.507e+03	0.0000	71990.0	15.30%	45561.9	9.97%
	7	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	1e-2804	-6.459e+03	0.0000	29382.0	6.25%	13774.8	3.02%
	8	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-2669	-6.147e+03	0.0000	13775.0	2.93%	4411.0	0.97%
	9	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2661	-6.129e+03	0.0000	70093.0	14.90%	44666.7	9.78%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2479	-5.710e+03	0.0000	52185.0	11.09%	31220.0	6.83%



Epigenome Analysis Platform

Report

SRR1658309

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets	# Background Sequences	% of Background
	1	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3782	-8.710e+03	0.0000	35673.0	6.91%	16084.7	3.20%
	2	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-3472	-7.995e+03	0.0000	16471.0	3.19%	5005.1	0.99%
	3	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	1e-3258	-7.504e+03	0.0000	34581.0	6.70%	16382.1	3.26%
	4	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3253	-7.490e+03	0.0000	87257.0	16.90%	56282.9	11.18%
	5	IRF1(IRF)/PBMC-IRF1-ChIP-Seq(GSE43036)/Homer	1e-3181	-7.325e+03	0.0000	19823.0	3.84%	7181.6	1.43%
	6	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-2913	-6.708e+03	0.0000	97138.0	18.82%	65836.8	13.08%
	7	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2802	-6.453e+03	0.0000	86504.0	16.76%	57501.2	11.43%
	8	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2767	-6.372e+03	0.0000	68845.0	13.34%	43329.1	8.61%
	9	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2697	-6.212e+03	0.0000	75362.0	14.60%	48833.7	9.70%
	10	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2602	-5.993e+03	0.0000	74008.0	14.34%	48121.3	9.56%



Epigenome Analysis Platform

Report

SRR1658228

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Sequences with Motif	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3225	-7.426e+03	0.0000	68270.0	17.81%	42050.4	11.15%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-2945	-6.781e+03	0.0000	76644.0	20.00%	49861.8	13.22%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2851	-6.566e+03	0.0000	67320.0	17.56%	42591.7	11.30%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2836	-6.531e+03	0.0000	54789.0	14.29%	32675.4	8.67%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2774	-6.390e+03	0.0000	59910.0	15.63%	36913.1	9.79%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2710	-6.241e+03	0.0000	59311.0	15.47%	36659.5	9.72%
	7	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2576	-5.932e+03	0.0000	25970.0	6.78%	12157.6	3.22%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2491	-5.737e+03	0.0000	82970.0	21.65%	57032.8	15.13%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2302	-5.301e+03	0.0000	52040.0	13.58%	32301.8	8.57%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2137	-4.921e+03	0.0000	39166.0	10.22%	22805.2	6.05%



Epigenome Analysis Platform

Report

SRR1658183

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Background sequences	% of Background
						Sequences with Motif	Sequences with Motif	Sequences with Motif	Sequences with Motif
	1	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-4049	-9.326e+03	0.0000	36496.0	7.32%	16297.7	3.32%
	2	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-3711	-8.545e+03	0.0000	16862.0	3.38%	5020.5	1.02%
	3	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	1e-3567	-8.214e+03	0.0000	35512.0	7.12%	16556.3	3.37%
	4	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3493	-8.045e+03	0.0000	84651.0	16.97%	53840.7	10.97%
	5	IRF1(IRF)/PBMC-IRF1-ChIP-Seq(GSE43036)/Homer	1e-3391	-7.809e+03	0.0000	20426.0	4.09%	7328.3	1.49%
	6	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3138	-7.227e+03	0.0000	94998.0	19.04%	63762.3	12.99%
	7	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3042	-7.005e+03	0.0000	83565.0	16.75%	54686.3	11.14%
	8	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3027	-6.970e+03	0.0000	67498.0	13.53%	41759.7	8.51%
	9	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2966	-6.831e+03	0.0000	74120.0	14.86%	47284.8	9.63%
	10	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2864	-6.596e+03	0.0000	72894.0	14.61%	46680.7	9.51%



Epigenome Analysis Platform

Report

SRR1658264

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Tar- get Se- quences	% of Tar- gets Se- quences with Mo- tif	# Back- ground Se- quences with Mo- tif	% of Back- ground Se- quences with Mo- tif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3551	-8.177e+03	0.0000	100118.0	16.61%	65080.8	11.11%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3216	-7.406e+03	0.0000	112589.0	18.68%	76802.6	13.11%
	3	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3153	-7.261e+03	0.0000	37418.0	6.21%	18450.9	3.15%
	4	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3102	-7.144e+03	0.0000	99668.0	16.53%	66589.7	11.36%
	5	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3066	-7.062e+03	0.0000	79535.0	13.19%	50398.8	8.60%
	6	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2994	-6.896e+03	0.0000	87153.0	14.46%	56812.7	9.69%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2849	-6.562e+03	0.0000	85514.0	14.19%	56084.5	9.57%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2769	-6.377e+03	0.0000	122346.0	20.30%	87243.2	14.89%
	9	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	1e-2629	-6.055e+03	0.0000	16181.0	2.68%	5783.0	0.99%
	10	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2601	-5.990e+03	0.0000	76096.0	12.62%	49490.9	8.45%



Epigenome Analysis Platform

Report

SRR1658318

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
						Sequences	Targets	Sequences	Background
						with Motif	with Motif	with Motif	with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-4765	-1.097e+04	0.0000	95698.0	17.67%	58146.6	10.91%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-4349	-1.002e+04	0.0000	107524.0	19.86%	69144.6	12.97%
	3	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-4205	-9.684e+03	0.0000	84687.0	15.64%	51260.0	9.62%
	4	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-4169	-9.600e+03	0.0000	94084.0	17.38%	58874.6	11.05%
	5	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-4154	-9.567e+03	0.0000	76581.0	14.14%	45082.8	8.46%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-3923	-9.035e+03	0.0000	83112.0	15.35%	50953.4	9.56%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-3782	-8.711e+03	0.0000	117724.0	21.74%	79898.6	14.99%
	8	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3611	-8.316e+03	0.0000	36974.0	6.83%	17432.2	3.27%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-3604	-8.299e+03	0.0000	74459.0	13.75%	45191.3	8.48%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-3089	-7.114e+03	0.0000	54450.0	10.06%	31348.6	5.88%



Epigenome Analysis Platform

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SRR1658192

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
						Sequences	Targets	Sequences	Background
						with Motif	with Motif	with Motif	ground Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3459	-7.966e+03	0.0000	85909.0	17.20%	54869.0	11.19%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3139	-7.229e+03	0.0000	96151.0	19.25%	64580.0	13.17%
	3	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-3072	-7.076e+03	0.0000	32950.0	6.60%	15786.7	3.22%
	4	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3065	-7.059e+03	0.0000	85451.0	17.11%	56020.1	11.42%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3027	-6.971e+03	0.0000	75150.0	15.05%	47781.0	9.74%
	6	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2941	-6.773e+03	0.0000	68178.0	13.65%	42511.7	8.67%
	7	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2851	-6.567e+03	0.0000	73704.0	14.76%	47280.9	9.64%
	8	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2672	-6.154e+03	0.0000	104104.0	20.84%	73439.5	14.97%
	9	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	1e-2560	-5.895e+03	0.0000	31913.0	6.39%	16199.4	3.30%
	10	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2533	-5.833e+03	0.0000	65238.0	13.06%	41676.1	8.50%



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SRR1658130

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences	% of Targets with Motif	# Background Sequences	% of Background with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3154	-7.264e+03	0.0000	82806.0	17.83%	53148.9	11.76%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-2903	-6.685e+03	0.0000	91595.0	19.72%	61384.4	13.58%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2807	-6.465e+03	0.0000	83322.0	17.94%	54951.2	12.16%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2760	-6.356e+03	0.0000	65643.0	14.13%	40856.1	9.04%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2583	-5.948e+03	0.0000	70434.0	15.17%	45358.4	10.04%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2512	-5.785e+03	0.0000	68877.0	14.83%	44381.1	9.82%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2379	-5.479e+03	0.0000	97374.0	20.97%	68675.1	15.20%
	8	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2218	-5.109e+03	0.0000	50386.0	10.85%	30794.7	6.81%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2208	-5.085e+03	0.0000	60819.0	13.10%	39099.7	8.65%
	10	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2182	-5.025e+03	0.0000	27444.0	5.91%	13832.9	3.06%



Epigenome Analysis Platform

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SRR1658310

Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
						Sequences	Targets	Sequences	Background
						with Motif	with Motif	with Motif	with Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-2765	-6.369e+03	0.0000	85750.0	16.84%	56817.4	11.49%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-2499	-5.755e+03	0.0000	95546.0	18.76%	66165.7	13.38%
	3	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-2399	-5.524e+03	0.0000	85996.0	16.89%	58652.2	11.86%
	4	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-2282	-5.256e+03	0.0000	67408.0	13.24%	43912.8	8.88%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-2147	-4.945e+03	0.0000	72743.0	14.28%	48847.9	9.88%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2131	-4.909e+03	0.0000	71902.0	14.12%	48227.5	9.76%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2012	-4.633e+03	0.0000	102175.0	20.06%	74361.0	15.04%
	8	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-1933	-4.453e+03	0.0000	51459.0	10.10%	32558.2	6.59%
	9	Elk4(ETS)/Hela-Elk4-ChIP-Seq(GSE31477)/Homer	1e-1898	-4.372e+03	0.0000	51597.0	10.13%	32806.2	6.64%
	10	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-1886	-4.345e+03	0.0000	63224.0	12.41%	42225.5	8.54%



SRR1658202

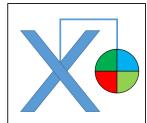
Motif	Rank	Name	P-value	log P-value	q-value (Benjamini)	# Target sequences	% of Targets	# Sequences with Motif	% of Background
						Sequences	Sequences	Sequences	Background
						with Motif	with Motif	with Motif	ground Motif
	1	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	1e-3707	-8.537e+03	0.0000	90261.0	17.48%	57182.4	11.33%
	2	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	1e-3403	-7.837e+03	0.0000	100772.0	19.52%	66974.5	13.26%
	3	GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	1e-3274	-7.540e+03	0.0000	71878.0	13.92%	44055.4	8.73%
	4	ETV4(ETS)/HepG2-ETV4-ChIP-Seq(ENCODE)/Homer	1e-3239	-7.459e+03	0.0000	90025.0	17.44%	58782.4	11.64%
	5	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	1e-3121	-7.187e+03	0.0000	78052.0	15.12%	49522.5	9.81%
	6	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer	1e-2987	-6.880e+03	0.0000	76670.0	14.85%	48915.8	9.69%
	7	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	1e-2832	-6.523e+03	0.0000	108473.0	21.01%	76006.2	15.05%
	8	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	1e-2788	-6.421e+03	0.0000	32404.0	6.28%	15949.4	3.16%
	9	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer	1e-2697	-6.210e+03	0.0000	67904.0	13.15%	42984.1	8.51%
	10	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	1e-2503	-5.765e+03	0.0000	53305.0	10.33%	32169.9	6.37%



6.2 de novo motif enrichment

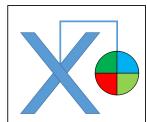
The table below shows the de novo motif enrichment results using homer. (*) denotes possible false positive)
SRR1658122

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3490	- 8.038e+03	22.31%	15.41%	55.4bp (60.2bp)	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer(0.946)
	2	1e-2403	- 5.535e+03	5.58%	2.78%	55.5bp (60.6bp)	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer(0.957)
	3	1e-1136	- 2.616e+03	48.75%	43.60%	55.3bp (59.7bp)	ORB2(RRM)/Drosophila_melanogaster-RNCMPT00126-PBM/HughesRNA(0.813)
	4	1e-1057	- 2.436e+03	56.73%	51.75%	56.2bp (62.8bp)	MYB98(MYB)/col-MYB98-DAP-Seq(GSE60143)/Homer(0.848)
	5	1e-1007	- 2.320e+03	54.06%	49.19%	55.9bp (62.4bp)	RUNX2/MA0511.2/Jaspar(0.793)
	6	1e-911	- 2.099e+03	24.82%	20.97%	56.0bp (60.1bp)	NRF(NRF)/Promoter/Homer(0.72)
	7	1e-787	- 1.813e+03	45.40%	41.14%	55.5bp (60.7bp)	AT-GTL1/MA1661.1/Jaspar(0.756)
	8	1e-783	- 1.804e+03	46.81%	42.55%	56.6bp (63.5bp)	bZIP910/MA0096.1/Jaspar(0.702)
	9	1e-751	- 1.729e+03	40.67%	36.59%	56.5bp (64.3bp)	YRM1/MA0438.1/Jaspar(0.761)
	10	1e-723	- 1.666e+03	35.89%	32.01%	56.1bp (60.8bp)	ZNF711(Zf)/SHSY5Y-ZNF711-ChIP-Seq(GSE20673)/Homer(0.865)



SRR1658320

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3709	- 8.541e+03	22.12%	15.21%	56.5bp (61.8bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.961)
	2	1e-2645	- 6.093e+03	6.45%	3.34%	55.6bp (61.0bp)	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer(0.898)
	3	1e-1429	- 3.293e+03	53.73%	48.06%	55.3bp (60.2bp)	DOF5.7/MA0984.1/Jaspar(0.797)
	4	1e-969	- 2.233e+03	51.13%	46.47%	56.0bp (60.1bp)	RPH1/MA0372.1/Jaspar(0.738)
	5	1e-962	- 2.217e+03	48.20%	43.58%	55.7bp (59.4bp)	PB0013.1_Eomes_1/Jaspar(0.689)
	6	1e-758	- 1.747e+03	29.45%	25.79%	56.0bp (60.1bp)	ovo/dmmpmm(Bergman)/fly(0.787)
	7	1e-704	- 1.622e+03	38.41%	34.60%	56.4bp (59.0bp)	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer(0.858)
	8	1e-665	- 1.531e+03	10.45%	8.25%	55.1bp (58.9bp)	NFkB-p65(RHD)/GM12787-p65-ChIP-Seq(GSE19485)/Homer(0.846)
	9	1e-639	- 1.472e+03	17.06%	14.34%	56.0bp (61.2bp)	CG7903(RRM)/Drosophila_melanogaster_RNCMPT00144-PBM/HughesRNA(0.736)
	10	1e-626	- 1.444e+03	42.20%	38.53%	56.9bp (59.2bp)	CG14718(RRM)/Drosophila_melanogaster_RNCMPT00006-PBM/HughesRNA(0.777)

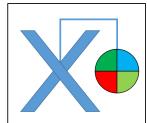


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SRR1658140

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3576	-8.235e+03	27.72%	20.17%	54.7bp (60.0bp)	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer(0.871)
	2	1e-1279	-2.946e+03	43.50%	38.21%	55.8bp (59.8bp)	DOF5.7/MA0984.1/Jaspar(0.729)
	3	1e-1017	-2.344e+03	38.50%	33.89%	55.8bp (59.5bp)	ZNF711(Zf)/SHSY5Y-ZNF711-ChIP-Seq(GSE20673)/Homer(0.669)
	4	1e-912	-2.101e+03	32.31%	28.15%	55.8bp (61.4bp)	prd/dmmpmm(Down)/fly(0.812)
	5	1e-863	-1.989e+03	42.30%	37.96%	56.3bp (58.7bp)	RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer(0.810)
	6	1e-848	-1.954e+03	53.99%	49.60%	55.2bp (60.0bp)	AT-GTL1/MA1661.1/Jaspar(0.768)
	7	1e-767	-1.768e+03	40.39%	36.33%	56.4bp (62.0bp)	MYB119/MA1176.1/Jaspar(0.865)
	8	1e-758	-1.748e+03	9.32%	7.09%	55.3bp (57.9bp)	NFkB-p65(RHD)/GM12787-p65-ChIP-Seq(GSE19485)/Homer(0.985)
	9	1e-741	-1.707e+03	47.79%	43.70%	56.7bp (59.2bp)	YAP7/YAP7_H2O2Hi/[](Harbison)/Y
	10	1e-715	-1.647e+03	34.51%	30.75%	55.6bp (57.9bp)	ZNF768(Zf)/Rajj-ZNF768-ChIP-Seq(GSE111879)/Homer(0.618)



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SRR1658131

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3563	-8.206e+03	21.20%	14.52%	55.1bp (60.1bp)	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer(0.886)
	2	1e-2044	-4.708e+03	3.08%	1.28%	57.3bp (61.1bp)	PU.1:IRF8(ETS:IRF)/pDC-Irf8-ChIP-Seq(GSE66899)/Homer(0.854)
	3	1e-1379	-3.178e+03	50.46%	44.90%	55.1bp (60.3bp)	kni/dmmpmm(Down)/fly(0.798)
	4	1e-1281	-2.952e+03	54.54%	49.17%	55.8bp (63.7bp)	AT2G15740(C2H2)/col-AT2G15740-DAP-Seq(GSE60143)/Homer(0.821)
	5	1e-962	-2.217e+03	43.55%	38.98%	56.3bp (60.7bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.691)
	6	1e-735	-1.694e+03	31.12%	27.44%	56.4bp (60.0bp)	Zac1(Zf)/Neuro2A-Plagl1-ChIP-Seq(GSE75942)/Homer(0.828)
	7	1e-715	-1.647e+03	29.40%	25.84%	56.2bp (57.3bp)	RUNX-AML(Runt)/CD4+-PolII-ChIP-Seq(Barski_et_al.)/Homer(0.844)
	8	1e-551	-1.271e+03	39.57%	36.17%	56.3bp (58.7bp)	CEP3/MA0282.1/Jaspar(0.697)
	9	1e-496	-1.144e+03	20.20%	17.61%	56.2bp (59.0bp)	E2F4/MA0470.2/Jaspar(0.744)
	10	1e-487	-1.123e+03	2.13%	1.31%	57.1bp (55.4bp)	BATF(bZIP)/Th17-BATF-ChIP-Seq(GSE39756)/Homer(0.995)

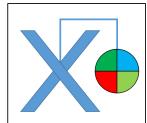


Epigenome Analysis Platform

Report

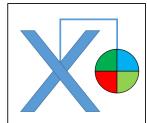
SRR1658311

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-4488	- 1.034e+04	30.21%	21.62%	54.8bp (59.9bp)	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer(0.933)
	2	1e-4225	- 9.729e+03	6.38%	2.69%	54.5bp (60.7bp)	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer(0.962)
	3	1e-1208	- 2.783e+03	56.81%	51.63%	55.2bp (59.9bp)	dof42(C2C2dof)/col-dof42-DAP-Seq(GSE60143)/Homer(0.827)
	4	1e-1096	- 2.525e+03	76.27%	71.90%	56.7bp (61.1bp)	ERT1/MA0420.1/Jaspar(0.701)
	5	1e-896	- 2.065e+03	27.84%	23.96%	55.9bp (58.2bp)	RUNX(Runt)/HPC7-Runx1-ChIP-Seq(GSE22178)/Homer(0.940)
	6	1e-844	- 1.944e+03	6.33%	4.43%	56.4bp (56.8bp)	Fra1(bZIP)/BT549-Fra1-ChIP-Seq(GSE46166)/Homer(0.991)
	7	1e-835	- 1.923e+03	54.94%	50.63%	56.4bp (59.6bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.686)
	8	1e-821	- 1.892e+03	7.30%	5.28%	55.4bp (57.8bp)	NFkB-p65(RHD)/GM12787-p65-ChIP-Seq(GSE19485)/Homer(0.990)
	9	1e-751	- 1.730e+03	35.19%	31.36%	56.5bp (60.6bp)	MYB98(MYB)/col-MYB98-DAP-Seq(GSE60143)/Homer(0.886)
	10	1e-618	- 1.425e+03	37.67%	34.12%	56.4bp (59.4bp)	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer(0.827)



