

Homoeologous non-reciprocal translocation explains a major QTL for seed lignin content in oilseed rape (*Brassica napus* L.)

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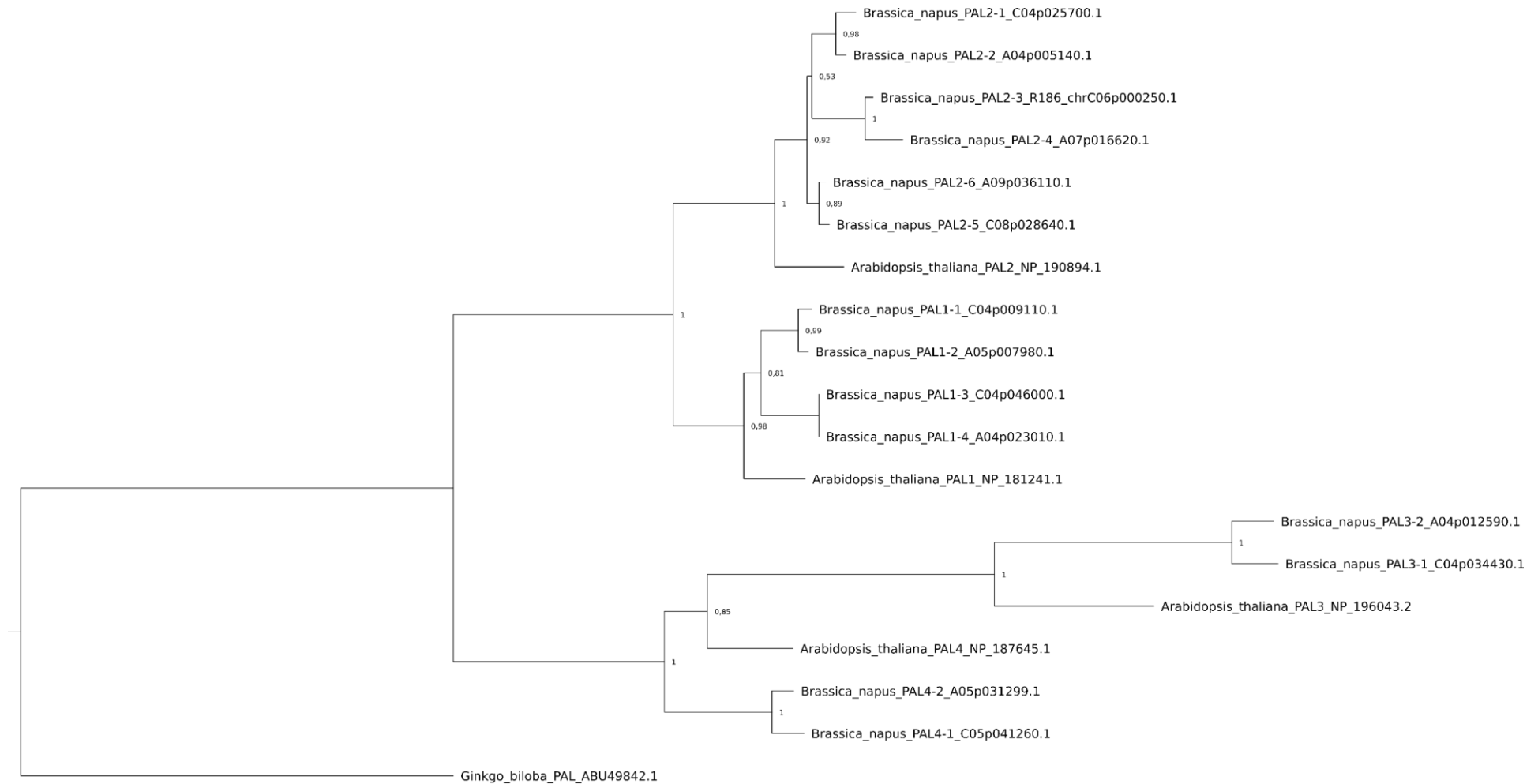
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Theoretical and Applied Genetics



Supplementary Figure 4: Phylogeny of PAL candidates of *B. napus* Express 617 and previously described PAL sequences. The maximum-likelihood tree was constructed with FastTree using 10,000 bootstraps and relative bootstrap-values are shown next to relevant nodes. The phylogenetic tree is based on amino acid sequences. The *Ginkgo biloba* PAL sequence was used to root the tree. The GenBank ID of the respective sequence or the Express 617 gene ID is given for each sequence.

