

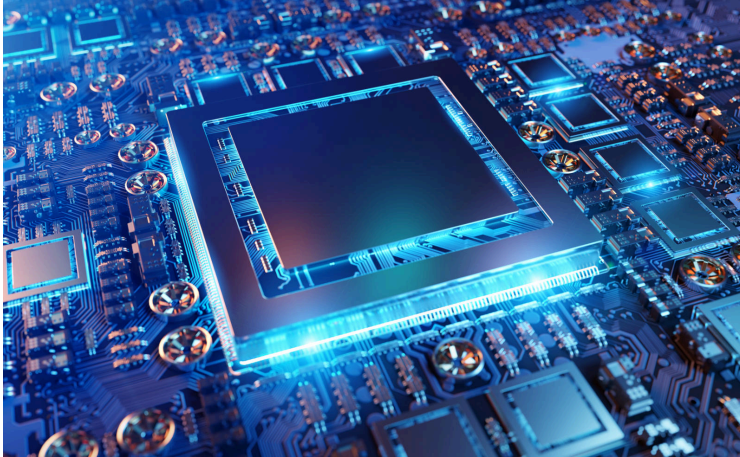
ATAC-seq

Thomas Juettemann, EMBL-EBI

Lars Grønvold, NMBU



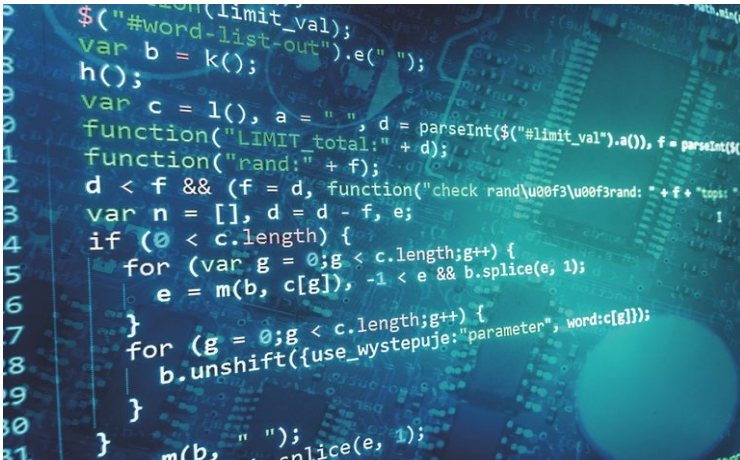
Genome & Epigenome = Hardware & Software



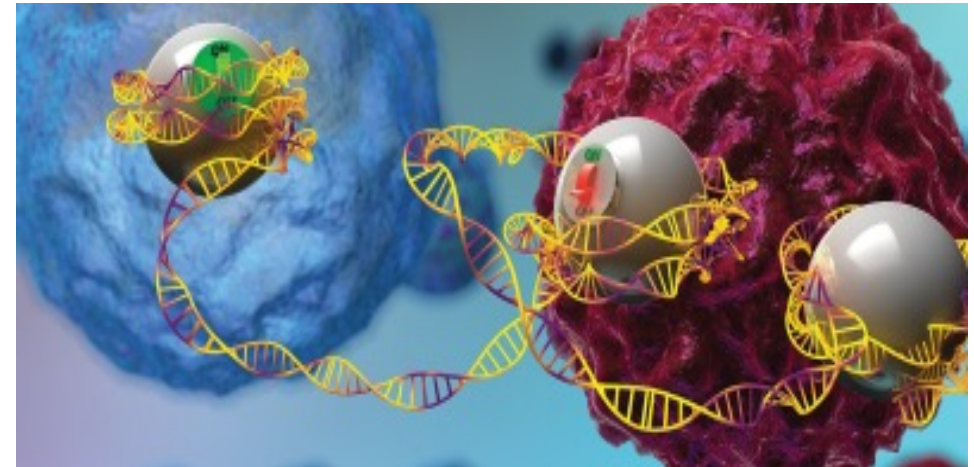
<https://www.javelin-tech.com/blog/2020/10/solidworks-2021-hardware-recommendations/>



