

INTERNATIONAL SYMPOSIUM

GU-Alliance for Research and Development



PRESENCIAL RETRANSMITIDO EN DIRECTO FACE-TO-FACE AND LIVE STREAMING

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Espacio Maldonado, Madrid



Talapro-2

¿A qué pacientes debemos testar? ¿Cuáles son candidatos a tratamiento?

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- Employment: None
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TALAPRO-2. Who should we test? Who is the ideal candidate for treatment?

Who to test?

Do PARPi – NHA combinations eliminate the need for testing?

Who is the ideal candidate for treatment?

What, where and when to test?



Who to test? Test everybody!!

Testing has <u>prognostic</u> implications (outcome)

Testing has implications for the <u>family risk</u> of cancer Testing has predictive implications (treatment selection)

Do PARPi - NHA combinations eliminate the need for testing?

Who is the ideal candidate for treatment?

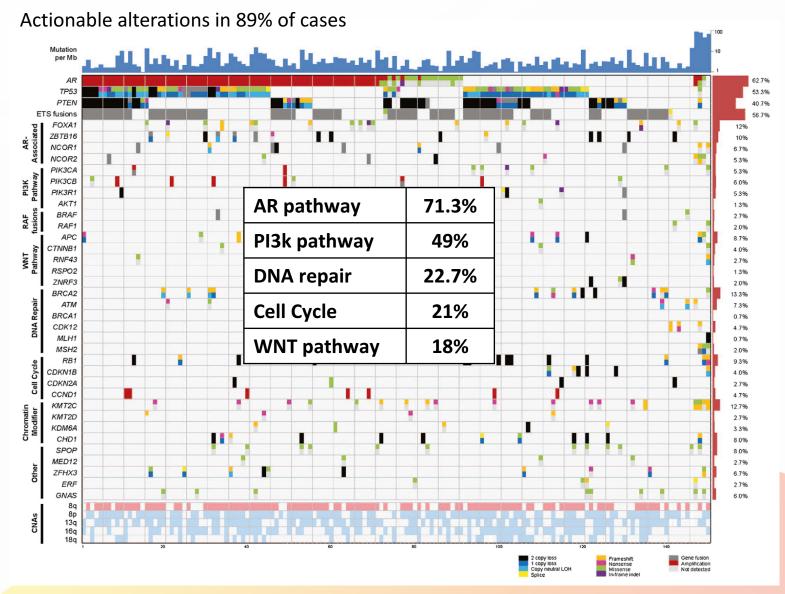
The ideal candidate is the one that <u>reflects the clinical trial population</u> expected benefit is greater than anticipated tox<u>icity</u> (disease burden)

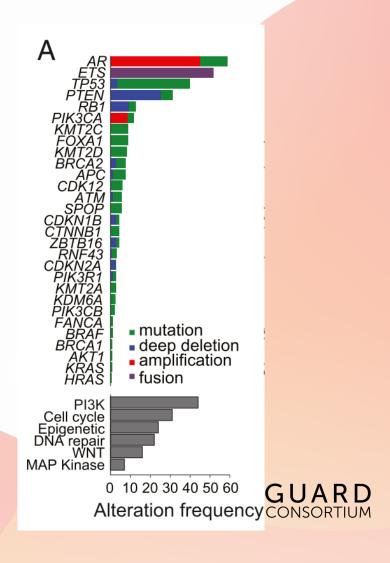
ECOG PS 0-1, adequate hematic-renal function, metastases defined by CT/Bone scar

What, where and when to test?



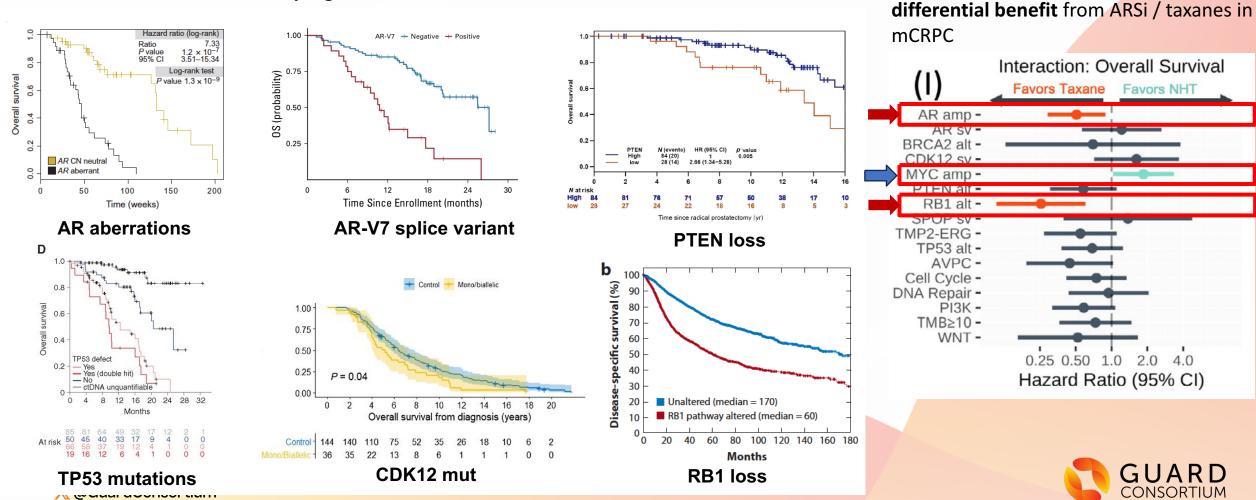
Molecular characterization in advanced prostate cancer





Clinical utility of genomic profiling in mCRPC

AR aberrations, loss of tumor suppressors (TP53, RB1, PTEN), DNA repair alterations... all **associated with adverse prognosis**

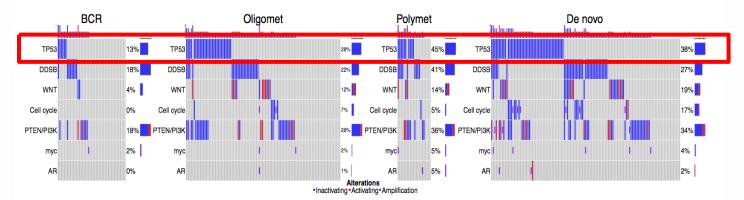


Some alterations could be associated with

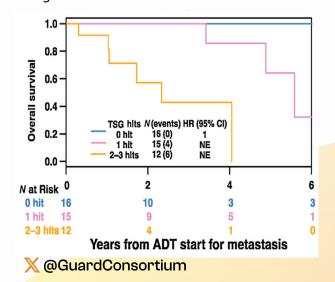
Genomic alterations and prognosis in mHSPC

Loss of function of tumor supressors is associated with adverse prognosis

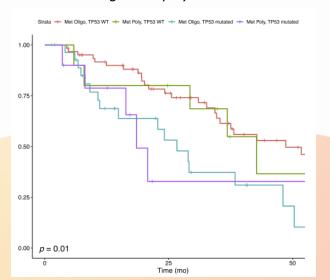
Increased TP53 alterations with higher volume of metastatic disease



Mutations in the TP53, RB1 and PTEN suppressor genes associated with adverse outcome

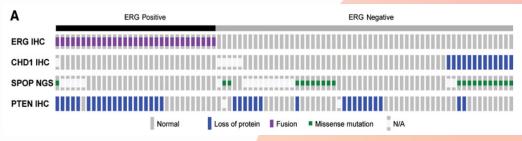


TP53 mutations associated with adverse prognosis in both oligo- and polymetastatic disease

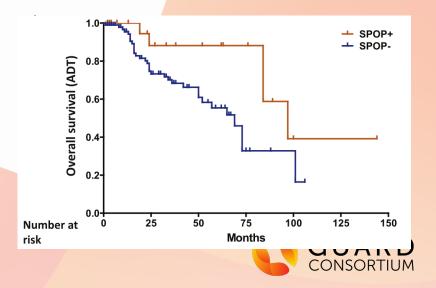


SPOP mutations associated with favorable prognosis

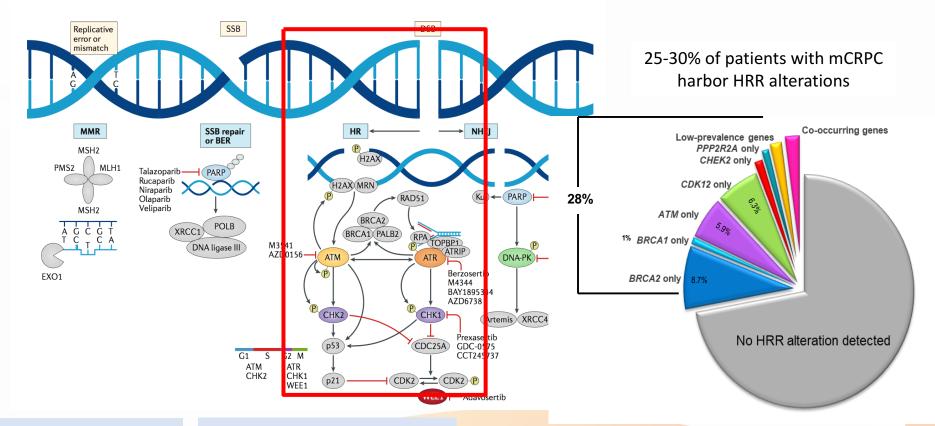
Most frequently mutated gene in prostate cancer Mutations in the MATH domain



SPOP mutation associated with higher response rate and time on abiraterone in mCRPC



DNA repair alterations in advanced prostate cancer



Mismatch Repair

Base Excision Repair (BER)

Non-homologous end-joining

Homologous recombination (HR)

#guardsymposium2025

X@GuardC Yap et al. Nat Rev Oncol 2019. De Bono et al. N Eng J Med 2020. Olmos et al Ann Oncol 2024. Olmos et al Ann Oncol 2025.