Supplementary Table 6: Amino acid and coding sequences of *B. napus* Express 617 PALs.

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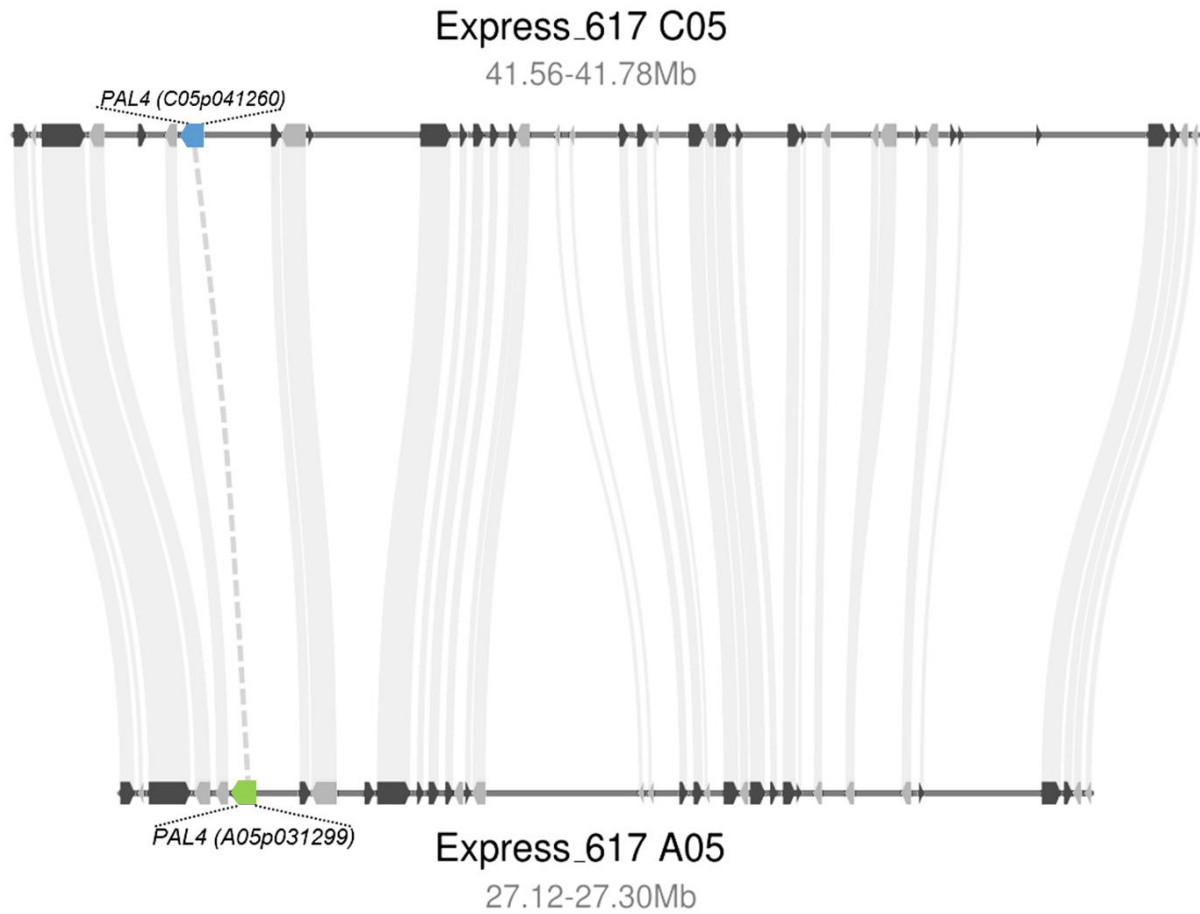
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Supplementary Table 7: Organ-specific expression of *B. napus* Express 617 PAL candidate genes. The median transcripts per millions (TPMs) of each PAL candidate gene per organ is listed. Paired-end RNA-Seq data generated in this study derived from seeds (35 DAF) of Express 617 (E617) and SGD14 (S14) are marked with an asterisk. Publicly available paired-end *B. napus* RNA-Seq data sets were used for the remaining organs. The number of analysed data sets per organ is stated via (n = X). The colour gradient from white to blue indicates the expression strength with dark blue symbolising high expression. DAF, days after flowering; DAP, days after pollination; SAM, shoot apical meristem.