SRR1658328

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
ACTTCCGGTT	1	1e-2976	- 6.854e+03	36.58%	28.70%	55.4bp (61.4bp)	ETV1(ETS)/GIST48- ETV1-ChIP- Seq(GSE22441)/Homer(0.891)
GCGCGAAAG	2	1e-1224	- 2.820e+03	49.36%	43.92%	55.8bp (60.5bp)	LBD18/MA1673.1/Jaspar(0.667)
GGGGCCCTTT	3	1e-1029	- 2.372e+03	35.50%	30.81%	55.0bp (60.0bp)	d1/MA0022.1/Jaspar(0.763)
GTGCCTTC	4	1e-1006	- 2.318e+03	42.31%	37.48%	56.4bp (59.9bp)	RUNX1(Runt)/Jurkat- RUNX1-ChIP- Seq(GSE29180)/Homer(0.801)
ATTTACTG	5	1e-928	- 2.137e+03	73.94%	69.64%	56.3bp (60.3bp)	AT5G47660(Trihelix)/colamp- AT5G47660-DAP- Seq(GSE60143)/Homer(0.776)
CGTTTGC GG	6	1e-879	- 2.024e+03	47.13%	42.54%	56.0bp (59.8bp)	CG7903(RRM)/Drosophila_melanogaster_RNCMPT00144-PBM/HughesRNA(0.732)
TAGGGCCT	7	1e-850	- 1.959e+03	34.99%	30.75%	56.6bp (59.0bp)	ZNF711(Zf)/SHSY5Y-ZNF711-ChIP- Seq(GSE20673)/Homer(0.889)
AGGCCGCTT	8	1e-846	- 1.949e+03	50.98%	46.45%	56.0bp (59.7bp)	ERF15(AP2ERE吕布)/colamp- ERF15-DAP- Seq(GSE60143)/Homer(0.728)
ACCCATTCGGC	9	1e-830	- 1.913e+03	43.85%	39.43%	55.1bp (58.6bp)	prd/dmmpmm(Pollard)/fly(0.696)
CGCATTCGAA	10	1e-818	- 1.885e+03	33.73%	29.61%	55.8bp (62.3bp)	AT5G22990(C2H2)/colamp- AT5G22990-DAP- Seq(GSE60143)/Homer(0.844)

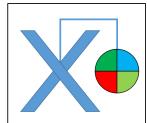


Epigenome Analysis Platform

Report

SRR1658247

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3771	-8.684e+03	25.78%	17.98%	54.9bp (60.0bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.865)
	2	1e-1062	-2.446e+03	44.75%	39.70%	56.4bp (61.9bp)	MYB119/MA1176.1/Jaspar(0.794)
	3	1e-941	-2.168e+03	59.74%	54.95%	55.9bp (59.0bp)	SKN7(MacIsaac)/Yeast(0.801)
	4	1e-871	-2.008e+03	35.95%	31.58%	55.5bp (60.1bp)	DOF5.7/MA0984.1/Jaspar(0.745)
	5	1e-830	-1.913e+03	36.61%	32.33%	55.9bp (60.4bp)	CG7903(RRM)/Drosophila_melanogaster_RNCMPT00144-PBM/HughesRNA(0.726)
	6	1e-760	-1.752e+03	41.92%	37.68%	55.2bp (60.4bp)	AT-GTL1/MA1661.1/Jaspar(0.825)
	7	1e-690	-1.589e+03	25.71%	22.21%	56.5bp (59.9bp)	OSR2/MA1646.1/Jaspar(0.735)
	8	1e-559	-1.288e+03	18.65%	15.87%	56.4bp (61.1bp)	SWI4(MacIsaac)/Yeast(0.766)
	9	1e-554	-1.278e+03	32.71%	29.30%	56.5bp (59.0bp)	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer(0.904)
	10	1e-547	-1.261e+03	1.88%	1.05%	57.4bp (55.7bp)	JunB(bZIP)/DendriticCells-Junb-ChIP-Seq(GSE36099)/Homer(0.995)

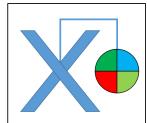


Epigenome Analysis Platform

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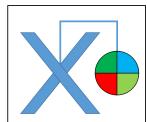
SRR1658229

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3542	-8.156e+03	22.78%	16.13%	54.7bp (59.8bp)	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer(0.881)
	2	1e-1276	-2.938e+03	56.11%	50.94%	55.9bp (60.0bp)	dof42(C2C2dof)/coldof42-DAP-Seq(GSE60143)/Homer(0.750)
	3	1e-961	-2.214e+03	55.61%	51.13%	56.3bp (60.3bp)	TBP3(MYBrelated)/coldTBP3-DAP-Seq(GSE60143)/Homer(0.774)
	4	1e-888	-2.045e+03	55.62%	51.32%	56.2bp (58.7bp)	CEP3/MA0282.1/Jaspar(0.660)
	5	1e-884	-2.037e+03	38.30%	34.18%	55.7bp (60.7bp)	AT-GTL1/MA1661.1/Jaspar(0.839)
	6	1e-852	-1.964e+03	28.60%	24.88%	56.1bp (60.9bp)	CG7903(RRM)/Drosophila_melanogaster-RNCMPT00144-PBM/HughesRNA(0.729)
	7	1e-830	-1.912e+03	54.11%	49.94%	55.3bp (59.5bp)	MYB65(MYB)/coldMYB65-DAP-Seq(GSE60143)/Homer(0.712)
	8	1e-812	-1.871e+03	41.42%	37.40%	55.6bp (58.9bp)	HNF1b(Homeobox)/PDAC-HNF1B-ChIP-Seq(GSE64557)/Homer(0.779)
	9	1e-805	-1.854e+03	59.69%	55.62%	56.8bp (61.1bp)	TFAP2A/MA0003.4/Jaspar(0.724)
	10	1e-782	-1.801e+03	48.78%	44.75%	56.4bp (59.8bp)	Dof2/MA0020.1/Jaspar(0.799)



SRR1658184

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3197	- 7.361e+03	28.86%	21.50%	55.6bp (60.6bp)	ETV1(ETS)/GIST48- ETV1-ChIP- Seq(GSE22441)/Homer(0.887)
	2	1e-1341	- 3.089e+03	17.61%	13.63%	55.8bp (60.9bp)	IRF5/MA1420.1/Jaspar(0.661)
	3	1e-1284	- 2.958e+03	40.64%	35.35%	55.7bp (60.1bp)	prd/dmmpmm(Down)/fly(0.801)
	4	1e-967	- 2.228e+03	55.51%	50.77%	56.0bp (59.0bp)	TBP3(MYBrelated)/col- TBP3-DAP- Seq(GSE60143)/Homer(0.764)
	5	1e-925	- 2.130e+03	43.71%	39.14%	56.2bp (59.8bp)	Dof2/MA0020.1/Jaspar(0.801)
	6	1e-776	- 1.787e+03	42.98%	38.81%	54.8bp (57.9bp)	ZFX(Zf)/mES-Zfx-ChIP- Seq(GSE11431)/Homer(0.723)
	7	1e-773	- 1.782e+03	36.92%	32.89%	55.8bp (58.8bp)	Mef2a(MADS)/HL1- Mef2a.biотин-ChIP- Seq(GSE21529)/Homer(0.776)
	8	1e-730	- 1.682e+03	47.34%	43.23%	55.4bp (60.1bp)	AT- GTL1/MA1661.1/Jaspar(0.845)
	9	1e-659	- 1.518e+03	43.43%	39.58%	56.3bp (58.6bp)	Nkx2- 5(var.2)/MA0503.1/Jaspar(0.669)
	10	1e-656	- 1.512e+03	54.89%	50.98%	56.8bp (59.4bp)	EBF3/MA1637.1/Jaspar(0.821)



Epigenome Analysis Platform

Report

SRR1658265

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3858	- 8.886e+03	46.21%	37.17%	56.0bp (63.1bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.923)
	2	1e-2631	- 6.059e+03	7.34%	4.02%	55.6bp (61.6bp)	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer(0.963)
	3	1e-1250	- 2.879e+03	50.08%	44.85%	55.3bp (59.9bp)	DOF5.7/MA0984.1/Jaspar(0.735)
	4	1e-1201	- 2.767e+03	54.69%	49.56%	56.3bp (61.6bp)	Dof2/MA0020.1/Jaspar(0.790)
	5	1e-772	- 1.779e+03	37.99%	34.05%	56.2bp (61.8bp)	SKN7(MacIsaac)/Yeast(0.701)
	6	1e-695	- 1.601e+03	24.97%	21.69%	56.1bp (62.0bp)	Pp_0229(RRM)/Physcomitrella_pRNCMPT00229-PBM/HughesRNA(0.688)
	7	1e-685	- 1.579e+03	45.76%	41.91%	56.4bp (58.4bp)	CDC5(MYB)/Arabidopsis thaliana/AthaMap(0.691)
	8	1e-667	- 1.538e+03	49.62%	45.80%	56.3bp (61.1bp)	Unknown3/Arabidopsis-Promoters/Homer(0.840)
	9	1e-667	- 1.538e+03	22.18%	19.10%	56.0bp (64.3bp)	AT2G15740(C2H2)/col-AT2G15740-DAP-Seq(GSE60143)/Homer(0.703)
	10	1e-663	- 1.528e+03	5.29%	3.75%	56.7bp (56.1bp)	AP-1(bZIP)/ThioMac-PU.1-ChIP-Seq(GSE21512)/Homer(0.991)



Epigenome Analysis Platform

Report

SRR1658319

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3399	- 7.828e+03	30.28%	21.30%	55.9bp (62.1bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.960)
	2	1e-2264	- 5.215e+03	7.66%	3.92%	55.3bp (61.9bp)	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer(0.896)
	3	1e-1320	- 3.041e+03	45.64%	39.20%	55.2bp (60.8bp)	prd/dmmpmm(Down)/fly(0.741)
	4	1e-1078	- 2.484e+03	29.15%	23.98%	56.1bp (65.3bp)	ETS2/MA1484.1/Jaspar(0.775)
	5	1e-988	- 2.275e+03	57.70%	52.07%	55.9bp (58.8bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.767)
	6	1e-687	- 1.582e+03	37.81%	33.31%	56.5bp (59.0bp)	RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer(0.867)
	7	1e-683	- 1.573e+03	16.57%	13.28%	55.5bp (61.9bp)	SWI4(MacIsaac)/Yeast(0.815)
	8	1e-672	- 1.548e+03	27.51%	23.48%	55.6bp (61.8bp)	GTL1(Trihelix)/colamp-GTL1-DAP-Seq(GSE60143)/Homer(0.853)
	9	1e-632	- 1.456e+03	61.03%	56.57%	55.1bp (59.1bp)	RO3G_00049(RRM)/Rhizopus_oryzae-RNCMPT00205-PBM/HughesRNA(0.758)
	10	1e-582	- 1.340e+03	34.63%	30.59%	56.4bp (60.1bp)	CG14718(RRM)/Drosophila_melanogaster-RNCMPT00006-PBM/HughesRNA(0.790)

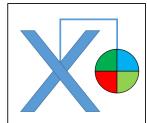


Epigenome Analysis Platform

Report

SRR1658126

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-4179	-9.624e+03	20.74%	13.55%	54.9bp (59.9bp)	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer(0.878)
	2	1e-1266	-2.917e+03	33.86%	28.86%	56.3bp (61.6bp)	UPC2/MA0411.1/Jaspar(0.826)
	3	1e-1226	-2.825e+03	44.57%	39.32%	55.9bp (58.4bp)	twi/dmmpmm(Papatsenko)/fly(0.665)
	4	1e-1198	-2.760e+03	44.97%	39.76%	55.0bp (59.5bp)	ROX8(RRM)/Drosophila_melanog RNCMPT00148-PBM/HughesRNA(0.775)
	5	1e-906	-2.087e+03	34.01%	29.76%	56.0bp (61.8bp)	SWI6/SWI6YPD/9-SWI4,9-SWI6(Harbison)/Yeast(0.840)
	6	1e-888	-2.046e+03	51.18%	46.64%	56.3bp (58.9bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.730)
	7	1e-859	-1.978e+03	22.81%	19.21%	56.1bp (59.5bp)	RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer(0.814)
	8	1e-714	-1.645e+03	51.68%	47.60%	56.3bp (58.4bp)	ZNF768(Zf)/Rajj-ZNF768-ChIP-Seq(GSE111879)/Homer(0.681)
	9	1e-634	-1.461e+03	34.20%	30.62%	56.7bp (60.1bp)	EBF3/MA1637.1/Jaspar(0.803)
	10	1e-616	-1.420e+03	4.07%	2.75%	56.9bp (56.7bp)	BATF(bZIP)/Th17-BATF-ChIP-Seq(GSE39756)/Homer(0.987)



Epigenome Analysis Platform

Report

SRR1658324

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-4273	-9.841e+03	8.91%	4.18%	54.7bp (61.9bp)	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer(0.979)
	2	1e-3152	-7.258e+03	19.25%	12.93%	55.2bp (59.7bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.944)
	3	1e-1117	-2.574e+03	38.42%	33.39%	55.8bp (60.4bp)	dof42(C2C2dof)/col-dof42-DAP-Seq(GSE60143)/Homer(0.735)
	4	1e-1108	-2.553e+03	63.84%	58.70%	56.7bp (58.9bp)	CG14718(RRM)/Drosophila_melanogaster-RNCMPT00006-PBM/HughesRNA(0.748)
	5	1e-1095	-2.523e+03	62.64%	57.50%	56.3bp (62.0bp)	MYB98(MYB)/col-MYB98-DAP-Seq(GSE60143)/Homer(0.930)
	6	1e-1037	-2.390e+03	28.50%	24.07%	55.5bp (59.0bp)	RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer(0.898)
	7	1e-807	-1.859e+03	48.97%	44.50%	55.6bp (59.5bp)	ZNF711(Zf)/SHSY5Y-ZNF711-ChIP-Seq(GSE20673)/Homer(0.760)
	8	1e-777	-1.791e+03	4.54%	2.94%	56.3bp (56.3bp)	JunB(bZIP)/DendriticCells-Junb-ChIP-Seq(GSE36099)/Homer(0.994)
	9	1e-690	-1.589e+03	44.20%	40.11%	55.7bp (58.5bp)	Tb_0251(RRM)/Trypanosoma_brucei-RNCMPT00251-PBM/HughesRNA(0.754)
	10	1e-472	-1.087e+03	25.28%	22.38%	56.6bp (59.2bp)	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer(0.828)

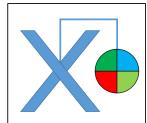


Epigenome Analysis Platform

Report

SRR1658243

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3890	-8.959e+03	23.17%	16.04%	54.6bp (59.9bp)	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer(0.886)
	2	1e-1050	-2.419e+03	64.81%	60.15%	56.8bp (60.0bp)	EBF3/MA1637.1/Jaspar(0.779)
	3	1e-934	-2.152e+03	36.76%	32.47%	55.6bp (60.4bp)	MYB(HTH)/ERMYB-Myb-ChIPSeq(GSE22095)/Homer(0.750)
	4	1e-901	-2.077e+03	55.62%	51.18%	56.1bp (61.5bp)	GTL1(Trihelix)/colamp-GTL1-DAP-Seq(GSE60143)/Homer(0.812)
	5	1e-871	-2.006e+03	46.83%	42.50%	55.8bp (60.3bp)	CG7903(RRM)/Drosophila_melanog-RNCMPT00144-PBM/HughesRNA(0.733)
	6	1e-866	-1.994e+03	43.62%	39.34%	56.3bp (59.2bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.742)
	7	1e-847	-1.952e+03	25.40%	21.77%	56.3bp (59.8bp)	SUM1(MacIsaac)/Yeast(0.734)
	8	1e-673	-1.551e+03	24.61%	21.41%	56.3bp (59.8bp)	ARR1/Literature(Harbison)/Yeast
	9	1e-660	-1.520e+03	20.76%	17.79%	57.2bp (56.1bp)	RUNX2(Runt)/PCa-RUNX2-ChIP-Seq(GSE33889)/Homer(0.961)
	10	1e-633	-1.459e+03	21.24%	18.31%	56.1bp (61.2bp)	SWI6/SWI6YPD/9-SWI4,9-SWI6(Harbison)/Yeast(0.868)

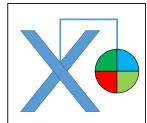


Epigenome Analysis Platform

Report

SRR1658306

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-4791	- 1.103e+04	7.75%	3.45%	55.1bp (60.8bp)	IRF2(IRF)/Erythroblas- IRF2-ChIP- Seq(GSE36985)/Homer(0.962)
	2	1e-1554	- 3.580e+03	53.92%	48.13%	55.6bp (60.7bp)	AT2G31460(REMB3)/col- AT2G31460-DAP- Seq(GSE60143)/Homer(0.807)
	3	1e-1129	- 2.601e+03	44.57%	39.71%	56.1bp (61.0bp)	Bgb::run/MA0242.1/Jaspar(0.739)
	4	1e-1087	- 2.505e+03	55.77%	50.94%	56.4bp (61.3bp)	MYB98(MYB)/col- MYB98-DAP- Seq(GSE60143)/Homer(0.918)
	5	1e-941	- 2.167e+03	34.66%	30.46%	56.3bp (61.6bp)	LBD18/MA1673.1/Jaspar(0.685)
	6	1e-936	- 2.157e+03	2.87%	1.61%	55.7bp (59.2bp)	NFkB- p65(RHD)/GM12787- p65-ChIP- Seq(GSE19485)/Homer(0.969)
	7	1e-843	- 1.943e+03	17.52%	14.44%	56.0bp (58.9bp)	ETV1/MA0761.2/Jaspar(0.681)
	8	1e-769	- 1.772e+03	32.68%	28.94%	55.6bp (59.7bp)	NCU02404(RRM)/Neurospora_cra- RNCMPT00238- PBM/HughesRNA(0.757)
	9	1e-766	- 1.765e+03	4.96%	3.39%	56.1bp (56.1bp)	AP-1(bZIP)/ThioMac- PU.1-ChIP- Seq(GSE21512)/Homer(0.979)
	10	1e-750	- 1.727e+03	42.85%	38.91%	55.7bp (60.2bp)	TBP3(MYBrelated)/col- TBP3-DAP- Seq(GSE60143)/Homer(0.796)



Epigenome Analysis Platform

Report

SRR1658342

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3177	-7.316e+03	27.21%	19.72%	54.8bp (59.6bp)	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer(0.884)
	2	1e-1148	-2.645e+03	53.93%	48.51%	56.1bp (60.7bp)	DEL2(E2FDP)/col-DEL2-DAP-Seq(GSE60143)/Homer(0.685)
	3	1e-1077	-2.482e+03	39.75%	34.69%	55.6bp (60.5bp)	dof42(C2C2dof)/col-dof42-DAP-Seq(GSE60143)/Homer(0.766)
	4	1e-980	-2.258e+03	36.30%	31.58%	55.9bp (61.7bp)	PABP(RRM)/Drosophila_melanog RNCMPT00139-PBM/HughesRNA(0.717)
	5	1e-728	-1.678e+03	4.64%	3.04%	56.4bp (56.0bp)	Fra1(bZIP)/BT549-Fra1-ChIP-Seq(GSE46166)/Homer(0.986)
	6	1e-716	-1.650e+03	24.49%	20.94%	56.2bp (57.5bp)	RUNX1/MA0002.2/Jaspar(0.847)
	7	1e-661	-1.523e+03	35.40%	31.53%	55.9bp (57.7bp)	PB0086.1_Tcfap2b_1/Jaspar(0.796)
	8	1e-640	-1.474e+03	42.82%	38.85%	56.4bp (58.8bp)	CDC5(MYB)/Arabidopsis thaliana/AthaMap(0.668)
	9	1e-603	-1.390e+03	39.68%	35.88%	55.9bp (58.2bp)	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer(0.794)
	10	1e-555	-1.278e+03	36.25%	32.68%	56.0bp (62.8bp)	che-1/MA0260.1/Jaspar(0.755)