<https://www.wallpaperflare.com/blue-dna-strand-wallpaper-32045>



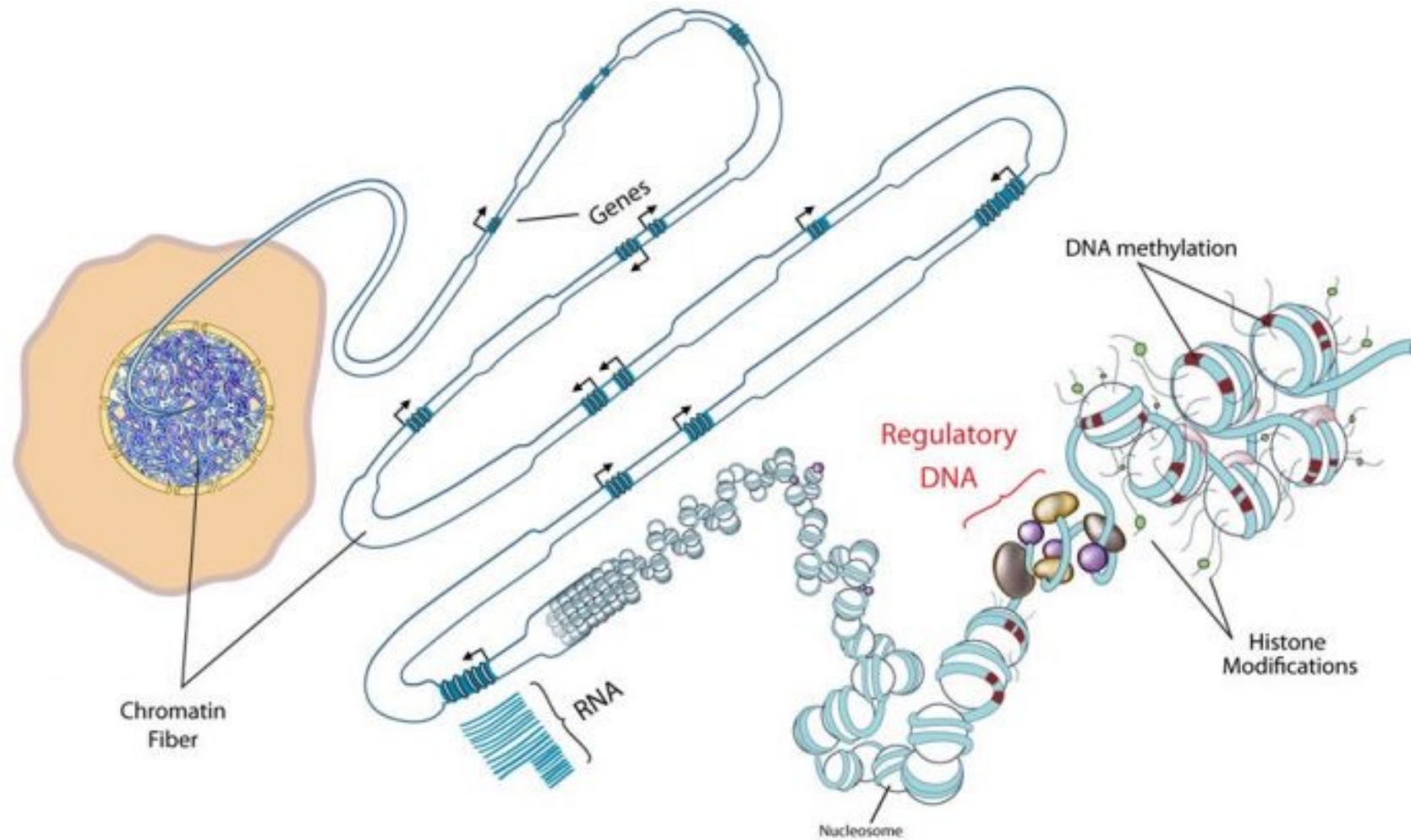
<https://informatics.tuwien.ac.at/bachelor/software-and-information-engineering/>



<https://www.the-scientist.com/lab-tools/researchers-engineer-epigenome-editors-to-study-how-gene-expression-affects-disease-65250>

