Tiling Path File (TPF) Specification v1.4: 2/15/2011

What it is: A TPF specifies the order of a set of sequences along a larger molecule(s). Gap types and sizes can be specified. The molecule can be as large as a chromosome and as small as a sequence contig made up of one smaller sequence. A TPF can have one or more sequences/clones.

What it is not: A TPF does not specify the particular version of a sequence, nor does it specify the switch points between adjacent clones in a given scaffold/contig.

Header Information: Header information is provided in a key-value type of structure. Each header field will be prefixed with ##. These fields are available:

- ##Organism (Required)
- ##Assembly Name (Required)
- ##Chromosome (Required)
- ##Strain/Haplotype/Cultivar (Optional)
- ##Type (controlled vocabulary) (Required)
- ##Version (Calculated by Database, Required)
- ##Comment (Optional)

Additional information will be calculated at submission.

- ##Submitter
- ##Create date
- ##Update date

Here is an example header:
##ORGANISM: Mus musculus
##ASSEMBLY NAME: Reference
##CHROMOSOME: 1
##STRAIN/HAPLOTYPE/CULTIVAR: C57BL/6J
##TYPE: Complete Chromosome
##Version: 1
##Comment: some useful information here.
##SUBMITTER: Tina Graves, WUGSC
##CREATE DATE: Nov 3 2006 12:16PM
##UPDATE DATE: Nov 5 2006 12:12PM

The data defining the actual tiling path should be flanked in header and footer lines to minimize the chance of file truncation. The header and footer lines shall have the following format:

All header "## TAG: value" pairs must occur before this line:

##=== Beginning of TPF Data ===

Required after the TPF data rows:
##=== End of TPF Data ===

Column definitions for sequence lines:
Column 1: accession number. This must be a valid accession assigned by the International DNA Sequence Database (GenBank/EMBL/DDBJ). No version number should be used. It is assumed that the current version of the accession is what is intended. **OPTIONAL**, use "?" if unknown.
Column 2: clone name. If the sequence is defined by a clone, then the clone name should be specified here. Ideally, standard Clone Registry nomenclature will be used. If a sequence is derived from more than one clone, the clone name can be given as "MULTIPLE". **OPTIONAL**, use "?" if unknown.
Column 3: local contig identifier. Name given to the scaffold/contig generated by assembling the listed sequences. **REQUIRED.**

- **NOTE: Use of "." (the "dot" character) is not allowed in contig identifiers.**
- **NOTE: A local contig identifier may only be used once per assembly.**

Column 4: contained status. This line is only used to specify clones that are known to be contained within another clone on the TPF. The only values allowed are 'CONTAINED' and 'CONTAINED_TURNOUT'. **REQUIRED for contained clones, otherwise OPTIONAL.**
Column 5: accession number. This must be a valid accession assigned by the INSDC. No version number should be used. It is assumed that the current version of the accession is what is intended. The accession provided in this column must be in column 1 on another line of the same TPF and must also belong to the same local contig (column 3) as the contained clone. See below for requirements. **REQUIRED if COLUMN 4 is CONTAINED or CONTAINED_TURNOUT, otherwise not valid.**
Column 6: clone name. The clone name used in this column should correspond to the accession listed in column 5, if the sequence is derived from a clone. Ideally, standard Clone Registry nomenclature will be used. See below for requirements. **REQUIRED IF COLUMN 4 is CONTAINED or CONTAINED_TURNOUT, otherwise not valid.**
NOTE1: Columns 5 and 6- these are similar to columns 1 and 2 in that at least one, but not both, requires a value. However, if both are known, please supply both values.
NOTE2: If column 4 is not populated in a sequence line, do not populate columns 4, 5 or 6. If column 4 is populated, then provide values or "?" for columns 5 and 6.

