rtStar™ tRNA-optimized First-Strand cDNA Synthesis Kit

The highly efficient system for cDNA synthesis from tRNA

tRNAs undergo by far the greatest number of and the most chemically diverse post-transcriptional modifications, which badly affect tRNA cDNA synthesis efficiency. Methylation, one of the most prevalent modifications, is the main obstacle that hinder transcriptional elongation and thus leads to noneffective cDNA conversion and qPCR. By using an excellent RNA demethylase, Arraystar developed rtStar™ tRNA-optimized First-Strand cDNA Synthesis Kit (Cat# AS-FS-004), a highly efficient system that removes methylations on the RNA to obtain a new level of accuracy on the tRNA detection.

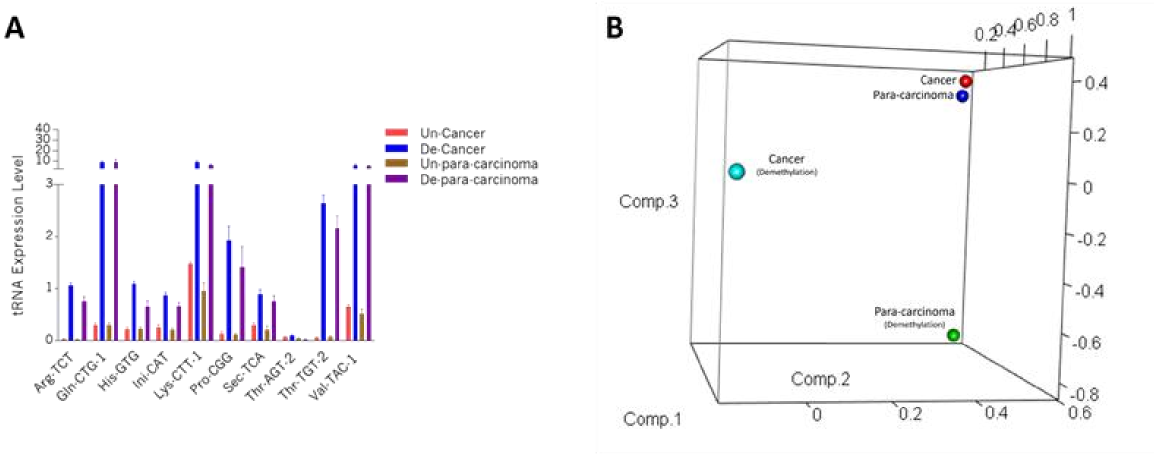

Figure 1. tRNA demethylation treatment dramatically increased PCR assay performance. A. tRNA levels in 3 pancreatic carcinomas and 3 matched para-carcinoma RNA samples with or without the RNA demethylation treatment. Error bars indicate SEM (n=3). De: demethylation, Un: untreated with demethyation. B. Principle component analysis (PCA) analysis of tRNA profiles for the pancreatic carcinoma and para-carcinoma tissues. The Cancer (Demethylation) and Para-carcinoma (Demethylation) samples are well separated, whereas the Cancer and Para-carcinoma samples without the demethylation treatment are indistinguishable.