

Non-immune molecular predictors of treatment response in gastric cancer (GC)

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DECLARATION OF INTERESTS

Personal financial interest of scientific consultancy for BMS, Lilly, MSD and Servier
Honorarium for speaking issues from Amgen, BMS, Lilly, MSD, Roche and Servier
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Outline

Introduction: inter- and intra-patient heterogeneity

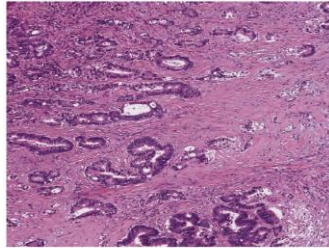
Main phase III trials with targeted therapies in GC

New strategies

Conclusions

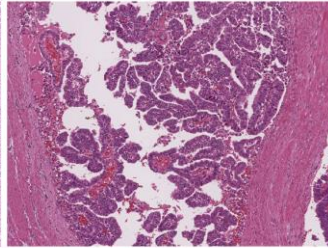
Inter-patient heterogeneity of GC

Histological subtypes



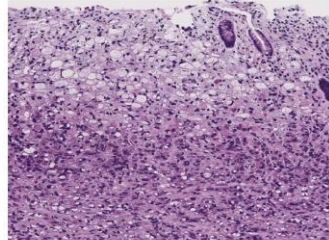
Tubular adenocarcinoma

The tumour is composed of dilated tubules invading the muscle layer.



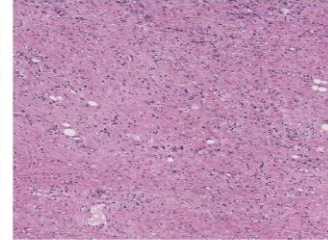
Papillary carcinoma

The tumour consists of elongated finger-like processes with fibrovascular connective tissue cores, lined by columnar cells.



Poorly cohesive carcinoma, signet-ring cell type

The tumour is composed predominantly of signet-ring cells, the neoplastic cells are larger at the superficial part of the mucosa



Poorly cohesive carcinoma NOS

The tumour consists of poorly cohesive cells of non-signet-ring cell type that invade the gastric wall widely, with marked desmoplasia.

GC is not one disease

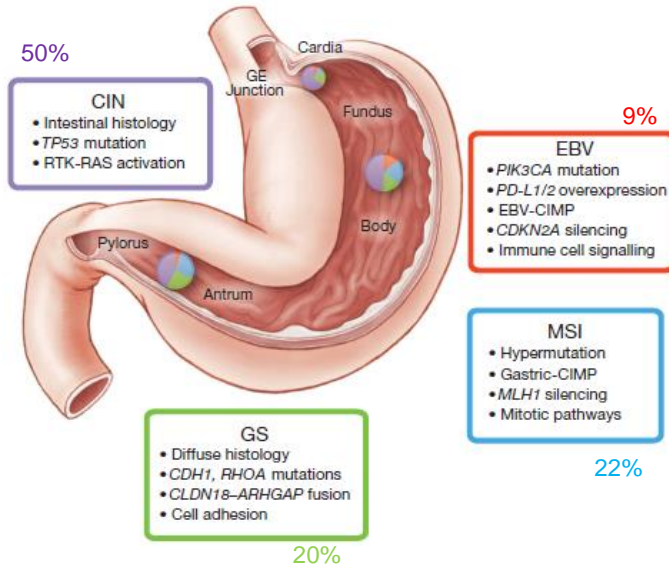
Different histological subtypes

Not prognostic

Not predictive of response

Inter-patient heterogeneity of GC

Molecular subtypes



GC is not one disease

4 different molecular subtypes

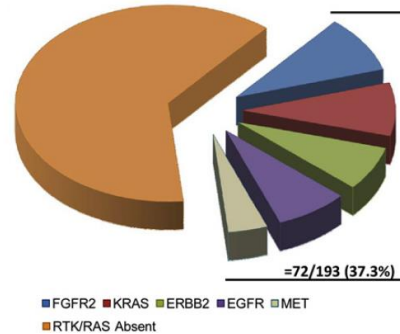
(Prognostic)

Not predictive of response (except MSI)

Targeted therapies

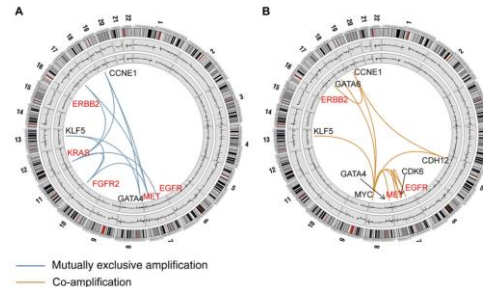
Main phase 3 trials in GC

- First molecular characterization of GC distinguish up to 40% of tumors harboring amplifications on FGFR2, KRAS, HER2, EGFR and MET (mutually exclusive)

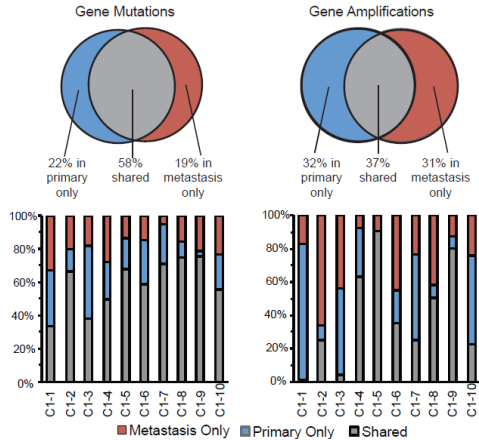


A Amplifications		B Deletions	
Esophageal	Gastric	Esophageal	
<i>MCL1</i> *	1p36.22	1q44	2q33.2
<i>PRKCI</i>	1q42.3	7q32.1	4q35.1
<i>MYB</i> *	<i>EPHB3</i>	7q36.3	6p25.3
<i>CDK6</i>	11q13.4	8p23.3	<i>PTPRD</i> *
7q22.1	<i>VEGFA</i> *	<i>CDKN2A</i> *	<i>FHIT</i> *
<i>MET</i>	<i>EGFR</i> *	<i>ATM</i> *	<i>FAM190A</i> *
7q34	<i>GATA4</i>	11q25	<i>PDE4D</i> *
9p13.3	<i>CCND1</i> *	21q11.2	<i>PARK2</i> *
10q22.2	<i>KRAS</i> *	<i>RUNX1</i>	<i>WWOX</i> *
<i>FGFR2</i>	<i>MDM2</i> *	1p36.11	<i>MACROD2</i> *
11p14.2*	<i>CCNE1</i> *	<i>CASP3</i> *	<i>SMAD4</i>
13q13.1	<i>MYC</i> *	1p13.2	10q11.23
13q14.1	<i>ERBB2</i> *	5q21.1	<i>PTEN</i> *
17q21.2	<i>GATA6</i>	<i>APC</i> *	<i>CASP7</i>
18q11.2	<i>FGFR1</i> *	<i>A2BP1</i> *	Colorectal
Colorectal	13q12.2		

