Unravelling the *Brassica napus* epigenetic network with an integrated multi-omics approach

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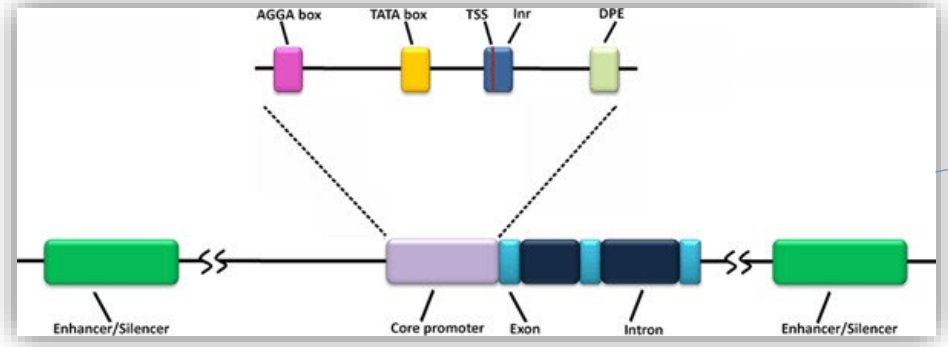
Cis-regulatory elements (CREs) and their highly dynamic activity

Promoters



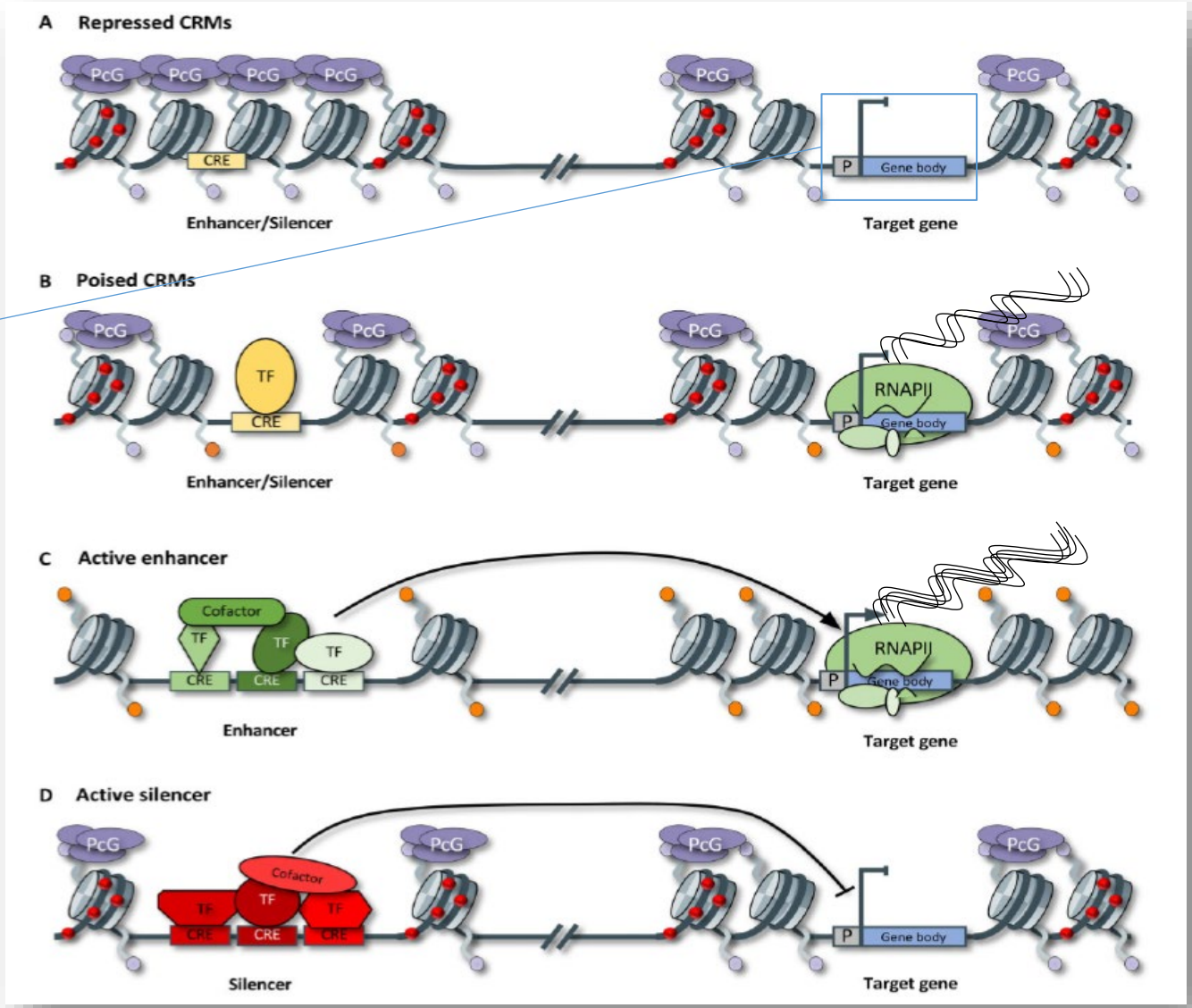
(Bilas et al., 2016)

