

Tutorial 2: Using Map Resources

1. Please click on the “Available Maps” link under “maps” in the dark green navigation bar to begin.

MapView Resources

Genetic Maps

- Maps available in CMap (comparative map viewer)
 - Apple: MNY75441-58 | MNY75441-87 | MWijcik_McIntosh | MRomeBeauty | MRomeBeauty_2 | MWhiteAngel | MWhiteAngel_2 | Fiesta x Discovery apple 2006
 - Pear: Bartlett | Housui | Kinchaku1a | Kinchaku1b
 - Prunus: Prunus bin map 2005 | TxE almond x peach F2 2004 | Myrobalan Plum x Almond-Peach hybrid 2004 | GxN almond x peach F2 2001 | Prunus Transcriptome Map | Prunus Resistance Map
 - Almond: Almond FxT 2000 | Almond FxB F1 1998
 - Apricot: Apricot GxV F1 2002 | Apricot LxL F2 2003 | Apricot LxB 2007
 - Cherry (Sour cherry): PoerasusEB | PoerasusRS
 - Peach: Peach AxJ 2005 | Peach PMP2 2005 | Peach peach x P. ferganensis BC1 PxF 2005 | Peach JxF 2004 | Peach So x B 1998 | Guardian x Nemaguard 2007 | Lovell x Nemared 1998 | NJ Pillar x KV 77119 1998
 - Raspberry: Red Raspberry L x Gm 2006 | Red Raspberry MJ x MO 2007
 - Rose: Diploid Rose D10 x E15 F1 2005
 - Strawberry: FVxFN diploid Fragaria reference map | 815x903BC diploid Fragaria 2006
- Major Prunus trait loci anchored to the reference TxE map
— View the description of the major Prunus trait loci anchored to TxE map. Links to CMap.
- Template for for data submission is available with the effort to develop more extensive map/marker database.

Peach Transcriptome Map

- Peach transcriptome map project page
- View transcriptome map in CMap (ESTs anchored to TxE map)

Peach Physical Map

- Peach physical mapping project page
- View Peach Physical Map (WebFPC or WebChrom)
View the contigs of BAC clones of peach physical map. Markers and BACs are linked to GDR sites.
- Interactive TxE general prunus map with anchored BACs and ESTs
Interactive map viewer that displays anchored BACs and ESTs to markers in each linkage group.

This page is the starting point for all of the mapping resources for GDR. This page shows what maps are available in GDR and provides direct links to each genetic map in CMap, peach transcriptome map, and peach physical map. There are also links to project pages for peach physical mapping and transcriptome development that have details of the projects and more links to the related data. This tutorial will explore all the graphical interfaces to maps and illustrate how they are integrated into each data detail page.

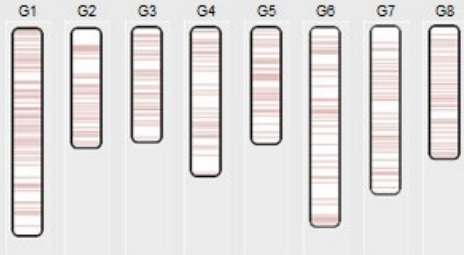
2. Please continue by clicking on the “CMap” link under “maps” in the dark green navigation bar to begin.

CMap is a very important mapping tool that allows comparisons between genetic and physical maps. This software is developed and provided by the researchers at Gramene (www.gramene.org). The CMap section of the mapping resources is complex and has its own tutorial and help page. These can be found listed at the top of the CMap page.