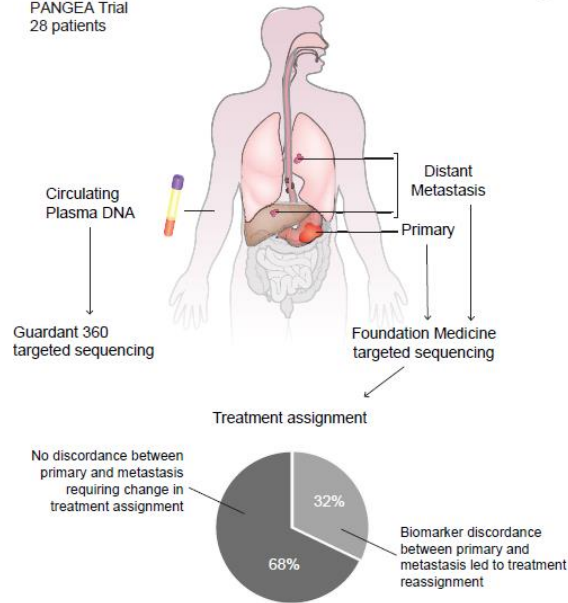
■ Esophageal
■ Gastric
■ Colorectal
■ Esophageal/gastric
■ Esophageal/colon
■ Esophageal/gastric/colon



Intra-patient heterogeneity of GC



PANGEA Trial
28 patients



≈ 30% of discordance between primary and metastases (tissue)
ctDNA is more similar to metastatic tissue

... should we rely on the primary tumor for biomarker guided therapies?

Targeted therapies

Main phase 3 trials in GC

- Only 4 of 19 positive trials

Pathway	Trial	Line	Screening	Agent	mOS	Hazard ratio
HER2	ToGA	1 st	HER2 (FISH)	Trastuzumab	13.8 vs. 11.1 m	HR 0.74
	LOGIC	1 st	HER2 (FISH)	Lapatinib	12.2 vs. 10.5 m	HR 0.91
	JACOB	1 st	HER2 3+, or HER2+&ISH+	Trastuzumab + Pertuzumab	17.5 vs. 14.2 m	HR 0.84
	TyTAN	2 nd	HER2 (FISH)	Lapatinib	11.0 vs. 8.9 m	HR 0.84
	GATSBY	2 nd	HER2 3+, or HER2+&ISH+	T-DM1	7.9 vs. 8.6 m	HR 1.15
EGFR	REAL-3	1 st	-	Panitumumab	8.8 vs. 11.3 m	HR 1.37
	EXPAND	1 st	-	Cetuximab	9.4 vs. 10.7 m	HR 1.00
	GOG	1 st	-	Gefitinib	3.73 vs. 3.67 m	HR 0.90
mTOR	GRANITE-1	2 nd & 3 rd	-	Everolimus	5.4 vs. 4.3 m	HR 0.90
MET	RILOMET1	1 st	MET (IHC)	Rilotumumab	8.8 vs. 10.7 m	HR 1.34
	METGastric	1 st	MET (IHC)	Onartuzumab	11.0 vs. 11.3 m	HR 0.82
VEGF	AVAGAST	1 st	-	Bevacizumab	12.1 vs. 10.1 m	HR 0.87
	RAINFALL	1 st	-	Ramucirumab	11.2 vs. 10.7 m	HR 0.96
	RAINBOW	2 nd	-	Ramucirumab	9.6 vs. 7.4 m	HR 0.80
	REGARD	2 nd	-	Ramucirumab	5.2 vs. 3.8 m	HR 0.77
	Li et al.	3 rd	-	Apatinib	6.5 vs. 4.7 m	HR 0.70
PARP	GOLD	2 nd	ATM (IHC)	Olaparib	12 vs. 10 m	HR 0.73
STAT3	BRIGHTER	2 nd	-	Napabucasin	6.93 vs. 7.36 m	HR 1.01

Targeted therapies

HER2

- HER2 is overexpressed in 15-25% of GC
- The ToGA trial demonstrated clinically meaningful survival results only in HER2-positive with IHC3+ or IHC2+&ISH+
- None other phase 3 clinical trial could demonstrate benefit in HER2-positive population

HER2	Trial	Rank	HER2 (FISH)	Treatment	OS (m)	HR
	ToGA	1 st	HER2 (FISH)	Trastuzumab	13.8 vs. 11.1 m	HR 0.74
	ToGA	1 st	HER2 3+, or HER2+&ISH+	Trastuzumab	16.0 vs. 11.8	HR 0.65
	LOGIC	1 st	HER2 (FISH)	Lapatinib	12.2 vs. 10.5 m	HR 0.91
	JACOB	1 st	HER2 3+, or HER2+&ISH+	Trastuzumab + Pertuzumab	17.5 vs. 14.2 m	HR 0.84
	JACOB - final analysis	1 st	HER2 3+, or HER2+&ISH+	Trastuzumab + Pertuzumab	18.1 vs. 14.2 m	HR 0.85
	TyTAN	2 nd	HER2 (FISH)	Lapatinib	11.0 vs. 8.9 m	HR 0.84
	GATSBY	2 nd	HER2 3+, or HER2+&ISH+	T-DM1	7.9 vs. 8.6 m	HR 1.15

Better selection

*Clinical activity do exist: final analysis confirm a **15% reduction in the risk of death** by adding pertuzumab*

*Biomarker analysis: **lower efficacy of T-DM1 in pts with heterogeneous HER2 expression**, compared with those with more homogeneous expression ($\geq 80\%$)*

HER2 expression

- Definition of the HER2 positivity
 - IHC 3+ or IHC 2+ (ISH positive)
- Intra-tumoral heterogeneity
 - High *HER2* amplification levels have been associated with a superior benefit of trastuzumab
 - HER2 protein levels have been associated with a superior benefit of trastuzumab
 - Quantification of the HER2 protein levels may identify the true HER2 positive patients
- Up front and secondary resistance
 - Up to 55% had other genomic events (cell cycle, PI3K, RTK)
- Loss of HER2
 - Described in 30-70% of the patients, after trastuzumab therapy

