excluderanges

April 29, 2025

`T2T.CHM13.chm13.draft_v1.1.telomere`
T2T.CHM13.chm13.draft_v1.1.telomere

Description

Telomere identified by the VGP pipeline (v1.1)

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`T2T.CHM13.chm13.draft_v2.0.cen_mask`
T2T.CHM13.chm13.draft_v2.0.cen_mask

Description

Centromeric satellite masking bed file (v2.0)

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`T2T.Lareau.chm13v2.0_peaks`
T2T.Lareau.chm13v2.0_peaks

Description

Regions of high homology to mtDNA (NUMT regions) defined by caleblareau/mitoblacklist

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`T2T.UCSC.censat` *T2T.UCSC.censat*

Description

T2T peri/centromeric satellite annotation (v2.0, 20220329, CHM13 v2.0)

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`T2T.UCSC.gap` *T2T.UCSC.gap*

Description

Locations of assembly gaps, as determine by strings of 'N' characters (v1.0)

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`T2T.UCSC.hgUnique.hg38` *T2T.UCSC.hgUnique.hg38*

Description

Regions unique to the T2T-CHM13 v2.0 assembly compared to the GRCh38/hg38 and GRCh37/hg19 reference assemblies

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`T2T.excluderanges` *T2T.excluderanges*

Description

Defined by the Boyle-Lab/Blacklist software, High Signal and Low Mappability regions

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`TAIR10.Klasfeld.arabidopsis_Excludable_20inputs`
TAIR10.Klasfeld.arabidopsis_Excludable_20inputs

Description

Defined by the Boyle-Lab/Blacklist software, High Signal and Low Mappability regions (DOI: 10.1101/2022.02.27.482177)

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`TAIR10.Klasfeld.arabidopsis_greenscreen_20inputs`
TAIR10.Klasfeld.arabidopsis_greenscreen_20inputs

Description

Defined by the green screen pipeline (DOI: 10.1101/2022.02.27.482177)

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`TAIR10.UCSC.araTha1.gap`
TAIR10.UCSC.araTha1.gap

Description

Gaps in the May 2011 Arabidopsis thaliana genome assembly

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`TAIR10.Wimberley.predicted_excluded_list_sorted_0.6`
TAIR10.Wimberley.predicted_excluded_list_sorted_0.6

Description

Defined by the ewimberley/peakPass software

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`ce10.Boyle.ce10-Excludable.v2`

ce10.Boyle.ce10-Excludable.v2

Description

Defined by the Boyle-Lab/Blacklist software, High Signal and Low Mappability regions

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`ce10.Kundaje.ce10-Excludable`

ce10.Kundaje.ce10-Excludable

Description

Defined by Anshul Kundaje, superseded by ce10.Boyle.ce10-Excludable.v2

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`ce11.Boyle.ce11-Excludable.v2`

ce11.Boyle.ce11-Excludable.v2

Description

Defined by the Boyle-Lab/Blacklist software, High Signal and Low Mappability regions

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`danRer10.Domingues.Excludableed`

danRer10.Domingues.Excludableed

Description

Defined manually using total RNA-seq.

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`danRer10.UCSC.contig` *danRer10.UCSC.contig*

Description

Gaps between contigs in scaffolds

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`danRer10.UCSC.scaffold` *danRer10.UCSC.scaffold*

Description

Gaps between scaffolds in chromosome assemblies

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`danRer10.Yang.Supplemental_Table_19.ChIP-seq_black_list_in_the_zebrafish_genome` *danRer10.Yang.Supplemental_Table_19.ChIP-seq_black_list_in_the_zebrafish_genome*

Description

Defined via MACS2 peak calling using ChIP-seq (PMID: 33239788)

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`dm3.Boyle.dm3-Excludable.v2` *dm3.Boyle.dm3-Excludable.v2*

Description

Defined by the Boyle-Lab/Blacklist software, High Signal and Low Mappability regions

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`dm3.Kundaje.dm3-Excludable` *dm3.Kundaje.dm3-Excludable*

Description

Defined by Anshul Kundaje. Contains heterochromatin chromosomes chr2LHet. Superseded by dm3.Boyle.dm3-Excludable.v2

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`dm3.UCSC.contig` *dm3.UCSC.contig*

