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Types of self-assembling of length Intron RNA presented in the regions of homologue chromosomes somatic pairing

Amongst different types of chromosome pairing (meiotic, somatic, sister chromatids pairing) initiation stages are less elucidated. In somatic homolog pairing initiation the long intron RNA intron products interference may play the essential role.

- 1. Homologue chromosomes somatic pairing in *Drosophila melanogaster***
- 2. Somatic pairing for GABA locus in 15 chromosome ; Alu repeats role**
- 3. Alu repeats enrichment of enlarged version of REST transcription factor gene**

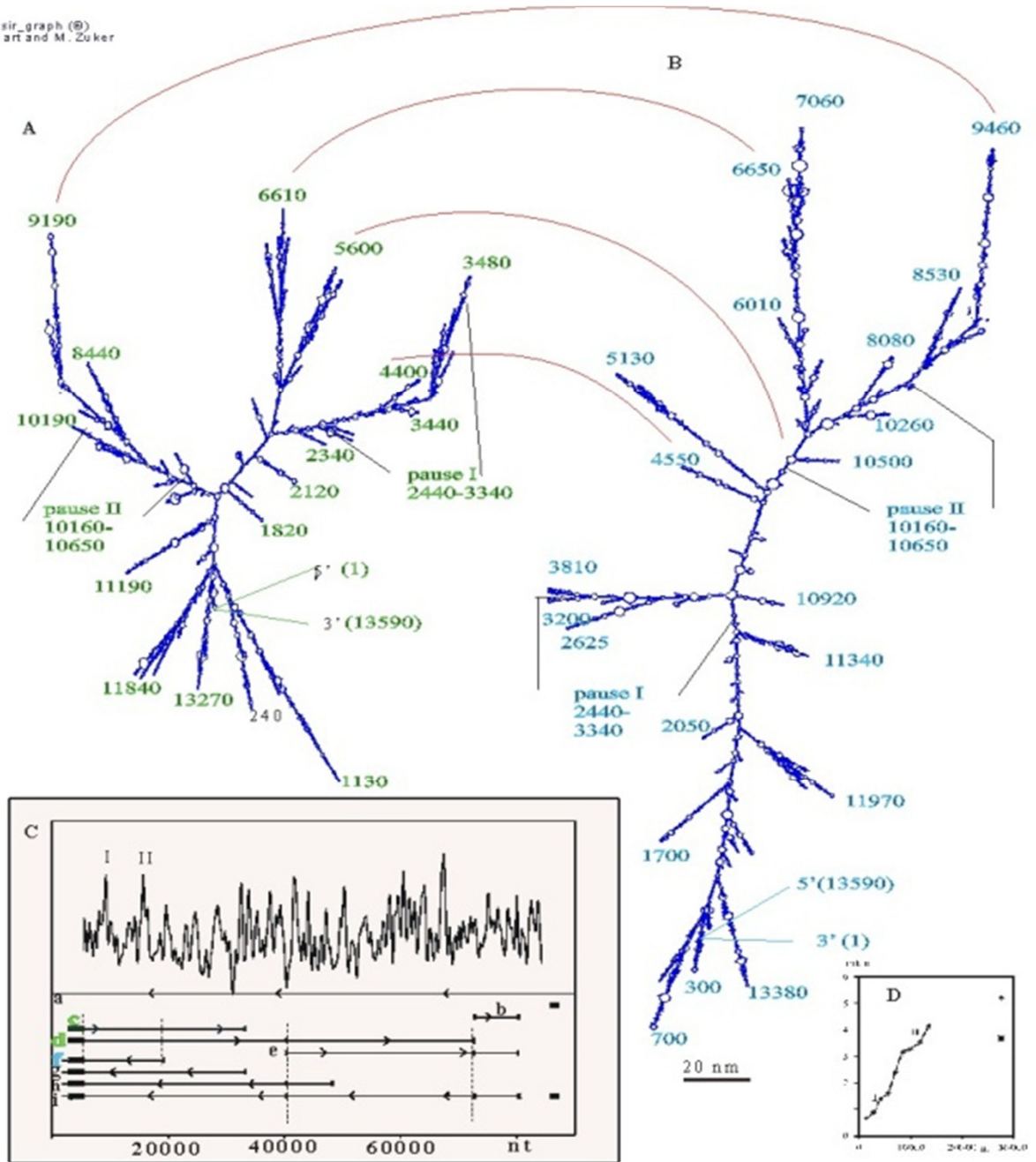
Table.1 Correlation of stretched forms parameters of long intron RNA folding and chromosome pairing

Locus *(FISH probe), chromatin state, genes, their cytological map	Pairing profile (tetraploid cell)*	Long intron length (sequence identical to plus or minus DNA strand (GenBank))	Parameters of stretched forms (3'5' – apex, μm)
28B1-B2, 2L euchromatin Rapgap1 28B1-B2	~ 88%	13700nt plus sense 13700nt minus strand (part of 27677 minus strand) antisense 27677 nt plus (AF023478) sense 27677 nt minus (DQ327805) antisense 32100nt plus (JV12284) sense	4,151 2,256; 2,100 5,245; 3,680 5,976 6,955
21E3-E4, euchromatin 2L ia2 21E3-E3 s 21E4-E4	~ 82%	14361 plus (BT010107)sense 14361 minus (JV226177)antisense 14611 nt plus (JV215331)sense 14611nt minus	2,365; 2,31; 2,2 2,822 5,395 not annotated in DB
16E1, X, euchromatin CG6398 16D5-D7 Mnb 16E4-F1	~77%	9012 nt plus (JV211954) antisense 9012 nt minus (FJ631303) sense 7888 nt plus (X70798)sense 7888 nt minus (JV212371)antisense	1,785; 1,509 2,313; 2,174 2,422 2,128

