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Detecting the genes controlling homologous recombination in *Brassica napus*

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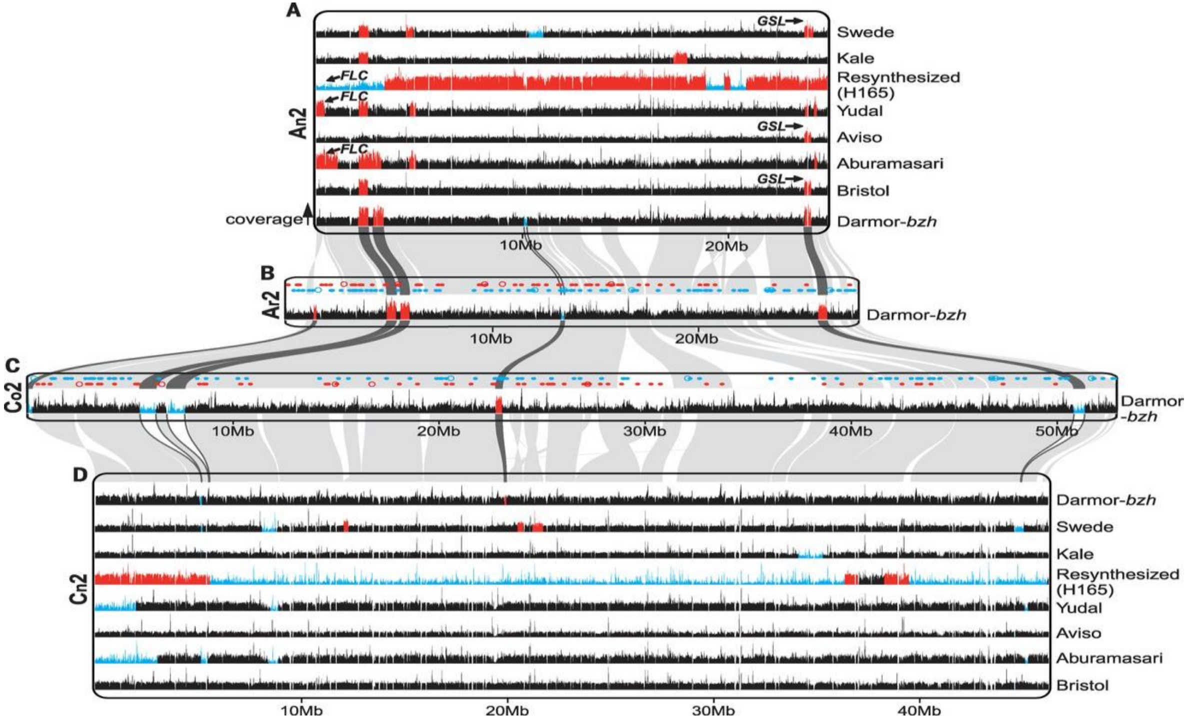
Canada

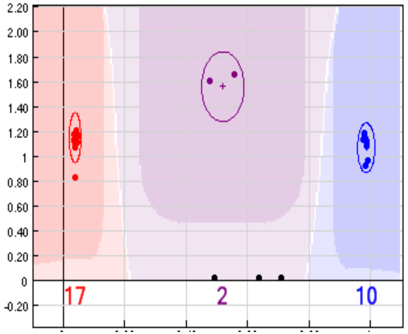
Homoeologous recombination is an on-going mechanism creating variation in *B. napus*

