MYC PROBES

MULTICOLOR DNA PROBE PANELS

MYC has been described as a master regulator of cell function, with its effects ranging from ribosome biogenesis to cell cycle and metabolism control.[1] Due to its critical role in cell maintenance, mutations in MYC can be far-reaching and severe. In fact, MYC is one of the most frequently mutated oncogenes in human cancer, with multiple meta-analyses estimating that the gene is amplified in approximately 14% of cases across 12 major cancer types,[1] including:

Burkitt Lymphoma

MYC translocations are found in virtually 100% of BL; t(8;14) (q24; q32) is the most frequent rearrangement, and accounts for about 85% of cases. Other less common translocations, such as t(2; 8) (p12; q24) and t(8; 22) (q24; q11), make up the other 15%.[2]

Multiple Myeloma

A recent large-scale study found MYC translocations in 25% (323/1280) of MM patients. Translocations occurred most frequently as inter-chromosomal rearrangements involving 2-5 chromosomes (90%, or 291/323 cases).[3]

Breast Cancer

The Molecular Taxonomy of Breast Cancer International Consortium (METABRIC) and the Cancer Genome Atlas Project (TCGA) conducted two of the largest genomic studies on breast cancer, analyzing more than 3000 breast tumors. MYC amplifications were identified in 26.6% and 21.9% of samples, respectively.[1]

Ovarian and Endometrial Cancer

TCGA analyses of ovarian carcinomas (n=557) and endometrial carcinomas (n=373) detected MYC amplification in 30.7% and 10.8% of tumors, respectively. In ovarian cancer, MYC amplification is correlated with inactivation of the BRCA and RB1 pathways.[1]

Colorectal Cancer

Colorectal cancer has four molecular subtypes. TCGA analysis (n=220) and a larger meta-analysis (n=503) identified the frequency of MYC amplification at 6% overall, with frequencies in the different subtypes ranging from 5% to 11%.[1]

Lung Cancer

In a recent study, 183 non-small cell lung cancer adenocarcinomas were analyzed using whole-exome/genome sequencing. Of the 25 genetic alterations identified, MYC amplification was observed in 31% of cases.[1]

Let Empire Genomics help you confirm MYC amplifications, rearrangements and fusions with our MYC gene-specific, break-apart, and fusion probes, which can detect copy number variations, translocations, and fusions, respectively. Our fusion probes can also be customized to detect MYC fusions with any human gene.

PROBE NAME	LOCATION	DYE COLOR	SKU
MYC FISH Probe	8q24.21		MYC-20-OR
MYC Break-Apart Probe	8q24.21		MYCBA-20-ORGR
IGH-MYC Fusion Probe	14q32.33/8q24.21		IGH-MYC-20-GROR

To View Our MYC FISH Probes

visit www.empiregenomics.com/MYC or call (716) 856-3873

1. Kalkat, Manpreet, et al. "MYC deregulation in primary human cancers." Genes 8.6 (2017): 151.
2. Nwanze, Julum, et al. "MYC immunohistochemistry Predicts MYC rearrangements by Fish." Frontiers in oncology 7 (2017): 209.
3.Mikulasova, Aneta, et al. "MYC Rearrangements in Multiple Myeloma Are Complex and Correlate with Increased Expression of MYC." (2017): 65-65.