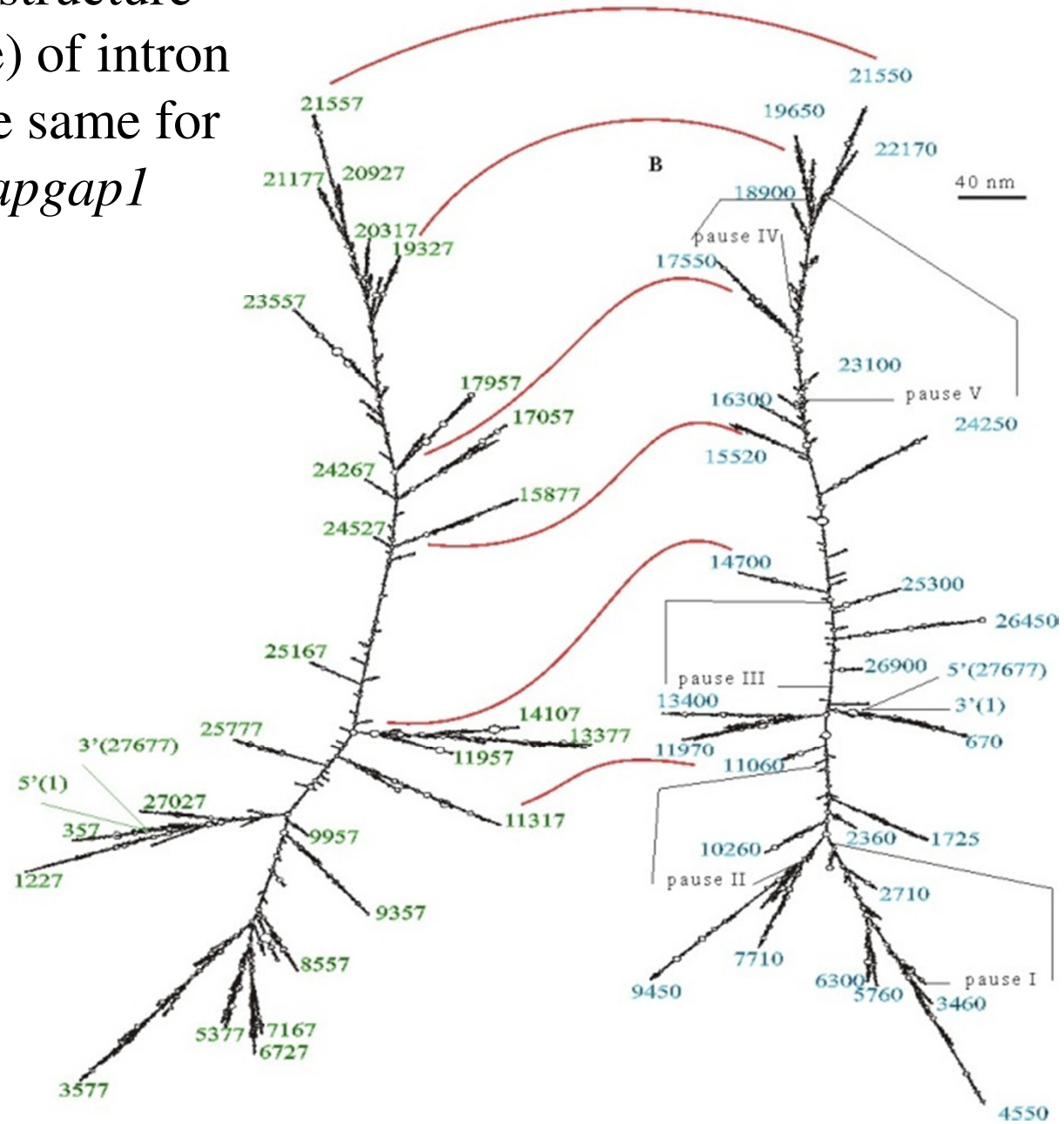
<p>8C8, X, euchromatin</p> <p>CG42388 8C4</p> <p>CG10962 8C1-C4 rdgA 8C1-C4</p>	<p>~74%</p>	<p>10722 nt minus (BT133107) sense 10722 nt plus (part of intron,JV208221) antisense 10144nt minus (BT133107) sense 9144 nt plus (JV208221) antisense</p> <p>12708 nt plus (JV209098) sense 12708 nt minus (D17315) sense</p>	<p>2,752 2,794 3,157 3,512 3,022 2,982; 2,788; 2,449</p>
<p>69C2-C8, 3L, euchr</p> <p>Ncc 69 69B3</p> <p>CG32103 69B4-B5</p>	<p>~75%</p>	<p>11682 nt plus (JV219927) sense 11682 nt minus (JV211796)anti- sense 6812 nt plus (BTO44506)sense 6812 nt minus (JV215063)antisense</p>	<p>1,742; 1,562 1,65; 1,42; 1,81; 1,1 1,912 2,044; 1,773</p>
<p>40A2-A3, 2L, heterochromatin step 40A1-39F3</p> <p>1. CG31612 40A2-A3</p>	<p>~ 52%</p>	<p>12522 nt plus (FJ632818) sense 12522 nt minus (JV212396) antisense 5883 nt plus strand (BTO30162) sense (part of 12522 nt) 6839 plus strand (AY089601) sense 6839 minus strand</p>	<p>2,896 2,665;2,461 2,975 1,55; 1,21 not annotated in DB</p>

