AccuGenomics
A higher standard of accuracy

PRODUCT INFORMATION

Accukit™ ONCO1LB
Accukit™ ONCO2ST
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 standard mixtures (ISM™) 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 covary and undergo the same processing, handling and reaction conditions as the native template 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 risk of false results. SNAQ™-SEQ is optimally designed for low target concentration applications such as ctDNA and pathogen monitoring and provides confidence in the results — including negatives.

SNAQ™-SEQ INTERNAL STANDARD MIXTURES (ISM™):

» Improves assay accuracy
  - Provides limit of blank (LOB) for EACH variant position in EACH sample

» Eliminate false positives (FP) and improve sensitivity by reducing False Negatives (FN)

» QC result for EACH sample in the run
  - Control for stochastic, technical, and operator errors; monitor for reagent drift

» Provides higher confidence in a negative result

» Identify CNVs with dPCR-like resolution

» Improves sample throughput
  - Standards are in the sample, so more room on the flow cell for samples

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

- IVD Manufacturers
- CRO
- CLIA-labs
- CDx

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

Accukit™ ONCO1LB and Accukit™ ONCO2ST

Available fragmented or unfragmented, each Accukit contains a blend of 13 synthetic DNA ISM™ to clinically important oncogenic regions of the genome (Table 1). The mixtures (either fragmented to an average size of ~165bp for cell-free DNA assays, or unfragmented for solid tissue samples) are suitable for use as routine spike-in standards. When spiked into the sample prior to library prep, the ONCO1LB and ONCO2ST SNAQ™-SEQ Accukit standards will provide a 'background' reference call for each of the matching regions of the genome, providing accurate and true LOD, LOB and sample specific performance metrics.

Product Name and Description		ISM™ Targets	
		Gene	Location
Accukit ONCO1LB Cat #: 1207	Accukit ONCO2ST Cat #: 1208	BRAF	chr7:140453075-140453193
Format: ctDNA, fragmented	Format: solid tissue, unfragmented	EGFR exon 19	chr7:55242415-55242513
		EGFR exon 20	chr7:55248986-55249171
		EGFR exon 21	chr7:55259412-55259567
		KRAS exon 2	chr12:25398209-25398318
Concentration: 10,000 copies/ul	Concentration: 10,000 copies/ul	KRAS exon 3	chr12:25380169-25380346
		PIK3CA exon 21	chr3:178951883-178952152
		EML4-ALKv1	AB274722.1 (RefseqID)
Volume: 2 x 50ul vials	Volume: 2 x 50ul vials	TPM3-NTRK1	X03541.1 (RefseqID)
		ERBB2 exon 7	chr17:37863244-37863457
Compatibility* TST170 (ILMN); Oncomine Pan-Cancer cfNA Assay (TMO), other panels	Compatibility* TST170 (ILMN); Oncomine Pan-Cancer cfNA Assay (TMO), other panels	ERBB2 exon 13	chr17:37868182-37868300
		ERBB2 exon 22	chr17:37879573-37879710
		ERBB2 exon 29	chr17:37882816-37882912

Table 1: Accukit ONCO1LB (Fragmented for use with liquid biopsy), and Accukit ONCO2ST (Unfragmented, for use with solid tissue), same ISM target regions for liquid biopsy or solid tissue NGS applications

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

USES:

- *Sensitivity control (true LOD)*
- *Internal run QC*
- *Abundance Control*
- *Control for systemic and technical errors*
- *LOB determination*
- *Spike into the sample or the purified nucleic acid prior to library prep, process sample as normal*

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