Glossary

Tab	Description
Samples & Antibodies	List of samples and antibodies used for CUT&RUN
Mapping & Peak Calling	Summary of read mapping, peak calling, and FRiP (Fraction of Reads in Peaks) score.
Summary Pearson's Correlation	Pearson correlation coefficients for the indicated sample comparisons.
Summary Consensus Peaks	Summary of the number of significant consensus peaks identified per condition.
Browser visualization	Visualization of HIF1 binding sites at some genes involved in proteoglycan and glycosaminoglycan pathways.

Antibodies for CUT&RUN

Target	Catalog Number	Lot No.	Company
HIF1A	GTX127309	44714	GeneTex
IgG (negative ctrl)	53180 (part of CUT&RUN assay kit)	24115219	Active Motif
H3K4me3 (positive ctrl)	53180 (part of CUT&RUN assay kit)	24115219	Active Motif

Cell lines used

Sample Name	Description
NA	Non acidic - control for AA
AA	Acidic adapted
CtrlSF	Control for DMOG- and TGFB-treated
DMOG	DMOG-treated
TGFB	TGFb-treated

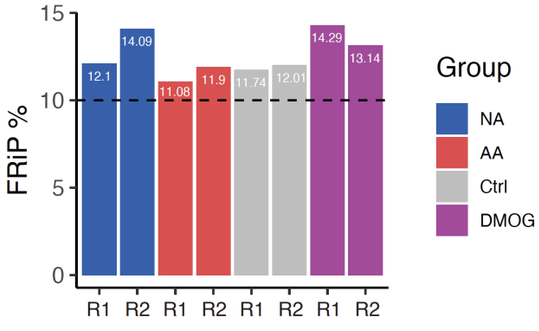
Replicates
R1: Replicate 1
R2: Replicate 2

CUT&RUN

Number of sequencing reads, mapped reads, called peaks and FRiP score

sampleName	sample name with R1 and R2 ending denoting replicate 1 and 2
total PE reads	Total sequencing read pairs obtained
% mapping (hg38)	Percentage of total aligned reads recorded by Bowtie2 to GRCh38.p14 genome (Gencode v47)
% mapping (dmel)	Percentage of total aligned reads recorded by Bowtie2 to dmel genome (Flybase: dmel_r6.62_FB2025_01)
	calculated as the ratio of aligned reads to Drosophila melanopgaster in sample vs reads
	aligned to Drosophila melanogaster in IgG control, to scale genome coverage for hg38
Scaling factor	alignment for peak calling with SEACR
FRiP	Percentage of fraction of reads in Peaks assesed by Subread FeatureCounts
Called Peaks	Number of significantly called peaks using SEACR with on scaled bedGraphs parameters: norm 0.01 stringent

sampleName	total PE reads	% mapping (hg38)	% mapping (dmel)	Scaling factor	FrIP	CalledPeaks
AA_HIF1A_R1	34 679 573	81,42	3,73	0,2	11,08	57779
AA_HIF1A_R2	31 649 960	88,39	6,35	0,3	11,90	50337
NA_HIF1A_R1	21 175 964	83,86	7,65	0,3	12,10	42708
NA_HIF1A_R2	56 525 036	84,55	15,45	1,0	14,09	47917
NA_IgG	25 421 838	72,25	24,07	1,0		
Ctrl_HIF1A_R1	21 188 863	64,79	10,69	1,0	11,74	36487
Ctrl_HIF1A_R2	16 860 777	64,53	12,36	1,0	12,01	26928
Ctrl_IgG	17 889 173	64,93	9,79	1,0		
Ctrl_H3K4me3	50 104 386	73,22	26,78	1,0	19,12	42706
DMOG_HIF1A_R1	29 124 642	83,02	11,45	1,0	14,29	39586
DMOG_HIF1A_R2	24 134 702	79,32	14,67	1,0	13,14	30878

