

Biomarker Updates

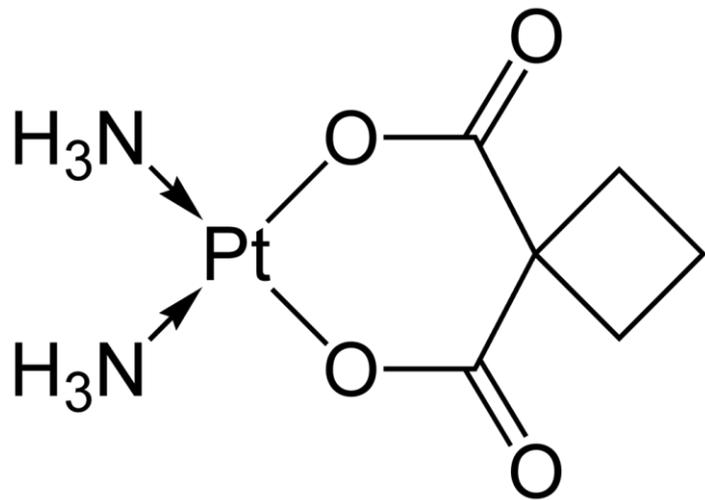
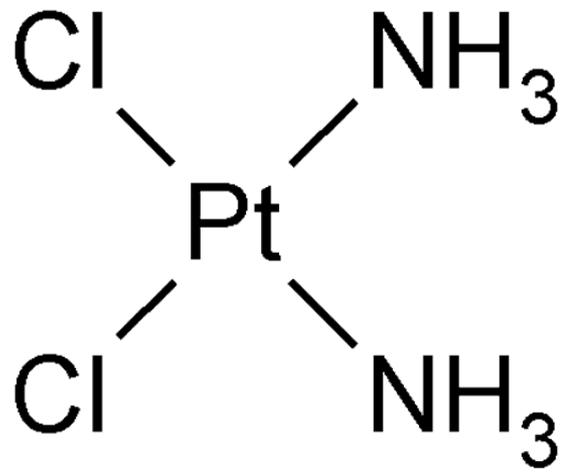
Thomas Powles

Director of Barts Cancer Center.
Professor of Urology Cancer, Barts Cancer Institute.



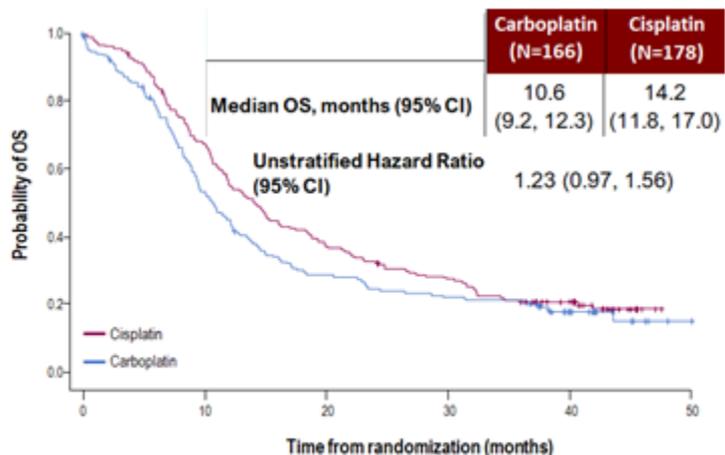
DISCLOSURES

- **Consulting Fees: AstraZeneca, BMS, Exelixis, Incyte, Ipsen, Merck, MSD, Novartis, Pfizer, Seattle Genetics, Merck Serono, Astellas, Johnson & Johnson, Eisai, Roche**
- **Contracted Research: AstraZeneca, BMS, Exelixis, Ipsen, Merck, MSD, Novartis, Pfizer, Seattle Genetics, Merck Serono, Astellas, Johnson & Johnson, Eisai, Roche**
- **Other (Travel/Accommodation/Expenses): Roche, Pfizer, MSD, AstraZeneca, Ipsen**

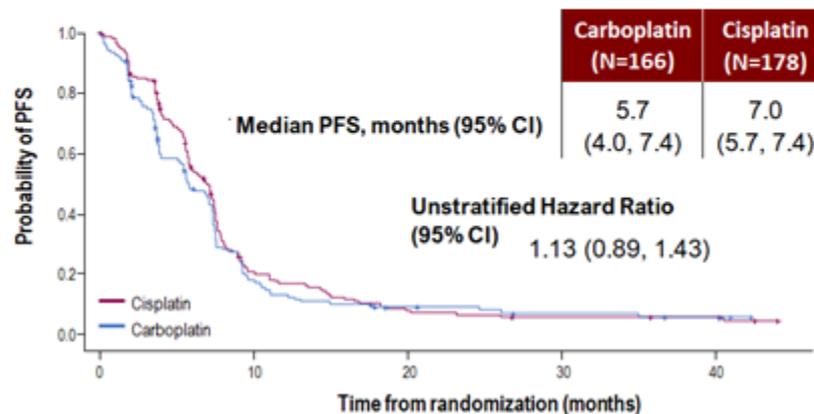


Indirect comparison of cisplatin and carboplatin in bladder cancer

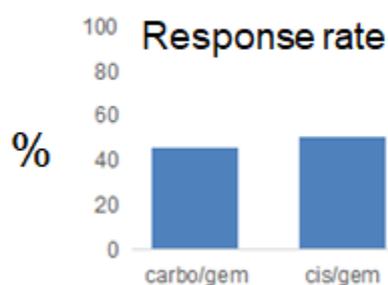
	Carboplatin (N = 166)	Cisplatin (N = 178)
Liver metastasis at baseline		
Yes	53 (31.9)	40 (22.5)
No	113 (68.1)	138 (77.5)
Number of Bellmunt risk factors		
0	53 (31.9)	77 (43.3)
1	74 (44.6)	74 (41.6)
2	33 (19.9)	21 (11.8)



Carboplatin	166	140	123	93	70	54	45	42	37	35	33	32	32	20	12	6	2	0
Cisplatin	178	171	150	123	98	82	74	65	58	51	48	39	36	26	15	5	0	



Carboplatin	166	103	63	35	17	13	10	8	8	5	5	5	4	3	1	0
Cisplatin	178	146	88	43	26	20	16	11	10	8	8	8	7	6	4	0

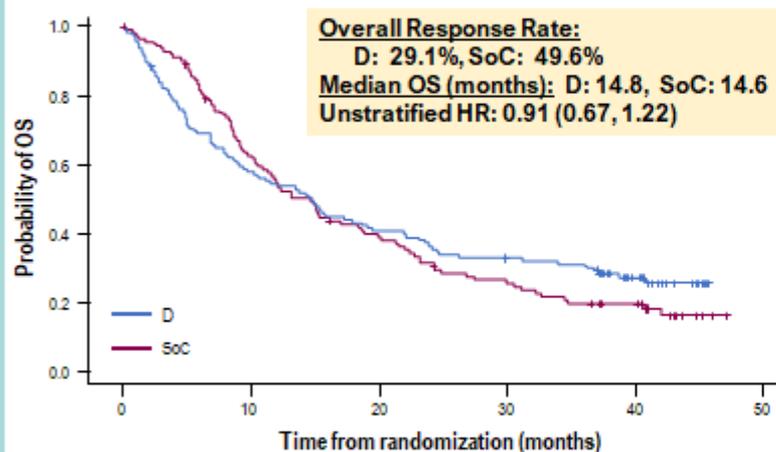


Method:
Adhoc analysis of the control
arm from DANUBE
RIII study 1st line UC trial.

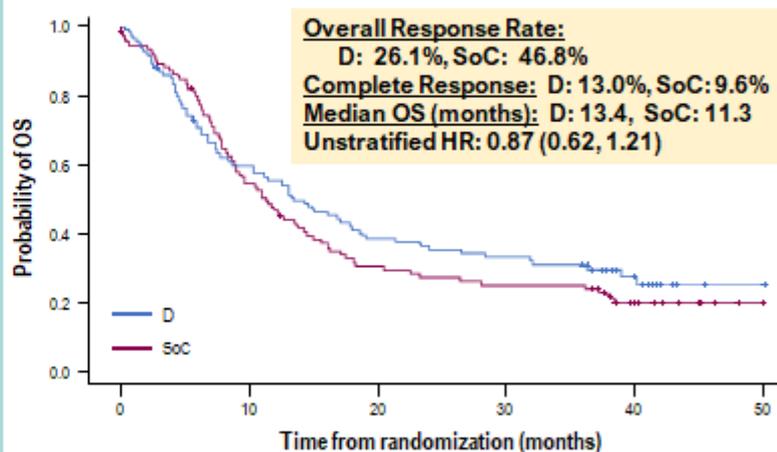
Powles et al EAU 2021

Overall Survival by Cisplatin-Eligibility, PD-L1 High *Durvalumab vs. SoC*

Cisplatin-eligible population



Cisplatin-ineligible population



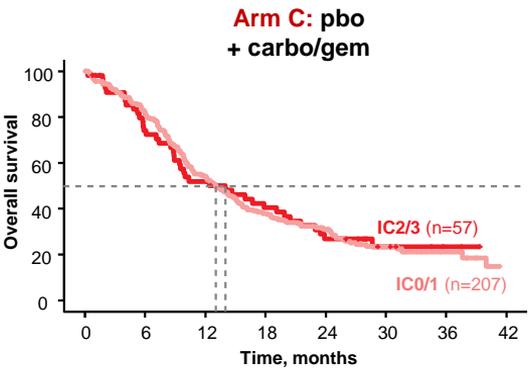
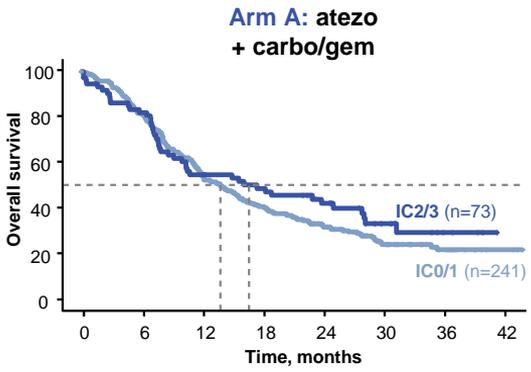
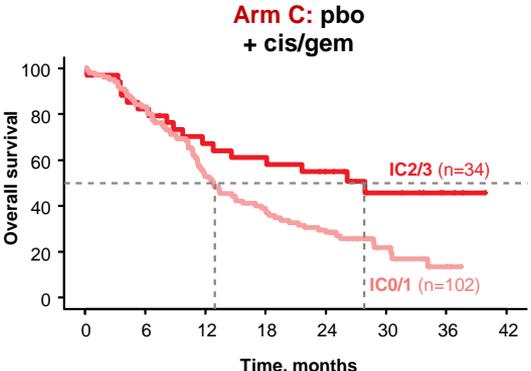
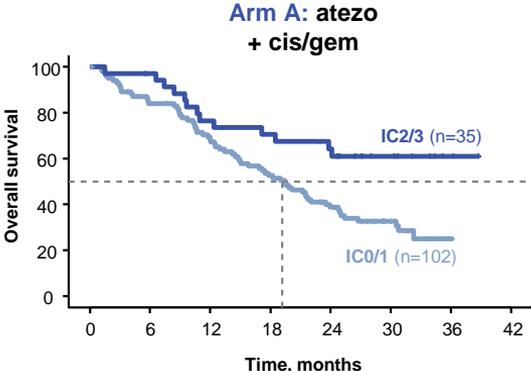
Cisplatin-related immunomodulation and efficacy with atezolizumab + cisplatin- vs carboplatin-based chemotherapy in metastatic urothelial cancer

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Effects of cisplatin ± atezo on OS are most prominent in patients with PD-L1 IC-high tumours



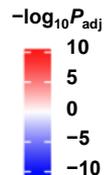
IMvigor130: OS by PD-L1 status and chemo

	mOS, mo		OS HR (95% CI)
	IC0/1	IC2/3	
Arm A	Atezo + cis/gem	19.5	NR (0.25, 0.83)
	carbo/gem	13.9	16.6 (0.61, 1.17)
Arm C	Pbo + cis/gem	12.8	27.9 (0.30, 0.86)
	carbo/gem	13.0	14.0 (0.71, 1.42)



Cisplatin vs carboplatin leads to gene expression changes suggestive of induction of innate and adaptive immunity

- IMvigor130:** Cis- vs carbo-treated patients showed on-treatment enrichment of TNF- α signalling via NF κ B, inflammatory response gene sets and interferon response gene sets across immune cell clusters
- Neoadjuvant cohort:** TNF α signaling via NF κ B was also enriched in paired tumour samples (post- vs pre-cis/gem)

