Volume 16 Number 8 1988 Nucleic Acids Research

Apa I and Sst I RFLPs at the insulin-like growth factor II (IGF2) locus on chromosome 11

K.Xiang, N.J.Cox and G.I.Bell

The Howard Hughes Medical Institute, The University of Chicago, 920 East 58th St., Chicago, IL 60637, USA

SOURCE/DESCRIPTION: phigf2-11 (vector - pBR327) is a cDNA clone containing a 1.9 kbp EcoRI insert that encodes amino acids -23 to 156 of the human IGF-II precursor as well as a 3'-untranslated region of ~1.35 kbp (this latter region has not been completely sequenced).

POLYMORPHISM: Apa I digestion reveals polymorphic fragments of 3.6 kbp (allele 1) and 2.3 and 1.3 kbp (allele 2). Sst I digestion reveals an invariant fragment of 2.7 kbp and polymorphic fragments of 12.5 kbp (allele 1) and 8.5 kbp (allele 2).

FREQUENCY: Ascertained in Chinese.

	Allele 1	Allele 2
Apa I (N=84)	0.46	0.54
Sst I (N=79)	0.46	0.54

CHROMOSOMAL LOCALISATION: 11p15.5

MENDELIAN INHERITANCE: Co-dominant segregation observed in one three-generation pedigree.

PROBE AVAILABILITY: Contact G.I. Bell

OTHER COMMENTS: There is significant linkage disequilibrium between the Apa I and Sst I sites; the linkage disquilibrium parameter D=0.20 which is 81% of its theoretical maximum for these RFLPs. Faintly hybridizing fragments, presumably due to cross-hybridization of sequences in the 3'-untranslated portion of the probe with related sequences, are evident when normal post-hybridization washing conditions (0.1 X SSC and 0.1% SDS, 50°C, 60 min) are used.