# VII SIMPOSIO NACIONAL de ONCOLOGÍA de PRECISIÓN

Vigo, 20 y 21 de febrero de 2025



Dr. Ovidio Fernández Calvo Servicio Oncología Médica Complexo Hospitalario Universitario de Ourense Vigo 21 Febrero 2025

## **Disclosures**

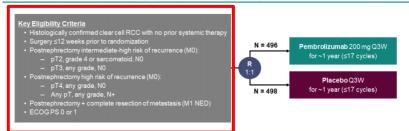
• Consultant or Advisory Role: Astellas Pharma, Pfizer, Bristol-Myers-Squibb, Ipsen, Merck, Eisai

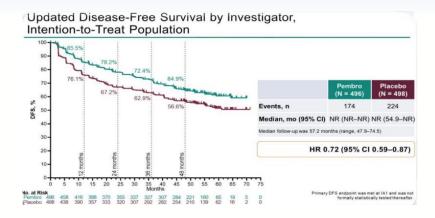
• Speaking honoraria: Novartis, Bristol-Myers-Squibb, Ipsen, Roche, Astellas Pharma, Bayer

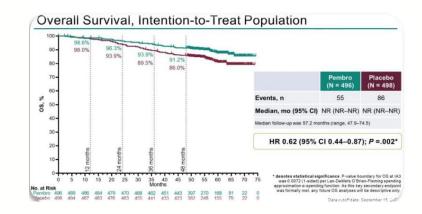
• Travel/Accommodations: Bristol-Myers-Squibb, Ipsen, Astellas

## Keynote 564

### KEYNOTE-564 Study (NCT03142334)



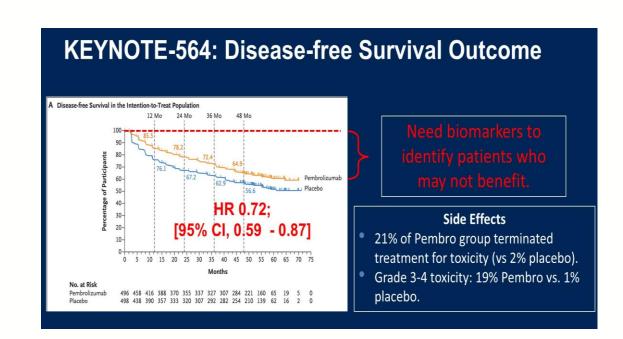




## Keynote 564

## Improvement in both **DFS** and **OS** but......

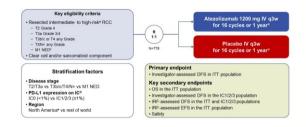
- Overtreatment
- Toxicity
- We need to select patients based on biomarkers



## IMMotion010: Kim-1

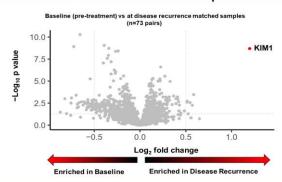
Circulating kidney injury molecule-1 (KIM-1) biomarker analysis in IMmotion010, a randomized Phase 3 study of adjuvant atezolizumab vs placebo in patients with renal cell carcinoma at increased risk of recurrence after resection

### IMmotion010 Study design (NCT03024996)



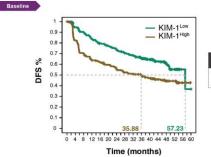
### Circulating biomarker analysis scheme Biomarker identification Association of circulating KIM-1 with DFS outcomes A high-sensitivity, quantitative, electrochemiluminescence A high throughput proteomics analysis was assay was used to evaluate circulating KIM-1 in all performed using an affinity-based proximity extension available baseline, on-treatment, treatment assay panel of approximately 3000 proteins discontinuation and disease recurrence serum samples Circulating proteins with differential abundance A serum KIM-1 cutoff was selected based on optimal and patterns in matched baseline vs disease recurrence stable differentiation of clinical benefit between treatment samples (n=73 pairs) were identified arms Study Treatment: Atezolizumab or Placebo At Disease Recurrence(n=103) Baseline (Pre-treatment) On treatment Or At Discontinuation without (n=752) Disease Recurrence (n=371)

