
Molekylær diagnostikk og presisjonsmedisin innen kreft – IMPRESS-Norway

Farmasidagene 2022

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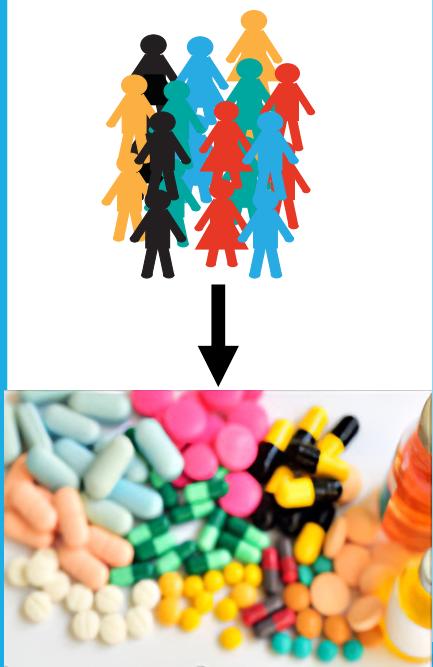
Conflicts of interest

Have participated in advisory boards and meetings arranged by pharmaceutical companies. No personal honorarium, but to institution (ABBVIE, Roche, AstraZeneca, Bayer, Janssen, Pfizer, Takeda, BMS, Merck, Novartis, Sanofi, Eli Lilly)

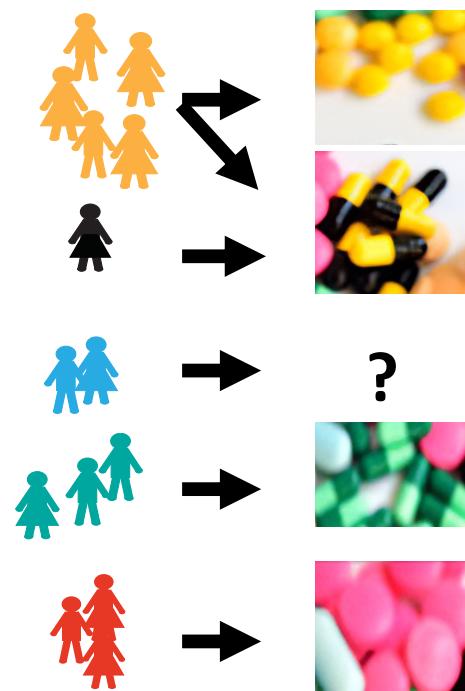
Have received research funding (drug / funds): Roche, AstraZeneca, Novartis, Incyte, Eli Lilly, BMS, Ultimovacs

Kreftbehandling – store endringer siste tiden

One size fits all



Precision Medicine



Requirements:

Sufficient molecular diagnostics available

Knowledge on new drugs and mechanisms

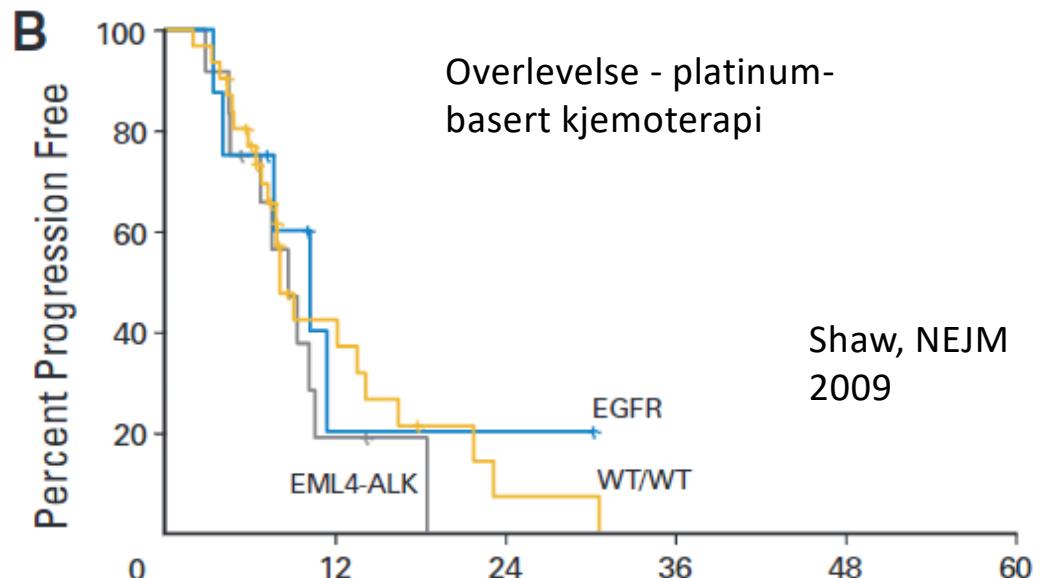
Available drugs



«The genes, not only the tissue, will steer the treatment»
Dr John Mendelsohn,
Past President, MDACC,
Texas

ALK-positiv sykdom

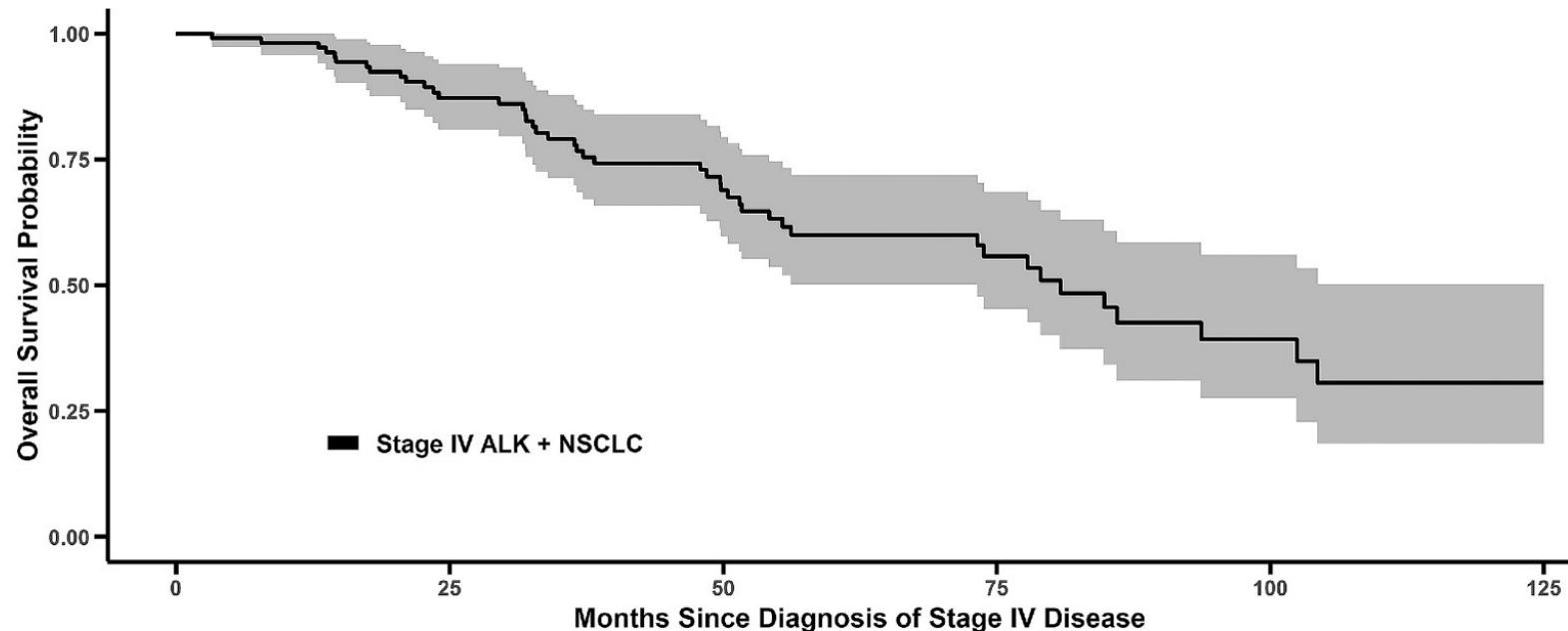
2-5% av pasientene med NSCLC



Cancer in Norway 2016

Table 8.1: Five-year relative survival by primary site, stage and period of diagnosis, 1977–2016, **males**

