

# **GDR in Drupal**

**facilitating community building and  
efficient maintenance**



# GDR (Genome Database for Rosaceae)

is a web-based community database of Rosaceae genetics and genomics data and analysis tools facilitating utilization of the data among member species

[www.rosaceae.org](http://www.rosaceae.org)



# Topics

- GDR News
- Major objectives for the next grant period
  - Content
  - Infrastructure using Chado/Drupal (Demo)
- Data/tools currently available from GDR
- How to access the data and tools (Demo)

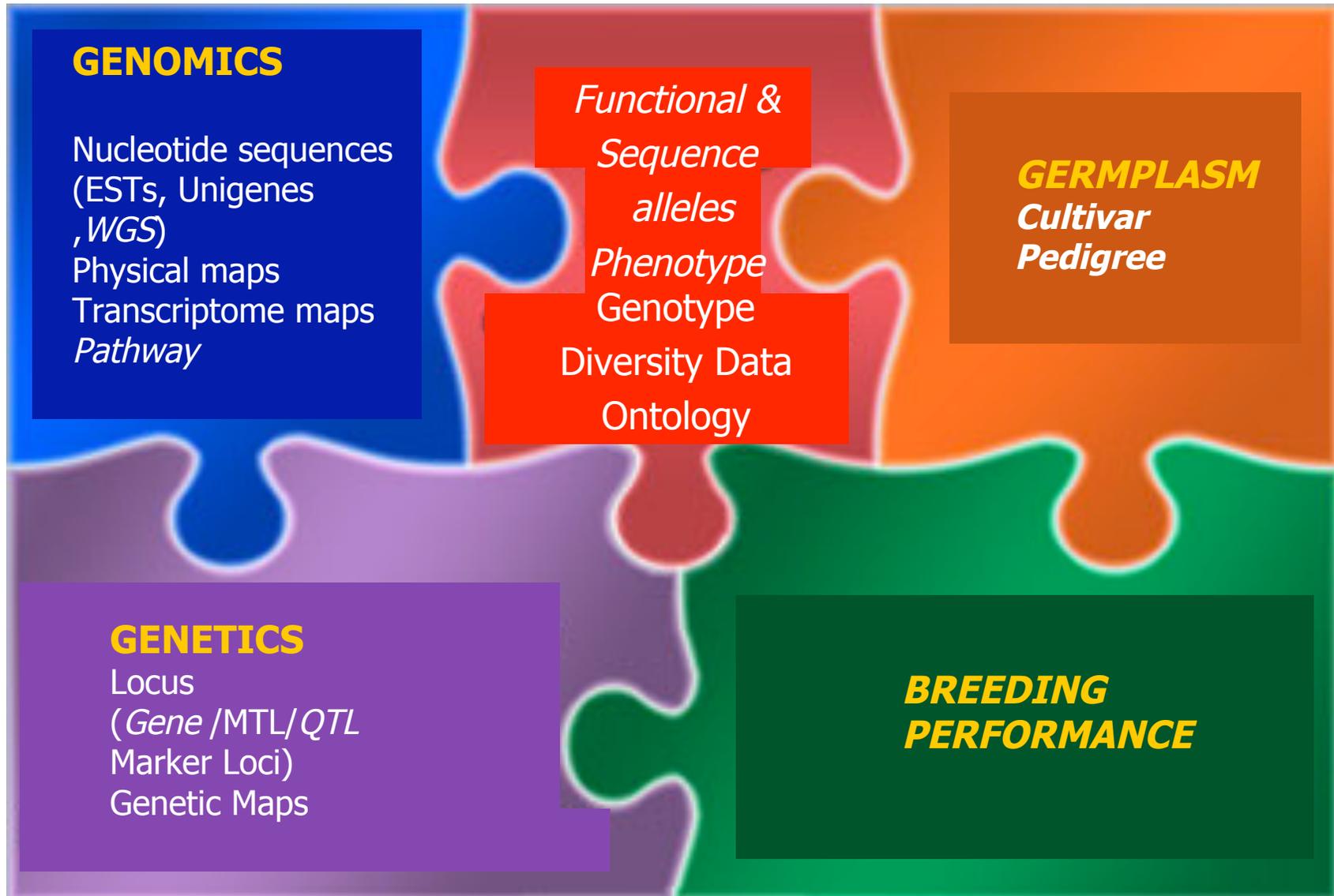
# GDR News

- GDR receives funding from Sept 2009 to Aug 2013 from the USDA Specialty Crop Research Initiative program 😊
- Tree fruit Genome Database Resources (tfGDR) will expand GDR to include Citrus.
- Whole genome sequence of peach in GBrowse (will go public in Apr 1)
  - apple and strawberry data to follow
- GDR is implemented in Drupal.
- Project site developed for RosBreed.

