

2nd generation test that more comprehensively informs treatment decisions.

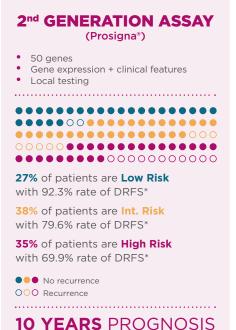


More Accurate
Prognostic
Score

Intrinsic Subtype Identified Clinicopathological Factors Integrated

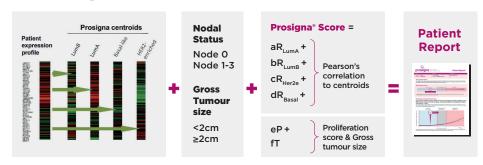


Prosigna® more accurately identifies the low-risk group with better outcomes and the high-risk group with worse outcomes¹.



1st GENERATION ASSAY 21 genes Gene expression only Samples need to be sent to the US 5 with 85.4% rate of DRFS* 31% of patients are Low Risk with 79.8% rate of DRFS* 19% of patients are High Risk with 74.9% rate of DRFS* No recurrence OO Recurrence

Clinically Validated Algorithm Generates a Prosigna® Score for Each Patient.

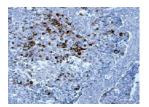


*DRFS: Distant Recurrence Free Survival.

The probability of developing recurrence were obtained from a bespoke data analysis of the TransATAC study (Sestak I, Dowsett M, Cuzick J. NICE Request – TransATAC Data Analysis –2017. Illustration adapted from Harnan S, et al. Tumour profiling tests to guide adjuvant chemotherapy decisions in early breast cancer Health Technol Assess. 2019 Jun;23(30):1-328.

How does the Prosigna® Assay work?

Extract RNA from FFPE* tumour sample



Test RNA using
Prosigna® Assay
on the nCounter
Analysis System





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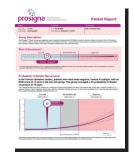
Capture expression profile of patient's tumour





Patient Report

- Intrinsic Subtype identified
- Risk of Recurence (ROR) within 10 years
- Risk of Recurence (ROR) 5-10 years (late relapse)
- Clinicopathological factors like tumour size and nodal status incorporated in the score



More comprehensive information for better treatment decisions.





Provides more accurate prognosis which is the foundation of treatment recommendations¹.



Prosigna® combines tumour gene expression and clinico-pathological factors in a single 10-year Risk of distant Recurrence (ROR) score^{2,3}.



The only breast cancer prognostic test identifying the four PAM50 molecular subtypes.



Easy access to local testing with faster turnaround times.

- Sestak I, Buus R, Cuzick J, et al. JAMA Oncol. 2018; 4(4):545-553
 Kos et al. Breast Cancer Res, 2014, 16:103
 Alexandre et al. Cancer Manag Res, 2019; 11: 10353-10373

