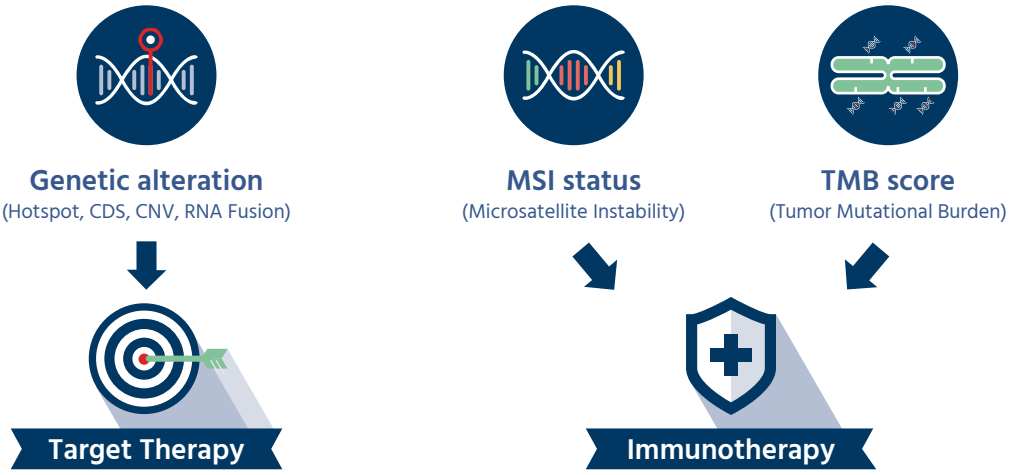
Discover all you need to know for
Target Therapy and Immunotherapy of Cancer

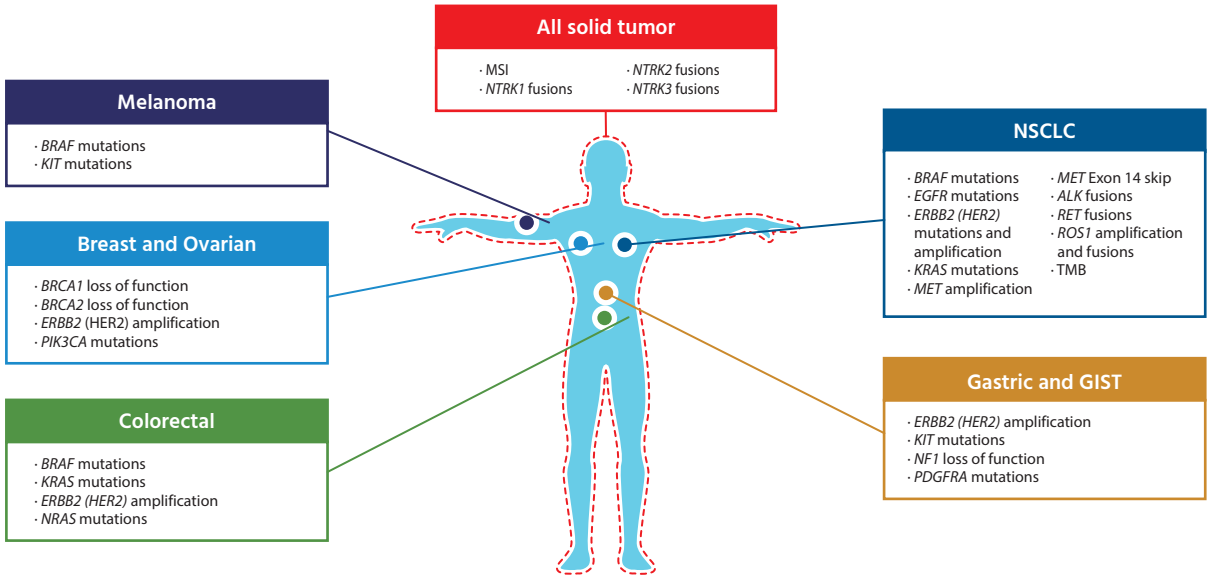
Solid Tumor Panel

What is the Solid Tumor Panel?



The solid tumor panel is a specialized genetic test that analyzes the genetic alterations present in various types of solid tumors, such as lung, breast, and colon. This test examines genetic regions that are frequently mutated in solid tumors.
It provides a comprehensive understanding of the genetic makeup of the tumor cells, enabling informed treatment decisions and improving patient outcome.

