

## Guidelines for submitting RNA samples extracted from FFPE tissue, or for samples with small quantities of RNA.

Labeling Protocol	Manufacture's Recommendation	GEGF's Recommendation
<b>NuGen Ovation PicoSL WTA (cartridge and peg)</b>	Total RNA required: 500 pg to 50 ng in in 5 ul. High quality total RNA required: with DNase treatment but without nucleic acid based carriers during RNA purification.	10-20 ng/ul in 5ul
<b>SensationPlus FFPE 3' IVT labeling (cartridge)</b>	Total RNA required: 20 ng to 200 ng FFPE total RNA in 5 ul.	100 ng in 5 ul
<b>SensationPlus FFPE WT labeling (cartridge)</b>	Total RNA required: 20 ng to 200 ng FFPE total RNA in 5 ul.	100 ng in 5ul

**SensationPlus™ FFPE Amplification and WT Labeling Kit** is designed for one round of whole transcriptome amplification using both random and dT primers in the first cDNA Synthesis step allowing researchers to perform global gene expression analysis on archives of degraded RNA derived from FFPE samples samples for further use in expression analysis experiments such as microarrays, quantitative RT-PCR, or other relevant RNA-based applications. The system is comprised of reagents and a protocol for amplification of 20 to 200 ng of total RNA derived from FFPE samples into labeled double-stranded cDNA. The cDNA can then be analyzed on Affymetrix® Whole-Transcript Expression Arrays.

**SensationPlus™ 3' IVT FFPE Amplification and Labeling Kit** is designed for one round of whole transcriptome amplification using both random and dT primers in the first cDNA Synthesis step allowing researchers to perform global gene expression analysis on archives of degraded RNA derived from FFPE samples samples for further use in expression analysis experiments such as microarrays, quantitative RT-PCR, or other relevant RNA-based applications. The system is comprised of reagents and a protocol for amplification of 20 to 200 ng of total RNA derived from FFPE samples into labeled cDNA. The cDNA can then be analyzed on Affymetrix® 3' IVT Expression Arrays.

The GeneChip® miRNA 2.0 Array provides the most sensitive, accurate, and complete measurement of small non-coding RNA transcripts involved in gene regulation. 100-1000 ng of total RNA in 8 ul is required.



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