Targeted therapies

EGFR

- 5-10% of GC have *EGFR* amp or EGFR overexpression
- None of the phase 3 clinical trial could demonstrate benefit in unselected GC population

EGFR	REAL-3	1 st	-	Panitumumab	8.8 vs. 11.3 m	HR 1.37
	EXPAND	1 st	-	Cetuximab	9.4 vs. 10.7 m	HR 1.00
	GOG	1 st	-	Gefitinib	3.73 vs. 3.67 m	HR 0.90

Post-hoc biomarker analysis suggest meaningful efficacy in pts with high levels of EGFR

Targeted therapies

MET

- MET overexpression found in 25-65% of GC, although not fully correlated with the pathway function
- Aberrant c-MET pathway activation could occur due to MET overexpression, *MET* amp or ↑ HGF
- Two phase 3 trials could not demonstrate enough efficacy when blocking the MET pathway

MET	RILOMET1	1 st	MET (IHC)	Rilotumumab	8.8 vs. 10.7 m	HR 1.34
	METGastric	1 st	MET (IHC)	Onartuzumab	11.0 vs. 11.3 m	HR 0.82

Patients with moderate (2+) and strong (3+) MET staining on ≥ 50% of tumor cells tended to live longer with onartuzumab

Targeted therapies

Why did they failure?

- In part because of a non-adequate study design:
 - Inter-patient variability: GC is not a unique disease
 - Lack of a biomarker
 - Lack of an adequate biomarker
 - Difficulties in measuring the biomarker
- In part because of the intrinsic characteristics of GC:
 - Intra-patient variability: spatial and temporal heterogeneity

New strategies

Novel HER2-directed therapies

Antibody-drug conjugates

- Trastuzumab deruxtecan (T-Dxd) (DS-8201a)
- RC48-ADC: ongoing phase 2 trial (NCT03556345)

Monoclonal antibodies

- Margetuximab (+ PD-1 inhibitor)

Bispecific antibodies

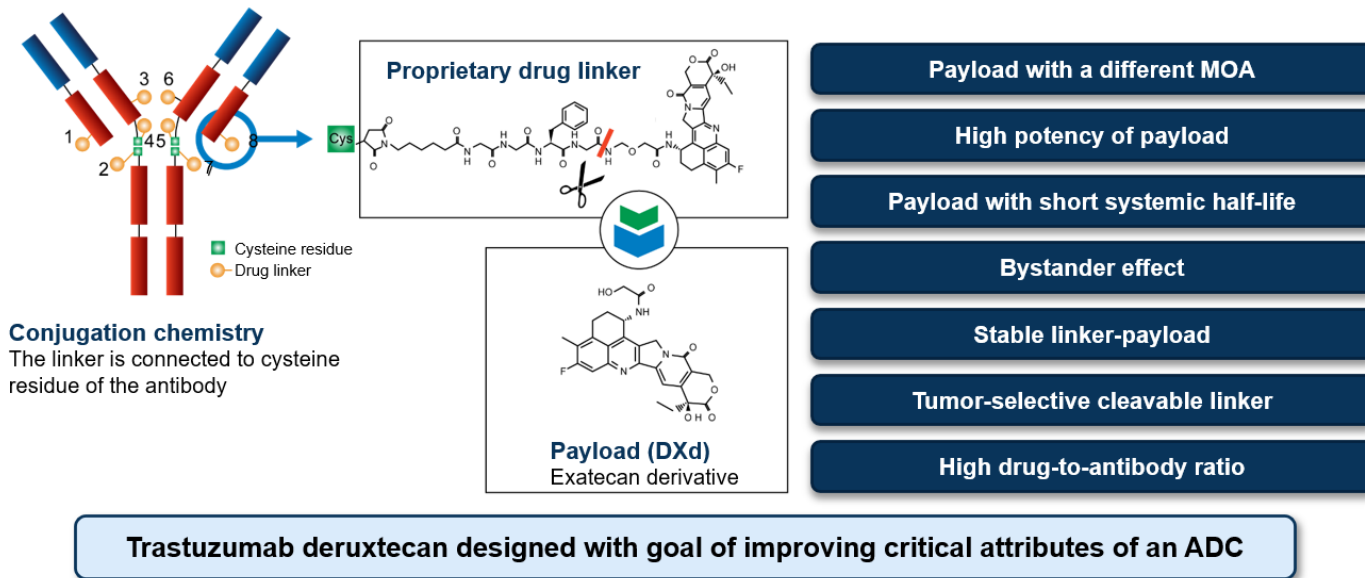
- Zanidatamab (ZW25); targets two areas on HER2 (phase 2 in combination with SOC chemo [NCT03929666], and phase 1/2 with chemo and PD-1 inhibitor [NCT04276493])

Combination with immune checkpoint inhibitors

- With durvalumab, nivolumab, and pembrolizumab (phase 3 KEYNOTE-811)