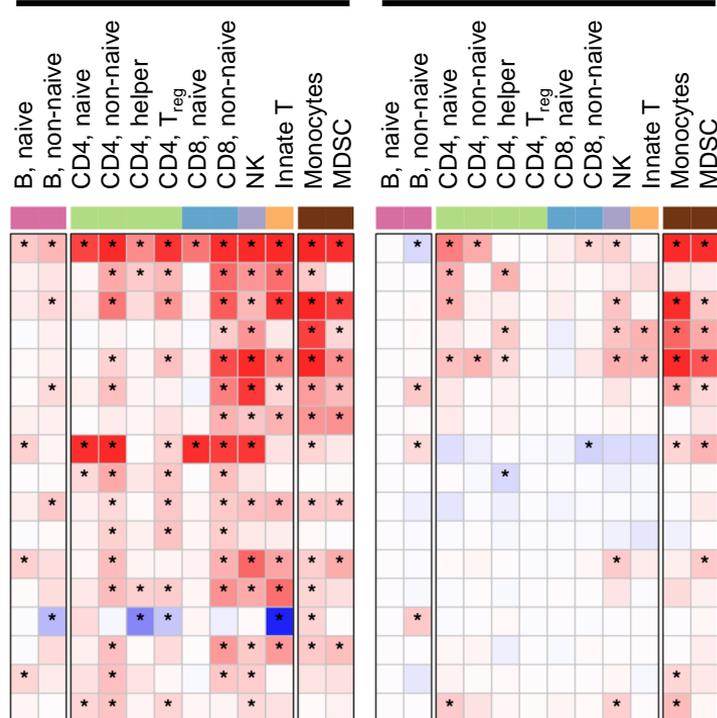


Gene sets

TNFA_SIGNALING_VIA_NFKB
 IL2_STAT5_SIGNALING
 INFLAMMATORY_RESPONSE
 INTERFERON_ALPHA_RESPONSE
 INTERFERON_GAMMA_RESPONSE
 ALLOGRAFT_REJECTION
 IL6_JAK_STAT3_SIGNALING
 MYC_TARGETS_V1
 G2M_CHECKPOINT
 P53_PATHWAY
 MITOTIC_SPINDLE
 APOPTOSIS
 HYPOXIA
 OXIDATIVE_PHOSPHORYLATION
 KRAS_SIGNALING_UP
 ANDROGEN_RESPONSE
 MTORC1_SIGNALING

Arm A (C3D1 vs C1D1):
 atezo + cis/gem
 vs atezo + carbo/gem

Arm C (C3D1 vs C1D1):
 pbo + cis/gem
 vs pbo + carbo/gem

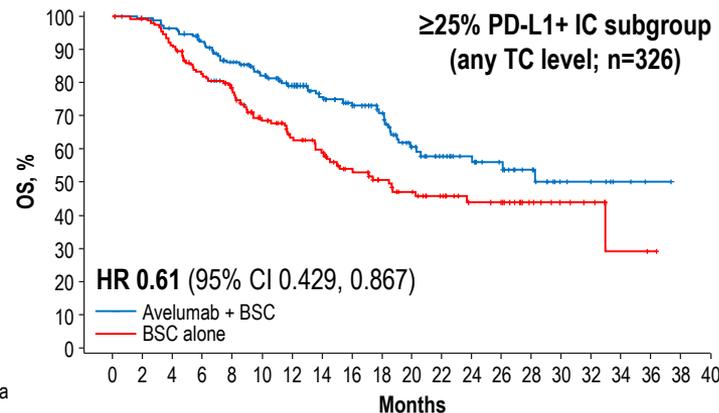
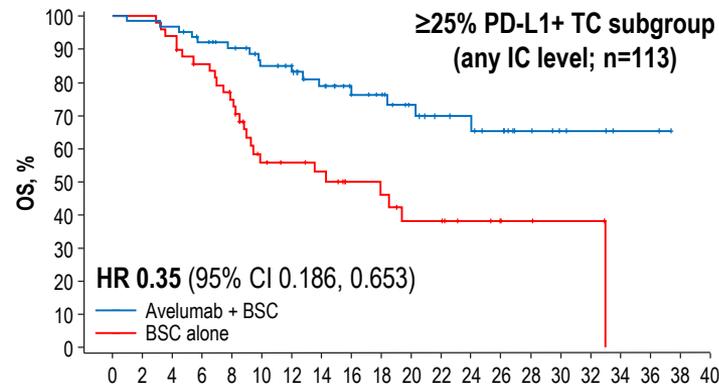
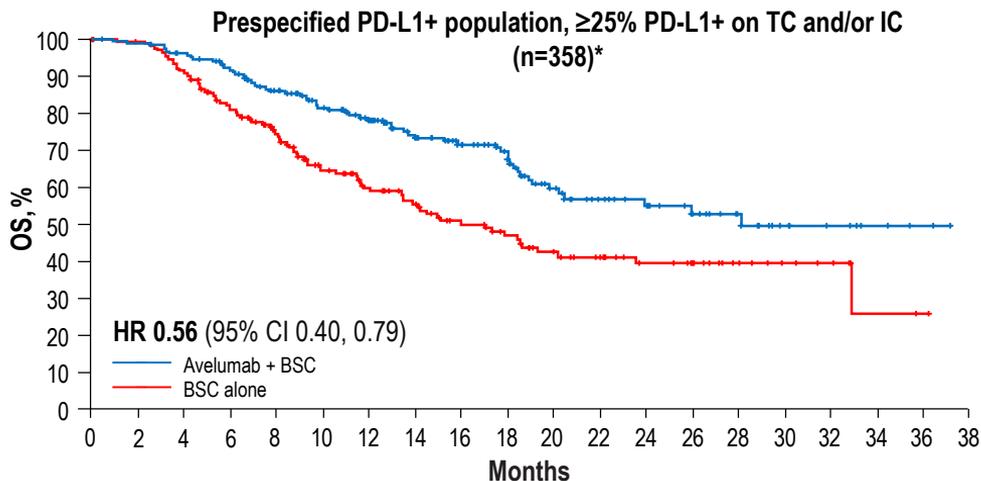


The PD-L1 biomarker consists of many different biomarker and should be considered as such.

Randomized trials testing PD-L1 in UC

Drug	setting	Result
atezolizumab	Platinum refractory	-ve
atezolizumab	Adjuvant	-ve
Durvalumab	1 st line	-ve
Pembrolizumab	1 st line	-ve
nivolumab	adjuvant	+ve for ITT and PD-L1+ve
Avelumab	1 st line maintenance	+ve for ITT and PD-L1+ve

PD-L1 biomarker: TC vs IC component

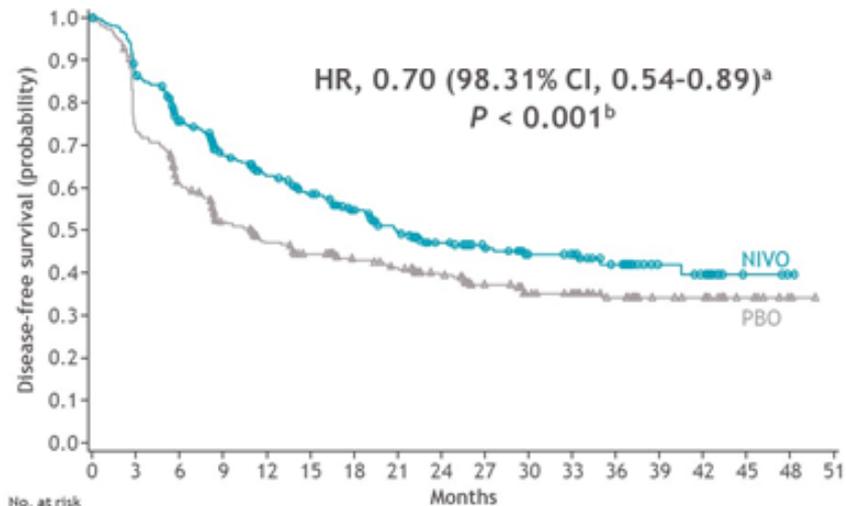


Neither PD-L1+ TC nor IC alone fully predicts OS benefit

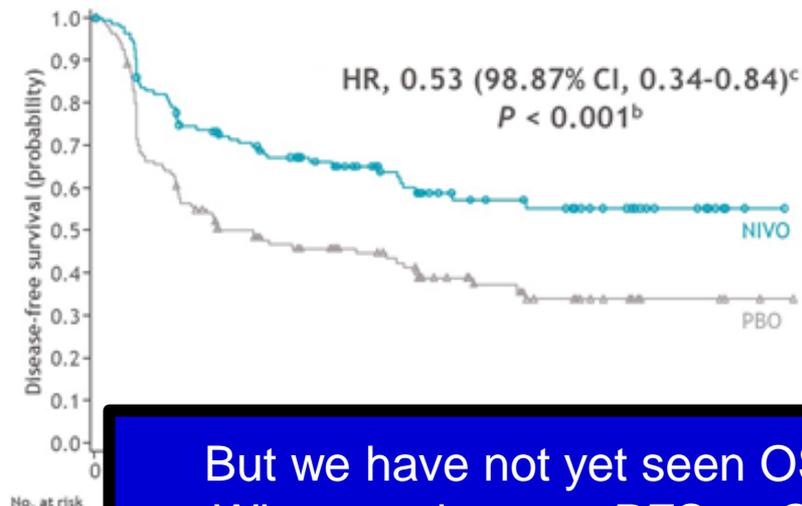
•TC, tumor cell; IC, immune cell; NE, not evaluable.
 *PD-L1 expression in $\geq 25\%$ of TC or in $\geq 25\%$ or 100% of IC if the percentage of IC was $>1\%$ or $\leq 1\%$, respectively, using the Ventana SP263 assay.

Adjuvant nivolumab in high-risk urothelial cancer.

ITT



PD-L1 $\geq 1\%$

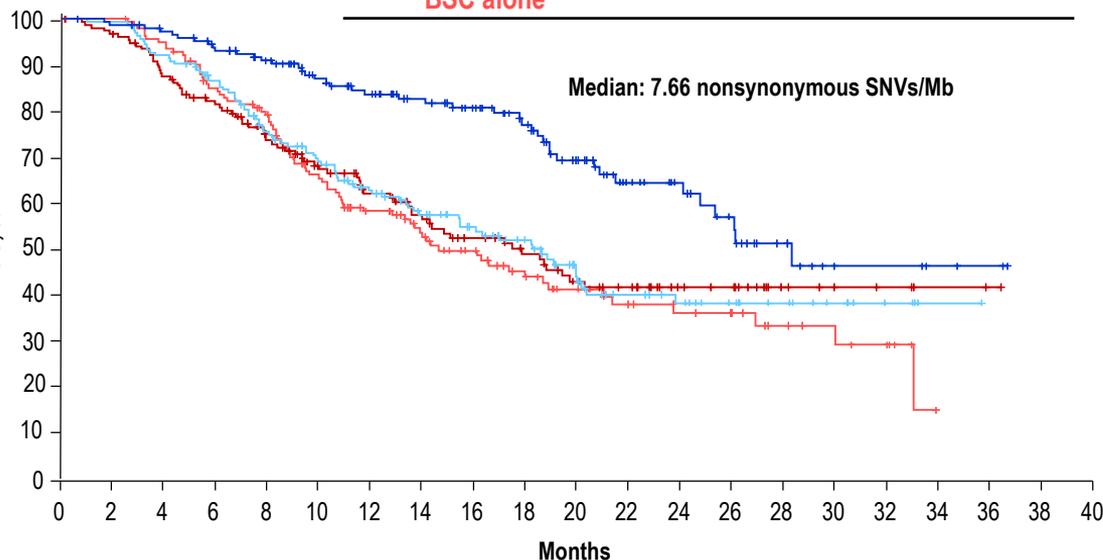


But we have not yet seen OS?
Why was there no PFS or OS
advantage for atezolizumab?
Why didn't the biomarker work with
atezo?