BRCA genes are the most frequently mutated

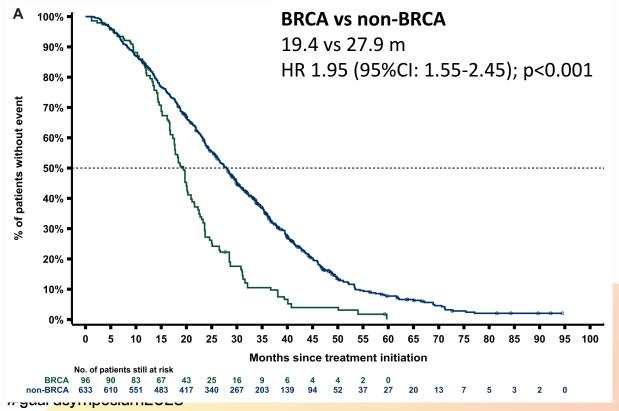
| mCRPC | mHSPC | | |
|-------|--|--|--|
| 8.4% | 7.9% | | |
| 2.6% | 1.1% | | |
| 10.7% | 11.3% | | |
| 1.9% | 1.6% | | |
| 2.1% | 2% | | |
| 1.5% | 3% | | |
| 5.2% | 3.6% | | |
| 2.9% | 2.9% | | |
| 0.5% | 1.3% | | |
| 0.4% | 1.1% | | |
| 0.7% | 1.3% | | |
| | 8.4% 2.6% 10.7% 1.9% 2.1% 1.5% 5.2% 2.9% 0.5% 0.4% | | |



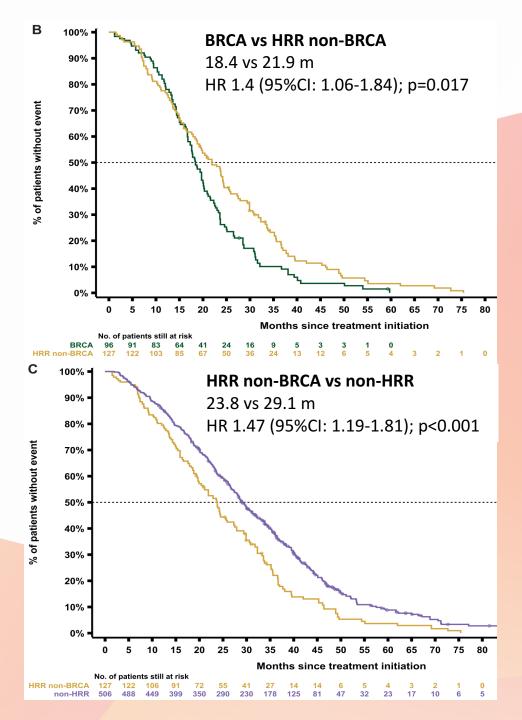
HRR alterations and prognosis The CAPTURE study - Cohort 1 (mCRPC)

N=729. mCRPC undergoing 1st L therapy. 1L ARSi (64.6%) 1L Taxanes (35.4%)

| BRCA | Non-BRCA HRR | Non- HRR | |
|-------|-----------------|-------------|--|
| 13.2% | 17.4% | 69.4% | |



X @GuardConsortium
Olmos et al. Ann Oncol 2024

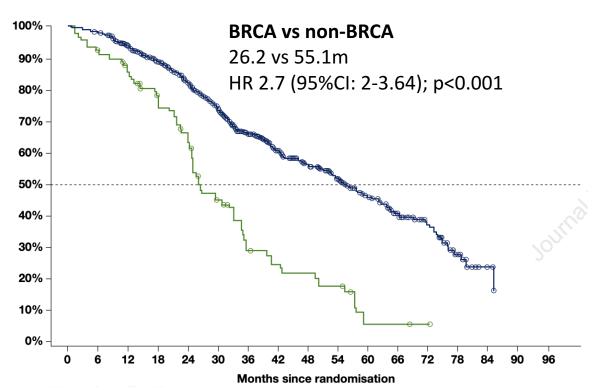


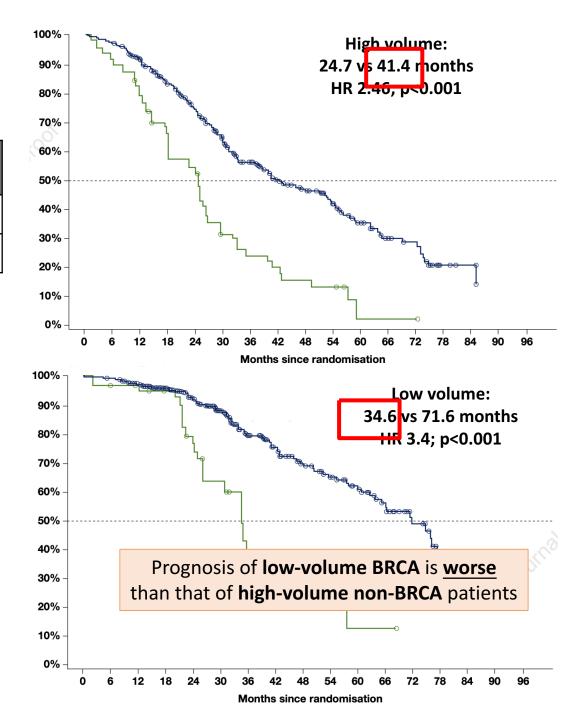
HRR alterations and prognosis The CAPTURE study - Cohort 2 (mHSPC)

The CAPTURE study

N=556. mHSPC patients. Hi Vol 55%. ADT alone (13%), ADT + ARSi (45%), ADT + Docetaxel (30%), ADT + ARSi + Docetaxel (11%)

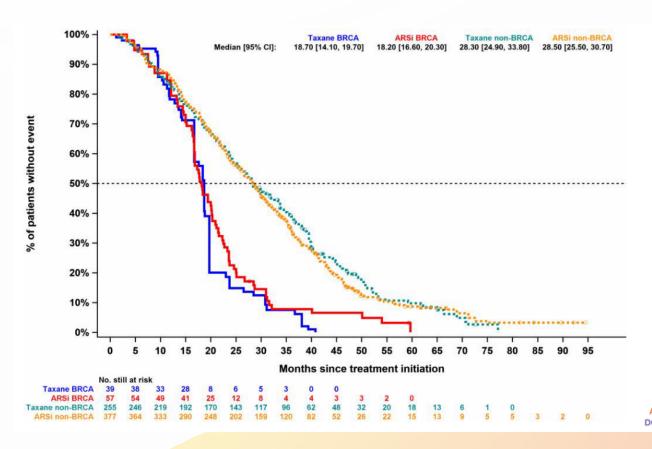
| | All pts | Hi Vol | Low Vol |
|------|---------|-----------|------------|
| BRCA | 13.3% | 13.7% | 12.8% |
| HRR | 28.4% | 28.1% | 28.8% |



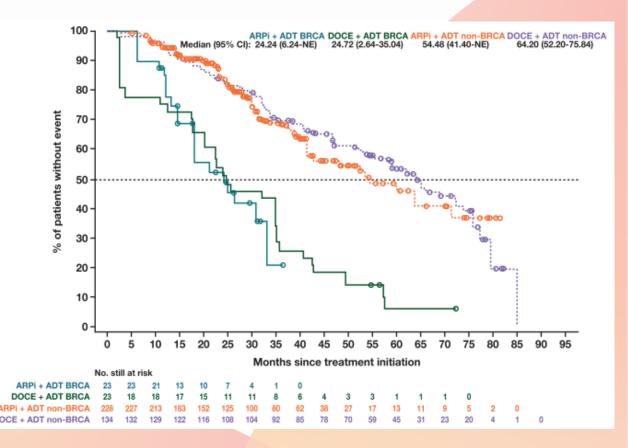


Conventional therapy is ineffective in BRCA mutants

mCRPC: no OS difference 1st line taxane vs ARSi



mHSPC: no OS difference ADT+ARSi vs ADT+Taxane







Non-BRCA HRR is a heterogeneous subgroup

Impact of **individual non-BRCA HRR alterations** on outcome in patients treated with ARSIs or taxanes as first-line therapy for mCRPC (CAPTURE Cohort 1)

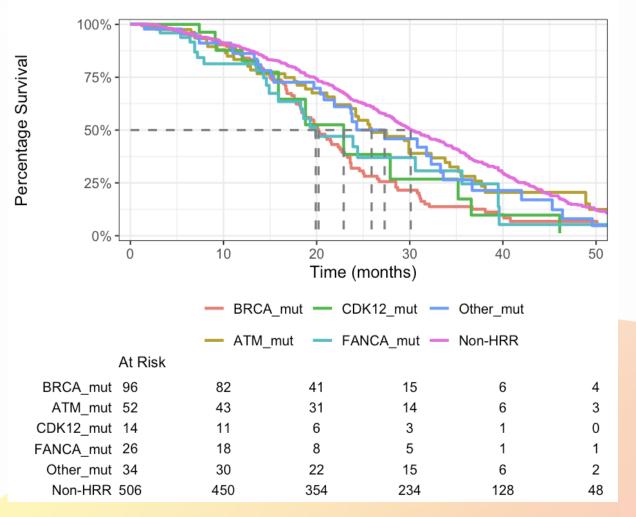


TABLE 1. PATIENT CHARACTERISTICS

| | | Non-HRR (N=506) | BRCA (N=96) | ATM (N=52) | CDK12 (N=14) | FANCA (N=26) | Other (N=34) |
|---|----------------|--------------------|----------------|---------------|-----------------|-----------------|-----------------|
| | <65 | 114 (23%) | 16 (17%) | 18 (35%) | 5 (36%) | 7 (27%) | 5 (15%) |
| Age (yr) | 65-75 | 201 (40%) | 41 (43%) | 20 (39%) | 2 (14%) | 11 (42%) | 14 (41%) |
| *** | >=75 | 191 (38%) | 39 (41%) | 14 (27%) | 7 (50%) | 8 (31%) | 15 (44%) |
| Stage I | V at diagnosis | 244 (48%) | 41 (43%) | 22 (42%) | 5 (36%) | 18 (69%) | 13 (38%) |
| Albu | min < 4 g/dL | 181 (36%) | 46 (48%) | 13 (25%) | 5 (36%) | 12 (46%) | 14 (41%) |
| Α | LP≥ULN | 237 (47%) | 58 (60%) | 35 (67%) | 6 (43%) | 15 (58%) | 13 (38%) |
| H | lb ≤ 12.5 | 185 (37%) | 40 (42%) | 16 (31%) | 6 (43%) | 10 (39%) | 11 (32%) |
| LI | DH ≥ ULN | 225 (45%) | 46 (48%) | 31 (60%) | 7 (50%) | 14 (54%) | 17 (50%) |
| PSA | > 50 ng/dL | 180 (36%) | 41 (43%) | 23 (44%) | 8 (57%) | 13 (50%) | 11 (32%) |
| ECOG | >=1 | 268 (53%) | 52 (54%) | 28 (54%) | 8 (57%) | 14 (54%) | 16 (47%) |
| ECOG | 0 | 238 (47%) | 44 (46%) | 24 (46%) | 6 (43%) | 12 (46%) | 18 (53%) |
| Gleas | on Score >= 8 | 318 (63%) | 63 (66%) | 33 (64%) | 11 (79%) | 22 (85%) | 15 (44%) |
| Bone metastases > 10 Visceral metastases Time to mCRPC ≥ median | | 86 (17%) | 18 (19%) | 8 (15%) | 3 (21%) | 9 (35%) | 4 (12%) |
| | | 70 (14%) | 9 (9%) | 3 (6%) | 5 (36%) | 4 (15%) | 6 (18%) |
| | | 268 (53%) | 42 (44%) | 20 (39%) | 8 (57%) | 8 (31%) | 20 (59%) |
| 1st line | Taxanes | 200 (40%) | 34 (35%) | 25 (48%) | 5 (36%) | 13 (50%) | 12 (35%) |
| therapy | ARSIs | 306 (60%) | 62 (65%) | 28 (52%) | 9 (64%) | 13 (50%) | 22 (65%) |

TABLE 2. IMPACT OF NON-BRCA MUTATION STATUS ON OS AND RPFS (MULTIVARIABLE MODEL)

| | Median (95%CI) | HR (95%CI) vs BRCA | HR (95%CI) vs non-HRR | |
|------------------------|-------------------------|---------------------------|--|--|
| OVERALL SURVIVA | L | | | |
| Non-HRR | 29.6 m (27.9-32.1) | - | - | |
| BRCA | 18.4 m (16.7-20.2) | - | - | |
| ATM | 24.2 m (17.9-29.4) | 0.65 (0.43-0.97); p=0.035 | 1.25 (0.9-1.7); p=0.17 | |
| CDK12 | 17.4 m (9.2-35.2) | 1.38 (0.68-2.8); p=0.37 | 2.1 (1.2-3.6); p=0.015 | |
| FANCA | FANCA 17.1 m (7.9-23.9) | 0.97 (0.58-1.62); p=0.91 | 1.9 (1.2-2.9); p=0.003 1.3 (0.9-1.9); p=0.139 | |
| Other | 24 m (15-33) | 0.66 (0.4-1); p=0.07 | | |
| RADIOGRAPHIC PR | ROGRESSION-FREE SURVIV | AL . | | |
| Non-HRR | 11 m (10.1-12) | - | - | |
| BRCA | 7.1 m (6.2-8.5) | - | - | |
| ATM | 7.7 m (6.4-10.3) | 0.76 (0.5-1.2); p=0.194 | 1.37 (0.98-1.9); p=0.07 | |
| CDK12 | 9.2 (3.1-12.2) | 1.33 (0.6-2.9); p=0.48 | 1.54 (0.8-2.9); p=0.167 | |
| FANCA | 7.1 (3.6-11) | 1.1 (0.64-1.8); p=0.77 | 1.9 (1.2-3); p=0.004 | |
| Other | 11 (7.3-15.2) | 0.81 (0.5-1.3); p=0.386 | 1.4 (0.97-2.1); p=0.07 | |

Lorente et al. ESMO 2024

Who to test? Test everybody!!

