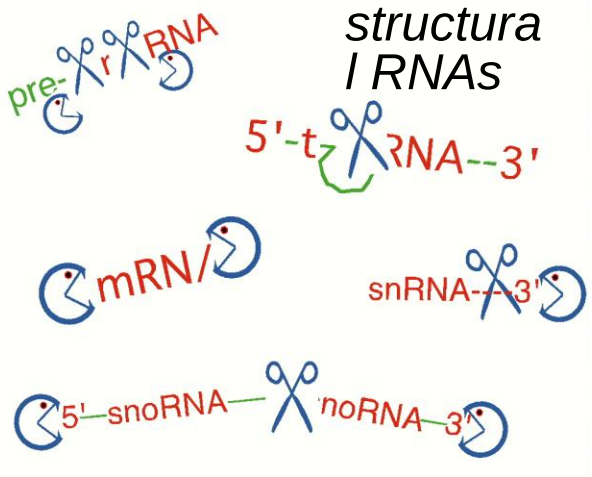
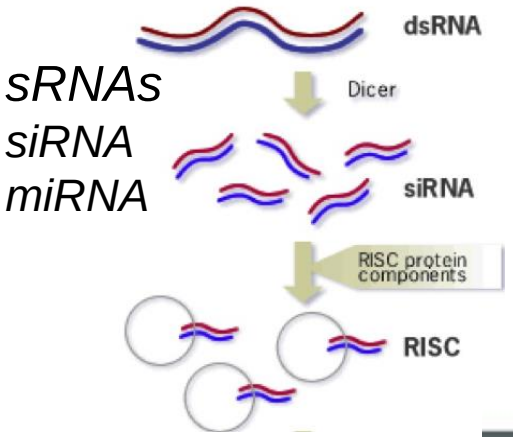
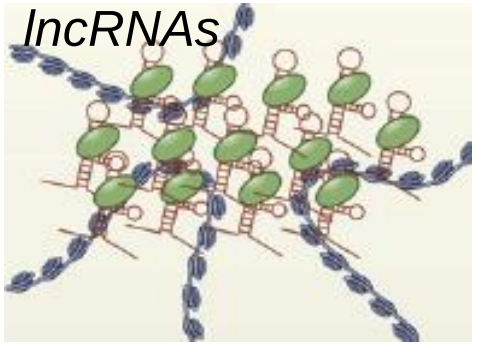
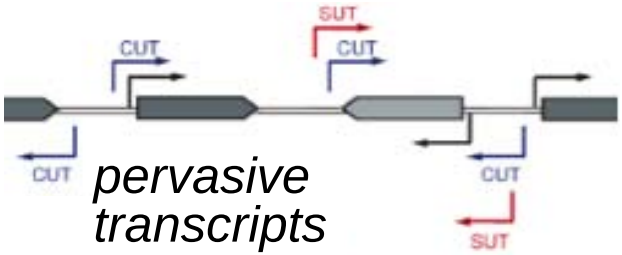
ncRNAs
czyli RNA są różniste, kuliste, w kształcie grzyba i cygara









– Czy może nam pani powiedzieć, na terenie jakiego zakładu się obecnie znajdujemy?

– Tego ni mogę powiedzieć, bo to jest tajemnica państwowa! Mogę tylko powiedzieć, że mam 5 złotych od bombki.

– Czy pani jeszcze może nam powiedzieć, jakie bombki produkujecie?

– Panie, różne, różniste. Tu się robi tak: kuliste, w kształcie grzyba i cygara.

– Cały czas mowa o o bombkach choinkowych.

– Też. A, a wie pan, jaki mamy asortyment? Od A do N...

ncRNA

• Housekeeping

- constitutively expressed
- required for normal function and cell viability

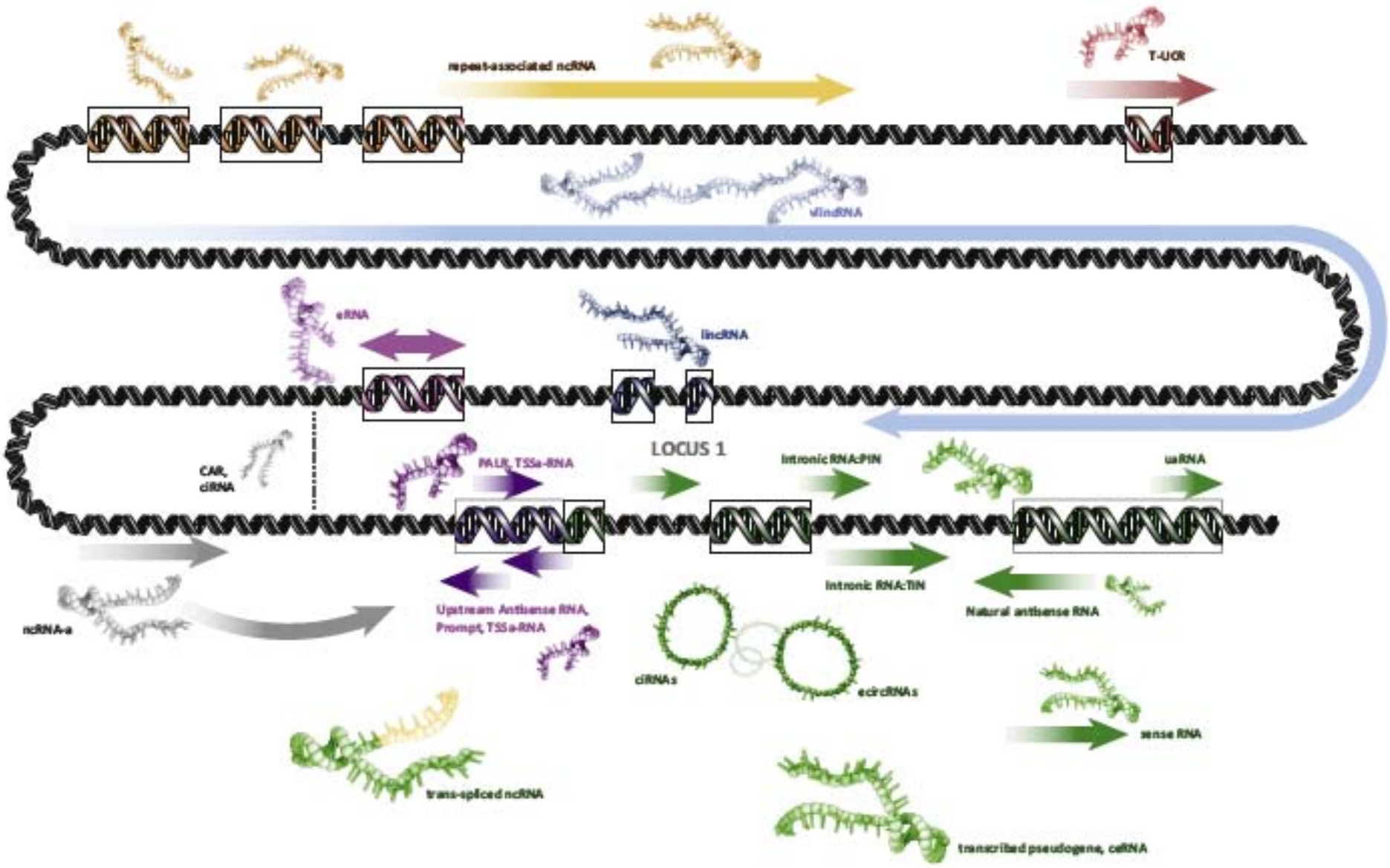
- **tRNA** and **rRNA** – translation
- **snRNA** – splicesosome components, pre-mRNA splicing
- **snoRNA** – rRNA processing and modification, scaRNA (CB specific)
- RNA components of **RNase P** and **RNase MRP** – endonucleases: tRNA and rRNA processing
- Signal Recognition Particle **SRP RNA** – protein secretion to ER
- **tmRNA** tRNA-mRNA hybrid- targeting nascent proteins for degradation
- **gRNA** – guide RNA in RNA editing
- **telomerase RNA** – synthesis of telomers

• Regulatory

- expressed temporarily (development, response to stimuli)
- affect gene expression at the level of transcription or translation

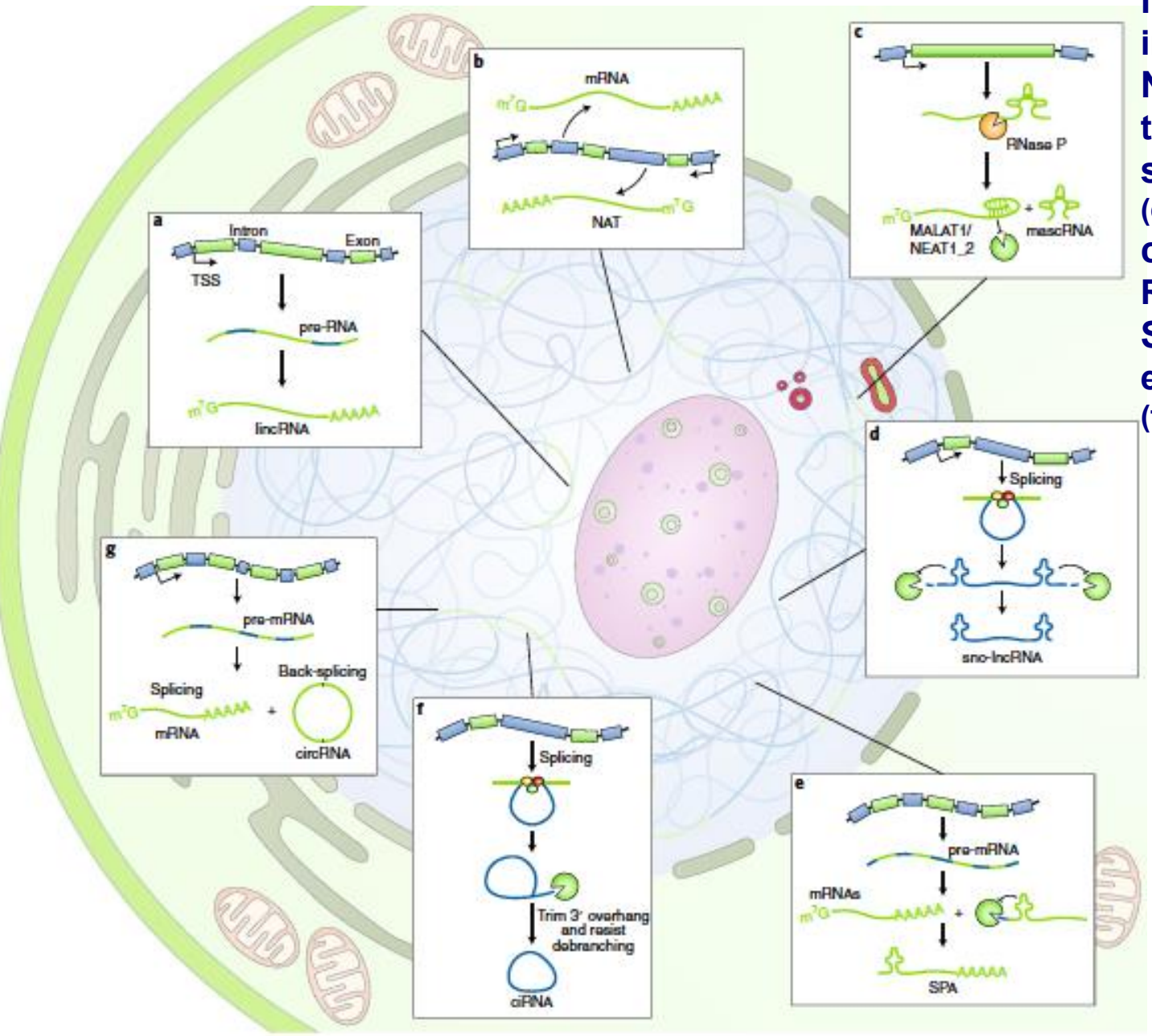
- **sRNAs: siRNA** (exo-siRNAs and endo-siRNAs; ta-siRNA; nat-siRNA; lsiRNAs); **miRNA**; **piRNA** – act in TGS or PTGS
- **lncRNAs** – much less known, usually act in TGS (chromatin level)

LONG ncRNAs



Laurent at al, TiG 2015

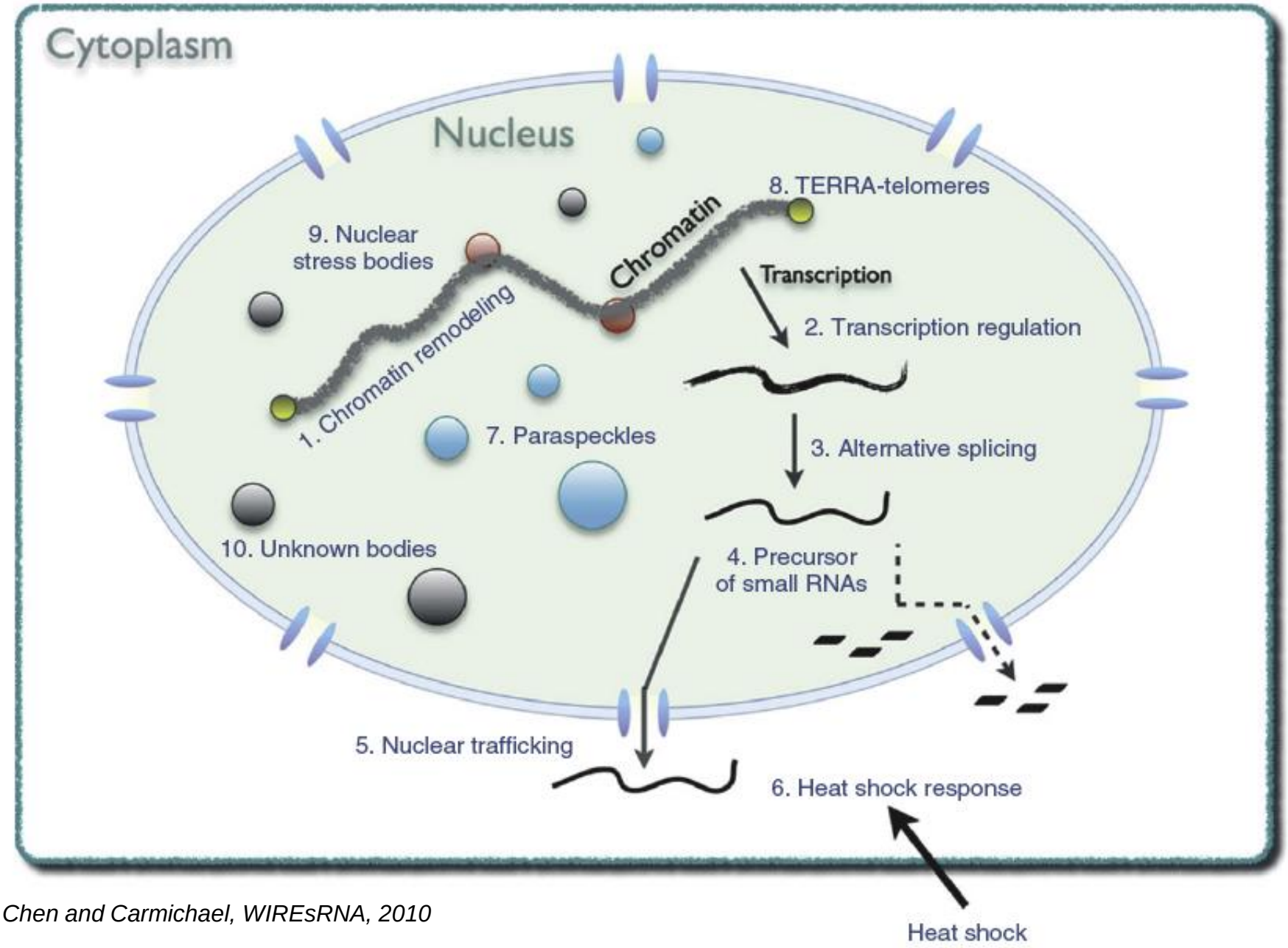
The diversity of lncRNAs



lincRNAs - long inergenic transcipts
NAT - natural antisense transcripts
snoRNA-lncRNA (excised from introns)
circRNAs - circular RNAs
SPA RNAs – snoRNA 5' ended polyA RNAs (from readthrough RNAs)

