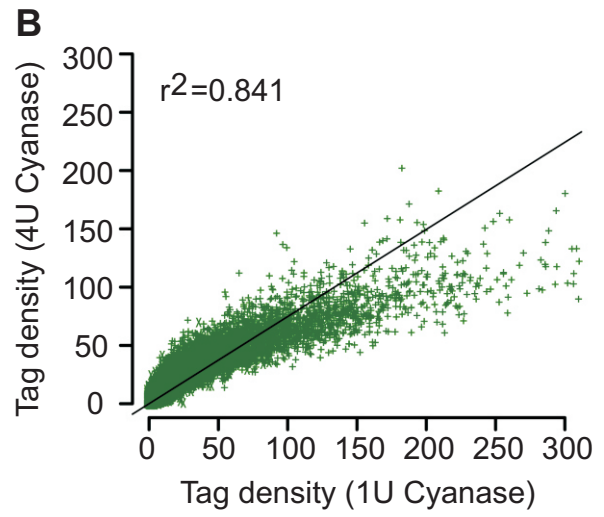
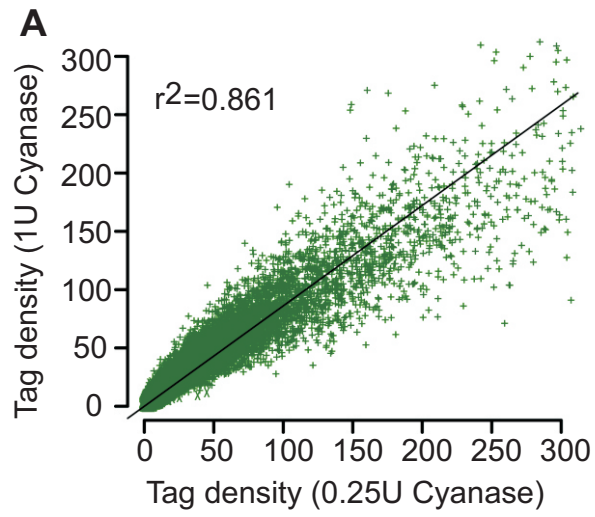


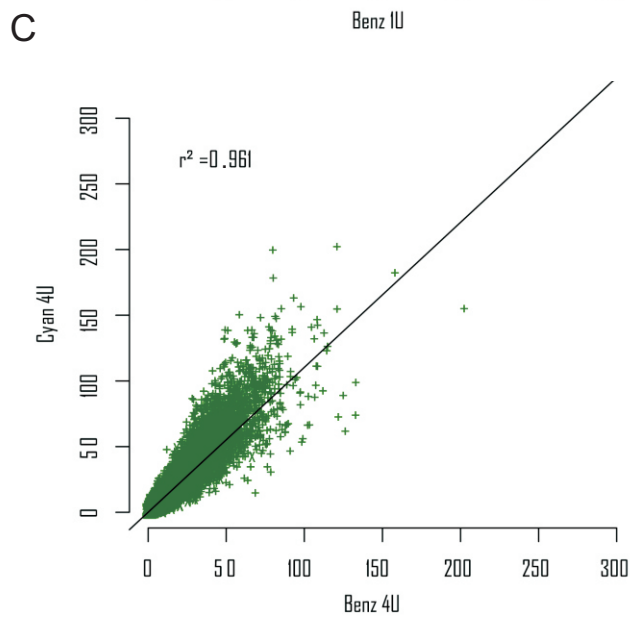
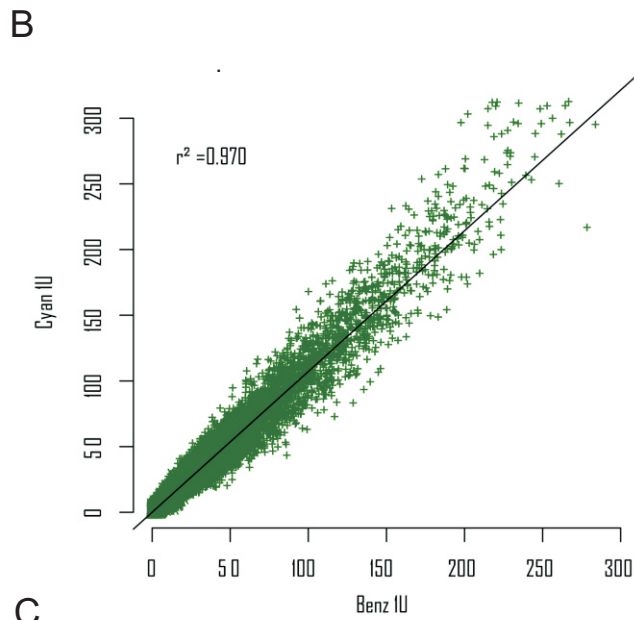
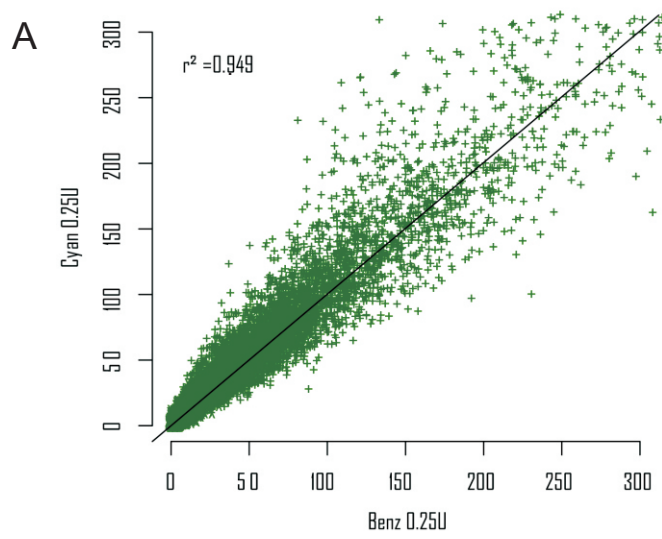
Grontved_Supplementary_Fig1