## KIM-1 was identified as the most significantly enriched circulating protein in recurrence vs baseline serum samples in IMmotion010



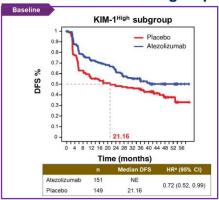
## IMMotion010: Kim-1

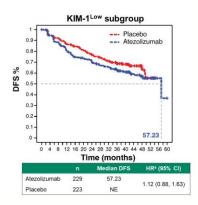
## KIM-1 High status at baseline was associated with worse DFS in IMmotion 010 $\,$



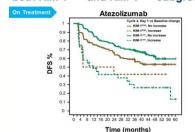
		Median DFS (months)	HR* (95% CI)
KIM-1 <sup>High</sup>	300	35.88	4.75 (4.40.0.47)
KIM-1Low	452	57.23	1.75 (1.40, 2.17)

## Atezolizumab improved DFS vs Placebo in the baseline KIM-1<sup>High</sup> subgroup

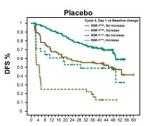




## On-treatment increase in KIM-1 was associated with worse DFS in both KIM-1 $^{\rm High}$ and KIM-1 $^{\rm Low}$ subgroups

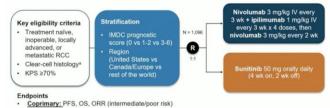


Baseline	On-treatment		Median DFS	HR (95% CI)
KIM-1 <sup>High</sup> Incr	Increase <sup>a</sup>	12	14.8	
KIM-1	No increase	126	NE	1.68 (0.77, 3.69)
KIM-1Low	Increase <sup>a</sup>	34	11.5	
	No increase	179	NE	3.56 (2.21, 5.75)



Time (months)					
Baseline	On-treatment	n	Median DFS	HR (95% CI)	
KIM-1 <sup>Hgh</sup> Increase <sup>®</sup> No increase	Increase*	36	4.8		
	No increase	105	45.4	3.53 (2.24, 5.58)	
KIM-1Low	Increase <sup>a</sup>	28	29.0		
	No increase	179	NE	2.51 (1.42, 4.44)	

## Checkmate-214: Kim-1

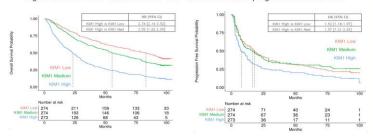


- · Secondary: PFS, OS, ORR (ITT)
- · Exploratory: PFS, OS, ORR (favorable risk)

CheckMate 214

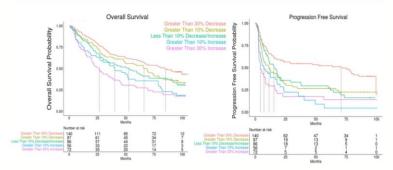
### Baseline KIM-1 levels and clinical outcomes

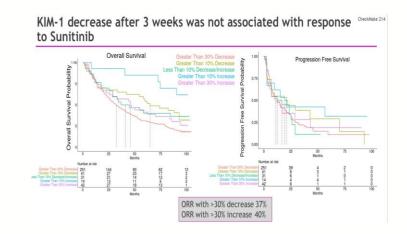
· Higher baseline KIM-1 was associated with worse overall and progression free survival

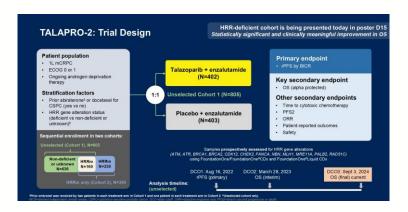


KIM-1 association with outcomes remains significant after adjustment for

### Early KIM-1 decrease associated with PFS & OS in Nivo+lpi arm



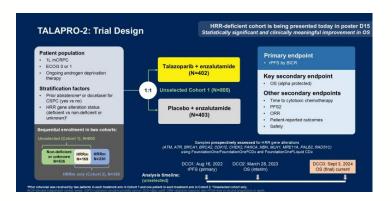




Prior abiraterone <sup>a</sup> or docetaxel, n (%)		109 (27.1)	110 (27.3)
	Abiraterone	21 (5.2)	25 (6.2)
	Docetaxel	86 (21.4)	93 (23.1)
HRR gene alteration status <sup>b</sup> , n (%)	Deficient	85 (21.1)	84 (20.8)
	Non-deficient or unknown	317 (78.9)	319 (79.2)

