



University of Glasgow | College of Medical,
Veterinary & Life Sciences

Molecular Phenotype Guided Therapy for Pancreatic Cancer

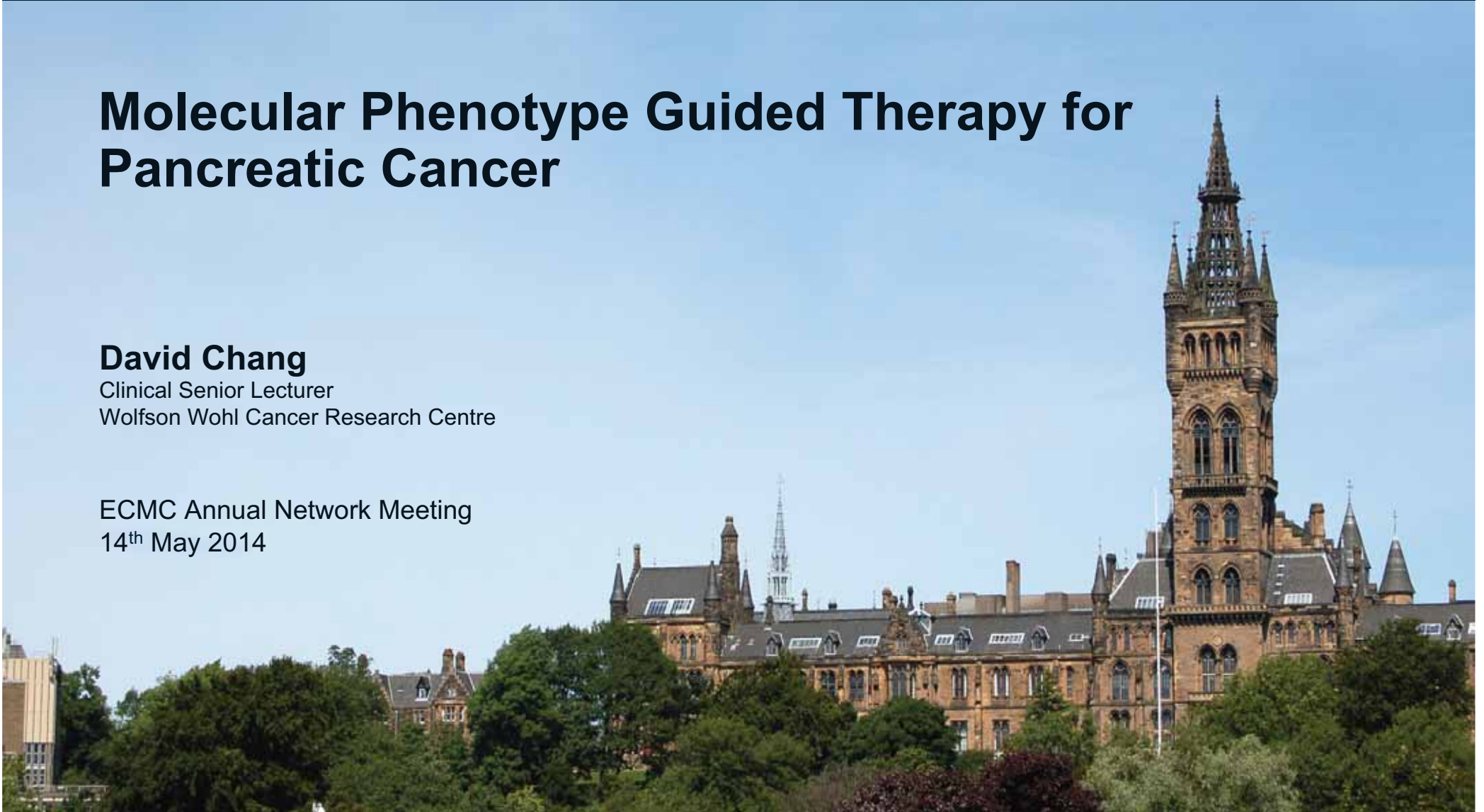
David Chang

Clinical Senior Lecturer

Wolfson Wohl Cancer Research Centre

ECMC Annual Network Meeting

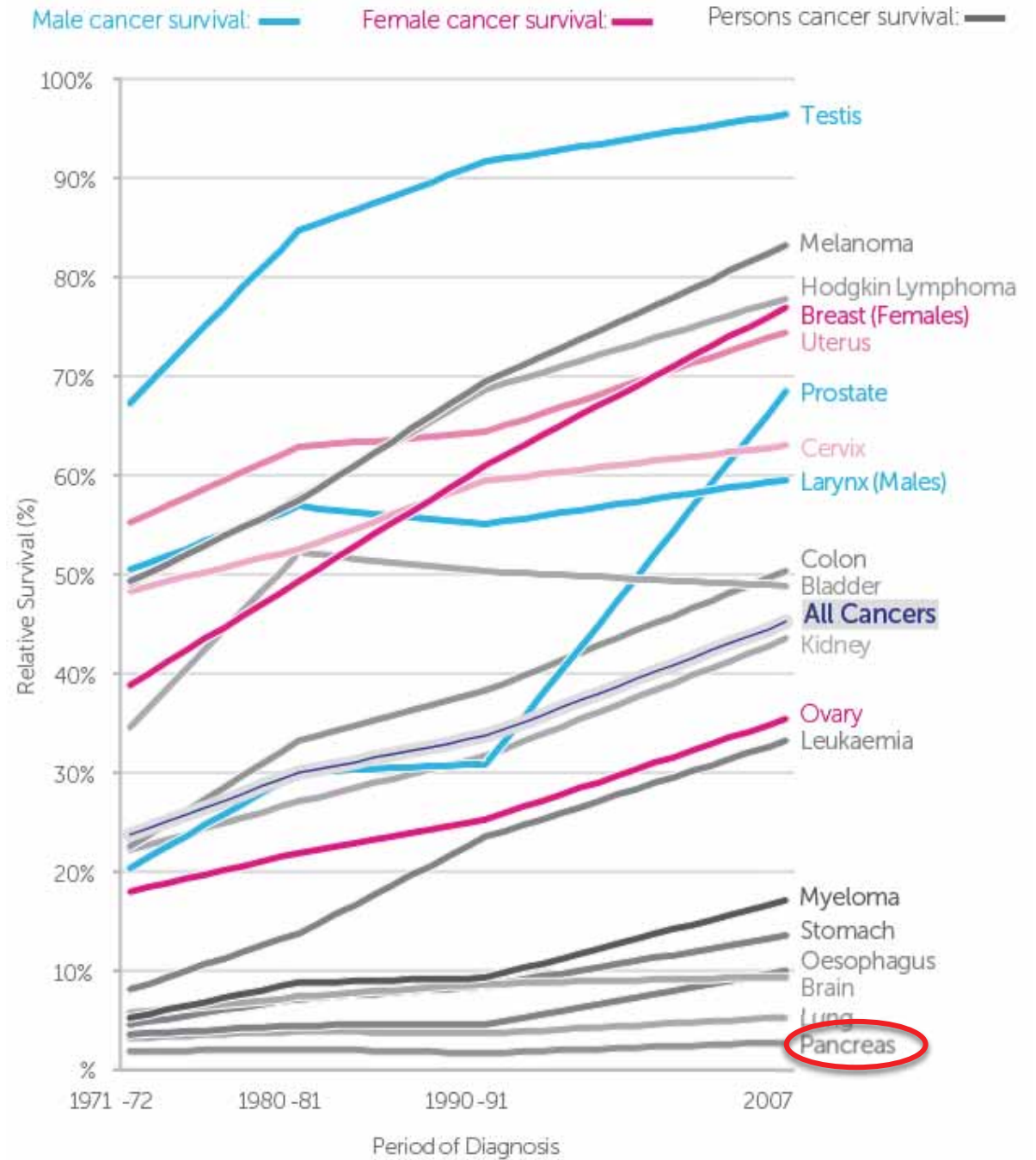
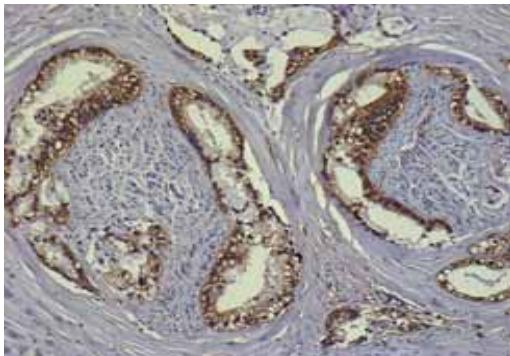
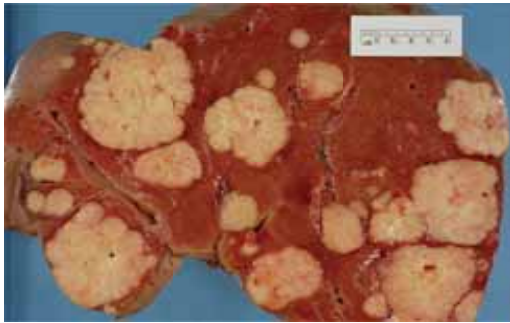
14th May 2014





