C) *IBM* (*increase in BONSAI methylation 1*): a mechanism to remove silent mark from transcribed sequences.

BONSAI locus is not methylated in wild type Arabidopsis, but it is hyper-methylated in mutants with genome-wide hypomethylation[1]. To understand this enigmatic phenomenon, we screened mutants with increased DNA methylation at the *BONSAI* locus[2, 3].

One of the trans-acting locus identified, *IBM1* (*increase in BONSAI methylation 1*) encodes a histone demethylase[2]. Methylation of histone H3 lysine 9 (H3K9me) is normally found in transposons and not in genes. In the *ibm1* mutant, H3K9me accumulates in active genes. The ectopic H3K9me accumulates progressively over generations. In addition, *ibm1* mutant shows developmental abnormalities, which also become more and more severe over generations (Fig 1).

Epigenome analyses revealed that IBM1 removes H3K9me2 from thousands of transcribed genes[4-6] (Fig 2). This activity ensures robust expression of active genes.

Through screening mutants suppressing the *ibm1*-induced developmental defects, we identified H3K4me1 in gene body as a downstream factor for the silencing by body H3K9me[7]. (Detail in D)。

WT *ibm1* WT *ibm1*

Fig 1 Developmental defects induced by *ibm1*. The *ibm1* mutation induces phenotypes such as leaf deformation (left), reduced fertility (center), and dwarf (right). The phenotypes become progressively severe over generations.

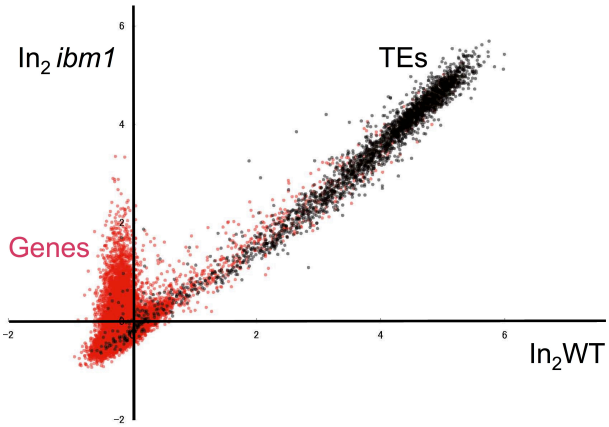

Fig 2　Accumulation of H3K9me2 in genes in *ibm1* mutant.

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