

Supplementary Materials

Supplementary Tables

Supplementary Table 1: Mapping statistics for datasets in this study

Library	Raw frag- ments	Unique non-chrM reads	Unique non-chrM reads af- ter dedup	Complexity	chrM frac- tion	TSS ratio
SK-L001-GM12878-ATAC-1	25,204,077	39,693,750	33,191,786	0.79	0.22	9.23
SK-L002-GM12878-ATAC-2	21,019,294	32,301,936	24,852,942	0.70	0.32	12.80
SK-L005-GM12878-ATAC_Kethoxal-1	26,967,412	42,349,494	34,720,194	0.76	0.22	11.92
SK-L006-GM12878-ATAC_Kethoxal-2	28,083,530	43,996,380	35,745,648	0.75	0.23	12.35
SK-L007-GM12878- ATAC_Kethoxal_biotin_pulldown-1	30,391,595	48,649,648	3,367,986	0.06	0.24	9.84
SK-L008-GM12878- ATAC_Kethoxal_biotin_pulldown-2	36,320,602	58,638,602	3,595,220	0.05	0.25	8.92
SK-L009-GM12878- ATAC_Kethoxal_input-1	13,002,248	20,324,336	7,296,094	0.33	0.24	13.81
SK-L010-GM12878- ATAC_Kethoxal_input-2	11,984,129	18,941,686	8,168,106	0.40	0.22	11.07
SK-L011-HEK293T-ATAC_Kethoxal-1	12,576,111	19,216,260	14,670,352	0.69	0.41	15.20
SK-L012-HEK293T-ATAC_Kethoxal-2	13,567,064	20,905,448	16,161,544	0.70	0.40	14.42
SK-L013-HEK293T- ATAC_Kethoxal_with_biotin_enriched-1	46,013,562	72,318,598	12,153,228	0.14	0.39	11.95
SK-L014-HEK293T- ATAC_Kethoxal_with_biotin_enriched-2	61,750,300	97,499,704	13,715,198	0.12	0.39	11.04
SK-L015-HEK293T- ATAC_Kethoxal_pulldown_supernatant-1	11,382,288	17,461,940	13,582,016	0.70	0.40	15.20
SK-L016-HEK293T- ATAC_Kethoxal_pulldown_supernatant-2	7,632,787	11,717,616	9,312,228	0.72	0.41	14.96
SK-L017-HEK293T- ATAC_Kethoxal_input-1	6,738,330	10,606,360	8,108,918	0.69	0.36	15.09
SK-L018-HEK293T- ATAC_Kethoxal_input-2	7,382,103	11,648,988	8,897,006	0.70	0.35	13.88
SK-L019-HEK293T-ATAC-Kethoxal-1	5,662,131	7,893,954	5,029,326	0.56	0.52	16.02
SK-L020-HEK293T-ATAC-Kethoxal-2	9,081,011	12,362,796	6,974,112	0.49	0.54	15.36
SK-L024-HEK293T- Biotin_ATAC_600k_pulldown	224,738,071	310,871,120	27,191,952	0.07	0.52	17.25
SK-L025-HEK293T-KAS_ATAC- 600k_supernatant	17,108,823	23,408,630	12,589,982	0.46	0.53	23.35
SK-L027-HEK293T-KAS_ATAC- 600k_input	175,596,606	255,157,430	59,741,052	0.20	0.49	19.18
SK-L028-HEK293T-KAS_ATAC- 600k_Kethoxal_supernatant	35,921,381	50,662,014	28,053,546	0.48	0.52	18.66
SK-L029-HEK293T-KAS_ATAC- 600k_Kethoxal_pulldown	66,158,532	100,347,548	13,280,000	0.11	0.49	23.81

Supplementary Table 2: ENCODE accession IDs for TF ChIP-seq datasets used in this study

Cell line and TF	ENCODE ID
GM12878 ARID3A	ENCFF531CLQ
GM12878 ARNT	ENCFF596RIT
GM12878 ATF3	ENCFF882AEU
GM12878 ATF7	ENCFF277FJJ
GM12878 BACH1	ENCFF631RZH
GM12878 BATF	ENCFF728KFD
GM12878 BCL11A	ENCFF824QXX
GM12878 BHLHE40	ENCFF445XYV
GM12878 BRCA1	ENCFF303GOQ
GM12878 CBF3	ENCFF876CUT
GM12878 CEBPB	ENCFF864EON
GM12878 CEBPZ	ENCFF639KLW
GM12878 CREB1	ENCFF053UZX
GM12878 CREM	ENCFF294IGP
GM12878 CTCF	ENCFF796WRU
GM12878 CUX1	ENCFF451AII
GM12878 E2F4	ENCFF744QAC
GM12878 E2F8	ENCFF961ZFW
GM12878 E4F1	ENCFF855PXT
GM12878 EBF1	ENCFF895MHN
GM12878 EGR1	ENCFF612EIU
GM12878 ELF1	ENCFF146SYU
GM12878 ELK1	ENCFF164MPE
GM12878 ESRRA	ENCFF660PIB
GM12878 ETS1	ENCFF568AZT
GM12878 ETV6	ENCFF151UJT
GM12878 FOS	ENCFF571DGT
GM12878 FOXM1	ENCFF549GKZ
GM12878 GABPA	ENCFF093KLR
GM12878 HSF1	ENCFF663ODL
GM12878 IRF3	ENCFF785MSW
GM12878 IRF4	ENCFF113VGD
GM12878 IRF5	ENCFF478SRO
GM12878 JUNB	ENCFF912OPT
GM12878 JUND	ENCFF023QWA
GM12878 KLF5	ENCFF992IBT
GM12878 MAFK	ENCFF436SJS
GM12878 MAX	ENCFF361EVH
GM12878 MAZ	ENCFF250FJC
GM12878 MEF2A	ENCFF826GQU
GM12878 MEF2B	ENCFF884QQW
GM12878 MEF2C	ENCFF238UKB
GM12878 MXI1	ENCFF376AEL
GM12878 MYB	ENCFF705CGM
GM12878 MYC	ENCFF214XPD
GM12878 NFATC1	ENCFF172KBM
GM12878 NFATC3	ENCFF002XEC
GM12878 NFYA	ENCFF937QTP
GM12878 NFYB	ENCFF156MUM
GM12878 NR2C1	ENCFF626EEU
GM12878 NR2C2	ENCFF782KRV
GM12878 NR2F1	ENCFF118UKC
GM12878 NRF1	ENCFF864EBU

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Supplementary Table 2 – *Continued from previous page*