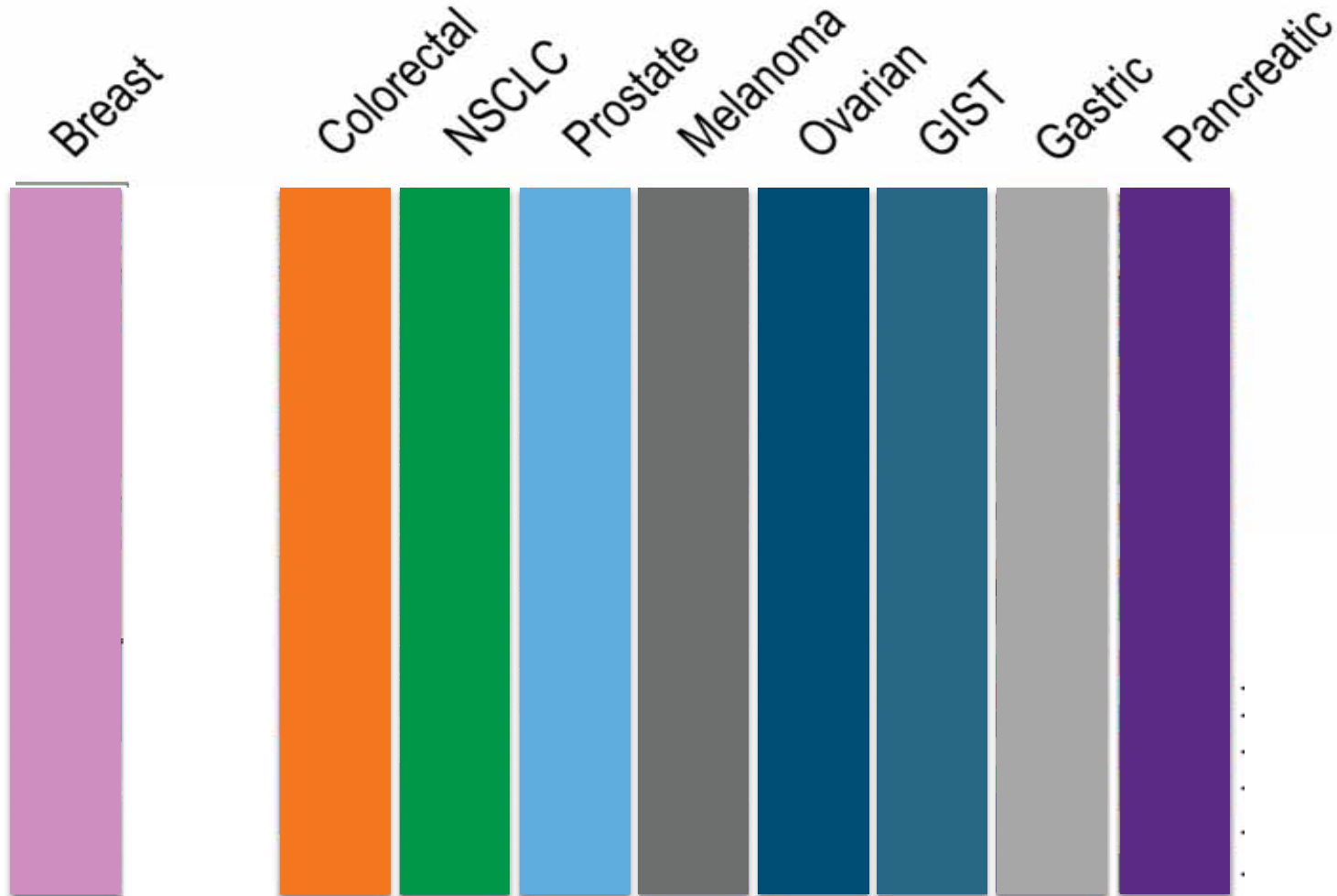
Outline

- Cancer is heterogeneous
 - APGI sequencing project (mutational landscape)
 - Therapeutic implications
 - DNA-damaging agents responsive phenotype
- Lesson learnt so far and challenges ahead

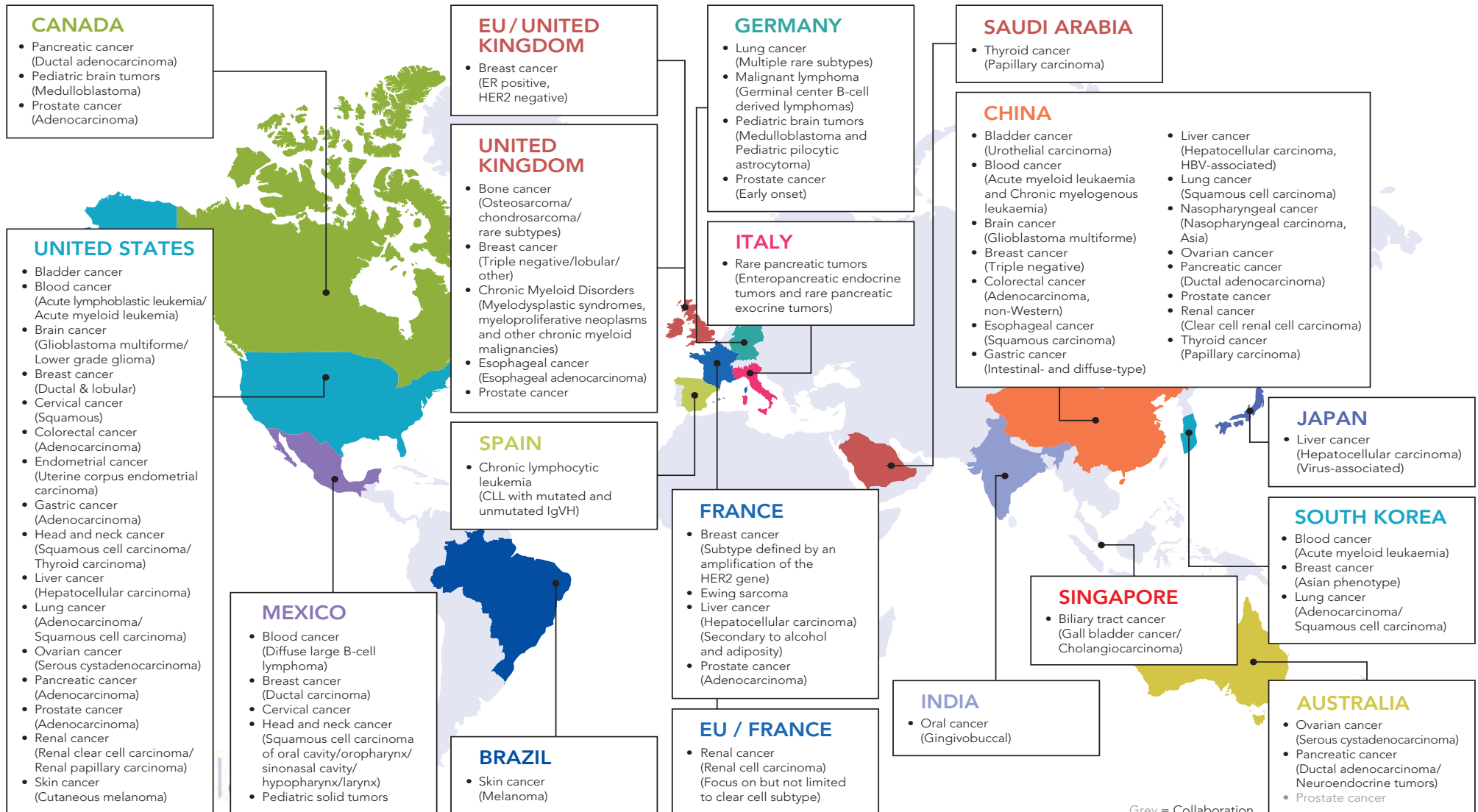




Cancer is complex & Heterogeneous



International Cancer Genome Consortium (ICGC)



Australian Pancreatic Cancer Genome Initiative (APGI)



Prospective observational cohort study design (350 PDAC)

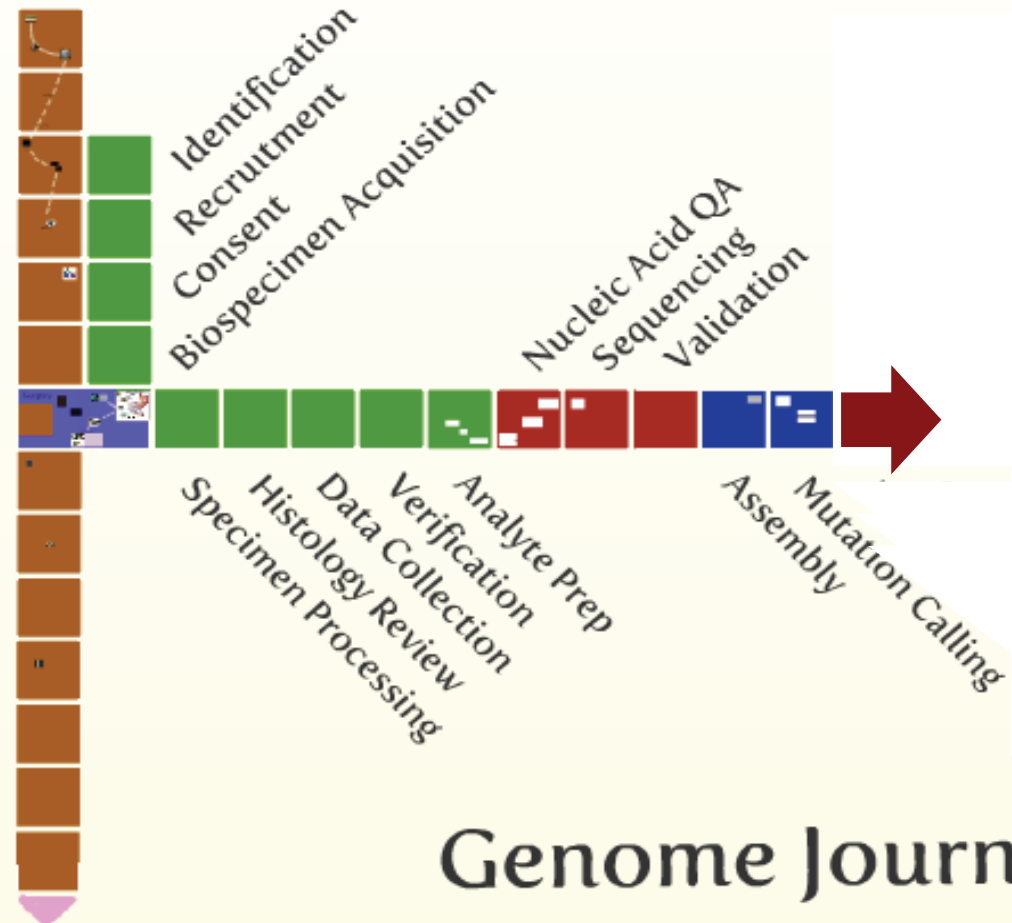


Biankin

Grimmond

Patient Journey

- Symptoms
- Specialist
- More Tests
- Diagnosis
- Treatment Plan
- Preparation
- Surgery
- Recovery
- Adjuvant Therapy
- Follow-up
- Recurrence
- Palliation
- Death
- Post Mortem

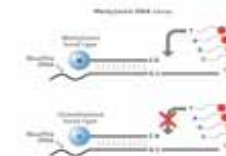
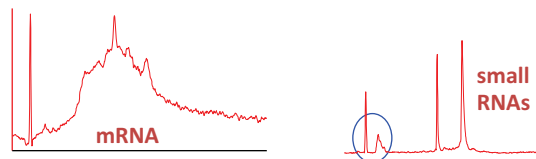
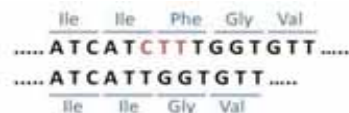
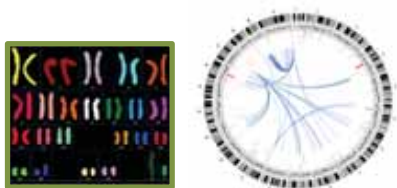


Genome Journey



ICGC Data Portal
"ICGCMart"

Data Generation strategy:



Genome

Exome

Transcriptome

Epigenome



SNP/CNV Chip analysis,
gDNA sequencing

40-100% Cellularity

Exome sequencing

>20% cellularity

Expression array,
mRNAseq,
miRNAseq

Methyl Miner
enrichment, methyl
seq

Tumor
& normal
40x /80x fold

Tumor & normal
>95% 20x
~250x

Tumor tissue
& adjacent normal
~100 million reads

Tumor & adjacent
normal : 450K
array

Genomic Landscape of PDAC

- Whole Exome Capture and Sequencing + CNV (n=142)
(Biankin et al., *Nature* 2012)

- 38 of 79 (> 1 mutations) identified by Jones *et al.* (2008 n=24)
- 186 of 998 of Jones *et al.* (2008)
- 19% overlap
- 1456 novel genes mutated

