Genome Plasticity: A Key to Regula Function

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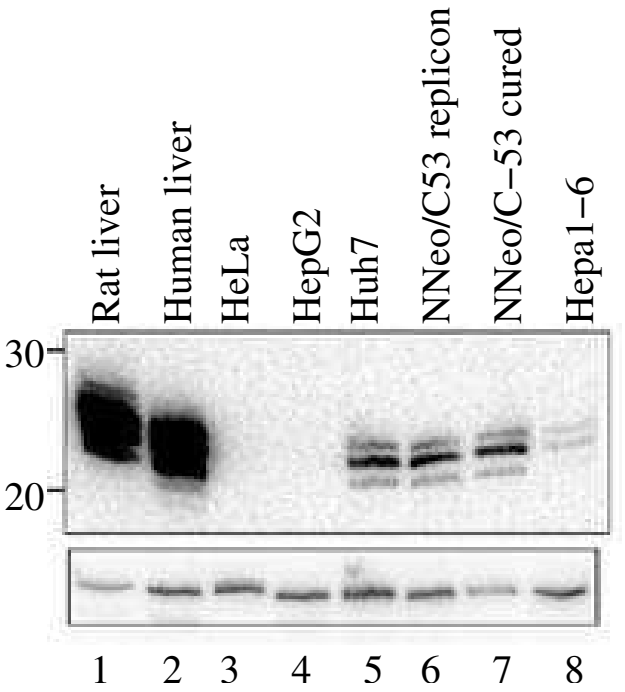
