Assembly and comparison of two closely related *Brassica napus* genomes

Authors: Philipp E. Bayer1, Bhavna Hurgobin1,2, Agnieszka A. Golicz2, Chon-Kit Kenneth Chan1, Yuxuan Yuan1, HueyTyng Lee1,2, Michael Renton1, Jinling Meng3, Ruiyuan Li3, Yan Long3, Jun Zou3, Ian Bancroft4, Boulos Chalhoub5, Graham J. King3,6, Jacqueline Batley1, David Edwards1

Author affiliations:

1 School of Plant Biology, The University of Western Australia, Stirling Highway, Crawley, WA 6009, Australia

2 Australian Centre for Plant Functional Genomics, School of Agriculture and Food Sciences, University of Queensland, St. Lucia, QLD 4072, Australia

3 National Key Laboratory of Crop Genetic Improvement, Key Laboratory of Rapeseed Genetic Improvement, Ministry of Agriculture P. R. China, Huazhong Agricultural University, Wuhan, China

4 Department of Biology, University of York, York, UK

5 Organization and Evolution of Plant Genomes, Unité de Recherche en Génomique Végétale, Unité Mixte de Recherche 1165 (Institut National de Recherche Agronomique, Centre National de la Recherche Scientifique, Université Evry Val d’Essonne), Evry 91057, France

6 Southern Cross Plant Science, Southern Cross University, Lismore, NSW 2480, Australia

Corresponding author: David Edwards, School of Plant Biology, The University of Western Australia, Stirling Highway, Crawley, WA 6009, Australia. Tel: +61 (0)8 6488 2415 E-mail: [dave.edwards@uwa.edu.au](mailto:dave.edwards@uwa.edu.au)

Word count: 5,704

E-mail addresses in order of authors

philipp.bayer@uwa.edu.au

b.hurgobin@uq.edu.au

agnieszka.golicz@uq.net.au

kenneth.chan@uwa.edu.au

yuxuan.yuan@research.uwa.edu.au

h.lee12@uq.edu.au

michael.renton@uwa.edu.au

jmeng@mail.hzau.edu.cn

ruiyuan.li@gznu.edu.cn

longyan@caas.cn

zoujun@mail.hzau.edu.cn

ian.bancroft@york.ac.uk

chalhoub@evry.inra.fr

Graham.King@scu.edu.au

jacqueline.batley@uwa.edu.au

dave.edwards@uwa.edu.au

Running title: Assembly of *Brassica napus* genomes

Keywords: Genome assembly, whole genome comparison, genotyping by sequencing, genome assembly improvement, *Brassica napus*, Tapidor, contigPlacer

# Abstract

As an increasing number of plant genome sequences become available, it is clear that gene content varies between individuals, and the challenge arises to predict the gene content of a species. However, genome comparison is often confounded by variation in assembly and annotation. Differentiating between true gene absence and variation in assembly or annotation is essential for the accurate identification of conserved and variable genes in a species.

Here we present the *de novo* assembly of the *B. napus* cultivar Tapidor and comparison with an improved assembly of the *B. napus* cultivar Darmor*-bzh*. Both cultivars were annotated using the same method to allow comparison of gene content. We identified genes unique to each cultivar and differentiate these from artefacts due to variation in the assembly and annotation. We demonstrate that using a common annotation pipeline can result in different gene predictions, even for closely related cultivars, and repeat regions which collapse during assembly impact whole genome comparison. After accounting for differences in assembly and annotation, we demonstrate that the genome of Darmor*-bzh* contains a greater number of genes than the genome of Tapidor.

Our results are the first step towards comparison of the true differences between *B. napus* genomes and highlight the potential sources of error in the future production of a *B. napus* pangenome.

