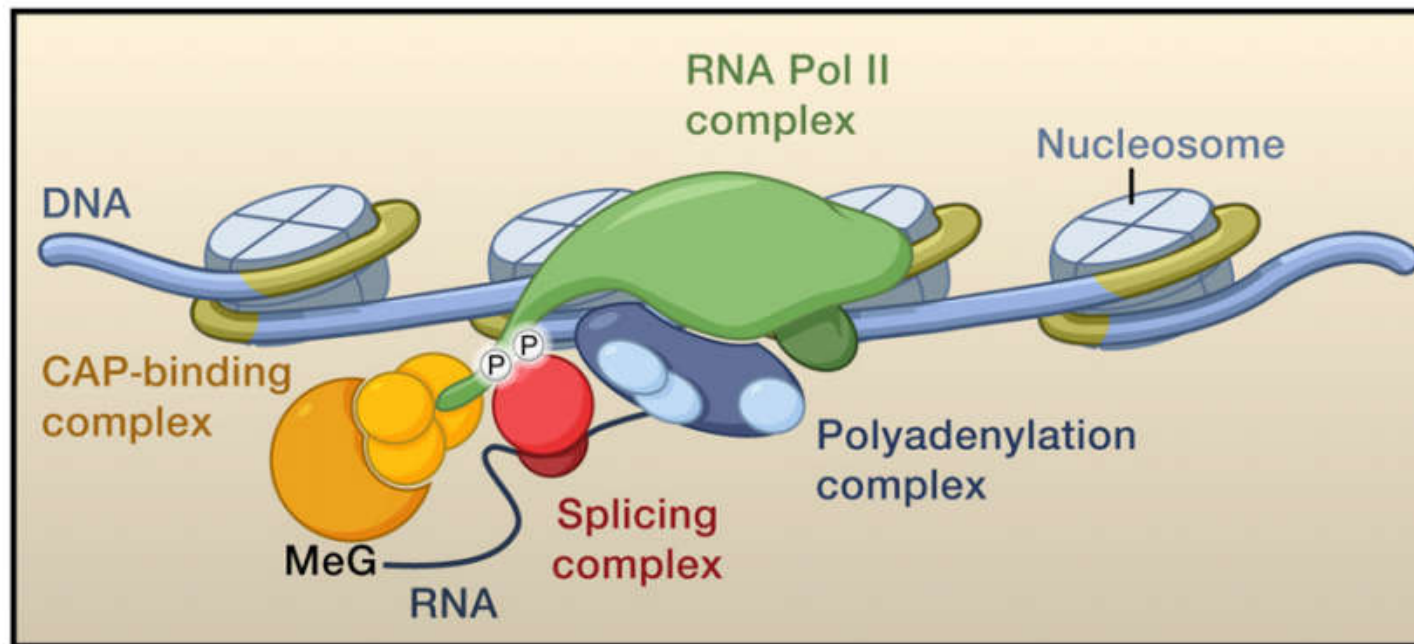


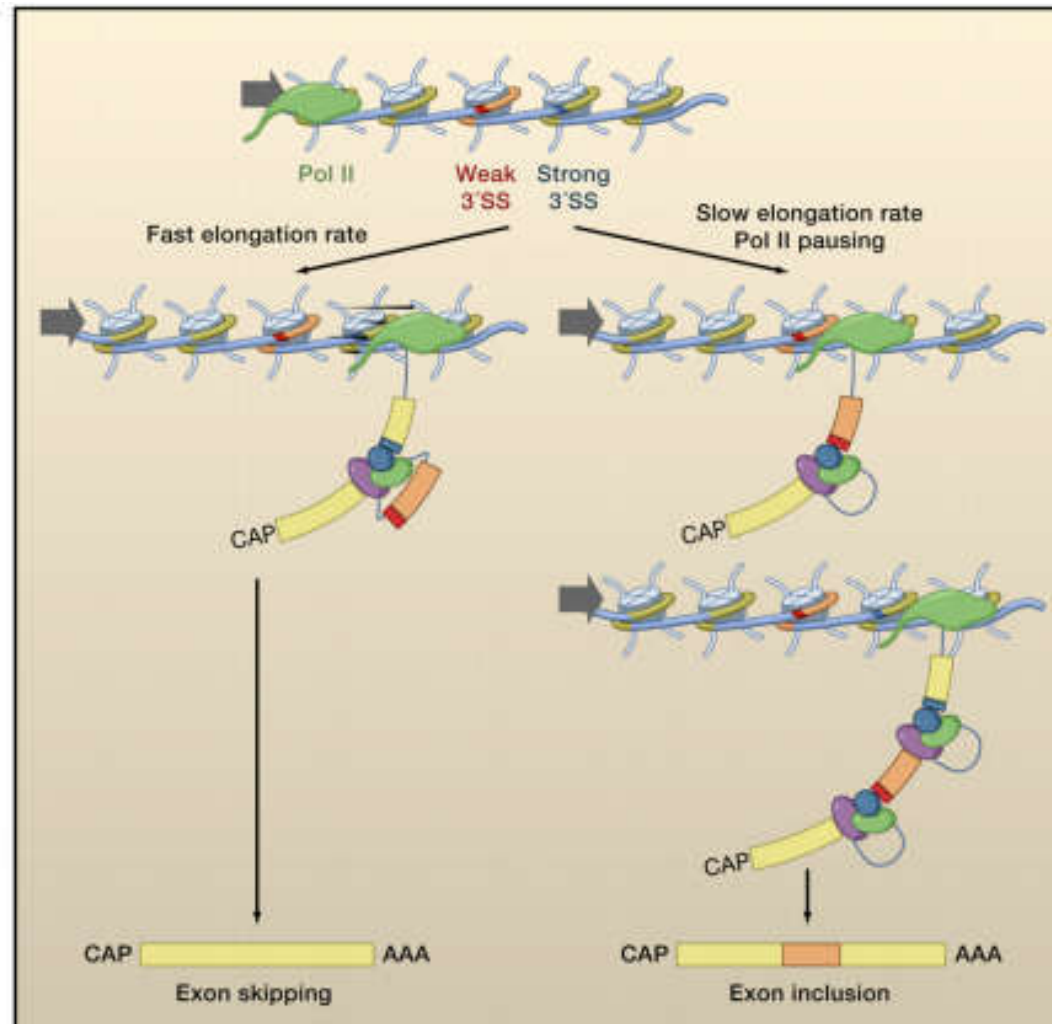
Epigenetic regulation of alternative splicing