Tissue source for <u>prospective</u> HRR gene alteration testing, n (%)	Talazoparib + Enzalutamide (N=402)	Placebo + Enzalutamide (N=403)
Tumor tissue	402 (100.0)	403 (100.0)
Tumor tissue and blood (circulating tumor DNA)	57 (14.2)	58 (14.4)

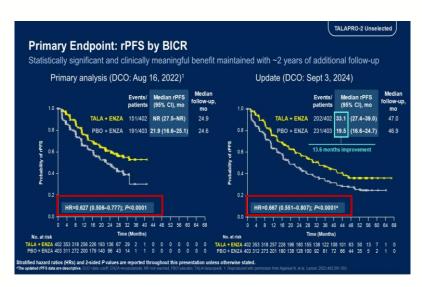
HRR gene alterations by prospective tumor tissue testing, n (%)	Talazoparib + Enzalutamide (N=402)	Placebo + Enzalutamide (N=403)
1 or more alterations in the corresponding gene	85 (21.1)	82 (20.3)
CDK12	23 (5.7)	29 (7.2)
BRCA2	23 (5.7)	28 (6.9)
ATM	23 (5.7)	14 (3.5)
CHEK2	6 (1.5)	5 (1.2)
BRCA1	5 (1.2)	4 (1.0)
Other (ATR, FANCA, MLH1, MRE11A, NBN, PALB2, RAD51C)	14 (3.5)	13 (3.2)

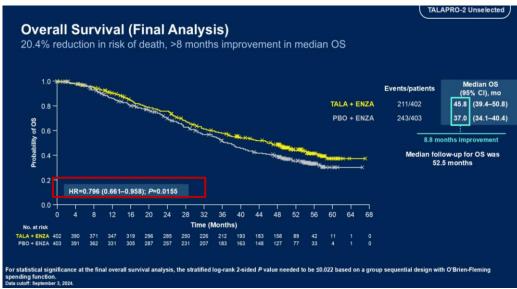


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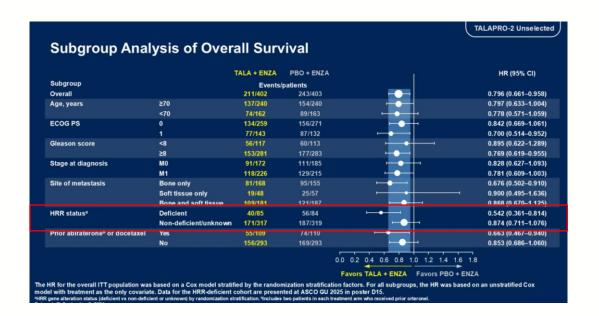
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HRR gene alterations by prospective tumor tissue testing, n (%)¹	Talazoparib + Enzalutamide (N=402)	Placebo + Enzalutamide (N=403)
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CDK12	23 (5.7)	29 (7.2)
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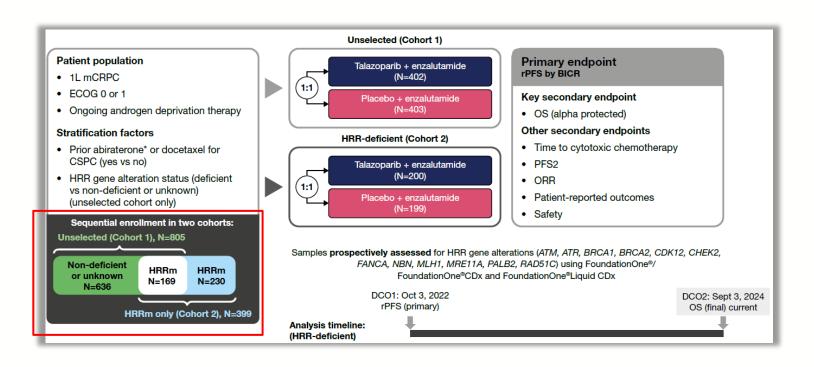