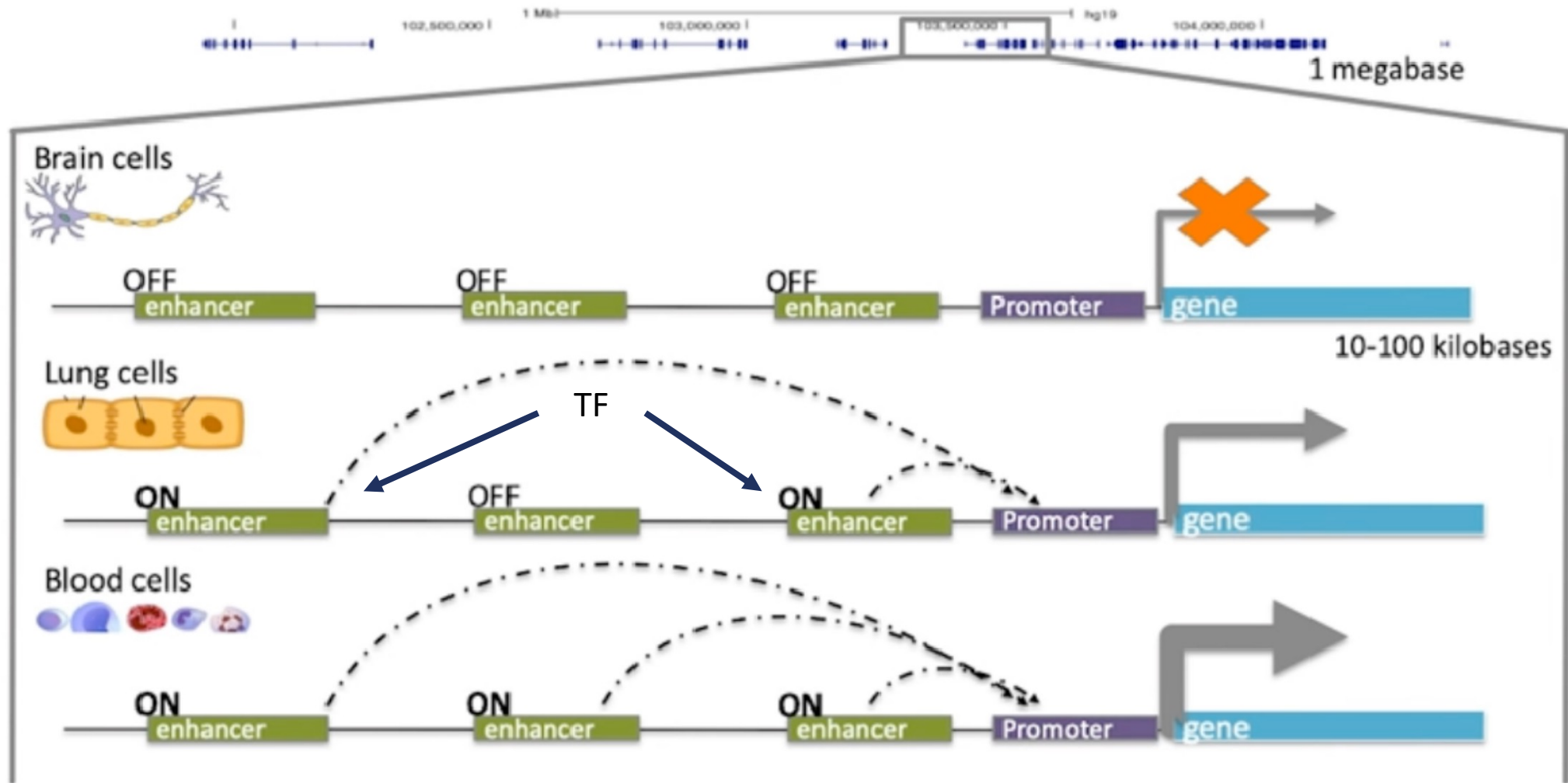


Hierarchical folding of chromatin defines the physical memory of the cell

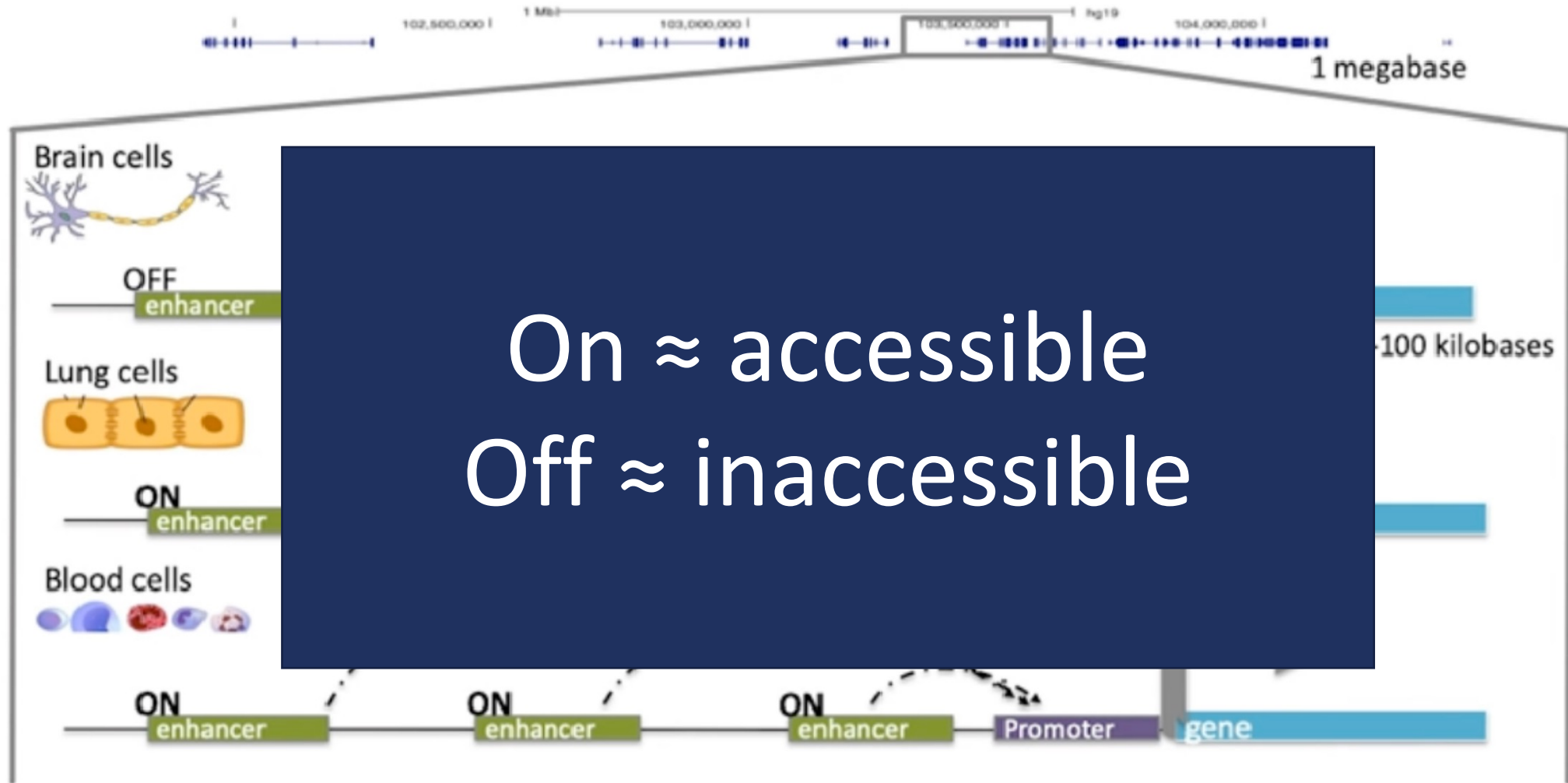


<http://www.roadmapepigenomics.org/>