- Coupling of Transcription and RNA Processing



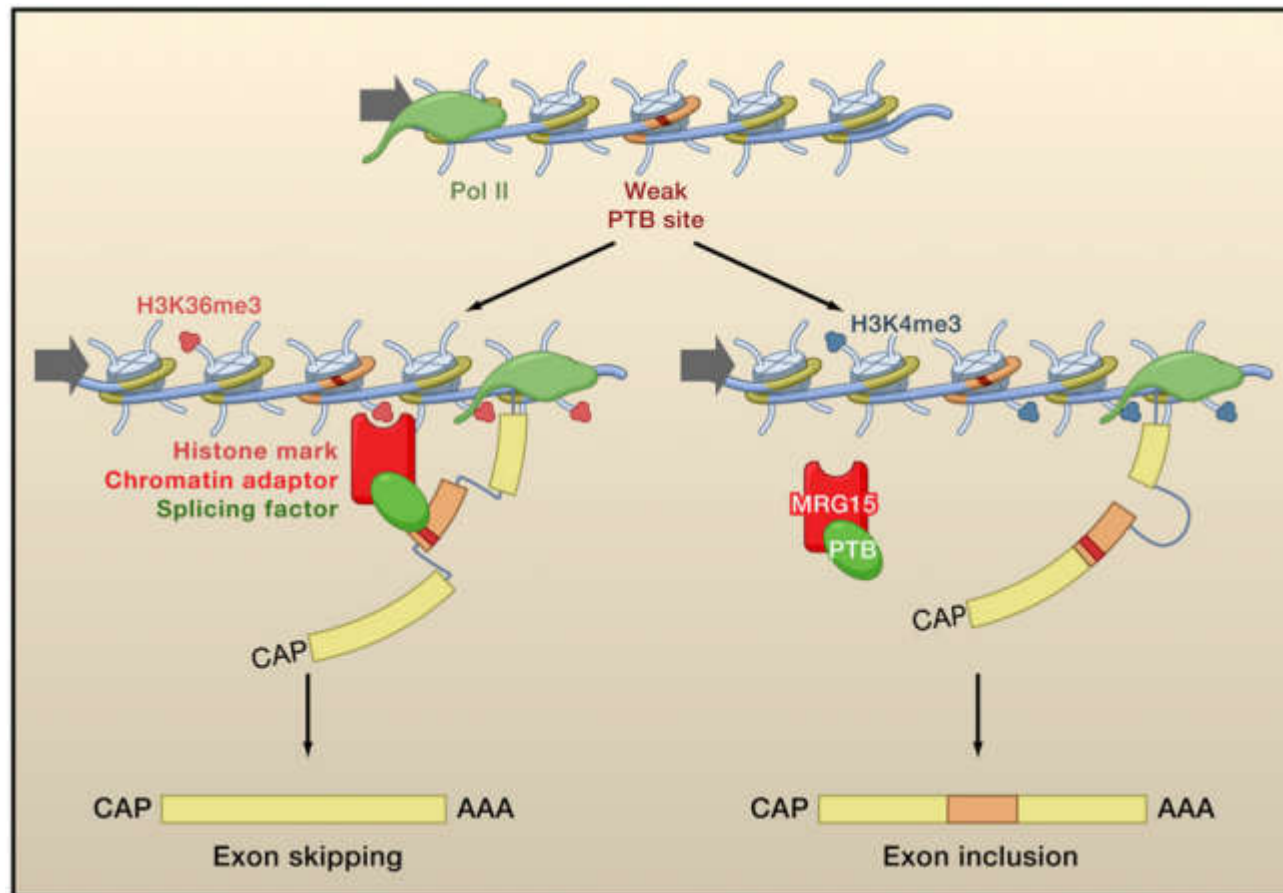
(Reini F. Luco et al., 2010, Cell)

