

Figure S1. Evolutionary analysis of *HMT* (SDG, PRMT) and *HDM* (JMJ, HDMA) in representative species of the major lineage of green plants. *HMT*: Histone methyltransferases, *SDG*: SET domain group, *PRMT*: protein arginine methyltransferases, *HDM*: Histone demethylases, *HDMA*: SWIRM and C-terminal domain, *JMJ*: JmjC domain-containing proteins.

PRMT

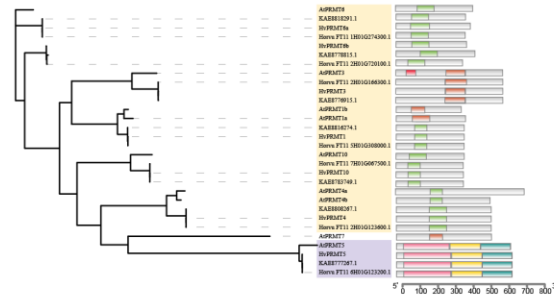
Tree scale: 1

Colored ranges

I

II

PrrA
PRMT5
PRMT5_TIM
PRMT5_C
zf-C2H2_2
Methyltransf_25



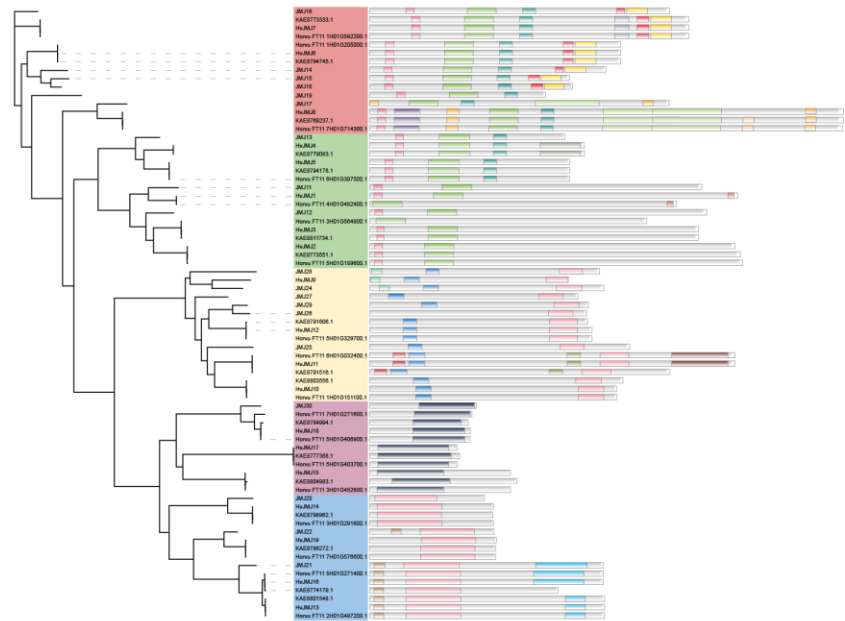
JMJ

Tree scale: 1

Colored ranges

KDM5
KDM3
JMJD6
JmjC-only
KDM4

JmjC
FYRC
JmjN
zf-C5HC2
FYRN
Plasmodium_HRP
PLI-1
PHD
ARID
zf-RING_2
SPICE
zf-H2C2_2
WRC
cupin_RmlC-like
zf-4CXXC_R1
SRBM_C
DUF5401
Bactofilin
Cupin_5
F-box-like
APH