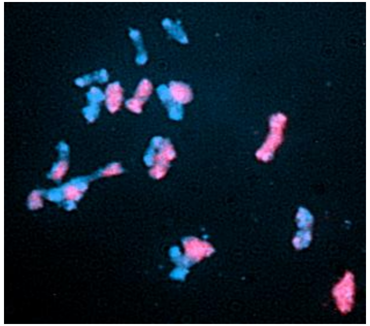


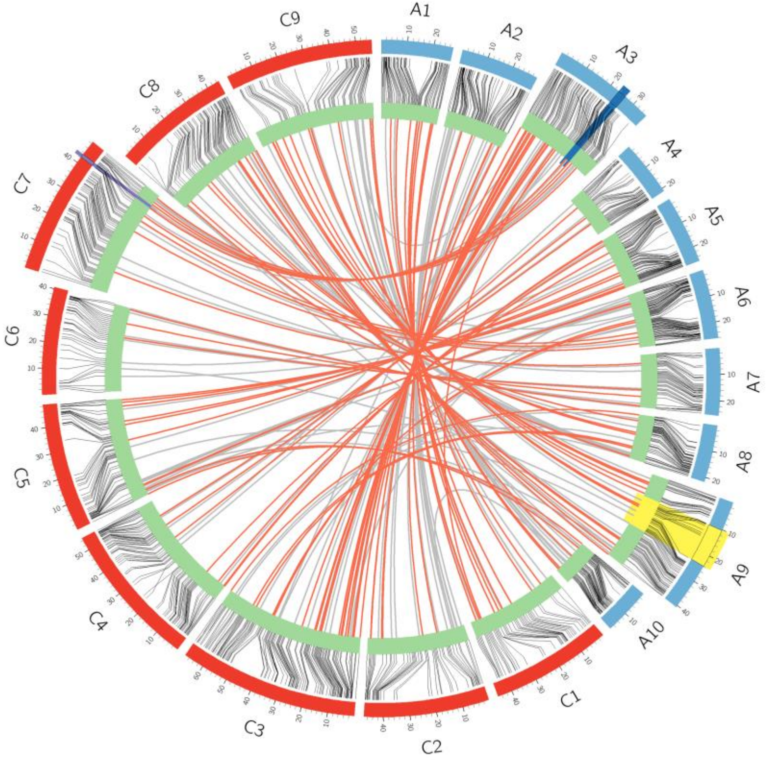
Chalhoub et al Science 2014

A major quantitative trait locus on chromosome A9, *BnaPh1*, controls homoeologous recombination

SNP genotyping and cytological assessment of segregating lines identified one major and two minor QTL loci controlling levels of homoeologous recombination

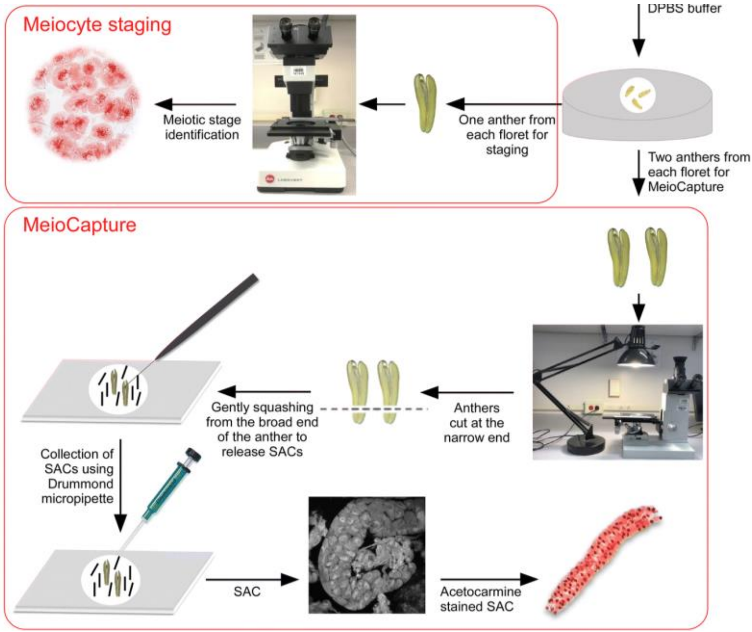






Higgins et al, 2021, New Phytol. 229: 3281-3293

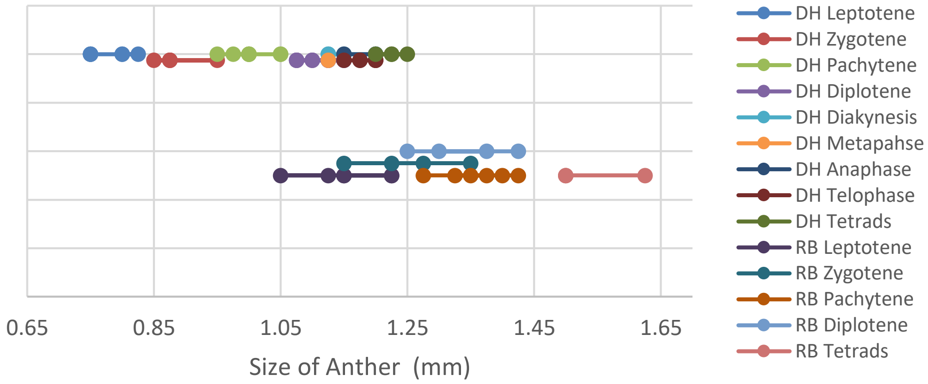
Gene expression analyses of meiocytes



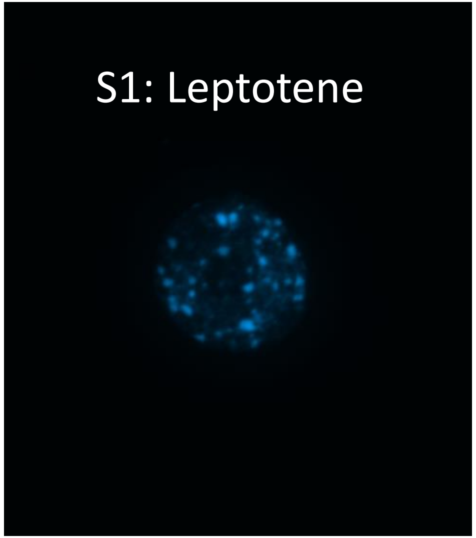
Shunmugam et al. (2018) BMC Plant Biol 18, 293.