OS benefit in subgroups defined by Tumor Mutation Burden (TMB) and PD-L1 status

Arm	TMB	HR (95% CI)
Avelumab + BSC	>Median	0.48 (0.332, 0.707)
BSC alone		
Avelumab + BSC	≤Median	0.88 (0.643, 1.197)
BSC alone		

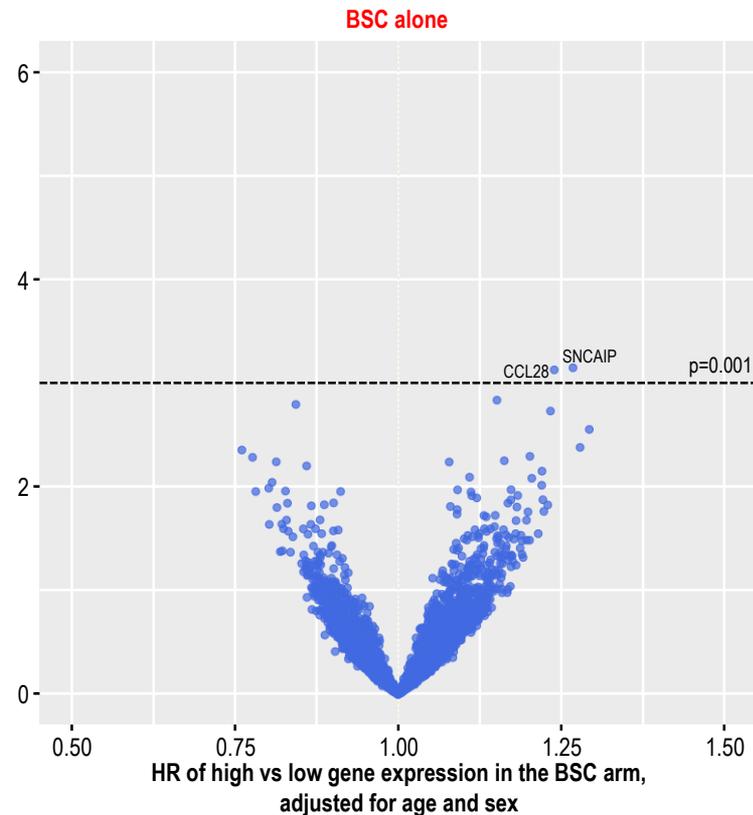
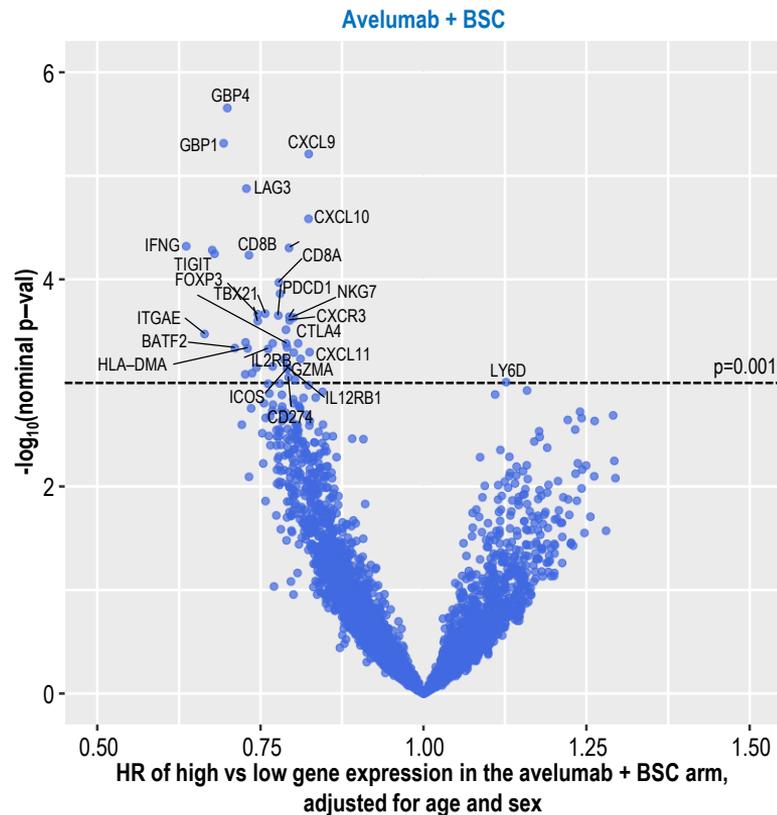
Subgroup	HR (95% CI) Avelumab + BSC vs BSC alone
PD-L1+	0.56 (0.400, 0.790)
PD-L1-	0.85 (0.616, 1.181)
TMB-high	0.46 (0.321, 0.673)
TMB-low	0.93 (0.665, 1.289)
TMB-high, PDL1+ (n=190)	0.49 (0.291, 0.812)
TMB-high PDL1- (n=105)	0.42 (0.247, 0.732)
TMB-low PDL1+ (n=148)	0.62 (0.389, 0.995)
TMB-low, PDL1- (n=140)	1.40 (0.871, 2.252)



Neither TMB nor PD-L1 status alone fully predict OS benefit

EAU2021

- Tumor gene expression data can identify genes that may be associated with OS benefit from avelumab
- Immune-related genes are associated with OS benefit from avelumab



• Genes of interest with $p < 0.001$ are labeled

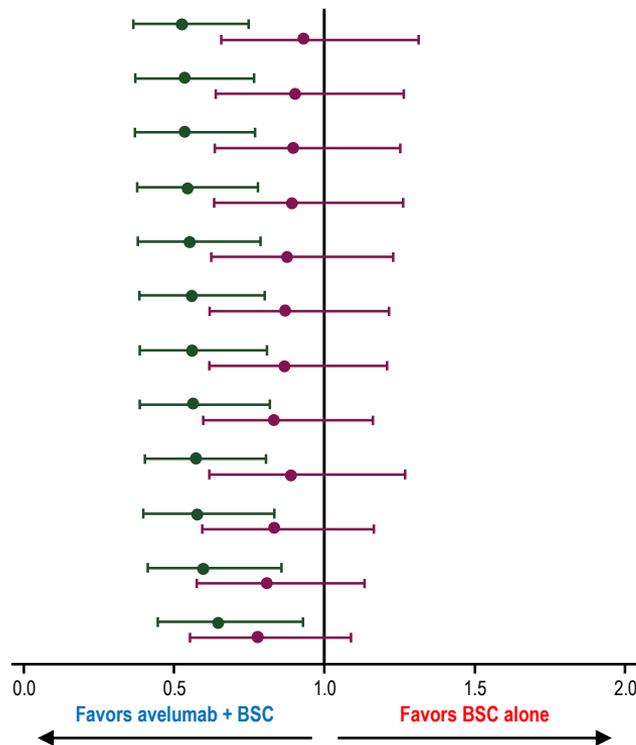
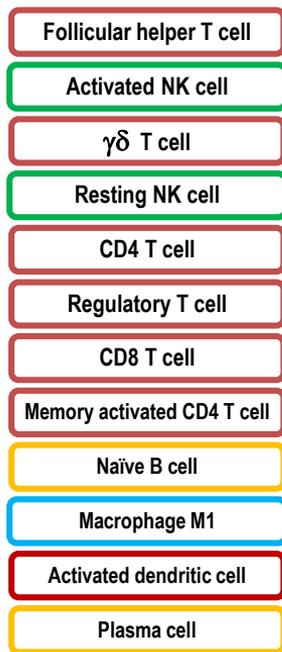
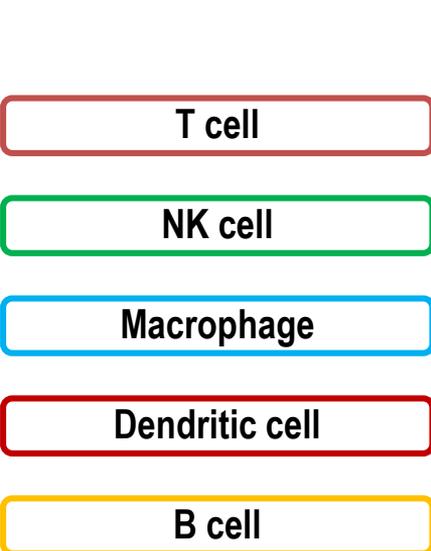
Relationship between immune cell gene expression signatures and OS with avelumab

Multiple immune cell signatures may predict OS benefit with avelumab

Signatures with interaction term $p < 0.15$

>Median vs ≤Median

HR (95% CI)

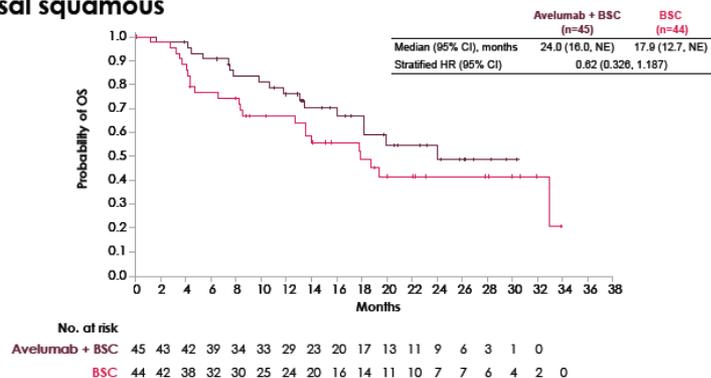


0.53 (0.367, 0.757)
0.92 (0.650, 1.297)
0.53 (0.365, 0.760)
0.90 (0.641, 1.268)
0.52 (0.362, 0.759)
0.90 (0.642, 1.263)
0.54 (0.374, 0.774)
0.90 (0.638, 1.272)
0.55 (0.384, 0.800)
0.86 (0.614, 1.211)
0.54 (0.375, 0.785)
0.88 (0.629, 1.234)
0.55 (0.379, 0.794)
0.88 (0.628, 1.230)
0.56 (0.382, 0.810)
0.84 (0.602, 1.173)
0.57 (0.400, 0.803)
0.89 (0.619, 1.269)
0.56 (0.388, 0.817)
0.84 (0.603, 1.181)
0.59 (0.405, 0.846)
0.82 (0.581, 1.143)
0.64 (0.443, 0.921)
0.78 (0.558, 1.099)

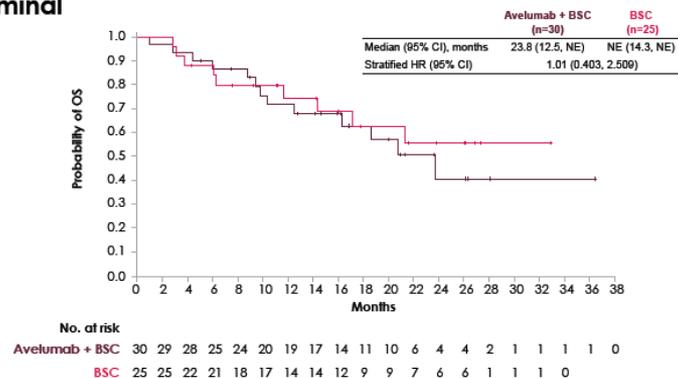
Gene signatures are from the Leukocyte gene signature matrix (LM22), Newman et al (2015) Nature Methods, <https://doi.org/10.1038/nmeth.3337>

Outcome of avelumab in TCGA subtypes.

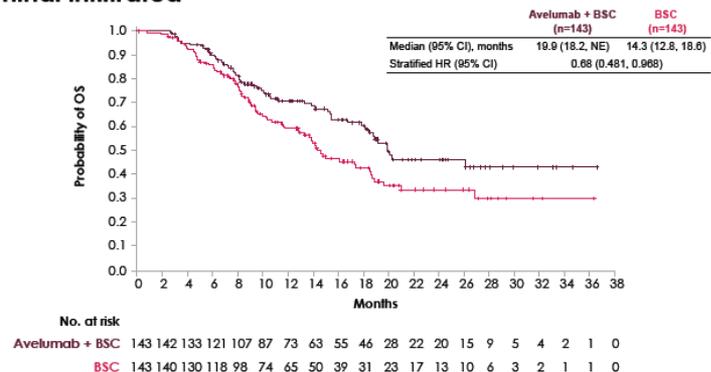
A. Basal squamous



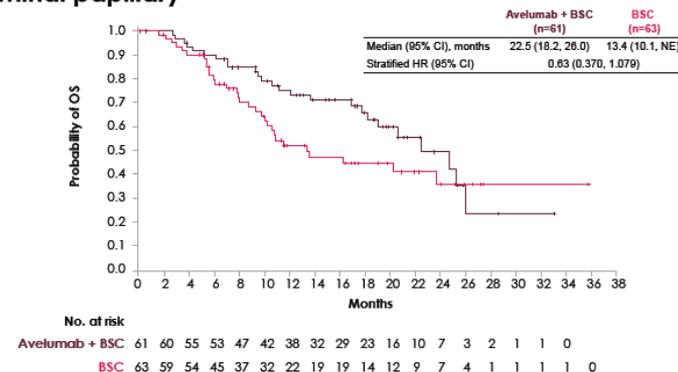
B. Luminal



C. Luminal infiltrated

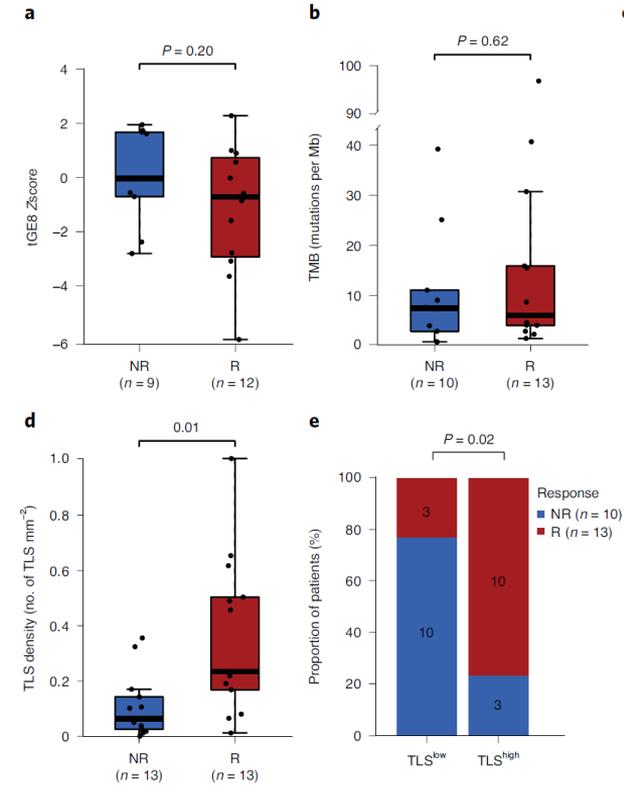
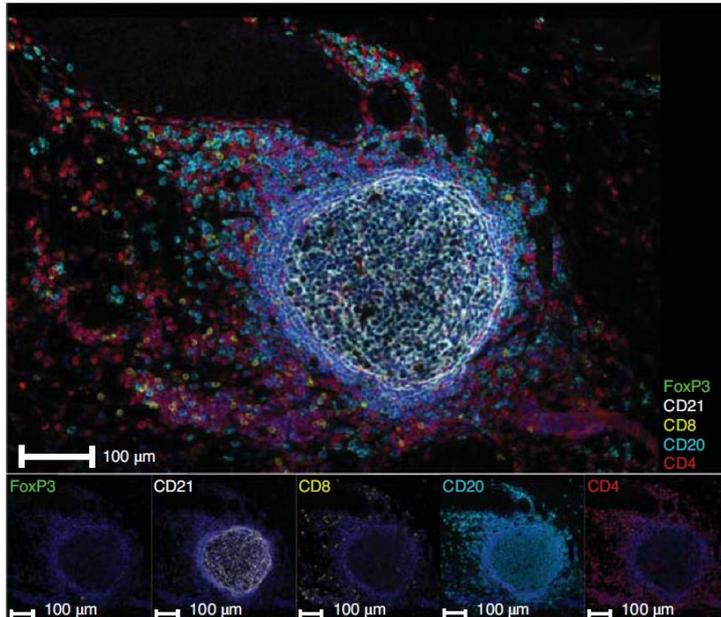


