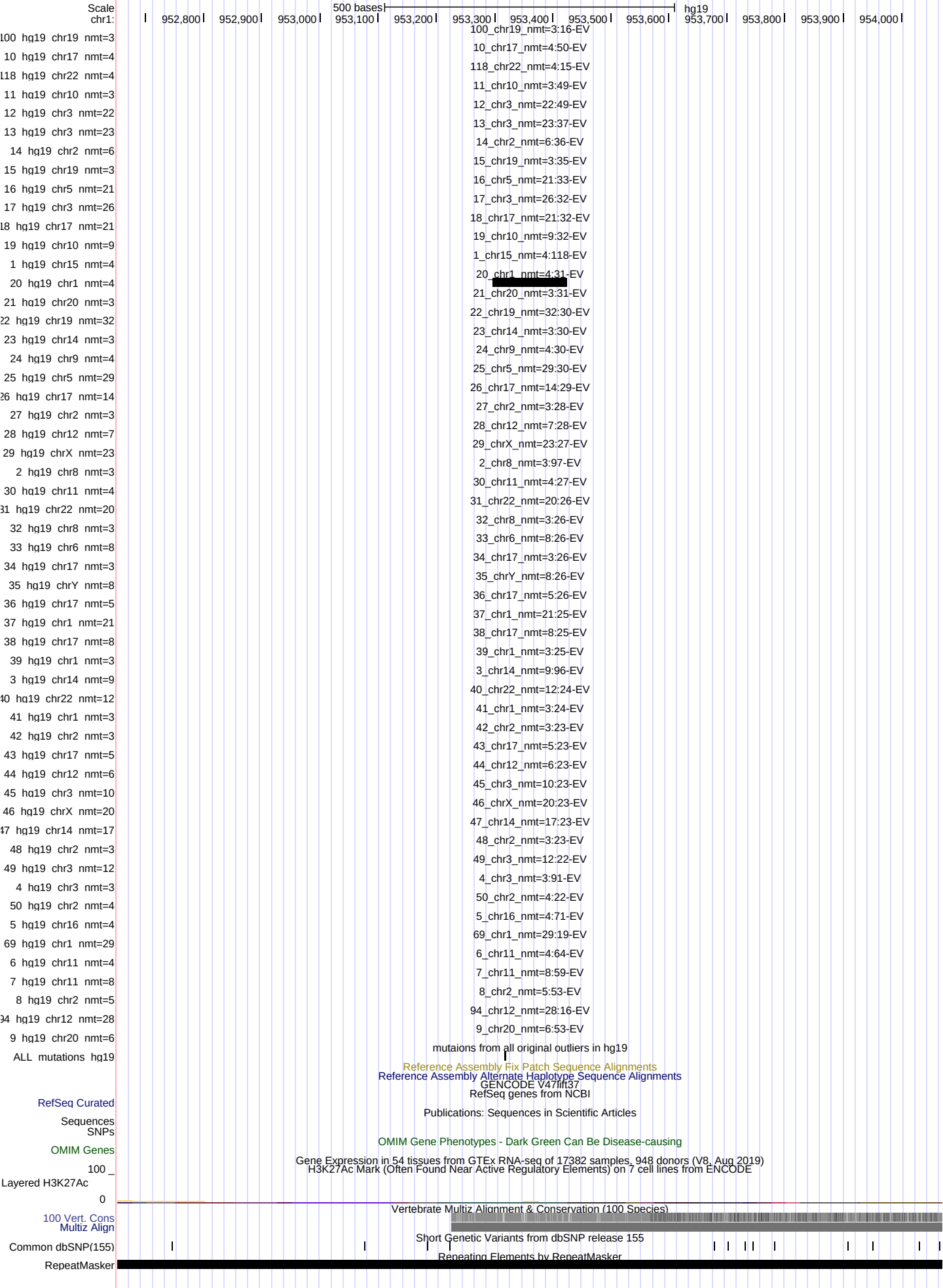
Scale
chr1:
500 bases
hg19
952,800
952,900
953,000
953,100
953,200
953,300
953,400
953,500
953,600
953,700
953,800
953,900
954,000
100_chr19_nmt=3:16-EV
10_chr17_nmt=4:50-EV
118_chr22_nmt=4:15-EV
11_chr10_nmt=3:49-EV
12_chr3_nmt=22:49-EV
13_chr3_nmt=23:37-EV
14_chr2_nmt=6:36-EV
15_chr19_nmt=3:35-EV
16_chr5_nmt=21:33-EV
17_chr3_nmt=26:32-EV
18_chr17_nmt=21:32-EV
19_chr10_nmt=9:32-EV
1_chr15_nmt=4:118-EV
20_chr1_nmt=4:31-EV
21_chr20_nmt=3:31-EV
22_chr19_nmt=32:30-EV
23_chr14_nmt=3:30-EV
24_chr9_nmt=4:30-EV
25_chr5_nmt=29:30-EV
26_chr17_nmt=14:29-EV
27_chr2_nmt=3:28-EV
28_chr12_nmt=7:28-EV
29_chrX_nmt=23:27-EV
2_chr8_nmt=3:97-EV
30_chr11_nmt=4:27-EV
31_chr22_nmt=20:26-EV
32_chr8_nmt=3:26-EV
33_chr6_nmt=8:26-EV
34_chr17_nmt=3:26-EV
35_chrY_nmt=8:26-EV
36_chr17_nmt=5:26-EV
37_chr1_nmt=21:25-EV
38_chr17_nmt=8:25-EV
39_chr1_nmt=3:25-EV
3_chr14_nmt=9:96-EV
40_chr22_nmt=12:24-EV
41_chr1_nmt=3:24-EV
42_chr2_nmt=3:23-EV
43_chr17_nmt=5:23-EV
44_chr12_nmt=6:23-EV
45_chr3_nmt=10:23-EV
46_chrX_nmt=20:23-EV
47_chr14_nmt=17:23-EV
48_chr2_nmt=3:23-EV
49_chr3_nmt=12:22-EV
4_chr3_nmt=3:91-EV
50_chr2_nmt=4:22-EV
5_chr16_nmt=4:71-EV
69_chr1_nmt=29:19-EV
6_chr11_nmt=4:64-EV
7_chr11_nmt=8:59-EV
8_chr2_nmt=5:53-EV
94_chr12_nmt=28:16-EV
9_chr20_nmt=6:53-EV
mutaions from all original outliers in hg19
ALL mutations hg19
Reference Assembly Fix Patch Sequence Alignments
Reference Assembly Alternate Haplotype Sequence Alignments
GENCODE V47lift37
RefSeq genes from NCBI
RefSeq Curated
Publications: Sequences in Scientific Articles
Sequences
SNPs
OMIM Genes
OMIM Gene Phenotypes - Dark Green Can Be Disease-causing
Gene Expression in 54 tissues from GTEx RNA-seq of 17382 samples, 948 donors (V8, Aug 2019)
H3K27Ac Mark (Often Found Near Active Regulatory Elements) on 7 cell lines from ENCODE
100
Layered H3K27Ac
0
Vertebrate Multiz Alignment & Conservation (100 Species)
100 Vert. Cons
Multiz Align
Short Genetic Variants from dbSNP release 155
Common dbSNP(155)
Repeating Elements by RepeatMasker
RepeatMasker