

A



Whole Genome Alignments
.axtNet



Baseline RNA-seq
.bigwig



10 COMMON MARKS
PCSD + SRA

H. ACETYLATION

H3K9ac
H3K27ac

H. METHYLATION

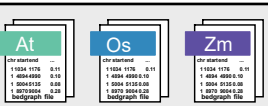
H3K4me2 H3K27me2
H3K4me3 H3K36me3
H3K9me2

H. VARIANT

H2A.Z

5mC

CHROMATIN ACCESS



Functional genomics
conservation score

Inter species-CS

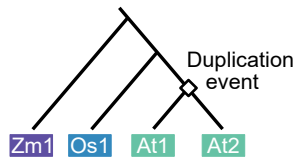


Paralog modelling

LECIF-score

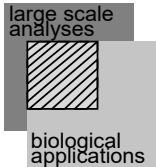
HYPOTHESIS

Highlight regions with high
phenotypic similarity



one2many gene pairs
ancestral function?

RESOURCE



Tracks and applications
available in a database

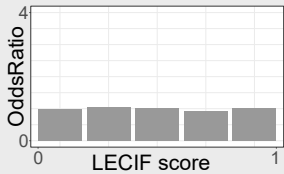


Arabidopsis thaliana

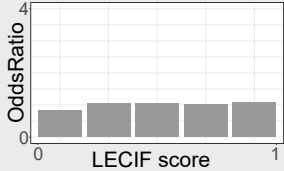
Genetic Variability

B Enrichment of At GWAS variants
in LECIF binned regions

Oryza: top side



Zea: bot side

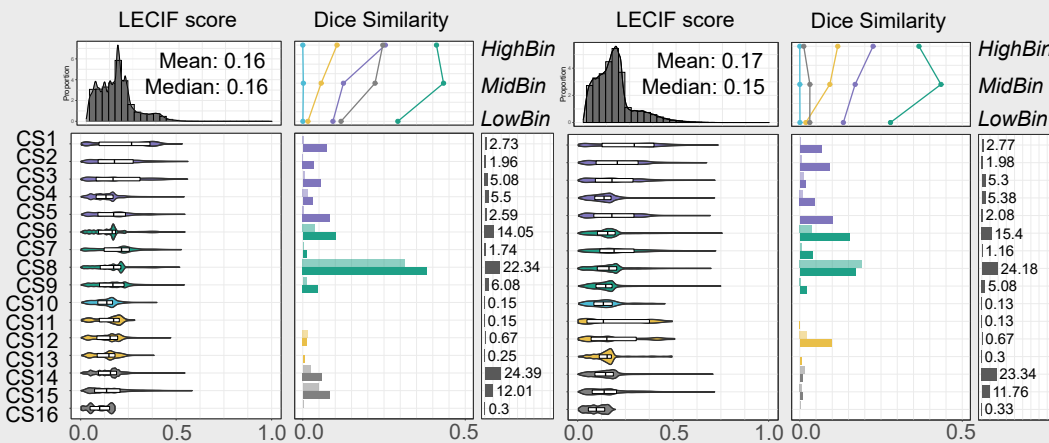


Chromatin States

E

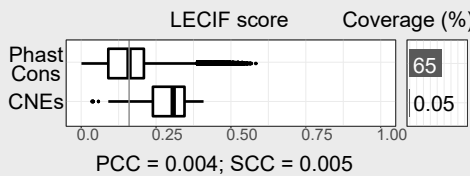
Oryza: left side

Zea: right side

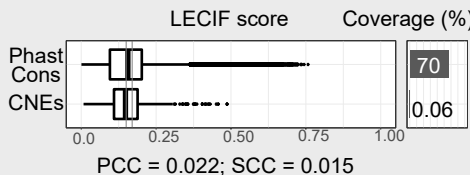