D. Luminal papillary



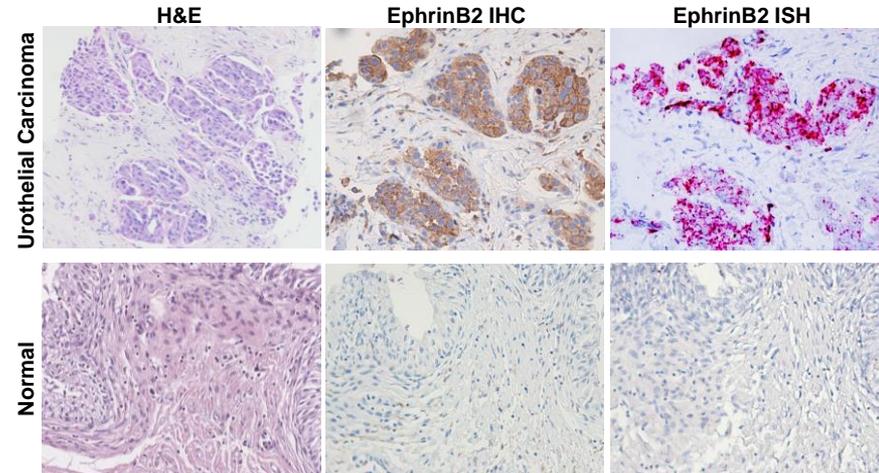


Neoadjuvant PD-L1 plus CTLA-4 blockade in patients with cisplatin-ineligible operable high-risk urothelial carcinoma



Phase II trial of pembrolizumab (P) in combination with sEphB4-HSA (B4) in previously treated metastatic urothelial carcinoma (mUC)

- EphrinB2 is a transmembrane protein expressed in developing arterial capillary endothelium; it is minimally expressed in adults but re-expressed in tumors and tumor blood vessels
- EphB4, the high affinity cognate receptor, is also expressed in developing venous endothelium and is re-induced in tumors and tumor vessels
- EphrinB2-EphB4 interaction activates bidirectional signaling to promote development and tumor progression by direct effects on tumor cell viability, tumor angiogenesis and immune cell response
- EphrinB2 and EphB4 are highly expressed in urothelial tumors and are negative prognostic markers¹

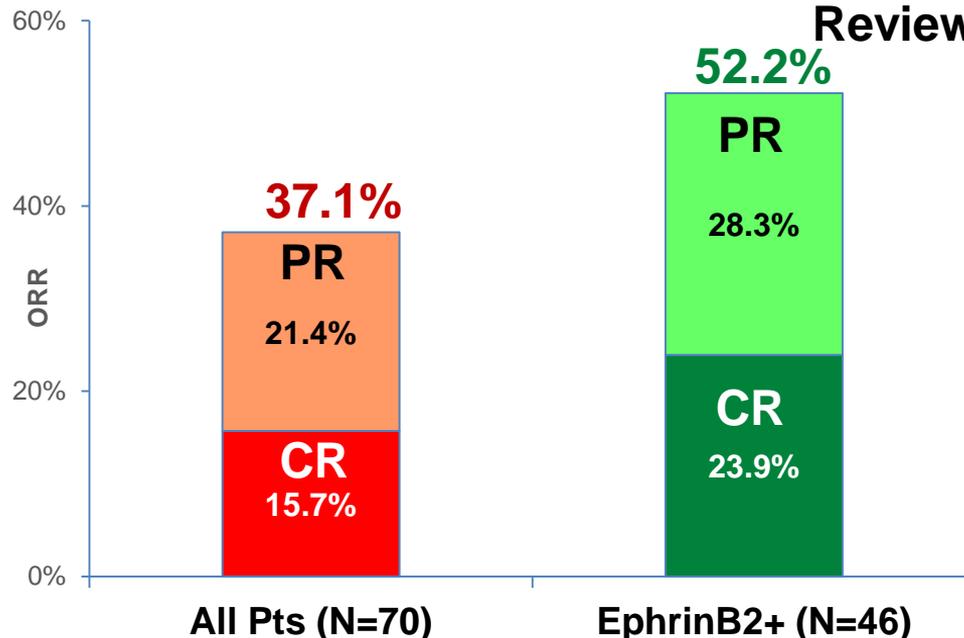


EphrinB2 membrane staining
≥ 1% is considered positive

1. Chandrashekar et al, Neoplasia 2017, PMID 28732212

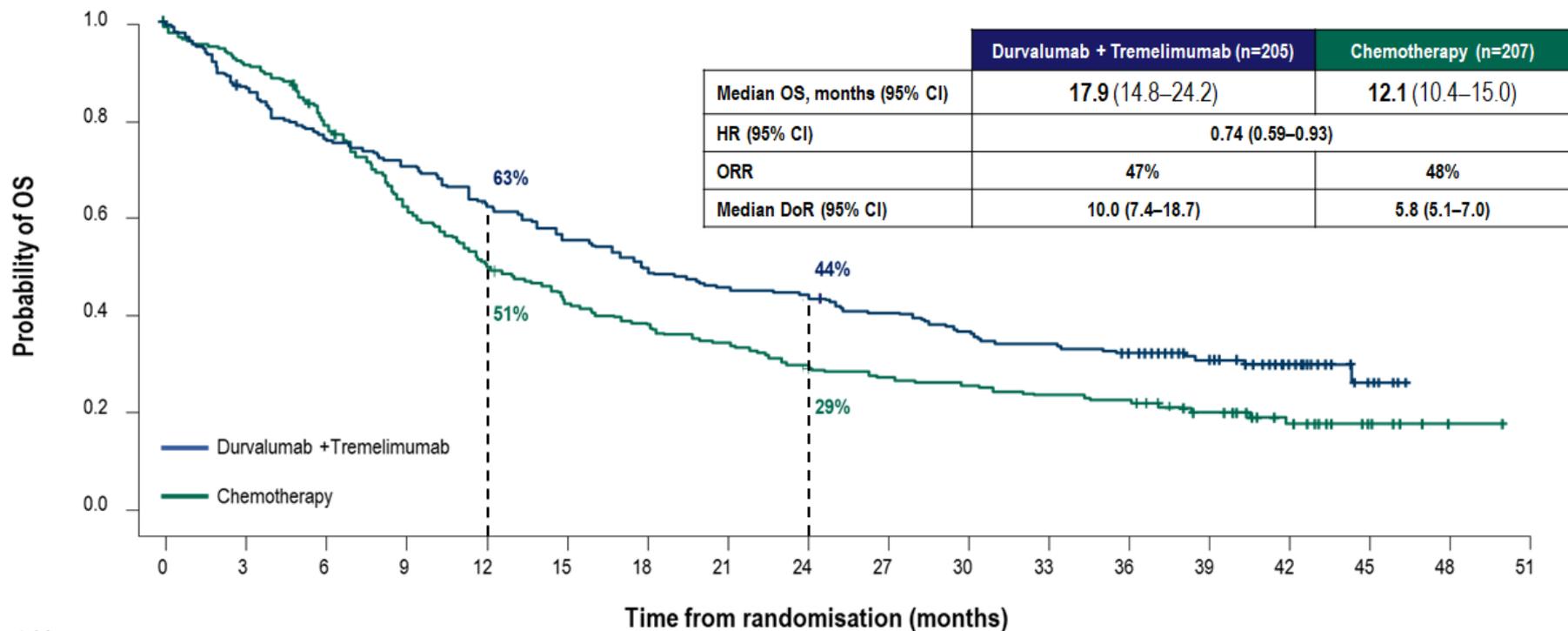
Intent to Treat Confirmed ORR and DOR (Independent Review)

Median follow up
23.0 months
95% CI (18.1, 36.3)



Median DOR (95% CI), months	All Pts (N=70)	EphrinB2+ (N=46)
	Not Reached (13.3, NE)	Not Reached (11.9, NE)

OS With Durvalumab + Tremelimumab vs Chemotherapy in the PD-L1 High Population (Secondary Endpoint)



Number at risk

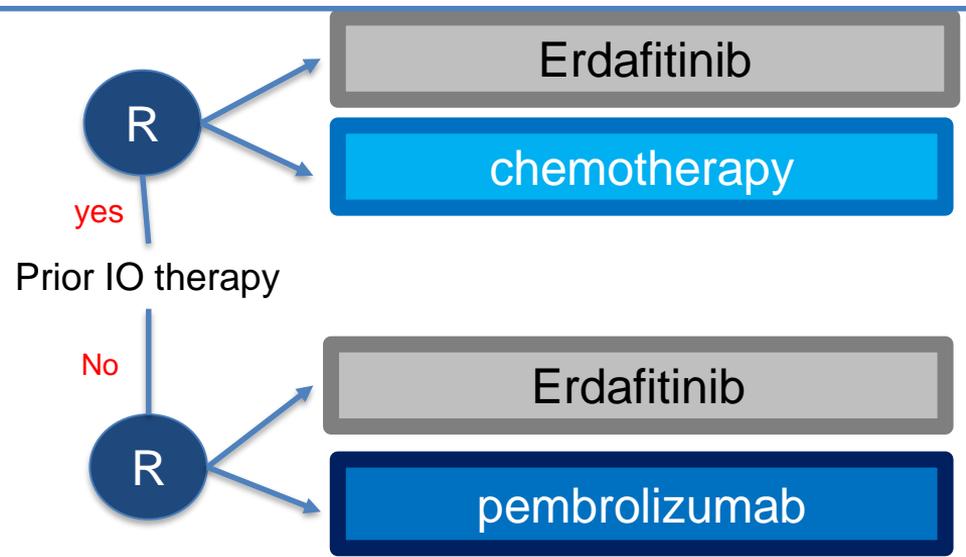
Durvalumab+Tremelimumab	205	177	156	144	129	114	101	92	89	81	73	68	63	41	21	6	0	0
Chemotherapy	207	186	161	126	101	86	74	66	57	51	48	44	42	27	16	8	2	0 18

FGF-3 inhibitor in selected patients with urothelial cancer.

