

Research & Updated TS0500 ctDNA Version



Updated TS0500 ctDNA Version

Illumina updated its TS0500 ctDNA assay from version 1(v1) to version 2(v2). This update has several advantages, including an improved sensitivity to detect somatic mutations at low frequencies. The new version has the same comprehensive content of 523 analyzed genes and a panel size of 1.94 Mb. However, the chemistry and the workflow are improved to facilitate a higher analytical sensitivity.

Illumina compared the two versions and published their results in an <u>application note</u>. They identified an increased analytical sensitivity for the detection of single nucleotide variants (SNVs) in v2 compared to v1: While variants with a variant allele frequency (VAF) of 0.5% could be detected with a sensitivity of 95% in v1, variants with a VAF of 0.4% could be detected with a sensitivity of 95% in v2. Thus, variants with a lower variant allele frequency can be detected with the same sensitivity with v2 compared to v1. Even variants with a VAF of 0.2% could be detected with a sensitivity of 90% with v2. In addition, the analytical specificity also increased for SNVs: from \ge 95% for v1 to 99.995% for v2. For the tumor mutational burden (TMB), a high concordance between v1 and v2 exists. Thus, v2 offers the same comprehensive context and a high concordance between the assays with the advantage of a higher sensitivity for variants with low allele frequencies.



Want to Discover More? We invite you to take a look at our website. www.cegat.com/TS0500 We also tested and compared the two versions in our laboratory. As stated in Illumina's application note, we observed similar results: The sensitivity for SNV detection increased from v1 to v2. When comparing all variants, including SNVs, indels, and fusions, the overall sensitivity slightly increases from 87% in v1 to 87.5% in v2 (see figure 1).



Figure 1| Sensitivity comparison. The sensitivity slightly increased in v2 compared to v1 when considering all variants.



About Us

CeGaT was founded in 2009 in Tübingen, Germany. Our scientists are specialized in next-generation sequencing (NGS) for genetic diagnostics, and we also provide a variety of sequencing services for research purposes and pharma solutions. Our sequencing service portfolio is complemented by analyses suited for microbiome, immunology, and translational oncology studies.

Our dedicated project management team of scientists and bioinformaticians works closely with you to develop the best strategy to realize your project. Depending on its scope, we select the most suitable library preparation and conditions on our sequencing platforms.

We would be pleased to provide you with our excellent service. Contact us today to start planning your next project.



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