- RNA Pol II elongation rate control alternative splicing model



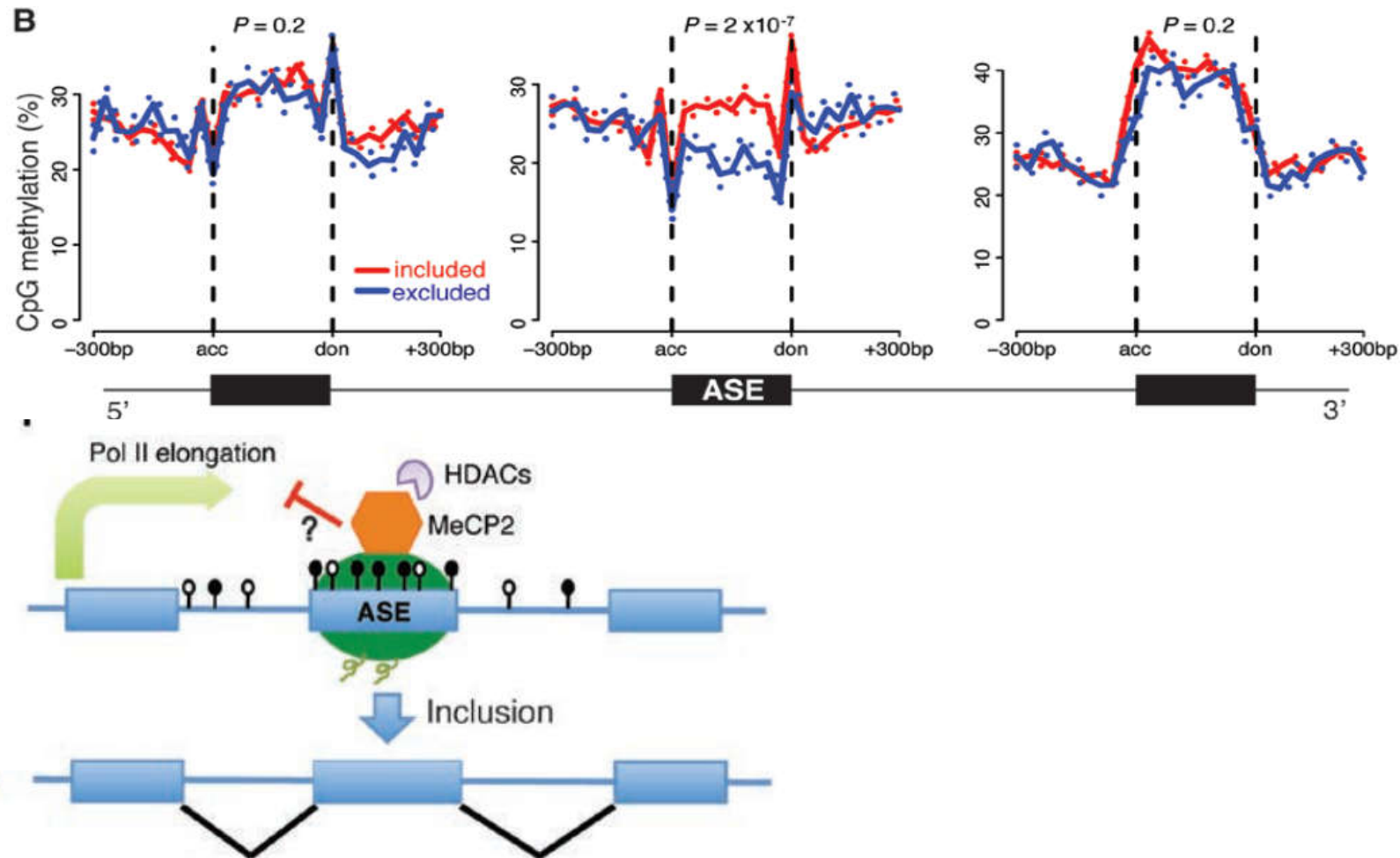
(Reini F. Luco et al., 2010, Cell)

