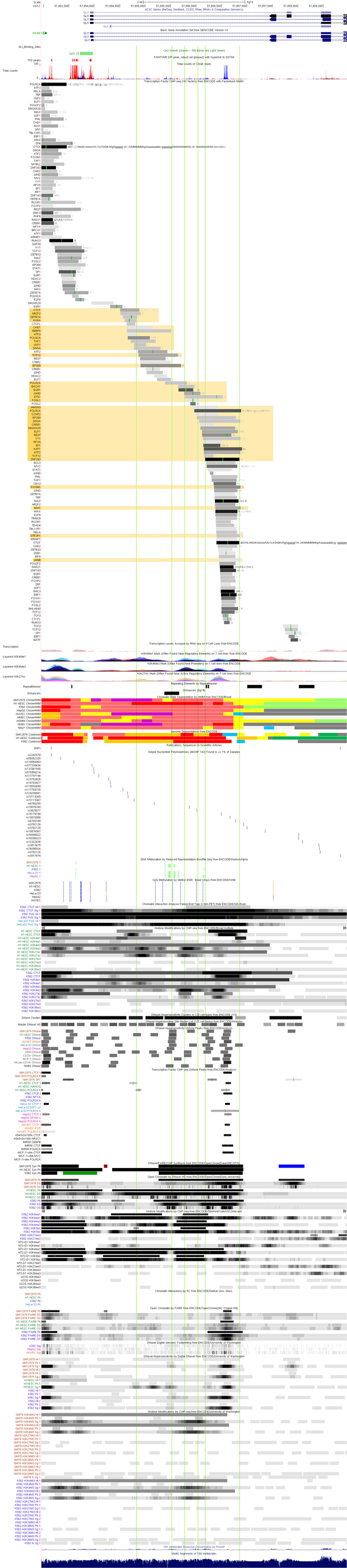
Scale
chr12
hg19
UCSC Genes (RefSeq, GenBank, CCDS, Rfam, tRNAs & Comparative Genomics)
Basic Gene Annotation Set from GENCODE Version 19
GLI_Binding_Sites
CpG islands (islands < 300 Bases are Light Green)
FANTOMS DPI peak, robust set (phase2) with hyperlink to SSTAR
Total counts of ChIP-Seq reads
Total counts
Transcription Factor ChIP-seq (161 factors) from ENCODE with Factorbook Motifs
Transcription
Transcription Levels Assayed by RNA-seq on 9 Cell Lines from ENCODE
Layered H3K4Me1
H3K4Me1 Mark (Often Found Near Regulatory Elements) on 7 cell lines from ENCODE
Layered H3K4Me3
H3K4Me3 Mark (Often Found Near Promoters) on 7 cell lines from ENCODE
Layered H3K27Ac
H3K27Ac Mark (Often Found Near Active Regulatory Elements) on 7 cell lines from ENCODE
RepeatMasker
Repeating Elements by RepeatMasker
Enhancers
Enhancers (hg19)
Chromatin State Segmentation by HMM from ENCODE/Broad
Genome Segmentations from ENCODE
Publications: Sequences in Scientific Articles
Single Nucleotide Polymorphisms (dbSNP 142) Found in >= 1% of Samples
DNA Methylation by Reduced Representation Bisulfite-Seq from ENCODE/HudsonAlpha
CpG Methylation by Methyl 450K. Bead Arrays from ENCODE/HAIB
Chromatin Interaction Analysis Paired-End Tags (ChIA-PET) from ENCODE/GIS-Ruan
Histone Modifications by ChIP-seq from ENCODE/Broad Institute
DNase Clusters
Master DNase HS
Transcription Factor ChIP-seq Uniform Peaks from ENCODE Analysis
Open Chromatin by DNase HS from ENCODE/Open Chromatin/UNC Chapel Hill
Histone Modifications by ChIP-seq from ENCODE/Stanford/Yale/USC/Harvard
Chromatin Interactions by 5C from ENCODE/Dekker Univ. Mass
Open Chromatin by FAIRE from ENCODE/OpenChromatin/UNC Chapel Hill
DNase Digital Genomic Footprinting from ENCODE/University of Washington
DNase Hypersensitivity by Digital DNase from ENCODE/University of Washington
Histone Modifications by ChIP-seq from ENCODE/University of Washington
100 Vertebrates Basewise Conservation by PhyloP
Multiz Alignments of 100 Vertebrates