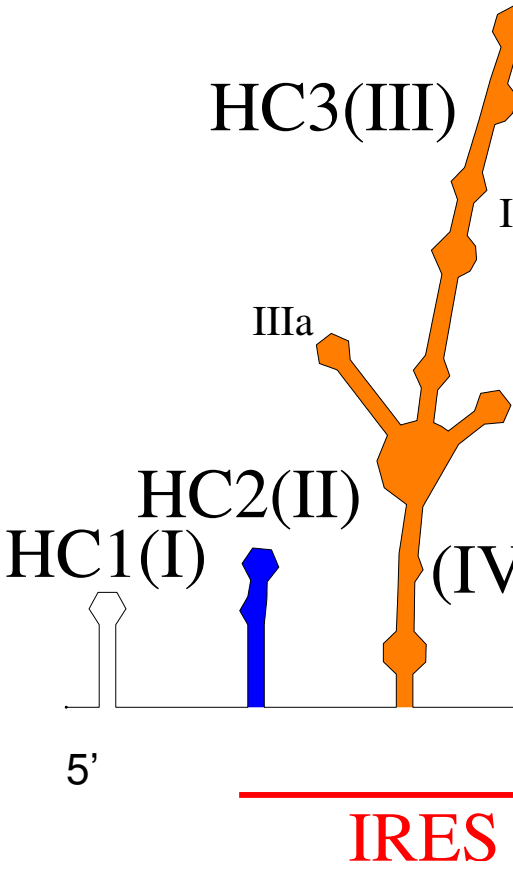
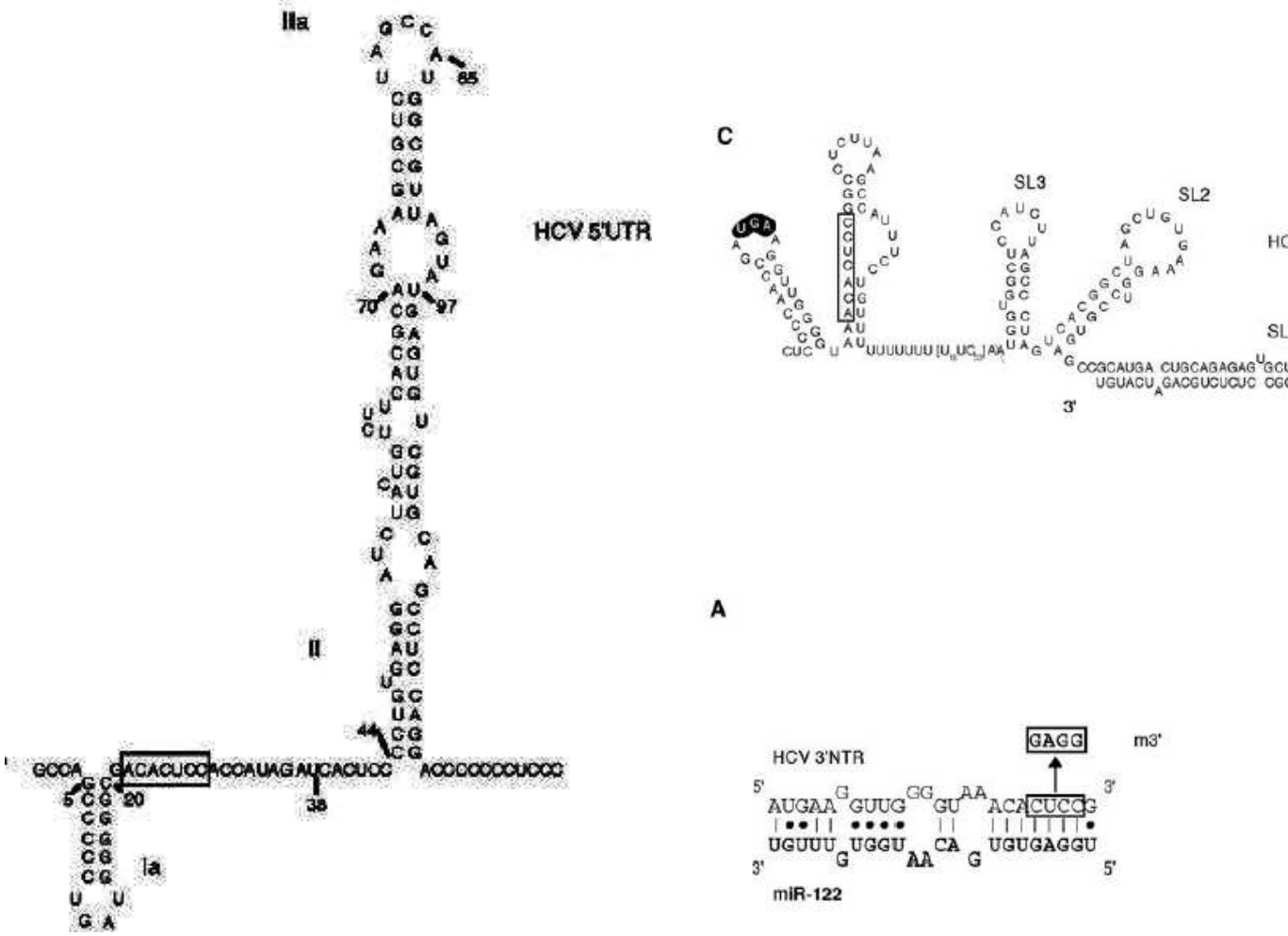
21^{st} TBI Meeting in Bled, 2006