ICD-10	Site	Stage	Relative survival (%)							
			1977–81	1982–86	1987–91	1992–96	1997–01	2002–06	2007–11	2012–16*
C33-34	Lung, trachea	Total	6.1	7.5	7.3	8.1	8.9	10.3	13.0	16.0
		Localised	13.8	17.4	16.1	22.5	33.7	41.1	44.6	53.3
		Regional	5.9	8.0	9.4	8.4	9.3	11.8	15.4	19.4
		Distant	0.7	0.5	0.8	0.5	0.7	1.1	1.9	1.8



Number at risk

■ 110 80 50 25 10 1



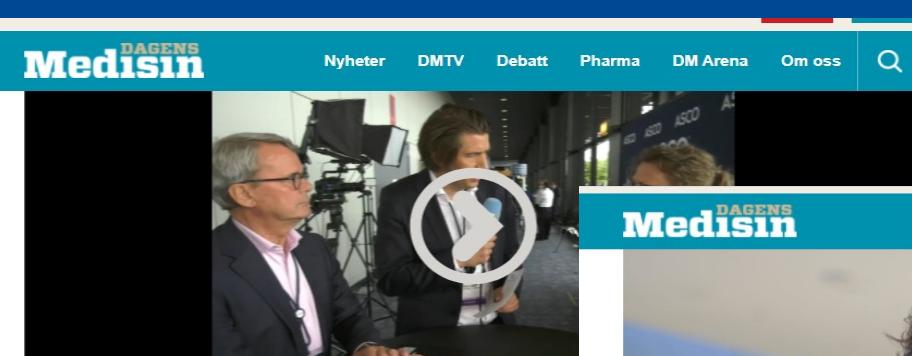
Pacheco et al, *Journal of Thoracic Oncology* 2019 14, 691-700 DOI: (10.1016/j.jtho.2018.12.014)

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Overlevelse stadium IV
ALK-positiv lungekreft:
**Median Overlevelse
(OS) 81 måneder (6.8 år)**

Hjernemetastaser på
diagnosetidspunkt
påvirket ikke
overlevelsen signifikant

Nasjonal enighet om behov for bedret molekylærdiagnostikk



– Vi er nødt til å vurdere pasientene med gensekvensering

Melanom, lungekrest og ASCO-oppsummering er temaer for denne sesjonen.

Lasse Moe
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Publisert: 2019-06-03 — 23.34

HASTER: – Det blir stadig nye tumor-agnostiske markører, som kan utnyttes i behandling. Vi trenger et raskt system for NGS (gensekvensering), sier overlege Christian Kersten ved Sørlandet Sykehus. Her avbildet under ESMO 2018, i München. Foto: Lasse Moe

Overlegen Per Eystein Lønning (t.v.) og Hans Petter Eikesdal mener norske myndigheter er for mye i tiden med gensekvensering

– I dag må jeg stadig oftere si til pasientene at jeg ikke kan tilby den beste utredningen, rett og slett fordi vi ikke tar de nødvendige testene, sier overlege Christian Kersten ved Sørlandet Sykehus.

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Kritisk til treg innføring av gentesting

– I dag må jeg stadig oftere si til pasientene at jeg ikke kan tilby den beste utredningen, rett og slett fordi vi ikke tar de nødvendige testene, sier overlege Christian Kersten ved Sørlandet Sykehus.

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Strategisk arbeid mot en nasjonal klinisk studie



Bottom up:

- White paper for Norwegian concept, National PI (Åslaug Helland)
- Buy-in from oncology, haematology, pathology environments in all Norwegian health regions -> National approach



Top down:

- Dialogue with health authorities (regional health care systems, ministry)
- Engaging key national stakeholders: NoMa, NIPH, HDIR, Cancer Registry, Cancer Society



International: Joined DRUP network and building Nordic Task Force



Public-private: Dialogue with industry partners: trial participation and consortium formation for public-private partnership



Parallel development of diagnostic platforms (InPreD), PCM PPP (CONNECT) and research on RWE & controls, health economy & HTA, ethics, legal & org. of PCM (INSIGHT)

DRUP, drug discovery protocol; HDIR, Directorate of Health; HTA, health technology assessment; NIPH, Norwegian Institute of Public Health; NoMa, Norwegian Medicines Agency; PCM, precision cancer medicine; PI, principal investigator; PPP, public-private partnerships; RWE, real-world evidence.

Molekylærpatologi i Norge

De fleste patologiavdelinger utfører molekylære analyser
(n=17)

- Enkeltmarkør analyser

10 av 17 avdelinger har tatt i bruk « neste generasjons sekvensering », NGS:

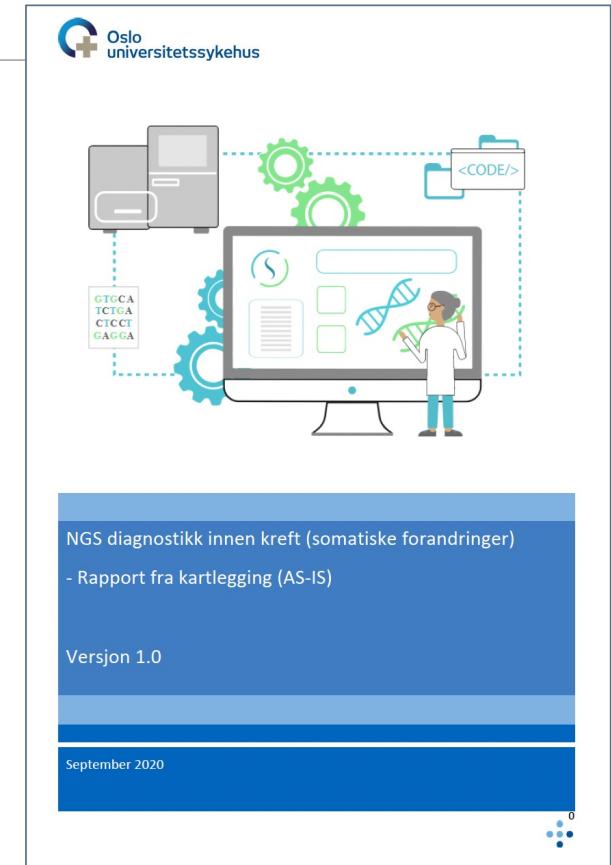
- Kan analysere mange gener samtidig for samme prøve
- Kan ha samme analyse på tvers av tumortyper

Teknologi: to ulike teknologier benyttes:

- Illumina (store sykehus) & Thermo Fisher (IonTorrent)

Genpaneler: ulike størrelser

- Små paneler (50-100 gener), mellomstore (100-400 gener), store (mer enn 400 gener)



Kartlegging utført av NGS undernettverkt i Nasjonalt kompetansenettverk for personilpasset medisin – presisjonsmedisin 2020

NGS: store versus små genpaneler

Små genpanel:

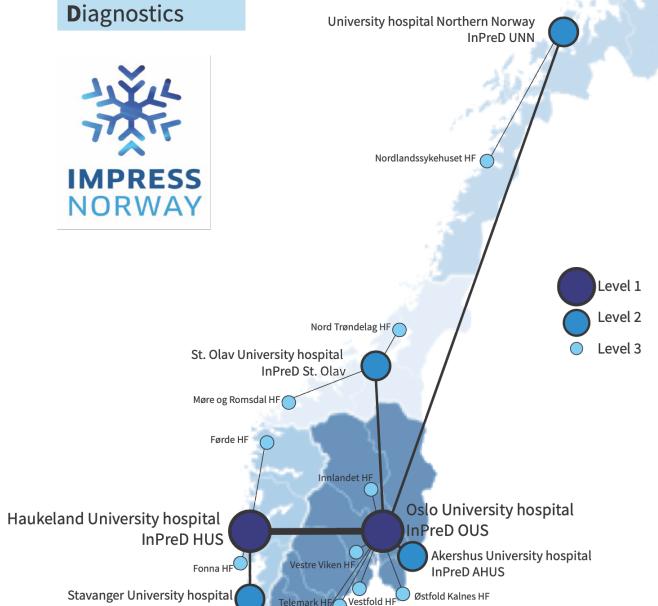
- Kan ikke identifisere «profiler», eks. Tumor mutasjons byrde (TMB) eller genomisk ustabilitet (GI)
- Egnet for gener som man undersøker ofte for og i mange krefttyper
- Raskere og mer automatisert (sekvenseringen)
- Krever mindre kompetanse da det er «kjente» forandringer man leter etter
- Mindre krav til tilpasset IT struktur

