



Figure 3. Epigenetic alterations involving DNA methylation can lead to cancer by various mechanisms. Loss of DNA cytosine methylation (white hexagons) illustrated in the hypo column results in genome instability. Focal hypermethylation (pink hexagons) at gene promoters shown in the hyper column causes heritable silencing and, therefore, inactivation of tumor suppressors and other genes. Additionally, methylated CpG sites (pink hexagons) are prone to mutation: They are hot spots for C to T transition mutations caused by spontaneous hydrolytic deamination; or methylation of CpG sites can increase the binding of some chemical carcinogens to DNA; and it increases the rate of UV-induced mutations.