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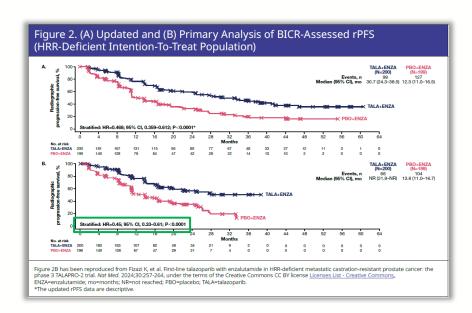


TEAEs, n (%)	TALA + ENZA (N=398)	PBO + ENZA (N=401)	No new safety findings were
Any TEAE	394 (99.0)	384 (95.8)	identified after an additional 2 years of follow-up
Treatment-related	360 (90.5)	286 (71.3)	No additional cases of MDS or
SAEs	182 (45.7)	126 (31.4)	AML in the talazoparib group;
Treatment-related	85 (21.4)	13 (3.2)	n=1 of each previously reported
Grade 3–4 TEAEs	302 (75.9)	179 (44.6)	Rate of discontinuation of
Grade 5 TEAEs	14 (3.5)	20 (5.0)	talazoparib due to AEs was
Treatment-related	1 (0.3)	2 (0.5)	similar to that in the primary
Dose interruption of talazoparib or placebo due to AE	260 (65.3)	99 (24.7)	<ul> <li>analysis</li> <li>In exposure-adjusted analyses,</li> </ul>
Dose reduction of talazoparib or placebo due to AE <sup>a</sup>	217 (54.5)	29 (7.2)	rate of venous embolic and thrombotic events was
Discontinuation of talazoparib or placebo due to AE	86 (21.6)	52 (13.0)	(2.4 per 100 participant-years)



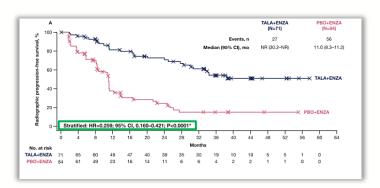


### rPFS HRR population

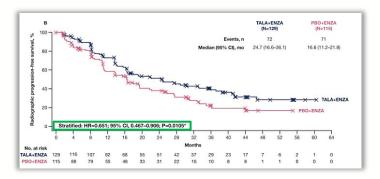


rPFS favored TALA plus ENZA in patients with and without BRCA1/2 alterations

### rPFS BRCA1/2



### rPFS Non-BRCA1/2 HRRm



### Overall Survival HRR (Final Analysis)<sup>1</sup>

TALAPRO-2 HRRm

PBO+ENZA

(N=199)

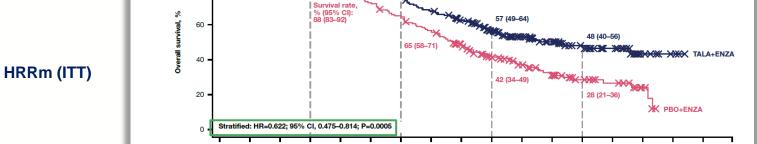
31.1 (27.3-35.4)

TALA+ENZA

(N=200)

45.1 (35.4-NR)

Events, n Median (95% CI), mo



A. Any HRR Gene Alterations (HRR-Deficient Intention-To-Treat Population)

80

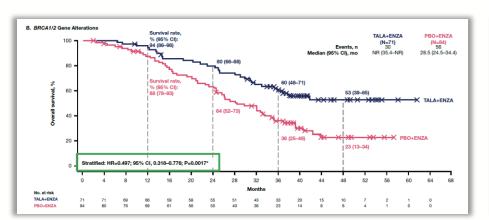
Survival rate,

% (95% CI):

