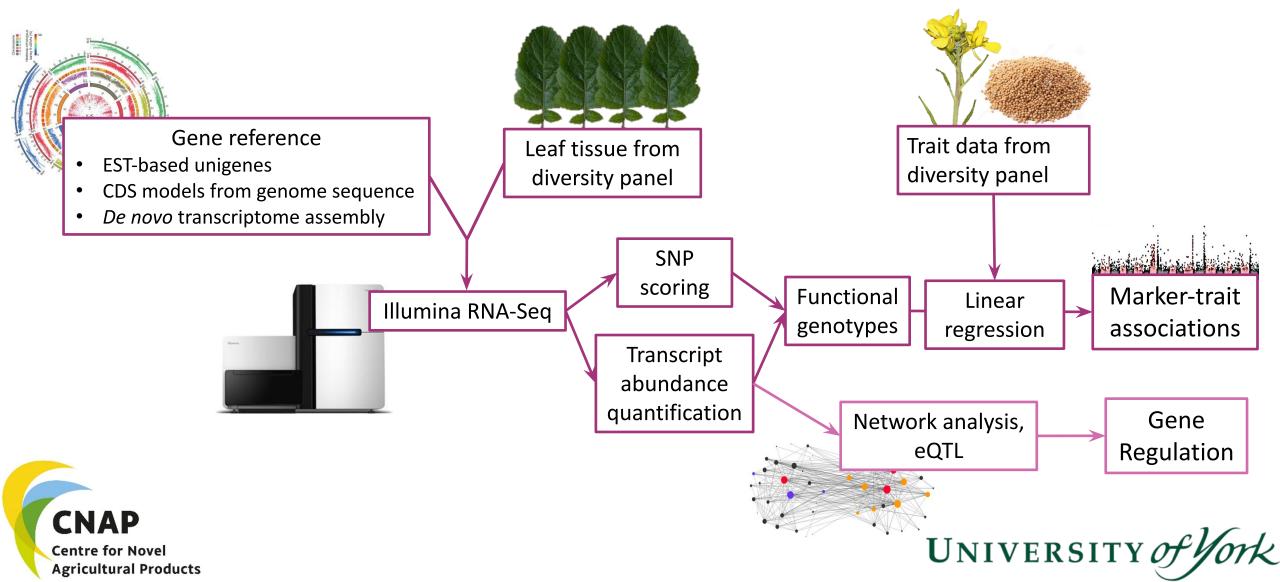
# Mapping the genetic basis of yield and quality traits in *Brassica juncea*

Andrea Harper UK-BRC, 24<sup>th</sup> November 2020



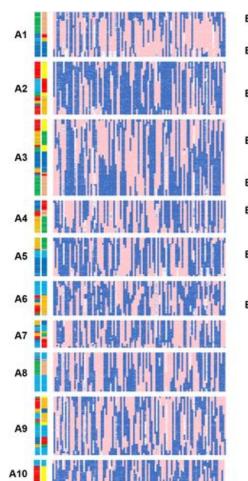


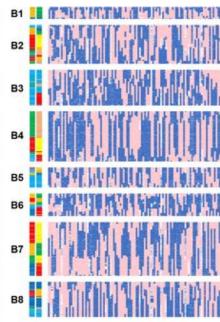
#### **Associative Transcriptomics pipeline**



#### AB pan-transcriptome reference

- Pseudomolecules built for the A and B genomes using published B. rapa Chiifu v2.0 (Cai et al., 2017) and B. nigra YZ12151 (Yang et al., 2016) genome sequences
- Corrected using high-density transcriptome SNP-based linkage mapping
- Published *B. rapa* Chiifu v2.0 and *B. nigra* YZ12151 CDS gene models mapped onto the pseudomolecules
- Additional B. juncea T84-66 CDS models interpolated into the A and B genomes respectively using collinear flanking genes
- The final AB pan-transcriptome resource comprises 93,963 hypothetically ordered CDS models (50,427 on the A genome and 43,536 on the B genome)





Genome-Ordered Graphical Genotypes (GOGGs) for VNDH population





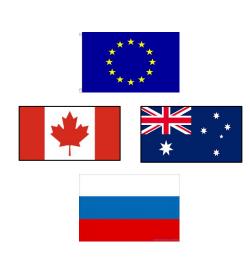
#### Diversity panel, markers and traits

