Scale
chr7: 155,593,000 155,594,000 155,595,000 155,596,000 155,597,000 155,598,000 155,599,000 155,600,000 155,601,000 155,602,000 155,603,000 155,604,000 155,605,000

5 kb hg19

Reference Assembly Fix Patch Sequence Alignments
Reference Assembly Alternate Haplotype Sequence Alignments
GENCODE V47lift37 (4 items filtered out)

SHH
ENSG00000296779

RefSeq Curated
RefSeq genes from NCBI

Merged 143 items
351575
DECIPHER CNVs (not updated anymore - use the hg38 track) (Merged 143 items)
260327
340409

Sequences
SNPs
Publications: Sequences in Scientific Articles

DECIPHER SNVs (not updated anymore - use the hg38 track)
267605
261040
305825
293438
286699
287358
286794

OMIM Genes
OMIM Gene Phenotypes - Dark Green Can Be Disease-causing

DECIPHER: Population CNVs
26138

ClinVar Short Variants < 50bp

Merged 85 items
ClinVar Copy Number Variants >= 50bp (Merged 85 items)
nssv13646018
dup
del
nssv582923
nssv581931
nssv3395559
nssv582111
del

ClinVar interp
ClinVar SNVs submitted interpretations and evidence
P
LP
VUS
LB
B
OTH

Common dbSNP(155)
Short Genetic Variants from dbSNP release 155

Database of Genomic Variants: Structural Var Regions (CNV, Inversion, In/del)
nsv509227
nsv951662
esv2663062
nsv1075489

Database of Genomic Variants: Supporting Structural Var (CNV, Inversion, In/del)
nssv619502
nssv2998639
essv5397101
essv5400478
essv5402442
essv5493244
essv5494377
essv5506176
essv5511052
essv5514690
essv5523287
essv5530479
essv5566249
essv5576785
essv5580872
essv5588729
essv5660014
essv5660241
essv5710063
essv5740812
essv5781026
essv5788685
essv5844632
essv5851131
essv5860235
essv5868466
essv5899722
essv5906910
essv5927592
essv5941723
essv5943960
essv5979289
essv6016565
essv6019480
essv6026214
essv6027336
essv6069215
essv6070138
essv6095056
essv6155638
essv6204521
essv6205181
essv6261530
essv6291431
essv6311257
essv6386713
essv6459515
essv6477702
essv6489126
essv6496444
essv6505792
essv6533217
essv6584788
essv6586369
nssv3772350

Database of Genomic Variants: Gold Standard Variants
Gene Expression in 54 tissues from GTEx RNA-seq of 17382 samples, 948 donors (V8, Aug 2019)

SHH

Layered H3K27Ac
H3K27Ac Mark (Often Found Near Active Regulatory Elements) on 7 cell lines from ENCODE

100 Vert. Cons
4.88
-4.5
100 vertebrates Basewise Conservation by PhyloP

Multiz Alignments of 100 Vertebrates
Rhesus
Mouse
Dog
Elephant
Chicken
X_tropicalis
Zebrafish

RepeatMasker
Repeating Elements by RepeatMasker