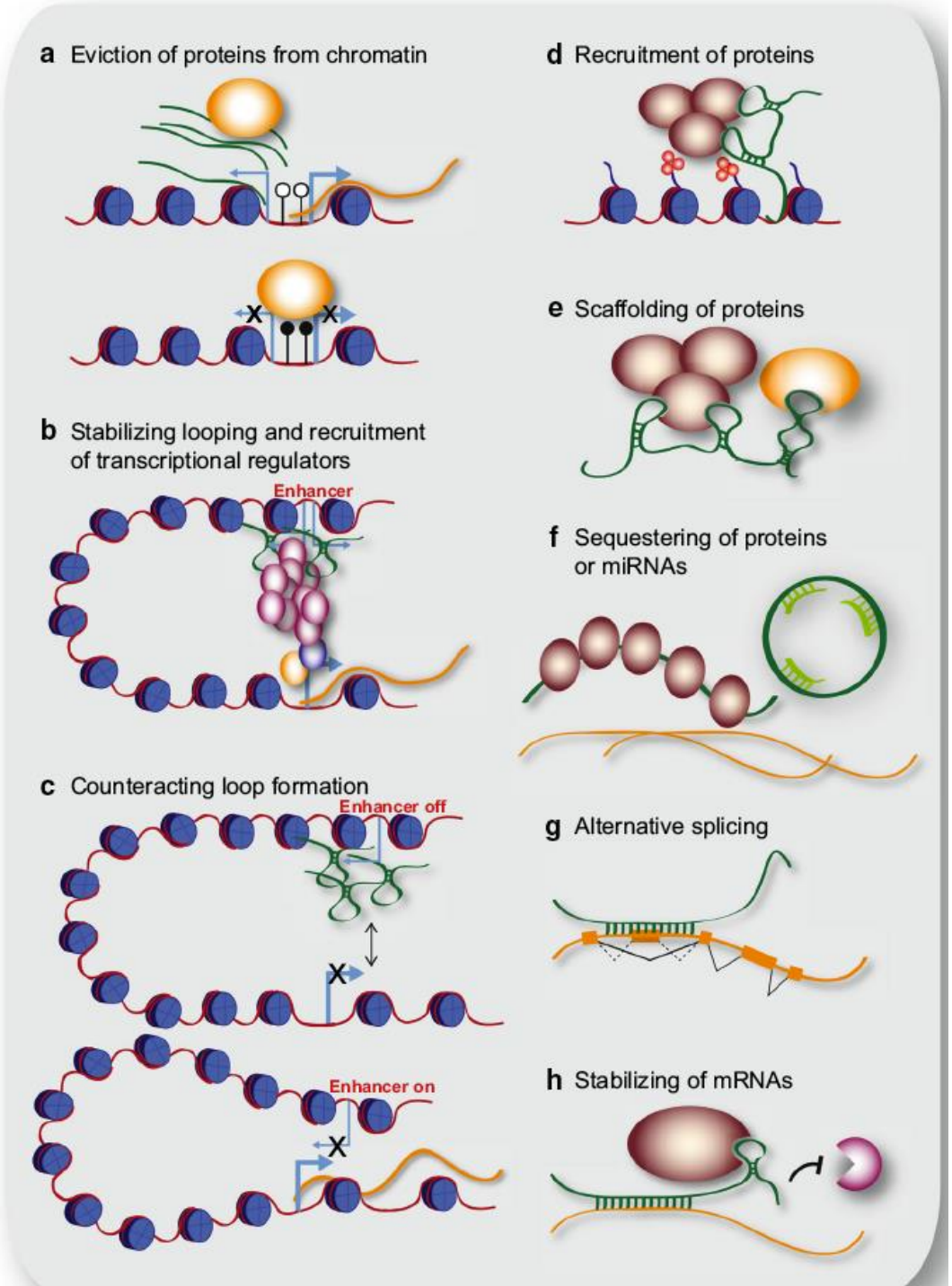
You et al., Nat Cell Biol, 2010

FUNCTIONS of LONG ncRNAs

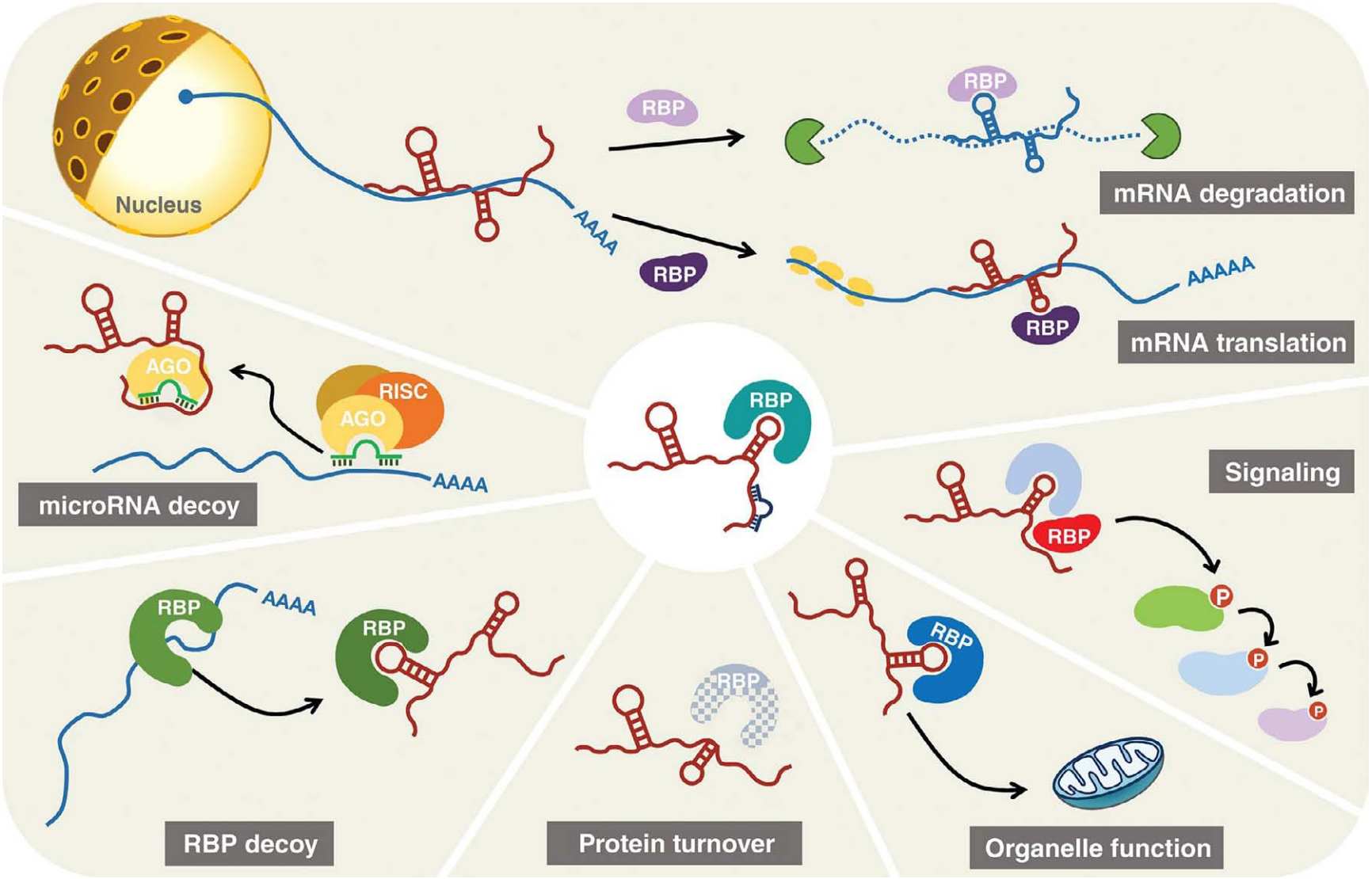


Chen and Carmichael, WIREsRNA, 2010

FUNCTIONS of LONG ncRNAs

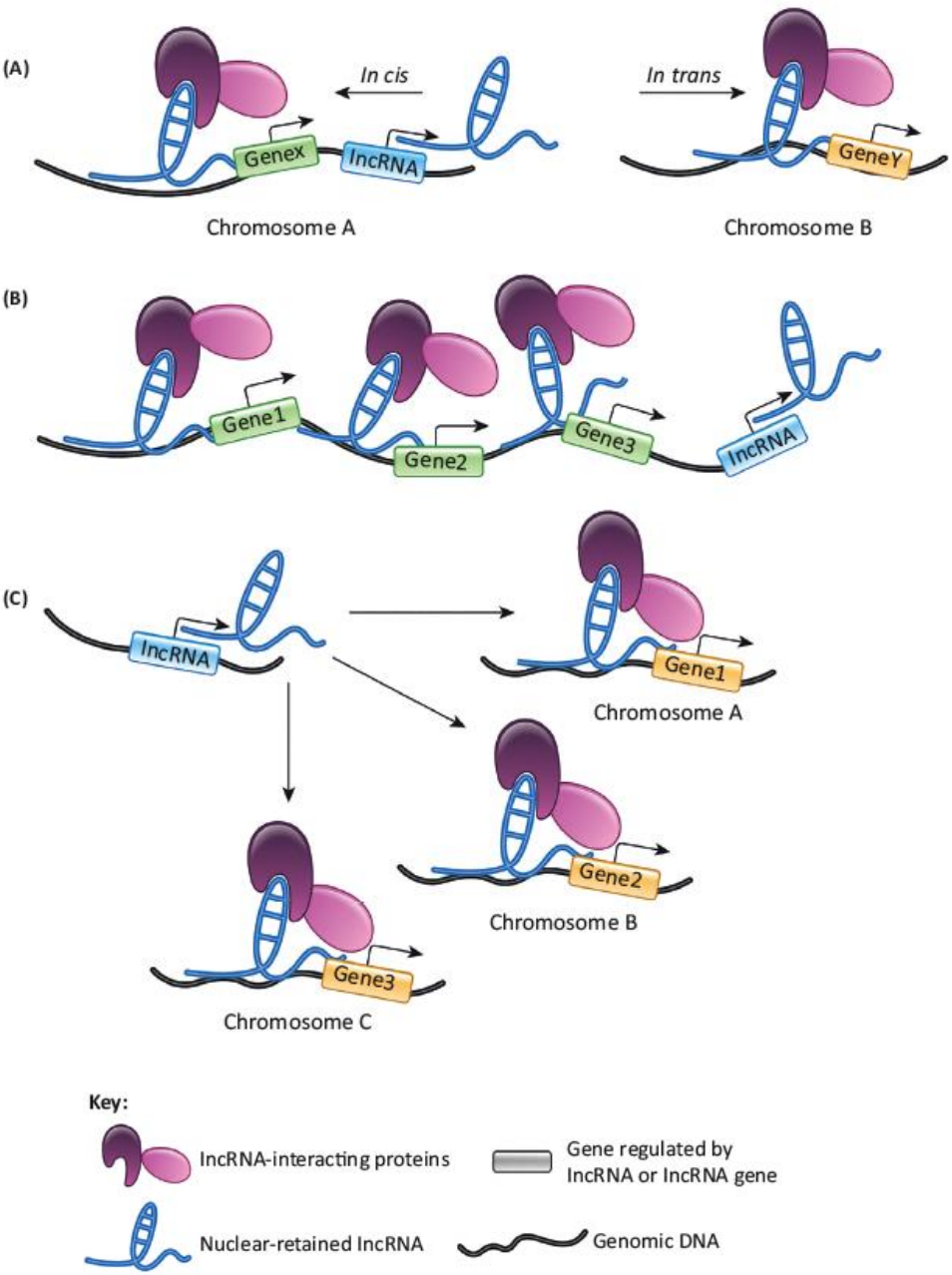


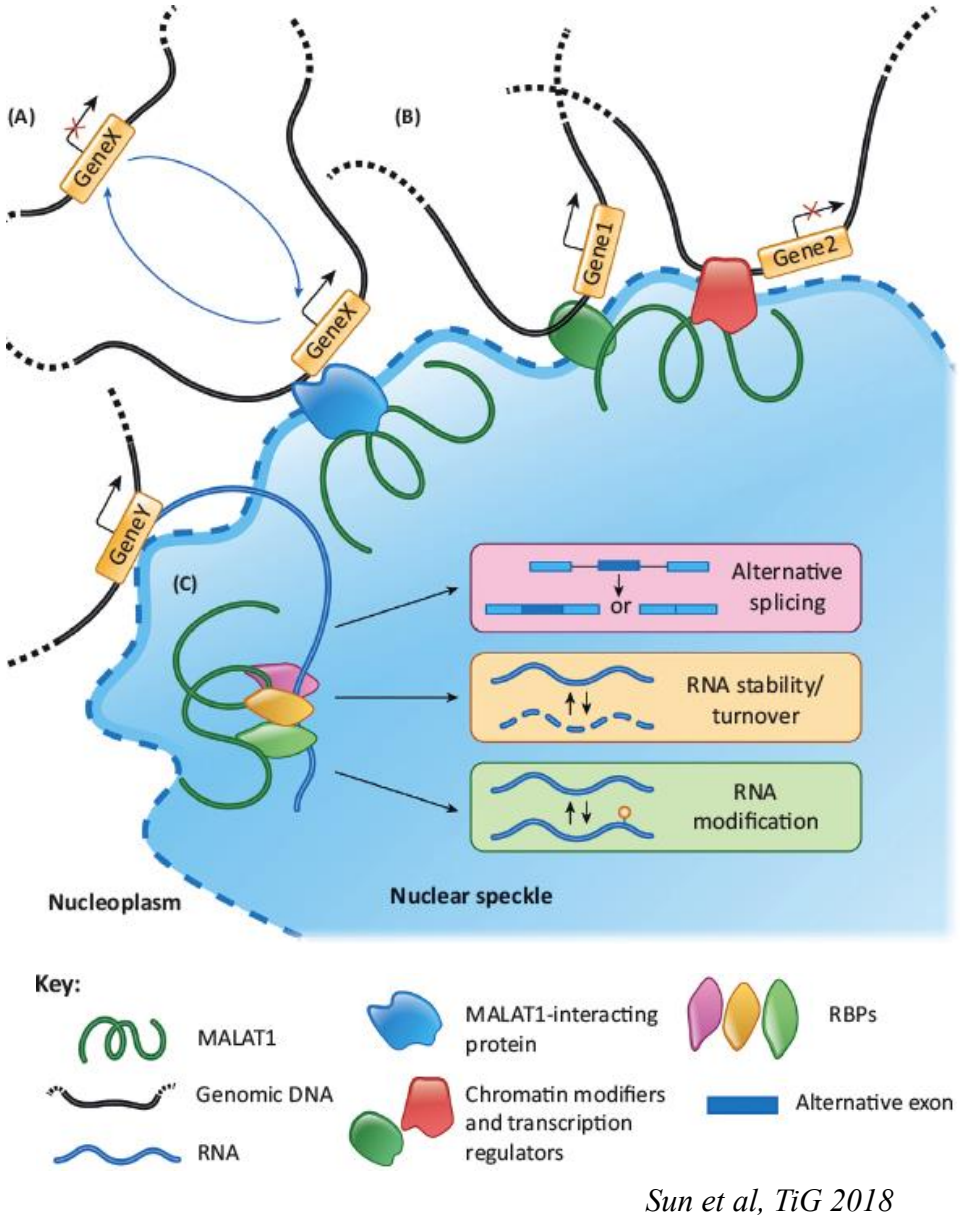
CYTPLASMIC FUNCTIONS of LONG ncRNAs



Noh et al, WIREsRNA, 2018

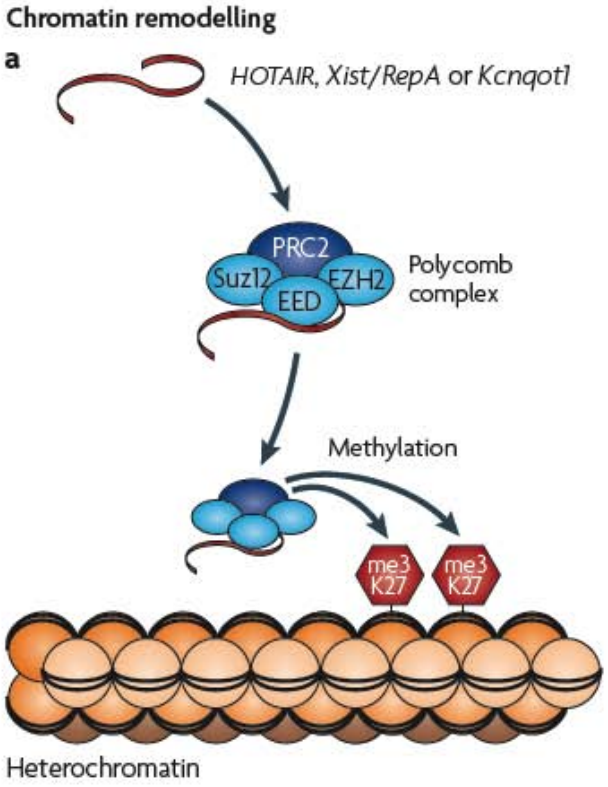
lncRNAs and regulation of gene expression

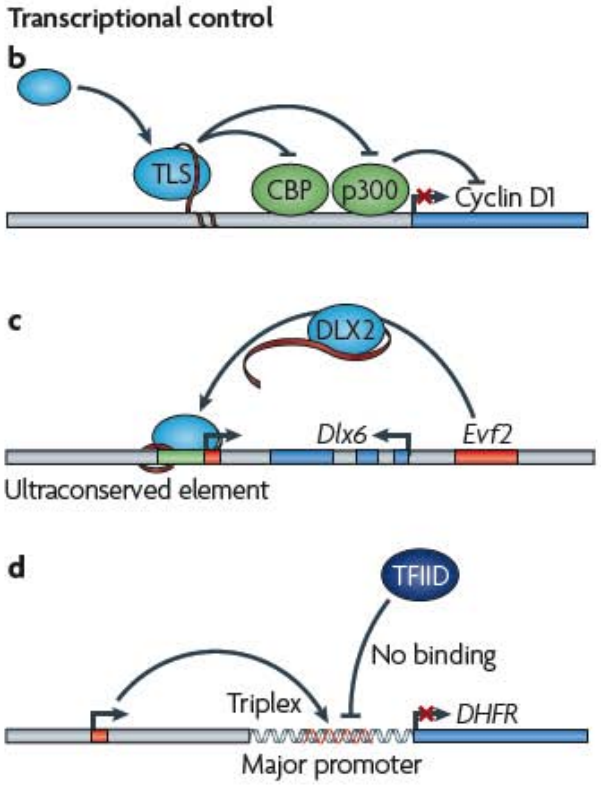


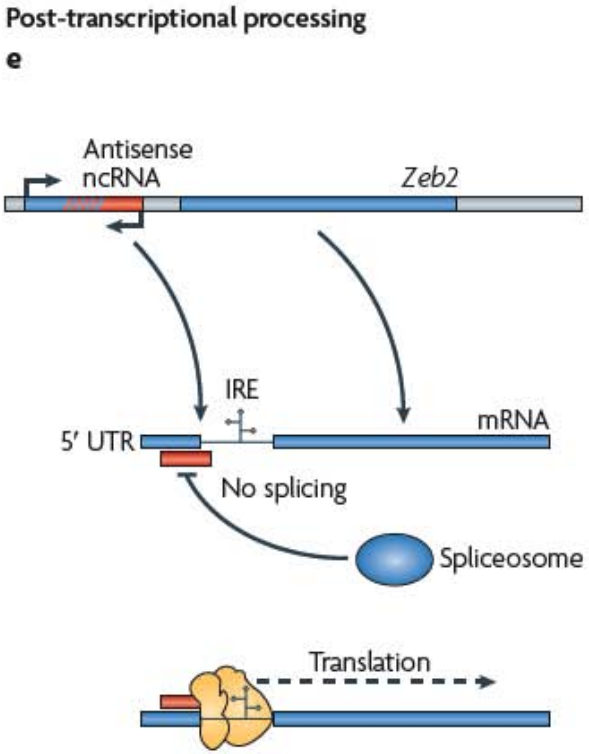


Sun et al, TiG 2018

MECHANISM of ACTION of LONG ncRNAs







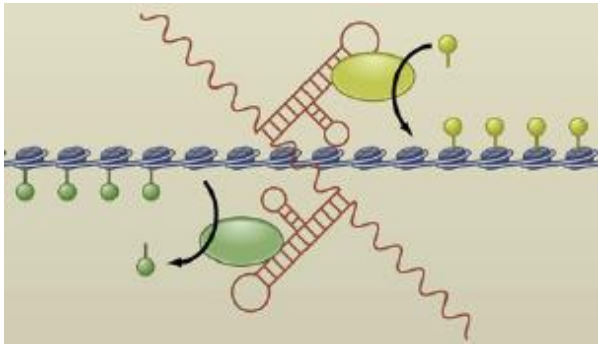
ncRNAs recruit chromatin modifying complex to genes, resulting in histone modifications (H3meK27) and heterochromatin formation

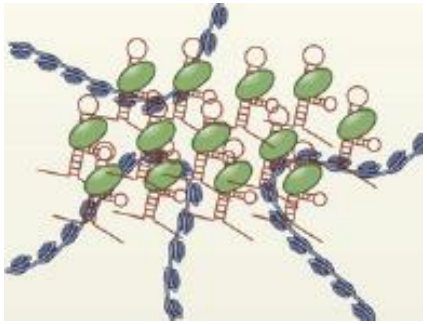
- ncRNAs act as repressors or enhancers of transcription via binding to protein factors or DNA;
- may act as decoys to titrate trx factors away from genes

ncRNAs mask 5' splice site resulting in intron retention, recognition of IRE and translation

Mercer et al., Nat. Rev. Genet., 2007

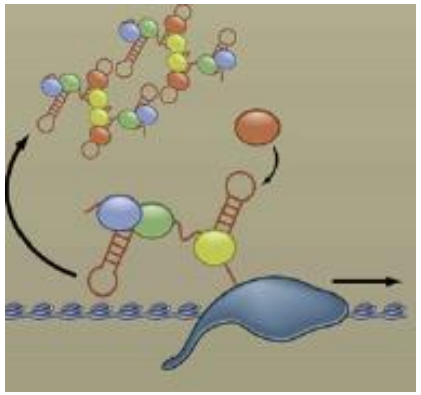
MECHANISM of ACTION of LONG ncRNAs



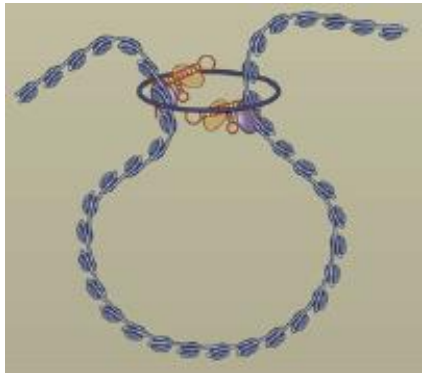


Cotranscriptional recruitment of chromatin-modifying factors.

Nucleation of chromatin.



Dynamic assembly of nuclear structures: paraspecles, nuclear bodies

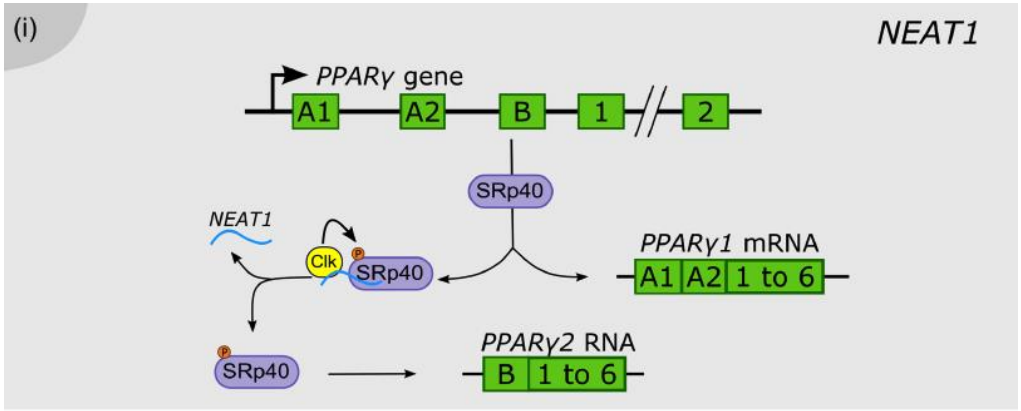


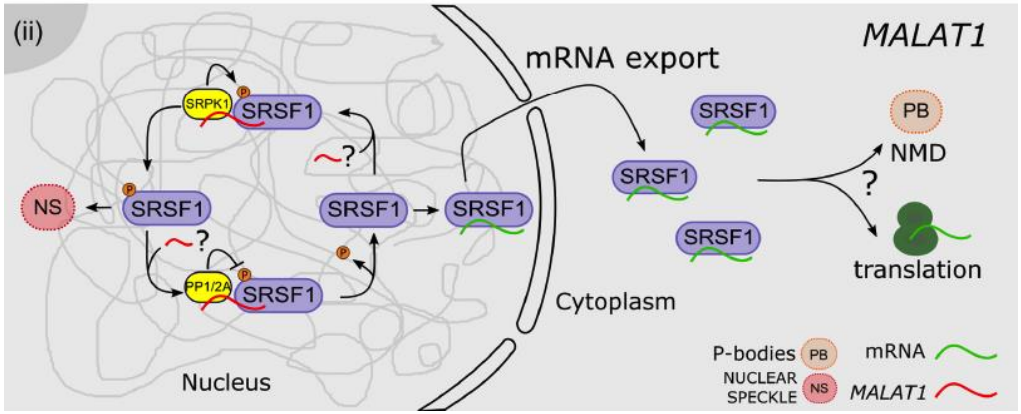
Formation of higher-order chromatin loops

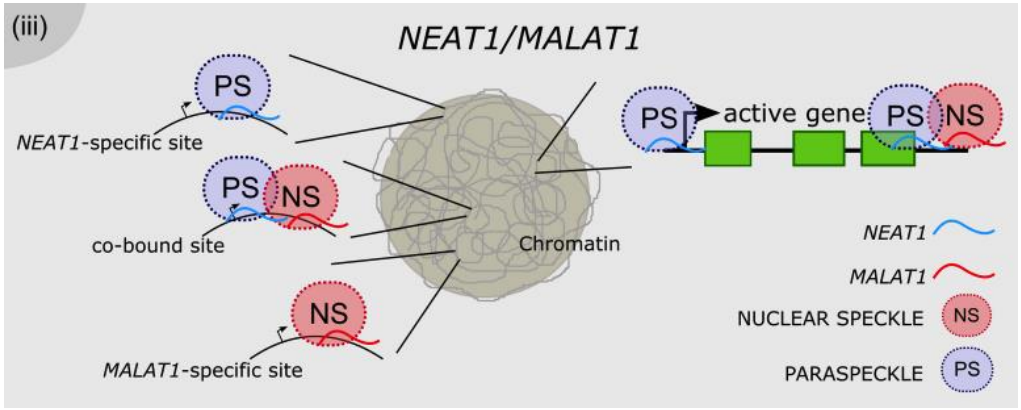
- **GUIDES** (chromatin modifyiers)
- **TRX FACTORS**
- **SCAFFOLDS** (RNP structures)

Nagano and Fraser, Cell, 2011

NEAT and MALAT1



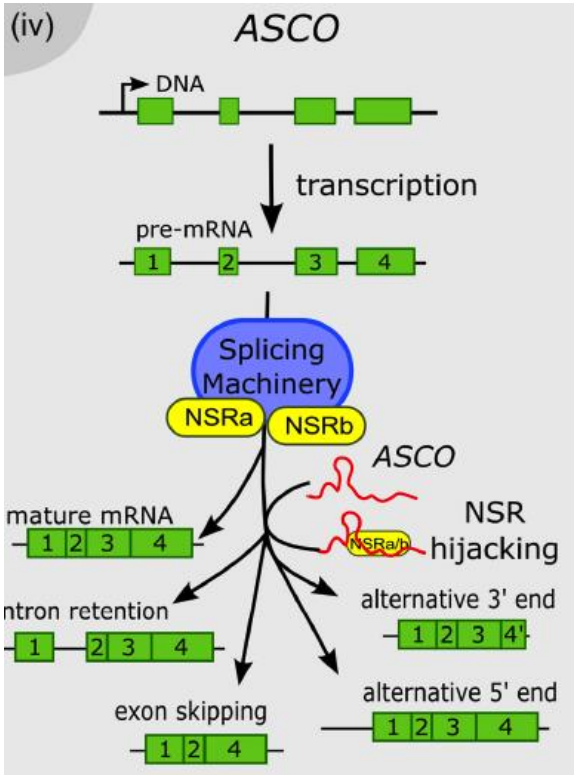


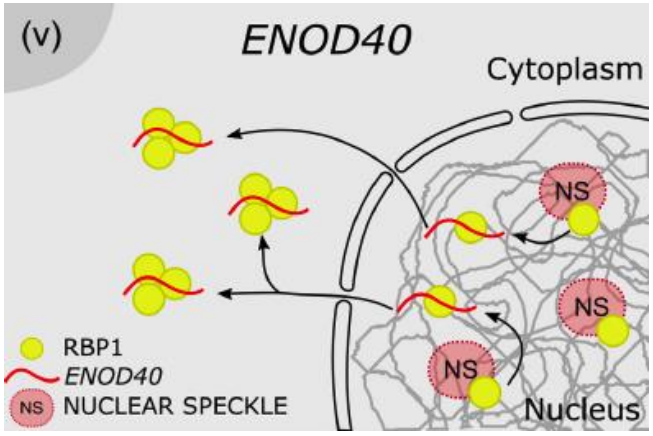


Regulate the phosphorylation status of splicing factors

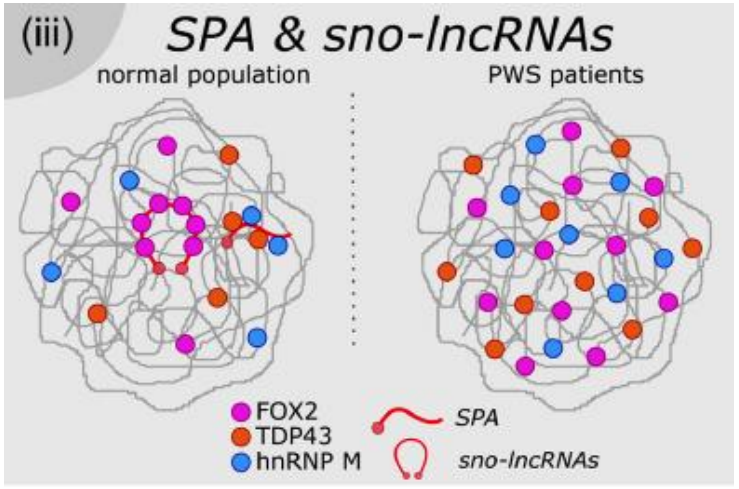
Bind to common and distinct actively transcribed loci across the genome

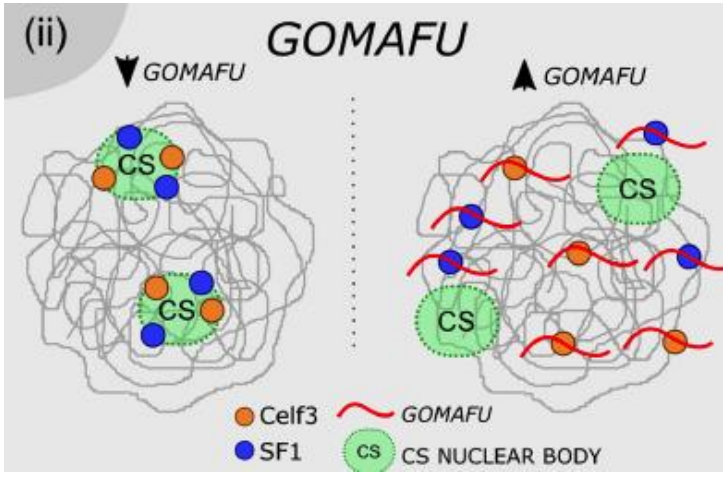
LncRNA and splicing regulation





lncRNAs act as splicing factor hijackers





INVISIBLE RNAs

Cell, Vol. 121, 725–737, June 3, 2005, Copyright ©2005 by Elsevier Inc. DOI 10.1016/j.cell.2005.04.030

Cryptic Pol II Transcripts Are Degraded by a Nuclear Quality Control Pathway Involving a New Poly(A) Polymerase

Françoise Wyers,[4,5,7] Mathieu Rougemaille,[5,7] Gwenaël Badis,[1] Jean-Claude Rousselle,[2] Marie-Elisabeth Dufour,[4] Jocelyne Boulay,[5] Béatrice Régnault,[3] Frédéric Devaux,[6] Abdelkader Namane,[2] Bertrand Séraphin,[2,5,*] Domenico Libri,[5,*] and Alain Jacquier[1,*]

3262–3267 | PNAS | February 28, 2006 | vol. 103 | no. 9

Accumulation of unstable promoter-associated transcripts upon loss of the nuclear exosome subunit Rrp6p in *Saccharomyces cerevisiae*

Carrie Anne Davis and Manuel Ares, Jr.*

Vol 457|19 February 2009|doi:10.1038/nature07728

Bidirectional promoters generate pervasive transcription in yeast

Zhenyu Xu[1]*, Wu Wei[1]*, Julien Gagneur[1], Fabiana Perocchi[1], Sandra Clauder-Münster[1], Jurgi Camblong[2], Elisa Guffanti[3], Françoise Stutz[3], Wolfgang Huber[4] & Lars M. Steinmetz[1]

Vol 457|19 February 2009|doi:10.1038/nature07747

Widespread bidirectional promoters are the major source of cryptic transcripts in yeast

Helen Neil[1], Christophe Malabat[1], Yves d'Aubenton-Carafa[2], Zhenyu Xu[3], Lars M. Steinmetz[3] & Alain Jacquier[1]

INVISIBLE RNAs

SCIENCE VOL 322 19 DECEMBER 2008

RNA Exosome Depletion Reveals Transcription Upstream of Active Human Promoters

Pascal Preker,[1] Jesper Nielsen,[2] Susanne Kammler,[1]* Søren Lykke-Andersen,[1] Marianne S. Christensen,[1] Christophe K. Mapendano,[1] Mikkel H. Schierup,[2] Torben Heick Jensen[1]†

SCIENCE VOL 322 19 DECEMBER 2008

Divergent Transcription from Active Promoters

Amy C. Seila,[1]* J. Mauro Calabrese,[1,2]*† Stuart S. Levine,[3] Gene W. Yeo,[4]‡ Peter B. Rahl,[3] Ryan A. Flynn,[1] Richard A. Young,[2,3] Phillip A. Sharp[1,2]§

Vol 457|19 February 2009|doi:10.1038/nature07759

Post-transcriptional processing generates a diversity of 5′-modified long and short RNAs