Output of sir_graph (B)
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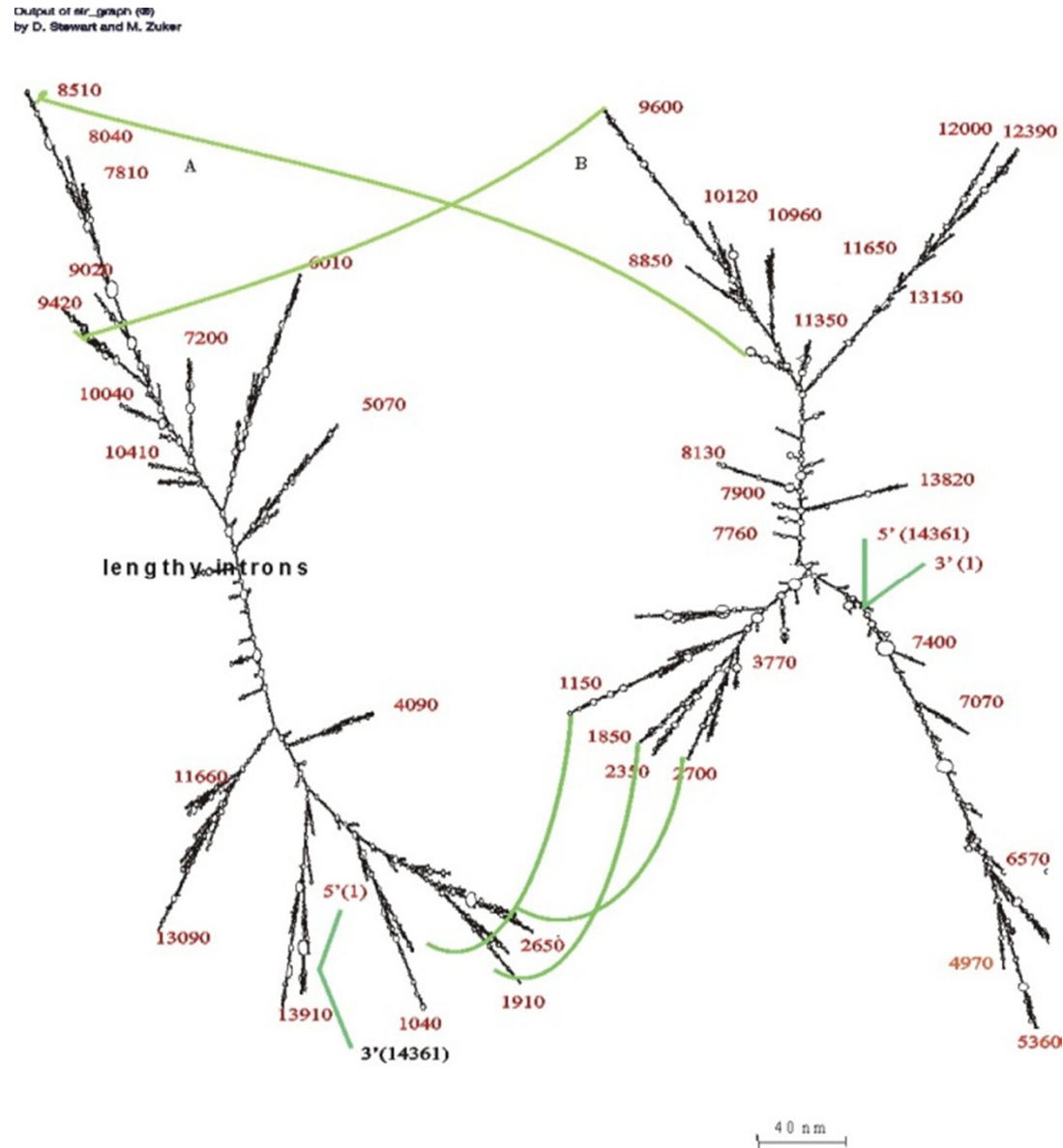
Folded secondary structure of (*sense*) RNA intron product (13590 nt) and the same for RNA (*antisense*) of intron portion (*Rapgap1* gene, 28B1-B2 locus); scheme of 28B1-B2 locus; folded structure linear dimension dependence upon nascent RNA length in nt