# Introduction

*Brassica* is a genus which contains economically important crop species, including condiments such as mustards; vegetable crops including broccoli, Brussels sprouts, cabbage, cauliflower; and commercially important oilseeds which are used as both a food and biofuel. The genomes of the *Brassica* family are related as described in the triangle of U (Nagaharu 1935). There are three diploid *Brassica*-species, *B. rapa* (AA, n=10), *B. nigra* (BB, n=8), and *B. oleracea* (CC, n=9), and these genomes evolved from a common ancestor which underwent at least one whole genome triplication (Lysak et al. 2005). Combinations of these genomes result in three amphidiploid *Brassica* species: *B. juncea* (AABB, n=18), *B. carinata* (BBCC, n=17) and *B. napus* (AACC, n=19). Several *Brassica* genome assemblies have now been published, including the A genome of the *B. rapa* cultivar Chiifu (Wang et al. 2011), the C genome of the *B. oleracea* cultivars A2 (Liu et al. 2014) and TO1000 (Parkin et al. 2014), the AACC genome of the *B. napus* cultivar Darmor*-bzh* (Chalhoub et al. 2014) and the BB and AABB genome of *B. nigra* and *B. juncea* (Yang et al. 2016).

Early indications of significant differences in genome content between individuals was apparent from data obtained from RFLP and SSR analysis in *Brassica* species, where a relatively large number of null alleles were detected with co-dominant molecular assays (Udall et al. 2005). With the increased application of next generation DNA sequencing technology, these genomic differences are becoming more apparent and there is a growing understanding that a single genome does not reflect the gene content of a species. Following the production of reference genome assemblies, searchers are moving towards the characterisation of pangenomes, representing the gene content of a species, including core genes which are found in all individuals and variable genes which are only present in some individuals (Golicz et al. 2015). Variable genes can be split into two groups: copy number variations (CNVs), in which the number of copies of a gene differs between individuals, and presence/absence variations (PAVs), an extreme form of CNV in which a gene is present in some individuals but absent in others (Saxena et al. 2014, Golicz et al. 2016).

Gene presence/absence variation is important for crop improvement as some variable genes have been shown to be associated with agronomic traits. In rice, comparison of three divergent lines led to the identification of several variable genes including the submergence tolerance gene *Sub1A* which is absent in submergence intolerant lines (Schatz et al. 2014). A recent study investigated the pangenome for 1,483 rice accessions and found 1,913 high confidence dispensable genes, out of which 1,489 were expressed (Yao et al. 2015). A genome wide association study (GWAS) with SNPs for those rice accessions found that 23.5% of metabolic traits had higher association signals with SNPs located on dispensable genes than with SNPs located on the core reference genome. Similarly, comparison of three *Brassica rapa* morphological variations (turnip, rapid cycling, Chinese cabbage) revealed around 1,224 unique genes in each of the three genomes (Lin et al. 2014), while another recent study produced low coverage sequence data for 199 *B. rapa* and 119 *B. oleracea* accessions to identify SNPs and trace parallel selection signals in the two subgenomes (Cheng et al. 2016). Regions undergoing positive selection could be identified (25 in *B. rapa* and 58 in *B. oleracea*), out of which 9 were shared between the genomes.

In chickpea, the re-sequencing of 16 lines identified up to 32 genes absent in each line (Thudi et al. 2016), while a comparison of 503 inbred maize lines demonstrated that only 16.4% out of 8,681 representative transcripts were expressed in all lines (Hirsch et al. 2014). Recently, Golicz et al (2016) identified 61,379 genes in a *Brassica oleracea* pangenome study, of which 18.7% demonstrated presence/absence variation among individuals, and with the variable genes being enriched for annotations associated with important agronomic traits.

The repetitive content of plant genomes makes genome assembly and validation a challenge (Edwards et al., 2013). Assemblers often cannot accurately assign sequence reads from repetitive regions to their correct genomic location, and repeat sequences in the genome frequently collapse into a single copy in the assembly. In addition, different annotation results may confound comparative analyses as some genes may not be predicted in some cultivars even if they share significant sequence identify with genes predicted in other cultivars. These factors impact the direct comparison of whole genome assemblies for complex crop genomes and make the assessment of species pangenomes a major challenge.

Here we describe the *de novo* assembly and annotation of the amphidiploid *B. napus* cultivar Tapidor and comparison with an improved and reannotated assembly of the published *B. napus* cultivar Darmor*-bzh* (Chalhoub et al. 2014). Comparison of the gene content between Darmor*-bzh* and Tapidor identified genes that are conserved or unique to each cultivar. In addition, we identified genes which appear to be absent in one or other cultivar due to variation in assembly or annotation. Our results present a detailed assessment and comparison of assemblies for complex *B. napus* genomes, the first step towards establishing a *B. napus* pangenome. These finding highlight the differences which may be observed between cultivars and demonstrate the challenges in producing a future *B. napus* pangenome.