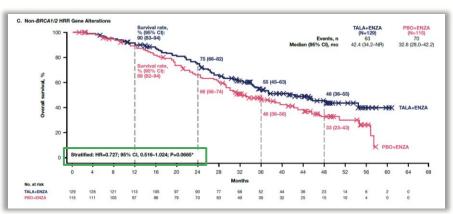
At a median follow-up of 44.2 months, treatment with TALA plus ENZA resulted in a 38% reduced risk of death vs ENZA plus PBO for patients with HRR-deficient mCRPC

### Overall Survival BRCA1/2 (Final Analysis)<sup>1</sup>

### BRCA1/2



### Non-BRCA1/2 HRRm



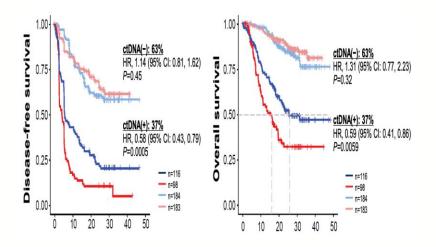
 Patients with BRCA1/2 gene alterations had a 50% reduction in risk of death and those with non-BRCA1/2 HRR gene alterations had a 27% lower risk of death with TALA plus ENZA vs ENZA plus PBO

<sup>\*</sup>The P values are nominal and descriptive for the subgroup analyses.

Tissue sample for PD-L1 testing

## Imvigor 010: ctDNA exploratory analysis

# Key eligibility<sup>a</sup> High-risk MIUC (bladder, renal pelvis, ureter) Radical cystectomy/nephroureterectomy with LN dissection within ≤ 14 weeks - ypT2-T4a or ypN+ for patients treated with NACb - pT3-T4a or pN+ for patients not treated with NACb No postsurgical radiation or AC If no prior NAC given, patient had to be ineligible for, or declined, cisplatin-based AC ECOG PS 0-2 Observation<sup>c</sup> q3w



### Study desing

#### Screening Surveillance Treatment Follow-Up · High-risk MIBC Atezolizumab Primary ctDNA+ - (y)pT2-T4a N0 M0 or (y)pT0-T4a N+ × 1 y analysis Treatment M0 at cystectomy population: Serial plasma collection Follow-Up Received or did not receive prior NAC Placebo g6w for 6 mo Not included Eligible or not eligible for AC post-cystectomy; $\times 1 y$ in analysis g12w for months 6-12 Cystectomy within past 6-24 weeks with no evidence of residual disease Radiographic imaging No known PD-L1 status for adjuvant q12w for up to 12 mo Surveillance Radiographic Survival follow-up post-cystectomy aroup: Included imaging q6m for 2 y q6m for 2 y Available tumour sample for PD-L1 status<sup>a</sup> in analysis and WES and matched blood sample ctDNA- definition: Primary endpoint: · Disease-free status at baseline Investigator-assessed DFS ≥1 ctDNA- result and no ctDNA+ result Key secondary endpoint: ≥1 post-baseline diseases assessment OS . Completed ≥12 mo of surveillance post-cystectomy or discontinued surveillance <12 mo with no ctDNA+ result