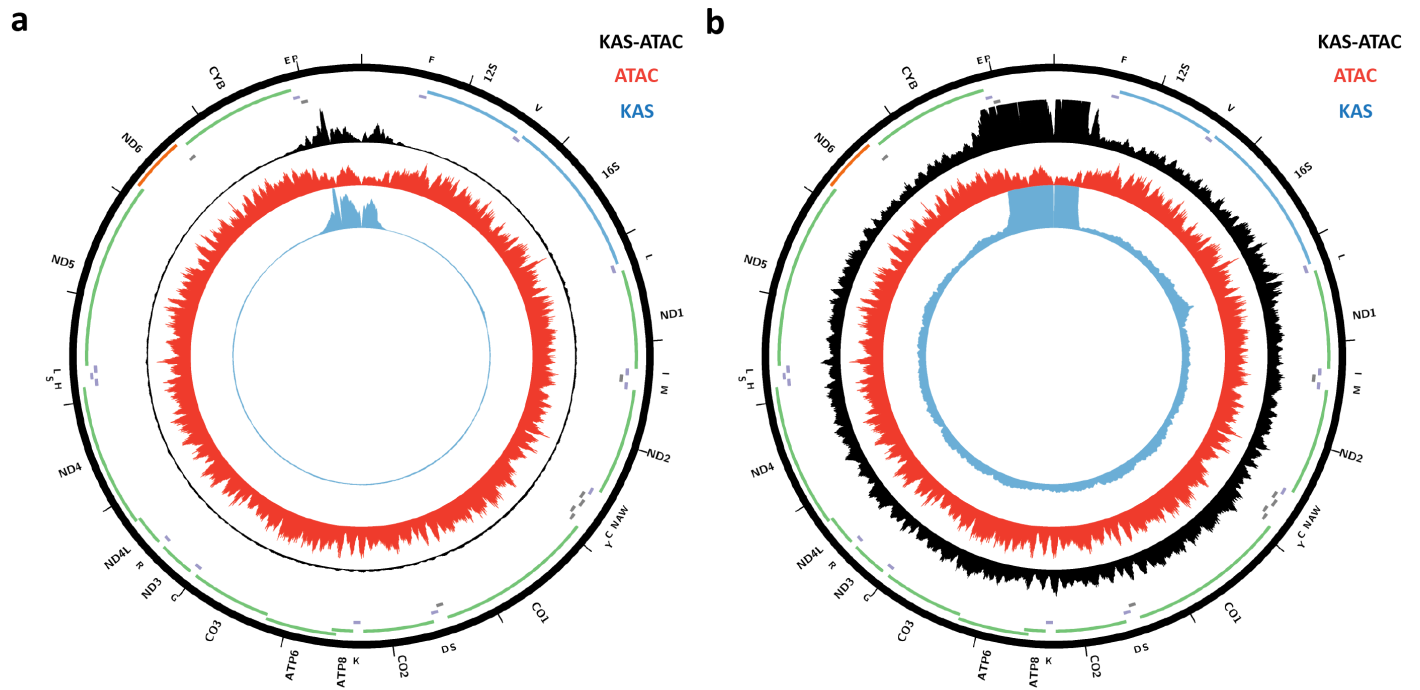
Cell line and TF	ENCODE ID
GM12878 PAX5	ENCFF192WNJ
GM12878 PAX8	ENCFF934NVD
GM12878 PBX3	ENCFF402DQD
GM12878 PKNOX1	ENCFF946JFA
GM12878 POU2F2	ENCFF934JFA
GM12878 RELA	ENCFF141SMI
GM12878 RELB	ENCFF968MBN
GM12878 REST	ENCFF262MRD
GM12878 RFX5	ENCFF601WHE
GM12878 RUNX3	ENCFF346JDW
GM12878 RXRA	ENCFF063KLF
GM12878 SIX5	ENCFF878FBM
GM12878 SMAD1	ENCFF033MGN
GM12878 SP1	ENCFF038AVV
GM12878 SPI1	ENCFF492ZRZ
GM12878 SREBF1	ENCFF397YRO
GM12878 SREBF2	ENCFF896MPE
GM12878 SRF	ENCFF089YRX
GM12878 STAT1	ENCFF896SEI
GM12878 STAT3	ENCFF029PAA
GM12878 STAT5A	ENCFF006GSY
GM12878 TBX21	ENCFF170IZO
GM12878 TCF12	ENCFF068YYR
GM12878 TCF3	ENCFF700TAS
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GM12878 USF2	ENCFF196JQW
GM12878 YBX1	ENCFF488IGF
GM12878 YY1	ENCFF258UEW
GM12878 ZBED1	ENCFF753UAX
GM12878 ZBTB33	ENCFF845VSZ
GM12878 ZBTB4	ENCFF880BEK
GM12878 ZEB1	ENCFF703XCL
GM12878 ZNF274	ENCFF034UEJ
GM12878 ZNF384	ENCFF955FRU
HEK293 BCL11A	ENCFF972WFM
HEK293 BCL6B	ENCFF884UOX
HEK293 CTCF	ENCFF071FSR
HEK293 EGR2	ENCFF501WRO
HEK293 ELK4	ENCFF226QHL
HEK293 GFI1B	ENCFF199YAZ
HEK293 GLI2	ENCFF576SDC
HEK293 GLIS1	ENCFF628APG
HEK293 GLIS2	ENCFF311QUH
HEK293 HIC1	ENCFF979QGX
HEK293 HOXA7	ENCFF521UKW
HEK293 HOXB7	ENCFF610SSK
HEK293 HOXC10	ENCFF722GPK
HEK293 HOXD13	ENCFF223BOC
HEK293 KLF16	ENCFF585OJO
HEK293 KLF1	ENCFF103JPK
HEK293 KLF8	ENCFF790TTV
HEK293 MAZ	ENCFF529XTF
HEK293 MEIS1	ENCFF628KKY

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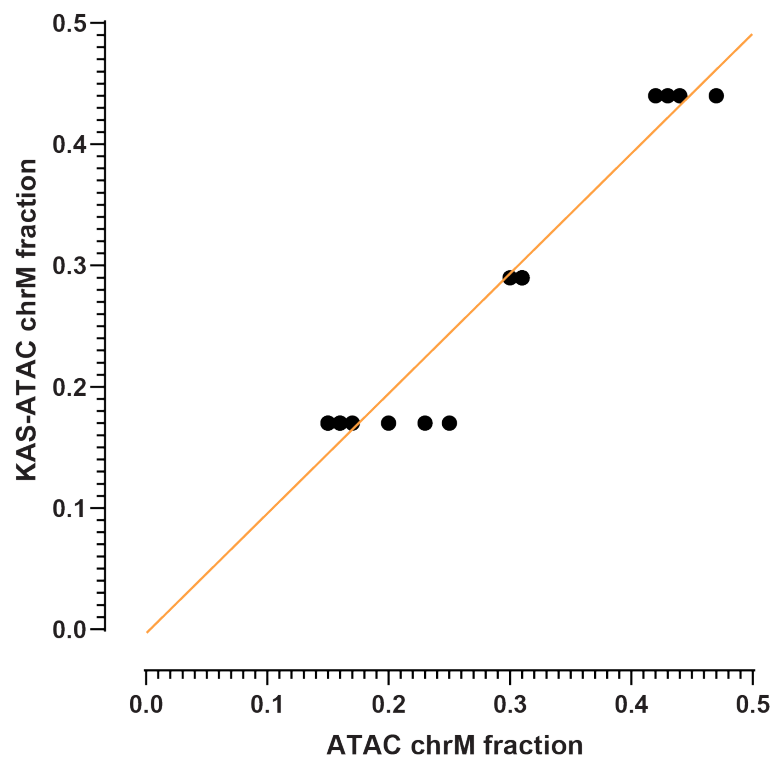
Supplementary Table 2 – *Continued from previous page*

Cell line and TF	ENCODE ID
HEK293 MZF1	ENCFF669FUB
HEK293 PBX3	ENCFF851ZEB
HEK293 PRDM1	ENCFF753PSU
HEK293 PRDM4	ENCFF351OYP
HEK293 REST	ENCFF437IAR
HEK293 SCRT1	ENCFF424QVD
HEK293 SCRT2	ENCFF916ITG
HEK293 SP2	ENCFF444VWF
HEK293 SP3	ENCFF663PCO
HEK293 TCF7L2	ENCFF136SOA
HEK293 WT1	ENCFF006ZKN
HEK293 YY1	ENCFF430PDB
HEK293 YY2	ENCFF755NLD
HEK293 ZBTB49	ENCFF066ZQN
HEK293 ZBTB6	ENCFF139IGE
HEK293 ZBTB7A	ENCFF114DGV
HEK293 ZEB1	ENCFF079WZH
HEK293 ZFHX2	ENCFF153XOB
HEK293 ZIC2	ENCFF359GIY
HEK293 ZNF148	ENCFF410SFG
HEK293 ZNF263	ENCFF108NXV
HEK293 ZNF274	ENCFF315BAF
HEK293 ZNF350	ENCFF064ZJO
HEK293 ZNF423	ENCFF222HPT
HEK293 ZSCAN16	ENCFF180POM
HEK293 ZSCAN4	ENCFF952OOU