Collected meiocytes from staged anthers of:

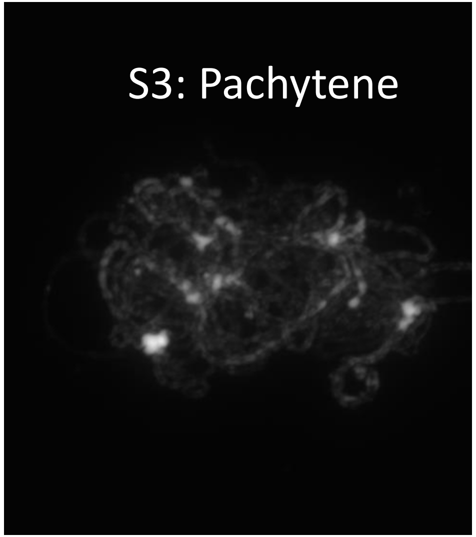
- DH12075
- Resynthesised *B. napus* (RB1)

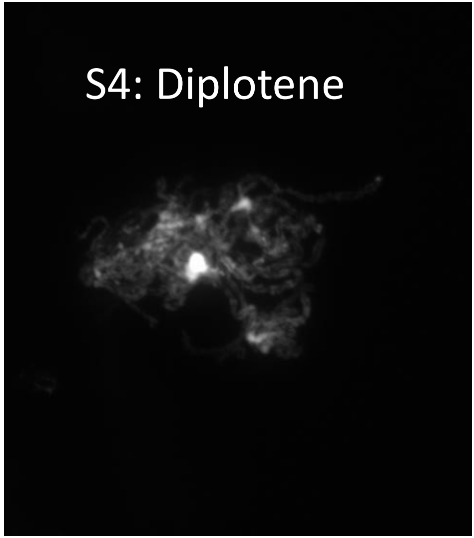


Monitoring gene expression throughout Prophase I and Metaphase I of *Brassica napus*

