

## Introduction of Cancer Precision Medicine and Biobank Consortium Collaboration Pilot Project

This is a Public Private Partnerships (PPP) project to build up a real world data (RWD) with comprehensive genetic testing and detailed medical records. This database is also friendly for industrial applications.

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National Biobank Consortium of Taiwan (NBCT)

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National Health Research Institutes,
Department of Medical Affairs, Ministry of Health and Welfare
(20190601-20231231)



## The Biobank Management Act

### was enforced in Taiwan in 2010

- > Biobank can legally obtain broad consent from participants
- > Biobanks are requested to have strict data safety managment.
- Business use of biobank specimens or data should give commercial benefit feedback, which is an important clause for industrial applications.

Above are the 3 most important niches of the Biobanks in Taiwan. The 35 biobanks should become big fortunes for biomedical researchers and industries in Taiwan.



## The establishment of National Biobank Consortium of Taiwan (NBCT)

- ➤ To improve the performance and function of Biobanks in Taiwan, a National Biobanks was suggested.
- Through the cooperation of all biobanks in Taiwan, with uniform quality and clinical data content, a large and comprehensive human biobank network can be quickly established.
- Under such design, National Biobank Consortium of Taiwan (NBCT) was established through the fund support and governance from Ministry of Health and Welfare.
- ➤ All Alliance should follow the same SOP for the biomaterial collection and have the same quality of the biosamples and data when submitted to the applicants.



簡介~ 合作機構 收案內容 申請作業~ 訊息公告~ 台灣人體生物資料庫 聯絡我們



NBCT was formally established on 2019-10-30

## 國家級人體生物資料庫整合平台 National Biobank Consortium of Taiwan (NBCT)







NBCT is a **virtual biobank**, the specimens and data are stored in each biobank (decentralized storage)

Researchers can applied the biospecimens and data from various biobanks though NBCT (one stop service)

## Currently NBCT is composed of 34 biobanks, 29 belonged to medical hospitals, 4 belonged to research institutes, 1 is in the University