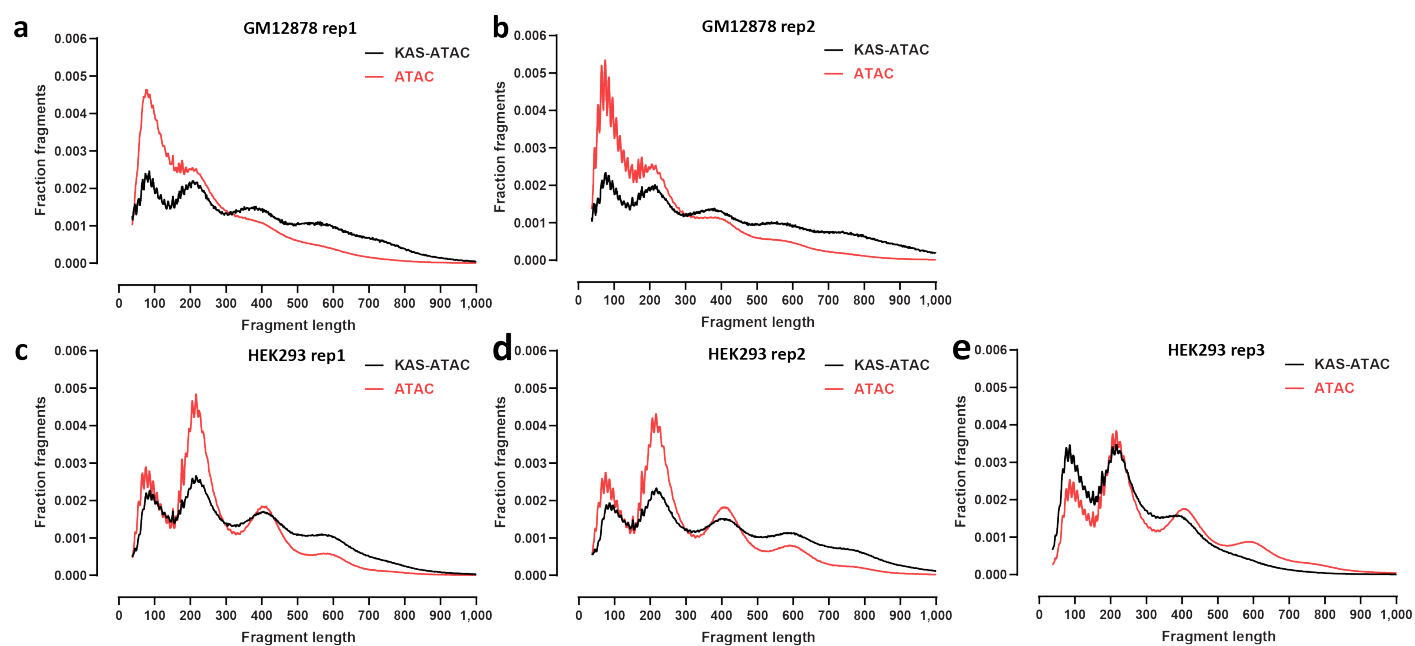
Supplementary Figures



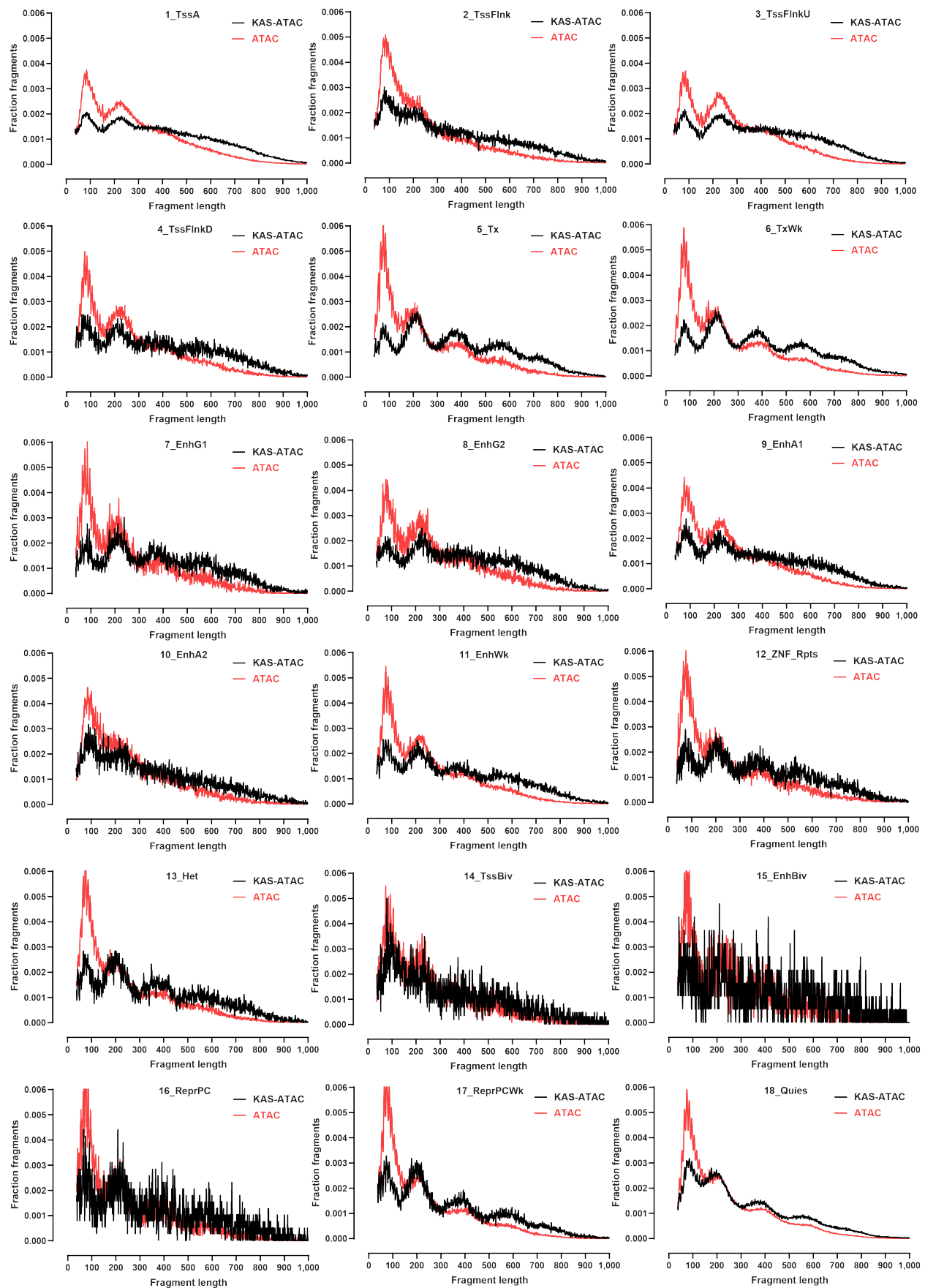
Supplementary Figure 1: KAS-seq, ATAC-seq, and KAS-ATAC mitochondrial genome profiles in human GM12878 cells. (a) Shown are KAS-seq, ATAC-seq, and KAS-ATAC mitochondrial genome profiles (b) Shown are KAS-seq, ATAC-seq, and KAS-ATAC mitochondrial genome profiles with signal capped so that differences outside the D-loop can be visualized.



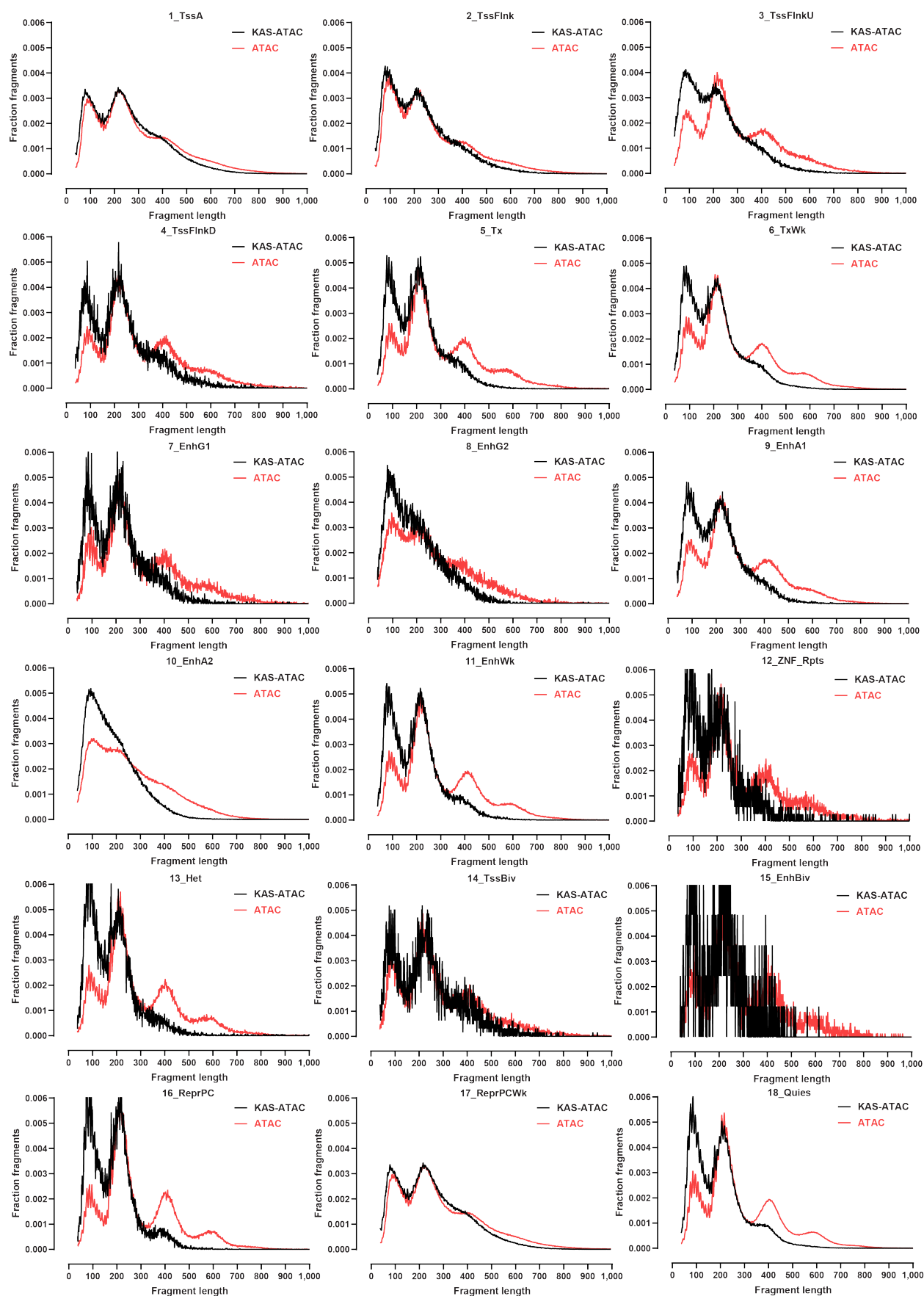
Supplementary Figure 2: Fraction of mitochondrial reads in ATAC-seq and KAS-ATAC libraries.