Column definitions for non-sequence lines:

Column 1: GAP. This is the term used and it should always be capitalized. Used to note the gap lines. **REQUIRED**
Column 2: gap type. Specifies the type of gap. **REQUIRED**
Values are:

- TYPE-1: [Deprecated]- was a place-holder for a picked clone.
- TYPE-2: clone gap
- TYPE-3: contig gap- unable to close using available technology
- Biological Gap: If there is a biological gap such as a centromere, etc. then use the name rather than type-4. This is a controlled vocabulary:
  - CENTROMERE
  - TELOMERE
  - HETEROCHROMATIN
  - SHORT-ARM
- PAR: (Y-chromosome only) The pseudoautosomal regions of the Y chromosome are represented by PAR gaps. Accessions for chr. X-derived PAR sequences are omitted from the chr. Y TPF, but are present in the chr. Y AGP. Switch points for PAR boundary clones will be curated manually.
  - Note: The comments section of the header should be used to provide the bp positions at which the PAR region begins and ends in the relevant accessions. Header comments are entered via the web-based form at the time of submission. This information will be inserted into the ##COMMENT line of the header. It will also be stored in the database and can be retrieved for future use.

Column 3:

- For TYPE-2, TYPE-3 or Biological gap: Gap size. Estimated size x gap. In the absence of submitted gap sizes a default of 50,000 bp will be used for clone and contig gaps. **OPTIONAL**, unless the gap type is 'Biological' then required.
- For PAR gap: accession number of the first sequence to contain the PAR region, as defined on the X chromosome (this accession may contain both non-PAR and PAR sequence)

Column 4:

- For TYPE-2, TYPE-3 or Biological gap: Method used to determine gap size. If a gap size has been estimated experimentally, the method should be noted here. Currently acceptable values:
  - FISH
  - OPTICAL MAP
  - ALIGNMENT
  - PCR
  - FINGERPRINT

    - Multiple methods may be entered for a single gap. Methods should be separated by a semi-colon (Example: FISH;OPTICAL MAP;ALIGNMENT).
    - **REQUIRED if column 3 is populated and gap type is not biological, otherwise not valid.**
- For PAR gap: accession number of the last sequence to contain the PAR region, as defined on the X chromosome (this accession may contain both non-PAR and PAR sequence)

All columns are tab delimited and lines are terminated by a newline. Lines beginning with a single "#" can occur anywhere within the file, are comments and can be ignored by parsers. Lines beginning with "##" can be ignored by simple parsers but contain structured information about the TPF.
Each file should have only one header, so all of the objects described in a file should have common header information.

Validation:
For sequence based lines:

- If column 1 is populated with a valid accession, column 2 may be unpopulated (using "?" as a placeholder). Ideally, this will only occur in the case where a sequence is not based on a defined clone and will have no other easily identified name.
- If an accession is supplied, it must be valid according to the IDNSC.
- A given accession cannot be used more than once per assembly, but may be used in >1 assembly. (The assembly name is listed in row 3 of the TPF header).
- If column 1 is not populated (using "?" as a placeholder) then column 2 should be populated.
- Use of the "." character is not permitted in column 3.
- If there is not enough information to populate column 1 or 2, then a gap line should be used.
- If column 4 is populated, then columns 5 and 6 must be populated.
- If column 4 is not populated, then columns 5 and 6 must not be populated.
- If column 4 = CONTAINED or CONTAINED_TURNOUT, the accession provided in column 5 must be present in the same local contig (column 3) as the accession in column 1.

For gap lines:

- Gap type-1 lines are no longer allowed.
- Gap type-2 lines will default to 50Kb if no other data is provided.
- Gap type-2 lines may not be adjacent to one another.
- Gap type-3 lines will default to 50 Kb if no data is provided.
- Gap type-3 lines may not be adjacent to one another.