Epigenome Analysis Platform

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SRR1658270

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-4176	- 9.617e+03	33.25%	25.00%	55.6bp (61.9bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.944)
	2	1e-3410	- 7.854e+03	7.32%	3.75%	55.5bp (61.2bp)	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer(0.946)
	3	1e-1429	- 3.290e+03	53.24%	47.85%	55.8bp (62.0bp)	prd/dmmpmm(Down)/fly(0.799)
	4	1e-1070	- 2.465e+03	36.86%	32.44%	56.3bp (59.8bp)	NFkB-p65-Rel(RHD)/ThioMac-LPS-Expression(GSE23622)/Homer(0.62)
	5	1e-1013	- 2.334e+03	51.17%	46.63%	56.0bp (61.3bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.768)
	6	1e-911	- 2.100e+03	43.96%	39.72%	55.2bp (60.4bp)	AT-GTL1/MA1661.1/Jaspar(0.736)
	7	1e-844	- 1.946e+03	56.61%	52.48%	56.2bp (63.2bp)	MYB98(MYB)/col-MYB98-DAP-Seq(GSE60143)/Homer(0.844)
	8	1e-780	- 1.797e+03	35.88%	32.13%	56.4bp (60.5bp)	CEP3/MA0282.1/Jaspar(0.717)
	9	1e-759	- 1.749e+03	3.25%	2.04%	56.7bp (55.7bp)	BATF(bZIP)/Th17-BATF-ChIP-Seq(GSE39756)/Homer(0.992)
	10	1e-712	- 1.642e+03	21.43%	18.42%	56.5bp (57.7bp)	RUNX(Runt)/HPC7-Runx1-ChIP-Seq(GSE22178)/Homer(0.960)



Epigenome Analysis Platform

Report

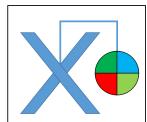
SRR1658269

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3811	-8.776e+03	21.03%	13.56%	56.4bp (60.5bp)	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer(0.971)
	2	1e-2807	-6.465e+03	7.18%	3.51%	55.2bp (60.4bp)	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer(0.925)
	3	1e-1041	-2.399e+03	42.43%	37.22%	55.0bp (59.0bp)	dof42(C2C2dof)/col-dof42-DAP-Seq(GSE60143)/Homer(0.772)
	4	1e-959	-2.210e+03	3.94%	2.26%	55.6bp (58.6bp)	NFkB-p65(RHD)/GM12787-p65-ChIP-Seq(GSE19485)/Homer(0.974)
	5	1e-942	-2.171e+03	41.35%	36.41%	56.1bp (61.3bp)	DEL2(E2FDP)/col-DEL2-DAP-Seq(GSE60143)/Homer(0.741)
	6	1e-898	-2.069e+03	24.42%	20.34%	56.5bp (60.3bp)	Dof2/MA0020.1/Jaspar(0.832)
	7	1e-863	-1.987e+03	59.06%	54.24%	56.8bp (59.6bp)	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer(0.859)
	8	1e-770	-1.775e+03	56.10%	51.51%	56.2bp (60.1bp)	AT3G10030(Trihelix)/colamp-AT3G10030-DAP-Seq(GSE60143)/Homer(0.876)
	9	1e-762	-1.756e+03	18.64%	15.26%	55.8bp (59.1bp)	SWI4(MacIsaac)/Yeast(0.826)
	10	1e-746	-1.719e+03	40.89%	36.50%	56.3bp (58.3bp)	ZNF768(Zf)/Raji-ZNF768-ChIP-Seq(GSE111879)/Homer(0.655)



SRR1658296

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-4261	-9.811e+03	20.98%	14.09%	55.1bp (59.2bp)	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer(0.951)
	2	1e-1891	-4.356e+03	8.73%	5.64%	56.2bp (61.3bp)	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer(0.867)
	3	1e-1268	-2.920e+03	46.51%	41.46%	55.2bp (59.5bp)	prd/dmmpmm(Down)/fly(0.757)
	4	1e-1141	-2.627e+03	55.50%	50.67%	55.9bp (60.1bp)	che-1/MA0260.1/Jaspar(0.721)
	5	1e-934	-2.151e+03	46.55%	42.22%	55.8bp (59.9bp)	ZNF711(Zf)/SHSY5Y-ZNF711-ChIP-Seq(GSE20673)/Homer(0.696)
	6	1e-920	-2.119e+03	48.23%	43.91%	56.7bp (58.9bp)	ANAC046(NAC)/colamp-ANAC046-DAP-Seq(GSE60143)/Homer(0.608)
	7	1e-798	-1.840e+03	42.75%	38.79%	56.6bp (64.1bp)	AT2G15740(C2H2)/col-AT2G15740-DAP-Seq(GSE60143)/Homer(0.844)
	8	1e-786	-1.810e+03	5.27%	3.67%	56.5bp (56.8bp)	Fra1(bZIP)/BT549-Fra1-ChIP-Seq(GSE46166)/Homer(0.991)
	9	1e-714	-1.646e+03	20.10%	17.16%	56.6bp (58.0bp)	RUNX(Runt)/HPC7-Runx1-ChIP-Seq(GSE22178)/Homer(0.957)
	10	1e-697	-1.607e+03	57.49%	53.73%	56.5bp (62.1bp)	NAC025/MA0935.1/Jaspar(0.863)



Epigenome Analysis Platform

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SRR1658197

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3454	-7.954e+03	27.10%	19.75%	55.2bp (60.8bp)	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer(0.972)
	2	1e-1366	-3.147e+03	30.14%	25.20%	56.3bp (66.4bp)	ERT1/MA0420.1/Jaspar(0.750)
	3	1e-1178	-2.713e+03	13.85%	10.54%	55.5bp (59.4bp)	ISRE(IRF)/ThioMac-LPS-Expression(GSE23622)/Homer(0.896)
	4	1e-1170	-2.694e+03	57.20%	52.06%	56.1bp (61.2bp)	DOF5.7/MA0984.1/Jaspar(0.767)
	5	1e-954	-2.198e+03	41.97%	37.43%	55.9bp (59.8bp)	ARF16(ARF)/col-ARF16-DAP-Seq(GSE60143)/Homer(0.803)
	6	1e-881	-2.029e+03	36.95%	32.71%	55.7bp (62.3bp)	StBRC1/MA1410.1/Jaspar(0.676)
	7	1e-871	-2.008e+03	35.63%	31.45%	55.8bp (59.6bp)	PRDM4/MA1647.1/Jaspar(0.796)
	8	1e-813	-1.874e+03	46.00%	41.74%	55.7bp (61.8bp)	GTL1(Trihelix)/colamp-GTL1-DAP-Seq(GSE60143)/Homer(0.733)
	9	1e-750	-1.729e+03	4.48%	2.97%	56.4bp (55.4bp)	Fos(bZIP)/TSC-Fos-ChIP-Seq(GSE110950)/Homer(0.990)
	10	1e-698	-1.609e+03	35.80%	32.05%	56.3bp (65.8bp)	STP1/MA0394.1/Jaspar(0.674)

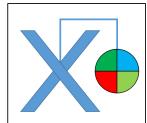


Epigenome Analysis Platform

Report

SRR1658278

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3531	- 8.131e+03	33.59%	25.61%	55.9bp (62.0bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.905)
	2	1e-2697	- 6.212e+03	6.88%	3.63%	54.9bp (61.5bp)	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer(0.933)
	3	1e-1448	- 3.335e+03	45.18%	39.58%	56.3bp (60.5bp)	prd/dmmpmm(Down)/fly(0.700)
	4	1e-1224	- 2.819e+03	50.31%	45.10%	56.7bp (62.4bp)	CAMTA1(CAMTA)/col-CAMTA1-DAP-Seq(GSE60143)/Homer(0.756)
	5	1e-1144	- 2.636e+03	44.06%	39.10%	55.6bp (60.6bp)	dof42(C2C2dof)/col-dof42-DAP-Seq(GSE60143)/Homer(0.784)
	6	1e-974	- 2.244e+03	48.39%	43.75%	55.6bp (60.6bp)	AT3G10030(Trihelix)/colamp-AT3G10030-DAP-Seq(GSE60143)/Homer(0.694)
	7	1e-899	- 2.070e+03	63.07%	58.69%	56.5bp (60.0bp)	ZNF711(Zf)/SHSY5Y-ZNF711-ChIP-Seq(GSE20673)/Homer(0.872)
	8	1e-891	- 2.053e+03	34.19%	30.05%	56.7bp (64.0bp)	MYB98(MYB)/col-MYB98-DAP-Seq(GSE60143)/Homer(0.896)
	9	1e-879	- 2.025e+03	38.46%	34.22%	56.0bp (61.0bp)	Dof2/MA0020.1/Jaspar(0.902)
	10	1e-769	- 1.772e+03	24.17%	20.75%	56.7bp (58.2bp)	RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer(0.943)

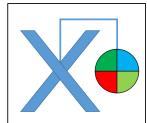


Epigenome Analysis Platform

Report

SRR1658205

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3483	-8.021e+03	27.64%	20.18%	55.2bp (59.8bp)	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer(0.948)
	2	1e-1554	-3.580e+03	8.26%	5.37%	54.6bp (61.2bp)	IRF8/MA0652.1/Jaspar(0.960)
	3	1e-1123	-2.588e+03	36.47%	31.69%	55.3bp (59.7bp)	ROX8(RRM)/Drosophila_melanogaster-RNCMPT00148-PBM/HughesRNA(0.745)
	4	1e-1089	-2.510e+03	6.13%	4.02%	55.9bp (60.7bp)	PU.1:IRF8(ETS:IRF)/pDC-Irf8-ChIP-Seq(GSE66899)/Homer(0.871)
	5	1e-985	-2.268e+03	41.73%	37.11%	56.4bp (60.7bp)	SWI4/SWI4YPD/29-SWI4,29-SWI6(Harbison)/Yeast(0.805)
	6	1e-971	-2.237e+03	40.51%	35.95%	56.5bp (62.3bp)	Dof2/MA0020.1/Jaspar(0.783)
	7	1e-969	-2.233e+03	42.32%	37.72%	55.6bp (61.3bp)	Deaf1/dmmpmm(Pollard)/fly(0.752)
	8	1e-931	-2.144e+03	49.22%	44.62%	55.9bp (60.9bp)	CG7903(RRM)/Drosophila_melanogaster-RNCMPT00144-PBM/HughesRNA(0.725)
	9	1e-764	-1.759e+03	52.75%	48.57%	56.5bp (61.7bp)	MYB118(MYB)/colamp-MYB118-DAP-Seq(GSE60143)/Homer(0.851)
	10	1e-644	-1.483e+03	2.80%	1.71%	57.2bp (56.3bp)	AP-1(bZIP)/ThioMac-PU.1-ChIP-Seq(GSE21512)/Homer(0.989)

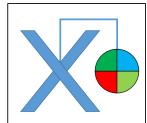


Epigenome Analysis Platform

Report

SRR1658142

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-4075	- 9.384e+03	27.80%	19.59%	55.4bp (61.3bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.951)
	2	1e-1442	- 3.321e+03	40.75%	35.07%	55.6bp (62.3bp)	AT1G76870/MA1367.1/Jaspar(0.79)
	3	1e-1189	- 2.740e+03	46.69%	41.40%	56.1bp (61.9bp)	ORB2(RRM)/Drosophila_melanogaster_RNCMPT00126-PBM/HughesRNA(0.721)
	4	1e-1036	- 2.387e+03	36.50%	31.80%	55.0bp (60.3bp)	dof42(C2C2dof)/coldof42-DAP-Seq(GSE60143)/Homer(0.733)
	5	1e-815	- 1.878e+03	53.11%	48.69%	56.6bp (60.4bp)	POL010.1_DCE_S_III/Jaspar(0.716)
	6	1e-720	- 1.658e+03	44.14%	40.05%	55.8bp (57.9bp)	Nkx2-5(var.2)/MA0503.1/Jaspar(0.702)
	7	1e-696	- 1.604e+03	5.58%	3.90%	55.8bp (56.5bp)	Fra1(bZIP)/BT549-Fra1-ChIP-Seq(GSE46166)/Homer(0.983)
	8	1e-578	- 1.332e+03	29.90%	26.57%	56.7bp (62.5bp)	NAC025/MA0935.1/Jaspar(0.848)
	9	1e-577	- 1.330e+03	2.43%	1.46%	52.9bp (57.3bp)	YY1(Zf)/Promoter/Homer(0.904)
	10	1e-565	- 1.302e+03	21.32%	18.41%	56.4bp (62.4bp)	Dof2/MA0020.1/Jaspar(0.729)

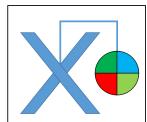


Epigenome Analysis Platform

Report

SRR1658340

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-4728	- 1.089e+04	18.43%	11.63%	55.1bp (59.3bp)	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer(0.961)
	2	1e-3565	- 8.211e+03	10.30%	5.87%	54.9bp (60.5bp)	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer(0.902)
	3	1e-1063	- 2.450e+03	55.91%	51.23%	56.7bp (60.0bp)	BMYB(HTH)/Hela-BMYB-ChIP-Seq(GSE27030)/Homer(0.915)
	4	1e-1033	- 2.380e+03	40.59%	36.12%	55.8bp (60.1bp)	hkb/dmmpmm(Papatsenko)/fly(0.683)
	5	1e-1006	- 2.319e+03	20.02%	16.55%	55.8bp (61.5bp)	SWI4(MacIsaac)/Yeast(0.840)
	6	1e-864	- 1.990e+03	49.97%	45.76%	55.5bp (58.4bp)	STAT5(Stat)/mCD4+-Stat5-ChIP-Seq(GSE12346)/Homer(0.683)
	7	1e-846	- 1.949e+03	48.81%	44.65%	56.8bp (60.2bp)	EBF3/MA1637.1/Jaspar(0.787)
	8	1e-772	- 1.779e+03	4.84%	3.32%	56.3bp (56.7bp)	AP-1(bZIP)/ThioMac-PU.1-ChIP-Seq(GSE21512)/Homer(0.985)
	9	1e-726	- 1.672e+03	32.43%	28.89%	56.4bp (60.3bp)	Bgb::run/MA0242.1/Jaspar(0.741)
	10	1e-712	- 1.641e+03	4.10%	2.76%	52.6bp (55.9bp)	YY1/MA0095.2/Jaspar(0.947)

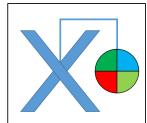


Epigenome Analysis Platform

Report

SRR1658133

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-4033	-9.287e+03	29.11%	21.32%	56.4bp (60.6bp)	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer(0.930)
	2	1e-3177	-7.317e+03	7.62%	4.04%	55.7bp (60.4bp)	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer(0.940)
	3	1e-1231	-2.836e+03	38.69%	33.85%	55.6bp (59.9bp)	ROX8(RRM)/Drosophila_melanogaster-RNCMPT00148-PBM/HughesRNA(0.745)
	4	1e-1226	-2.823e+03	54.90%	49.86%	56.7bp (61.6bp)	MIG1(MacIsaac)/Yeast(0.675)
	5	1e-1078	-2.483e+03	46.58%	41.88%	56.5bp (64.6bp)	MYB98(MYB)/col-MYB98-DAP-Seq(GSE60143)/Homer(0.910)
	6	1e-1042	-2.400e+03	46.46%	41.85%	56.4bp (61.0bp)	CG7903(RRM)/Drosophila_melanogaster-RNCMPT00144-PBM/HughesRNA(0.739)
	7	1e-1026	-2.363e+03	51.27%	46.66%	56.2bp (60.2bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.741)
	8	1e-879	-2.025e+03	36.29%	32.25%	55.3bp (64.0bp)	At5g18450(AP2ERE吕布)/col-At5g18450-DAP-Seq(GSE60143)/Homer(0.707)
	9	1e-841	-1.937e+03	26.54%	22.96%	56.4bp (58.5bp)	RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer(0.846)
	10	1e-788	-1.816e+03	50.73%	46.69%	56.4bp (58.9bp)	AtGRF6(GRF)/col-AtGRF6-DAP-Seq(GSE60143)/Homer(0.675)



Epigenome Analysis Platform

Report

SRR1658214

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3238	- 7.456e+03	25.33%	18.36%	56.1bp (62.2bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.925)
	2	1e-1342	- 3.091e+03	3.72%	1.99%	56.5bp (61.2bp)	PU.1-IRF(ETS:IRF)/Bcell-PU.1-ChIP-Seq(GSE21512)/Homer(0.925)
	3	1e-1304	- 3.004e+03	57.58%	52.12%	55.0bp (59.5bp)	ROX8(RRM)/Drosophila_melanogaster-RNCMPT00148-PBM/HughesRNA(0.759)
	4	1e-1172	- 2.700e+03	49.80%	44.63%	56.4bp (61.2bp)	Unknown3/Arabidopsis-Promoters/Homer(0.739)
	5	1e-1008	- 2.322e+03	63.09%	58.38%	55.9bp (61.0bp)	AT3G10030(Trihelix)/colamp-AT3G10030-DAP-Seq(GSE60143)/Homer(0.774)
	6	1e-993	- 2.287e+03	56.41%	51.64%	56.1bp (59.3bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.769)
	7	1e-981	- 2.259e+03	50.15%	45.42%	56.0bp (60.6bp)	prd/dmmpmm(Down)/fly(0.729)
	8	1e-670	- 1.544e+03	27.46%	24.06%	57.1bp (56.5bp)	MET32/MA0334.1/Jaspar(0.887)
	9	1e-654	- 1.507e+03	5.89%	4.24%	56.7bp (56.8bp)	Fra1(bZIP)/BT549-Fra1-ChIP-Seq(GSE46166)/Homer(0.989)
	10	1e-566	- 1.304e+03	23.18%	20.23%	56.4bp (58.8bp)	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer(0.902)

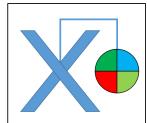


Epigenome Analysis Platform

Report

SRR1658232

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3178	-7.318e+03	21.06%	14.44%	54.6bp (59.6bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.886)
	2	1e-1003	-2.312e+03	57.79%	52.81%	55.5bp (58.0bp)	TCF7/MA0769.2/Jaspar(0.646)
	3	1e-996	-2.296e+03	43.61%	38.72%	56.7bp (62.2bp)	AT2G15740(C2H2)/col-AT2G15740-DAP-Seq(GSE60143)/Homer(0.800)
	4	1e-971	-2.238e+03	50.76%	45.85%	56.0bp (60.5bp)	GTL1(Trihelix)/colamp-GTL1-DAP-Seq(GSE60143)/Homer(0.792)
	5	1e-895	-2.062e+03	31.60%	27.32%	55.0bp (59.7bp)	dof42(C2C2dof)/col-dof42-DAP-Seq(GSE60143)/Homer(0.754)
	6	1e-790	-1.821e+03	23.34%	19.73%	55.7bp (60.8bp)	KHDRBS1(KH)/Mus_musculus-RNCMPT00062-PBM/HughesRNA(0.801)
	7	1e-752	-1.733e+03	33.02%	29.04%	56.0bp (58.1bp)	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer(0.858)
	8	1e-746	-1.720e+03	38.53%	34.39%	55.4bp (59.3bp)	BMYB(HTH)/Hela-BMYB-ChIP-Seq(GSE27030)/Homer(0.692)
	9	1e-740	-1.705e+03	4.47%	2.91%	56.2bp (55.9bp)	BATF(bZIP)/Th17-BATF-ChIP-Seq(GSE39756)/Homer(0.987)
	10	1e-640	-1.475e+03	2.10%	1.15%	51.6bp (55.0bp)	YY1/MA0095.2/Jaspar(0.912)



