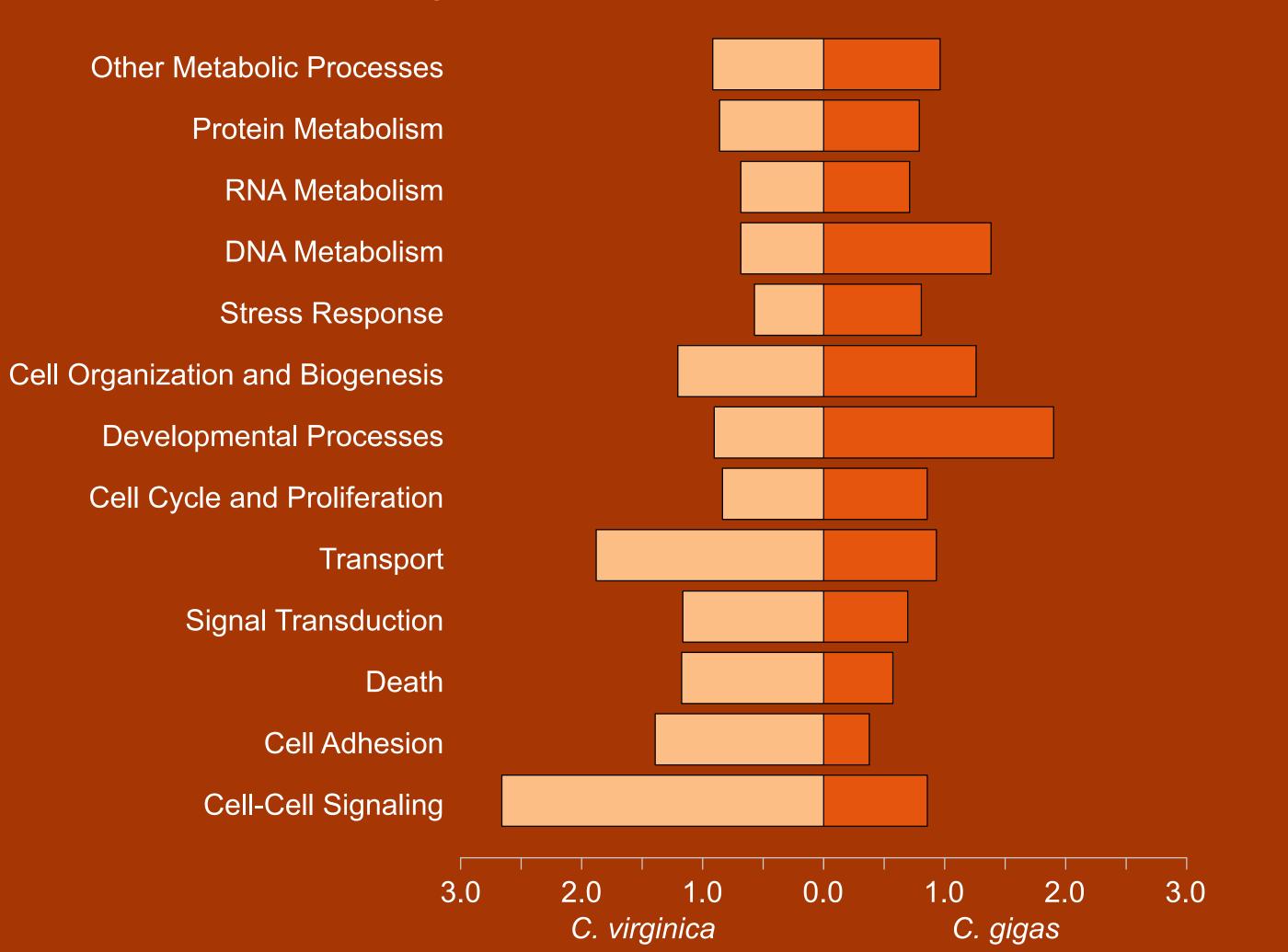
Similar methylation landscapes and environmental responses in congeneric oysters

	C. virginica	C. gigas
Overall percent methylation	15-20%	15-20%
Number of Genes	39,493	33,784
Number of methylation islands	37,063	23,173
Number of DML	598	628

Is there a functional role?