Testing has <u>prognostic</u> implications (outcome)
Testing has implications for the family risk of cancer

Testing has predictive implications (treatment selection)

Do PARPi – NHA combinations eliminate the need for testing?

Who is the ideal candidate for treatment?

The ideal candidate is the one that <u>reflects the clinical trial population</u> expected <u>benefit</u> is <u>greater than anticipated toxicity</u> (disease burden

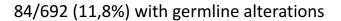
ECOG PS 0-1, adequate hematic-renal function, metastases defined by CT/Bone scan

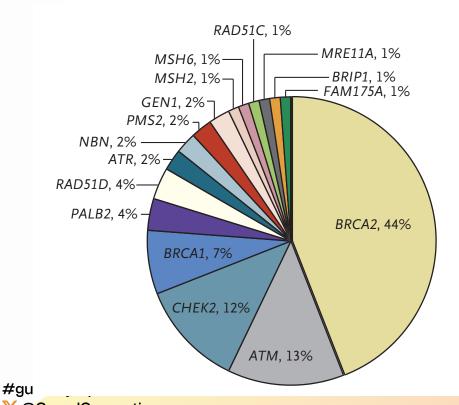
What, where and when to test?

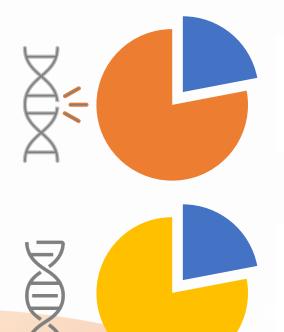


Germline BRCA alterations

692 men with metastatic prostate cancer unselected for family history of cancer or age at diagnosis were assessed for mutations in 20 DNA repair genes







Among 72 men with germline DNA-repair mutations

22% had a family history of PC

Among 537 men without germline DNA-repair mutations

22% had a family history of PC

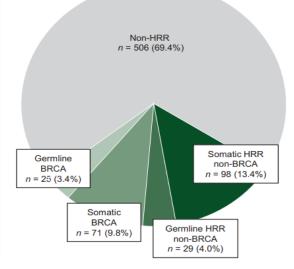


Germline alterations vary across populations

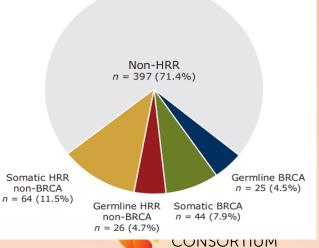
Metastatic prostate cancer (CAPTURE, spanish population)

| Gene | European Ancestry N=692 | Spanish N=419 | African- American N=2669 | Chinese N=1836 | LATAM N=379 |
|--------|-------------------------------|------------------|--------------------------------|-------------------|----------------|
| ATM | 1.6 | 1.9 | 0.97 | 1.04 | 0.8 |
| ATR | 0.3 | 0 | - | 0.29 | 0 |
| BRCA1 | 0.9 | 0.9 | 1.41 | 0.21 | 0.3 |
| BRCA2 | 5.3 | 3.3 | 2.8 | 4.3 | 0.8 |
| BRIP1 | 0.14 | 0 | 0 | 0.06 | 0.5 |
| CHEK2 | 1.4 | 0.5 | 0.48 | 0.17 | 1 |
| MLH1 | 0 | 0 | 0 | - | - |
| MSH2 | 0.14 | 0.2 | 0 | 0.45 | - |
| MSH6 | 0.14 | 0 | 0 | 0.17 | - |
| NBN | 0.3 | 0 | 0 | 0.06 | 0 |
| PALB2 | 0.4 | 0 | 1.1 | 0.67 | 0 |
| PMS2 | 0.3 | 0 | 0.47 | 0.06 | - |
| RAD51C | 0.14 | 0 | 0.68 | 0.06 | 0 |
| RAD51D | 0.4 | 0 | 0 | 0.25 | 0 |

| mCRPC | |
|-----------|------|
| BRCAg | 3.4% |
| Non-BRCAg | 4% |



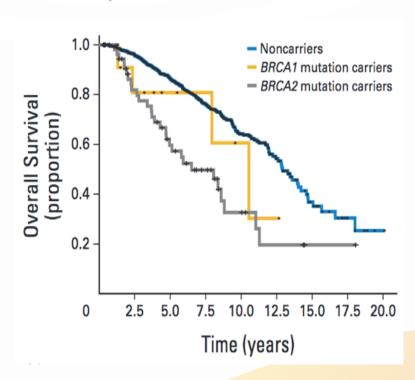
| mHSPC | |
|-----------|------|
| BRCAg | 4.5% |
| Non-BRCAg | 4.7% |



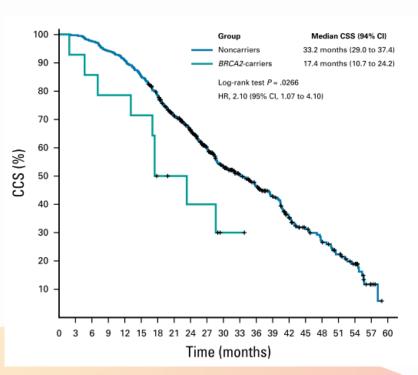
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Germline BRCA mutations are associated with adverse prognosis

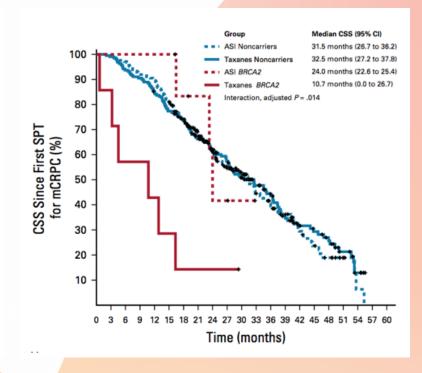
Localized prostate cancers



mCRPC



mCRPC: worse outcome in pts treated with taxanes







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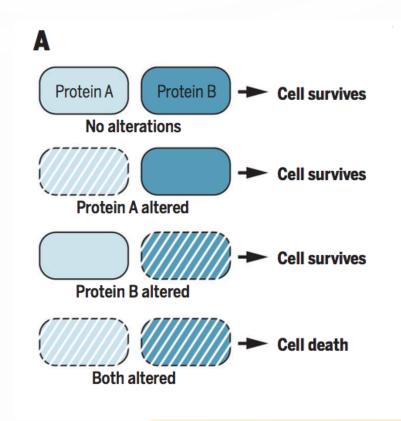
ECOG PS 0-1, adequate hematic-renal function, metastases defined by CT/Bone scar

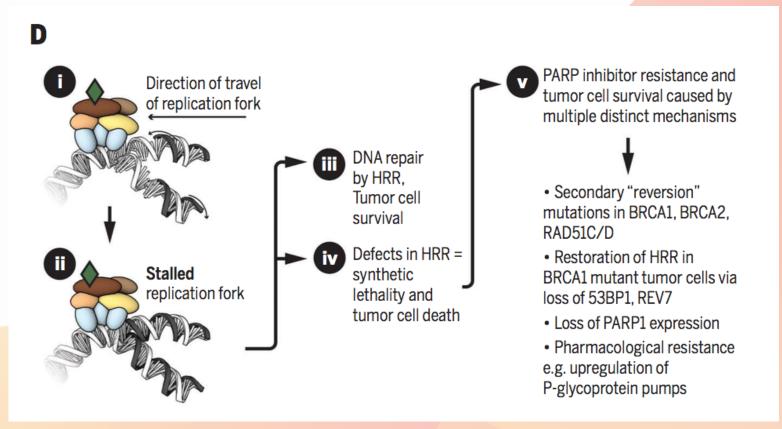
What, where and when to test?



Patients with BRCA/HRR alterations are sensitive to PARPi

Synthetic letality





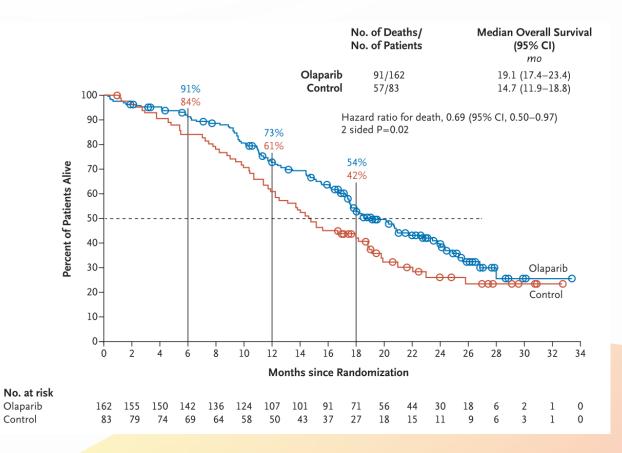




BRCA alterations are predictive biomarkers of PARPi efficacy

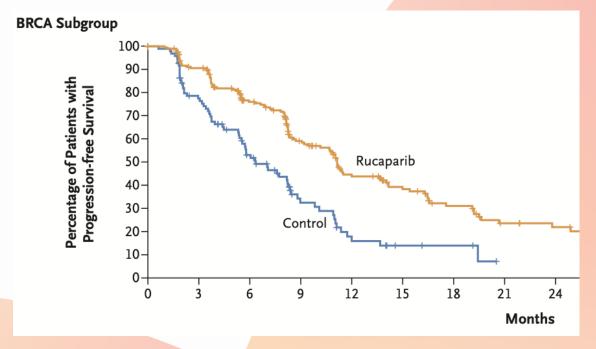
PROFOUND (randomized phase III):

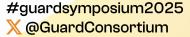
Olaparib improves OS vs 2nd hormonal agent in BRCA/ATM pts



TRITON2 (randomized phase III):

