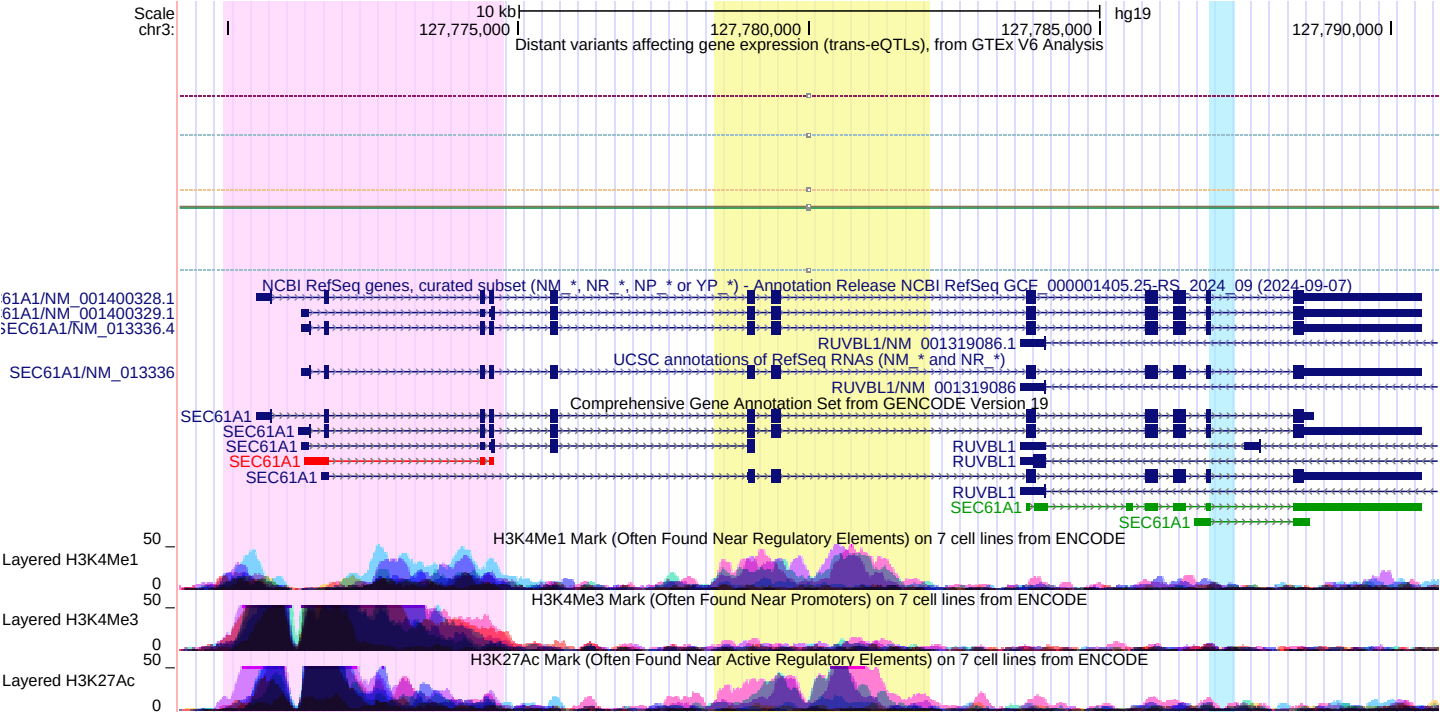
Scale
chr3:
10 kb
hg19
127,775,000
127,780,000
127,785,000
127,790,000
Distant variants affecting gene expression (trans-eQTLs), from GTEx V6 Analysis
NCBI RefSeq genes, curated subset (NM_*, NR_*, NP_* or YP_*) - Annotation Release NCBI RefSeq GCF_000001405.25-RS_2024_09 (2024-09-07)
61A1/NM_001400328.1
61A1/NM_001400329.1
SEC61A1/NM_013336.4
RUVBL1/NM_001319086.1
UCSC annotations of RefSeq RNAs (NM_* and NR_*)
SEC61A1/NM_013336
RUVBL1/NM_001319086
Comprehensive Gene Annotation Set from GENCODE Version 19
SEC61A1
SEC61A1
SEC61A1
SEC61A1
SEC61A1
RUVBL1
RUVBL1
RUVBL1
SEC61A1
SEC61A1
50
H3K4Me1 Mark (Often Found Near Regulatory Elements) on 7 cell lines from ENCODE
Layered H3K4Me1
0
50
H3K4Me3 Mark (Often Found Near Promoters) on 7 cell lines from ENCODE
Layered H3K4Me3
0
50
H3K27Ac Mark (Often Found Near Active Regulatory Elements) on 7 cell lines from ENCODE
Layered H3K27Ac
0