3. Please continue by clicking on the “GDR MapViewer Peach” link under the “maps” in the dark green navigation bar.

View BACs and ESTs anchored to the prunus TxE map

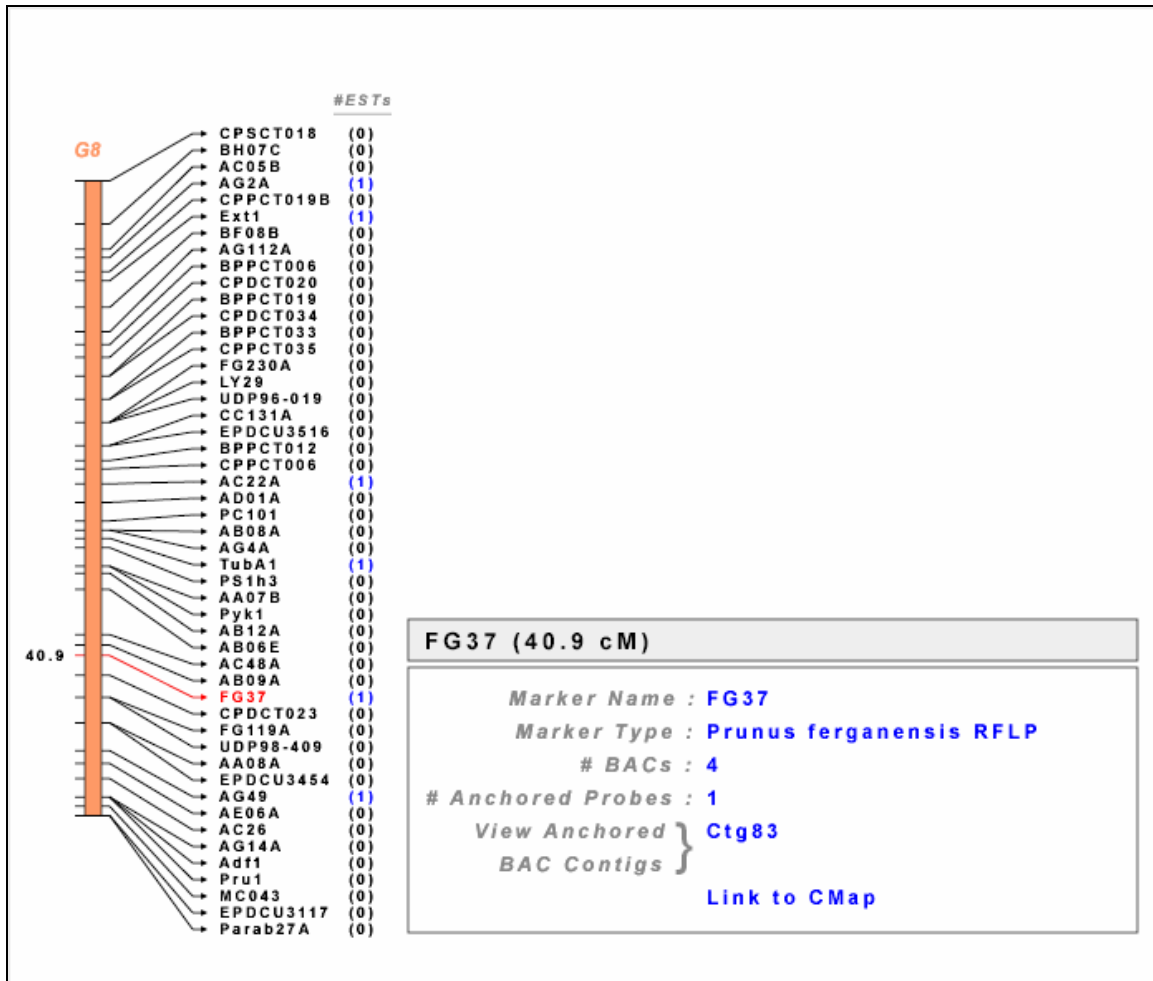
The eight linkage groups of the general Prunus map (TxE) are shown. Click any linkage group to get the information of the markers, and BACs and ESTs anchored to loci. Only the markers that are used for BAC hybridization are shown.



Instructions:

- To view the linkage group in details, you need SVG Viewer plug-in for your web browser.
- To check whether you have SVG plug-in, [click here](#).
- To download the plug-in, go to [Adobe Website](#).
- If you have any SVG viewer problems, please mail to [web database developer](#).