# Major goals for the next 4 years

- To integrate **whole genome sequences**, large-scale phenotyping/genotyping data, and **breeding data** with the current GDR data
- To develop an infrastructure using chado and drupal (tripal) that is easy to develop, implement and maintain

# Data to be integrated..



# Plan for Building an Efficient Database



**Content Management System**



Demo by Stephen Ficklin  
Jan 13<sup>th</sup> (Tue) 2:30 pm

**Drupal modules as web front-end for Chado**



**Chado**

**Generic Database schema**

# Advantages of using Drupal

## For Database Developers

- Easy to use and update
  - Provides functionality for community building – forums, calendars, project pages etc
- **Open Source, popular, robust, secure and modular**
- Users/Roles/Access Control

## For Users – control your own page/site!

- You can create/edit pages and upload data
  - for meetings/conference/employment
  - for project/lab sites
  - as editors for gene, QTL, breeding data, etc
  - access private data securely before publication



# Editing a project page

**GDR** | Genome Database  
For Rosaceae

Logged in as: sook | [Log Out](#)

[General Info](#) | [Species](#) | [Projects](#) | [Maps](#) | [Search](#) | [Tools](#) | [Community](#) | [Contact Us](#) | [Administer](#)

## Candidate Genes for Fruit Softening in Prunus

NRI Award #2005-35300-15463

PI: Cameron P. Peace  
Department of Horticulture  
Washington State University  
E-mail: [cpeace@wsu.edu](mailto:cpeace@wsu.edu)  
Telephone: 509-335-4800

### Candidate Genes for Fruit Softening in Prunus

**Title: \***

**Accomplishments:**  
[Menu settings](#)

Show summary in full view

**Body:**  
  
cpeace@wsu.edu  
Telephone: 509-335-6899"/>  
**Accomplishments:**

- Re-screening of two identified numerous: organization of the than 50-kb and per target endoPG gen

The first goal of the p

The second goal is to

# Creating a new page

The image shows a screenshot of the GDR Genome Database For Rosaceae website. The top navigation bar includes links for General Info, Species, Projects, Maps, Search, Tools, Community, Contact Us, and Administer. A search bar and a user login status (Logged in as: sook | Log Out) are also present. The main content area displays the title "Genetic Diversity of Wild Apple Accessions in the National Plant Germ" with "View" and "Edit" buttons. Below the title, there is contact information for Gayle Volk and Christopher Richards. A sidebar on the left lists "Accomplishments" and "Broad Impacts". The "Administer" menu is open, showing options like "Create content", "Content management", "Site building", "Site configuration", "User management", and "Reports". The "Create Page" form is visible, with the title "Gayle Volk Project II" and a rich text editor containing the text "Link back to Gayle Volk NRI project".

**GDR | Genome Database For Rosaceae**

Logged in as: sook | Log Out

General Info | Species | Projects | Maps | Search | Tools | Community | Contact Us | Administer

**Genetic Diversity of Wild Apple Accessions in the National Plant Germ**

View Edit

NRI Award #2005-35300-15466

PI: Gayle Volk, CoPI: Christopher Richards, Collaborator: Phil Forsline  
USDA-ARS-National Center for Genetic Resources Preservation  
Plant Germplasm Preservation Research Unit  
Ft. Collins, CO 80525  
E-mail: gvolk@lamar.colostate.edu  
Telephone: 970-495-3205

**Accomplishments:**

- Quantify and apportion genetic diversity of wild apple accessions. This objective has been completed.
- Identify a group of individuals for genotyping. This objective has been completed.

