Disease Probes

FOR MULTIPLE MYELOMA

Empire Genomics' **Multiple Myeloma FISH Panel** is made up of probes for detecting 6 major genetic lesions found in 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]
RB1/LAMP1	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]
MYC	MYC rearrangements are complex in MM, occurring as translocations, inversions and insertions. Studies show they could be found in up to 50% of patients.[4]
CCND1/IGH	CCND1 is found fused to IGH in approximately 20% of MM cases. As with other IGH fusions, CCND1/IGH results in overexpression of the IGH fusion partner.[5]
TP53	Found in just under 10% of newly diagnosed MM patients, TP53 deletions result in haploinsufficiency of this important tumor suppressor.[6]

Probes	Location	Dye Color	Catalog Number
1p1q	1p32.3/1q21.3		1p1q-20-GROR
IGH break apart	14q32.33		IGHBA-20-ORGR
RB1/LAMP1	13q14.2/13q34		RB1-LAMP1-20-ORGR
MYC break apart	8q24.21		MYCBA-20-ORGR
CCND1/IGH fusion	11q13.3/14q32.33		CCND1-IGH-Split-20-ORGR
TP53	17p13.1		TP53-20-OR

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. Affer M *et al.* (2014) Leukemia 28.8: 1725-1735. 5. Kuroda J *et al.* Acta haematologica 120.3: 177-181. 6. Teoh PJ *et al.* (2014) Leukemia 28.10: 2066-2074.

800.715.5880
3370 Walden Avenue Suite 114
Depew, NY 14043

www.empiregenomics.com

MM-Probes
011924