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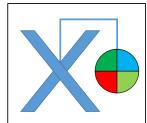
SRR1658168

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3039	-7.000e+03	22.82%	16.27%	55.3bp (60.9bp)	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer(0.908)
	2	1e-1305	-3.007e+03	45.82%	40.35%	55.0bp (59.6bp)	ROX8(RRM)/Drosophila_melanog RNCMPT00148-PBM/HughesRNA(0.783)
	3	1e-867	-1.998e+03	46.14%	41.67%	56.4bp (58.8bp)	ZNF711(Zf)/SHSY5Y-ZNF711-ChIP-Seq(GSE20673)/Homer(0.821)
	4	1e-846	-1.948e+03	35.72%	31.53%	55.7bp (59.0bp)	AT5G22990(C2H2)/col-AT5G22990-DAP-Seq(GSE60143)/Homer(0.658)
	5	1e-839	-1.934e+03	4.96%	3.26%	55.2bp (58.7bp)	MF0003.1_REL_class/Jaspar(0.965)
	6	1e-830	-1.912e+03	57.03%	52.63%	56.5bp (61.8bp)	NAC025/MA0935.1/Jaspar(0.759)
	7	1e-747	-1.722e+03	49.20%	45.02%	55.7bp (61.2bp)	ERF15(AP2ERE吕布)/colamp-ERF15-DAP-Seq(GSE60143)/Homer(0.673)
	8	1e-682	-1.573e+03	18.85%	15.85%	56.1bp (60.1bp)	IRF4(IRF)/GM12878-IRF4-ChIP-Seq(GSE32465)/Homer(0.849)
	9	1e-673	-1.552e+03	56.88%	52.91%	56.2bp (58.7bp)	CG14718(RRM)/Drosophila_melanog RNCMPT00006-PBM/HughesRNA(0.655)
	10	1e-609	-1.403e+03	50.28%	46.50%	56.1bp (61.2bp)	SWI4/SWI4YPD/29-SWI4,29-SWI6(Harbison)/Yeast(0.793)



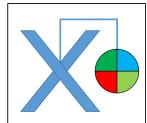
SRR1658267

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-4040	- 9.305e+03	44.53%	35.52%	55.5bp (61.3bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.956)
	2	1e-1981	- 4.562e+03	3.66%	1.72%	56.1bp (61.3bp)	PU.1-IRF(ETS:IRF)/Bcell-PU.1-ChIP-Seq(GSE21512)/Homer(0.922)
	3	1e-1269	- 2.923e+03	49.27%	44.10%	56.0bp (61.0bp)	prd/dmmpmm(Down)/fly(0.794)
	4	1e-1057	- 2.435e+03	56.12%	51.39%	55.2bp (59.2bp)	dof42(C2C2dof)/col-dof42-DAP-Seq(GSE60143)/Homer(0.785)
	5	1e-925	- 2.132e+03	50.01%	45.58%	56.2bp (59.5bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.763)
	6	1e-788	- 1.816e+03	19.39%	16.29%	56.5bp (59.0bp)	RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer(0.831)
	7	1e-747	- 1.721e+03	37.74%	33.94%	55.4bp (60.3bp)	AT-GTL1/MA1661.1/Jaspar(0.825)
	8	1e-729	- 1.681e+03	18.72%	15.78%	55.8bp (62.0bp)	PABP(RRM)/Drosophila_melanogRNCMPT00139-PBM/HughesRNA(0.719)
	9	1e-689	- 1.588e+03	4.96%	3.47%	56.5bp (56.4bp)	JunB(bZIP)/DendriticCells-Junb-ChIP-Seq(GSE36099)/Homer(0.991)
	10	1e-638	- 1.471e+03	42.88%	39.27%	56.3bp (58.3bp)	ZNF768(Zf)/Rajj-ZNF768-ChIP-Seq(GSE111879)/Homer(0.693)



SRR1658177

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3542	- 8.156e+03	34.12%	24.54%	55.7bp (60.4bp)	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer(0.945)
	2	1e-2237	- 5.152e+03	5.32%	2.33%	55.1bp (62.2bp)	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer(0.897)
	3	1e-914	- 2.105e+03	58.09%	52.66%	55.8bp (61.3bp)	BMYB(HTH)/Hela-BMYB-ChIP-Seq(GSE27030)/Homer(0.868)
	4	1e-831	- 1.915e+03	48.40%	43.23%	56.4bp (58.3bp)	CDC5(MYB)/Arabidopsis thaliana/AthaMap(0.676)
	5	1e-802	- 1.848e+03	35.21%	30.45%	56.9bp (61.3bp)	ASG1/MA0275.1/Jaspar(0.750)
	6	1e-732	- 1.687e+03	53.33%	48.46%	56.2bp (59.3bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.762)
	7	1e-677	- 1.559e+03	48.41%	43.74%	55.5bp (57.6bp)	MSN4/MA0342.1/Jaspar(0.789)
	8	1e-618	- 1.425e+03	59.30%	54.85%	56.0bp (59.1bp)	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer(0.753)
	9	1e-613	- 1.414e+03	2.96%	1.69%	51.8bp (55.4bp)	YY1/MA0095.2/Jaspar(0.961)
	10	1e-580	- 1.336e+03	5.45%	3.70%	56.3bp (57.5bp)	Fra1(bZIP)/BT549-Fra1-ChIP-Seq(GSE46166)/Homer(0.985)



SRR1658339

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3416	-7.867e+03	20.82%	14.30%	55.0bp (59.0bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.937)
	2	1e-2386	-5.495e+03	3.43%	1.39%	56.6bp (63.5bp)	IRF1(IRF)/PBMC-IRF1-ChIP-Seq(GSE43036)/Homer(0.899)
	3	1e-1251	-2.881e+03	52.91%	47.58%	56.6bp (62.2bp)	PF10_0214(RRM)/Plasmodium_falciparum-RNCMPT00240-PBM/HughesRNA(0.725)
	4	1e-1031	-2.375e+03	57.12%	52.30%	55.9bp (57.2bp)	REI1/MA0364.1/Jaspar(0.624)
	5	1e-983	-2.264e+03	25.88%	21.89%	55.8bp (61.2bp)	BMYB(HTH)/Helab-BMYB-ChIP-Seq(GSE27030)/Homer(0.802)
	6	1e-981	-2.261e+03	55.35%	50.63%	55.0bp (59.2bp)	Hnrnpr(RRM)/Xenopus_tropicalis-RNCMPT00289-PBM/HughesRNA(0.748)
	7	1e-913	-2.103e+03	8.89%	6.53%	55.7bp (57.8bp)	NFkB-p65(RHD)/GM12787-p65-ChIP-Seq(GSE19485)/Homer(0.976)
	8	1e-868	-2.000e+03	46.95%	42.54%	55.9bp (60.1bp)	PRDM4/MA1647.1/Jaspar(0.732)
	9	1e-799	-1.842e+03	4.58%	3.01%	56.9bp (56.3bp)	BATF(bZIP)/Th17-BATF-ChIP-Seq(GSE39756)/Homer(0.991)
	10	1e-789	-1.819e+03	44.14%	39.97%	56.4bp (60.4bp)	SWI6/SWI6YPD/9-SWI4,9-SWI6(Harbison)/Yeast(0.832)

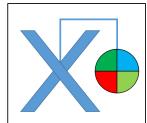


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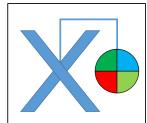
SRR1658276

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3968	-9.139e+03	24.59%	16.95%	55.2bp (59.8bp)	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer(0.956)
	2	1e-1206	-2.777e+03	45.00%	39.75%	55.1bp (60.4bp)	DOF5.7/MA0984.1/Jaspar(0.814)
	3	1e-819	-1.887e+03	42.11%	37.82%	56.3bp (61.8bp)	MYB98(MYB)/col-MYB98-DAP-Seq(GSE60143)/Homer(0.912)
	4	1e-770	-1.773e+03	15.19%	12.31%	56.0bp (62.1bp)	SWI4(MacIsaac)/Yeast(0.831)
	5	1e-760	-1.750e+03	46.77%	42.57%	56.2bp (60.2bp)	ZNF711(Zf)/SHSY5Y-ZNF711-ChIP-Seq(GSE20673)/Homer(0.894)
	6	1e-734	-1.692e+03	11.30%	8.84%	54.9bp (58.7bp)	SpiB(ETS)/OCILY3-SPIB-ChIP-Seq(GSE56857)/Homer(0.717)
	7	1e-682	-1.572e+03	36.00%	32.22%	56.8bp (62.5bp)	STP3/MA0396.1/Jaspar(0.749)
	8	1e-669	-1.541e+03	34.11%	30.42%	55.2bp (58.3bp)	OSR2/MA1646.1/Jaspar(0.725)
	9	1e-629	-1.449e+03	32.51%	28.98%	55.7bp (59.8bp)	Foxn1/MA1684.1/Jaspar(0.628)
	10	1e-621	-1.431e+03	1.88%	1.02%	52.0bp (56.1bp)	YY1(Zf)/Promoter/Homer(0.978)



SRR1658128

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
CAC TTT CCGTTT AAG GGG TTT TTT	1	1e-4075	-9.385e+03	25.46%	18.31%	55.1bp (59.7bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.884)
CGT TTT TTT GCGG AAT TTT TTT TTT	2	1e-1117	-2.572e+03	41.65%	37.14%	55.8bp (61.0bp)	ORB2(RRM)/Drosophila_melanog RNCMPT00126-PBM/HughesRNA(0.754)
GGG GAA ACC GGA Aac Gtt Ttt Ttt	3	1e-1084	-2.498e+03	37.56%	33.22%	55.1bp (62.6bp)	IRF5/MA1420.1/Jaspar(0.753)
AAA CGG CC Ttt Gaa Ccc Ccc	4	1e-1039	-2.393e+03	38.98%	34.69%	55.8bp (61.5bp)	MYB(HTH)/ERMYB-Myb-ChIPSeq(GSE22095)/Homer(0.725)
CGT GAC CAG TT Aca Ctt Taa	5	1e-1005	-2.316e+03	53.71%	49.31%	56.8bp (59.6bp)	BMYB(HTH)/Hela-BMYB-ChIP- Seq(GSE27030)/Homer(0.847)
GGCCCTAA Agt Gcc Tgg	6	1e-935	-2.154e+03	56.50%	52.27%	56.2bp (61.8bp)	TBP3(MYBrelated)/col-TBP3-DAP- Seq(GSE60143)/Homer(0.779)
GTT ACT GATT Ttt Aat Ttt Ttt	7	1e-761	-1.752e+03	45.91%	42.13%	56.0bp (58.5bp)	HNF1b/Homeobox)/PDAC-HNF1B-ChIP- Seq(GSE64557)/Homer(0.743)
AGGCCTCT Agt Gcc Tgg	8	1e-754	-1.737e+03	39.80%	36.13%	56.3bp (59.9bp)	ZFX(Zf)/mES-Zfx-ChIP- Seq(GSE11431)/Homer(0.882)
GTG GTT AAC Agt Gtt Ttt Aac	9	1e-720	-1.660e+03	32.89%	29.46%	56.3bp (58.6bp)	RUNX1(Runt)/Jurkat-RUNX1-ChIP- Seq(GSE29180)/Homer(0.797)
CGTTACGT Agt Gtt Ttt Aac	10	1e-713	-1.643e+03	48.17%	44.49%	56.4bp (62.5bp)	NAC025/MA0935.1/Jaspar(0.855)



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SRR1658245

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-4297	- 9.895e+03	28.02%	19.47%	55.7bp (61.2bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.967)
	2	1e-2877	- 6.626e+03	4.21%	1.65%	55.6bp (61.4bp)	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer(0.961)
	3	1e-1097	- 2.526e+03	48.99%	43.81%	56.5bp (63.9bp)	AT2G15740(C2H2)/col-AT2G15740-DAP-Seq(GSE60143)/Homer(0.726)
	4	1e-1022	- 2.354e+03	42.96%	38.04%	55.7bp (61.5bp)	dof42(C2C2dof)/col-dof42-DAP-Seq(GSE60143)/Homer(0.754)
	5	1e-810	- 1.866e+03	23.15%	19.53%	56.8bp (59.7bp)	RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer(0.761)
	6	1e-732	- 1.686e+03	33.02%	29.11%	55.0bp (58.5bp)	PU.1:IRF8(ETS:IRF)/pDC-Irf8-ChIP-Seq(GSE66899)/Homer(0.776)
	7	1e-725	- 1.671e+03	22.14%	18.76%	56.0bp (59.8bp)	che-1/MA0260.1/Jaspar(0.751)
	8	1e-686	- 1.581e+03	57.37%	53.28%	55.7bp (59.1bp)	MYB116(MYB)/colamp-MYB116-DAP-Seq(GSE60143)/Homer(0.742)
	9	1e-681	- 1.569e+03	47.99%	43.91%	57.0bp (60.1bp)	STB1(MacIsaac)/Yeast(0.669)
	10	1e-670	- 1.545e+03	30.95%	27.28%	55.8bp (60.5bp)	URC2/MA0422.1/Jaspar(0.821)



SRR1658227

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-4073	- 9.380e+03	25.82%	18.10%	55.7bp (60.4bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.969)
	2	1e-1918	- 4.418e+03	11.02%	7.36%	55.7bp (62.2bp)	IRF2(IRF)/Erythrobias-IRF2-ChIP-Seq(GSE36985)/Homer(0.911)
	3	1e-1311	- 3.019e+03	45.23%	39.88%	54.9bp (59.6bp)	ROX8(RRM)/Drosophila_melanogaster-RNCMPT00148-PBM/HughesRNA(0.752)
	4	1e-1026	- 2.364e+03	50.08%	45.29%	56.8bp (59.0bp)	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer(0.930)
	5	1e-979	- 2.255e+03	40.91%	36.36%	55.7bp (59.9bp)	Deaf1/dmmpmm(Pollard)/fly(0.743)
	6	1e-835	- 1.924e+03	37.39%	33.28%	55.9bp (60.1bp)	CG7903(RRM)/Drosophila_melanogaster-RNCMPT00144-PBM/HughesRNA(0.723)
	7	1e-801	- 1.845e+03	36.37%	32.37%	56.3bp (58.9bp)	RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer(0.849)
	8	1e-752	- 1.733e+03	25.30%	21.85%	55.8bp (59.4bp)	NRF(NRF)/Promoter/Homer(0.77)
	9	1e-738	- 1.701e+03	49.94%	45.88%	56.1bp (58.7bp)	HNRNPA1L2(RRM)/Homo_sapiens-RNCMPT00023-PBM/HughesRNA(0.754)
	10	1e-665	- 1.533e+03	26.73%	23.41%	55.2bp (60.3bp)	AT-GTL1/MA1661.1/Jaspar(0.822)



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SRR1658182

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3737	-8.606e+03	26.60%	19.61%	54.9bp (59.8bp)	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer(0.873)
	2	1e-1249	-2.876e+03	27.82%	23.59%	56.1bp (59.3bp)	ELF3/MA0640.2/Jaspar(0.721)
	3	1e-1202	-2.769e+03	47.50%	42.73%	55.7bp (61.4bp)	BMYB(HTH)/Hela-BMYB-ChIP-Seq(GSE27030)/Homer(0.777)
	4	1e-1014	-2.337e+03	43.65%	39.31%	55.4bp (60.2bp)	AT5G47660(Trihelix)/colamp-AT5G47660-DAP-Seq(GSE60143)/Homer(0.720)
	5	1e-960	-2.211e+03	43.01%	38.80%	55.8bp (63.5bp)	Deaf1/dmmpmm(Pollard)/fly(0.742)
	6	1e-902	-2.078e+03	26.89%	23.32%	56.1bp (61.3bp)	KHDRBS1(KH)/Mus_musculus-RNCMPT00062-PBM/HughesRNA(0.765)
	7	1e-821	-1.892e+03	45.97%	42.04%	56.1bp (58.3bp)	ZNF768(Zf)/Rajj-ZNF768-ChIP-Seq(GSE111879)/Homer(0.713)
	8	1e-752	-1.733e+03	17.00%	14.28%	56.8bp (57.6bp)	RUNX(Runt)/HPC7-Runx1-ChIP-Seq(GSE22178)/Homer(0.955)
	9	1e-729	-1.681e+03	48.50%	44.77%	56.4bp (62.3bp)	STP3/MA0396.1/Jaspar(0.775)
	10	1e-722	-1.663e+03	5.05%	3.59%	56.8bp (56.7bp)	Fra1(bZIP)/BT549-Fra1-ChIP-Seq(GSE46166)/Homer(0.981)

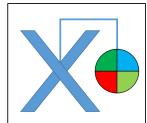


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SRR1658263

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-4075	-9.385e+03	18.42%	11.71%	55.1bp (58.4bp)	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer(0.965)
	2	1e-3522	-8.111e+03	5.40%	2.24%	55.3bp (60.9bp)	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer(0.960)
	3	1e-1010	-2.327e+03	43.38%	38.63%	55.6bp (61.1bp)	AT3G10030(Trihelix)/colamp-AT3G10030-DAP-Seq(GSE60143)/Homer(0.826)
	4	1e-934	-2.151e+03	51.51%	46.85%	56.7bp (59.5bp)	EBF3/MA1637.1/Jaspar(0.774)
	5	1e-932	-2.148e+03	6.27%	4.27%	56.5bp (57.2bp)	Fra1(bZIP)/BT549-Fra1-ChIP-Seq(GSE46166)/Homer(0.989)
	6	1e-908	-2.092e+03	33.29%	29.06%	56.2bp (59.8bp)	ORB2(RRM)/Drosophila_melanog RNCMPT00126-PBM/HughesRNA(0.720)
	7	1e-880	-2.028e+03	41.27%	36.88%	56.2bp (58.5bp)	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer(0.690)
	8	1e-846	-1.950e+03	44.45%	40.08%	55.6bp (62.5bp)	ASG1/MA0275.1/Jaspar(0.791)
	9	1e-744	-1.715e+03	20.55%	17.33%	56.2bp (58.8bp)	bHLH80/MA1357.1/Jaspar(0.725)
	10	1e-625	-1.439e+03	37.27%	33.65%	56.4bp (58.8bp)	CDC5(MYB)/Arabidopsis thaliana/AthaMap(0.668)



SRR1658173

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-4011	- 9.236e+03	40.27%	31.34%	55.5bp (61.5bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.945)
	2	1e-2832	- 6.522e+03	7.78%	4.23%	55.4bp (61.1bp)	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer(0.928)
	3	1e-1111	- 2.560e+03	43.33%	38.47%	55.9bp (60.4bp)	dof42(C2C2dof)/col-dof42-DAP-Seq(GSE60143)/Homer(0.729)
	4	1e-1082	- 2.493e+03	59.15%	54.29%	55.8bp (62.9bp)	SWI6/SWI6YPD/9-SWI4,9-SWI6(Harbison)/Yeast(0.972)
	5	1e-907	- 2.090e+03	33.36%	29.23%	56.5bp (59.1bp)	RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer(0.798)
	6	1e-872	- 2.009e+03	49.52%	45.14%	56.9bp (60.1bp)	EBF3/MA1637.1/Jaspar(0.790)
	7	1e-791	- 1.823e+03	4.04%	2.60%	56.1bp (55.6bp)	AP-1(bZIP)/ThioMac-PU.1-ChIP-Seq(GSE21512)/Homer(0.978)
	8	1e-722	- 1.663e+03	45.31%	41.36%	56.9bp (61.1bp)	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer(0.714)
	9	1e-717	- 1.653e+03	43.47%	39.56%	55.8bp (58.2bp)	AtGRF6(GRF)/col-AtGRF6-DAP-Seq(GSE60143)/Homer(0.660)
	10	1e-712	- 1.640e+03	40.93%	37.07%	55.7bp (60.6bp)	AT-GTL1/MA1661.1/Jaspar(0.841)