H Comparative Genomics
Conservation

Oryza: top side



Zea: bot side

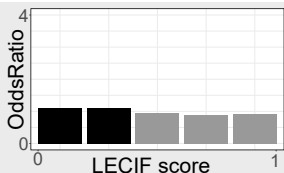


Oryza sativa

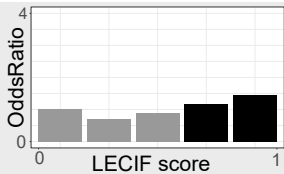
Genetic Variability

C Enrichment of Os GWAS variants
in LECIF binned regions

Arabidopsis: top side



Zea: bot side

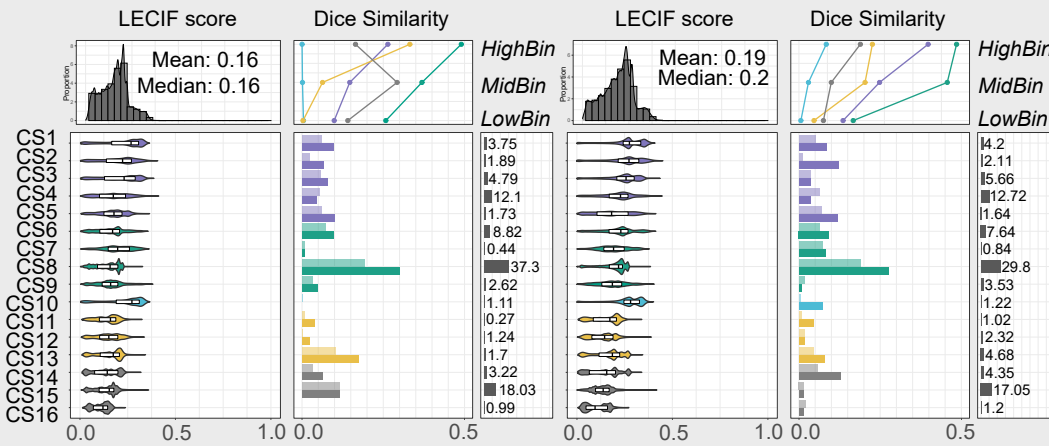


Chromatin States

F

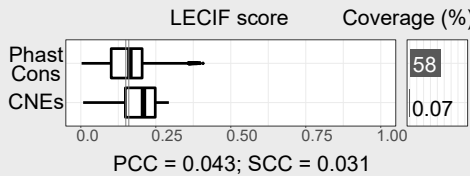
Arabidopsis: left side

Zea: right side

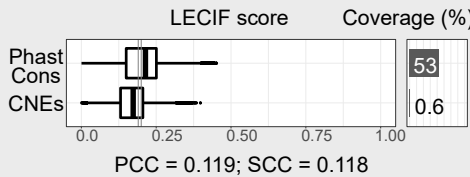


I Comparative Genomics
Conservation

Arabidopsis: top side



Zea: bot side

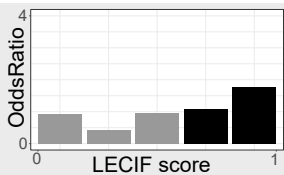


Zea mays

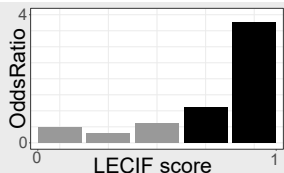
Genetic Variability

D Enrichment of Zm GWAS variants
in LECIF binned regions

Arabidopsis: top side



Oryza: bot side

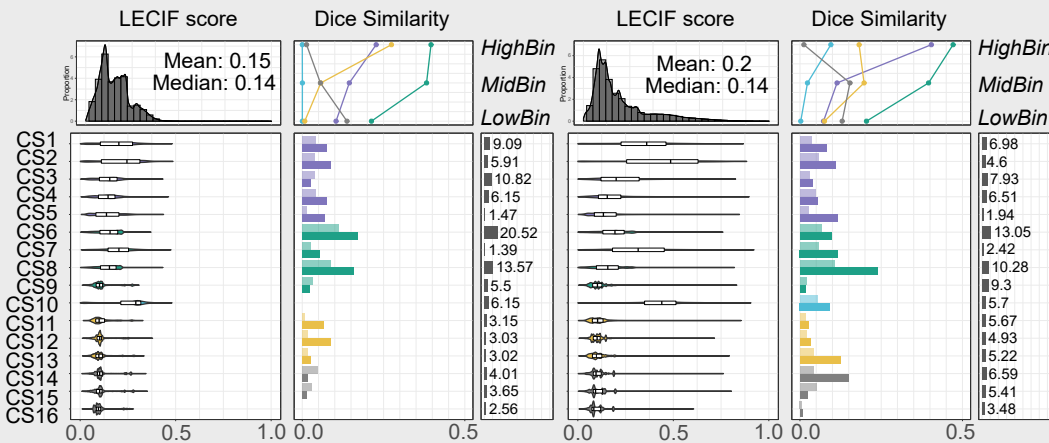


Chromatin States

G

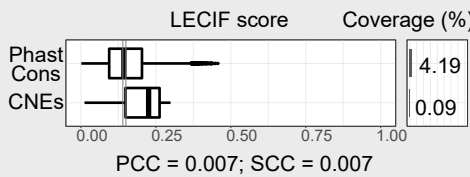
Arabidopsis: left side

Oryza: right side



J Comparative Genomics
Conservation

Arabidopsis: top side



Oryza: bot side