Affymetrix/Cold Spring Harbor Laboratory ENCODE Transcriptome Project*

Cold Spring Harbor Laboratory Katalin Fejes-Toth[1,2]*, Vihra Sotirova[1,2], Ravi Sachidanandam[1]†, Gordon Assaf[1,2], Gregory J. Hannon[1,2]; **Affymetrix** Philipp Kapranov[3]*, Sylvain Foissac[3], Aarron T. Willingham[3], Radha Duttagupta[3], Erica Dumais[3] & Thomas R. Gingeras[1,3]

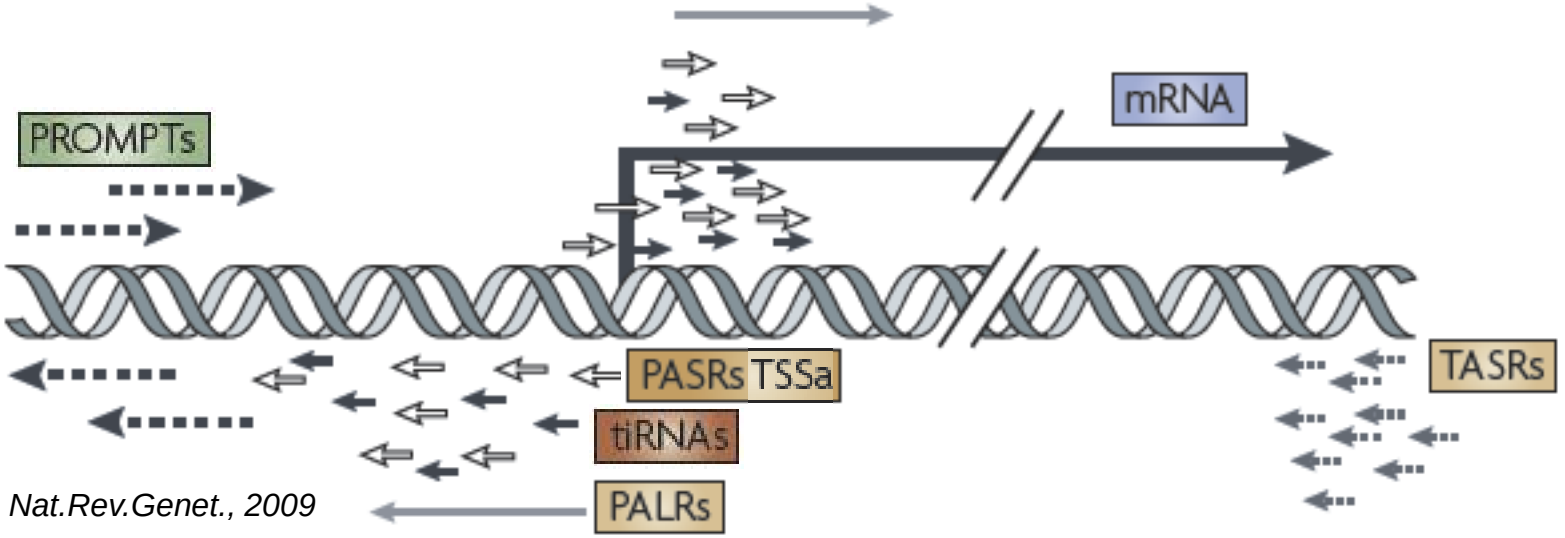
Cell *131*, 1340–1353, December 28, 2007

Genome-Wide High-Resolution Mapping of Exosome Substrates Reveals Hidden Features in the *Arabidopsis* Transcriptome

Julia A. Chekanova,[1,2,8,13] Brian D. Gregory,[3,4,8] Sergei V. Reverdatto,[2] Huaming Chen,[4] Ravi Kumar,[1] Tanya Hooker,[1] Junshi Yazaki,[3,4] Pinghua Li,[2,10] Nikolai Skiba,[5,9] Qian Peng,[3,6] Jose Alonso,[3,11] Vladimir Brukhin,[7,12] Ueli Grossniklaus,[7] Joseph R. Ecker,[3,4,*] and Dmitry A. Belostotsky[1,2,13,*]

PERVASIVE TRANSCRIPTION OF THE GENOME

All possible types of RNAs, detected by tiling microarrays and "deep sequencing", SAGE and GRO, accompany major coding transcripts



Jacquier, Nat.Rev.Genet., 2009

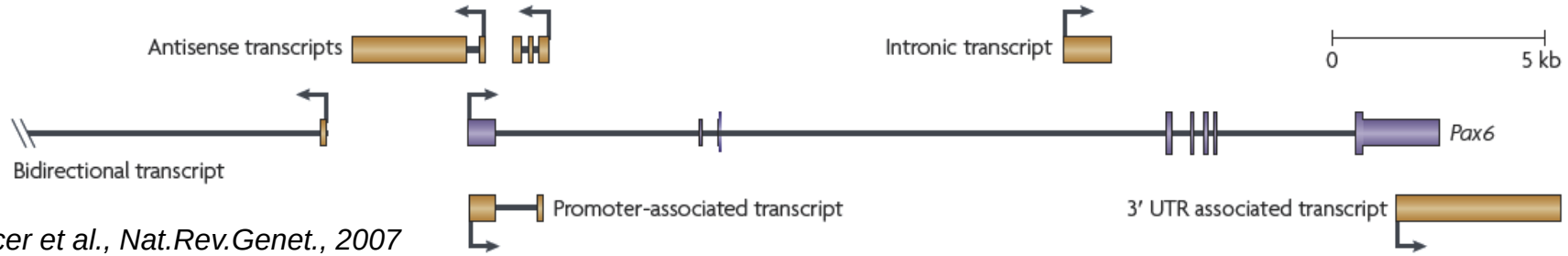
(1) protein-coding mRNA; (2) PROMPT - promoter upstream transcripts (short); (3) PASR- promoter-associated sRNAs (< 200 nts); (4) TSSa transcription start site-associated RNAs (20-90 nts); (5) TASR –terminator associated sRNAs (< 200 nts); (6) PARL - promoter-associated long RNAs (> 200 nts); (7) tiRNAs - tiny transcription-initiation RNAs (18 nts)

SAGE, CAGE, GRO tags

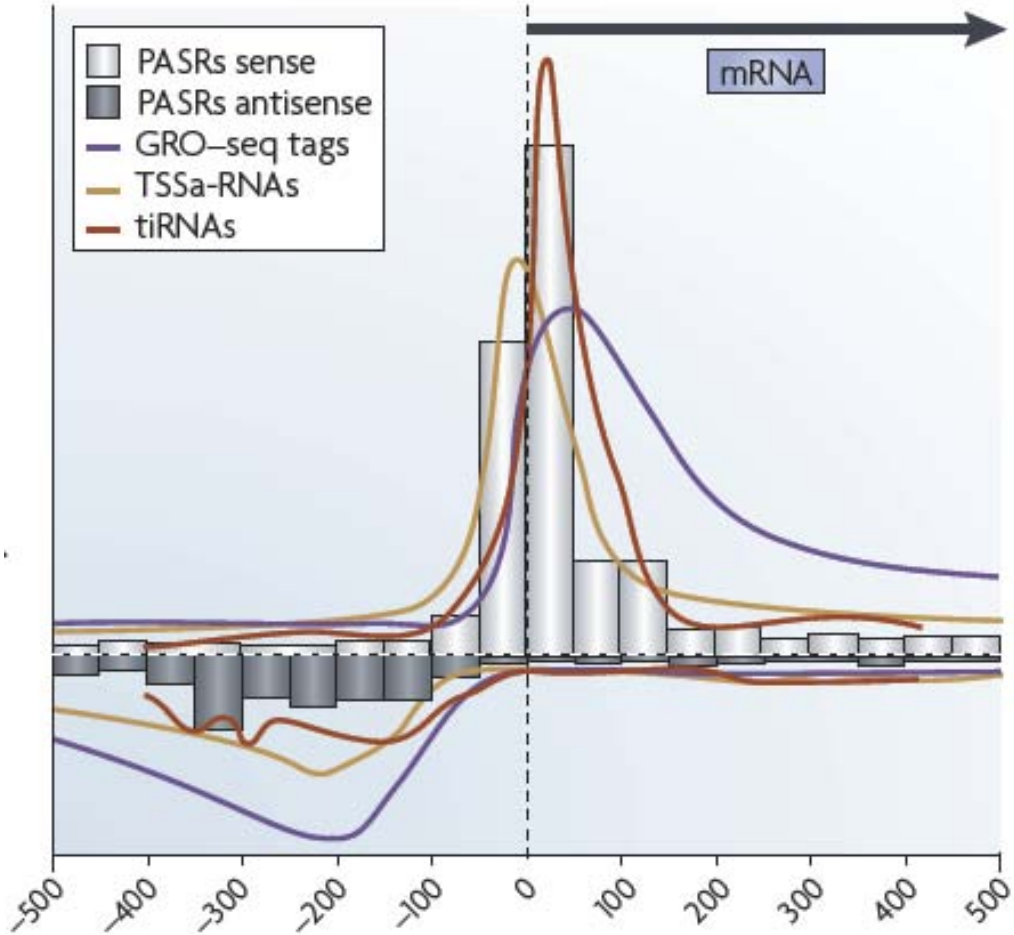
antisense RNAs (can be long)

CUTs, SUTs - cryptic unstable or stable unannotated transcripts (200-600 nts)

PRESENCE of ncRNAs



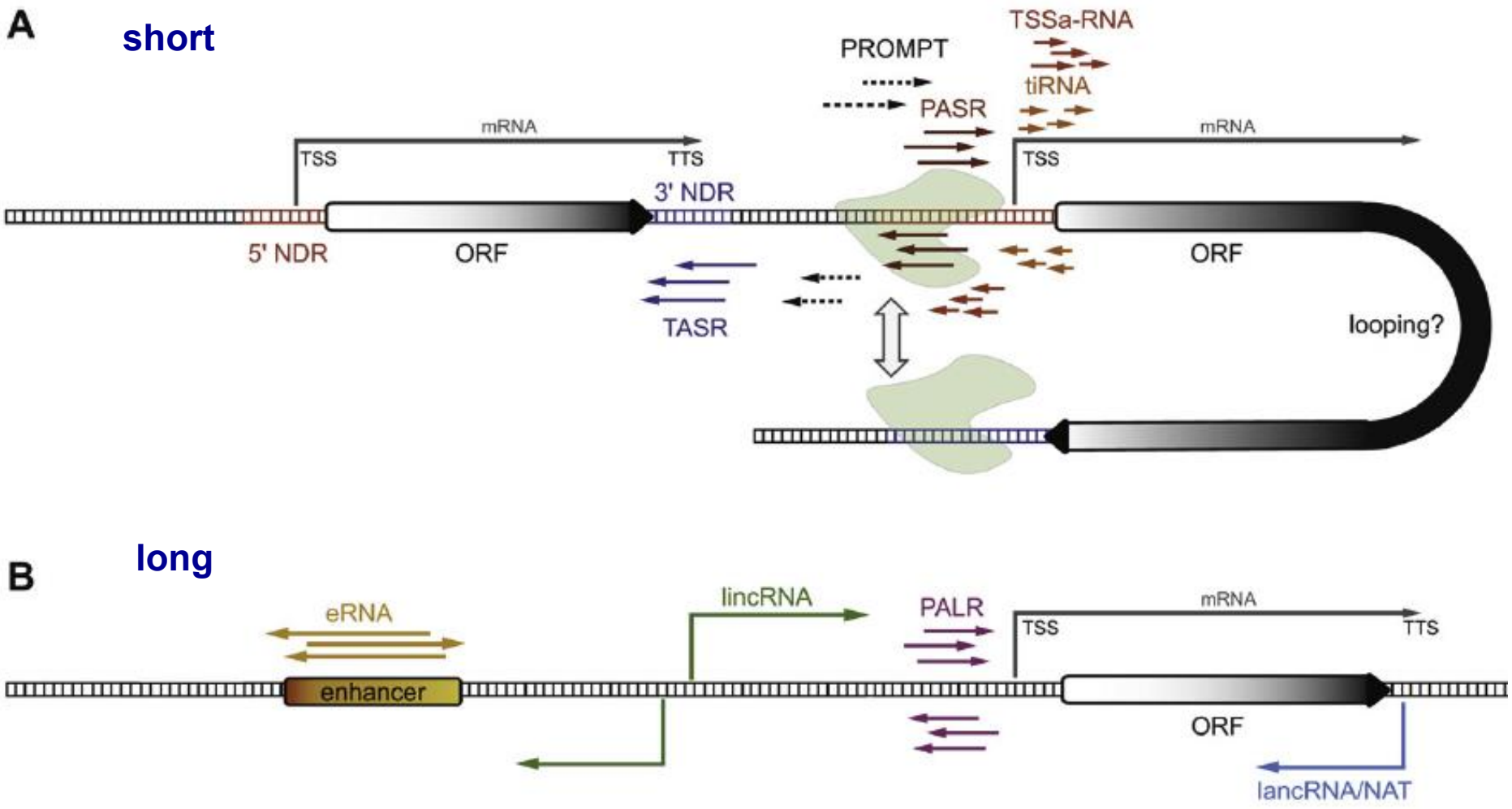
Mercer et al., Nat.Rev.Genet., 2007



DENSITY of small RNAs

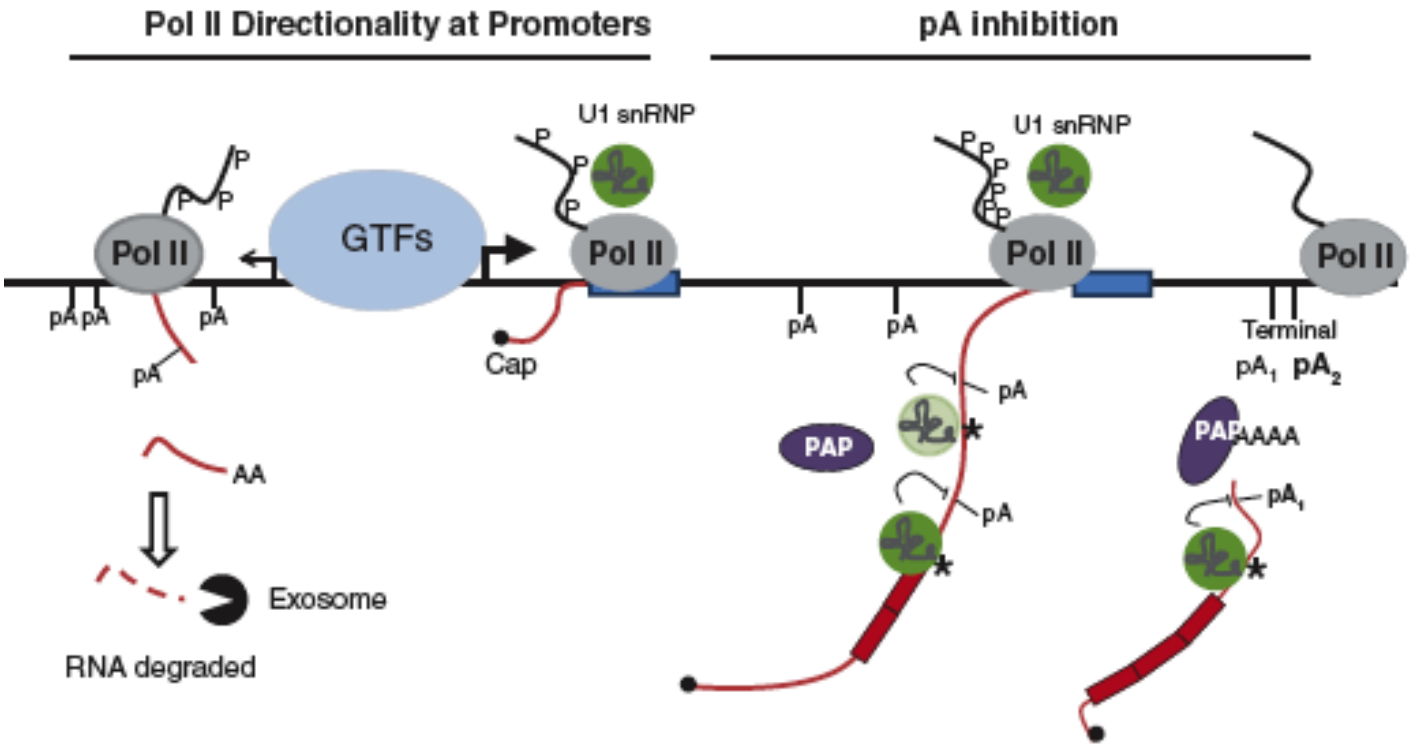
Jacquier, Nat.Rev.Genet., 2009

GENOMIC ORGANIZATION of ncRNA

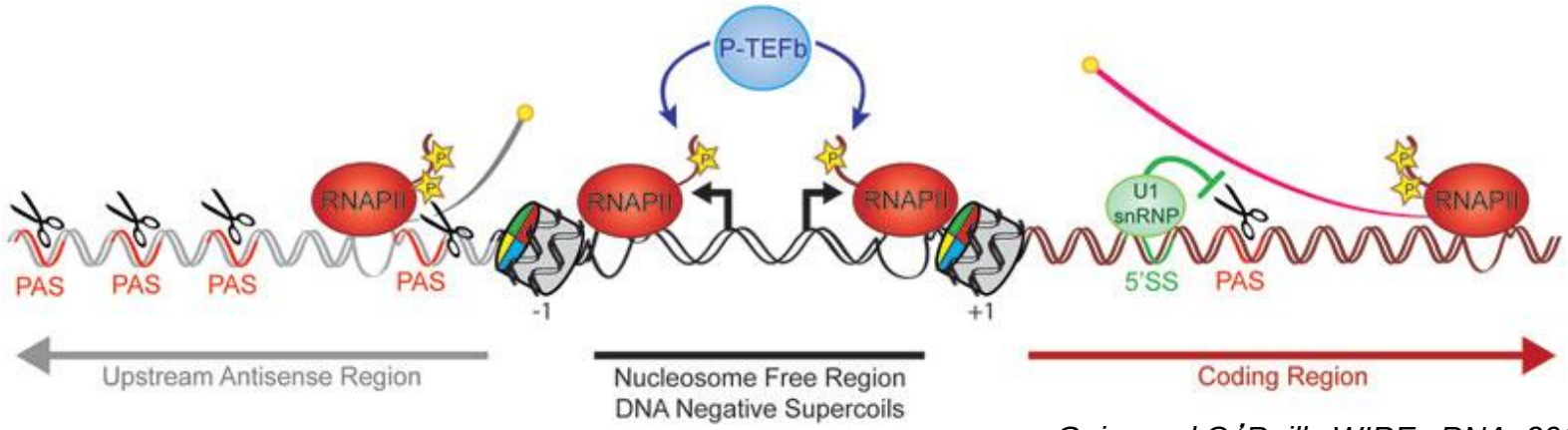


Tisseur et al., Biochemie, 2011

U1 and non-coding transcription



U1 participates in pA site selection and Pol II directionality at promoters



Guiro and O'Reilly WIREs RNA, 2015

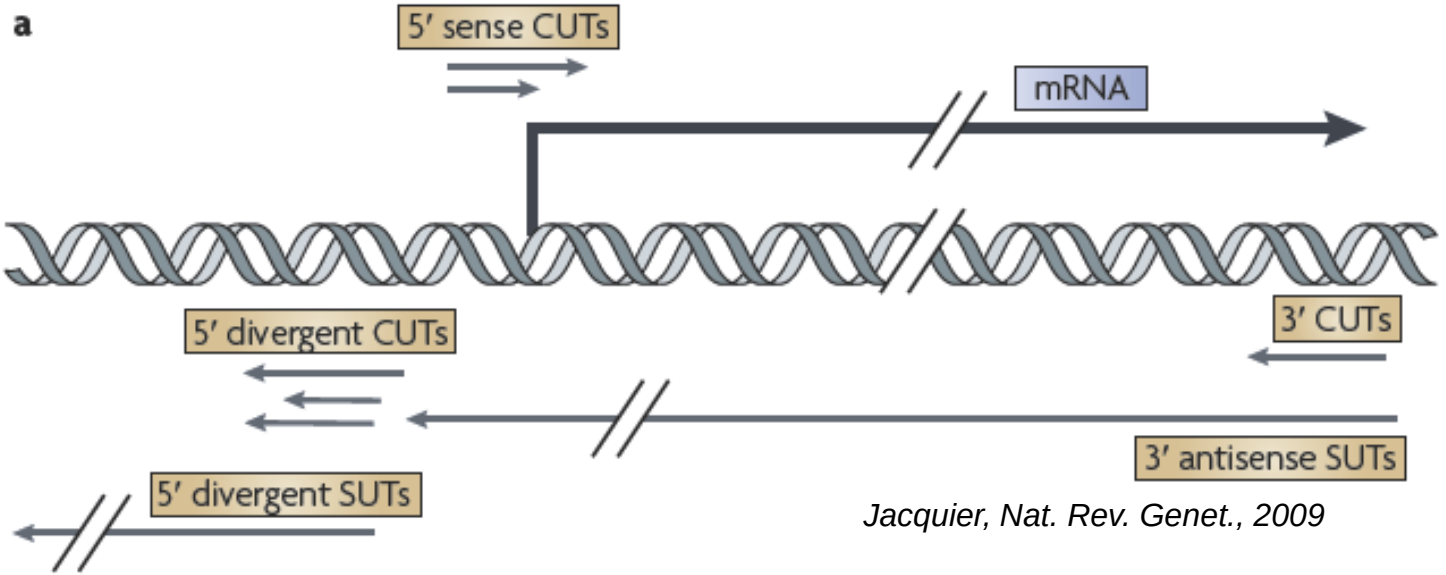
CUTs, SUTs, XUTs, MUTs and ALL THAT JAZZ

CUT = Cryptic Unstable Transcripts
SUT = Stable Unannotated Transcripts
SAT = Ssu72-associated Transcripts
XUT = Xrn1-dependent UnstableTranscripts
MUT = Meiotic Unstable Transcripts

NO LONGER TRANSCRIPTIONAL NOISE

(yeast, mammals, worms, plants - all organisms?)