Gene expression control



Gene expression control

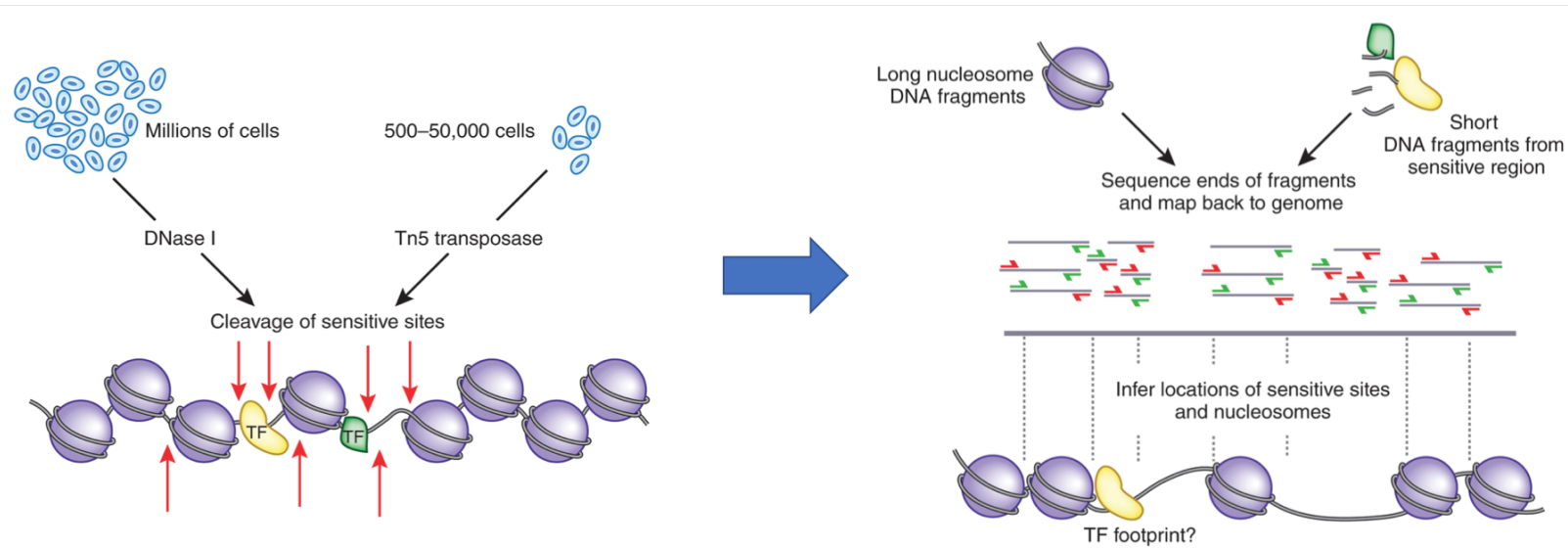


Assay of Transposase Accessible Chromatin sequencing

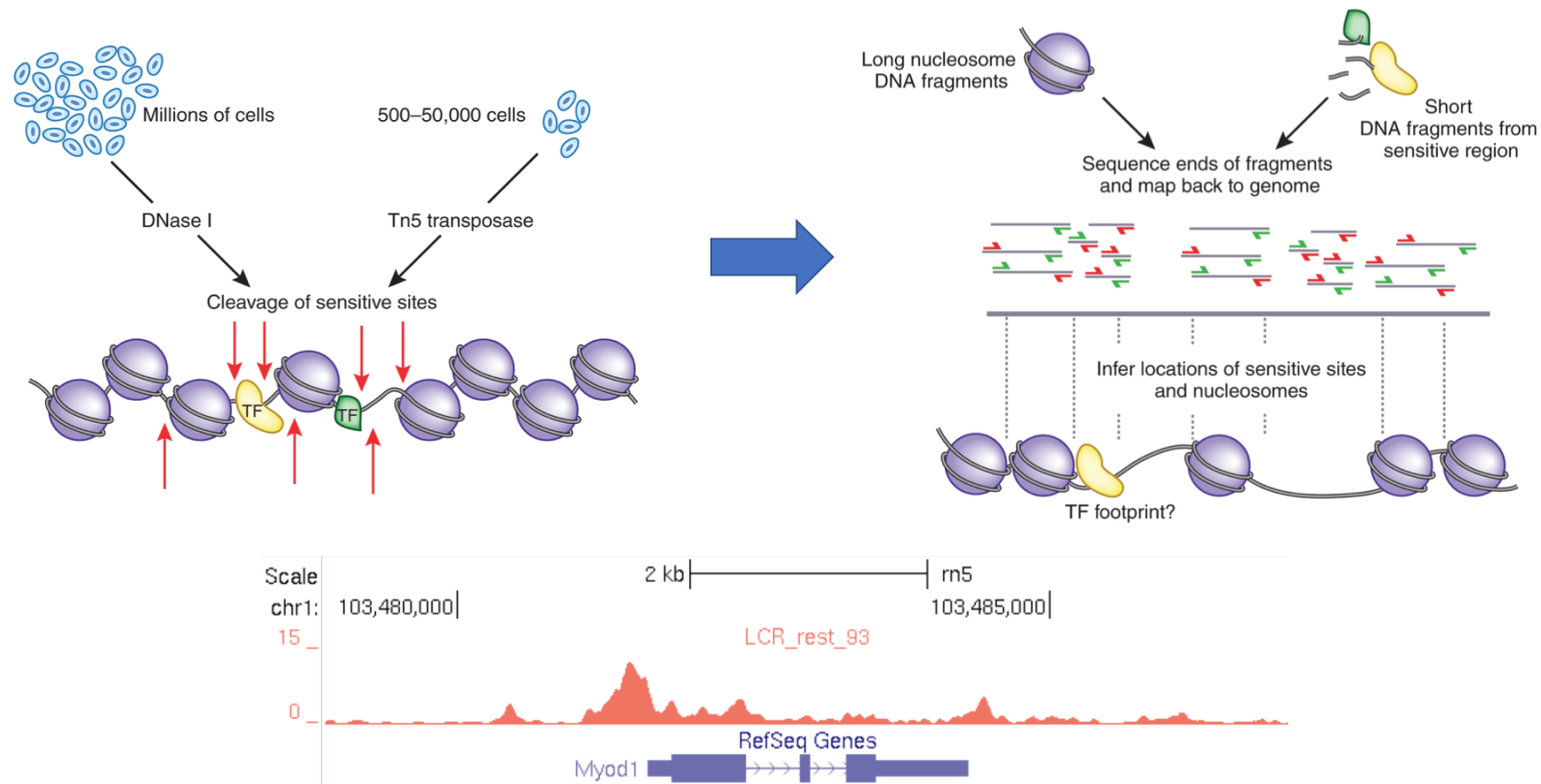
(ATAC-seq)