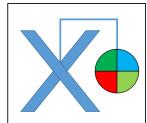


Epigenome Analysis Platform

Report

SRR1658155

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3544	- 8.162e+03	38.06%	29.49%	55.8bp (62.2bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.883)
	2	1e-2403	- 5.535e+03	7.76%	4.35%	55.1bp (61.2bp)	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer(0.922)
	3	1e-1249	- 2.878e+03	57.22%	51.80%	55.8bp (60.1bp)	dof42(C2C2dof)/col-dof42-DAP-Seq(GSE60143)/Homer(0.745)
	4	1e-907	- 2.089e+03	58.66%	54.06%	56.1bp (60.2bp)	GTL1(Trihelix)/colamp-GTL1-DAP-Seq(GSE60143)/Homer(0.781)
	5	1e-871	- 2.006e+03	49.10%	44.57%	56.4bp (59.9bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.812)
	6	1e-841	- 1.939e+03	4.98%	3.27%	57.1bp (56.6bp)	Fra1(bZIP)/BT549-Fra1-ChIP-Seq(GSE46166)/Homer(0.991)
	7	1e-781	- 1.799e+03	29.17%	25.37%	56.6bp (60.2bp)	Dof2/MA0020.1/Jaspar(0.862)
	8	1e-739	- 1.703e+03	32.03%	28.22%	56.1bp (59.9bp)	CG7903(RRM)/Drosophila_melanogaster-RNCMPT00144-PBM/HughesRNA(0.730)
	9	1e-719	- 1.656e+03	55.88%	51.77%	56.3bp (58.6bp)	ZNF768(Zf)/Raji-ZNF768-ChIP-Seq(GSE111879)/Homer(0.623)
	10	1e-714	- 1.644e+03	35.07%	31.22%	55.6bp (59.0bp)	HNF1b/Homeobox)/PDAC-HNF1B-ChIP-Seq(GSE64557)/Homer(0.746)

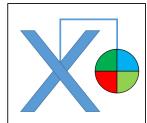


Epigenome Analysis Platform

Report

SRR1658317

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3935	-9.062e+03	18.40%	11.84%	55.4bp (60.5bp)	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer(0.950)
	2	1e-1654	-3.809e+03	3.59%	1.75%	56.1bp (60.4bp)	PU.1:IRF8(ETS:IRF)/pDC-Irf8-ChIP-Seq(GSE66899)/Homer(0.878)
	3	1e-1367	-3.149e+03	49.15%	43.59%	55.2bp (60.4bp)	REL/MA0101.1/Jaspar(0.793)
	4	1e-1205	-2.775e+03	46.61%	41.41%	56.1bp (60.6bp)	RPH1/MA0372.1/Jaspar(0.660)
	5	1e-1133	-2.609e+03	13.25%	10.06%	55.3bp (62.3bp)	IRF5/MA1420.1/Jaspar(0.908)
	6	1e-1018	-2.344e+03	57.44%	52.64%	56.3bp (61.2bp)	MYB98(MYB)/col-MYB98-DAP-Seq(GSE60143)/Homer(0.888)
	7	1e-733	-1.690e+03	41.27%	37.28%	55.8bp (57.9bp)	RUNX-AML(Runt)/CD4+-PolII-ChIP-Seq(Barski_et_al.)/Homer(0.851)
	8	1e-714	-1.644e+03	33.58%	29.85%	56.8bp (59.0bp)	ZNF711(Zf)/SHSY5Y-ZNF711-ChIP-Seq(GSE20673)/Homer(0.940)
	9	1e-701	-1.615e+03	5.61%	3.96%	56.6bp (56.9bp)	Fra1(bZIP)/BT549-Fra1-ChIP-Seq(GSE46166)/Homer(0.992)
	10	1e-686	-1.580e+03	50.66%	46.70%	56.9bp (59.3bp)	EBF3/MA1637.1/Jaspar(0.857)



Epigenome Analysis Platform

Report

SRR1658191

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3444	-7.931e+03	20.63%	13.81%	55.7bp (60.6bp)	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer(0.956)
	2	1e-1804	-4.156e+03	9.68%	6.18%	55.9bp (61.5bp)	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer(0.862)
	3	1e-1072	-2.470e+03	44.13%	39.02%	55.0bp (59.3bp)	RAP212(AP2ERE吕布)/col-RAP212-DAP-Seq(GSE60143)/Homer(0.828)
	4	1e-1032	-2.378e+03	10.19%	7.38%	56.0bp (58.8bp)	MF0003.1_REL_class/Jaspar(0.95)
	5	1e-967	-2.227e+03	5.57%	3.59%	56.9bp (57.0bp)	JunB(bZIP)/DendriticCells-Junb-ChIP-Seq(GSE36099)/Homer(0.994)
	6	1e-858	-1.976e+03	50.09%	45.45%	56.3bp (59.1bp)	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer(0.866)
	7	1e-784	-1.807e+03	53.38%	48.93%	56.0bp (60.2bp)	AT3G10030(Trihelix)/colamp-AT3G10030-DAP-Seq(GSE60143)/Homer(0.831)
	8	1e-748	-1.723e+03	24.78%	21.16%	56.0bp (60.5bp)	CG7903(RRM)/Drosophila_melanogaster-RNCMPT00144-PBM/HughesRNA(0.730)
	9	1e-658	-1.517e+03	41.73%	37.76%	56.3bp (59.8bp)	AtGRF6(GRF)/col-AtGRF6-DAP-Seq(GSE60143)/Homer(0.742)
	10	1e-604	-1.393e+03	39.40%	35.63%	56.2bp (60.9bp)	Unknown3/Arabidopsis-Promoters/Homer(0.836)

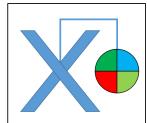


Epigenome Analysis Platform

Report

SRR1658210

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3510	-8.083e+03	27.84%	20.45%	55.0bp (59.5bp)	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer(0.975)
	2	1e-2281	-5.253e+03	8.29%	4.93%	56.0bp (60.4bp)	PU.1:IRF8(ETS:IRF)/pDC-Irf8-ChIP-Seq(GSE66899)/Homer(0.905)
	3	1e-1583	-3.646e+03	48.60%	42.72%	55.9bp (61.3bp)	prd/dmmpmm(Down)/fly(0.854)
	4	1e-929	-2.140e+03	41.30%	36.89%	55.7bp (60.8bp)	Deaf1/dmmpmm(Pollard)/fly(0.753)
	5	1e-928	-2.139e+03	33.53%	29.35%	56.5bp (63.1bp)	CG7903(RRM)/Drosophila_melanogaster-RNCMPT00144-PBM/HughesRNA(0.723)
	6	1e-767	-1.768e+03	44.47%	40.40%	55.6bp (60.1bp)	MNB1A/MA0053.1/Jaspar(0.682)
	7	1e-766	-1.764e+03	7.93%	5.89%	55.3bp (58.1bp)	NFkB-p65(RHD)/GM12787-p65-ChIP-Seq(GSE19485)/Homer(0.904)
	8	1e-750	-1.727e+03	42.10%	38.12%	56.3bp (58.5bp)	ZNF768(Zf)/Rajj-ZNF768-ChIP-Seq(GSE111879)/Homer(0.716)
	9	1e-749	-1.725e+03	45.51%	41.48%	56.2bp (58.3bp)	ZNF711(Zf)/SHSY5Y-ZNF711-ChIP-Seq(GSE20673)/Homer(0.876)
	10	1e-640	-1.476e+03	3.98%	2.68%	56.9bp (56.2bp)	Fra1(bZIP)/BT549-Fra1-ChIP-Seq(GSE46166)/Homer(0.991)



SRR1658111

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
 ACTTCCGGTT	1	1e-3938	-9.069e+03	19.43%	12.48%	55.6bp (60.5bp)	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer(0.952)
 TTTCAGCTTC	2	1e-2716	-6.256e+03	9.86%	5.70%	54.9bp (61.1bp)	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer(0.855)
 CGAAAACCG	3	1e-1383	-3.185e+03	42.76%	37.07%	56.1bp (60.9bp)	prd/dmmpmm(Down)/fly(0.850)
 TTTCCGTA	4	1e-1276	-2.940e+03	32.49%	27.40%	56.6bp (62.4bp)	NAM(NAC)/col-NAM-DAP-Seq(GSE60143)/Homer(0.758)
 TCTGTGGC	5	1e-880	-2.028e+03	45.76%	41.16%	56.9bp (57.1bp)	RUNX1/MA0002.2/Jaspar(0.850)
 GTTACTGATT	6	1e-841	-1.938e+03	35.83%	31.55%	55.8bp (59.5bp)	HNF1b/Homeobox)/PDAC-HNF1B-ChIP-Seq(GSE64557)/Homer(0.711)
 AGGCCCTTA	7	1e-826	-1.904e+03	37.77%	33.47%	56.3bp (59.3bp)	ZNF711(Zf)/SHSY5Y-ZNF711-ChIP-Seq(GSE20673)/Homer(0.892)
 GCTTCCGCCTT	8	1e-763	-1.757e+03	56.33%	52.01%	55.2bp (61.5bp)	RDR1/MA0360.1/Jaspar(0.671)
 CTCAGAGA	9	1e-726	-1.672e+03	56.89%	52.69%	56.2bp (58.7bp)	CEP3/MA0282.1/Jaspar(0.658)
 CGGATTTG	10	1e-686	-1.580e+03	48.71%	44.62%	56.1bp (59.3bp)	HNRNPR(RRM)/Gallus_gallus-RNCMPT00288-PBM/HughesRNA(0.735)



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SRR1658201

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3477	-8.008e+03	24.29%	16.78%	55.3bp (59.5bp)	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer(0.956)
	2	1e-2492	-5.739e+03	10.15%	5.96%	56.2bp (62.1bp)	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer(0.916)
	3	1e-1128	-2.600e+03	48.27%	42.87%	55.8bp (61.0bp)	prd/dmmpmm(Down)/fly(0.794)
	4	1e-1089	-2.509e+03	48.36%	43.05%	56.4bp (62.8bp)	STB2(MacIsaac)/Yeast(0.692)
	5	1e-800	-1.843e+03	44.72%	40.20%	55.7bp (59.5bp)	MF0003.1_REL_class/Jaspar(0.785)
	6	1e-705	-1.625e+03	44.66%	40.42%	55.8bp (57.9bp)	ZNF768(Zf)/Rajj-ZNF768-ChIP-Seq(GSE111879)/Homer(0.657)
	7	1e-665	-1.532e+03	4.65%	3.10%	56.8bp (57.0bp)	AP-1(bZIP)/ThioMac-PU.1-ChIP-Seq(GSE21512)/Homer(0.985)
	8	1e-605	-1.395e+03	24.98%	21.64%	56.9bp (58.0bp)	RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer(0.911)
	9	1e-577	-1.329e+03	46.39%	42.54%	56.6bp (59.5bp)	MYB(HTH)/ERMYB-Myb-ChIPSeq(GSE22095)/Homer(0.902)
	10	1e-519	-1.195e+03	23.37%	20.35%	55.8bp (61.0bp)	STAT1/MA0137.3/Jaspar(0.804)

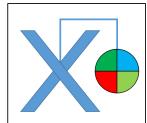


Epigenome Analysis Platform

Report

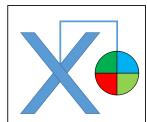
SRR1658240

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-4040	-9.303e+03	25.92%	18.40%	55.1bp (59.8bp)	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer(0.961)
	2	1e-2907	-6.694e+03	6.14%	3.07%	55.0bp (61.8bp)	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer(0.965)
	3	1e-1059	-2.440e+03	38.59%	34.05%	55.7bp (60.7bp)	DOF5.7/MA0984.1/Jaspar(0.757)
	4	1e-994	-2.290e+03	56.36%	51.78%	56.1bp (62.0bp)	GTL1(Trihelix)/colamp-GTL1-DAP-Seq(GSE60143)/Homer(0.826)
	5	1e-974	-2.244e+03	37.82%	33.49%	55.8bp (61.0bp)	SWI4/SWI4_YPD/29-SWI4,29-SWI6(Harbison)/Yeast(0.711)
	6	1e-956	-2.202e+03	57.11%	52.62%	56.2bp (61.3bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.780)
	7	1e-912	-2.102e+03	44.11%	39.78%	57.0bp (62.7bp)	OVOL2/MA1545.1/Jaspar(0.698)
	8	1e-889	-2.047e+03	35.97%	31.88%	56.1bp (63.6bp)	GTL1(Trihelix)/colamp-GTL1-DAP-Seq(GSE60143)/Homer(0.674)
	9	1e-729	-1.680e+03	4.45%	3.01%	57.0bp (55.7bp)	Fra1(bZIP)/BT549-Fra1-ChIP-Seq(GSE46166)/Homer(0.990)
	10	1e-692	-1.595e+03	28.28%	24.91%	56.5bp (60.9bp)	RDR1/MA0360.1/Jaspar(0.825)



SRR1658141

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
ACTTCCGGTT	1	1e-3628	-8.354e+03	19.37%	12.94%	55.6bp (61.0bp)	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer(0.947)
GTTTCAGTTTCA	2	1e-1610	-3.707e+03	8.72%	5.72%	55.1bp (60.2bp)	ISRE(IRF)/ThioMac-LPS-Expression(GSE23622)/Homer(0.90)
GGGGCCCGTTT	3	1e-1521	-3.504e+03	49.59%	43.77%	55.4bp (60.7bp)	kni/dmmpmm(Down)/fly(0.780)
TCAACGATTCTCGCTAACG	4	1e-1358	-3.127e+03	26.88%	22.19%	56.0bp (65.7bp)	AT2G15740(C2H2)/col-AT2G15740-DAP-Seq(GSE60143)/Homer(0.774)
AAAGCCGC	5	1e-882	-2.031e+03	45.19%	40.80%	56.5bp (64.9bp)	STP1/MA0394.1/Jaspar(0.711)
GGGCCTAA	6	1e-811	-1.869e+03	39.55%	35.44%	56.4bp (63.2bp)	ZNF711(Zf)/SHSY5Y-ZNF711-ChIP-Seq(GSE20673)/Homer(0.874)
TGTCGCTT	7	1e-780	-1.797e+03	6.87%	4.95%	57.2bp (62.9bp)	SWI6/SWI6YPD/9-SWI4,9-SWI6(Harbison)/Yeast(0.795)
CCGGTAAAAA	8	1e-692	-1.595e+03	40.03%	36.22%	55.4bp (60.7bp)	AT-GTL1/MA1661.1/Jaspar(0.832)
CCCGCCATTGG	9	1e-624	-1.438e+03	2.38%	1.41%	52.7bp (58.2bp)	YY1/MA0095.2/Jaspar(0.961)
CGTTTCCGG	10	1e-612	-1.411e+03	15.75%	13.18%	56.0bp (63.0bp)	CG7903(RRM)/Drosophila_melanogaster-RNCMPT00144-PBM/HughesRNA(0.738)



SRR1658303

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
ACTTCCGGTT	1	1e-2104	- 4.845e+03	38.61%	30.57%	55.2bp (62.3bp)	ETV1(ETS)/GIST48- ETV1-ChIP- Seq(GSE22441)/Homer(0.945)
CGACGAATACG	2	1e-1259	- 2.900e+03	49.18%	42.61%	55.0bp (63.3bp)	AT2G15740(C2H2)/col- AT2G15740-DAP- Seq(GSE60143)/Homer(0.675)
AAA TGGCGCC	3	1e-1255	- 2.892e+03	46.82%	40.30%	55.0bp (60.9bp)	ROX8(RRM)/Drosophila_melanogast- RNCMPT00148- PBM/HughesRNA(0.764)
CGTTTTTCGG	4	1e-973	- 2.241e+03	52.36%	46.56%	55.8bp (62.2bp)	PABP(RRM)/Drosophila_melanog- RNCMPT00139- PBM/HughesRNA(0.714)
CGCGAAAT	5	1e-884	- 2.037e+03	27.66%	22.90%	55.7bp (63.4bp)	SWI4(MacIsaac)/Yeast(0.917)
GGCCCTAA	6	1e-864	- 1.990e+03	51.98%	46.51%	56.3bp (59.8bp)	TBP3(MYBrelated)/col- TBP3-DAP- Seq(GSE60143)/Homer(0.756)
AGCGGTAA	7	1e-746	- 1.718e+03	43.86%	38.87%	56.5bp (62.7bp)	MYB65(MYB)/colamp- MYB65-DAP- Seq(GSE60143)/Homer(0.770)
GTTCACTTC	8	1e-713	- 1.643e+03	2.00%	0.91%	56.5bp (62.0bp)	PU.1- IRF(ETS:IRF)/Bcell- PU.1-ChIP- Seq(GSE21512)/Homer(0.924)
GAAAGCAC	9	1e-675	- 1.554e+03	29.61%	25.33%	56.3bp (60.1bp)	Dof2/MA0020.1/Jaspar(0.779)
CGGATTAA	10	1e-637	- 1.467e+03	31.29%	27.06%	56.1bp (61.5bp)	URC2/MA0422.1/Jaspar(0.839)



Epigenome Analysis Platform

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SRR1658312

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3786	-8.718e+03	28.75%	21.28%	54.9bp (59.7bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.858)
	2	1e-1325	-3.053e+03	27.17%	22.71%	56.1bp (61.1bp)	ERT1/MA0420.1/Jaspar(0.764)
	3	1e-1233	-2.840e+03	57.10%	52.10%	55.8bp (59.7bp)	dof42(C2C2dof)/col-dof42-DAP-Seq(GSE60143)/Homer(0.739)
	4	1e-992	-2.284e+03	58.56%	54.09%	56.3bp (59.5bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.780)
	5	1e-953	-2.195e+03	55.70%	51.29%	57.0bp (59.5bp)	EBF3/MA1637.1/Jaspar(0.788)
	6	1e-926	-2.133e+03	42.93%	38.67%	55.4bp (60.3bp)	AT-GTL1/MA1661.1/Jaspar(0.806)
	7	1e-918	-2.115e+03	47.23%	42.92%	56.0bp (60.4bp)	CG7903(RRM)/Drosophila_melanogaster-RNCMPT00144-PBM/HughesRNA(0.741)
	8	1e-893	-2.058e+03	39.40%	35.28%	56.5bp (59.4bp)	SIX1/MA1118.1/Jaspar(0.736)
	9	1e-883	-2.034e+03	4.39%	2.86%	56.1bp (55.8bp)	BATF(bZIP)/Th17-BATF-ChIP-Seq(GSE39756)/Homer(0.979)
	10	1e-798	-1.839e+03	32.62%	28.91%	56.5bp (58.9bp)	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer(0.810)



SRR1658114

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3612	-8.319e+03	20.67%	13.72%	54.6bp (60.2bp)	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer(0.867)
	2	1e-1279	-2.946e+03	40.04%	34.60%	56.8bp (65.5bp)	Unknown3/Arabidopsis-Promoters/Homer(0.842)
	3	1e-1026	-2.364e+03	43.00%	38.04%	56.3bp (62.5bp)	AT3G10030(Trihelix)/colamp-AT3G10030-DAP-Seq(GSE60143)/Homer(0.720)
	4	1e-931	-2.145e+03	27.86%	23.68%	56.3bp (59.7bp)	AT1G76870/MA1367.1/Jaspar(0.76)
	5	1e-879	-2.026e+03	54.40%	49.71%	56.3bp (61.3bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.782)
	6	1e-804	-1.853e+03	26.32%	22.51%	55.9bp (61.2bp)	CG7903(RRM)/Drosophila_melanogaster-RNCMPT00144-PBM/HughesRNA(0.738)
	7	1e-662	-1.526e+03	60.66%	56.64%	56.1bp (62.8bp)	NAC025/MA0935.1/Jaspar(0.862)
	8	1e-641	-1.477e+03	3.60%	2.31%	52.5bp (57.3bp)	YY1/MA0095.2/Jaspar(0.959)
	9	1e-635	-1.463e+03	39.58%	35.74%	55.9bp (61.8bp)	MNB1A/MA0053.1/Jaspar(0.698)
	10	1e-634	-1.460e+03	6.03%	4.32%	56.2bp (57.0bp)	Fra1(bZIP)/BT549-Fra1-ChIP-Seq(GSE46166)/Homer(0.992)