- The Chromatin-adaptor model of alternative splicing



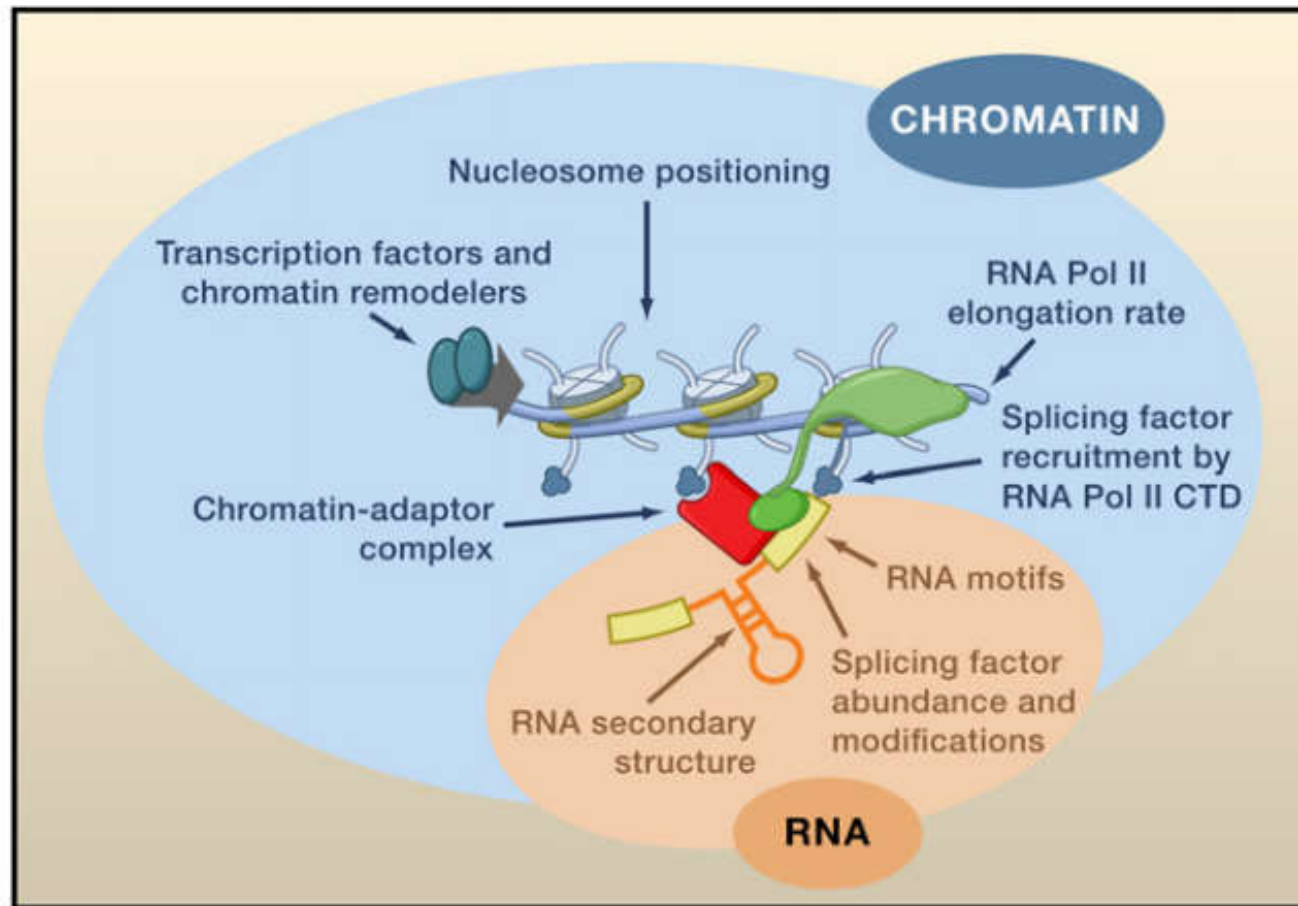
(Reini F. Luco et al., Cell)

- DNA methylation shapes the exon and intron boundaries and regulates AS by methyl-CpG-binding protein.



(Alika K et al., 2013, Cell research)

