

# **Informatics Update: Progress Towards Precision Cancer Surveillance**

Eric B. Durbin, DrPH, MS

Assistant Professor, Division of Biomedical Informatics, College of Medicine  
Director, Cancer Research Informatics Shared Resource Facility, Markey Cancer Center  
Director, Kentucky Cancer Registry  
University of Kentucky

Thirty-second Annual Advanced Cancer Registrars Workshop  
August 16, 2018

HOW'S THE  
BIG DATA PROJECT  
COMING ALONG,  
Isaac?



© D.Fletcher for CloudTweaks.com

# Topics to be Covered

- Growing evidence supporting precision medicine in cancer
- Implications for cancer surveillance and public health
- KCR informatics initiatives that are enhancing precision medicine data capture in registries
- Using precision cancer surveillance data
- Future plans

# Growing Evidence Supporting Precision Medicine Initiatives

Dictionary

precision medicine

pre·ci·sion med·i·cine

*noun*

medical care designed to optimize efficiency or therapeutic benefit for particular groups of patients, especially by using genetic or molecular profiling.  
"current research is focused around precision medicine—classifying patients on their tumor's molecular changes"

Translations, word origin, and more definitions

Feedback

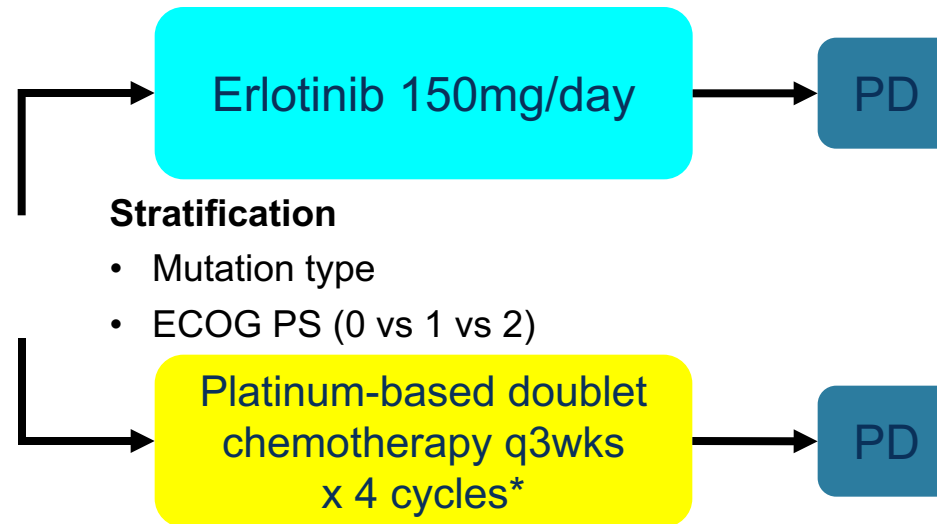


# EURTAC Study Design

- Chemonaïve
- Stage IIIB/IV NSCLC
- *EGFR* exon 19 deletion or exon 21 L858R mutation
- ECOG PS 0–2  
(n=174)

## Primary endpoint

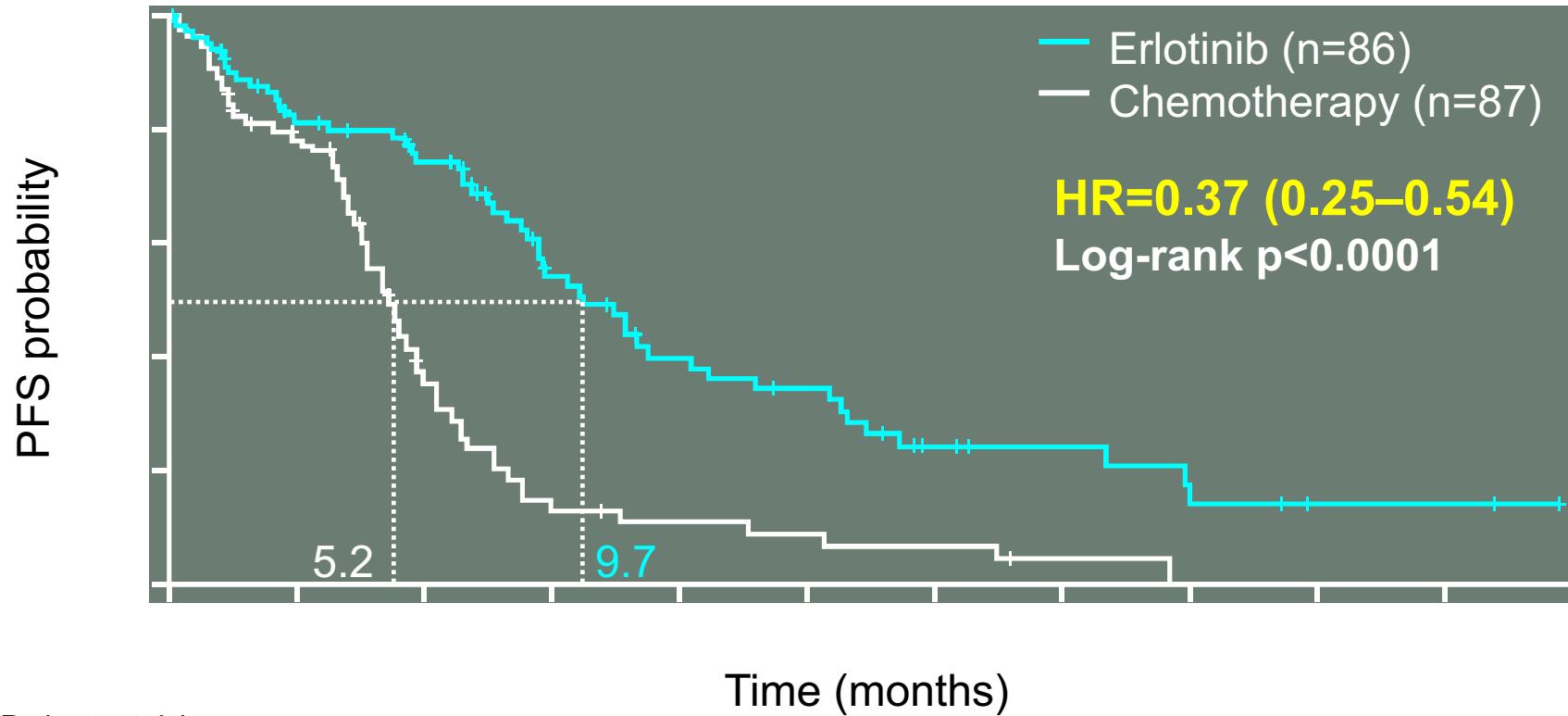
- Progression-free survival (PFS)
  - interim analysis planned at 88 events
- Patients enrolled between 2007 and 2011



## Secondary endpoints

- Objective response rate
- Overall survival (OS)
- Location of progression
- Safety
- *EGFR* mutation analysis in serum
- Quality of life

