FBrf00 90025 90025

CARNEGIE INSTITUTION

Department of Embryology
115 West University Parkway
Baltimore, Maryland 21210
[redacted] telephone
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FAX

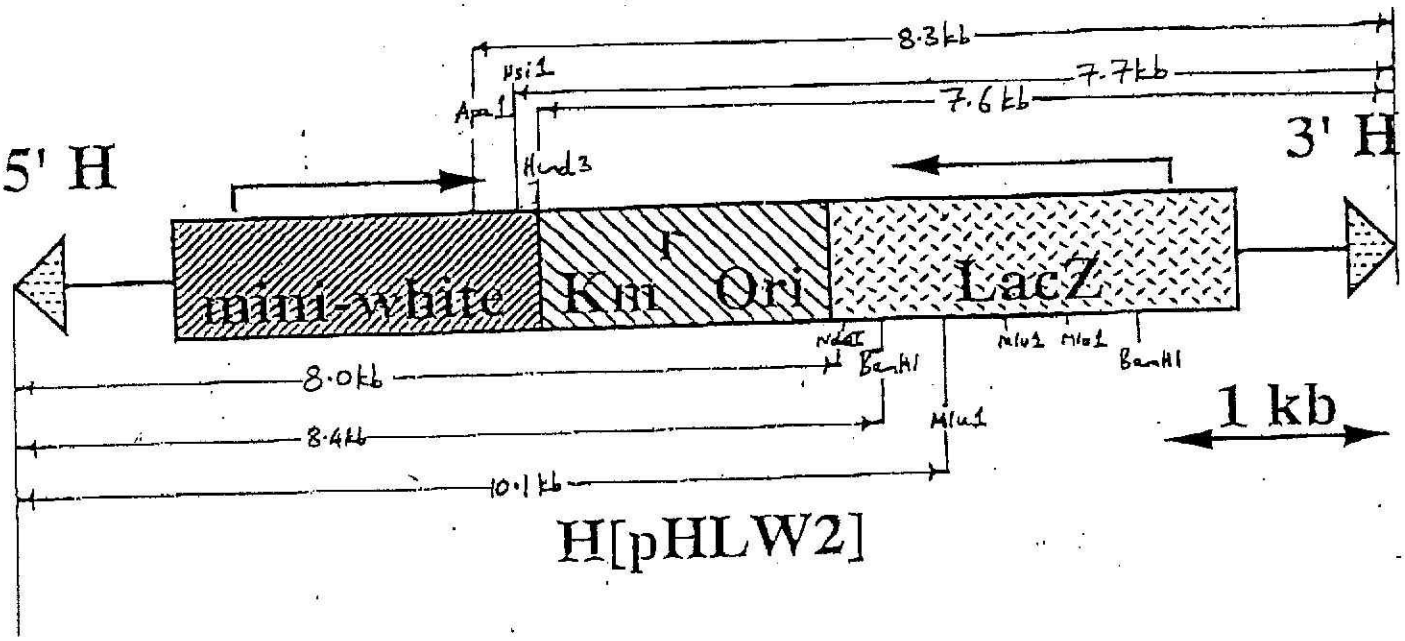
DATE: 5/7/96 TIME: _____ No. OF PAGES: 9 (including cover sheet)

TO: Lynn Crosby
Flybase

FROM: Brian Calvi

MESSAGE: Happy Computing

a hobo enhancer trap



(1) The LacZ gene is driven by the hsp 70 TATA box which acts as a weak promoter and is therefore an effective enhancer trap. The lacZ gene is fused to the hsp70 trailer. (3' untranslated region)

