# Solid Tumor Panel

Providing Knowledge to Battle Cancer

PRODUCT SHEET

# Solid Tumor Panel

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.

CENTOGENE's Solid Tumor Panel with at total of 149 genes 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 as 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. Furthermore, somatic variants with an impact on prognosis of the individual tumor or on the efficacy of standard anti-tumor therapy are captured and reported.

## The CENTOGENE Advantage

Curated to **provide the most valuable information** for diagnostic decisions, prognosis, and therapeutic approaches

Powered by CENTOGENE's Biodatabank, **the world's largest real-world data repository** for rare and neurodegenerative diseases

The most **up-to-date panel gene content** with the latest medical and in-house findings

**High-quality analysis for precise clinical interpretation** using advanced bioinformatics and artificial intelligence-powered tools

## Genes Included (149)

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, FANCD2, FANCI, FBXW7, FGFR1, FGFR2, FGFR3, FGFR4, GNA11, GNAQ, GNAS, HNF1A, HRAS, IDH1, IDH2, KDR, KEAP1, KIT, KMT2A, KMT2C, KMT2D, KRAS, MAO2K1, 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*

# Key Features and Performance

| | |
|---|---|
| **COVERAGE** | ≥ 97.0 % targeted regions covered at ≥ 200 x |
| **VARIANT TYPES** | • Sensitivity<br>SNVs and InDels (≤ 50 bp)* > 97.2 %<br>• Accuracy of > 96.2 %<br>• Specificity of ≥ 99.9 % guaranteed for all reported variants. Variants with low quality and/or unclear zygosity are confirmed by orthogonal methods** |
| **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 the standards and guidelines for the Interpretation and reporting of sequence variants in cancer.*** |
| **REQUESTED MATERIAL** | FFPE tissue (block or sections)**** or fresh tumor tissue |
| **TAT** | 10 business days |

SNVs: single nucleotide variants; InDels: small insertions/deletions
* SNV detection down to 5% allele frequency
** Variants with low quality and / or unclear zygosity are confirmed by orthogonal methods, i.e.: SNVs and InDels by Sanger sequencing
*** Li et al. 2017, PMID: 27993330
**** Formalin-Fixed Paraffin Embedded (FFPE) Block or ≥10 sections of 10µm thickness with control slide

# Common Directed Therapies Covered by Solid Tumor Panel

| BIOMARKER* | MECHANISM | EVIDENCE LEVEL / GUIDELINES |
|---|---|---|
| ABL1 (T315I) | BCR-ABL inhibitor 3rd gen&Pan-TK inhibitor | FDA |
| BRAF (V600E) | BRAF inhibitor | FDA |
| BRAF (V600E,V600K) | BRAF inhibitor;MEK inhibitor | FDA |
| BRAF (V600E,V600K) | MEK inhibitor | FDA |
| BRAF (V600E) | BRAF inhibitor | FDA |
| BRAF (V600E,V600K) | BRAF inhibitor;MEK inhibitor | FDA |
| BRCA1 oncogenic mutations (complete gene covered) | PARP inhibitor | FDA |
| BRCA2 oncogenic mutations (complete gene covered) | PARP inhibitor | FDA |
| EGFR exon 19 deletions | ERBB2 inhibitor&EGFR inhibitor 2nd gen | FDA |
| EGFR (L858R,L861Q,G719A,G719S,G719C,G719D,L747S,S768I,L861P,L861Q,L861R) | ERBB2 inhibitor&EGFR inhibitor 2nd gen | FDA |
| EGFR exon 19 deletions | EGFR inhibitor 1st gen | FDA |
| EGFR (L858R) | EGFR inhibitor 1st gen | FDA |
| EGFR exon 19 deletions | EGFR inhibitor 1st gen | FDA |
| EGFR (L858R,L861Q,G719A,G719S,G719C,G719D,L747S,S768I,L861P,L861Q,L861R) | EGFR inhibitor 1st gen | FDA |
| EGFR (T790M) | EGFR inhibitor 3rd gen | FDA |
| JAK2 (V617F) | JAK inhibitor | FDA |
| KIT mutation in exon 9,11,13,14 or 17 | BCR-ABL inhibitor 1st gen&KIT inhibitor | FDA |
| KIT mutation in exon 9,11,13,14 or 17 | Pan-kinase inhibitor | FDA |
| KIT mutation in exon 9,11,13,14 or 17 | Pan-TK inhibitor | FDA |
| PTCH1 oncogenic mutations (complete gene covered) | SHH inhibitor | FDA |
| RET (618,620,634,768,791,891,918,C634W,M918T) | Pan-TK inhibitor | FDA |
| TSC1 oncogenic mutations (complete gene covered) | MTOR inhibitor | FDA |
| TSC1 oncogenic mutations (complete gene covered) | MTOR inhibitor | FDA |
| TSC2 oncogenic mutations (complete gene covered) | MTOR inhibitor | FDA |
| ABL1 (T315A,F317L,F317V,F317I,F317C,F317I,Y253H,E255K,E255V,F359V,F359C,F359I) | BCR-ABL inhibitor 3rd gen | NCCN |
| ABL1 (F359V,F359C,F359I,Y253H,E255K,E255V) | BCR-ABL inhibitor 2nd gen | NCCN |
| ABL1 (T315A,F317L,F317V,F317I,F317C,V299L) | BCR-ABL inhibitor 2nd gen | NCCN |
| ABL1 (T315I) | BCR-ABL inhibitor 3rd gen&Pan-TK inhibitor | NCCN |
| BRAF (V600D,V600K,V600M,V600G,V600R) | BRAF inhibitor | NCCN |
| BRAF (V600E,V600D,V600K,V600M,V600G,V600R) | BRAF inhibitor | NCCN |
| EGFR (L861Q,G719A,G719S,G719C,G719D,L747S,S768I,L861P,L861Q,L861R) | ERBB2 inhibitor&EGFR inhibitor 2nd gen | NCCN |
| EGFR (L858R,L861,G719,S768I) | EGFR inhibitor 1st gen | NCCN |
| EGFR (L861Q,G719A,G719S,G719C,G719D,L747S,S768I,L861P,L861Q,L861R) | EGFR inhibitor 1st gen | NCCN |
| KIT mutation in exon 9,11,13,14 or 17 | BCR-ABL inhibitor 1st gen&KIT inhibitor | NCCN |
| PDGFRA inframe deletion (I843) | BCR-ABL inhibitor 1st gen&KIT inhibitor | NCCN |
| PDGFRA (552-596,631-668,814-854) | BCR-ABL inhibitor 1st gen&KIT inhibitor | NCCN |
| PDGFRA (552-596,631-668,814-854) | Pan-kinase inhibitor | NCCN |
| PDGFRA (552-596,631-668,814-854) | Pan-TK inhibitor | NCCN |

*based on the CGI Cancer Biomarkers database (2018/01/17 data)