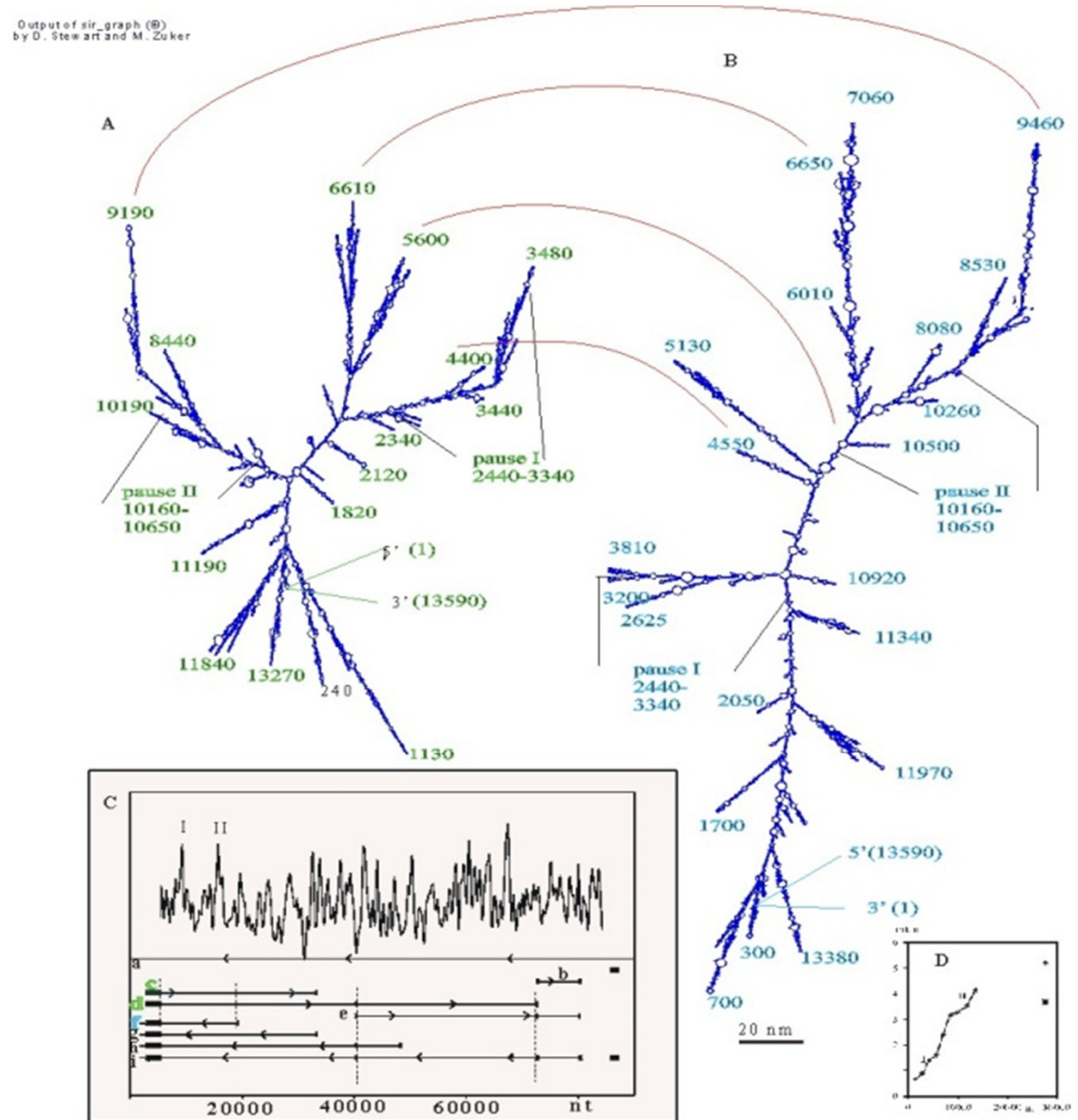
Folded secondary structure of RNA (*antisense*) of intron (27677 nt) and the same for RNA (*sense*) of *Rapgap1* (28B1-B2)



Folded secondary structure of RNA (*antisense*) of intron (14361 nt) and the same for RNA (*sense*) of *ia2* gene (locus 21E3-E3)



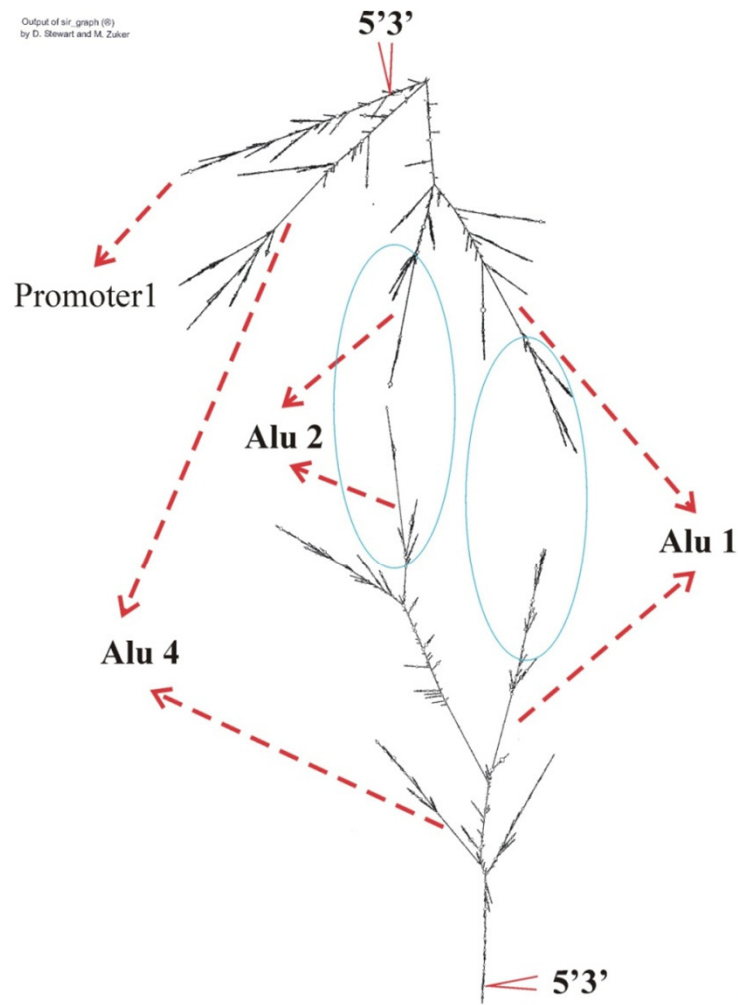
Folded secondary structure of RNA (*sense*) of intron (13590 nt) and the same for RNA (*antisense*) of of intron portion (*Rapgap1*, 28B1-B2) ; scheme of 28B1-B2 locus; folded structure length dependence upon nascent RNA intron product length in nt



