BIOCARE MEDICAL

HematoFISH™ Probe Panels | Hematology / Oncology

The use of FISH (Fluorescence *in situ* Hybridization) in the study of hematological cancers has grown significantly in the last decade. All the major hematologic malignancies have been associated with an array of genetic anomalies that are readily revealed by FISH. Thus we are now in an era of FISH probe "panels" that can be routinely applied to understand the underlying genetics of these cancers. This information is useful in predicting cancer progression and aggressiveness.

Chronic Lymphocytic Leukemia

Over the past decade, several prognostic fluorescence *in situ* hybridization (FISH) cytogenetic markers have shown great utility for chronic lymphocytic leukemia (CLL). A specific panel of chromosomal aberrations has been shown to have predictive value for patient course and outcome[1,2]. This panel includes probes for the detection of deletion at 13q14, trisomy of chromosome 12, deletion at 11q22, and deletion at 17p13, listed in order of decreasing survival time[3,4]. The variable region of the immunoglobulin heavy chain (IgH – 14q32) gene is another predictive marker useful for CLL, showing a high correlation between non-mutated IgH status and poor survival and, correspondingly, better prognosis in cases with mutations in IgH[5,6,7]. CLL with a deletion at 6q21-q23 is associated with elevated atypical morphology, intermediate incidence of IgH hypermutation, and overall intermediate risk[8].

Multiple Myeloma

Multiple myeloma (MM) is the second most common hematologic malignancy. FISH can help stratification and prognosis in newly diagnosed MM patients[9]. Many MM mutations are translocations involving the immunoglobulin heavy chain (IgH) gene10. IgH (14q32) translocations involve three main partners: 11q13 (CCND1), 4p16 (FGFR3), and 16q23 (MAF)11. In general, the t(4;14) [IGH/FGFR3] or t(14;16) [IGH/MAF] translocation is considered a high-risk group, while the t(11;14) [IGH/CCND1] is considered a better prognostic group[12]. As MM advances, a number of secondary chromosomal aberrations develop: deletion of 17p13, chromosome 13 and chromosome 1 abnormalities[13,14]. Patients with 17p13 deletions have more aggressive disease and overall shorter survival[15]. Chromosome 13 aberrations, monosomy 13 or 13q14 deletion, are associated with a poor prognosis[16]. Chromosome 1 mutations, 1q gain and 1p loss, are associated with shorter survival[17].

Ordering Information

Products for Chronic Lymphocytic Leukemia	Intended Use	Volume (mL)	Colors	Catalog Number
D13S25 (13q14.3) Orange	ASR	0.1		HFA 7266 A
D13S319 (13q14.2) Orange	ASR	0.1		HFA 7267 A
RB1 (13q14.2) Orange	ASR	0.1		HFA 7298 A
RB1 (13q14.2) Green	ASR	0.1		HFA 7315 A
LAMP1 (13q34) Green	ASR	0.1		HFA 7281 A
LAMP1 (13q34) Aqua	ASR	0.1		HFA 7282 A
Copy Control 12 Green	ASR	0.1		HFA 7210 A
Copy Control 12 Aqua	ASR	0.1		HFA 7211 A
ATM (11q22.3) Orange	ASR	0.1		HFA 7262 A
TP53 (17p13) Orange	ASR	0.1		HFA 7306 A
IGH (14q32) Constant Orange	ASR	0.1		HFA 7278 A
IGH (14q32) Variable Green	ASR	0.1		HFA 7279 A
CCND1 (11q13) Orange	ASR	0.1		HFA 7260 A
MYB (6q23) Orange	ASR	0.1		HFA 7283 A
6q21 Green	ASR	0.1		HFA 7309 A

Products for Multiple Myeloma	Intended Use	Volume (mL)	Colors	Catalog Number
CCND1 (11q13) Orange	ASR	0.1		HFA 7260 A
FGFR3 (4p16.3) Aqua	ASR	0.1		HFA 7276 A
FGFR3 (4p16.3) Orange	ASR	0.1		HFA 7277 A
D13S25 (13q14.3) Orange	ASR	0.1		HFA 7266 A
D13S319 (13q14.2) Orange	ASR	0.1		HFA 7267 A
RB1 (13q14.2) Orange	ASR	0.1		HFA 7298 A
RB1 (13q14.2) Green	ASR	0.1		HFA 7315 A
LAMP1 (13q34) Green	ASR	0.1		HFA 7281 A
LAMP1 (13q34) Aqua	ASR	0.1		HFA 7282 A
TP53 (17p13) Orange	ASR	0.1		HFA 7306 A
Copy Control 17 Green	ASR	0.1		HFA 7225 A
1p21.2 Green	ASR	0.1		HFA 7307 A
1q21.3 Orange	ASR	0.1		HFA 7308 A

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800.799.9499
4040 Pike Lane
Concord CA 94520
www.biocare.net