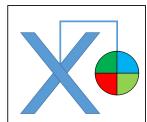


Epigenome Analysis Platform

Report

SRR1658149

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3553	-8.183e+03	26.69%	18.64%	54.5bp (60.2bp)	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer(0.865)
	2	1e-908	-2.091e+03	52.03%	47.06%	56.1bp (59.1bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.771)
	3	1e-875	-2.017e+03	32.92%	28.44%	55.6bp (60.0bp)	pho/dmmpmm(Bergman)/fly(0.798)
	4	1e-740	-1.706e+03	42.25%	37.86%	55.5bp (60.4bp)	AT-GTL1/MA1661.1/Jaspar(0.788)
	5	1e-625	-1.439e+03	21.66%	18.39%	55.8bp (57.8bp)	Oct6(POU,Homeobox)/NPC-Pou3f1-ChIP-Seq(GSE35496)/Homer(0.680)
	6	1e-597	-1.375e+03	33.42%	29.69%	56.4bp (58.8bp)	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer(0.890)
	7	1e-571	-1.315e+03	35.61%	31.90%	56.8bp (59.0bp)	NKX2-2/MA1645.1/Jaspar(0.734)
	8	1e-525	-1.210e+03	4.70%	3.27%	55.9bp (56.2bp)	Fra1(bZIP)/BT549-Fra1-ChIP-Seq(GSE46166)/Homer(0.986)
	9	1e-490	-1.130e+03	38.33%	34.82%	56.1bp (59.0bp)	CDC5(MYB)/Arabidopsis thaliana/AthaMap(0.678)
	10	1e-457	-1.053e+03	27.46%	24.39%	56.9bp (60.3bp)	Znf281/MA1630.1/Jaspar(0.712)

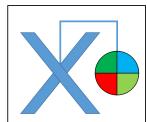


Epigenome Analysis Platform

Report

SRR1658176

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-4231	-9.744e+03	20.13%	13.22%	54.7bp (59.8bp)	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer(0.886)
	2	1e-1407	-3.241e+03	49.05%	43.54%	56.0bp (61.4bp)	prd/dmmpmm(Down)/fly(0.806)
	3	1e-1329	-3.061e+03	37.75%	32.65%	56.7bp (63.7bp)	PF10_0214(RRM)/Plasmodium_falciparum_RNCMPT00240-PBM/HughesRNA(0.815)
	4	1e-1015	-2.338e+03	46.67%	42.02%	55.4bp (59.7bp)	dof42(C2C2dof)/coldof42-DAP-Seq(GSE60143)/Homer(0.783)
	5	1e-950	-2.188e+03	54.10%	49.56%	56.2bp (60.2bp)	TBP3(MYBrelated)/coldTBP3-DAP-Seq(GSE60143)/Homer(0.756)
	6	1e-939	-2.163e+03	33.54%	29.37%	56.2bp (64.2bp)	SWI4(MacIsaac)/Yeast(0.855)
	7	1e-860	-1.981e+03	63.72%	59.51%	56.3bp (62.1bp)	NAC025/MA0935.1/Jaspar(0.864)
	8	1e-758	-1.747e+03	4.13%	2.71%	55.9bp (55.6bp)	Fra1(bZIP)/BT549-Fra1-ChIP-Seq(GSE46166)/Homer(0.979)
	9	1e-652	-1.502e+03	37.33%	33.75%	55.9bp (57.9bp)	ZNF768(Zf)/Rajj-ZNF768-ChIP-Seq(GSE111879)/Homer(0.641)
	10	1e-598	-1.377e+03	1.89%	1.07%	51.7bp (56.6bp)	YY1/MA0095.2/Jaspar(0.975)

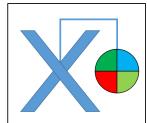


Epigenome Analysis Platform

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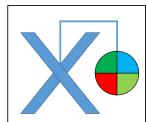
SRR1658127

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
AAACAGGAAACTCTCACTGGAAAGTC	1	1e-4378	-1.008e+04	26.06%	17.84%	55.0bp (59.6bp)	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer(0.959)
CGAAACCGGAACTCTCACTGGAAAGTC	2	1e-1505	-3.467e+03	23.07%	18.30%	55.6bp (62.5bp)	IRF5/MA1420.1/Jaspar(0.904)
CCCCGCCATTTCTCACTGGAAAGTC	3	1e-1261	-2.904e+03	40.88%	35.59%	55.1bp (59.8bp)	prd/dmmpmm(Down)/fly(0.770)
TTTCAAGTTCTCTCACTGGAAAGTC	4	1e-992	-2.285e+03	27.84%	23.64%	54.5bp (59.9bp)	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer(0.783)
GGCCCTAAACCGGAAAGTC	5	1e-982	-2.263e+03	48.12%	43.32%	56.2bp (59.8bp)	RPH1/MA0372.1/Jaspar(0.712)
CTCAGAGCTAGTAGAA	6	1e-910	-2.097e+03	52.53%	47.88%	56.3bp (58.5bp)	CDC5(MYB)/Arabidopsis thaliana/AthaMap(0.667)
CCGGTTAAAAA	7	1e-874	-2.015e+03	44.53%	40.04%	55.4bp (60.5bp)	AT-GTL1/MA1661.1/Jaspar(0.839)
TTTACCGTAAACCACTGG	8	1e-845	-1.947e+03	30.49%	26.48%	56.7bp (64.1bp)	PF10_0214(RRM)/Plasmodium_falciparum_RNCMPT00240-PBM/HughesRNA(0.765)
GGCGGCCCTTAACTCACTGG	9	1e-753	-1.734e+03	32.29%	28.43%	56.1bp (61.1bp)	pho/MA1460.1/Jaspar(0.718)
GGGGATTTCCTCACTGG	10	1e-717	-1.652e+03	2.19%	1.19%	55.2bp (59.4bp)	NFkB-p65(RHD)/GM12787-p65-ChIP-Seq(GSE19485)/Homer(0.973)



SRR1658208

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3080	- 7.093e+03	25.23%	18.63%	55.9bp (60.8bp)	ETV1(ETS)/GIST48- ETV1-ChIP- Seq(GSE22441)/Homer(0.915)
	2	1e-1075	- 2.476e+03	41.28%	36.61%	56.6bp (64.5bp)	SWI4(MacIsaac)/Yeast(0.771)
	3	1e-1052	- 2.424e+03	61.79%	57.11%	56.0bp (60.7bp)	prd/dmmpmm(Down)/fly(0.790)
	4	1e-975	- 2.247e+03	55.28%	50.71%	56.1bp (61.0bp)	TBP3(MYBrelated)/col- TBP3-DAP- Seq(GSE60143)/Homer(0.762)
	5	1e-845	- 1.946e+03	35.48%	31.49%	55.9bp (61.1bp)	CG7903(RRM)/Drosophila_melanogaster- RNCMPT00144- PBM/HughesRNA(0.742)
	6	1e-685	- 1.578e+03	33.27%	29.73%	56.6bp (57.7bp)	RUNX2(Runt)/PCa- RUNX2-ChIP- Seq(GSE33889)/Homer(0.845)
	7	1e-616	- 1.420e+03	22.90%	19.95%	55.1bp (59.4bp)	NFkB- p65(RHD)/GM12787-p65- ChIP- Seq(GSE19485)/Homer(0.899)
	8	1e-546	- 1.259e+03	31.58%	28.46%	55.8bp (57.0bp)	Su(H)/dmmpmm(Bergman)/fly(0.66)
	9	1e-522	- 1.203e+03	1.95%	1.16%	57.1bp (55.8bp)	BATF(bZIP)/Th17-BATF- ChIP- Seq(GSE39756)/Homer(0.991)
	10	1e-432	- 9.950e+02	1.78%	1.09%	52.8bp (58.1bp)	YY1(Zf)/Promoter/Homer(0.959)

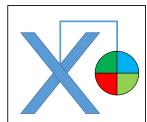


Epigenome Analysis Platform

Report

SRR1658325

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-2985	- 6.874e+03	23.29%	16.83%	56.4bp (60.8bp)	ETV5/MA0765.2/Jaspar(0.945)
	2	1e-1311	- 3.020e+03	8.70%	5.95%	54.8bp (60.7bp)	ISRE(IRF)/ThioMac-LPS-Expression(GSE23622)/Homer(0.90)
	3	1e-1205	- 2.776e+03	42.53%	37.42%	55.0bp (60.2bp)	kni/dmmpmm(Down)/fly(0.835)
	4	1e-1063	- 2.449e+03	4.23%	2.54%	55.9bp (58.3bp)	NFkB-p65(RHD)/GM12787-p65-ChIP-Seq(GSE19485)/Homer(0.973)
	5	1e-954	- 2.197e+03	46.11%	41.50%	55.6bp (58.3bp)	ZNF711(Zf)/SHSY5Y-ZNF711-ChIP-Seq(GSE20673)/Homer(0.693)
	6	1e-904	- 2.084e+03	62.74%	58.29%	56.7bp (60.0bp)	Dof2/MA0020.1/Jaspar(0.745)
	7	1e-870	- 2.003e+03	43.36%	38.99%	55.9bp (59.9bp)	CG7903(RRM)/Drosophila_melanogaster-RNCMPT00144-PBM/HughesRNA(0.735)
	8	1e-723	- 1.666e+03	43.71%	39.72%	56.9bp (59.9bp)	STB1(MacIsaac)/Yeast(0.699)
	9	1e-696	- 1.605e+03	31.12%	27.52%	56.6bp (59.9bp)	Gfi1b/MA0483.1/Jaspar(0.664)
	10	1e-650	- 1.497e+03	43.86%	40.07%	56.5bp (58.2bp)	z/dmmpmm(Bigfoot)/fly(0.691)

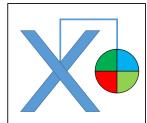


Epigenome Analysis Platform

Report

SRR1658244

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
ACTTCCGGTT	1	1e-2784	- 6.412e+03	27.36%	20.72%	55.5bp (61.0bp)	ETV1(ETS)/GIST48- ETV1-ChIP- Seq(GSE22441)/Homer(0.929)
CCGAAACG	2	1e-1466	- 3.377e+03	53.81%	48.08%	56.0bp (61.8bp)	IRF6/MA1509.1/Jaspar(0.799)
TTTAGGCCCT	3	1e-1043	- 2.402e+03	56.07%	51.24%	55.7bp (58.9bp)	PLAGL2/MA1548.1/Jaspar(0.654)
GCGGCC	4	1e-1023	- 2.357e+03	62.64%	57.94%	56.8bp (60.9bp)	Dof2/MA0020.1/Jaspar(0.669)
AAACACAGGCCT	5	1e-848	- 1.954e+03	56.21%	51.86%	55.0bp (57.3bp)	ZFX(Zf)/mES-Zfx-ChIP- Seq(GSE11431)/Homer(0.893)
ATTTCGCG	6	1e-778	- 1.792e+03	39.67%	35.64%	56.4bp (63.8bp)	STB1(MacIsaac)/Yeast(0.779)
CCCACAGTTA	7	1e-738	- 1.701e+03	45.04%	41.02%	56.3bp (58.6bp)	MET32(MacIsaac)/Yeast(0.865)
CCCTTGAG	8	1e-727	- 1.676e+03	50.94%	46.90%	56.8bp (59.5bp)	EBF3/MA1637.1/Jaspar(0.790)
GGAAATCCCC	9	1e-646	- 1.489e+03	18.62%	15.78%	55.0bp (58.9bp)	MF0003.1_REL_class/Jaspar(0.913)
CTCACAGA	10	1e-644	- 1.483e+03	41.74%	38.03%	56.8bp (56.8bp)	MET28/MA0332.1/Jaspar(0.730)

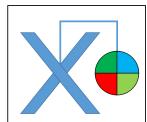


Epigenome Analysis Platform

Report

SRR1658181

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3075	- 7.083e+03	27.17%	20.14%	55.5bp (60.9bp)	ETV1(ETS)/GIST48- ETV1-ChIP- Seq(GSE22441)/Homer(0.917)
	2	1e-1326	- 3.054e+03	49.26%	43.75%	55.1bp (59.9bp)	DOF5.7/MA0984.1/Jaspar(0.820)
	3	1e-896	- 2.064e+03	39.09%	34.72%	56.0bp (59.2bp)	TBP3(MYBrelated)/col- TBP3-DAP- Seq(GSE60143)/Homer(0.731)
	4	1e-874	- 2.013e+03	44.39%	39.97%	55.3bp (60.4bp)	AT- GTL1/MA1661.1/Jaspar(0.822)
	5	1e-795	- 1.831e+03	38.95%	34.84%	56.1bp (60.4bp)	CG7903(RRM)/Drosophila_melanogaster RNCMPT00144- PBM/HughesRNA(0.738)
	6	1e-783	- 1.803e+03	41.94%	37.80%	56.9bp (59.0bp)	MEC- 8(RRM)/Caenorhabditis_elegans RNCMPT00181- PBM/HughesRNA(0.748)
	7	1e-738	- 1.701e+03	45.54%	41.46%	55.5bp (58.5bp)	STAT5(Stat)/mCD4+- Stat5-ChIP- Seq(GSE12346)/Homer(0.688)
	8	1e-723	- 1.666e+03	54.02%	49.94%	54.6bp (58.9bp)	gt/dmmpmm(SeSiMCMC)/fly(0.71)
	9	1e-654	- 1.508e+03	36.09%	32.42%	54.8bp (57.7bp)	ZFX(Zf)/mES-Zfx-ChIP- Seq(GSE11431)/Homer(0.754)
	10	1e-630	- 1.451e+03	1.83%	0.99%	50.1bp (55.3bp)	YY1/MA0095.2/Jaspar(0.956)

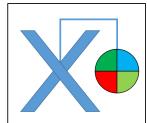


Epigenome Analysis Platform

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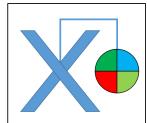
SRR1658288

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-2818	- 6.490e+03	19.56%	13.56%	55.7bp (60.9bp)	ETV1(ETS)/GIST48- ETV1-ChIP- Seq(GSE22441)/Homer(0.923)
	2	1e-1786	- 4.114e+03	54.13%	47.53%	56.1bp (62.2bp)	prd/dmmpmm(Down)/fly(0.859)
	3	1e-1330	- 3.063e+03	46.68%	41.05%	55.5bp (61.4bp)	DEL2(E2FDP)/col-DEL2- DAP- Seq(GSE60143)/Homer(0.694)
	4	1e-909	- 2.094e+03	46.18%	41.52%	54.7bp (59.2bp)	bin/dmmpnm(Bergman)/fly(0.716)
	5	1e-851	- 1.960e+03	56.02%	51.48%	56.1bp (60.5bp)	HNRNPA1(RRM)/Homo_sapiens- RNCMPT00022- PBM/HughesRNA(0.732)
	6	1e-751	- 1.731e+03	30.35%	26.52%	55.8bp (59.4bp)	SWI4(MacIsaac)/Yeast(0.733)
	7	1e-737	- 1.698e+03	15.66%	12.75%	56.0bp (62.6bp)	CG7903(RRM)/Drosophila_melanogaster- RNCMPT00144- PBM/HughesRNA(0.735)
	8	1e-670	- 1.544e+03	41.59%	37.65%	56.8bp (57.2bp)	SUP- 12(RRM)/Caenorhabditis_elegans- RNCMPT00179- PBM/HughesRNA(0.831)
	9	1e-662	- 1.525e+03	44.12%	40.16%	56.5bp (59.7bp)	STB4/MA0391.1/Jaspar(0.801)
	10	1e-653	- 1.506e+03	25.12%	21.77%	56.4bp (59.9bp)	RUNX1(Runt)/Jurkat- RUNX1-ChIP- Seq(GSE29180)/Homer(0.761)



SRR1658110

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3416	- 7.868e+03	22.91%	15.97%	54.8bp (60.2bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.948)
	2	1e-2226	- 5.126e+03	9.06%	5.46%	54.8bp (60.6bp)	ISRE(IRF)/ThioMac-LPS-Expression(GSE23622)/Homer(0.90)
	3	1e-1253	- 2.886e+03	59.66%	54.24%	56.6bp (60.1bp)	MIG1(MacIsaac)/Yeast(0.728)
	4	1e-1162	- 2.677e+03	56.36%	51.12%	56.0bp (61.1bp)	BMYB(HTH)/Hela-BMYB-ChIP-Seq(GSE27030)/Homer(0.778)
	5	1e-1031	- 2.375e+03	43.76%	38.90%	56.1bp (61.8bp)	DEL2(E2FDP)/col-DEL2-DAP-Seq(GSE60143)/Homer(0.748)
	6	1e-1028	- 2.368e+03	50.57%	45.64%	56.1bp (59.9bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.768)
	7	1e-977	- 2.252e+03	27.38%	23.24%	55.0bp (62.8bp)	RDR1/MA0360.1/Jaspar(0.741)
	8	1e-895	- 2.061e+03	21.99%	18.34%	56.7bp (64.0bp)	AT2G15740(C2H2)/col-AT2G15740-DAP-Seq(GSE60143)/Homer(0.776)
	9	1e-848	- 1.954e+03	34.41%	30.24%	56.4bp (59.9bp)	CST6(MacIsaac)/Yeast(0.793)
	10	1e-824	- 1.899e+03	33.08%	29.01%	55.9bp (59.6bp)	Oct6(POU,Homeobox)/NPC-Pou3f1-ChIP-Seq(GSE35496)/Homer(0.688)



SRR1658161

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
CAC TTT CCG GGG A G G A C T T C A G G A G	1	1e-4318	- 9.943e+03	26.04%	18.43%	54.9bp (60.0bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.853)
TAA AAC CGGC G G G T T C C C T T T T T T	2	1e-1165	- 2.684e+03	47.52%	42.69%	55.8bp (60.9bp)	BARHL2/MA0635.1/Jaspar(0.756)
TCA ATT CGCG A A C A C T A C T A	3	1e-918	- 2.115e+03	28.09%	24.32%	55.7bp (61.1bp)	SWI4/SWI4_YPD/29-SWI4,29-SWI6(Harbison)/Yeast(0.795)
ATG ACT CTC A T G A C T C A C A	4	1e-899	- 2.071e+03	5.46%	3.73%	56.7bp (56.8bp)	Fos(bZIP)/TSC-Fos-ChIP-Seq(GSE110950)/Homer(0.986)
TGT GGT TTT G C G C G G A G	5	1e-884	- 2.037e+03	39.48%	35.39%	56.6bp (57.6bp)	RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer(0.931)
CTT AAC CGG C C C I G G G T	6	1e-846	- 1.948e+03	48.24%	44.12%	56.5bp (61.5bp)	ovo/dmmpmm(Bigfoot)/fly(0.690)
TT AGGG CCT C A G A T C G A	7	1e-776	- 1.787e+03	34.78%	31.07%	56.2bp (58.6bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.789)
AGG CCT TCT A G G C C T C T	8	1e-682	- 1.572e+03	59.22%	55.53%	56.4bp (59.4bp)	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer(0.856)
CCCC AGGG AAA C C C A G G G A A A	9	1e-657	- 1.514e+03	44.34%	40.74%	55.5bp (58.2bp)	EBF1(EBF)/Near-E2A-ChIP-Seq(GSE21512)/Homer(0.890)
AAAT CCCCC A A A T C C C C C	10	1e-646	- 1.488e+03	24.81%	21.77%	56.2bp (59.1bp)	MZF1/MA0056.2/Jaspar(0.856)



