

DNAaseI hypersensitive sites (DHSs): “The accessible Chromatin Landscape of the Human Genome”

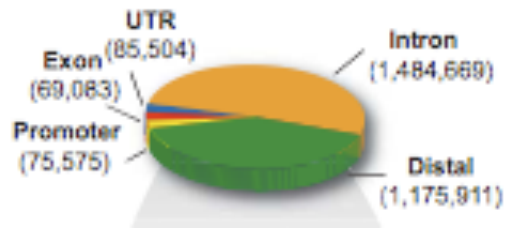
Thurman et al, submitted to Nature

Summary by EK

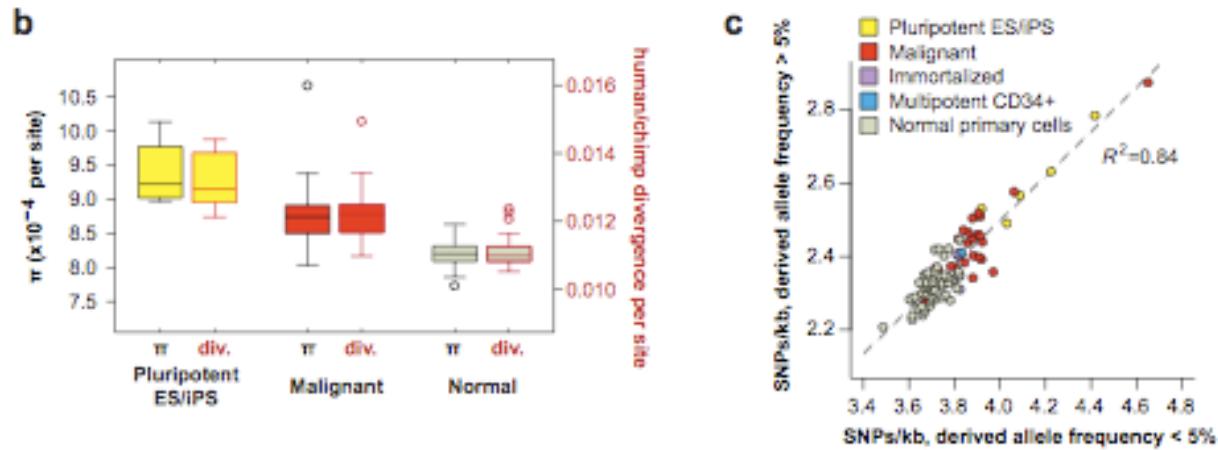
Data

- 125 diverse human cell and tissue types
 - 71 normal differentiated primary cells
 - 16 immortalized primary lines
 - 30 malignancy derived cell lines
 - 8 multipotent and pluripotent progenitor cells
- ~2.8 million DHS sites
 - ~0.9 million specific to single cell type
 - ~1.9 million active in two or more cell types
 - ~3000 detected in all cell types

Results



- DHSs overlapping Gencode promoters found in many cell types while distal DHSs are largely cell-type and lineage specific
- They find enhancer-promoter pairings by correlation of distal DHSs with promoter DHSs



Variation and DHSs

- Differences in diversity and divergence with chimp for different cell types are identical suggesting different mutation rates
- positive correlation of rare and common SNPs (~62% of SNPs in all cell lines are rare): implying different mutation rates
- consistent with increased germ-line mutation rates