(1) Accessible/Open

(2) Unmethylated

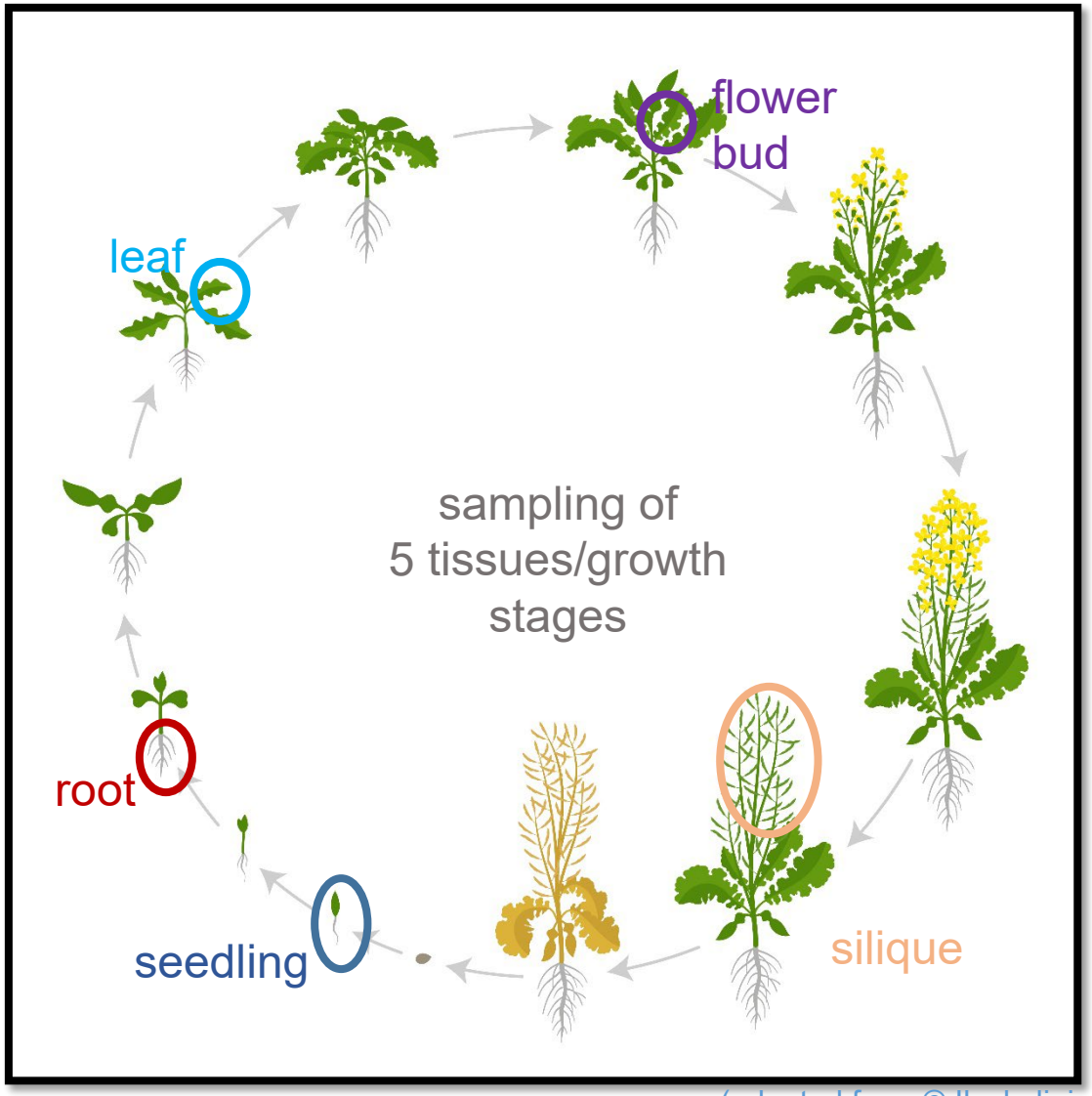
(3) Regulating/ed

Silencers & Enhancers

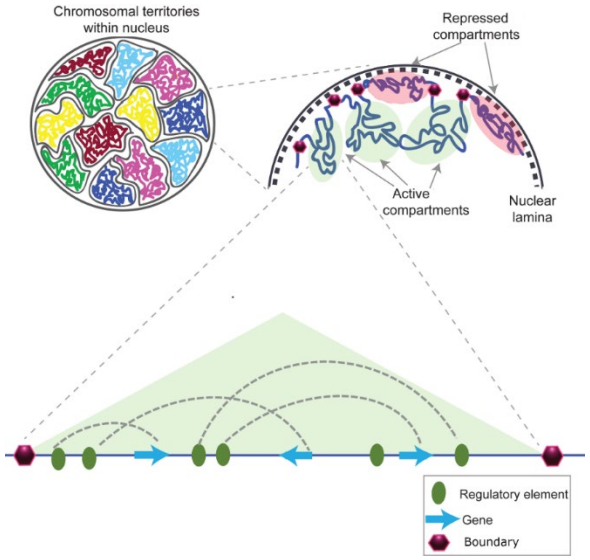


(Schmitz et al., 2022)

Mapping of the CREs architecture in *Brassica napus*



(adapted from © Ilyakalinin)