Store genpanel:

- Trengs for å identifisere «profiler», eks. Tumor mutasjons byrde (TMB) eller genomisk ustabilitet (GI)
- Viktig for å finne lavfrekvente varianter
- Kostbare og tar tid (sekvenseringen)
- Krever kompetanse (bioinformatikk, molekylærbiologi, patologi og onkologi)
- Krever tilpasset IT struktur

Utvikling innen molekylærpatologi – del av tjenesten

InPreD - Norway
Infrastructure for
Precision
Diagnostics



The six pathology departments at the university hospitals as core of InPreD-Norway

- Network for NGS accessible for all pathology departments being established
- Patient recruitment to biomarker driven clinical trials is available for all hospitals

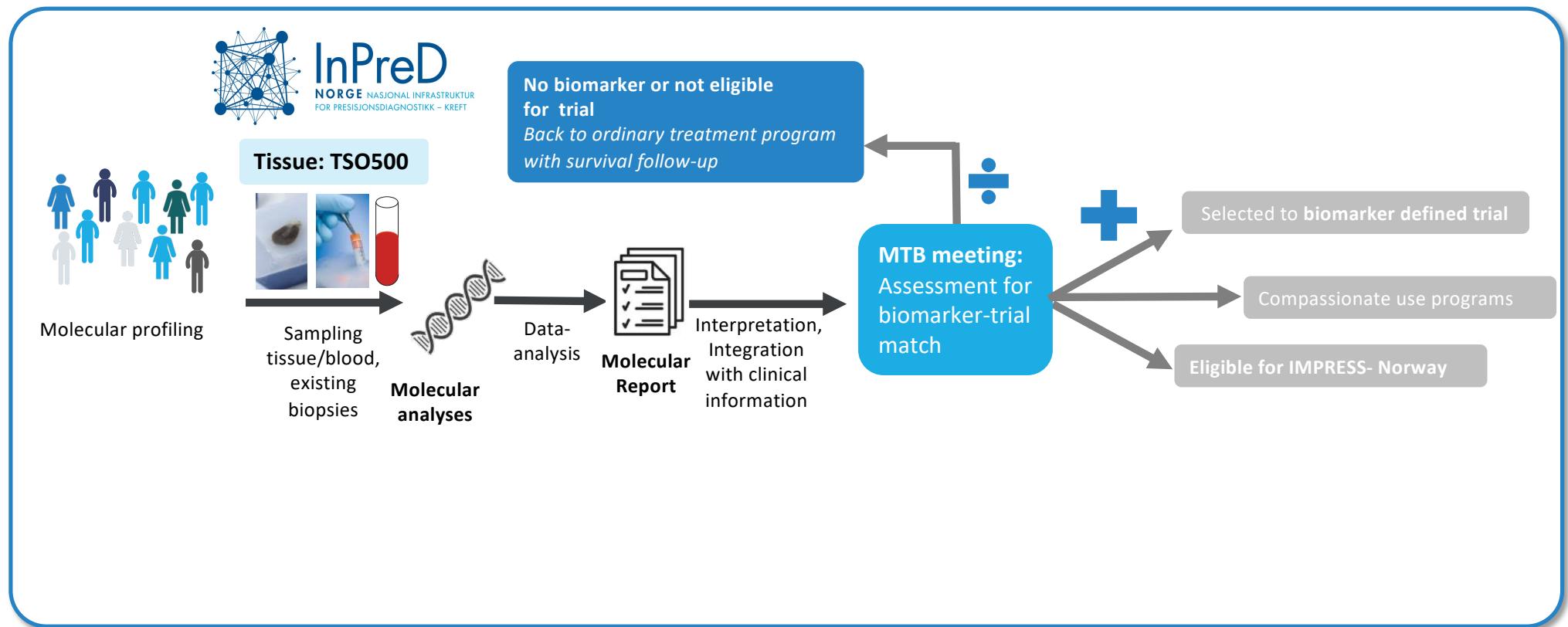
Funding:

- 100 MNOK ++ from regional health authorities
- Large gene panel reimbursed

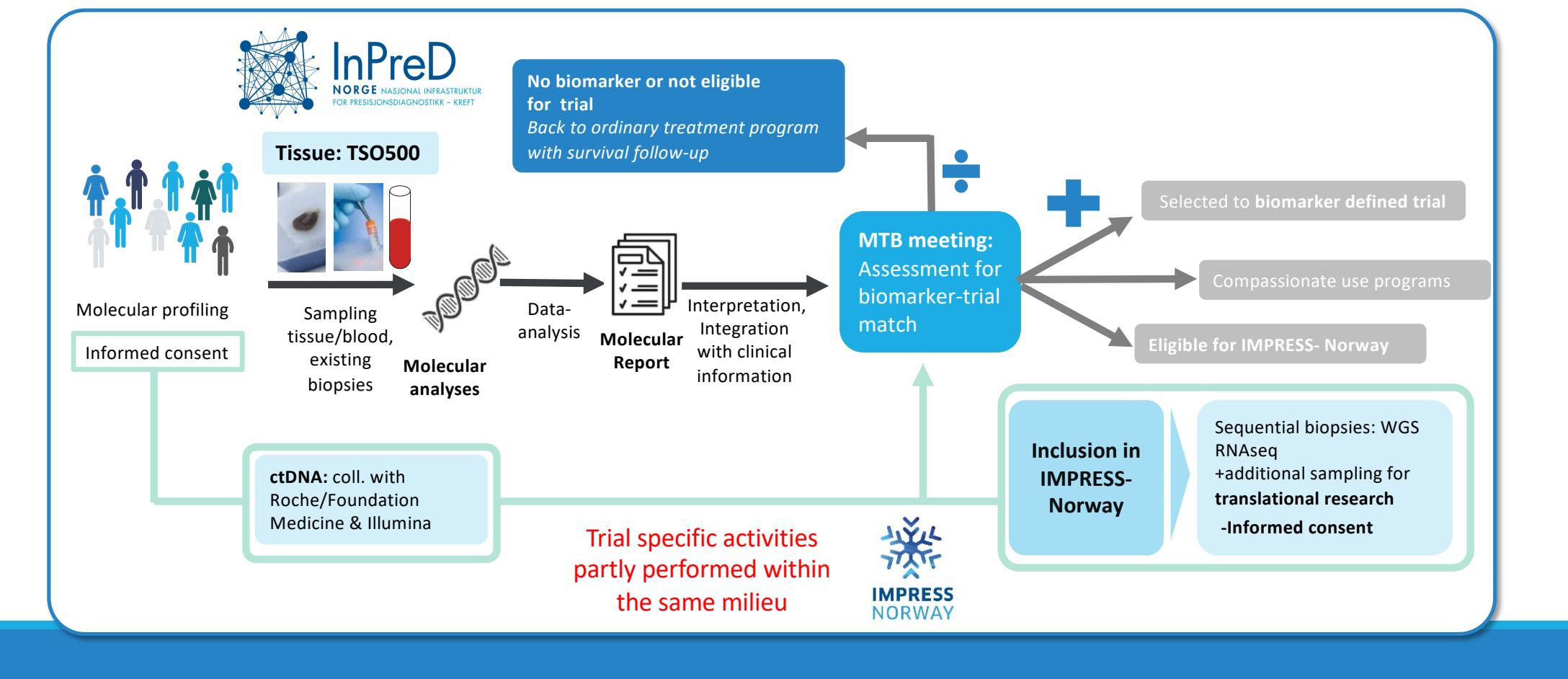
Aim: Equal access to expanded molecular testing – and experimental treatment for cancer patients



