Sema4 Signal®: Personalizing cancer care with data-driven precision oncology solutions

Germline mutations play a significant role in the treatment and management of cancer

Pathogenic germline mutations are prevalent across diverse cancer types, genes, and patient ages

**PERCENTAGE % OF GERMLINE MUTATIONS IN DIFFERENT TYPES OF CANCER**

<table>
<thead>
<tr>
<th>Cancer Type</th>
<th>Percentage</th>
</tr>
</thead>
<tbody>
<tr>
<td>Colorectal</td>
<td>18%</td>
</tr>
<tr>
<td>Breast</td>
<td>12%</td>
</tr>
<tr>
<td>Ovarian</td>
<td>24%</td>
</tr>
<tr>
<td>Prostate</td>
<td>17%</td>
</tr>
<tr>
<td>Pancreatic</td>
<td>15%</td>
</tr>
</tbody>
</table>

**SEMA4 SIGNAL: COMPREHENSIVE SOMATIC AND GERMLINE OPTIONS FOR ALL CANCERS**

<table>
<thead>
<tr>
<th>Sema4 Signal Hereditary Cancer (HC)</th>
<th>Sema4 Signal Whole Exome/Transcriptome Sequencing for all cancers (WES/WTS)</th>
<th>Sema4 Signal Solid Tumor Panel</th>
</tr>
</thead>
<tbody>
<tr>
<td>Enables flexible testing options, including our 73 gene Comprehensive panel, each delivered via Sema4 Traversa™ genomic platform optimized for germline variants</td>
<td>Delivers comprehensive genomic profiling, leveraging an -18,500 exome and transcriptome platform to provide the most comprehensive molecular picture of a patient's cancer to inform the care plan today and provide insights for the future</td>
<td>Targets 161 of the most clinically relevant and actionable cancer genes using as little as 10-20ng of DNA for rapid turnaround time</td>
</tr>
</tbody>
</table>

*Cancer type-specific sub-panels available that include up to 113 total genes
†Germline actionable findings are reported; VUS are not reported
The value of Sema4 Signal Whole Exome/Transcriptome Sequencing (WES/WTS) for comprehensive genomic profiling

**Personalize clinical care today**
- Germline variant detection
- Gold standard tumor mutational burden (TMB)

**Maximize clinical trial eligibility**
- Germline-based clinical trial inclusion criteria

**Inform clinical care tomorrow**
- Novel germline and RNA-based biomarkers for risk stratification and treatment

**Tumor-normal advantage**
- RNA sequencing increases detection of actionable fusions by >10%.\(^2\)

**Bringing RNA to the clinic**
- RNA expression to inform clinical trial inclusion

**Actionable insights based on clinical guidelines and scientific evidence**\(^4\)

<table>
<thead>
<tr>
<th>165+</th>
<th>200+</th>
<th>130+</th>
</tr>
</thead>
<tbody>
<tr>
<td>Targeted genes mentioned in NCCN guidelines(^3) for cancer treatment, detection, prevention, and risk reduction</td>
<td>Genes included in active clinical trials in the United States</td>
<td>Genes associated with diagnostic and prognostic relevance</td>
</tr>
</tbody>
</table>

**Sema4 Signal Whole Exome/Transcriptome Sequencing (WES/WTS) can help providers:**
- Determine diagnoses and prognoses
- Identify and select available targeted therapies
- Find current available clinical trials
- Learn about certain hereditary contributions to various cancer types

**Why Consider Whole Exome/Transcriptome Sequencing (WES/WTS) + Hereditary Cancer Solutions by Sema4**

<table>
<thead>
<tr>
<th>If your patient has</th>
<th>Then Consider</th>
<th>Why Consider</th>
</tr>
</thead>
<tbody>
<tr>
<td>A cancer with FDA-approved treatments based on germline biomarkers</td>
<td>Sema4 Signal Hereditary Cancer may identify actionable germline variants that cannot be detected with exome-based sequencing alone(^3)</td>
<td>Sema4 Signal Hereditary Cancer Panel(^6)</td>
</tr>
<tr>
<td>Met societal guidelines for hereditary cancer screening</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Everybody else</td>
<td></td>
<td>Over 20% of patients with germline variants do not meet standard clinical guidelines for hereditary cancer(^7)</td>
</tr>
</tbody>
</table>

**Our unparalleled support includes:**
- Genetic counseling for patients\(^6\)
- Patient education tools
- Extensive insurance network coverage & support
- Seamless workflow integration

To learn more about Sema4 Signal, please call 833-486-6260, email ClientServicesOncology@sema4.com, or visit sema4.com/oncology

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\(^1\) Tumor-normal sequencing may reveal hereditary cancer predisposition as well as non-cancer genes, as per ACMG guidelines

\(^2\) Genetic counseling available for germline findings

\(^3\) Over 20% of patients with germline variants do not meet standard clinical guidelines for hereditary cancer

\(^4\) RNA sequencing increases detection of actionable fusions by >10%.
References:


14. Figures updated March 2022

15. NCCN Clinical Practice Guidelines In Oncology (NCCN Guidelines®) Referenced with permission from the NCCN Clinical Practice Guidelines in Oncology (NCCN Guidelines) for Guideline Name V.X.2019. © National Comprehensive Cancer Network, Inc. 2020. All rights reserved. Accessed January 10, 2020. To view the most recent and complete version of the guideline, go online to NCCN.org. NCCN makes no warranties of any kind whatsoever regarding their content, use or application and disclaims any responsibility of their application or use in any way.


About Sema4:

Sema4 is a patient-centered health intelligence company dedicated to advancing healthcare through data-driven insights. Sema4 is transforming healthcare by applying AI and machine learning to multidimensional, longitudinal clinical and genomic data to build dynamic models of human health and defining optimal, individualized health trajectories. Centrellis®, our innovative health intelligence platform, is enabling us to generate a more complete understanding of disease and wellness and to provide science-driven solutions to the most pressing medical needs. Sema4 believes that patients should be treated as partners, and that data should be shared for the benefit of all.