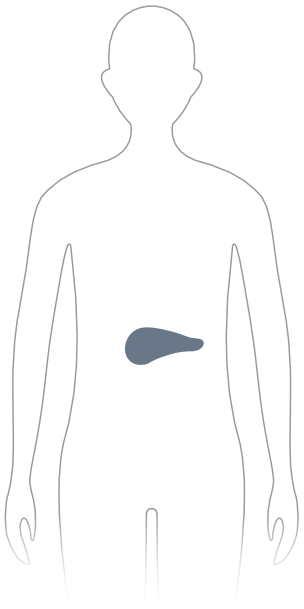
Patient		Sample		Physician	
Name	**Jane Jones**	Specimen Type	**Blood**	Ordering Physician	**John Smith**
Date of Birth (Age)	**11/27/1940 (85 yrs)**	Collection Date	**08/22/2026**	Medical Facility	**BillionToOne Inc**
Assigned Sex at Birth	**Female**	Receipt Date	**08/24/2026**	Address	**1035 O'Brien Drive Menlo Park, California 94025**
Diagnosis	**Cancer of unknown primary**	Accession ID	**V010900AA001-1**	Phone	**(833) 537-1819**
Medical Record #	**ID400231**	Report Date	**08/29/2026**	Fax	**(833) 874-0918**
Internal Patient ID	**10000090**				

Northstar Origin™ Results

Tissue of Origin Molecular Analysis



Primary Prediction	Predicted Probability
Pancreatic	**79%**

Lower Probability Predictions	
Gastroesophageal	**12%**

Ruled Out at 95% Confidence: Bladder, Breast, Colorectal

Interpretation

The Primary Prediction represents the tissue type most strongly supported by the methylation profile and/or somatic variant profile detected in cell-free DNA (cfDNA). Tissue types reported as Lower Probability Predictions remain compatible with the methylation profile, and tissue types reported as Ruled Out with 95% Confidence can be excluded as tissue of origin with 95% confidence based upon the methylation profile. These results should be interpreted in conjunction with the patient's clinical, radiologic, pathologic, and other laboratory findings. If the tissue of origin presented in the Primary Prediction does not correlate with other clinical findings, the Lower Probability Predictions can be considered. Clinical correlation is recommended.

Patient Name	**Jane Jones**	Date of Birth (Age)	**11/27/1940 (85 yrs)**	Assigned Sex at Birth	**Female**
Diagnosis	**Cancer of unknown primary**	Internal Patient ID	**10000090**	Report Date	**08/29/2026**

Methods and Limitations

Northstar Origin™ is a next generation sequencing (NGS)-based test designed to identify the likely tissue of origin of a solid tumor from a blood draw. Northstar Origin classifies the methylation patterns of circulating-tumor DNA (ctDNA) isolated from cell-free DNA (cfDNA) using a model trained on samples from patients with tumors of known tissue origin.

Plasma and buffy coat were isolated from whole blood collected in a Streck cfDNA tube. cfDNA was extracted from the plasma, and genomic DNA (gDNA) was extracted from the buffy coat. Methylated molecules were quantified in both cfDNA and gDNA. Methylation detected in the gDNA was used to adjust the cfDNA methylation signal, accounting for background from non-tumor DNA. Background-adjusted per-locus methylation signals and somatic variants reported by Northstar Select® are used as input to a classification model. The model outputs the probability that each of 12 tumor tissue classes (Biliary, bladder, breast, colorectal, cutaneous, gastroesophageal, gynecological [including cervical, ovarian, uterine, vaginal, or vulvar], kidney, liver, lung, pancreatic, prostate) is the tumor's tissue of origin.

Results may not be reported when the sample contains an insufficient amount of cfDNA, when the aggregate methylated ctDNA signal specific to tissue of origin is insufficient, when the model does not provide a sufficient primary prediction, or when quality control requirements are not met. A low molecular signal result indicates that methylated ctDNA was detected but the aggregate signal for tissue of origin prediction or the model's primary prediction was insufficient for a standalone tissue of origin determination. In these cases, the patient's submitted pathology report findings may be incorporated into the tissue of origin determination: the model-predicted tissue supported by these findings is reported as the most likely tissue of origin, and other predicted tissues are noted in the interpretation as tissues of origin that cannot be excluded. Low molecular signal results should be interpreted in the context of all available clinical information. The assay is validated to identify the 12 tissue classes as previously listed and cannot determine the tissue of origin of tumors arising from other sites. Northstar Origin is validated for patients with advanced solid tumors; results involving hematological malignancies such as leukemias are not valid. Northstar Origin is not validated for patients with multiple primaries. Results may vary or be invalid if the patient is pregnant, has undergone recent blood transfusion, stem cell transplant, or other procedures that may significantly affect the composition of the cfDNA or buffy coat gDNA. Northstar Origin predictions are probabilistic and do not represent a definitive determination of tissue of origin; the reported prediction may not correspond to the tumor's true tissue of origin. A low predicted probability does not exclude a tissue as the site of origin unless that class is specifically reported as ruled out, and the true tissue of origin may not be among the classes evaluated. Northstar Origin results are intended to supplement, not replace, standard pathologic, laboratory, and clinical evaluation and should not be used as the sole basis for diagnosis or treatment decisions. Results should be interpreted by a qualified medical professional in the context of the patient's clinical, radiologic, pathologic, and laboratory findings.

This NGS-based assay was developed and its performance characteristics determined by BillionToOne, Inc. It has not been cleared or approved by the U.S. Food and Drug Administration. BillionToOne, Inc. is regulated under CLIA. This test is used for clinical purposes. It should not be regarded as investigational or for research.

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