How does data flow

- **Samples**
  - GA IIx
  - Real Time Analysis (RTA)

- **DATA STORAGE**
  - Analyzer Cluster ...
  - GenomicsCore
  - Genomics (11TBs)

- **Pipeline**
  - Novoalign
  - Variant casava

- **DATA BACKUP**
  - atmost8/genomicscore

- **CLUSTER**
  - raw & test (5TBs)

- **cslxgenomics01**
  - Computational: SVA

- **cslxgenomics02**
  - NGS LIMS

- **cshsgenomics03**
  - CLCBio / Visualization

- **http://genomics.csmc.edu**
How does data flow

Analysis Cluster
.../cluster/GenomicsCore

DATA STORAGE
/rcgenomics (11TBs)

Pipeline
Novoalign
Variant
casava

CLUSTER
/raw & test (5TBs)

DATA BACKUP
/atmost8/genomicscore

Real Time Analysis (RTA)

GA IIx

500GBs

cslxgenomics01
Computational: SVA

genomics.csmc.edu
NGS LIMS

cshsgenomics03
CLCBio / Visualization

ATTGCC - ATT - G
ATTGCC - ATT - G
ATC – CA – ATTT G

ATTGCC - ATT - G
ATTGCC - ATT - G
ATC – CA – ATTT G

2-3 TBs
Thank you

- **Genomics Core**
  - Vincent Funari, Ph.D
  - Yuan Xue, Ph.D
  - Samuel P. Strom, Ph.D
  - Jordan Brown

- **BioTeam**
  - Michele Clamp, Ph.D
  - Chris Dagdigian

- **EIS Team**
  - Spencer Soohoo, Ph.D
  - Stuart Noah
  - James Chen
  - Jeff Tesch

- **Illumina Team**
  - Joseph Aman
  - Hsin-Lung Lo, Ph.D
How to find us?

- Get direct Access into Genomics Core internal web site.
  - http://genomics.csmc.edu
  - http://genomics

- You need to have VPN (Virtual Private Network) if you are out site the CSMC network.
Welcome to the Genomics Core Facility

Next Gen Sequencing Open House on Thursday 1/13/2011, lunch is provided.

The rapid evolution of genomic technology is allowing unparalleled advances in gene discovery, molecular pathogenesis, mutation detection, and molecular diagnosis. The Cedars Sinai Genomics Core was created to empower Cedars Sinai’s research investigators with the opportunity to access these types of data. We are an affordable full service facility performing quality control, sample preparation, data acquisition and interpretation. We also actively educate, consult, and advise campus faculty and staff in the utility and validity of these array-based and next generation sequencer technologies.

Contact Us

Mailing Address:
Genomics Core
8723 Alden Dr
Steven Spielberg Building Room 141
Los Angeles, California 90048

Lab Phone: (310) 423–4066
Fax: (310) 248–8141
Email: genomics@csmc.edu (all inquiries)
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Contact Us

The Team

**Vincent Funari, Ph.D.**
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Assistant Professor II, Department of Pediatrics, UCLA School of Medicine
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Email: funariv@csghs.org

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Email: xuey@csghs.org

**Samuel Strom, Ph.D.**
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Email: stroms@csghs.org

**Jordan Brown**
Research Assistant
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Email: jordan.brown@csghs.org

**Quocinh Nguyen**
Informatics
Phone: 310-248-8056
Email: quocinh.nguyen@csghs.org
### User Account

#### Users and Roles

<table>
<thead>
<tr>
<th>Username</th>
<th>Role</th>
<th>Password</th>
<th>Retype Password</th>
<th>Group</th>
<th>Remove Login</th>
<th>Delete</th>
</tr>
</thead>
<tbody>
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<td>Admin</td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Guest</td>
<td>Read Only</td>
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<td></td>
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<tr>
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<td>FUNARI</td>
<td></td>
<td></td>
</tr>
<tr>
<td>funari-read</td>
<td>Read Only</td>
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<td>FUNARI</td>
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<tr>
<td>funari-user</td>
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<tr>
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<td>KIM</td>
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<tr>
<td>xyue</td>
<td>Admin</td>
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<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>jordon</td>
<td>User</td>
<td>******</td>
<td>******</td>
<td>FUNARI</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Add User
- Save Users
LIMS at the Genomics Core

Laboratory Information Management System

You must enter your valid **username** and **password** to access the LIMS systems. If your account has not been created, please contact your PI or contact us to get one.