This page shows the eight linkage groups of the general Prunus map (TxE). To use the GDR MapViewer feature, the SVG Viewer plug-in is required. Instructions for obtaining this free software are listed below the linkage groups. To select a linkage group, click on the picture. It will link you directly to a page with the markers shown:



The linkage group is shown in orange along the left side of the screen. Each marker is listed to the right. The number of ESTs anchored to it shown in brackets. The ESTs shown are anchored to the map by hybridizing to the same BACs to which the marker has hybridized. Moving your pointer over the markers will show the location of the marker in centiMorgans along the left side of the linkage group picture. By clicking on the marker name, detailed information about this marker will show up in the main box.

Clicking on the marker name opens a page with detailed marker information:

Marker Information

Marker Name : FG37
 Marker Alias : NA
 Genbank ID : NA
 Marker Type : RFLP

Source ↗

source organism	Prunus ferganensis
source cultivar	NA
source description	Genomic DNA
source genbank id	NA
source marker	NA

Detection ↗

PCR condition	NA
screening method	NA
product length	NA
restriction enzyme	BamHI, DraI, EcoRI, HindIII, MvaI

Associated Sequences
 Monomorphic Population
 Polymorphism Data

Map Position ↗

map name	linkage group	bin	start	stop	locus name	view in CMap
Prunus Bin Map	G8	8:41	40.9	NA	FG37	CMap
GxN	G8	NA	29	NA	FG37	CMap
TxE	G8	NA	40.9	NA	FG37	CMap

Click locus name or the CMap link to view markers in the GDR map viewer or CMap. Click map name for more information of the map.

Contact ↗

contact name	email
I. Verde	email

Publication ↗

title	year	citation
Construction of a saturated linkage map for Prunus using an almond x peach F2 progeny.	1998	Theoretical and applied genetics. Theor. appl. genet. Nov 1998. v. 97 (7) p. 1034-1041. ISSN 0040-5752; THAGA6

The anchored BACs and the anchored ESTs can be explored by clicking on the headings in the light grey bar to the right of the main information.

If you return to the main linkage group page and click on a BAC or anchored probe associated with a marker, these links will open pages with further information.

AG106 (37.1 cM)

Marker Name : [AG106](#)
 Marker Type : [Prunus amygdalus RFLP](#)
 # BACs : [3](#)
 # Anchored Probes : [1](#)
 View Anchored } [Ctg37](#)
 BAC Contigs }
[Link to CMap](#)

BAC information link:

BACs Hybridized to Probe AG106

Click the BAC clone name for more data such as hybridized probes, BAC library, BAC contigs and link to Genetic and Physical maps.

Probe Name	:	AG106
Probe Type	:	almond RFLP
Probe provided by	:	P. Arus
BAC Clones	:	014I11
	:	022L02
	:	098F17

This page shows the BAC clones hybridized to the marker. Click on the BAC name for detailed information on the BAC clone.

Anchored Probe information link:

Other probes anchored to the locus AG106 (anchored by hybridization to the same BACs)

Probe Name	Probe Origin	Probe Type
LF55	Prunus persica	EST

This page shows other probes (eg. genetic markers and ESTs) that hybridized to the same BAC the marker hybridized to. Click on the probe name for further information on the probe.

If you return to the main linkage group page and click on the BAC contig name in “View Anchored BAC Contigs” field, it will open a WebFPC page for the BAC contig. This feature allows you to go from the TxE Prunus genetic map to the peach physical map.