**Broad Impacts:**

**Administer**

- Create content
- Content management
- Site building
- Site configuration
- User management
- Reports

**GDR | Genome Database For Rosaceae**

Logged in as: sook | Log Out

General Info | Species | Projects | Maps | Search | Tools | Community | Contact Us | Administer

**Create Page**

Title: \*  
Gayle Volk Project II

Menu settings

Show summary in full view

**Body:**

Source

Format Normal B I U ABC x<sub>2</sub> x<sup>2</sup>

Link back to Gayle Volk NRI project

Project

a. description

b.more description|

# User Management

**GDR | Genome Database For Rosaceae**

Logged in as: sook | [Log Out](#)

[General Info](#) [Species](#) [Projects](#) [Maps](#) [Search](#) [Tools](#) [Community](#) [Contact Us](#) [Administer](#)

## Roles

Roles allow you to fine tune the security and administration of Drupal. A role defines a group of users that have certain user permissions. Examples of roles include: anonymous user, authenticated user, and administrator. To delete a role choose the role and click the delete button.

By default, Drupal comes with the following roles:

- Anonymous user: this role is used for users who are not logged in.
- Authenticated user: this role is used for users who are logged in.

**Name**

- anonymous user
- authenticated user
- gdr admin user
- peach guest

**Permissions**

Permissions let you control what users can do on your site. Each user role (defined on the [user roles page](#)) has its own set of permissions. For example, you could give users classified as "Administrators" permission to "administer nodes" but deny this power to ordinary, "authenticated" users. You can use permissions to reveal new features to privileged users (those with subscriptions, for example). Permissions also allow trusted users to share the administrative burden of running a busy site.

Permission	peach guest
<b>block module</b>	
administer blocks	<input type="checkbox"/>
use PHP for block visibility	<input type="checkbox"/>
<b>comment module</b>	
access comments	<input type="checkbox"/>
administer comments	<input type="checkbox"/>
post comments	<input type="checkbox"/>
post comments without approval	<input type="checkbox"/>
<b>contact module</b>	
access site-wide contact form	<input checked="" type="checkbox"/>
administer site-wide contact form	<input type="checkbox"/>
<b>fckeditor module</b>	
access fckeditor	<input type="checkbox"/>

# Genomics Data

- Unigene for family Rosaceae and for genus of malus, prunus, fragaria, pyrus and rosa ESTs.
- EST annotation includes unigene set, homology, SSRs, ORF, SNPs, unique oligo sets for unigene microarray
- NCBI/Swiss-Prot/TremBL Rosaceae protein data

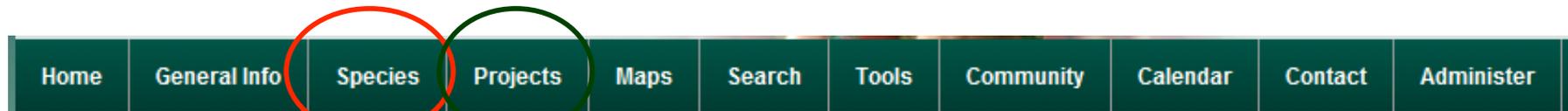
**Coming Soon – Whole Genome Sequence of Peach, Strawberry and Apple 😊**

# Genetics Data

- Locus (marker loci and MTL)
  - Over 1400 locus data available from marker/trait search site
- Maps and Genetic Diversity Data
  - 39 Rosaceae genetic maps in CMap
  - polymorphism/diversity search site
  - Genetically anchored peach physical and transcriptome map
  - Hybridization data between probes (ESTs and genetic markers) and peach BACs
- Publications
  - relevant to Rosaceae genetics and genomics



# Access the data from



**species page**

Apple	
Pear	
Prunus	Almond
Raspberry	Cherry
Rose	Apricot
Strawberry	Peach

Prunus Data

or

**projects page**

Rosaceae EST Unigene
Individual EST Project
Peach Physical Map
Peach Transcriptome Map
NRI Projects
Organelle
Proteins
BACs

# Or go directly to

Home	General Info	Species	Projects	Maps	Search	Tools	Community	Calendar	Contact	Administer
------	--------------	---------	----------	------	--------	-------	-----------	----------	---------	------------