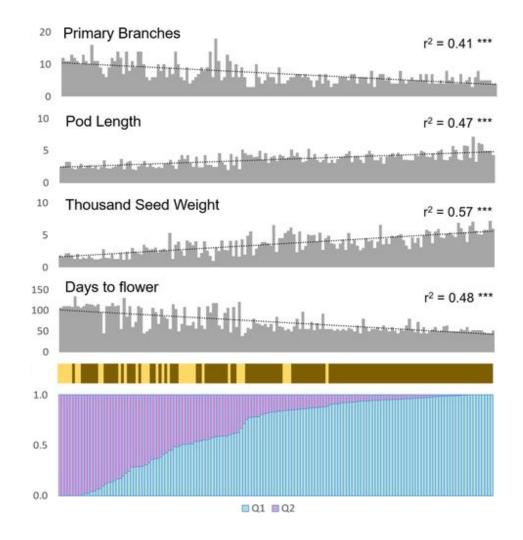
- 151 B. juncea accessions used for AT
- 101 Indian accessions, 6 Australian, 13 Canadian, 6 Chinese, 19 European, 6 resynthesised
- 171,196 SNPs with minor allele frequencies > 0.05
- Significant expression detected for 48,975 CDS models
- Traits measured in India field trials architecture, yield, phenology, seed size, oil content, tocopherols





## Population structure correlates with many important traits



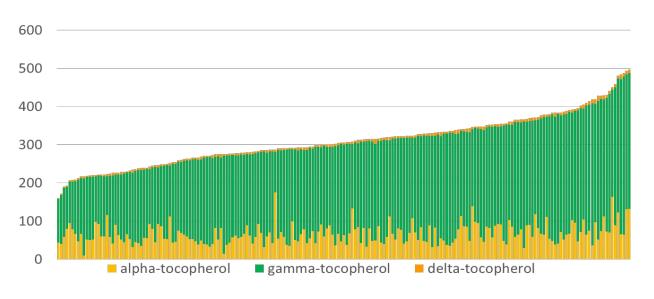


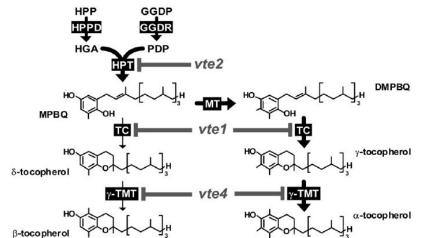




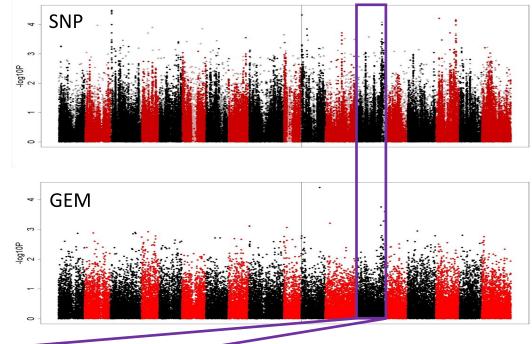


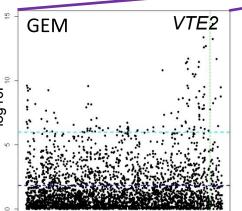
#### Seed quality in Brassica juncea





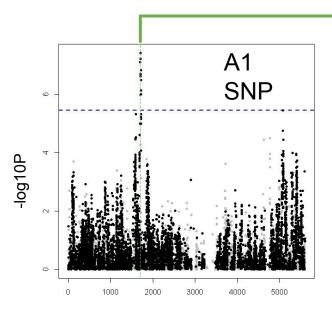
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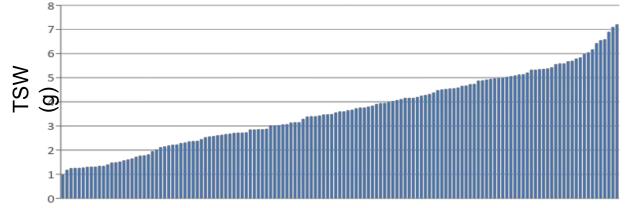
#### TSW in Brassica juncea

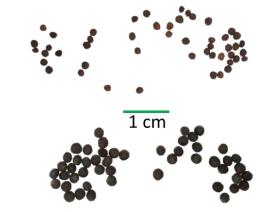


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Key regulator of endosperm nuclear division TTL

- Seed growth mainly coupled to endosperm and integument growth
- Early endosperm development involves nuclear division without cytokinesis, producing large, multinucleate endosperm cells.





Predictions showed 1.7 fold weight difference between single SNP marker alleles (p=0.004)



#### Acknowledgements



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#### the plant journal



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Validation of an Associative Transcriptomics platform in the polyploid crop species *Brassica juncea* by dissection of the genetic architecture of agronomic and quality traits

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#### TSW in Brassica juncea