- Gap type-2 and type-3 lines may not be adjacent to one another.
- TYPE-3 gaps may not be contained within a contig
- Biological gaps must provide a size estimate in column 3; they do not need to have a method in column 4.
- Biological gaps may not be contained within a contig
- There can be consecutive biological gap lines of different types.
- If a gap size is provided in column 3, the method used to determine this size must be provided in column 4, unless column 2 is a biological gap.
- PAR gaps are only permitted on the Y chromosome TPF.
- If the gap type is PAR, the beginning and ending accessions for this region must be listed in columns 3 and 4, respectively.
- If the gap type is PAR, columns 3 and 4 must both contain valid accessions that are found in column 1 on the chromosome X TPF.

CONTAINED COMPONENTS

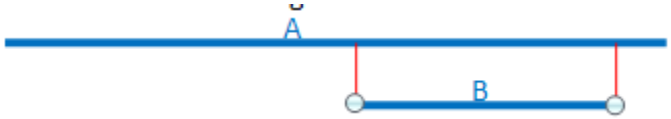
Types of Contained Components

A component is considered "contained" when its entire sequence can be aligned to another component on the TPF (excluding any internal alignment gaps). A contained component MUST be marked on a TPF if it is to be included in the corresponding AGP. There are two designators that can be used to mark contained components on the TPF: CONTAINED and CONTAINED_TURNOUT. The designators differ in the switch point selection rules applied to the contained component during AGP production.

A. CONTAINED

TPF components marked with the "CONTAINED" designator will follow the default switching rules during AGP production. Examples for usage are shown.

Example A1: Single contained clone

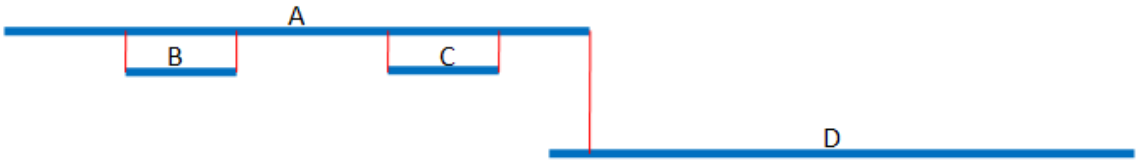


TPF shows:

A

B CONTAINED A

Example A2: Multiple non-overlapping contained clones



TPF shows:

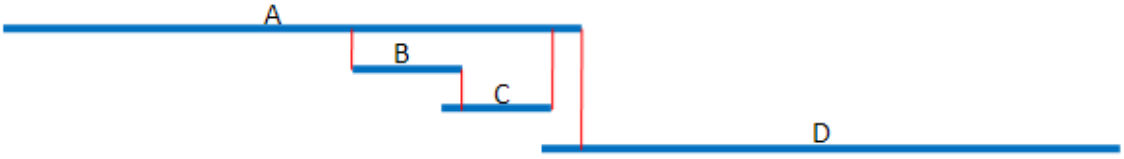
A

B CONTAINED A

C CONTAINED A

D

Example A3: Multiple overlapping contained clones



TPF shows:

A

B CONTAINED A

C CONTAINED A

D

Note that the TPF mark-ups for examples A2 and A3 are identical. The software that produces the AGPs will determine the relationship between clones B and C and produce the appropriate switch points.

IMPORTANT: If the last clone in a chain of contained clones will switch back to the container, all clones in the chain should be marked CONTAINED.

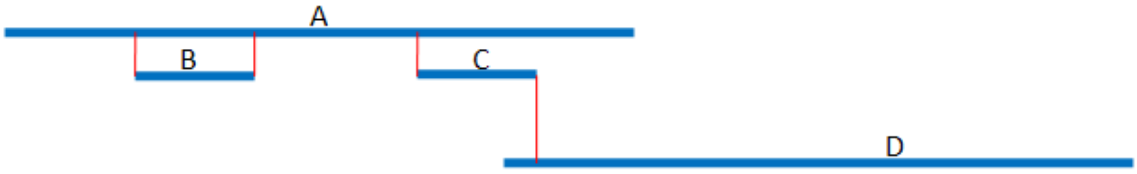
B. CONTAINED_TURNOUT

TPF components marked with the "CONTAINED_TURNOUT" designator will follow alternate switching rules during AGP production. Examples for usage are shown.

