



**Figure 8.** Packaging of active genes in chromosome 4, pericentric heterochromatin, and euchromatin. The plots show  $\log_2$  enrichment ( $y$ -axis) for RNA Pol II (green), H3K36me3 (pink), H3K9me2 (yellow), H3K9me3 (purple), SU(VAR)3-9 (blue), POF (brown), and HP1a (red) for a scaled metagene and 2 kb flanking region created by averaging data for all active genes in a given compartment. Fourth chromosome (*top*) and pericentric (*middle*) genes show a similar depletion in silencing marks at the TSS; these marks reappear over the body of the gene only in the case of the fourth chromosome. As expected, euchromatic genes do not show association with any of the silencing marks (*bottom*). (Adapted from Riddle et al. 2012.)