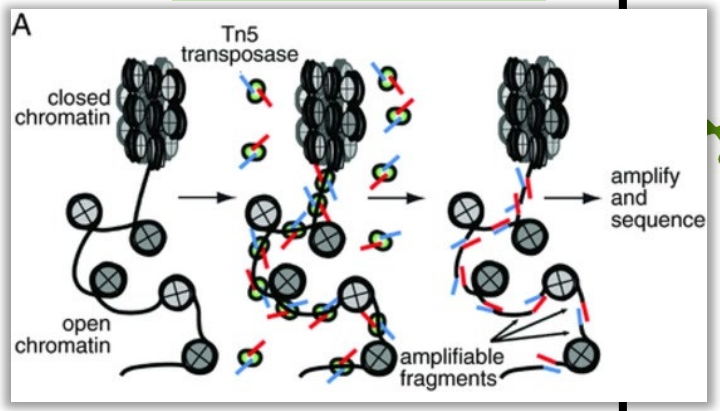


Experimental setup

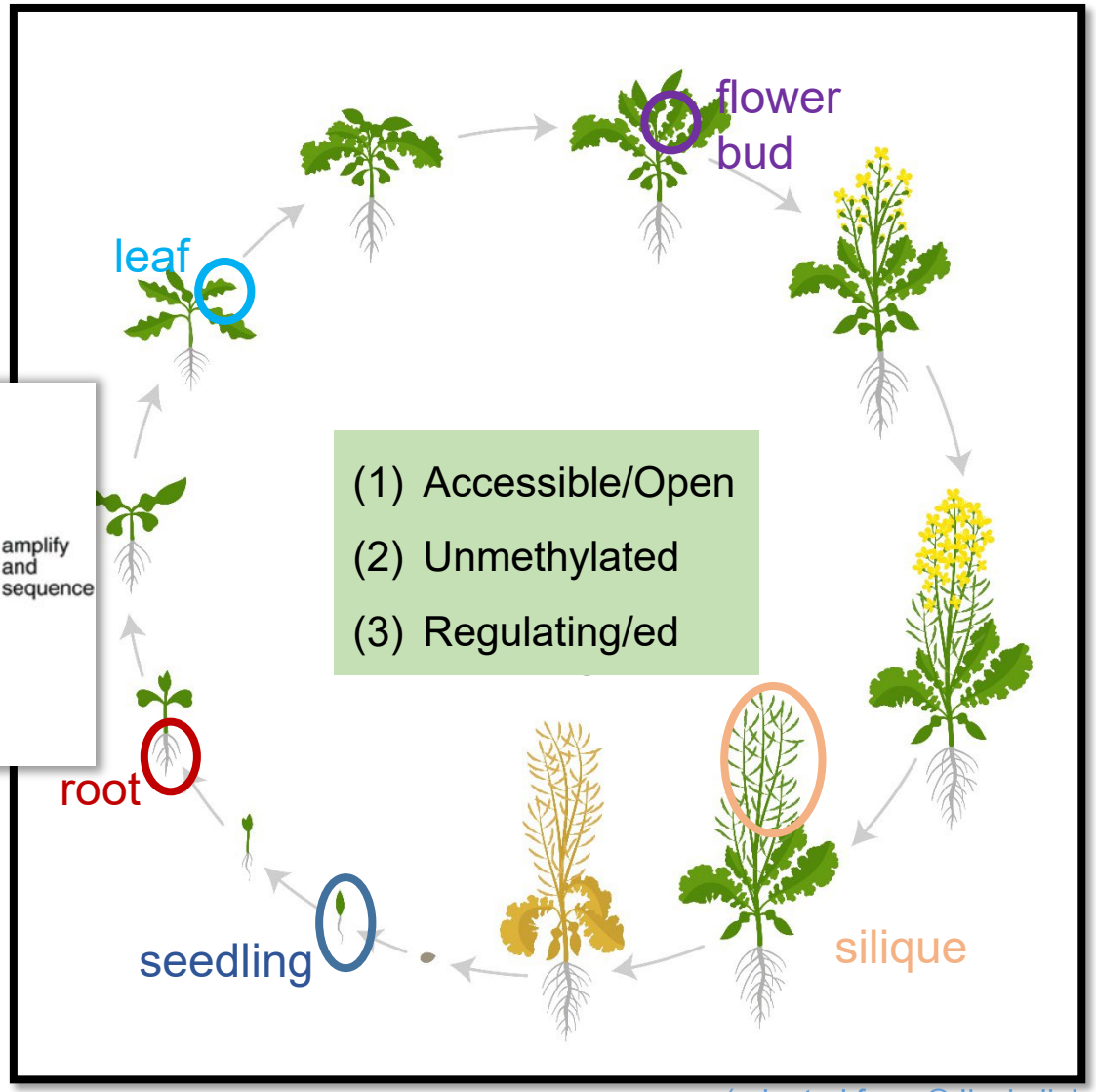
Mapping of the CREs architecture in *Brassica napus*

Experimental setup

(1) ATAC-seq

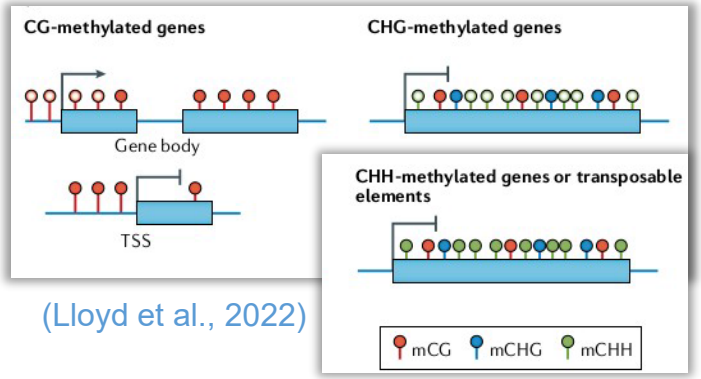


(Buenrostro *et al.*, 2015)



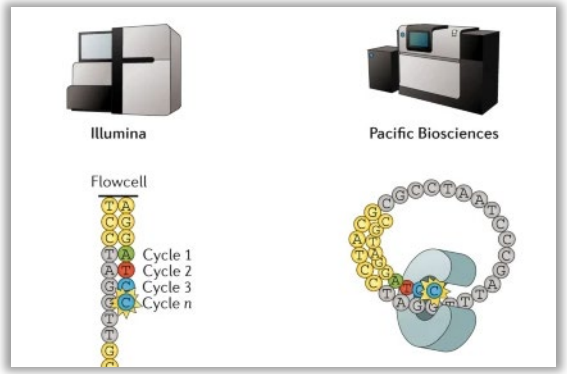
(adapted from © Ilyakalinin)