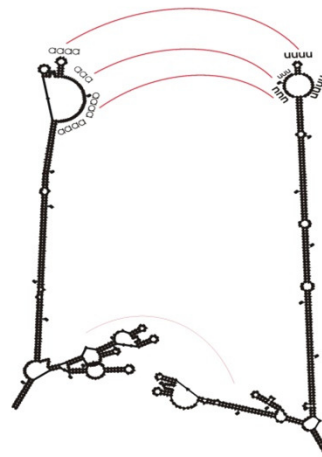
Peculiarity of locus 15q12 containing genes of GABRB3(beta3) and GABRA5 (alfa5) receptor subunits

- a) divergent character of transcriptional directions of these genes
- b) multi-variance of transcriptional isoforms of gene GABRB3 (β 3 subunit): isoforms differ one from the other by long introns and so that their multiple promoters are arranged in a ladder manner
- c) existence of lengthy fusion transcriptional isoform of GABRB3 including of both genes; in addition annotated isoforms there also putative genes of both directions deduced by GenScan on the basis of EST (Expression Sequence Tags) including unspliced in both directions. The annotated as well as putative isoforms demonstrate the alteration of bidirectional and mono-directional regions of transcription
- d) asymmetric transcription of the locus, e.g. the main promoters P1-P5 may be active on the maternal chromosome , but only P6 is active on the paternal chromosome, where P1-P5 are closed via the methylation of CpG islets in vicinity.
- e) coincidence of the two incidents such as syndrome of autism and chromosome pairing abrogation as consequence of large deletions beyond the gene GABRB3 gene.

Output of sir_graph (8)
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see apices of Alu 2



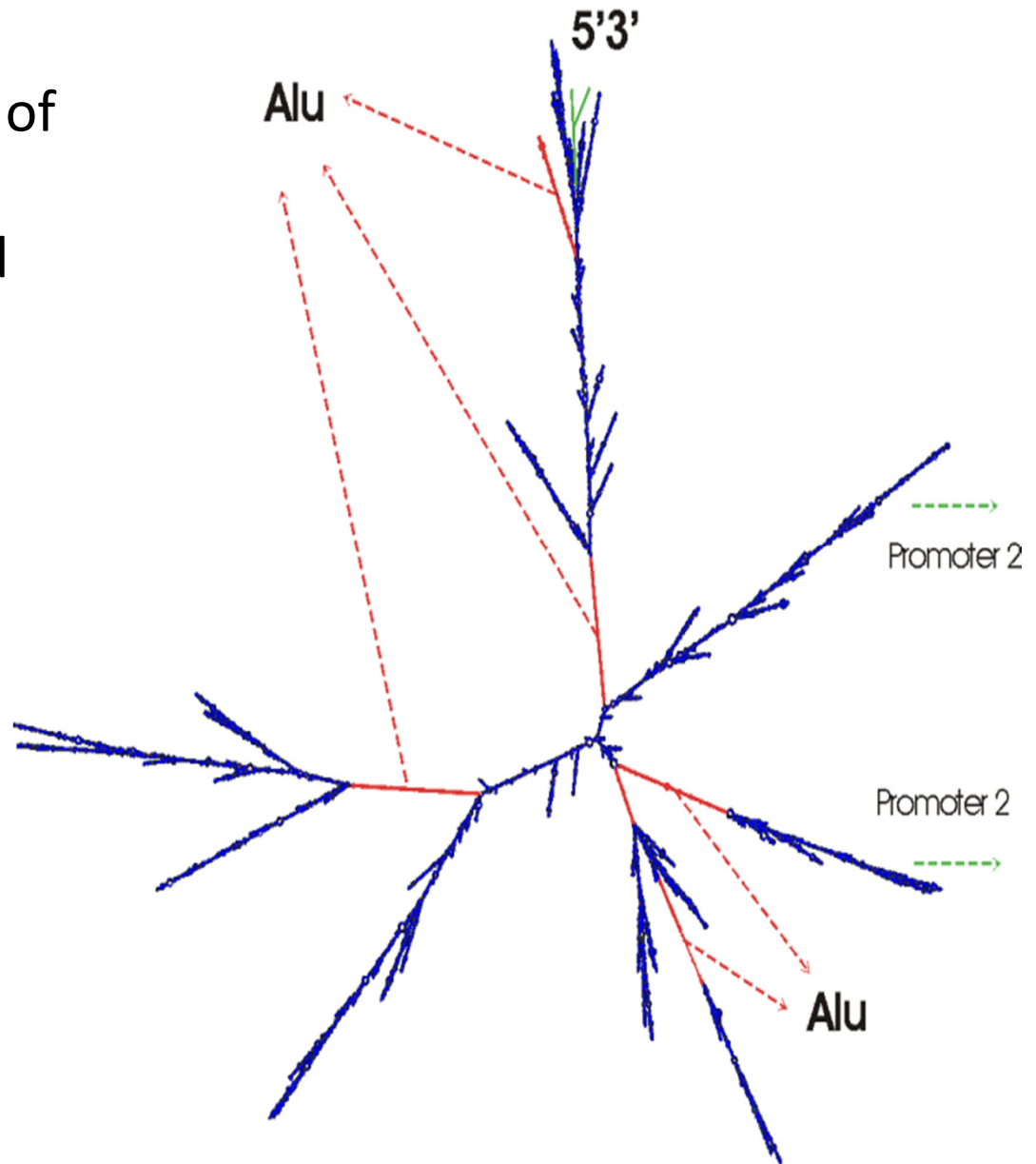
Sequences Alu1(-)loops

ata
 acat
 gtc
 agg
 aaa*n
 agg
 ata
 actta
 aagaa
 aagagg
 agaaataa
 actaacttt
 aggtaaa