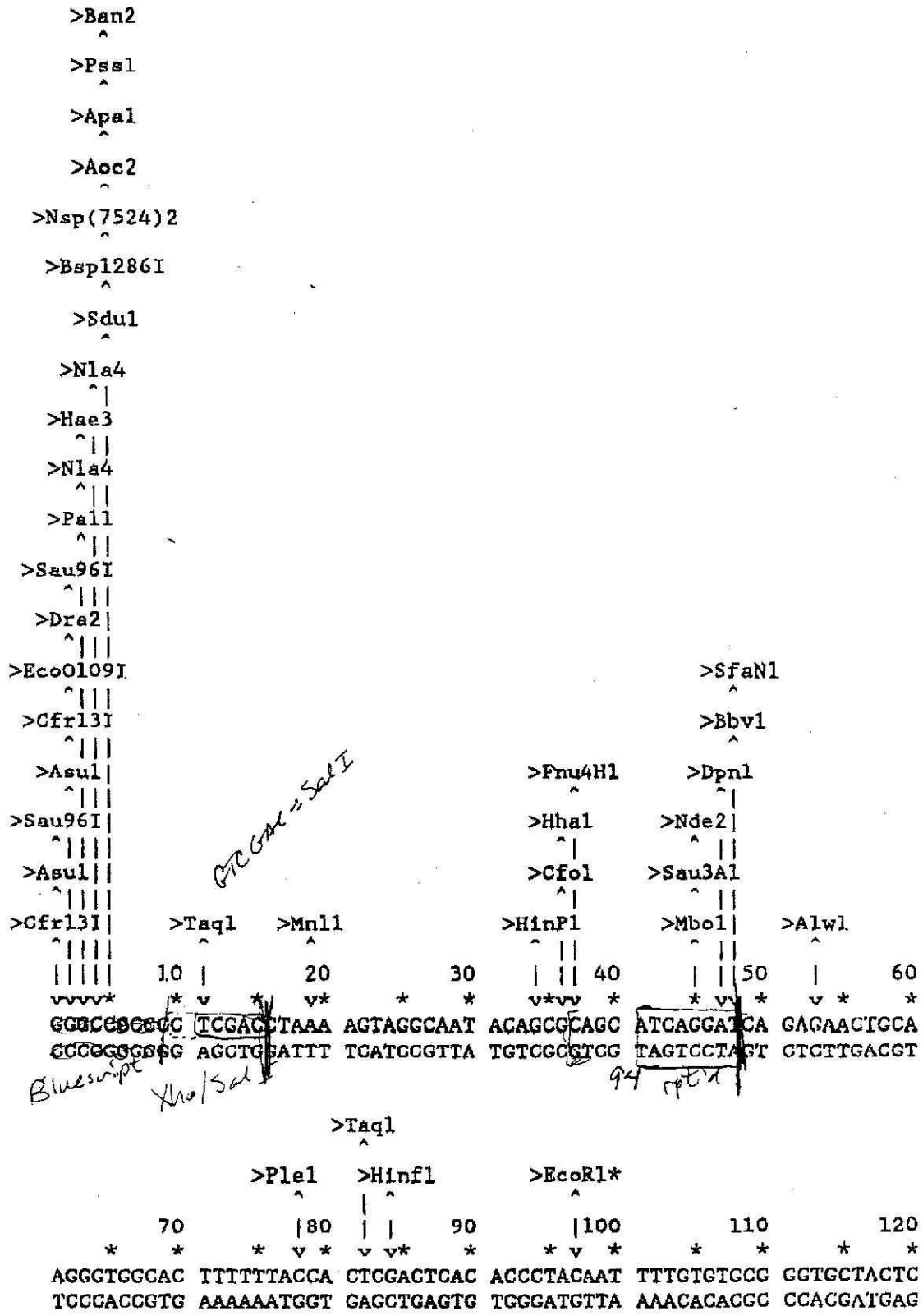
(2) The transposon contains plasmid rescue sequences. Six restriction enzymes (Apa I, Nsi I, Hind 3, Nde I, BamHI and MluI) good for plasmid rescue are shown. The rescue plasmid is pHS67 (Seufert et al. PNAS, 1986, 83, 735 - 739), which is Kanamycin resistant.