(2) WGBS



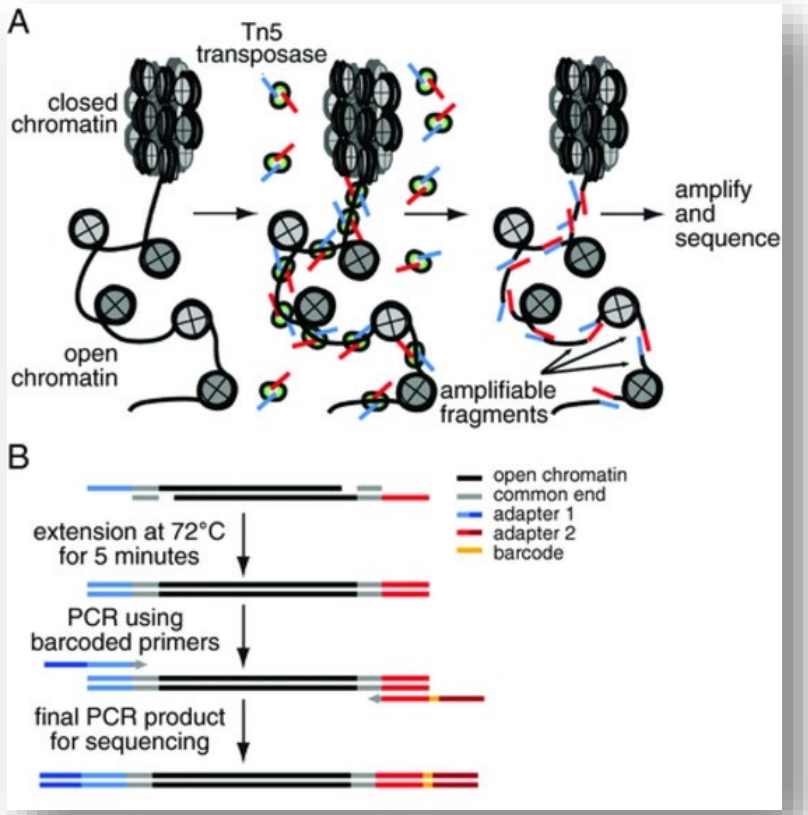
(Lloyd et al., 2022)

(3) mRNA-seq



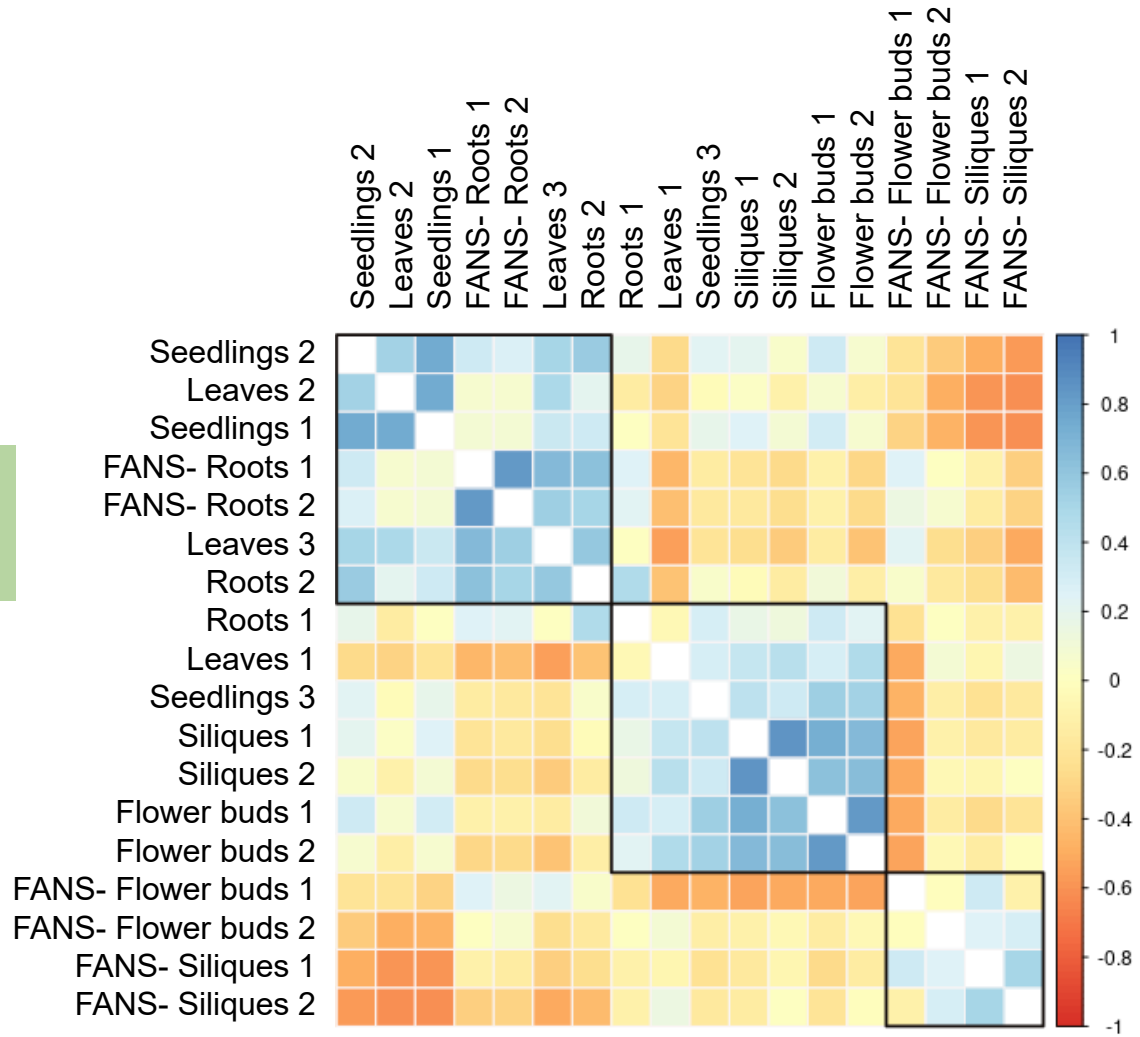
(Stark et al., 2019)

ATACseq – Open Chromatin Regions identification



(Buenrostro *et al.*, 2015).