## maps

CMap
GDR MapViewer Peach
WebChrom Peach
WebFPC Peach

## search

Mapped BACs
Markers
Traits
ESTs
Publications
Polymorphism
GO Terms

## Tools to blast against or download

NCBI BLAST
Batch BLAST
FASTA
SSR
EST Assembly
Remote Analysis Tools
Download Data

# Maps

<a href="#">Home</a>	<a href="#">General Info</a>	<a href="#">Species</a>	<a href="#">Projects</a>	<a href="#">Maps</a>	<a href="#">Search</a>	<a href="#">Tools</a>	<a href="#">Community</a>	<a href="#">Calendar</a>	<a href="#">Contact</a>	<a href="#">Administer</a>
----------------------	------------------------------	-------------------------	--------------------------	----------------------	------------------------	-----------------------	---------------------------	--------------------------	-------------------------	----------------------------

- CMap
- GDR MapViewer Peach
- WebChrom Peach
- WebFPC Peach

# CMap (comparative map viewer)

**Map Viewer :**

Ref. Species : Prunus (Prunus) Submit

Ref. Set : Prunus - Prunus Bin Map Submit

Ref. Map : G1 Submit

Start :

End :

Highlight :

Comp. Map == Genetic Maps ==

(Right) : Almond - FxT 2000 (All) [139]  
G1F [40]  
G1T [35]

Current Maps : Almond-FxT 2000-G1F [ Delete ]  
Prunus-Prunus Bin Map-G1 (Ref.)  
Prunus-TxE 2004-G1 [ Delete ]

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

: Almond - FxT 2000 (All) [90]  
G1T [35]  
G2T [4]

Image Size :  Small  Medium  Large

Font Size :  Small  Medium  Large

Image Type :  PNG  JPEG  GIF  SVG \*

Show Labels :  None  Landmarks  All

Collapse Overlapping :  No  Yes

Features :

Min. No.

Correspondences :

Include Feature Types : --All--  
Anchored EST (BAC contig)  
Anchored EST (BAC)  
Anchored Gene (Tentative)

Include Correspondence Types : --All--  
Automated name-based Hybridization

Almond  
FxT 2000  
G1F

I ? M X F N

PP\_Lea0015C01f OPE7  
PP\_Lea0008E03f AG53  
PP\_Lea0009H16f AC24B  
PP\_Lea0036D15f  
PP\_Lea0004K13f  
PP\_Lea0012K02f  
PP\_Lea0016L07f  
PP\_Lea0030I08f  
PP\_Lea0016D17f  
PP\_Lea0028D01f  
PP\_Lea0030M11f  
PP\_Lea0015I13f  
PP\_Lea0014H18f  
PP\_Lea0034016f  
PP\_Lea0028C01f  
PP\_Lea0035B03f  
PP\_Lea0008B15f  
PP\_Lea0002J03f  
PP\_Lea0021L13f  
PP\_Lea0006D08f  
PP\_Lea0003J12f  
PP\_Lea0021L08f  
PP\_Lea0005N09f  
PP\_Lea0021G04f  
PP\_Lea0020D21f  
PP\_Lea0022F24f  
PP\_Lea0026017f  
PP\_Lea0033A07f  
PP\_Lea0025002f  
PP\_Lea0009I05f  
PP\_Lea0003P06f  
PP\_Lea0006I23f  
PP\_Lea0009F11f  
PP\_Lea0001D16f  
PP\_Lea0010K23f  
PP\_Lea0005L17f  
PP\_Lea0001H20f  
PP\_Lea0004G19f

