

organism	RNA signal:	Effector:	chromatin/DNA modification:	Outcome:
<i>A. thaliana</i>	sRNA →	Ago/Piwi	histone H3K9me DNA 5mC	TGS
<i>S. pombe</i>	sRNA →	Ago/Piwi	histone H3K9me	TGS, CTGS
<i>C. elegans</i>	sRNA →	Ago/Piwi	histone H3K9me	TGS, CTGS
<i>Drosophila</i> (germline)	sRNA →	Ago/Piwi	histone H3K9me	TGS
<i>M. musculus</i> (germline)	sRNA →	Ago/Piwi	histone H3K9me DNA 5mC	TGS
<i>T. thermophila</i>	sRNA →	Ago/Piwi	histone H3K9me	DNA elimination
<i>S. pombe, M. musculus</i>	lncRNA mRNA →	RBD	histone H3K9me	TGS, CTGS

**Supplementary information S1 (figure). Conservation and divergence of RNA silencing pathways.** RNA silencing mechanisms are usually composed of an RNA signal (sRNA or sequence within lncRNA) that recruits an effector protein. For sRNAs, the effector is a member of the conserved Argonaute/Piwi (Ago/Piwi) family of proteins, whereas for lncRNAs it is an RNA-binding protein (RBD). The effector then recruits enzymes that either methylate histone H3 on lysine 9 (H3K9) or cytosine in DNA (5mC) resulting in transcriptional gene silencing (TGS) and in some cases also co-transcriptional gene silencing (CTGS), involving degradation of targeted nascent transcripts. In *S. pombe* and *A. thaliana*, sRNA amplification and the downstream histone or DNA methylation events are interdependent and form self-reinforcing positive feedback loops (denoted by forward and reverse arrows).