Description

dm3.UCSC.contig

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`dm3.UCSC.scaffold` *dm3.UCSC.scaffold*

Description

Gaps between scaffolds in chromosome assemblies

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`dm6.Boyle.dm6-Excludable.v2` *dm6.Boyle.dm6-Excludable.v2*

Description

Defined by the Boyle-Lab/Blacklist software, High Signal and Low Mappability regions

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`dm6.UCSC.other` *dm6.UCSC.other*

Description

Sequence of Ns in the assembly that were not marked as gaps in the AGP (A Golden Path) assembly definition file

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`excluderanges` *excluderanges: Genomic coordinates of problematic genomic regions*

Description

Genomic coordinates of problematic genomic regions that should be avoided when working with genomic data. GRanges of exclusion regions (formerly known as blacklisted), Nuclear Mitochondrial Sequences (NUMTs), centromeres, telomeres, known heterochromatin regions, etc. (UCSC 'gap' table data). In addition to data for human (hg19/hg38) and mouse (mm9/mm10) genome assemblies, it provides excludable regions for the latest T2T and mm39 assemblies. Data for C. elegans, D. melanogaster, D. rerio, A. thaliana also included.

`hg19.Bernstein.Mint_Excludable_hg19` *hg19.Bernstein.Mint_Excludable_hg19*

Description

Defined from Mint-ChIP (low input, multiplexed ChIP-seq) data

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg19.Birney.wgEncodeDacMapabilityConsensusExcludable` *hg19.Birney.wgEncodeDacMapabilityConsensusExcludable*

Description

Defined by the ENCODE consortium, includes satellite repeats (CATTC, GAATG, GAGTG, ACRO1), RepeatMasker repeats (ALR/Alpha, BSR/Beta), centromeric r epeats, chrM, High/Low mappability islands

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg19.Boyle.hg19-Excludable.v2`

hg19.Boyle.hg19-Excludable.v2

Description

Defined by the Boyle-Lab/Blacklist software, High Signal and Low Mappability regions

Author(s)

Mikhail Dozmorov `<mikhail.dozmorov@gmail.com>`

`hg19.Crawford.wgEncodeDukeMapabilityRegionsExcludable`

hg19.Crawford.wgEncodeDukeMapabilityRegionsExcludable

Description

Defined by the ENCODE consortium, includes satellite repeats (CATTC, GAATG, GAGTG, ACRO1), RepeatMasker repeats (ALR/Alpha, BSR/Beta), human satellite repeat HSATII, chrM, ribosomal subunit consensus sequences LSU-rRNA_Hsa, SSU-rRNA_Hsa. Has extra chromosomes, use keepStandardChromosomes() filtering

Author(s)

Mikhail Dozmorov `<mikhail.dozmorov@gmail.com>`

`hg19.Lareau.hg19.full.Excludable`

hg19.Lareau.hg19.full.Excludable

Description

ENCODE excludable regions combined with regions of high homology to mtDNA (NUMT regions)

Author(s)

Mikhail Dozmorov `<mikhail.dozmorov@gmail.com>`

`hg19.Lareau.hg19_peaks` *hg19.Lareau.hg19_peaks*

Description

Regions of high homology to mtDNA (NUMT regions) defined by caleblareau/mitoblacklist

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg19.UCSC.centromere` *hg19.UCSC.centromere*

Description

Gaps from centromeres

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg19.UCSC.clone` *hg19.UCSC.clone*

Description

Gaps between clones in the same map contig. Has extra chromosomes, use keepStandardChromosomes() filtering

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg19.UCSC.contig` *hg19.UCSC.contig*

Description

Gaps between contigs in scaffolds

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg19.UCSC.heterochromatin` *hg19.UCSC.heterochromatin*

Description

Gaps from large blocks of heterochromatin

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg19.UCSC.numtS` *hg19.UCSC.numtS*

Description

Human NumtS mitochondrial sequence

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg19.UCSC.scaffold` *hg19.UCSC.scaffold*

Description

Gaps between scaffolds in chromosome assemblies. Only non-autosomal chromosomes

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg19.UCSC.short_arm` *hg19.UCSC.short_arm*

Description

Gaps on the short arm of the chromosome

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg19.UCSC.telomere` *hg19.UCSC.telomere*

