

# Big Data and Cancer: Transforming Patient Care by Turning Data into Decisions



CANCER  
**PROGRESS**  
*by Defined Health*

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Conrad New York

# Big Data and Cancer: Transforming Patient Care by Turning Data into Decisions

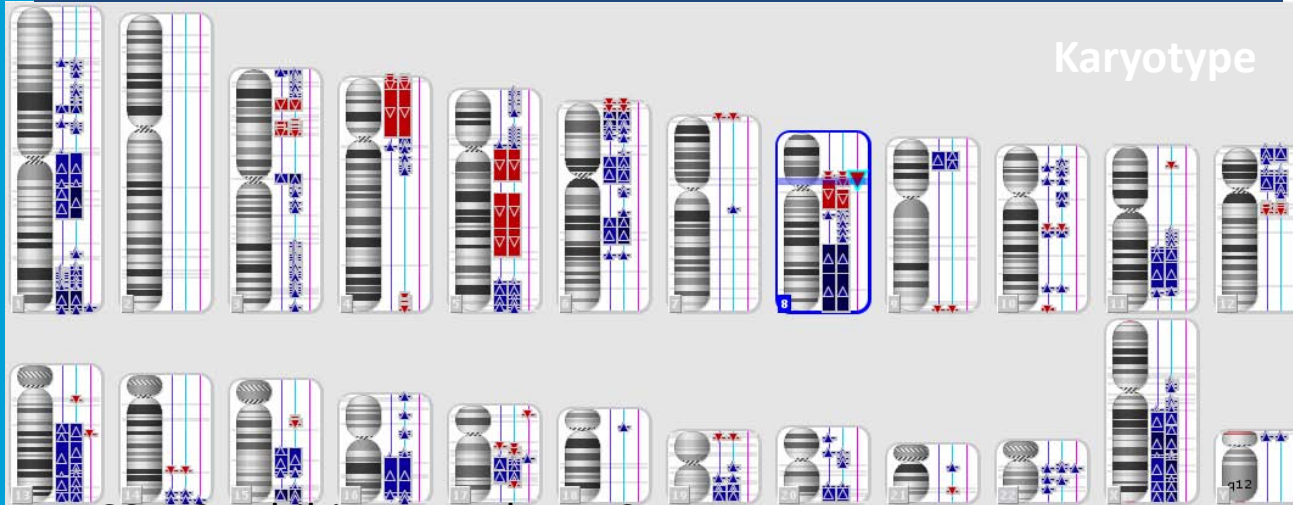
## Moderator:

- Colin Hill, Chief Executive Officer, President & Chairman, GNS Healthcare

## Panelists:

- Alexis Borisy, Entrepreneur in Residence, Third Rock Ventures
- Joel Dudley, PhD, Director of Biomedical Informatics and Assistant Professor of Genetics and Genomics Sciences, Icahn School of Medicine at Mount Sinai
- Brian Leyland-Jones, MD, VP, Molecular and Experimental Medicine, Avera Health
- Michael Kolodziej, MD, National Medical Director, Oncology Strategies, Aetna Ventures, LLC
- Timothy J. Thompson, CEO, Intervention Insights

# SSKT2 Basic CNV Report



SSKT2 exhibits some large CNV

changes, particularly on chromosomes 1, 4, 5, 6, 8, 13, and X. You'll note the two sets of bars (in a few cases 3). The first two bars are the replicate samples. 85% of the CNVs were concordant between the two tumor samples. Highlighted is chr 8 where there was a homozygous loss of ADAM 3A and 5P in all three samples, it has recently been linked to glioma development.