Rucaparib improves rPFS vs 2nd hormonal agent or Docetaxel in BRCA mutant pts





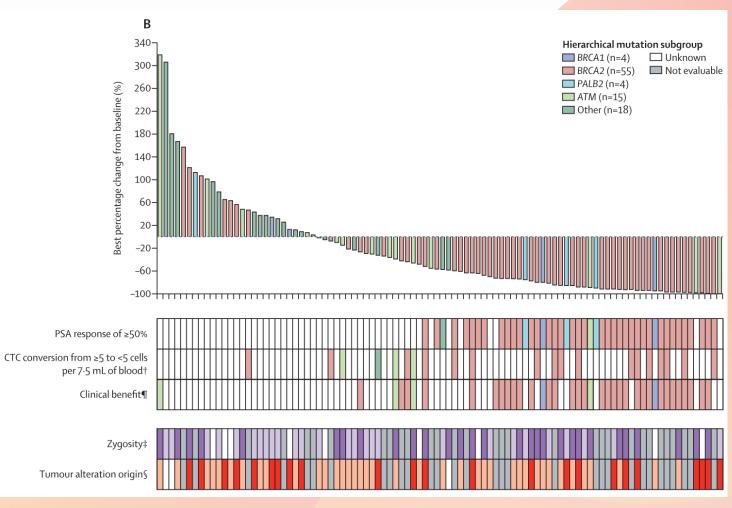


BRCA alterations are predictive biomarkers of PARPi efficacy

Antitumor activity in BRCA mutated patients of PARPi in monotherapy

| | PSA-50 RR | RECIST | rPFS |
|----------------------------|-----------|--------|--------|
| Olaparib (PROFOUND) | 61.7% | 43.9% | 9.8 m |
| Rucaparib (TRITON3) | 55% | 45% | 11.2 m |
| Talazoparib (TALAPRO-1) | 66% | 46% | 11.2 m |
| Niraparib (GALAHAD) | 43% | 34% | 8.1 m |

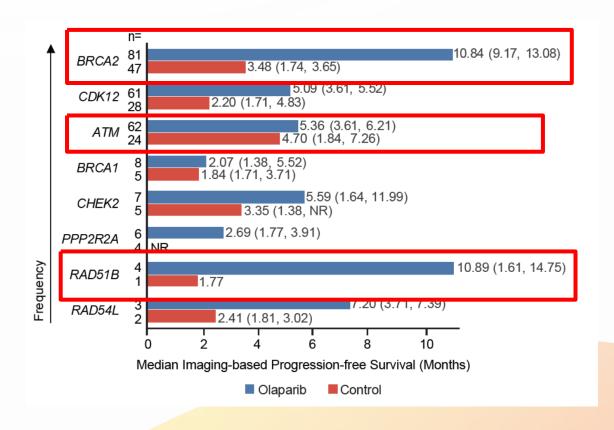
TALAPRO-1 trial: Talazoparib monotherapy 1 mg c/24h



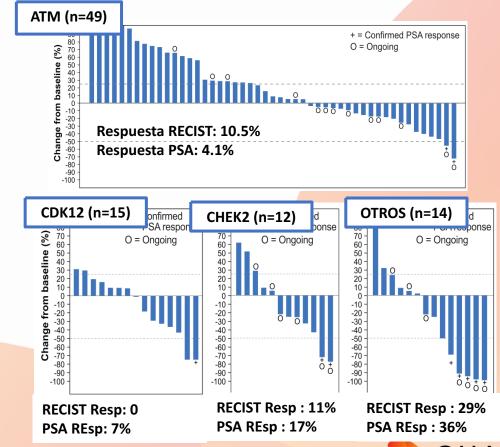
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Non-HRR is heterogeneous

PROFOUND: OS with different genomic alterations



Antitumor activity of Rucaparib in the non-BRCA cohort of the TRITON2 trial







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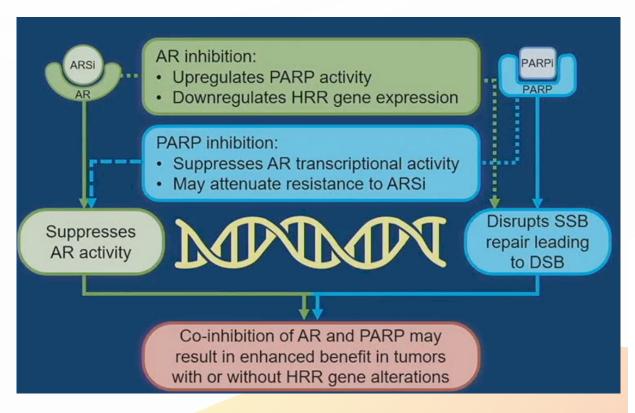
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What, where and when to test?

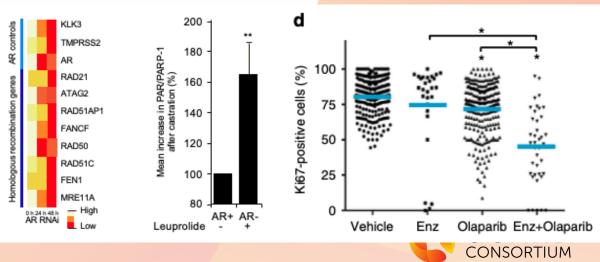


Do PARPi + ARSi doublets abrogate the need for testing?

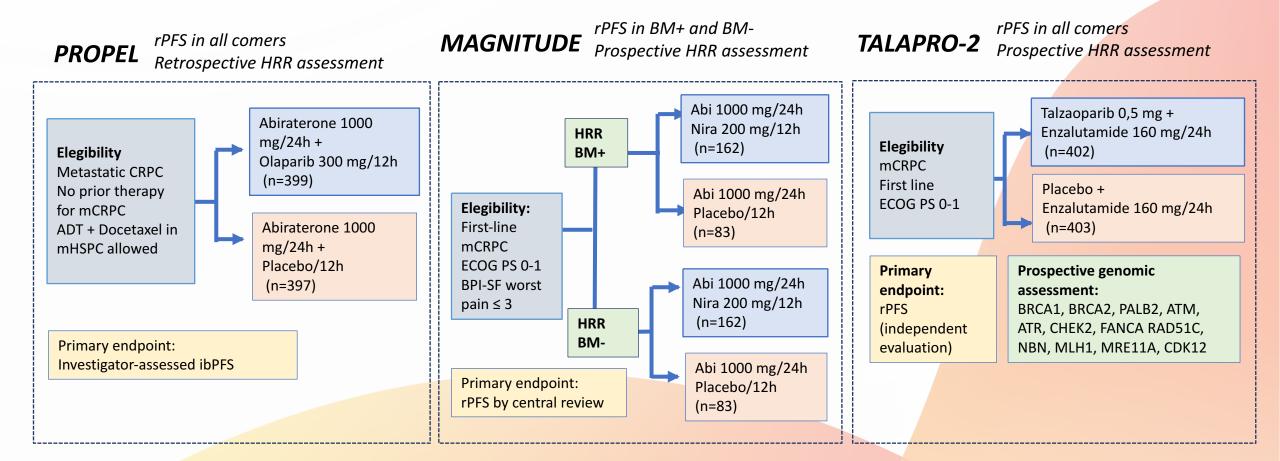


- ADT can inhibit homologous recombination
 Upregulation of DNA repair pathways dependent on PARP with androgen deprivation
- PARP-1 activity is critical for chromatin occupation by the androgen receptor

In vivo PARP inhibition is sufficient to supress AR activity



What is the evidence?



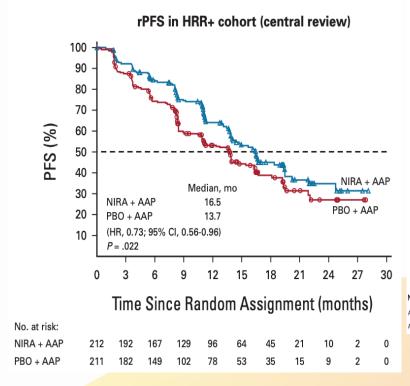




3 positive trials (primary endpoint)

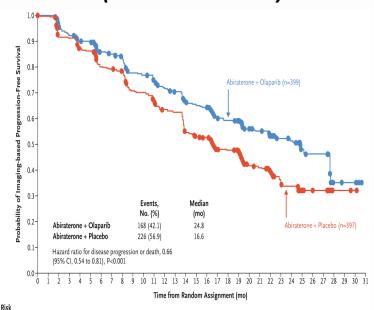
MAGNITUDE

All HRRm: rPFS HR 0.73 (95%CI: 0.56-0.96)



PROPEL

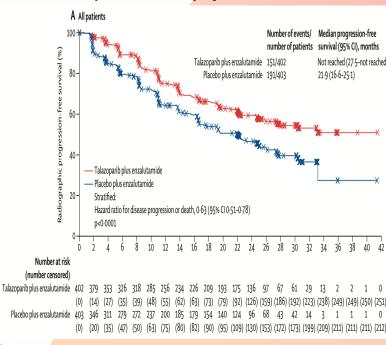
All comers: rPFS HR 0.73 (95%CI: 0.56-0.96)

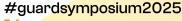


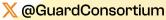
No. at Risk No. at Risk

TALAPRO-2

All comers: rPFS HR 0.63 (0.51-0.78); p<0.001





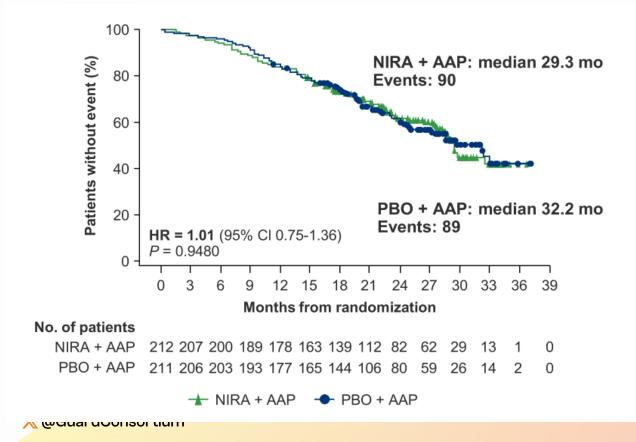




Overall survival



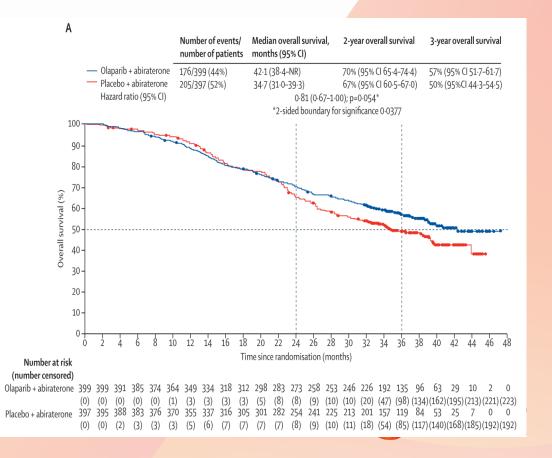
HR 1.01 (95%CI: 0.75-1.36)



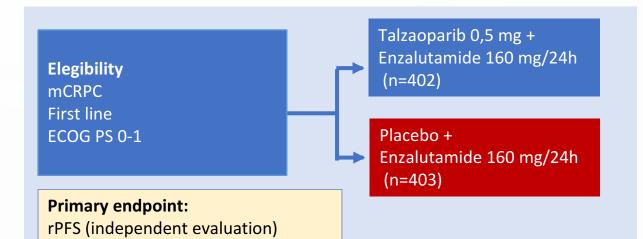


HR 0.81 (95%CI 0.67-1); p=0.054

2-sided boundary for significance: 0.037



The TALAPRO-2 trial



Secondary endpoints:

Time to chemotherapy PFS2 Response rate

Patient-reported outcomes

Safety

Stratification:

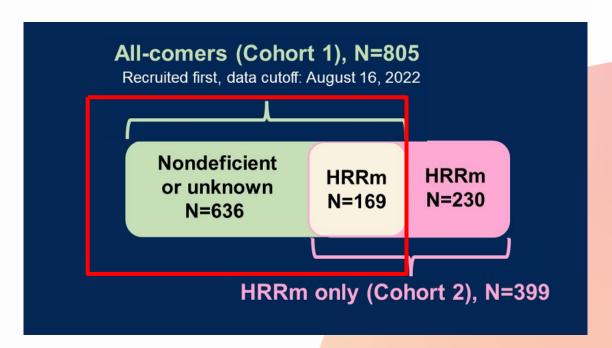
- Treatment with Docetaxel or hormonal agents in CPHSm
- HRR alteration (present vs absent vs unknown)

Prospective genomic assessment:

BRCA1, BRCA2, PALB2, ATM, ATR, CHEK2, FANCA RAD51C, NBN, MLH1, MRE11A, CDK12

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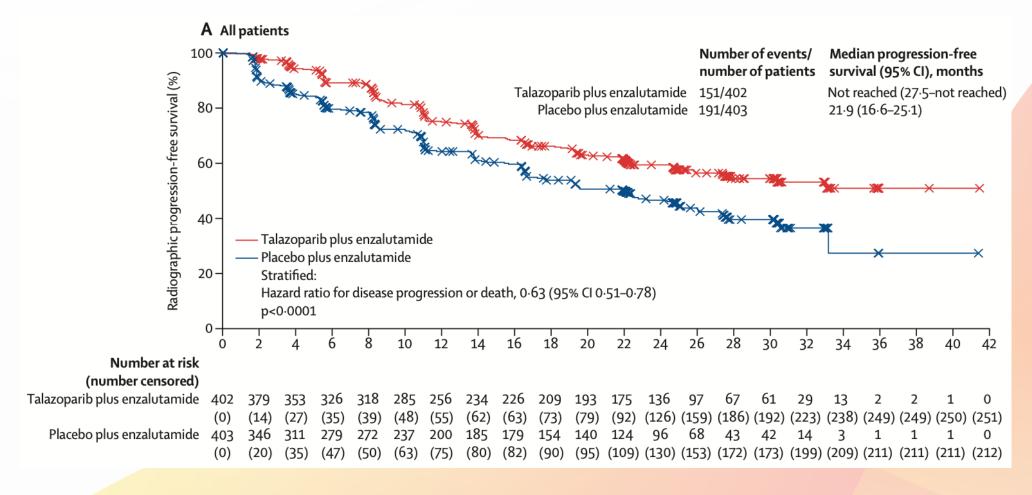
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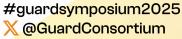


| | Enza + Talazo | Enza + Placebo |
|--------------------|---------------|----------------|
| Docetaxel mHSPC | 86 (21%) | 93 (23%) |
| Prior NHA | 23 (6%) | 27 (7%) |
| HRRm status | | |
| HRRm | 85 (21%) | 20.8% |
| Non-HRRm | 207 (51%) | 53.1% |
| HRRm unk | 110 (27%) | 26.1% |
| BRCA1/2 alteration | 27 (7%) | 32 (8%) |
| | | GUARD |

CONSORTIUM

Primary endpoint: significant increase in rPFS (all comers)

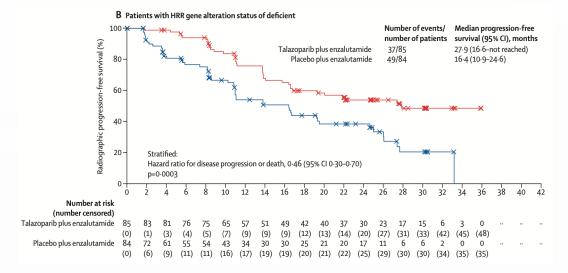






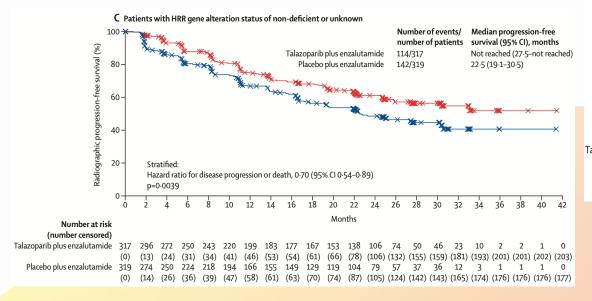
HRR biomarker positive:

HR 0.45 (95%CI 0.30-0.70); p=0.003



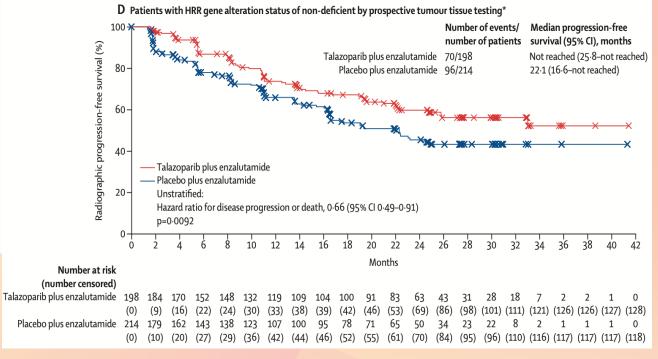
HRR biomarker negative/unknown:

HR 0.70 (95%CI 0.54-0.89); p=0.004



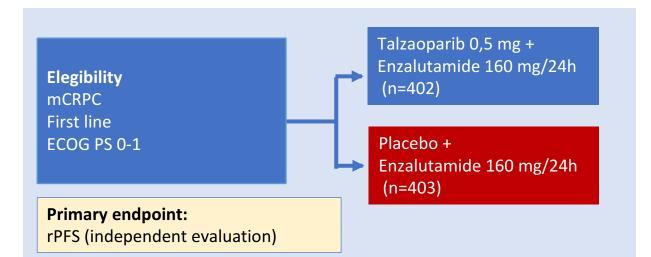
HRR biomarker negative (excluding unknown status):

HR 0.66 (95%CI 0.49-0.91); p=0.009





The TALAPRO-2 trial



Secondary endpoints:

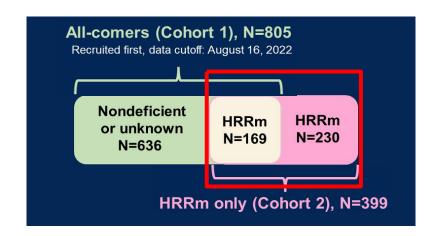
Time to chemotherapy
PFS2
Response rate
Patient-reported outcomes
Safety

Stratification:

 Treatment with Docetaxel or hormonal agents in CPHSm

Prospective genomic assessment:

BRCA1, BRCA2, PALB2, ATM, ATR, CHEK2, FANCA RAD51C, NBN, MLH1, MRE11A, CDK12

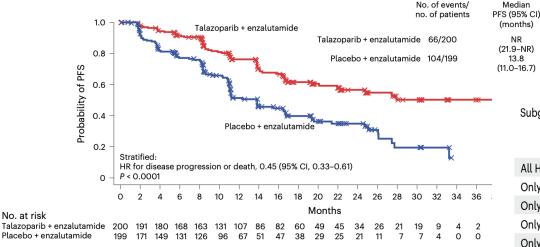


| | Enza + Talazo | Enza + Placebo | |
|---|-------------------------------------|-------------------------------------|--|
| Docetaxel mHSPC | 57 (28.5%) | 60 (30.2%) | |
| Prior NHA | 16 (8%) | 16 (8%) | |
| Tissue source Tissue only Tissue & ctDNA ctDNA only | 76 (38%) 121 (60.5%) 3 (1.5%) | 80 (40.2%) 115 (57.8%) 4 (2%) | |
| BRCA1 mutant | 5.5% | 6% | |
| BRCA2 mutant | 31% | 36.7% | |

TALAPRO-2: Cohort 2 results

HRR gene alteration: rPFS

HR 0.45 (95%CI 0.30-0.70); p=0.003



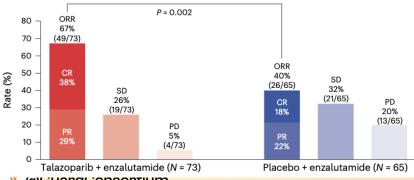
Subgroup analysis (rPFS) by gene alteration

| | Subgroup | Talazoparib + enzalutamide | Placebo + enzalutamide | Talazoparib + enzalutamide | Placebo + enzalutamide | | Hazard ratio (95% CI) | Two-sided <i>P</i> value |
|-----|--------------------|-------------------------------|---------------------------|-------------------------------|---------------------------|--------------|-----------------------|--------------------------|
| | | No. of events/ | no. of patients | Median (| months) | | | |
| | All HRR-deficient | 65/198 | 104/197 | NR | 13.8 | l ⊕ l | 0.44 (0.32-0.60) | <0.0001 |
| | Only BRCA1 | 2/8 | 5/9 | 20.0 | 11.7 | • | 0.17 (0.02-1.51) | 0.07 |
| | Only BRCA2 | 11/55 | 40/60 | NR | 11.0 | ⊢●⊣ | 0.19 (0.10-0.38) | <0.0001 |
| | Only PALB2 | 3/6 | 4/5 | NR | 8.6 | — | 0.56 (0.12-2.51) | 0.44 |
| | Only CDK12 | 12/28 | 18/30 | 21.9 | 13.8 | ⊢ • | 0.49 (0.23-1.02) | 0.05 |
| | Only ATM | 12/35 | 7/22 | NR | 27.7 | ⊢ | 0.76 (0.30-1.94) | 0.58 |
| | Only CHEK2 | 8/24 | 8/24 | 22.1 | NR | ⊢ • | 0.90 (0.34-2.39) | 0.83 |
| | | | | | | | | |
| | BRCA cluster | 15/71 | 54/84 | NR | 11.0 | ⊢●⊣ | 0.20 (0.11-0.36) | <0.0001 |
| | PALB2 cluster | 3/7 | 6/8 | NR | 8.3 | — | 0.46 (0.12-1.87) | 0.27 |
| | CDK12 cluster | 13/35 | 23/36 | 21.9 | 13.8 | \vdash | 0.38 (0.19-0.76) | 0.004 |
| Ī | ATM cluster | 16/43 | 9/29 | 27.9 | 27.7 | ⊢ | 0.90 (0.39-2.04) | 0.80 |
| ↓ I | Other gene cluster | 18/42 | 12/40 | 22.1 | NR | — | 1.51 (0.73–3.15) | 0.26 |
| | | | | | 0.01 | 0.10 1.00 | 10.00 | |

Favors talazoparib + enzalutamide Favors placebo + enzalutamide



Objective response rate

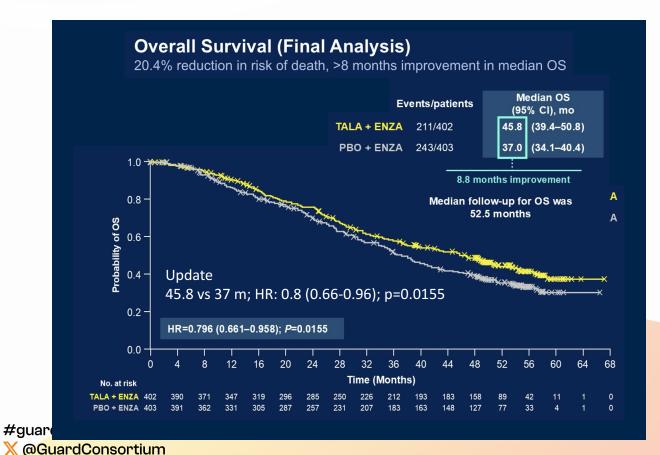


No. at risk

TALAPRO-2: Updated Overall Survival (ASCO GU 2025)