InPreD: Diagnosis and assessment for cancer patients where experimental treatment and clinical trial inclusion is an option



InPreD: Diagnosis and assessment for cancer patients where experimental treatment and clinical trial inclusion is an option



XX
DECMTB
OUS

IPD00xx Ovarial cancer

TS0500

DNA
RNAXX
NOVMTB
Report

Pipeline: 2.0.0.70/ 0.8.4/GRCh37/Tumor only

F/43y

Patient

Ovarian cancer

Y of D: 20xx

Tumor type

Metastasis

FF
Sample type

~30%

Tumor content

IPD0011-D01/R03/M01-F03

SUMMARY OF KEY FINDINGS

TMB		MSI	Stable
SNVs/ indels	Total nr of SNVs/indels in protein coding sequence: alter protein coding sequence 20 14 8	Copy number variants (>4, loss)	No reportable CNVs Gene fusions RNA None reported by pipeline

Biomarkers potentially
relevant for immune therapy

High TMB

Gene	Variant	Type	VAF
BRCA2	Q3047X	stop_gained	0.32
BRAF	E695Q	missense	0.26
CYLD	V500M	missense	0.31
XPO1	S387C	missense	0.31
MTOR	E1336K	missense	0.27
STAT3	E272K	missense	0.25
ESR1	Q226X	stop_gained	0.38

In COSMIC- hotspot

In COSMIC

Novel

In COSMIC and GL_DB

Additional results: Variants of unknown significance (VUS) in treatment relevant genes					
Gene	Variant	Functional Domain	Comments		
BRAF	Glu695Gln	Kinase domain	The sensitivity to BRAFi of this variant is unknown. V600 BRAF mutated tumors can be targeted by BRAF inhibitors..		
FGFR2	Glu1336Lys	none	The variant is of unknown functional consequence. Sensitivity to mTOR inhibitors is unknown.		
MTOR	Glu1336Lys	none	The variant is of unknown functional consequence. Sensitivity to mTOR inhibitors is unknown.		

Content courtesy of, and based on personal experience and observations of, Prof Kjetil Taskén.

Små pasientgrupper – samarbeid nødvendig for å lære mest mulig



Expanded use of existing anticancer drugs

ProTarget

A Danish Nationwide Clinical Trial
on Targeted Anti-Cancer Treatment
based on Molecular Profiling

FINPROVE

DRUG REDISCOVERY
PROGRAM IN FINLAND



Canadian Profiling and Targeted Agent
Utilization Trial (CAPTUR)



The Drup-trial

LETTER

<https://doi.org/10.1038/s41586-019-1600-x>

The Drug Rediscovery protocol facilitates the expanded use of existing anticancer drugs

D. L. van der Velden^{1,2,21}, L. R. Hoes^{1,2,3,21}, H. van der Wijngaart^{2,3,4,21}, J. M. van Berge Henegouwen^{2,3,5,21}, E. van Werkhoven⁶, P. Roepman⁷, R. L. Schilsky⁸, W. W. J. de Leng⁹, A. D. R. Huittema^{10,11}, B. Nuijen¹¹, P. M. Nederlof¹², C. M. L. van Herpen¹³, D. J. A. de Groot¹⁴, L. A. Devriese¹⁵, A. Hoeben¹⁶, M. J. A. de Jonge¹⁷, M. Chalabi^{1,18}, E. F. Smit^{2,19}, A. J. de Langen¹⁹, N. Mehra¹³, M. Labots⁴, E. Kapiteijn⁵, S. Sleijfer^{2,17}, E. Cuppen^{3,7,20}, H. M. W. Verheul^{4,13}, H. Gelderblom⁵ & E. E. Voest^{1,2,3*}

The large-scale genetic profiling of tumours can identify potentially actionable molecular variants for which approved anticancer drugs are available^{1–3}. However, when patients with such variants are treated with drugs outside of their approved label, successes and failures of targeted therapy are not systematically collected or shared. We therefore initiated the Drug Rediscovery protocol, an adaptive, precision-oncology trial that aims to identify signals of activity in cohorts of patients, with defined tumour types and molecular variants, who are being treated with anticancer drugs outside of their approved label. To be eligible for the trial, patients have to have exhausted or declined standard therapies, and have malignancies with potentially actionable variants for which no approved anticancer drugs are available. Here we show an overall rate of clinical benefit—defined as complete or partial response, or as stable disease beyond 16 weeks—of 34% in 215 treated patients, comprising 136 patients who received targeted therapies and 79 patients who received immunotherapy. The overall median duration of clinical benefit was 9 months (95% confidence interval of 8–11 months), including 26 patients who were experiencing ongoing clinical benefit at data cut-off. The potential of the Drug Rediscovery protocol is illustrated by the identification of a successful cohort of patients with microsatellite instable tumours who received nivolumab (clinical benefit rate of 63%), and a cohort of patients with colorectal cancer with relatively low mutational load who experienced only limited clinical benefit from immunotherapy. The Drug Rediscovery protocol facilitates the defined use of approved drugs beyond their labels in rare subgroups of cancer, identifies early signals of activity in these subgroups, accelerates the clinical translation of new insights into the use of anticancer drugs outside of their approved label, and creates a publicly available repository of knowledge for future decision-making.

is taken into consideration. However, with regards to drug sensitivity, the importance of a given genetic or molecular variant is usually tested in the subtype of cancer that most frequently contains this variant. The importance of the same variant in other cancers often remains unknown. Third, as drug development is challenging for rare subtypes of cancer, this can create inequality in care¹². Finally, with growing pressure from society to increase the success rate of drug-development trials¹³, there is hesitation amongst payers to reimburse large-scale sequencing efforts before they have proof that these efforts will make healthcare more sustainable. As a result, we are not using the full potential of rapidly expanding technological advances, knowledge of biomarkers and the spectrum of approved anticancer drugs for our patients.

The Center for Personalized Cancer Treatment was founded in 2010¹⁴ to address these issues. In this network (which now connects 45 hospitals in the Netherlands), patients with all types of metastatic cancer are offered the opportunity to undergo a fresh tumour biopsy for whole-genome sequencing (WGS) before starting systemic anticancer treatment. The WGS results are combined with treatment outcomes in a national, centralized database for research purposes, and returned to the physician who is treating the patient for future planning of treatment. This initiative has contributed to the identification of potentially actionable variants in cancers that are not routinely tested for these variants. To provide treatment opportunities for patients in whom such variants were identified (while simultaneously collecting clinical outcomes), we began the Drug Rediscovery protocol (DRUP), in which we seek to expand the use of targeted therapies that have been approved by the European Medicines Agency (EMA) and/or US Food and Drug Administration (FDA) beyond the approved indications of these therapies.