Description

Gaps from telomeres

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg19.Wold.hg19mitoExcludable` *hg19.Wold.hg19mitoExcludable*

Description

Definition method unknown

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg19.Yeo.eCLIP_Excludableregions.hg19` *hg19.Yeo.eCLIP_Excludableregions.hg19*

Description

Defined from eCLIP data, includes skyscraper, rRNA pseudogene, unreliably mapped satellite repeat, and low complexity skyscraper peak regions

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg38.Bernstein.Mint_Excludable_GRCh38` *hg38.Bernstein.Mint_Excludable_GRCh38*

Description

Defined from Mint-ChIP (low input, multiplexed ChIP-seq) data

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg38.Boyle.hg38-Excludable.v2`

hg38.Boyle.hg38-Excludable.v2

Description

Defined by the Boyle-Lab/Blacklist software, High Signal and Low Mappability regions

Author(s)

Mikhail Dozmorov `<mikhail.dozmorov@gmail.com>`

`hg38.Kundaje.GRCh38.Excludable`

hg38.Kundaje.GRCh38.Excludable

Description

Defined by Anshul Kundaje as a part of ENCODE and modENCODE consortia

Author(s)

Mikhail Dozmorov `<mikhail.dozmorov@gmail.com>`

`hg38.Kundaje.GRCh38_unified_Excludable`

hg38.Kundaje.GRCh38_unified_Excludable

Description

Defined as a combination of hg38.Lareau.hg38_peaks, hg38.Boyle.hg38-Excludable.v2, and hg38.Wimberley.peakPass6
followed by manual curation. Supersedes hg38.Kundaje.GRCh38.Excludable.

Author(s)

Mikhail Dozmorov `<mikhail.dozmorov@gmail.com>`

`hg38.Lareau.hg38.full.Excludable`

hg38.Lareau.hg38.full.Excludable

Description

ENCODE excludable regions combined with regions of high homology to mtDNA (NUMT regions)

Author(s)

Mikhail Dozmorov `<mikhail.dozmorov@gmail.com>`

`hg38.Lareau.hg38_peaks` *hg38.Lareau.hg38_peaks*

Description

Regions of high homology to mtDNA (NUMT regions) defined by caleblareau/mitoblacklist

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg38.Reddy.wgEncodeDacMapabilityConsensusExcludable.hg38` *hg38.Reddy.wgEncodeDacMapabilityConsensusExcludable.hg38*

Description

Defined by the ENCODE consortium, includes satellite repeats (CATTC, GAATG, GAGTG, ACRO1), RepeatMasker repeats (ALR/Alpha, BSR/Beta), centromeric repeats, chrM, High/Low mappability islands. Has extra chromosomes, use keepStandardChromosomes() filtering

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg38.UCSC.centromere` *hg38.UCSC.centromere*

Description

Gaps from centromeres

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg38.UCSC.contig` *hg38.UCSC.contig*

Description

Gaps between contigs in scaffolds

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg38.UCSC.heterochromatin` *hg38.UCSC.heterochromatin*

Description

Gaps from large blocks of heterochromatin

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg38.UCSC.scaffold` *hg38.UCSC.scaffold*

Description

Gaps between scaffolds in chromosome assemblies. Has extra chromosomes, use keepStandardChromosomes() filtering

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg38.UCSC.short_arm` *hg38.UCSC.short_arm*

Description

Gaps on the short arm of the chromosome

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg38.UCSC.telomere` *hg38.UCSC.telomere*

Description

Gaps from telomeres

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg38.Wimberley.peakPass60Perc_sorted`
hg38.Wimberley.peakPass60Perc_sorted

Description

Defined by the ewimberley/peakPass software

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg38.Wold.hg38mitoExcludable`
hg38.Wold.hg38mitoExcludable

Description

Definition method unknown

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`hg38.Yeo.eCLIP_Excludableregions.hg38liftover.bed.fixed`
hg38.Yeo.eCLIP_Excludableregions.hg38liftover.bed.fixed

Description

Defined from eCLIP data

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm10.Boyle.mm10-Excludable.v2`
mm10.Boyle.mm10-Excludable.v2

Description

Defined by the Boyle-Lab/Blacklist software, High Signal and Low Mappability regions