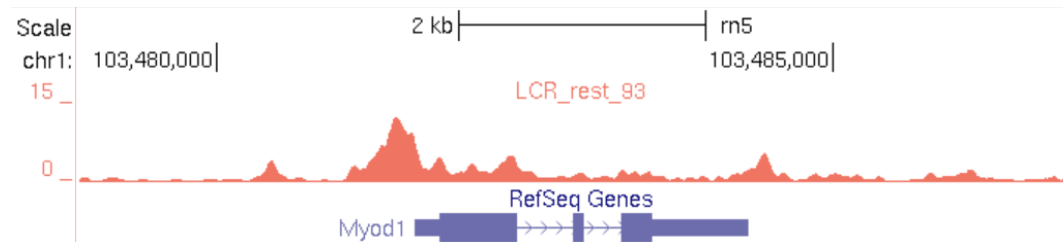
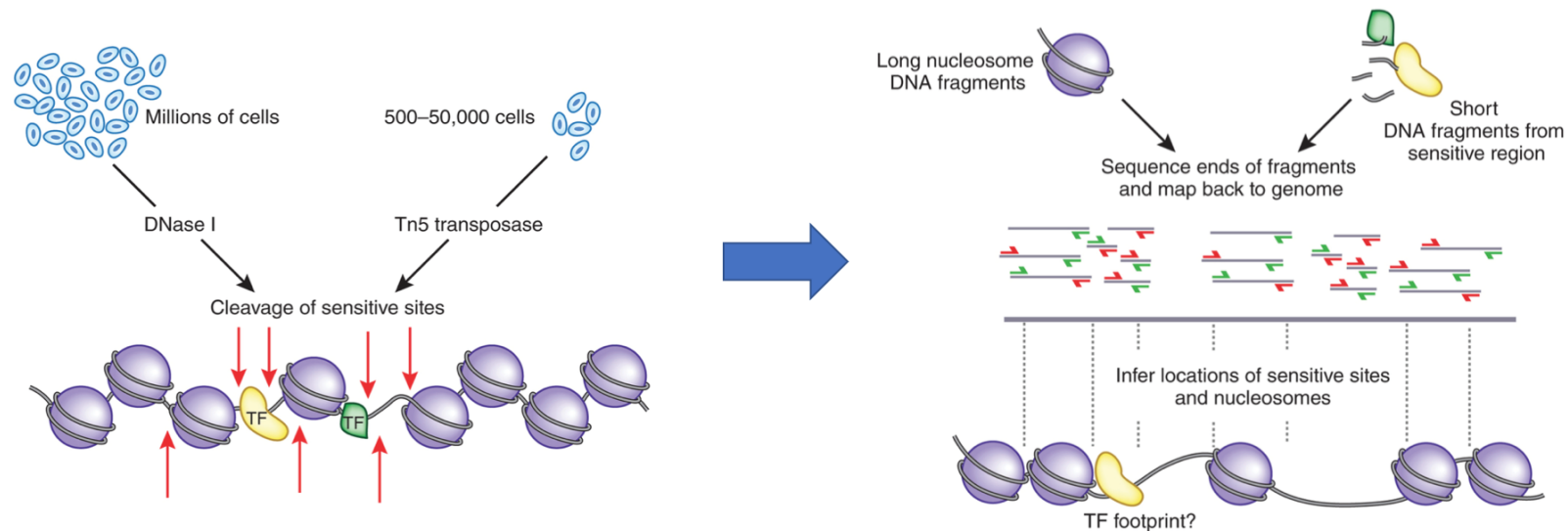
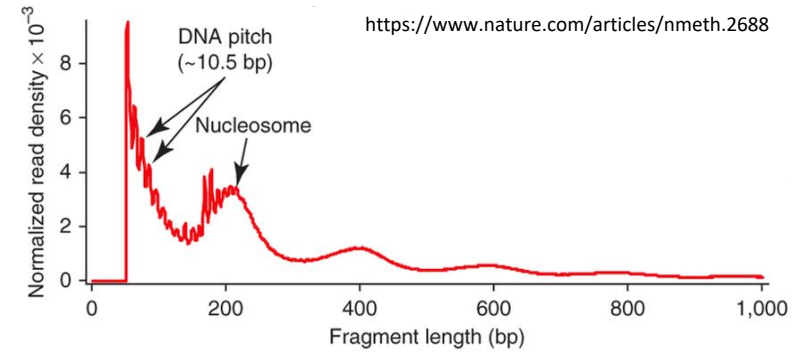
ATAC-seq