- **not visible in normal wild-type cells**
- **accumulate in RNA degradation mutants (EXOSOME, XRN family, TRAMP) or various metabolic conditions (aging, nutrient change, cell cycle etc)**
- **originate from widespread bidirectional promoters**
- **„mRNA-like" Pol II transcripts (capped, polyadenylated)**



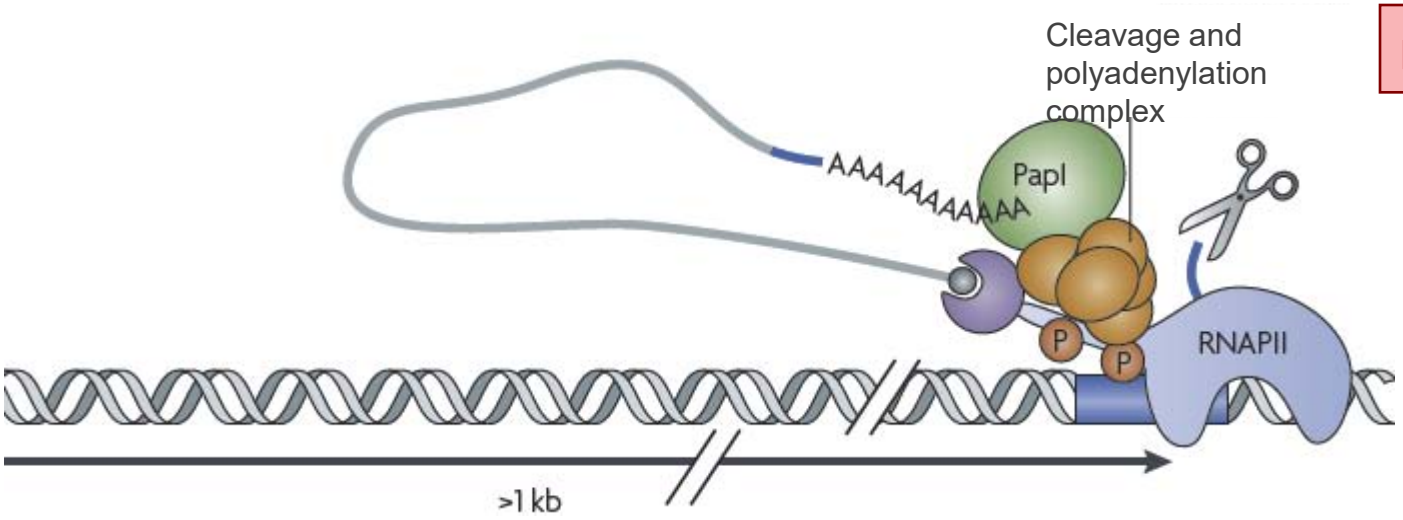
Jacquier, Nat. Rev. Genet., 2009

ncRNA instability and their termination mode

3’ end CLEAVAGE and POLYADENYLATION (CP)

mRNAs, SUTs

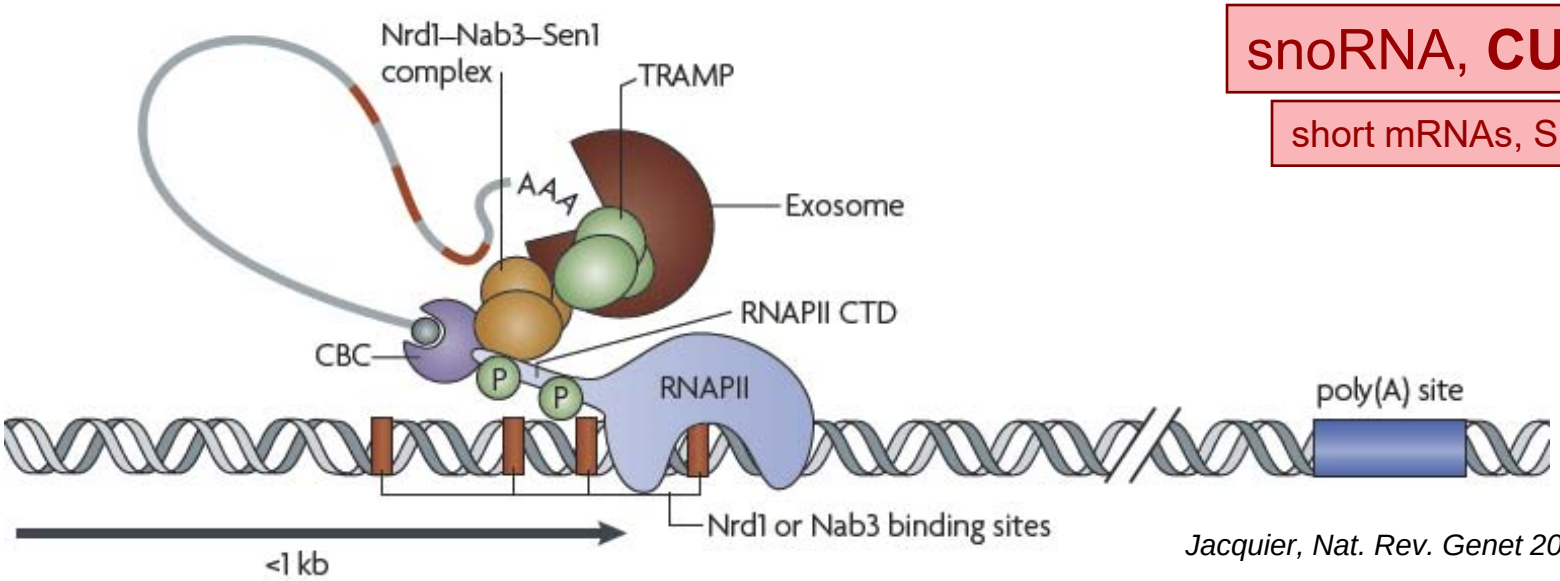
snoRNAs, CUTs



Nrd1/Nab3/Sen1-dependent termination

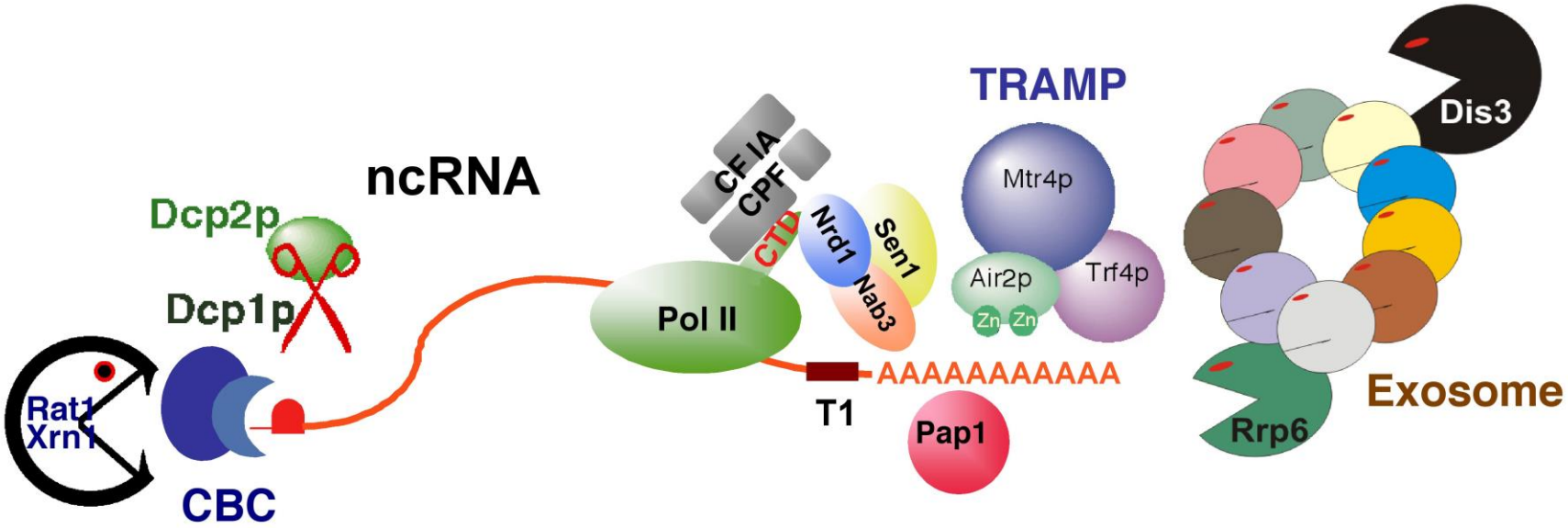
snoRNA, **CUTs**

short mRNAs, SUTs



Jacquier, Nat. Rev. Genet 2009

ncRNA instability and their termination mode



Unstable CUTs (*versus more stable SUTs*)
- are detected in TRAMP or exosome mutants
- are terminated by Nrd1/Nab3-dependent mechanism and polyadenylated by Trf4/TRAMP
- Nrd1/Nab3, TRAMP and exosome complexes interact

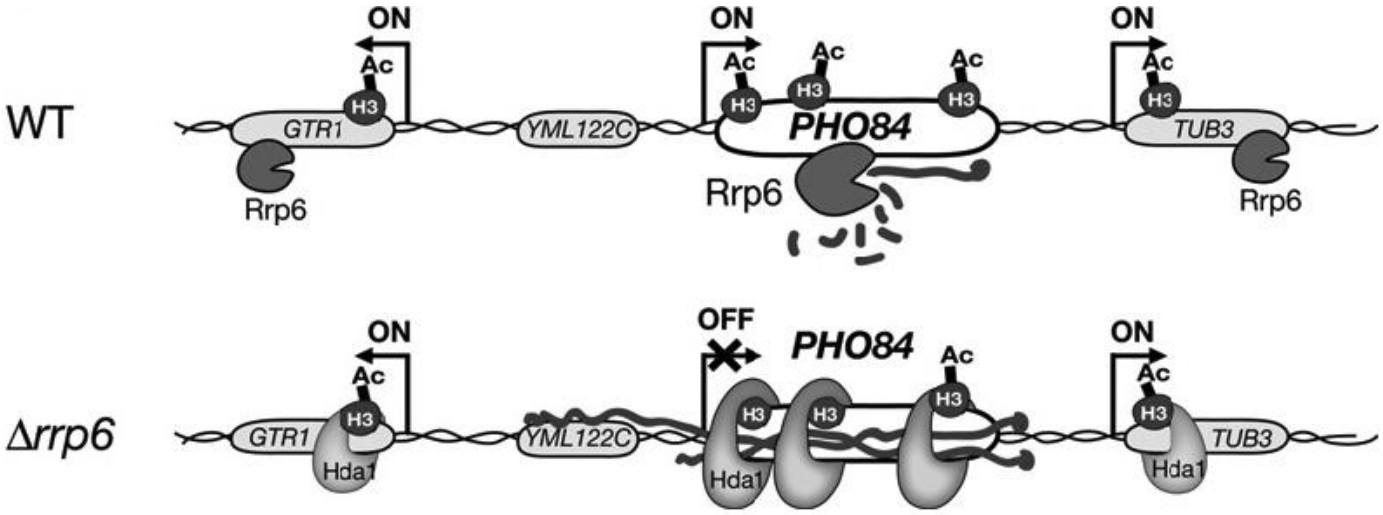
- some CUTs (SRG1, IGS1-R) are polyadenylated by Pap1
- some CUTs are exported to the cytoplasm (XUTs) and degraded by Xrn1
- ncRNP composition is largely unknown

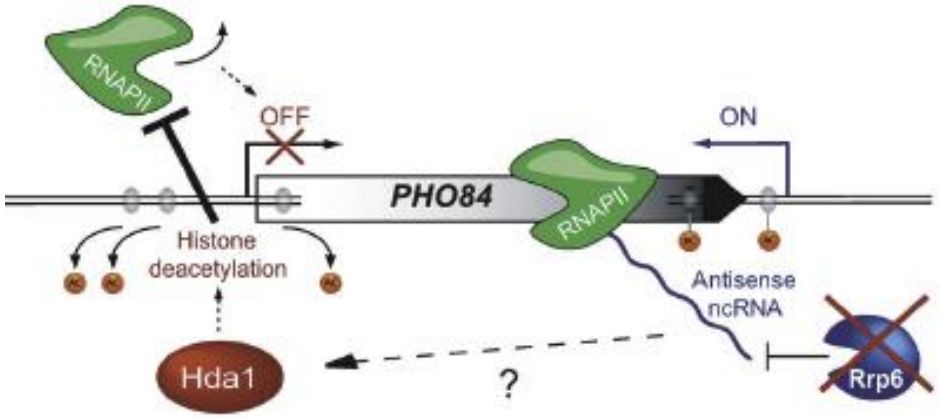
Wyers et al., Cell, 2005; Arigo et al., Mol.Cell, 2006a; Thiebaut et al., Mol.Cell, 2006, 2008; Houseley et al., EMBO J, 2007; Camblong et al., Cell, 2007; Thompson and Parker, Mol.Cell. Biol., 2007; Houseley et al., Mol. Cell, 2008; Vasiljeva et al., Mol.Cell, 2008; Luke et al., Mol. Cell, 2008; Berretta et al., Gene Dev., 2008; Preker et al., Science, 2008; Seila et al., Science, 2008; Xu et al., Nature, 2009; Neil et al., Nature, 2009

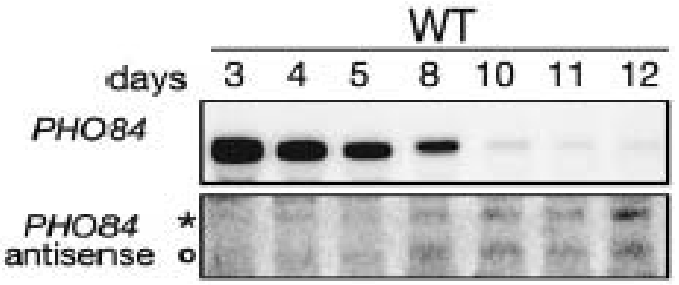
PHYSIOLOGICAL FUNCTIONS of CUTs

Regulation of gene expression via antisense RNA and epigenetic modification: *PHO84* (inorganic phosphate transporter)

Stabilization of as CUT leads to H3K18 deacetylation by Hda1 at *PHO84* promoter







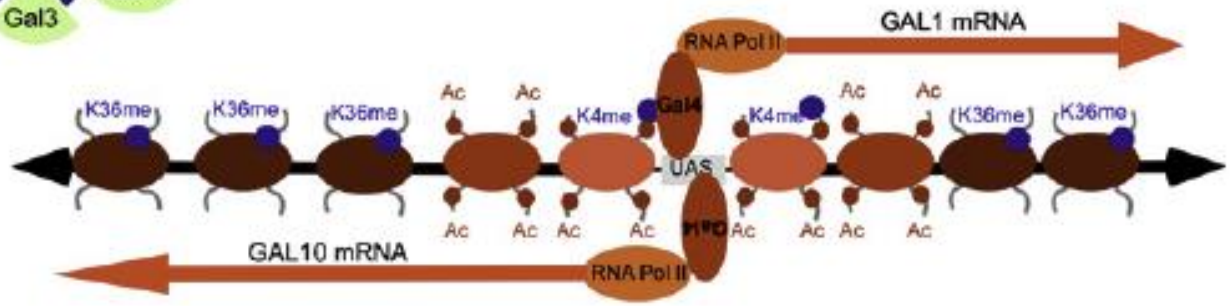
Similar *PHO84* silencing occurs in aging yeast

Camblong et al., Cell, 2007; Wery et al., WIREsSMB ’11

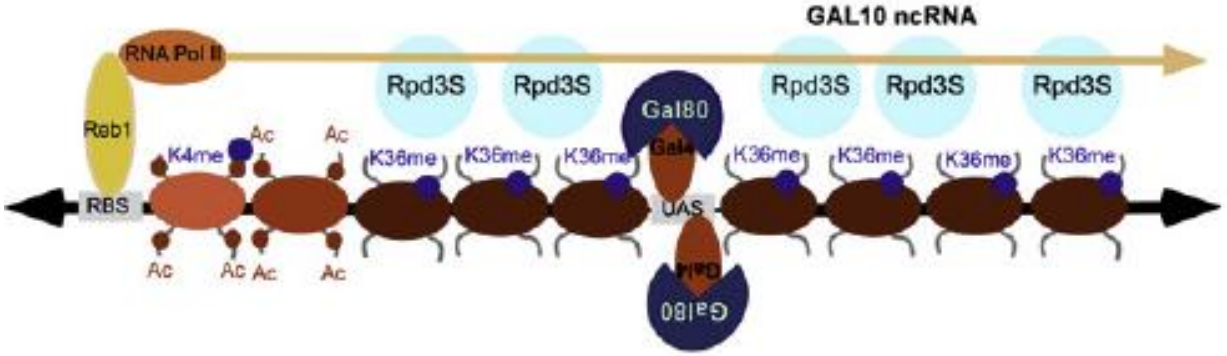
PHYSIOLOGICAL FUNCTIONS of CUTs

Regulation of gene expression via antisense RNA and epigenetic modification: *GAL10-GAL1* locus

Induction (galactose) – full transcription of GAL1/GAL10 mRNAs



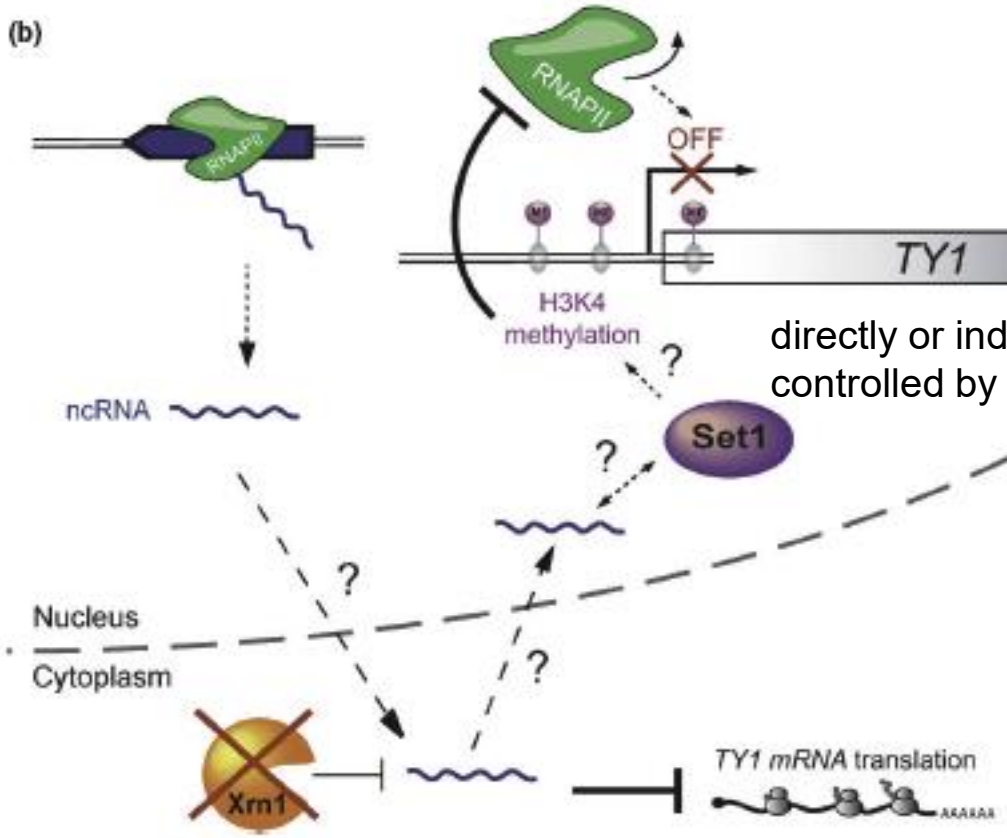
Repression (glucose) – Gal80/4 inhibitor binding at UAS inhibits transcription of GAL1/GAL10 mRNAs and allows Reb1 binding within GAL10 gene. This induces transcription of CUT RNA, which in turn leads toH3K36 histone methylation by HTM Set1 and Set2, histone deacetylation via recruitment of histone deacelylase complex Rpd3S, and further inhibition of mRNA transcription



Houseley et al., Mol.Cell, 2008

PHYSIOLOGICAL FUNCTIONS of XUTs

Transcriptional silencing of the Ty1 transposon

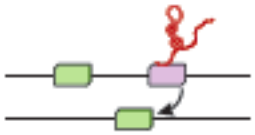
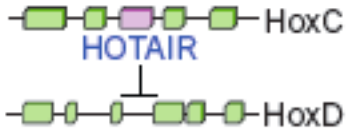
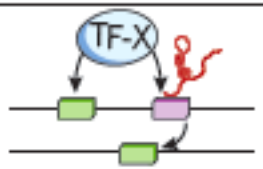
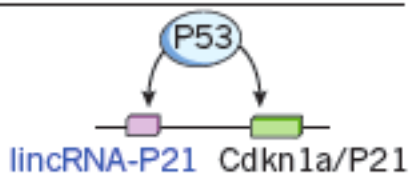
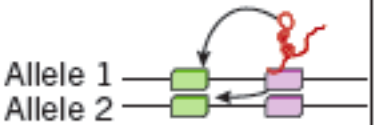
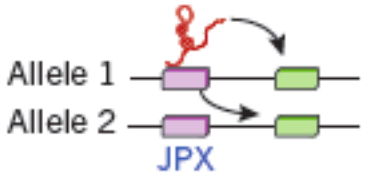
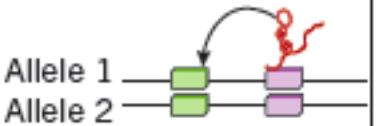


antisense *TY1* XUT

- **polyadenylated Pol II transcript**
- **antisense to TY1 promoter**
- **degraded by cytoplasmic Xrn1**
- **silences TY1 expression by promoting histone deacetylation and trimethylation (by Set1)**
- **can act *in-trans***

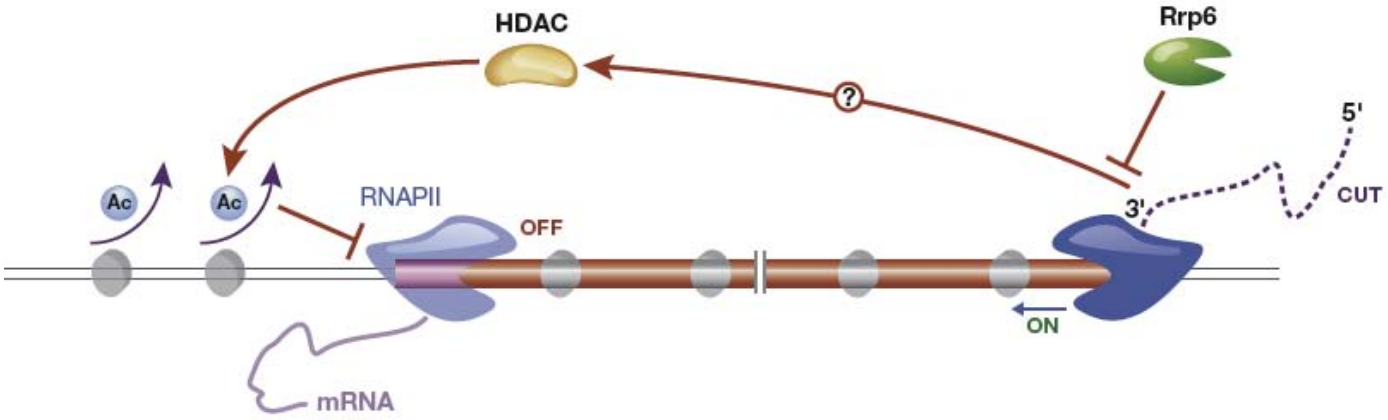
Berretta et al., Gene Dev, 2008; Wery et al., WIREsSMB´11

ncRNA ACTION *in-cis* or *in-trans*

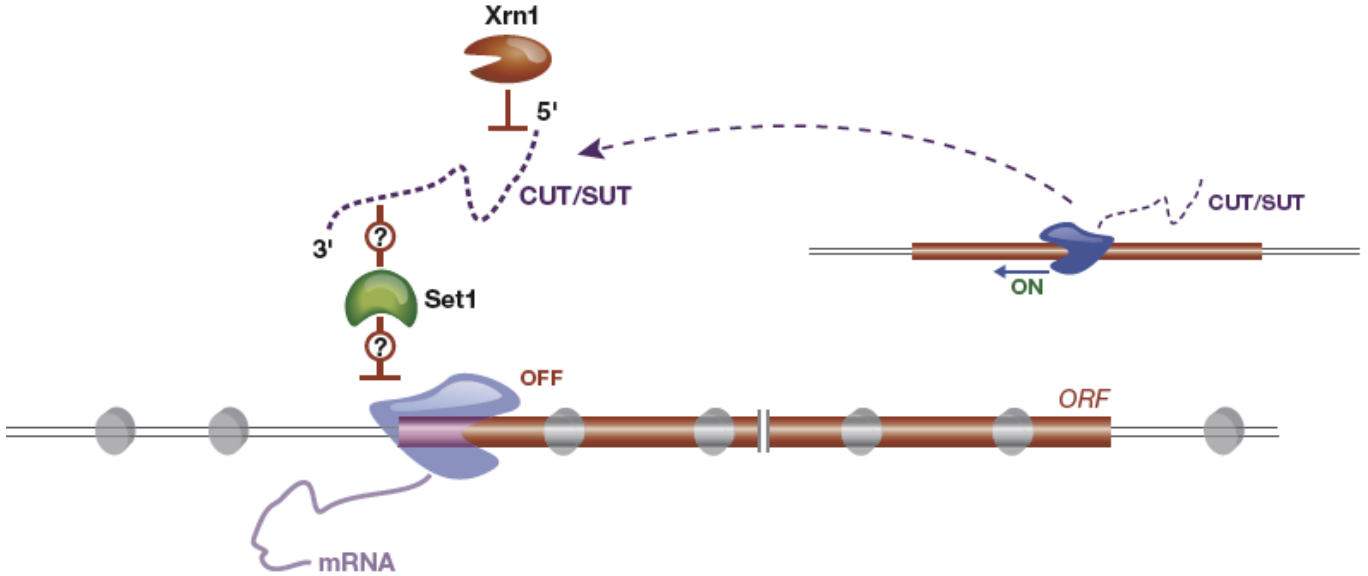
	Regulatory model	Expression correlation	Perturbation effect	Allele-specific regulation	Known ncRNA examples
trans		✗	✗	✗	
trans		✓	✗	✗	
trans		✓	✓	✗	Unknown
trans		✓	✓	✗	
cis		✓	✓	✓	
		✓ Neighbour affected		✗ Neighbour unaffected	

Guttman and Rinn, Nature, 2012

CUT ACTION *in-cis* or *in-trans*



CUT transcribed *in-cis*, when stabilized, recruits chromatin modification enzymes (HDAC) to gene promoter

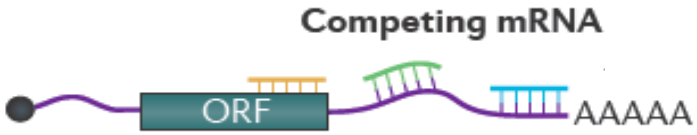


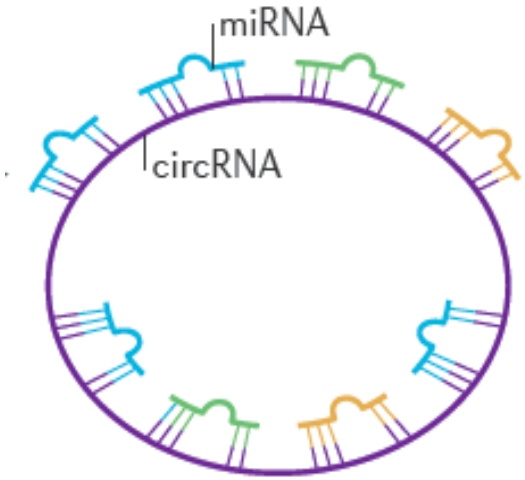
CUT transcribed from a distant locus, when stabilized, recruits chromatin modification enzymes (HTM) to inhibit transcrition

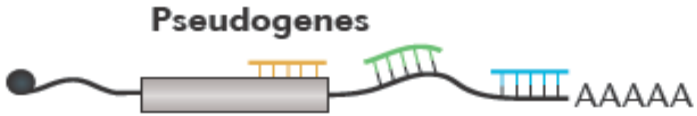
Berretta and Morillon, Embo Rep. 2009

miRNA sponges

Non-coding or coding competing RNAs that bind and sequester miRNAs and in this way stabilize their mRNA targets