17,000-50,000 OCRs per sample type



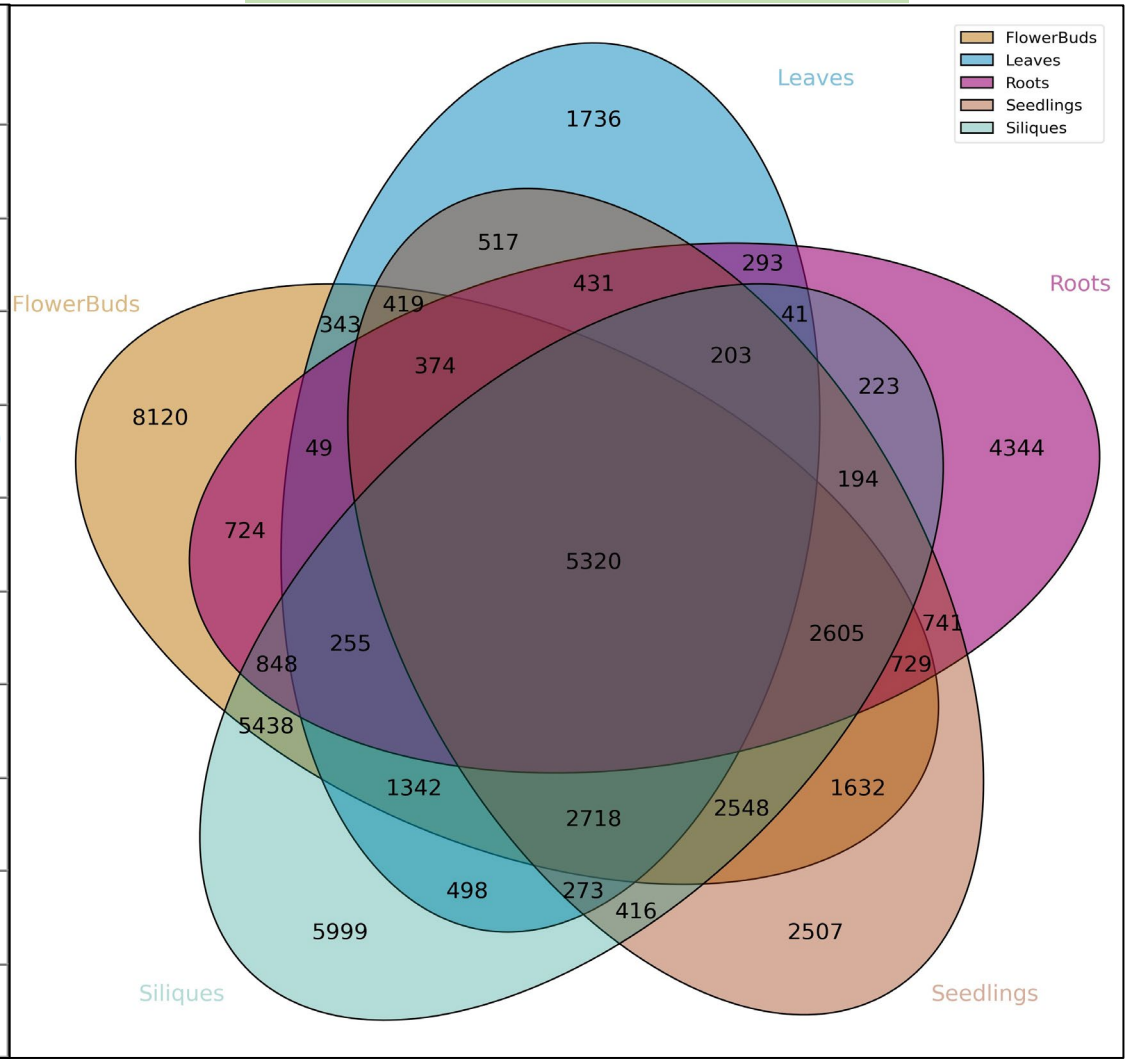
ATAC-seq - OCRs

ATACseq – OCRs features and conservation

OCRs TF annotation - HOMER

Rank	Motif	Name
1		PCF/Arabidopsis-Promoters/Homer
2		E-box/Arabidopsis-Promoters/Homer
3		ABF1(bZIP)/Arabidopsis-ABF1-ChIP-Seq(GSE80564)/Homer
4		ABI5(bZIP)/col-ABI5-DAP-Seq(GSE60143)/Homer
5		c-Myc(bHLH)/LNCAP-cMyc-ChIP-Seq(Unpublished)/Homer
6		CLOCK(bHLH)/Liver-Clock-ChIP-Seq(GSE39860)/Homer
7		SPCH(bHLH)/Seedling-SPCH-ChIP-Seq(GSE57497)/Homer
8		ABF2(bZIP)/col-ABF2-DAP-Seq(GSE60143)/Homer
9		At1g78700(BZR)/col-At1g78700-DAP-Seq(GSE60143)/Homer
10		At4g36780(BZR)/col-At4g36780-DAP-Seq(GSE60143)/Homer