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SRR1658323

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-4573	- 1.053e+04	32.53%	23.37%	56.2bp (60.8bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.981)
	2	1e-3434	- 7.909e+03	7.55%	3.68%	55.2bp (61.2bp)	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer(0.890)
	3	1e-945	- 2.177e+03	55.78%	51.05%	55.7bp (59.9bp)	BMYB(HTH)/Hela-BMYB-ChIP-Seq(GSE27030)/Homer(0.776)
	4	1e-796	- 1.835e+03	42.11%	37.87%	55.3bp (60.1bp)	Bgb::run/MA0242.1/Jaspar(0.635)
	5	1e-765	- 1.762e+03	46.92%	42.69%	56.3bp (58.2bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.769)
	6	1e-698	- 1.608e+03	62.05%	58.05%	56.5bp (61.0bp)	MYB33/MA1391.2/Jaspar(0.894)
	7	1e-681	- 1.570e+03	24.58%	21.23%	55.9bp (59.2bp)	HNF1b/Homeobox)/PDAC-HNF1B-ChIP-Seq(GSE64557)/Homer(0.718)
	8	1e-673	- 1.550e+03	34.14%	30.43%	56.1bp (57.5bp)	MET4(MacIsaac)/Yeast(0.882)
	9	1e-636	- 1.467e+03	50.86%	46.99%	56.2bp (58.8bp)	Nkx2-5(var.2)/MA0503.1/Jaspar(0.651)
	10	1e-588	- 1.355e+03	34.23%	30.76%	56.8bp (58.9bp)	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer(0.880)

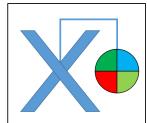


Epigenome Analysis Platform

Report

SRR1658242

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3169	-7.299e+03	18.60%	12.78%	55.3bp (60.3bp)	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer(0.941)
	2	1e-1487	-3.424e+03	61.70%	56.13%	55.8bp (59.9bp)	AT5G22990(C2H2)/col-AT5G22990-DAP-Seq(GSE60143)/Homer(0.665)
	3	1e-1193	-2.748e+03	60.65%	55.64%	56.2bp (61.4bp)	STB1(MacIsaac)/Yeast(0.803)
	4	1e-1023	-2.357e+03	43.59%	38.99%	55.7bp (61.6bp)	BMYB(HTH)/Hela-BMYB-ChIP-Seq(GSE27030)/Homer(0.839)
	5	1e-945	-2.178e+03	12.31%	9.55%	54.8bp (59.2bp)	SpiB(ETS)/OCILY3-SPIB-ChIP-Seq(GSE56857)/Homer(0.775)
	6	1e-903	-2.080e+03	51.95%	47.55%	56.4bp (63.8bp)	MYB98(MYB)/col-MYB98-DAP-Seq(GSE60143)/Homer(0.839)
	7	1e-893	-2.056e+03	38.58%	34.38%	56.2bp (60.4bp)	ZNF711(Zf)/SHSY5Y-ZNF711-ChIP-Seq(GSE20673)/Homer(0.852)
	8	1e-870	-2.004e+03	57.59%	53.29%	56.4bp (61.2bp)	DEL2(E2FDP)/col-DEL2-DAP-Seq(GSE60143)/Homer(0.800)
	9	1e-824	-1.899e+03	42.89%	38.77%	56.5bp (58.6bp)	RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer(0.770)
	10	1e-768	-1.771e+03	4.34%	2.88%	55.8bp (58.4bp)	IRF1(IRF)/PBMC-IRF1-ChIP-Seq(GSE43036)/Homer(0.831)



SRR1658224

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3200	- 7.370e+03	24.98%	18.55%	56.2bp (61.0bp)	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer(0.897)
	2	1e-2178	- 5.016e+03	4.74%	2.45%	56.7bp (62.0bp)	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer(0.910)
	3	1e-1003	- 2.311e+03	40.16%	35.85%	56.0bp (62.2bp)	BMYB(HTH)/Hela-BMYB-ChIP-Seq(GSE27030)/Homer(0.842)
	4	1e-1001	- 2.307e+03	56.22%	51.79%	56.7bp (60.2bp)	DOF2(C2C2(Zn) Dof)/Zea mays/AthaMap(0.692)
	5	1e-991	- 2.284e+03	38.87%	34.62%	55.6bp (61.3bp)	Deaf1/dmmpmm(Pollard)/fly(0.742)
	6	1e-945	- 2.176e+03	47.29%	42.99%	55.8bp (60.6bp)	CG7903(RRM)/Drosophila_melanogaster_RNCMPT00144-PBM/HughesRNA(0.724)
	7	1e-730	- 1.683e+03	16.30%	13.62%	55.9bp (57.3bp)	POL002.1_INR/Jaspar(0.745)
	8	1e-712	- 1.640e+03	39.78%	36.15%	56.0bp (57.7bp)	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer(0.794)
	9	1e-698	- 1.608e+03	2.95%	1.87%	55.5bp (58.9bp)	MF0003.1_REL_class/Jaspar(0.899)
	10	1e-638	- 1.470e+03	20.86%	18.07%	56.8bp (58.5bp)	RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer(0.907)



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SRR1658341

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3454	-7.954e+03	25.74%	18.53%	55.0bp (60.2bp)	Elf4(ETS)/BMDM-Elf4-ChIP-Seq(GSE88699)/Homer(0.869)
	2	1e-1250	-2.880e+03	49.80%	44.47%	55.9bp (62.4bp)	BMYB(HTH)/Hela-BMYB-ChIP-Seq(GSE27030)/Homer(0.757)
	3	1e-1165	-2.684e+03	66.07%	61.08%	56.3bp (63.5bp)	MYB98(MYB)/col-MYB98-DAP-Seq(GSE60143)/Homer(0.896)
	4	1e-1026	-2.363e+03	29.31%	25.05%	55.8bp (60.1bp)	AT5G22990(C2H2)/col-AT5G22990-DAP-Seq(GSE60143)/Homer(0.705)
	5	1e-946	-2.180e+03	43.16%	38.60%	56.4bp (60.0bp)	PCF/Arabidopsis-Promoters/Homer(0.735)
	6	1e-817	-1.883e+03	37.70%	33.59%	56.6bp (60.4bp)	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer(0.881)
	7	1e-780	-1.797e+03	44.19%	40.04%	56.7bp (61.3bp)	MYB65(MYB)/col-MYB65-DAP-Seq(GSE60143)/Homer(0.763)
	8	1e-751	-1.731e+03	32.99%	29.18%	56.3bp (58.7bp)	RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer(0.893)
	9	1e-742	-1.710e+03	21.59%	18.34%	55.2bp (64.6bp)	FLI1/MA0475.2/Jaspar(0.740)
	10	1e-709	-1.633e+03	6.00%	4.28%	56.3bp (56.0bp)	BATF(bZIP)/Th17-BATF-ChIP-Seq(GSE39756)/Homer(0.987)



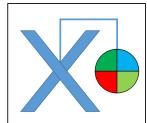
SRR1658215

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3437	- 7.916e+03	23.33%	16.62%	55.1bp (60.4bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.839)
	2	1e-1440	- 3.316e+03	52.80%	47.24%	56.2bp (62.9bp)	MYB98(MYB)/col-MYB98-DAP-Seq(GSE60143)/Homer(0.865)
	3	1e-929	- 2.140e+03	37.66%	33.40%	55.6bp (59.8bp)	Bgb::run/MA0242.1/Jaspar(0.865)
	4	1e-822	- 1.894e+03	41.65%	37.55%	56.1bp (59.8bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.762)
	5	1e-728	- 1.678e+03	37.07%	33.31%	56.9bp (60.6bp)	MIG1(MacIsaac)/Yeast(0.775)
	6	1e-693	- 1.597e+03	26.25%	22.95%	56.2bp (58.9bp)	Lm_0212(RRM)/Leishmania_maj_RNCMPT00212-PBM/HughesRNA(0.790)
	7	1e-662	- 1.525e+03	2.41%	1.43%	57.1bp (56.1bp)	BATF(bZIP)/Th17-BATF-ChIP-Seq(GSE39756)/Homer(0.994)
	8	1e-644	- 1.485e+03	29.23%	25.92%	55.8bp (61.1bp)	RRTF1(AP2ERE吕布)/colamp-RRTF1-DAP-Seq(GSE60143)/Homer(0.689)
	9	1e-632	- 1.457e+03	36.15%	32.66%	56.7bp (61.1bp)	EBF3/MA1637.1/Jaspar(0.820)
	10	1e-603	- 1.390e+03	35.61%	32.22%	56.3bp (59.3bp)	CEP3/MA0282.1/Jaspar(0.713)



SRR1658170

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3198	-7.364e+03	24.28%	17.14%	54.9bp (59.7bp)	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer(0.943)
	2	1e-1719	-3.959e+03	2.73%	1.09%	56.1bp (61.7bp)	PU.1:IRF8(ETS:IRF)/pDC-Irf8-ChIP-Seq(GSE66899)/Homer(0.863)
	3	1e-1311	-3.020e+03	49.17%	43.41%	55.0bp (59.7bp)	ROX8(RRM)/Drosophila_melanogaster-RNCMPT00148-PBM/HughesRNA(0.777)
	4	1e-1202	-2.768e+03	41.15%	35.79%	55.7bp (63.6bp)	AT2G15740(C2H2)/col-AT2G15740-DAP-Seq(GSE60143)/Homer(0.773)
	5	1e-951	-2.191e+03	56.44%	51.52%	56.1bp (59.6bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.772)
	6	1e-757	-1.745e+03	4.89%	3.23%	56.9bp (56.5bp)	BATF(bZIP)/Th17-BATF-ChIP-Seq(GSE39756)/Homer(0.992)
	7	1e-718	-1.653e+03	30.22%	26.39%	56.3bp (63.9bp)	AT1G77200(AP2EREBP)/colamp-AT1G77200-DAP-Seq(GSE60143)/Homer(0.687)
	8	1e-699	-1.610e+03	33.28%	29.39%	55.7bp (60.7bp)	ERF115(AP2EREBP)/colamp-ERF115-DAP-Seq(GSE60143)/Homer(0.819)
	9	1e-686	-1.580e+03	2.68%	1.54%	55.7bp (58.9bp)	MF0003.1_REL_class/Jaspar(0.962)
	10	1e-677	-1.559e+03	51.12%	46.97%	55.8bp (57.0bp)	ZNF768(Zf)/Rajj-ZNF768-ChIP-Seq(GSE111879)/Homer(0.730)

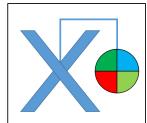


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SRR1658152

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
ACTTCCGGTT	1	1e-2561	-5.897e+03	28.07%	20.43%	55.7bp (60.7bp)	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer(0.931)
AAAATGGCGGC	2	1e-1018	-2.345e+03	44.69%	39.05%	55.0bp (59.4bp)	RAP212(AP2ERE吕布)/col-RAP212-DAP-Seq(GSE60143)/Homer(0.804)
ATTTCCCCCG	3	1e-857	-1.974e+03	58.83%	53.60%	55.6bp (60.8bp)	E2F7(E2F)/Hela-E2F7-ChIP-Seq(GSE32673)/Homer(0.779)
GTTTCAGTTTCA	4	1e-831	-1.915e+03	7.77%	5.29%	55.1bp (60.2bp)	ISRE(IRF)/ThioMac-LPS-Expression(GSE23622)/Homer(0.91)
CC CGG A T CCG	5	1e-829	-1.911e+03	39.25%	34.28%	55.7bp (59.1bp)	TBS1/MA0404.1/Jaspar(0.763)
CGGATTAA	6	1e-685	-1.579e+03	49.61%	44.92%	56.0bp (59.9bp)	Dof2/MA0020.1/Jaspar(0.695)
GGCCTCTGAG	7	1e-678	-1.562e+03	57.44%	52.78%	55.9bp (57.0bp)	Zac1(Zf)/Neuro2A-Plagl1-ChIP-Seq(GSE75942)/Homer(0.705)
TTAGGGCC	8	1e-629	-1.449e+03	42.55%	38.14%	56.3bp (58.3bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.786)
GCACAAAT	9	1e-580	-1.338e+03	44.62%	40.35%	56.7bp (58.5bp)	DAL82/MA0291.1/Jaspar(0.762)
TTAAGAAACCCC	10	1e-553	-1.275e+03	60.47%	56.30%	54.8bp (59.6bp)	che-1/MA0260.1/Jaspar(0.750)



SRR1658295

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3754	- 8.644e+03	20.43%	13.22%	54.8bp (59.7bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.947)
	2	1e-3014	- 6.941e+03	6.03%	2.68%	54.9bp (62.5bp)	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer(0.964)
	3	1e-1161	- 2.674e+03	18.69%	14.64%	56.8bp (63.0bp)	Deaf1/dmmpmm(Pollard)/fly(0.731)
	4	1e-1036	- 2.387e+03	40.89%	35.83%	54.9bp (60.0bp)	DOF5.7/MA0984.1/Jaspar(0.779)
	5	1e-865	- 1.993e+03	54.13%	49.35%	56.3bp (59.0bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.761)
	6	1e-860	- 1.982e+03	47.65%	42.91%	55.7bp (61.0bp)	CG7903(RRM)/Drosophila_melanogaster-RNCMPT00144-PBM/HughesRNA(0.739)
	7	1e-841	- 1.937e+03	49.11%	44.42%	56.4bp (63.2bp)	MYB98(MYB)/col-MYB98-DAP-Seq(GSE60143)/Homer(0.816)
	8	1e-701	- 1.615e+03	30.10%	26.26%	55.7bp (59.4bp)	RUNX(Runt)/HPC7-Runx1-ChIP-Seq(GSE22178)/Homer(0.849)
	9	1e-680	- 1.566e+03	55.45%	51.22%	55.9bp (57.6bp)	CG14718(RRM)/Drosophila_melanogaster-RNCMPT00006-PBM/HughesRNA(0.661)
	10	1e-615	- 1.417e+03	4.44%	2.97%	56.6bp (56.9bp)	JunB(bZIP)/DendriticCells-Junb-ChIP-Seq(GSE36099)/Homer(0.992)

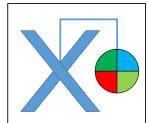


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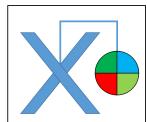
SRR1658277

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3206	-7.384e+03	17.51%	11.60%	55.4bp (59.1bp)	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer(0.963)
	2	1e-1287	-2.965e+03	43.81%	38.42%	55.1bp (60.4bp)	DOF5.7/MA0984.1/Jaspar(0.762)
	3	1e-1278	-2.944e+03	3.28%	1.69%	56.1bp (58.5bp)	MF0003.1_REL_class/Jaspar(0.956)
	4	1e-1179	-2.716e+03	4.02%	2.29%	55.6bp (61.0bp)	PU.1-IRF(ETS:IRF)/Bcell-PU.1-ChIP-Seq(GSE21512)/Homer(0.914)
	5	1e-865	-1.993e+03	49.95%	45.46%	55.7bp (60.7bp)	Deaf1/dmmpmm(Pollard)/fly(0.749)
	6	1e-704	-1.621e+03	33.39%	29.64%	56.2bp (58.5bp)	RUNX-AML(Runt)/CD4+-PolII-ChIP-Seq(Barski_et_al.)/Homer(0.790)
	7	1e-696	-1.605e+03	25.29%	21.89%	57.0bp (62.6bp)	MYB119/MA1176.1/Jaspar(0.695)
	8	1e-677	-1.561e+03	29.38%	25.84%	54.9bp (64.1bp)	AT2G15740(C2H2)/col-AT2G15740-DAP-Seq(GSE60143)/Homer(0.809)
	9	1e-627	-1.444e+03	21.71%	18.67%	56.8bp (64.4bp)	PF10_0214(RRM)/Plasmodium_falciparum-RNCMPT00240-PBM/HughesRNA(0.776)
	10	1e-602	-1.388e+03	35.59%	32.05%	56.6bp (62.3bp)	MYB98(MYB)/col-MYB98-DAP-Seq(GSE60143)/Homer(0.740)



SRR1658246

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3894	- 8.968e+03	27.90%	19.77%	55.4bp (63.1bp)	Elk4(ETS)/Hela-Elk4-ChIP-Seq(GSE31477)/Homer(0.949)
	2	1e-1994	- 4.592e+03	10.32%	6.59%	56.2bp (61.7bp)	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer(0.820)
	3	1e-1226	- 2.823e+03	66.01%	60.71%	56.3bp (64.3bp)	MYB98(MYB)/col-MYB98-DAP-Seq(GSE60143)/Homer(0.906)
	4	1e-1123	- 2.587e+03	51.94%	46.70%	55.1bp (60.9bp)	Dof3/MA0021.1/Jaspar(0.818)
	5	1e-954	- 2.197e+03	41.82%	37.12%	56.1bp (61.6bp)	CG7903(RRM)/Drosophila_melanogaster-RNCMPT00144-PBM/HughesRNA(0.747)
	6	1e-886	- 2.042e+03	51.99%	47.34%	56.4bp (61.3bp)	DOF2(C2C2(Zn)) Dof/Zea mays/AthaMap(0.711)
	7	1e-855	- 1.969e+03	36.06%	31.76%	56.2bp (60.3bp)	ZNF711(Zf)/SHSY5Y-ZNF711-ChIP-Seq(GSE20673)/Homer(0.886)
	8	1e-841	- 1.937e+03	21.03%	17.50%	56.3bp (61.4bp)	IRF5/MA1420.1/Jaspar(0.791)
	9	1e-726	- 1.673e+03	33.10%	29.22%	55.7bp (62.5bp)	AT-GTL1/MA1661.1/Jaspar(0.831)
	10	1e-720	- 1.659e+03	30.84%	27.07%	56.5bp (57.0bp)	RUNX2(Runt)/PCa-RUNX2-ChIP-Seq(GSE33889)/Homer(0.927)

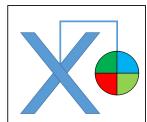


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SRR1658309

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-4075	-9.384e+03	21.65%	14.53%	55.8bp (61.4bp)	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer(0.950)
	2	1e-2293	-5.281e+03	6.86%	3.83%	55.8bp (60.4bp)	IRF4(IRF)/GM12878-IRF4-ChIP-Seq(GSE32465)/Homer(0.916)
	3	1e-1198	-2.760e+03	61.43%	56.33%	56.6bp (62.7bp)	MYB98(MYB)/col-MYB98-DAP-Seq(GSE60143)/Homer(0.903)
	4	1e-1109	-2.555e+03	62.37%	57.49%	56.4bp (60.7bp)	dl(var.2)/MA0023.1/Jaspar(0.746)
	5	1e-1102	-2.538e+03	56.12%	51.17%	55.8bp (61.5bp)	BMYB(HTH)/Hela-BMYB-ChIP-Seq(GSE27030)/Homer(0.771)
	6	1e-991	-2.284e+03	50.87%	46.18%	55.5bp (61.3bp)	DEL2(E2FDP)/col-DEL2-DAP-Seq(GSE60143)/Homer(0.700)
	7	1e-790	-1.821e+03	36.42%	32.46%	55.9bp (57.7bp)	RUNX1/MA0002.2/Jaspar(0.873)
	8	1e-686	-1.581e+03	51.09%	47.19%	56.4bp (61.8bp)	DPL-1(E2F)/cElegans-Adult-ChIP-Seq(modEncode)/Homer(0.695)
	9	1e-669	-1.542e+03	1.97%	1.08%	57.1bp (55.9bp)	BATF(bZIP)/Th17-BATF-ChIP-Seq(GSE39756)/Homer(0.990)
	10	1e-572	-1.318e+03	41.45%	37.97%	56.5bp (58.8bp)	CEP3/MA0282.1/Jaspar(0.680)