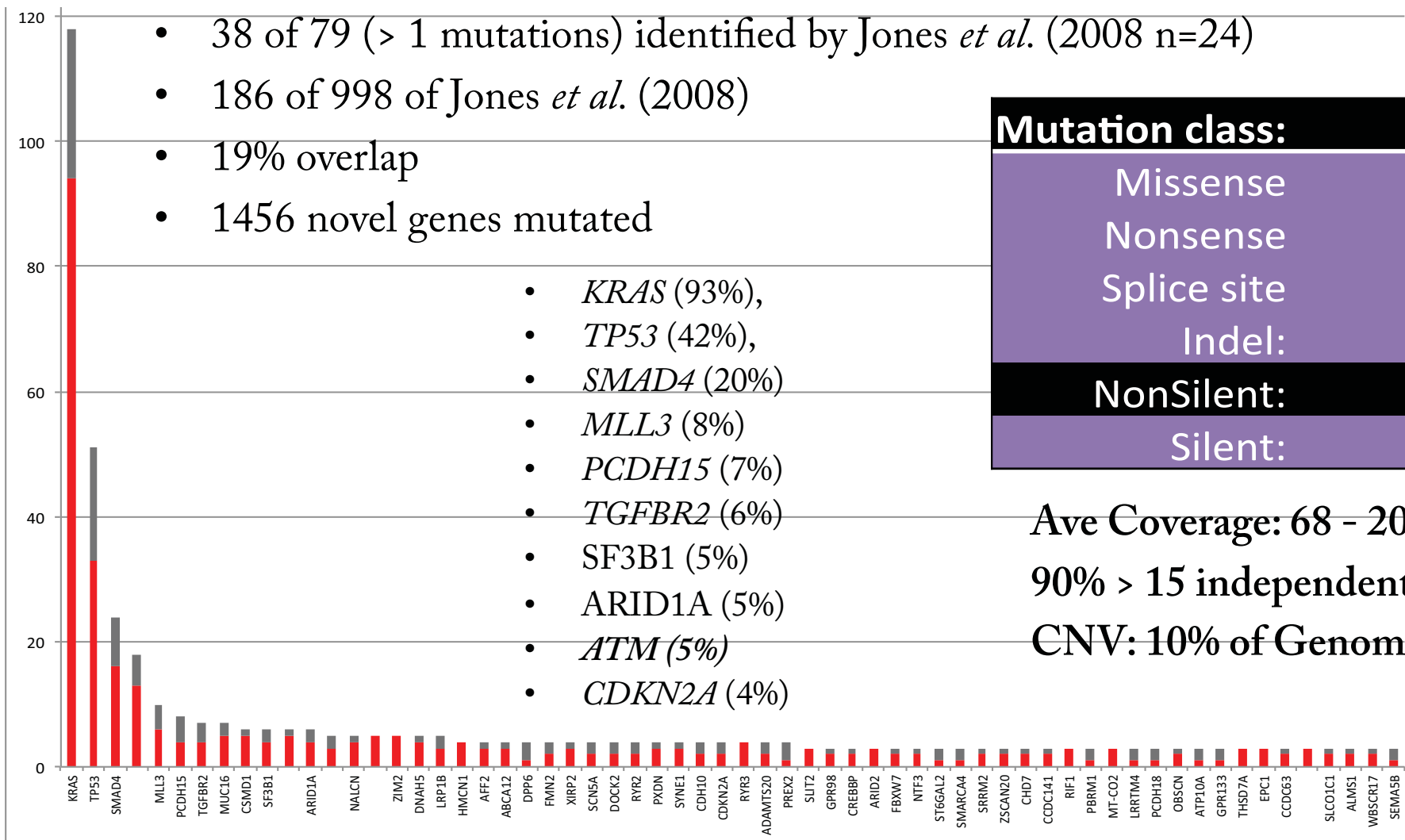
Mutation class:	Total:
Missense	1684
Nonsense	99
Splice site	89
Indel:	144
NonSilent:	2016
Silent:	611

- *KRAS* (93%),
- *TP53* (42%),
- *SMAD4* (20%)
- *MLL3* (8%)
- *PCDH15* (7%)
- *TGFBR2* (6%)
- *SF3B1* (5%)
- *ARID1A* (5%)
- *ATM* (5%)
- *CDKN2A* (4%)

Ave Coverage: 68 - 200x

90% > 15 independent reads

CNV: 10% of Genome



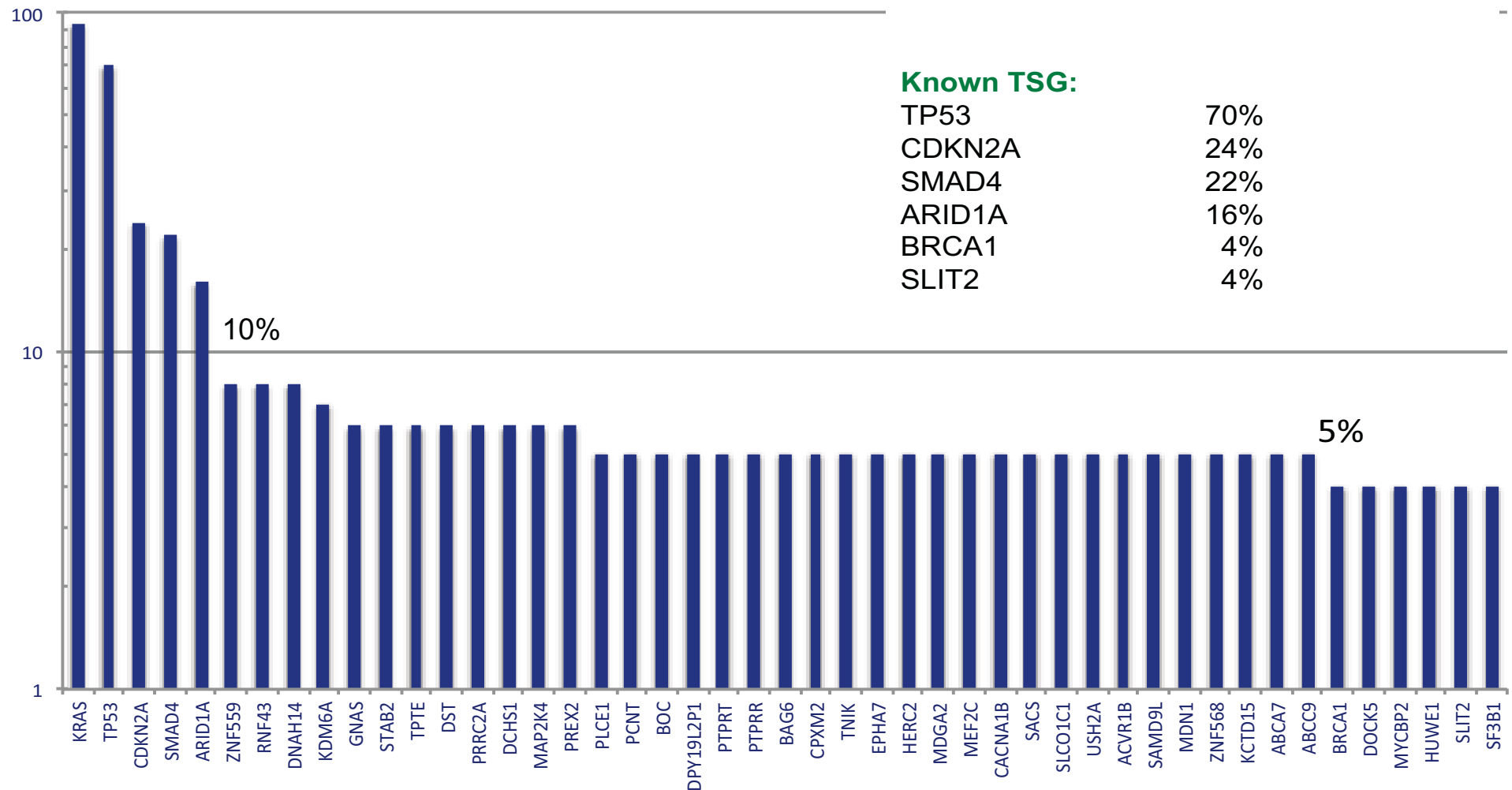
Non-Silent Point Mutations in PDAC (WGS)

Known oncogenes:

KRAS:	93%
GNAS:	7%
SF3B1:	4%

Known TSG:

TP53	70%
CDKN2A	24%
SMAD4	22%
ARID1A	16%
BRCA1	4%
SLIT2	4%





Heterogeneity = Therapeutic development implications

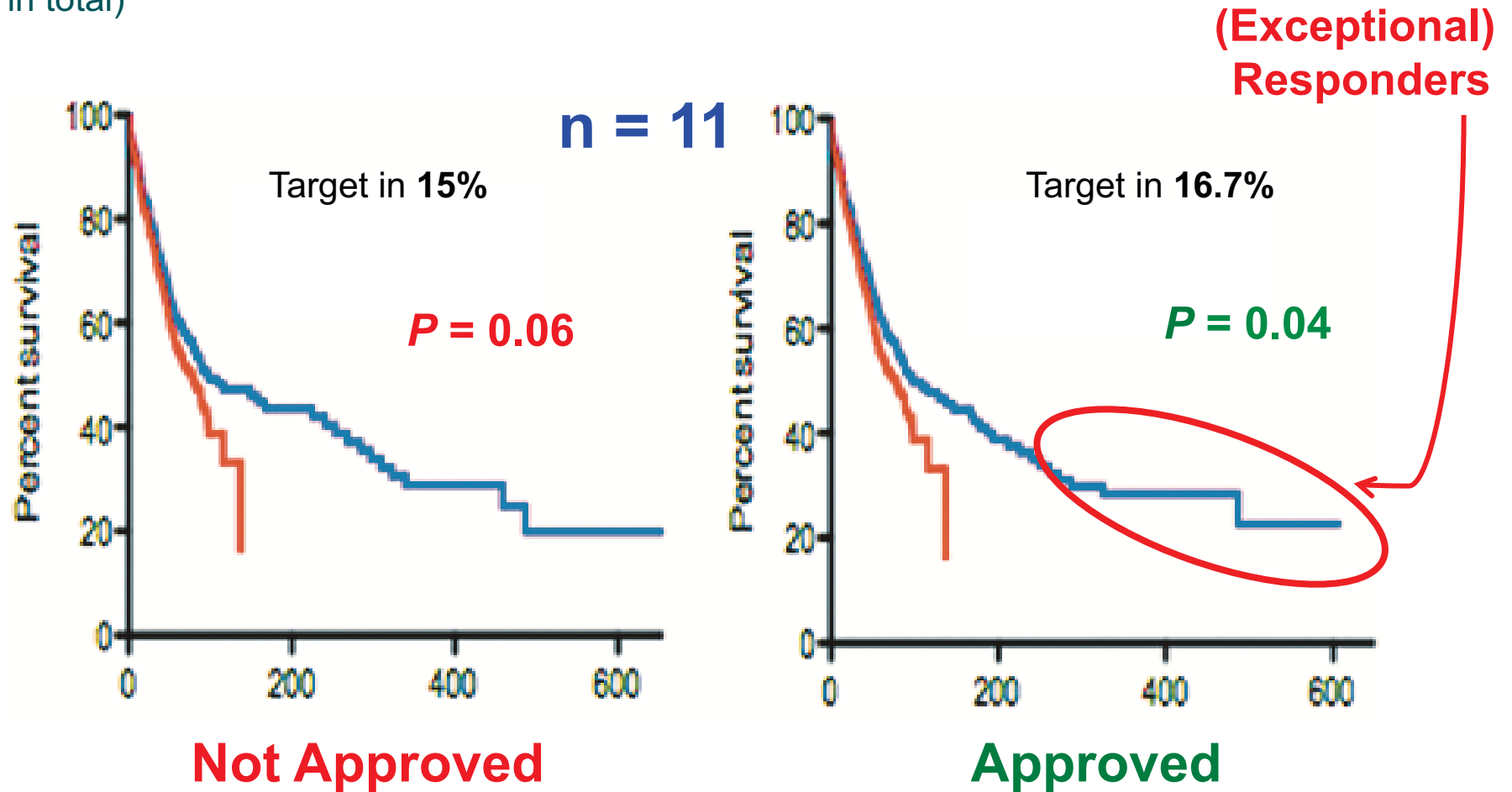
The Second Rule of Clinical Trials:

"It (the drug) must be used on a simple, not a composite, disease."