The DRUP is an ongoing, prospective multi-drug and pan-cancer

High inclusion rate (46%)

High level of clinical benefit (34%)

IMPRESS-Norway:

Improving public cancer care by implementing precision medicine in Norway



Study-design: combined umbrella-basket, Simon two-stage model

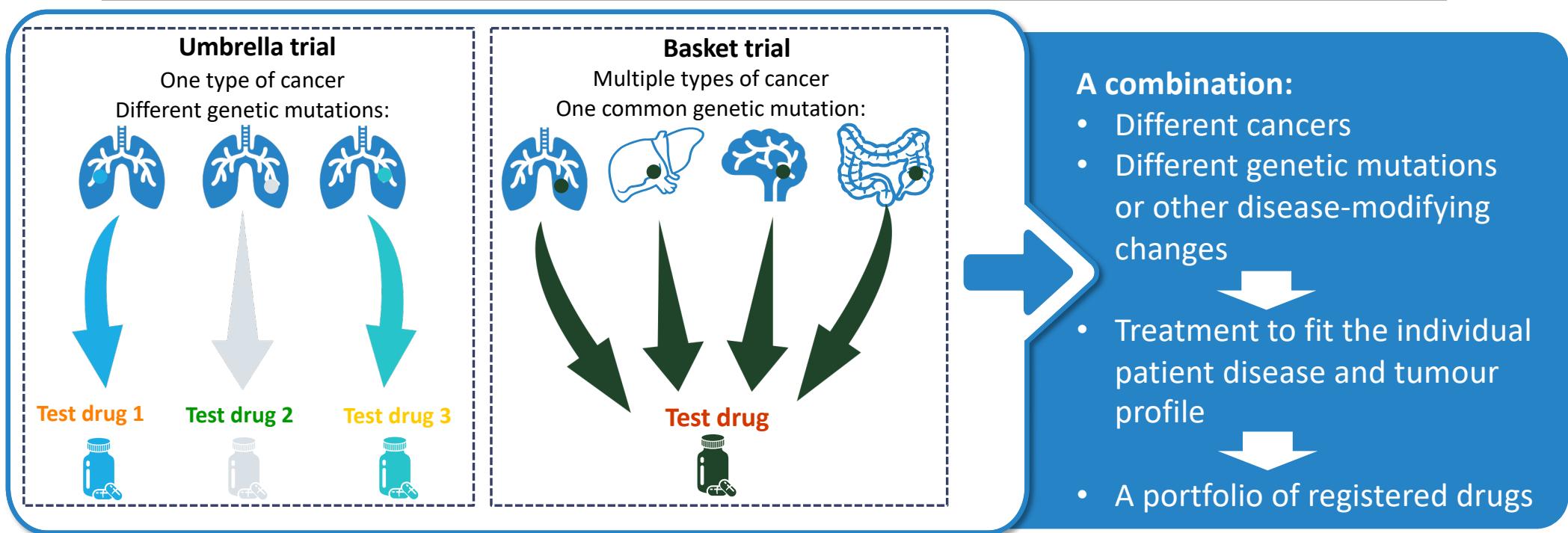
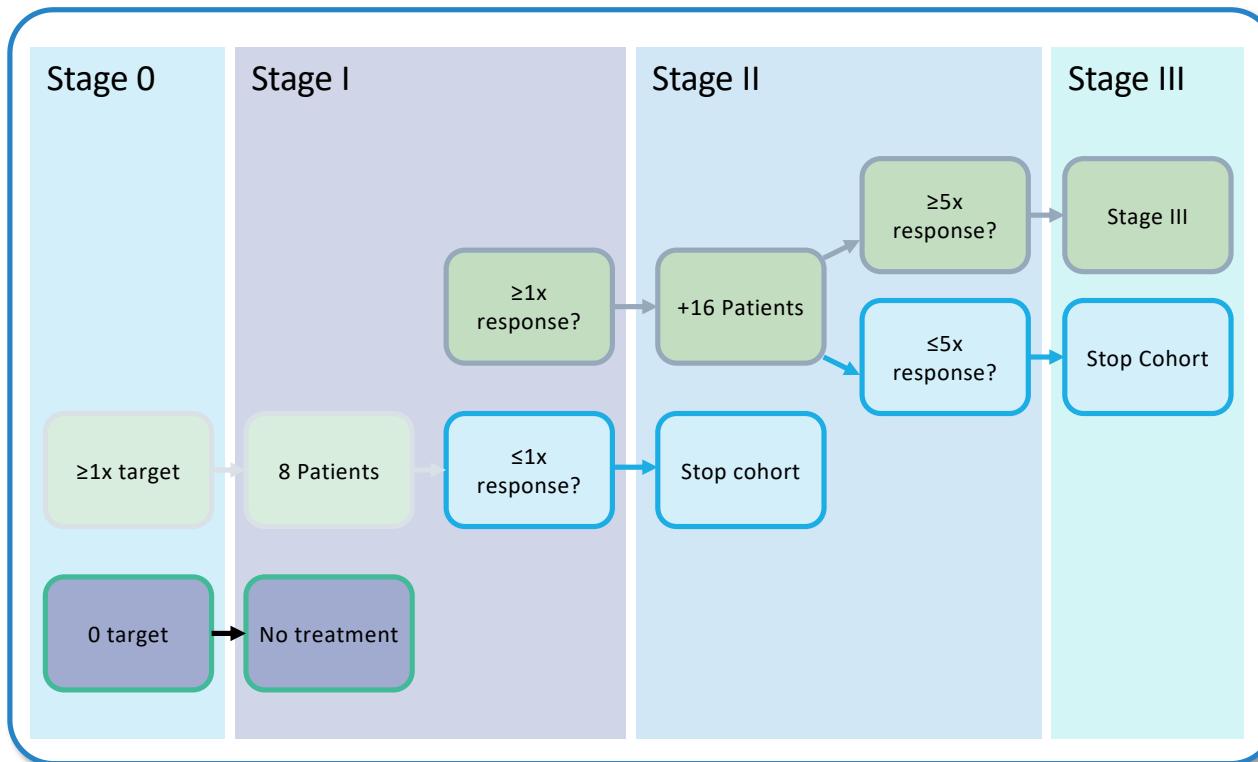


Figure adapted from: West HJ. *JAMA Oncology* 2017; **3**:423.

Study-design: combined umbrella-basket, Simon two-stage model



Eligible patients with identified actionable targets with matching drug from the study drug portfolio will be included in an IMPRESS-Norway cohort

A cohort will consist of patients with the same indication and same actionable target.

Stage 3 - ekspansjonskohort

- Aktuelt når ≥ 5 av 24 pasienter i en kohort har nytte av behandlingen etter 16 ukerts behandling
 - Da har man data på effekt, median/gjennomsnittlig varighet av behandlingen
 - Legemiddelet har en kjent pris / er allerede godkjent
 - Legemiddelet har kjent bivirkningsprofil
 - Frekvensen / forventet antall pasienter er kjent
-
- Firma betaler behandling i 16 uker (+50000 per pasient til sykehuset som behandler),
 - Det offentlige overtar finansieringen av legemiddelet etter 16 uker
 - Nylig vedtak på Olaparib / biallelisk inaktivert BRCA1/2

Unntak på gruppenivå for olaparib som monoterapi til behandling av pasienter med biallelisk BRCA1/2-mutasjoner (inaktivering) for pasienter som er deltakere i IMPRESS-Norway

Fagdirektørene i de regionale helseforetakene besluttet 14. februar 2022 å gi unntak på gruppenivå for olaparib som monoterapi til behandling av pasienter med metastatisk kreft og biallelisk BRCA1/2-mutasjoner (inaktivering) som har progrediert på standard behandling, og som er deltakere i IMPRESS-Norway.

Behandlingen er aktuell ved alle kreftformer med unntak for pasientgrupper der olaparib allerede har markedsføringstillatelse.

Pasientene skal følges opp i en særskilt behandlingskohort i den nasjonale studien IMPRESS-Norway, for å fremskaffe dokumentasjon om effektene av slik behandling.