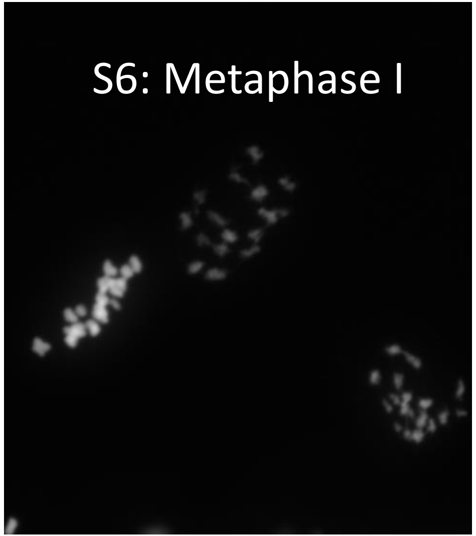

S1: Leptotene


S2: Zygotene

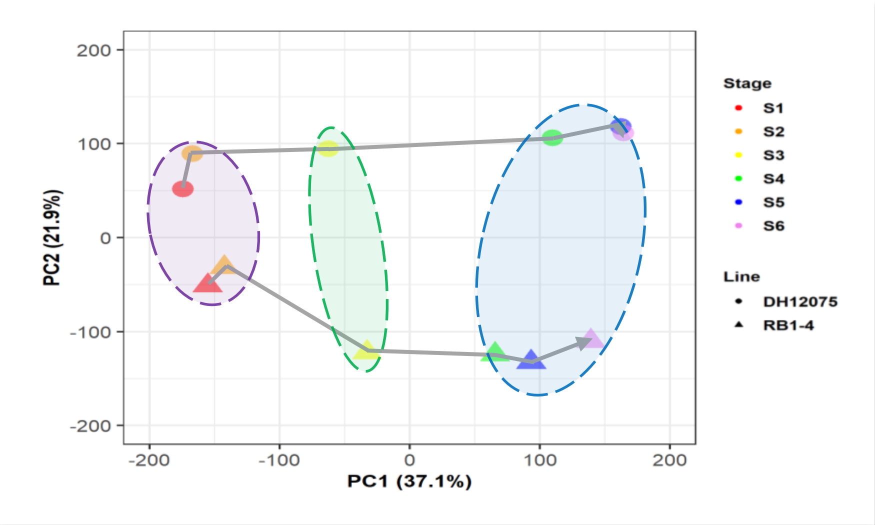

S3: Pachytene

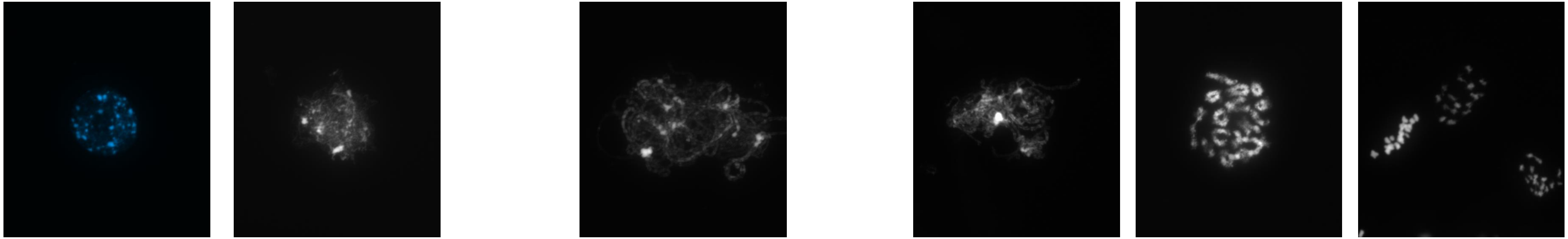

S4: Diplotene


S5: Diakinesis

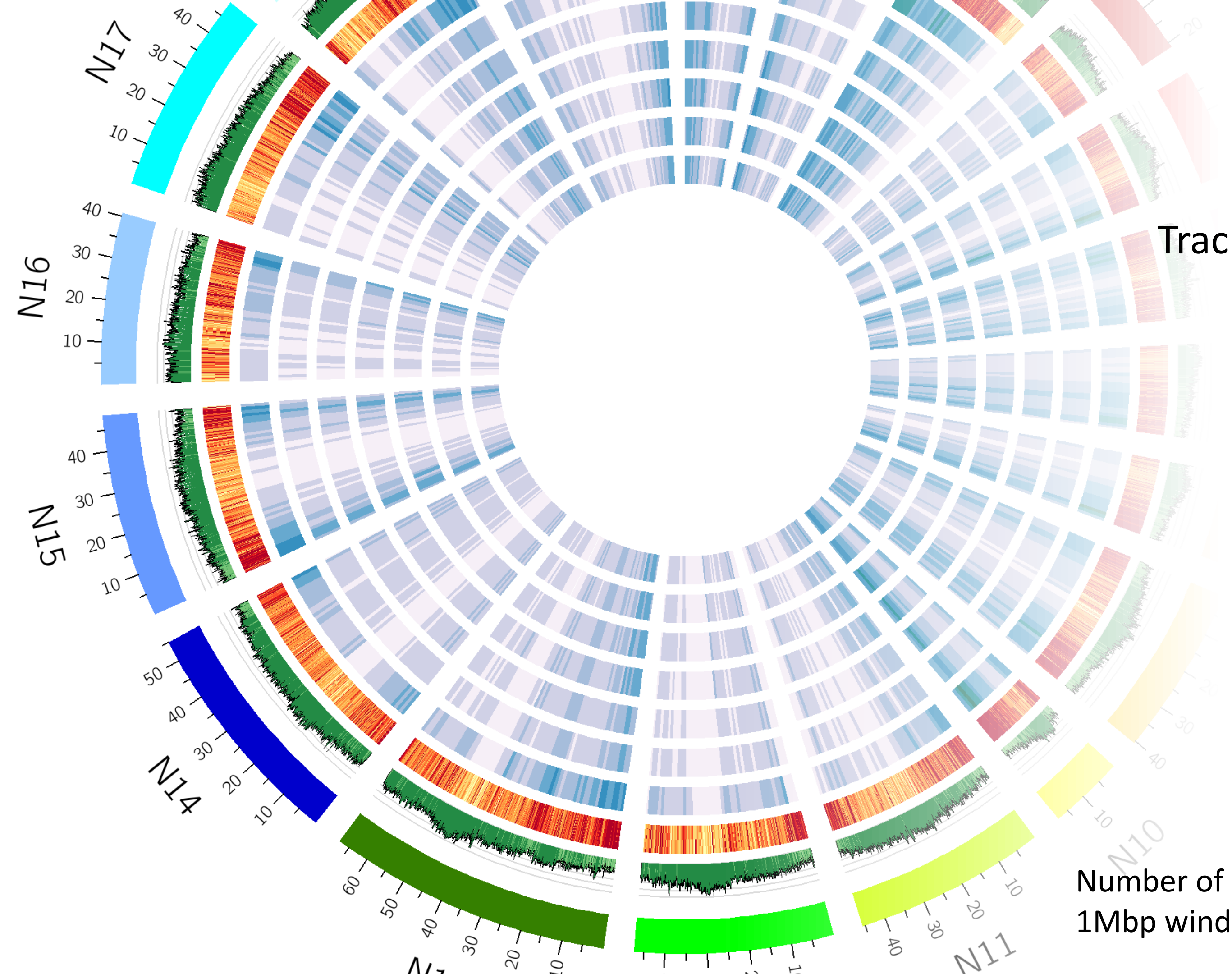

S6: Metaphase I

Three distinct phases of gene expression during meiosis