**SEQUENCING LIMS**

<table>
<thead>
<tr>
<th>Field</th>
<th>Value</th>
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</thead>
<tbody>
<tr>
<td>Username</td>
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<tr>
<td>Password</td>
<td></td>
</tr>
<tr>
<td>Login</td>
<td></td>
</tr>
</tbody>
</table>

**MICROARRAY LIMS**

<table>
<thead>
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<th>Field</th>
<th>Value</th>
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</thead>
<tbody>
<tr>
<td>Username</td>
<td>Available Soon ...</td>
</tr>
<tr>
<td>Password</td>
<td></td>
</tr>
<tr>
<td>Login</td>
<td></td>
</tr>
</tbody>
</table>
How to Access the LIMS?

Laboratory Information Management System

You must enter your valid **username** and **password** to access the LIMS systems. If your account has not been created, please contact your PI or **contact us** to get one.

**SEQUENCING LIMS**

- **Username**: funariv
- **Password**: ........

**Login**

**MICROARRAY LIMS**

- **Username**: Available Soon ...
- **Password**: 

**Login**
How to Access the LIMS?

- It could get wrong at a first try

- LDAP login will be implemented in next phase
  (LDAP: Lightweight Directory Access Protocol)
What is LIMS?

- LIMS = Laboratory Management Information System
- Software, database, hardware
- Enables centralization of information
- Capture, manage, search, retrieve data
You logged in

Group: CSMC

Groups are headed by PIs and contain one or more Group Members. Members can create new Samples and Libraries for sequencing and PIs can add also new Members and Projects.

Total kbases sequenced 0

People in the CSMC Group

<table>
<thead>
<tr>
<th>Group Member</th>
<th>funanv, sam-pl</th>
</tr>
</thead>
<tbody>
<tr>
<td>PI</td>
<td>sam-pl</td>
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</tbody>
</table>

Projects from the CSMC Group
No results found

List of entries that reference this page

Group CSMC.
Enter Meta Data

Adding Project

* Name: Mouse Genomes Project
  The Mouse Genomes Project - next generation sequencing and variations analysis of 17 mouse strains.

* Group: FUNARR

* Group Member: funarr

* Required field
Enter Meta Data

Adding Sample

* Name: Exome
BioAnalyzer QC File: Browse...
Bioanalyzer QC: Y
Comments:
DNA Made By: funariv
Description:
DNA Concentration: 6
Fragment Size: 250
* Group: FUNARI

* Group Member:
- funariv
- funariv-phytol
- funariv-user
- jordan

* Library Made: Y
Library Made By: funariv
* Project: Mouse Genomes Project
* Species: Mouse
* Status: IN PROGRESS
Type: mRNA

* = Required field

Cancel | Add now Sample
Where is my data?
One week later
Where is my data

Laboratory Information Management System

You must enter your valid **username** and **password** to access the LIMS systems. If your account has not been created, please contact your PI or **contact us** to get one.

**SEQUENCING LIMS**

- Username: funariv
- Password: 

**Login**

**MICROARRAY LIMS**

- Username: Available Soon ...
- Password: 

**Login**
Your profile

Group: FUNARI

Groups are headed by PIs and contain one or more Group Members. Members can create new Samples and Libraries for sequencing and PIs can also add new Members and Projects.

Total kbases sequenced 0

People in the FUNARI Group

<table>
<thead>
<tr>
<th>Group Member</th>
</tr>
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<tbody>
<tr>
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<tr>
<td>funari-road</td>
</tr>
<tr>
<td>funari-user</td>
</tr>
<tr>
<td>funari-jordon</td>
</tr>
<tr>
<td>PI</td>
</tr>
<tr>
<td>funari-pl</td>
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</table>

