BASAL TRANSCRIPTIONAL MACHINERY MommeD9 & 31: Trim28 **Active** locus CHROMATIN-REMODELING COMPLEXES—opening HISTONE DEACETYLATION MommeD10 & 16: Baz1b part of chromatin-remodeling complexes MommeD5: HDAC1 MommeD4, 35 & 37: Smarca5 SWI/SNF chromatin remodeler Naïve locus **DNA METHYLATION** HISTONE METHYLATION MommeD2 & 32: Dnmt1 maintenance DNA methyltransferase MommeD13 & 17: Setdb1 H3K9 methyltransferases Momme D14: Dnmt3b de novo DNA methyltransferase MommeD33: Suv39h1 MommeD1, 23, & 36: Smchd1 may direct DNA methylation? CHROMATIN REMODELLING COMPLEXES—closing MommeD19: Smarcc1 SWI/SNF chromatin remodeler MommeD27: Pbrm1 DNA binding unit of SWI/SNF TRANSCRIPTION FACTOR MommeD11: Klf Inactive histone methylation A Histone acetylation **Inactive** locus Methylated CpG residue

Figure 2. Summary of the point of action of *MommeD* mutants. An active, naïve, and inactive chromatin template are shown, and all of the *MommeD*s in Table 2 are indicated; red indicates that they are suppressor mutations and so the wild-type protein represses expression, whereas green indicates that they are enhancer mutations and so the wild-type protein activates expression.

Epigenetics, Second Edition © 2015 Cold Spring Harbor Laboratory Press