**Tiling Path File (TPF) Specification v1.8**

**Date: Nov. 6, 2013**

**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, along with the desired orientation of the component sequences. 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 header information will be calculated upon 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 by 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 DB nomenclature will be used. **OPTIONAL**.

* If a sequence is derived from more than one clone, the clone name can be given as “MULTIPLE”.
* Use “?“ if clone name unknown or component is not a clone.

**Column 3:** local contig identifier. The name given to the scaffold/contig generated by assembling the listed sequences. **REQUIRED.**

* **NOTE: A local contig identifier may only be used once per assembly.**

**Column 4:** contained status or component orientation. This column is only used to specify clones that are known to be contained within another clone on the TPF, or to indicate the desired orientation of a component within the contig.

* For contained components, the only values allowed are "CONTAINED" and "CONTAINED\_TURNOUT". **Use: REQUIRED for contained components, otherwise OPTIONAL.**
* When indicating orientation, the only allowed values are "PLUS" and "MINUS". **Use: OPTIONAL.**
	+ **Note:** If no orientation is specified for a singleton component, a default orientation of “PLUS” is assumed
	+ **Note:** Orientation cannot be specified for components marked as contained

**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 DB 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 with CONTAINED or CONTAINED\_TURNOUT in a sequence line, do not populate columns 5 or 6. If column 4 is populated with CONTAINED or CONTAINED\_TURNOUT, 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.
* Biological Feature: If there are TPF components providing representation of a biological feature (e.g. centromere, heterochromatin), use the following terms to flank the first and last such components on the TPF. **NOTE: No gap will be inserted at these lines; they are used for TPF mark-up only.**
	+ CENTROMERE\_DATA\_START
	+ CENTROMERE\_DATA\_END
	+ HETEROCHROMATIN\_DATA\_START
	+ HETEROCHROMATIN\_DATA\_END

**Column 3:**

* For TYPE-2, TYPE-3 or Biological gap: Gap size. Estimated size of gap. In the absence of submitted gap sizes, a pre-defined species-specific gap size 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
		- RADIATION HYBRID
		- PCR
		- FINGERPRINT
		- PAIRED ENDS
		- ALIGN GENUS
		- ALIGN XGENUS
		- ALIGN TRNSCPT
	+ Multiple methods may be entered for a single gap. Methods should be separated by a semi-colon (Example: FISH;OPTICAL MAP;ALIGN GENUS).
	+ **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 has 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 = CONTAINED or CONTAINED\_TURNOUT, then columns 5 and 6 must be populated.
* If column 4 = PLUS or MINUS, then columns 5 and 6 must not 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 a species-specific preset size if no sizing data is provided.
* Gap type-2 lines may not be adjacent to one another.
* Gap type-3 lines will default to a species-specific preset size if no sizing 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.

**Specifying Orientation for TPF Components**

Component orientation may be optionally specified in TPF column 4 (PLUS or MINUS).

* If the TPF component with specified orientation is a singleton, the specified orientation will be used in the AGP.
* If no orientation is specified for singleton TPF components, they will be placed in “plus” orientation in the AGP by default.

Although there is no need to specify orientation for non-singleton TPF components (their orientation is defined automatically via the alignments with neighboring components), this is allowed. This can be useful for cases where a TPF component is flanked by phase 1 or “?” components and will thus appear as a singleton in the AGP.

* If the TPF component with specified orientation appears as a singleton in the AGP, the specified orientation will be used in the AGP.
* If the TPF component with specified orientation does not appear as a singleton in the AGP, the orientation derived from its alignments will still be used for the purposes of contig building. However, if the component orientation in the AGP conflicts with the orientation specified on the TPF, a warning/error message will be reported.

Orientations cannot be specified on the TPF for contained components. Their orientation will always be derived from the alignment with the container clone.

 **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

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

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

AL805928 RP23-136C12 Mmchr2\_ctg1

AL929257 RP23-75A23 Mmchr2\_ctg1

AL929064 RP23-442A7 Mmchr2\_ctg1

AL929036 RP24-548P4 Mmchr2\_ctg1

GAP TYPE-3 20000 ALIGN XGENUS

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

AL732526 RP23-338O4 Mmchr2\_ctg2

AL845267 RP23-426D2 Mmchr2\_ctg2

AL772379 RP23-170D24 Mmchr2\_ctg2

AL772213 RP23-104G16 Mmchr2\_ctg2

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