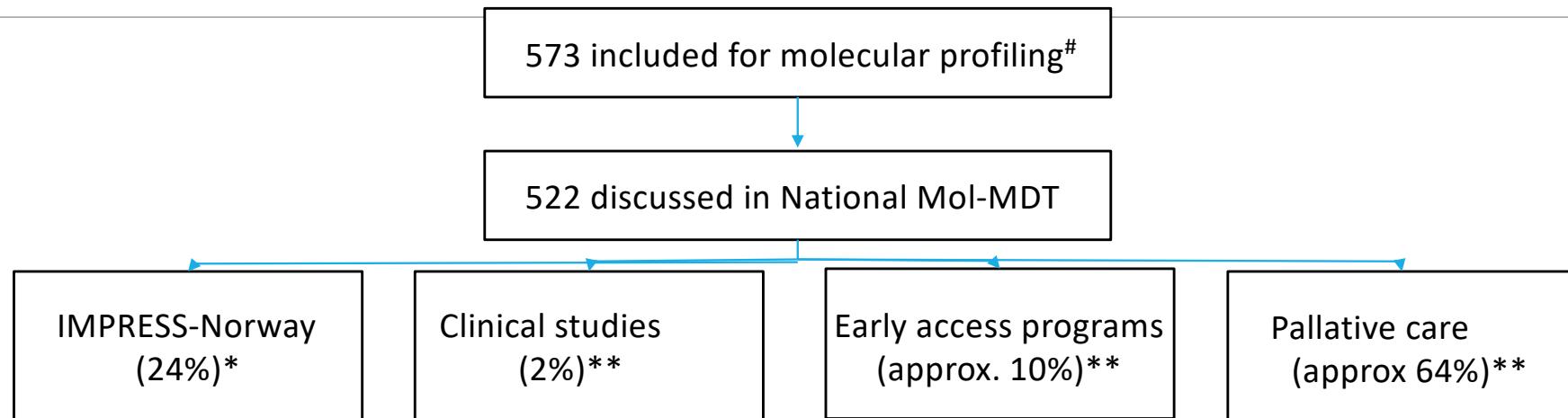
IMPRESS-Norway



- Aktuelt for pasienter med avansert kreftsykdom etter standard behandling
- Aktuelle pasienter screenes med utvidet genpanel – pt TSO500 + ctDNA analyser
- En hovedprotokoll og medikamentspesifikke manualer
- Resultater diskutes i nasjonalt molekylært MDT-møte
- Hvis funn indikerer inklusjon i annen klinisk studie eller IMPRESS-Norway kohort -> henvisning til studieinklusjon
- Farmaceutisk / diagnostisk industri deltar med legemiddel / diagnostikk
- Alle medikamenter er godkjent av EMA / FDA – brukes utenfor indikasjon
- Biobanking (WGS, RNAseq), livskvalitetsmålinger
- Standard responsevaluering(RECIST osv) og monitorering – GCP
- Kopling til helseregister - helseøkonomianalyser

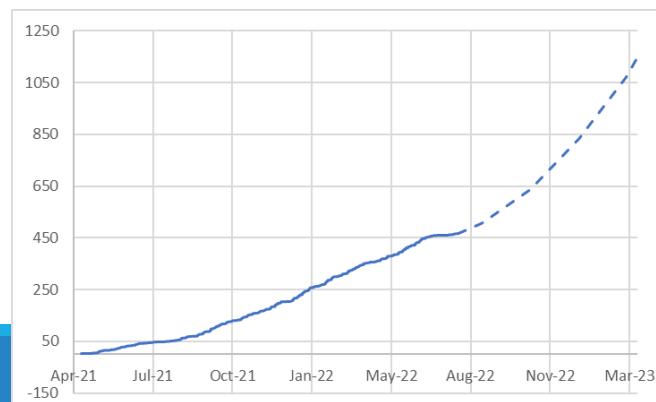
Infrastructure for precision diagnostics

01.04.2021 – 12.10.2022



* 127 patients included in a cohort of 522 discussed in National Mol-MDT

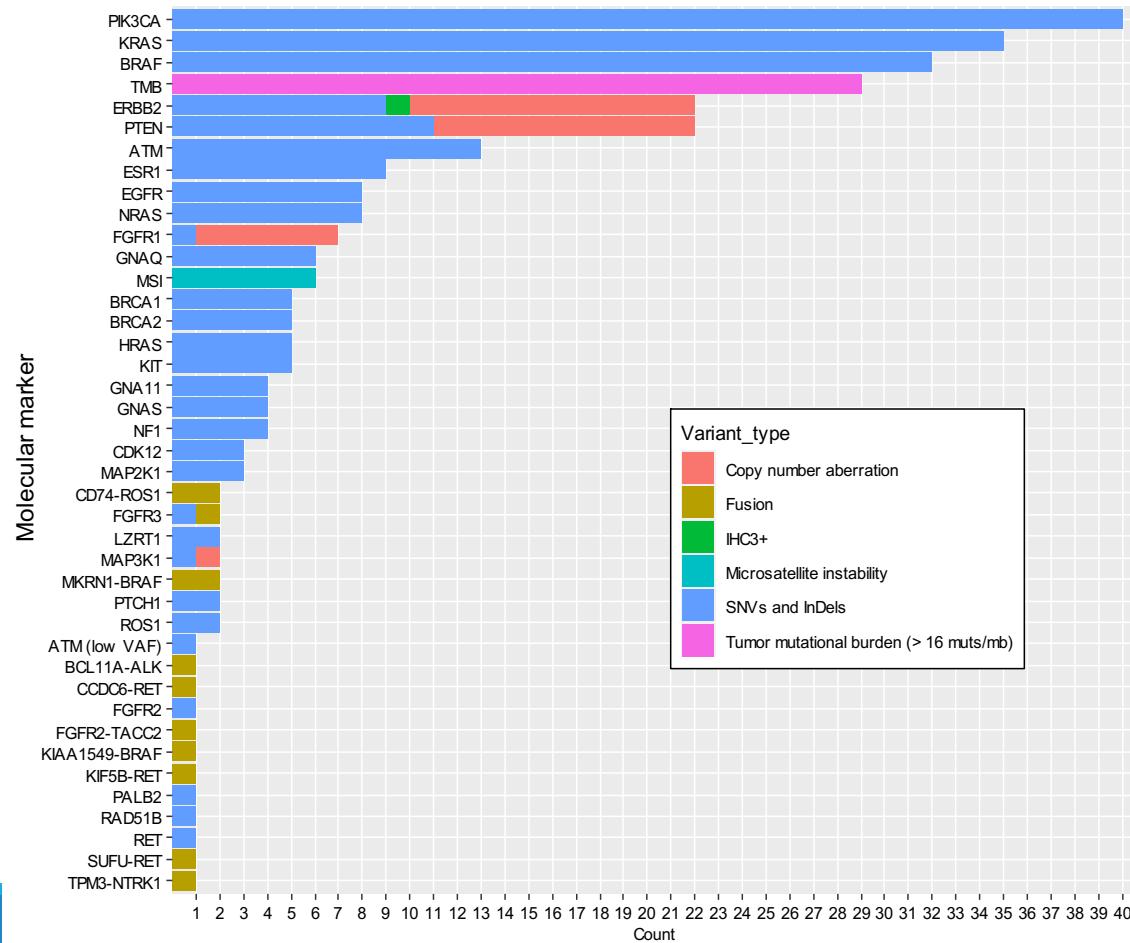
** lag time for screening before inclusion into clinical trials and early access program giving uncertain no. of actual included.



Graph: No. Of patients included for molecular profiling as function of time. Solid line are patients included to date and stippled lined is expected no. of patient included. Capacity increase mainly due to opening of new site (HUS) and planned automation.