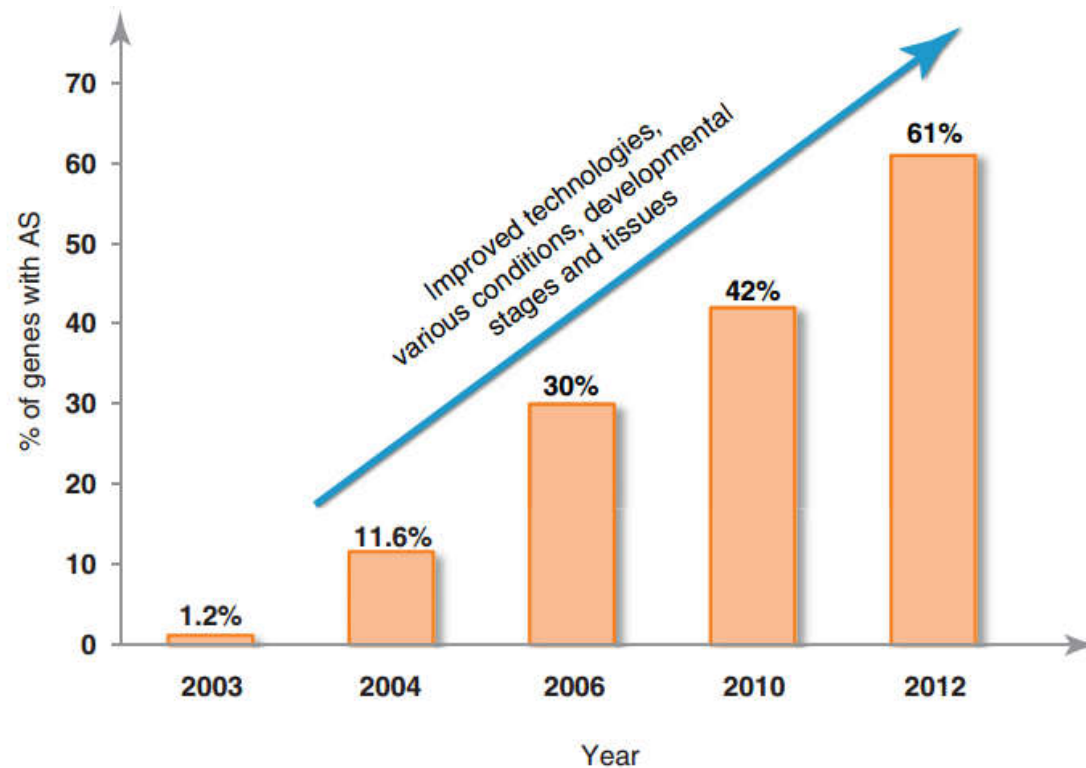
- An Integrated Model for the Regulation of Alternative Splicing



(Reini F. Luco et al., Cell)

Alternative splicing in plants is totally underestimated

- Increasing frequency of occurrence of alternative splicing (AS) in Arabidopsis with time.



(Naeem H et al., 2012, Cell)

- Most of the components in Chromatin-adaptor model are conserved between Arabidopsis and animals

Chromatin-Adaptor Complex	Conservation
H3K36me3/MRG15/PTB(Luco et al., 2010)	Both Conserved
H3acetyl/Gcn5/U2 snRNP(Li, 2009)	Both Conserved
H3K4me3/CHD1/U2 snRNP(Sims et al., 2007)	CHD1 not find
H3K9me3/HP1a/hnRNPs(Piacentini et al., 2009)	Both Conserved