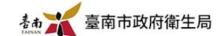
























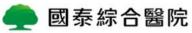






































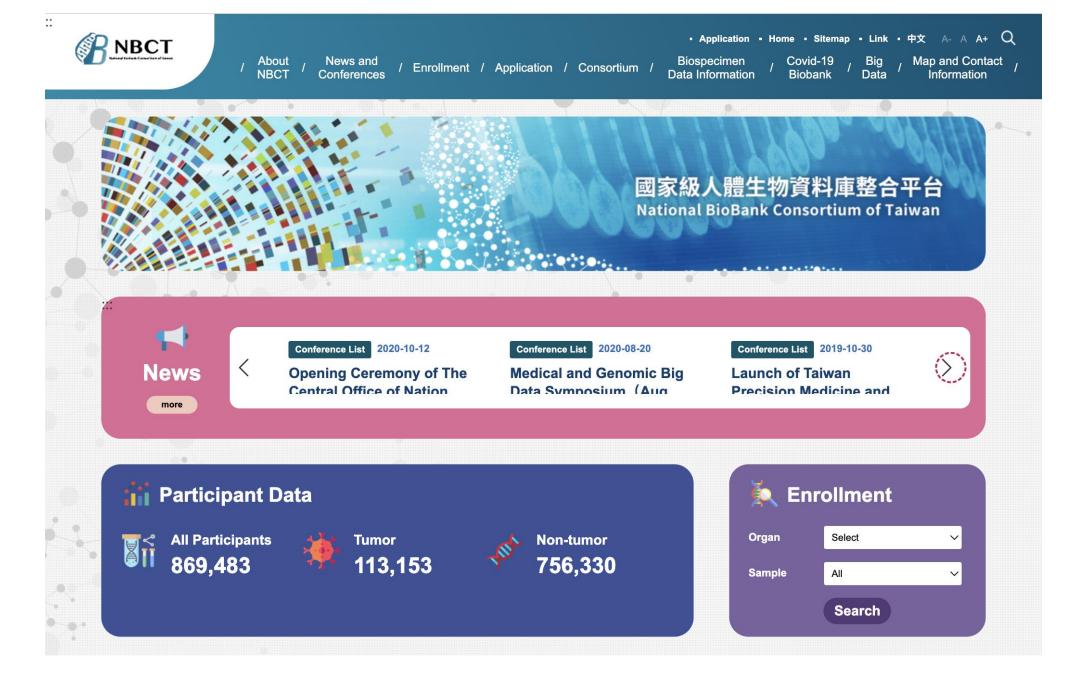






#### **Detailed Executive Plans**

- Facilitate the cooperation of the nationwide biobanks to utilize the specimen and related information.
- ➤ Improve the management standards of all biobanks to promote the quality consistency of biobank specimens and related information.
- Combined with value-added services for all biobanks to increase the application incentives from all biomedical researchers.
- ➤ The goal is to become the most important resource for biotechnology medicine and the healthcare industry.

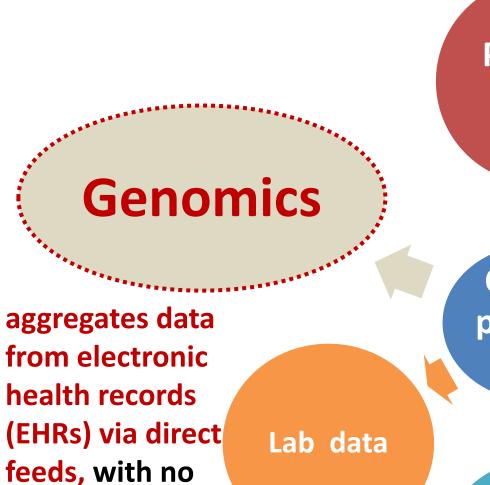


https://nbct.nhri.org.tw

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## Establish 12 Standard operation procedures (SOP) for the application procedures and specimen's Quality

- 1) Application for NBCT Specimens and Information
- 2) Review of NBCT Specimens and Information
- 3) Confidentiality and Conflict of Interest Avoidance
- 4) NBCT Specimens Procedure of the Fresh Frozen Tissue Collection and DNA Extraction
- 5) NBCT Specimens Procedure of the Tissue RNA Extraction
- 6) NBCT Procedure of the Blood Specimens Processing
- 7) NBCT Procedure of the Blood Specimens DNA Extraction
- 8) NBCT Procedure of the Paraffin Blocks and Blank Section Specimens Making
- 9) NBCT Procedure of the Pleural Fluid, Ascites, Spinal Fluid, and Cerebrospinal Fluid Specimens Collection and Processing
- 10) NBCT Procedure of the Urine Specimens Collection and Processing
- 11) NBCT Standard Operating Procedure of the Specimens Delivery I Refrigeration Shipping
- 12) NBCT Standard Operating Procedure of the Specimens Delivery  $\Pi$  Room Temperature Shipping