Siefker-Radtke et al ASCO 2018
Powles T ESMO 2018 (Review)

	Erdafitinib	INCB054828
Population	Platinum refractory	Platinum refractory
Number	99	100
Phase	II	II
biomarker	Mutations and fusions	Mixed (2 cohorts)
RR	40%	25%
PFS months	5.5 months (4.2-6)	na
Toxicity (grade 3)	Stomatitis Nail tox. Hypophosphatemia	Alopecia Fatigue Hypophosphatemia.
Median OS	9.5 months (8-19)	NA

THOR: Randomised phase III erdafitinib vs chemotherapy or pembrolizumab in biomarker +ve UC



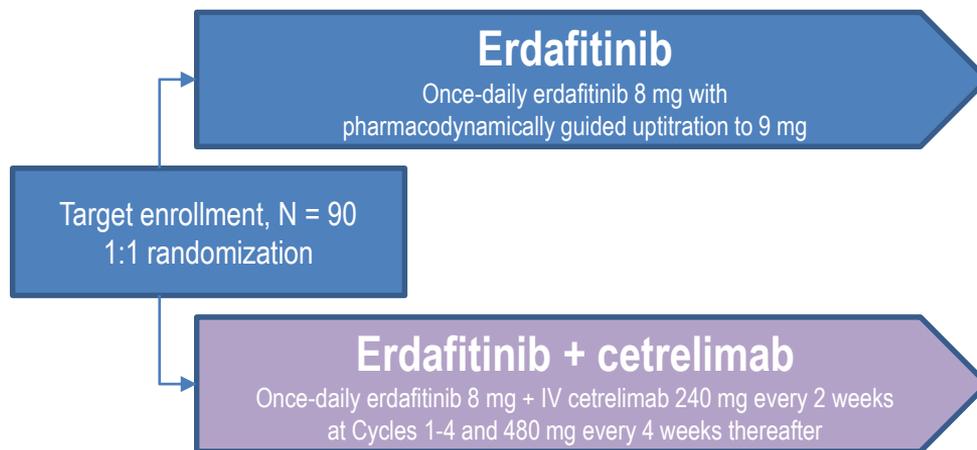
NORSE Phase 2 Study Design^a



Key eligibility criteria

- Age \geq 18 years
- mUC diagnosis
- Ineligible for cisplatin
- Select *FGFRa* (mutation/fusion)
- Measurable disease
- No prior systemic therapy for mUC

Patients with any PD-L1 status could be enrolled



Primary end points

- ORR
- Safety

Key secondary end points

- DCR
- DOR
- Time to response

No formal statistical comparisons between arms are prespecified

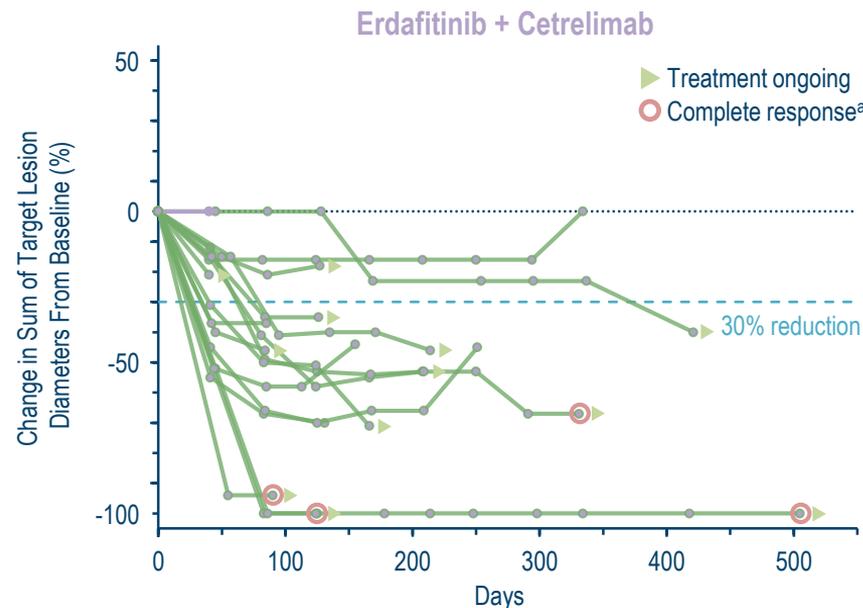
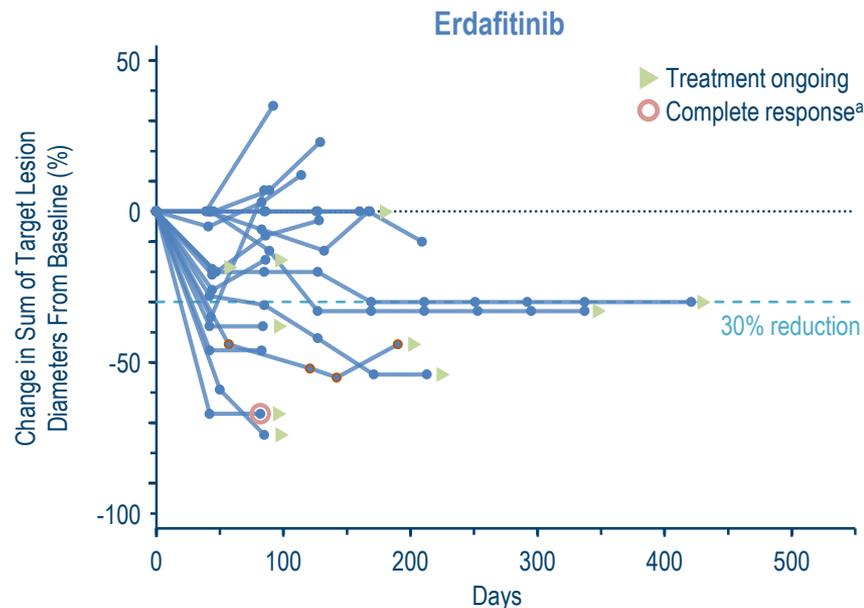
Point estimates along with 95% CI will be presented for each arm.

- *Sample size determination:* Assuming a true ORR of 45% in the erdafitinib arm and 55% in the erdafitinib + cetrelimab arm, $n \approx 45$ patients in each arm would result in an estimated ORR that is above a 95% CI lower bound of 30% and 40%, respectively
- A review of safety and efficacy data was planned per the data review committee charter when ~ 40 patients were response-evaluable

DCR, disease control rate; DOR, duration of response; IV, intravenous; ORR, overall response rate.

^aEnrollment began in April 2018. The data cut-off for this analysis was July 19, 2021.

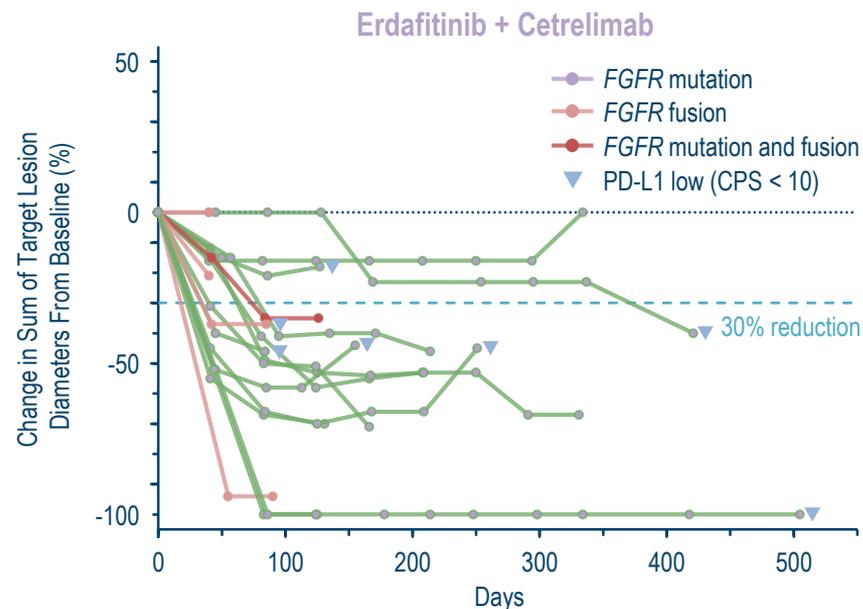
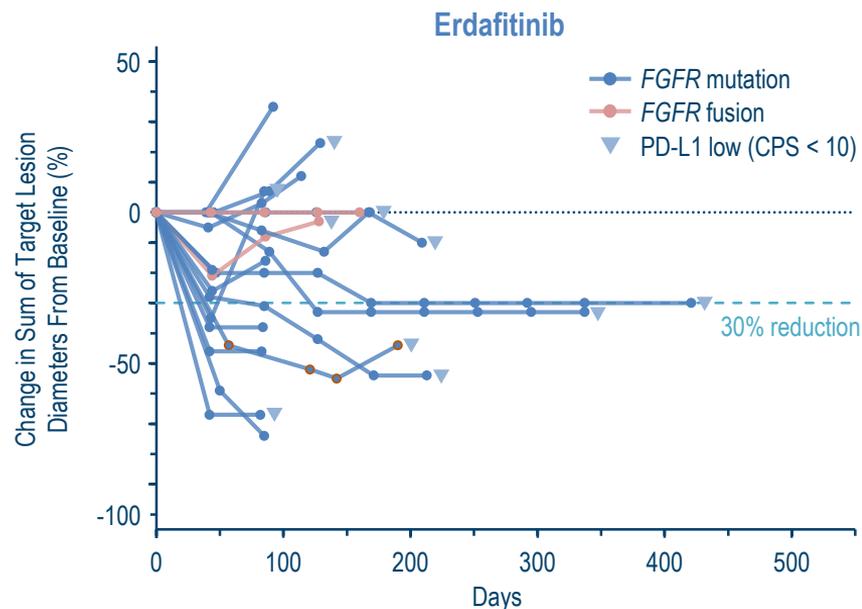
NORSE: Antitumor Activity Over Time



- Patients in both treatment arms had a durable reduction in the sum of target lesion diameters over time
- Median of the maximum reduction in the sum of target lesion diameters was 28% in the erdafitinib arm and 51% in the erdafitinib + cetrelimab arm

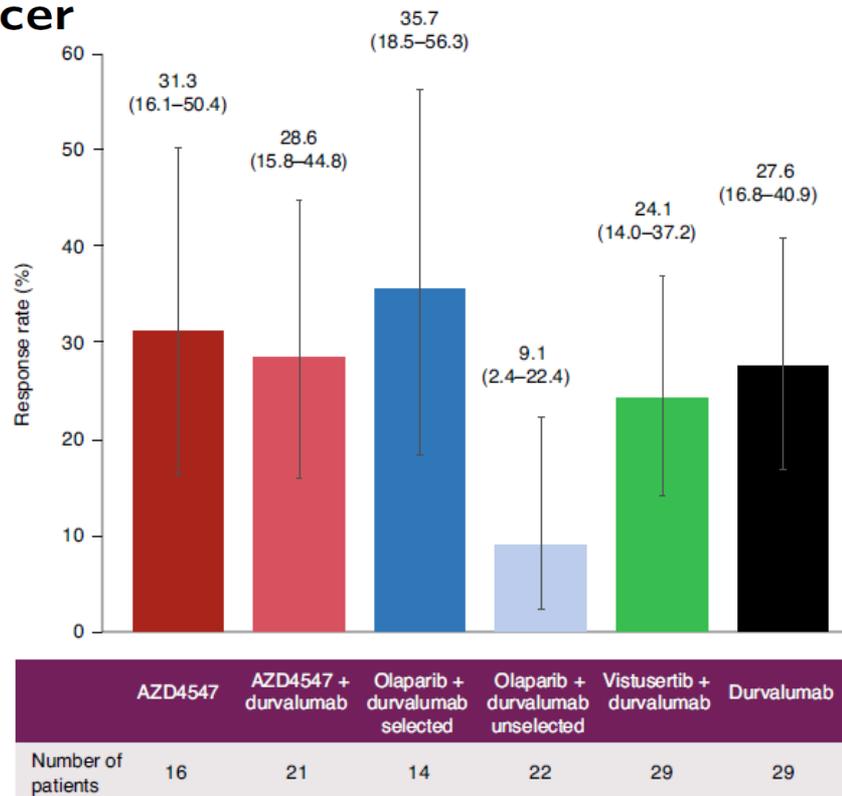
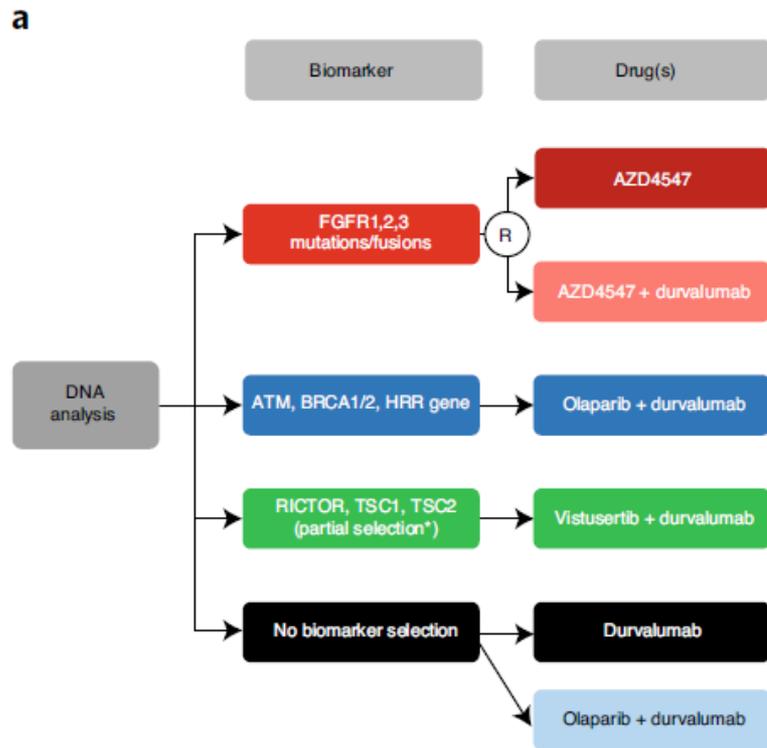
^aComplete responses include patients who had sum of target lesions > 0 mm; in patients with lymph node target lesions, a diameter < 10 mm is required for complete response per RECIST 1.1.