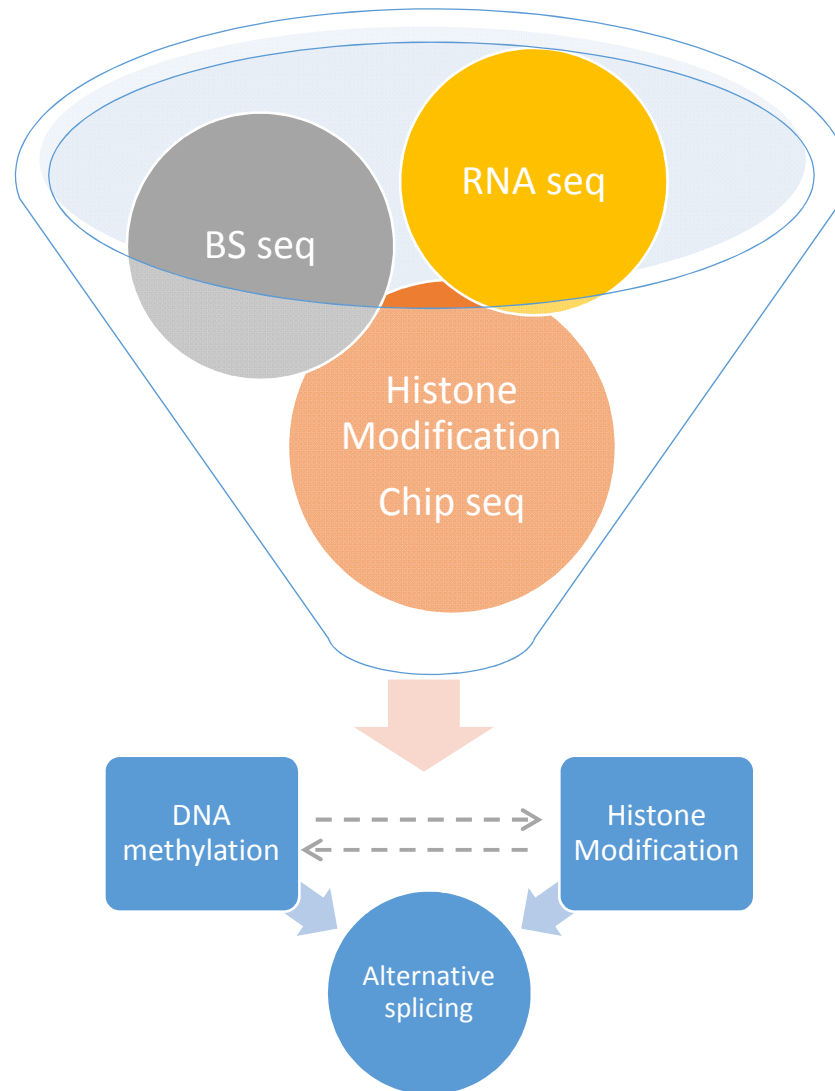
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AtMBD5 :31 DD---NHLPPDNRTEIRVRTSGTKAGTVDFYIE--PITGRKFRSKNEVLY-YLEHGTPKKSVKTAENGDSHS--- 98
AtMBD6 :80 D----NHLPPGHRVEDKIRTSAGTASVDKYIE--PNTGRKFRSRTVLY-YLEHGTSKRGTKKAENTY-FNPD--- 143
AtMBD1 :107 DKPLPRTPRGFKRSLILRKD---YSKMDAYYIT--P-TGKKLRSRNEIAAFI-DANQDYKY-ALLGDENFTVP--- 173
AtMBD4 :86 DKPLPKTPKGFKRSLILRKD---YSKMDTYFT--P-TGKKLRSRNEIAAFV-EANPEFRN--APLGDENFTVPK- 152
AtMBD3 :97 DEHSIPKTPQGLKRVLVRTN---CVKVDVYVESLAP-RRKRFKSIKEVATFI-EDKEEFKQ-MTLEEVSFAAPK- 165
AtMBD2 :50 DKPNISRPPAGQRLLRIRGEGG-TRFADVYVA--P-SGKKLRSTVEQK-YLNDNSEYIGGVKLSQSFQI--- 118
AtMBD7A:109 YASKGFRLPQGISVEEVPRKN---SHYIDXYVER---KGRFRSLVSVER-YLRESRNSIEQQLRVLQNRGH--- 176
AtMBD8A:123 LRSLFNVDSNQSKEEEDGEELEDNEGQIHNSYV-YORPNLDSTQNVLIQGTSGNKI-KRKRGRPRKKIRNPSE- 196
MeCP2 :96 DD---PILPEGNTKRLKOKSGRSAGKYDV-YLIN-P-QGKAFRSKVE-LIAYFEKVGDTSLD---PNDQFTVTGR 162
-----P-GW-----R-SG--AG--D--YI---P--G--FRSK---L--Y-----F-----

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(Mikako Ito et al.,2003, Plant Physiology)

- A data-mining work on AS in epigenetic scope could and should be done



CMT family and DRM family

CMT family:

CMT3,(CMT1),CMT2(Chromomethyltransferase)

Uniq for plants, related to Dnmt1,activity associated with H3K9 methylation, maintenance methylation of CHG methylation

DRM family:

DRM2(DMR1) (domain rearranged methyltransferase)

De novo methylation of all sequence

- Mutant of *drm12*, *cmt2*, *cmt3* have distinct attribution on DNA methylation and gene expression

CMT3 prefer to methylating DNA in the CHG site

CMT2 methylated CHG and CHH equally ,methylated CHG in a redundant way

CMT2 and DRM methylated CHH sites completely in non-overlapping ways

CMT3 and DRM2 cooperatively regulated protein-coding genes
DNA methylation