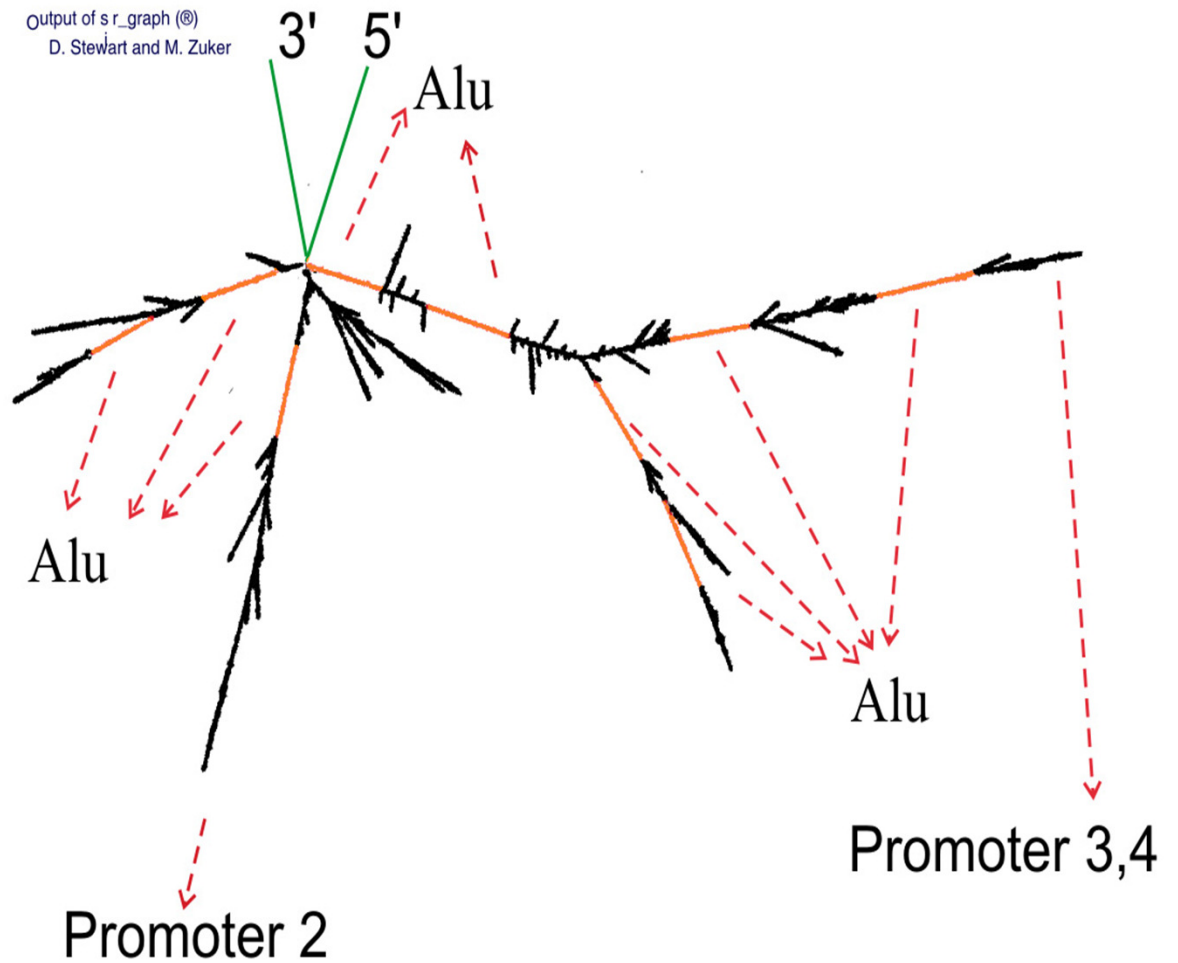
Sequences Alu1(+)loops

tattt
 acat
 ggact
 tcc
 tt*n
 cctc
 tatat
 actta
 tct
 ttctaca
 actaacttt
 tctaate
 ctgcct