requirement for

capture the data in

a specific format

the clinician to

**Patient** staus Cancer patientt S

Outcome
Survival
/progression
free

Disease

Diagnosis and staging

**Treatment** 

# Electronic health records (EHR):

First stage

Structured data

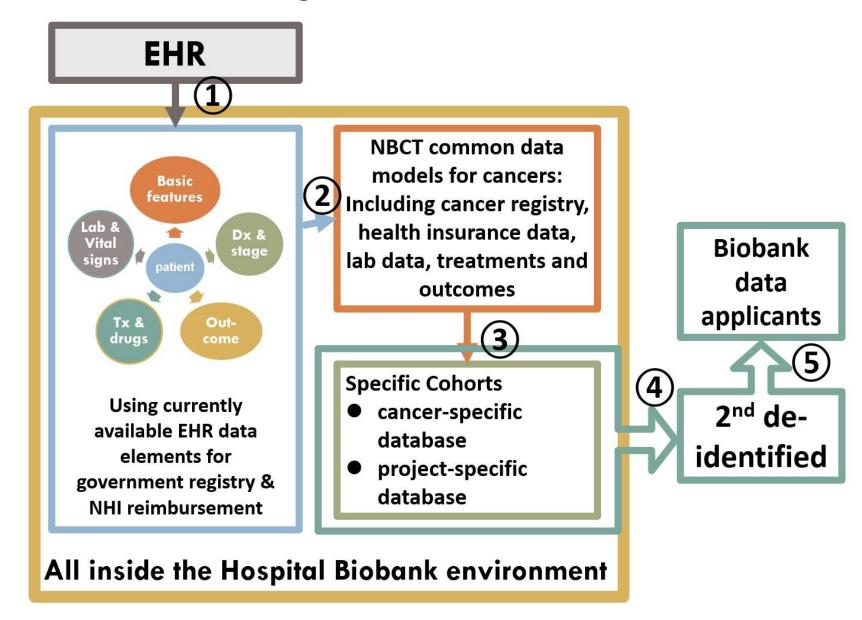
2<sup>nd</sup> stage

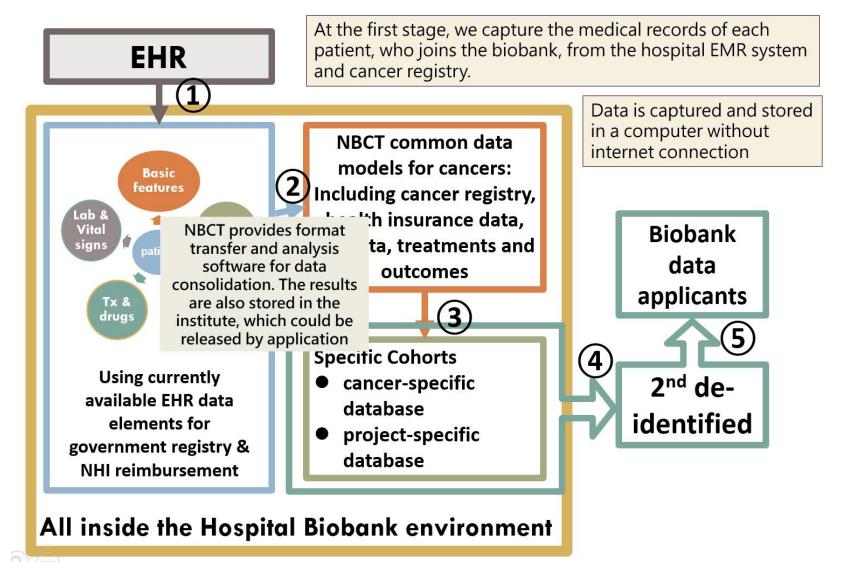
- Unstructured data
  - free text
  - image

### Establish the Common Data Model in each hospital's biobank (NBCT CDM)

To build up standardized medical big data for future collaboration

Since Taiwan has only one universal health insurance system, it became a big niche to build up a CDM from the electronic health record (EHR).





The establishment of CDM has been successful in more than 15 hospitals. This becomes **one big achievement** of NBCT and **the important base for RWD** 



## National Biobank Consortium of Taiwan

Success in promoting the precision medicine ecosystem Unleash the Potential of the Epidemic Prevention Industry

#### By the end of August. 2023:

34 Biobanks

869,000 participants

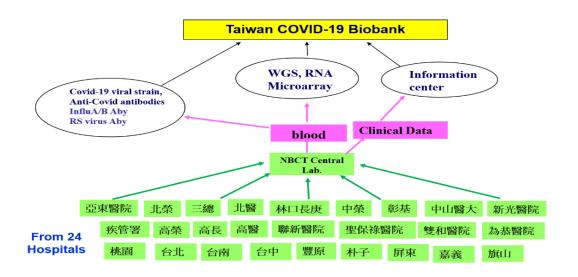
12 SOP 142
Academic applications

26
Industrial applications

#### Cancer Precision Medicine and Biobank Consortium Collaboration Pilot Project



MOHW · NHRI (NBCT) & Roche Collaboration for Precision Medicine Eco system



## Cancer Precision Medicine and Biobank Consortium Collaboration Pilot Project



MOHW · NHRI (NBCT) & Roche Collaboration for Precision Medicine Eco system

## Recruitment of 2000 participants with late stage cancers

- Patients of late stage cancer patients with no prior systemic anti-cancer treatment
- Patients with recurrence of cancer disease who received prior neo-adjuvant, adjuvant or CCRT at least 12 months ago
- only adults older than 18 years can be recruited.
- All participants need to agree for medical data collection and stored in the Hospital biobanks

Cancer types	Stage	
Non-small cell carcinoma ( needs to be EGFR、ALK and ROS1 negative ) IIIB以上		
Esophageal carcinoma	IIIB以上	
Gall bladder carcinoma	IIIB以上	
Gastric carcinoma	IIIB以上	
cholangiocarcinoma	IIIB以上	
Pancreatic carcinoma	III以上	

All participant can get one free comprehensive genetic test composed of 324 genes (FoundationOne® CDx) for their tumor tissue.