Trastuzumab Deruxtecan in Advanced HER2+ GC

Phase 2 DESTINY-Gastric01 Trial



Trastuzumab Deruxtecan in Advanced HER2+ GC

Phase 2 DESTINY-Gastric01 Trial

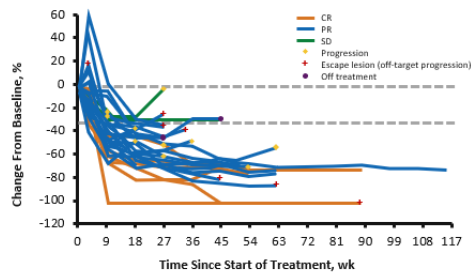
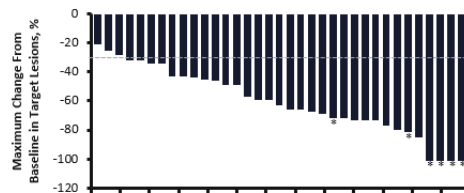
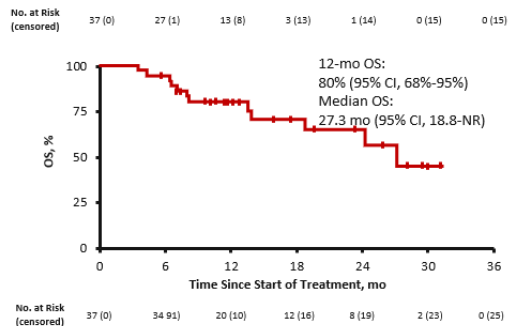
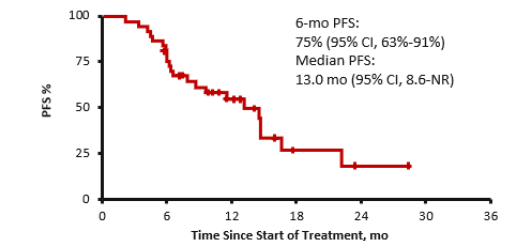
	Primary Cohort ¹		Exploratory Cohorts	
	T-DXd (n = 119)	PC Overall (n = 56)	Cohort 1 IHC 2+/ISH- (n = 19)	Cohort 2 IHC 1+ (n = 21)
ORR by ICR (CR + PR)	51.3% (n = 61) 95% CI, 41.9-60.5; P < .0001*	14.3% (n = 8) 95% CI, 6.4-26.2	36.8% (n = 7) 95% CI, 16.3%-61.6%	19.0% (n = 4) 95% CI, 5.4%-41.9%
Confirmed ORR by ICR (CR + PR)	42.9% (n = 51) 95% CI, 33.8-52.3	12.5% (n = 7) 95% CI, 5.2-24.1	26.3% (n = 5) 95% CI, 9.1%-51.2%	9.5% (n = 2) 95% CI, 1.2%-30.4%
CR	8.4% (n = 10)	0	0	0
PR	34.5% (n = 41)	12.5% (n = 7)	26.3% (n = 5)	9.5% (n = 2)
SD	42.9% (n = 51)	50.0% (n = 28)	63.2% (n = 12)	61.9% (n = 13)
PD	11.8% (n = 14)	30.4% (n = 17)	10.5% (n = 2)	28.6% (n = 6)
NE	2.5% (n = 3)	7.1% (n = 4)	0	0
Confirmed DCR (CR + PR + SD)	85.7% (n = 102) 95% CI, 78.1-91.5	62.5% (n = 35) 95% CI, 48.5-75.1	89.5% (n = 17) 95% CI, 66.9%-98.7%	71.4% (n = 15) 95% CI, 47.8%-88.7%
Median confirmed DOR	11.3 months 95% CI, 5.6 months-NE	3.9 months 95% CI, 3.0-4.9 months	7.6 months 95% CI, 4.1 months-NE	12.5 months 95% CI, NE-NE

Primary cohort: HER2+ and progressed on trastuzumab-containing regimen

Exploratory: in ≤20 patients with naive HER2-low disease (IHC 2+/ISH- and IHC 1+)

Combinations with immune checkpoints inhibitors

Pembrolizumab + trastuzumab + platin + fluoropyrimidine



N = 37 patients; most received cape/ox

- 6-mo PFS: 75%; median: 13 mo
- Median OS: 27.3 mo
- RR: 83%

Ongoing phase 3
KEYNOTE-811
(NCT03615326)

New strategies

FGFR2

Ph II SHINE Study (AZD4547)

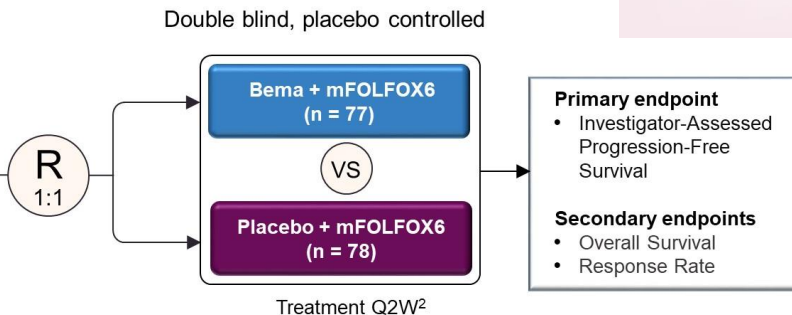
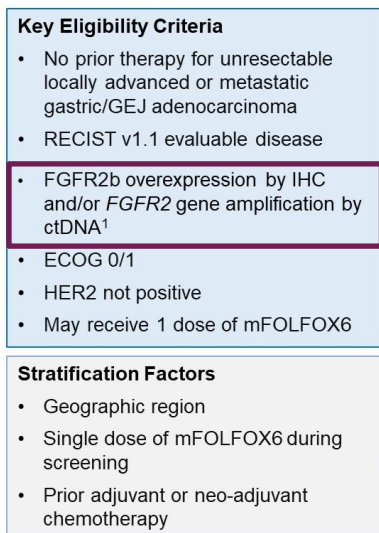
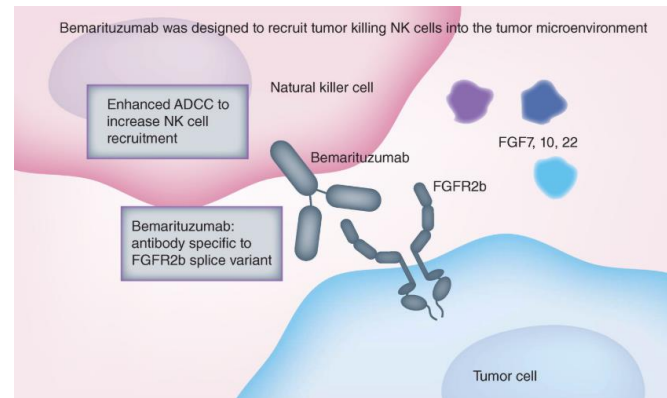
- 2nd line: paclitaxel vs AZD4547
- Patients selected based on *FGFR2* gene amplification or *FGFR2* polysomy

Negative

- *FGFR2* gene amplification showed high intratumor heterogeneity
- *FGFR2* CNV (in tumor and in plasma) predicted response to AZD4547
- Homogeneity of *FGFR2* amplification required to respond to AZD4547

New strategies

FGFR2: Bemarituzumab Phase 2 study



Statistical Plan

Trial initially designed as registrational Phase 3 (n=548) with 2-sided α 0.05 Amended after enrolling n = 155 to a proof-of-concept Phase 2 with pre-specified statistical assumptions of:

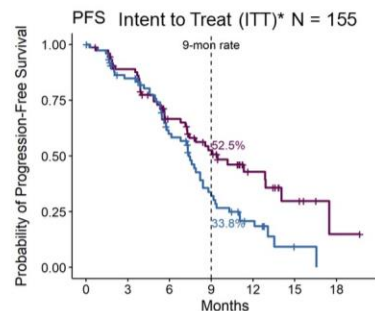
- Hierarchical sequential testing: PFS, then OS/ORR
- ≥ 84 events to demonstrate benefit at a $HR \leq 0.76$ for PFS at 2-sided α of 0.2

1 Central testing: Immunohistochemical stain (Ventana): cut-off any 2+/3+; circulating tumor DNA (PGDx): cut-off 1.5X
2 15mg/kg Q2W with a single 7.5mg/kg dose on Cycle 1 Day 8²

New strategies

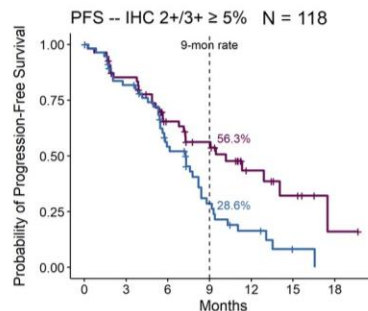
FGFR2: Bemarituzumab Phase 2 study

Progression-Free Survival Benefit Increased with Higher Levels of FGFR2b Overexpression



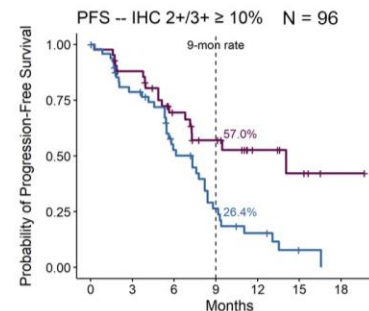
	Number at risk	
BEMA	77	78
PLACEBO	78	78
	0	3
	6	12
	9	18
	12	15
	15	18
	18	18

	Bema N = 77	Placebo N = 78
mPFS, mo (95% CI)	9.5 (7.3, 12.9)	7.4 (5.8, 8.4)
	P=0.0727	
HR (95% CI)	0.68 (0.44, 1.04)	



	Number at risk	
BEMA	58	60
PLACEBO	60	60
	0	3
	6	12
	9	18
	12	15
	15	18
	18	18

	Bema N = 58	Placebo N = 60
mPFS, mo (95% CI)	10.2 (6.8, 14.1)	7.3 (5.5, 8.2)
HR (95% CI)	0.54 (0.33, 0.87)	



	Number at risk	
BEMA	44	52
PLACEBO	52	52
	0	3
	6	12
	9	18
	12	15
	15	18
	18	18

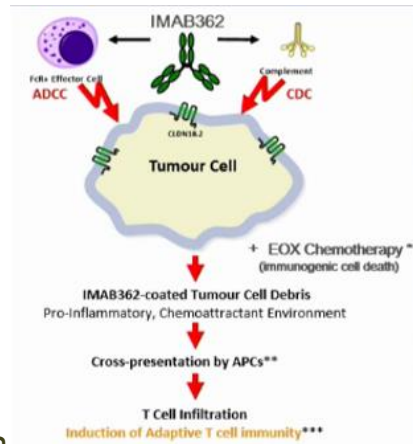
	Bema N = 44	Placebo N = 52
mPFS, mo (95% CI)	14.1 (6.8, NR)	7.3 (5.4, 8.2)
HR (95% CI)	0.44 (0.25, 0.77)	

*ITT = 149 with IHC 2+/3+ and 6 pts with IHC <2+ or not available who were enrolled based on ctDNA alone

New strategies

Claudine 18.2

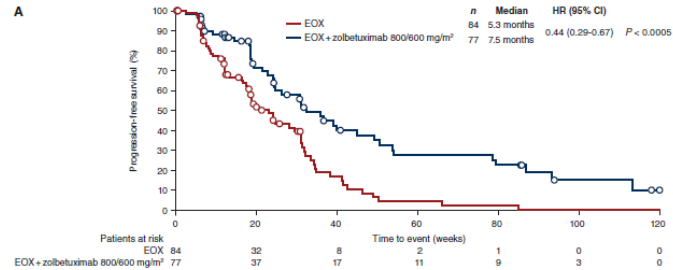
- Claudine 18.2 is a major structural component of tight junctions
 - Broadly expressed in GC, not in healthy tissues except in the stomach mucosa
- Zolbetuximab (IMAB362) is a chimeric IgG1 specific for CLDN18.2
 - Antibody-dependent cellular cytotoxicity (ADCC)
 - Complement-dependent cytotoxicity (CDC)
 - In combination with chemo, enhances T-cell infiltration and induces pro-inflammatory cytokines



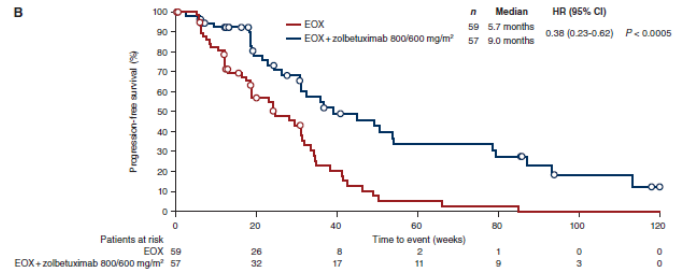
New strategies

Claudine 18.2: Phase II FAST Trial

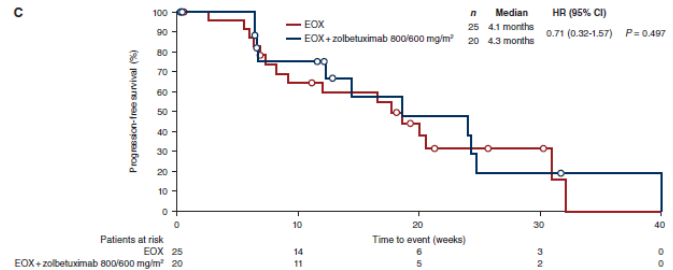
- Randomized Ph II Trial, 1st Line GC
- CLN18.2 positive patients (2+/3+ IHC staining in $\geq 40\%$ of tumor cells)
 - Positive trial (PFS)
 - Subgroup analysis: better PFS in moderate to strong CLDN18.2 expression in $\geq 70\%$ of tumor cells