Projects from the FUNARI Group

<table>
<thead>
<tr>
<th>Project</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mouse Genomes Project</td>
<td>The Mouse Genomes Project - next generation sequencing and variations analysis of 17 mouse strains.</td>
</tr>
<tr>
<td>skeleton</td>
<td>The skeleton contains three specific cell types: chondrocytes in cartilage and osteoblasts and osteoclasts in bone. Our understanding of the transcriptional mechanisms that lead to cell differentiation along these three lineages has increased considerably.</td>
</tr>
</tbody>
</table>

List of entries that reference this page
The illumina run summary

### Illumina Run: 101230 HWUSI-EAS1764 00004 FC

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
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</thead>
<tbody>
<tr>
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<td>All.htm</td>
</tr>
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<td>Clusters</td>
<td>345,495,190</td>
</tr>
<tr>
<td>Date Created</td>
<td>01-10-2011</td>
</tr>
<tr>
<td>Full All Html</td>
<td>FullAll.htm</td>
</tr>
<tr>
<td>IVC Html</td>
<td>IVC.htm</td>
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<tr>
<td>Illumina Flowcell</td>
<td>63089AAXX</td>
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<tr>
<td>Kb Sequenced</td>
<td>10,291</td>
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<td>Machine</td>
<td>EAS1764</td>
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<tr>
<td>Passing Clusters Percent</td>
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<tr>
<td>Perfect</td>
<td>FullPerfect.htm</td>
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<td>Run Date</td>
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<td>Status</td>
<td>HAS SEQUENCE</td>
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<td>Summary</td>
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<tr>
<td>Summary File</td>
<td>BustardSummary.xml</td>
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<tr>
<td>Yield</td>
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#### Lanes and Libraries for run

<table>
<thead>
<tr>
<th>Illumina Lane</th>
<th>Library</th>
<th>Type</th>
<th>Fragment Size</th>
<th>Read Length</th>
<th>Species</th>
<th>Yield</th>
<th>Passing Clusters Percent</th>
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<tbody>
<tr>
<td>63089AAXX Lane 1</td>
<td>fuanriv Phix (14)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1,398,870</td>
<td>80.13</td>
</tr>
<tr>
<td>63089AAXX Lane 2</td>
<td>fuanriv N1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1,477,936</td>
<td>72.50</td>
</tr>
<tr>
<td>63089AAXX Lane 3</td>
<td>fuanriv Phix (10)</td>
<td></td>
<td></td>
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<td></td>
<td>1,379,959</td>
<td>81.86</td>
</tr>
<tr>
<td>63089AAXX Lane 4</td>
<td>fuanriv Exome</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1,404,263</td>
<td>84.11</td>
</tr>
<tr>
<td>63089AAXX Lane 5</td>
<td>fuanriv Phix (8)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1,220,013</td>
<td>86.30</td>
</tr>
<tr>
<td>63089AAXX Lane 6</td>
<td>fuanriv Phix (6)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1,101,545</td>
<td>86.83</td>
</tr>
<tr>
<td>63089AAXX Lane 7</td>
<td>fuanriv N2 plus DSN(6)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1,074,809</td>
<td>89.63</td>
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<tr>
<td>63089AAXX Lane 8</td>
<td>fuanriv N2 plus DSN (10)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1,234,163</td>
<td>87.08</td>
</tr>
</tbody>
</table>
Your data

Illumina Flowcell: 63089AAXX

Illumina Flowcells are prepared with up to 12 sample in 8 lanes ready for sequencing. As sequencing runs finish the output data is automatically uploaded - a summary.

<table>
<thead>
<tr>
<th>Library Type</th>
<th>Single Read</th>
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<tbody>
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<td>Y</td>
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<td>Read Length</td>
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Get SampleSheet

<table>
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<th>Lanes</th>
<th>Library</th>
<th>Yield</th>
<th>Passing Clusters Percent</th>
<th>Species</th>
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<tbody>
<tr>
<td>63089AAXX Lane 1</td>
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<td></td>
<td></td>
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<tr>
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<td>72.50</td>
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<td></td>
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<tr>
<td>63089AAXX Lane 3</td>
<td>funaniv Phix (10)</td>
<td>1,379,959</td>
<td>81.86</td>
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<td></td>
</tr>
<tr>
<td>63089AAXX Lane 4</td>
<td>funaniv Exome</td>
<td>1,404,203</td>
<td>84.11</td>
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<tr>
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<td>funaniv Phix (8)</td>
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<tr>
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<td>1,234,163</td>
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</table>