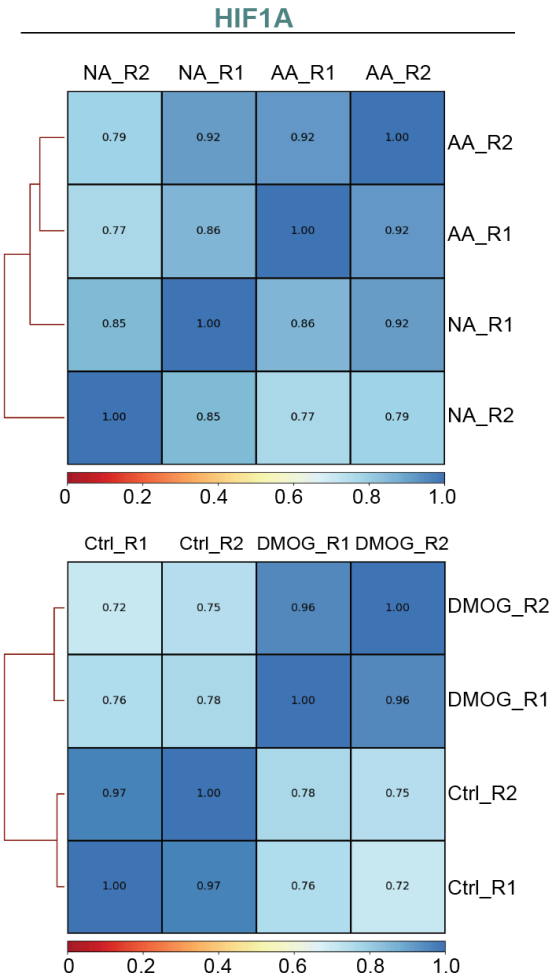


Pearson's correlation analysis

Reads Per Genomic Content (RPGC)-normalized genome coverage files were scaled using a spike-in normalized scaling factor.

Pearson correlation coefficients were calculated for NA vs. AA samples (Fig. 2 N–Q) and Ctrl vs. DMOG (Fig. S5 J–N) using deepTools v3.5.5 over normalized, scaled signal genomic coverage.

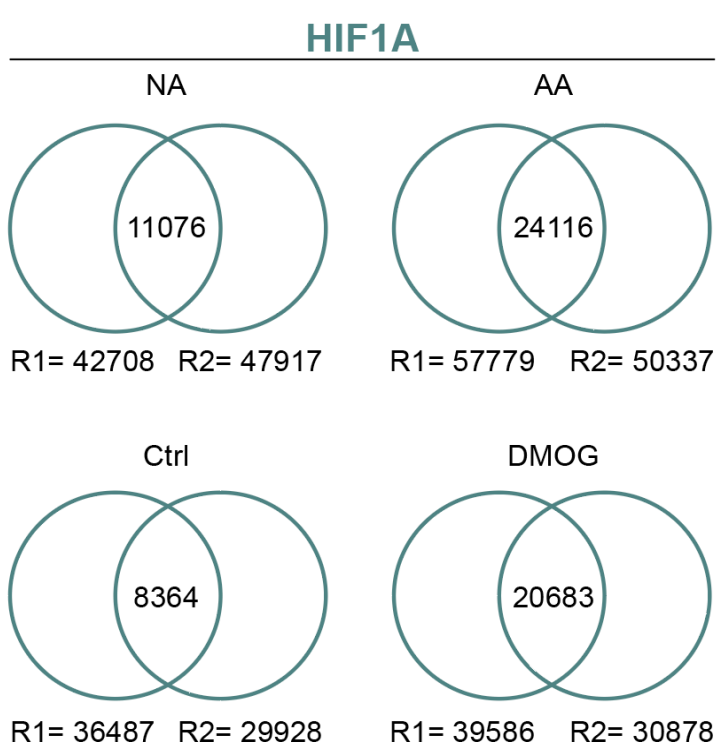
The numbers in the boxes represent the correlation coefficients between the samples in the corresponding rows and columns. "_R1" and "_R2" denote replicates 1 and 2, respectively, for each comparison.



Consensus Peak analysis

sampleName	Name of the sample, with "_R1" and "_R2" indicating replicate 1 and replicate 2, respectively.
consensus Peaks	Peaks called by SEACR (FDR 0.01) that are present in both replicates. Peaks were identified independently in each replicate using SEACR at FDR 0.01, and overlapping peaks between replicates were determined using the findOverlapOfPeaks function from the R package ChIPpeakAnno (Bioconductor v3.20).

sampleName	consensus Peaks
AA_HIF1A_R1	
AA_HIF1A_R2	24116
NA_HIF1A_R1	
NA_HIF1A_R2	11076
Ctrl_HIF1A_R1	
Ctrl_HIF1A_R2	8364
DMOG_HIF1A_R1	
DMOG_HIF1A_R2	20683



Browser view

A,B and C Visualization of HIF1 binding sites at the *GPC5* , *SULF2* , and *VCAN* loci under NA and AA conditions.

D,E, and F Visualization of HIF1 binding sites at the *DSE* , *DSEL* , and *EXT1* loci under Ctrl and DMOG conditions.