prosigna®
Breast cancer
prognostic gene signature assay

CE

See the difference with **Prosigna®**

Breast Cancer Prognostic Gene Signature Assay

- **PAM50-based report of intrinsic subtype**

- **The first genomic breast cancer assay that can be run in your local lab**

- **CE marked for FFPE tissue**

CE Product Summary Sheet

Prosigna is an in vitro diagnostic assay that uses the gene expression profile of cells found in breast tissue to assess a patient's risk of distant recurrence. The assay measures the gene expression profile using RNA extracted from Formalin-Fixed, Paraffin-Embedded (FFPE) breast tumour tissue. The gene expression data are weighted together with clinical variables to generate both a subtype (luminal A, luminal B, Her2-enriched, or basal-like) and a score indicative of the probability of distant recurrence of disease. The assay is performed on the NanoString nCounter® Dx Analysis System using FFPE breast tumour tissue previously diagnosed as invasive breast carcinoma.

nanoString™

For detailed information see the Prosigna package insert or visit: **www.prosigna.com**
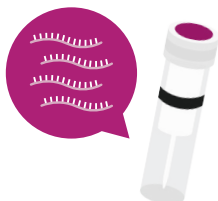
Prosigna Sample Requirements

Block Selected

H&E stain to identify tumour area and cellularity

Tumour area transposed to unstained slides and macrodissected

RNA extracted with manual kit

The Prosigna assay is performed on RNA isolated from FFPE breast tumour tissue. A pathologist examines a hematoxylin and eosin (H&E) stained slide and identifies (and marks) the area of invasive breast carcinoma suitable for the test. The pathologist also measures the tumour surface area, which determines the number of unstained slides required for the test, and the tumour cellularity to ensure the presence of sufficient tumour tissue for the test. A trained technician macrodissects the area on the unstained slides corresponding to the marked tumour area on the H&E-stained slide and isolates RNA from the tissue. The isolated RNA is then tested on the NanoString nCounter Dx Analysis System to provide test results including the Prosigna Score and risk category.

Specimen Attribute	Requirement
Tissue input	Viable invasive breast carcinoma (ductal, lobular, mixed, or NOS)
Tissue input format	Macro-dissected 10-micron-thick slide-mounted tissue sections
Minimum tumour size	4 mm^2 tumour area
Minimum tumour cellularity	10% within tumour area
Minimum RNA amount	125 ng (12.5 ng/µL)
Tumour area	≥ 100 mm^2 1 slide 20 – 99 mm^2 3 slides 4 – 19 mm^2 6 slides

Prosigna Algorithm and Output

The test is based on the PAM50 gene expression profile, and is performed on the nCounter Analysis system using RNA extracted from formalin fixed paraffin embedded (FFPE) breast tumour tissue samples. The algorithm uses a 50-gene expression profile to assign breast cancer to one of four PAM50 molecular subtypes determined by the tumour's molecular profile. The prototypical gene expression profiles (e.g. centroids) of the four PAM50 molecular subtypes were retrained on the nCounter Dx Analysis System using FFPE breast tumour samples collected from multiple clinical sites in North America. After performing the assay on a patient test sample, a computational algorithm based on a Pearson's correlation compares the normalized 50-gene expression profile of the patient test sample to the prototypical expression profiles of the four breast cancer intrinsic subtypes. The patient test sample is assigned the subtype with the highest Pearson's correlation.

The algorithm reports a Risk of Recurrence (ROR) score on a 0–100 scale, which is correlated with the probability of distant recurrence at ten years for post-menopausal women with hormone receptor-positive, early stage breast cancer. The report also provides a risk category (low, intermediate, or high). The ROR score is calculated using coefficients from a Cox model that includes the Pearson correlation to a 46-gene subset of the 50 genes[1] used to calculate each intrinsic subtype, a proliferation score, and tumour size. The test variables are multiplied by the corresponding coefficients from the Cox model to generate the score, which is then adjusted to a 0–100 scale based on coefficients generated from the training set of FFPE breast tumour samples. Risk categories are also reported based on cut-offs for ROR determined in a clinical validation study.
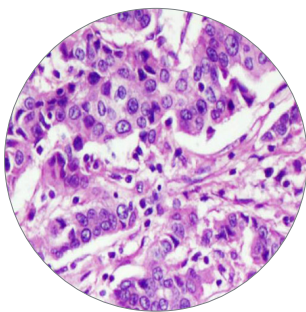
Extract RNA from FFPE tumour sample

Run RNA and Prosigna CodeSet on nCounter Dx Analysis System
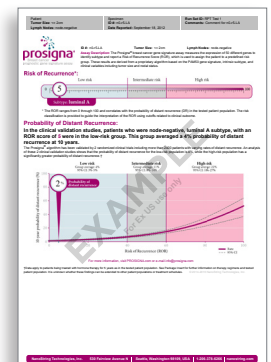
Patient specific expression profile

---

[1] *The 50-gene ROR and 46-gene ROR are functionally identical with a very high R-squared value equal to 0.997. Wallden et al. BMC Medical Genomics (2015) 8:54*

prosigna® Breast cancer prognostic gene signature assay

PRODUCT DESCRIPTION	CATALOG NUMBER	UNIT
Prosigna® Gene Signature Assay Complete kit for running Prosigna tests. Includes all CodeSet and Master Kit components; does not include RNA Isolation Kit.	PROSIGNA-001 PROSIGNA-002 PROSIGNA-003 PROSIGNA-004 PROSIGNA-010	One kit of 1 patient assay One kit of 2 patient assays One kit of 3 patient assays One kit of 4 patient assays One kit of 10 patient assays
Roche FFPET RNA Isolation Kit Includes 25 isolations per kit.	Roche-FFPET-025	Each

CONTACT

email: info@prosigna.com

For more information and details on how to offer Prosigna at your institution, please contact:

EU Authorized Rep.
Emergo Europe
Prinsessegracht 20
2514 AP The Hague
The Netherlands
EU +31.70.345.8570

NanoString Technologies, Inc.
530 Fairview Ave N
Seattle, WA 98109
Phone: 888-358-NANO
(888-358-6266)

For more information, please visit **www.prosigna.com**

nanoString™