Avicenna, The Canon of Medicine, 1025AD

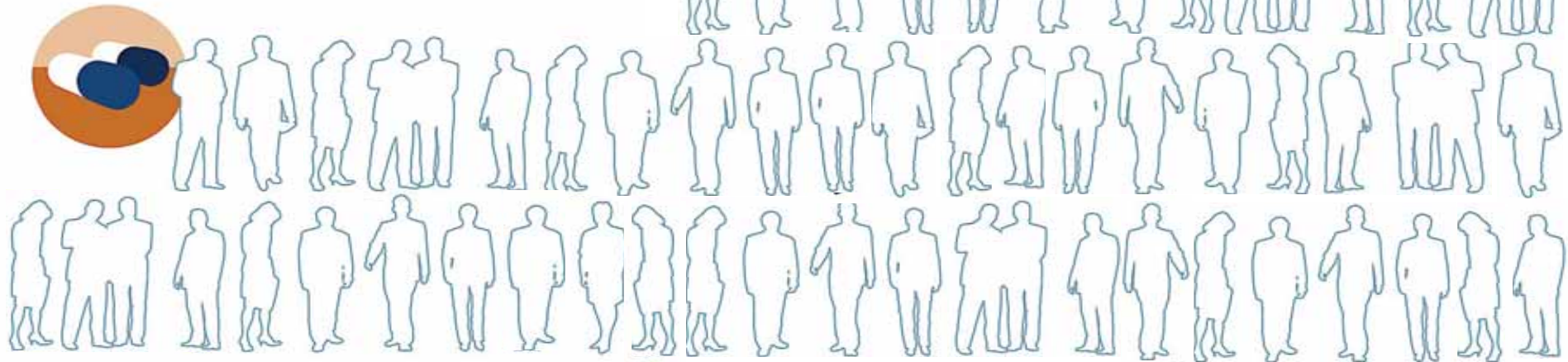
Fool's Gold or Lost Treasures??

Simulation of 334 NSCLC patients (actual survival) in each arm (668 in total)

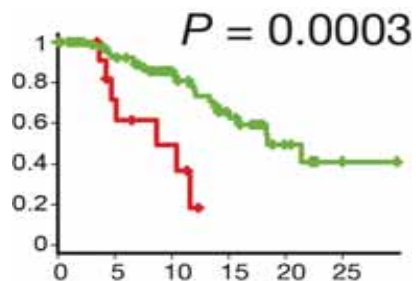


Smaller Trials, Greater Chance of Success

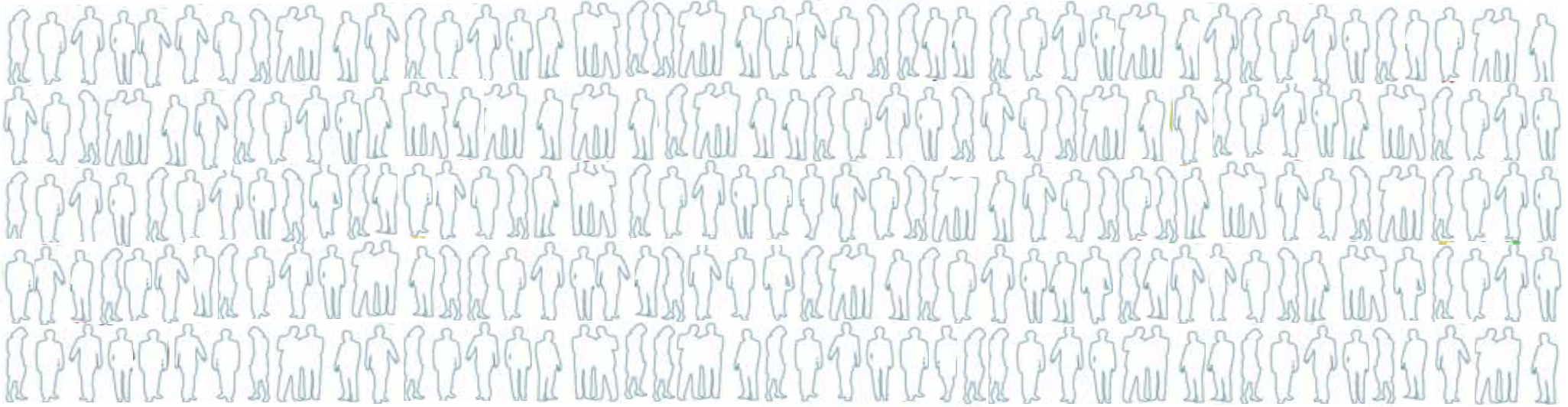
OLD MODEL: Large numbers of patients, not selected by molecular characteristics; lower chance of demonstrating effectiveness, since many participants do not have the molecular defects being targeted



NEW MODEL: Small patient populations, all with the relevant mutations or genetic defects; greater chance of desired results, since all participants have the potential to respond



Personalising Cancer Care



Trial of Drug A



Trial of Drug B

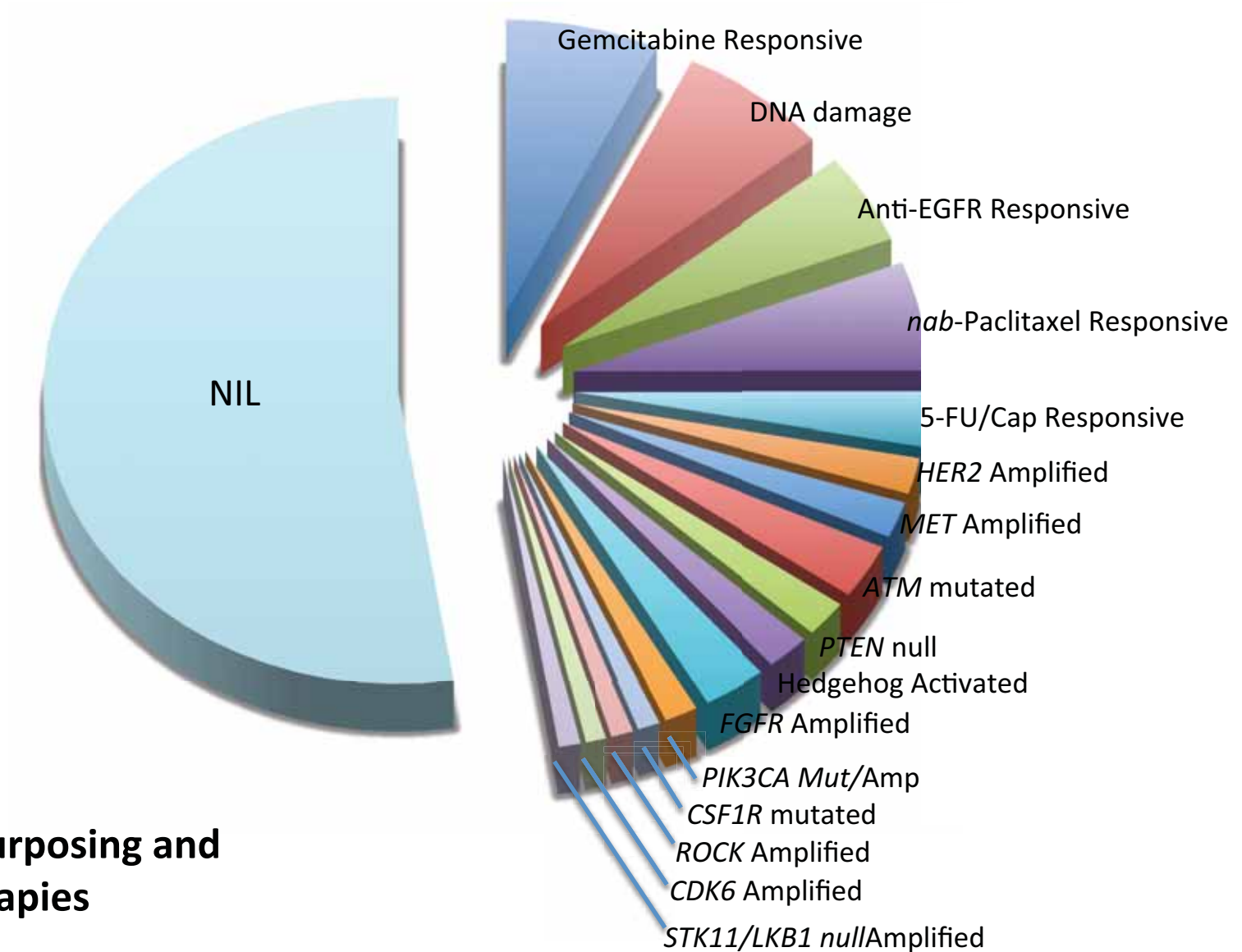
Test each person to choose the right treatment

