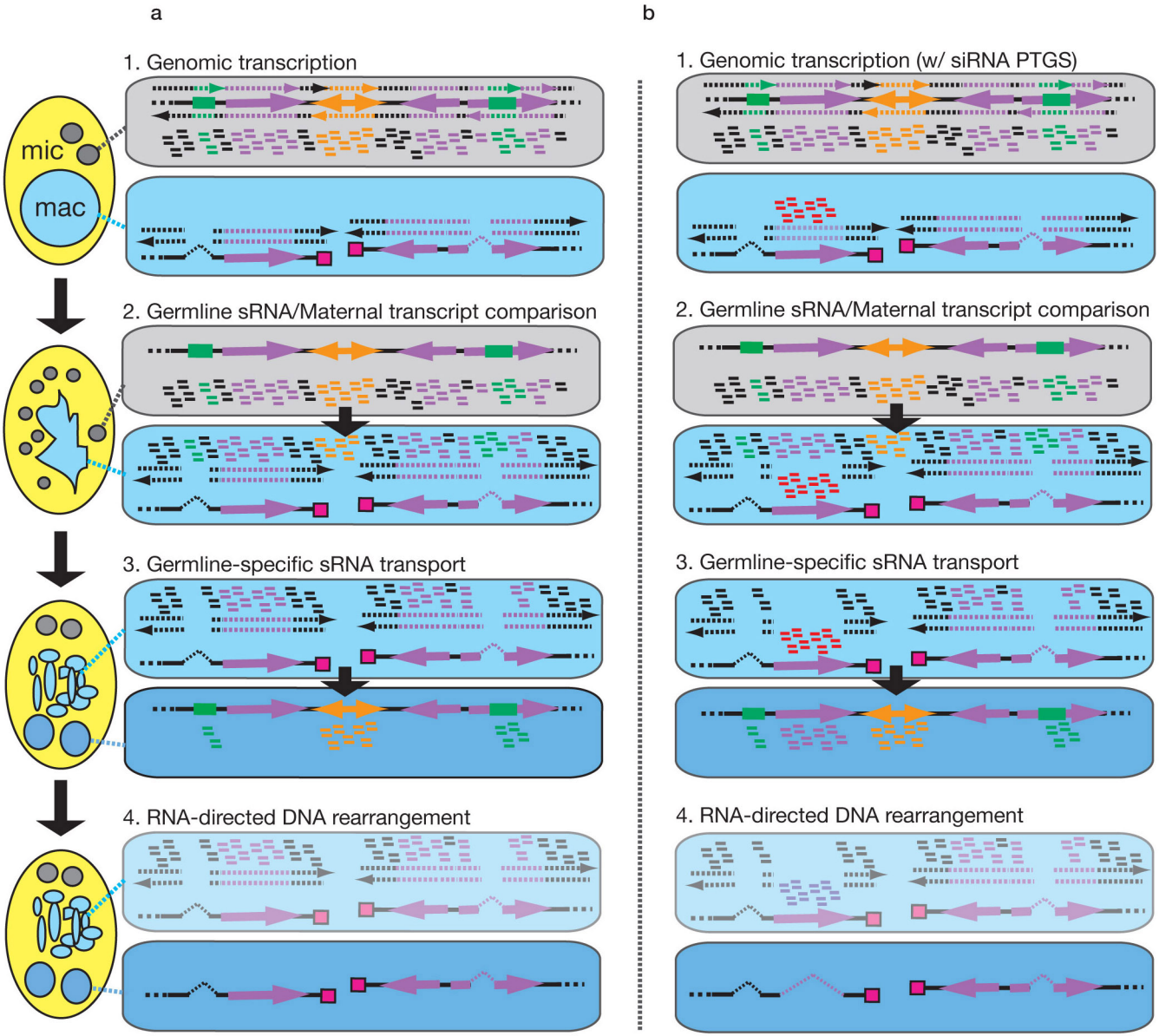

Figure 10. The Transcriptome Scanning Model for the Comparison of Germ-line and Somatic Genomes

(*a*) Default regulation. (*1*) Upon initiating meiosis, most or all of the macronuclear and micronuclear genomes is transcribed; the dashed lines in the macronucleus represent uncharacterized transcripts. In the micronucleus, transcription is bidirectional, resulting in the production of scnRNAs (short double-stranded molecules) for all types of sequences (cellular genes, *light purple arrows*; transposons, *orange double arrow*; IES, *green boxes*). (*2*) The scnRNAs are exported to the maternal macronucleus, where they may pair with homologous somatic transcripts. Pairing may also occur in the cytoplasm. (*3*) scnRNAs that pair with homologous transcripts are sequestered or destroyed, while the micronucleus-specific ones are re-exported to the developing zygotic macronucleus, where they pair with homologous sequences (DNA or nascent transcripts), thus targeting H3K9 methylation to micronuclear-specific sequences (transposons and IESs). (*4*) The marked sequences are eliminated. (*b*) Effects of posttranscriptional silencing of a gene in the maternal macronucleus. Experimental induction of posttranscriptional silencing by high-copy transgenes or dsRNA results in the production of double-stranded siRNAs homologous to that gene (in *red*). These siRNAs degrade the homologous maternal somatic transcripts, so that homologous scnRNAs will not be inactivated and will be free to target the deletion of the gene in the developing zygotic macronucleus.