

Sydney Rock Oyster  
Draft (Genome)

SAT  
Am  
Before  
Lunch

Daniel Powell

km  
n  
200  
200  
homozygous  
peak  
3 years  
Market  
Size

km freq  $k=21$   
Level of hetero 3.51%  
C. gas 1.4%

Genome 784 Mb  
Size

PK  
MP  
Chicago Library  
Dovetail

Workflow

Merqulous2 = kmcr 55  
PK  $\leftrightarrow$  MP

90k scaffolds  
not portion

270k contigs

Isolation of single  
haplotypes Haplomerger

⇒ 4712 Scaff  
139k contigs

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✗ Dovetail Chicago Library

Final Scaffolds = 12,592

NSD 806 Kb

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Gap filling using Gap Closer

# Scaffolds - 10,107

% genome gaps - 5.3%

contigs  
NSD

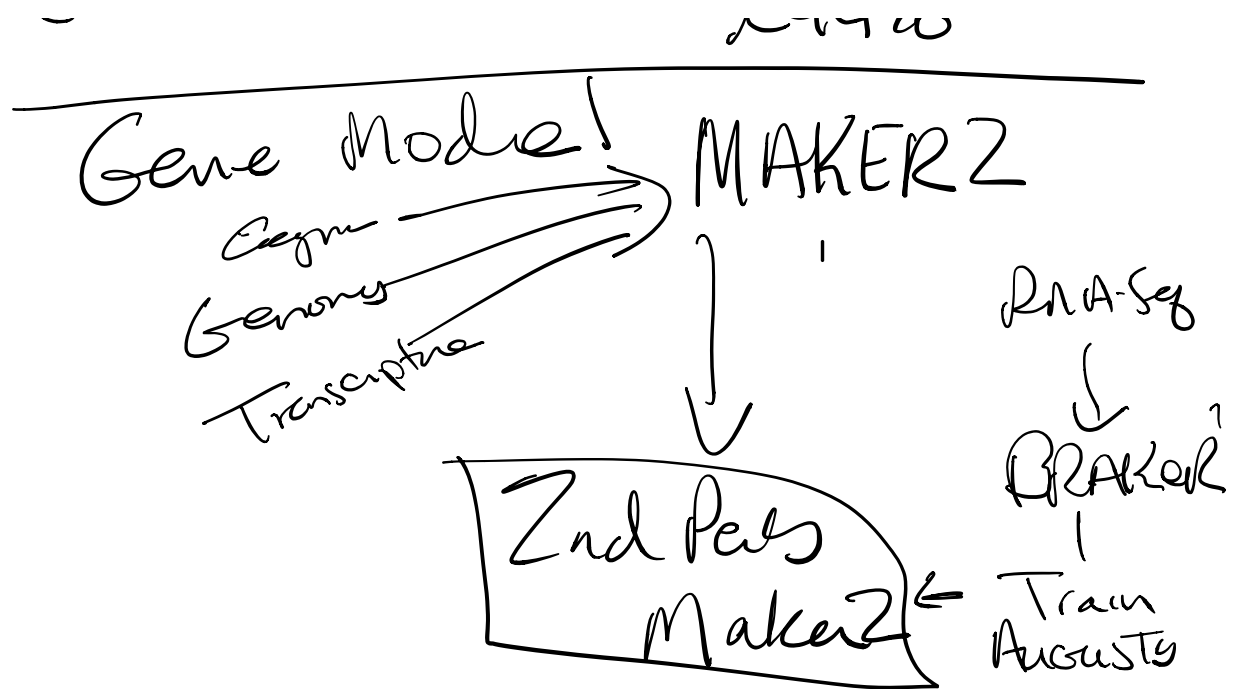
- 39k

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Completeness 91% <sup>reps</sup> mapped

70% transcriptome  
mapped

CEGMA BUSCO. all ok



Summer 10K Scaffolds

↳ Dovetail scaffolding

30,313 gene models

↳ Hi-C

40-50%  
Genome  
Repetitive