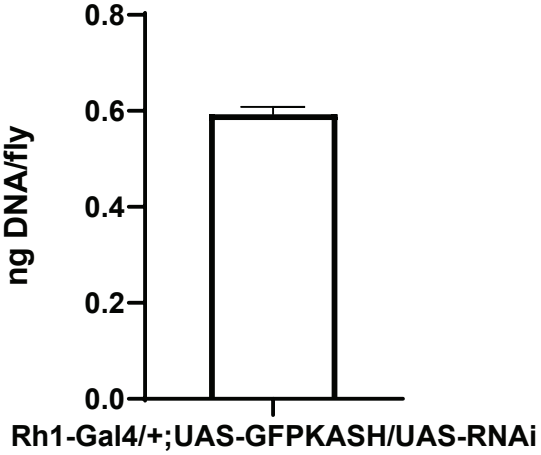
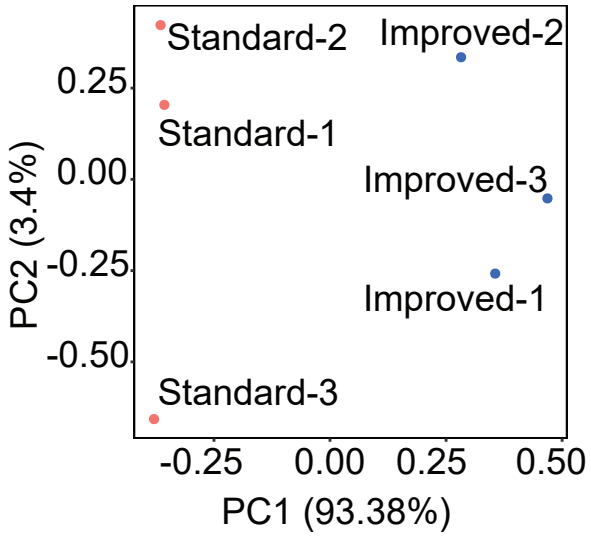
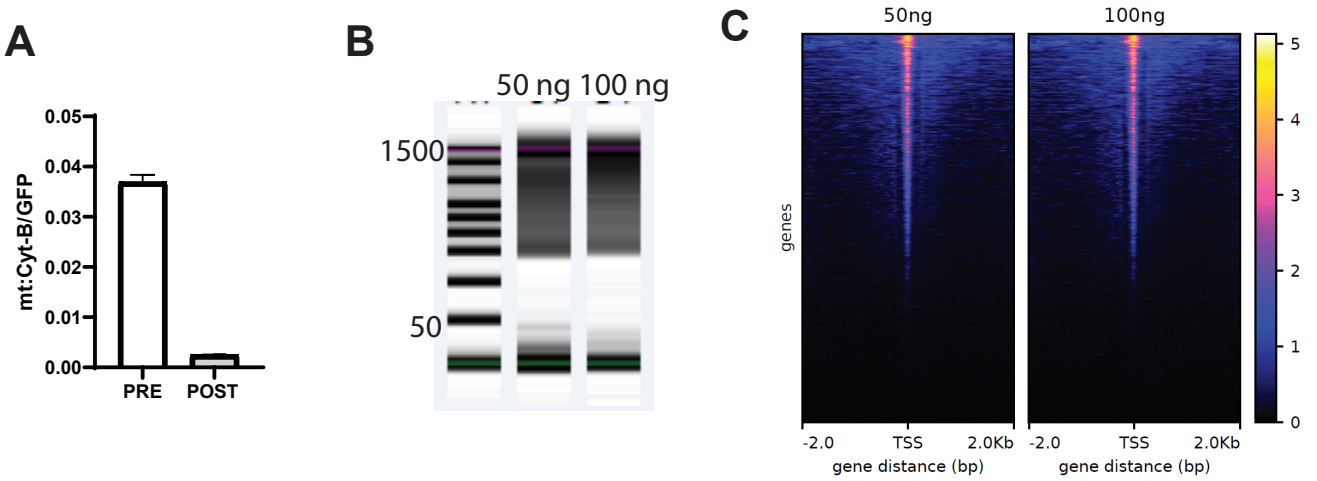

0.8
0.6
0.4
0.2
0.0
ng DNA/fly
Rh1-Gal4/+;UAS-GFPKASH/UAS-RNAi

A


Standard-2
Improved-2
Standard-1
Improved-3
Improved-1
Standard-3
0.25
0.00
-0.25
-0.50
PC2 (3.4%)
-0.25
0.00
0.25
0.50
PC1 (93.38%)