# Results

## The *B. napus* Darmor*-bzh* and Tapidor genome assemblies

The published Darmor*-bzh* assembly (Chalhoub et al. 2014) consists of 19 pseudomolecules anchored to a high resolution genetic map, as well as 19 collections of contigs assigned to a chromosome but not placed, and 3 collections of contigs that are not assigned to any pseudomolecule. In total, the 19 pseudomolecules have a combined length of 850 Mbp which includes 204 Mbp remaining in 22 unplaced collections. K-mer based predictions for both assembly size and genome size were calculated. Using all Darmor*-bzh* reads and all Tapidor reads as input, k-mer based genome assembly size prediction estimated an assembly size of 808 Mbp for Darmor*-bzh* and 697 Mbp for Tapidor, while k-mer based genome size prediction suggested a genome size of 1,345 Mbp for Darmor*-bzh* and 1,335 Mbp for Tapidor.

The SkimGBS pipeline (Bayer et al. 2015) was applied to improve the published Darmor*-bzh* assembly. This predicted 1,006,985 SNPs and called 38,471,969 genotypes across 92 individuals of the Tapidor x Ningyou-7 population, using the published Darmor*-bzh* assembly as the reference. Using this data, contigPlacer added 8,820 previously unplaced contigs into the Darmor*-bzh* pseudomolecules, increasing their length by 153 Mbp (23.6%) (Table 1). It was not possible to place 10,981 contigs (51.3 Mbp), out of which 10,486 carried no SNPs, and 495 had conflicting pseudomolecule locations. Unplaced contigs placed on two different pseudo-molecules had an average size of 7,244 bp ranging from 2,004 bp to 98,348 bp. Of the contigs with a previously assigned pseudomolecule, 98% were placed within their predicted pseudomolecule (Supplementary Table 1).

The *B. napus* cultivar Tapidor was assembled *de novo* using paired end and mate paired Illumina sequencing data with a range of insert sizes. The sequence data was first cleaned prior to assembly. From 417,527,199 Tapidor read pairs, 54,030,058 (12.9%) were identified as clonal and removed. Quality control using sickle (Joshi and Fass 2011) discarded a further 414,133 read pairs and 2,917,744 single reads, while computational normalization using khmer (Brown et al. 2012, Crusoe et al. 2015) removed another 134,597,316 read pairs bringing the final number of read pairs for assembly to 258,028,009. These were assembled using VelvetOptimiser (Gladman and Seemann 2012) in conjunction with Velvet (Zerbino et al. 2008) and a k-mer value of 71. After removal of contigs smaller than 1000 bp the assembly contained 21,280 contigs with an N50 of 197,031 bp and a total size of 634.19 Mbp.

To produce pseudomolecules for Tapidor, the contigs were sorted by comparison with the improved Darmor*-bzh* pseudomolecules, placing 18,087 contigs into 19 pseudomolecules with a total length of 616.7 Mbp, with 3,193 (19.5 Mbp) unplaced contigs. Using this Tapidor assembly, the SkimGBS pipeline predicted 945,406 SNPs and called 35,829,337 genotypes for the Tapidor x Ningyou-7 population. ContigPlacer then placed an additional 452 Tapidor contigs into pseudomolecules, bringing the total size of the Tapidor pseudomolecules to 625.9 Mbp, with 2,741 contigs (8.2 Mbp) remaining unplaced, none of which contained SNPs (Table 1, Supplementary Table 1). A comparison of the Darmor*-bzh* and Tapidor assemblies showed a near perfect overlap, with secondary overlaps due to sequence identity between homeologous chromosomes (Supplementary Figure 1). A high resolution genetic map using the Tapidor x Ningyou-7 DH population and MSTMap (Wu et al. 2008) placed 318.9 Mbp (50.1%) of the Tapidor assembly into 19 linkage groups, and the order of these contigs agreed with the placement of contigs using the Darmor*-bzh* reference (Supplementary Figure 2).