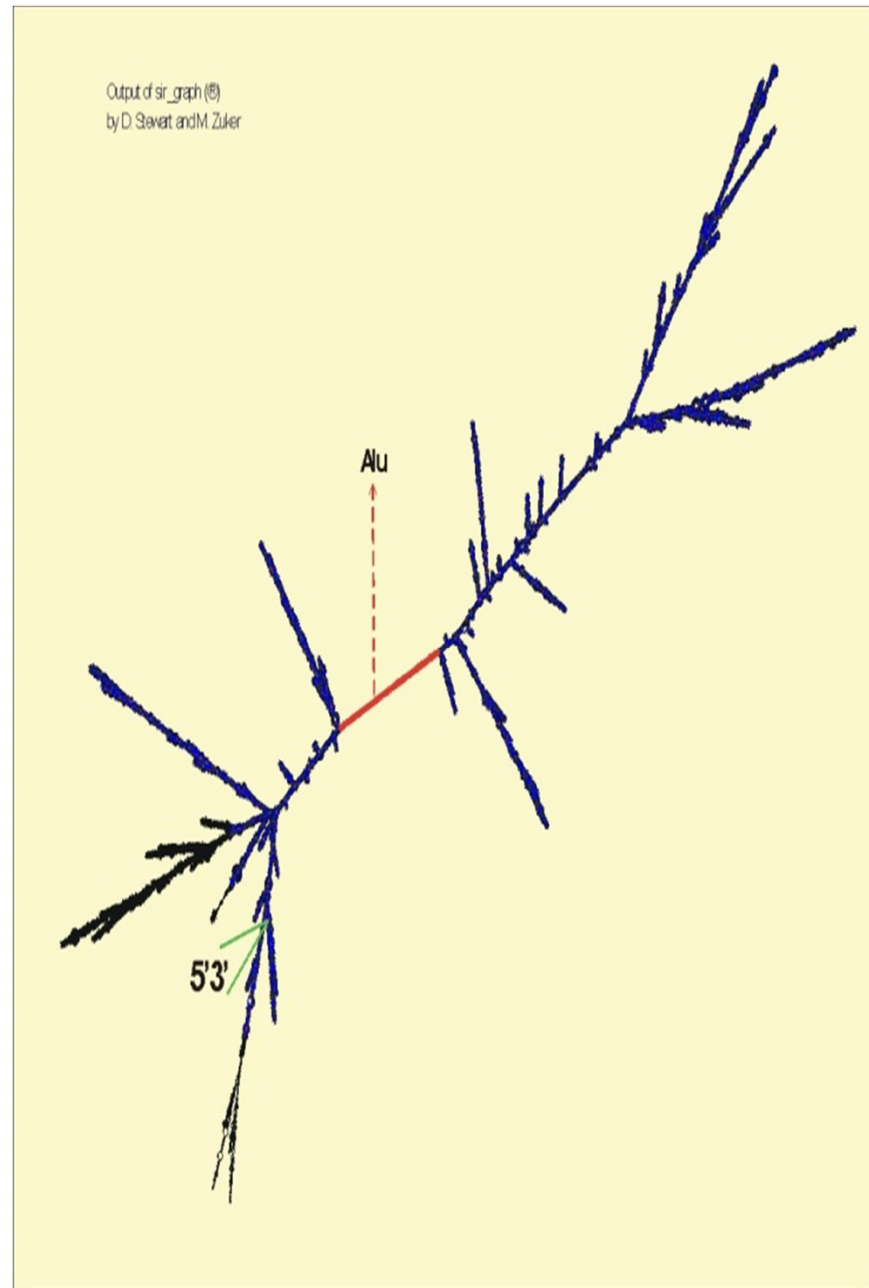
Folded structure of
RNA intron
product adjoined
Promoter2



Folded
structure of
RNA intron
portion
between
Promoter2
and
Promoter3,4
enriched by
Alu repeats

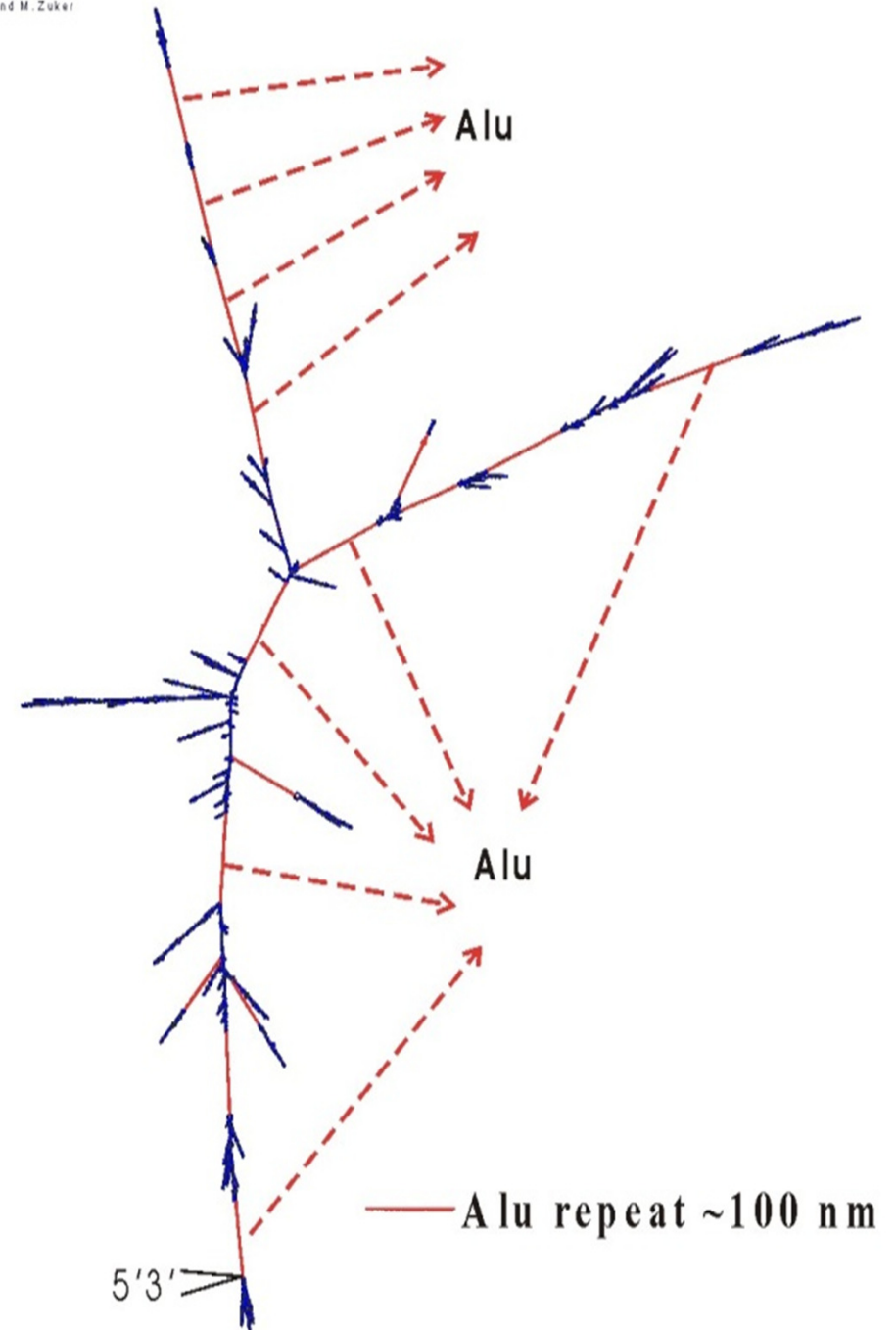


Folded secondary of
(+)RNA(31240nt)
product of inner
intron of main gene
body for GABRA5
(26883560_26914806
of *H.s.*15chr)



