

Tiling Path File (TPF) Specification v1.4

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**

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.
- ✚ 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



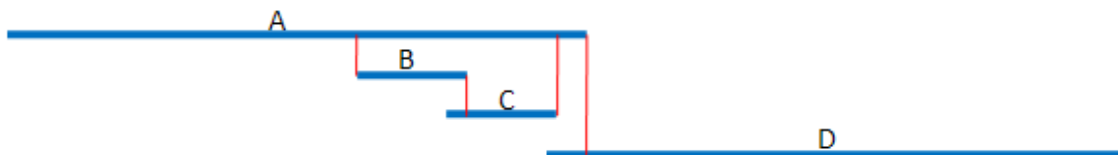
Example A2: Multiple non-overlapping contained clones



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

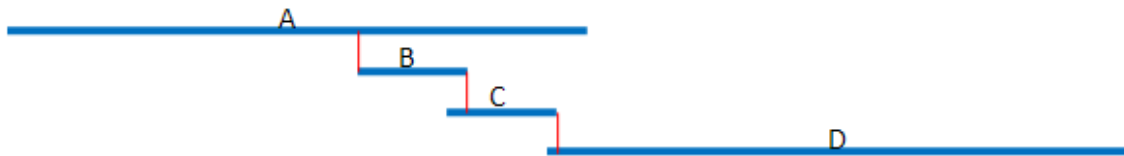


Example B2: Multiple non-overlapping contained clones



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  CENTROMERE3000000
?    WI1-1974M19      Mmchr2_ctg1
?    WI1-923N3        Mmchr2_ctg1
CU207330  WI1-2764C4Mmchr2_ctg1
AL928883  RP23-60E18Mmchr2_ctg1
AL732620  RP23-167G19      Mmchr2_ctg1
```

AL929080 RP24-129J15 Mmchr2_ctg1
AL732328 RP23-106P4Mmchr2_ctg1
AL844530 RP23-248L2Mmchr2_ctg1
CU181741 WI1-2132D7 Mmchr2_ctg1 CONTAINED AL845441 RP23-327I5
AL845441 RP23-327I5Mmchr2_ctg1
AL935139 RP23-74F20Mmchr2_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 RP23-198G1Mmchr2_ctg1
BX682541 RP23-349P20 Mmchr2_ctg1
AL928662 RP23-379M5Mmchr2_ctg1
AL732403 RP23-119L20 Mmchr2_ctg1
BX323054 RP23-329P15 Mmchr2_ctg1
AL928940 RP23-94J17Mmchr2_ctg1
AL929142 RP23-340A13 Mmchr2_ctg1
AL928958 RP23-344N23 Mmchr2_ctg1
AL928924 RP23-307E15 Mmchr2_ctg1
CR388026 RP23-39L16Mmchr2_ctg1
AL928735 RP23-413M3Mmchr2_ctg1
BX842658 RP23-86F17Mmchr2_ctg1
AL845275 RP23-112F5Mmchr2_ctg1
AL845515 RP23-256D19 Mmchr2_ctg1
AL845492 RP23-222P7Mmchr2_ctg1
AL929240 RP23-245A10 Mmchr2_ctg1
AL772190 RP23-124P7Mmchr2_ctg1
CR936244 RP24-562B12 Mmchr2_ctg1
CU207293 WI1-632G16Mmchr2_ctg1
AL845485 RP23-237D23 Mmchr2_ctg1
BX649227 RP23-114C18 Mmchr2_ctg1
AL840637 RP23-113H3Mmchr2_ctg1
AL845488 RP23-215P8Mmchr2_ctg1
AL928600 RP23-348O19 Mmchr2_ctg1
AL929143 RP23-339G18 Mmchr2_ctg1
AL773590 RP23-181A13 Mmchr2_ctg1
BX005023 RP24-316N23 Mmchr2_ctg1
AL928713 RP23-399M5Mmchr2_ctg1
AL929149 RP23-93B24Mmchr2_ctg1
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 RP23-119N4Mmchr2_ctg1

AL953853 RP23-6M16 Mmchr2_ctg1
AL772216 RP23-153M22 Mmchr2_ctg1
AL844485 RP23-436D21 Mmchr2_ctg1
AL845264 RP23-116F18 Mmchr2_ctg1
AL772352 RP23-147F6Mmchr2_ctg1
AL928715 RP23-373D16 Mmchr2_ctg1
AL929020 RP23-291L24 Mmchr2_ctg1
BX679665 RP23-247J17 Mmchr2_ctg1