Is there a connection between expression pattern o
different cells and the HCV specific viability only in

Yes there is! two possible binding sites active bindi

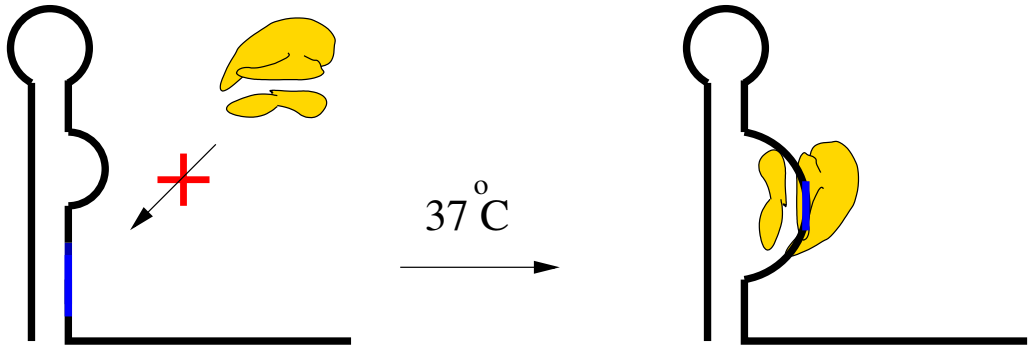


Jopling et al. *Science* (39), 2005

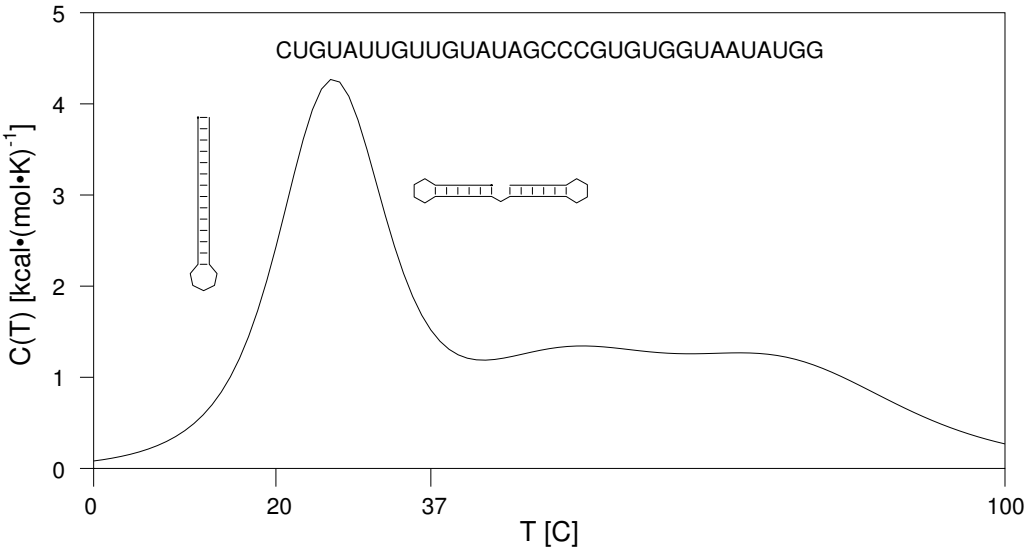
Host pathogen interaction via ncRNAs a gener

Pathogen	Host	ncRNA
Bacterium		
Yersinia pestis	mammals	*lcrF*mRNA the
Listeria monocytogenes	mammals	*PfrA*mRNA th
Staphylococcus aureus	mammals	RNAIII
Clostridium perfringens	mammals	VR-RNA
Streptococcus pyrogenes		*pel*
Vibrio cholerae	mammals	4 ncRNAs
Vibrio angullarum	fish	RNAα
Erwinia carotovora	plants	RsmB'
Epstein-Barr virus	human	BHRF1-1/-2/- BART1/2
simian virus 40	simians	SV40miRNAs
HCV	human liver cells	miRNA122
Flock House virus	C. elegans	RNAi
Flock House virus	C. elegans	RNAi

L. monocytogenes' thermosensor



xtofs thermosensors



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simian virus 40	simians	SV40miRNAs
HCV	human liver cells	miRNA122
Flock House virus	C. elegans	RNAi
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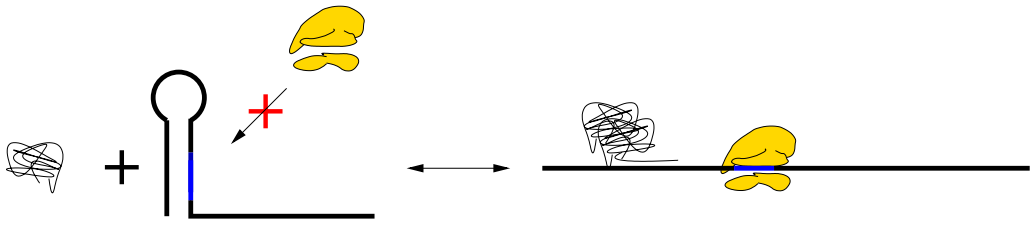
RNAIII 512 nucleotide transcript, highly structured

Functions:

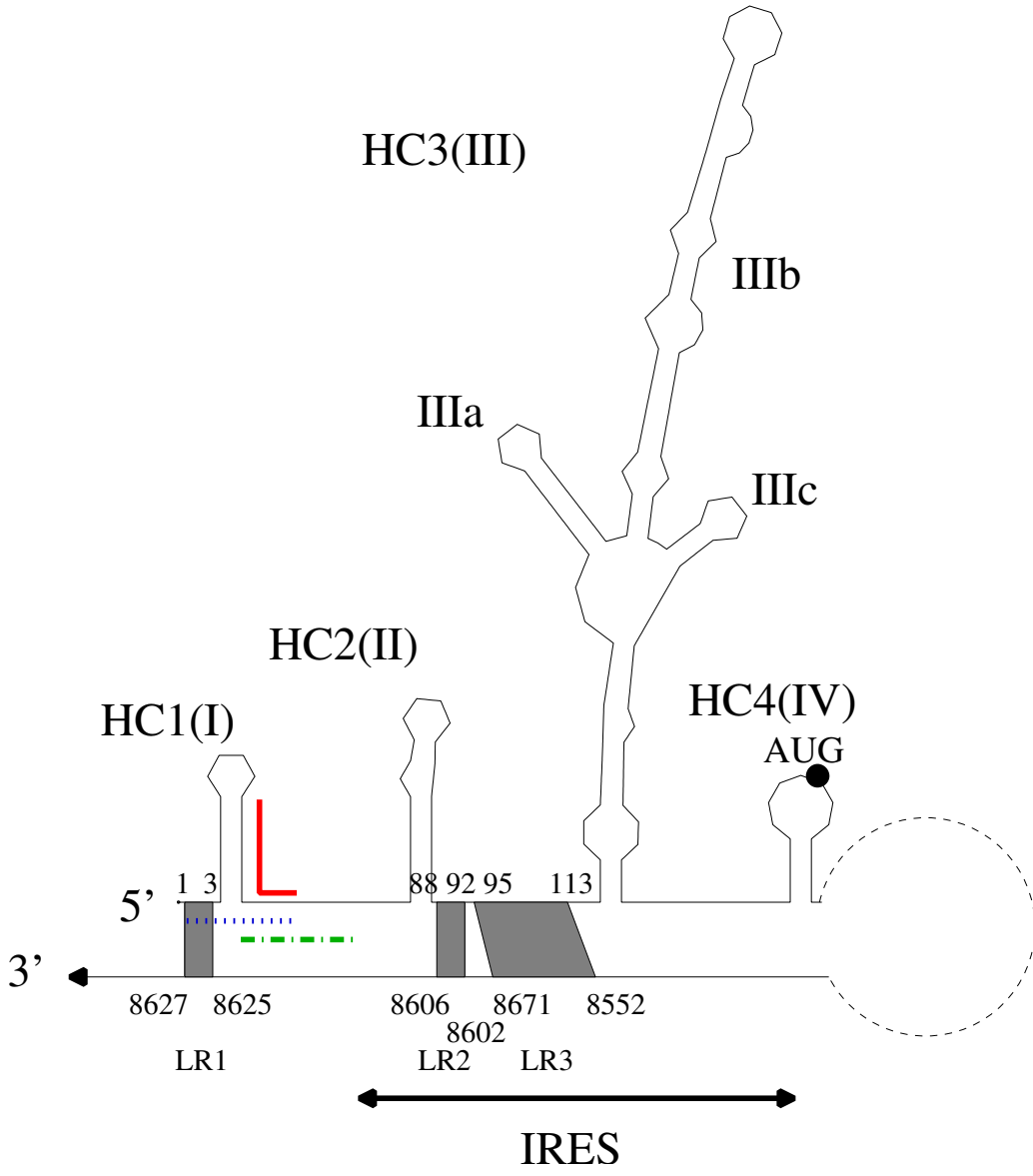
- activates expression of secreted proteins
  RNAIII5'end *prf*-mRNA encoding α-hemolysin