NORSE: Antitumor Activity Over Time, by *FGFRa* type and PD-L1 status

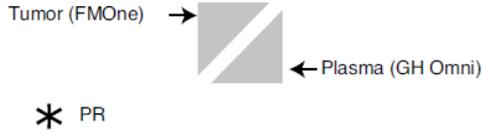
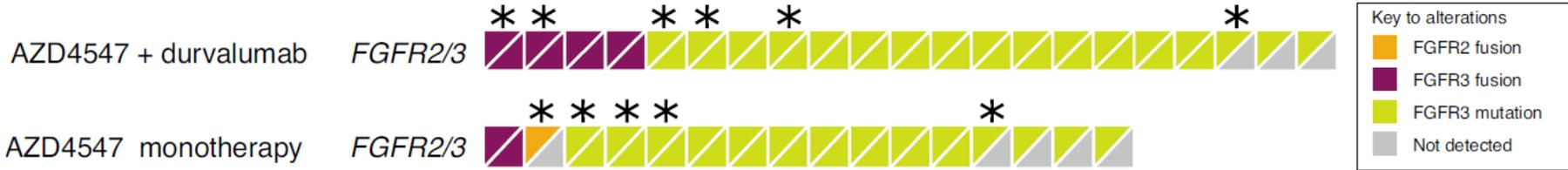


- Responses were observed in patients with both *FGFR* mutations and fusions
- In patients with PD-L1 low status, responses were observed in 50% in the erdafitinib arm (5 of 10) and in 71% patients in the erdafitinib + cetrelimab arm (5 of 7); few patients with PD-L1 positive status had available data at the time of this analysis

An adaptive, biomarker-directed platform study of durvalumab in combination with targeted therapies in advanced urothelial cancer

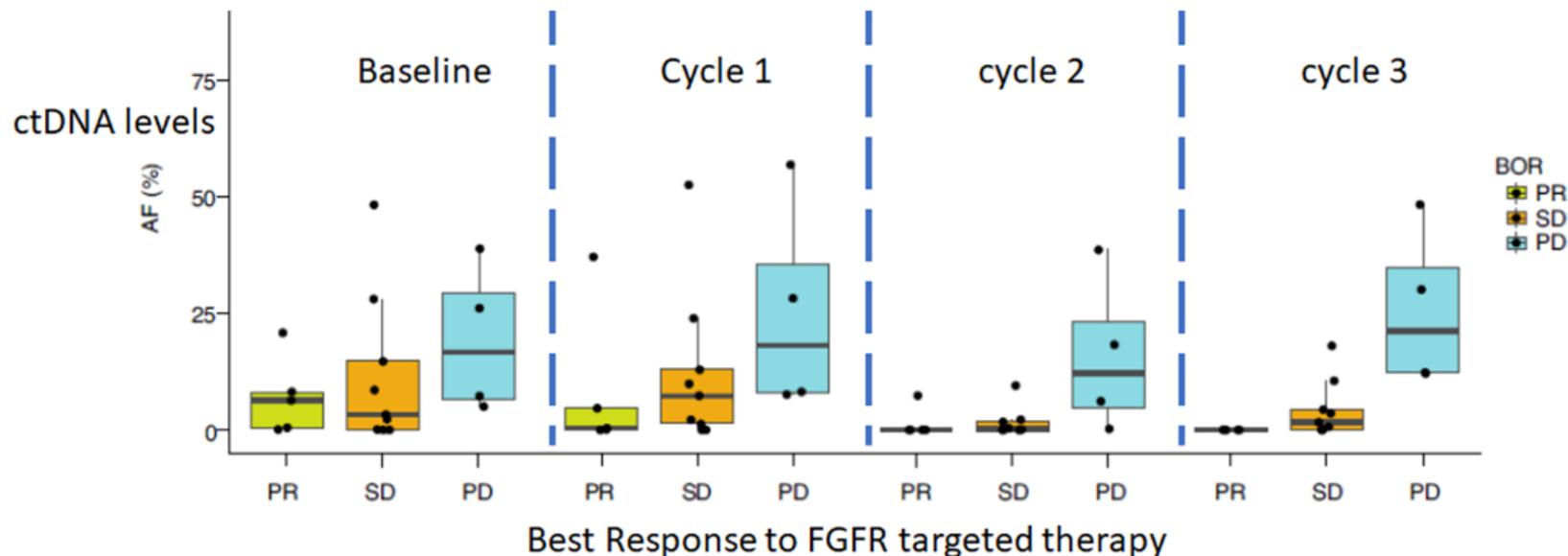


FGFR DNA alterations from tissue at ctDNA strongly correlate

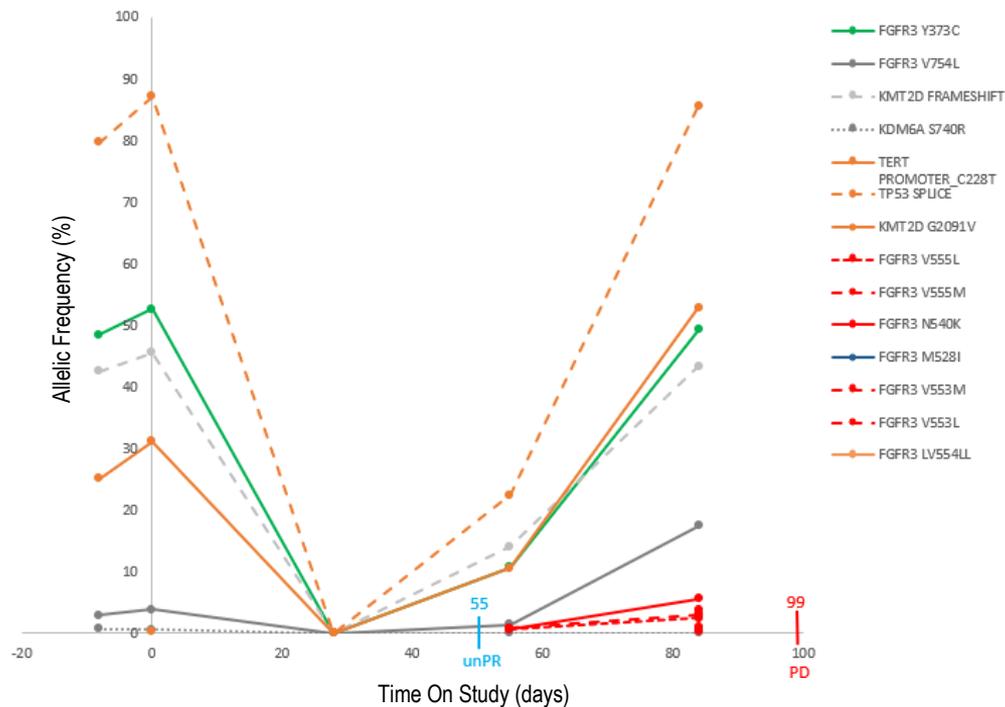


An adaptive, biomarker-directed platform study of durvalumab in combination with targeted therapies in advanced urothelial cancer

Response to FGFR targeted therapy correlating with changes to tracked FGFR mutations



Presence of new FGFR3 clones at progression on FGFR using personalised ctDNA analysis.

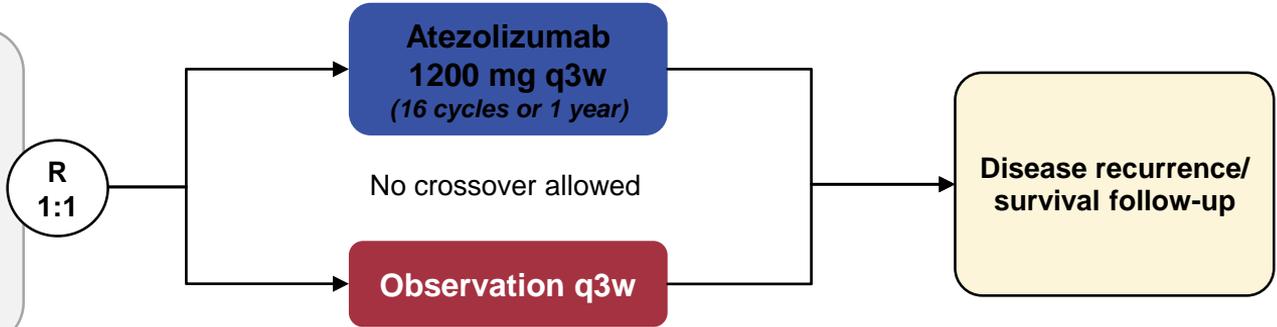


Patient BISCAY76

Phase 3 IMvigor010 adjuvant study in MIUC

Key eligibility

- High-risk MIUC (bladder or upper tract)
- Radical surgery with lymph node dissection within ≤ 14 weeks
- Tissue sample for PD-L1 testing

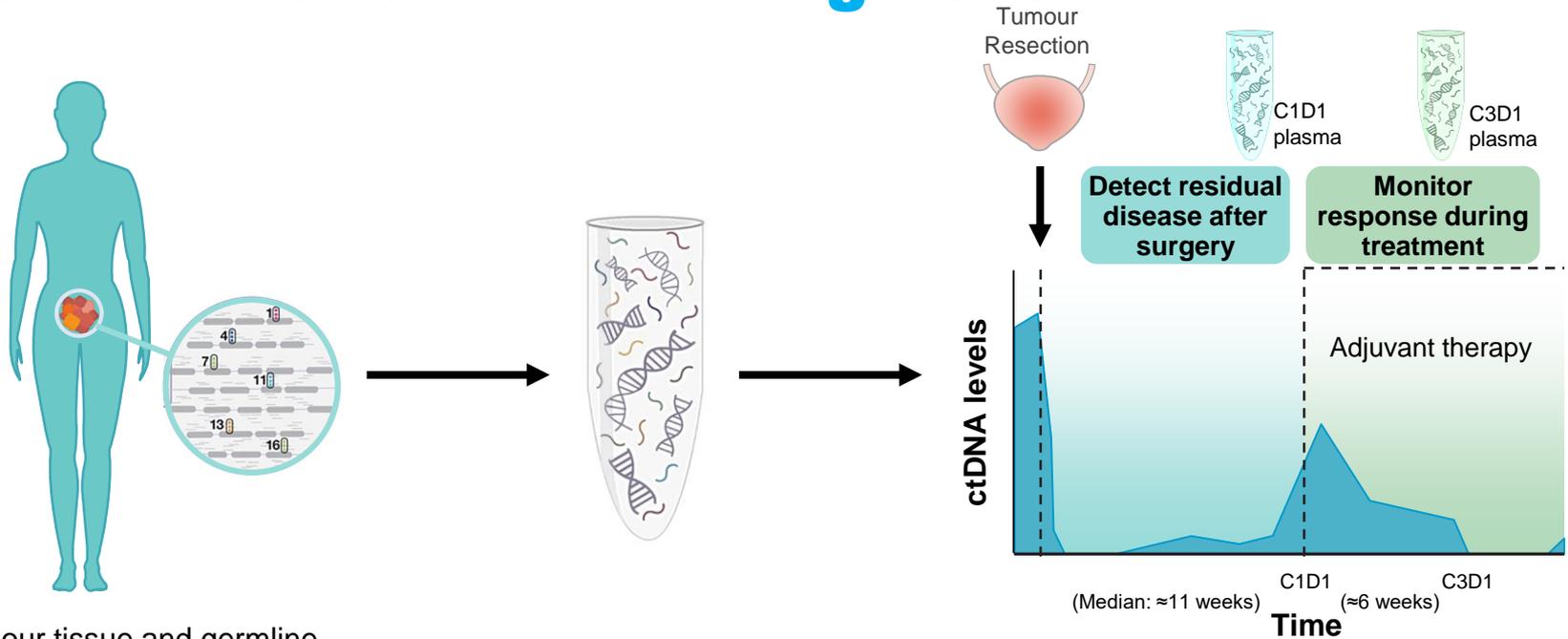


Endpoints

- Primary: DFS (ITT population)
- Key secondary: OS (ITT population)
- Other: Safety
- **Exploratory: predictive, prognostic and pharmacodynamic biomarkers in tumour tissue and blood and their association with disease recurrence**

- IMvigor010 did not meet its primary endpoint (DFS in the ITT population)¹
 - A pre-planned interim OS analysis was performed but could not be formally tested
 - OS follow-up is immature and ongoing in the ITT population
- The PD-L1 and TMB biomarkers did not identify patients benefitting from atezolizumab vs observation in the ITT population
- A pre-specified ctDNA biomarker analysis was performed

Evaluation of ctDNA in IMvigor010



1. Tumour tissue and germline material were sequenced (whole exome sequencing)
2. Up to 16 mutations for personalised mPCR ctDNA assay were identified for each patient

