AccuGenomics
A higher standard of accuracy

PRODUCT INFORMATION

Accukit™ ONCO1LB
SNAQ™-SEQ Spike-in QC Standards

Standardized Nucleic Acid Quantification for Sequencing (SNAQ-SEQ) is an innovative QC method that uses mixtures of synthetic DNA or RNA internal standards (MIS™) spiked into each sample prior to NGS library prep.[1] Being mixed with the sample and biochemically identical to the regions of interest, these standards undergo the same processing, handling and reaction conditions as the sample does, to provide the ideal run control approach for NGS-based assays. SNAQ-SEQ is compatible with hybrid capture and amplicon-based library prep chemistries and with multiple sample types, tissues, blood and plasma (cfDNA).

Expand your limit of detection

Detecting low allele frequency variants, even using error correction, is challenging and has higher risks of false results. SNAQ-SEQ is optimally designed for low target concentration applications such as ctDNA and pathogen monitoring by enhancing confidence in the results—including negatives.

SNAQ-SEQ INTERNAL STANDARDS MIXTURES (ISM™):

- Improves assay accuracy
  - Provides limit of blank (LOB) for EACH variant position in EACH sample
- Eliminate false positives (FP) and improves sensitivity (FN)
- QC result for EACH sample in the run
  - Control stochastic, operator and technical errors
- Provides higher confidence in the negative result
- Identify CNVs with dPCR-like resolution
- Improves sample throughput
  - Controls in the sample = more room on the flow cell

SNAQ-SEQ INTERNAL STANDARDS ARE AN IDEAL TOOL FOR ALL NGS-ASSAYS DEVELOPERS INCLUDING:

- IVD Manufacturers
- CRO
- CLIA-labs

Optimal run controls for NGS assays

SNAQ-SEQ is a powerful and easy to use QC system that is optimized to deliver the highest accuracy, sensitivity and specificity for quantitative and high-sensitivity NGS-assays such as cell-free DNA.

[1] Blomquist, Thomas et al. "Control for stochastic sampling variation and qualitative sequencing error in next generation sequencing." *Biomolecular detection and quantification* vol. 5 (2015): 30-37. doi:10.1016/j.bdq.2015.08.003

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Contains a blend of 13 synthetic DNA ISM™ to clinically important oncogenic regions of the genome *(Table 1)*. The mixtures are fragmented to an average size of ~165bp and are suitable for use as routine spike-in controls for cell-free DNA assays. When spiked into the sample prior to library prep, the Accukit ONCO1LB SNAQ-SEQ controls will provide a *'background'* reference call for each of the matching regions of the genome, providing accurate LOB and performance information.

USES:

- Run QC, LOB Determination, Sensitivity control, Control for Systemic and Technical errors
- Spike into sample DNA just prior to library prep step and process sample as normal

Product Name	MIS™ Targets		Format◆	Concentration	Volume	Catalog No.	Compatibility*
Accukit ONCO1LB	Gene	Location	ctDNA	10,000 copies/ul	50ul	1207	TST170 (ILMN); Oncomine Pan-Cancer cfNA Assay (TMO)
	BRAF	chr7:140453075-140453193					
	EGFR exon 19	chr7:55242415-55242513					
	EGFR exon 20	chr7:55248986-55249171					
	EGFR exon 21	chr7:55259412-55259567					
	KRAS exon 2	chr12:25398209-25398318					
	KRAS exon 3	chr12:25380169-25380346					
	PIK3CA exon 21	chr3:178951883-178952152					
	EML4-ALKv1	AB274722.1 (RefseqID)					
	TPM3-NTRK1	X03541.1 (RefseqID)					
	ERBB2 exon 7	chr17:37863244-37863457					
	ERBB2 exon 13	chr17:37868182-37868300					
	ERBB2 exon 22	chr17:37879573-37879710					
	ERBB2 exon 29	chr17:37882816-37882912					

Table 1: Accukit ONCO1 LB Target Regions

◆Solid Tissue formats available (non-fragmented).

*.bed files available upon request to determine assay compatibility.

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