

## Tiling Path File (TPF) Specification v1.9

### Date: Feb. 25, 2019

**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", "CONTAINED\_TURNOUT" and "CONTAINED\_SUBSEQ". **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 or CONTAINED\_SUBSEQ, 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 or CONTAINED\_SUBSEQ, 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 or CONTAINED\_SUBSEQ in a sequence line, do not populate columns 5 or 6. If column 4 is populated with CONTAINED or CONTAINED\_TURNOUT or CONTAINED\_SUBSEQ, then provide values or "?" for columns 5 and 6.

**Column 7:** Sequence start. This column must contain a positive numerical value. This column is only used if column 4 is populated with CONTAINED\_SUBSEQ. This column is only used to provide the START coordinate of accession in column 1 at which switch occurs from CONTAINER to CONTAINED\_SUBSEQ (in 1-base coordinates).

**Column 8:** Sequence stop. This column must contain a positive numerical value. This column is only used if column 4 is populated with CONTAINED\_SUBSEQ. This column is only used to provide the STOP coordinate of accession in column 1 at which switch occurs from CONTAINED\_SUBSEQ to CONTAINER (in 1-base coordinates).

### **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 or CONTAINED\_SUBSEQ, then columns 5 and 6 must be populated.
- If column 4 = CONTAINED\_SUBSEQ, then columns 7 and 8 must be populated.
- If column 4 = CONTAINED\_SUBSEQ, then columns 7 and 8 must be numerical values.
- If column 4 = CONTAINED\_SUBSEQ, then columns 7 and 8 cannot be zero or negative values.
- If column 4 = CONTAINED\_SUBSEQ, then numerical value in column 7 must be smaller than numerical value in column 8.
- If column 4 = CONTAINED\_SUBSEQ, then numerical values in columns 7 and 8 must be within range of sequence specified in column 1.

- If column 4 = PLUS or MINUS, then columns 5, 6, 7 and 8 must not be populated.
- If column 4 is not populated, then columns 5, 6, 7 and 8 must not be populated.
- If column 4 = CONTAINED or CONTAINED\_TURNOUT or CONTAINED\_SUBSEQ, 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 three designators that can be used to mark contained components on the TPF: CONTAINED, CONTAINED\_TURNOUT, and CONTAINED\_SUBSEQ. The designators differ in the switch point selection rules applied to the contained component during AGP production. The rule of full alignment of contained to container does not apply to CONTAINED\_SUBSEQ.

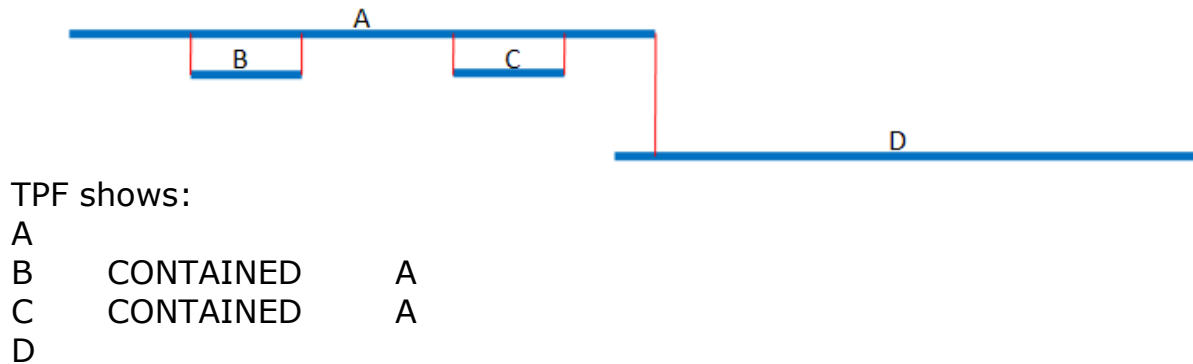
#### A. CONTAINED

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

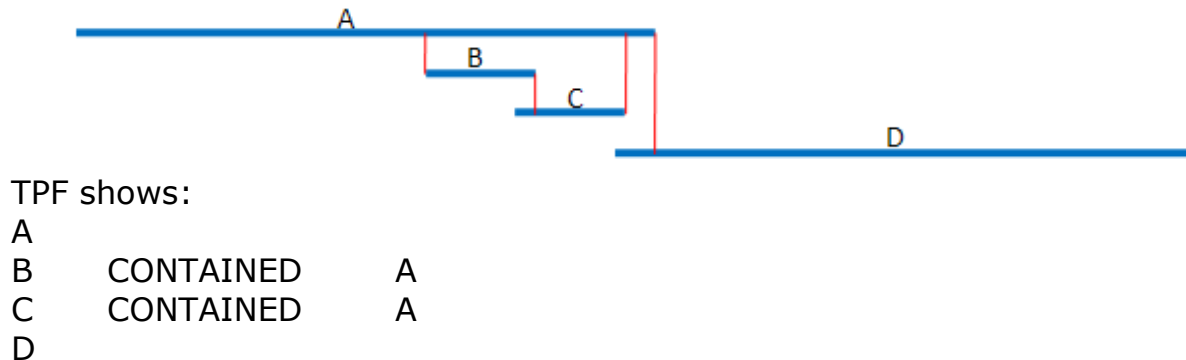
##### Example A1: Single contained clone



##### Example A2: Multiple non-overlapping contained clones



##### Example A3: Multiple overlapping contained clones



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

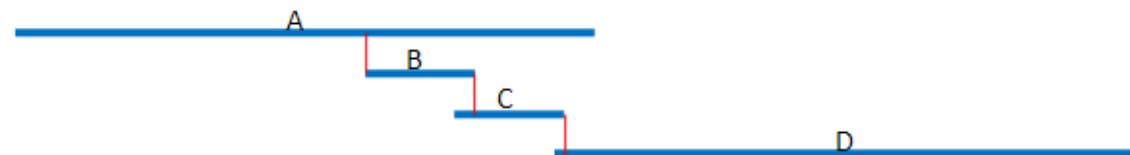


TPF shows:

```

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.**

### C. CONTAINED\_SUBSEQ

TPF components marked with the "CONTAINED\_SUBSEQ" designator will follow using the switch points provided in columns 7 and 8 during AGP production. Example for usage is shown.

**Example C1: Small sequence of a long-read inserted into a clone**



The software will use the switch points provided in columns 7 and 8 to produce the AGP.

### 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 or CONTAINED\_SUBSEQ, 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
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