



# Trimmer-2 cDNA normalization kit

In an eukaryotic cell, the mRNA population constitutes approximately 1% of total RNA with the number of transcripts varying from several thousand to several tens of thousands. Normally, the high abundance transcripts (several thousand mRNA copies per cell) of as few as 5-10 genes account for 20% of the cellular mRNA. The intermediate abundance transcripts (several hundred copies per cell) of 500-2000 genes constitute about 40-60% of the cellular mRNA. The remaining 20-40% of mRNA is represented by rare transcripts (from one to several dozen mRNA copies per cell) [Alberts *et al.*, 1994]. Such an enormous difference in abundance complicates large-scale transcriptome analysis, which results in recurrent sequencing of more abundant cDNAs.

cDNA normalization decreases the prevalence of high abundance transcripts and equalizes transcript concentrations in a cDNA sample, thereby dramatically increasing the efficiency of sequencing and rare gene discovery.

Trimmer-2 kit is designed to normalize amplified full-length-enriched cDNA prepared using Evrogen Mint-2 cDNA synthesis kit (cat. # SK005). The resulting cDNA contains equalized abundance of different transcripts and can be used for construction of cDNA libraries and for direct sequencing, including high-throughput sequencing on the next generation sequencing platforms (e.g. Illumina).

## Features

- Rapid and reliable way to remove repeated transcripts from cDNA library
- Equalization of full-length-enriched cDNA before library cloning
- Simple procedure, no physical separation steps
- Fully compatible with NGS sequencing protocols

## Available products

Product	Cat.#	Size
Trimmer-2 kit	NK003	10 rxn

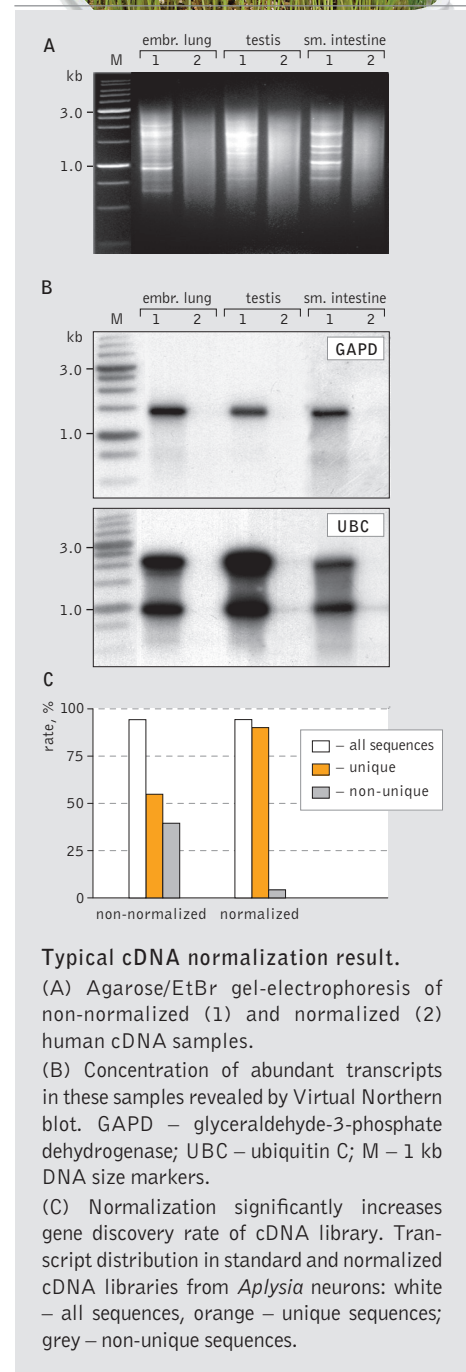
Storage: -20°C.

Kit is intended for research purposes only.

For more information, please visit our web-site:

**[www.evrogen.com](http://www.evrogen.com)**

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## References

Alberts B, Bray D, Lewis J, Raff M, Roberts K, Watson JD. Molecular biology of the cell. 3rd ed., Garland Publishing, New York. 1994.