EXPRESSMED LABORATORIES

CAP ACCREDITED COLLEGE of AMERICAN PATHOLOGISTS

FISH Probes List

Solid Tumors			
Target	Probe Type	Locus	Disease/Application
19q13/19p13	Deletion	19q13	Deletions affecting the long arm of chromosome 19 (19q) are frequently found in human malignant gliomas as well as in neuroblastomas and epithelial ovarian cancers.
1p36/1q25	Deletion	1p36	Deletions affecting the short arm of chromosome 1 (1p) are frequently found in human gliomas and neuroblastomas. Loss of 1p is a strong prognostic factor in patients with neuroblastoma.
ALK (2p23)	Break apart	2p23	ALK translocations are frequently found in anaplastic large cell lymphoma (ALCL), an aggressive non-Hodgkin lymphoma. Additionally, inversions [inv(2)(p21p23)] affecting the ALK gene have been frequently detected in non-small cell lung cancer (NSCLC) and lead to the formation of EML4-ALK fusion transcripts.
DDIT3	Break apart	12q13	DDIT3 is consistently rearranged in myxoid liposarcomas.
EGFR/CEN7	Amplification	7p11	EGFR gene amplification frequently observed in solid neoplasms including non-small-cell lung cancer (NSCLC) and glioblastoma.
EWSR1	Break apart	22q12	Translocations involving the chromosomal region 22q12.2 are found in 90-95% of patients with Ewing sarcoma or peripheral primitive neuroectodermal tumors (PNET).
FOXO1	Break apart	13q14	Detection of specific translocations involving the chromosomal region 13q14.11 harboring the FOXO1 gene characteristic for alveolar rhabdomyosarcoma.
FUS	Break apart	16p11	FUS gene rearrangements have been shown to be involved in both solid tumors and leukemias. Occurring in over 90% of myxoid liposarcomas
HER2(ERBB2)/CEN17	Amplification	17q12	Amplification of proto-oncogene HER2 (ERBB2) in breast and gastric cancers

MDM2/CEN 12	Amplification	12q15	MDM2 amplification is regarded as a valuable tool for the differential diagnosis between WDLPS and lipomas.
N-MYC	Amplification	2p24	Amplification of the MYCN gene is found in about 25% of primary neuroblastomas and is strongly associated with rapid tumor progression, advanced stages of the disease, and poor prognosis.
RET	Break apart	10q11	RET gene rearrangements is observed e.g. in lung adenocarcinoma.
ROS1	Break apart	6q22	Translocations affecting ROS1 have been detected in various tumors including non-small cell lung cancer (NSCLC). Administration of ROS1 kinase inhibitors may represent a very effective therapeutic strategy in NSCLC patients harboring activating ROS1 rearrangements.
SS18	Break apart	18q11	Translocations involving the region 18q11.2 are found in over 90% of synovial sarcoma.
TFE3	Break apart	Xp11	Translocations involving the chromosomal region Xp11.2 are frequently detected in renal cell carcinomas (RCCs) which usually affect children and adolescents.
WWTR1	Break apart	3q25	The recurrent translocation t(1;3)(p36.3;q25.1) was identified in approximately 90% of epithelioid hemangioendothelioma (EHE) cases, but not in other vascular tumors.

Lymphomas			
Target	Probe Type	Locus	Disease/Application
BCL2	Break apart	18q21	Translocations involving the BCL2 gene are commonly identified in B-cell lymphomas. In particular, the translocation t(14;18)(q32.3;q21.3) has been identified in about 80% of follicular lymphoma.
BCL2/IGH	Fusion	t(14;18)	Translocations involving the BCL2 gene and the IGH gene are considered to be cytogenetic hallmarks for follicular lymphoma (FL).
BCL6	Break apart	3q27	Chromosomal rearrangements of the BCL6 gene region were found to occur in different types of non-Hodgkin lymphoma (NHL), including diffuse large B-cell lymphoma (DLBCL) and follicular lymphoma (FL).
BIRC3/MALT1	Fusion	t(11;18)	The recurrent translocation t(11;18) (q22.2;q21.3) is frequently found in mucosa-associated lymphoid tissue lymphoma which represents the most common extranodal B-cell tumor and accounts for 5-10% of all non-Hodgkin lymphoma.
CCND1	Break apart	11q13	Translocations involving the chromosomal region t(11;14) (q13.3;q32.3) are considered to be characteristic for mantle cell lymphomas but have also been identified in other lymphoproliferative disorders, such as B-prolymphocytic leukemia, in plasma cell myelomas and B-cell chronic lymphocytic leukemia.
CCND1/IGH	Fusion	t(11;14)	The translocation t(11;14)(q13.3;q32.3) that involves the CCND1 and IGH gene regions is detected in up to 95% of patients with mantle cell lymphomas.
IGH	Break apart	14q32	Rearrangements involving the IGH gene are considered to be cytogenetic hallmarks for non-Hodgkin lymphoma (NHL).
IRF4,DUSP22	Break apart	6p25	Rearrangements of the IRF4/DUSP22 chromosomal region have been detected in various B-cell and T-cell lymphomas. Large B-cell lymphoma (LBCL) with IRF4 rearrangement is considered a distinct new

			provisional entity. Most cases have IG/IRF4 fusions and have a favorable prognosis. Moreover, IRF4 translocation has a high specificity for cutaneous cutaneous anaplastic large cell lymphoma (ALCL) supporting the clinical utility of FISH for IRF4 in the differential diagnosis of T-cell lymphoproliferative disorders.
MALT1	Break apart	18q21	The most common translocations affecting the MALT1 gene are t(11;18)(q22.2;q21.3) and t(14;18)(q32.3;q21.3) occurring in 50% and 15-20% of MALT lymphomas, respectively.
MYC	Break apart	8q24	Translocations involving the MYC gene are considered to be cytogenetic hallmarks for Burkitt Lymphoma but are also found in other types of lymphomas.
MYC/IGH	Fusion	t(8;14)	The most frequent translocation involving the MYC gene region t(8;14)(q24.21;q32.3) can be found in approx. 80% of the Burkitt's lymphoma cases and juxtaposes the MYC gene next to the IgH (immunoglobulin heavy chain) locus.