Example B1: Single contained clone

TPF shows:
A
B CONTAINED_TURNOUT A

Example B2: Multiple non-overlapping contained clones



TPF shows:
A
B CONTAINED A
C CONTAINED_TURNOUT A
D

Example B3: Multiple overlapping contained clones

TPF shows:
A
B CONTAINED_TURNOUT A
C CONTAINED_TURNOUT A
D

IMPORTANT: In Example B3, note the use of CONTAINED_TURNOUT for both components, and contrast to Example A3. **If the last clone in a chain of contained clones will not switch back to the container, the entire chain should be marked as CONTAINED_TURNOUT.**

Additional Info for TPF Representation of Contained Components

- A component can only be contained by another component present in the same TPF contig
  - If column 4 = CONTAINED or CONTAINED_TURNOUT, the accession provided in column 5 must be present in the same local contig (column 3) as the accession in column 1.
- In situations of hierarchical containments, the TPF should always display the nearest contained relationship for any contained sequences.
  - Example:
    - A ----------
    - B ----------
    - C --------
  - TPF should report:
    - B contained in A
    - C contained in B
- In situations of hierarchical containments the order of the contained sequences on the TPF does not need to reflect the desired sequence order on the AGP.
- In situations where multiple sequences are contained within the same sequences (but are not hierarchical), the order of the contained sequences on the TPF does not need to reflect the desired sequence order on the AGP.

Specific TPF examples:

1. A TPF may contain one or more partial contigs. For example:

```
##ORGANISM: Mus musculus
##CHROMOSOME: 1
##ASSEMBLY NAME: NOD/MrkTac
##STRAIN/HAPLOTYPE/CULTIVAR: NOD/MrkTac
##TYPE: Contig
##VERSION: 1
##COMMENT: EXAMPLE TPF ONLY
##SUBMITTER: Schneider, NCBI
##CREATE DATE: Nov 3 2006 12:16PM
##UPDATE DATE: Nov 3 2006 12:16PM

##=== Beginning of TPF Data ===

AL645951        DN-29B18        NCBI_Mmchr1_ctg163678
AL596283        DN-257N2        NCBI_Mmchr1_ctg163678
CR936839        DN-120A16       NCBI_Mmchr1_ctg37199
CR936842        DN-189K17       NCBI_Mmchr1_ctg37199
#
AL671997        DN-396O20       NCBI_Mmchr1_ctg163206
AL672024        DN-378G17       NCBI_Mmchr1_ctg163206

##=== End of TPF Data ===
```

The absence of gap lines implies there is no known order for these contigs. Note that contigs may be separated by"#". This is not required and is only done to facilitate reading of the TPF by individuals.