Relative proportions of GOSlim terms in genes with DML









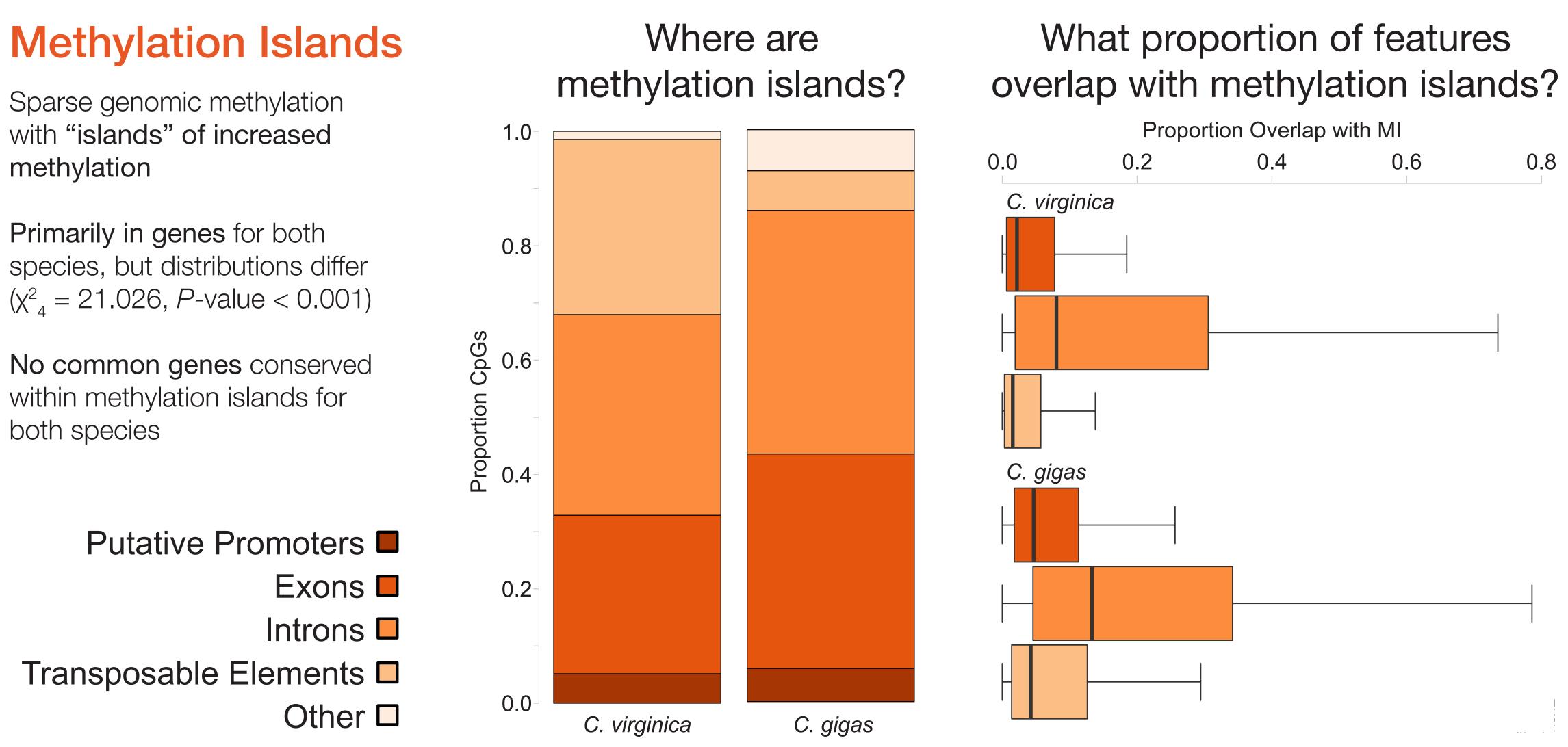
Influence of ocean acidfication on eastern (Crassostrea virginica) and Pacific oyster (Crassostrea gigas) DNA methylation

