

Example .bed file format for multi-genome gene model input

chromosome ID	start coordinate	stop coordinate	gene model ID	genome ID	strand
chr1	34617	40204	Zm00001eb000010	B73	+
chr1	41214	46762	Zm00001eb000020	B73	-
chr1	47662	53272	Zm00030ab000010	Ki11	+
chr1	54156	59780	Zm00030ab000020	Ki11	-
chr1	99852	104723	Zm00040ab000020	P39	-
chr1	104584	115154	Zm00040ab000030	P39	-

This .bed file format is the required input for the multi-genome database build. Chromosomal coordinates make up the first three columns, followed by gene model ID, the genome ID (this genome ID will correspond to the genome IDs manually entered in the multi-genome “Genes in an Interval” genome drop-down menu; see Supplemental Figure S1), and strand. Genome ID can be either a genome’s official ID or an alias.

Example metadata format

File_handle	Data_id	Source	Type	Link	Description
eightDAS_root	Root 8 days after sowing	NAM Consortium	Expression	https://nam-genomes.org/	Plants were either field- or greenhouse-grown and roots were collected eight days after sowing.
sixteenDAP_embryo	Embryo 16 days after pollination	NAM Consortium	Expression	https://nam-genomes.org/	Plants were either field- or greenhouse-grown and embryos were collected 16 days after pollination.
whole_seed_24_days_after_pollination	whole seed 24 days after pollination	Diepenbrock 2017 [DellaPenna Lab]	Expression	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5774569/	All plants in each plot were self-pollinated, and pollination dates were recorded. A single ear from a given plot was harvested at (each of) 12, 24, and 36 DAP. Immediately after harvest, whole ears were frozen in liquid nitrogen. The ears were stored at -80 degrees C until kernels could be removed from the still-frozen ears, placed in test tubes, and maintained at -80 degrees C.

whole_seed_1 2_days_after_ pollination	whole seed 12 days after pollination	Diepenbrock 2017 [DellaPenna Lab]	Expression	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5774569/	All plants in each plot were self-pollinated, and pollination dates were recorded. A single ear from a given plot was harvested at (each of) 12, 24, and 36 DAP. Immediately after harvest, whole ears were frozen in liquid nitrogen. The ears were stored at -80 degrees C until kernels could be removed from the still-frozen ears, placed in test tubes, and maintained at -80 degrees C.
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This is the required metadata .csv format for the database build, including the column headers File_handle, Data_id, Source, Type, Link, and Description. File_handle must have the exact same name as the abundance file, minus the file extension. For instance, the file_handle “eightDAS_root” corresponds to an abundance .txt file named “eightDAS_root.txt”. Note that file_handle IDs and their associated .txt or .fpkm_tracking files cannot begin with a numeral, and cannot contain any non-alphanumeric character except an underscore (“_”). File handles can be descriptive, such as eightDAS_root, or have SRA numbers from NCBI (i.e. SRR12345 corresponding to a file called SRR12345.fpkm_tracking). “Source” is the name of the consortium or project that originally sequenced the data; “Link” contains the URL that links the Source to the project publication or the project website. “Description” contains general methods used to generate the library.

Example abundance .txt file format

Gene model ID	abundance
Zm00001eb000010	1.700325
Zm00001eb000020	52.9438
Zm00001eb000030	0.080943
Zm00030ab061810	0.0817445
Zm00030ab061820	16.4987
Zm00030ab061830	0
Zm00040ab201460	0.6890385
Zm00040ab201470	0.428948
Zm00040ab201490	0.29024503

Above is a subset of the “eightDAS_root.txt” input for the multi-genome database build. Gene model IDs for all genomes (distinguished by the prefixes Zm00001eb = B73, Zm00030ab =

Ki11, and Zm00040 = P39) are in Column A, and abundances (in this case, RNA-Seq fpkm values calculated by Cufflinks) is in Column B.

Drop-down organization for PHP files

The diagram illustrates the configuration of drop-down menus in PHP files for genome selection. It is divided into two main sections, labeled 1 and 2, with arrows indicating the mapping from code to form elements.

Section 1 (Bottom Left): This section shows the configuration for the "Genes in an Interval" Chromosome ID drop-down menu. The code defines a set of options for chromosomes 1 through 10, and an "all" option. The code is as follows:

```
<b><font color="green">Genome Version: <select name='filtered'>
<option value="genomeselect">select genome</option>
<option value="B73">B73_refgen5</option>
<option value="Ki11">Ki11</option>
<option value="P39">P39</option>
</select><br>
Chromosome: <select name='chr'>
<option value="chr1">Chromosome 1</option>
<option value="chr2">Chromosome 2</option>
<option value="chr3">Chromosome 3</option>
<option value="chr4">Chromosome 4</option>
<option value="chr5">Chromosome 5</option>
<option value="chr6">Chromosome 6</option>
<option value="chr7">Chromosome 7</option>
<option value="chr8">Chromosome 8</option>
<option value="chr9">Chromosome 9</option>
<option value="chr10">Chromosome 10</option>
<option value="all">All Chromosomes</option>
```

Section 2 (Top Right): This section shows the configuration for the "Genome Version" drop-down menu. The code defines a set of options for genome versions B73_refgen5, Ki11, and P39. The code is as follows:

```
<b><font color="green">Genome Version: <select name='filtered'>
<option value="genomeselect">select genome</option>
<option value="B73">B73_refgen5</option>
<option value="Ki11">Ki11</option>
<option value="P39">P39</option>
</select><br>
Chromosome: <select name='chr'>
<option value="chr1">Chromosome 1</option>
<option value="chr2">Chromosome 2</option>
<option value="chr3">Chromosome 3</option>
<option value="chr4">Chromosome 4</option>
<option value="chr5">Chromosome 5</option>
<option value="chr6">Chromosome 6</option>
<option value="chr7">Chromosome 7</option>
<option value="chr8">Chromosome 8</option>
<option value="chr9">Chromosome 9</option>
<option value="chr10">Chromosome 10</option>
<option value="all">All Chromosomes</option>
```

Form Elements: The form elements on the right show the visual representation of these configurations. The "Genome Version" drop-down menu is shown with options B73_refgen5, Ki11, and P39. The "Chromosome" drop-down menu is shown with options Chromosome 1 through Chromosome 10, and All Chromosomes. The "Genome Start Position" and "Genome End Position (bp)" fields are also visible.

Drop-down menu changes for chromosome ID (1) that must be manually edited in index_singlegenome.php, index_multigenome.php, and Protein_index.php files. Above is an example of the drop-down configurations for index_multigenome.php file on the left. At the bottom left (1) is the chromosome ID configuration for the "Genes in an Interval" Chromosome ID drop-down (lower right); this chromosome ID script is in all three different index_*.php files and must be edited in each to reflect the chromosome IDs of the target genome(s). For index_multigenome.php only (2), the Genome Version drop-down menu must be edited to reflect the genomes from the multi-genome bed file (described in Supplemental Table S1). Note that <option value= for the Genome Version dropdown menu in the php file corresponds to the genome ID listed in Column 5 of the bed file described in Supplemental Table S1.