2. A TPF may specify an entire chromosome. For example:

```
##ORGANISM: Mus musculus
##CHROMOSOME: 2
##ASSEMBLY NAME: Reference
##STRAIN/HAPLOTYPE/CULTIVAR: C57BL/6J
##TYPE: Complete Chromosome
##VERSION: 2
##COMMENT: EXAMPLE TPF ONLY
##SUBMITTER: Schneider, NCBI
##CREATE DATE: Oct 29 2007 04:39PM
##UPDATE DATE: Oct 29 2007 04:39PM

##=== Beginning of TPF Data ===

GAP  CENTROMERE     3000000
```

```
?    WI1-1974M19    Mmchr2_ctg1
?    WI1-923N3 Mmchr2_ctg1
CU207330  WI1-2764C4     Mmchr2_ctg1
AL928883  RP23-60E18     Mmchr2_ctg1
AL732620  RP23-167G19    Mmchr2_ctg1
AL929080  RP24-129J15    Mmchr2_ctg1
AL732328  RP23-106P4     Mmchr2_ctg1
AL844530  RP23-248L2     Mmchr2_ctg1
CU181741  WI1-2132D7 Mmchr2_ctg1   CONTAINED AL845441 RP23-327I5
AL845441  RP23-327I5     Mmchr2_ctg1
AL935139  RP23-74F20     Mmchr2_ctg1
AL954325  RP23-416H10    Mmchr2_ctg1
AL928978  RP23-95M7 Mmchr2_ctg1 CONTAINED_TURNOUT AL954325 RP23-
416H10
AL928947  RP23-69N1 Mmchr2_ctg1 CONTAINED_TURNOUT AL954325 RP23-
416H10
AL807832  RP23-198D21    Mmchr2_ctg1
AL928550  RP23-272I15    Mmchr2_ctg1
AL807778  RP23-198G1     Mmchr2_ctg1
BX682541  RP23-349P20    Mmchr2_ctg1
AL928662  RP23-379M5     Mmchr2_ctg1
AL732403  RP23-119L20    Mmchr2_ctg1
BX323054  RP23-329P15    Mmchr2_ctg1
AL928940  RP23-94J17     Mmchr2_ctg1
AL929142  RP23-340A13    Mmchr2_ctg1
AL928958  RP23-344N23    Mmchr2_ctg1
AL928924  RP23-307E15    Mmchr2_ctg1
CR388026  RP23-39L16     Mmchr2_ctg1
AL928735  RP23-413M3     Mmchr2_ctg1
BX842658  RP23-86F17     Mmchr2_ctg1
AL845275  RP23-112F5     Mmchr2_ctg1
AL845515  RP23-256D19    Mmchr2_ctg1
AL845492  RP23-222P7     Mmchr2_ctg1
AL929240  RP23-245A10    Mmchr2_ctg1
AL772190  RP23-124P7     Mmchr2_ctg1
CR936244  RP24-562B12    Mmchr2_ctg1
CU207293  WI1-632G16     Mmchr2_ctg1
AL845485  RP23-237D23    Mmchr2_ctg1
BX649227  RP23-114C18    Mmchr2_ctg1
AL840637  RP23-113H3     Mmchr2_ctg1
AL845488  RP23-215P8     Mmchr2_ctg1
AL928600  RP23-348O19    Mmchr2_ctg1
AL929143  RP23-339G18    Mmchr2_ctg1
AL773590  RP23-181A13    Mmchr2_ctg1
BX005023  RP24-316N23    Mmchr2_ctg1
AL928713  RP23-399M5     Mmchr2_ctg1
AL929149  RP23-93B24     Mmchr2_ctg1
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BX293551  RP23-107O21    Mmchr2_ctg1
AL929043  RP23-58H6 Mmchr2_ctg1    CONTAINED BX293551 RP23-107O21
AL929187  RP23-8G6  Mmchr2_ctg1    CONTAINED AL929043 RP23-58H6
BX294115  RP24-465I11    Mmchr2_ctg1
AL929440  RP23-292F11    Mmchr2_ctg1
AL928665  RP23-294O23    Mmchr2_ctg1
AL928832  RP23-261N18    Mmchr2_ctg1