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm10.Hardison.Excludable.full`
mm10.Hardison.Excludable.full

Description

Definition method unknown

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm10.Hardison.psuExcludable.mm10`
mm10.Hardison.psuExcludable.mm10

Description

Definition method unknown

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm10.Kundaje.anshul.Excludable.mm10`
mm10.Kundaje.anshul.Excludable.mm10

Description

Defined by Anshul Kundaje as a part of ENCODE and modENCODE consortia

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm10.Kundaje.mm10.Excludable`
mm10.Kundaje.mm10.Excludable

Description

Defined by Anshul Kundaje as a part of ENCODE and modENCODE consortia

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm10.Lareau.mm10.full.Excludable` *mm10.Lareau.mm10.full.Excludable*

Description

ENCODE excludable regions combined with regions of high homology to mtDNA (NUMT regions)

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm10.Lareau.mm10_peaks` *mm10.Lareau.mm10_peaks*

Description

Regions of high homology to mtDNA (NUMT regions) defined by caleblareau/mitoblacklist

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm10.UCSC.centromere` *mm10.UCSC.centromere*

Description

Gaps from centromeres

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm10.UCSC.clone` *mm10.UCSC.clone*

Description

Gaps between clones in the same map contig. Has extra chromosomes, use keepStandardChromosomes() filtering

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm10.UCSC.contig` *mm10.UCSC.contig*

Description

Gaps between contigs in scaffolds

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm10.UCSC.fragment` *mm10.UCSC.fragment*

Description

A single gap of 31 bases in chrX_GL456233_random

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm10.UCSC.other` *mm10.UCSC.other*

Description

Sequence of Ns in the assembly that were not marked as gaps in the AGP (A Golden Path) assembly definition file. Has extra chromosomes, use keepStandardChromosomes() filtering

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm10.UCSC.scaffold` *mm10.UCSC.scaffold*

Description

Gaps between scaffolds in chromosome assemblies

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm10.UCSC.short_arm` *mm10.UCSC.short_arm*

Description

Gaps on the short arm of the chromosome

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm10.UCSC.telomere` *mm10.UCSC.telomere*

Description

Gaps from telomeres

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm10.Wold.mm10mitoExcludable` *mm10.Wold.mm10mitoExcludable*

Description

Definition method unknown

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm39.UCSC.centromere` *mm39.UCSC.centromere*

Description

Gaps from centromeres

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm39.UCSC.contig` *mm39.UCSC.contig*

Description

Gaps between contigs in scaffolds

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm39.UCSC.scaffold` *mm39.UCSC.scaffold*

Description

Gaps between scaffolds in chromosome assemblies

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm39.UCSC.short_arm` *mm39.UCSC.short_arm*

Description

Gaps on the short arm of the chromosome

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm39.UCSC.telomere` *mm39.UCSC.telomere*

Description

Gaps from telomeres

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm39.excluderanges` *mm39.excluderanges*

Description

Defined by the Boyle-Lab/Blacklist software, High Signal and Low Mappability regions

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm9.Lareau.mm9.full.Excludable`
mm9.Lareau.mm9.full.Excludable

Description

ENCODE excludable regions combined with regions of high homology to mtDNA (NUMT regions)

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm9.Lareau.mm9_peaks` *mm9.Lareau.mm9_peaks*

Description

Regions of high homology to mtDNA (NUMT regions) defined by caleblareau/mitoblacklist

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm9.UCSC.centromere` *mm9.UCSC.centromere*

Description

Gaps from centromeres

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm9.UCSC.contig` *mm9.UCSC.contig*

Description

Gaps between contigs in scaffolds. Has extra chromosomes, use keepStandardChromosomes() filtering

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm9.UCSC.fragment` *mm9.UCSC.fragment*

Description

Gaps between the contigs of a draft clone. (In this context, a contig is a set of overlapping sequence reads). Has extra chromosomes, use keepStandardChromosomes() filtering

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm9.UCSC.numtS` *mm9.UCSC.numtS*

Description

Mouse NumtS mitochondrial sequence

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

`mm9.Wold.mm9mitoExcludable` *mm9.Wold.mm9mitoExcludable*

Description

Definition method unknown

Author(s)

Mikhail Dozmorov <`mikhail.dozmorov@gmail.com`>

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