Overall population



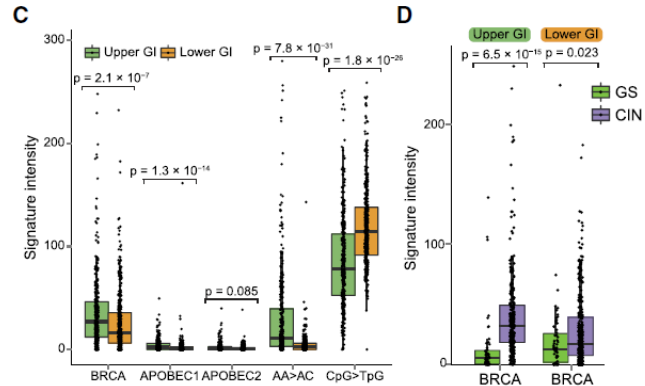
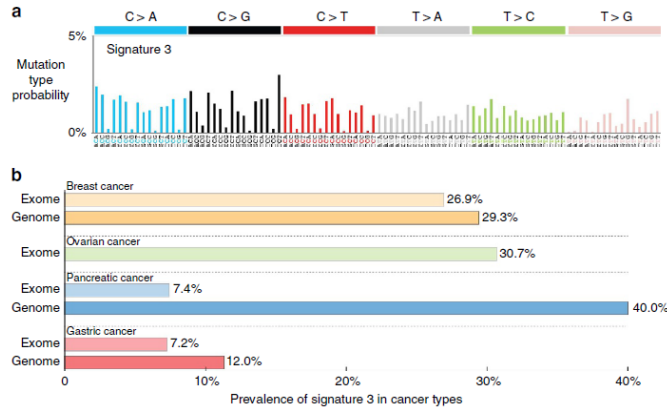
$\geq 70\%$ of tumor cells positive for CLDN18.2



40-69% of tumor cells positive for CLDN18.2

New strategies

DNA damaging agents

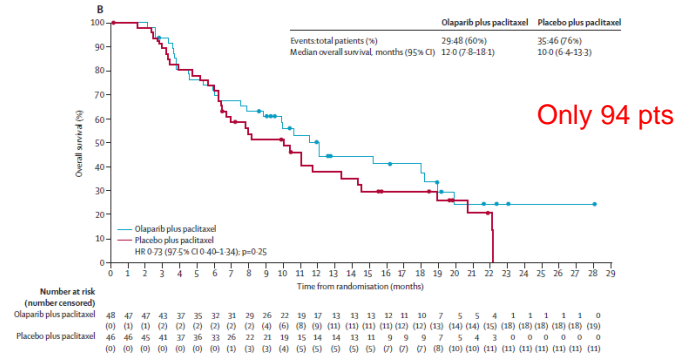
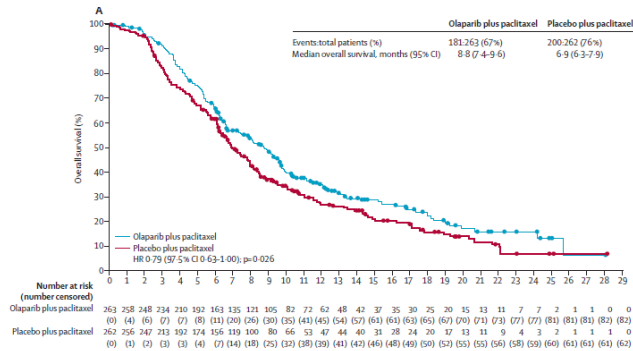


- 7-12% of GC have defective double-strand DNA break repair by homologous recombination and may benefit from either platinum therapy or PARPi

New strategies

DNA damaging agents

- Ph II with Paclitaxel + Olaparib showed improvement of OS in ATM-neg pts
- Ph III GOLD Study (2nd Line)
 - Paclitaxel + Olaparib/Placebo 100 mg BID
 - Co-primary end points: OS in All patients (525 pts) and in ATM-neg patients



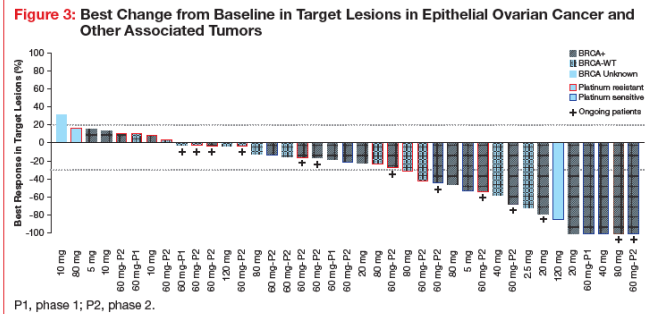
New strategies

DNA damaging agents

- **Pamiparib**: a selective PARP 1/2 inhibitor that crosses the blood-brain barrier

Antitumor Activity of BGB-290 in Epithelial Ovarian Cancer and Other Solid Tumors

- A total of 39 patients were evaluable per RECIST V1.1
 - 23 patients were BRCA-mutation positive (BRCA+), 13 patients had wild-type BRCA (BRCA-WT), and 3 were of unknown BRCA status



Ph III Trial ongoing (NCT03427814)

BeiGene, Ltd., BGB-290-303, A Phase 3, Double-blind, Randomized Study of BGB-290 versus Placebo as Maintenance Therapy in Patients with Inoperable Locally Advanced or Metastatic Gastric Cancer that Responded to Platinum-based First-line Chemotherapy.

Conclusions

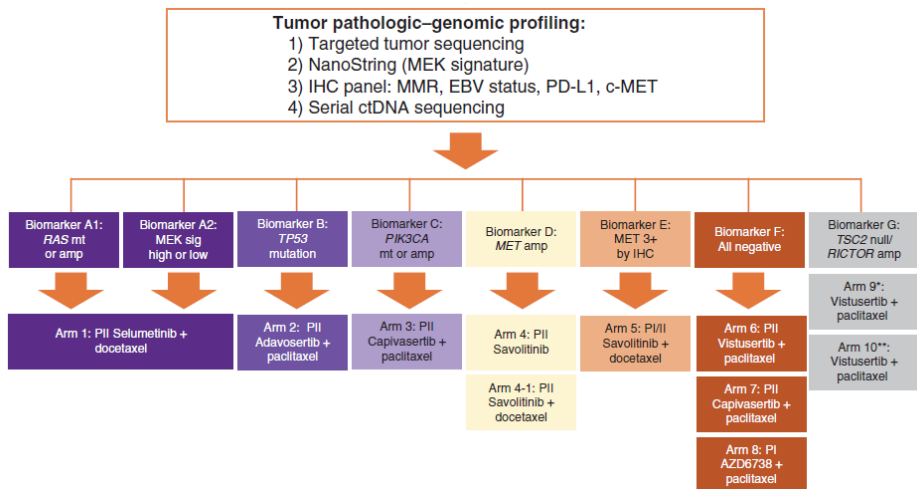
- **HER2** is a well-defined target in mGC with trastuzumab already approved in the 1st line setting, and other drugs/combinations being actively validated
- **FGFR** (FGFR2b) is being revisited as a target in this setting, encouraging data with bemarituzumab.
- **Claudine 18.2** is a validated target in mGC. Zolbetuximab is being evaluated in the high-expressing population.
- **Response to a first line platinum-based therapy** may become a potential biomarker for DNA damaging. Pamiparib is being evaluated in the maintenance setting.