Gene Information



- ▶ Hotspot mutation genes (165 genes)
  : *ALK, BRAF, EGFR, ERBB2(HER2), IDH1, IDH2, KIT, KRAS, MYC, MYCN, NRAS, PDGFRB, PIK3CA, NTRK1, NTRK2, NTRK3, MET, RET, ROS1, FGFR2,* etc.
- ▶ CDS genes, full exon sequencing (227 genes)
  : *BRCA1, BRCA2, NF1,* etc.
- ▶ CNV (127 genes)
  : *ALK, BRAF, EGFR, ERBB2(HER2), IDH2, KIT, KRAS, MYC, MYCN, NRAS, PDGFRB, PIK3CA, NTRK1, NTRK3, MET, RET, ROS1, FGFR2,* etc.
- ▶ RNA Fusion genes (49 genes)
  : *AKT1, AKT2, AKT3, ALK, AR, BRAF, BRCA1, CDKN2A, EGFR, ERBB2, ERBB4, ERG, ESR1, ETV1, ETV4, ETV5, FGFR1, FGFR2, FGFR3, MAP3K8,* etc.

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Competitive Advantages

- Comprehensive genomic profiling covering more than 400+ genes
- Full exon sequencing for 227 genes
- Providing OKR (Oncomine Knowledge Report) containing relevant therapeutic & clinical trial information
- Available for genetic counseling for the result from medical specialist

Service features

Test & Code	Oncomine Comprehensive Assay Plus (TMB/MSI) (incl. RNA) [ON124] Oncomine Comprehensive Assay Plus (TMB/MSI) (excl. RNA) [ON125]		
Specimen	**[Formalin-fixed, paraffin-embedded (FFPE) slide]** – 10 unstained sections from one block (10 μm x 10 sections) & H&E 1 slide – tissue size : 4 mm x 4 mm **[Needle biopsy]** – 20 unstained sections from one block (10 μm x 20 sections) & H&E 1 slide **Both FFPE slide and needle biopsy specimen are acceptable.*		
Method	NGS (Next Generation Sequencing)	**TAT**	14 days
Sample storage	Room temperature (Refrigerated is recommended.)		
Test description	This test is for the treatment decision of malignant solid cancers such as gastric cancer, lung cancer, colon cancer, breast cancer, ovarian cancer, melanoma, gastrointestinal stromal tumor, cerebral spinal cord malignancies, childhood neuroblastoma, and unknown primary cancer. DNA and RNA are extracted from tumor tissues and FFPE specimens, and mutation information of about 400 genes is analyzed. Also, SNV, small indel, copy number variant are detected. In case of the test including RNA option, RNA fusion is also detected. TMB score and MSI status are additionally reported. However, when reporting the results, only the mutations corresponding to tier 1 and tier 2 are reported, and tier 3 and tier 4 are not reported.		
Caution & Limitation	• This test was performed using sequencing analysis, and can detect SNP and small-indel variants within the analyzed region. The test cannot detect any variants in the region not covered by the test. • The limit of detection for SNV and small-indel variants is approximately 5%. • The detection rate of certain regions such as homopolymer and repeat regions may be lower due to limitation of DNA sequencing method, and certain target region may have lower coverage. • The detected variants in this test are not confirmed by Sanger sequencing, ddPCR or other confirmation methods. • This test does not distinguish between germline and somatic variants. If the variant allele frequency of the mutation is close to 50% or 100%, the possibility of germline variant cannot be excluded. • The variants detected in this test are classified into four stages (tier 1~4) according to the 2017 JMD guideline, and tier 4 variants are not reported. • If the MAPD (Median of the Absolute values of all Pairwise Differences) score, a QC index for CNV calling, exceed 0.5, CNV analysis will not be performed. If the MAPD score exceed 0.3, the reliability is considered low. • For CNV analysis, only copy number gain is reported. The detection limit of copy number gain is about 4 copy gain. • MSI status is reported as MSI-High or MSS. If the 76 MSI biomarkers are not covered enough, MSI status may be reported as no call or QC fail. Validation of MSI status from the manufacturer, using 192 samples, showed sensitivity of 96% and specificity of 99%. • TMB score is the number of mutations detected per 106 base pair. The classification for TMB-low and TMB-high is not yet defined.		

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