Trial of Drug C

Trial of Drug D

New Targets and Drugs

Actionable Phenotypes in Pancreatic Cancer

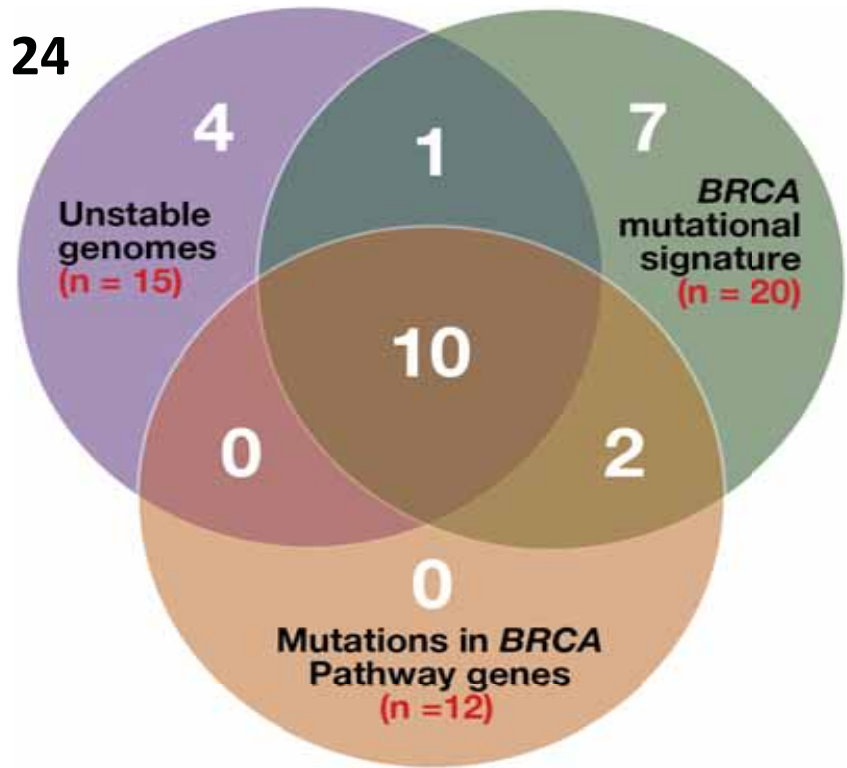


Rescuing, Repurposing and Emerging Therapies

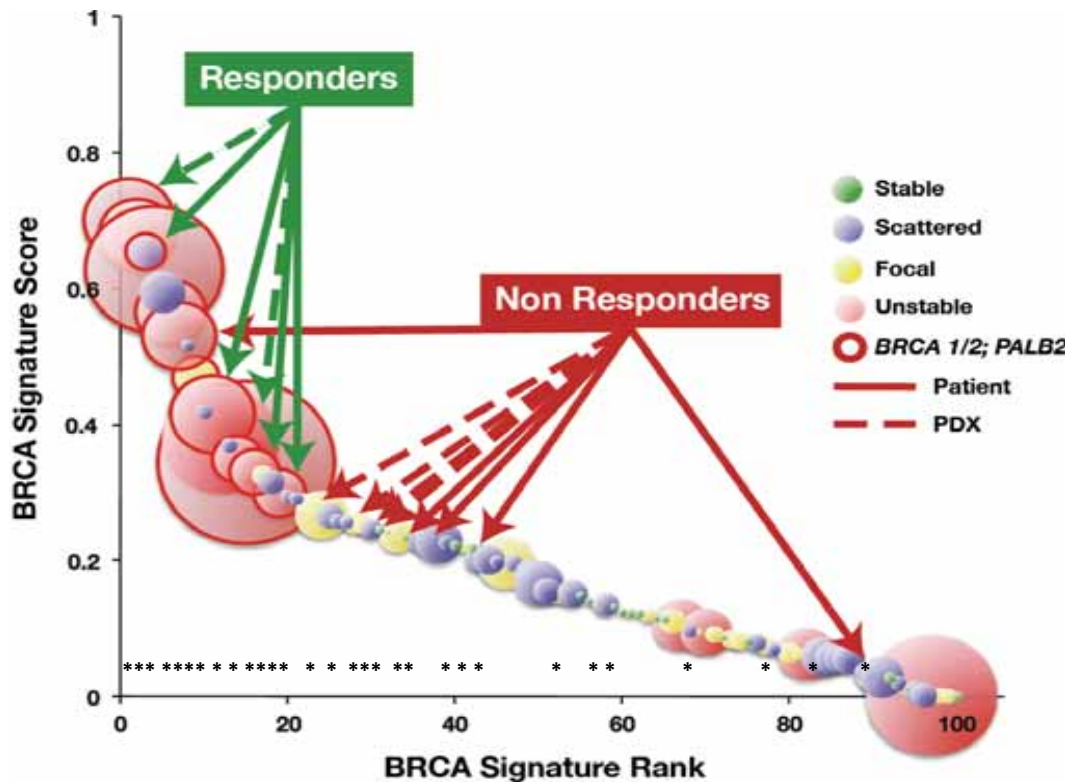
Approach

- N = 100 WGS
- Phenotype-to-genotype analysis
- DNA-damaging agent responsive phenotype is potentially substantially larger than previously believed.

N = 24



- Platinum responders are enriched by high *BRCA* signature ranking with overlapping unstable genomes and mutations in *BRCA* DNA maintenance pathway genes



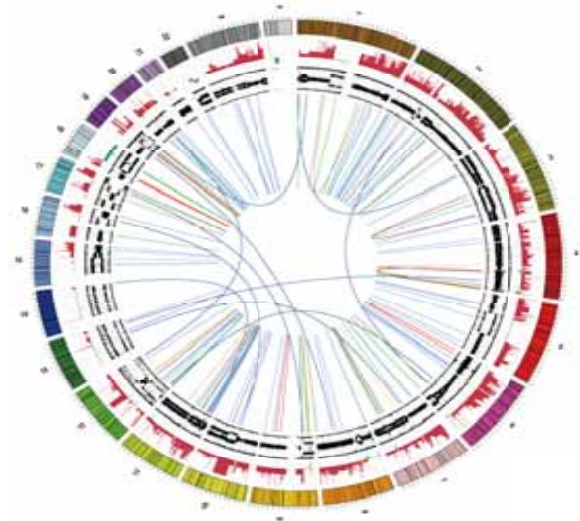
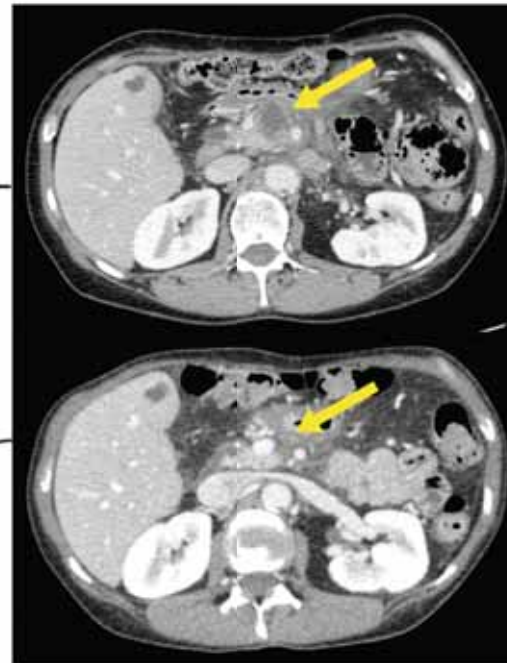
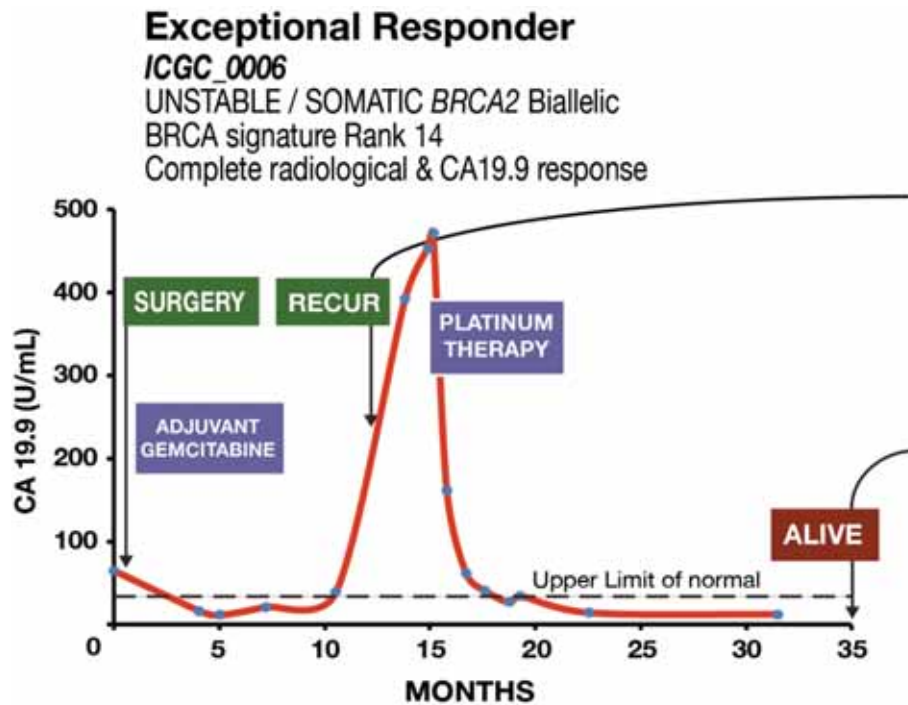
Studying Exceptional Responders

Mining the genomes of exceptional responders

David K. Chang¹⁻⁵, Sean M. Grimmond^{1,6}, T. R. Jeffry Evans¹ and Andrew V. Biankin¹⁻⁵

Abstract | The National Cancer Institute of the United States recently announced a major new initiative in understanding the genomes or, more broadly, the molecular phenotypes of exceptional responders. What can we expect to learn from exceptional responders? What are the potential benefits, and how do we approach studying them?

Chang et al, *Nat Rev Cancer*, 2014



Pajic & Chang et al, in preparation

Targeting Actionable Molecular Phenotypes

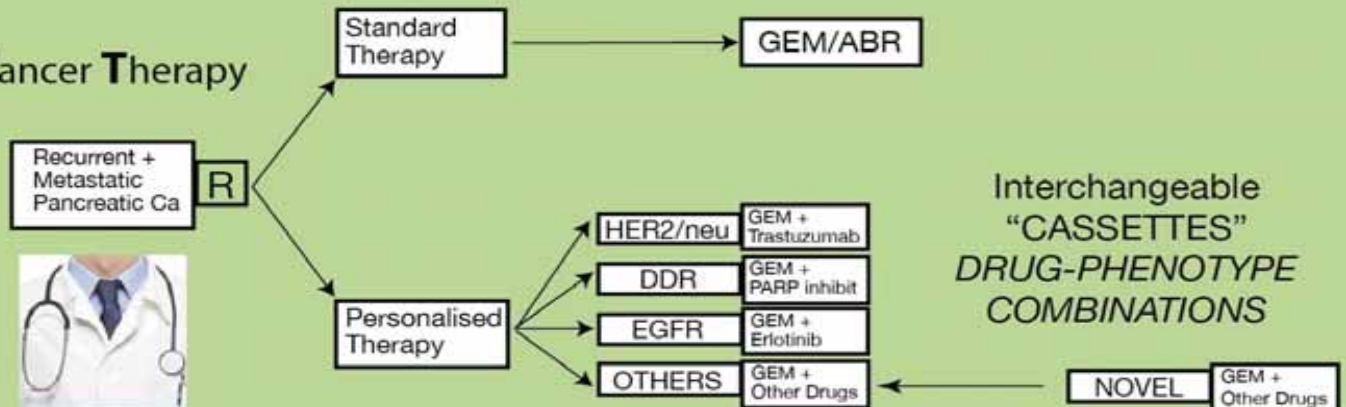


*Initially direct recruitment of ICGC patients
Then panel-based screening*

IMPACT Clinical Trial

Individualised Molecular Pancreatic Cancer Therapy

Patients are screened for actionable mutations, recruited and randomised between standard therapy and a biomarker driven "Individualised" strategy which evolves and adapts as new information comes to light.