FoundationOne® CDx has been approved by FDA of USA for diagnostic practice.

## The first project of NBCT combined with Precision Medicine

- ➤ This project will collect the genetic data and clinical medical data (real world data) of the 2000 participants.
- ➤ The comprehensive genetic testing reports and detailed medical records will be stored and managed in each hospitals' biobank.
- ➤ The EHR data in each biobank after transformed into NBCT CDM, will be combined with the XML data of FoundationOne® CDx report, and build up a cancer genetic and medical dataset of each patient.
- ➤ Through one stop service of NBCT, researchers can apply all of the 2000 patients' data together. Hereinafter referred to as **the large cancer genetic** and medical database.

## The goal of this first pilot project of NBCT combined with Precision Medicine

- ➤ This large database will help strengthen Taiwan's medical quality and provide clinicians with more reference for decision-making.
- ➤ This large database can be applied by the industrial researchers directly to accelerate industrial upgrading.
- ➤ In addition, through this project, the use of real-world evidence (RWE) can be promoted in the future as a mechanism for drug research and development, drug marketing registration and health insurance reimbursement evaluation.

## The medical records collected in this pilot project

(Red words mean the data are collected directly from EHR)

- 1 Patient demographic
- 2-1 Cancer characteristic (newly diagnosis)
- 2-2 Cancer characteristic (recurrence)
- **3 Performance status**
- 4. Co-morbidities
- 5. Laboratory results
- 6. Biomarker test
- 7. Cancer related medication
- 7-1 Stopping reason for cancer related medication (inpatient)
- 7-2 Stopping reason for cancer related medication (outpatient)
- 8. Co-medication

- 9. Cancer related radiotherapy
- 10 Cancer related surgery
- 11. Cancer treatment outcome
- 12. Follow-ups
- 13. Death data
- 14. Value indicator of the project

## **Establishment of Molecular Tumor Board (MTB)**

Molecular guided treatment options for personalized medicine by comprehensive genetic testing has become a new trend. The drugs may be matched with the gene targets, but not in the approved condition by TFDA (off-label use).

- > Set up a MTB becomes necessary to help for the best treatment decision.
- > MTB needs to be a multidisciplinary Practice.

#### The responsibility of MTB in this pilot project

- \* Provide consultation service for attending doctors in this project
- \* Decide the feasibility of the compassionate use of the free drugs matched with the gene targets
- This pilot project has successfully established in-house Molecular Tumor Board in each participating hospital, and a central molecular tumor board.
- This is a big step forward in the promotion of cancer precision medicine in Taiwan.

### Compassionate use of the drugs matched with the gene targets

Roche, Merk, Chugai, and Lily also join the pilot project, will give free drugs for patients according to their genetic testing results in this project and after approval by MTB.

Roche 羅氏藥廠贈藥品項	對應基因
賀癌寧®凍晶注射劑/ Kadcyla® Vial 100mg/ 160mg	HER2
賀癌平®凍晶注射劑/ Herceptin® Vial 440mg	HER2
得舒緩®膜衣錠/ Tarceva® Film-coated Tablets 150mg/100mg	EGFR
日沛樂®膜衣錠/ Zelboraf® Film-coated 240mg	BRAF
可泰利 <sup>®</sup> 膜衣錠/ Cotellic <sup>®</sup> Film-coated tablets 20mg	BRAF
羅思克®膠囊/ Rozlytrek® hard capsules 200mg	ROS1
羅思克®膠囊/ Rozlytrek® hard capsules 200mg	NTRK

Lilly	
禮來公司之贈藥	對應基因
Selpercatinib	RET
<b>♦</b> MERCK	
默克藥廠之贈藥	對應基因
Tepotinib	MET
CHUGAI	
中外製藥之贈藥	對應基因
ALECENSA®	ALK

Through the comprehensive genetic testing, and the decision of the molecular tumor board (MTB), the compassionate use of these drugs matched with the gene targets has been successful in practice. It becomes a win-win-win strategy for cancer patients, attending doctors, and the pharma.

