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December 20, 1990

John Merriam
UCLA Drosophila Genmaps Database
DEPARTMENT OF BIOLOGY
405 HILGARD AVENUE
LOS ANGELES, CALIFORNIA 90024-1606
FAX [redacted]

FAX [redacted]

Q180 Df(3R)D1-A143
Df(3R)D1-AD28
In(3LR)D1-KX12

Lehmann, Ruth
MIT Whitehead Institute
9 Cambridge Center
Cambridge, MA 02142

Dear Colleagues:

I would like to use information from the clone list to construct a "physical map" of the Drosophila genome. You have (a) clone(s) listed, as described below, so I would like to enlist your help. What I need for this project are the names and locations of chromosome rearrangement breakpoints that lie within the region of your clone/walk. Mapping breakpoints is the most reliable way of connecting the molecular with the cytological scales.

As you know, the clone list has been useful to Drosophila workers in finding starting points for their walks. The database is organized by references, so that the original cloning paper from a lab is cited as key #1, with subsequent papers cited by subject (key #5 is sequence information, for example). The clone list is therefore also a gene-by-gene literature index. The clone list is now mounted on the Indiana University BioArchive computer bulletin board in the FLY subdirectory. Use Internet address 129.79.1.101 and your local File Transfer Program.

Please take a few minutes to complete this form and return to me by FAX or mail. It will be most useful if you can update your clone sizes and make more exact your clone locations. Make any other changes you want also. List the rearrangements and which breakpoints you have identified. Any cytologically visible rearrangement (deletion, inversion, translocation, transposition, duplication) is useful. Please indicate if the same citation is the best reference, or indicate a better one (or a personal communication).

I thank you for your help as always. With your prompt and generous support I can expect to show you the results in March at the Chicago fly meeting.

List Rearrangements :	Breakpoint found:	Other breakpoints:

CHANGE or CONFIRM indexing for original clone cit'n: Locations __ Clone sizes __ Names/Products __

Wang C and Lehmann R (1989) 30th Annual Dros. Conference

Location	Key	kb gen/cDNA	Gene name (abbreviation) product rearrangements...
91F	1,6	30 0	nanos (nos)

1,4,5,6 olC SW 616

Return to John Merriam, UCLA Biology, LA 90024 FAX [redacted]
REFERENCE: Wang C and Lehmann R (1989) 30th Annual Dros. Conference

NAME: Charlotte Wang / Ruth Lehmann PHONE [redacted] FAX # [redacted]

1. GENE: How do you describe the gene you are reporting on?

mutant name (if any) nanos

abbreviation nos

biochemical name (if any) _____

upgrade

2. LOCATION: Where is your clone/walk located? 91F13 6
(If you are using a clone from a more extended walk, what is the location of your gene? _____)

3. SIZE: How many kb did you clone? (round to nearest kb)

genomic 120 Kb vector/library name Charon vector, Maniatis library

cDNA 2.3 Kb vector/library name pNB40 (Nic Brown library) 6

4. METHOD: Describe the entry point for your clone/walk

prior clone HP 5.3 from Delta region (H. Vässin) transposon tag _____

expression _____ differential screen ✓

microclone _____ oligonucleotide _____ PCR? _____

homology _____

5. SEQUENCE: round to the nearest 10th the kb sequenced

genomic 3.0 accession # not yet

cDNA 2.3 accession # submitted ✓

PRODUCT: How many amino acids in the ORF? 400

no homologies

List above the predicted function or homology group of the ORF

List above the key words that describe domains in the ORF

6. TRANSCRIPTS: round m RNA sizes to nearest 10th kb, list largest first 2.4 When/where found? Ovaries, 0-4 hr embryos, 9F5 (maternal expn)

7. PROTEIN (antibody detection) Where found? _____

8. LAC Z FUSION stain Where found? _____

9. MORE DETAILS: _____

Breakpoints for Df(3R)DL-HD28, 91F; 92B Df(3R)DL-KX12 + In(3LR)67CD; 91F, Df(3R)DL-A143 have been mapped on genomic walk 6

key 2 for understand