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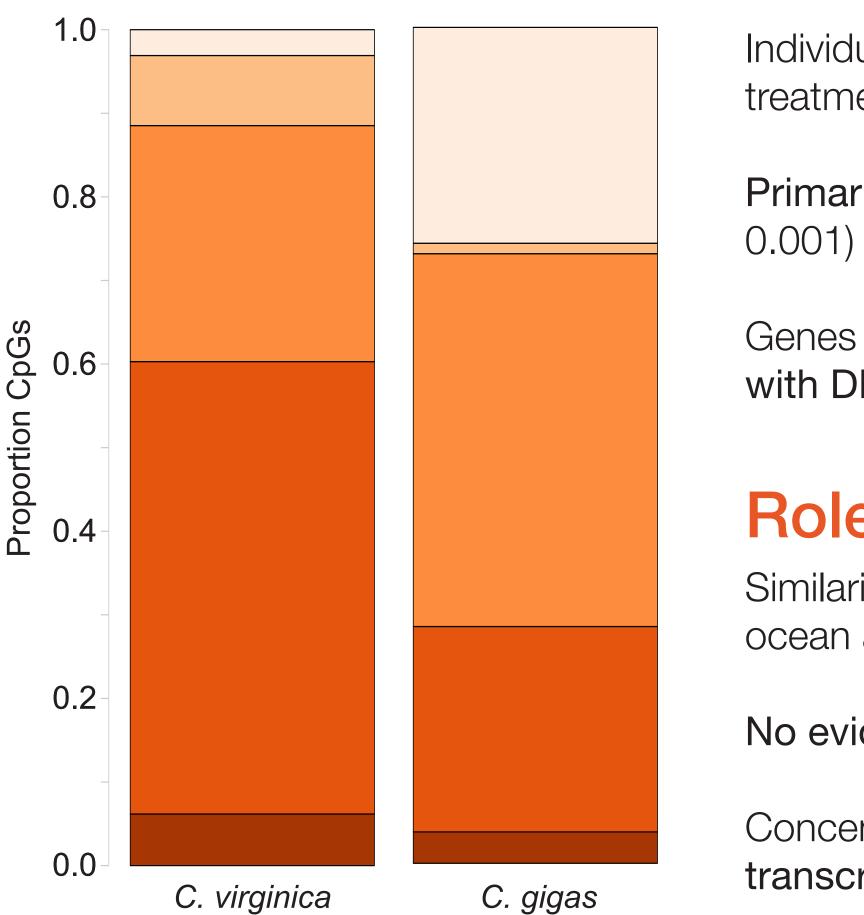
Introduction

DNA methylation is a **possible mechanism for** intergenerational plasticity

Understanding the parental gonad epigenome can inform characterization of methylation inheritance



Where in the genome are DML found?







Pacific oyster carryover effect

Methods

C. virginica: control: $pCO_2 = 492 \mu atm$, treatment: $pCO_2 = 2552 \mu atm$, 4 weeks, 10 samples, MBD-BSseq

C. gigas: control: $pCO_{2} = 863 \mu atm$, treatment: $pCO_2 = 3344 \mu atm$, 7 weeks, 2 pooled samples, WGBS

Differentially Methylated Loci (DML)

Individual CpG loci with significantly different methylation levels between control and treatment conditions

Primarily in genes for both species, but distributions differ (χ^2_{1} = 38.516, *P*-value <

Genes with DML are invovled in various biological processes, with 81 common genes with DML between species

Role of Methylation in Environmental Response

Similarities between *C. virginica* and *C. gigas* methylation landscapes and responses to ocean acidification could indicate conserved role of methylation

No evidence for genes with DML to be associated with distinct biological processes.

Concentration of DML in gene bodies suggests influence on gene activity or transcriptional control in response to ocean acidification.

8.0 0.6