Prunus  
Prunus Bin Map  
G1

I ? M F N

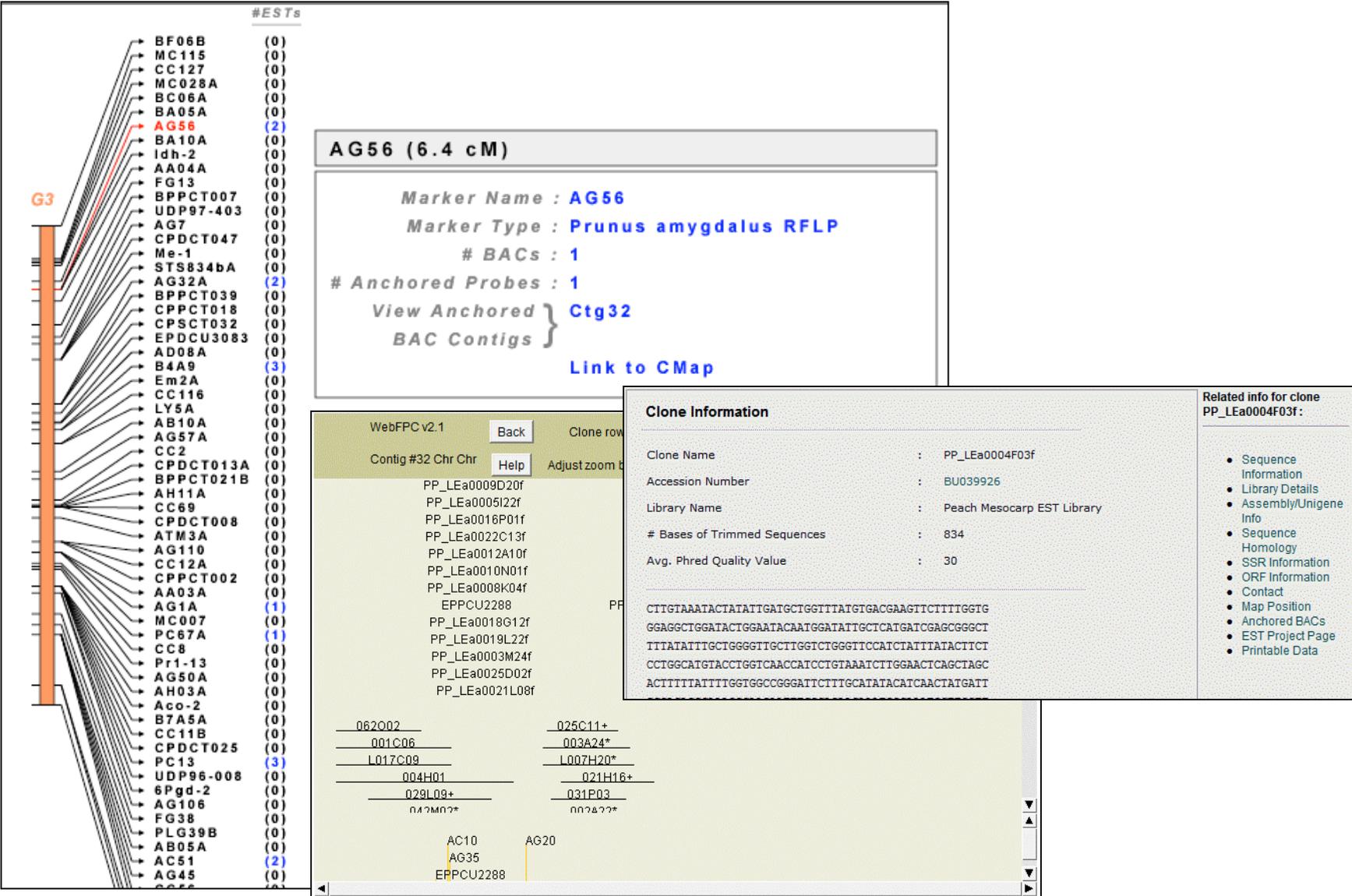
AA08B  
1:14  
pchmes4  
CC23  
EPDCU5100  
1:15  
AG116A  
1:26  
AC47  
PceGR59  
PC32  
PC30  
BPPCT042B  
AG29A  
CPSCT036  
CPSCT027  
UDP96-005  
CPDCT019  
CPPCT049  
AG29A  
CPSCT036  
1:34  
PC85  
MC044  
1:50  
TSR2  
LY37  
1:55  
AB08B  
Lap-1