Molecular biomarkers identified during screening phase

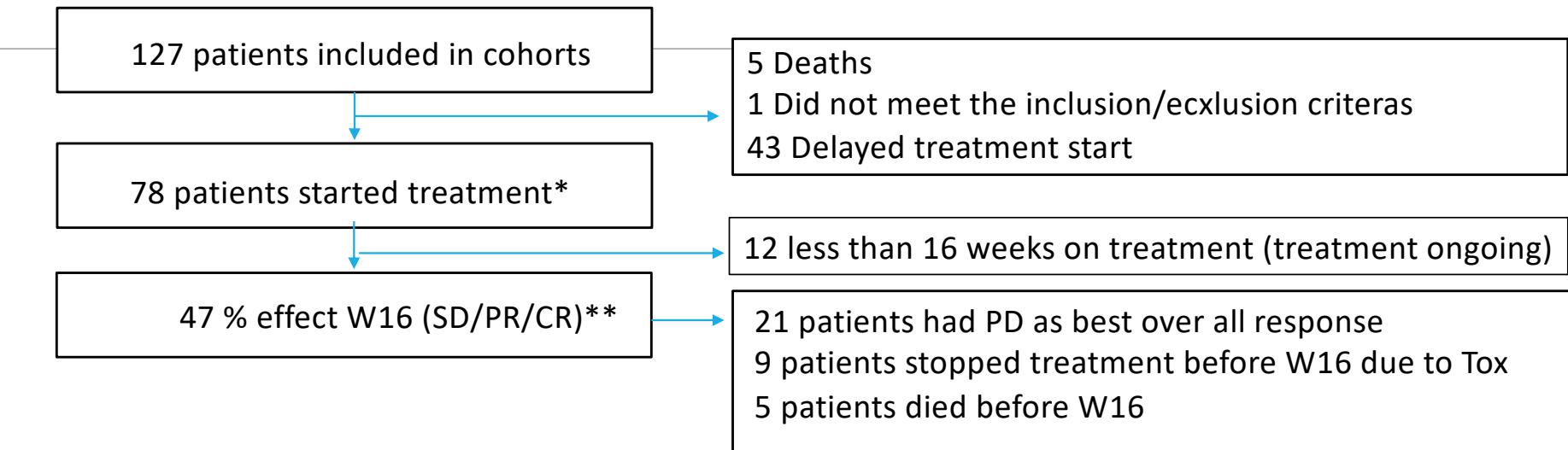
Biomarkers in IMPRESS-OUS patients (n = 328)



Alterations in PI3K/AKT/ mTOR and RAS/MAPK pathways, changes in ERBB2, FGFR, HRR genes and high tumor mutational burden (TMB) are the most commonly detected biomarkers.

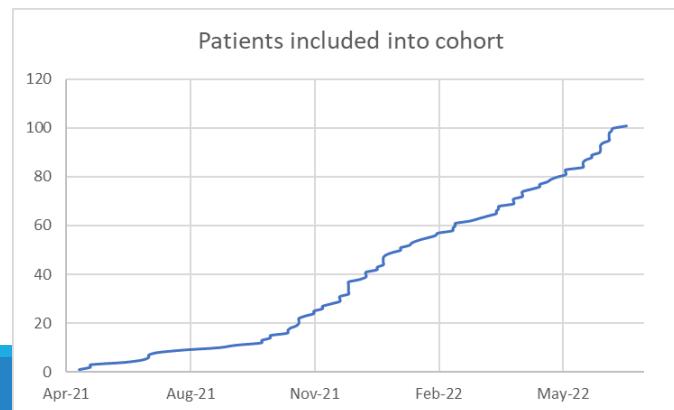
IMPRESS-Norway - oppdatering

01.04.2021 – 12.10.2022

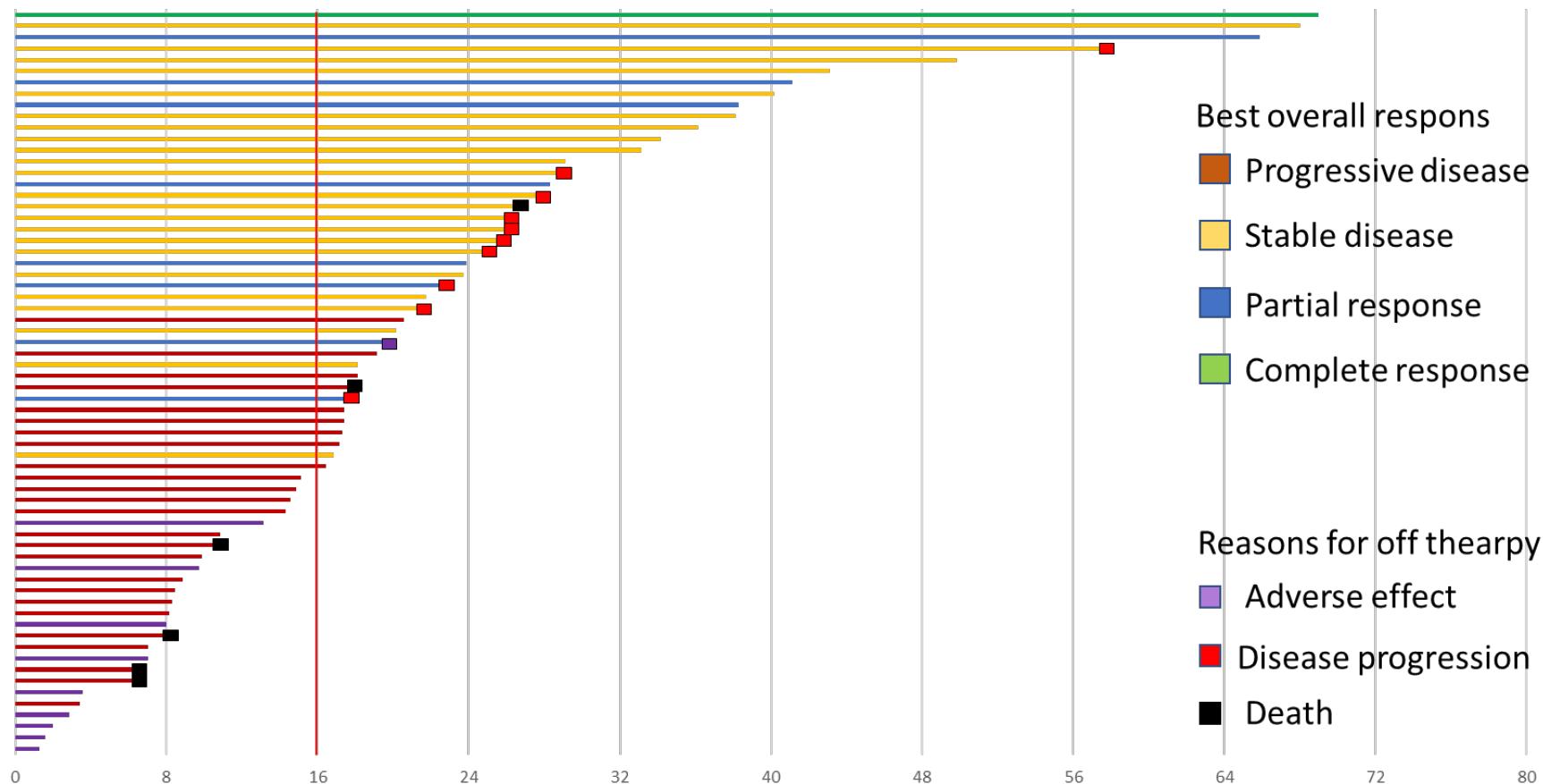


* Lag time between included into cohort and start treatment mainly due to still effect of last line of treatment.

** 31/66 patients clinical effect at W16



Graph: No. of patients included into cohort as function of time. The inclusion rate is mainly effected by capacity for molecular profiling and access to drugs. Increase end 2021 due to inclusion of Novartis drugs.