ATAC-seq

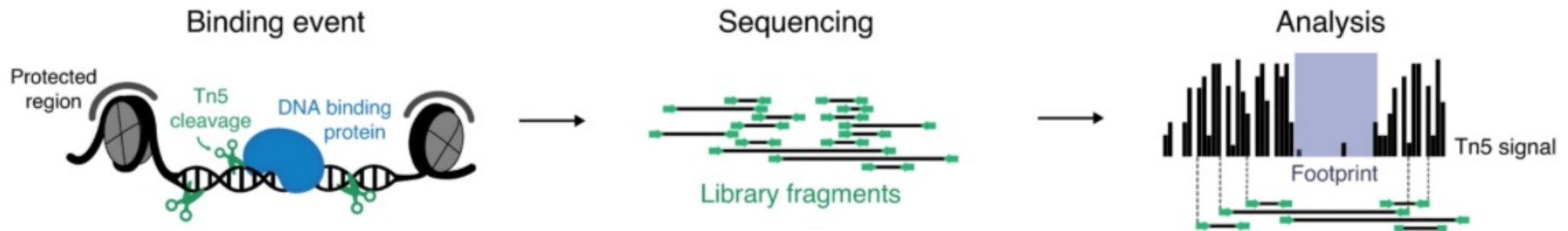


ATAC-seq

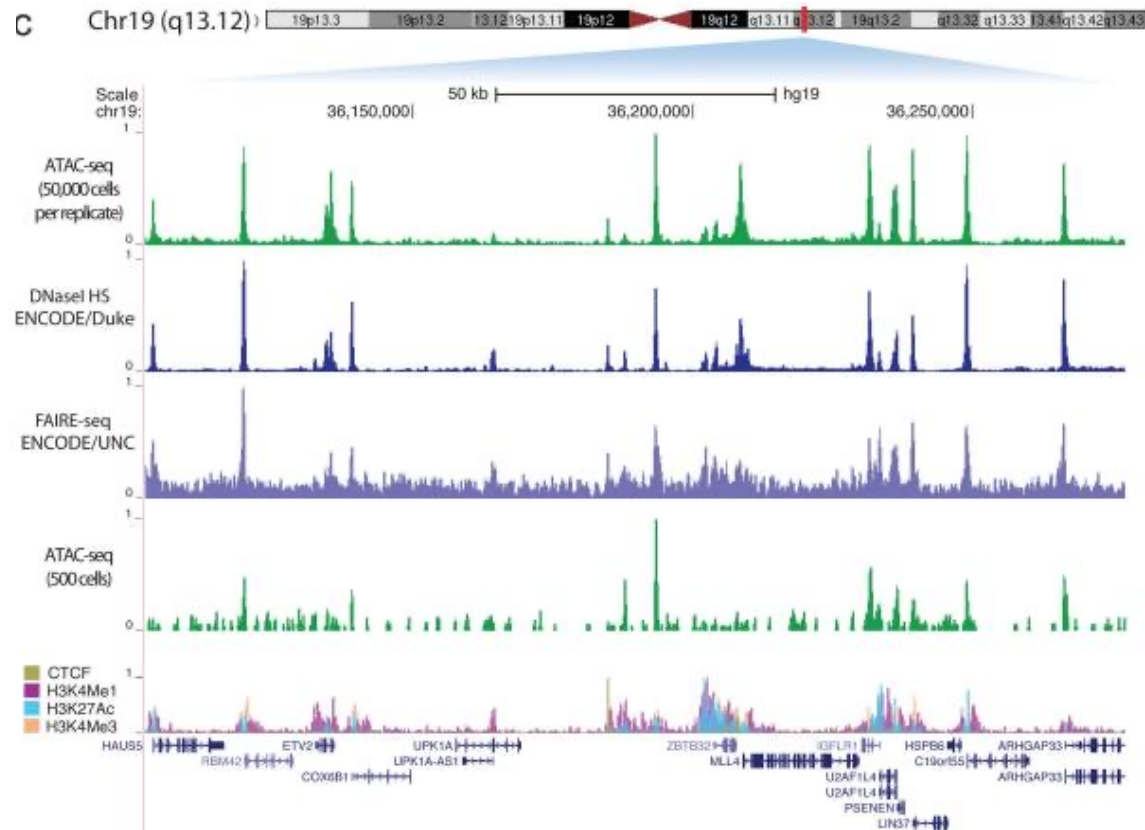
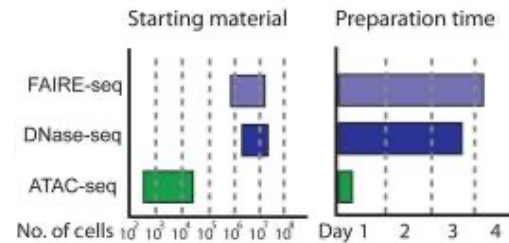


Common use cases

- Mapping regions of open chromatin
- Mapping nucleosome positions
- Transcription factor footprinting



Comparison



<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3959825/#R10>



Qualities of good ATAC-seq data

Enrichment of signal around transcription start sites (TSS enrichment)

High enrichment of reads in ATAC-seq peaks

'Sensible' fragment length distribution (may depend on use case)

Low mitochondrial contamination (common problem in ATAC-seq)

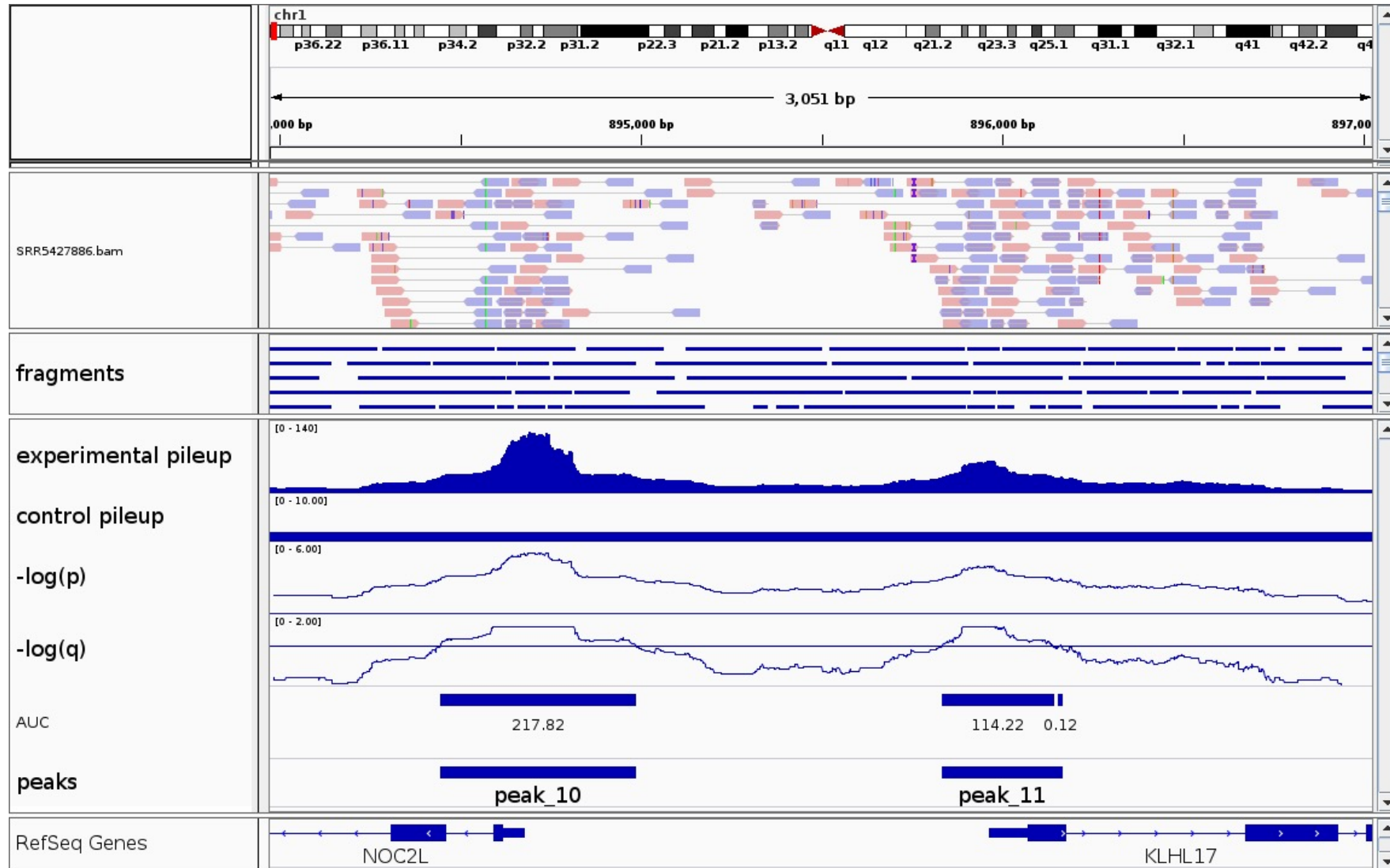
All of the other stuff you would look for in many other NGS data types (good alignment rate, duplication rate/library complexity, etc)