Prunus  
TxE 2004  
G1

I ? M X F N

PP\_Lea0015C01f  
PP\_Lea0022I08f  
PP\_Lea0009H16f  
PP\_Lea0012K02f  
PP\_Lea0004K13f  
PP\_Lea0008E03f  
PP\_Lea0036D15f  
PP\_Lea0016L07f  
PP\_Lea0030I08f  
PP\_Lea0003I01f  
PP\_Lea0009A14f  
PP\_Lea0017M09f  
PP\_Lea0016D20f  
PP\_Lea0027G07f  
PP\_Lea0010I06f  
PP\_Lea0007M11f  
PP\_Lea0003E19f  
PP\_Lea0030E14f  
PP\_Lea0005L17f  
PP\_Lea0021G04f  
PP\_Lea0003P06f  
PP\_Lea0005N09f  
PP\_Lea0033A07f  
PP\_Lea0026017f  
PP\_Lea0020D21f  
PP\_Lea0006I23f  
PP\_Lea0010K23f  
PP\_Lea0009F11f  
PP\_Lea0009I05f  
PP\_Lea0013K20f  
PP\_Lea0011H02f  
PP\_Lea0013L04f  
PP\_Lea0003G23f  
PP\_Lea0013L10f  
PP\_Lea0013A14f  
PP\_Lea0027D06f  
PP\_Lea0009014f  
PP\_Lea0022021f  
PP\_Lea0003H21f  
PP\_Lea0009H21f  
PP\_Lea0027M15f  
PP\_Lea0009K13f  
PP\_Lea0009C17f  
PP\_Lea0013C10f  
PP\_Lea0012002f  
PP\_Lea0003L17f  
PP\_Lea0012P01f  
PP\_Lea0028N01f  
PP\_Lea0013D03f  
PP\_Lea0005P03f  
PP\_Lea0002B13f

# Genetic, Physical, and Transcriptome Map



# search engine

<a href="#">Home</a>	<a href="#">General Info</a>	<a href="#">Species</a>	<a href="#">Projects</a>	<a href="#">Maps</a>	<a href="#">Search</a>	<a href="#">Tools</a>	<a href="#">Community</a>	<a href="#">Calendar</a>	<a href="#">Contact</a>	<a href="#">Administer</a>
----------------------	------------------------------	-------------------------	--------------------------	----------------------	------------------------	-----------------------	---------------------------	--------------------------	-------------------------	----------------------------

[NCBI BLAST](#)

[Batch BLAST](#)

[FASTA](#)

[SSR](#)

[EST Assembly](#)

[Remote Analysis Tools](#)

[Download Data](#)



## Search EST

[Click here to Search Unigene Contigs](#)

Select database and search ESTs by clone name and other features. [Visit each description page for more information on each EST database.](#) More search options such as the unigene name, putative function and anchored map.

Prunus    Fragaria    Rosa    R

**Search EST by Name**

Accession No. ▾ Enter text

**Search EST by Features**

Has SSRs

Represents a Unigene From\*

\*This feature will return the unigene version 3 (Jun. 2006) and version

**Search EST by Taxonomy**

Taxonomy :

**Search EST by Tissue**

Tissue (curated) :

**Search EST by Putative Function**

All  
Carpel  
Flower  
Fruit Mesocarp  
Fruit  
Fruit Ep  
Fruit Ep  
Fruit Ep  
Fruit M  
Gynoe  
Inflores  
Leaf  
Petal  
Phloem  
Recept  
Recept  
Root  
Seed  
Shoot  
Unspec  
Vegeta  
Whole  
Xylem  
All

### Contig Search

Select database and search  
[Return to EST Search Page.](#)

#### Search Contig

Unigene

Enter text

### Contig Information

Contig Name : Rosa\_v4\_Contig1008  
Length of Consensus Sequence : 591  
Assembly Name : Rosa Unigene Version 4  
Date Created : 02-MAY-08  
Number of Member Sequences : 8

```
ATAGCAAGCAAGCAAAGCAATTCATTAATCAAAGCAAAACCCATTTTC
AGTTACTCAAATCCAATCAGCACCATGCTCGAAAGTGGGCAACTGTGA
CTGCTCTGACGCTTCCAGTGCACCAAGAAGGAAACAGTTTGGTCATTG
TTGAGACTGAGAAGAGCTACGACACTGTTGTTATGGATGCACCAGCTGCC
GAGAACGGCGGAAAATGCAAAATGCGGCACCACCTGCTCTTGATCGACTG
CAAAATGTGGAAATTAAGTCCCCTATTCCAGACCAATGGCTGCCATATAAC
TATGTGGTGATAAAAATGTGGAGTCTCGTCAATAAAGGATTTGTGAGAA
TCAAATAACTCCTCTGTTTATTGTGATAGTAGTTTGATCGAGTCTGTGA
GTGAGTGGGTGAAAGATGACTCTACTGTACGTATGTGTGCAATCATAT
CTGTGTTCTTTAGTAGCTTGTAAAGGTTCTTGATCTGGCCATTATCTGTGG
CCTTGTGATTATGTTTAAATTAATGAAATTACTGTTTCGTATACATGCTGAT
TTTACCTCTTTAGCTGINTCTAATATTTTNTCAAATAAAAA
```