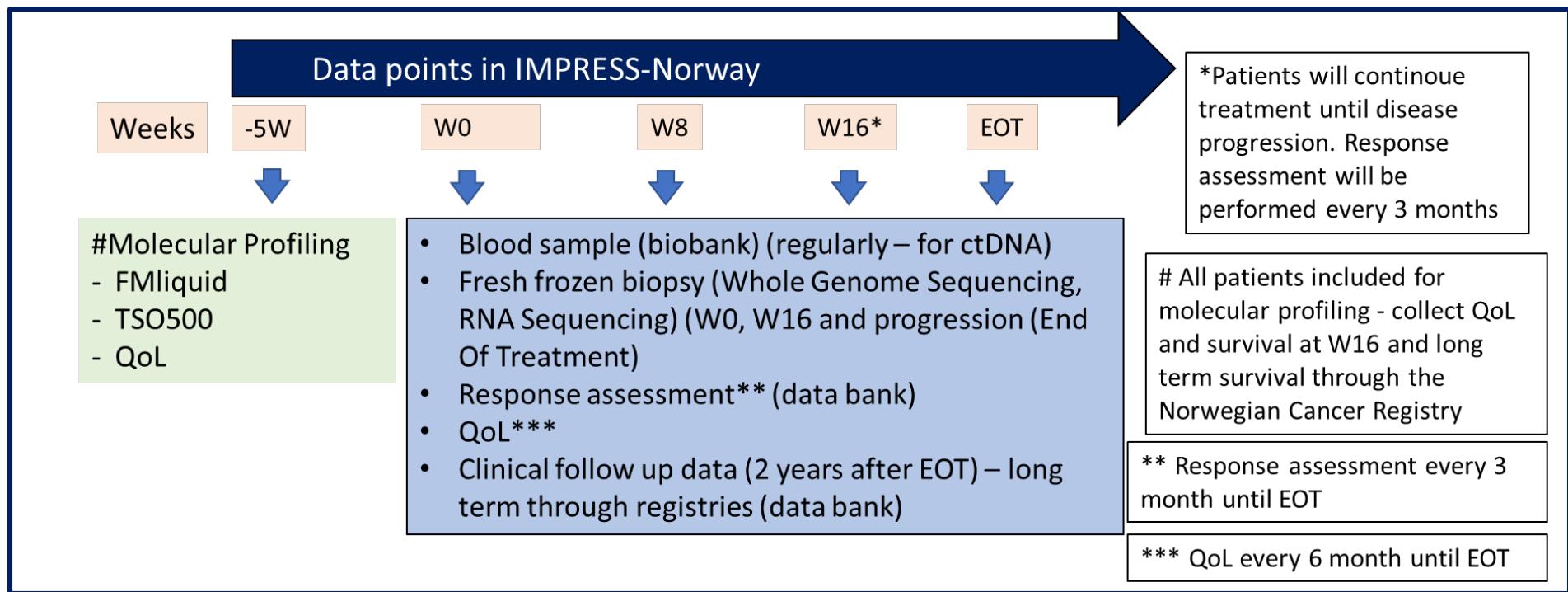


66 patients evaluated at W16. 5 patients died before W16, 9 patients stopped treatment before W16 due to toxicity and 21 patients had progressive disease as best overall response. 31/66 patients had effect according to protocol at W16. 1 patients had complete response at W16, 8 patients had partial response at W16 and 22 patients had stable disease at W16.

Medikamenter

	Drug	Company	Status
1	Alecensa	Roche	Included
2	Phesgo (Pertuzumab and Trastuzumab)	Roche	Included
3	Tecentriq (Atezolizumab)	Roche	Included
4	Avastin (Bevacizumab)	Roche	Included
5	Cotellic (Cobimetinib)	Roche	Included
6	Zelboraf (Vemurafenib)	Roche	Included
7	Erivegde (Vismodegib)	Roche	Included
8	Rozlytrek (Entrectinib)	Roche	Included
9			
10	Tafinlar (dabrafenib)	Novartis	Included
11	Mekinist (trametinib)	Novartis	Included
12	Piqray (alpelisib)	Novartis	Included
13	Tabrecta (capmatinib)	Novartis	Exp. 1 November 2022
14			
15			
16	Lynparza (olaparib)	Astra Zeneca	Included
17			
18	Retsevmo (selpercatinib)	Eli Lilly	Exp. 1. January 2023
19	Pemazyre (Pemigatinib)	Incyte	Exp. 1. Nov 2022
20	Melfalan	Generisk	Included
21	Imatinib	Generisk	Included
22	Bortezomib (KLL)	Generisk	
23	Actinomycin D og hydroxyurea (AML)	Generisk	

Extensive collection of data



A national precision cancer medicine implementation initiative for Norway

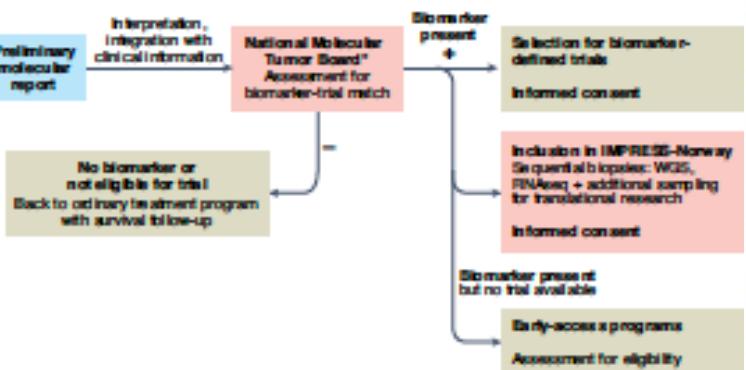
Patients with advanced disease referred for molecular profiling

Informed consent

Breast biopsy samples → Extended molecular analysis → Data analysis → Preliminary molecular report → Interpretation, integration with clinical information → National Molecular Tumor Board Assessment for biomarker-trial match

*National Molecular Tumor Board Weekly virtual meeting with regular staff (oncologist, pathologist, hematologist, molecular biologist, bioinformatician, medical geneticist)

Standardized reporting format and dialogue with local clinicians



correspondence

Table 1 | CONNECT: a public-private partnership of stakeholders in precision cancer medicine

CONNECT working-groups interfacing

InPreD (WG1)	IMPRESS (WG2)	Innovative Implementation methods (WG3)	Data governance, storage and sharing for secondary use and analysis (WG4)
InPreD national testing Infrastructure	IMPRESS-Norway national PCM trial	INSIGHT-INCLUDE: Impact of precision cancer medicine health economics and regulatory framework for implementation	INSIGHT-INCLUDE legal framework; InPreD ICT solution; IMPRESS aggregation of data in Europe

CONNECT is operationalized via working groups (WG1-WG4) that engage experts from the public and private sector. p: ICT, information and communications technology; PCM, precision cancer medicine.

Kjetil Taskén^{1,2,3}, Hege E. G. Russnes^{2,4}, Elise Aas⁵, Line Bjørge^{1,6}, Egil S. Blitx⁷, CONNECT Public-Private Partnership Consortium⁸, Espen Enerly⁹, Gro L. Fagereng¹⁰, Asmund Fløbak¹⁰, Bjørnar Gilje¹¹, Bjørn T. Gjertsen^{1,12,13}, Tommod K. Guren¹¹, Jutta Heitz¹⁴, Elvind Hovig^{15,16}, Randi Hovland¹⁷, InPreD-Norway and National Molecular Tumor Board Consortium¹⁸, IMPRESS-Norway Consortium¹⁹, Per E. Lanning^{20,21}, Leonardo A. Meza-Zepeda^{20,22}, Per M. Mæhle²³, Hilde L. Nilsen²³, Steinar Ø. Thoresen²³, Ketil Widerberg²³, Sigbjørn Smeland²³ and Åslaug Helland^{1,2,10}

CONNECT Public-Private Partnership Consortium

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Published online: 05 May 2022

<https://doi.org/10.1038/s41591-022-01777-4>

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Acknowledgments

The authors are grateful for public funding to the precision cancer medicine ecosystem from the Regional Health Authorities for South-Trøndelag, Western, Middle and Northern Norway, the Norwegian Clinical Treatment Research Programme (CLINIEHØYR), the Norwegian Cancer Society, the Nordic Trial Alliance/Nordic, the Radhus Hospital Foundation and other regional funds, as well as company contributions received so far from Roche, Novartis, Eli Lilly, Incyte and collaboration projects with Roche Foundation Medicine and Ambrx. The Norwegian Medicines Agency represented by Martti Hyttest participated in CONNECT as an observer.

Author contributions

KJ wrote the manuscript and integrated edits from other authors. Important discussions and contributions to the initiatives described were made by all authors. All authors have approved the final version of the text.

Competing interests

Participation in the CONNECT Public-Private Partnership is regulated by a consortium agreement that handles conflicts of interest and regulates interaction with the publicly funded infrastructure InPreD-Norway and the investigator-initiated and publicly funded trial IMPRESS-Norway. IMPRESS-Norway (principal investigator Å.T.) has currency contributions from Roche, Novartis, Incyte and Eli Lilly and collaboration projects with Roche Foundation Medicine and Ambrx. The Norwegian Medicines Agency represented by Martti Hyttest participated in CONNECT as an observer.



Takk for oppmerksomheten