Expression Landscape

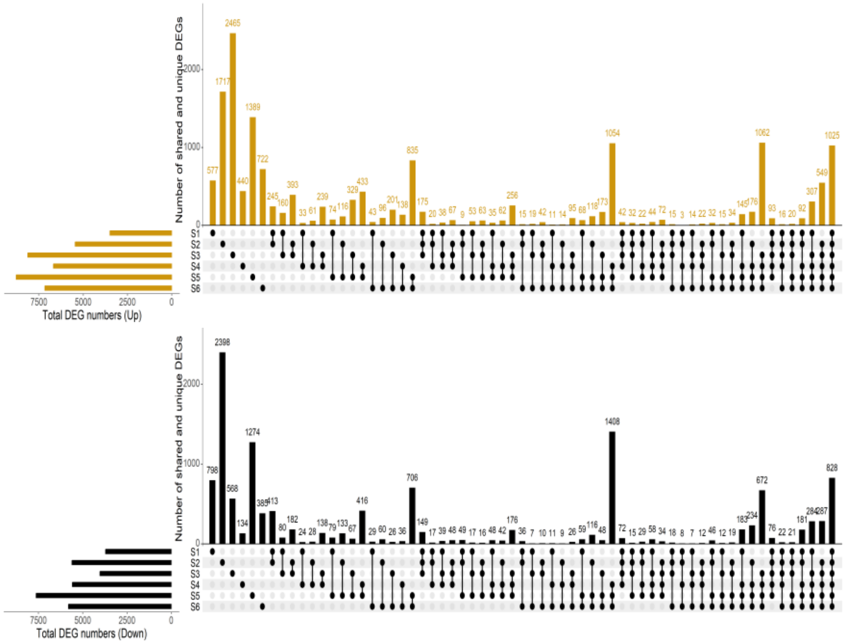


Tracks:

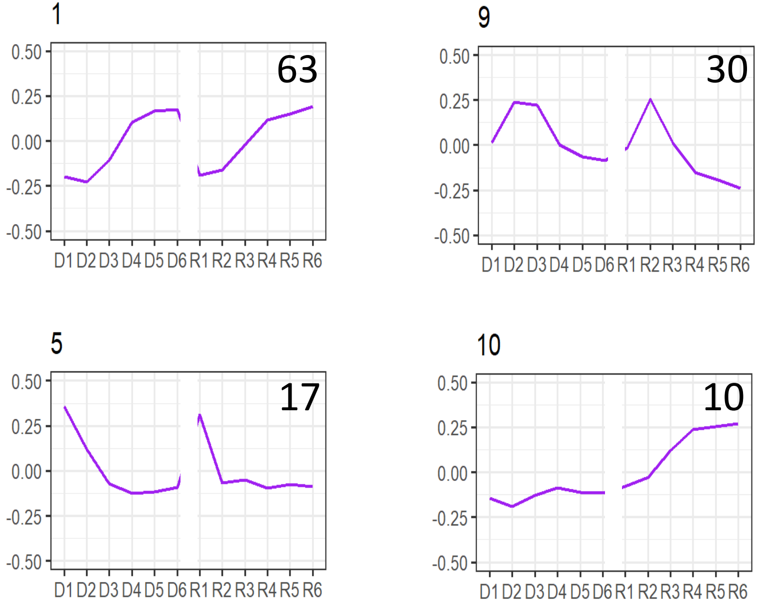
- Transposable Elements
- Gene
- Leaf tissue
- Leptotene
- Zygotene
- Pachytene
- Diplotene
- Diakenesis
- Metaphase I

Number of expressed genes mean(TPM)>0.1 in 1Mbp window, min. 0, max. 200.