# EUROTAC: First-line Treatment in EGFR Mutation Positive NSCLC

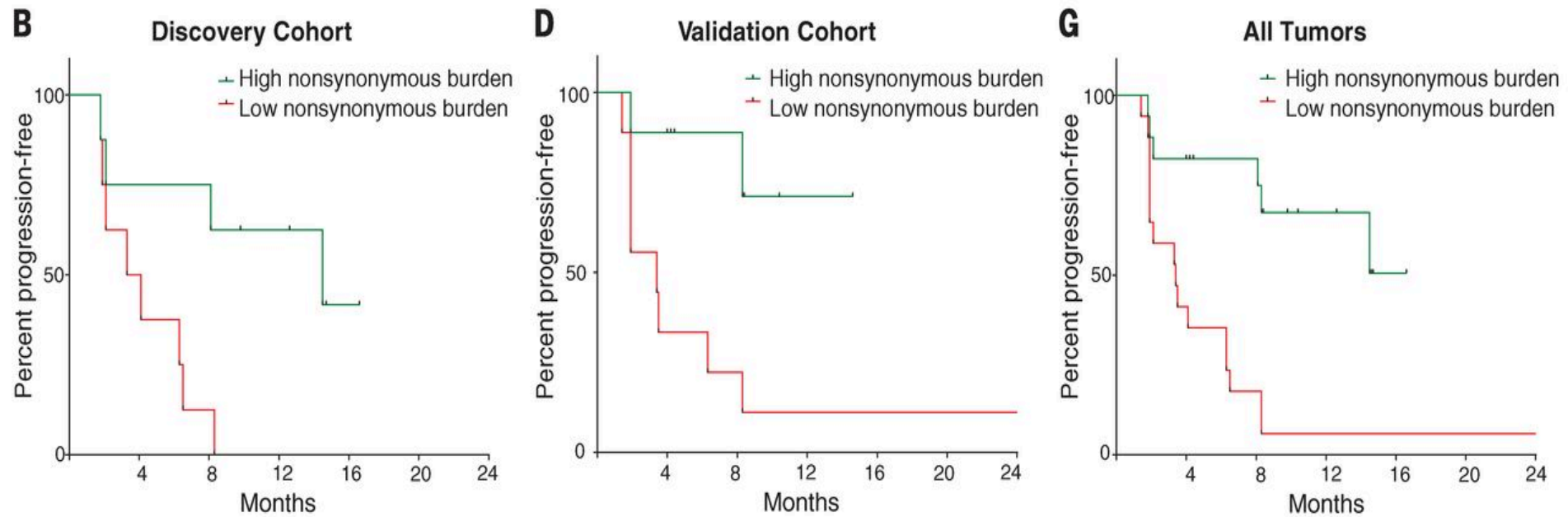


Patients at risk

Erlotinib	86	63	54	32	21	17	9	7	4	2	2	0
Chemo	87	49	20	8	5	4	3	1	0	0	0	0

# Immuno-therapy with PD-1 Targeted Pembrolizumab

**Nonsynonymous mutation burden associated with clinical benefit of anti-PD-1 therapy in non-small cell lung cancer.**

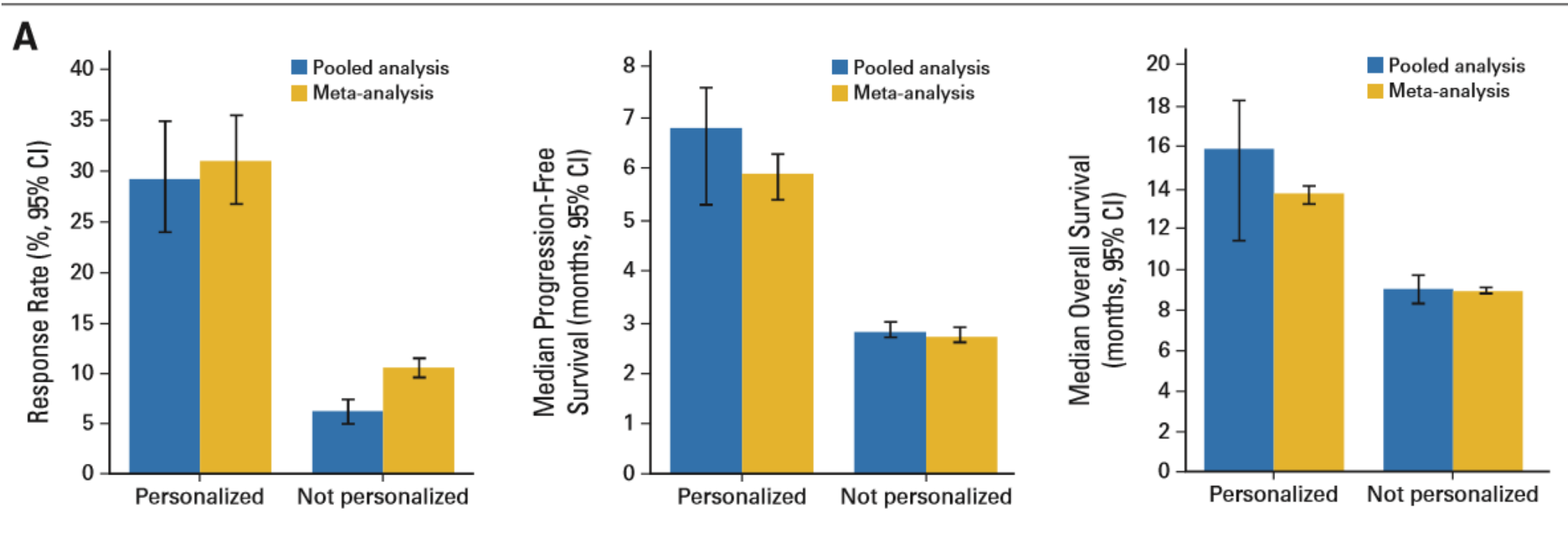


Naiyer A. Rizvi et al. *Science* 2015;348:124-128



**Study Conclusions: More Mutations Predict Better Efficacy**

# Pooled Analysis of 570 Phase II Trials of Single Agent Targeted Therapies



Schwaederle, MM, et al. JCO 2015

# The Precision Medicine Paradigm Shift

Implications for Cancer Surveillance and Public Health

# Shifting Paradigm in Lung Cancer Treatment

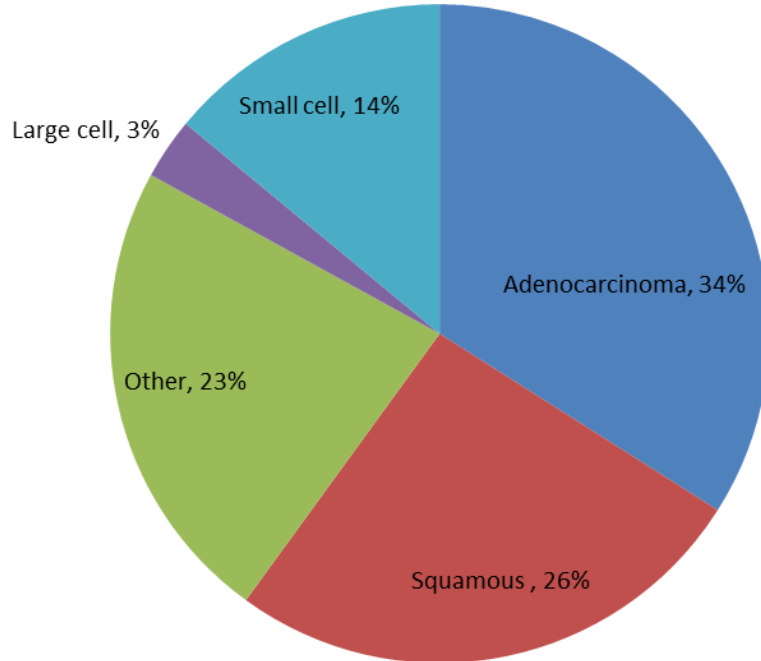
Old Way ->

**Traditional: Based on histology**

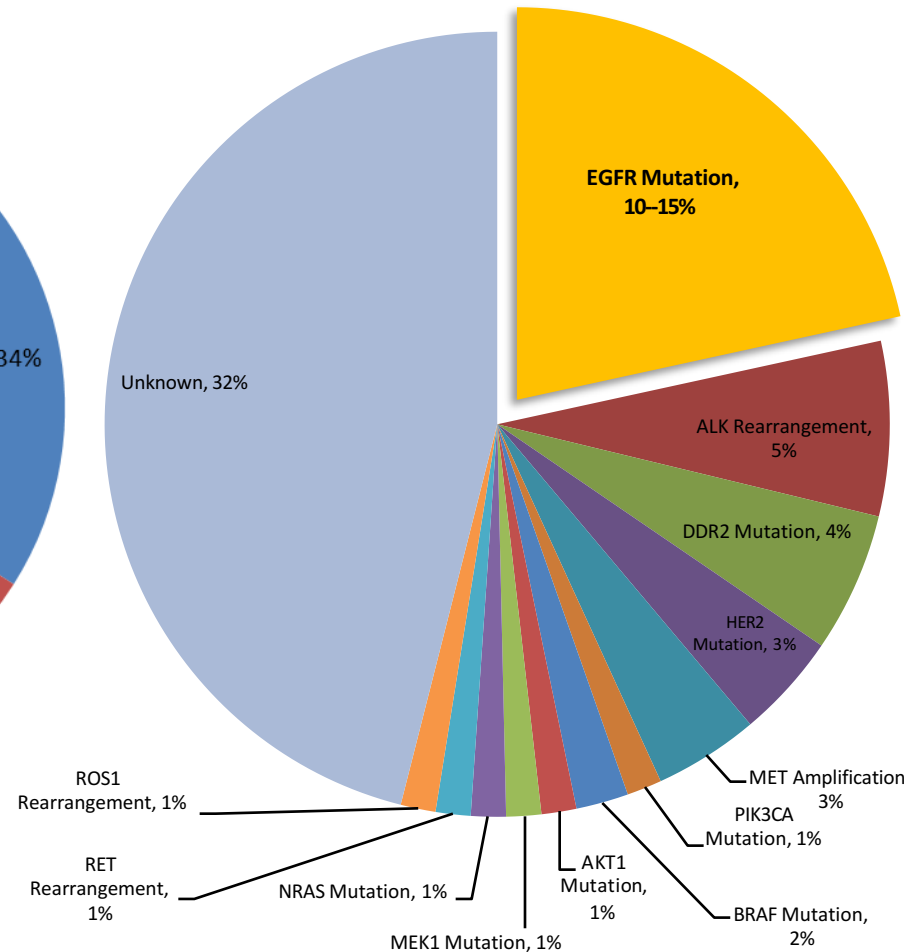
**Molecular: Based on genomic profile**

<- New Way

Chemotherapy



"Targeted" therapy



# Role of Precision Cancer Surveillance

1. Capture data that accurately measures the implementation and use of precision medicine in clinical settings
2. Evaluate the adoption of precision medicine and impact on the population
3. Leverage population-based data to ensure maximum benefit to the entire population through evidence-based cancer prevention and control
4. Leverage population-based data to accelerate further advances in precision medicine
  - a) Basic research
  - b) Clinical research
  - c) Population research

} Translational Science

# From Precision Medicine to Precision Cancer Surveillance

pre · ci · sion sur · veil · lance

Cancer surveillance designed to optimize efficiency in medical care or predict therapeutic benefit for particular groups of patients, especially by using genetic or molecular profiling across entire populations of patients

“Current KCR research is focused around precision surveillance – how to develop informatics methods to deliver efficiencies in registry operations in order to capture additional information so that we may classify all cancer patients by their tumor’s molecular changes”



# Capturing the Data (The Very Big Data)

Implications for Hospital Cancer Registries

# It All Begins with E-Path...

**onPath** SURGICAL PATHOLOGY REPORT  
 INTERNAL MEDICINE SPECIALISTS, INC.  
 1234 Holbrook Avenue, Teriwee, Georgia 25487  
 Phone 555.265.5547 fax 555.265.9898

PATIENT: John Q. Browne IM-09-192  
 DOB: 02/09/1955 Date Of Service: 11/11/2009  
 SEX: Male  
 CHART ID: 124887

PHYSICIAN: Sensosia W. Pintela  
 LOCATION: Westside Surgical Center  
 SPECIMEN: 1. TRANSVERSE COLON POLYP X2  
 2. DESCENDING COLON POLYP  
 3. SIGMOID COLON POLYP X2

PROCEDURE:  
 PREOP DX:  
 POSTOP DX:  
 HISTORY: HX OF POLYPS

**DIAGNOSIS**

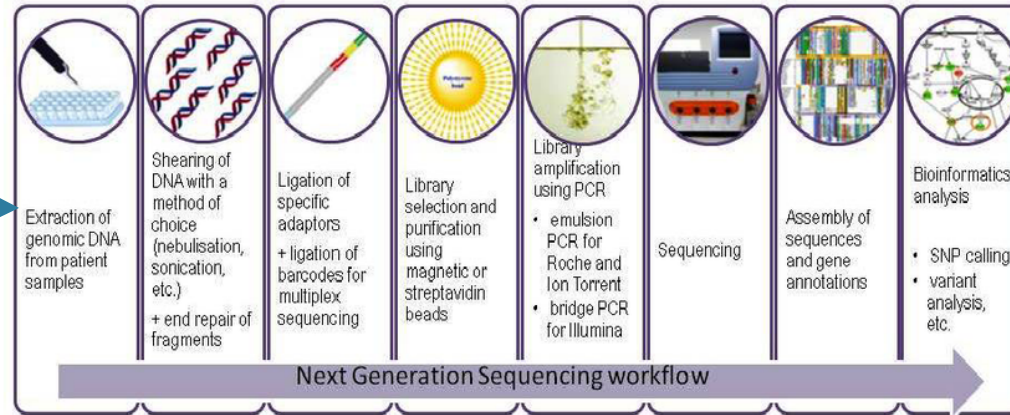
1. TRANSVERSE COLON POLYP X2: HYPERPLASTIC POLYP.  
 2. DESCENDING COLON POLYP: FRAGMENTS OF TUBULAR ADENOMA.  
 3. SIGMOID COLON POLYP X2: HYPERPLASTIC POLYP.