Sample	Aligned tags (millions)	Aligned tags to mito genome (millions)
DNase I (rep1)	27.8	0.33
DNase I (rep 2)	27.0	0.44
Benzonase 0.25U/ml	21.7	3.52
Benzonase 1U/ml	22.3	4.21
Benzonase 4U/ml	23.4	3.98
Cyanase 0.25U/ml	17.1	3.83
Cyanase 1U/ml	20.7	4.91
Cyanase 4U/ml	23.9	6.43

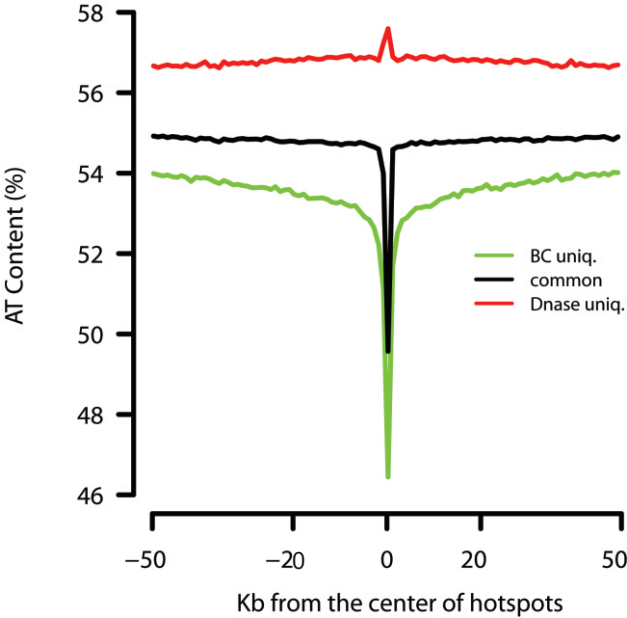
Grontved_Supplementary_Fig2



Grontved_Supplementary_Fig3



Grontved_Supplementary_Fig4



Supplementary figure legends_Grontved et al

Supplementary figure 1. Aligned tags from DNase I, Benzonase and Cyanase digestions of chromatin from nuclei and frozen mouse liver tissue. Tags were aligned to mm9 and to the mitochondrial (mito) genome.

Supplementary figure 2. Scatter plot of hotspot tag density from liver tissue digested with Cyanase. (A) 0.25U/ml vs. 1U/ml. (B) 1U/ml vs. 4U/ml.

Supplementary figure 3. Scatter plot of hotspot tag density from liver tissue digested with different concentrations of Benzonase and Cyanase. (A) 0.25U/ml Benzonase vs. Cyanase. (B) 1U/ml Benzonase vs. Cyanase. (C) 4U/ml Benzonase vs. Cyanase.

Supplementary figure 4. Distribution of AT percentage surrounding DNase I/Benzonase/Cyanase (common), DNase I unique and Benzonase/Cyanase unique hotspots.