### Related info for Rosa\_v4\_Contig1008

- Sequence Information
- Comprising ESTs
- Sequence Homology
- Sequence GO Terms
- SSR/ORF Information
- View AutoSNP output

### Search Contig by Features

Has SSRs

Has SNPs

(Only Genera Unigenes have SNPs available. The Rosaceae Unigene does not.)

### Search Contig by Putative Function

Match Description :

Match Organism :

GO Term (id number or name) :

\*Please click [here](#) to browse available GO Terms.  
(Only Version 3 Contigs have GO Terms.)

Submit

Clear

# Marker Search

Search molecular markers by name or by marker is mapped, map position and the simply-inherited traits. Some of the mark probes in BAC hybridization, so some ES associated BAC clones and EST clones as positions. [Template for data submission](#) i

Search by Name

Marker Type

Marker description

Marker mapped in species

Map Position

Map Name

Linkage Group

Bin Name

## Marker Information

Marker Name	BPPCT028
Marker Alias	N/A
Genbank ID	N/A
Marker Type	SSR

### Source

source organism	Prunus persica
source cultivar	O Henry
source description	Genomic DNA
source genbank id	AF374944
source marker	N/A

### Detection

PCR condition	94 C 1 min, 94 C 45 sec, 57 C 45 sec, 72 C 2 min. 35 cycles, 72 C
---------------	---

## Related info for BPPCT028

- Marker Information
- Associated BACs
- Associated ESTs

## Associated BACs

BACs are associated with some markers as the source of the marker, by hybridizing to the marker, and/or by hybridizing to the EST that is the source of the marker. Click the BAC name for more data.

**BPPCT028 is hybridized to the BACs**

clone name
024G18

Monomorphic Population

Polymorphism Data

### Map Position

map name	linkage group	bin	start	stop	locus name	view in CMap
TxE	G1	N/A	77.4	N/A	BPPCT028	CMap
JxF	G1	N/A	124.1	N/A	BPPCT028	CMap
P2175 x GN	P2175G1	N/A	119.9	N/A	BPPCT028	CMap
P2175 x GN	GN1	N/A	133.7	N/A	BPPCT028	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.

## Trait

<b>trait name</b>	Root-knot nematode resistance
<b>trait alias</b>	RKN resistance
<b>trait category</b>	Biotic stress
<b>published symbol</b>	Mi
<b>taxon</b>	peach
<b>trait description</b>	The search for peach rootstocks resistant to root-knot nematodes has been a long and continuing project in the United States and other countries. Some rootstocks, such as Nemaguard, Nemared, Flordaguard, Guardian, Okinawa, and Higama, show various levels of resistance to root-knot nematodes. Lu et al. (1997) were the first to propose a two-gene model for
<b>screening method</b>	Bioassays were used to measure nematode resistance: each F2 genotype was scored for number of galls and egg masses.

### Map Position

map name	linkage group	position	comments
TxE	G2	0 - 1 cM	tentatively anchored to the position from the position in other maps with common markers

### References

author	title	year	citation
Lu, Z.X., Sosinski, B., Reighard, G.L.	Construction of a genetic linkage map and identification of AFLP markers for resistance	1998	Genome / Genome Apr 1998. v. 41 (2) p. 199-207. ISSN 0831-2796; GENOE3

## Search Peach BAC

Peach BACs that have been hybridized to a probe (genetic markers or peach ESTs) and those that have been used in fingerprinting can be searched in this site. Search options include BAC clone name and the marker probe specifications such as map name, linkage group, probe source organism and probe type. BAC data page provides data such as hybridized markers and ESTs, BAC library details and BAC contig assembly results.

Below are the prunus BAC clones of which sequences are publicly available.