AL929179 RP23-428M4Mmchr2_ctg1
AL831794 RP23-114B13 Mmchr2_ctg1
AL845548 RP23-307N14 Mmchr2_ctg1
AL928795 RP23-38B1 Mmchr2_ctg1
AL928909 RP23-320I18 Mmchr2_ctg1
AL845313 RP23-202C2Mmchr2_ctg1
AL845533 RP23-232K16 Mmchr2_ctg1
AL772342 RP23-105D19 Mmchr2_ctg1
AL928641 RP23-272N6Mmchr2_ctg1
AL928560 RP23-353N23 Mmchr2_ctg1
BX649225 RP23-104N16 Mmchr2_ctg1
AL929209 RP23-415C3Mmchr2_ctg1
AL935271 RP23-336A16 Mmchr2_ctg1
AL928807 RP23-97D20Mmchr2_ctg1
AL773538 RP23-14I24Mmchr2_ctg1
AL772303 RP23-185P20 Mmchr2_ctg1
BX322642 RP24-363O9Mmchr2_ctg1
AL928918 RP23-403G13 Mmchr2_ctg1
AL844560 RP23-334M9Mmchr2_ctg1
AL845434 RP23-211O3Mmchr2_ctg1
AL845290 RP23-201A19 Mmchr2_ctg1
AL844558 RP23-378I2Mmchr2_ctg1
BX649230 RP23-157J23 Mmchr2_ctg1
AL935312 RP23-56A7 Mmchr2_ctg1
AL929165 RP23-446D4Mmchr2_ctg1
AL928632 RP23-303M15 Mmchr2_ctg1
AL929268 RP23-379F6Mmchr2_ctg1
AL929158 RP23-92O15Mmchr2_ctg1
AL844166 RP23-107K21 Mmchr2_ctg1
AL845417 RP23-20I9 Mmchr2_ctg1
AL928841 RP23-95M4 Mmchr2_ctg1
AL844839 RP23-191F2Mmchr2_ctg1
AL845543 RP23-257O6Mmchr2_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 RP23-55O12Mmchr2_ctg1
AL928545 RP23-218A13 Mmchr2_ctg1
AL935297 RP23-419K8Mmchr2_ctg1
AL772218 RP23-129K21 Mmchr2_ctg1
AL845498 RP23-222D20 Mmchr2_ctg1

AL954131 RP23-32H12Mmchr2_ctg1
AL928589 RP23-350C1Mmchr2_ctg1
AL928557 RP23-349H7Mmchr2_ctg1
AL928620 RP23-319M16 Mmchr2_ctg1
AL845265 RP23-158O8Mmchr2_ctg1
AL928904 RP23-463M17 Mmchr2_ctg1
AL928680 RP23-396N6Mmchr2_ctg1
AL928653 RP23-410F9Mmchr2_ctg1
AL844855 RP23-113K9Mmchr2_ctg1
AL929034 RP23-90F9 Mmchr2_ctg1
AL928806 RP23-34E4 Mmchr2_ctg1
BX649213 RP24-189E15 Mmchr2_ctg1
AL928877 RP23-52D18Mmchr2_ctg1
AL928860 RP23-5I15 Mmchr2_ctg1
BX571892 RP23-207B21 Mmchr2_ctg1
AL928572 RP23-333P17 Mmchr2_ctg1
AL845528 RP23-25P15Mmchr2_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 RP23-442K5Mmchr2_ctg1
AL928939 RP23-294B13 Mmchr2_ctg1
AL929311 RP23-291N2Mmchr2_ctg1
BX294442 RP23-310O19 Mmchr2_ctg1
AL772387 RP23-133B16 Mmchr2_ctg1
AL805928 RP23-136C12 Mmchr2_ctg1
AL929257 RP23-75A23Mmchr2_ctg1
AL929064 RP23-442A7Mmchr2_ctg1
AL929036 RP24-548P4Mmchr2_ctg1
GAP TYPE-3 20000 ALIGNMENT
AL928693 RP23-407K8Mmchr2_ctg2
BX649461 RP23-114M13 Mmchr2_ctg2
CT030013 RP23-282P19 Mmchr2_ctg2
