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Supplementary information S1. Summary of key long noncoding RNAs (lncRNAs) discussed in this Review

Name	Function and phenotype	Molecular and cellular function	Structure–function of RNA domains	Major proteins associated with or recruited by the lncRNA	Localization to DNA	Nuclear compartment
Xist	Dosage compensation in eutherians; knockout is embryonic lethal in females	Recruits chromatin regulators and reorganizes nuclear structure to silence gene expression from the Xi*	RNA structural features and functions of some domains are known	hnRNP-U (DNA localization); SHARP, PRC1, PRC2 (chromatin regulation); LBR (chromosomal architecture); many others identified through unbiased proteomics	Localizes broadly across Xi (localization controlled primarily by 3D proximity to the lncRNA genomic locus)	Xi*
TERC	Telomere maintenance; knockout leads to premature aging	Required scaffold for proteins in the telomerase complex; catalyzes and templates the extension of telomeric DNA	3D structure solved for RNA–protein complex; domains extensively characterized through mutagenesis	TERT, DKC1, TEP1, TCAB1, NOP10 (telomerase complex)	Functions at telomeres (localization controlled primarily by affinity interactions with DNA-binding proteins)	Cajal bodies (when not at telomeres)
Kcnq1ot1	Knockout leads to growth deficiencies	Silences imprinted genes in the CDKN1C locus in *cis*; also silences KCNQ1 through transcriptional interference	Some functional RNA domains are known	G9a, Dnmt1, PRC2 (chromatin regulation)	Functions to silence gene expression in *cis*; localization not mapped at high resolution (proximity)	Kcnq1ot1 RNA cloud, which contains the Kcnq1 imprinted domain
Malat1	Mouse knockout normal; knockout affects proliferation of cancer cell lines	Affects localization of some nuclear speckle proteins — unknown how	Some specific protein binding sites are known, although functions remain unclear	SR proteins, U1 snRNP (RNA processing); many others identified through unbiased	Localizes to chromatin at many sites throughout the nucleus	nuclear speckles

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		this connects to cellular or organismal function		proteomics	and genome (affinity)	
Neat1	Mouse knockout has defects in mammary and ovarian development	Required for the formation of paraspeckles; unknown how this connects to cellular or organismal function	Unknown	PSF, PSP1, PSP2, P54, NONO (RNA processing); many others identified through unbiased proteomics	Localizes to chromatin at many sites throughout nucleus and genome (affinity)	paraspeckles
Firre	Required for murine adipogenesis *in vitro*	Formation of interchromosomal contacts; unknown how this connects to cellular or organismal function	Repeated RNA domains are known to mediate nuclear localization	SAF-A (DNA localization); many others identified through unbiased proteomics	Localizes to the X chromosome and specific sites on other chromosome s (proximity and affinity)	Firre RNA compartment, which includes sites on other chromosomes
roX	Dosage compensation in *Drosophila* spp.; knockout is lethal in males	Activates gene expression on the single X chromosome in males by recruiting the male-specific lethal (MSL) complex	Domains have been extensively characterized through RNA structure mapping and mutagenesis	MSL1, MSL2, MSL3, MOF, MLE (MSL complex); CLAMP (DNA localization)	Localizes to specific CLAMP motifs on the X chromosome (affinity)	X chromosome
HOTTIP	Mouse knockout has muscle and skeletal defects	Activates HoxA genes in *cis*	Unknown	WDR5 (chromatin regulation)	Regulates genes close to its genomic locus (proximity)	None; very low expression

* Xi, inactive X chromosome