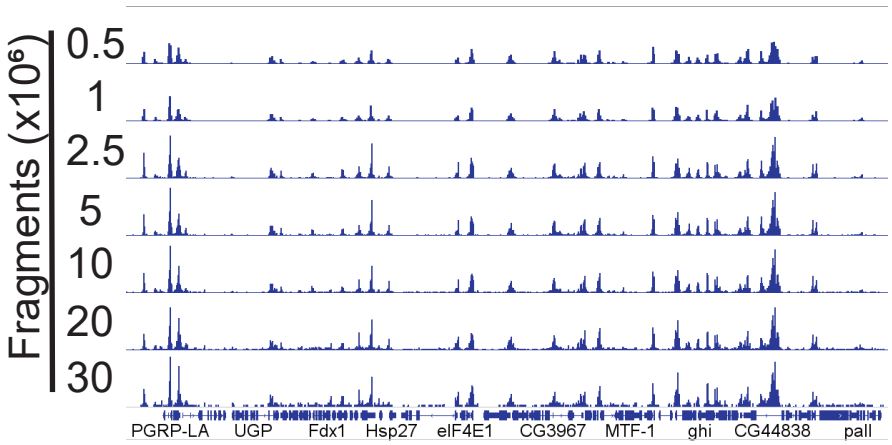

A
mt:Cyt-B/GFP
0.05
0.04
0.03
0.02
0.01
0.00
PRE
POST
B
50 ng 100 ng
1500
50
C
50ng
100ng
genes
-2.0
TSS
2.0Kb
gene distance (bp)
-2.0
TSS
2.0Kb
gene distance (bp)
5
4
3
2
1
0

