The Cancer Genome Atlas (TCGA)

National Human Genome Research Institute
National Cancer Institute

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Cancer in the U.S.

- >10,000,000 in the US have cancer (1 in 30 people)
- ~1,400,000 people will be diagnosed this year
- ~700,000 will die from cancer this year (a death every 45 seconds)
Comprehensive genomic analysis in large numbers of cancer specimens is now technically and economically feasible.
TCGA Project Pipeline

Tissue Sample

Pathology QC

DNA & RNA Isolation, QC

Sequencing

Expression, CNA & LOH, Epigenetics

Data and Results Storage & QC

Integrative Analysis

Comprehensive Knowledge of a Cancer

= Process

= Data

= Results

= BCR

= GSCs

= CGCCs

= DCC

= Collaborators
**OVARIAN**

Coverage(T/N) Callable Purity Ploidy
31x / 30x 81% 90% 2.8

**Point Mutations**

- **Rate/Mb**: 0.75
- **Total**: 1786
- **Coding**: 9

**Chr. Aberrations**

- **CNA Breaks**: ---
- **TX-Inter**: 9
- **TX-Intra**: 15

**Lost BRCA1 germline indel**

**HIGHLIGHTS**

<table>
<thead>
<tr>
<th>GENE</th>
<th>MUTATION</th>
<th>FUNCTION</th>
</tr>
</thead>
<tbody>
<tr>
<td>TP53</td>
<td>Insertion</td>
<td>Tumor suppressor</td>
</tr>
<tr>
<td>EXOC6B</td>
<td>Missense</td>
<td>protein transport, exocytosis</td>
</tr>
<tr>
<td>ANKRD6</td>
<td>Missense</td>
<td>ankyrin</td>
</tr>
<tr>
<td>AHNAK</td>
<td>Missense</td>
<td>CNS development</td>
</tr>
<tr>
<td>C11orf52</td>
<td>Nonsense</td>
<td>?</td>
</tr>
<tr>
<td>GABRB3</td>
<td>Missense</td>
<td>GABA receptor</td>
</tr>
</tbody>
</table>

**HIGHLIGHTS**

NF1-EFCAB5 fusion gene probably inactivating validated by RNA-seq

Courtesy of Gaddy Getz – Unpublished, Analysis in Process
TCGA Tumor Projects

Projects with comprehensive data available
- Glioblastoma (brain)
- Ovarian

Projects anticipated to begin in 2010-2011
- Breast (multiple types)
- Bladder
- Cervical
- Head and neck
- Hepatocellular (liver)
- Lymphoma
- Melanoma
- Multiple myeloma
- Pancreatic
- Prostate
- Sarcoma
- Stomach
- Thyroid
- Uterine (endometrial)

Projects in progress (partial data sets available)
- Acute Myeloid Leukemia
- Colon Adenocarcinoma
- Rectal Carcinoma
- Lung Adenocarcinoma
- Lung Squamous Cell Carcinoma
- Renal Clear Cell Carcinoma
International Cancer Genome Consortium Projects (June, 2010)

- USA
  - TCGA projects
- Canada
  - pancreatic*
  - prostate
- Australia
  - pancreatic*
  - ovarian
- China
  - stomach
- EU/France
  - renal carcinomas
- EU/United Kingdom
  - breast cancers*
- France
  - breast cancers*
  - hepatic (alcohol-associated)
- Germany
  - pediatric brain cancers
- India
  - oral
- Italy
  - rare pancreatic types
- Japan
  - hepatic (virus-associated)
- Spain
  - chronic lymphocytic leukemia
- United Kingdom
  - breast cancers*

*collaborative project
Cancer Research and Treatment in the Future

- TCGA can reveal all of the mutated genes that are functionally important for a specific tumor type (even if that gene is mutated in <5% of patients)
- TCGA will reveal new tumor biomarkers, new therapeutic targets
- Individualized approaches to therapy will be enabled; customized treatment based on the genetics of the tumor
- TCGA is breaking ground for new approaches to genomic and cancer research; methods to analyze and make sense of exceedingly massive and complex genomic data sets
- Cancer patients soon, and forever, will benefit