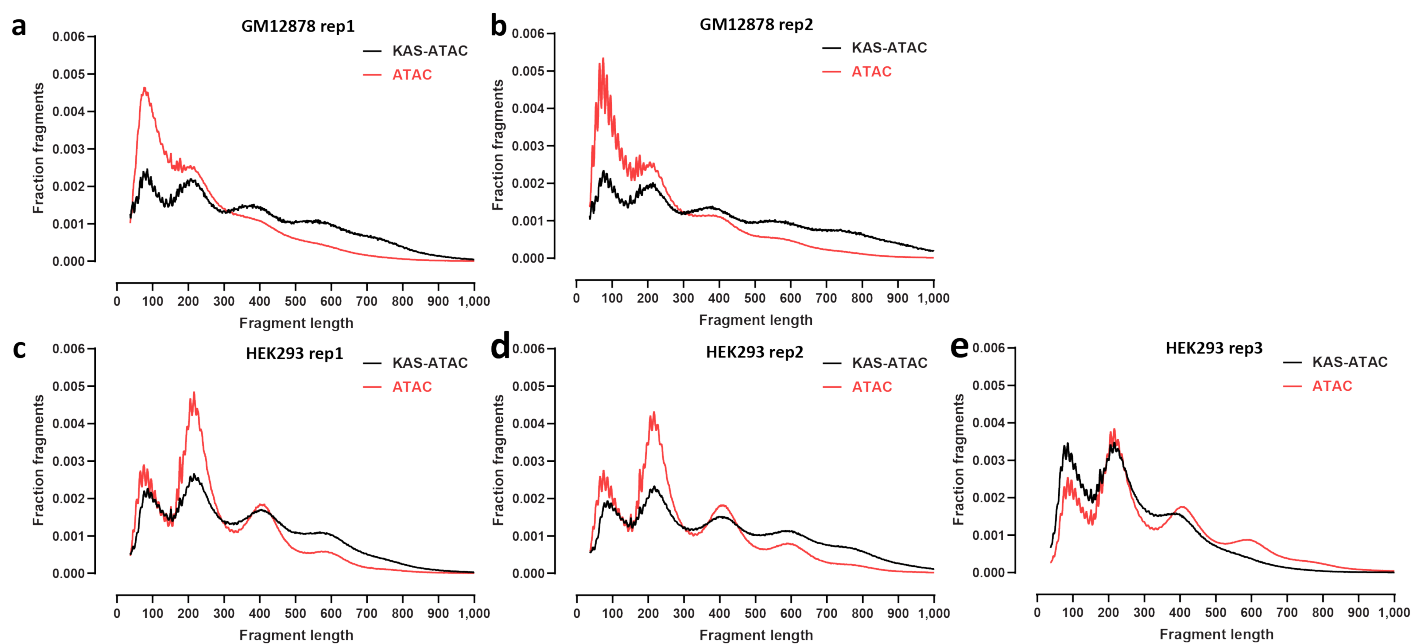
Supplementary Figure 3: Fragment length distribution in ATAC-seq and KAS-ATAC. (a) GM12878 cells, replicate 1; (b) GM12878 cells, replicate 2; (c) HEK293 cells, replicate 1; (d) HEK293 cells, replicate 2; (e) HEK293 cells, replicate 3.



Supplementary Figure 4: Distribution of KAS-ATAC and ATAC-seq fragment lengths in different chromatin states in GM12878 (replicate 1) cells.



Supplementary Figure 5: Distribution of KAS-ATAC and ATAC-seq fragment lengths in different chromatin states in HEK293 (replicate 3) cells.



Supplementary Figure 6: Genome-wide TSS metaprofiles for ATAC-seq and KAS-ATAC libraries. (a) GM12878 cells, replicate 1; (b) GM12878 cells, replicate 2; (c) HEK293 cells, replicate 1; (d) HEK293 cells, replicate 2; (e) HEK293 cells, replicate 3.

promoters

	GM12878-PRO-seq-GSM6603472	HEK293-PRO-seq-batch1-rep1-GSM4160108	HEK293-PRO-seq-batch1-rep2-GSM4160109	HEK293-PRO-seq-batch2-rep1-GSM4160114	HEK293-PRO-seq-batch2-rep2-GSM4160115	HEK293-PRO-seq-batch2-rep3-GSM4160116	GM12878 KAS-seq	HEK293-KAS-seq	GM12868-ATAC	GM12868-KAS-ATAC	HEK293-ATAC	HEK293-KAS-ATAC
GM12878-PRO-seq-GSM6603472	1.00	0.51	0.51	0.40	0.41	0.40	0.18	0.29	0.24	0.33	0.28	0.31
HEK293-PRO-seq-batch1-rep1-GSM4160108	0.51	1.00	0.99	0.90	0.87	0.89	0.21	0.32	0.31	0.29	0.45	0.38
HEK293-PRO-seq-batch1-rep2-GSM4160109	0.51	0.99	1.00	0.89	0.87	0.88	0.27	0.38	0.37	0.35	0.50	0.44
HEK293-PRO-seq-batch2-rep1-GSM4160114	0.40	0.90	0.89	1.00	0.98	0.99	0.38	0.45	0.43	0.41	0.57	0.50
HEK293-PRO-seq-batch2-rep2-GSM4160115	0.41	0.87	0.87	0.98	1.00	0.98	0.52	0.59	0.54	0.54	0.65	0.61
HEK293-PRO-seq-batch2-rep3-GSM4160116	0.40	0.89	0.88	0.99	0.98	1.00	0.40	0.47	0.44	0.43	0.58	0.51
GM12878 KAS-seq	0.18	0.21	0.27	0.38	0.52	0.40	1.00	0.97	0.88	0.96	0.80	0.90
HEK293-KAS-seq	0.29	0.32	0.38	0.45	0.59	0.47	0.97	1.00	0.88	0.96	0.83	0.93
GM12868-ATAC	0.24	0.31	0.37	0.43	0.54	0.44	0.88	0.88	1.00	0.94	0.94	0.95
GM12868-KAS-ATAC	0.33	0.29	0.35	0.41	0.54	0.43	0.96	0.96	0.94	1.00	0.87	0.95
HEK293-ATAC	0.28	0.45	0.50	0.57	0.65	0.58	0.80	0.83	0.94	0.87	1.00	0.94
HEK293-KAS-ATAC	0.31	0.38	0.44	0.50	0.61	0.51	0.90	0.93	0.95	0.95	0.94	1.00

enhancers

	GM12878-PRO-seq-GSM6603472	GM12878-KAS	GM12878-ATAC	GM12878-KAS-ATAC
GM12878-PRO-seq-GSM6603472	1.00	0.67	0.14	0.64
GM12878-KAS	0.67	1.00	0.27	0.80
GM12878-ATAC	0.14	0.27	1.00	0.45
GM12878-KAS-ATAC	0.64	0.80	0.45	1.00