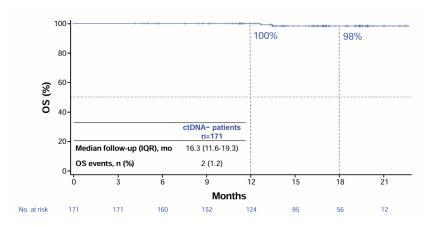
### ctDNA- population

Characteristic		All ctDNA- patients n=171
Median age (range), y		69 (40-90)
Race, n (%)	White	96 (56.1)
	Asian	63 (36.8)
	Othera	12 (7.0)
Male, n (%)		135 (78.9)
ECOG PS at	0	115 (67.3)
screening, n (%)	1	49 (28.7)
<b>o</b>	2	7 (4.1)
Histology at radical	UC	142 (83.0)
resection, n (%)	UC with mixed histology	29 (17.0)
Tumour stage, n (%)b	<t2< td=""><td>18 (10.7)</td></t2<>	18 (10.7)
	T2	59 (34.9)
	T3	74 (43.8)
	T4	18 (10.7)
Nodal stage, n (%)	N0	135 (78.9)
_	N+	36 (21.1)
PD-L1 status, n (%)c	IC0/1	98 (57.6)
	IC2/3	72 (42.4)
Lymph nodes	<10	37 (22.2)
removed, n (%)d	≥10	130 (77.8)
Lymph node density,	<20	162 (97.0)
n (%)d	≥20	5 (3.0)
Prior neoadjuvant	Yes	83 (48.5)
chemotherapy, n (%)	No	88 (51.5)

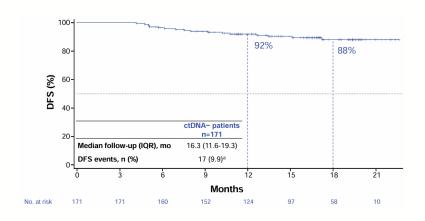
### **DFS** in the ctDNA-population



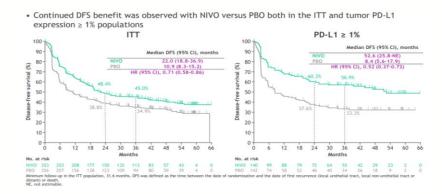
### OS in the ctDNA-population



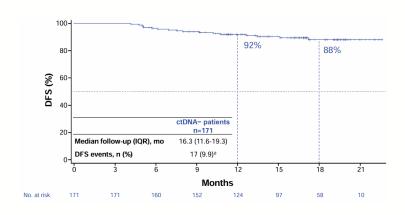
### **DFS** in the ctDNA-population



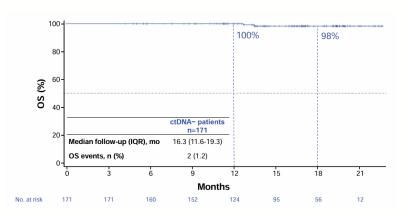
### **DFS in Checkmate274**



### **DFS** in the ctDNA-population

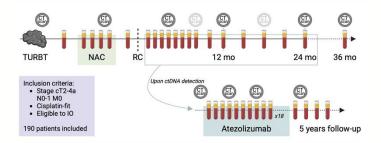


### OS in the ctDNA-population



- We need longer follow-up in both arms
- Has ctDNA negative a negative predictive value?
- Serial ctDNA testing may have greater clinical hability than landmark ctDNA as a risk stratification tool using Natera Signature

## **Tombola Trial**



### Primary objective:

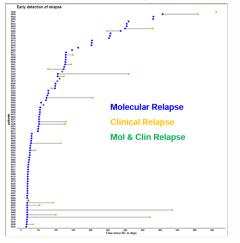
 Complete response (CR) after treatment with investigational agent initiated by ctDNA positive status after radical cystectomy.

CR defined as NED = negative ctDNA and no visible metastasis on CT

### Secondary objectives:

- Duration of freedom from clinical relapse
- Overall survival
- Cancer specific survival

### Relapse following cystectomy



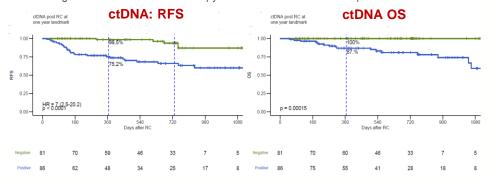
56% were ctDNA+ post-RC

75% were detected < 4 months post RC

Of the ctDNA- patients, only 2 (3%) developed metastases on CT-scan during follow-up