HER2 Amplified (2%): GEM + Trastuzumab

KRAS wild type (5%): GEM + Erlotinib

BRCA2 Germ Line mutant (3%): MMC + Capecitabine

Lessons Learnt (@#\$% !)

- Logistically demanding: tissue acquisition, QC, drugs
- Patients randomised to standard of care withdraw and buy drug themselves
- Screening time (main problem is sample delivery)
- Sample variability (different path labs)
- Low prevalence phenotypes (need to screen large numbers)
- Screening cost (genome maybe cheaper, bioinformatics still the same)

Lessons Learnt (@#\$% !)

- Patients without an actionable phenotype (what is best SOC?)
- Social and ethical implications with sequencing (framework for return of results)
- Change of technology (re-validation)
- Lots more to be learnt & lots more challenges ahead

Biobanking & QC



International
Cancer Genome
Consortium



Perth

- St John of God Hospital
- PathWest Laboratory Medicine
- Fremantle Hospital

- Adelaide**
- Royal Adelaide Hospital
 - Flinders Medical Centre



Melbourne

- Peter MacCallum Cancer Centre
- Victorian Cancer Biobank
- Austin Hospital
- Cancer 2015



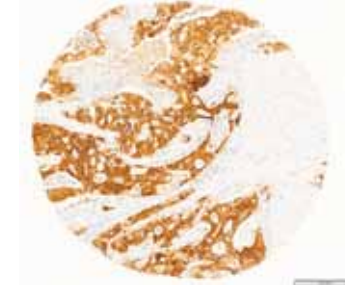
Brisbane

- Queensland Centre for Medical Genomics
- Greenslopes Private Hospital
- Princess Alexandra Hospital

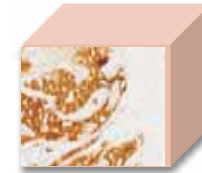


Sydney

- The Kinghorn Cancer Centre
- Sydney Cancer Centre
- NHMRC Clinical Trials Centre
- AGITG • Bankstown Hospital
- Westmead Hospital
- Royal North Shore Hospital



1. Independent Pathological review
in Australia, Italy and USA.



2. 5mm³ frozen blocks of Tumour are sectioned to
locate non-tumour tissue.



3. Tumour rich regions are dissected form block
and DNA/RNA extracted

~ 700 cases

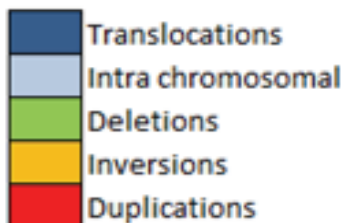
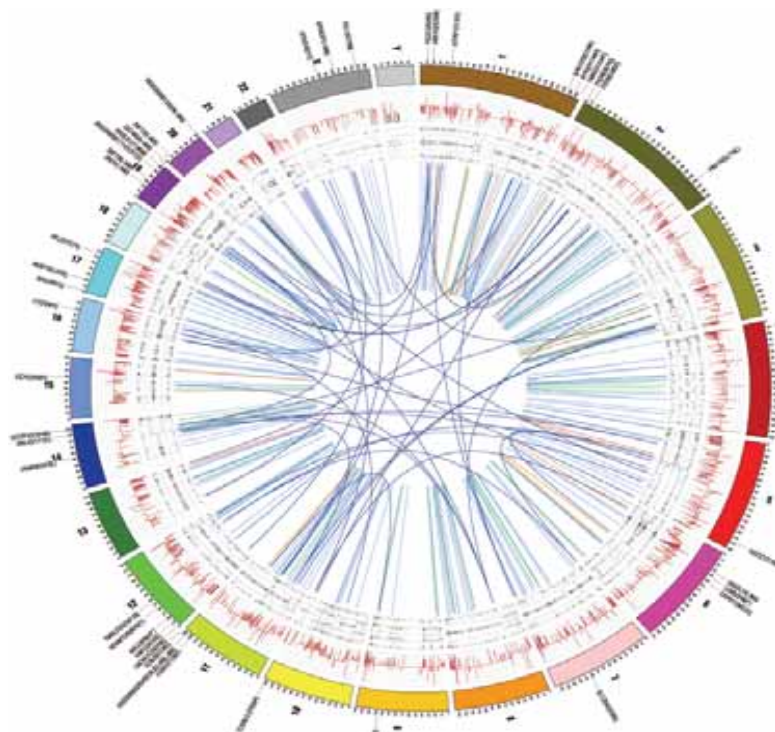
Amber Johns and Team



How to integrate detailed molecular information into clinical practice: Molecular MDT

Patient Cancer Genome Report:

APGI-1992



Somatic simple mutations

- ABCC9
- ADAMTS20
- AMAC1L2
- B3GALT4
- BLID
- BRCC3
- C3orf62
- C11orf94
- CACNA1C
- CAPN11
- CENPE
- COLEC11
- CTCF
- FRMD6
- GPR137B
- IQCH
- KIR3DX1
- KLKB1
- LEMD2
- PIK3CD
- PXDN
- RPA1
- SIGLECP3
- SLC26A5
- TIMELESS
- ZNF432
- ZNF132

Genes affected by Inter-chromosomal translocations

- FGFR1 (bi-allelic)
- LYPD6B
- NRXN3
- SFTPB
- TNPO1
- TP53BP2
- ZNF468

Genes affected by intra-chromosomal breakpoint

133 genes

Expressed Fusion transcript

ATE1 – KLRAQ1

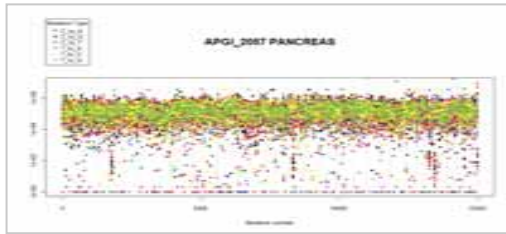
Differential Methylation & Expression

1800 genes

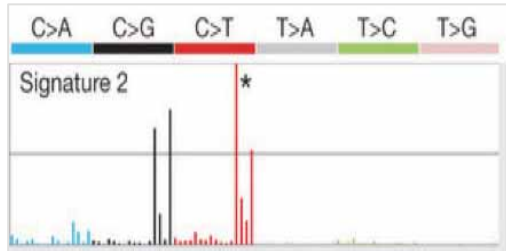
Preclinical models?

Xenograft
Cell Line

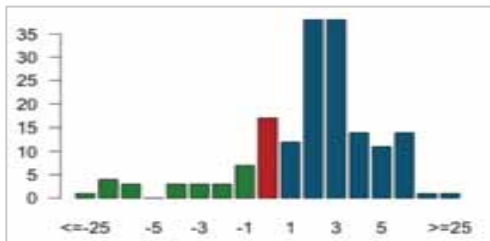
Comprehensive Cancer Genome analysis: (<3 days)



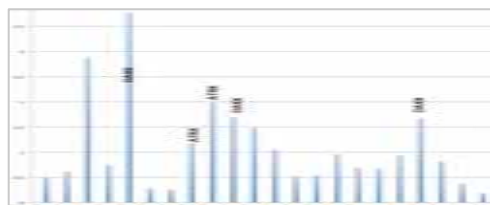
Mutation burden



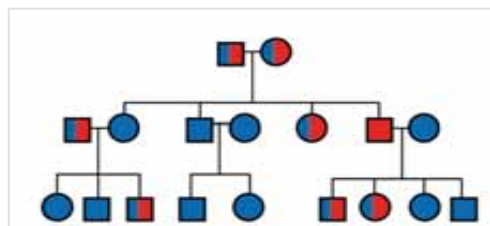
Mutational Signature



Breakpoint Signature

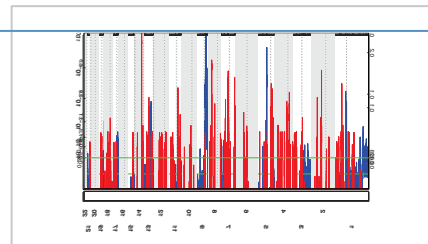
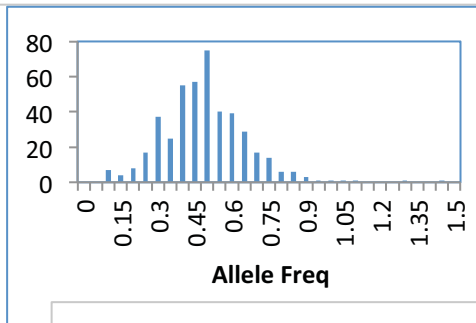


Telomere status

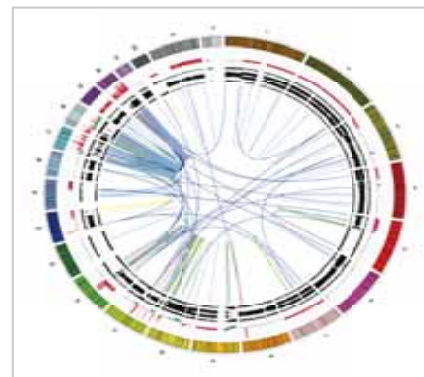


Germline/Inheritance

ABCC9, ADAMTS20, AMAC1L2,, BLID, BRCC3, CACNA1C, CAPN11, CENPE, COLEC11, CTCF, FRMD6, GPR137B, LEMD2, PIK3CD, PXDN, RPA1..