Conclusions

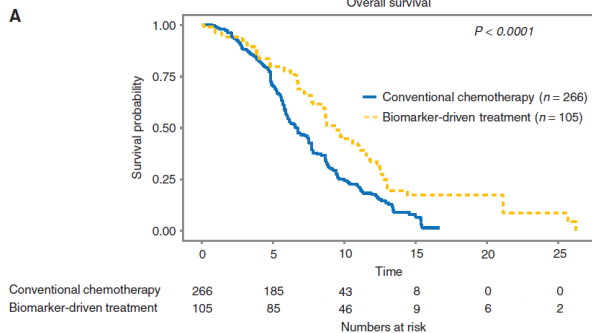
- While the majority of old phase 3 trials failed, due to
 - **Inexistent or poor biomarker selection**
 - High inter-patient heterogeneity: **GC is not a unique entity** (different histology, different molecular subtypes with intrinsic aberrant pathways)
 - High **intra-patient heterogeneity: spatial** (different tumor areas) and **temporal** (acquired resistances to targeted therapies)
- Precision medicine needs **better designed clinical trials** with **better validated biomarkers** and **patient stratification**

The VIKTORY Trial

Targeted therapies based on patient genomic profile



- Umbrella trail
- 2nd line treatment of mGC pts based on eight biomarkers
- Prolonged PFS and OS in pts receiving a biomarker-guided therapy, compared with conventional chemotherapy



The PANGEA Trial

Targeted therapies based on patient genomic profile

- Personalized treatment strategy applied at 1st diagnosis and then serially over up to three ttx lines

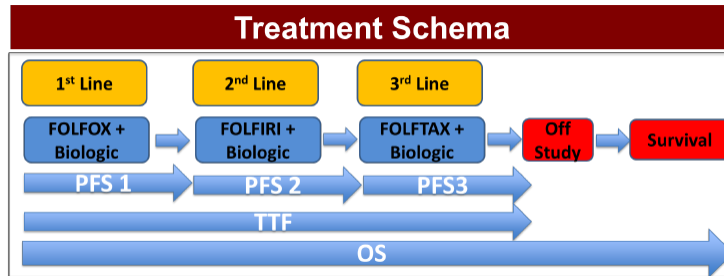


Table 2. Biomarker prioritization and treatment assignment algorithm.

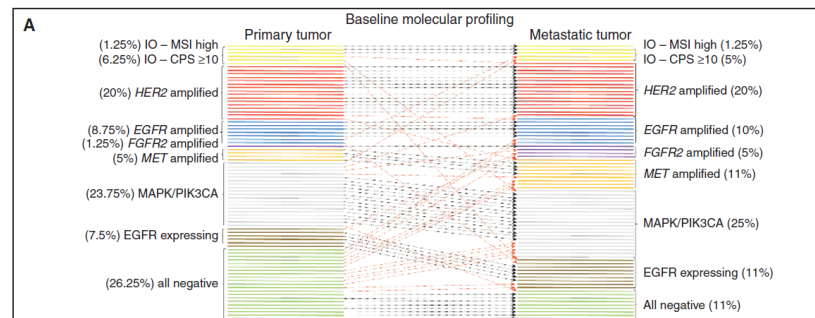
Biomarker Group & Description*	Treatment Arm	Antibody Therapy
1) IO**	Anti-PD-1	nivolumab
2) <i>HER2</i> amplified***	Anti-HER2	trastuzumab
3) <i>EGFR</i> amplified***	Anti-EGFR	ABT-806
4) <i>FGFR2</i> amplified***	Anti-FGFR2	bemarituzumab [^]
5) <i>MET</i> amplified***	Anti-MET	none available ^{^^}
6) MAPK/PIK3CA aberrant	Anti-VEGFR2	ramucirumab
7) EGFR expressing	Anti-EGFR	ABT-806
8) All negative	Anti-VEGFR2	ramucirumab

The PANGEA Trial

Targeted therapies based on patient genomic profile

Spatial and temporal heterogeneity:

- Spatial heterogeneity (primary → metastasis)
 - 28 of 80 (35%) ttx changed
- Temporal heterogeneity (1st line → 2nd line)
 - 27 of 55 (49%) patients
- Temporal heterogeneity (2nd line → 3rd line)
 - 13 of 27 (48%) patients