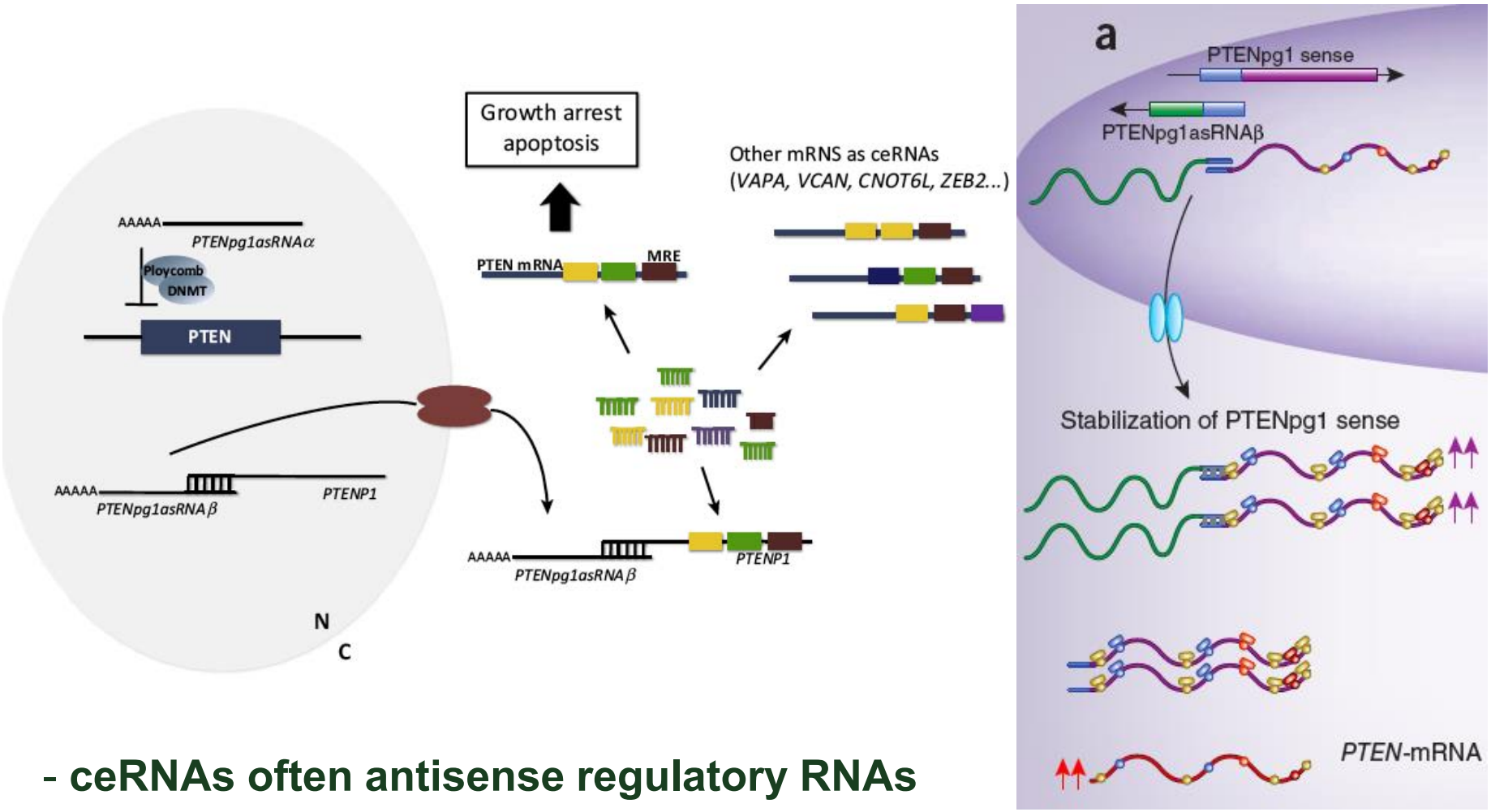






Hausser and Zavolan, NatRevGent, 2015

Competing endogenous RNAs: ceRNAs

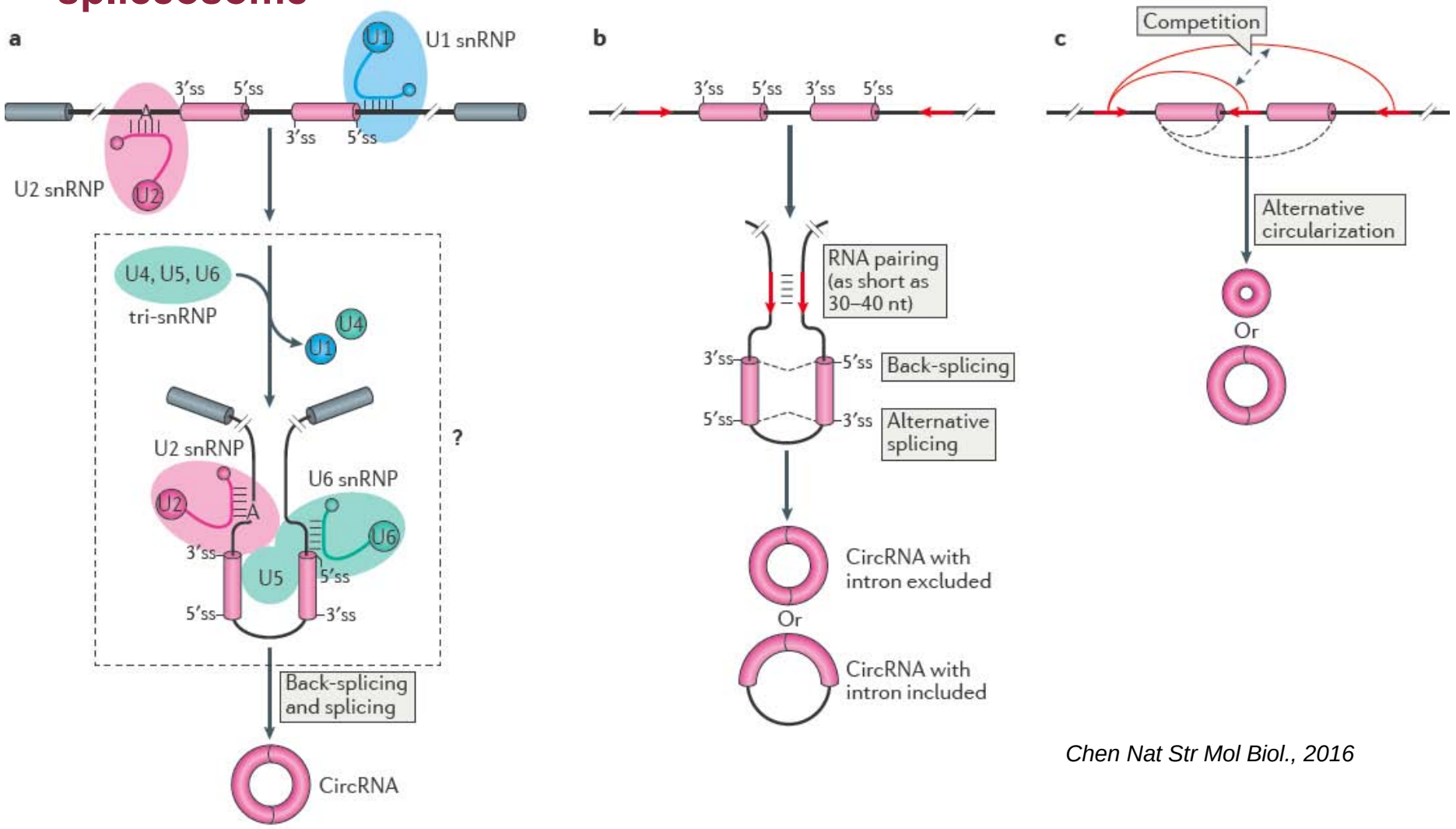


- ceRNAs often antisense regulatory RNAs
- stabilize mRNA by sequestering miRNAs that target mRNA
- implicated in cancer

Guil and Esteller, TiBS 2015

Circular RNAs: circRNAs

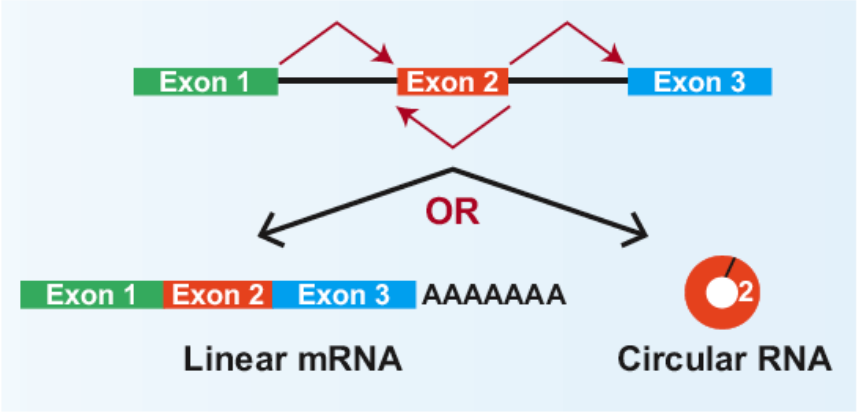
Made of exons, arise by noncanonical back splicing catalysed by the spliceosome



Chen Nat Str Mol Biol., 2016

CircRNA synthesis may be stimulated by some RNA binding proteins (Mbl, QKI) that bind to intronic sequences and stabilize short hairpins

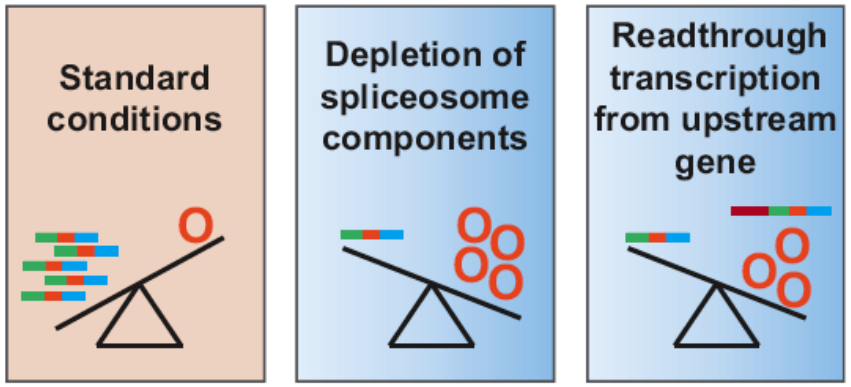
circRNA expression

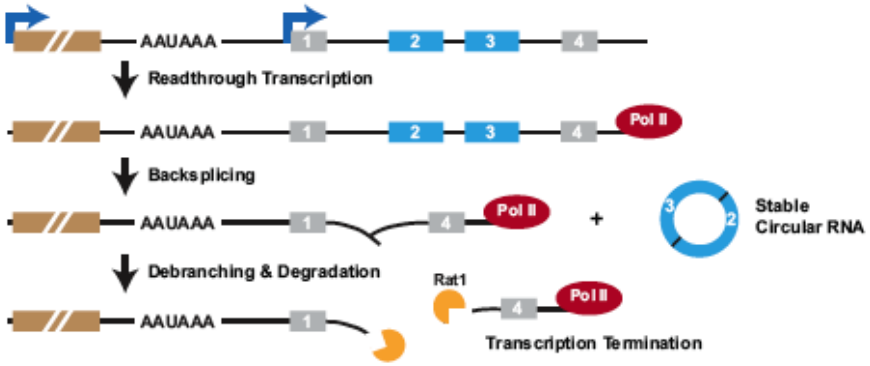


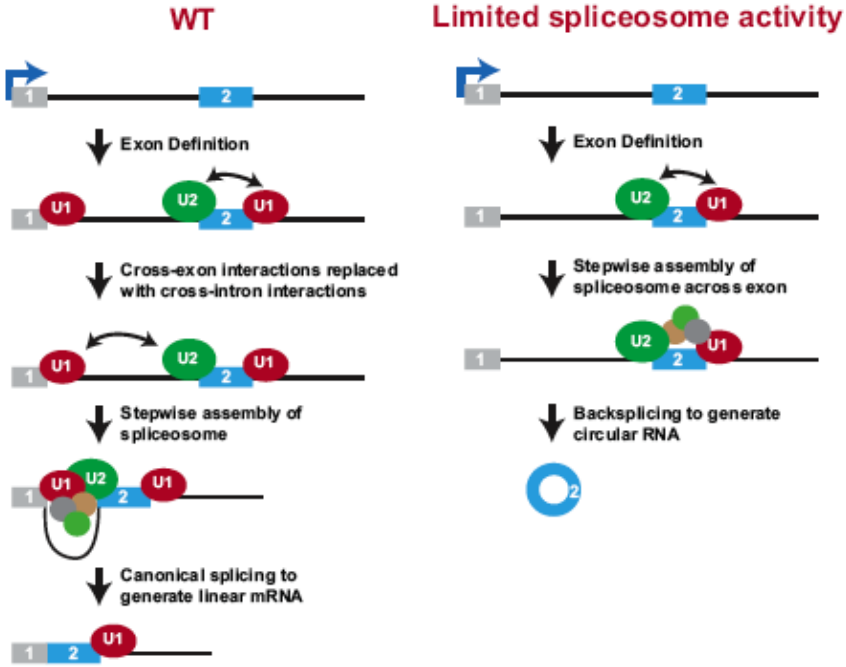
circRNA expression is stimulated by

- inhibition of canonical splicing (depletion of spliceosome components)
- readthrough transcription

The amounts of linear vs. circular RNA can be modulated:



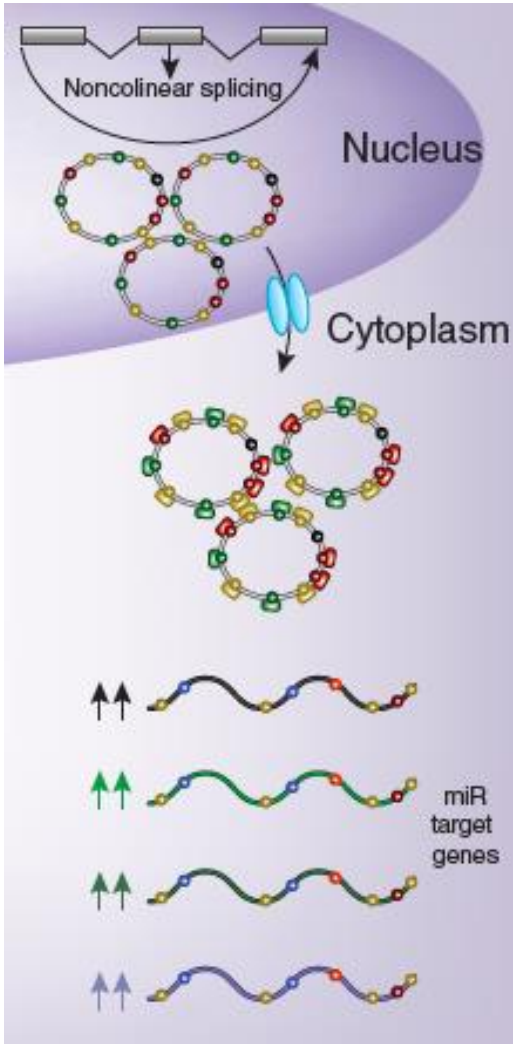


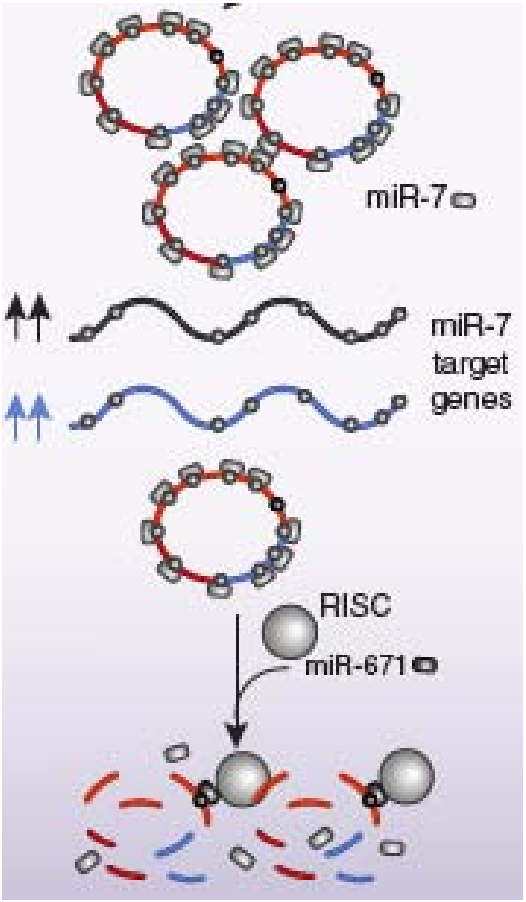


Liang Mol Cell., 2017

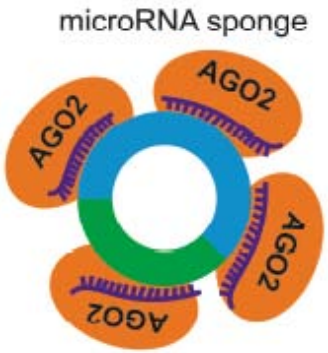
circRNAs: functions

Some circRNAs contain miR-responsive elements and sequester miRNAs
Are often regulated via miRNAs and degraded by Ago2 Slicer
CircRNAs with distinct MREs may sequester different miRNAs
CircRNAs may also sequester proteins





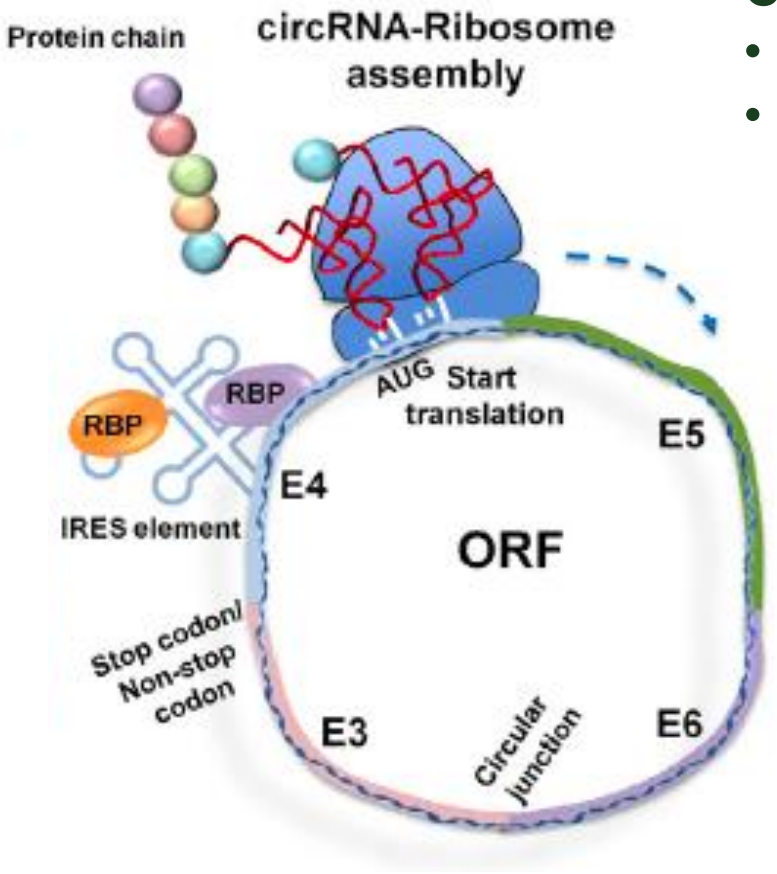
Taulli et al., Nat Str Mol Biol., 2013
Cortes-Lopez and Miura, YJBM, 2016



circRNA	microRNA sponged
CDR1as	miR-7 (+70 sites) miR-671
circRNA-Sry	miR-138 (38 sites)
circRNA-CER	miR-136
circRNA-001569	miR-145
circ-HRCR	miR-223
circ-Foxo3	miR-36, miR-49, miR-433, and 5 other miRNAs.
circHIPK3	miR-124 and 8 other miRNAs.

circRNA	Interacting Proteins
circ-Foxo3	ID-1, E2F1, FAK, HIF1α p21-CDK2

but circRNAs can be translated...



CircRNA translation:

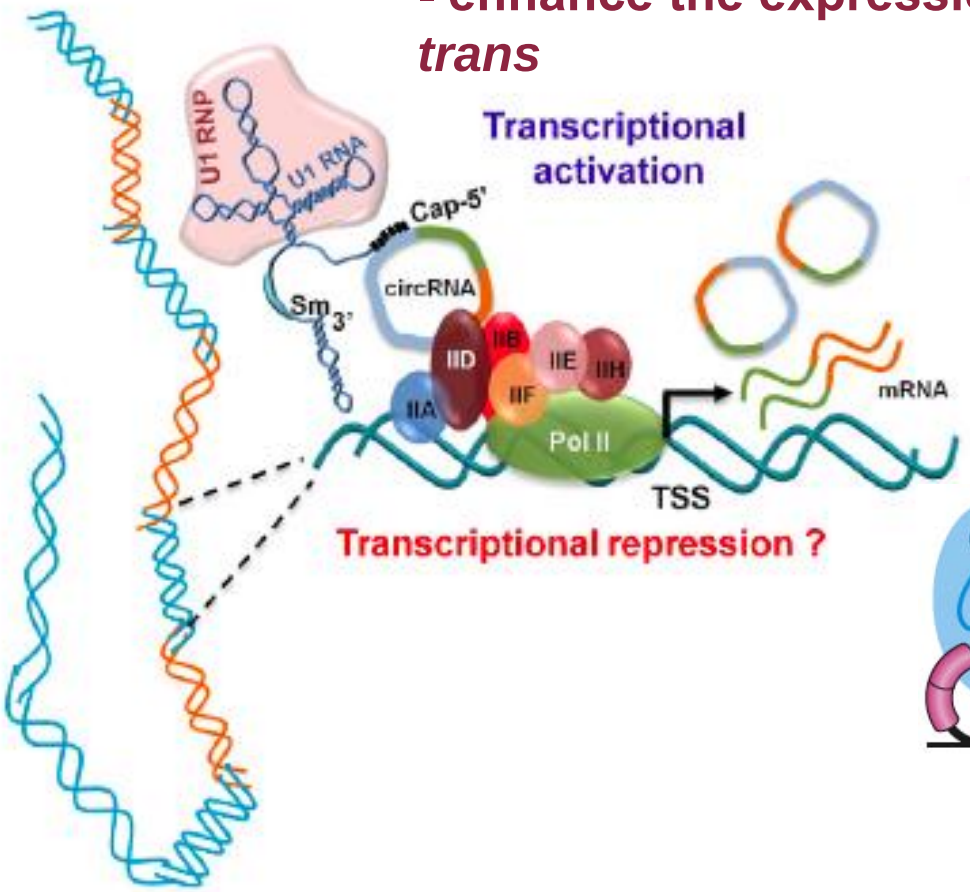
- **in a cap-independent manner (IRES)**
- **often driven by m^{6}A modification**

Model	CircRNA feature	Sequence feature	Peptide/protein
Virus			
Hepatitis delta (δ) virus (HDV)	Circular single-stranded RNA	OFR with a TGA stop codon	Protein of 122 amino acids
Rice yellow mottle virus	Covalently closed circular RNA (220 nt)	Infinite ORF, IRES-dependent sequence	16-kDa highly basic protein
Bacteria			
Escherichia coli	795-nt circular mRNA	Infinite GFP ORF, IRES-independent sequence	GFP
Mammals			
HEK-293 cells	Single exon minigene	IRES-dependent sequence	GFP
HEK-293 cells	Exonic	Poly-A tail-independent translation	NH2-terminal portion of NCX1 protein (70-kDa)
Rabbit reticulocyte lysate	Exonic	Cap-independent translation, IRES-independent sequence, poly-A tail-independent translation	EGF, IGF-1, IGF-2
HeLa cells	Exonic		

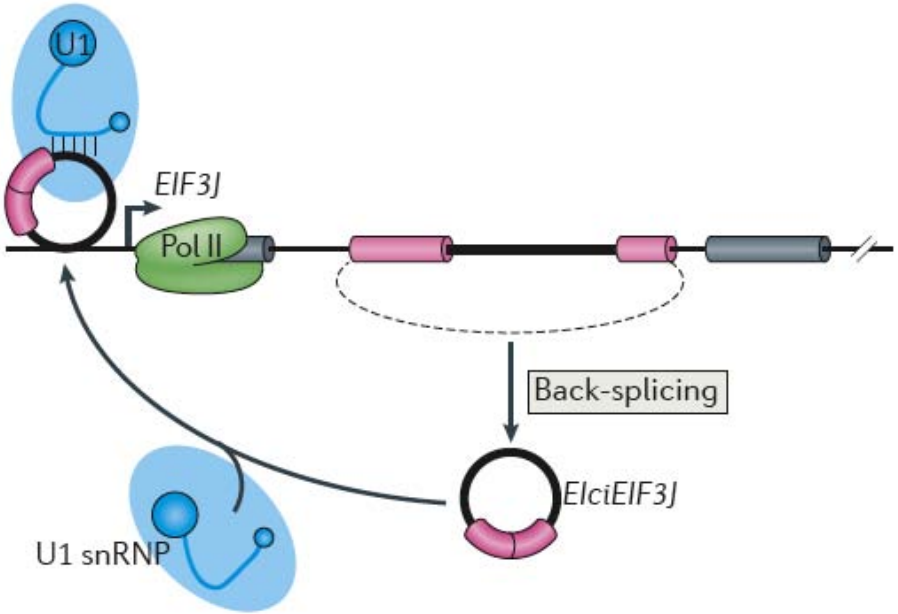
Granados-Riveron and Aquino-Jarquin, BBA., 2016

circRNAs may regulate transcription

exon-intron circRNAs (ElciRNAs)
- associate with U1 snRNP in the nucleus
- enhance the expression of their parental gene *in trans*