enhancers

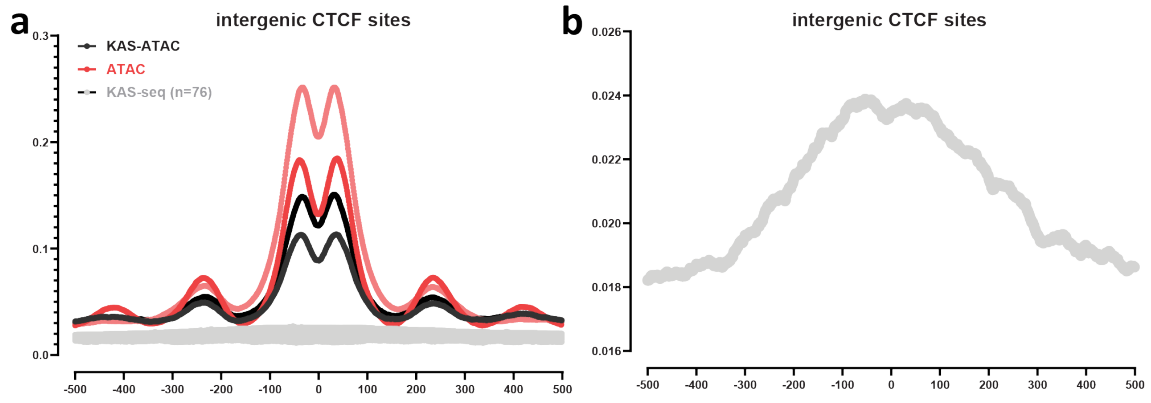
	HEK293-PRO-seq-batch1-rep1-GSM4160108	HEK293-PRO-seq-batch1-rep2-GSM4160109	HEK293-PRO-seq-batch2-rep1-GSM4160114	HEK293-PRO-seq-batch2-rep2-GSM4160115	HEK293-PRO-seq-batch2-rep3-GSM4160116	HEK293-KAS	HEK293-ATAC	HEK293-KAS-ATAC
HEK293-PRO-seq-batch1-rep1-GSM4160108	1.00	0.99	0.86	0.88	0.85	0.50	0.43	0.55
HEK293-PRO-seq-batch1-rep2-GSM4160109	0.99	1.00	0.87	0.89	0.86	0.47	0.44	0.53
HEK293-PRO-seq-batch2-rep1-GSM4160114	0.86	0.87	1.00	0.98	0.97	0.42	0.48	0.51
HEK293-PRO-seq-batch2-rep2-GSM4160115	0.88	0.89	0.98	1.00	0.98	0.46	0.46	0.52
HEK293-PRO-seq-batch2-rep3-GSM4160116	0.85	0.86	0.97	0.98	1.00	0.47	0.46	0.52
HEK293-KAS	0.50	0.47	0.42	0.46	0.47	1.00	0.27	0.71
HEK293-ATAC	0.43	0.44	0.48	0.46	0.46	0.27	1.00	0.61
HEK293-KAS-ATAC	0.55	0.53	0.51	0.52	0.52	0.71	0.61	1.00

Supplementary Figure 7: Correlation between KAS-seq, ATAC-seq, KAS-ATAC and PRO-seq datasets. Enhancer elements were defined as the outersection of ENCODE DNase peaks for each cell line (ENCODE ID ENCFF759OLD for GM12878 and ENCODE ID ENCFF285OXK for HEK293) and annotated TSSs (RefSeq). PRO-seq datasets were obtained from the indicated GEO accession IDs.

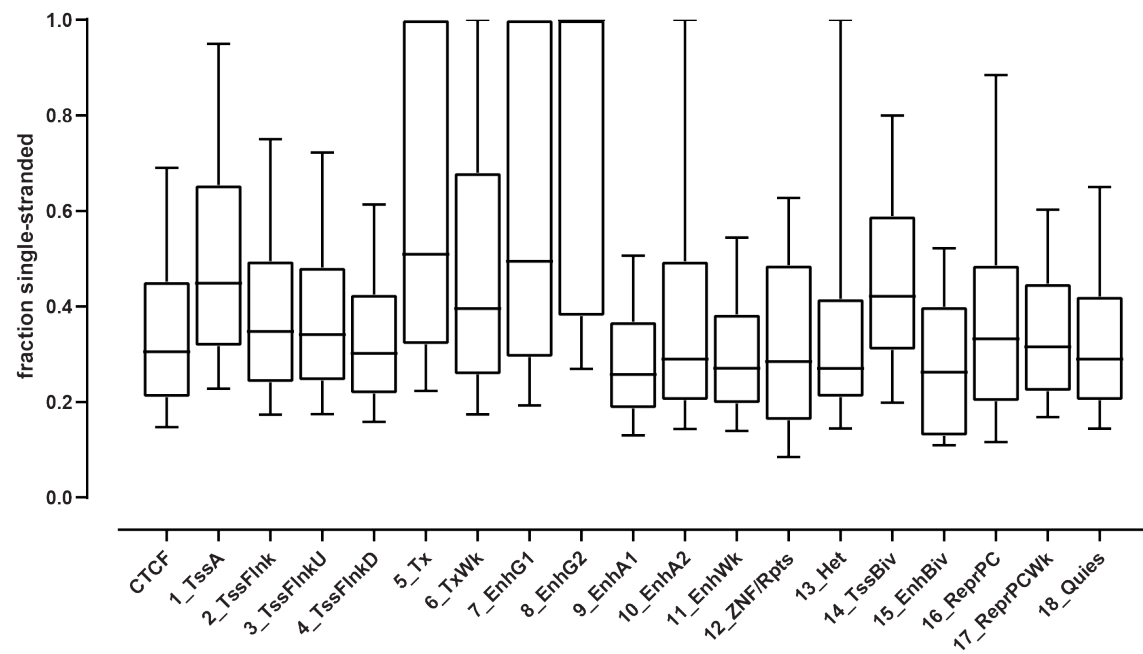
	GM12878-polyA-ENCSR843RJV-ENCFF700JWD	GM12878-polyA-ENCSR843RJV-ENCFF935TRK	GM12878-total-ENCSR820PHH-ENCFF345SHY	GM12878-total-ENCSR820PHH-ENCFF873VWU	ATAC	KAS	KAS-ATAC	PRO-seq
GM12878-polyA-ENCSR843RJV-ENCFF700JWD	1.00	0.97	0.93	0.93	0.45	0.42	0.43	0.42
GM12878-polyA-ENCSR843RJV-ENCFF935TRK	0.97	1.00	0.93	0.93	0.45	0.42	0.43	0.42
GM12878-total-ENCSR820PHH-ENCFF345SHY	0.93	0.93	1.00	0.98	0.48	0.45	0.46	0.45
GM12878-total-ENCSR820PHH-ENCFF873VWU	0.93	0.93	0.98	1.00	0.47	0.45	0.45	0.45
ATAC	0.45	0.45	0.48	0.47	1.00	0.95	0.95	0.90
KAS	0.42	0.42	0.45	0.45	0.95	1.00	0.98	0.95
KAS-ATAC	0.43	0.43	0.46	0.45	0.95	0.98	1.00	0.95
PRO-seq	0.42	0.42	0.45	0.45	0.90	0.95	0.95	1.00