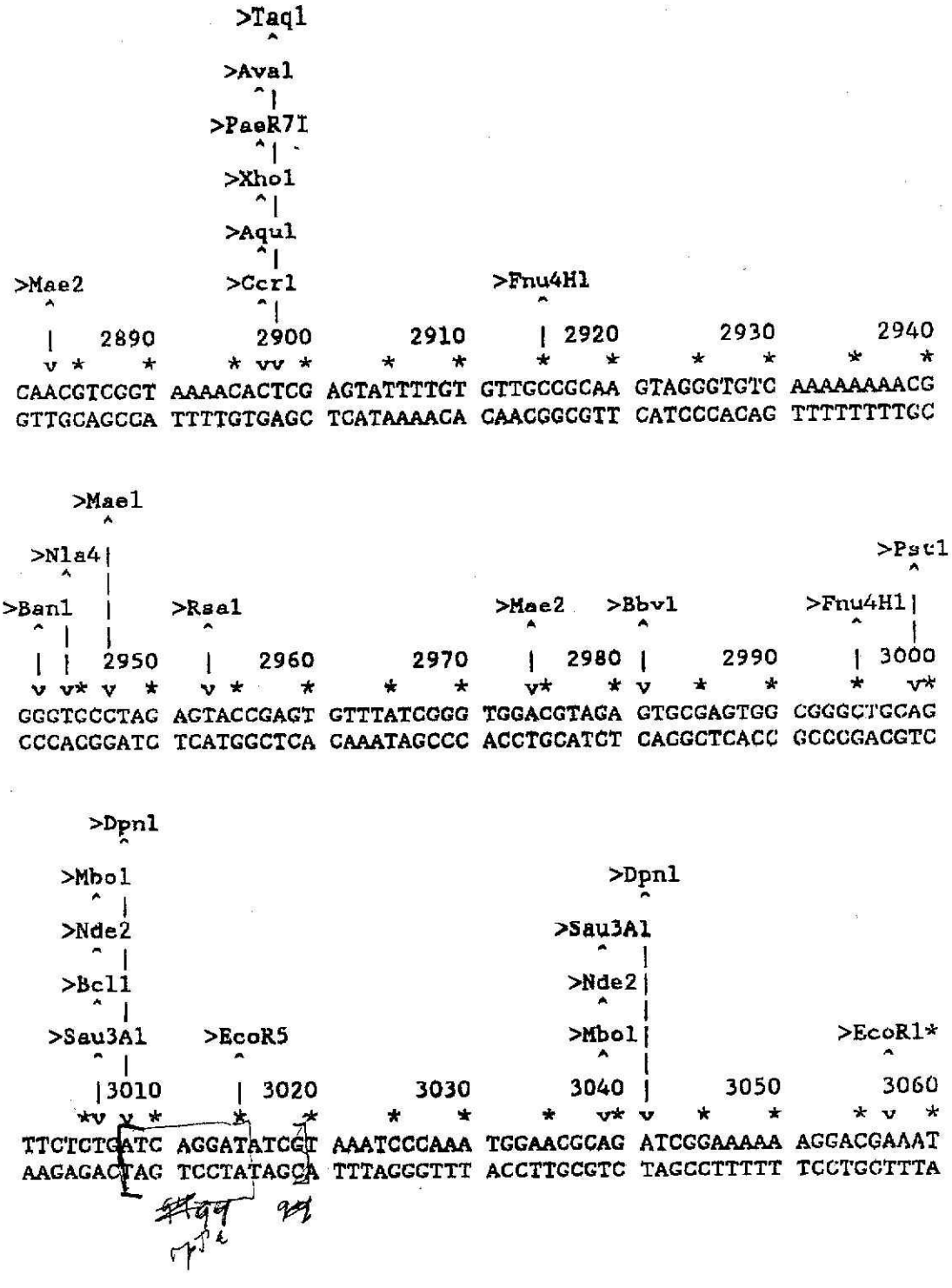
(3) The transposon is genetically marked with the mini-white gene.