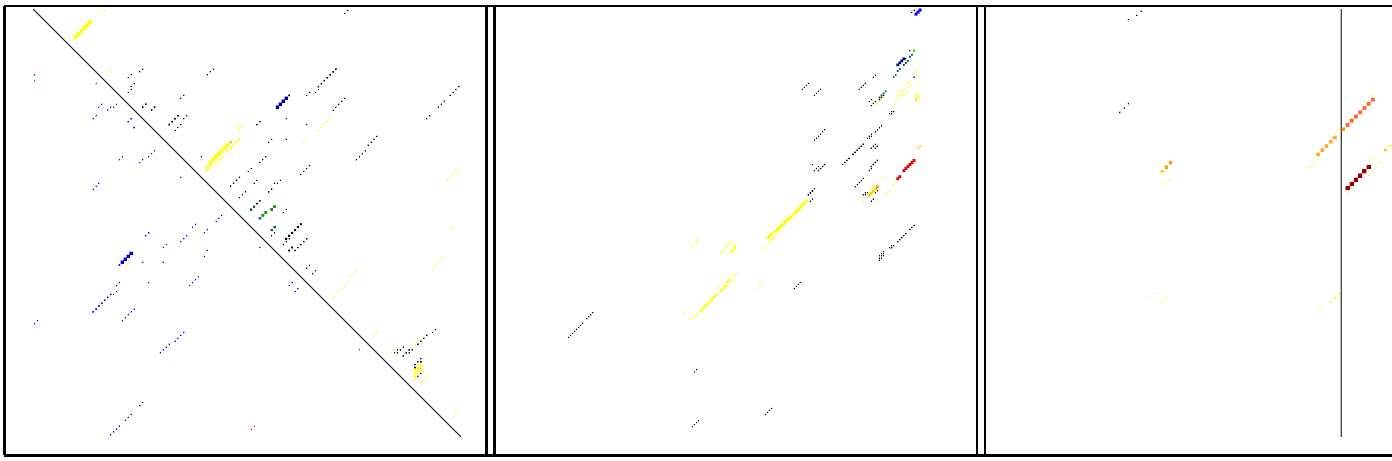
- encodes δ-hemolysin on 5'end

- represses expression of surface proteins
  p.ex.: 3'end represses expression of δ-hemolysin
  3'end represses expression of *spa* encoding prot

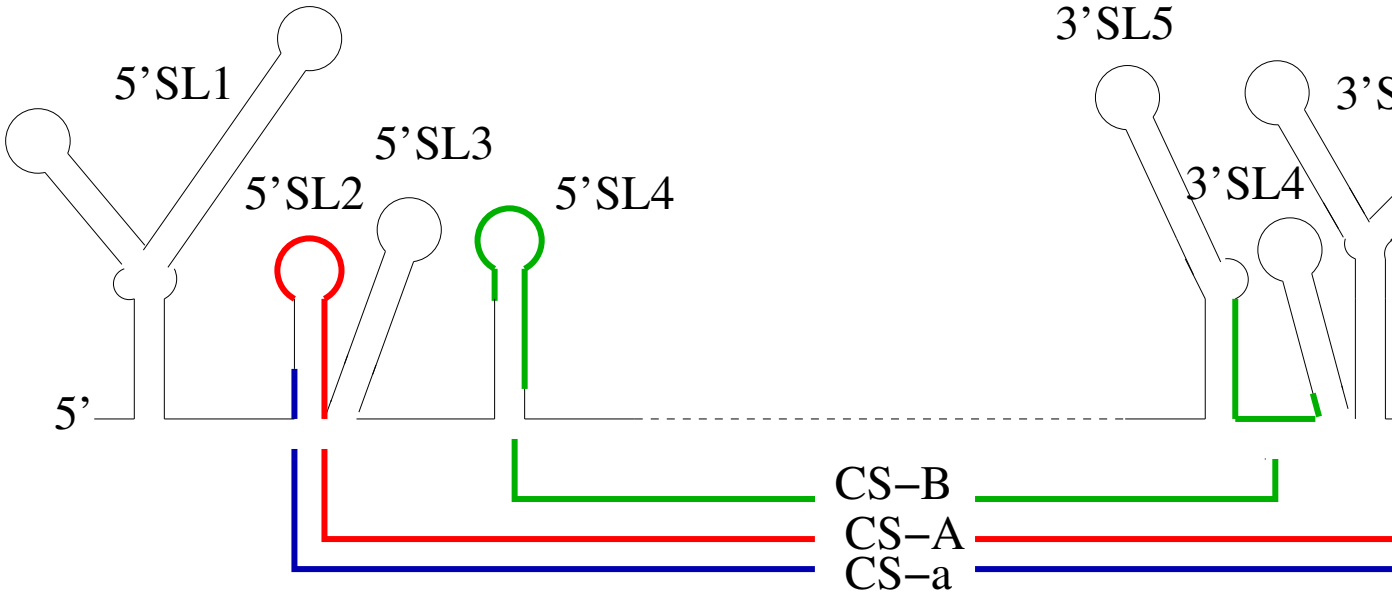
Can we find this too?