CytoRegion	Chromosom e	CN State
APC	5	1
BAP1	3	1
<b>FGFR3</b>	4	1
IRF4	6	1
MAP3K1	5	1
MLL2	12	1
MYST3	8	1
PBRM1	3	1
<b>PIK3R1</b>	5	1
<b>PRKDC</b>	8	1
RAD50	5	1
SETD2	3	1
<b>TGFB2</b>	3	1

CNV Losses

CNV Gains



CytoRegion	Chromosom e	CN State
AKT3	1	4
BTK	X	4
IGF1R	15	4
PAK3	X	4
ARFRP1	20	3
ATM	11	3
<b>AURKA</b>	20	3
BCORL1	X	3
<b>BRIP1</b>	17	3
CBFB	16	3
CCND2	12	3
CD79B	17	3
CDH1	16	3
<b>CDKN2A</b>	9	3
CDKN2B	9	3
CTCF	16	3
DDR2	1	3
EPHA3	3	3
FGF14	13	3
FGF23	12	3
FGF6	12	3
FGFR4	5	3
FLT4	5	3
GNA13	17	3
GNAS	20	3
IRS2	13	3
KDM5A	12	3
KRAS	12	3
MAP2K1	15	3
MCL1	1	3
MRE11A	11	3
NOTCH2	1	3
NPM1	5	3
NTRK1	1	3
NUP93	16	3
PPP2R1A	19	3
PRDM1	6	3
RB1	13	3
RNF43	17	3
SPOP	17	3
STAG2	X	3

# RNA Seq (sample #1)

Drug	Target_Expressed	Target_Expressed_FC
Adriamycin	TOP2A	4.52
Alitretinoin	RXRB	-1.01
AMG337	MET	-2.65
BGJ398	FGFR1	-1.86
Crizotinib	MET	-2.65
Dacarbazine	POLA2	0.94
Etoposide	TOP2A	4.52
GSK2141795 (GSK795)		
Interferon		
MLN8237	AURKA	4.2
Paclitaxel		
Pemetrexed	DHFR GART	2.68 1.18
Sorefenib	BRAF	1.58
Tamoxifen	ESR1	-3.72
Temsirolimus	MTOR	1.16
Vinblastine		
Vorinostat		
XL184	MET	-2.65

# RNA seq (sample #2)

Drug	Target_Expressed	Target_Expressed_FC
Adriamycin	TOP2A	4.95
BGJ398	FGFR1	-3.43
Crizotinib	ALK ROS1	4.95 11.13
Dacarbazine	POLA2	0.85
Etoposide	TOP2A	4.95
GSK2141795 (GSK795)		
MLN8237	AURKA	4.49
Paclitaxel	TUBB3	4.53
Pemetrexed	GART	0.99
PF-00299804	KRAS	1.1
Sorefenib	PDGFRB	-2.33
Vinblastine	TUBB3	4.53
Vorinostat	HDAC2	1

# Tumor 1

# SSKT 2

# Tumor 2

**BRAF (1.6) -Sorefenib**

**CDK2 (1.3) -Bosutinib**

DHFR (2.7)

DIO1 (6.6)

**ESR1 (-3.7)**

GSK3B (1)

IDE (2)

IKBKB (1.5)

**JAK2 (2)**

KCNN3 (3.9)

MMP11 (3.2)

MR1 (1.6)

**MTOR (1.2) -Everolimus**

PDE4D (2.4)

POLE2 (4.6)

**PPARD (-0.8)**

PTK2 (1.2)

RRM2 (4.7)

**RXRΒ (-1) -Alitretinoin et al.**

**SDC2 (-2.4)**

SLC12A1 (8.2)

SLC18A2 (5.4)

CTPS1 (2.3 / 1.7)

DNMT1 (2.5 / 1.6)

POLA1 (1.4 / 1.2)

SLC6A4 (5.4 / 6.3)

SQLE (2.7 / 3.9)

**THRA (-1.5 / -1.8)**

**TOP2A (4.5 / 5)-  
Adriamycin/Etoposide**

POLA2 (1 / 0.9)

**AURKA (4.2/ 4.5) -  
MLN8237 (Alisertib)**

GART (1.2 / 1)

KCNH2 (4.2)

SLC6A2 (6)

CACNA1B (8.9)

**TUBB3 (4.5) -Paclitaxel/Vinblast**

AODRA2A (2.3)

CA9 (9.7)

FDPS (1.3)