Supplementary Figure 8: Comparison of Activity-By-Contact (ABC) modeling of promoter output using different data modalities. Shown are Spearman r correlation scores between ABC scores and RNA-seq output for GM12878 cells using ENCODE datasets (accession IDs for RNA-seq are indicated in the figure). ABC scores were calculated for each human gene following the previously described approach (Fulco et al. 2019) and using all ENCODE Hi-C datasets for GM12878 cells (accession IDs ENCFF194JDI, ENCFF955UVZ, ENCFF387IXM, ENCFF668TPL, ENCFF938ACB, ENCFF160PIP, ENCFF475GWB, ENCFF229MEW, ENCFF410FUO, ENCFF592GYT, ENCFF779SSO, ENCFF717LOV, ENCFF982XTF, ENCFF037PYX, ENCFF639IHA, ENCFF925SSJ, ENCFF005XHG, ENCFF457BVX, ENCFF131MFY, ENCFF512XPV, ENCFF837MNZ, ENCFF908NNJ, ENCFF558LDH, ENCFF558LDH, ENCFF991GHV, ENCFF075YWD, ENCFF290KPE, ENCFF930OVW, ENCFF515UDW, ENCFF916NSQ, ENCFF613NZE, ENCFF104TDF, ENCFF811VCC, ENCFF665QXT, ENCFF682LLL, ENCFF789MTX, ENCFF993IGW, ENCFF784LIP, ENCFF372XCU, ENCFF949VQC, ENCFF275RDF, ENCFF409YJA, ENCFF800UMS, ENCFF905EYO, ENCFF856SNL, ENCFF103ZBU, ENCFF064AOF, ENCFF693AYH, ENCFF825CNB, ENCFF825CNB, ENCFF591GZA, ENCFF361ECG, ENCFF625ZDB, ENCFF649NLE, ENCFF238SIE, ENCFF688XZY, ENCFF416CVP, ENCFF997OUB, ENCFF170SLP, ENCFF989YDB, ENCFF127QEU, ENCFF791APL, ENCFF572CHW, ENCFF346VTM, ENCFF690OEX, ENCFF360RWN, ENCFF849BZT, ENCFF610VEI, ENCFF748NRZ, ENCFF610VEI, ENCFF748NRZ, ENCFF847SEP, ENCFF568AYH, ENCFF149TDN, ENCFF871DEB, ENCFF814SHU, ENCFF907SUU, ENCFF659EAO, ENCFF677FWQ, ENCFF975DWR, ENCFF030WIP, ENCFF975DWR, ENCFF030WIP, ENCFF652INK, ENCFF551PHE, ENCFF021GFH, ENCFF931LZN, ENCFF377VFH, ENCFF779SSO, ENCFF717LOV, ENCFF982XTF, and ENCFF037PYX), which were processed separately and merged into a single map for maximum coverage using Jucor (Durand et al. 2016). ABC scores were calculated for each data modality for all elements within a radius of 2.5 Mbp of a gene promoter as $ABC(P_i) = \sum_j A(E_j) \times C(P_i, E_j)$ where

$A(E_j)$ is the ATAC/KAS/KAS-ATAC/PRO-seq signal at enhancer element E_j within the specified neighborhood of the promoter and $C(P_i, E_j)$ is the Hi-C interaction density between each enhancer E_j and the promoter P_i .



Supplementary Figure 9: KAS-seq, KAS-ATAC and KAS levels (normalized to RPM) around intergenic ($\geq 1,000$ bp away from genes) CTCF sites in HEK293 cells. (a) All three modalities. KAS-seq libraries used are from Marinov & Kim et al. 2023; (b) Representative KAS-seq dataset only.



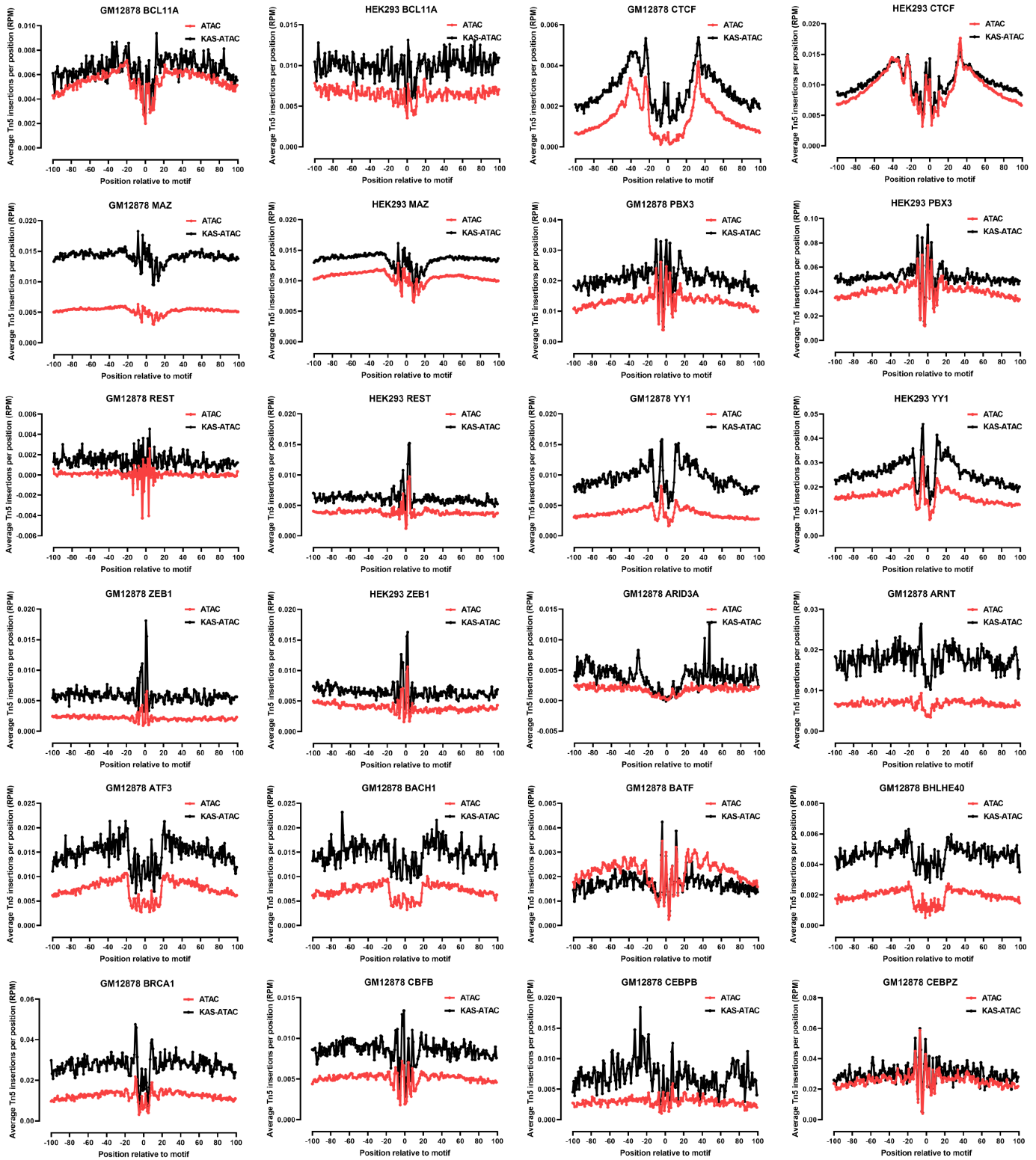
Supplementary Figure 10: Estimating absolute levels of single-stranded accessible DNA. Distribution of the ratios between the number of KAS-ATAC molecules and ATAC molecules for ATAC-seq peaks found in different chromatin states and for CTCF occupancy sites.