Copy number changes



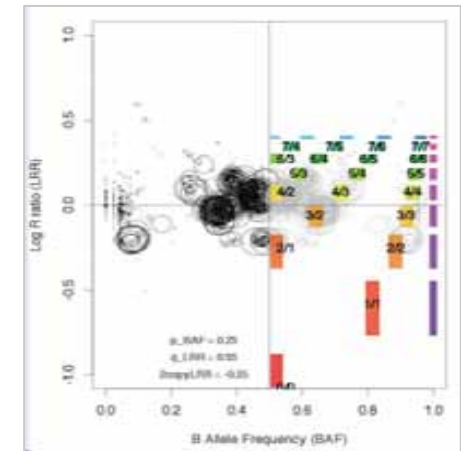
Genome organization

Mutations

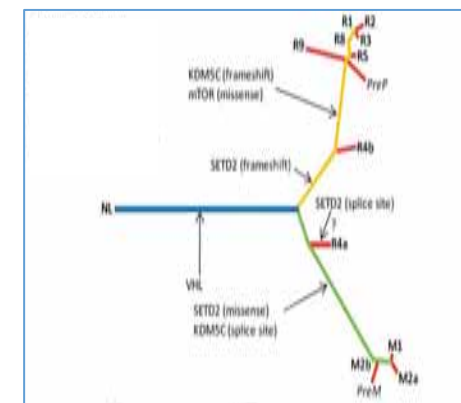
Break counts >50 = 846	Ploidy detected = 4
Chromosome counts = 85	% base state = 42
Centromere counts = 156	% '1' copy loss = 8
DNA index = 1.71	%acquired homo = 17

Chr	Copy	B allele	SNPs	Chr	Copy	B allele	SNPs
1 p	4	2	7891	12 p	5	0	476
1 q	3	0	121	12 q	4	0	364
2 p	4	2	14304	13 q	4	2	79
2 q	4	2	254	14 q	3	0	44
3 p	3	2	96	15 q	3	0	74
3 q	3	2	506	16 p	2	2	302
4 p	4	2	2505	16 q	2	2	19651
4 q	4	2	25045	17 p	3	3	302
5 p	4	0	775	17 q	3	0	154
5 q	3	0	214	18 p	3	2	7842
6 p	2	2	144	18 q	3	2	1295
6 q	4	2	8198	19 p	4	0	170
7 p	3	0	45	19 q	8	0	1204
7 q	4	2	781	20 p	5	0	233
8 p	3	0	616	20 q	4	0	160
8 q	3	0	826	21 p	3	0	13
9 p	3	3	156	21 q	6	4	112
9 q	3	3	194	22 q	4	4	62
10 p	4	0	504	23 p	3	0	3437
10 q	4	0	245	23 q	4	0	354
11 p	3	2	8127	24 p	3	3	10
11 q	3	2	694	24 q	2	2	13

Ploidy



Clonality

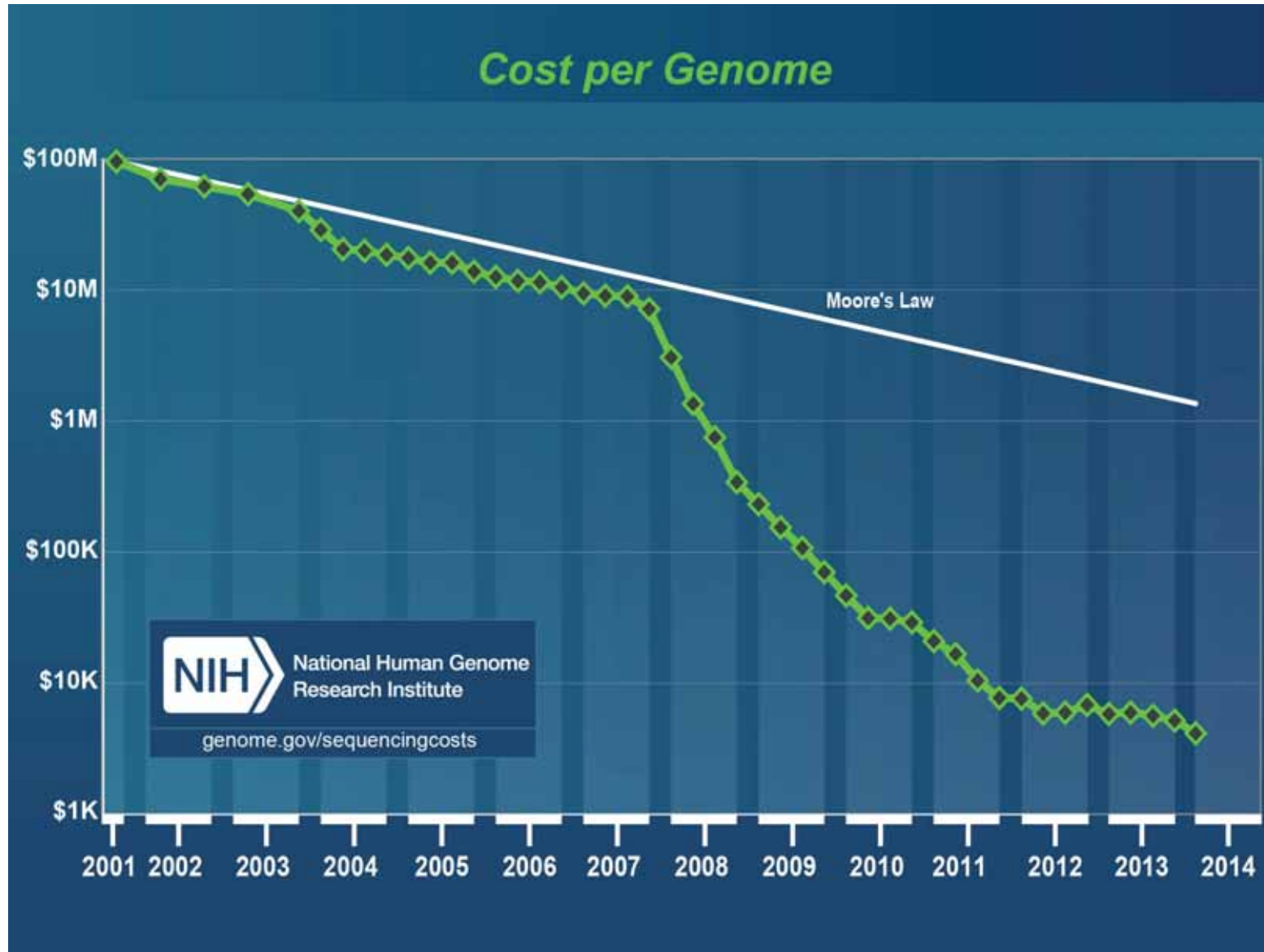


Evolution

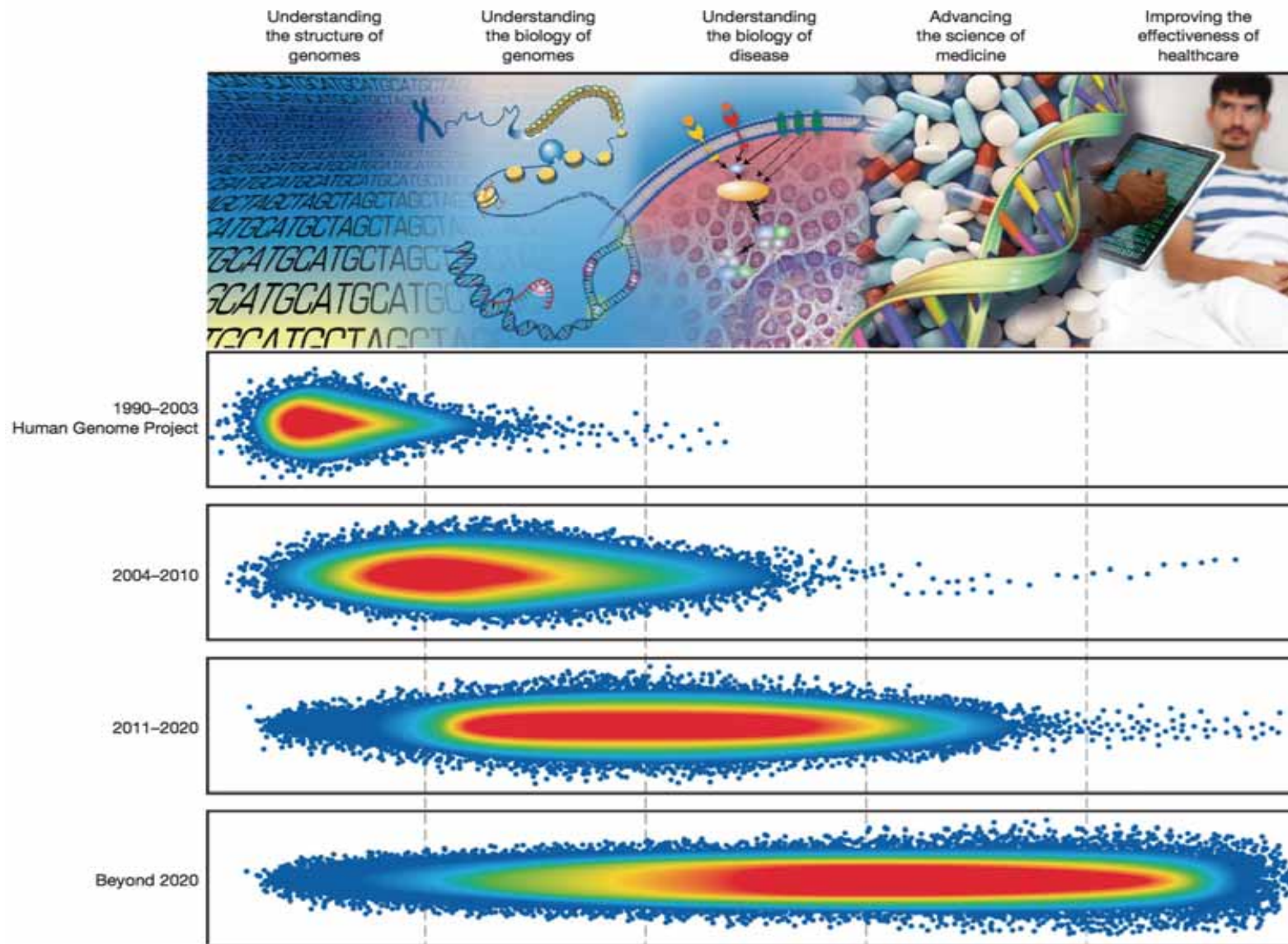
Staying ahead of the latest Technology



Cost of Sequencing is dropping dramatically (technology is here!!)