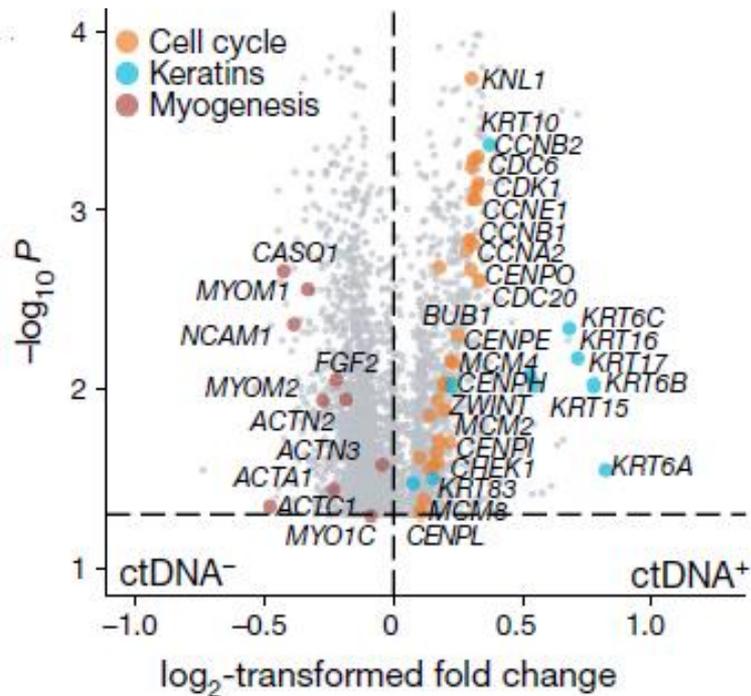
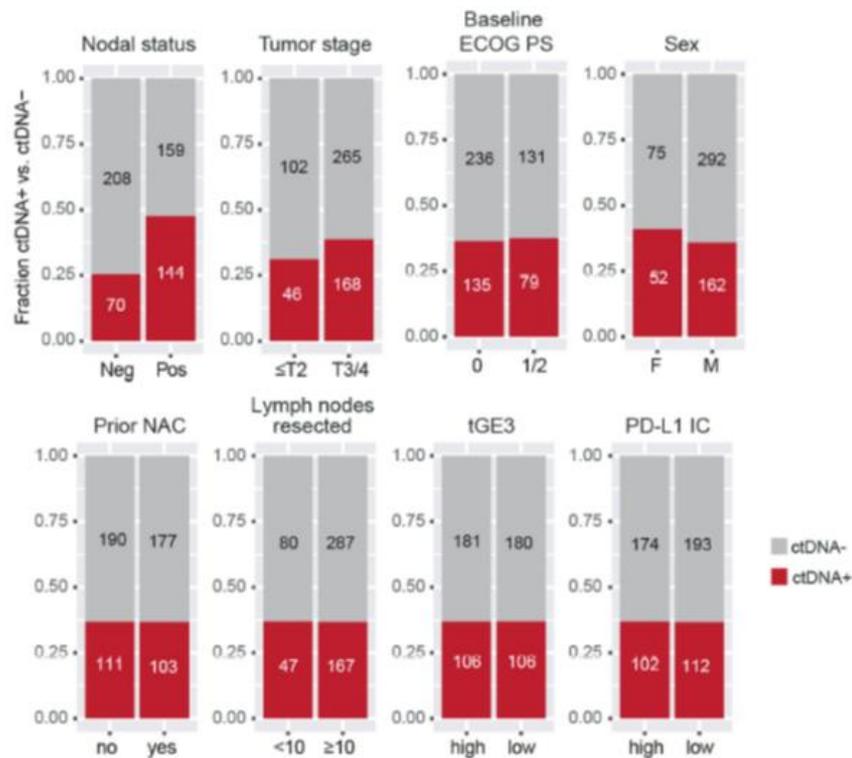
3. Plasma samples were sequenced to $\approx 100,000\times$
4. If ≥ 2 mutations were detected, sample was defined as ctDNA(+)

5. MRD sample timepoint before adjuvant treatment (C1D1) was collected
6. On-treatment sample (C3D1; week 6) was also collected

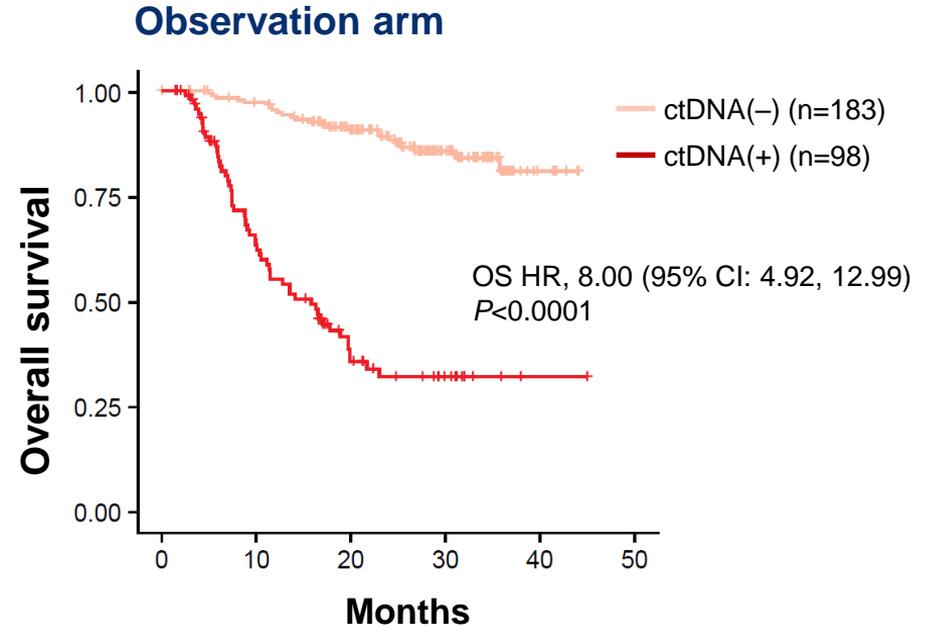
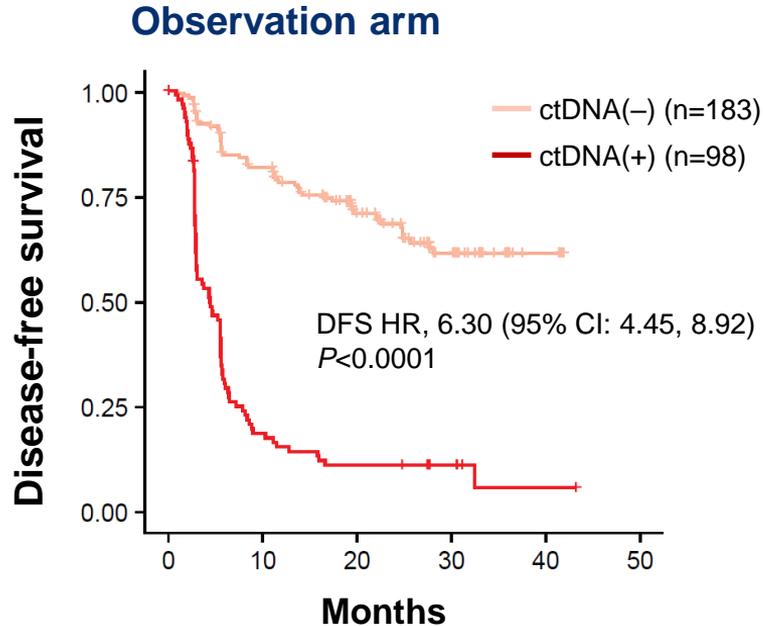
C, cycle; D, day;

29

ctDNA is expressed across broad clinical subgroups and have high expression of cell cycle and keratin genes.

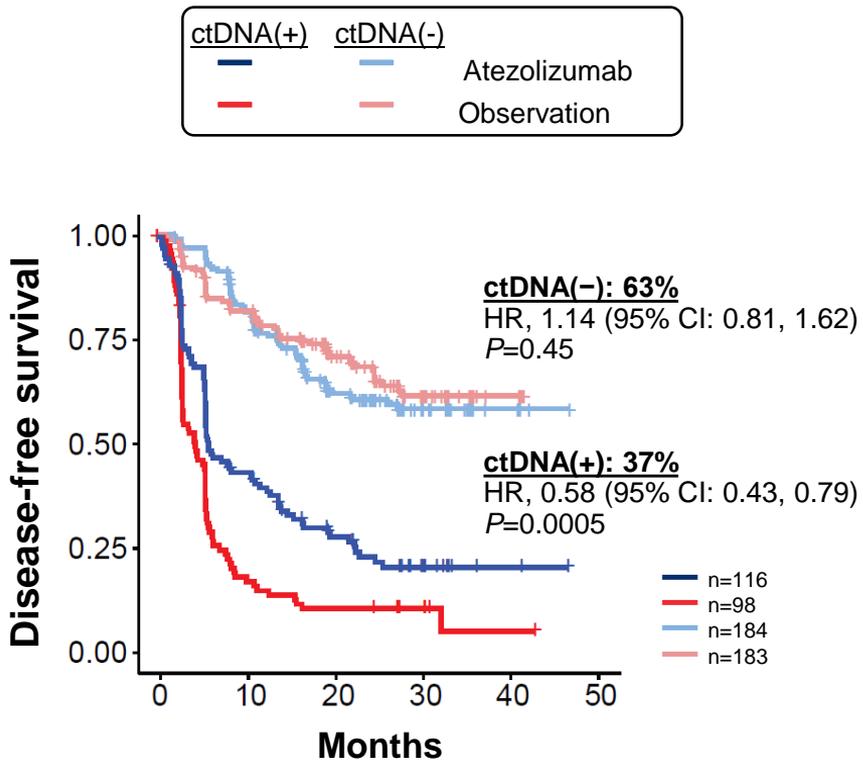


ctDNA(+) patients have poor prognosis

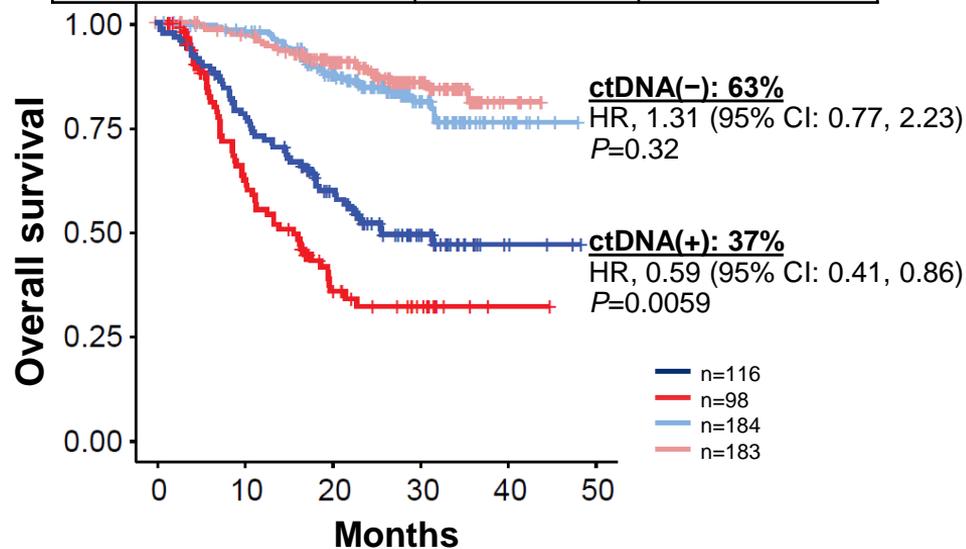


- IMvigor010 confirmed the prognostic value of ctDNA status

ctDNA(+) patients in the BEP had improved DFS and OS with atezolizumab vs observation

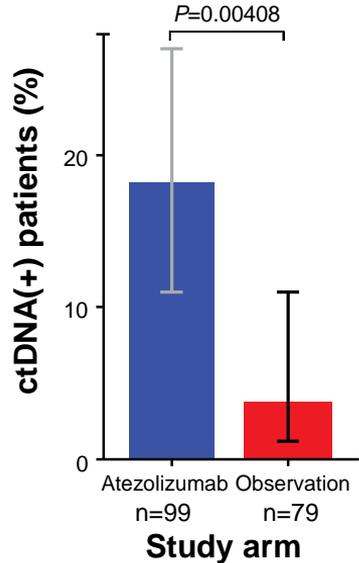


	ctDNA(+) patients	
	Atezolizumab	Observation
Median DFS (95% CI), mo	5.9 (5.6, 11.2)	4.4 (2.9, 5.6)
Median OS (95% CI), mo	25.8 (20.5, NR)	15.8 (10.5, 19.7)