082I18 (GenBank) | 028F08 (GenBank) | pPn31C7(GenBank) | PpN018G07(GenBank) 045O02 (GDR) | 058P04 (GDR) | 080O24 (GDR) | AprC27 (GDR)

### Search by BAC name

(eg. Select "Starts with" and type in "101C" to get all the BACs with name that begins with "101C".)

Starts with ▼ 10

Submit Query

[New BAC Search](#)

Page 1 of 19 | [Next](#)

#### BAC Name

108J24	106J18	101B06
108J12	106N10	101D04
104K22	106N19	101K07
108J15	107H19	102D05
109L12	107L19	102D13
103C03	107O02	102H12
104N01	108A10	102F06
105N07	108F09	109J03
106F04	100G24	102P08
106I20	100K08	105A12

(Select the four categories)

#### Map Name

FVxFN  
ExB

## Hybridized Probes / ESTs

Data of probes/ESTs that hybridized to the BAC clone is provided below.  
Marker or EST name is linked to a page with detailed information.  
No genetically linked probes have been hybridized to this clone.

Probe Name	Probe Type	Source Organism	Hybridization Date	Hybridization Done By
------------	------------	-----------------	--------------------	-----------------------

PP\_LEa0035B0

### Related info for BAC clone 100A08 :

- [Hybridized Probes/ESTs](#)
- [Library Details](#)
- [Contig Assembly](#)

## BAC Contig Assembly

The BAC clone 100A08 belongs to a contig.

(For peach physical map development, BAC clones are being assembled into contigs using an approach that combines hybridization of mapped markers and BAC fingerprinting. We use Image for band-calling and FPC for the automatic assembly of the bands.)

### Contig Number

### FPC file Name

### Date of FPC assembly

### FPC done by

### [View Contig in WebFPC](#)

### [BAC Clones in Contig](#)

### Related info for BAC clone 100A08 :

- [Hybridized Probes/ESTs](#)
- [Library Details](#)
- [Contig Assembly](#)

WebFPC v2.1

[Back](#)

Clone rows

Show Clones

[Marker Remarks](#)

[Clone Remarks 2](#)

Contig #360 Chr Chr

[Help](#)

Adjust zoom by

Zoom

[In](#)

[Out](#)

[Marker hiding](#)

PP\_LEa0016G14f  
PP\_LEa0018C02f  
PP\_LEa0005G18f  
PP\_LEa0012D19f  
PP\_LEa0026O16f  
PP\_LEa0014N03f

\_\_\_\_\_  
L009D06

\_\_\_\_\_  
L003I21\*

\_\_\_\_\_  
009K13

\_\_\_\_\_  
098H02

\_\_\_\_\_  
074Q18

\_\_\_\_\_  
020N17

\_\_\_\_\_  
100B08

\_\_\_\_\_  
L082K12

\_\_\_\_\_  
L006I16

\_\_\_\_\_  
048F17

\_\_\_\_\_  
L003J03

\_\_\_\_\_  
065L16

# Rosaceae Community Resources

<a href="#">Home</a>	<a href="#">General Info</a>	<a href="#">Species</a>	<a href="#">Projects</a>	<a href="#">Maps</a>	<a href="#">Search</a>	<a href="#">Tools</a>	<a href="#">Community</a>	<a href="#">Calendar</a>	<a href="#">Contact</a>	<a href="#">Administer</a>
----------------------	------------------------------	-------------------------	--------------------------	----------------------	------------------------	-----------------------	---------------------------	--------------------------	-------------------------	----------------------------

- [RosIGI](#)
- [USRosExec](#)
- [NRI Projects](#)
- [Conferences](#)
- [Employment](#)
- [Mailing Lists](#)
- [Message Boards](#)
- [Links](#)



# Acknowledgements

- GDR Team – Dorrie Main, Sook Jung, Meg Staton, Randall Svancara, Taein Lee, Ping Zheng, Albert Abbott
- Previous members: Anna Blenda, Stephen Ficklin, Christopher Jesudurai
- Rosaceae Community
- NSF Plant Genome Program
- USDA Specialty Crop Research Initiative

# Thank you!

## Visit us at

- Plant Database Booth
  - Sunday 8-8:30 pm
  - Monday 10-10:30 am, 4-4:30 pm
- Poster C915
  - Monday 10 -11:30