Dynamic expression landscape during meiosis

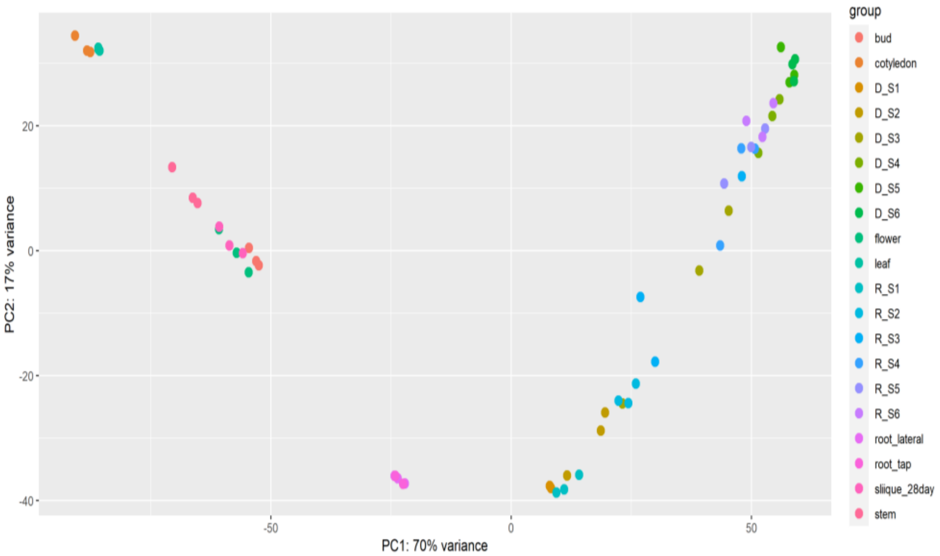


Differentially expressed genes in two lines



Patterns of gene expression across stages in two lines (WGCNA clusters)

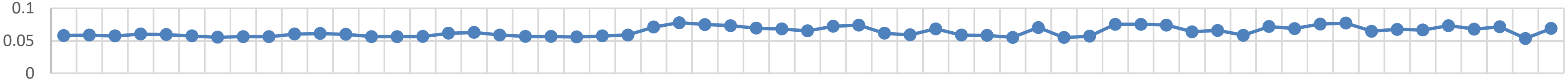
Meiosis specific gene expression

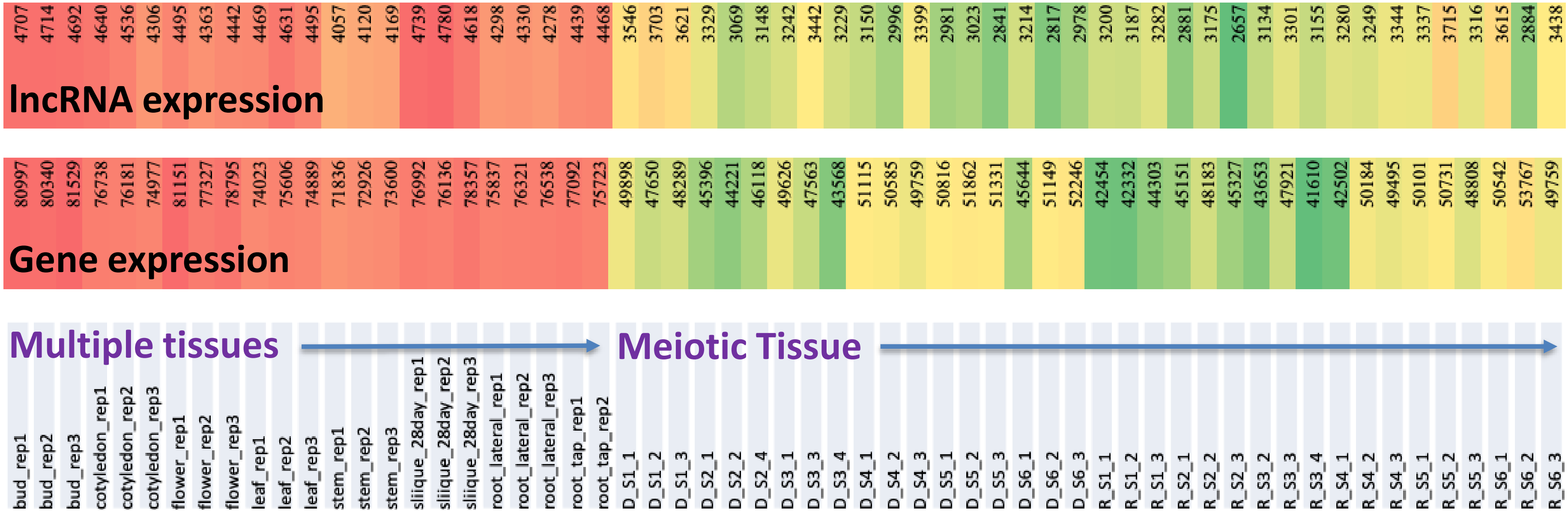


- 371 (574) orthologues of known meiosis genes were expressed in the meiocyte data
- 176 known meiotic genes were specifically expressed only in meiocyte tissue
- An additional 4743 genes were specifically expressed in meiocytes