**GROSS DESCRIPTION**

1. Received in formalin, 1.5 cm in greatest dimension, labeled "descending colon", which is sigmoid colon. Two are submitted in one block.



CPT Detail: 88

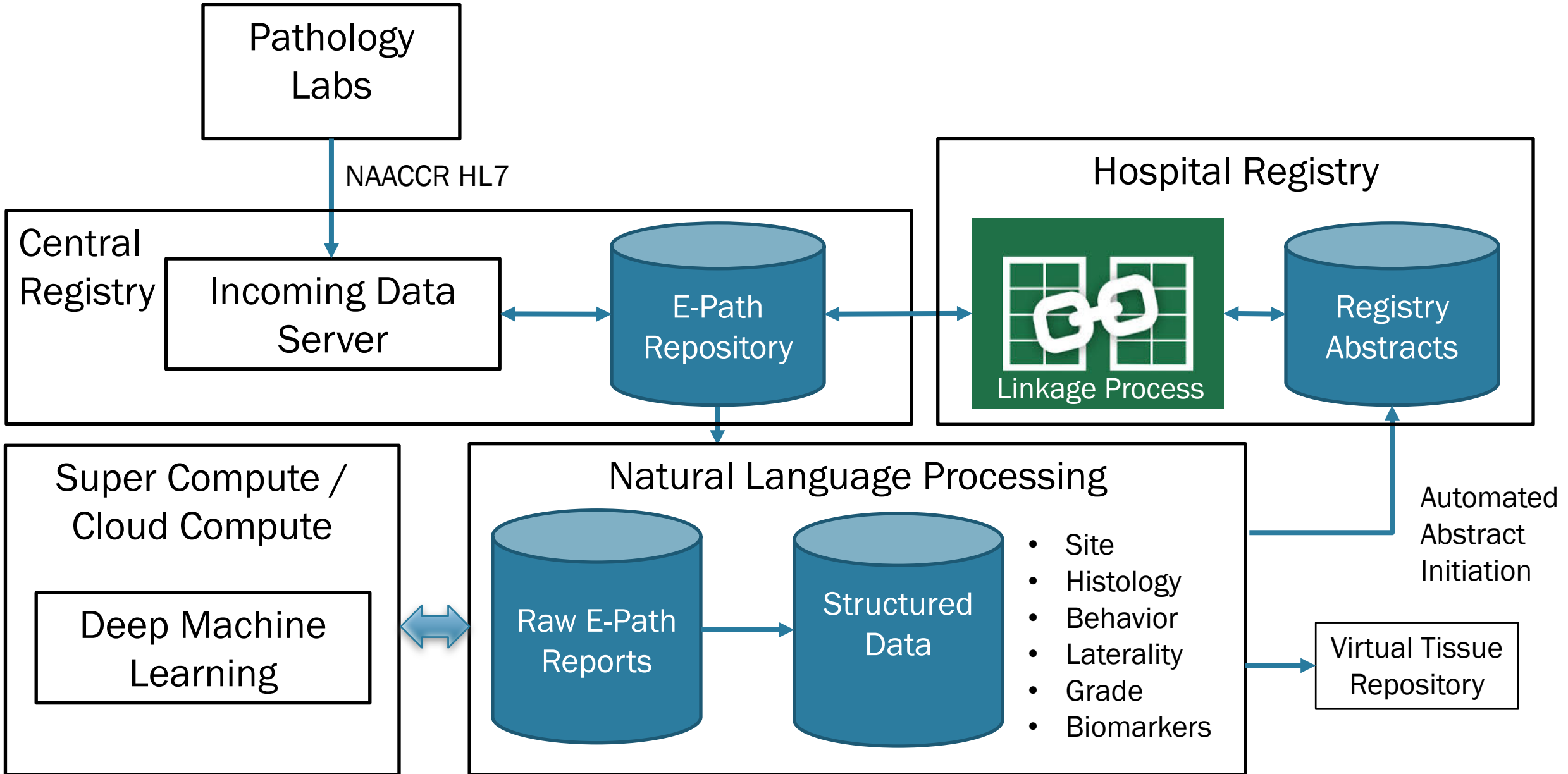


1

Tumor Molecular Report		
Alteration	Function	Oncogenic?
BRCA2 Q1782* (4.4%)	Tumor suppressor involved in the DNA damage response	Not previously reported, but frameshift at 1784 and 1738 are likely oncogenic and loss of function
BRAF D594N (2.2%)	Intracellular kinase	Hot spot, Likely oncogenic, gain of function
TP53 R337L (10.7%)	Tumor suppressor in the DNA damage pathway	Hot spot, likely oncogenic, loss of function

<sup>1</sup>Next generation sequencing applications for breast cancer research - Scientific Figure on ResearchGate. Available from: [https://www.researchgate.net/Overview-of-the-main-steps-in-Next-Generation-Sequencing-workflow\\_fig1\\_282061980](https://www.researchgate.net/Overview-of-the-main-steps-in-Next-Generation-Sequencing-workflow_fig1_282061980) [accessed 13 Aug, 2018]

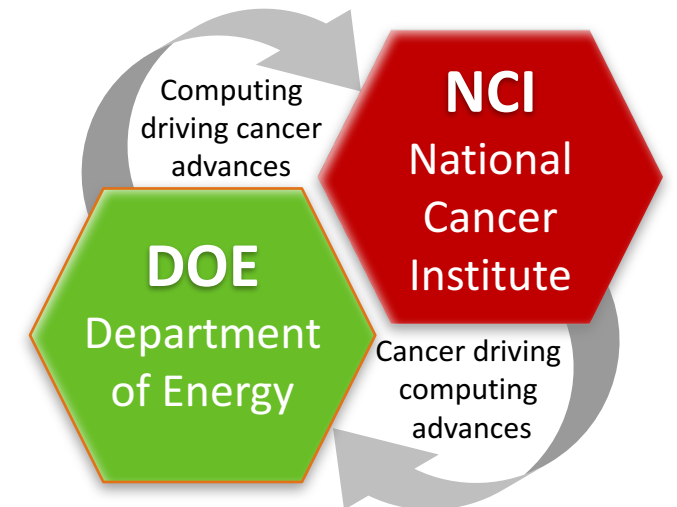
# Electronic Pathology Data Flow at KCR



# KCR Collaborating with National Cancer Institute and Department of Energy (DOE) on Major NLP Initiative

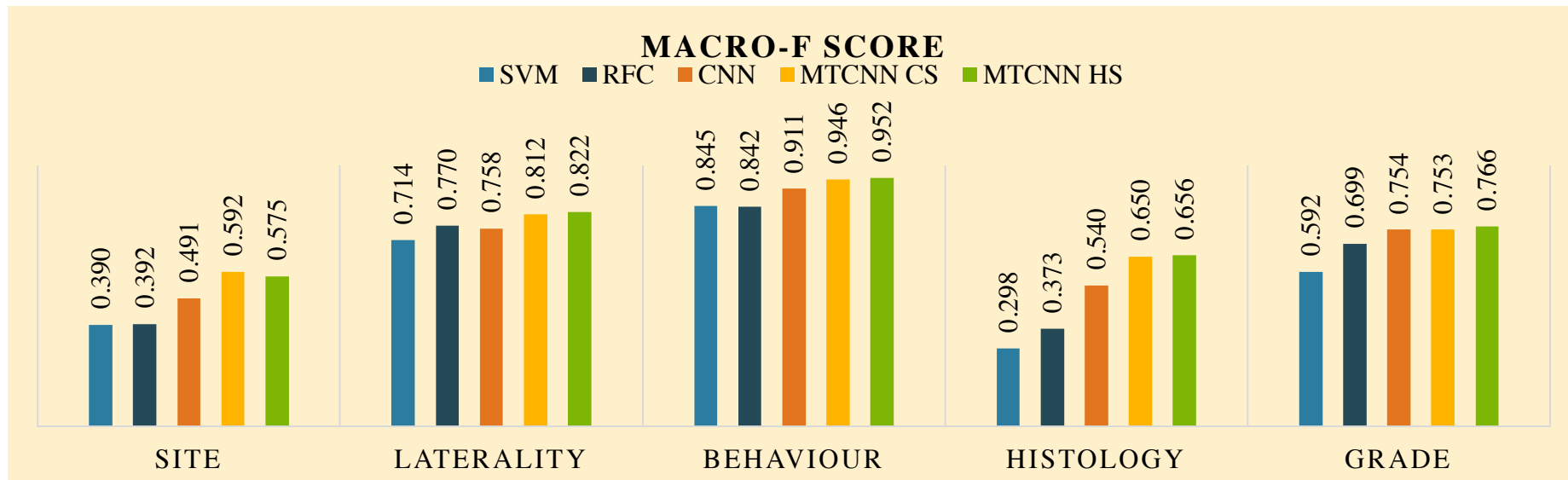
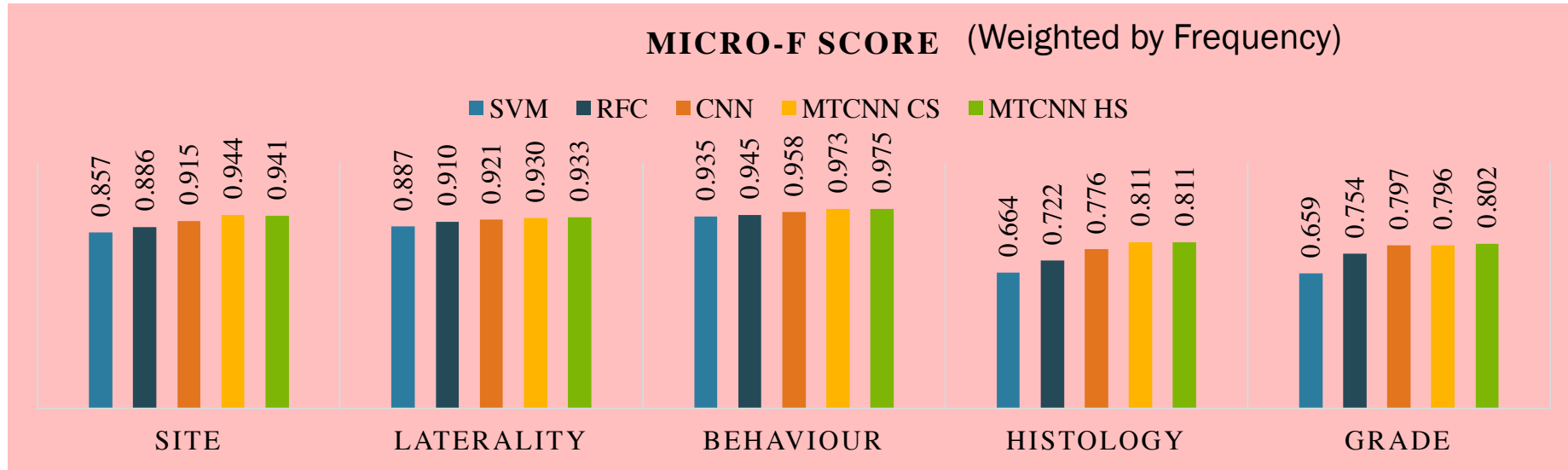
- KCR one of only four SEER registries chosen to participate
- Moonshot Initiative
  - Exascale CAncer Distributed Learning Environment (CANDLE)
- Pilot 3: Population Information Integration, Analysis, and Modeling
- Specific Aim: Deep NLP for Information Capture
  - Advanced machine learning for scalable patient information capture from unstructured clinical reports to semi-automate SEER data capture