AL845257 RP23-280K4Mmchr2_ctg2
AL928706 RP23-54E16Mmchr2_ctg2
CR847856 RP23-447G16 Mmchr2_ctg2
AL773534 RP23-183O12 Mmchr2_ctg2
AL928690 RP23-443L19 Mmchr2_ctg2
AL844844 RP23-103D7Mmchr2_ctg2
AL844838 RP23-263E15 Mmchr2_ctg2
BX005038 RP24-550O4Mmchr2_ctg2
AL732430 RP23-176J12 Mmchr2_ctg2
AL732528 RP23-218B17 Mmchr2_ctg2
AL732546 RP23-264D16 Mmchr2_ctg2
BX294112 RP24-316M2Mmchr2_ctg2
AL732525 RP23-358I10 Mmchr2_ctg2
AL935039 RP24-144B2Mmchr2_ctg2
AL732585 RP23-226M2Mmchr2_ctg2
AL732309 RP23-132N23 Mmchr2_ctg2
AL732557 RP23-47P18Mmchr2_ctg2
AL732590 RP23-464C2Mmchr2_ctg2

BX649340	RP23-225D24	Mmchr2_ctg2
AL731682	RP23-123F7Mmchr2_ctg2	
AL845455	RP23-325E4Mmchr2_ctg2	
AL773595	RP23-297I16	Mmchr2_ctg2
AL732541	RP23-306D20	Mmchr2_ctg2
BX649422	RP23-70A22Mmchr2_ctg2	
AL732311	RP23-125H15	Mmchr2_ctg2
AL773563	RP23-414L19	Mmchr2_ctg2
AL845266	RP23-449M10	Mmchr2_ctg2
AL954801	RP23-171K6Mmchr2_ctg2	
BX649202	RP24-157P15	Mmchr2_ctg2
AL731552	RP23-113K24	Mmchr2_ctg2
AL772282	RP23-328F3Mmchr2_ctg2	
AL772166	RP23-413I12	Mmchr2_ctg2
AL928953	RP24-83K6	Mmchr2_ctg2
AL732513	RP23-344B24	Mmchr2_ctg2
AL731778	RP23-475B13	Mmchr2_ctg2
AL732616	RP23-466D3Mmchr2_ctg2	
AL772249	RP23-430H1Mmchr2_ctg2	
AL928994	RP24-118E9Mmchr2_ctg2	
AL731851	RP23-362N19	Mmchr2_ctg2
AL732526	RP23-338O4Mmchr2_ctg2	
AL845267	RP23-426D2Mmchr2_ctg2	
AL772379	RP23-170D24	Mmchr2_ctg2
AL772213	RP23-104G16	Mmchr2_ctg2
AL929437	RP23-74P16Mmchr2_ctg2	
AL845323	RP23-304D11	Mmchr2_ctg2
BX294378	RP23-457B12	Mmchr2_ctg2
AL928926	RP23-443G7Mmchr2_ctg2	
BX005298	RP23-261D24	Mmchr2_ctg2
AL845258	RP23-315H12	Mmchr2_ctg2
AL954388	RP23-395P6Mmchr2_ctg2	
AL954299	RP23-399D3Mmchr2_ctg2	
AL928593	RP23-100E9Mmchr2_ctg2	
BX649430	RP24-553E7Mmchr2_ctg2	
AL844532	RP23-221O14	Mmchr2_ctg2
AL844546	RP23-243I3Mmchr2_ctg2	
AL732572	RP23-32C16Mmchr2_ctg2	
AL928861	RP24-153B19	Mmchr2_ctg2
AL732564	RP23-442G9Mmchr2_ctg2	
AL929275	RP23-65P13Mmchr2_ctg2	
BX511243	RP23-62N18Mmchr2_ctg2	
AL928893	RP23-55I14Mmchr2_ctg2	
AL808027	RP23-161B9Mmchr2_ctg2	
AL928669	RP23-375I1Mmchr2_ctg2	
AL928710	RP23-255P20	Mmchr2_ctg2
AL772271	RP23-17P12Mmchr2_ctg2	
AL845471	RP23-320N1Mmchr2_ctg2	
AL929154	RP23-94M9	Mmchr2_ctg2
AL731852	RP23-365F1Mmchr2_ctg2	
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