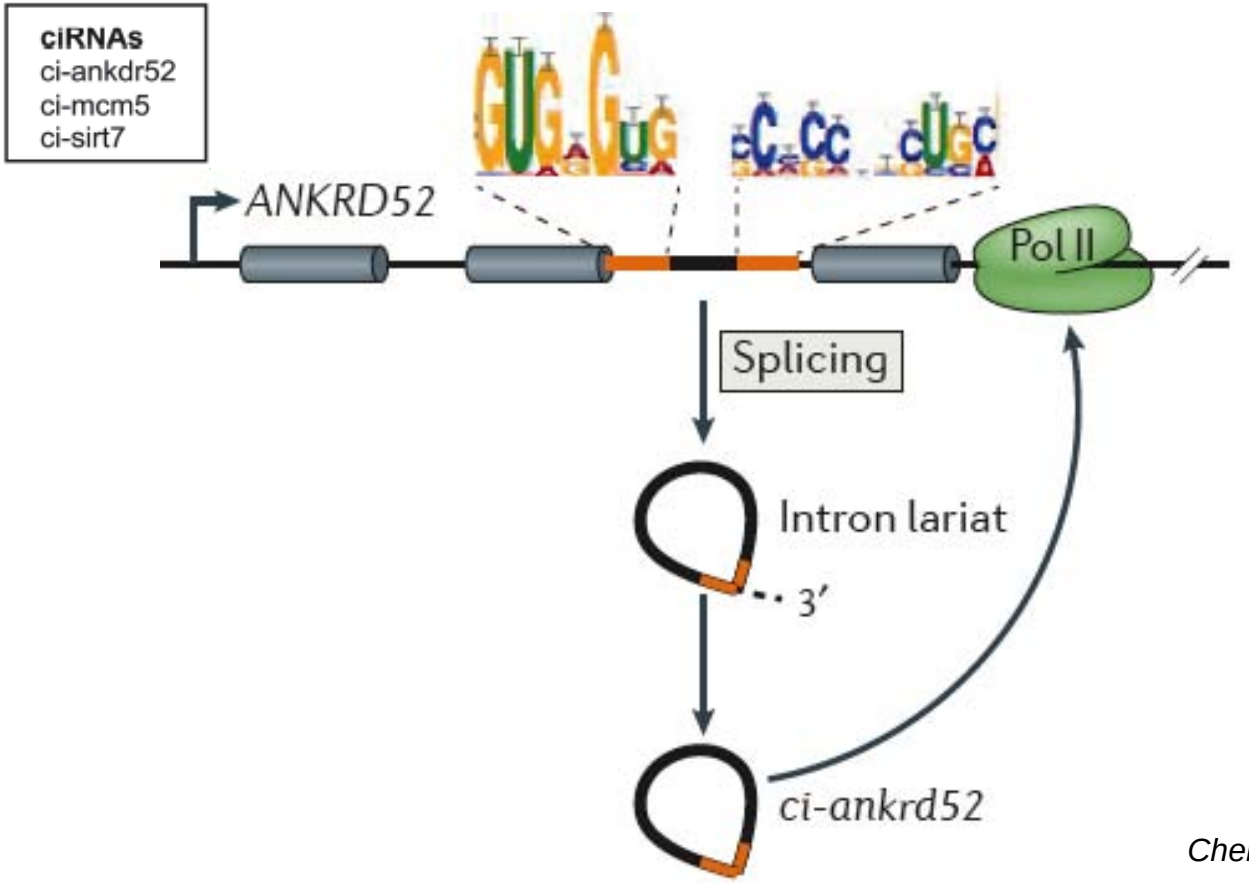
ElciRNAs
circRIF3J
circPAIP2



Li at al., Nat Struct Mol Biol, 2015;
Chen, NatRevMolCellBiol, 2016
Granados-Riveron and Aquino-Jarquin, BBA., 2016

Circular intron-derived ciRNAs
regulate transcription

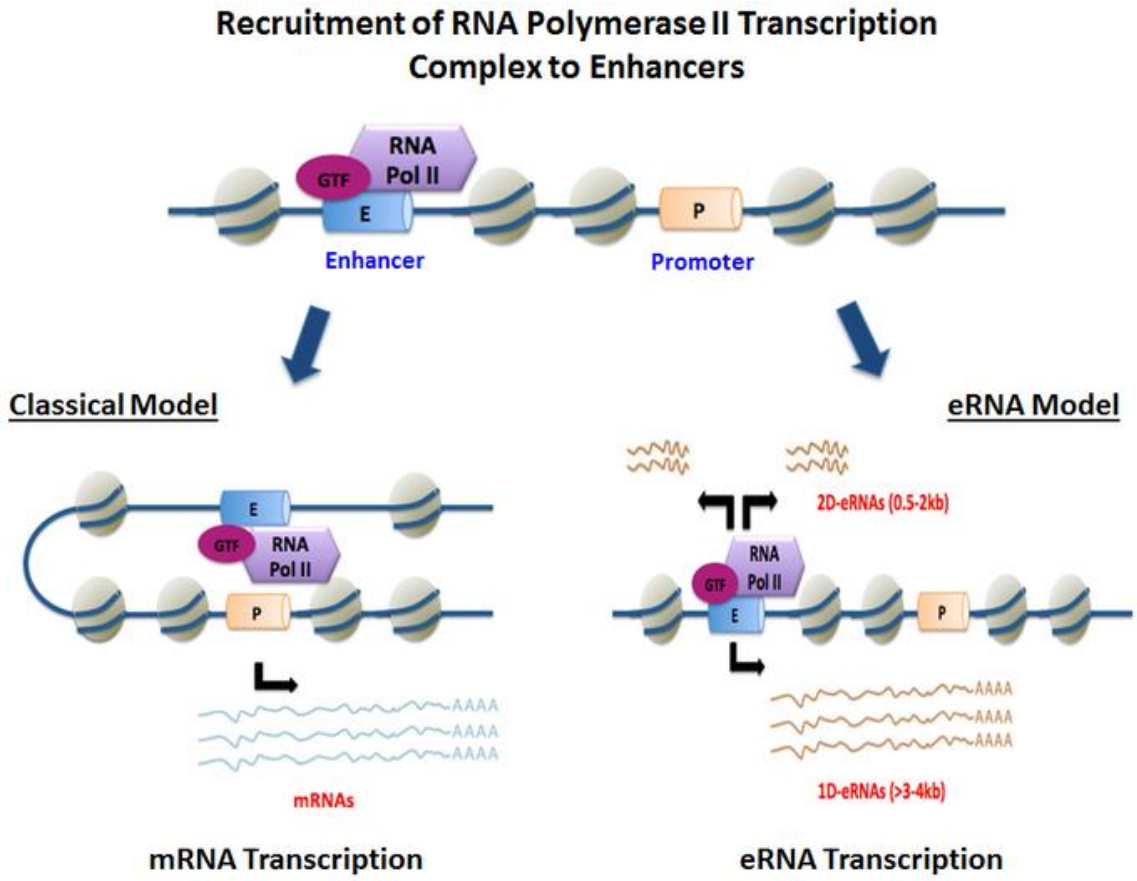
- accumulate in human cells due to lariat debranching defect, in the nucleus
- processing depends on GU-rich motive near 5' splice site and branchpoint
- interact with phosphorylated Pol II and modulate Pol II elongation
- regulate the expression of their parental gene

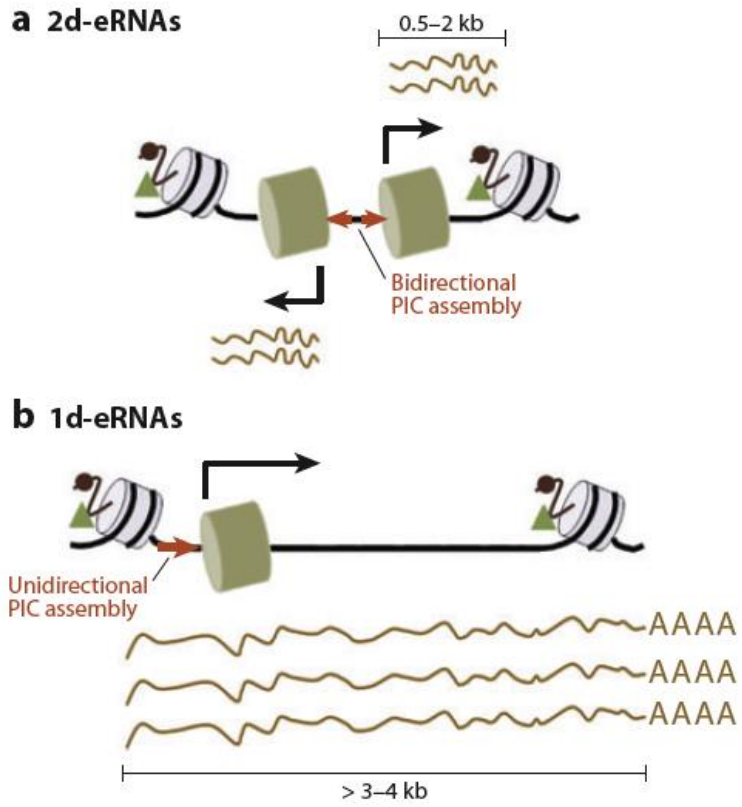


Chen, NatRevMolCellBiol, 2016

Enhancer RNAs: eRNAs

<u>eRNAs</u>: short (not always, up to 2 kb) **ncRNAs transcribed from enhancer regions**

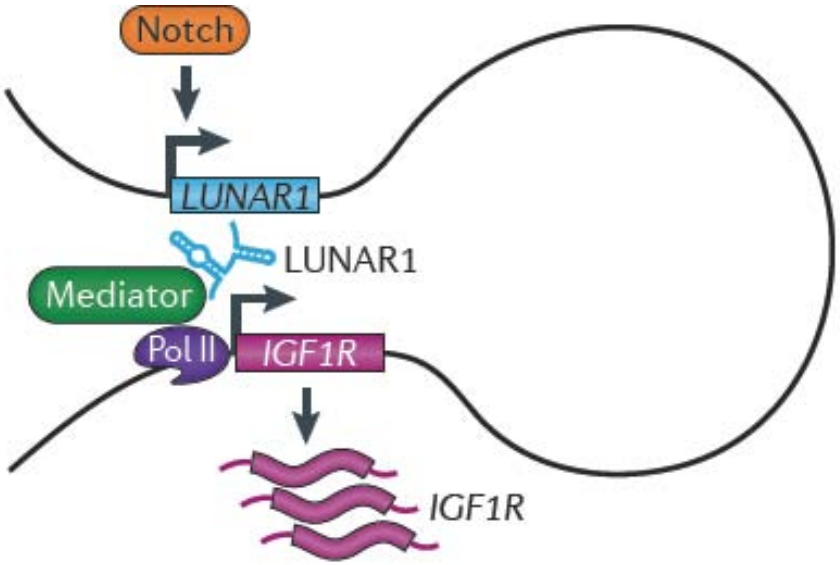


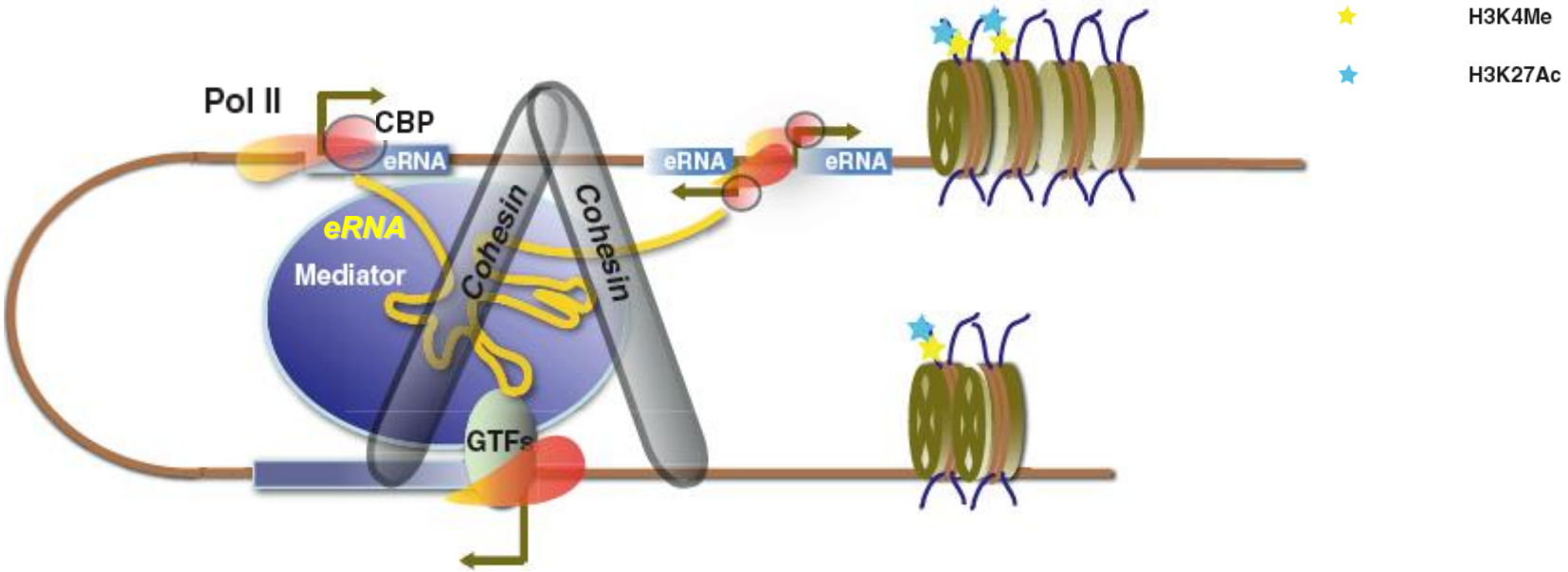


2d-eRNAs: bidirectional, comparatively short, nonpolyadenylated
1d-eRNAs: unidirectional, long, polyadenylated

Natoli and Andrau, Annu Rev Genet., 2012

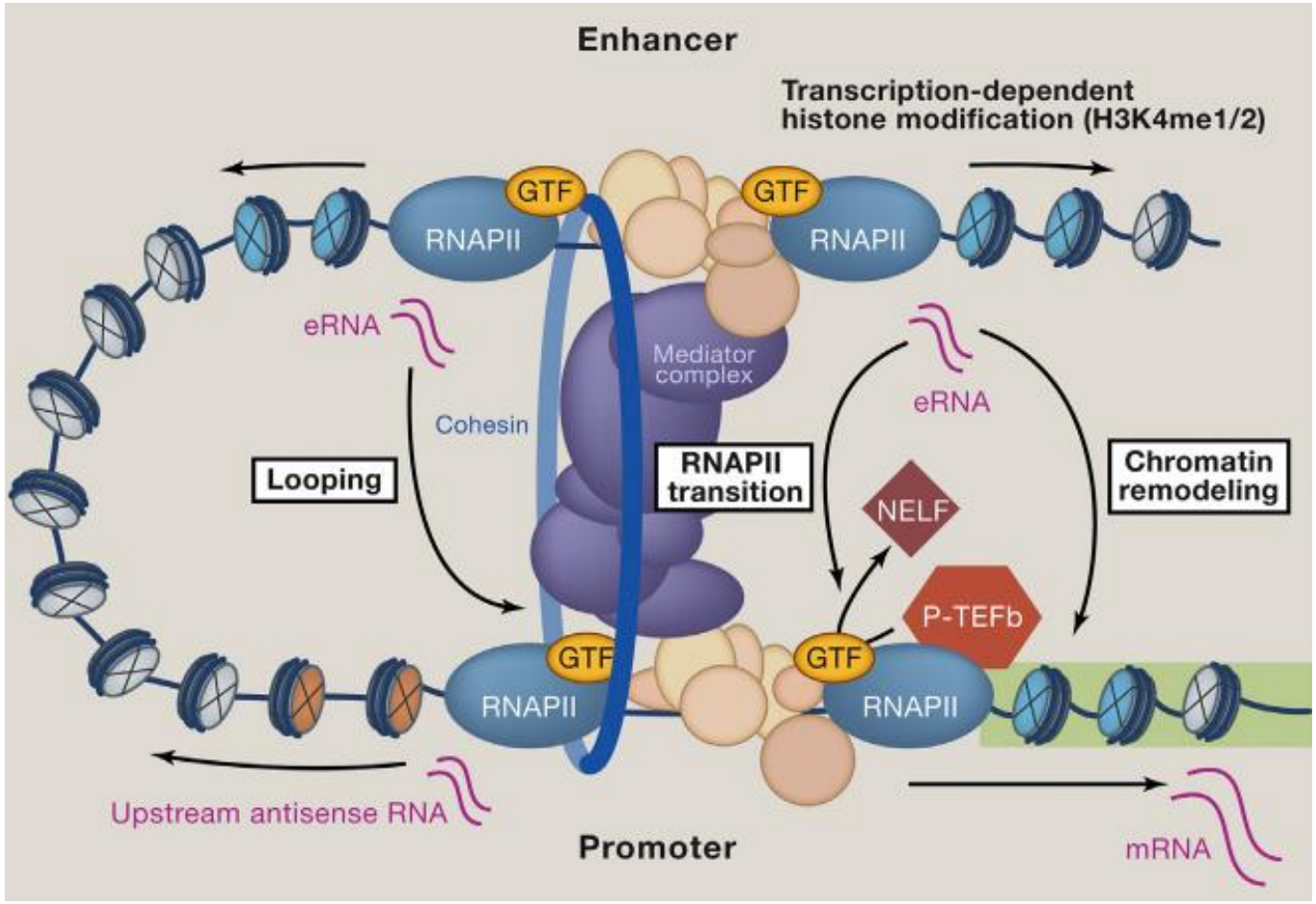
eRNAs: functions
Chromosome looping





Quinn and Chang, Nat Rev Genet 2015;
Lai and Shiekhattar, Curr Op Gene Dev 2014

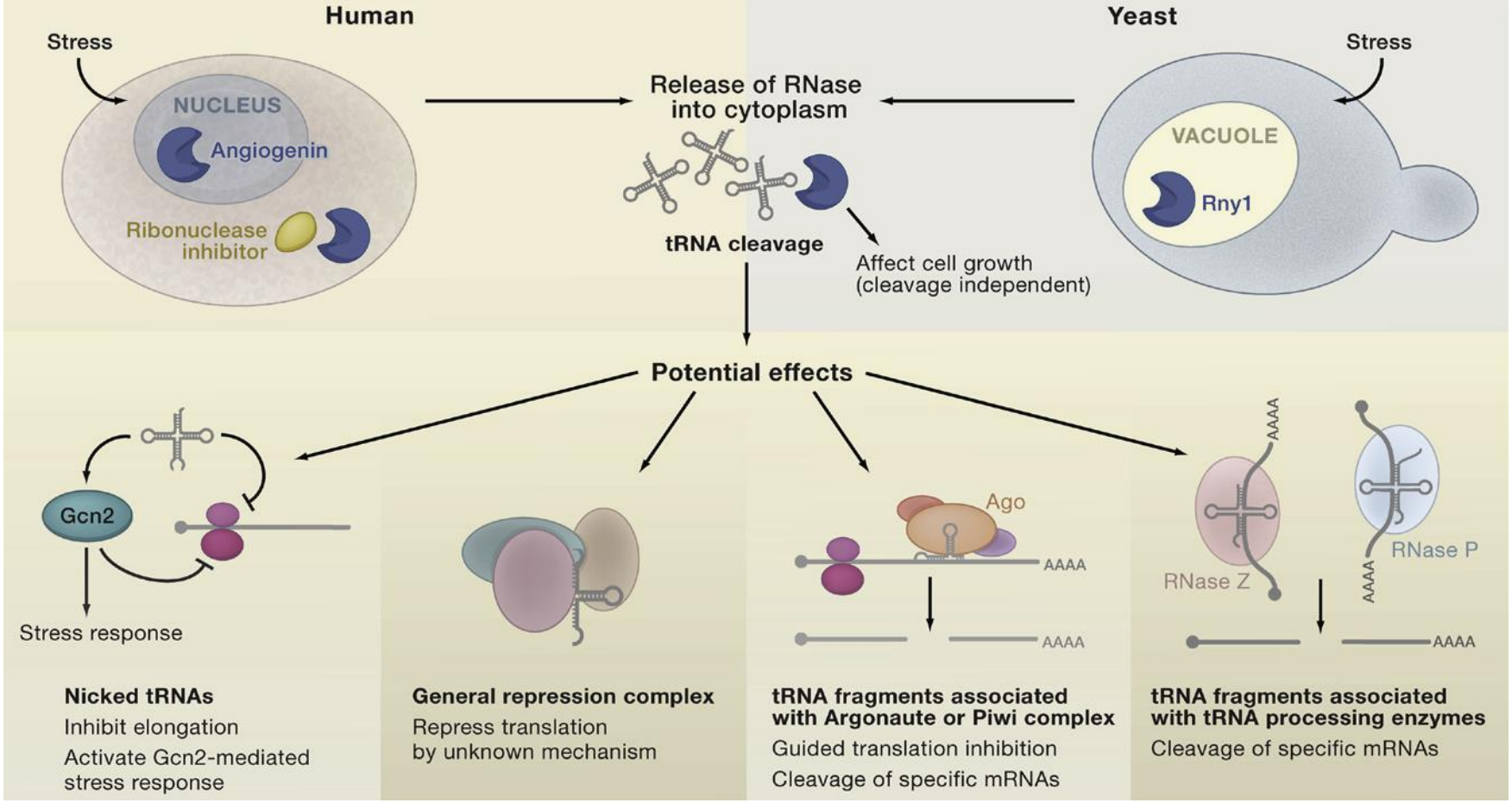
Enhancer RNAs: eRNAs



Unusual ncRNAs: tRFs tRNA-derived RNA fragments

Stress-induced enzymatic tRNA cleavage

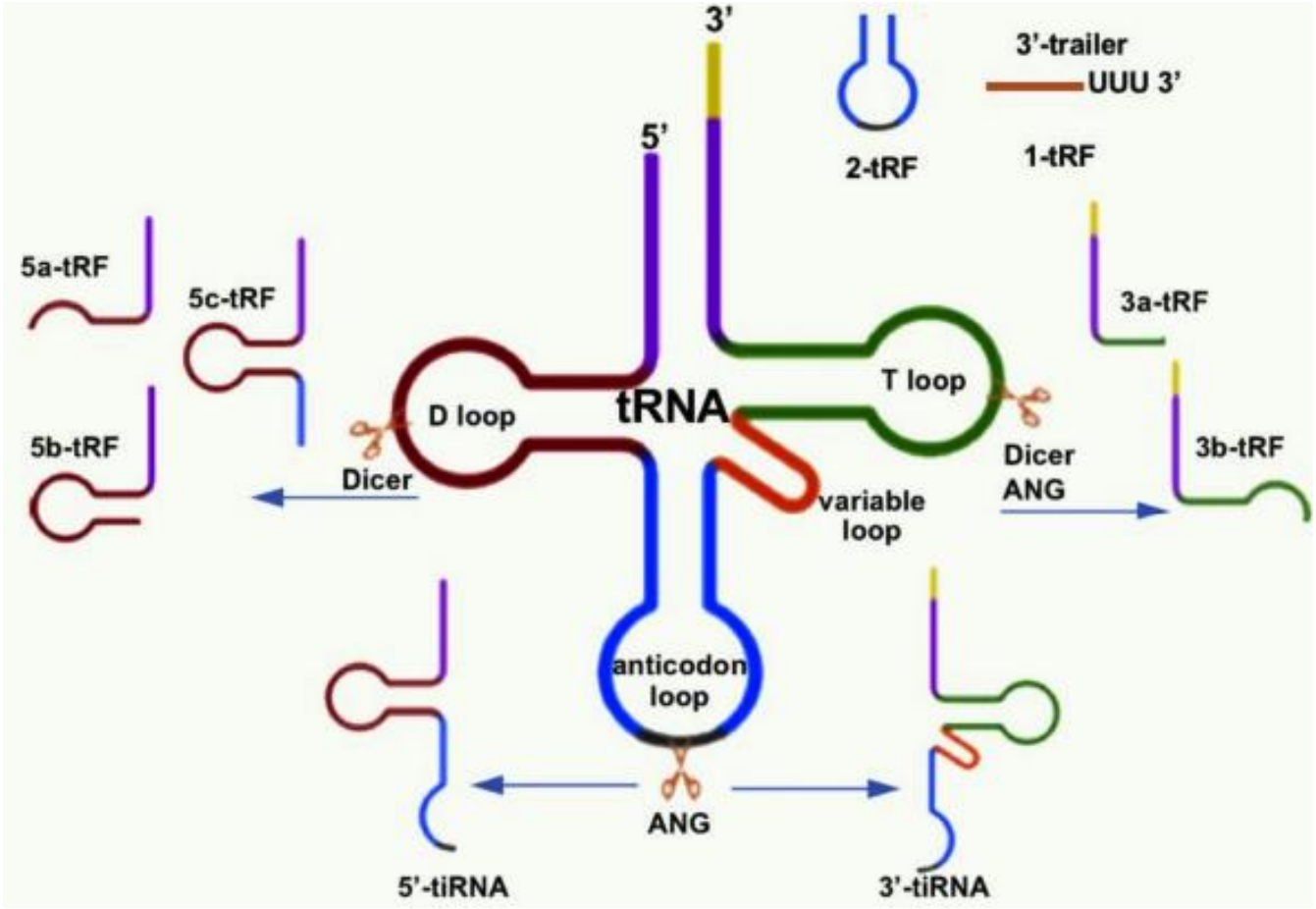
(*S. cerevisiae, D. melanogaster, A. thaliana, A. nidulans*, human cell lines)