*DOE-NCI partnership to advance exascale development through cancer research*



# Tumor-Level Analysis: 2-fold cross-validation 2004-2015 data (59,427 cases)

Pilot 3



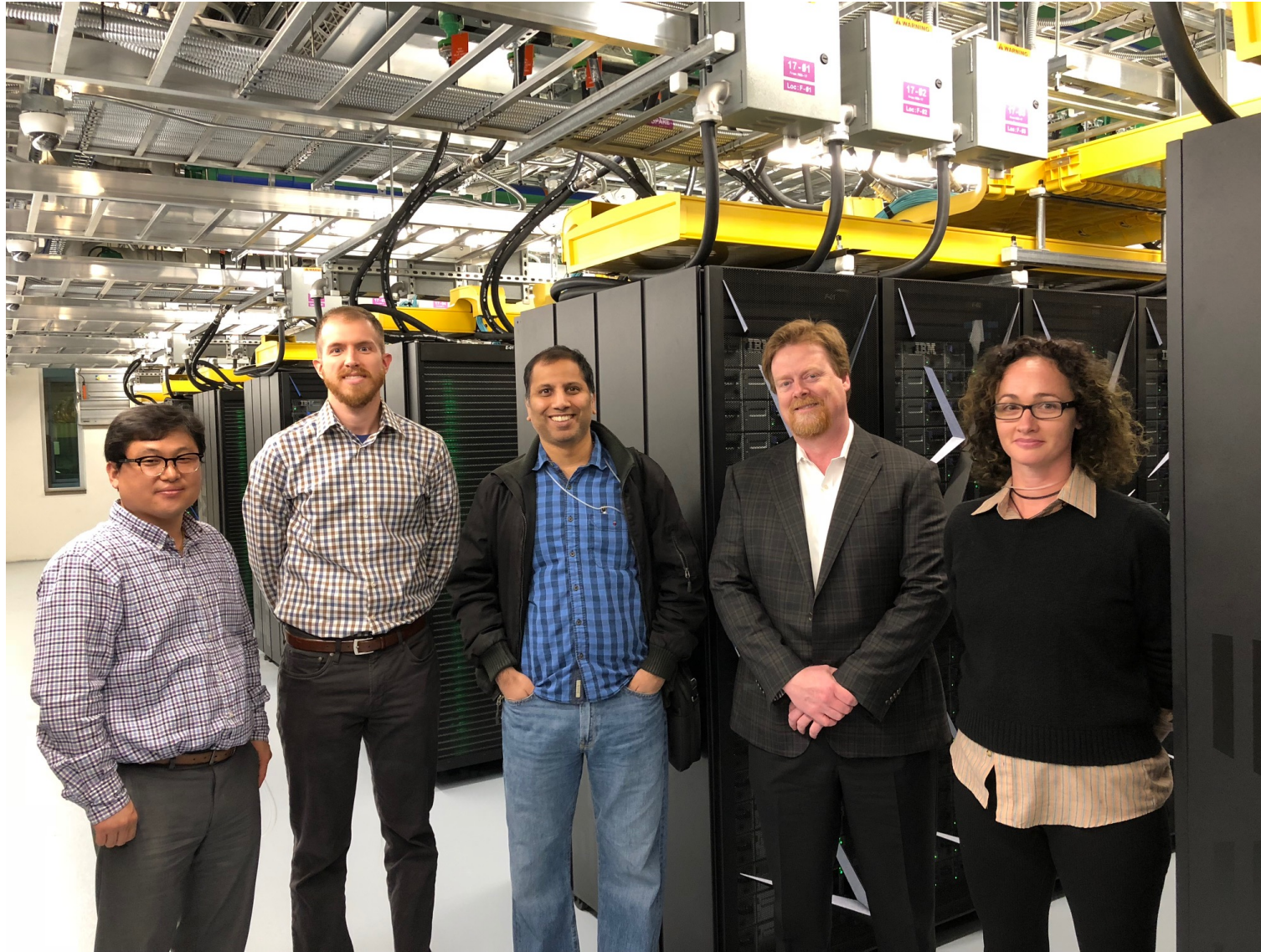
F Scores

>= .90 Good

>= .95 Very Good



# KCR/Markey Team at the Oakridge National Lab SUMMIT: Most Powerful Supercomputer on Earth



# Capturing Biomarkers

Natural Language Processing for Electronic Pathology Reports

# Capturing Molecular Biomarkers the Old-fashioned Way: Manual Abstraction of Site Specific Factors

- Brain and CNS
  - Brain molecular markers
  - Brain & CNS chromosome 1p and 19q
  - MGMT
- Breast
  - Ki-67
  - Oncotype DX
- Colon and Rectum
  - KRAS
  - Microsatellite Instability (MSI)
- Uveal Melanoma
  - Chromosome 3 and 8q status
- Oropharynx
  - HPV Status



# NLP to Enhance Automated Capture of Biomarkers

- NCCN Guidelines for EGFR and ALK Testing in Lung Cancer
  - EGFR
    - Epidermal growth factor receptor (EGFR) mutations cause new cancer cells to form quickly
    - Testing advised for metastatic lung adenocarcinomas, large-cell lung carcinomas and unknown subtypes
  - ALK
    - Anaplastic lymphoma kinase (ALK) gene re-arrangements makes an overactive ALK surface receptor that helps lung cancer cells grow
    - Testing advised for metastatic lung adenocarcinomas, large-cell lung carcinomas and unknown subtypes

# KCR Collaboration with the SEER Seattle Puget-Sound Registry and the Fred Hutchinson Cancer Research Center

## ■ Hypothesis

- NLP can be used to derive ALK and EGFR testing results from non-small cell lung cancer E-Path reports

## ■ Study Methods

- Each team selected 1000 random E-Path reports from their respective registry
  - Seattle ended up selecting over 3500 reports
- Lung cancer oncologists reviewed all E-Path reports to identify reports indicating ALK and EGFR testing and reporting of testing results
- Each team developed a machine-learned NLP model to derive tests and test results from E-Path reports
- Model tested on other team's cohort of E-Path reports

# Study Results

- Seattle and Kentucky achieved excellent results identifying EGFR and ALK testing was ordered
  - F-Scores 96.0 – 98.0
- Seattle performed better identifying positive test results
  - Seattle ALK/EGFR Positive Results F-Scores 97.0
  - Kentucky EGFR Positive Results F-Score 60.0
- Models did not perform well on the other site's E-Path reports
  - Seattle on KY Data: ALK/EGFR F-Scores 36.0, 4.0, respectively
  - Kentucky on Seattle Data: results pending
- Conclusions
  - Testing results not routinely reported
  - Pathology reporting terminology for biomarkers differs by region
  - Models perform better when trained on region specific data
  - More research needed

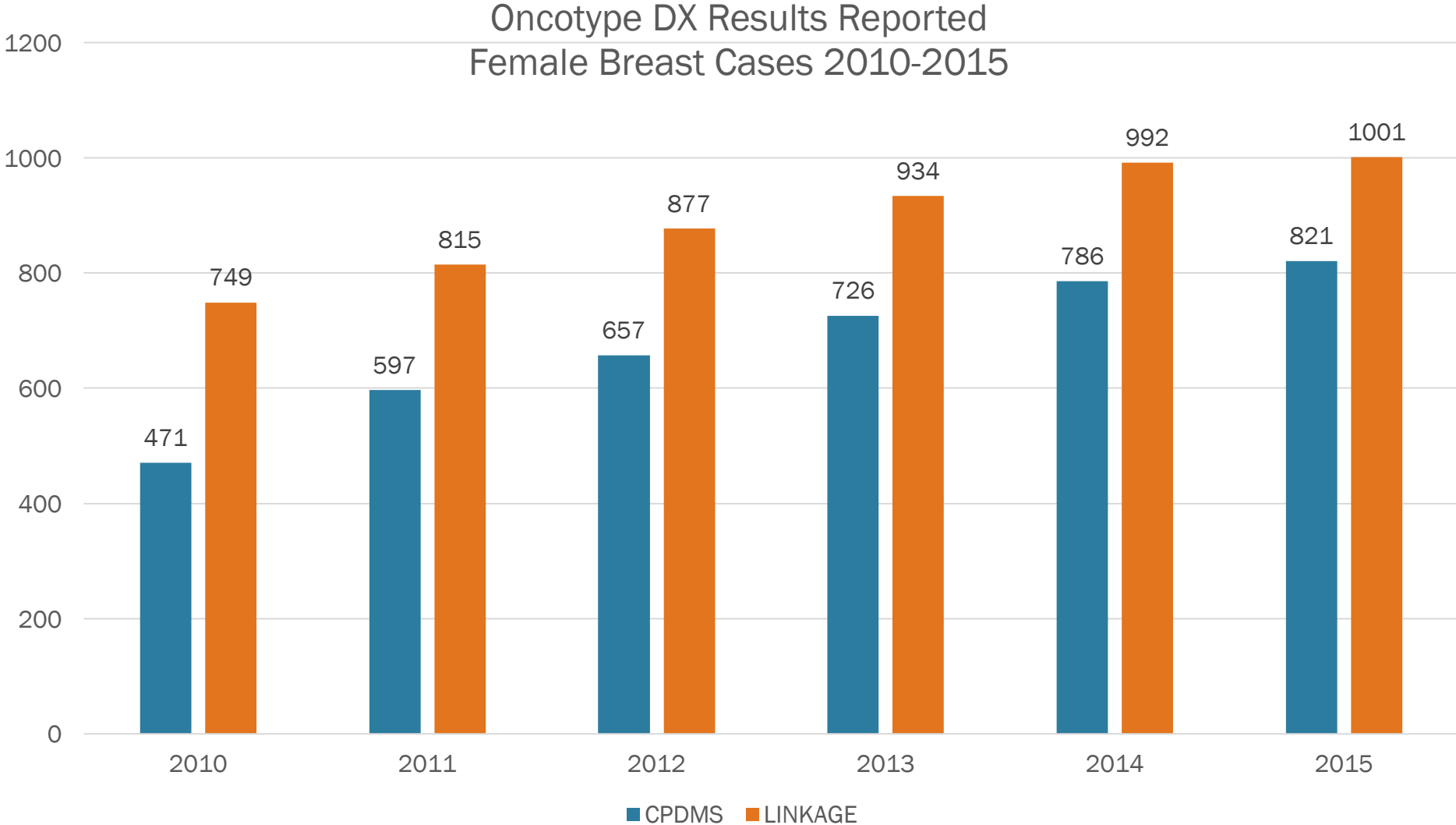
# Capturing Molecular Biomarkers at Scale

