A fragment of the human c-Ki-ras1 pseudogene (HGM9 gene symbol KRAS1P), localized to 6p12-p11, detects 3 allele, RFLP

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SOURCE AND DESCRIPTION OF CLONE: J819, 3.8kb low copy number fragment from human c-Ki-ras1, subcloned in the HindIII site of vector pBR322 from a Charon 4A λ phage-human genomic library. C-Ki-ras1 is localized to 6p12-p11 (Popescu et al., 1985). HGM9 gene symbol KRAS1P.

POLYMORPHISM: TaqI generates a 3 allele polymorphism, with allele 1 defined by a 22kb band, allele 2 by an 18kb band and allele 3 by a 19kb band.

FREQUENCY: Studied in the 80 parents of CEPH families, Caucasians.

allele 1	0.48 $\pm$ 0.04
allele 2	0.51 $\pm$ 0.04
allele 3	0.01 $\pm$ 0.01

NOT POLYMORPHIC FOR: PstI, EcoRV, BamHI, BglII, MspI, EcoRI, HindIII and PvuII, each screened with DNA from a panel of at least 10 unrelated Caucasian individuals.

CHROMOSOMAL LOCALIZATION: C-Ki-ras1 was localized to 6p23-q12 with a panel of human-rodent cell hybrids (Sakaguchi et al., 1984), and to 6p12-p11 by in-situ hybridization (Popescu et al., 1985).

MENDELIAN INHERITANCE: Co-dominant inheritance pattern observed in 32 informative matings (256 offspring) from CEPH family panel. No segregation distortion. No parental exclusions.

PROBE AVAILABILITY: Dr E. H. Chang, Uniformed Services University of Health Sciences, Bethesda, Maryland 20814, USA. ATCC catalogue number 41032.

OTHER COMMENTS: Hybridization with a 1.1kb BglII-HindIII segment of the insert of J819 is recommended, because the entire 3.8kb HindIII fragment contains a repetitive sequence. Satisfactory specific signal and low background with standard techniques and stringency conditions for rinsing and hybridization. Genomic DNA digests satisfactorily in 5-6 hours with 5-6 units TaqI per mcg, 65°C.

REFERENCES: Chang et al.: Proc. Natl. Acad. Sci. USA 79:4848-4852, 1982; Sakaguchi et al.: Mol. Cell. Biol. 4:989-993, 1984; Popescu et al.: Somatic Cell Mol. Genet. 11:149-155, 1985.

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