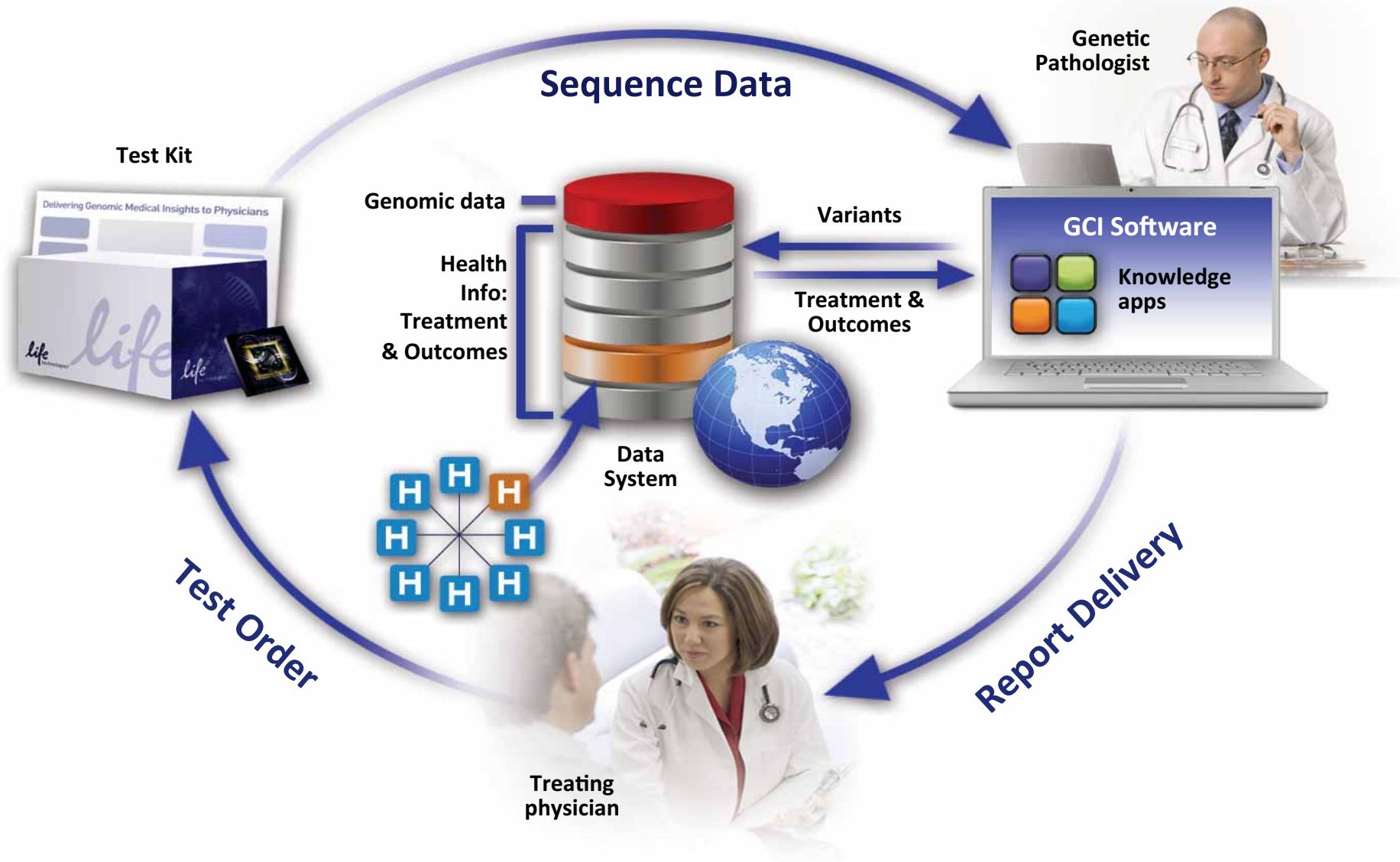


Harness the Technology: From Base Pairs to Bedside



Green & Guyer, *Nature* 2011

Knowledge Bank Approach



Data Sharing at a Global Scale



Global Alliance
for Genomics & Health

[Sign up for updates](#)

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CONTACT US

Collaborate. Innovate. Accelerate.

Working together to share knowledge, create networks and accelerate advances in genomics and health.

→ [Read our Partner Meeting and 2014 Goals Report](#)

<http://genomicsandhealth.org/>

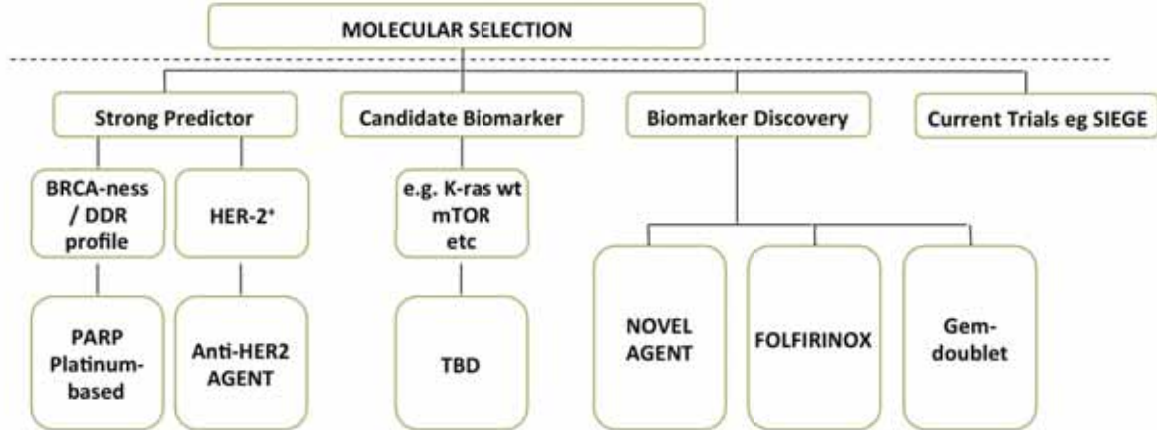
185 organisations, 26 countries
1st meeting March 2014

Smarter and more Nimble Trial Designs



- Locally-advanced* / metastatic (stratified)
- Histo-/cytologically confirmed adenocarcinoma (with available biopsy that can be adequately phenotyped)
- PS 0 or 1
- Consent for biomarker analysis

* Consider SCALOP-2



- Design Considerations:
- window study (FOLFIRINOX/Gem-doublet on PD)
 - a new combination may need phase I run-in

- End-points (clinical):**
Overall survival
Response rate
TTP

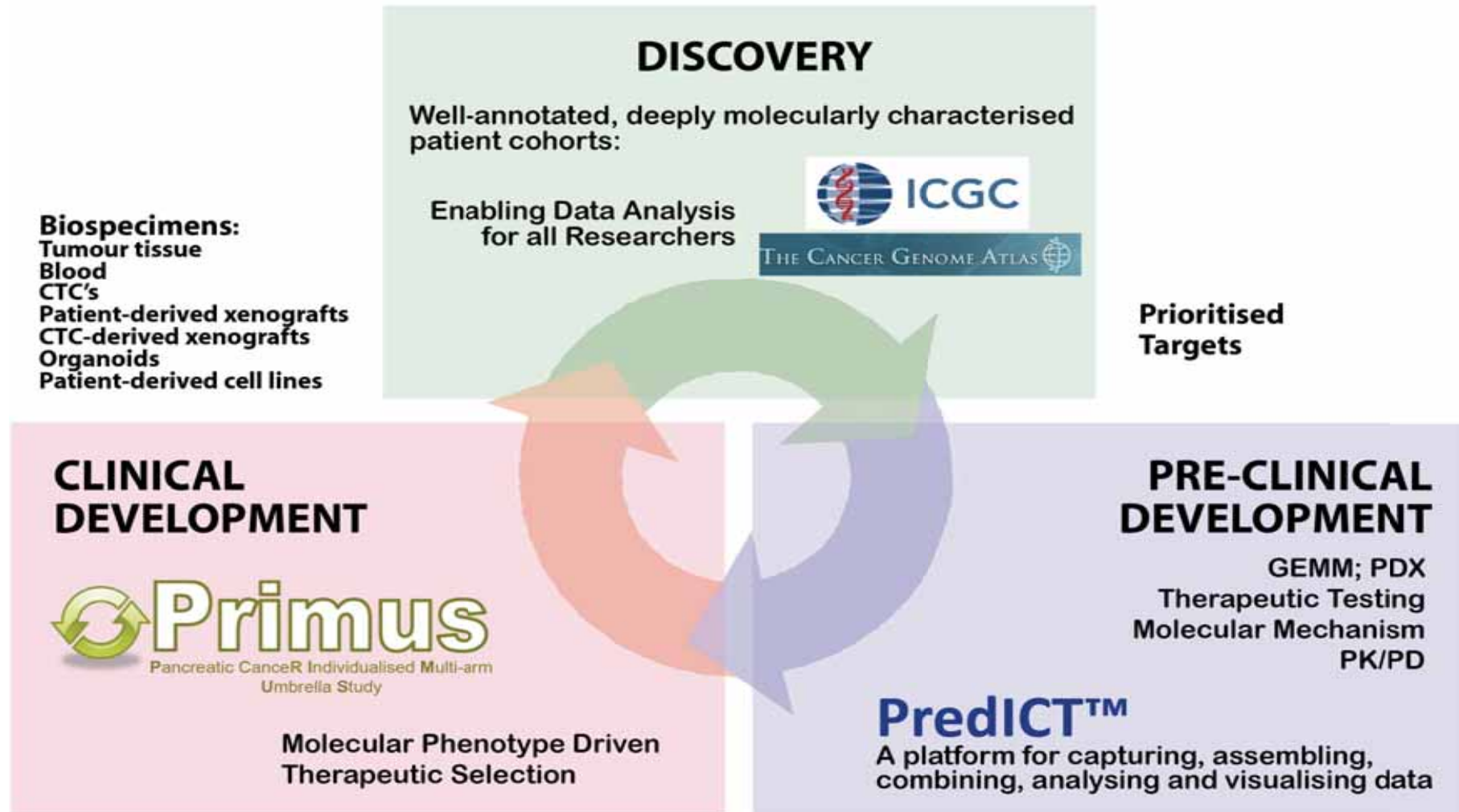
End-points (translational):
Predictive value of biomarker
Resistance mechanism



Jeff Evans
Juan Valle
Andrew Biankin
Sean Grimmond
and more.....

Better Integration between Key Elements

IMPACT-UK Framework (Individualised Molecular Pancreatic Cancer Therapy)



Translate Research Medicine to Routine Patient Care

- Funding bodies
- Regulatory bodies
- Consumer advocates
- Multiple pharma companies
- Intra-tumoral heterogeneity

- All challenges, but also a unique opportunity

QCMG: Sean Grimmond

Bioinformatics:

John Pearson
Lynn Fink
Darrin Taylor
David Wood
Conrad Leonard
Oliver Holmes
Christina Xu
Matthew Anderson
Scott Wood
Sarah Song
Felicity Newell

Genome Biology:

Nic Waddell
Karin Kassahn
Ann-Marie Patch
Katia Nones
Nicole Cloonan
Anita Steptoe
Shivangi Wani
Keerthana Krishnan
Jason Steen
Muhammad Fadlullah
Kelly Quek

GenomeSeq:

David Miller
Tim Bruxner
Craig Nourse
Ehsan Nourbakhsh
Suzanne Manning
Angelika Christ
Ivon Harliwong
Senel Idrisoglu

Garvan: Andrew Biankin

Rob Sutherland
Liz Musgrove
Roger Daly
James Kench

Chris Scarlett
Marc Jones
David Chang
Jianmin Wu
Anthony Gill
Page Tobelman
Jeremy Humphris
Mark Pinese
Mark Cowley
Angela Chou
Lorraine Chantrill
Adnan Nagrial
Venessa Chin

Amber Johns
Scott Mead
Michelle Thomas
Chris Toon
Mary-Anne Brancato
Cathy Axford

APGI collaborators & patients

Acknowledgements

Glasgow:

Ross Carter
Colin Mackay
Nigel Jamieson
Euan Dickson
Mark Duxbury
Karin Oien
Jane Hair
Fraser Duthie
Jeff Evans

Sanger:

Ludmil Alexandrov
Serena Nik-Zainal
Peter Campbell
Mike Stratton

Verona:

Aldo Scarpa
Claudio Bassi
Paolo Pederzoli
Rita Lawlor

Johns Hopkins:

Ralph Hruban
Jim Eshleman
Anirban Maitra
Chris Iacobuzio-Donahue



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Thank you for your attention