**Oncotype DX Linkages**

**NGS Multi-gene Panel Reporting**

# Results of Oncotype DX Linkage

## 32% Increase in Completeness



# Capturing Next Generation Sequencing (NGS) Multi-Gene Panel Biomarkers

- Clinical use of multi-gene panel sequencing of tumors is increasing rapidly
  - Molecular Tumor Boards
- Common service providers
  - Foundation Medicine
  - Caris Life Sciences
  - Guardant Health
  - OncoDNA
  - Tempus
  - Oncology Research Information Exchange Network (ORIEN) [Research]
  - Academic Clinical Labs
- Reports include mutations (both significant and of unknown significance)
  - Several providers are also willing to share raw data files (BAM)

# Foundation Medicine

- FoundationOne CDx
  - Next generation sequencing based in vitro diagnostic device for detection of substitutions, insertion and deletion alternations (indels), and copy number alterations (CNAs) in 324 genes
  - Select gene rearrangements
  - Genomic signatures
    - Microsatellite instability (MSi)
    - Tumor mutation burden (TMB)
- Uses DNA isolation from formalin-fixed paraffin embedded (FFPE) tumor tissue specimens
- FDA approved on November 30, 2017
- CMS coverage simultaneously proposed
  - Medicare beneficiaries with recurrent, metastatic or advanced state IV cancer, not previously NGS tested

# FoundationOne CDx

Table 1: Companion diagnostic indications

INDICATIONS	BIOMARKER	FDA-APPROVED THERAPY*
Non-Small Cell Lung Cancer (NSCLC)	<i>EGFR</i> exon 19 deletions and <i>EGFR</i> exon 21 L858R alterations	Gilotrif® (afatinib), Iressa® (gefitinib), or Tarceva® (erlotinib)
	<i>EGFR</i> exon 20 T790M alterations	Tagrisso® (osimertinib)
	<i>ALK</i> rearrangements	Alecensa® (alectinib), Xalkori® (crizotinib), or Zykadia® (ceritinib)
	<i>BRAF</i> V600E	Tafinlar® (dabrafenib) in combination with Mekinist® (trametinib)
Melanoma	<i>BRAF</i> V600E	Tafinlar® (dabrafenib) or Zelboraf® (vemurafenib)
	<i>BRAF</i> V600E or V600K	Mekinist® (trametinib) or Cotellic® (cobimetinib), in combination with Zelboraf® (vemurafenib)
Breast Cancer	<i>ERBB2</i> (HER2) amplification	Herceptin® (trastuzumab), Kadcylla® (ado-trastuzumab-emtansine), or Perjeta® (pertuzumab)
Colorectal Cancer	<i>KRAS</i> wild-type (absence of mutations in codons 12 and 13)	Erbitux® (cetuximab)
	<i>KRAS</i> wild-type (absence of mutations in exons 2, 3 and 4) and <i>NRAS</i> wild-type (absence of mutations in exons 2, 3 and 4)	Vectibix® (panitumumab)
Ovarian Cancer	<i>BRCA1/2</i> alterations	Rubraca® (rucaparib)

\* Tarceva® is the registered trademark of OSI Pharmaceuticals, LLC. Zelboraf®, Herceptin®, Perjeta®, Kadcylla®, and Cotellic® are registered trademarks of Genentech, Inc. Gilotrif® is a registered trademark of Boehringer Ingelheim International GmbH. Iressa® and Tagrisso® are registered trademarks of the AstraZeneca group of companies. Xalkori® is a registered trademark of Pfizer Inc. Zykadia®, Tafinlar®, and Mekinist® are registered trademarks of Novartis AG Corporation Switzerland. Erbitux® is a registered trademark of ImClone LLC, a wholly owned subsidiary of Eli Lilly and Company. Alecensa® is a registered trademark of Chugai Seiyaku Kabushiki Kaisha. Vectibix® is a registered trademark of Immunex Corporation. Rubraca® is a registered trademark of Clovis Oncology, Inc.



## Current Gene List<sup>2</sup>

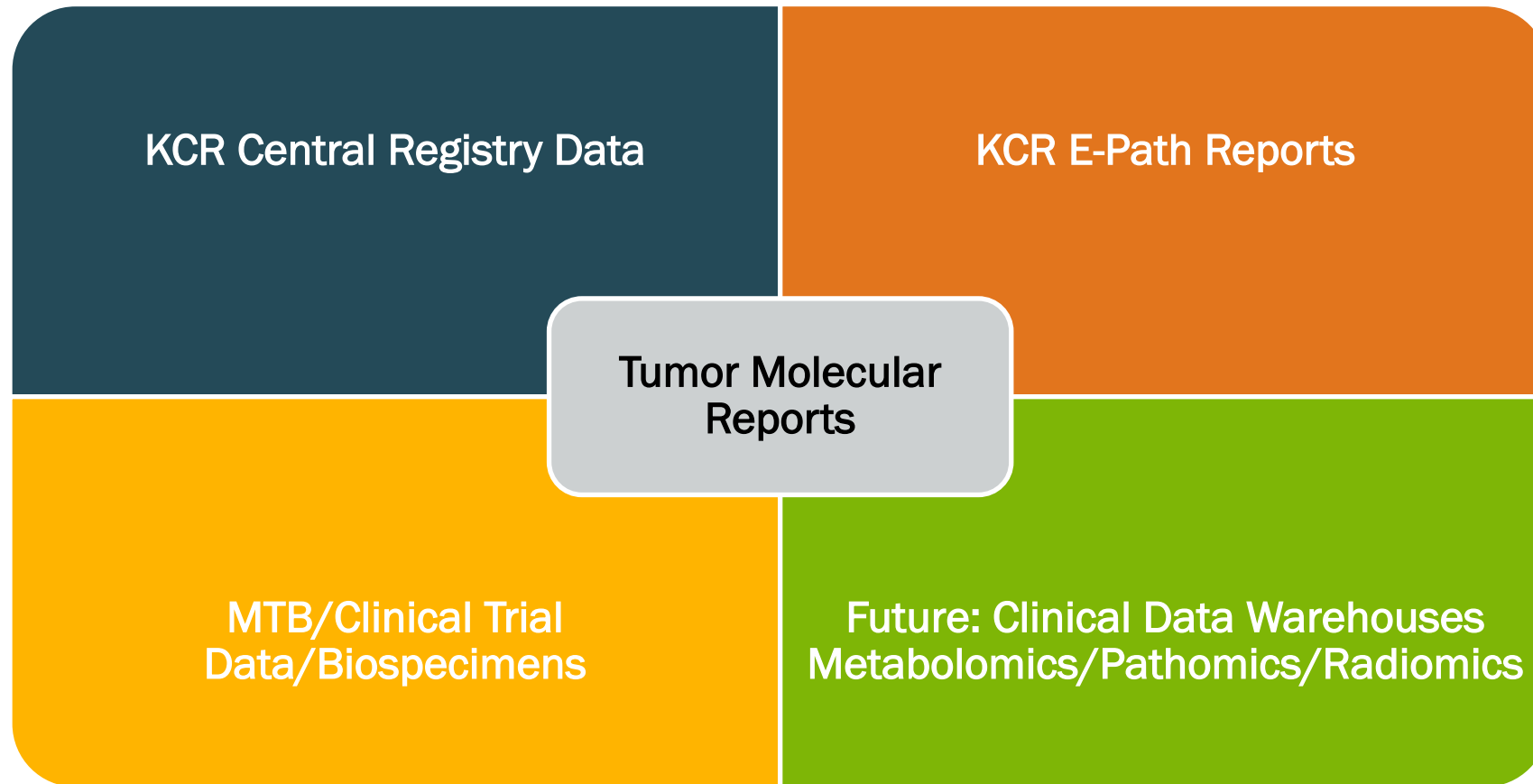
Genes with full coding exonic regions included in FoundationOne CDx for the detection of substitutions, insertion-deletions (indels), and copy-number alterations (CNAs).

