

Poseidon™ Repeat Free™ FGFR1 (8p12) Break probe

Introduction: Translocations affecting the chromosomal locus **FGFR1 (8p12)** are hallmarks of an atypical stem cell myeloproliferative disorder. These events disrupt the fibroblast growth factor receptor 1 (FGFR1) gene and fuse the FGFR1 C-terminal catalytic domain with unrelated proteins. FGFR1 amplification is also found in 8.7% of breast cancers and is an independent predictor of outcome.

Intended use: The **FGFR1 (8p12)** Break probe is optimized to detect translocations involving the FGFR1 gene region at 8p12 in a dual-color, split assay on metaphase/interphase spreads and paraffin embedded tissue sections.

The probe is recommended to be used in combination with a Poseidon FISH Kit providing necessary reagents to perform FISH (KBI-60002, KBI-60003 or KBI-60001) for optimal results.

Critical region 1 (red): The **distal FGFR1** gene region probe is direct-labeled with PlatinumBright550.

Critical region 2 (green): The **proximal FGFR1** gene region probe is direct-labeled with PlatinumBright495.

Reagent Poseidon probes are direct-labeled DNA probes provided in a ready-to-use format. Apply 10 µl of probe to a sample area of approximately 22 x 22 mm.

Please refer to the Instructions for Use for the entire Poseidon FISH protocol.

Poseidon Repeat Free probes do not contain Cot-1 DNA. Hybridization efficiency is therefore increased and background, due to unspecific binding, is highly reduced.

Interpretation: The **FGFR1 (8p12)** Break probe is designed as a dual-color split probe to detect translocations at 8p12. A break is defined when a red/green or yellow fusion signals (F) splits into separate red and green signals. Only red and green signals which are more than one signal diameter apart from each other are counted as a break. Co-localized red/green or yellow signals identify the normal chromosome(s) 8.

Signal patterns other than those described above may indicate variant translocations or other complex rearrangements. Investigators are advised to analyze metaphase cells for the interpretation of atypical signal patterns.

	Normal Signal Pattern	8p12 Split	8p12 Amplification
Expected Signals	2F	1F1R1G	3+F

References: Smedley et al, 1998, Hum Mol Genet. 7; 627-642.
Sohal et al, 2001, Genes Chrom. Cancer 32; 155-163.



Application Manual

**KBI-10737
ON FGFR1 (8p12) Break**

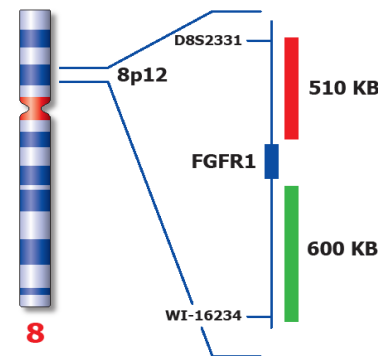


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Not to scale