Genome plasticity of HCV



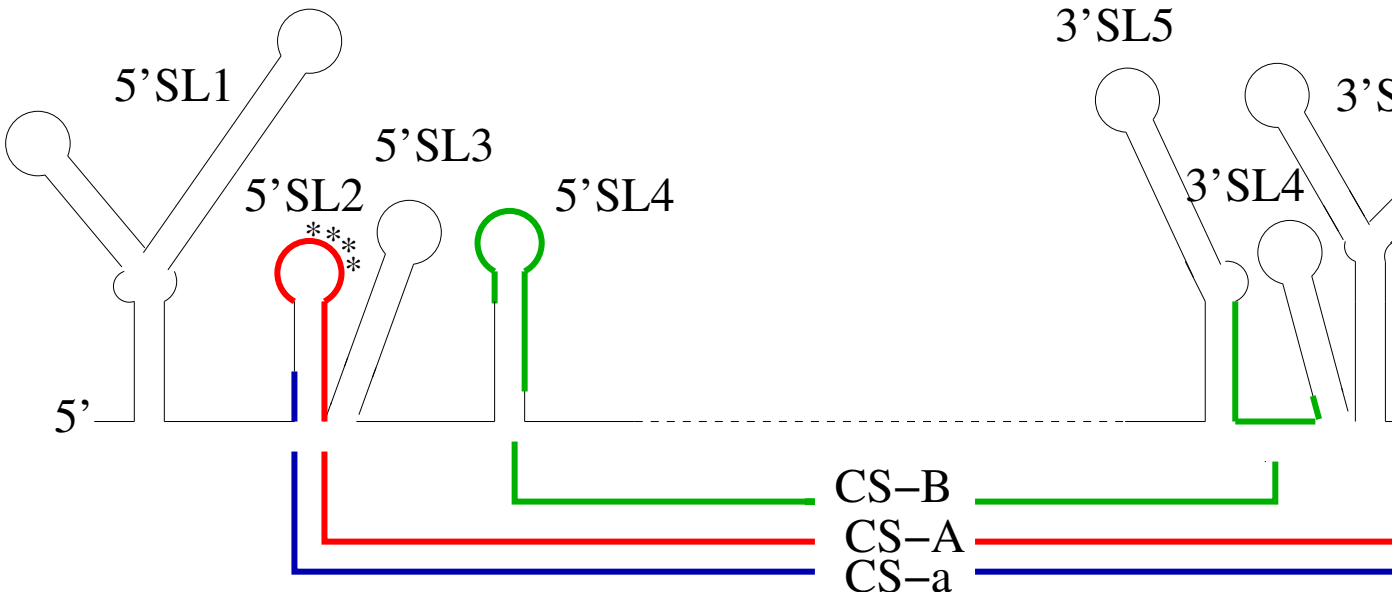
Tickborne Encephalitis virus



CS-B predicted by Khromykh et al., 2001 *J. Virol.* (75)

Point Mutations

5'SL2	3'SL1	AACA	viable
+	-	-	-
-	+	-	-
+	+	-	+
-	-	+	-/+
+	-	+	-
-	+	+	-
+	+	+	-/+



Collaboration with Christian Mandl and Regina Kofler, In
Medical University, Vienna; *J. Virol.* Apr. 2006

Genome plasticity of TBE