SRR1658228

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
 ACTTCCGGTT	1	1e-2896	- 6.669e+03	26.79%	19.13%	55.1bp (61.2bp)	ETV1(ETS)/GIST48- ETV1-ChIP- Seq(GSE22441)/Homer(0.918)
 AAAAACCGGC	2	1e-1214	- 2.796e+03	42.68%	36.81%	55.5bp (61.6bp)	prd/dmmpmm(Down)/fly(0.834)
 TTTAGGCCCT	3	1e-1051	- 2.422e+03	45.80%	40.26%	55.6bp (60.8bp)	cad/dmmpmm(SeSiMCMC)/fly(0.647)
 GCGGTAAA	4	1e-836	- 1.925e+03	49.79%	44.80%	56.0bp (61.9bp)	EMB1789(C3H)/col- EMB1789-DAP- Seq(GSE60143)/Homer(0.766)
 AGGAAGCCCTT	5	1e-770	- 1.775e+03	17.27%	13.85%	55.1bp (59.1bp)	ETV4/MA0764.2/Jaspar(0.871)
 AAAAATGGCC	6	1e-716	- 1.650e+03	2.51%	1.32%	51.5bp (55.5bp)	YY1/MA0095.2/Jaspar(0.913)
 GTTACTGATT	7	1e-698	- 1.608e+03	29.26%	25.23%	55.4bp (59.3bp)	HNF1b/Homeobox)/PDAC- HNF1B-ChIP- Seq(GSE64557)/Homer(0.699)
 GGGGATTT	8	1e-625	- 1.441e+03	36.37%	32.28%	56.1bp (59.5bp)	MZF1/MA0056.2/Jaspar(0.835)
 TCTCTGAG	9	1e-613	- 1.412e+03	41.07%	36.90%	56.2bp (59.3bp)	CDC5(MYB)/Arabidopsis thaliana/AthaMap(0.658)
 ATGACTCATC	10	1e-598	- 1.378e+03	5.26%	3.58%	56.7bp (56.9bp)	Fra1(bZIP)/BT549-Fra1- ChIP- Seq(GSE46166)/Homer(0.990)



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SRR1658183

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-4423	- 1.019e+04	10.58%	5.44%	54.6bp (61.0bp)	IRF2(IRF)/Erythroblas- IRF2-ChIP- Seq(GSE36985)/Homer(0.954)
	2	1e-1629	- 3.752e+03	23.50%	18.58%	55.7bp (59.7bp)	ELF3(ETS)/PDAC- ELF3-ChIP- Seq(GSE64557)/Homer(0.859)
	3	1e-1258	- 2.897e+03	59.54%	54.20%	56.3bp (61.4bp)	MYB98(MYB)/col- MYB98-DAP- Seq(GSE60143)/Homer(0.853)
	4	1e-1168	- 2.690e+03	25.05%	20.74%	56.8bp (60.8bp)	YRM1/MA0438.1/Jaspar(0.853)
	5	1e-1010	- 2.327e+03	34.57%	30.09%	55.1bp (59.5bp)	ROX8(RRM)/Drosophila_melanogast- RNCMPT00148- PBM/HughesRNA(0.759)
	6	1e-955	- 2.201e+03	48.41%	43.74%	56.2bp (60.0bp)	SKN7/MA0381.1/Jaspar(0.696)
	7	1e-837	- 1.929e+03	58.04%	53.67%	56.3bp (59.3bp)	Dof2/MA0020.1/Jaspar(0.835)
	8	1e-822	- 1.895e+03	10.53%	8.06%	55.8bp (59.1bp)	NFkB- p65(RHD)/GM12787- p65-ChIP- Seq(GSE19485)/Homer(0.949)
	9	1e-800	- 1.842e+03	5.05%	3.38%	56.5bp (56.7bp)	AP-1(bZIP)/ThioMac- PU.1-ChIP- Seq(GSE21512)/Homer(0.994)
	10	1e-731	- 1.683e+03	50.65%	46.56%	56.2bp (59.5bp)	Tb_0251(RRM)/Trypanosoma_br- RNCMPT00251- PBM/HughesRNA(0.857)

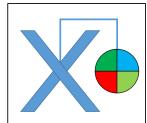


Epigenome Analysis Platform

Report

SRR1658264

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3794	-8.736e+03	23.62%	16.94%	55.2bp (59.9bp)	Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer(0.943)
	2	1e-2904	-6.688e+03	5.30%	2.60%	55.5bp (61.3bp)	IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer(0.955)
	3	1e-1519	-3.498e+03	52.17%	46.79%	55.2bp (60.3bp)	DOF5.7/MA0984.1/Jaspar(0.816)
	4	1e-1137	-2.618e+03	36.03%	31.65%	56.0bp (59.3bp)	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer(0.748)
	5	1e-1034	-2.382e+03	52.91%	48.47%	56.5bp (61.9bp)	MYB98(MYB)/col-MYB98-DAP-Seq(GSE60143)/Homer(0.922)
	6	1e-917	-2.112e+03	60.50%	56.37%	55.6bp (59.1bp)	MYB73(MYB)/col-MYB73-DAP-Seq(GSE60143)/Homer(0.666)
	7	1e-888	-2.045e+03	59.12%	55.04%	56.8bp (57.5bp)	MET28/MA0332.1/Jaspar(0.778)
	8	1e-773	-1.780e+03	33.49%	29.94%	56.9bp (66.0bp)	MYB33/MA1391.2/Jaspar(0.744)
	9	1e-763	-1.759e+03	34.30%	30.74%	55.9bp (58.4bp)	CST6(MacIsaac)/Yeast(0.751)
	10	1e-756	-1.743e+03	37.19%	33.57%	56.2bp (61.5bp)	REB1/MA0363.1/Jaspar(0.638)



SRR1658318

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-4333	-9.979e+03	19.63%	12.80%	55.2bp (60.2bp)	ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer(0.952)
	2	1e-1739	-4.006e+03	37.11%	31.38%	55.8bp (60.9bp)	MF0009.1_TRP(MYB)_class/Jaspar
	3	1e-1014	-2.336e+03	57.67%	53.05%	56.3bp (59.0bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.790)
	4	1e-966	-2.226e+03	38.05%	33.73%	55.4bp (58.2bp)	pho/MA1460.1/Jaspar(0.857)
	5	1e-935	-2.154e+03	42.73%	38.37%	55.2bp (60.2bp)	AT-GTL1/MA1661.1/Jaspar(0.826)
	6	1e-922	-2.125e+03	51.79%	47.37%	56.8bp (59.6bp)	EBF3/MA1637.1/Jaspar(0.783)
	7	1e-854	-1.969e+03	42.07%	37.91%	55.9bp (57.6bp)	ZNF768(Zf)/Rajj-ZNF768-ChIP-Seq(GSE111879)/Homer(0.751)
	8	1e-848	-1.955e+03	5.08%	3.43%	56.3bp (56.9bp)	BATF(bZIP)/Th17-BATF-ChIP-Seq(GSE39756)/Homer(0.970)
	9	1e-823	-1.897e+03	5.55%	3.84%	55.1bp (57.9bp)	MF0003.1_REL_class/Jaspar(0.971)
	10	1e-736	-1.695e+03	21.92%	18.77%	56.2bp (60.6bp)	Tb_0251(RRM)/Trypanosoma_br-RNCMPT00251-PBM/HughesRNA(0.797)



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SRR1658192

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-4133	- 9.517e+03	26.87%	18.87%	55.5bp (61.0bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.962)
	2	1e-1409	- 3.246e+03	44.90%	39.29%	55.0bp (59.5bp)	ROX8(RRM)/Drosophila_melanog RNCMPT00148-PBM/HughesRNA(0.764)
	3	1e-1247	- 2.873e+03	61.77%	56.49%	56.4bp (60.7bp)	MYB65(MYB)/colamp-MYB65-DAP-Seq(GSE60143)/Homer(0.839)
	4	1e-1037	- 2.388e+03	4.82%	3.01%	56.0bp (59.5bp)	MF0003.1_REL_class/Jaspar(0.93)
	5	1e-1030	- 2.372e+03	59.41%	54.59%	55.9bp (62.8bp)	SWI6/SWI6YPD/9-SWI4,9-SWI6(Harbison)/Yeast(0.972)
	6	1e-994	- 2.289e+03	47.30%	42.55%	56.8bp (59.7bp)	Tb_0220(RRM)/Trypanosoma_b RNCMPT00220-PBM/HughesRNA(0.822)
	7	1e-902	- 2.078e+03	47.96%	43.43%	55.4bp (60.3bp)	AT-GTL1/MA1661.1/Jaspar(0.746)
	8	1e-864	- 1.991e+03	11.88%	9.20%	56.0bp (60.9bp)	che-1/MA0260.1/Jaspar(0.739)
	9	1e-741	- 1.708e+03	2.63%	1.52%	56.8bp (56.2bp)	BATF(bZIP)/Th17-BATF-ChIP-Seq(GSE39756)/Homer(0.995)
	10	1e-715	- 1.648e+03	32.15%	28.45%	54.5bp (59.7bp)	PB0033.1_Irf3_1/Jaspar(0.724)

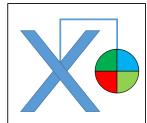


Epigenome Analysis Platform

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SRR1658130

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-2886	- 6.647e+03	23.82%	17.15%	55.3bp (61.2bp)	ETV1(ETS)/GIST48- ETV1-ChIP- Seq(GSE22441)/Homer(0.924)
	2	1e-1385	- 3.189e+03	60.36%	54.55%	55.9bp (62.7bp)	prd/dmmpmm(Down)/fly(0.800)
	3	1e-1157	- 2.666e+03	54.27%	48.92%	56.2bp (62.5bp)	SWI4(MacIsaac)/Yeast(0.866)
	4	1e-872	- 2.009e+03	50.89%	46.25%	56.0bp (59.7bp)	PCF/Arabidopsis- Promoters/Homer(0.713)
	5	1e-732	- 1.686e+03	32.45%	28.55%	56.1bp (62.8bp)	ACE2(MacIsaac)/Yeast(0.723)
	6	1e-688	- 1.584e+03	43.69%	39.63%	56.0bp (58.9bp)	ARF34/MA1693.1/Jaspar(0.765)
	7	1e-667	- 1.537e+03	33.47%	29.71%	56.5bp (61.3bp)	MYB98(MYB)/col- MYB98-DAP- Seq(GSE60143)/Homer(0.863)
	8	1e-667	- 1.536e+03	17.76%	14.80%	56.8bp (65.1bp)	DAL80/MA0289.1/Jaspar(0.741)
	9	1e-661	- 1.524e+03	2.54%	1.47%	56.2bp (55.1bp)	Atf3(bZIP)/GBM-ATF3- ChIP- Seq(GSE33912)/Homer(0.981)
	10	1e-564	- 1.300e+03	23.81%	20.73%	56.5bp (59.7bp)	dl(var.2)/MA0023.1/Jaspar(0.814)

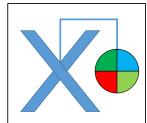


Epigenome Analysis Platform

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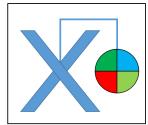
SRR1658310

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-2484	-5.720e+03	31.47%	24.83%	55.1bp (60.4bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.858)
	2	1e-1137	-2.620e+03	57.63%	52.59%	55.9bp (61.4bp)	BMYB(HTH)/Hela-BMYB-ChIP-Seq(GSE27030)/Homer(0.769)
	3	1e-1018	-2.345e+03	52.25%	47.45%	56.5bp (61.6bp)	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer(0.838)
	4	1e-921	-2.123e+03	45.47%	40.96%	55.9bp (61.3bp)	CG7903(RRM)/Drosophila_melanogaster-RNCMPT00144-PBM/HughesRNA(0.733)
	5	1e-895	-2.063e+03	43.72%	39.30%	55.6bp (63.1bp)	DEL2(E2FDP)/col-DEL2-DAP-Seq(GSE60143)/Homer(0.710)
	6	1e-863	-1.988e+03	15.78%	12.74%	55.1bp (59.8bp)	ISRE(IRF)/ThioMac-LPS-Expression(GSE23622)/Homer(0.903)
	7	1e-801	-1.846e+03	57.33%	53.09%	56.3bp (61.5bp)	Unknown3/Arabidopsis-Promoters/Homer(0.842)
	8	1e-797	-1.837e+03	39.90%	35.81%	56.0bp (61.4bp)	GTL1(Trihelix)/colamp-GTL1-DAP-Seq(GSE60143)/Homer(0.853)
	9	1e-742	-1.711e+03	51.57%	47.48%	56.4bp (59.2bp)	Dof2/MA0020.1/Jaspar(0.810)
	10	1e-709	-1.633e+03	33.98%	30.27%	56.3bp (59.8bp)	MZF1/MA0056.2/Jaspar(0.847)



SRR1658202

Motif	Rank	P-value	log P-pvalue	% of Targets	% of Back-ground	STD(Bg STD)	Best Match/Details
	1	1e-3550	- 8.175e+03	26.52%	19.21%	56.1bp (61.8bp)	Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer(0.938)
	2	1e-2336	- 5.379e+03	10.40%	6.55%	55.0bp (60.8bp)	IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer(0.952)
	3	1e-1088	- 2.505e+03	36.22%	31.58%	55.1bp (60.5bp)	dof42(C2C2dof)/col-dof42-DAP-Seq(GSE60143)/Homer(0.742)
	4	1e-1087	- 2.504e+03	55.48%	50.57%	55.6bp (59.0bp)	TBS1/MA0404.1/Jaspar(0.700)
	5	1e-1054	- 2.427e+03	65.21%	60.51%	56.7bp (63.4bp)	CRF10(AP2EREBP)/col100-CRF10-DAP-Seq(GSE60143)/Homer(0.767)
	6	1e-907	- 2.090e+03	60.37%	55.93%	56.0bp (60.1bp)	TBP3(MYBrelated)/col-TBP3-DAP-Seq(GSE60143)/Homer(0.759)
	7	1e-856	- 1.973e+03	63.63%	59.37%	55.5bp (59.7bp)	ct/MA0218.1/Jaspar(0.685)
	8	1e-714	- 1.645e+03	35.00%	31.27%	56.7bp (57.5bp)	RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer(0.932)
	9	1e-662	- 1.526e+03	27.42%	24.09%	55.7bp (61.1bp)	ZNF711(Zf)/SHSY5Y-ZNF711-ChIP-Seq(GSE20673)/Homer(0.691)
	10	1e-652	- 1.503e+03	47.92%	44.13%	56.1bp (58.8bp)	EWS:ERG-fusion(ETS)/CADO_ES1-EWS:ERG-ChIP-Seq(SRA014231)/Homer(0.705)

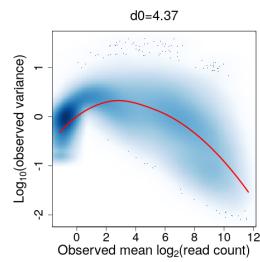


7 Differential analysis

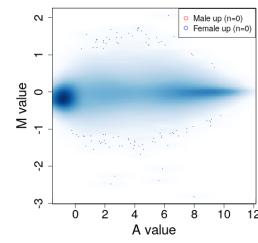
Here we first performed differential analysis based on the user specified variable of interest, then we performed differential TF motif enrichment based on those differential enriched/accessible peaks (DEPs/DAPs), identifying TF motifs that were enriched in one set of peaks regions relative to another set. Finally, we performed functional annotation to the nearest genes of DEPs/DAPs to identify enriched biological themes in different conditions. The figures below show the differential analysis and functional annotations for different comparisons.

Female_vs_Male

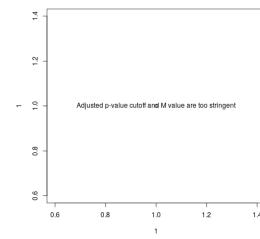
MVC plot



MA plot

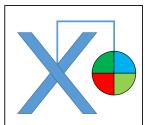


Differential motif enrichment

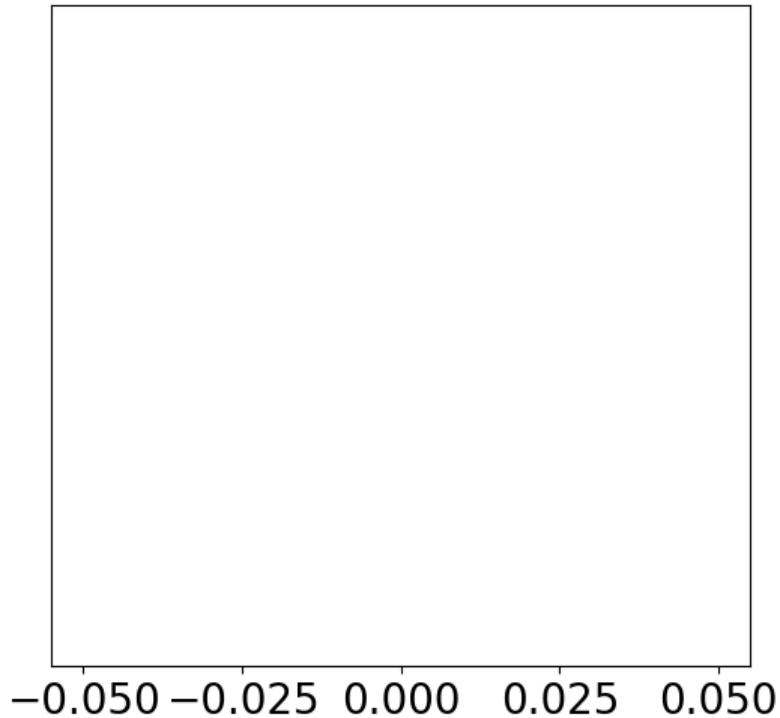


Female_vs_Male

Functional enrichment

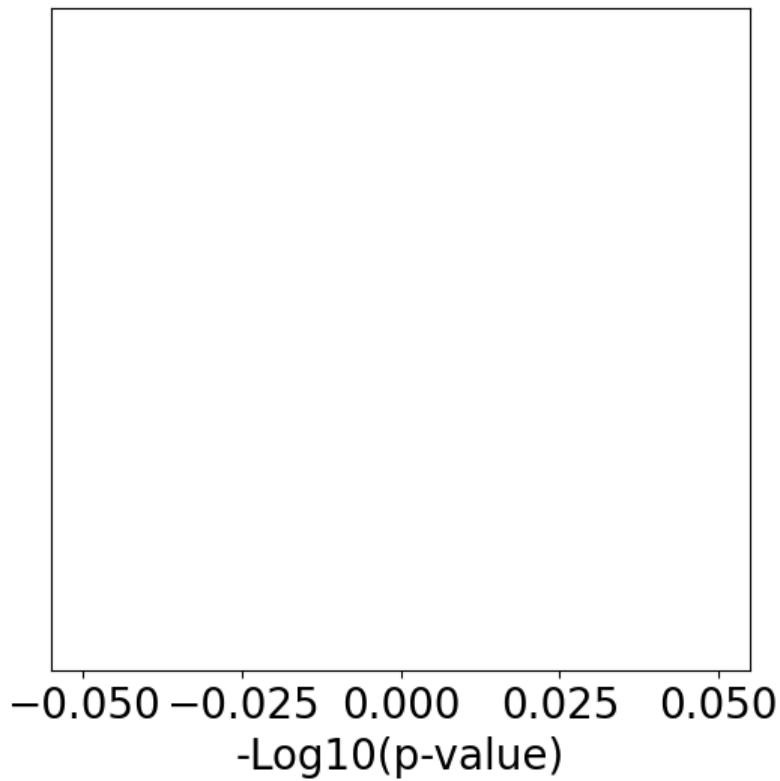


Female

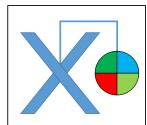


-Log10(p-value)

Male



-Log10(p-value)



8 References

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