<i>ABL1</i>	<i>ACVR1B</i>	<i>AKT1</i>	<i>AKT2</i>	<i>AKT3</i>	<i>ALK</i>	<i>ALOX12B</i>	<i>AMER1 (FAM123B)</i>	<i>APC</i>
<i>AR</i>	<i>ARAF</i>	<i>ARFRP1</i>	<i>ARID1A</i>	<i>ASXL1</i>	<i>ATM</i>	<i>ATR</i>	<i>ATRX</i>	<i>AURKA</i>
<i>AURKB</i>	<i>AXIN1</i>	<i>AXL</i>	<i>BAP1</i>	<i>BARD1</i>	<i>BCL2</i>	<i>BCL2L1</i>	<i>BCL2L2</i>	<i>BCL6</i>
<i>BCOR</i>	<i>BCORL1</i>	<i>BRAF</i>	<i>BRCA1</i>	<i>BRCA2</i>	<i>BRD4</i>	<i>BRIP1</i>	<i>BTG1</i>	<i>BTG2</i>
<i>BTK</i>	<i>C11orf30 (EMSY)</i>	<i>CALR</i>	<i>CARD11</i>	<i>CASP8</i>	<i>CBFB</i>	<i>CBL</i>	<i>CCND1</i>	<i>CCND2</i>
<i>CCND3</i>	<i>CCNE1</i>	<i>CD22</i>	<i>CD274 (PD-L1)</i>	<i>CD70</i>	<i>CD79A</i>	<i>CD79B</i>	<i>CDC73</i>	<i>CDH1</i>
<i>CDK12</i>	<i>CDK4</i>	<i>CDK6</i>	<i>CDK8</i>	<i>CDKN1A</i>	<i>CDKN1B</i>	<i>CDKN2A</i>	<i>CDKN2B</i>	<i>CDKN2C</i>
<i>CEBPA</i>	<i>CHEK1</i>	<i>CHEK2</i>	<i>CIC</i>	<i>CREBBP</i>	<i>CRKL</i>	<i>CSF1R</i>	<i>CSF3R</i>	<i>CTCF</i>
<i>CTNNA1</i>	<i>CTNNB1</i>	<i>CUL3</i>	<i>CUL4A</i>	<i>CXCR4</i>	<i>CYP17A1</i>	<i>DAXX</i>	<i>DDR1</i>	<i>DDR2</i>
<i>DIS3</i>	<i>DNMT3A</i>	<i>DOT1L</i>	<i>EED</i>	<i>EGFR</i>	<i>EP300</i>	<i>EPHA3</i>	<i>EPHB1</i>	<i>EPHB4</i>
<i>ERBB2</i>	<i>ERBB3</i>	<i>ERBB4</i>	<i>ERCC4</i>	<i>ERG</i>	<i>ERRF1</i>	<i>ESR1</i>	<i>EZH2</i>	<i>FAM46C</i>

## Poll: Who is interested in reviewing molecular reports and coding the mutations manually?

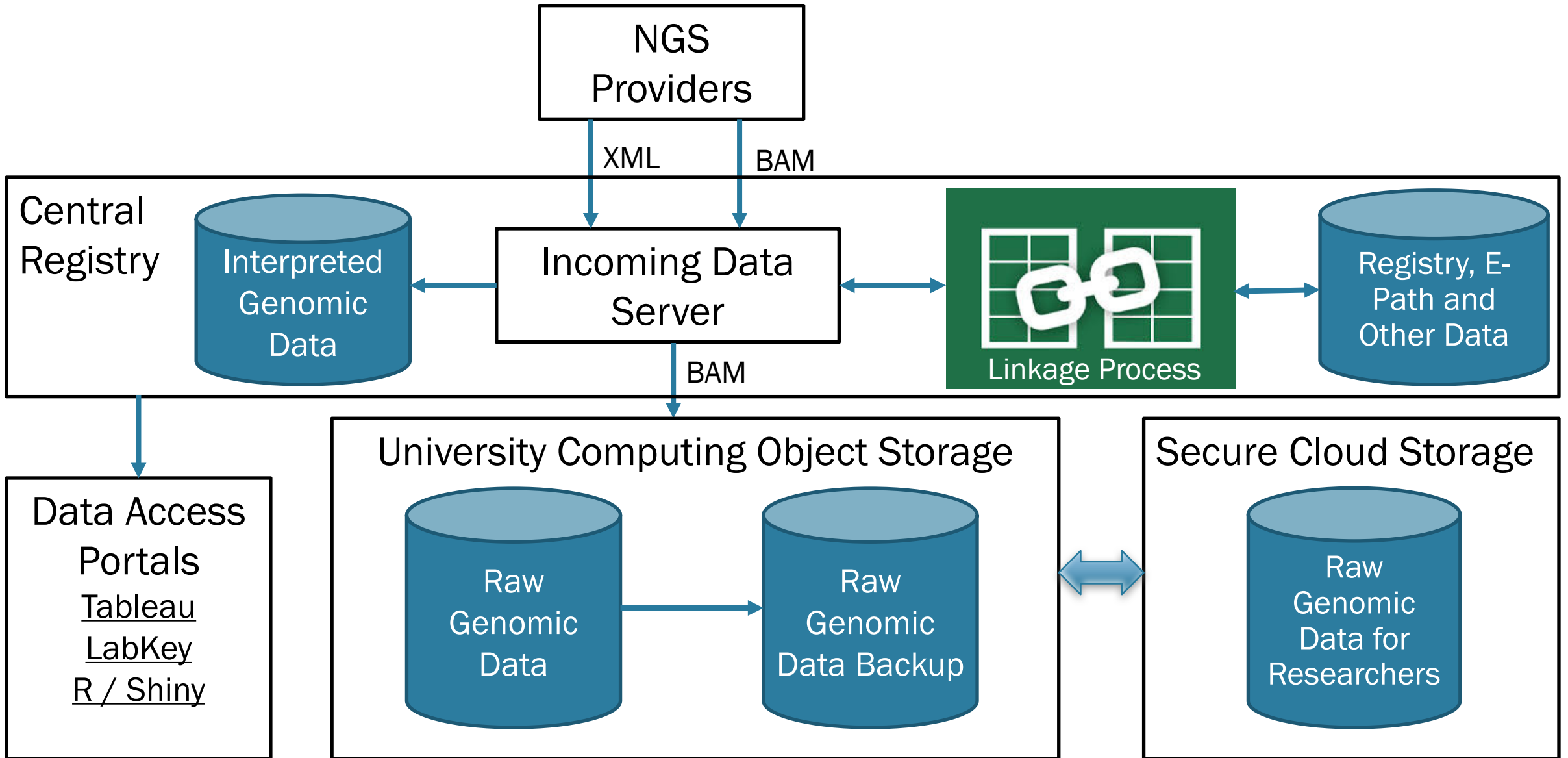
<i>JUN</i>	<i>KDM5A</i>	<i>KDM5C</i>	<i>KDM6A</i>	<i>KDR</i>	<i>KEAP1</i>	<i>KEL</i>	<i>KIT</i>	<i>KLHL6</i>
<i>KMT2A (MLL)</i>	<i>KMT2D (MLL2)</i>	<i>KRAS</i>	<i>LTK</i>	<i>LYN</i>	<i>MAF</i>	<i>MAP2K1 (MEK1)</i>	<i>MAP2K2 (MEK2)</i>	<i>MAP2K4</i>
<i>MAP3K1</i>	<i>MAP3K13</i>	<i>MAPK1</i>	<i>MCL1</i>	<i>MDM2</i>	<i>MDM4</i>	<i>MED12</i>	<i>MEF2B</i>	<i>MEN1</i>
<i>MERTK</i>	<i>MET</i>	<i>MITF</i>	<i>MKNK1</i>	<i>MLH1</i>	<i>MPL</i>	<i>MRE11A</i>	<i>MSH2</i>	<i>MSH3</i>
<i>MSH6</i>	<i>MST1R</i>	<i>MTAP</i>	<i>MTOR</i>	<i>MUTYH</i>	<i>MYC</i>	<i>MYCL (MYCL1)</i>	<i>MYCN</i>	<i>MYD88</i>
<i>NBN</i>	<i>NF1</i>	<i>NF2</i>	<i>NFE2L2</i>	<i>NFKBIA</i>	<i>NKX2-1</i>	<i>NOTCH1</i>	<i>NOTCH2</i>	<i>NOTCH3</i>
<i>NPM1</i>	<i>NRAS</i>	<i>NT5C2</i>	<i>NTRK1</i>	<i>NTRK2</i>	<i>NTRK3</i>	<i>P2RY8</i>	<i>PALB2</i>	<i>PARK2</i>
<i>PARP1</i>	<i>PARP2</i>	<i>PARP3</i>	<i>PAX5</i>	<i>PBRM1</i>	<i>PDCD1 (PD-1)</i>	<i>PDCD1LG2 (PD-L2)</i>		<i>PDGFRA</i>
<i>PDGFRB</i>	<i>PDK1</i>	<i>PIK3C2B</i>	<i>PIK3C2G</i>	<i>PIK3CA</i>	<i>PIK3CB</i>	<i>PIK3R1</i>	<i>PIM1</i>	<i>PMS2</i>
<i>POLD1</i>	<i>POLE</i>	<i>PPARG</i>	<i>PPP2R1A</i>	<i>PPP2R2A</i>	<i>PRDM1</i>	<i>PRKAR1A</i>	<i>PRKCI</i>	<i>PTCH1</i>
<i>PTEN</i>	<i>PTPN11</i>	<i>PTPRO</i>	<i>QKI</i>	<i>RAC1</i>	<i>RAD21</i>	<i>RAD51</i>	<i>RAD51B</i>	<i>RAD51C</i>
<i>RAD51D</i>	<i>RAD52</i>	<i>RAD54L</i>	<i>RAF1</i>	<i>RARA</i>	<i>RB1</i>	<i>RBM10</i>	<i>REL</i>	<i>RET</i>
<i>RICTOR</i>	<i>RNF43</i>	<i>ROS1</i>	<i>RPTOR</i>	<i>SDHA</i>	<i>SDHB</i>	<i>SDHC</i>	<i>SDHD</i>	<i>SETD2</i>
<i>SF3B1</i>	<i>SGK1</i>	<i>SMAD2</i>	<i>SMAD4</i>	<i>SMARCA4</i>	<i>SMARCB1</i>	<i>SMO</i>	<i>SNCAIP</i>	<i>SOCS1</i>
<i>SOX2</i>	<i>SOX9</i>	<i>SPEN</i>	<i>SPOP</i>	<i>SRC</i>	<i>STAG2</i>	<i>STAT3</i>	<i>STK11</i>	<i>SUFU</i>
<i>SYK</i>	<i>TBX3</i>	<i>TEK</i>	<i>TET2</i>	<i>TGFBP2</i>	<i>TIPARP</i>	<i>TNFAIP3</i>	<i>TNFRSF14</i>	<i>TP53</i>
<i>TSC1</i>	<i>TSC2</i>	<i>TYRO3</i>	<i>U2AF1</i>	<i>VEGFA</i>	<i>VHL</i>	<i>WHSC1 (MMSET)</i>	<i>WHSC1L1</i>	<i>WT1</i>
<i>XPO1</i>	<i>XRCC2</i>	<i>ZNF217</i>	<i>ZNF703</i>					

# Integration of Molecular, Registry, Pathology, MTB, Clinical Trial, Biorepository, Other Data



Integrated data to support Molecular Tumor Boards, Population Health and Research in Precision Medicine

# Genomic Data Flow into the Central Registry



# Additional Data Needed from Hospital Registrars

- Contextual information about specimen sent for testing
  - Primary site?
  - Recurrence?
  - Metastatic lesion?
  