**VEGFA (2.8) -Lenalidomide**

IMPA2 (2.1)

GRIN2A (6.6)

DHODH (2.4)

PTPN1 (0.7)

**HDAC2 (1) -Vorinostat**

**ALK (5) -Crizotinib**

**KRAS (1.1) -Dacomitinib**

**ROS1 (11.1) -Crizotinib**



downregulated  
upregulated

values: log2 fold change



# RNA-seq & CNV Concordance

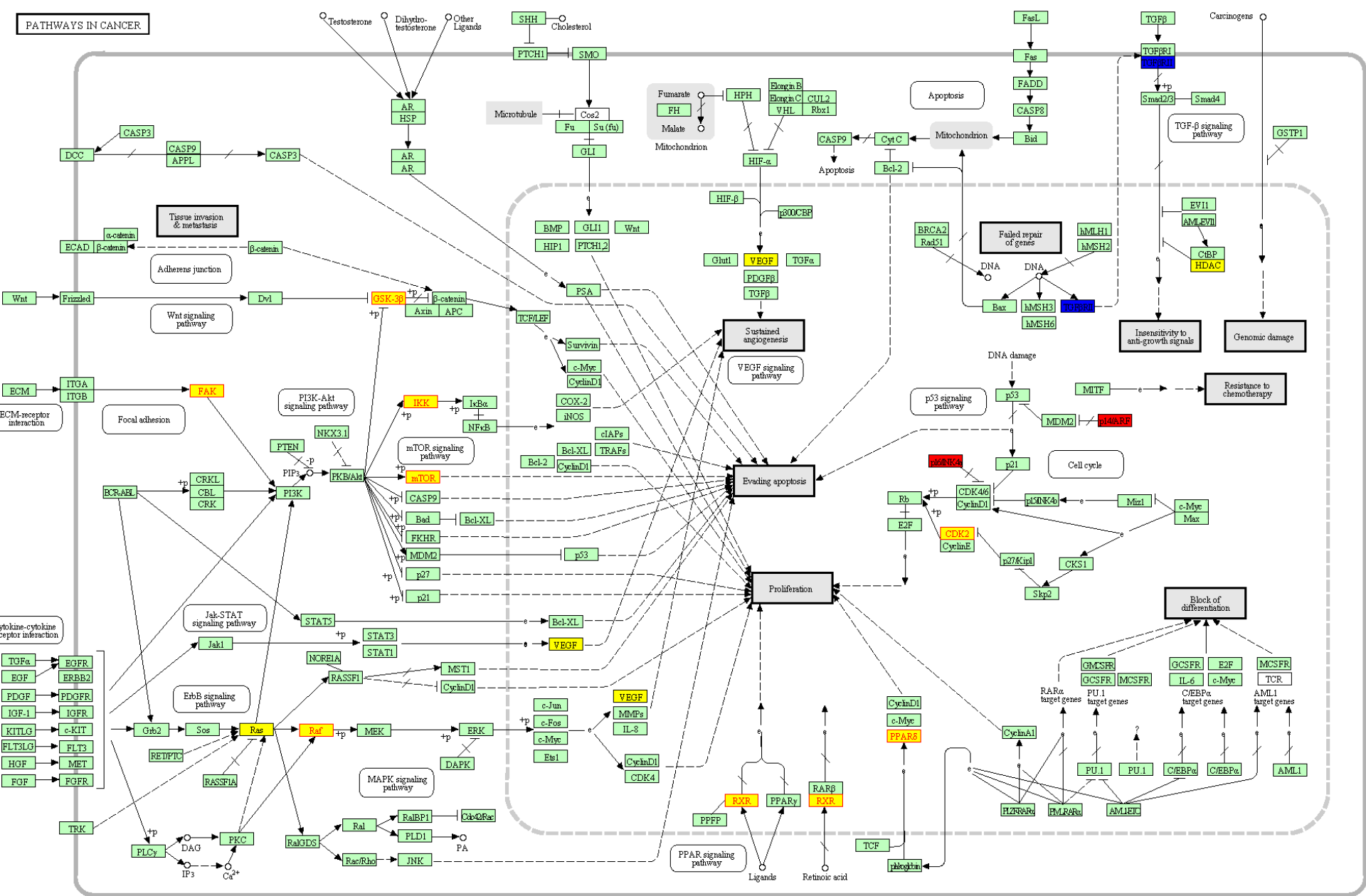
Gene	Chromosome	CN State	Gain/Loss	SSKT2_T1	SSKT2_T2
AURKA	20	3	Gain	Up (4.2)	up (4.5)
BRIP1	17	3	Gain	up (5)	up (5.8)
CDKN2A	9	3	Gain	up (4.4)	up (4.7)
FGFR3	4	1	Loss	up (3.5)	NA (1.4)
PIK3R1	5	1	Loss	NA (-0.1)	down (-2.3)
PRKDC	8	1	Loss	up (3.2)	NA (0.8)
TGFBR2	3	1	Loss	down (-2.5)	down (-2.9)