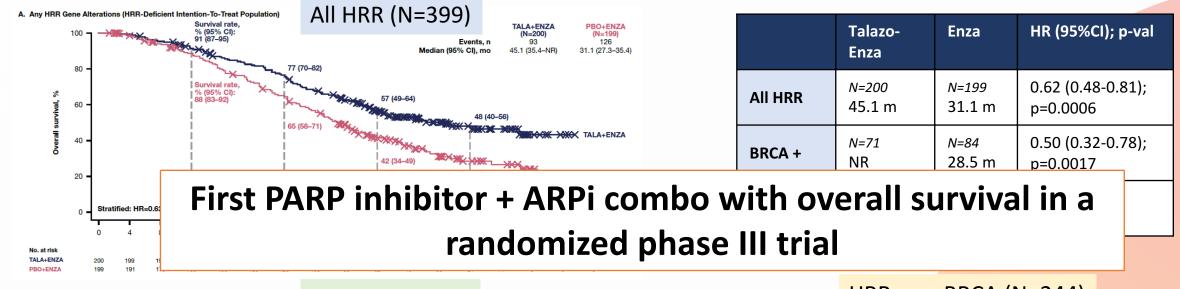
Cohort A (all comers)

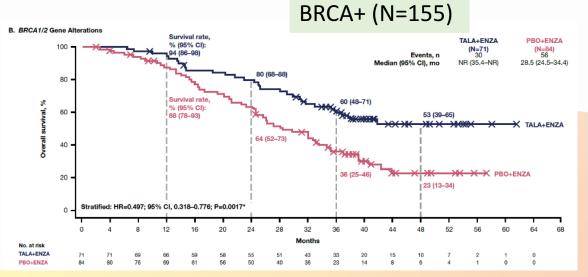
Primary analysis (Aug 16 2022) NR vs 36.4m; HR: 0.89 (0.69-1.14); p=0.35 Overall Survival in Subgroups With No Alterations Detected by Both ctDNA and Tumor Tissue (prospective & retrospective)



No BRCA alteration detected Events/ Median OS (95% CI), mo patients 114/219 48.4 (37.2-54.1) TALA + ENZA PBO + ENZA 137/220 37.1 (31.1–40.7) 0.8 Probability of OS 11.3 months improvement 0.4 0.2 HR=0.749 (95% CI, 0.582-0.963); P=0.0237a No. at risk TALA + ENZA 219 213 204 187 172 159 155 135 123 114 102 99 PBO + ENZA 220 214 196 179 164 155 135 121 110 98 84 75 63 39 No HRR alteration detected Median OS Events/ patients (95% CI), mo 46.6 (33.0-54.1) TALA + ENZA 82/154 PBO + ENZA 99/160 37.4 (30.0–40.9) 0.8 9.2 months improvement Probability of 0.6 0.4 0.2 HR=0.782 (0.582-1.050); P=0.1008a

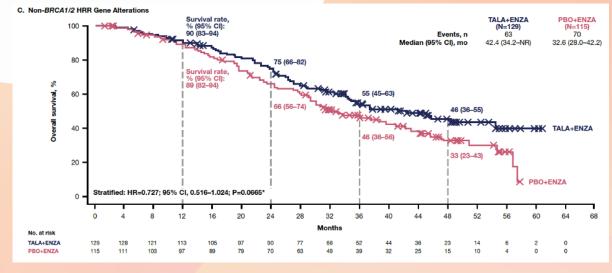
TALAPRO-2: Updated Overall Survival - Cohort B (HRR +) (ASCO GU 2025)



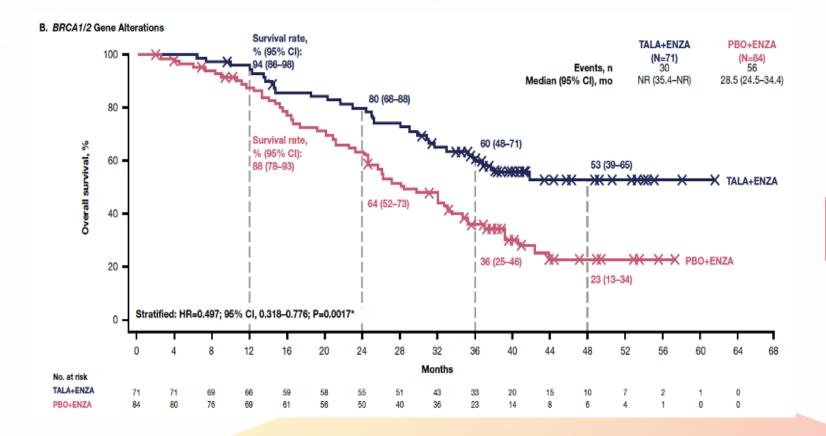


Fizazi et al. ASCO GU 2025





Benefit is greatest in patients with BRCA mutations



| | Talazo- Enza | Enza | HR (95%CI); p-val | |
|------------|-----------------|-------|-------------------------------|--|
| OS median | NR | 28.5m | 0.50 (0.32-0.78); p=0.0017 | |
| 2-yr OS | 80% | 64% | ΔOS: 16% | |
| 3-yr OS | 60% | 36% | ΔOS: 24% | |
| 4-yr OS | 53% | 23% | ΔOS: 30% | |
| PSA50 resp | 88.7% | 56.2% | - | |





Toxicity

Toxicity outcomes in the TALAPRO-2 trial

| All-grade toxicity | | TALAPRO-2 | | |
|--------------------|-------------|-------------|------|--|
| | | Tala + Enza | Enza | |
| Anemia | | 65% | 16% | |
| Neutropenia | | 32% | 7% | |
| Thrombopenia | | 23% | 3% | |
| Fatigue | | 33% | 27% | |
| Nausea | | 21% | 17% | |
| Hypertension | | 18% | 19% | |
| Thromboembo | olic events | - | - | |
| | | | | |
| Interruption. | PARPi/Pbo | 58% | 17% | |
| | ARSi | 34% | 16% | |
| Dose red | PARPi/Pbo | 52% | 6% | |
| | ARSi | 14% | 6% | |
| Discont PARPi/Pbo | | 10% | 7% | |
| เพตินสา นออกรอก แน | ARSi | 8% | 7% | |

Improved quality of life

| | Number of event | Number of events/number of patients | | Hazard ratio (95% CI) | p value |
|---|----------------------------------|-------------------------------------|--------------------|----------------------------|---------|
| | Talazoparib plus enzalutamide | Placebo plus enzalutamide | | | |
| GHS/QoL | 64/197 | 71/197 | • | 0.69 (0.49–0.97) | 0.032 |
| Physical functioning | 60/197 | 82/197 - | •- | 0.57 (0.41-0.80) | 0.0010 |
| Role functioning | 67/197 | 69/197 | • | 0.77 (0.55-1.08) | 0.12 |
| Emotional functioning | 39/197 | 57/197 → | - | 0.48 (0.32-0.72) | 0.0004 |
| Cognitive functioning | 66/197 | 73/197 | → | 0.70 (0.50-0.97) | 0.033 |
| Social functioning | 61/197 | 68/197 | • | 0.75 (0.53-1.06) | 0.10 |
| Fatigue | 88/197 | 88/197 | + | 0.85 (0.63-1.14) | 0.27 |
| Nausea and vomiting | 24/197 | 32/197 — | •— | 0.56 (0.33-0.95) | 0.030 |
| Pain | 52/197 | 74/197 - | •- | 0.56 (0.39-0.79) | 0.0011 |
| Dyspnoea | 45/197 | 50/197 | • | 0.68 (0.45-1.02) | 0.063 |
| Insomnia | 39/197 | 40/197 | • | 0.77 (0.50-1.21) | 0.26 |
| Appetite loss | 52/197 | 64/197 - | •- | 0.60 (0.41-0.87) | 0.0061 |
| Constipation | 33/197 | 48/197 - | - - | 0.52 (0.34-0.82) | 0.0037 |
| Diarrhoea | 19/197 | 21/197 — | • | 0.61 (0.32–1.15) | 0.12 |
| B EORTC QLQ-PR25 | | | | | |
| Urinary symptoms | 28/197 | 37/197 - | - | 0.56 (0.34-0.93) | 0.022 |
| Bowel symptoms | 16/197 | 21/197 — | - | 0.54 (0.28-1.05) | 0.064 |
| Hormonal treatment- related symptoms | 43/197 | 41/197 | • | 0.78 (0.50–1.20) | 0.25 |
| Incontinence aid | 16/197 | 14/197 | • | 1.16 (0.56–2.41) | 0.69 |
| | Favours talazopa | ib plus enzalutan | nide Favours place | 3 ebo plus enzalutamide | |

Do PARPi - NHA combinations eliminate the need for testing?

Who is the ideal candidate for treatment?

The ideal candidate is the one that <u>reflects the clinical trial population</u> expected <u>benefit</u> is <u>greater than anticipated toxicity</u> (disease burden)

ECOG PS 0-1, adequate hematic-renal function, metastases defined by CT/Bone scan



Do PARPi - NHA combinations eliminate the need for testing

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ECOG PS 0-1, adequate hematic-renal function, metastases defined by CT/B<mark>one scan</mark>

What about non-BRCA HRR alterations?



Prior therapy in PARPi + ARSi trials

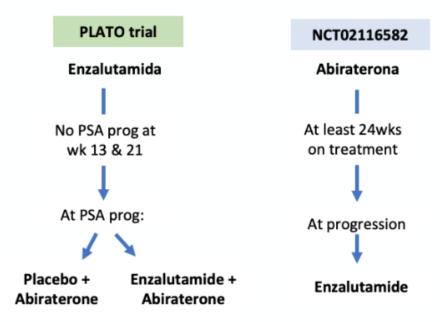
| | Prior ADT only | Prior Docetaxel | Prior ARPi | |
|-----------|---------------------|-----------------|------------|--|
| PROPEL | PROPEL 77.2% | | 0.3% | |
| MAGNITUDE | 76.8% | 20.1% | 3.1% | |
| TALAPRO-2 | TALAPRO-2 71% | | 7% | |

PARPi + NHA combinations



Are results applicable to patients treated with ARPIs in the mHSPC or nmCRPC setting?