- Timing/State of Disease
  - At time of diagnosis?
  - Before or after chemotherapy?
  - Following recurrence?
    - How long after remission?
  
- Additional treatment details
  - Specific targeted therapy
    - Selected from dropdown (searchable)
  
- Treatment response to targeted therapy

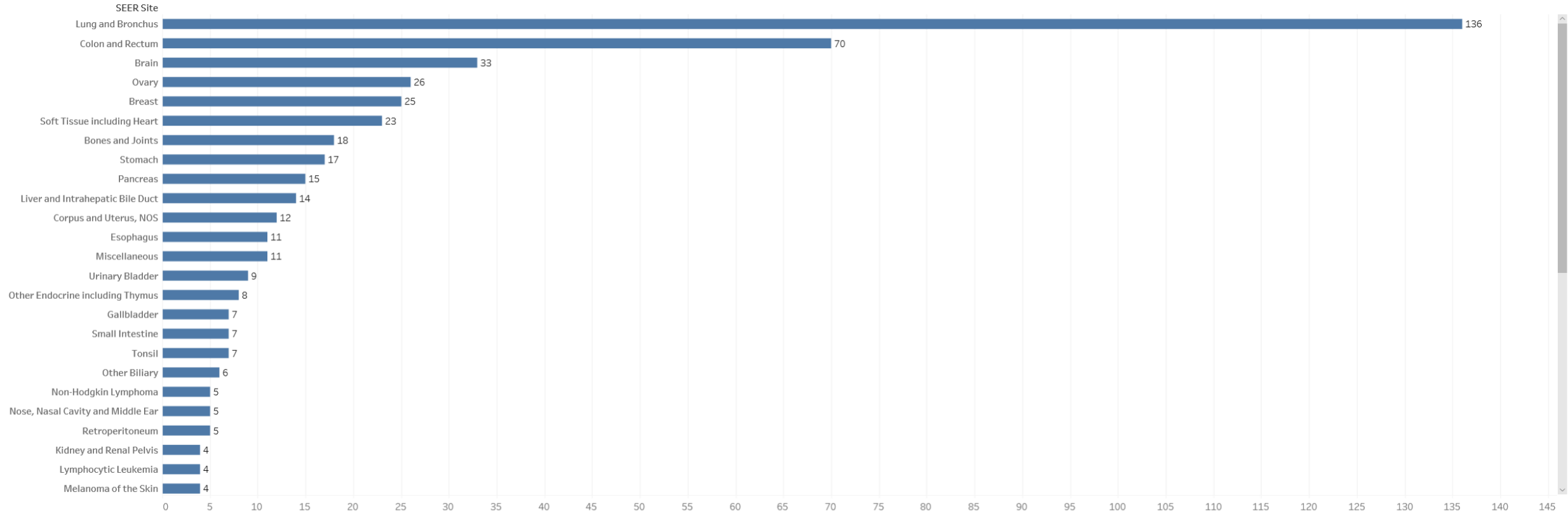
# Population Health and Research

Using population-based molecular report data

Total Primary Case Count: **518**

Cancer Cases with Molecular Reports by SEER Site

Updated: 5/18/2018 8:26:10 AM



Primary Case Count

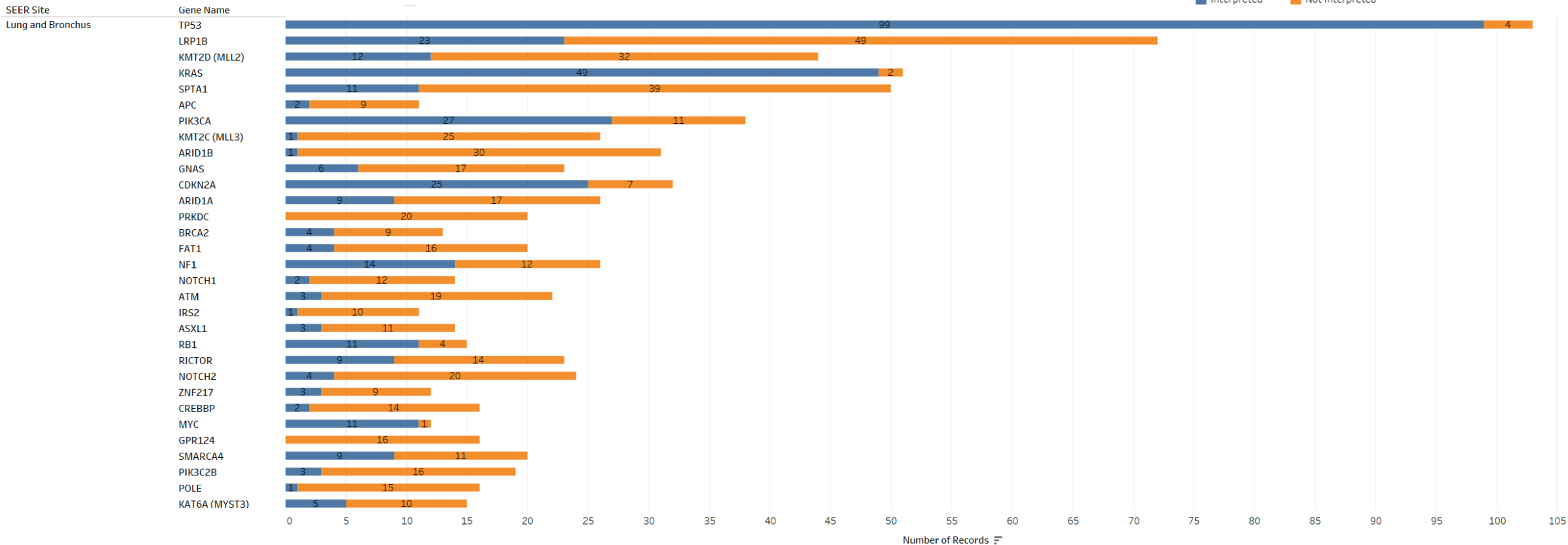
<b>Gene Interpretation</b> <input checked="" type="radio"/> (All) <input type="radio"/> Interpreted <input type="radio"/> Not Interpreted	<b>SEER Site</b> <input checked="" type="checkbox"/> (All) <input checked="" type="checkbox"/> Anus, Anal Canal and Anorectum <input checked="" type="checkbox"/> Bones and Joints <input checked="" type="checkbox"/> Brain <input checked="" type="checkbox"/> Breast <input checked="" type="checkbox"/> Cervix Uteri <input checked="" type="checkbox"/> Colon and Rectum <input checked="" type="checkbox"/> Corpus and Uterus, NOS <input checked="" type="checkbox"/> Cranial Nerves Other Nervous System <input checked="" type="checkbox"/> Esophagus <input checked="" type="checkbox"/> Eye and Orbit	<b>Histology</b> <input checked="" type="checkbox"/> (All) <input checked="" type="checkbox"/> ACINAR CELL CARCINOMA <input checked="" type="checkbox"/> ACUTE MYELOMONOCYTTIC LEUKEMIA <input checked="" type="checkbox"/> ADENOCAR W/MXD SUBTYPES <input checked="" type="checkbox"/> ADENO/ADENOMAT.POLYPOSIS COLI <input checked="" type="checkbox"/> ADENOCAR.IN VILLOUS ADENOMA <input checked="" type="checkbox"/> ADENOCAR.W/NEROENDOCR DIFFERNT <input checked="" type="checkbox"/> ADENOCAR/ADENOMATOUS POLYP <input checked="" type="checkbox"/> ADENOCAR/TUBULOVILLOUS ADENOMA <input checked="" type="checkbox"/> ADENOCARCINOMA, INTESTINAL TYP <input checked="" type="checkbox"/> ADENOCARCINOMA, NOS	<b>Behavior</b> <input checked="" type="checkbox"/> (All) <input checked="" type="checkbox"/> Benign <input checked="" type="checkbox"/> Borderline <input checked="" type="checkbox"/> Malignant	<b>Stage at Diagnosis</b> <input checked="" type="checkbox"/> (All) <input checked="" type="checkbox"/> Stage I <input checked="" type="checkbox"/> Stage II <input checked="" type="checkbox"/> Stage III <input checked="" type="checkbox"/> Stage IV <input checked="" type="checkbox"/> Stage Unknown	<b>Age at Diagnosis</b> 1 ————— 92	<b>Diagnosis Year</b> 1991 ————— 2017	<b>Vital Status</b> <input checked="" type="radio"/> (All) <input type="radio"/> Alive <input type="radio"/> Dead	<b>Gender</b> <input checked="" type="radio"/> (All) <input type="radio"/> Female <input type="radio"/> Male	<b>KY Appalachia</b> <input checked="" type="checkbox"/> (All) <input checked="" type="checkbox"/> Appalachia <input checked="" type="checkbox"/> non-Appalachia <input checked="" type="checkbox"/> Outside KY
--	---	--	---	---	---------------------------------------	--	--	---	---

Cancer Cases with Molecular Reports by SEER Site and Gene Mutation Counts

Updated: 5/18/2018 8:26:44 AM

Total Mutation Count: 8,342

Gene Interpretation  
 Interpreted  Not Interpreted



Gene Name:  (All),  ABL1,  ABL2,  ACTB,  ACVR1B,  AKT1,  AKT2,  AKT3,  ALK,  AMER1 (FAM123B),  APC

Gene Interpretation:  (All),  Interpreted,  Not Interpreted

SEER Site:  (All),  Anus, Anal Canal and Anorectum,  Bones and Joints,  Brain,  Breast,  Cervix Uteri,  Colon and Rectum,  Corpus and Uterus, NOS,  Cranial Nerves Other Nervous System,  Esophagus,  Eye and Orbit

Histology:  (All),  ACINAR CELL CARCINOMA,  ACUTE MYELOMONOCYTIC LEUKEMIA,  ADENOCAR W/MXD SUBTYPES,  ADENO/ADENOMAT.POLYPOSIS COLI,  ADENOCAR.IN VILLOUS ADENOMA,  ADENOCAR.W/NEROENDOCR DIFFERNT,  ADENOCAR/ADENOMATOUS POLYP,  ADENOCAR/TUBULOVILLOUS ADENOMA,  ADENOCARCINOMA, INTESTINAL TYP,  ADENOCARCINOMA, NOS