Red: Upregulated and Gain

Blue: Downregulated and loss

NA: not diff. expressed or no reliable expression value

PATHWAYS IN CANCER



Blue: Downregulated & CNV: Loss  
 Red: Upregulated & CNV: Gain





## **BRIP1 BRCA1 interacting protein C-terminal helicase 1 [ *Homo sapiens* (human) ]**

Gene ID: 83990, updated on 17-Nov-2013

### **Organism**

[Homo sapiens](#)

### **Lineage**

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo

### **Also known as**

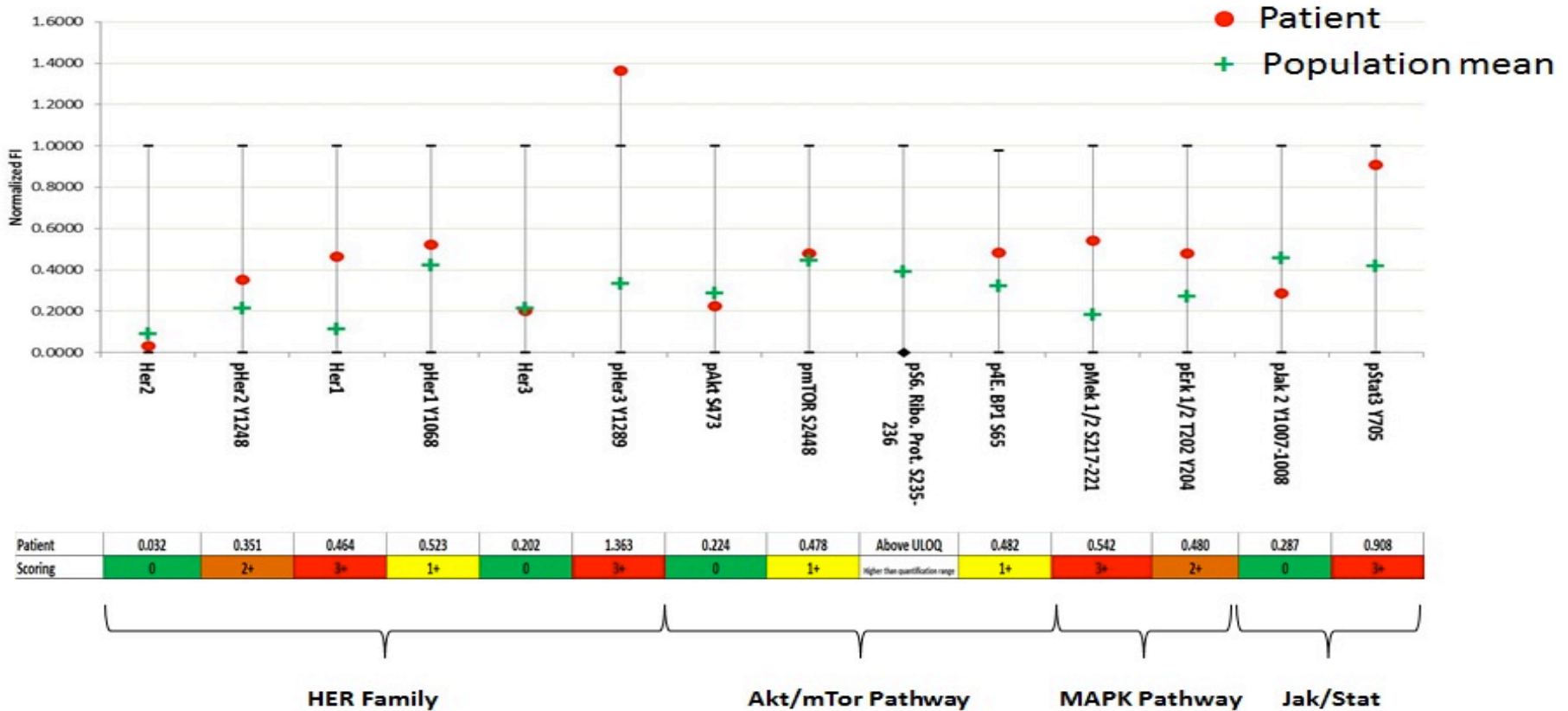
OF; BACH1; FANCI

### **Summary**

The protein encoded by this gene is a member of the RecQ DEAH helicase family and interacts with the BRCT repeats of breast cancer, type 1 (BRCA1). The bound complex is important in the normal double-strand break repair function of breast cancer, type 1 (BRCA1). This gene may be a target of germline cancer-inducing mutations. [provided by RefSeq, Jul 2008]

**Location: 17q22.2**

# TheraLink Results



# Summary

- Woman with triple negative breast cancer
  - Already has received multiple chemotherapy regimens: Including taxanes x 2, fluoropyrimidine, and anthracycline

# Recommended Treatment Schema

- Everolimus 10 mg/day po x 21 days of 28 day cycle plus one of the following:
- carboplatin (AUC 2) weekly (Day 1,8,15) or
- cisplatin 20mg/m<sup>2</sup> weekly (Day 1,8,15)

## References:

- Anticancer Res. 2012 Aug;32(8):3435-41. **The mTOR inhibitor everolimus in combination with carboplatin in metastatic breast cancer**
- Cancer Chemother Pharmacol. 2012 Mar;69(3):591-8. doi: 10.1007/s00280-011-1734-5. Epub 2011 Sep 13. **A phase I study of daily everolimus plus low-dose weekly cisplatin for patients with advanced solid tumors**

