



Figure 7. Chromatin annotation of the *D. melanogaster* genome. (A) A nine-state model of prevalent chromatin states was generated using data from S2 cells. Each chromatin state (row) is defined by a combinatorial pattern of enrichment (red) or depletion (blue) for specific histone modification marks. First (left) panel, color code for mapping; second panel, histone modification marks used (active marks labeled in green, repressive in blue, general in black); third panel, enrichment or depletion of chromosomal proteins found in that state; fourth (right) panel, fold over-/underrepresentation of genic and transcription start site (TSS)-proximal (± 1 kb) regions relative to the entire tiled genome. (B) A genome-wide karyotype view of the domains defined by the nine-state model in S2 cells. Centromeres are shown as open circles; dashed lines span gaps in the genome assembly. Note the association of pericentric heterochromatin and the fourth chromosome distal arm with state 7 and the association of state 5 with the male X chromosome. (Adapted, by permission from Macmillan Publishers Ltd: NATURE, from Kharchenko et al. 2011, © 2011.)