HDMA

Tree scale: 1

Colored ranges

LDL2-like
LDL3-like
FLD-like
LDL1-like

Amino_oxidase
SWIRM

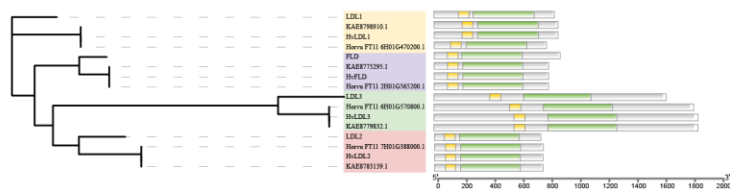
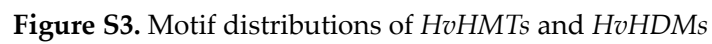
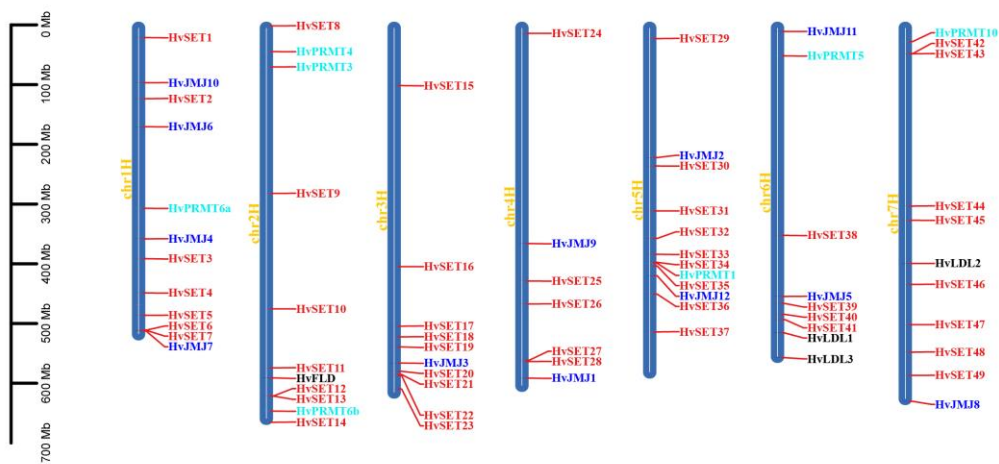


Figure S2. Phylogenetic and Conserved Domain Analysis of *PRMT*, *JMJ* and *HDMA*

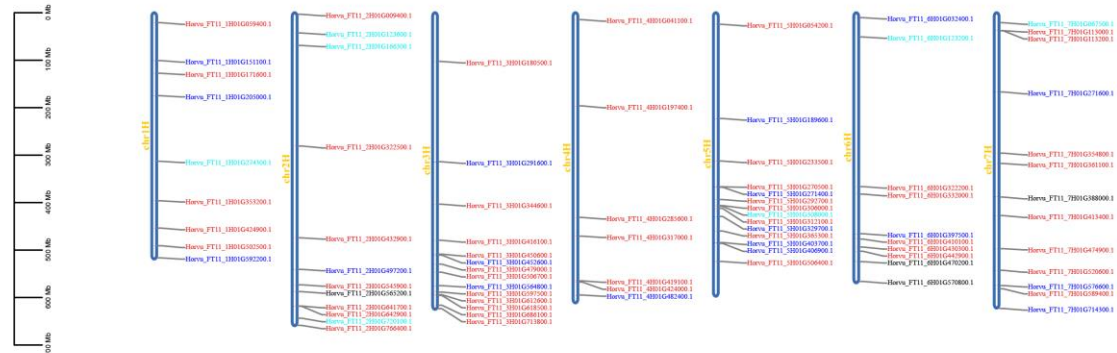
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Morex



B1K-04-12



OUN333

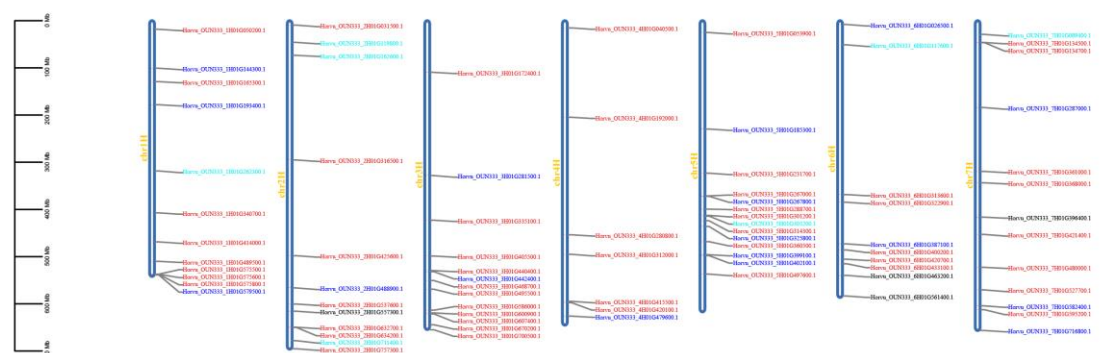


Figure S4. Chromosomal location analysis of *HMT* (*SDG*, *PRMT*) and *HDM* (*JMJ*, *HDMA*) families in different germplasms of barley. The red font is the *SDG* subfamily gene, the turquoise font is the *PRMT* subfamily gene, the blue font is the *JMJ* subfamily gene, and the black font is the *HDMA* subfamily gene