# Our values guide our approach to creating a better health care system

## Our cause

To make quality health care more affordable and more accessible

## Our strategy

To be the global leader in empowering people to live healthier lives



# Clinical Policy Unit Function

- Aetna's Clinical Policy Unit is responsible for evaluating medical technologies to determine whether they are “experimental and investigational” and “medically necessary” as defined in applicable coverage documents
- Aetna has developed more than 600 Clinical Policy Bulletins (CPBs).
- The goal is to develop objective, clinically supported and defensible determinations.

# Clinical Coverage Criteria

The following criteria are considered in evaluating a medical technology:

- The technology must have final approval from the appropriate governmental regulatory bodies, when required
- The scientific evidence must permit conclusions concerning the effect of the technology on health outcomes
- The technology must improve net health outcome
- The technology must be as beneficial as any established alternatives
- The improvement must be attainable outside investigational settings

# EVIDENCE

cost



# ASSESSING GENOMIC ASSAYS: ACCURACY AND CLINICAL RELEVANCE

**Analytical performance:** Is the quantification of the analyte(s) of interest reliable and reproducible?

**Clinical validity:** How well does the test relate to the clinical outcome of interest?

**Clinical utility:** Does the information provided make a contribution to and improve current optimal management of the patient's disease?

**Economic value:** Assessment of cost savings and/or cost-effectiveness

Measures are interrelated

Analytic performance must be evaluated in context of the clinical use

Clinical validity must be assessed in context of analytic performance