OCRs overlap between samples

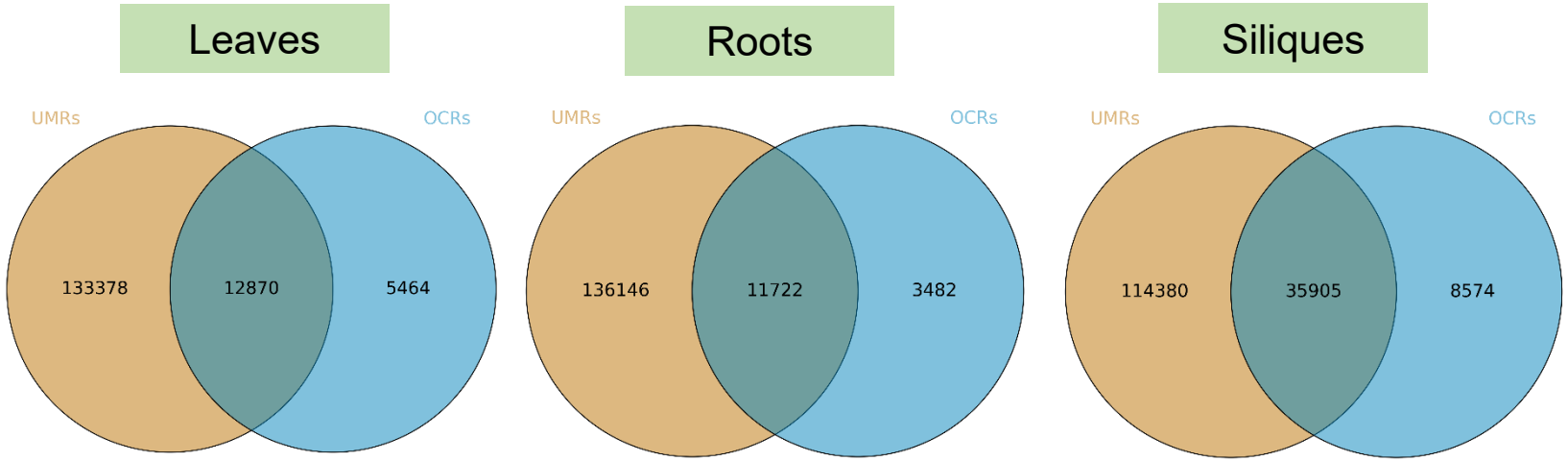


WGBS - UMRs identification and conservation

Vanessa Putland
Crisp Lab @UQ Crop Epigenomics

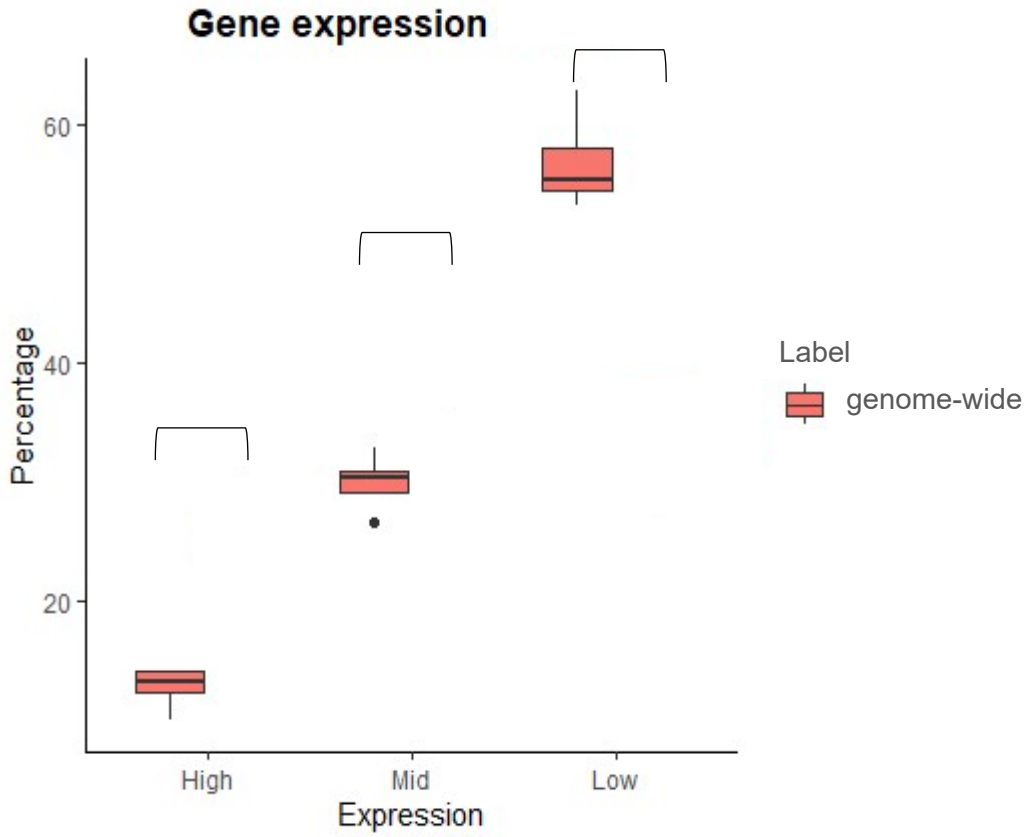
Tiles defined as “UMR” if CG, CHG and CHH <10%

Sample types	Total # UMRs	Total UMR space	Percent of genome UMR
Leaves	169,483	285 Mb	37%
Roots	167,494	285 Mb	37%
Siliques	164,458	280 Mb	37%



mRNA and OCRs

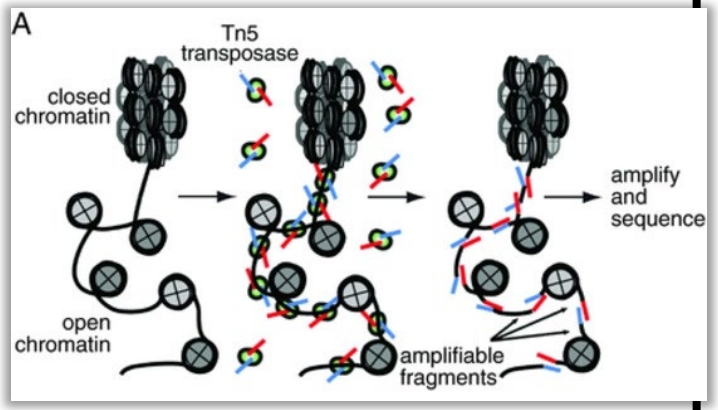
Sample types	Total High expression	Total Medium expression	Total Low to No expression
Leaves	10.2%	26.9%	62.9%
Roots	14.4%	31.2%	54.4%
Siliques	13.3%	30.4%	56.3%
Seedlings	14.4%	31.4%	54.2%
Flower Buds	13.3%	33.2%	53.5%