	ATAC	KAS-ATAC			
ARID3A-GM12878	0.12	0.11	NFYA-GM12878	0.33	0.31
ARNT-GM12878	0.27	0.29	NFYB-GM12878	0.35	0.33
ATF3-GM12878	0.21	0.24	NR2C1-GM12878	0.29	0.30
BACH1-GM12878	0.23	0.25	NR2C2-GM12878	0.26	0.28
BATF-GM12878	0.24	0.30	NR2F1-GM12878	0.30	0.31
BCL11A-GM12878	0.26	0.27	NRF1-GM12878	0.23	0.23
BCL11A-HEK293	0.26	0.26	PAX5-GM12878	0.35	0.34
BCL6B-HEK293	0.26	0.27	PAX8-GM12878	0.32	0.34
BHLHE40-GM12878	0.25	0.27	PBX3-GM12878	0.34	0.33
BRCA1-GM12878	0.28	0.27	PBX3-HEK293	0.33	0.31
CBFB-GM12878	0.27	0.27	PKNOX1-GM12878	0.31	0.31
CEBPB-GM12878	0.31	0.29	POU2F2-GM12878	0.25	0.25
CEBPZ-GM12878	0.33	0.31	PRDM1-HEK293	0.24	0.23
CREB1-GM12878	0.18	0.26	PRDM4-HEK293	0.27	0.27
CREM-GM12878	0.21	0.28	RELA-GM12878	0.23	0.28
CTCF-GM12878	0.21	0.24	RELB-GM12878	0.25	0.28
CTCF-HEK293	0.23	0.24	REST-GM12878	0.35	0.35
CUX1-GM12878	0.27	0.29	REST-HEK293	0.32	0.33
E2F4-GM12878	0.28	0.28	RFX5-GM12878	0.31	0.33
E2F8-GM12878	0.24	0.25	RUNX3-GM12878	0.27	0.26
E4F1-GM12878	0.15	0.24	RXRA-GM12878	0.30	0.39
EBF1-GM12878	0.27	0.30	SCRT1-HEK293	0.31	0.31
EGR1-GM12878	0.27	0.29	SCRT2-HEK293	0.29	0.30
EGR2-HEK293	0.29	0.27	SIX5-GM12878	0.33	0.32
ELF1-GM12878	0.30	0.29	SMAD1-GM12878	0.35	0.35
ELK1-GM12878	0.29	0.28	SP1-GM12878	0.26	0.28
ELK4-HEK293	0.28	0.27	SP2-HEK293	0.29	0.27
ESRRA-GM12878	0.33	0.34	SP3-HEK293	0.28	0.26
ETS1-GM12878	0.32	0.31	SPI1-GM12878	0.28	0.28
ETV6-GM12878	0.28	0.28	SREBF1-GM12878	0.32	0.34
FOS-GM12878	0.28	0.27	SREBF2-GM12878	0.36	0.33
FOXM1-GM12878	0.19	0.20	SRF-GM12878	0.32	0.28
GABPA-GM12878	0.29	0.28	STAT1-GM12878	0.22	0.23
GF11B-HEK293	0.27	0.27	STAT3-GM12878	0.26	0.27
GLI2-HEK293	0.41	0.57	STAT5A-GM12878	0.20	0.20
GLIS1-HEK293	0.28	0.27	TBX21-GM12878	0.33	0.31
GLIS2-HEK293	0.27	0.26	TCF12-GM12878	0.34	0.33
HIC1-HEK293	0.30	0.30	TCF3-GM12878	0.32	0.31
HOXA7-HEK293	0.64	0.62	TCF7-GM12878	0.29	0.27
HOXB7-HEK293	0.18	0.19	TCF7L2-HEK293	0.26	0.24
HOXC10-HEK293	0.20	0.19	USF1-GM12878	0.24	0.27
HOXD13-HEK293	0.26	0.23	USF2-GM12878	0.24	0.26
HSF1-GM12878	0.33	0.69	WT1-HEK293	0.29	0.28
IRF3-GM12878	0.23	0.21	YBX1-GM12878	0.30	0.36
IRF4-GM12878	0.25	0.28	YY1-GM12878	0.33	0.32
IRF5-GM12878	0.17	0.15	YY1-HEK293	0.30	0.33
JUNB-GM12878	0.29	0.35	YY2-HEK293	0.30	0.35
JUND-GM12878	0.27	0.33	ZBED1-GM12878	0.28	0.25
KLF16-HEK293	0.28	0.26	ZBTB33-GM12878	0.27	0.27
KLF1-HEK293	0.33	0.31	ZBTB49-HEK293	0.31	0.40
KLF5-GM12878	0.29	0.30	ZBTB4-GM12878	0.29	0.31
KLF8-HEK293	0.28	0.27	ZBTB6-HEK293	0.34	0.36
MAFK-GM12878	0.29	0.31	ZBTB7A-HEK293	0.28	0.27
MAX-GM12878	0.30	0.31	ZEB1-GM12878	0.31	0.32
MAZ-GM12878	0.26	0.27	ZEB1-HEK293	0.29	0.31
MAZ-HEK293	0.27	0.26	ZFHX2-HEK293	0.19	0.17
MEF2A-GM12878	0.21	0.20	ZIC2-HEK293	0.30	0.29
MEF2B-GM12878	0.21	0.20	ZNF148-HEK293	0.28	0.25
MEF2C-GM12878	0.21	0.19	ZNF263-HEK293	0.31	0.30
MEIS1-HEK293	0.25	0.26	ZNF274-GM12878	0.31	0.28
MXI1-GM12878	0.29	0.30	ZNF274-HEK293	0.32	0.27
MYB-GM12878	0.32	0.33	ZNF350-HEK293	0.29	0.29
MYC-GM12878	0.31	0.30	ZNF384-GM12878	0.19	0.19
MZF1-HEK293	0.29	0.29	ZNF423-HEK293	0.31	0.30
NFATC1-GM12878	0.19	0.20	ZSCAN16-HEK293	0.33	0.35
NFATC3-GM12878	0.20	0.20	ZSCAN4-HEK293	0.32	0.33

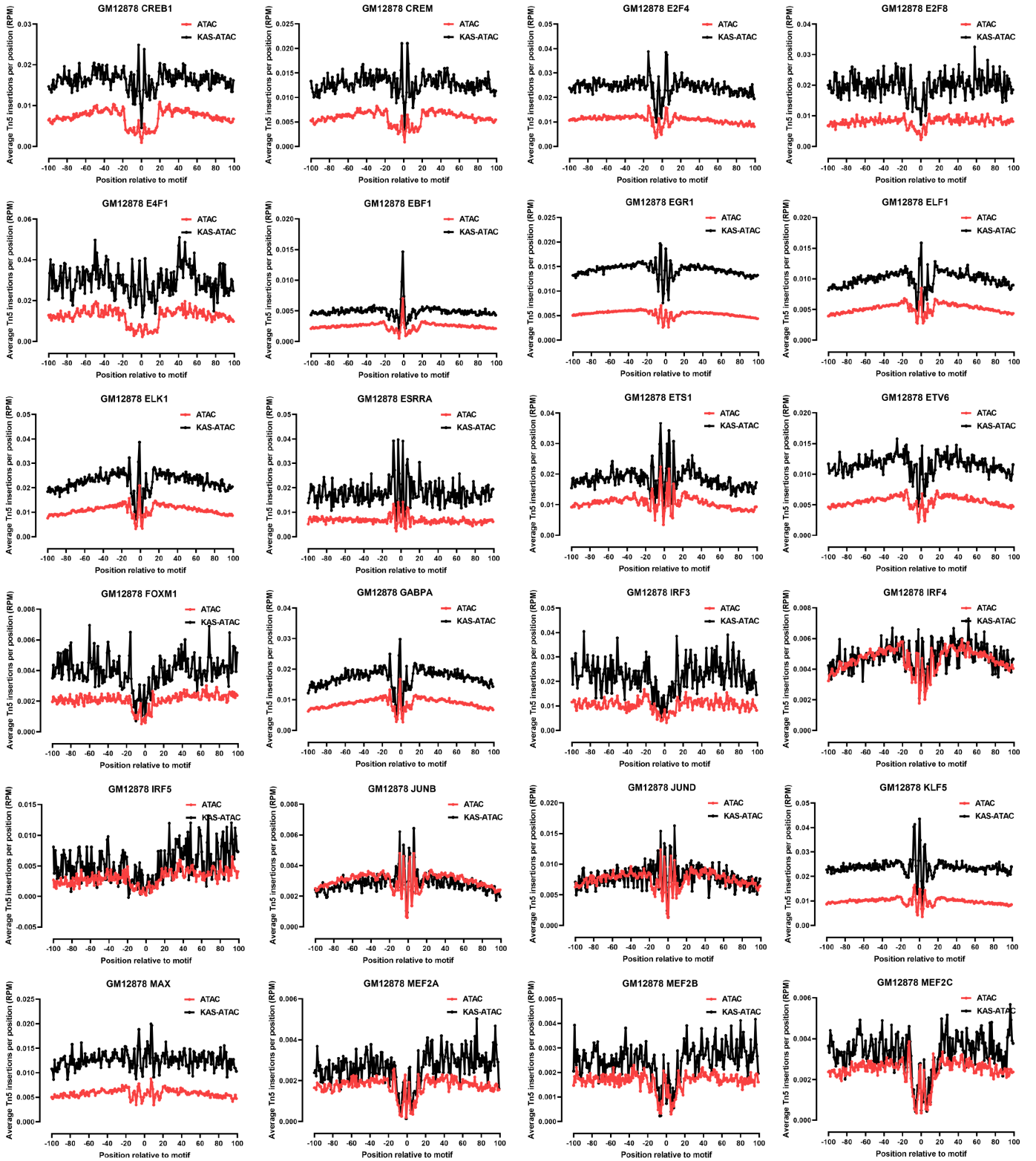
Supplementary Figure 11: Transcription factor footprint scores in KAS-ATAC and ATAC datasets. Footprint scores were calculated as

$$FPS = \frac{\sum_{i=a}^b C_i}{\sum_{i \leq c} C_i + \sum_{i \geq d} C_i}, \text{ where } C_i \text{ is}$$

