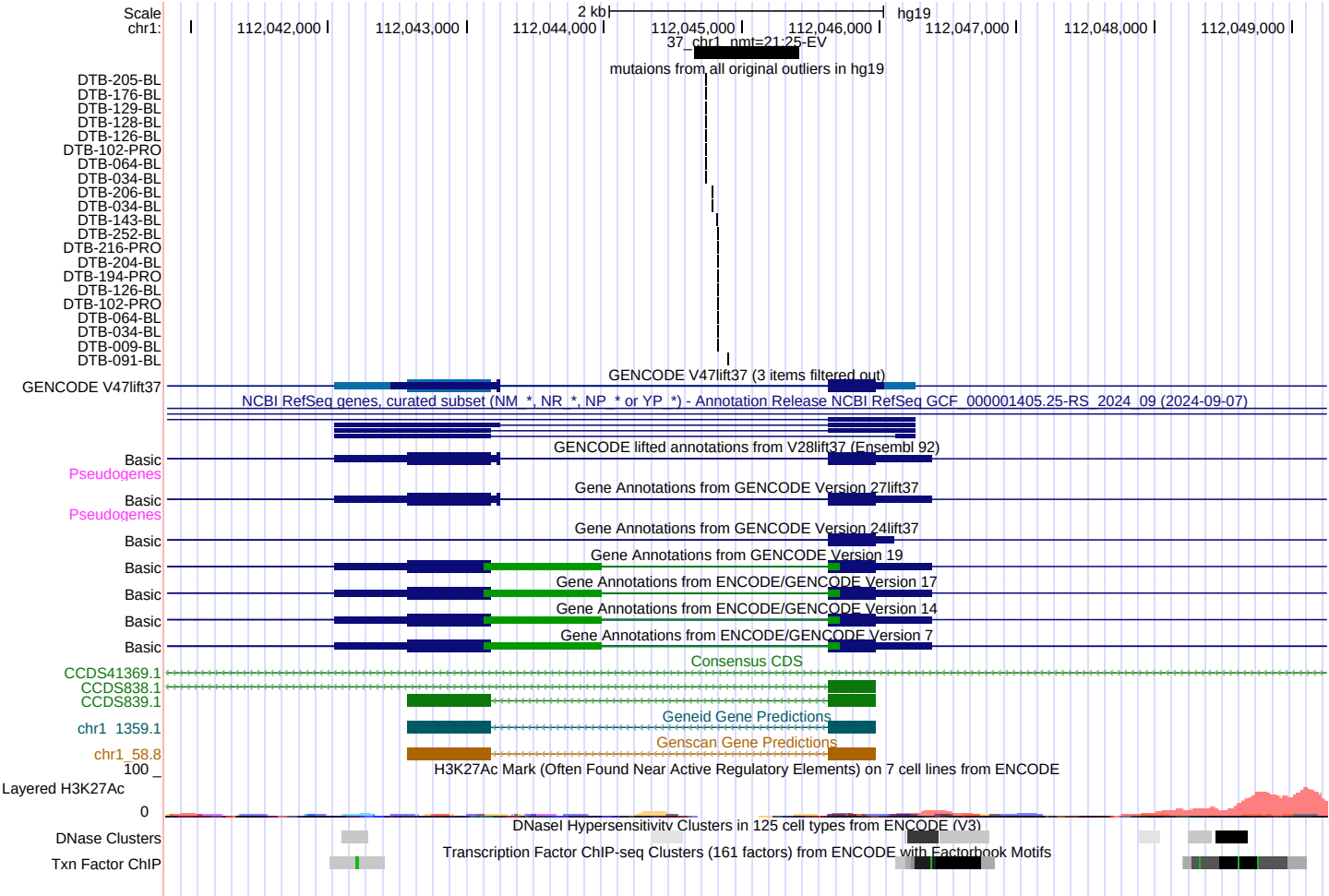
Scale
chr1:
2 kb
hg19
112,042,000
112,043,000
112,044,000
112,045,000
112,046,000
112,047,000
112,048,000
112,049,000
37_chr1_nmt=21:25-EV
mutaions from all original outliers in hg19
DTB-205-BL
DTB-176-BL
DTB-129-BL
DTB-128-BL
DTB-126-BL
DTB-102-PRO
DTB-064-BL
DTB-034-BL
DTB-206-BL
DTB-034-BL
DTB-143-BL
DTB-252-BL
DTB-216-PRO
DTB-204-BL
DTB-194-PRO
DTB-126-BL
DTB-102-PRO
DTB-064-BL
DTB-034-BL
DTB-009-BL
DTB-091-BL
GENCODE V47lift37
GENCODE V47lift37 (3 items filtered out)
NCBI RefSeq genes, curated subset (NM_*, NR_*, NP_* or YP_*) - Annotation Release NCBI RefSeq GCF_000001405.25-RS_2024_09 (2024-09-07)
Basic
Pseudogenes
GENCODE lifted annotations from V28lift37 (Ensembl 92)
Basic
Pseudogenes
Gene Annotations from GENCODE Version 27lift37
Basic
Gene Annotations from GENCODE Version 24lift37
Basic
Gene Annotations from GENCODE Version 19
Basic
Gene Annotations from ENCODE/GENCODE Version 17
Basic
Gene Annotations from ENCODE/GENCODE Version 14
Basic
Gene Annotations from ENCODE/GENCODE Version 7
Consensus CDS
CCDS41369.1
CCDS838.1
CCDS839.1
chr1_1359.1
Geneid Gene Predictions
chr1_58.8
Genscan Gene Predictions
100
H3K27Ac Mark (Often Found Near Active Regulatory Elements) on 7 cell lines from ENCODE
Layered H3K27Ac
0
DNaseI Hypersensitivity Clusters in 125 cell types from ENCODE (V3)
DNase Clusters
Transcription Factor ChIP-seq Clusters (161 factors) from ENCODE with Factorbook Motifs
Txn Factor ChIP