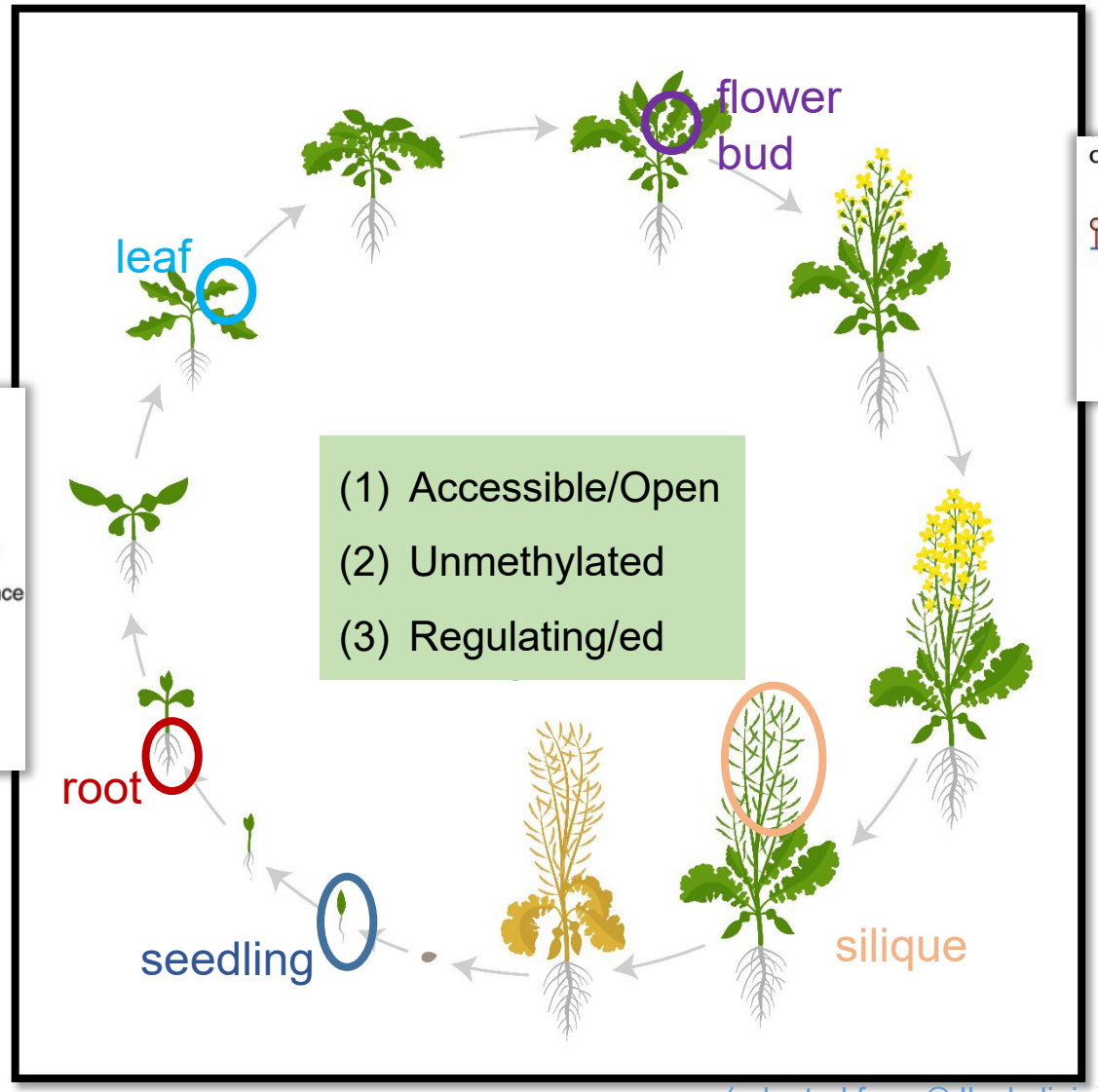
Map of the cis-regulatory architecture in *Brassica napus*

CREs map

(✓) ATAC-seq



(Buenrostro *et al.*, 2015)



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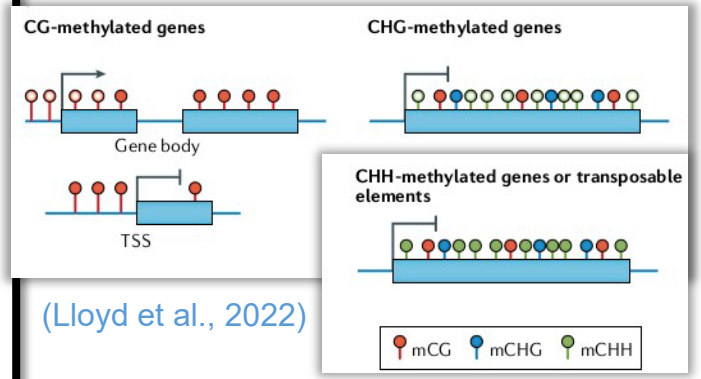
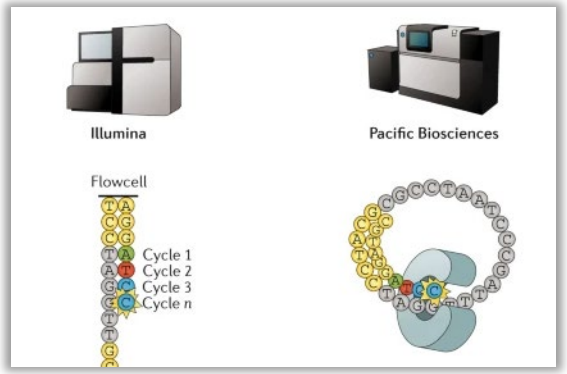
(✓) WGBS



(Lloyd et al., 2022)

(✓) mRNA-seq



(Stark et al., 2019)

eQTLs and OCR/CREs – functional (non) coding structural variants

Gözde Yildiz

57 *Brassica napus* genotypes (WOR)

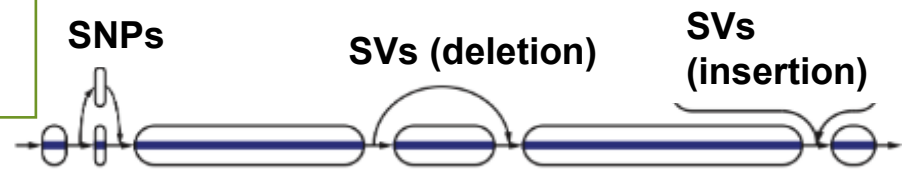
Short-reads (**n:57**) (Illumina sequencing)

RNAseq-reads (**n:57**) (Illumina sequencing)

Long reads (**n:57**) (ONT sequencing)

Single nucleotide polymorphism (**SNPs**)

Structural variations (**SVs**)