HER2 Baseline Spatial Heterogeneity

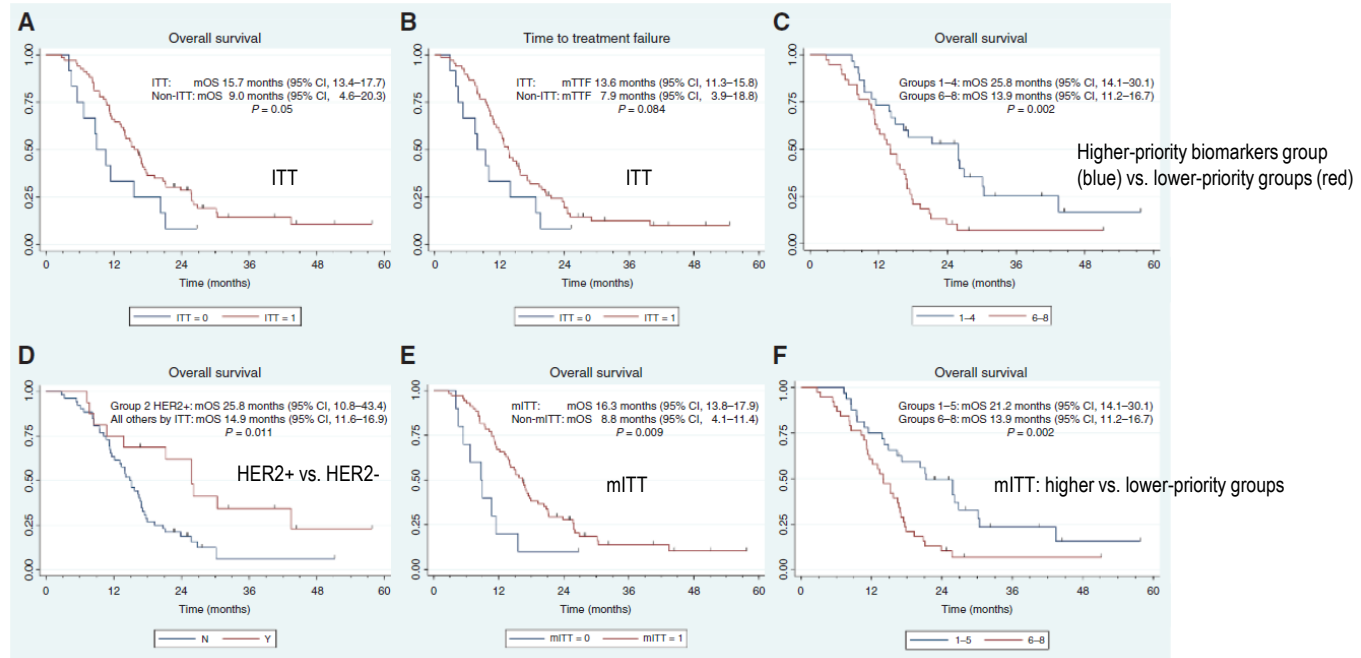
- 2/63 (3.2%) positive only in metastases
- 3/17 (17.6%) positive by primary tumor only

HER2 conversion

- ~45% converted to *HER2* negative over time

The PANGEA Trial

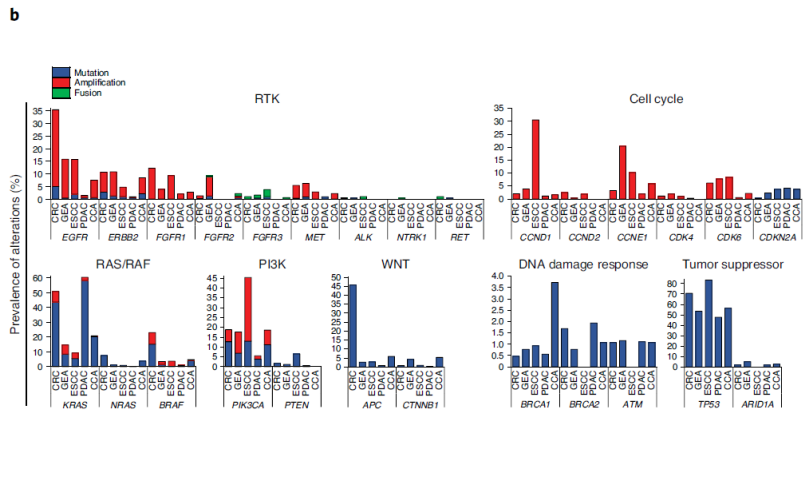
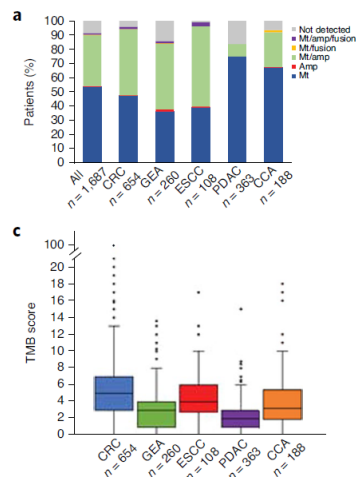
Targeted therapies based on patient genomic profile



SCRUM-Japan GI-SCREEN and GOZILA studies

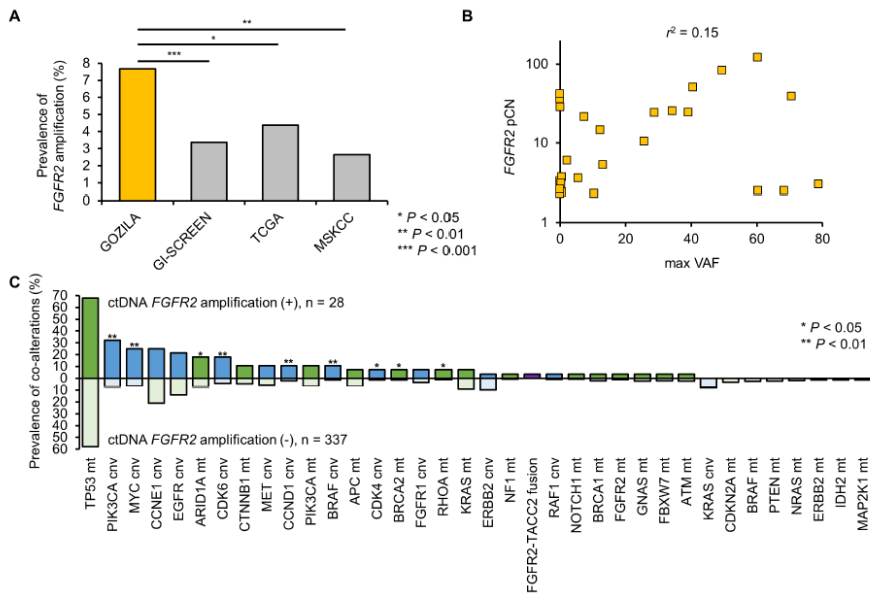
Large-scale sequencing to screen GC patients for trial eligibility

- Feasibility of large-scale sequencing for GC precision medicine
- ctDNA genotyping revealed the presence of rare molecular alterations



SCRUM-Japan GI-SCREEN and GOZILA studies

ctDNA detects *FGFR2* amp and concurrent genomic alterations associated with FGFR inhibitor efficacy



- *FGFR2* amp more freq in ctDNA (7.7%) than in tissue (4.4%)
- *FGFR2* amp associated with worse prognosis
- Two patients with normal *FGFR* in tissue but with amp in ctDNA after PD to 1st line ttx did respond to FGFRi
- One pt with *FGFR2* and *MET* co-amp (ctDNA) with limited benefit from FGFRi
- Large-scale sequencing of ctDNA allows to better understanding of the incidence, prognosis and predictive value of molecular alterations, as well as to identify those patients who can benefit from targeted therapies

Thank you very much!

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