## Lung adenocarcinoma, 86yr, male, ECOG=2

Sensitivity for the detection of copy number alterations is reduced due to sample quality.

## Biomarker Findings

Microsatellite status - MS-Stable
Tumor Mutational Burden - 1 Muts/Mb

### Genomic Findings

For a complete list of the genes assayed, please refer to the Appendix.

**MET** exon 14 splice site (2888-32\_2891del36)

7 Disease relevant genes with no reportable alterations: ALK, BRAF, EGFR, ERBB2, KRAS, RET, ROS1

## Lung adenocarcinoma, 62 yr male ECOG=1

## Biomarker Findings

Microsatellite status - MS-Stable
Tumor Mutational Burden - 7 Muts/Mb

### Genomic Findings

For a complete list of the genes assayed, please refer to the Appendix.

MET amplification copy-number="29"
NF1 I679fs\*21
FBXW7 K326\*
HGF amplification - equivocal†
KEAP1 deletion exons 4-5
TP53 Q144fs\*26 (VAF 26%)

7 Disease relevant genes with no reportable alterations: ALK, BRAF, EGFR, ERBB2, KRAS, RET, ROS1

## Gastric adenocarcinoma, 73 yr male, ECOG=1

### Biomarker Findings

Microsatellite status - MS-Stable
Tumor Mutational Burden - 2 Muts/Mb

## Genomic Findings

For a complete list of the genes assayed, please refer to the Appendix.

MET amplification
CCNE1 amplification
RAF1 amplification - equivocal<sup>†</sup>
TP53 E286\*

1 Disease relevant genes with no reportable alterations: *ERBB2* 

† See About the Test in appendix for details.

GENE

**MET** 

**ALTERATION** 

amplification

copy-number="15"

GENE

**TP53** 

**ALTERATION** 

E286\*

TRANSCRIPT ID

NM\_000546.4

**CODING SEQUENCE EFFECT** 

856G>T

VARIANT CHROMOSOMAL POSITION

chr17:7577082

**VARIANT ALLELE FREQUENCY (% VAF)** 

26.5%

GENE

CCNE1

**ALTERATION** 

amplification

copy-number="8"

### Esophageal carcinoma 62 male., ECOG=1

Sensitivity for the detection of copy number alterations is reduced due to sample quality.

#### Biomarker Findings

Microsatellite status - MS-Stable
Tumor Mutational Burden - 6 Muts/Mb

#### Genomic Findings

For a complete list of the genes assayed, please refer to the Appendix.

MET amplificationFGF3 amplificationCCND1 amplificationFGF4 amplificationFGFR1 amplificationMLL2 M5280fs\*6MTAP loss exons 2-8NSD3 (WHSC1L1)MYC amplificationamplification

*SOX2* amplification *TBX3* R269W - subclonal<sup>†</sup>

CDKN2A/B CDKN2B loss, TP53 K132R

CDKN2A loss ZNF703 amplification

FGF19 amplification

1 Disease relevant genes with no reportable alterations: *ERBB2* 

† See About the Test in appendix for details.

**GENE** 

MET

**ALTERATION** 

amplification

copy-number ="8"

**GENE** 

**TP53** 

**ALTERATION** 

K132R

TRANSCRIPT ID

NM\_000546.4

CODING SEQUENCE EFFECT

395A>G

VARIANT CHROMOSOMAL POSITION

chr17:7578535

**VARIANT ALLELE FREQUENCY (% VAF)** 

65.5%

### Lung adenocarcinoma, 80 yr male ECOG=1

Due to the low tumor purity, sensitivity for the detection of copy number alterations including ERBB2 is reduced due to sample quality. Refer to appendix for limitations statement. Sensitivity for the detection of other alterations and genomic signatures may also be reduced and the TMB score may be underreported.