Influence of long non-coding RNA

Ratio lncRNA/genes

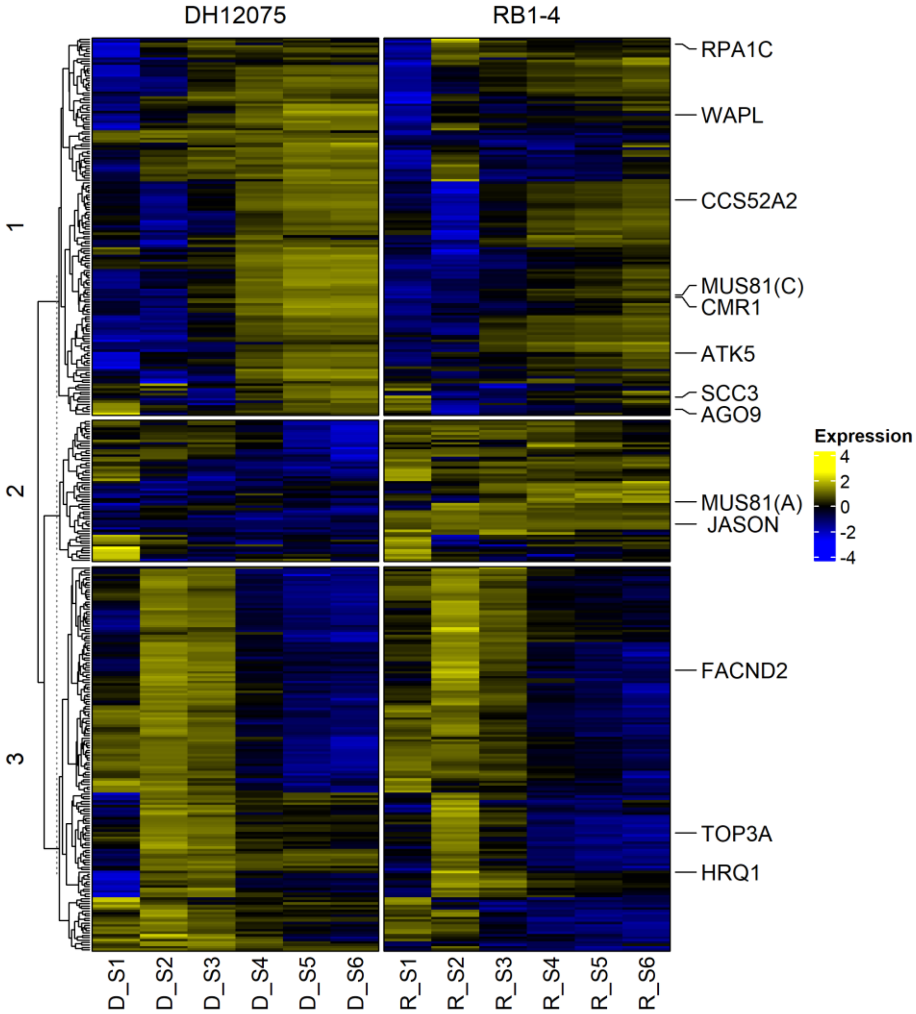




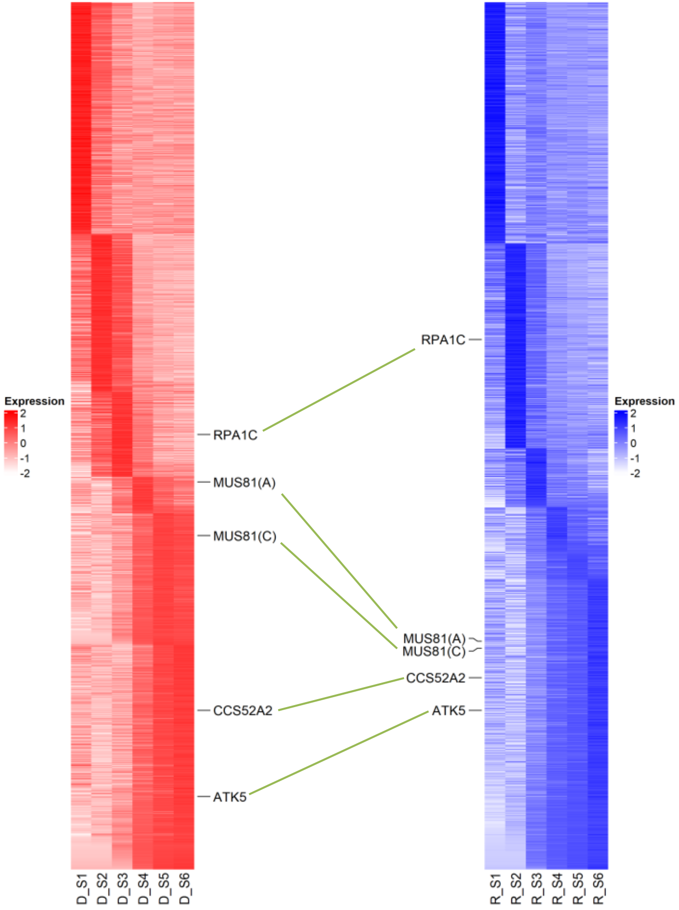
Multiple tissues → **Meiotic Tissue** →

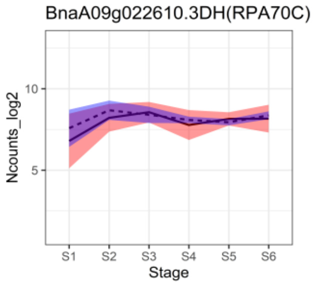
	lncRNA expression	Gene expression
bud_rep1	4707	80997
bud_rep2	4714	80340
bud_rep3	4692	81529
cotyledon_rep1	4640	76738
cotyledon_rep2	4536	76181
cotyledon_rep3	4306	74977
flower_rep1	4495	81151
flower_rep2	4363	77327
flower_rep3	4442	78795
leaf_rep1	4469	74023
leaf_rep2	4631	75606
leaf_rep3	4495	74889
stem_rep1	4057	71836
stem_rep2	4120	72926
stem_rep3	4169	73600
silique_28day_rep1	4739	76992
silique_28day_rep2	4780	76136
silique_28day_rep3	4618	78357
root_lateral_rep1	4298	75837
root_lateral_rep2	4330	76321
root_lateral_rep3	4278	76538
root_tap_rep1	4439	77092
root_tap_rep2	4468	75723
D_S1_1	3546	49898
D_S1_2	3703	47650
D_S1_3	3621	48289
D_S2_1	3329	45396
D_S2_2	3069	44221
D_S2_4	3148	46118
D_S3_1	3242	49626
D_S3_3	3442	47563
D_S3_4	3229	43568
D_S4_1	3150	51115
D_S4_2	2996	50585
D_S4_3	3399	49759
D_S5_1	2981	50816
D_S5_2	3023	51862
D_S5_3	2841	51331
D_S6_1	3214	45644
D_S6_2	2817	51149
D_S6_3	2978	52246
R_S1_1	3200	42454
R_S1_2	3187	42332
R_S1_3	3282	44303
R_S2_1	2881	45151
R_S2_2	3175	48183