Gerald Lanes

<table>
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<tr>
<th>Lanes</th>
<th>Gerald Lane</th>
<th>Library</th>
<th>Yield</th>
<th>Passed</th>
<th>Errors</th>
<th>Aligned</th>
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<th>SeqFile</th>
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<tbody>
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## Your data

### Gerald Lanes

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<th>Gerald Lane</th>
<th>Library</th>
<th>Yield</th>
<th>Passed</th>
<th>Errors</th>
<th>Aligned</th>
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<th>Seqfile</th>
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<tr>
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<td>GER 63089AAXX 1 1</td>
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<td>0.49</td>
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<td>funariv Phix (6)</td>
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<td>86.83</td>
<td>0.21</td>
<td>98.85</td>
<td>170.16</td>
<td>s_6_sequence.txt</td>
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<tr>
<td>63089AAXX Lane 7</td>
<td>GER 63089AAXX 1 7</td>
<td>funariv N2 plus DSN(6)</td>
<td>1,074,809</td>
<td>89.83</td>
<td>0.35</td>
<td>38.44</td>
<td>39.85</td>
<td>s_7_sequence.txt</td>
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<td>GER 63089AAXX 1 8</td>
<td>funariv N2 plus DSN (10)</td>
<td>1,234,163</td>
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<td>0.38</td>
<td>39.18</td>
<td>40.48</td>
<td>s_8_sequence.txt</td>
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# Your data

**Illumina Lane:** 63089AAXX Lane 1

<table>
<thead>
<tr>
<th>Clusters</th>
<th>411,121</th>
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<tbody>
<tr>
<td>Illumina Flowcell</td>
<td>63089AAXX</td>
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<tr>
<td>Lane Number</td>
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</tr>
<tr>
<td>Library 1</td>
<td>fuanliv Phix (14)</td>
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<td>Passing Clusters Percent</td>
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<tr>
<td>Yield</td>
<td>1,398,670</td>
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</table>

## Gerald Lanes

<table>
<thead>
<tr>
<th>Gerald Lane</th>
<th>Genome</th>
<th>Yield</th>
<th>Errors</th>
<th>Passed</th>
<th>Aligned</th>
<th>Seqfile</th>
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</thead>
<tbody>
<tr>
<td>GER 63089AAXX 1 1</td>
<td>Sequence Squashed</td>
<td>1,398,670</td>
<td>0.49</td>
<td>80.13</td>
<td>98.95</td>
<td>s_1_sequence.txt</td>
</tr>
</tbody>
</table>

## List of entries that reference this page

- Illumina Lane 63089AAXX Lane 1
- Gerald Lane GER 63089AAXX 1 1
How does data flow

Analysis Cluster
…/cluster/GenomicsCore

DATA STORAGE
/rcgenomics (11TBs)

Real Time Analysis (RTA)

500GBs

Pipeline
Novoalign
Variant
casava

CLUSTER
/raw & test (5TBs)

DATA BACKUP
/atmos8/genomicscore

2-3 TBs

cslxgenomics01
Computational: SVA

cslxgenomics02
NGS LIMS

cshsgenomics03
CLCBio / Visualization

ATTGCC  - ATT- - G
ATTGCC  - ATT- - G
ATC – CA – ATTT G

ATTGCC - ATT- - G
ATTGCC - ATT- - G
ATC – CA – ATTT G

ATTGATCGATATAG
CGCGATAGCGCG
GATATCGGGGATA

500GBs

GA IIx

500GBs

Real Time Analysis (RTA)
How does data flow

- **Samples**
- **GA IIx**
- **Real Time Analysis (RTA)**
- **DATA STORAGE**
  - /genomics (11TBs)
- **Analysis Cluster**
  - ../cluster/GenomicsCore
- **Pipeline**
  - Novoalign
  - Variant
casava
- **DATA BACKUP**
  - /atmost8/genomicscore
- **CLUSTER**
  - raw & test (5TBs)

- **cslxgenomics01**
  - Computational: SVA
- **cslxgenomics02**
  - NGS LIMS
- **cshsgenomics03**
  - CLCBio / Visualization

http://genomics.csmc.edu