AL929194  RP23-385L14    Mmchr2_ctg1
AL772377  RP23-141B15    Mmchr2_ctg1
AL845529  RP23-276D17    Mmchr2_ctg1
AL928704  RP23-393G10    Mmchr2_ctg1
AL772367  RP23-119N4     Mmchr2_ctg1
AL953853  RP23-6M16 Mmchr2_ctg1
AL772216  RP23-153M22    Mmchr2_ctg1
AL844485  RP23-436D21    Mmchr2_ctg1
AL845264  RP23-116F18    Mmchr2_ctg1
AL772352  RP23-147F6     Mmchr2_ctg1
AL928715  RP23-373D16    Mmchr2_ctg1
AL929020  RP23-291L24    Mmchr2_ctg1
BX679665  RP23-247J17    Mmchr2_ctg1
AL929179  RP23-428M4     Mmchr2_ctg1
AL831794  RP23-114B13    Mmchr2_ctg1
AL845548  RP23-307N14    Mmchr2_ctg1
AL928795  RP23-38B1 Mmchr2_ctg1
AL928909  RP23-320I18    Mmchr2_ctg1
AL845313  RP23-202C2     Mmchr2_ctg1
AL845533  RP23-232K16    Mmchr2_ctg1
AL772342  RP23-105D19    Mmchr2_ctg1
AL928641  RP23-272N6     Mmchr2_ctg1
AL928560  RP23-353N23    Mmchr2_ctg1
BX649225  RP23-104N16    Mmchr2_ctg1
AL929209  RP23-415C3     Mmchr2_ctg1
AL935271  RP23-336A16    Mmchr2_ctg1
AL928807  RP23-97D20     Mmchr2_ctg1
AL773538  RP23-14I24     Mmchr2_ctg1
AL772303  RP23-185P20    Mmchr2_ctg1
BX322642  RP24-363O9     Mmchr2_ctg1
AL928918  RP23-403G13    Mmchr2_ctg1
AL844560  RP23-334M9     Mmchr2_ctg1
AL845434  RP23-211O3     Mmchr2_ctg1
AL845290  RP23-201A19    Mmchr2_ctg1
AL844558  RP23-378I2     Mmchr2_ctg1
BX649230  RP23-157J23    Mmchr2_ctg1
AL935312  RP23-56A7 Mmchr2_ctg1
AL929165  RP23-446D4     Mmchr2_ctg1
AL928632  RP23-303M15    Mmchr2_ctg1
AL929268  RP23-379F6     Mmchr2_ctg1
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AL929158 RP23-92O15 Mmchr2_ctg1
AL844166 RP23-107K21 Mmchr2_ctg1
AL845417 RP23-20I9 Mmchr2_ctg1
AL928841 RP23-95M4 Mmchr2_ctg1
AL844839 RP23-191F2 Mmchr2_ctg1
AL845543 RP23-257O6 Mmchr2_ctg1
AL935116 RP23-59I2 Mmchr2_ctg1
AL772224 RP23-131N18 Mmchr2_ctg1
AL845271 RP23-119O19 Mmchr2_ctg1
AL928888 RP23-390M20 Mmchr2_ctg1
AL844888 RP23-193F18 Mmchr2_ctg1
AL845520 RP23-283C20 Mmchr2_ctg1
AL928882 RP23-281I20 Mmchr2_ctg1
BX510346 RP23-188D15 Mmchr2_ctg1
AL929011 RP23-55O12 Mmchr2_ctg1
AL928545 RP23-218A13 Mmchr2_ctg1
AL935297 RP23-419K8 Mmchr2_ctg1
AL772218 RP23-129K21 Mmchr2_ctg1
AL845498 RP23-222D20 Mmchr2_ctg1
AL954131 RP23-32H12 Mmchr2_ctg1
AL928589 RP23-350C1 Mmchr2_ctg1
AL928557 RP23-349H7 Mmchr2_ctg1
AL928620 RP23-319M16 Mmchr2_ctg1
AL845265 RP23-158O8 Mmchr2_ctg1
AL928904 RP23-463M17 Mmchr2_ctg1
AL928680 RP23-396N6 Mmchr2_ctg1
AL928653 RP23-410F9 Mmchr2_ctg1
AL844855 RP23-113K9 Mmchr2_ctg1
AL929034 RP23-90F9 Mmchr2_ctg1
AL928806 RP23-34E4 Mmchr2_ctg1