AG32A (18 cM)

Marker Name : **AG32**
Marker Type : **Prunus amygdalus RFLP**
BACs : **5**
Anchored Probes : **1**
View Anchored BAC Contigs } **Ctg102, Ctg240, Ctg242**
[Link to CMap](#)

WebFPC v2.1 Clone rows Show Clones

Contig #102 Chr Chr Adjust zoom by Zoom

AG25 PP_LEa0007M11f
PP_LEa0021L08f
AG23 PP_LEa0003E19f
AG32

013F04
L007N10
090I06
L010A13
011G17*
030J10
034H13+
013I06

AG25 AG32

The main linkage group page also has a direct link to CMap, where the marker of interest will appear highlighted in yellow:

AG56 (6.4 cM)

Marker Name : **AG56**

Marker Type : **Prunus amygdalus RFLP**

BACs : 1

Anchored Probes : 1

View Anchored } **Ctg32**
BAC Contigs }

[Link to CMap](#)

CMap

[CMap Home](#) | [Maps](#) | [Search](#) | [Matrix](#) | [Map Sets](#) | [Feature Types](#) | [Map Types](#) | [Evidence Types](#) | [Species](#) | [Help](#) | [Tutorial](#)

Map Viewer :

Ref. Species :

Ref. Set :

Ref. Map :

Start :

End :

Highlight :

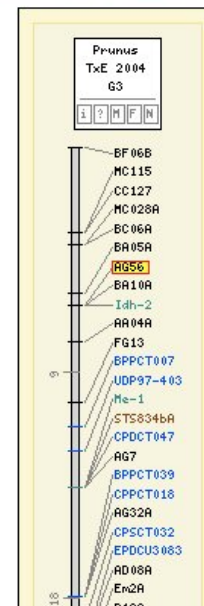
Comp. Map (Right) : == Genetic Maps ==

Current Maps : Prunus-TxE 2004-G3 (Ref.)

Comp. Map (Left) : == Genetic Maps ==

Image Size : Small Medium Large

Font Size : Small Medium Large



4. Please continue by clicking on the “WebChrom Peach” link under the “maps” in the dark green navigation bar.

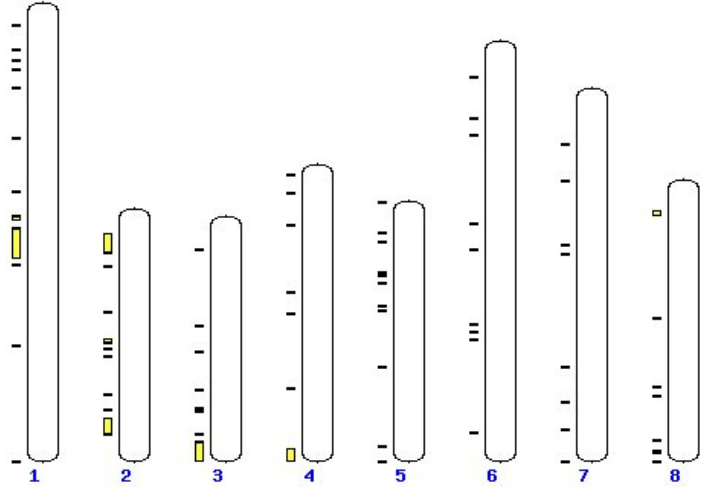
general info | species | projects | maps | search | tools | community

WebChrom: peach Chromosome

Home | WebFPC | WebChrom

WebChrom Search | WebChrom Help

Sequencing Status is shown by green bars in chromosome drawing
Click on a Chromosome to view further details.



The diagram displays eight vertical bars representing chromosomes, numbered 1 through 8. Each bar has a series of horizontal tick marks along its length. Small green rectangular bars are placed at various positions on the chromosomes to indicate sequencing status. Chromosome 1 has a green bar near the bottom. Chromosome 2 has a green bar near the top. Chromosome 3 has a green bar near the bottom. Chromosome 4 has a green bar near the bottom. Chromosome 5 has a green bar near the bottom. Chromosome 6 has a green bar near the top. Chromosome 7 has a green bar near the top. Chromosome 8 has a green bar near the top.

