

Solid Tumor Panel



Providing knowledge to battle cancer

Cancer is a genetic disease where inherited (germline) or new (somatic) mutations lead to uncontrolled growth of tumor cells in the body. Somatic mutations are acquired genetic modifications unique to an individual that can affect any type of cell in the body, except for the germ cells. Somatic mutations often also consist of known 'driver mutations', which sometimes can be targeted by highly specific and efficient drugs. The knowledge of those targetable mutations in tumor cells can therefore identify additional treatment options.

We have designed a sequencing test which covers such therapeutic targets in solid tumors. Our Solid Tumor Panel provides full sequencing of 106 selected cancer-associated genes as well as the hotspot analysis of relevant cancer regions in 43 genes. It detects over 5,000 validated oncogenic variants, and includes the latest evidence-based variants associated with treatment decisions in solid tumors. The panel covers more than 25 genetic variants with directed therapies which follow the FDA and NCCN guidelines as well as many that are currently being tested in clinical trials.¹ Furthermore, somatic variants with an impact on prognosis of the individual tumor or on the efficacy of standard anti-tumor therapy are captured.

Our Solid Tumor Panel can provide a better understanding of tumor behavior as well as its likelihood to respond to a treatment contributing to tailored medicine for the patient, thus frequently leading to a better outcome or reduced adverse effects.

¹doi: <https://doi.org/10.1101/140475>

Who should consider our Solid Tumor Panel?

Physicians searching in their patients for genetic identification of oncogenic variants in solid tumors as well as new therapeutic options:

- With aggressive, advanced, or metastasized forms of cancers
- Where the first-line treatment has failed
- With limited treatment options or relevant side-effects in standard treatment

What cancers are targeted by our Solid Tumor Panel?

The Solid Tumor Panel targets more than 100 different types of somatic cancers, including:

- | | | | |
|--------------------------|----------------------------|--------------|--------------|
| • Adrenal | • Colon | • Hepatic | • Prostate |
| • Biliary tract | • Endometrial | • Lung | • Renal |
| • Bone marrow | • Esophageal | • Lymphoma | • Skin |
| • Breast | • Gastrointestinal stromal | • Ovarian | • Testicular |
| • Central nervous system | • Glioma | • Pancreatic | • Thyroid |

What are the benefits of our Solid Tumor Panel?

- Identify oncogenic variant(s) by deep sequencing of key cancer genes
- Detect clinically actionable variants which link to new treatment options
- Guide towards the best therapeutic strategy for each patient, best efficacy, and minimum adverse effects
- Save precious time by analyzing large numbers of potentially relevant genes in parallel

Key panel features

CATEGORY	CHARACTERISTICS
COVERAGE	> 97% of targeted regions covered at $\geq 200\times$
SPECIFICITY	> 99.9% for all reported variants
METHOD	NGS capture targeted enrichment
SENSITIVITY	Single nucleotide variants (SNV) detection down to 5% allele frequency
REPORTING	Pathogenic and likely pathogenic variants are reported following ACMG classification guidelines recommendations Additionally, these variants are reported according to their actionability into Tier 1 (strong clinical significance) or Tier 2 (potential clinical significance) following AMP recommendations ²
REQUESTED MATERIAL	FFPE tissue (block or sections) ³ or fresh tumor tissue
TAT	10 business days

² <https://doi.org/10.1016/j.jmoldx.2016.10.002>

³ Formalin-Fixed Paraffin Embedded (FFPE) Block or ≥ 10 sections of 10 μm thickness with control slide

Genes included

Coverage of full coding regions for:

ABL1, AKT1, AKT2, AKT3, APC, AR, ARID1A, ASXL1, ATM, ATR, ATRX, BAP1, BRAF, BRCA1, BRCA2, CDH1, CDK12, CDK4, CDKN1B, CDKN2A, CDKN2B, CHEK1, CHEK2, CREBBP, CSF1R, CTNNB1, DDR2, EGFR, ERBB2, ERBB3, ERBB4, EZH2, FANCA, FANCD2, FANCI, FBXW7, FGFR1, FGFR2, FGFR3, FGFR4, GNA11, GNAQ, GNAS, HNF1A, HRAS, IDH1, IDH2, KDR, KEAP1, KIT, KMT2A, KMT2C, KMT2D, KRAS, MAP2K1, MAP2K2, MEN1, MET, MLH1, MPL, MRE11, MSH2, MSH6, MTOR, NBN, NF1, NF2, NFE2L2, NOTCH1, NOTCH2, NOTCH3, NRAS, NTRK3, PALB2, PDGFRA, PIK3CA, PIK3R1, PMS2, POLE, PTCH1, PTEN, PTPN11, RAD50, RAD51, RAD51B, RAD51C, RAD51D, RB1, RBM10, RET, RIT1, RNF43, SETD2, SLX4, SMAD4, SMARCA4, SMARCB1, SMO, SPOP, SRC, STK11, TP53, TSC1, TSC2, TSHR, VHL with +/- 2bp flanking intronic regions

Hotspot analysis targeting relevant cancer-associated regions for the following genes:

ALK, ARAF, AXL, BTK, CBL, CCND1, CDK6, ERCC2, ESR1, FLT3, FOXL2, GATA2, H3-3A, H3C2, JAK1, JAK2, JAK3, KNSTRN, MAGOH, MAP2K4, MAPK1, MAX, MDM4, MED12, MYC, MYCN, MYD88, NTRK1, NTRK2, PDGFRB, PIK3CB, PPP2R1A, RAC1, RAF1, RHEB, RHOA, ROS1, SF3B1, STAT3, TERT, TOP1, U2AF1, XPO1

CONTACT AND CUSTOMER SERVICE

Phone: +49 (0)381 80 113-416 Email: customer.support@centogene.com
Fax: +49 (0)381 80 113-401 www.centogene.com

CLIA #99D2049715