#### Biomarker Findings

Microsatellite status - Cannot Be Determined α
Tumor Mutational Burden - Cannot Be Determined

#### Genomic Findings

For a complete list of the genes assayed, please refer to the Appendix.

**BRAF** V600E **PIK3CA** H1047R **DNMT3A** splice site 2408+2T>C **TP53** S261fs\*84

7 Disease relevant genes with no reportable alterations: ALK, EGFR, ERBB2, KRAS, MET, RET, ROS1

† See About the Test in appendix for details.

α Patients with Microsatellite status of Cannot Be Determined should be re-tested with an orthogonal (alternative) method.

#### Report Highlights

- Targeted therapies with NCCN categories of evidence in this tumor type: Dabrafenib (p. 9), Dabrafenib + Trametinib (p. 8), Vemurafenib (p. 12)
- Evidence-matched clinical trial options based on this patient's genomic findings: (p. 14)
- Variants that may represent clonal hematopoiesis and may originate from non-tumor sources: DNMT3A splice site 2408+2T>C (p. 6)

GENOMIC FINDINGS	THERAPIES WITH CLINICAL RELEVANCE (IN PATIENT'S TUMOR TYPE)	THERAPIES WITH CLINICAL RELEVANCE (IN OTHER TUMOR TYPE)
BRAF - V600E	Dabrafenib + Trametinib	Dabrafenib 2A
		Vemurafenib 2A
		Encorafenib + Binimetinib
		Selumetinib
		Trametinib
10 Trials see p. 14		Vemurafenib + Cobimetinib
<b>PIK3CA -</b> H1047R	none	Everolimus
10 Trials see p. 16		Temsirolimus
		NCCN category

#### VARIANTS THAT MAY REPRESENT CLONAL HEMATOPOIESIS (CH)

Genomic findings below may include nontumor somatic alterations, such as CH. The efficacy of targeting such nontumor somatic alterations is unknown. This content should be interpreted based on clinical context. Refer to appendix for additional information on CH.

DNMT3A - splice site 2408+2T>C \_\_\_\_\_\_p.

## Adenocarcinoma of pancreas, 75 yr female, ECOG=0

#### Biomarker Findings

Microsatellite status - MS-Stable
Tumor Mutational Burden - 1 Muts/Mb

#### Genomic Findings

For a complete list of the genes assayed, please refer to the Appendix.

BRAF G469S

**PIK3CA M1043I** 

ARID1A Q1452fs\*39

MTAP loss exons 2-8

ACVR1B loss

CDKN2A/B CDKN2B loss, CDKN2A loss

NSD3 (WHSC1L1) amplification - equivocal

TP53 E336\*

ZNF703 amplification - equivocal<sup>†</sup>

2 Disease relevant genes with no reportable alterations: *BRCA1*, *BRCA2* 

† See About the Test in appendix for details.

#### Report Highlights

- Targeted therapies with potential clinical benefit approved in another tumor type: Everolimus (p. 10), Selumetinib (p. 10), Temsirolimus (p. 11), Trametinib (p. 12)
- Evidence-matched clinical trial options based on this patient's genomic findings: (p. 13)

GENE

#### **BRAF**

**ALTERATION** 

G469S

TRANSCRIPT ID

NM\_004333

CODING SEQUENCE EFFECT

1405\_1406GG>TC

**VARIANT ALLELE FREQUENCY (% VAF)** 

36.9%



BIOMARKER FINDINGS	THERAPY AND CLINICAL TRIAL IMPLICATIONS	
Microsatellite status - MS-Stable	No therapies or clinical trials. see Biomarker Findings section	
Tumor Mutational Burden - 1 Muts/Mb	No therapies or clinical trials. see Biomarker Findings section	
GENOMIC FINDINGS	THERAPIES WITH CLINICAL RELEVANCE (IN PATIENT'S TUMOR TYPE)	THERAPIES WITH CLINICAL RELEVANCE (IN OTHER TUMOR TYPE)
<b>BRAF</b> - G469S	none	Selumetinib
<b>10 Trials</b> see p. 15		Trametinib
<b>PIK3CA -</b> M1043I	none	Everolimus
<b>10 Trials</b> see p. 18		Temsirolimus
<b>ARID1A -</b> Q1452fs*39	none	none
8 Trials see p. 13		
MTAP - loss exons 2-8	none	none
1 Trial see p. 17		

#### Esophagus, SCC, 52 yr. male ECOG=1

#### Biomarker Findings

**Tumor Mutational Burden -** 12 Muts/Mb **Microsatellite status -** MS-Stable

#### Genomic Findings

For a complete list of the genes assayed, please refer to the Appendix.

