Scale
chr1:
500 bases
hg19
10,200
10,300
10,400
10,500
10,600
10,700
10,800
10,900
11,000
11,100
11,200
11,300
11,400
11,500
11,600
11,700
11,800
11,900
12,000
Amniotic_Homebrew_1
BALF_Homebrew_1
Bile_Homebrew_1
Bile_NEBNext_1
CellMedia_NEBNext_1
CSF_Homebrew_1
CSF_TruSeq_1
OvarianFF_Homebrew_1
Plasma_Homebrew_1
Plasma_LifeTech_1
Plasma_NEBNext_1
Plasma_NEXTflex_1
Saliva_Homebrew_1
Saliva_NEBNext_1
Saliva_TruSeq_1
Seminal_Homebrew_1
Serum_Homebrew_1
Serum_TruSeq_1
Sputum_Homebrew_1
Stool_NEBNext_1
Urine_Homebrew_1
Urine_NEBNext_1
Urine_TruSeq_1
Amniotic
BALF
Bile
Bile
CellMedia
CSF
CSF
OvarianFF
Plasma
Plasma
Plasma
Plasma
Saliva
Saliva
Saliva
Seminal
Serum
Serum
Sputum
Stool
Urine
Urine
Urine
Bam: 1000 Genomes read alignments (individual NA12878)
VCF: 1000 Genomes phase 1 interim SNVs
Reference Assembly Fix Patch Sequence Alignments
Reference Assembly Alternate Haplotype Sequence Alignments
GENCODE V47lift37 (26 items filtered out)
DDX11L16
RefSeq genes from NCBI
RefSeq Curated
Publications: Sequences in Scientific Articles
Sequences
SNPs
Short Genetic Variants from dbSNP release 153
Common dbSNP(153)
Simple Nucleotide Polymorphisms (dbSNP 151) Found in >= 1% of Samples
rs367896724
rs555500075
rs575272151
rs544419019
Gene Expression in 54 tissues from GTEx RNA-seq of 17382 samples, 948 donors (V8, Aug 2019)
DDX11L1
H3K27Ac Mark (Often Found Near Active Regulatory Elements) on 7 cell lines from ENCODE
Layered H3K27Ac
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
4.88
100 vertebrates Basewise Conservation by PhyloP
100 Vert. Cons
-4.5
Multiz Alignments of 100 Vertebrates
Rhesus
Mouse
Dog
Elephant
Chicken
X_tropicalis
Zebrafish
Repeating Elements by RepeatMasker
RepeatMasker