

Plasma-SeqSensei™ Melanoma RUO Kit



Plasma-SeqSensei™* (PSS) Melanoma RUO kits offer next-generation sequencing technology-based assays that enable highly sensitive and quantitative detection of mutations in circulating tumour DNA (ctDNA) from plasma and deliver results within two days as easy-to-read reports using Plasma-SeqSensei™ Software.

Key gene mutations covered include BRAF and NRAS to detect predictive markers, resistance mutations and frequently occurring clinically relevant genetic alterations in melanoma research settings.

Unique benefits for clinical researchers



High sensitivity at low frequencies

PSS workflow reduces sequencing error rate up to 100-fold employing unique molecular identifiers (UID), enabling detection of 0.07% and higher mutant allele frequencies (MAF) with 95% certainty in a background of 10,000 wildtype copies.

→ Confident mutant variant reporting



Absolute mutant quantification

Internal quantifier Quantispike enables absolute ctDNA quantification down to a limit of detection (LOD) of seven mutant molecules (MM) independent of actual sample DNA input.

→ Consistent quantification independent of cfDNA input.

Unique benefits for clinical research laboratory



Short and standardised workflow

Standardised workflow from cfDNA samples to results in two days, including sequencing time.



Fast and convenient data analysis

Locally installed software automates data analysis and provides an easy-to-read mutation report, requiring only minimal bioinformatic knowledge.

Key facts

- ✓ Highly sensitive down to 0.07% MAF
- ✓ Able to detect six mutant molecules with 95% confidence
- ✓ Fast turnaround time (two days)
- ✓ Easy-to-read report



Target regions for PSS Melanoma RUO Kit

Gene ID#	Transcript ID#	CDS start	CDS end
BRAF	ENST00000288602	1,383	1,431
BRAF	ENST00000288602	1,742	1,813
NRAS	ENST00000369535	162	210
NRAS	ENST00000369535	420	449
NRAS	ENST00000369535	1	52
NRAS	ENST00000369535	341	364

Product specifications

Feature	Description	
Starting sample	Whole blood and plasma	
Sample capacity	2–16 samples per kit	
QC function	Positive control and no template control (NTC) applied to every run	
Input DNA required	5.7–95 ng / 116 μL	
Number of amplicons	6	
Sensitivity	0.07% allele frequency with 95% certainty in 10,000 wildtype copies	
Cut-off	7 mutant molecules	
Compatible sequencing instruments	llumina MiSeq™ Illumina NextSeq 500/550™	

 $^{{}^{\}star}\,\mathsf{Plasma}\text{-}\mathsf{Seq}\mathsf{Sense}\mathsf{i}^{\intercal}\mathsf{M}\,\mathsf{Melanoma}\,\mathsf{RUO}\,\mathsf{Kit}\,\mathsf{is}\,\mathsf{for}\,\mathsf{Research}\,\mathsf{Use}\,\mathsf{Only}.\,\mathsf{Not}\,\mathsf{for}\,\mathsf{use}\,\mathsf{in}\,\mathsf{diagnostic}\,\mathsf{procedures}.$