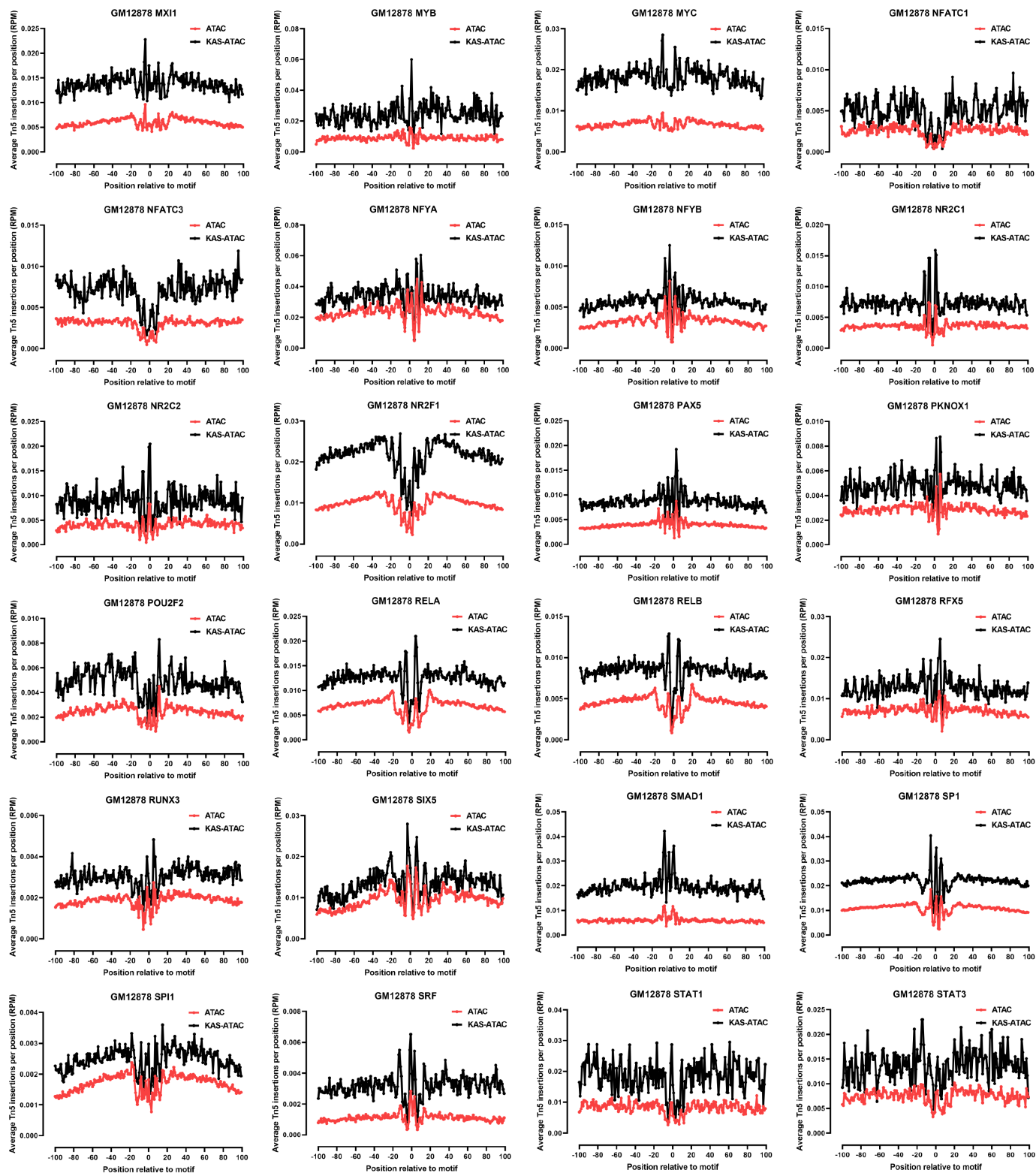
the coverage over a given position in the footprint metaprofile, and in this case $a = -20$, $b = +20$, $c = -30$, and $d = +30$.



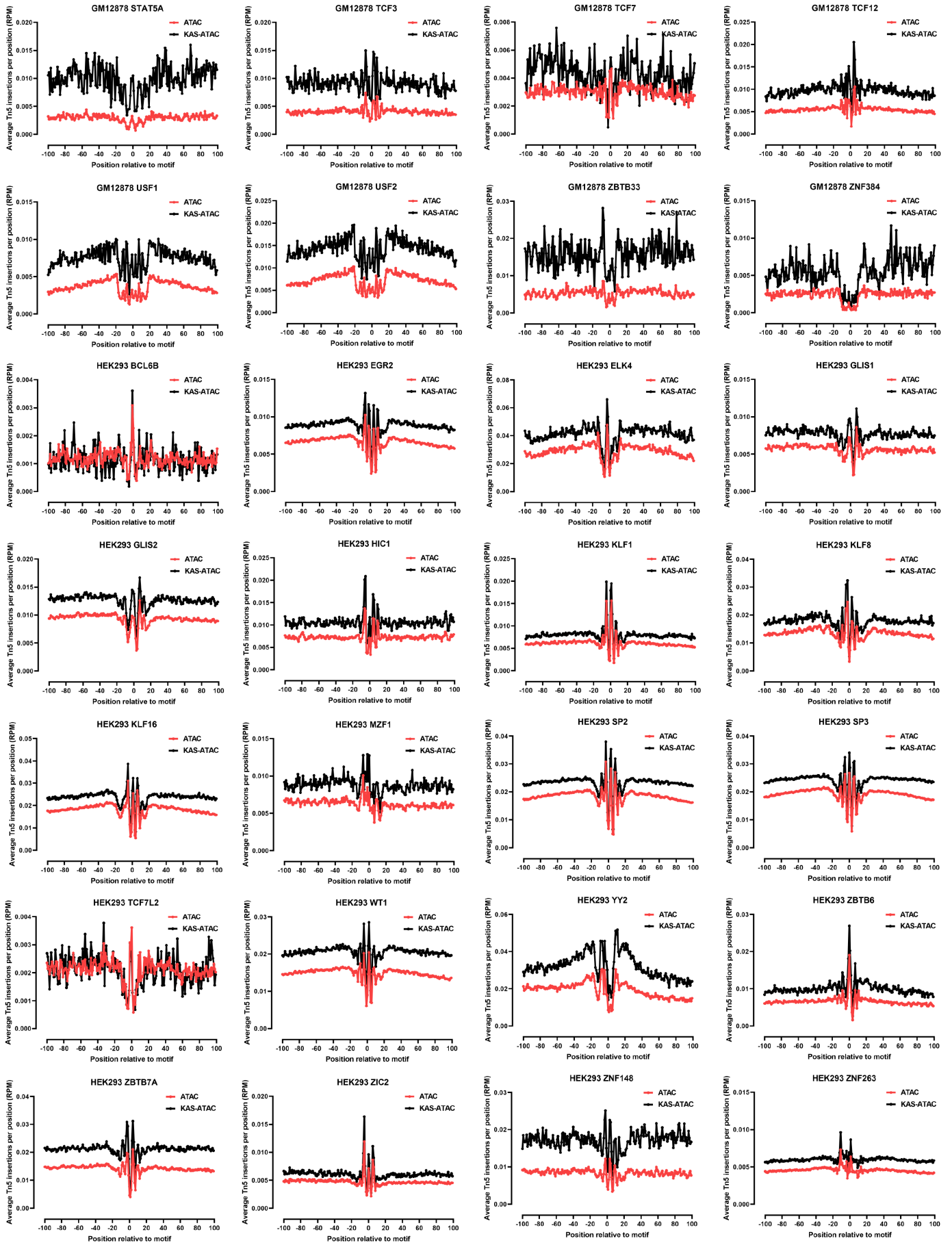
Supplementary Figure 12: Transcription factor footprints in KAS-ATAC and ATAC datasets. Shown are the average Tn5 insertion profiles (see Methods for details) around the motifs for the indicated factors that are located within ENCODE ChIP-seq peaks for the TF in the given cell line.



Supplementary Figure 13: Transcription factor footprints in KAS-ATAC and ATAC datasets. Shown are the average Tn5 insertion profiles (see Methods for details) around the motifs for the indicated factors that are located within ENCODE ChIP-seq peaks for the TF in the given cell line.



Supplementary Figure 14: Transcription factor footprints in KAS-ATAC and ATAC datasets. Shown are the average Tn5 insertion profiles (see Methods for details) around the motifs for the indicated factors that are located within ENCODE ChIP-seq peaks for the TF in the given cell line.



Supplementary Figure 15 (*preceding page*): Transcription factor footprints in KAS-ATAC and ATAC datasets. Shown are the average Tn5 insertion profiles (see Methods for details) around the motifs for the indicated factors that are located within ENCODE ChIP-seq peaks for the TF in the given cell line.