Activity of sequential ARPIs is substantially lower than on first-line



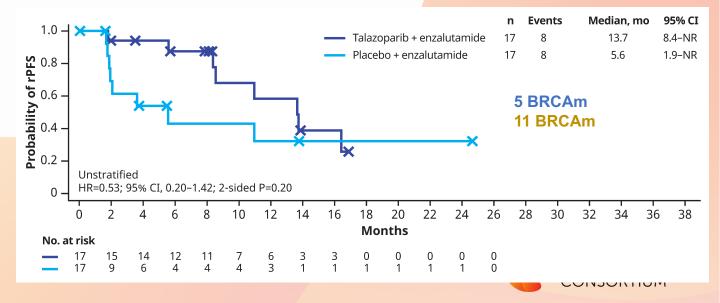
| | Enz→ Abi | Abi→ Enz |
|----------|----------|----------|
| N | 251 | 145 |
| PSA resp | 2% | 26% |
| PSA-PFS | 2.8 m | 5.7 m |
| rPFS | 7 m | 8.1 m |

TALAPRO-2: 50 pts received prior ARSI (abi or orteronel) in mHSPC

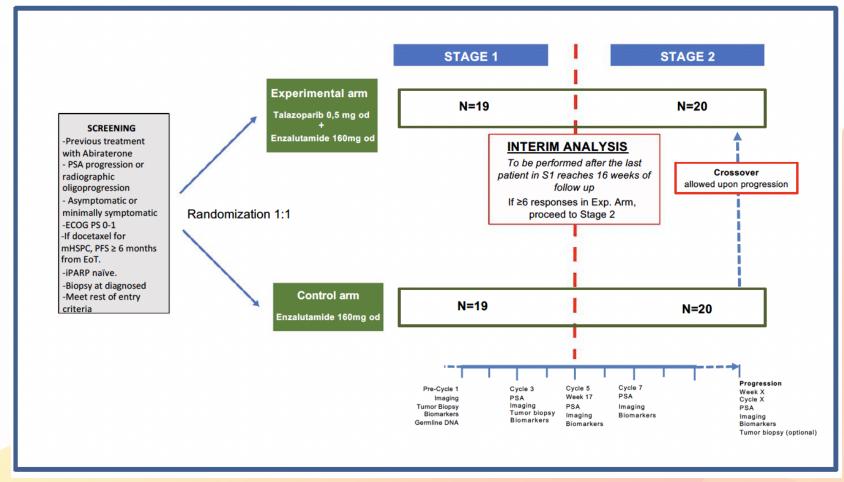
Table 4. rPFS by Previous Treatment With a Second-Generation Androgen Receptor Pathway Inhibitor or With Docetaxel (All-Comers ITT Population)

| | TALA + ENZA | PBO + ENZA | TALA + ENZA | PBO + ENZA | | |
|--------------------------------|--------------------|------------|--------------------|---------------------|---------------------|---------|
| | Even | ts*/N | Median | (95% CI) | HR (95% CI) | P Value |
| Prior abiraterone [†] | | | | | | |
| Yes | 15/23 [‡] | 16/27§ | 11.0 (5.6–16.4) | 1.9 (1.8–11.0) | 0.57 (0.28–1.16) | 0.12 |
| No | 135/376 | 172/373 | NR (30.4-NR) | 22.5 (17.7–26.1) | 0.64 (0.51-0.80) | 0.0001 |
| | | | | | | |

Prior ARPI



A multicenter, open label, randomized phase II trial to evaluate the efficacy of <u>T</u>alazoparib plus <u>E</u>nzalutamide as first line treatment for patients with <u>M</u>etastatic castration resistant <u>P</u>rostate <u>C</u>ancer following progression on <u>A</u>biraterone: TEAM PC study





Prior therapy in PARPi +/- ARSi trials

| | Prior ADT only | Prior Docetaxel | Prior ARPi |
|-----------|-------------------|-----------------|------------|
| PROPEL | 77.2% | 22.5% | 0.3% |
| MAGNITUDE | 76.8% | 20.1% | 3.1% |
| TALAPRO-2 | 71% | 22% | 7% |
| PROFOUND | 0 | 65% | 100% |
| TRITON-3 | 0 | 22% | 100% |
| TALAPRO-1 | 0 | 99% | 99% |
| GALAHAD | HAD 0 100% | | 100% |

PARPi + NHA combinations

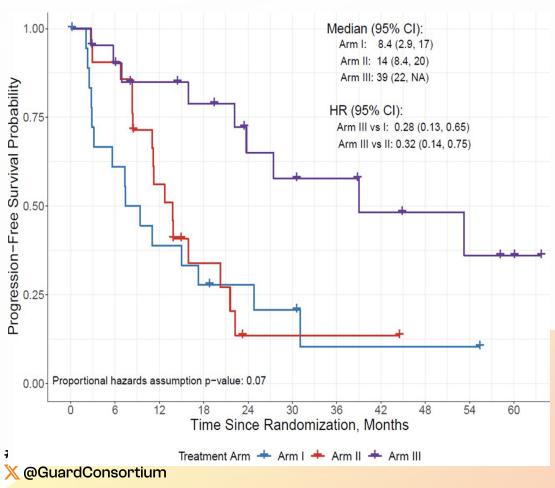
PARPi monotherapy



#guard<mark>s, researchese</mark> X @GuardConsortium

PARPi monotherapy & PARPi +/- NHT Combination or sequential therapy?

BRCAAWAY Abiraterone + Olaparib upfront vs Abiraterone → Olaparib vs Olaparib → Abiraterone



Primary endpoint: radiographic PFS

| | Arm I (n = 19) | Arm II (n = 21) | Arm III (n = 21) |
|---------------------------------|---------------------|--------------------|---------------------|
| Median PFS, months (95% CI) | 8.4 (2.9, 17) | 14 (8.4, 20) | 39 (22, NR) |
| Objective RR, % (95% CI) | 22 (6.4, 48) | 14 (3, 36) | 33 (15, 57) |
| PSA RR, % (95% CI) | 61 (36, 83) | 67 (43, 85) | 95 (76, 100) |
| Undetectable PSA RR, % (95% CI) | 17 (3.6, 41) | 14 (3, 36) | 33 (15, 57) |

16 patients crossed over at progression

| | Crossover to Olaparib (n = 8) | Crossover to Abiraterone (n = 8) |
|--|----------------------------------|----------------------------------|
| Median PFS from crossover, months (95% CI) | 8.3 (5.5, 15) | 7.2 (2.8, NR) |
| Median PFS from randomization, months (95% CI) | 16 (7.8, 25) | 16 (11, NR) |



Do PARPi – NHA combinations eliminate the need for testing

Who is the ideal candidate for treatment?

The ideal candidate is the one that <u>reflects the clinical trial population</u> expected <u>benefit</u> is <u>greater than</u> anticipated <u>toxicity</u> (disease burden)

ECOG PS 0-1, adequate hematic-renal function, metastases defined by CT/Bone scan

What about non-BRCA HRR alterations?



Benefit is greatest with BRCA mutations

| PROPEL | HR 0.23 (95%CI 0.12-0.43) |
|-----------|---------------------------|
| MAGNITUDE | HR 0.53 (95%CI 0.36-0.79) |
| TALAPRO-2 | HR 0.20 (95%CI0.11-0.36) |

Intermediate with **HRR mutations**

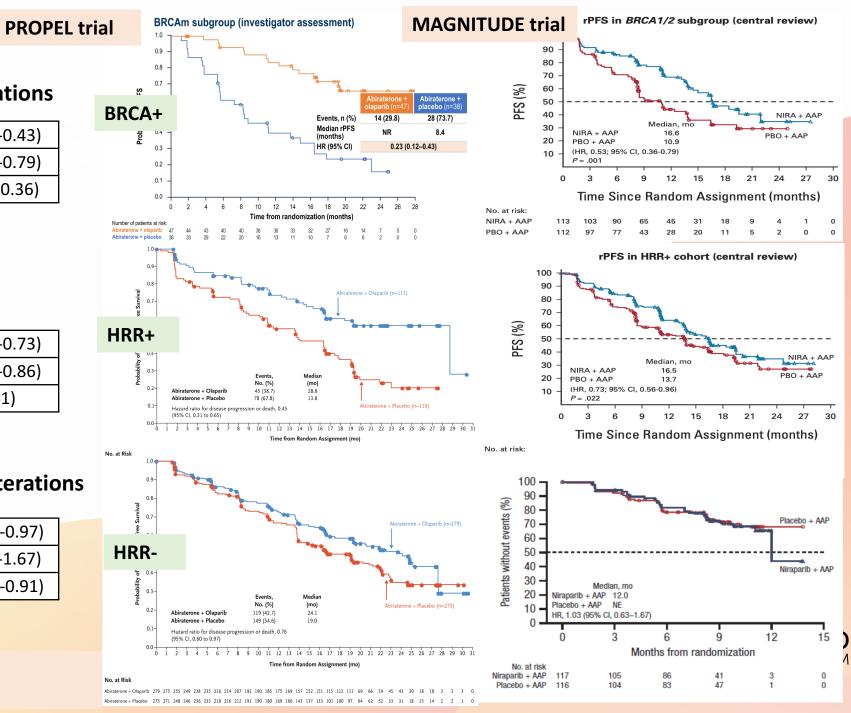
| PROPEL | HR 0.50 (95%CI 0.34-0.73) |
|-----------|---------------------------|
| MAGNITUDE | HR 0.64 (95%CI 0.49-0.86) |
| TALAPRO-2 | HR 0.45 (0.33-0.61) |

Lowest in patients without HRR alterations

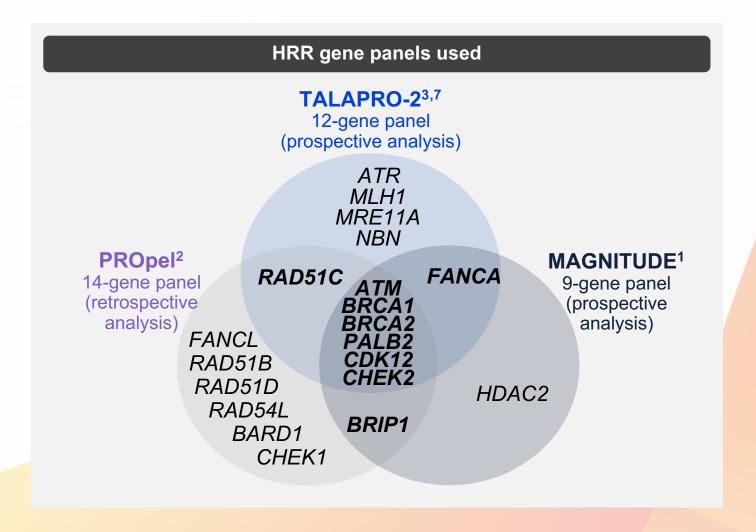
| PROPEL | HR 0.76 (95%CI: 0.60-0.97) |
|-----------|----------------------------|
| MAGNITUDE | HR 1.03 (95%CI 0.63-1.67) |
| TALAPRO-2 | HR 0.66 (95%CI: 0.49-0.91) |

#guardsymposium2025

Clarke et al. NEJM Evidence 2023. Saad et al. Lancet Oncol 2023. Chi et al. J Clin Oncol 2023. Chi et al. Ann Oncol 2023. Agarwal et al. Lancet Oncol 2023. Fizazi et al. Nature Med 2024.