Note: JavaScript must be enabled to utilize WebChrom most fully

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This page shows the eight linkage groups of the general Prunus map which was used as a framework for building peach physical map. To see the information for each, click on one of the pictures.

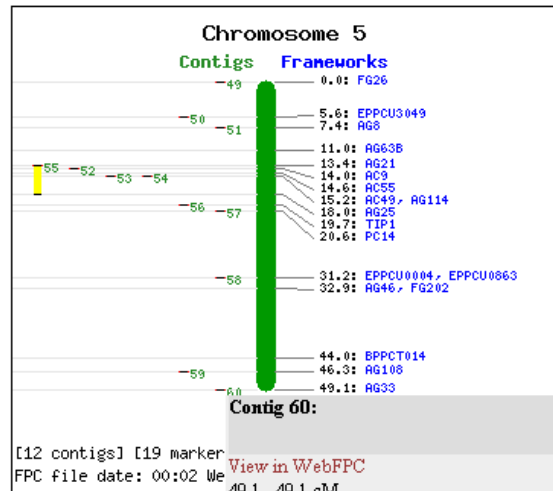
WebChrom: peach Chromosome 5

[Home](#) | [WebFPC](#) | [WebChrom](#)

[WebChrom Search](#) | [WebChrom Help](#)

Contigs / Frameworks

Click on a contig or framework for more detailed information.



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15 total clones
0 sequenced clones
2 unique markers hit
Max CB value: 95
CB 0 - 95 covered by FWs
1 framework(s) hit in this Chr.

To the left of the map are the contigs, which have been positioned by framework hits. The right of the map shows the markers with framework hits. Positioning your pointer over a marker or contig name will cause a pop-up box to show more information (see red arrow above). To make the box stay in place on the screen and not disappear, click on the “freeze” button. To make the box disappear, click on the “close” button.

The contig information box contains information such as length in centiMorgans, the number of clones in the contig, unique marker hits, etc. A link is provided to view the specific contig in WebFPC.

The marker information box (see below) shows information on position and the number of BAC clones hybridized to the marker in each anchored contig. Details on the contigs can be viewed by clicking the contig name. A link is provided to view the marker in WebFPC.

5. Please continue by clicking on the “WebFPC Peach” link under the “maps” in the dark green navigation bar.

The screenshot shows the WebFPC v2.1 web interface. At the top, it says "WebFPC: peach" and has navigation links for "Home", "WebFPC", and "WebChrom". The main heading is "WebFPC v2.1" with a "Help" button. There are two main sections: "Select Contig" and "Search for Contig".

The "Select Contig" section contains a table with the following data:

