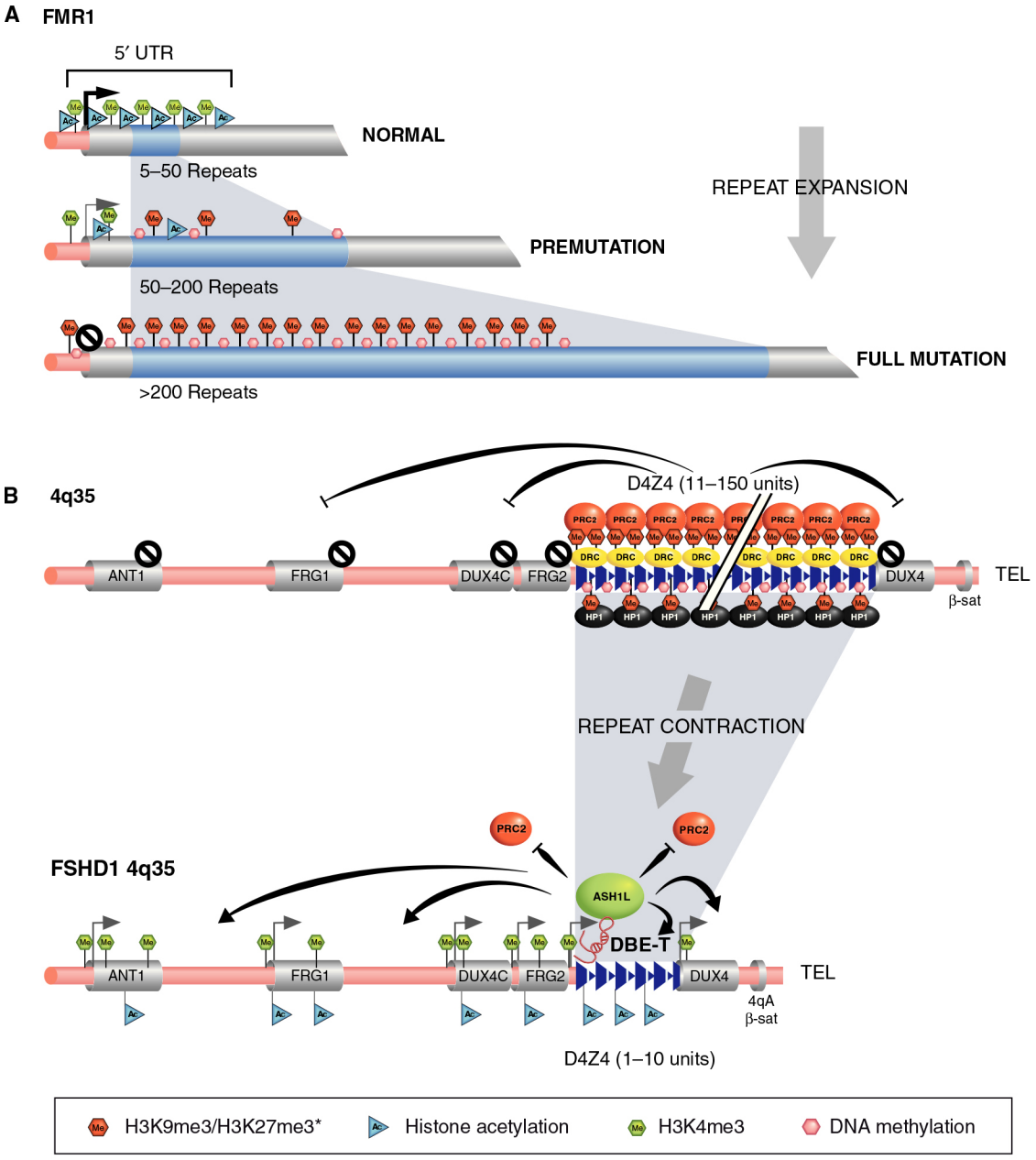

Figure 8. Human diseases showing genetic alterations in regions with triplet repeats, in the form of repeat expansion or contraction, with consequential in *cis* chromatin structural changes. (*A*) The 5′ region of the FMR1 gene is shown with the CGG triplet repeat (blue shading) in normal and fragile-X-affected individuals. The chromatin-associated features of the 5′ FMR1 region are indicated in each case. The normal repeat number range (5–50) typically shows active chromatin features, whereas fully expanded repeat alleles (more than 200) have heterochromatic features. (*B*) The 4q35 region associated with normal and facioscapulohumeral dystrophy individuals (FSHD1) is depicted. In the normal repeat number range (11–150 units), heterochromatinization is presumed to initiate from the D4Z4 repeats (blue triangles) and spread throughout the 4q35 region (chromatin marks not shown throughout), silencing all genes. The 4q35 region in FSHD1 individuals has a contracted number of D4Z4 repeats, which is permissive to transcription of the DBE-T lncRNA (indicated in red), recruiting ASH1L and associated factors to remodel, generating euchromatin and allowing gene expression from 4q35 genes with myopathic potential. PRC2, Polycomb repressive complex 2; DRC, D4Z4-repressing complex; HP1, heterochromatin protein 1; ASH1L, absent small and homeotic disks protein 1; DBE-T, D4Z4-binding element transcript.