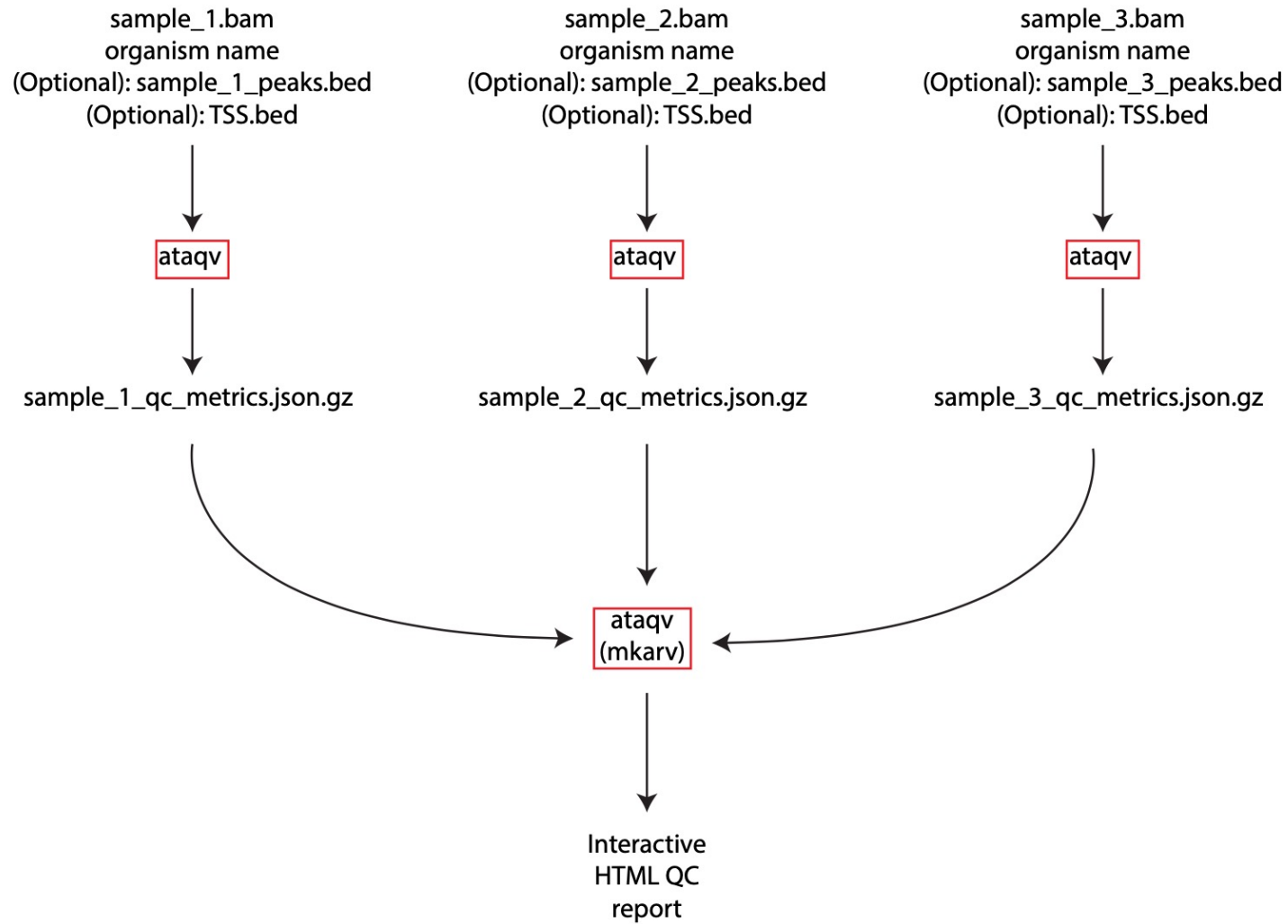


Quality control

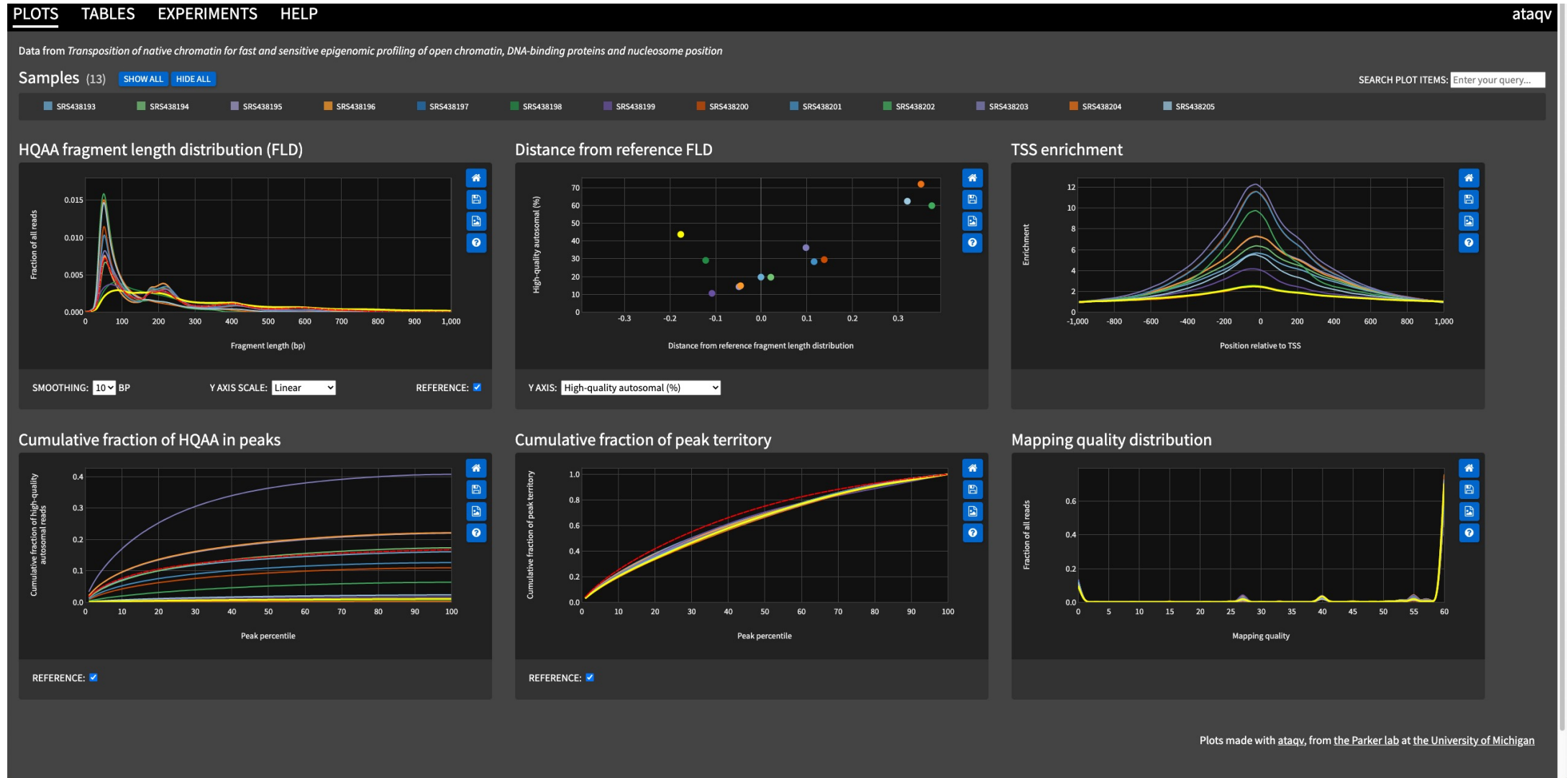


Genrich





Ataqv HTML report



<https://parkerlab.github.io/ataqv/demo/>

Ataqv HTML report

PLOTS

TABLES

EXPERIMENTS

HELP

ataqv

Data from Transposition of native chromatin for fast and sensitive epigenomic profiling of open chromatin, DNA-binding proteins and nucleosome position

Quality Indicators

CSVEXCEL

Search:

Name	Sample	Library	HQAA (%)	SMR	FLDD	TSS enrichment	Duplicate fraction in peaks	Duplicate fraction outside of peaks	Peak duplicate ratio
SRS438193_SRR891268_1	SRS438193	SRR891268	19.532	1.979	0	5.600	0.386	0.387	1.003
SRS438194_SRR891269_1	SRS438194	SRR891269	19.472	1.809	0.022	6.290	0.265	0.280	1.056
SRS438195_SRR891270_1	SRS438195	SRR891270	14.115	1.494	-0.048	7.171	0.097	0.145	1.493
SRS438196_SRR891271_1	SRS438196	SRR891271	14.692	1.506	-0.045	7.206	0.093	0.139	1.492
SRS438197_SRR891272_1	SRS438197	SRR891272	43.538	1.072	-0.176	2.397	0.320	0.292	0.913
SRS438198_SRR891273_1	SRS438198	SRR891273	28.939	1.501	-0.121	2.484	0.407	0.433	1.065
SRS438199_SRR891274_1	SRS438199	SRR891274	10.394	1.279	-0.107	3.995	0.569	0.572	1.004
SRS438200_SRR891275_1	SRS438200	SRR891275	29.353	2.297	0.139	11.315	0.019	0.036	1.857