BRCA2 K944\* - subclonal<sup>†</sup>

ERBB2 amplification - equivocal<sup>†</sup>

**CCND1** amplification

CASP8 deletion exons 4-9

CDKN2A/B CDKN2B loss, p14ARF loss exon 1

FGF12 amplification - equivocal

FGF19 amplification

FGF3 amplification

FGF4 amplification

TP53 E285V - subclonal, R248\_I251>L, Y205C<sup>†</sup>

† See About the Test in appendix for details.

GENE

#### BRCA2

**ALTERATION** 

K944\* - subclonal

**HGVS VARIANT** 

NM\_000059.3:c.2830A>T (p.K944\*)

VARIANT CHROMOSOMAL POSITION

chr13:32911322

**VARIANT ALLELE FREQUENCY (% VAF)** 

6.0%

GENE

#### **TP53**

**ALTERATION** 

E285V - subclonal, R248\_I251>L, Y205C

**HGVS VARIANT** 

NM\_000546.4:c.854A>T (p.E285V),

NM\_000546.4:c.743\_751del (p.R248\_l251delinsL),

NM\_000546.4:c.614A>G (p.Y205C)

VARIANT CHROMOSOMAL POSITION

chr17:7577084, chr17:7577529-7577538, chr17:7578235

**VARIANT ALLELE FREQUENCY (% VAF)** 

1.3%, 33.2%, 15.8%

**GENE** 

#### ERBB2

**ALTERATION** 

amplification - equivocal

copy-number="7"

**GENE** 

#### CCND1

**ALTERATION** 

amplification

copy-number="25"

GENE

FGF4

**ALTERATION** 

amplification

copy-number="29"

GENE

FGF3

ALTERATION

amplification

copy-number="29"

BIOMARKER FINDINGS	THERAPIES WITH CLINICAL RELEVA (IN PATIENT'S TUMOR TYPE)	NCE THERAPIES WITH CLINICAL RELEVANCE (IN OTHER TUMOR TYPE)
Tumor Mutational Burden - 12 Muts/Mb	Nivolumab 1	Atezolizumab
	Pembrolizumab 1	Avelumab
	Nivolumab + Ipilimumab	Cemiplimab
	Dostarlimab	Durvalumab
10 Trials see p. 22		Retifanlimab
Microsatellite status - MS-Stable	No therapies or clinical trials	s. See Biomarker Findings section
GENOMIC FINDINGS	THERAPIES WITH CLINICAL RELEVA (IN PATIENT'S TUMOR TYPE)	NCE THERAPIES WITH CLINICAL RELEVANCE (IN OTHER TUMOR TYPE)
<b>BRCA2 -</b> K944* - subclonal	none	Niraparib
		Olaparib
		Rucaparib
<b>10 Trials</b> see p. <u>24</u>		Talazoparib
ERBB2 - amplification - equivocal	none	Ado-trastuzumab emtansine
		Fam-trastuzumab
		deruxtecan
		Lapatinib
		Margetuximab
		Neratinib
10 Trials see p. 27		Trastuzumab
IO Iriais see p. ZZ		Trastuzumab + Pertuzumab
CCND1 - amplification	none	none
5 Trials see p. 26		