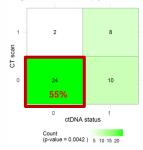
## **Tombola Trial**

Oncological outcome – immunotherapy at the time of molecular relapse



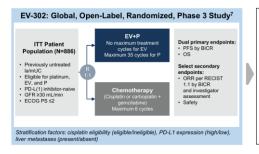
### **Primary endpoint**

NED (No evidense of disease) (CT and ctDNA-) following immunotherapy



# **EV-302: Exploratory Analysis Nectin-4 Expression**

### Study Design and Methods

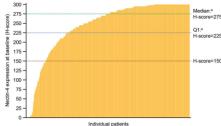


### Exploratory Nectin-4 Biomarker Analysis

- Retrospective assessment of Nectin-4 expression<sup>a</sup> by a CAP/CLIA validated Nectin-4 IHC assay in primary or metastatic tumor tissue<sup>b</sup>
- Nectin-4 expression and Nectin-4/PD-L1 expression were available for 800 of 886 randomized patients (EV+P: n=394; chemotherapy; n=406)
- PD-L1 expression status was determined as high (CPS ≥10) or low (CPS <10) using a validated PD-L1 IHC assay<sup>o</sup>
- Clinical efficacy (PFS, OS, and ORR) was assessed in Nectin-4 expression subgroups

### Distribution of Nectin-4 H-Scores Was Skewed Toward High Expression

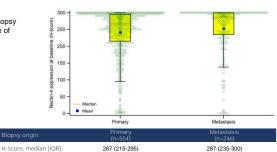




Variable	EV+P (n=394)	Chemotherapy (n=406)
H-score, median (IQR)	280 (230-298)	270 (215-297)
Subgroup, H-score, n (%)		
<150	38 (9.6)	50 (12.3)
≥150 to <225	50 (12.7)	56 (13.8)
≥225	306 (77.7)	300 (73.9)
Patients with H-score 0, n (%)	3 (0.8)	6 (1.5)

High Nectin-4 H-Scores Were Observed Regardless of the Biopsy Origin

 The majority (69%) of biopsy samples submitted were of primary origin<sup>a</sup>



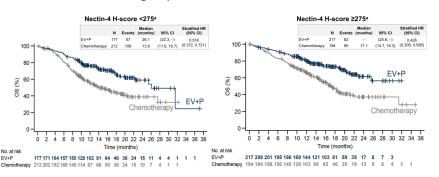
Data cutoff: 8 August 2023.

EV, enfortumab vedion; IOR, interquartile range; la/mUC, locally advanced or metastatic urothelial cancer; P, pembrolizumab.

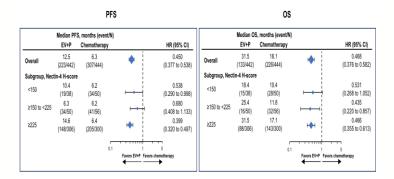
"These are not matched biopsies; one tumor tissue sample was submitted for each patient.

# **EV-302: Exploratory Analysis Nectin-4 Expression**

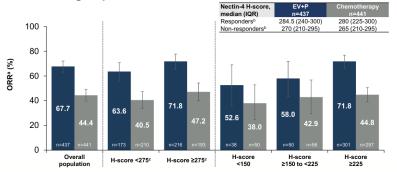
## Consistent OS Benefit with EV+P in Both <275 and ≥275 Nectin-4 H-Score Subgroups



## Consistent PFS and OS Benefit with EV+P Across Nectin-4 H-Score Subgroups



Consistent ORR Benefit with EV+P Across All Nectin-4 Subgroups



## Conclusions

Adjuvant Pembrolizumab treatment improves OS in High-Risk RCC patients

Kim-1 could be a biomarker to select which patients could benefit from adjuvant immmunotherapy

KIM- 1: Preliminary data in patients with advanced disease treated with IO show positivy results

Talapro2 (Talazoparib + Enzalutamide) demonstrate an improvement in OS in mCRP patients

The question is: what patients? All corners? HRR +? BRCA1/2? And others....

ctDNA is the most promising biomarker in UC (Adjuvant setting) but ......

We can not actually select treatment based on this results

EV +P improve OS independent on Nectin-4 expression

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Dr. Ovidio Fernández Calvo Servicio Oncología Médica Complexo Hospitalario Universitario de Ourense Vigo 21 Febrero 2025