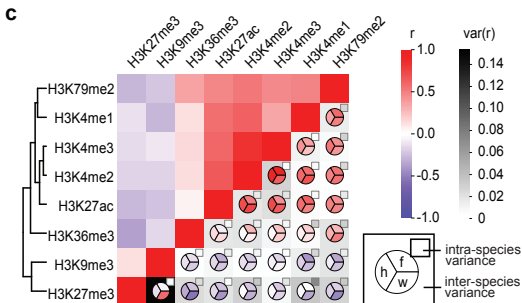
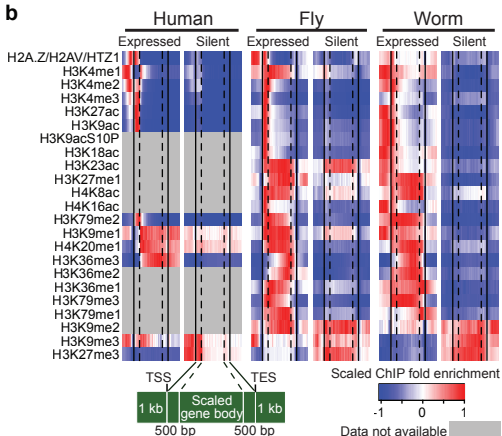
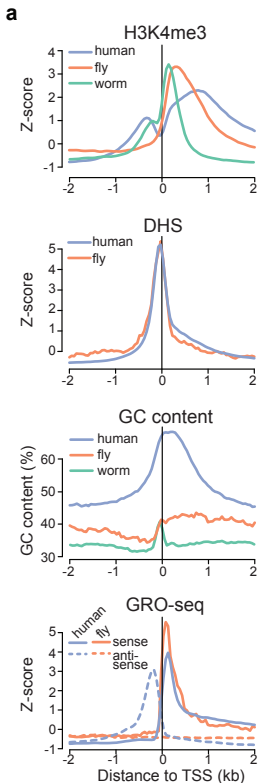


Chromatin features	Human	Fly	Worm	Figures
Promoters				
H3K4me3 enrichment pattern around TSS	Bimodal peak	Unimodal peak*	Weak bimodal peak	ED1a,b,S12
Well positioned +1 nucleosome at expressed genes	Yes	Yes	Yes	S13
Gene bodies				
Lower H3K36me3 in specifically expressed genes	Yes	Yes	Yes	S21-S23
Enhancers				
High H3K27ac sites are closer to expressed genes	Yes	Yes	Yes	S5-6
Higher nucleosome turnover at high H3K27ac sites	Yes	Yes	ND	S7
Nucleosome positioning				
10-bp periodicity profile	Yes	Yes	Yes	S19a
Positioning signal in genome	Weak	Weak	Less weak	S19b
LADs				
Histone modification in short LADs	H3K27me3	H3K27me3	H3K27me3	S17
Histone modification in long LADs	H3K9me3 internal, H3K27me3 borders	ND	H3K9me3 +H3K27me3	S15
Associated with late replication in S-phase	Yes	Yes	ND	S18
Genome-wide correlation				
Correlation between H3K27me3 and H3K9me3	Low	Low	High (in arms)	ED1c,ED3a
Chromatin state maps				
Similar marks and genomic features at each state	Yes	Yes	Yes	2,S29-32
Silent domains: constitutive heterochromatin				
Composition	H3K9me3	H3K9me3	H3K9me3 +H3K27me3	2,ED3b
Predominant location	Pericentric+chrY	Pericentric+chr4/Y	Arms	3a,ED3b
Depletion of H3K9me3 at TSS of expressed genes	Yes	Yes	Weak	ED2c
Silent domains: Polycomb-associated				
Composition	H3K27me3	H3K27me3	H3K27me3	2
Predominant location	Arms	Arms+Chr4	Arms+Centers	3a,ED3b
Topological domains				
Active promoters enriched at boundaries	Yes	Yes	ND	S38
Similar chromatin states are enriched in each domain	Yes	Yes	ND	S39

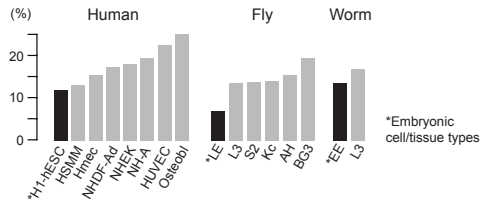
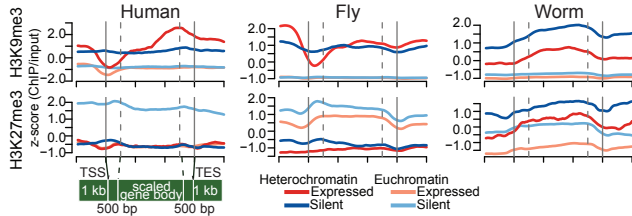
*Unimodal peak enriched downstream of TSS

ND: No Data



a

H3K9me3 coverage in mappable regions (%)

**c****b**