Disease Probes for Multiple Myeloma

Empire Genomics' **Multiple Myeloma FISH Panel** is made up of probes designed to hybridize to regions with 5 known aberrations associated with the disease.

1p-/1q+	On the p arm of chr. 1, loss of tumor suppressor CDKN2C triggers abnormal cell proliferation; on the q arm, extra copies of CKS1B cause genomic breakdown.[1]
IGH	Disease-initiating IGH translocations, found in about 40% of MM cases, result in fusions with partner genes that are upregulated by IGH enhancers.[2]
13q-	Chromosome 13q deletions are one of the most frequent alterations in MM, and often include loss of RB1 and LAMP1 at 13q14.2 and 13q34, respectively.[3]
Hyperdiploidy	H-MM is observed in 50 - 60% of multiple myeloma patients and is characterized by trisomies of the odd chromosomes, typically 3, 5, 7, 9, 11, 15, 19, or 21.[4]
17p-	Found in just under 10% of newly diagnosed MM patients, TP53 deletions result in haploinsufficiency of this important tumor suppressor.[5]

Probe Name	Location	Dye Color	Catalog Number
1p1q FISH Probe	1p32.3/1q21.3		1p1q-20-GO-R
IGH Break Apart FISH Probe	14q32.33		IGHBA-20-OG-R
RB1/LAMP1 Extended FISH Probe	13q14.2/13q34		RB1-LAMP1-EXT-20-OG-R
SMAD6/NR4A3/5p15 FISH Probe	15q22/9q22/5p15		SMAD6-NR4A3-5P15-20-OAG-R
TP53/CON17 FISH Probe	17p13.1/17q11.1		TP53-CHR17-20-OG-R

1. Chang H *et al.* (2010) Bone marrow transplantation 45.1: 117-121. 2. Kim Gina *et al.* (2014) Genes, Chromosomes and Cancer 53.6: 467-474. 3. Binder M *et al.* (2017) Blood cancer journal 7.9: e600-e600. 4. Kumar *et al.* (2009) Mayo Clin Proc 84:1095-1110. 5. Teoh PJ *et al.* (2014) Leukemia 28.10: 2066-2074.

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