BX649213 RP24-189E15 Mmchr2_ctg1
AL928877 RP23-52D18 Mmchr2_ctg1
AL928860 RP23-5I15 Mmchr2_ctg1
BX571892 RP23-207B21 Mmchr2_ctg1
AL928572 RP23-333P17 Mmchr2_ctg1
AL845528 RP23-25P15 Mmchr2_ctg1
BX276179 RP23-204B24 Mmchr2_ctg1
AL844538 RP23-289K19 Mmchr2_ctg1
BX649224 RP24-555L22 Mmchr2_ctg1
AL929100 RP23-436G18 Mmchr2_ctg1
BX649226 RP23-105O21 Mmchr2_ctg1
AL773540 RP23-177L19 Mmchr2_ctg1
AL929117 RP23-442K5 Mmchr2_ctg1
AL928939 RP23-294B13 Mmchr2_ctg1
AL929311 RP23-291N2 Mmchr2_ctg1
BX294442 RP23-310O19 Mmchr2_ctg1
AL772387 RP23-133B16 Mmchr2_ctg1

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AL805928  RP23-136C12    Mmchr2_ctg1
AL929257  RP23-75A23     Mmchr2_ctg1
AL929064  RP23-442A7     Mmchr2_ctg1
AL929036  RP24-548P4     Mmchr2_ctg1
GAP  TYPE-3    20000     ALIGNMENT
AL928693  RP23-407K8     Mmchr2_ctg2
BX649461  RP23-114M13    Mmchr2_ctg2
CT030013  RP23-282P19    Mmchr2_ctg2
AL845257  RP23-280K4     Mmchr2_ctg2
AL928706  RP23-54E16     Mmchr2_ctg2
CR847856  RP23-447G16    Mmchr2_ctg2
AL773534  RP23-183O12    Mmchr2_ctg2
AL928690  RP23-443L19    Mmchr2_ctg2
AL844844  RP23-103D7     Mmchr2_ctg2
AL844838  RP23-263E15    Mmchr2_ctg2
BX005038  RP24-550O4     Mmchr2_ctg2
AL732430  RP23-176J12    Mmchr2_ctg2
AL732528  RP23-218B17    Mmchr2_ctg2
AL732546  RP23-264D16    Mmchr2_ctg2
BX294112  RP24-316M2     Mmchr2_ctg2
AL732525  RP23-358I10    Mmchr2_ctg2
AL935039  RP24-144B2     Mmchr2_ctg2
AL732585  RP23-226M2     Mmchr2_ctg2
AL732309  RP23-132N23    Mmchr2_ctg2
AL732557  RP23-47P18     Mmchr2_ctg2
AL732590  RP23-464C2     Mmchr2_ctg2
BX649340  RP23-225D24    Mmchr2_ctg2
AL731682  RP23-123F7     Mmchr2_ctg2
AL845455  RP23-325E4     Mmchr2_ctg2
AL773595  RP23-297I16    Mmchr2_ctg2
AL732541  RP23-306D20    Mmchr2_ctg2
BX649422  RP23-70A22     Mmchr2_ctg2
AL732311  RP23-125H15    Mmchr2_ctg2
AL773563  RP23-414L19    Mmchr2_ctg2
AL845266  RP23-449M10    Mmchr2_ctg2
AL954801  RP23-171K6     Mmchr2_ctg2
BX649202  RP24-157P15    Mmchr2_ctg2
AL731552  RP23-113K24    Mmchr2_ctg2
AL772282  RP23-328F3     Mmchr2_ctg2
AL772166  RP23-413I12    Mmchr2_ctg2
AL928953  RP24-83K6 Mmchr2_ctg2
AL732513  RP23-344B24    Mmchr2_ctg2
AL731778  RP23-475B13    Mmchr2_ctg2
AL732616  RP23-466D3     Mmchr2_ctg2
AL772249  RP23-430H1     Mmchr2_ctg2
AL928994  RP24-118E9     Mmchr2_ctg2
AL731851  RP23-362N19    Mmchr2_ctg2
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AL732526 RP23-338O4 Mmchr2_ctg2
AL845267 RP23-426D2 Mmchr2_ctg2
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