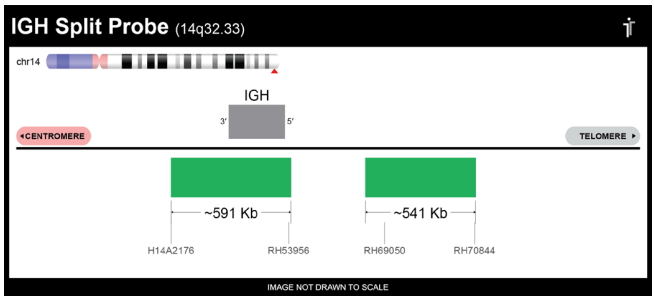
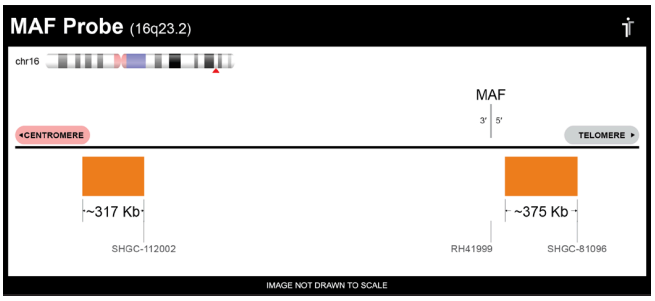
IGH Reflex Panel for Multiple Myeloma

IGH rearrangements are disease-initiating events in up to 40% of multiple myeloma (MM) cases, as well as the MM precursor, monoclonal gammopathy of undetermined significance (MGUS).1 These rearrangements result in fusions with several recurrent partner genes. Empire Genomics' IGH Reflex FISH Panel is designed to detect 4 major IGH fusions found in MM:

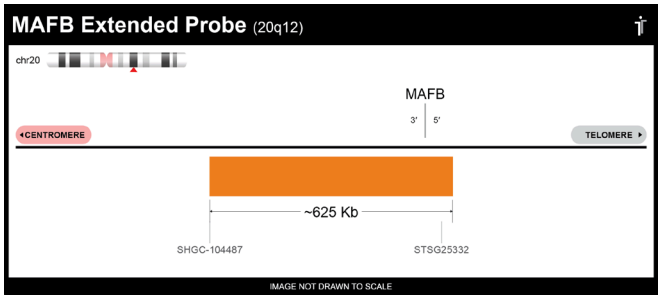
IGH/MAF (IGH-MAF-SPLIT-20-GO-R)





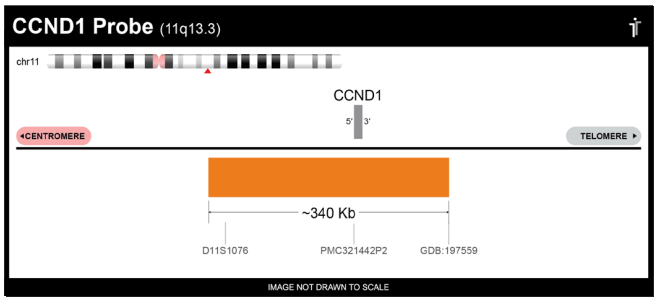
The cryptic IGH/MAF fusion subjects MAF to IGH's powerful enhancer, resulting in MAF upregulation in plasma cells. The abnormality occurs in 5% of MM and 1-5% of MGUS patients. It's considered an early stage biomarker for the disease.[2]

IGH/MAFB (IGH-MAFB-SPLIT-EXT-20-GO-R)



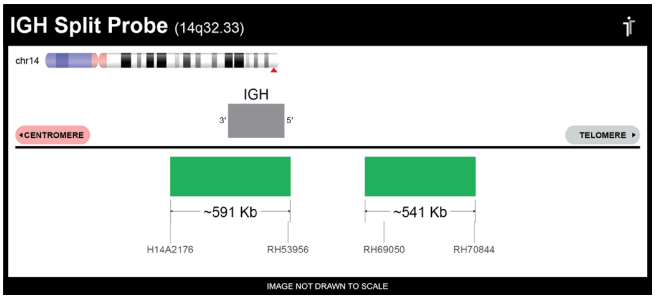
IGH/MAFB fusion is found in about 1% of MM.[3] Consistent with other IGH/MAF family fusions, it's considered a high-risk MM marker.[3] The fusion upregulates MAFB expression, which promotes transformation of fibroblasts and enhances tumor cell proliferation.[4]

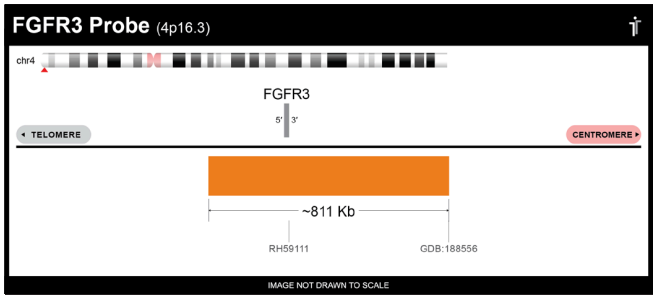
CCND1/IGH (CCND1-IGH-SPLIT-20-OG-R)



CCND1 is found fused to IGH in 15-20% of MM patients, representing the most frequent rearrangement in the disease. The fusion is usually balanced, and occurrs alongside monosomy 13 in about 25% of cases. It's considered a standard risk alteration in MM.[3]

FGFR3/IGH (FGFR3-IGH-SPLIT-20-OG-R)





IGH/FGFR3 fusion occurs in 15–20% of MM patients. It is frequently detected alongside chromosome 13q deletions. The percentage of plasma cells harboring IGH/FGFR3 increases significantly with disease progression, evidence that the alteration drives MM development.[5]

1. Kim G, *et al.* (2014) Genes, Chromosomes and Cancer 53.6: 467-474. 2. Atlas of Genetics & Cytogenetics in Oncology & Hematology (2018). DOI: 10.4267/2042/70210 3. Saxe D, *et al.* (2019) International Journal of Laboratory Hematology 41.1: 5-14. 4. Qiang YW, *et al.* (2018) BMC Cancer18.1: 724. 5. Kalff A & Spencer A (2012) Blood Cancer Journal 2.9: e89-e89

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