R_S2_3	2657	45327
R_S3_2	3134	43653
R_S3_3	3301	47921
R_S3_4	3155	41610
R_S4_1	3280	42502
R_S4_2	3249	50184
R_S4_3	3344	49495
R_S5_1	3337	50101
R_S5_2	3715	50731
R_S5_3	3316	48808
R_S6_1	3615	50542
R_S6_2	2884	53767
R_S6_3	3438	49759

Pattern of expression of orthologues of known meiosis genes

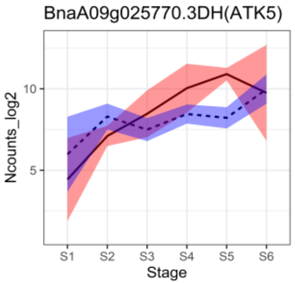


Meiosis genes underlying the A9 QTL





PCC = 0.893



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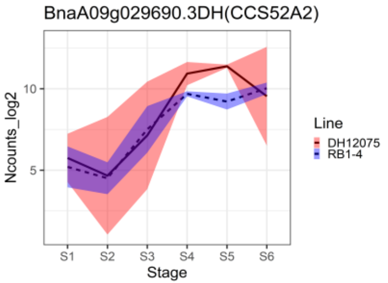
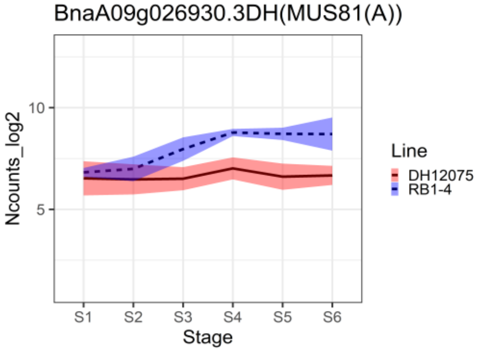
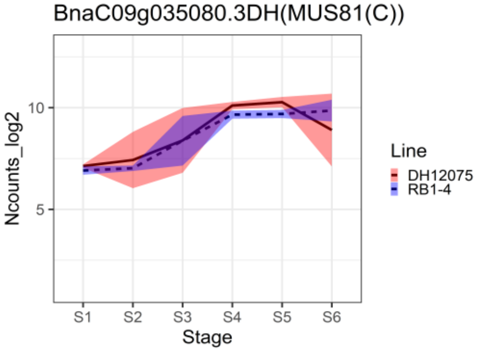


PCC = 0.972



PCC = 0.209



PCC = 0.963

Conclusions

- Active transcriptome landscape during meiosis
  - minimal evidence of lncRNA activity
- Orthologues of known meiotic genes followed similar patterns of expression in natural and resynthesized *B. napus*
  - Yet there were a number of key differences
- Only one orthologue of a known meiotic gene underlying the A9 QTL shows differential expression
- Many novel meiosis specific genes were identified and four that underly the QTL show dominant expression in DH12075

Acknowledgments

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DH12075 Genome

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