

Tiling Path File (TPF) Specification v1.1

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 is required and a supplied version will be ignored. 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. This line is only used to specify clones that are known to be contained within another clone on the TPF. The only value allowed is ‘contained’. **OPTIONAL**

Column 5: accession number. This must be a valid accession assigned by the INSDC. No version number is required and a supplied version will be ignored. 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. See below for requirements. **REQUIRED if COLUMN 4 is included, otherwise not valid.**

Column 6: 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. See below for requirements. **REQUIRED IF COLUMN 4 is included, 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, but if both are known, please supply both values.


NOTE2: If column 4 has no value, do not include the “?” for any of 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

Column 3: Gap size. Estimated size of 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.

Column 4: 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

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.

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.
- ✚ 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 a clone is contained, it should be listed immediately before or after (i.e.: adjacent to) the containing clone, or adjacent to other contained clones within the containing clone.
- ✚ The contained clone can come before or after the clone in which it is contained.

For gap lines:

- ✚ Gap type-1 lines will be allowed, but are not encouraged. There can be adjacent type-1 gap lines. Size will default to 50 Kb if no data provided. This gap type may be deprecated in future versions.
- ✚ Gap type-2 lines will default to 50Kb if no other data is provided. There can be two adjacent type-2 gap lines.
- ✚ Gap type-3 should not be adjacent. Size will default to 50 Kb if no data is provided.
- ✚ Biological Gaps must provide a size estimate, they do not need to define a method.
- ✚ TYPE-3 gaps may not be contained within a contig
- ✚ BIOLOGICAL gaps may not be contained within a contig
- ✚ There can be consecutive 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.

Specific examples:

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

```
##ORGANISM: Mus musculus
##CHROMOSOME: 1
##ASSEMBLY NAME: NOD
##STRAIN/HAPLOTYPE/CULTIVAR: NOD
##TYPE: Contig
##VERSION: 1
##COMMENT: Test TPF
##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_ctg163199
AL596283      DN-257N2      NCBI_Mmchr1_ctg163199
CR936839      CH29-120A16   NCBI_Mmchr1_ctg37199
CR936842      CH29-189K17   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.

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
AL928947  RP23-69N1 Mmchr2_ctg1
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
AL929187	RP23-8G6	Mmchr2_ctg1
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
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AL772224 RP23-131N18 Mmchr2_ctg1
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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
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AL929257 RP23-75A23Mmchr2_ctg1
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GAP TYPE-3 20000ALIGNMENT

AL928693	RP23-407K8Mmchr2_ctg2
BX649461	RP23-114M13 Mmchr2_ctg2
CT030013	RP23-282P19 Mmchr2_ctg2
AL845257	RP23-280K4Mmchr2_ctg2
AL928706	RP23-54E16Mmchr2_ctg2
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AL773534	RP23-183O12 Mmchr2_ctg2
AL928690	RP23-443L19 Mmchr2_ctg2
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AL929186 RP23-399K8Mmchr2_ctg2

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 AL844588 RP23-244N6Mmchr2_ctg2
 AL845350 RP23-322M5Mmchr2_ctg2
 AL928639 RP23-446O17 Mmchr2_ctg2
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 AL845159 RP23-263O22 Mmchr2_ctg2
 BX293566 RP23-441G5Mmchr2_ctg2
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 AL935162 RP24-463M4Mmchr2_ctg2
 AL840626 RP23-151M8Mmchr2_ctg2
 BX649304 RP23-273K8Mmchr2_ctg2
 BX000439 RP23-430L20 Mmchr2_ctg2
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 AL805948 RP23-18C13Mmchr2_ctg2
 AL844553 RP23-255J15 Mmchr2_ctg2
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 AL844898 RP23-346M17 Mmchr2_ctg2
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