Non-BRCA HRR is an elusive term

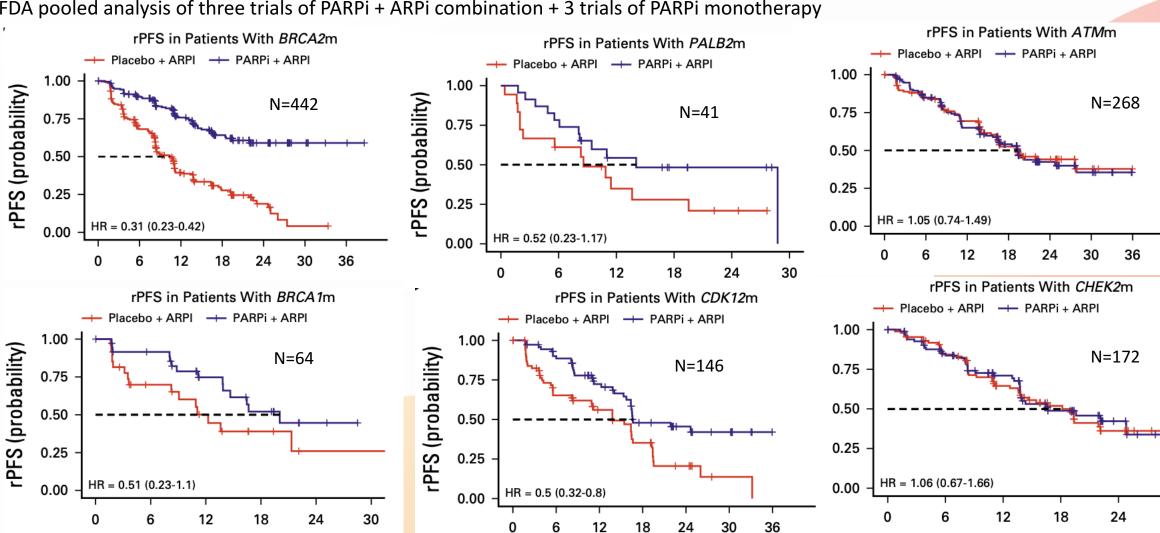






Patient selection for non-BRCA HRR

FDA pooled analysis of three trials of PARPi + ARPi combination + 3 trials of PARPi monotherapy

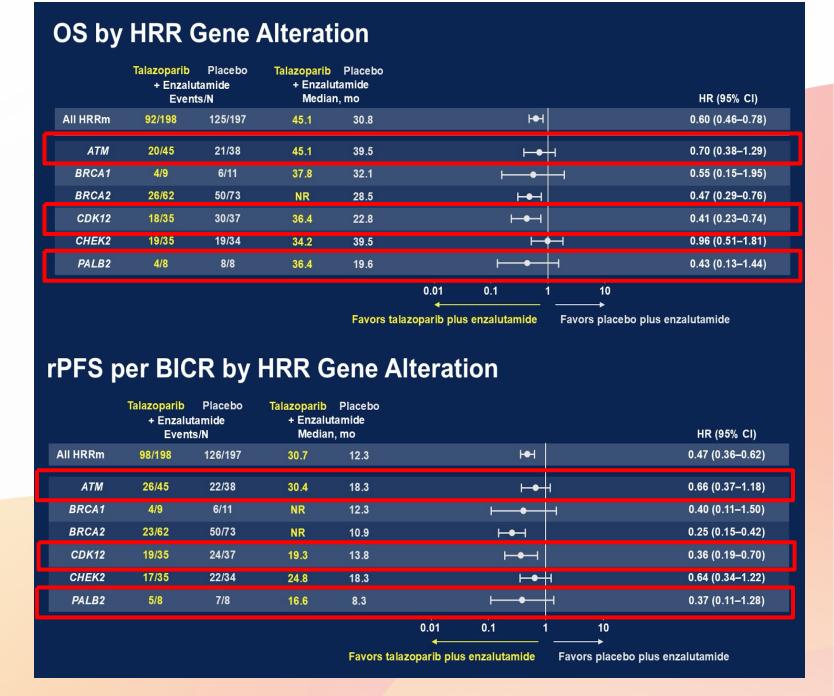


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TALAPRO-2: Benefit in individual non-BRCA HRR alterations

Benefit in some non-BRCA HRR alterations



Do PARPi - NHA combinations eliminate the need for testing?

Who is the ideal candidate for treatment?



Assessing DNA repair defects on tumor tissue

- Tumor testing is the gold standard (high clinical sensitivity)
- DNA repair alterations are early events
- Fresh or achival tumor samples can be used (older samples have lower success rates)
- Can capture both germline and somatic mutations

| PROFOUND study: primary vs metastatic tissue | HHR gene alteration prevalence % | |
|--|--|--|
| All patients | 27.9% | |
| All primary tumors Archived primary Newly collected primary | 27% 27% 26.5% | |
| All metastatic tumors Archived metastatic Newly collected metastatic | 32.3% 33.9% 29.7% | |

High failure rates (~30%)

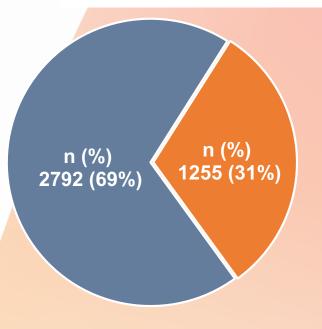
Rates of tissue failure

| Trial | (%) |
|----------------|-----|
| PROFOUND | 31% |
| TRITON2 | 32% |
| IPATENTIAL 150 | 33% |

Single-site biopsies do not capture intra-individual heterogeneity

Sample selection and optimisation of tissue collection is critical

PROFOUND study





Assessing DNA repair defects in ctDNA

Circulating tumor DNA assessment

Non-invasive, safer, serial analysis
Useful where no tissue is available
Can detect both germline and somatic mutations
Capture relative contribution of metastases in
different anatomical sites

But...

Biallelic deletions associated with greatest benefit to PARP inhibitors

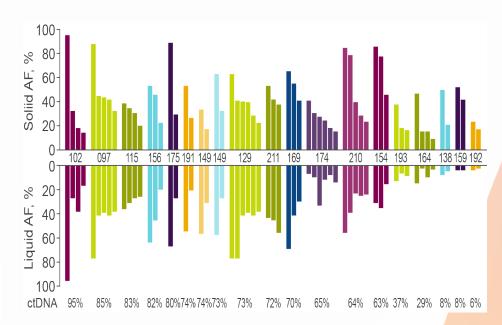
% pts with ctDNA fraction >20% was 47% (401/856) in TRITON2 & 28% (233/818) in TRITON3

ctDNA fraction may sharply decline only weeks after initial ADT (in mHSPC)

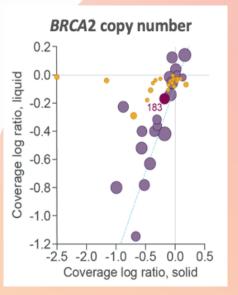
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X @GuardConsortium

Similar mutation profiles



Similar copy number alterations



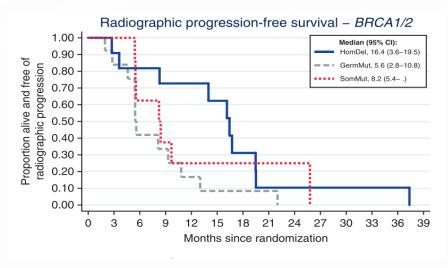
| | Mutations | Monoallelic deletions | Biallelic deletions | Amplific |
|-------------|-----------|-----------------------|------------------------|--------------|
| ctDNA, % | >0.1 | >5–10 | >10-15 | >2-5 |
| % mCRPC Pts | >80% | 50% | 40% | CN dependent |

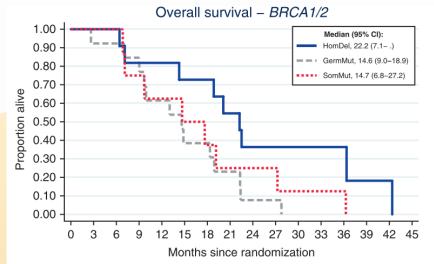
CONSORTIUM

Not all BRCA mutants are the same

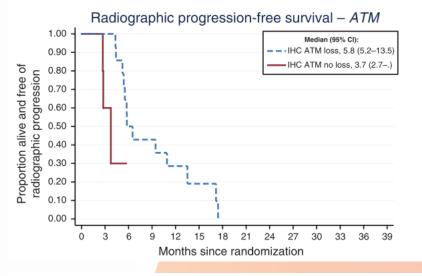
Biallelic BRCA2 mutations derive the greatest benefit from PARP inhibition

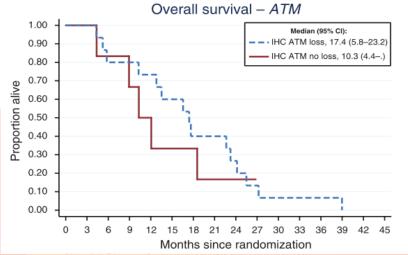
Homozygous BRCA deletions





ATM loss by IHC



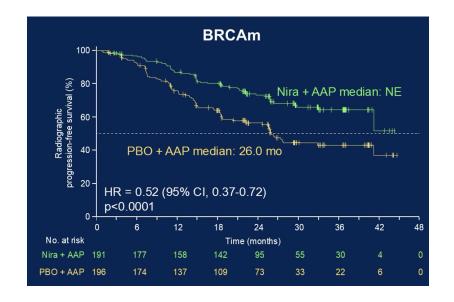


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Carreira et al. Cancer Discov 2021

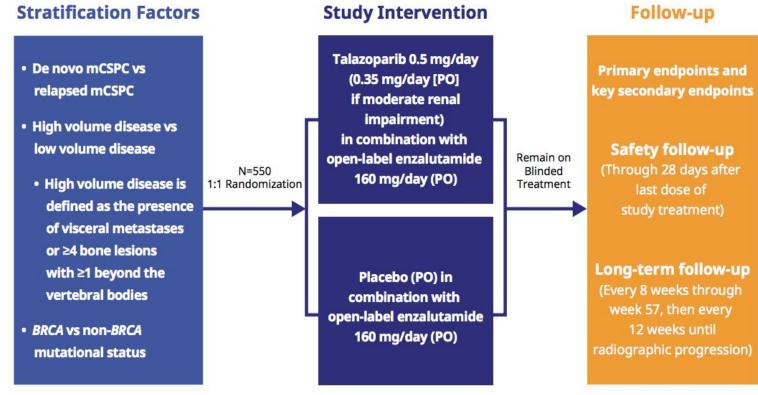
When to test?

ASCO 2025: Niraparib +
Abiraterone improves rPFS in
mHSPC HRR mutant population



TALAPRO-3: talazoparib plus enzalutamide versus placebo plus enzalutamide in men with mCSPC with DDR/HRR alterations.

- •Alterations in 12 DDR/HRR genes (ATM, ATR, BRCA1, BRCA2, CDK12, CHEK2, FANCA, MLH1, MRE11A, NBN, PALB2, RAD51C)
- Metastatic disease (no brain metastases)



TALAPRO-2. Who should we test? Who is the ideal candidate for treatment?

- Test <u>all metastatic patients</u> because testing has **prognostic, predictive and family risk** implications Test as soon as possible (currently mCRPC, implications for mHSPC therapy coming soon)
- Alterations in **HRR genes** identify candidates for treatment with PARP inhibitors (monotherapy or in combination with NHAs)
- Talazoparib + Enzalutamide is the only PARPi + NHA combo that has proven overall survival benefit in a randomized phase III trial

Greatest benefits in BRCA mutants but evidence of benefit with other alterations

- Outstanding issues when **finding the ideal candidate for treatment**What is the HRR alteration? What type of alteration (point mutation, biallelic deletion...)
What was the patient's prior therapy? Was the prior ARPi abiraterone or apa/enza/daro?
What is the patient's general status? What is the burden of disease?
What are the goals of treatment?



Thank you!





¡Gracias!