Thompson and Parker, Cell, 2009

- **act as miRNAs**
- **regulate translation**
- **regulate cellular stress response**
- **role in disease: cancer, viral infection, metabolic and neurological disease**

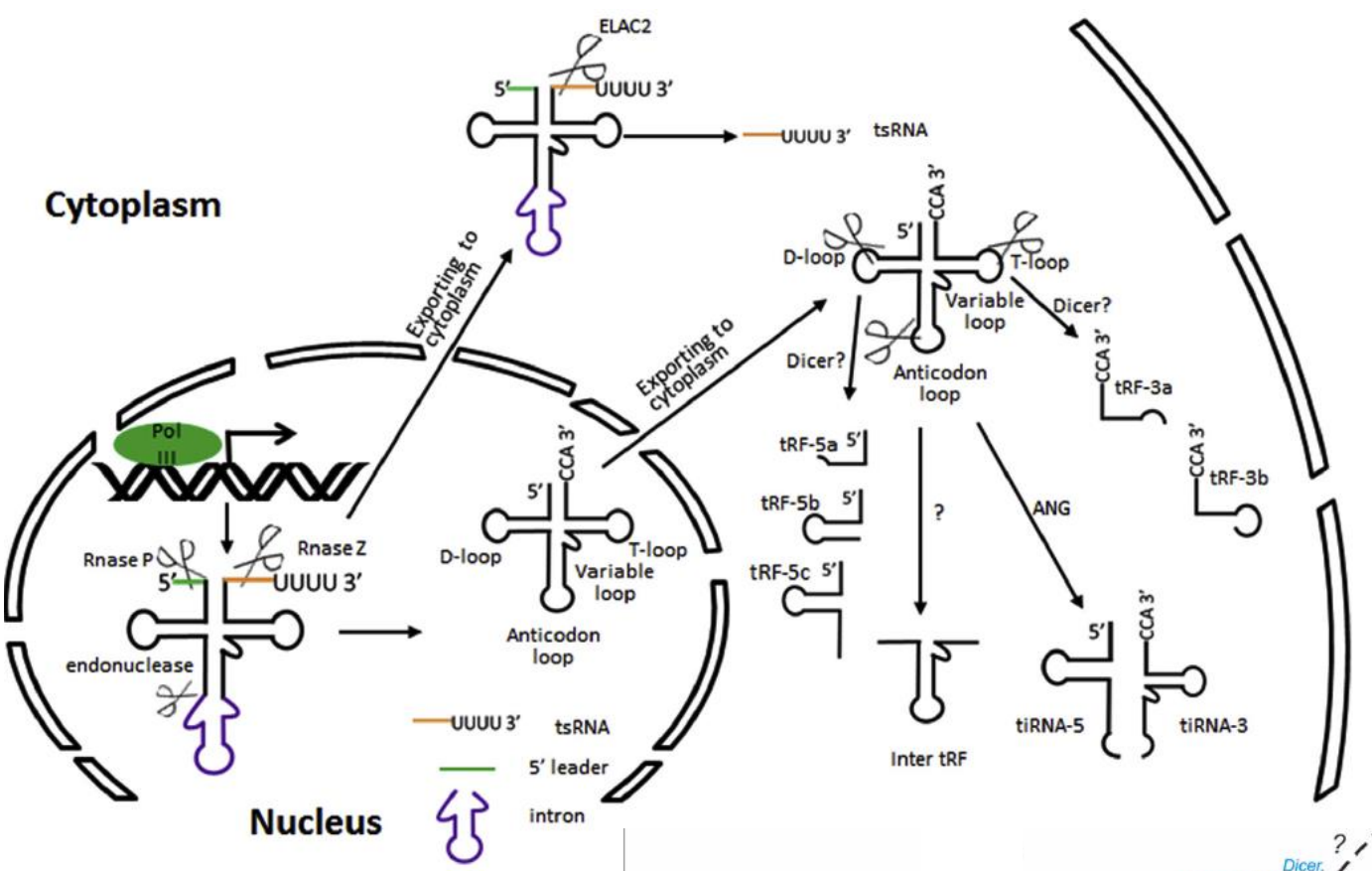
Unusual ncRNAs: tRFs tRNA-derived RNA fragments

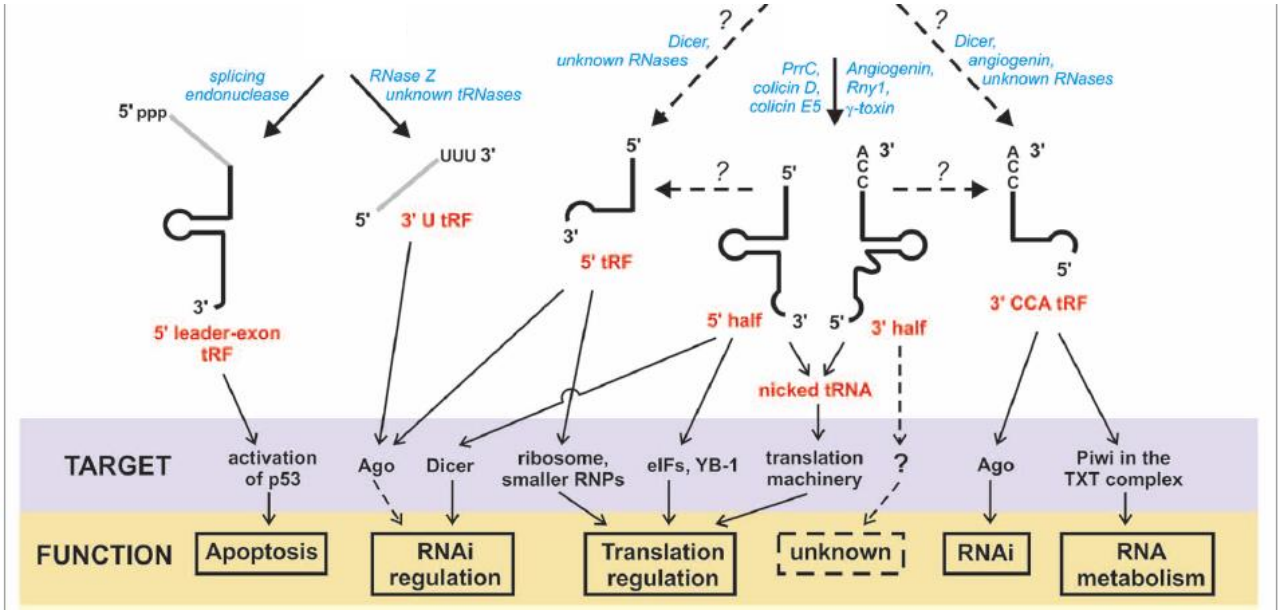


Li et al, Gene 2018

- **> 17 short abundant tRFs (13-26 nts), generated by RNase Z from mature (5' and 3' ends) and precursor (3' trailer) tRNAs (cytoplasm, prostate cancer).**
- **Abundant Dicer-dependent class I tRFs from mature 3' and 5' ends (HeLa)**
- **Class II tRFs from RNAseZ 3' cleavage to Pol III termination (cytoplas) associate with Ago2-3. Regulation of silencing via association with Ago proteins?**

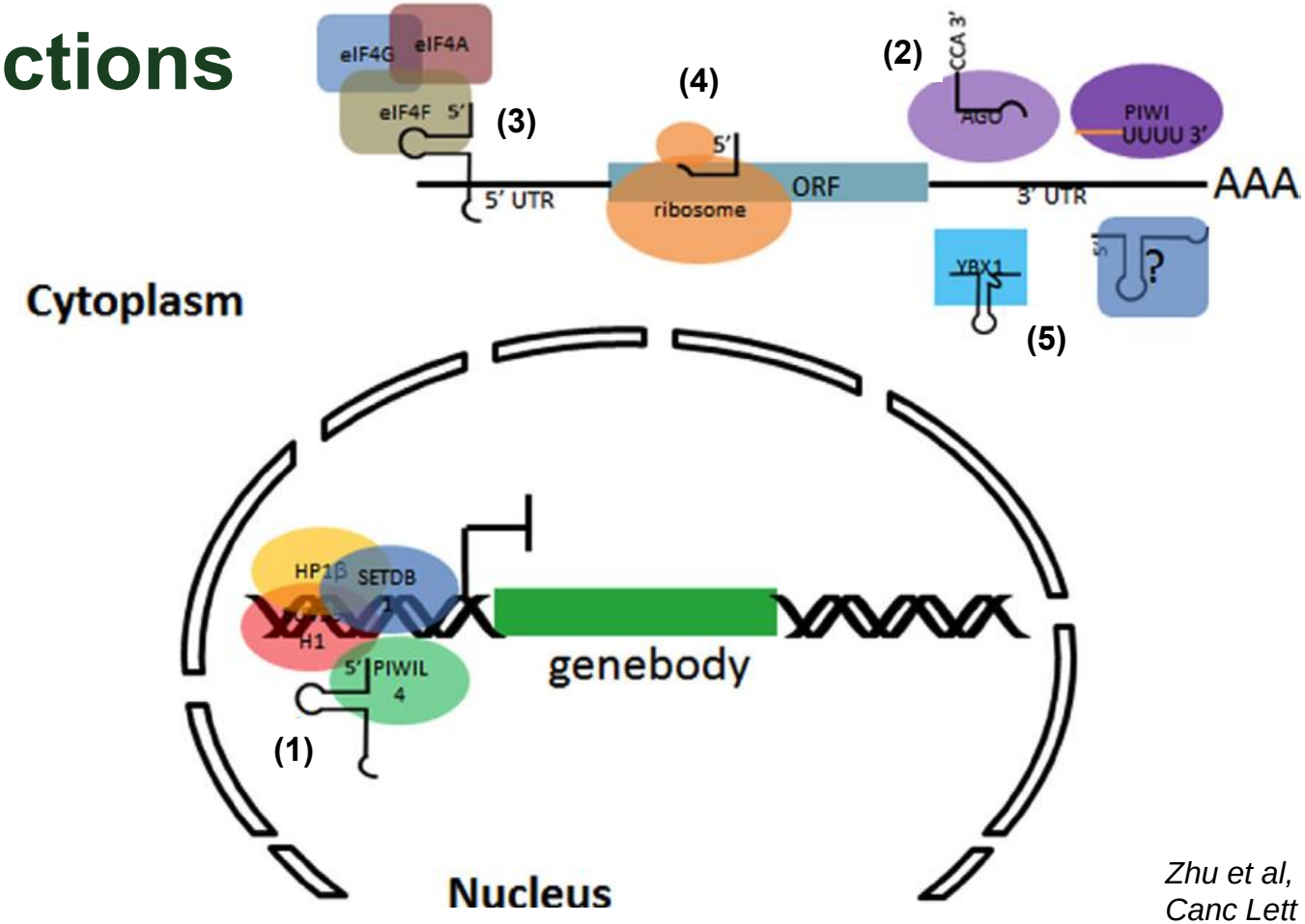
tRFs and tiRNAs





Zhu et al, Canc Lett 2018

tRFs: functions



Zhu et al,
Canc Lett 2018

(1) tiRNAs incorporated with Piwi suppress gene transcription

(2) tRFs associated with AGO/Piwi and suppress target gene expression.

(3) tiRNA inhibits translation by displacing translation initiation factor from mRNA

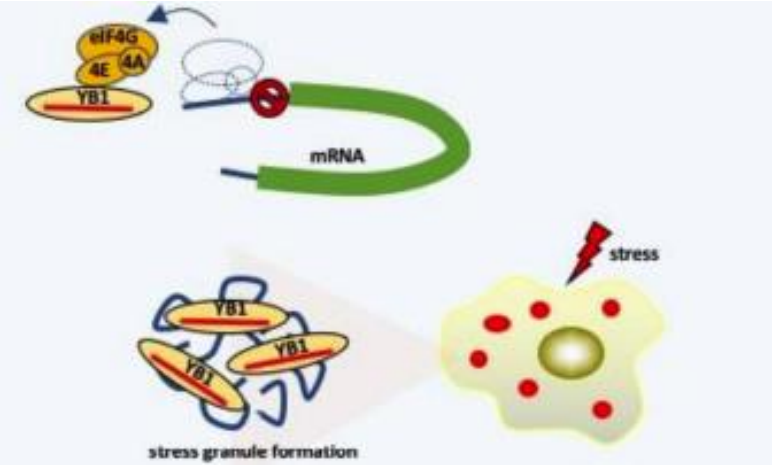
(4) tRFs can suppress translation through affecting ribosome elongation

(5) tRFs can reduce mRNA stability by displacing YBX1 from 3'UTR of mRNA

tRFs: functions

Translational repression by angiogenin-derived 5'-tiRNAs with terminal 5'-oligoG

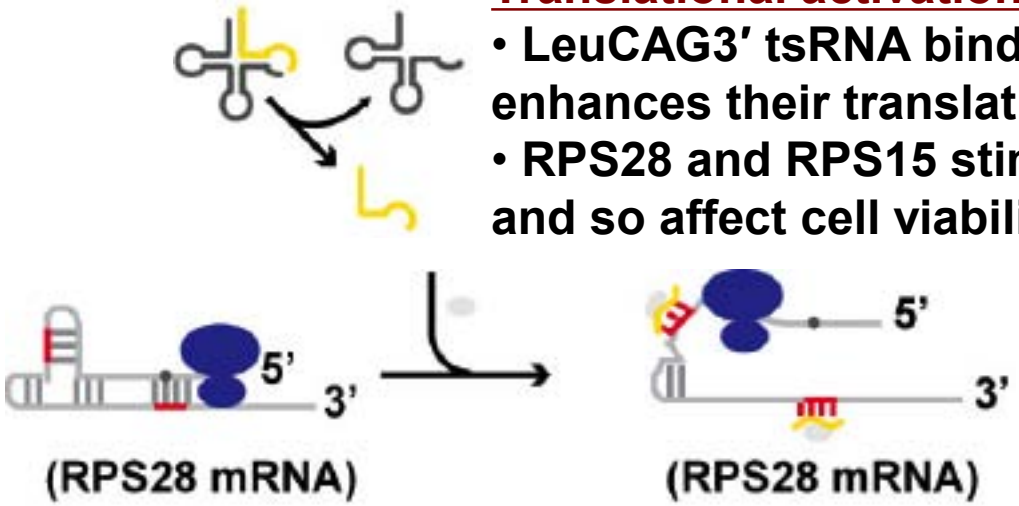
- represses translation *in vitro* and *in vivo*
- displaces eIF4G/eIF4A from uncapped transcripts and eIF4F from m^7G cap
- triggers formation of stress granules (SGs)
- translational repressor YB-1 contributes to tiRNA-mediated repression



Li et al, Gene 2018

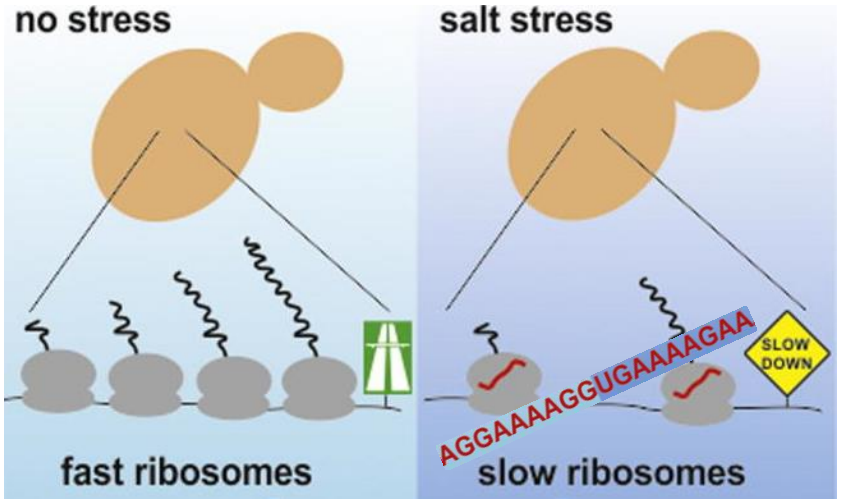
Translational activation by affecting ribosome biogenesis

- LeuCAG3′ tsRNA binds to *RPS28* and *RPS15* mRNAs and enhances their translation by disrupting secondary structure
- RPS28 and RPS15 stimulate biogenesis of 40S ribosome, and so affect cell viability and apoptosis



Kim et al, Nature 2017

Unusual ncRNAs: stress derived RNA fragments

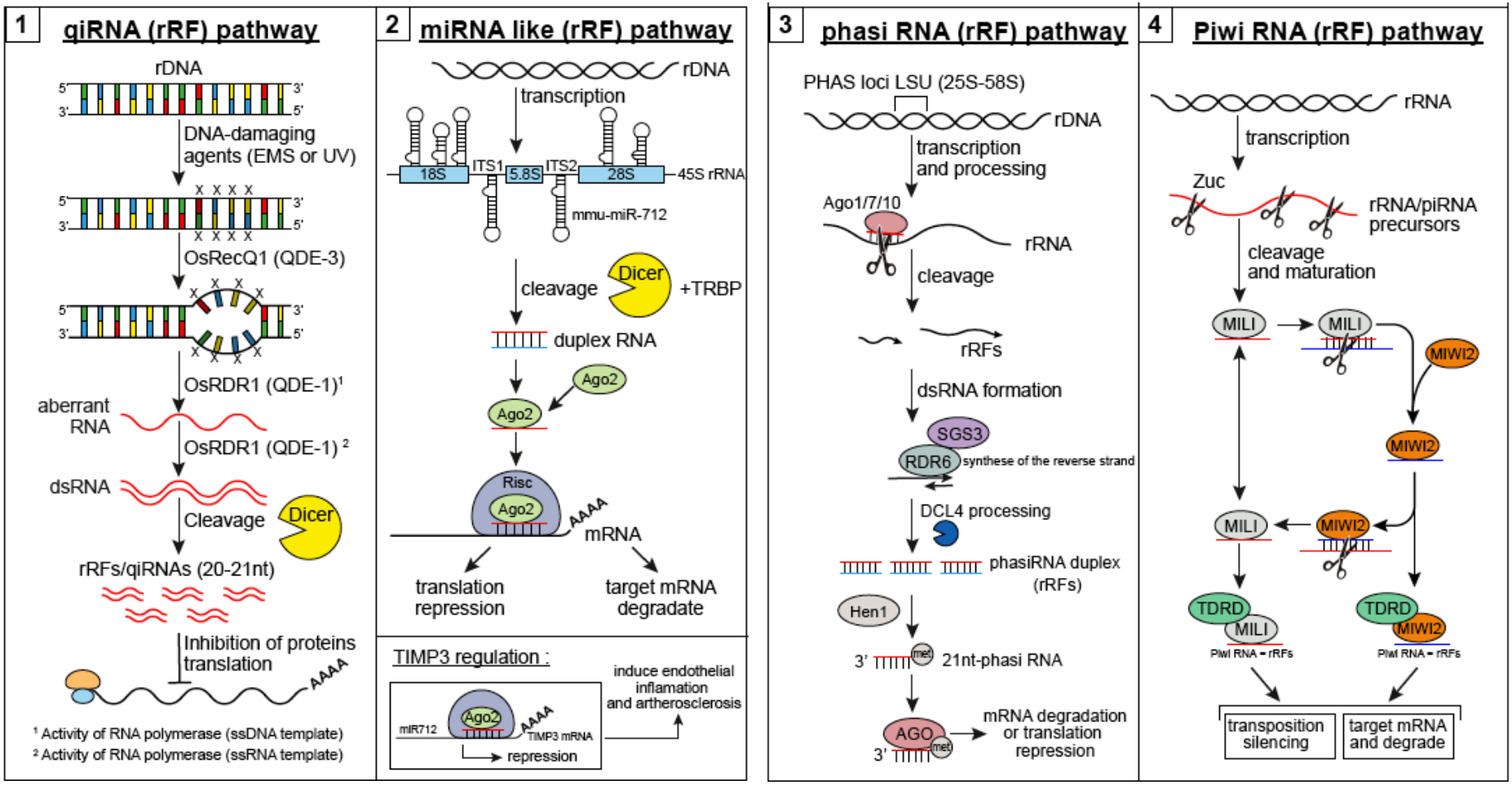


18-mer ncRNA derived from *TRM10* mRNA during salt stress in yeast

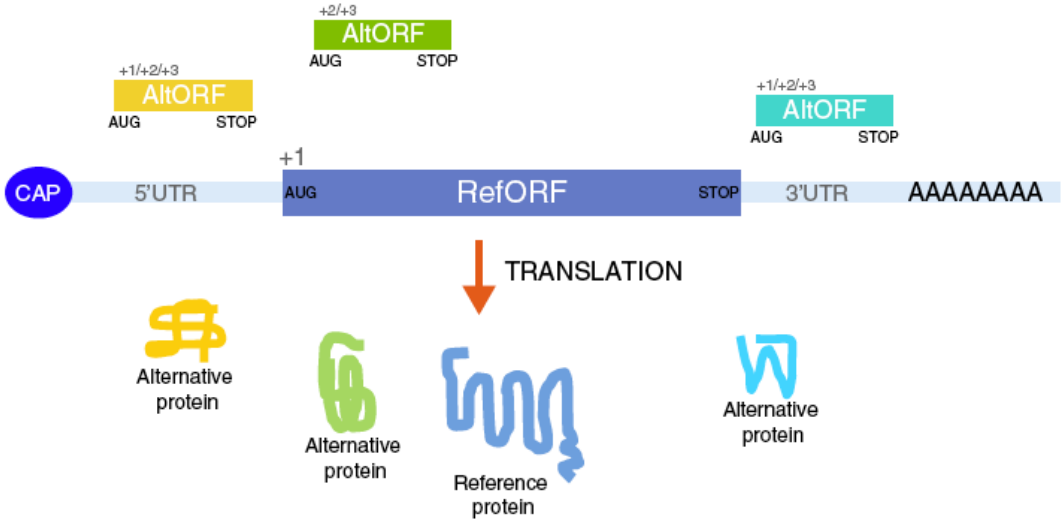
- **associates with polysomes**
- **inhibits general translation**

Pircher et al, Mol. Cell 2014
Gebetsberger and Polacek, RNA Biol., 2013

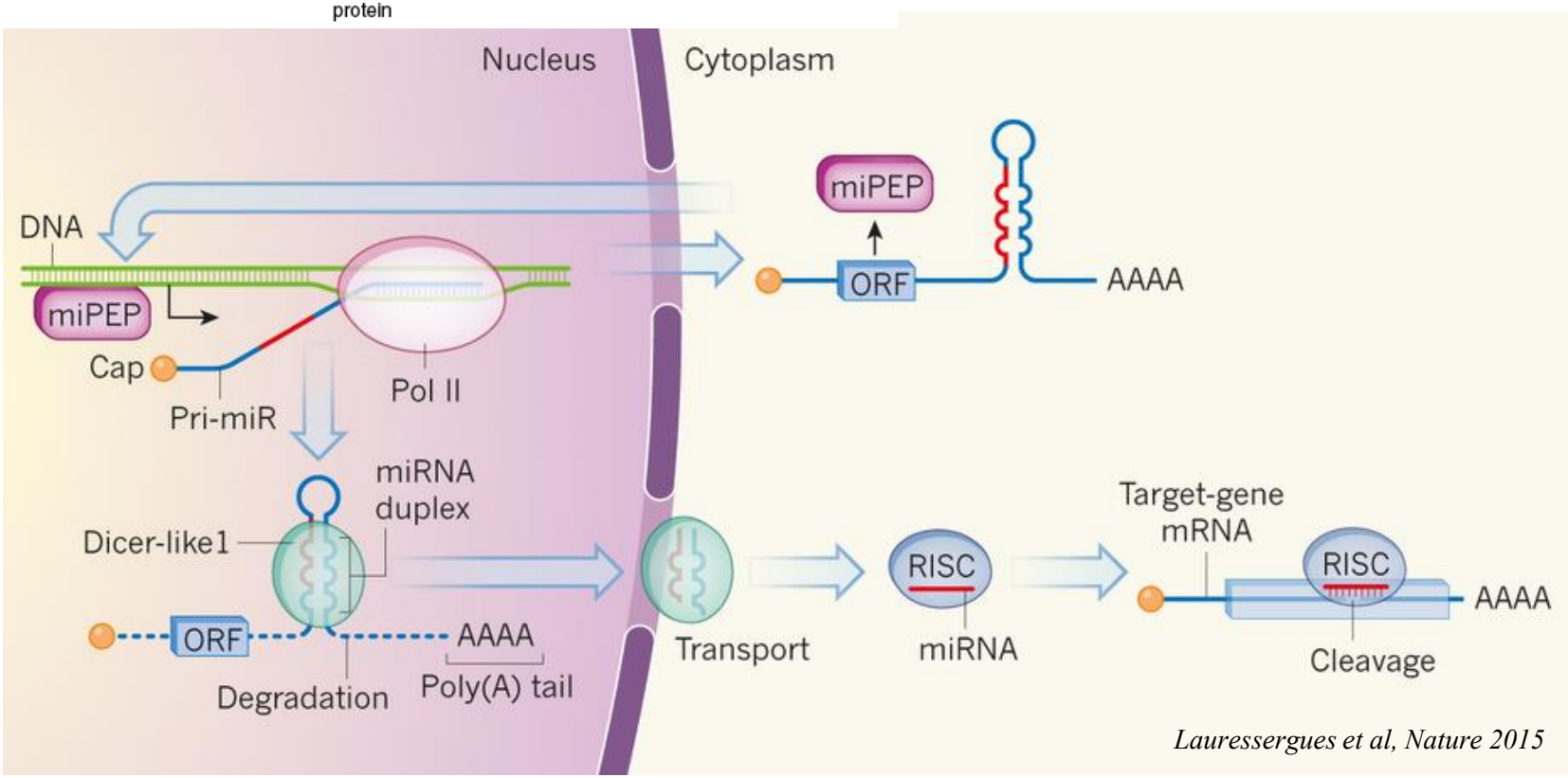
The biogenesis and function of ribosomal RNA-derived fragments.



