

# excluderanges

June 26, 2024

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T2T.CHM13.chm13.draft\_v1.1.telomere  
*T2T.CHM13.chm13.draft\_v1.1.telomere*

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## Description

Telomere identified by the VGP pipeline (v1.1)

## Author(s)

Mikhail Dozmorov <mikhail.dozmorov@gmail.com>

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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>

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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>

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excluderanges      *excluderanges: Genomic coordinates of problematic genomic regions*

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**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 (CATTTC, GAATG, GAGTG, ACRO1), RepeatMasker repeats (ALR/Alpha, BSR/Beta), centromeric repeats, 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.peakPass60Per 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 keepStandard-Chromosomes() 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*

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**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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