Behavior:  (All),  Benign,  Borderline,  Malignant

Best Stage Grouping:  (All),  Stage I,  Stage II,  Stage III,  Stage IV,  Stage Unknown

Age at Diagnosis: 0 to 92

Diagnosis Year: 1991 to 2017

Vital Status:  (All),  Alive,  Dead

Gender:  (All),  Female,  Male

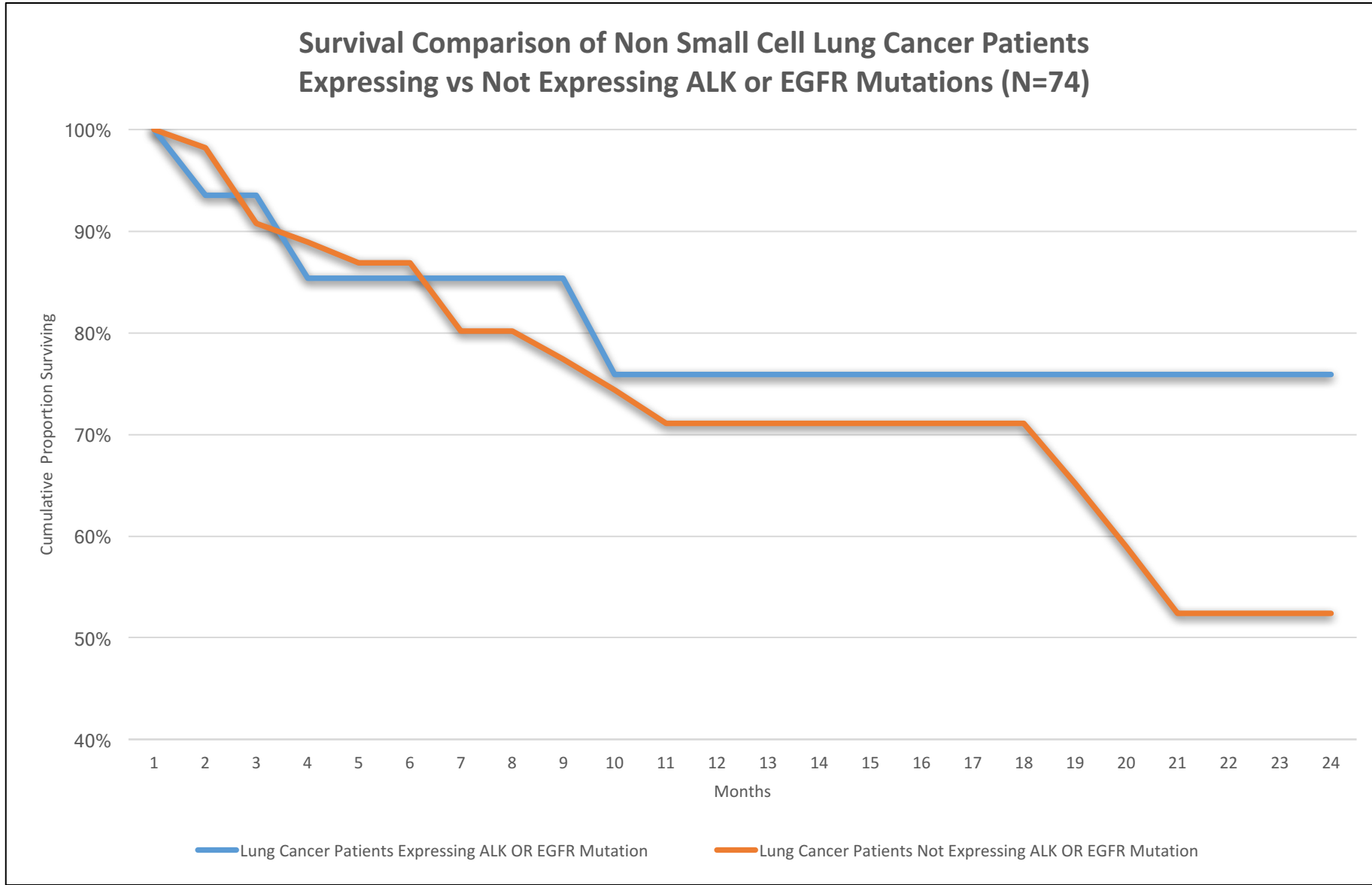
KY Appalachia:  (All),  Appalachia,  non-Appalachia,  Outside KY

# Identifying Molecular Disparities in the Population

- Recent study examined molecular profiles of 51 non-small cell lung cancer in Appalachian Kentucky compared to the Cancer Genome Atlas (TCGA)
- Certain tumor mutations were significantly higher among Appalachian Kentucky patients compared to the U.S.
  - PCMTD1
  - IDH1
- Does this represent a health disparity in Kentucky's underserved population?



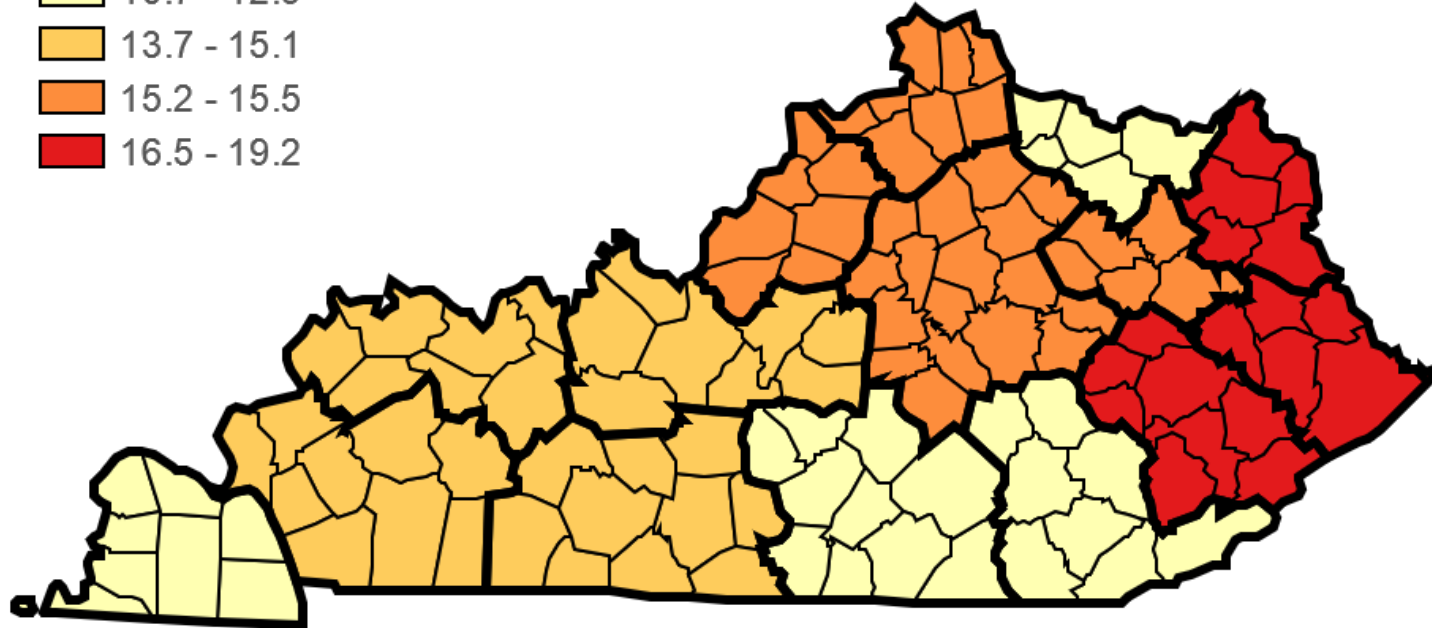
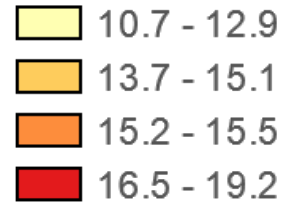
# Population Measures: How do Gene Mutations Impact Survival?



# Mapping Biomarker Data for Cancer Prevention and Control

Age-Adjusted Invasive Cancer Incidence Rates in Kentucky  
Triple Negative (HR-/HER2-) - Breast, Female, 2011 - 2015  
By Area Development District  
Age-Adjusted to the 2000 U.S. Standard Million Population

Kentucky Rate: 14.8 / per 100,000



All rates per 100,000.  
Data accessed May 16, 2018. Based on data released Nov 2017.  
© 2018 Kentucky Cancer Registry.

# Conclusions: Precision Cancer Surveillance is a Critical Role for Cancer Registries

- Capture and integration of Next Generation Sequencing (NGS) molecular test results is a major goal of the Kentucky Cancer Registry
- Informatics efforts are developing methods and tools to enhance e-Path reporting and other infrastructures needed to capture data for all patients who are tested
  - Cannot wait for site specific factors to emerge
  - Cancer registrar manual entry of 100s of molecular markers impossible
- Electronic transmissions of standardized molecular test results from NGS service providers is feasible and practical
  - Molecular test report data is no more challenging than electronic pathology reporting
  - Raw data file storage, however, requires more significant technical expertise and storage facilities
- Central cancer registries can be enhanced with **population-based** molecular test data within 2-4 years
- Advances will positively impact clinical decision making and evidence-based cancer prevention and control

# Acknowledgements:

## KCR/Markey Informatics Team

### ■ Software Team

- Isaac Hands
- Peter Ransdell
- Jason Jacob
- David Rust
- Roger Chui
- Clay Campbell
- Chaney Blu
- York Dobyns
- Luan Pham
- Bront Davis
- Justin Levens

### ■ Project Management

- Joseph Mueller

### ■ Systems Team

- Jenny Gregory
- John Williams
- Joel Wheeler
- Malissa Sullivan

### ■ Faculty

- Dr. JC Jeong
- Dr. Sally Ellingson
- Dr. Rama Kavuluru

# Questions/Discussion

## ■ Contact Information:

Eric B. Durbin, DrPH, MS

Telephone: 859-218-3182

E-mail: [ericd@kcr.uky.edu](mailto:ericd@kcr.uky.edu)

Web: <http://www.kcr.uky.edu>

## ■ Funding Acknowledgements

- Commonwealth of Kentucky
- University of Kentucky Markey Cancer Center
- CDC/NPCR/ECC: U58DP005400, U58DP006313
- NCI/SEER: HHSN261201000131, P30CA177558

Browse cancer incidence and mortality data on your iPad, iPhone, or iPod Touch



Available on the  
 App Store