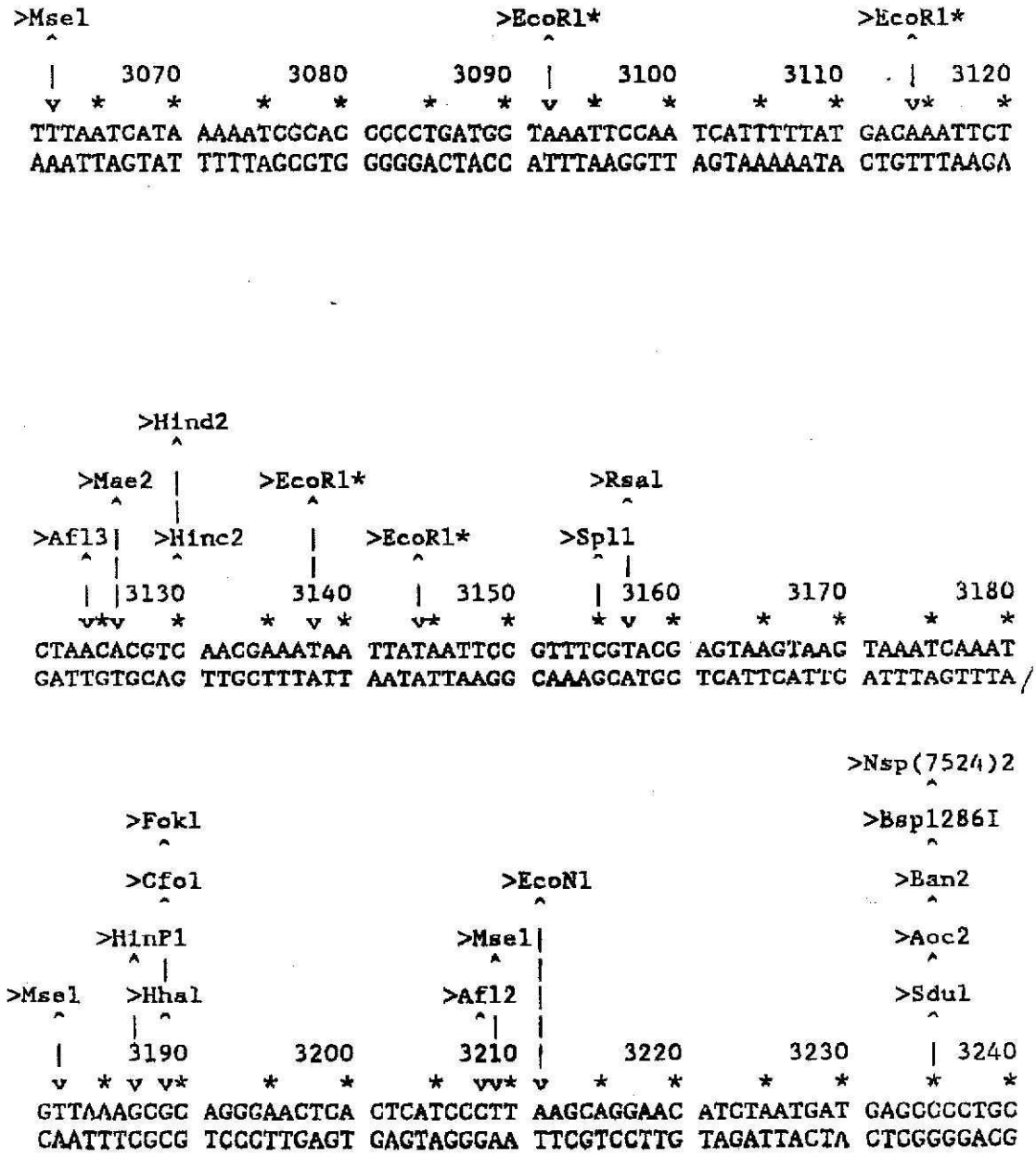
CHFL

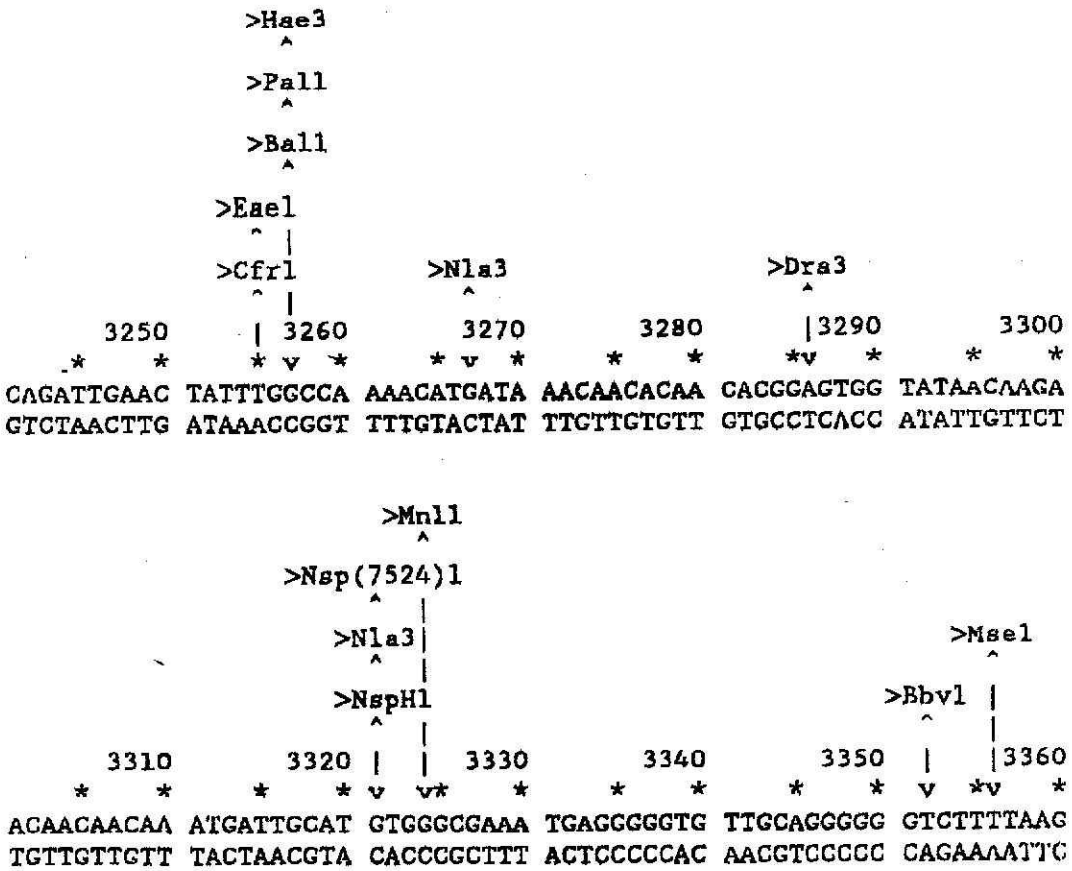
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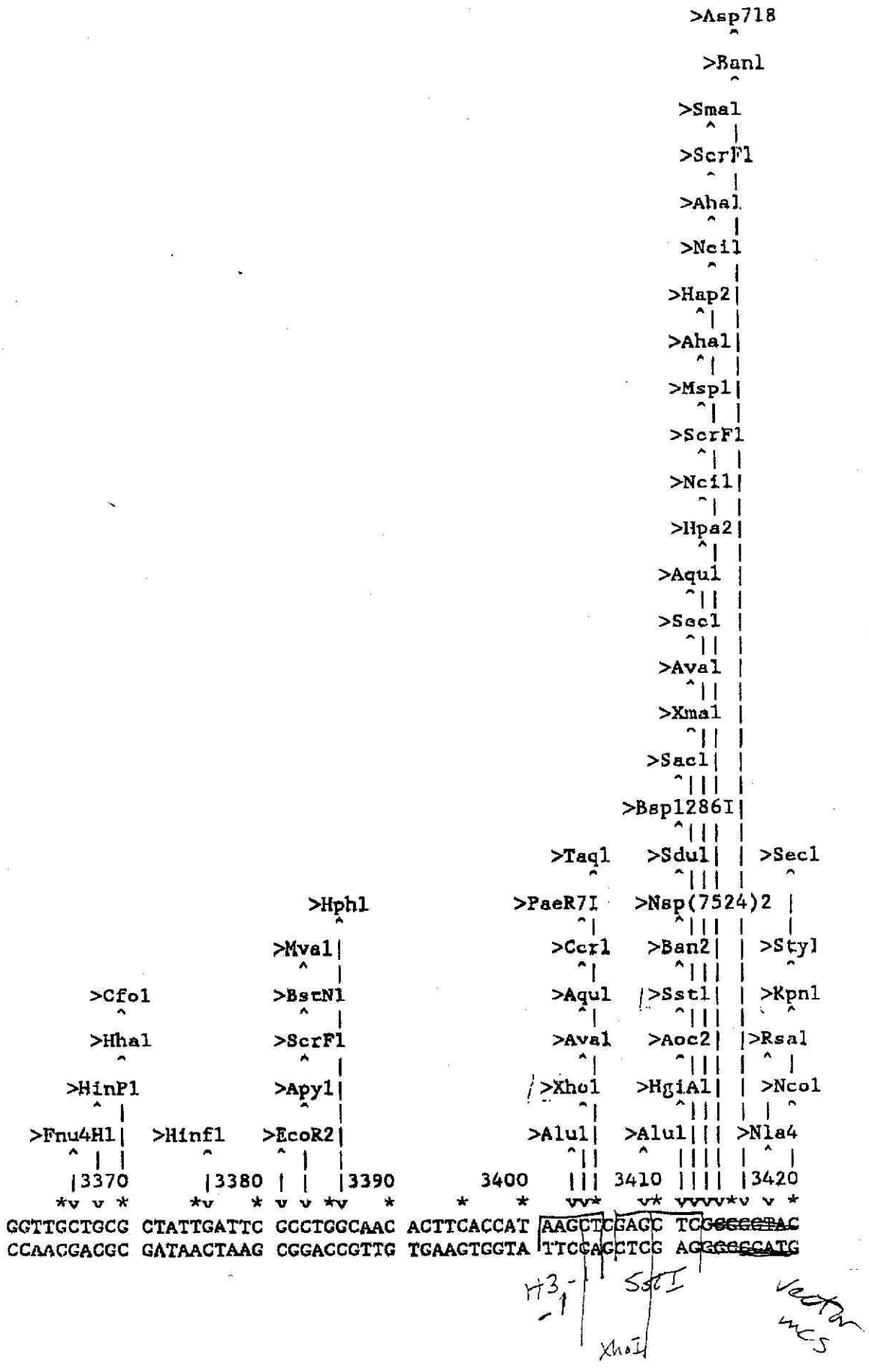
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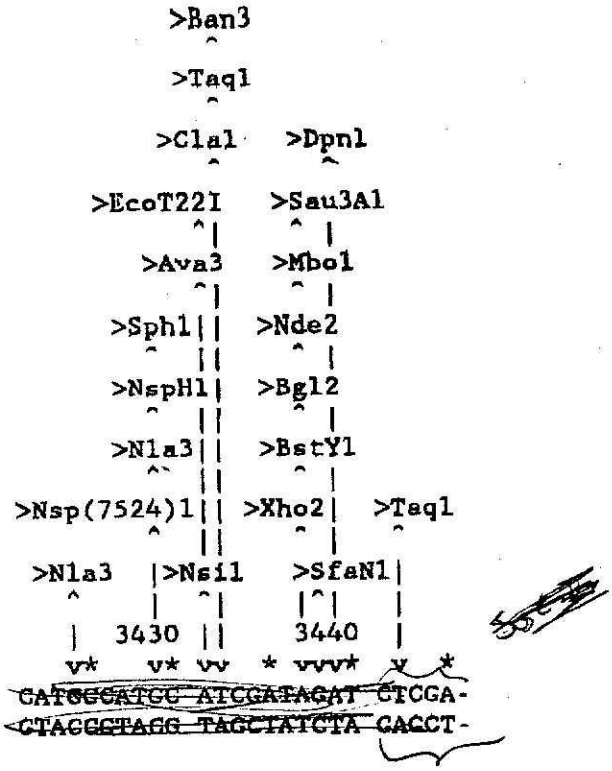

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From [redacted] Tue May 7 11:31:44 1996
Date: 7 May 1996 11:30:52 -0400
From: "Brian Calvi" <[redacted]>
Subject: Re: hobo constructs
To: "Madeline Crosby" <[redacted]>
X-Mailer: Mail*Link SMTP-QM 3.0.2
Content-Length: 4326

RE>>hobo constructs 5/7/96

Dear Lynn,
I have enclosed the sequence of cHFL, an early sequence that included the flanking 94E genomic DNA. The dashes represent ambiguities. I have the printout of a later version without ambiquities (hfl1seq) but can't find the file amongst my pile of old floppies despite an extensive archaelogical dig. I'll fax a hardcopy of the cHFL sequence and the 5' and 3' seq from hflseq along with my map of HLw2.There shouldn't be many changes so you can edit cHFL using HFLseq. If memory serves there should be about 49 bp 5' and 450 bp 3'; the ends of hobo can be found by a matrix against the genbank sequence. You may be right about pHSS6. Sorry I didn't get to talk to you more at the meeting, it gets crazier every year.
Brian

<<<<<< Attached TEXT file named "CHFL" follows >>>>>>
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