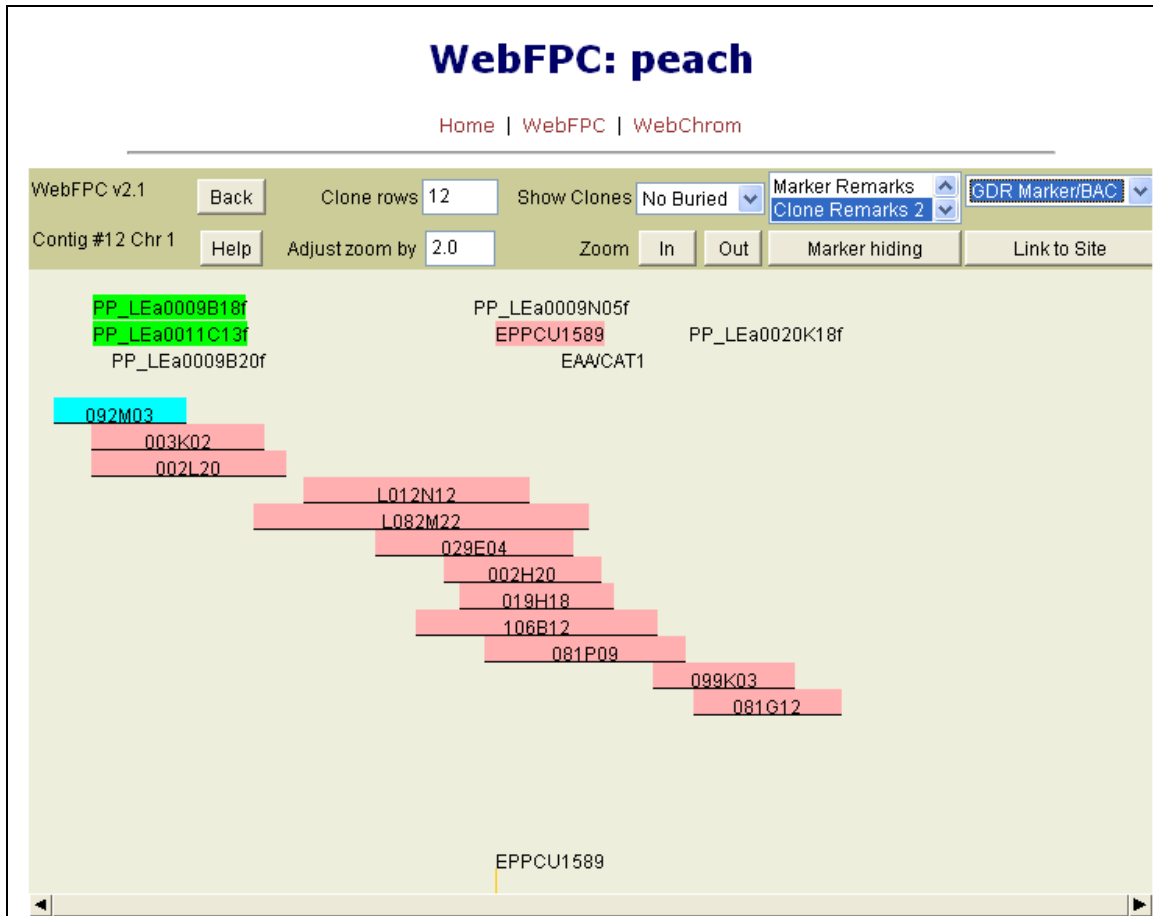
Contig	Clones	Markers	Sequence	Q #	Chr
1	6	3		0	1
2	15	4		3	1
3	8	1		0	1
4	2	1		0	1
5	2	1		0	1
6	14	12		2	1
7	10	3			1
8	2	2			1
9	16	4		3	1
10	13	2			1
11	15	10		4	1
12	12	7		0	1
13	17	8		1	1
14	10	2		0	1
15	7	3		0	1
16	13	6		1	1
17	8	3		0	1
18	13	10			2

The "Search for Contig" section has two search options: "Search By Marker" and "Search By Clone", each with an input field. Below these is a table with columns "Type", "Name", and "Ctg", which is currently empty. At the bottom of the interface, there are "Display" buttons under both the contig list and the search results table, and a "Clear" button next to the search results "Display" button.

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WebFPC lists the clones and markers associated with each contig on the peach physical map. This page allows users to search by marker or clone name in the upper left part of the page.

Selecting a contig and then clicking “Display” directly below the contig list will open a new page with more information on the contig.



The markers and clones are shown in relation to one another on the physical map. The clones can be hidden based on the selection beside “Hide Clones”. You can select the BACs or the probes (markers or ESTs) that are hybridized to the BACs, click “Link to Site” to go to the BAC, EST, or marker detail sites. You may zoom in or out on the contig in question by adjusting the zoom factor and clicking the “In” or “Out” buttons.

WebChrom/WebFPC program is developed by Arizona genomics computational laboratory (AGCoL) team. Detailed instruction on viewing WebFPC and WebChrom can be found in the manuals developed from the AGCoL team.

WebAGCoL (WebFPC/WebChrom) Users Manual

http://www.agcol.arizona.edu/software/webagcol/webagcol_installv2.2/Help_Dir/user.html