Folded secondary structure of (+)RNA(46200nt) intron product for enlarged gene version of REST transcription factor (4th chromosome of *Homo sapiens*, 56919700_56965900) enriched by numerous Alu repeats

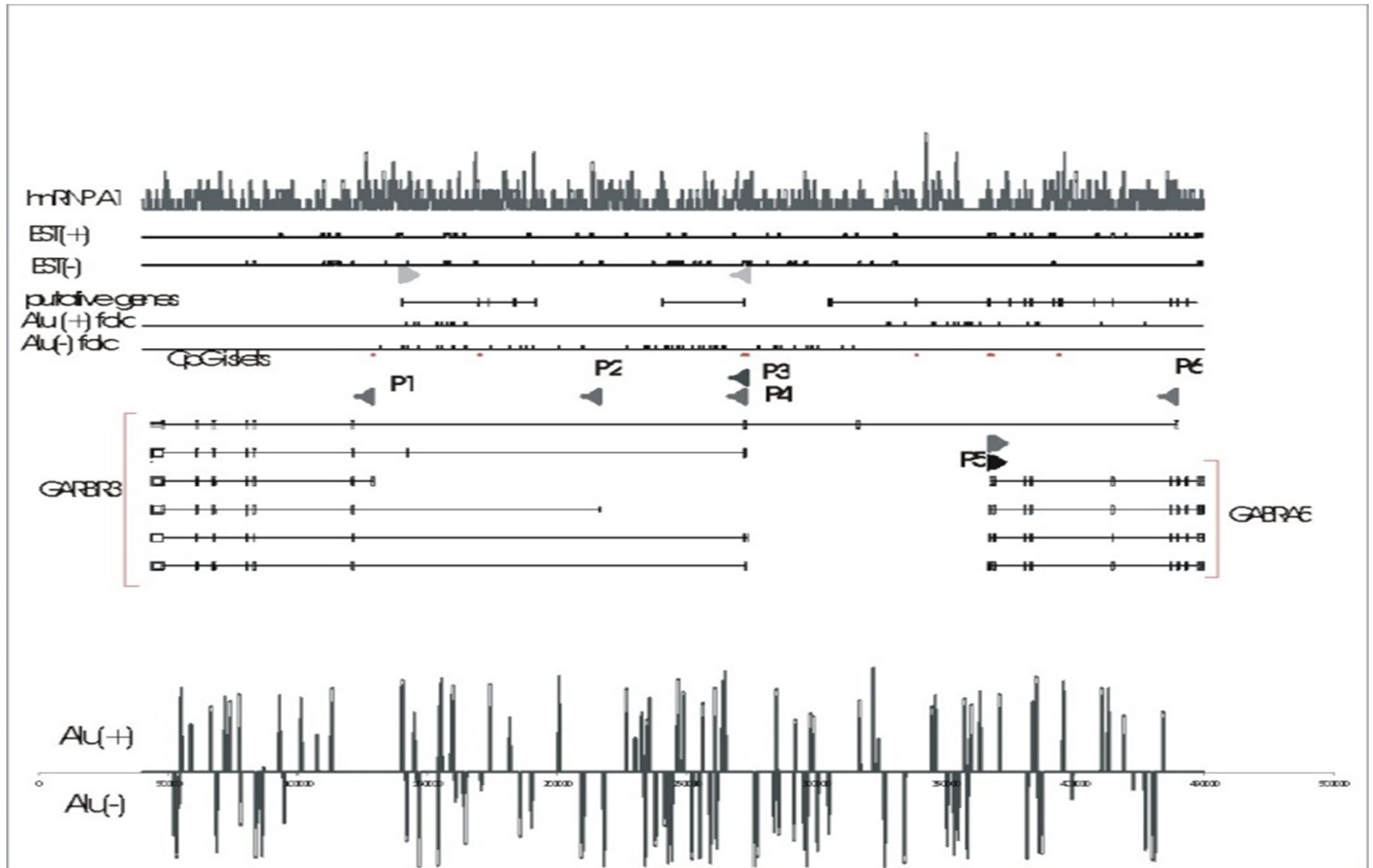
Output of sh_graph (8)
by D. Stewart and M. Zuker



Mostly stretched
folded structure of (-)
RNA intron product
(46200nt) with tandem of Alu
repeats (26772750_27818900
15 chromosome, GABA
locus)



Scheme of 15q12 locus (GABRB3 and GABRA5 genes)



Conclusion. The middle portion of inter-gene region without pairing is potential attractant for REST transcription factors and/or other proteins. Homolog pairing is maintained by edging interfered RNA intron products. Alu repeats at the level of pre-mRNA folding constitute the frame of stretched branches. ESTs that are usually single stranded present the counter-parts concerning double stranded Alu-repeats helices. Alu –repeat density is higher in the central portion of inter-gene region, where Alu(+) and Alu(-) repeat numbers are in approximate equilibrium.

IMG RAS LBI

35 years ago and now



Co-authors: Zharinova I, Ryazanskii S, Suzdaleva M, Protsevskii R.