SRS438201_SRR891276_1	SRS438201	SRR891276	28.213	1.970	0.116	11.238	0.026	0.044	1.662
SRS438202_SRR891277_1	SRS438202	SRR891277	59.693	5.540	0.374	9.420	0.014	0.013	0.907

Show

10

entries

< Previous

1

2

Next >

Showing 1 to 10 of 13 entries

Read Mapping Metrics

CSVEXCEL

Search:

Name	Sample	Library	Total reads	Properly paired and mapped (%)	Secondary (%)	Supplementary (%)	Duplicate (%)	Mean mapping quality	Median mapping quality
SRS438193_SRR891268_1	SRS438193	SRR891268	385,811,598	84.265	0.001	0	71.128	47.125	60
SRS438194_SRR891269_1	SRS438194	SRR891269	113,197,827	84.531	0.001	0	69.098	46.959	60
SRS438195_SRR891270_1	SRS438195	SRR891270	170,486,760	83.843	0.000	0	76.481	45.847	60
SRS438196_SRR891271_1	SRS438196	SRR891271	125,644,391	83.559	0.000	0	74.454	45.812	60
SRS438197_SRR891272_1	SRS438197	SRR891272	46,519,972	88.929	0.003	0	39.108	50.053	60
SRS438198_SRR891273_1	SRS438198	SRR891273	45,798,666	88.107	0.002	0	55.037	49.321	60
SRS438199_SRR891274_1	SRS438199	SRR891274	48,368,949	84.412	0.001	0	74.132	45.367	60
SRS438200_SRR891275_1	SRS438200	SRR891275	16,173,962	85.988	0.001	0	48.210	47.106	60
SRS438201_SRR891276_1	SRS438201	SRR891276	22,534,196	85.669	0.000	0	51.730	46.764	60



<https://parkerlab.github.io/ataqv/demo/>

Questions?