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SAM (n=16)	1.3	8.4	0.0	0.0	2.3	0.6	0.0	0.0	0.0	2.2	4.2	1.5	8.7	0.1
Anther prophase 1 (n=12)	0.1	0.8	0.0	0.0	3.1	2.4	0.0	0.0	0.0	3.7	0.1	0.0	0.1	0.2
Anther bolting (n=6)	0.7	54.0	0.0	0.1	3.0	1.8	0.0	0.0	0.0	4.5	27.9	14.8	19.9	0.0
Anther flowering (n=4)	0.0	70.0	0.0	0.0	9.0	5.8	0.0	0.0	0.0	13.1	33.1	31.6	25.8	20.5
Stamen (n=1)	0.1	30.5	0.0	0.0	0.4	1.0	0.0	0.0	0.0	1.1	9.3	1.5	13.4	4.1
Ovule (n=1)	0.8	135.2	0.0	0.0	18.3	20.6	0.0	0.0	0.0	19.5	25.4	9.1	72.7	17.5
Pistil (n=3)	7.1	11.9	0.0	0.0	4.6	2.8	0.0	0.0	0.0	6.7	12.2	7.0	26.4	3.7
Sepal (n=1)	0.0	2.0	0.0	0.0	7.8	5.9	3.1	0.0	0.0	19.6	6.9	0.0	5.9	0.0
Petal (n=2)	217.4	29.2	0.0	0.0	4.2	1.2	0.8	0.6	0.0	3.7	37.3	232.9	7.4	0.0
Siliques 10-20DAF (n=13)	9.4	22.3	0.0	0.0	10.3	6.0	0.0	0.0	0.0	12.8	29.1	12.1	13.7	7.7
Siliques 25DAF (n=6)	6.4	20.2	0.0	0.0	11.1	11.3	0.0	0.0	0.0	18.1	42.6	3.3	12.5	23.8
Siliques 30DAF (n=6)	10.7	33.8	0.0	0.0	13.7	13.1	0.0	0.0	0.0	18.7	44.7	6.1	11.0	17.6
Siliques 40DAF (n=2)	6.5	22.2	0.0	0.0	7.3	8.1	0.0	0.0	0.0	10.2	19.5	11.9	2.9	6.4
Seed_35DAF_E617* (n=3)	54.9	87.7	0.0	0.0	9.6	11.7	0.0	0.0	0.0	18.1	19.4	31.2	6.9	6.6
Seed_35DAF_S14* (n=3)	0.7	217.0	0.0	0.0	18.6	15.2	0.0	0.0	0.0	18.2	34.1	54.2	6.5	12.6
Seed coat 14DAF (n=7)	0.9	2.5	0.0	0.0	7.7	4.9	0.0	0.0	0.0	5.4	1.5	0.0	3.7	1.5
Seed coat 21DAF (n=6)	38.6	69.5	0.0	0.0	19.5	14.1	0.0	0.0	0.0	16.8	24.7	0.0	34.1	12.2
Seed coat 28DAF (n=6)	120.7	151.6	0.0	0.1	19.2	14.0	0.0	0.0	0.0	20.9	42.5	0.0	95.5	42.2
Seed coat 35DAF (n=6)	92.4	90.8	0.0	0.1	18.3	16.2	0.0	0.0	0.0	18.0	48.4	0.0	91.0	42.0
Seed coat 42DAF (n=6)	111.9	82.6	0.0	0.0	14.6	13.2	0.0	0.0	0.0	21.4	245.5	0.0	63.1	27.8
Embryo (n=6)	13.5	20.4	0.0	0.0	10.5	9.8	0.0	0.0	0.0	25.4	9.5	3.2	2.1	10.9
Endosperm (n=8)	15.2	33.4	0.0	0.0	4.7	4.1	0.0	0.0	0.0	5.5	3.1	3.0	10.4	1.3
Seedling (n=9)	0.2	7.5	0.0	0.1	13.2	10.5	0.0	0.0	0.0	23.6	15.5	10.9	18.6	0.0
Stem (n=19)	126.9	227.9	0.0	0.0	29.0	25.1	0.0	0.0	0.0	67.9	131.6	59.7	117.5	19.9
Shoot (n=2)	2.1	8.2	0.0	0.0	1.8	0.9	0.0	0.0	0.0	3.9	4.9	2.3	5.4	6.0
Shoot apex (n=2)	11.7	8.1	0.0	0.0	4.6	1.6	0.0	0.0	0.0	6.4	4.3	1.1	3.4	1.3
Root seedling (n=13)	8.4	7.6	0.0	0.5	18.4	14.1	0.0	0.0	0.0	56.7	44.3	25.8	31.2	3.6