ncRNAs or sPEP (small peptides)

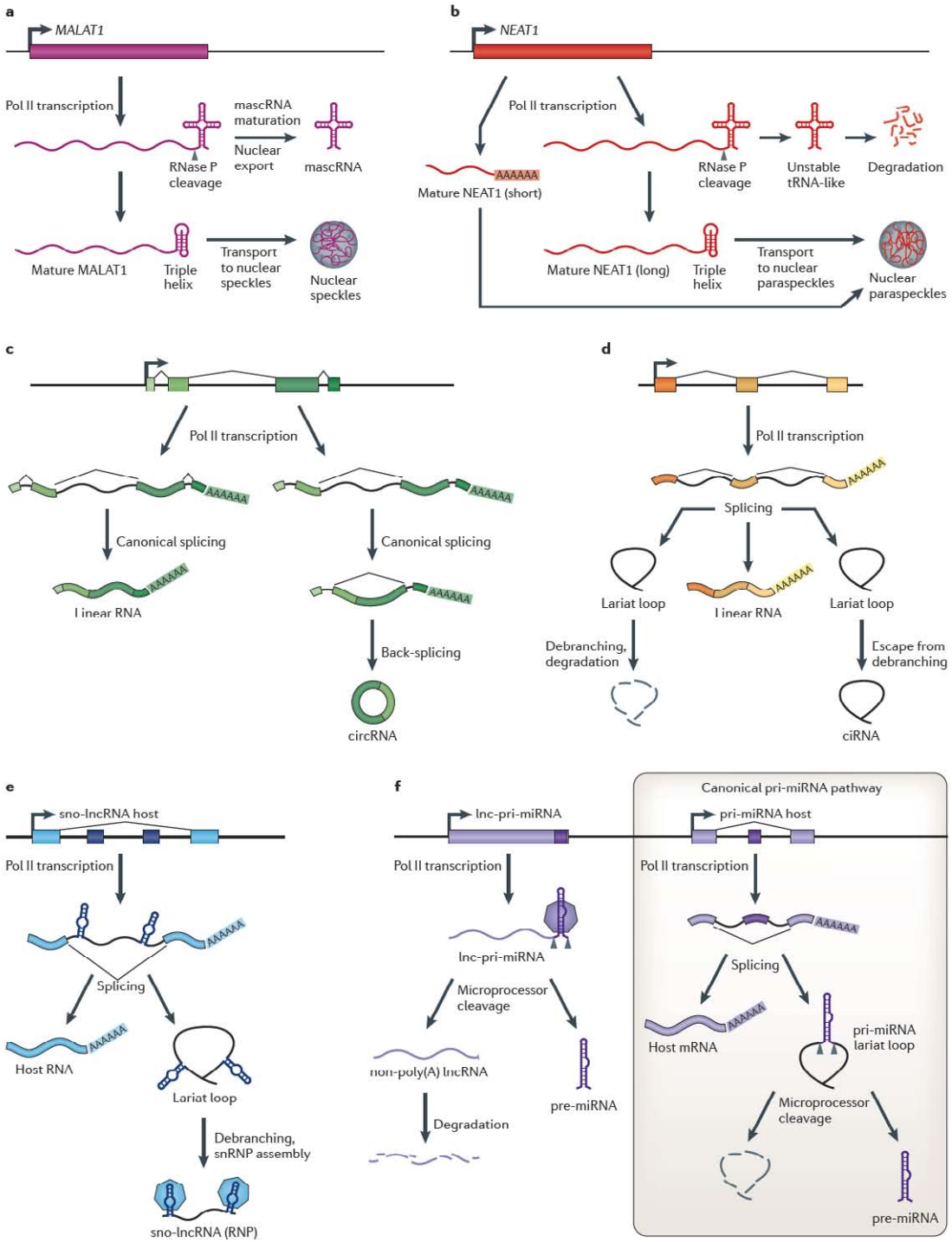


Alternative proteome
- uORFs, AltORFs
- some "ncRNAs" code for sPEP with functional potential



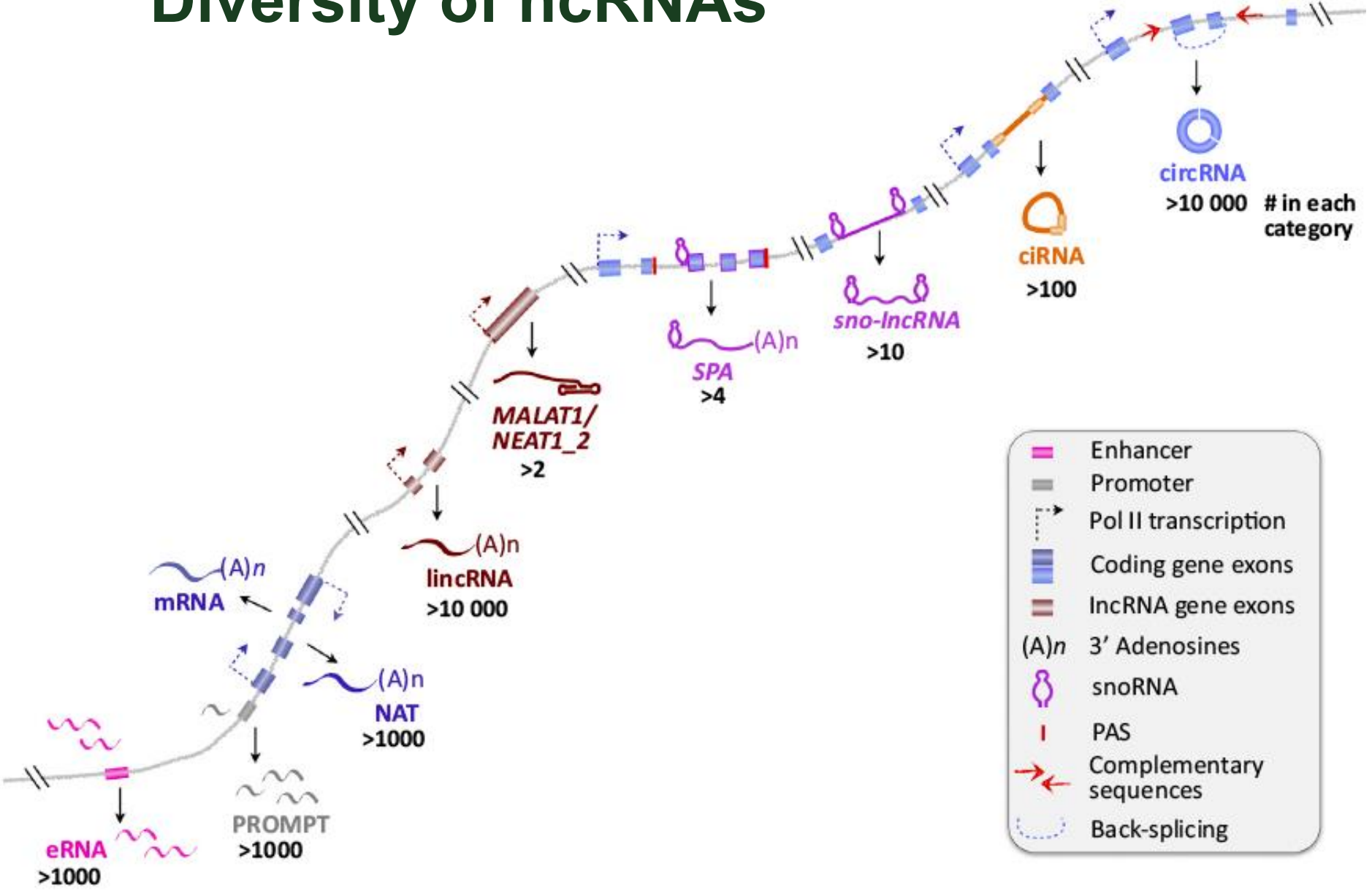
Lauressergues et al, Nature 2015

Unusual ways of ncRNAs



Quinn and Chang, Nat Rev Genet 2015

Diversity of ncRNAs



Wu et al, TiG, 2017

The Role of Non-coding RNAs in Oncology

Frank J. Slack[1,2,3,*] and Arul M. Chinnaiyan[4,5,6,7,8,*]

Cell *179*, November 14, 2019

Table 1. Oncogenic or Tumor-Suppressive Non-coding RNAs with *In Vivo* Experimental Evidence

Name	ncRNA Class	Cancer Types Examined	*In Vivo* Experimental Techniques Used	Cancer-Related Mechanisms and/or Functions of ncRNA	References
Oncogenic ncRNAs					
miR-10b	miRNA	breast, glioblastoma	antimiRs, CRISPR-Cas9 knockdown in mouse xenografts and allografts; transgenic knockout mouse models	targets several transcripts that encode regulators of cell-cycle progression, migration, invasion, and metastasis	Ma et al., 2010; Kim et al., 2016; El Fatimy et al., 2017
miR-21	miRNA	lung, B cell lymphoma	transgenic knockout, overexpression mouse models	targets transcripts that encode negative regulators of RAS signaling, leading to increased proliferation and decreased apoptosis	Hatley et al., 2010; Medina et al., 2010
miR-31	miRNA	lung, breast	overexpression in mouse xenografts; transgenic knockout, overexpression mouse models	targets transcripts that encode regulators of RAS, WNT, and TGF-β signaling to increase proliferation, stem cell renewal, and metastasis	Edmonds et al., 2016; Lv et al., 2017
miR-155	miRNA	lymphoma	transgenic overexpression mouse model, treatment with antimiRs	targets SHIP1 transcript, a negative regulator of AKT, to increase proliferation and survival	O'Connell et al., 2009; Babar et al., 2012; Cheng et al., 2015
miR-221	miRNA	liver	overexpression, treatment with antimiRs in mouse xenografts	targets transcripts of tumor suppressors and cell cycle inhibitors (e.g., p27, PTEN) to increase proliferation and decrease apoptosis	Pineau et al., 2010; Park et al., 2011
LeuCAG3′tsRNA	tsRNA	liver	LNA knockdown in PDX	enhances translation of transcripts encoding ribosomal proteins, leading to increased ribosome biogenesis and proliferation	Kim et al., 2017
ARLNC1	lncRNA	prostate	short hairpin RNA (shRNA) or ASO knockdown in mouse xenografts	interacts with the mRNA encoding AR, a nuclear receptor, to promote oncogenic AR signaling, proliferation, and survival	Zhang et al., 2018
CamK-A	lncRNA	breast	shRNA, small interfering RNA (siRNA) knockdown in mouse xenografts/PDX	interacts with and controls activity of kinases that modulate calcium-induced NF-KB signaling, leading to remodeling of the tumor microenvironment	Sang et al., 2018
CCAT1	lncRNA	colorectal, esophageal	shRNA, siRNA knockdown in mouse xenografts	interacts with transcription factors (e.g., SOX2, p63) to activate expression of genes involved in increasing proliferation and decreasing apoptosis	Kim et al., 2014; Jiang et al., 2018
CTBP1-AS	lncRNA	prostate	siRNA knockdown, overexpression in mouse xenografts	recruits chromatin modifying, splicing factors to promoter of a nuclear receptor corepressor (CTBP) to decrease its expression, leading to increased oncogenic AR activity	Takayama et al., 2013
DSCAM-AS1	lncRNA	breast	shRNA knockdown in mouse xenografts	interacts with proteins of the hnRNP complex involved in RNA processing and mediates proliferation, invasion, and metastasis	Niknafs et al., 2016
EPIC1	lncRNA	breast	shRNA knockdown in mouse xenografts	interacts with MYC transcription factor and increases its activation of target genes, leading to enhanced cell cycle progression	Wang et al., 2018
FAL1	lncRNA	ovarian, breast	shRNA, siRNA knockdown in mouse xenografts	stabilizes components of PRC1 chromatin modifying complex to mediate expression of genes involved in proliferation and survival	Hu et al., 2014
HOTAIR	lncRNA	breast	siRNA knockdown, overexpression in mouse xenografts	recruits PRC2, LSD1/CoREST/REST chromatin modifying complexes, scaffolds transcription factors at target promoters of genes involved in invasion, metastasis, and proliferation	Gupta et al., 2010; Li et al., 2016b
LINK-A	lncRNA	breast	shRNA knockdown in mouse xenografts; transgenic overexpression in mammary gland, LNA knockdown	interacts with kinases that control HIF1α activity, glycolysis; enhances degradation of tumor suppressors (RB, p53) and antigen peptide-loading complexes to promote immune evasion	Lin et al., 2016; Hu et al., 2019
lncARSR	lncRNA	RCC	shRNA knockdown, overexpression in mouse xenografts	interacts with transcriptional coactivator YAP and acts as a ceRNA for miRNAs that target RTK transcripts, leading to enhanced survival and propagation of tumor-initiating cells	Qu et al., 2016a, 2016b
PCAT-1	lncRNA	prostate	overexpression in mouse xenografts	represses expression of BRCA2 tumor suppressor to impact DNA damage repair	Prensner et al., 2014a
PVT 1	lncRNA	colorectal, gastric	CRISPR-Cas9 or shRNA knockdown, overexpression in mouse xenografts	activates oncogenic signaling (MYC, STAT3) and represses expression of tumor suppressors (p15, p16), resulting in increased proliferation, angiogenesis, and decreased apoptosis	Tseng et al., 2014; Kong et al., 2015; Zhao et al., 2018
SAMMSON	lncRNA	melanoma	GapmeR knockdown in PDX	interacts with and controls subcellular localization of proteins that regulate mitochondrial homeostasis and metabolism	Leucci et al., 2016

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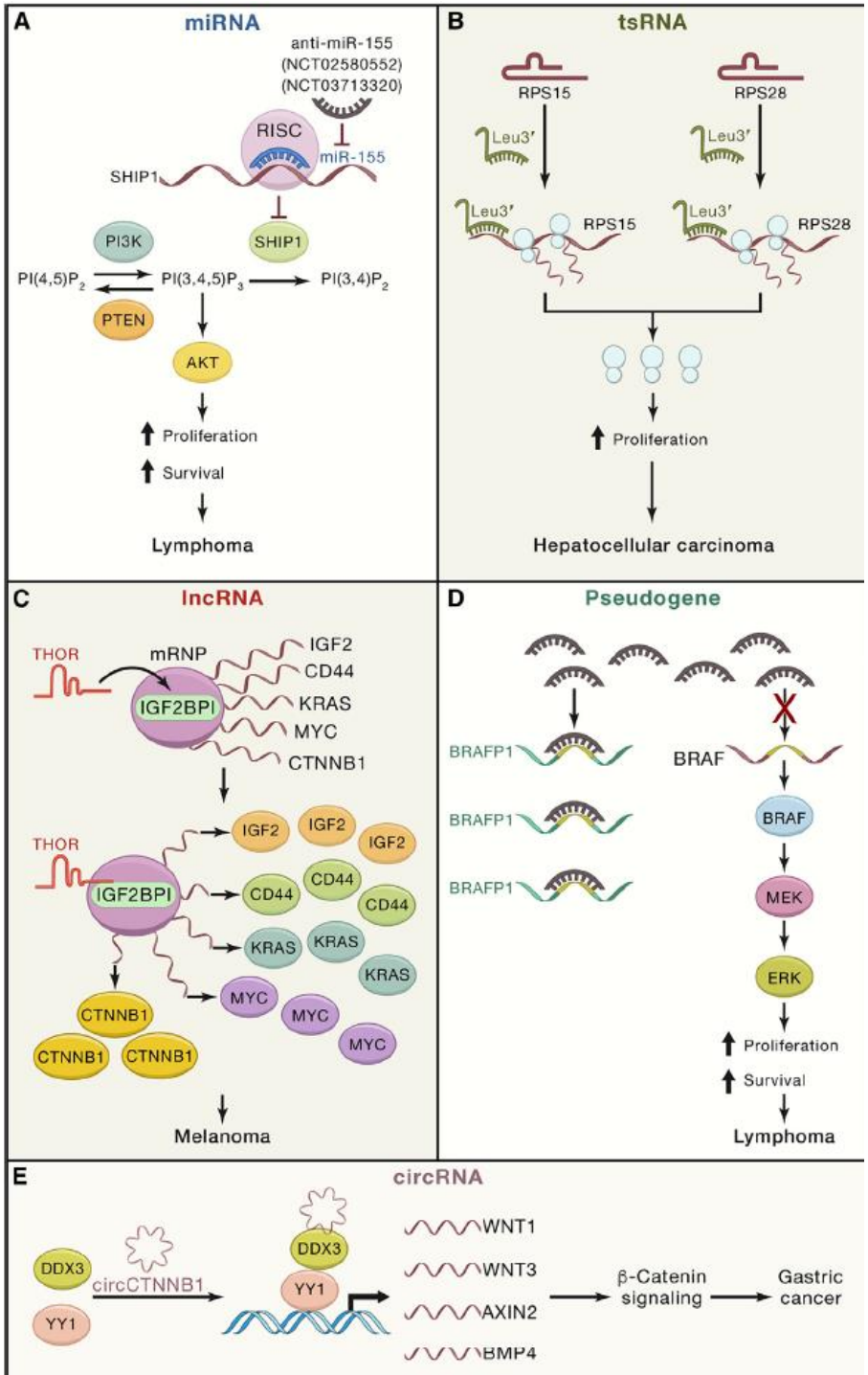
Oncogenic



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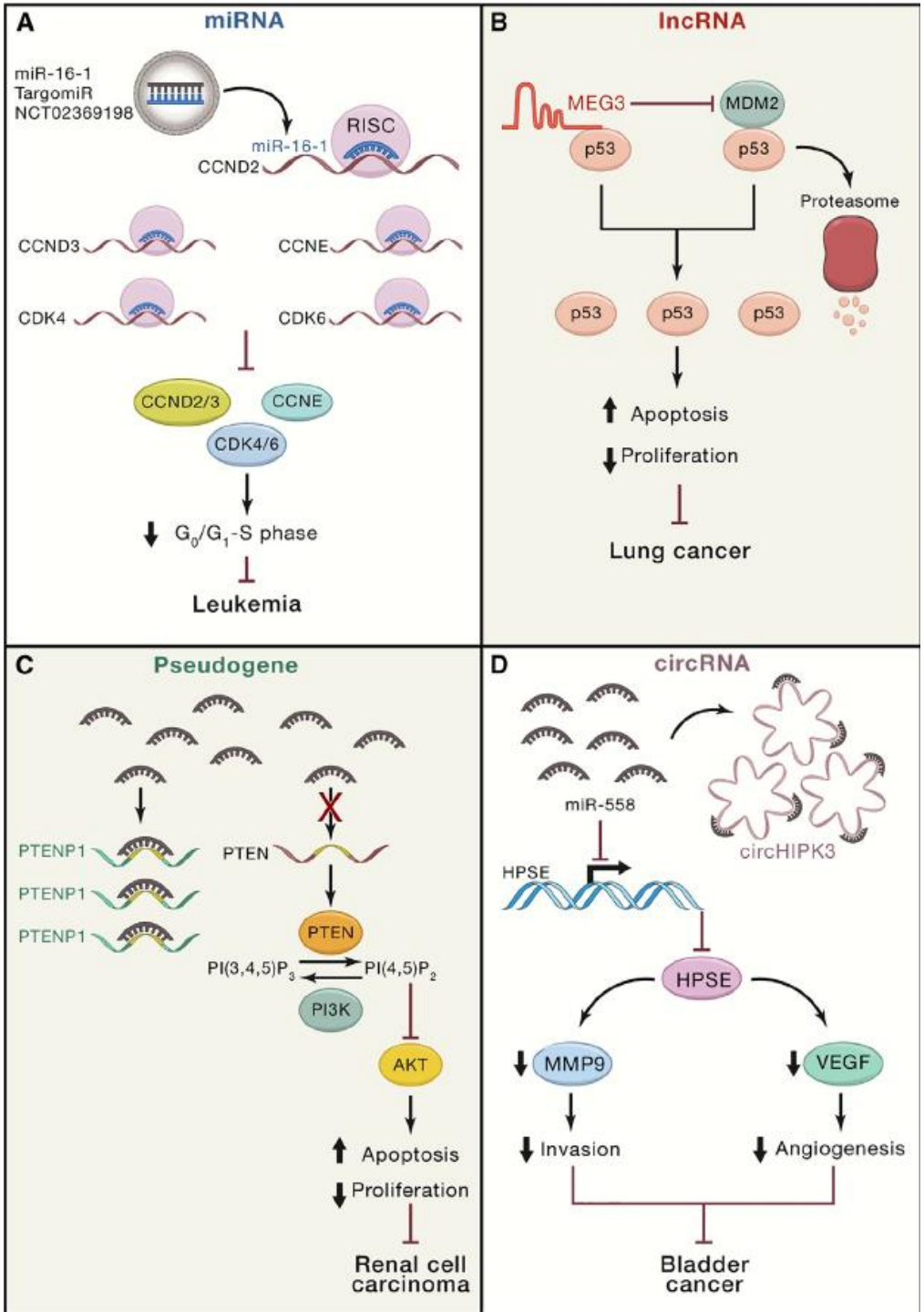
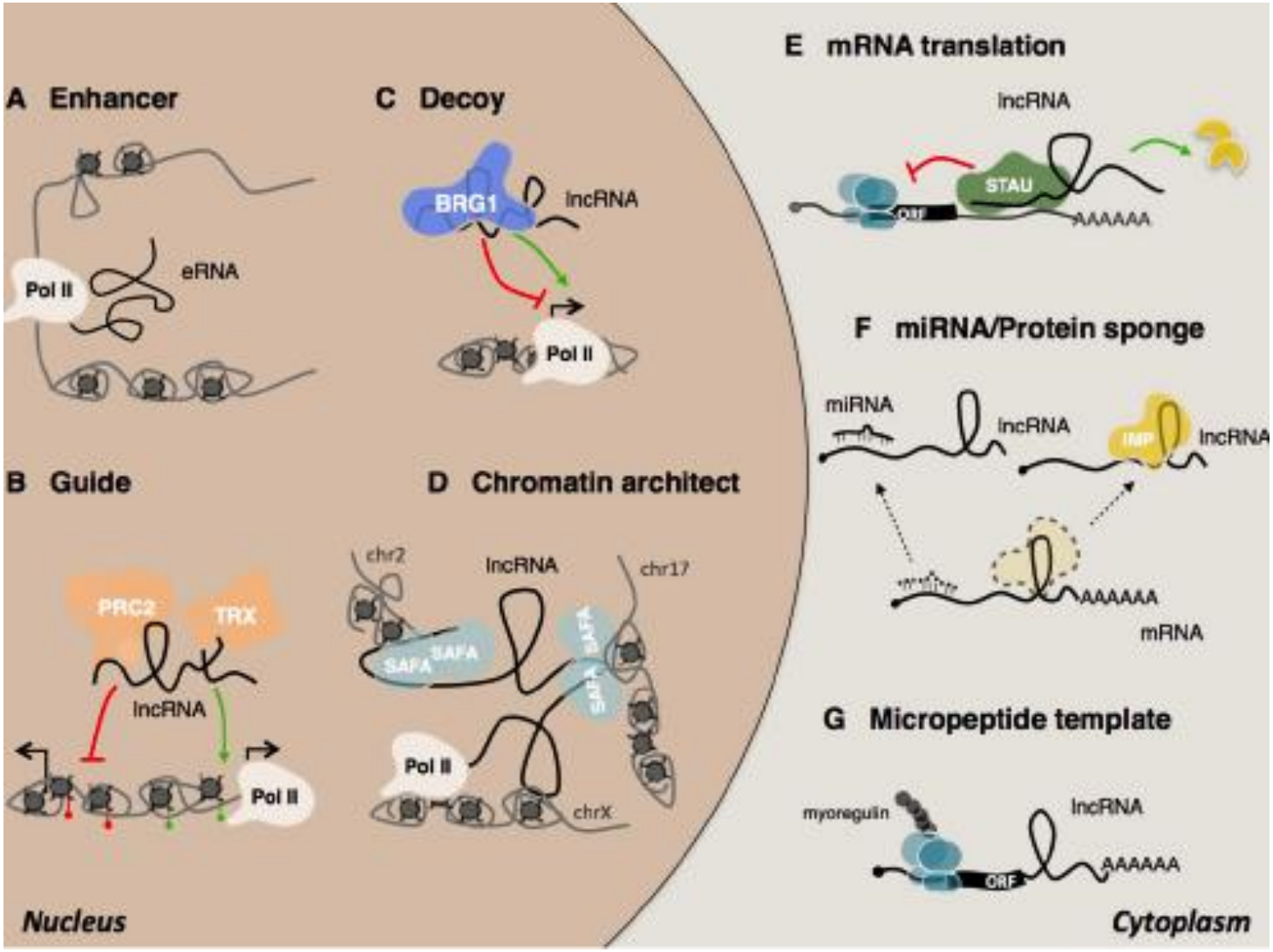


Tumor-suppressive

Diversity of ncRNA functions



TAKE-HOME MESSAGE

- **The majority of eukaryotic genomes are transcribed giving rise to a variety of RNAs**
- **At least some of the "invisible" transcripts in some conditions form functional ncRNAs**
- **These usually act in transcriptional silencing *in-cis* or *in-trans* by recruiting modifying enzymes (DNA, histones) to promoters or interacting with DNA (pRNA)**
- **Defects in ncRNA level or activity correlate with several diseases**