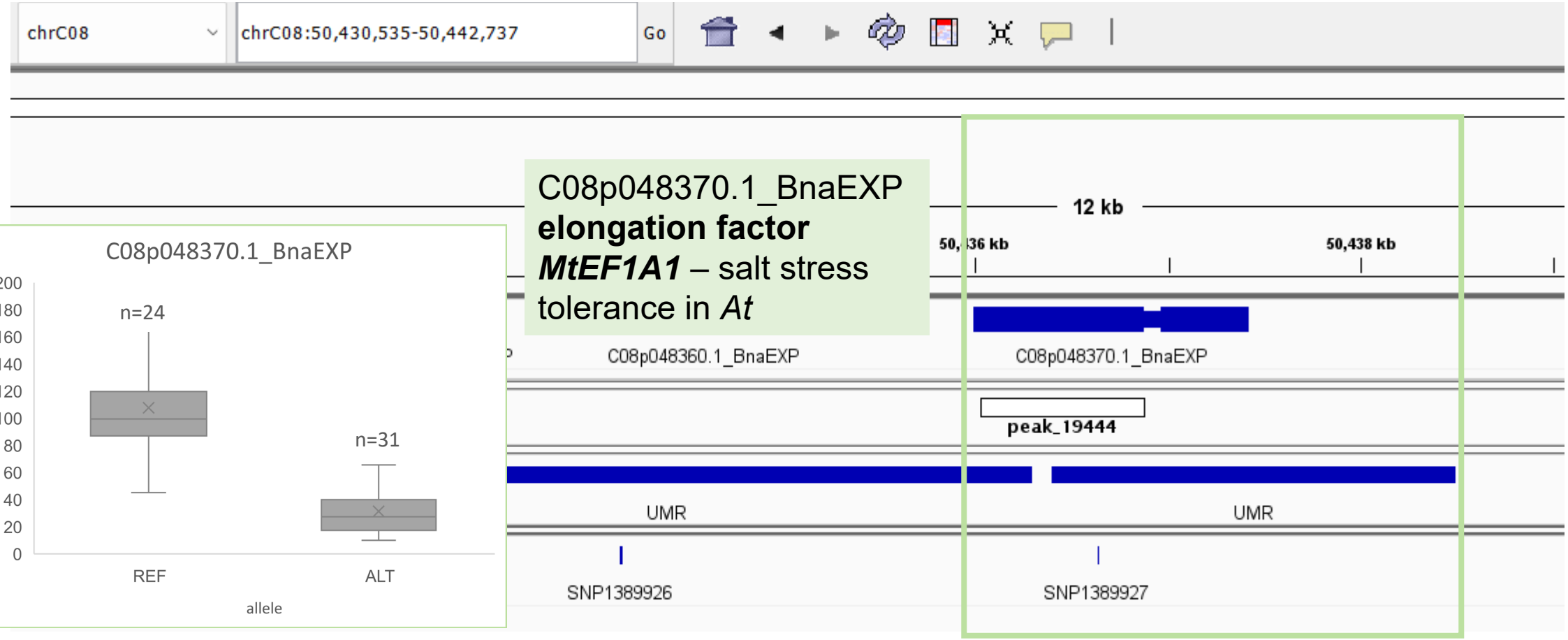
eQTL analysis

map of **active ORC/CREs** (leaves)

OCR/CRE-interacting eQTLs

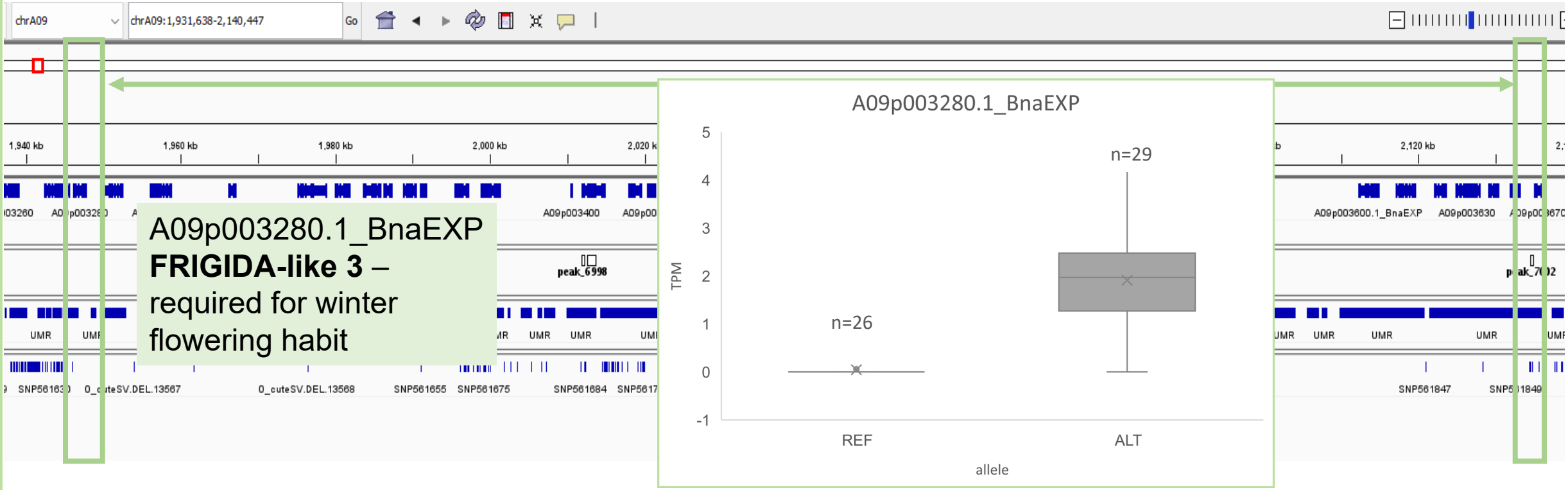
- 298 OCR/CRE-interacting **cis-eQTL** (294 SNPs, 4 SVs)
- 66 OCR/CRE-interacting **trans-eQTL** (66 SNPs)

OCR-interacting cis-eQTL



C08p048370.1_BnaEXP **elongation factor *MtEF1A1*** – salt stress tolerance in *At*

CRE-interacting trans-eQTL



A09p003280.1_BnaEXP
FRIGIDA-like 3 – required for winter flowering habit

Acknowledgments

Agrobioinformatics group (JLU)

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Vanessa Putland