Root 30DAP (n=20)	6.5	7.4	0.0	0.6	66.3	55.6	0.0	0.0	0.0	82.5	92.6	21.6	77.8	54.7
Root 60DAP (n=2)	0.5	13.8	0.0	0.2	132. 0	148. 0	8.0	0.0	0.0	252. 5	290. 0	17.5	364. 5	1.0



Supplementary Figure 5: *B. napus* Express 617 carries a previously not annotated A05 *PAL4* homolog and shows high local synteny between the homologous A05 region to the C05 region. The synteny plot was constructed based on the Express 617 assembly and covers the C05 region (41,56-41,78 million base pairs (Mb)) located inside the major low lignin QTL, as well as the corresponding homologous A05 region ranging from 27,12-27,30 million base pairs (Mb). Genes located on the forward strand are marked in black, while genes located on the reverse strand are marked in grey. The *PAL4* copy on C05 is highlighted in blue, while the manually annotated *PAL4* copy on A05 is marked in green. Respective novel syntenic genes are marked by a dashed line.

Supplementary Figure 6: The CDS with UTRs and upstream sequences of the A05, A05'', and C05 *PAL4* homologs. The CDS (light yellow box), UTRs (orange boxes) and 5'UTR upstream sequences (grey boxes) of the A05, A05'' and C05 *PAL4* homologs are shown. The A05'' *PAL4* sequence is identical to the A05 *PAL4* sequence except for the positions marked with red and purple rectangles. Subgenome-specific differences between A05 and A05'' *PAL4* to the C05 *PAL4* sequence can thus be inferred by all remaining positions lacking an asterisk underneath the alignment. Positions marked with a red rectangle stress A05'' specific SNPs, while purple rectangles mark SNPs, where the A05'' *PAL4* homolog carries the C05 *PAL4* allele. If one of these SNPs results in an amino acid exchange in the A05'' *PAL4* sequence compared to the A05 *PAL4* sequence a black box underneath each codon shows the respective exchange, e.g. at position 586 a valine was exchanged by isoleucine in the A05'' amino acid sequence. Amino acid exchanges derived from subgenome-specific SNPs are shown in cyan rectangles, e.g. at position 2, the aspartic acid (D) of A05 *PAL4* is changed to glutamic acid (E) in the C05 *PAL4*. Clustal Omega (Sievers et al. 2011) was applied for the construction of the sequence alignment.