A

peaks passing IDR < 0.05

R1	R2	R3	R4	
1.00	0.70	0.77	0.76	R1
	1.00	0.61	0.65	R2
		1.00	0.66	R3
			1.00	R4

B



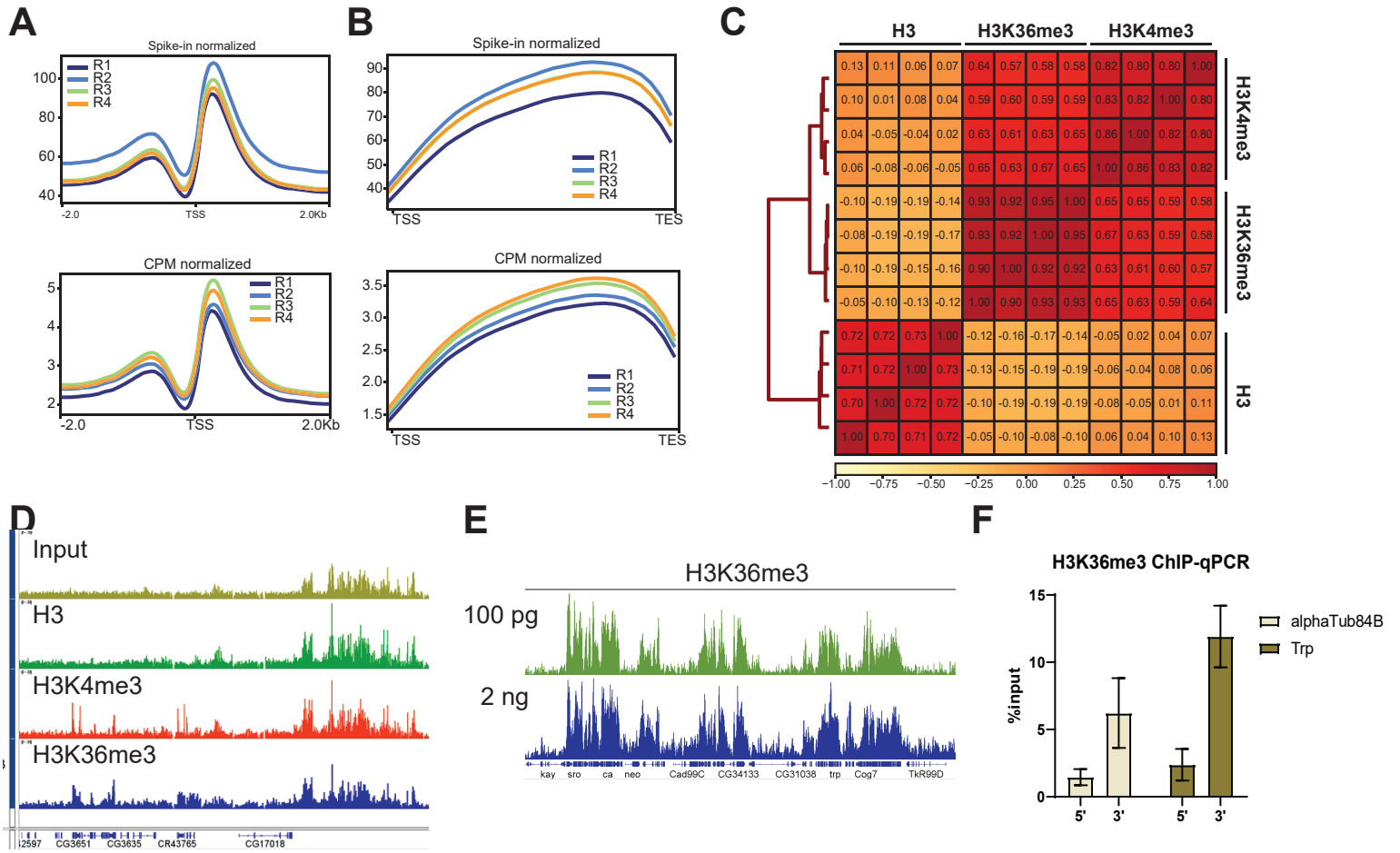

A
Spike-in normalized
R1
R2
R3
R4
100
80
60
40
-2.0
TSS
2.0Kb
CPM normalized
5
4
3
2
B
Spike-in normalized
90
80
70
60
50
40
TSS
TES
CPM normalized
3.5
3.0
2.5
2.0
1.5
C
H3
H3K36me3
H3K4me3
H3K4me3
H3K36me3
H3
−1.00
−0.75
−0.50
−0.25
0.00
0.25
0.50
0.75
1.00
D
Input
H3
H3K4me3
H3K36me3
CG3651
CG3635
CR43765
CG17018
E
H3K36me3
100 pg
2 ng
kay
sro
ca
neo
Cad99C
CG34133
CG31038
trp
Cog7
TkR99D
F
H3K36me3 ChIP-qPCR
%Input
15
10
5
0
5'
3'
5'
3'
alphaTub84B
Trp

Figure Supplemental legends

Figure Supplemental 1

Bar plot showing DNA yields when the “improved” NIE approach is used with flies heterozygous for both Rh1-Gal4 and UAS-GFP^{KASH} transgenes (mean ± standard deviation (SD), n=4)

Figure Supplemental 2.

Principal Component Analysis (PCA) of gene counts for RNA-seq data comparing the ‘standard’ and ‘improved’ datasets.

Figure Supplemental 3

A. Bar plot showing qPCR enrichment for GFP and mitochondrial DNA (mt:Cyt-B) in the PRE and POST-NIE. (Mean ± SD; n=3). B. Tapestation profiles of Omni-ATAC libraries prepared using 50 ng and 100 ng datasets. C. Heatmaps showing CPM-normalized Omni-ATAC signal for 50 ng- and 100 ng-associated datasets.

Figure Supplemental 4.

A. Pair-wise comparison of irreproducible discovery rate (IDR) values of peaks that pass the 0.05 threshold. B. Genome browser inspection of down-sampled CPM-normalized Omni-ATAC signal used for FRiP score analysis. Genes are shown in blue.

Figure Supplemental 5.

A. H3K4me3 Metaplots of Spike-in (top) and CPM normalized (bottom) data. B. H3K36me3 Metaplots of Spike-in (top) and CPM normalized (bottom) data. C. Spearman correlation heatmap of input-normalized ChIP-seq data comparing samples based on used antibody for each ChIP reaction. Spearman’s rank scores are based on read distribution over binned genome. D. Genome browser inspection of CPM-

normalized Input (Dark yellow), H3 (Green), H3K4me3 (Red) and H3K36me3 (blue) signal. E. Genome browser inspection of CPM-normalized H3K36me3 signal comparing libraries made with 100 pg or 2 ng of DNA as starting material. F. Bar plot showing H3K36me3 ChIP-qPCR enrichment as percentage chromatin input at the 5' and 3' ends of the housekeeping gene α*Tub84B* and the photoreceptor-specific gene *trp* (mean ± SD, n-3).