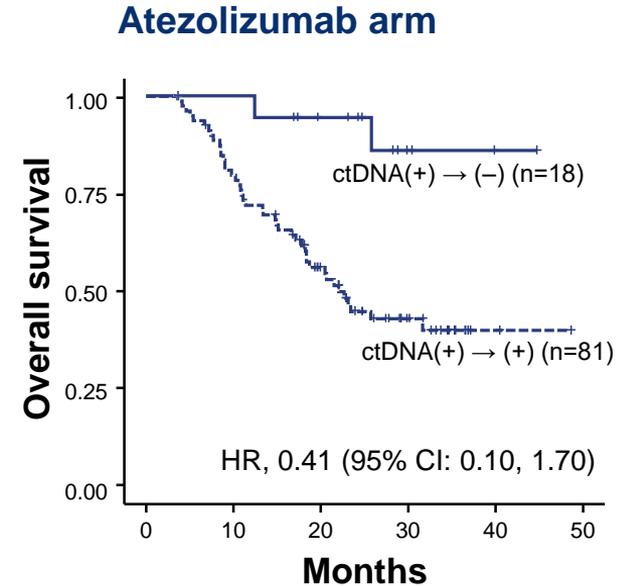
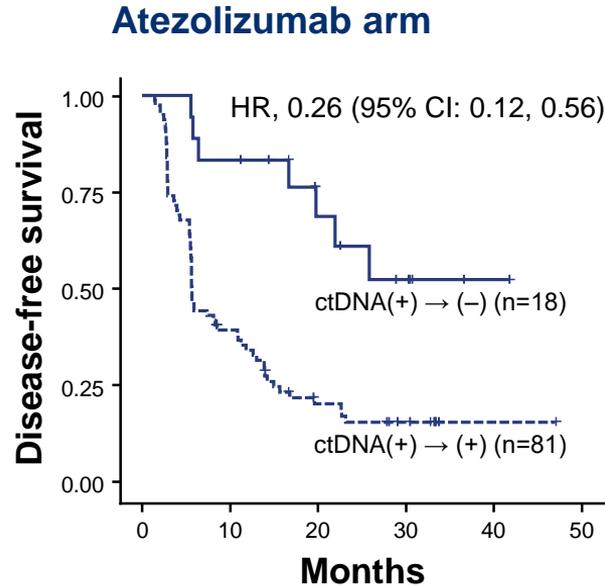
NR, not reached.

ctDNA clearance was associated with improved outcomes in the atezolizumab arm



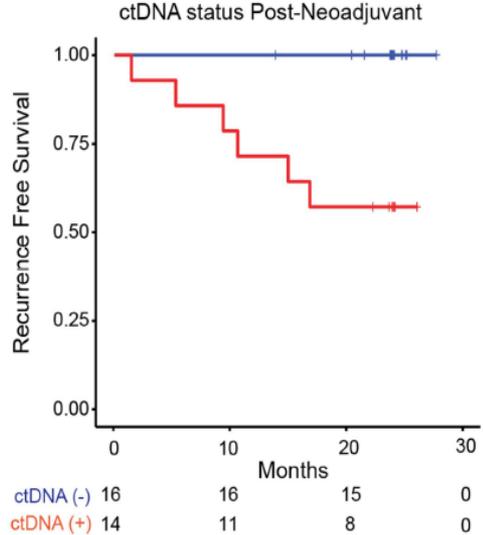
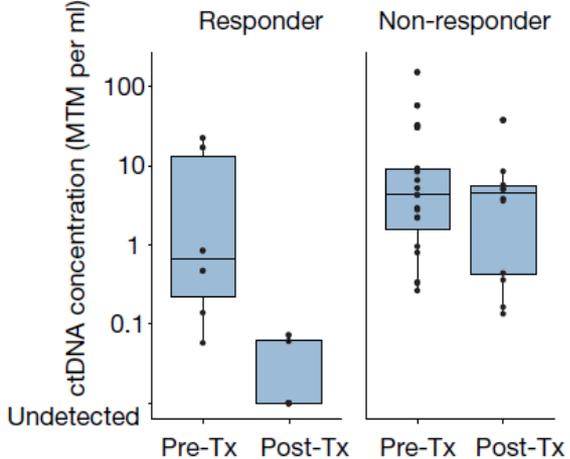
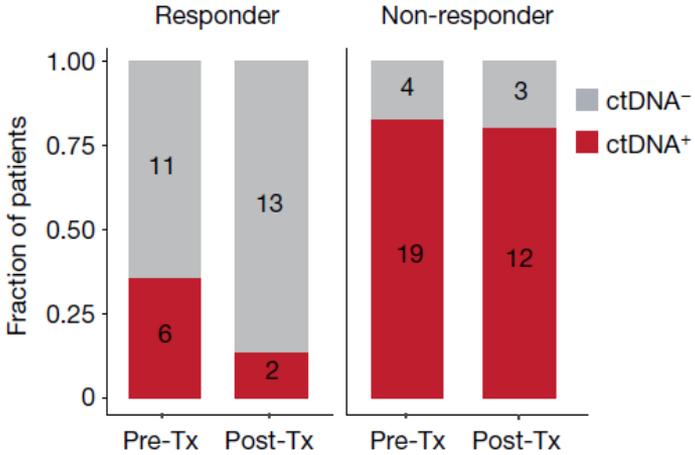
ctDNA(+) → (-)	18 (18.8%)	3 (3.8%)
ctDNA(+) → (+)	81 (81.82%)	76 (96.2%)

- ctDNA clearance occurs at a higher rate in the atezolizumab vs observation arm (C1 → C3)
Assessed using

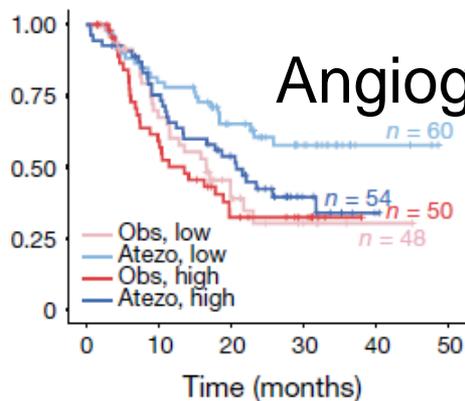
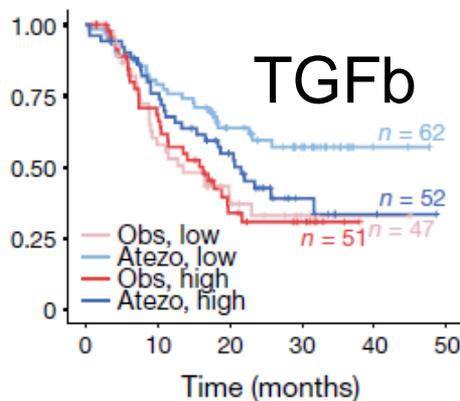
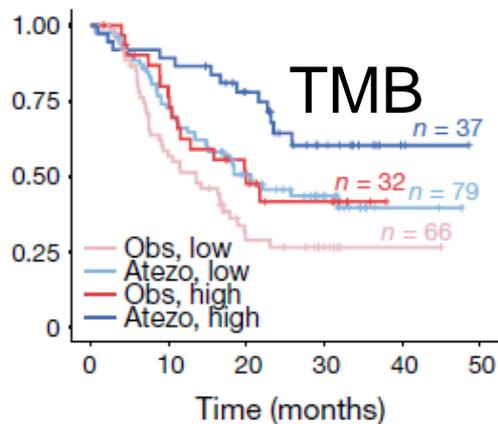
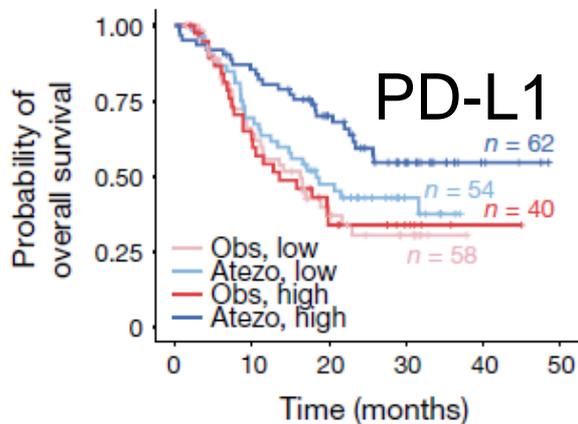


- ctDNA clearance was associated with improved DFS and OS outcomes in the atezolizumab arm

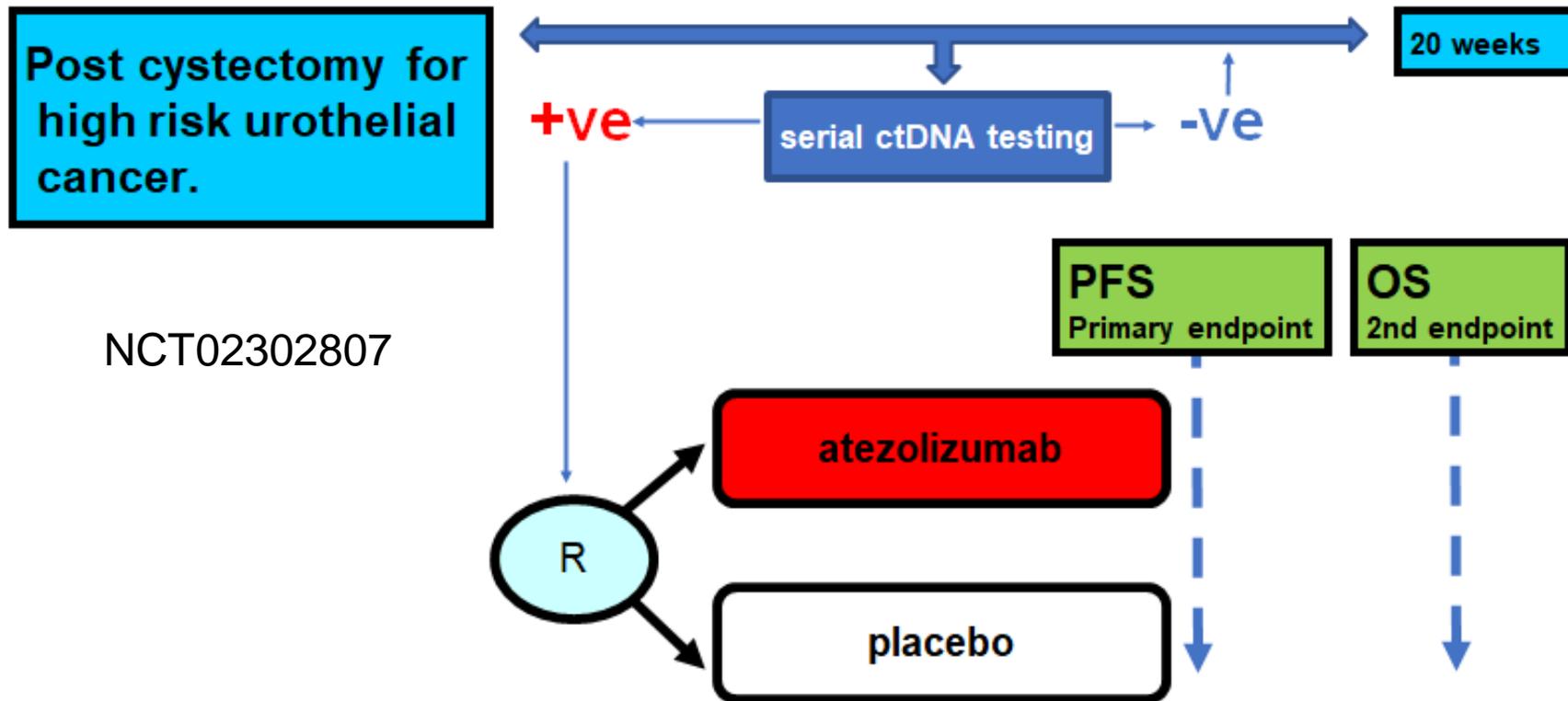
ctDNA levels also fall with neoadjuvant atezolizumab in MIBC.



Outcome in ctDNA+ve patients is related to tissue based immune biomarkers



Adjuvant Atezolizumab vs Placebo in High-Risk Muscle-Invasive Bladder Cancer Who Are ctDNA Positive Following Cystectomy (IMvigor011)



RC48-ADC in Advanced HER2+ Urothelial Cancer

- In an open-label, multicenter, single-arm, non-randomized phase II study 43 eligibility patients
- HER2-positive (IHC 2+ or 3+)
- 51% *confirmed objective response rate* (cORR) per independent central review.
- The most commonly observed treatment-related adverse events included hypoesthesia (numbness), alopecia and hemotoxicity.
- The presented results are expected to support a global late stage clinical trial, including

Summary

- The first generation of biomarkers for single agent ICIs (PD-L1 and TMB) have not changed therapy in metastatic disease. They may have a role in combination with other biomarkers or therapies.
- T effector gene RNA signatures continue to show a strong relationship with response but have not (and may not) be utilized.
- There is a rapid move towards circulating biomarkers with much promise.
- Novel combinations are developing new biomarkers. It would be good to not make the same mistakes.
- Tissue based and circulating biomarkers in combination may be transformative.