## Esophageal cancers

**BIOMARKER FINDINGS** THERAPY AND CLINICAL TRIAL IMPLICATIONS Microsatellite status - MS-Stable No therapies or clinical trials. see Biomarker Findings section Tumor Mutational Burden - 5 Muts/Mb No therapies or clinical trials. see Biomarker Findings section THERAPIES WITH CLINICAL THERAPIES WITH CLINICAL GENOMIC FINDINGS RELEVANCE RELEVANCE (IN PATIENT'S TUMOR TYPE) (IN OTHER TUMOR TYPE) Ado-trastuzumab Afatinib ERBB2 - A775\_G776insYVMA 2A emtansine Fam-trastuzumab 2A deruxtecan Trastuzumab Trastuzumab + Pertuzumab 10 Trials see p. 10 Lapatinib

## Gastric cancer

GENOMIC FINDINGS	THERAPIES WITH CLINICAL RELEVANCE (IN PATIENT'S TUMOR TYPE)	THERAPIES WITH CLINICAL RELEVANCE (IN OTHER TUMOR TYPE)
<b>ERBB2</b> - amplification - equivocal	Trastuzumab 1	Ado-trastuzumab emtansine
	Fam-trastuzumab deruxtecan	Afatinib
	Trastuzumab + Pembrolizumab	Dacomitinib
		Lapatinib
		Margetuximab
		Neratinib
10 Trials see p. 20		Trastuzumab + Pertuzumab
FBXW7 - Y545C - subclonal	none	Everolimus
9 Trials see p. 22		Temsirolimus
MET - amplification	none	Cabozantinib
		Capmatinib
		Crizotinib
10 Trials see p. 24		Tepotinib

## Adenocarcinoma of stomach 67 year male, ECOG=1

#### Biomarker Findings

Microsatellite status - MSI-High Tumor Mutational Burden - 74 Muts/Mb

#### Genomic Findings

For a complete list of the genes assayed, please refer to the Appendix.

ERBB2 L755S

APC K1182fs\*83,

R1463fs\*6

ARID1A D1850fs\*33,

G285fs\*78

EZH2 R213H - subclonal<sup>†</sup>

**PIK3CB** D1067Y

PIK3R1 | 128,7fs\*10 -

subclonal<sup>†</sup>

*STK11* N109fs\*20

CD70 G78fs\*33 -

subclonal<sup>†</sup>

CREBBP R1664C -

subclonal<sup>†</sup>

**GNAS** R201C, R160C -

subclonal<sup>†</sup>

HNF1A P291fs\*51

MAP3K1 N1305fs\*31

MLH1 loss exons 1-13

MLL2 A3552fs\*4

MSH3 K383fs\*32

PBRM1 R534\*, I279fs\*4

OKI K134fs\*14

SETD2 T305fs\*4

**SNCAIP** E852K

**SPEN** K943fs\*31

TGFBR2 K128fs\*3

TNFAIP3 C559\* -

subclonal<sup>†</sup>

TP53 K382fs\*40 subclonal, R273C<sup>†</sup>

WT1 R462Q - subclonal<sup>†</sup>



## Summary

Cancer Precision Medicine and Biobank Consortium
Collaboration Pilot Project has become the most successful example of private public partnership (PPP) model in Taiwan. It includes the participants of Ministry of Health and Welfare (MOHW), NBCT /NHRI, 14 medical hospitals, and 4 pharmaceutical companies.

## The important achievement of the Pilot project -1

- ✓ The program has successfully recruited 1164 participants by the end of August, 2023 and established the MTB of in 12 hospitals and a central MTB of clinical function level.
- ✓ More than 10% of the patients have found gene targets for free drugs. So far, 90 patients/times have applied for the drugs.
- ✓ This project has recruited a large number of GI cancer patients (224 pancreatic cancers, 158 esophageal cancers, 193 gastric cancers), which is not just beneficial for the patients, but also become precious domestic genetic & medical data, since quite few comprehensive genetic studies performed in these GI cancers due to lack of drug targets.

## The important achievement of the Pilot project -2

- ✓ This project also demonstrated that comprehensive NGS genetic testing can not only discover more gene variations, but also has future development, including new drug targets and analysis and identify of efficacy indicators.
- ✓ Through the establishment of CDM by NBCT, this pilot project have successfully integrated the genetic and medical data in each biobank.
- ✓ Integration of the genetic-medical big data of 500 patients from 7 cooperative hospitals has been achieved for the first time in Taiwan and have been sent to the applicant .





The working team of the NBCT Central Office

# THANKS For your attentions