

Test Performance

	Reporting Threshold		Analytical Sensitivity	Analytical Specificity
SNVs	0.1* - 0.5% (2~3 molecules)	LOD	< 1%	92.1-96.9%
			≥1%	100%
Indel	0.1* - 0.5% (2~3 molecules)	LOD	< 1%	92.1-96.9%
			≥1%	100%
Fusions	1.0% (2 molecules)		100%	100%
CNVs	2.3 - 4.0 copies (gain)		100%	100%
	1.0 copies (loss)			

* Based on cfDNA input of 20 ng

Service features

Test	Oncomine Pan-cancer Cell-free (LBx) Assay	Code	O004
Specimen	Streck Tube WB 20 ml (10 ml X 2ea)	TAT	14 days
Method	NGS (Next Generation Sequencing)	Sample Storage	Room temperature (Refrigerated is recommended.)
Test description	As a test that analyzes genetic alteration of circulating tumor DNA by extracting cell-free DNA from a blood sample, it can help determine the treatment policy for malignant tumors. It can be applied to various malignant tumors such as stomach cancer, lung cancer, colon cancer, breast cancer, ovarian cancer, and prostate cancer. It can detect SNV, small indel, copy number variant, and gene rearrangement of 55 genes, and the detection limit of SNV and small indel mutations is about 0.1 to 2.0% depending on the input cfDNA concentration.		
Caution & Limitation	<ul style="list-style-type: none"> This test was performed using DNA sequencing analysis, and it is possible to detect single nucleotide variant (SNV), small indel, copy number variation (CNV), gene rearrangement in the region included in the test. However it's not possible to detect any variants in the region not covered by the test. The detection limit of SNV and small-indel depends on the amount of DNA in the extracted sample and limit of detection (LOD) is about 0.1~2.0% depending on the concentration of cfDNA. And when the tumor proportion is low, variants may not be detected, so clinical correlaton is recommended. The four genes (APC, FBXW7, PTEN, TP53) corresponding to tumor suppressor genes among the selected genes included in this test do not cover the entire gene region, but include most of the major pathogenic variants. This test does not distinguish germline and somatic variations. If the variant allele frequency of the mutation is close to 50% or 100% in the gene associated with hereditary cancer syndrome, there is a possibility of germline mutation. The variants detected in this test are classified into four stages (tier 1 to 4) according to the 2017 JMD guideline (J Mol Diagn 2017; 19:313-327), and tier 4 variations are not reported. 		