To assess and compare the completeness of the two genome assemblies, CEGMA (Parra et al. 2007) was used to identify core eukaryotic genes (CEGs), and BUSCO (Simão et al 2015) was used with the Plants profile to identify Single-Copy Orthologs (SCOs). All 248 CEGs aligned completely with the Darmor*-bzh* assembly, while only 246 CEGs aligned completely with the Tapidor assembly, with the remaining two partially identified in the assembly. Of the 956 BUSCO groups, 925 and 904 appeared at least once in Darmor*-bzh* and Tapidor respectively. In Darmor*-bzh*, 862 BUSCOs appeared more than once with an average copy number of all BUSCOs of 2.2, while for Tapidor, 634 BUSCOs appeared more than once with an average copy number of 1.8. In Darmor*-bzh*, 26 BUSCOs were missing and 5 were fragmented, while in Tapidor 31 BUSCOs were missing with an additional 21 fragmented. RepeatModeler identified 310,192,450 bp (36.48%) repeats in Darmor*-bzh* and 223,636,559 bp (35.15%) repeats in Tapidor. LTR/Gypsy was the most common repetitive element in both assemblies, with 97,597 copies in Darmor*-bzh* and 92,747 copies in Tapidor (Supplementary Table 2).

## Gene-level comparison between Darmor*-bzh* and Tapidor

Both genome assemblies were annotated using identical publicly available gene, EST, RNA-Seq and protein data. Genes shorter than 100 bp, with an AED score of 1 (no evidence support for the annotation), or carrying transposase-related PFAM domains were removed.

The resulting AUGUSTUS high confidence gene sets contained 80,382 predicted genes for Darmor*-bzh* (37,220 on the A and 39,334 on the C pseudomolecules, 3,228 on unplaced contigs), and 70,162 predicted genes for Tapidor (31,969 on the A and 37,562 on C pseudomolecules, 631 on unplaced contigs) (Table 1).

We compared the gene content between assemblies across each pair of homologous chromosomes. In Darmor*-bzh*, 76,968 out of 77,154 genes (99.7%) located on pseudomolecules had sequence identity with Tapidor genes. Out of these, 65,280 were located in collinear blocks of at least 5 genes in the respective Tapidor pseudomolecule. Of the 11,688 genes with no partners in collinear blocks 2,458 matched sequence on the expected chromosome, out of which 701 matched the expected chromosomal region. In Tapidor, 69,372 out of 69,531 genes (99.7%) showed sequence identity with Darmor*-bzh* genes, with 59,099 genes in collinear blocks of at least five genes. Of the 10,903 genes with no partners in collinear blocks, 2,103 matched with the expected chromosome, out of which 524 matched within the expected range.

To further assess the differences in predicted gene content, we aligned sequence reads from both cultivars to each of the assemblies. Based on genomic read mapping, three Tapidor genes were predicted to be absent in Darmor*-bzh*, while 73 Darmor*-bzh* genes were predicted to be absent in Tapidor (Table 1). The genes predicted to be absent were compared with Darmor*-bzh*, Tapidor, Ningyou-7 and Tapidor x Ningyou-7 RNA-Seq data. Of the 73 genes, 21 (29%) showed no expression in Darmor-*bzh* or Tapidor, 19 (26%) were expressed in Darmor-*bzh* but neither Tapidor nor Ningyou-7, 27 (37%) were expressed in Darmor-*bzh* and Ningyou-7 but not in Tapidor, and expression segregated in the Tapidor x Ningyou-7 DH population, 2 (2.7%) were expressed in Tapidor and Ningyou-7 but not in Darmor-*bzh*, while 4 (5.5%) were expressed in all tissues in cases (Supplementary Table 3). The 3 genes predicted to be absent in Darmor-*bzh* but not in Tapidor were not expressed in Darmor-*bzh*, Ningyou-7 or Tapidor (Supplementary Table 4).

Proteins encoded by genes predicted to be absent in one of the two cultivars were compared with Swiss-Prot and checked for enriched GO-terms. In genes present in Darmor*-bzh* but not in Tapidor, terms such as ‘RNA splicing’ and ‘floral meristem growth’ were enriched (p < 0.05, Supplementary Table 5). The 3 genes predicted to be present in Tapidor but not in Darmor*-bzh* had no Swiss-Prot hits and therefore, transfer of GO annotation was not possible.

## Assessment of repetitive and collapsed assembly regions

Using the differential comparative read mapping pipeline CoReFinder, we identified 30,200 and 26,812 collapsed regions longer than 50 bp, with a total length of 12,495,844 bp and 10,522,089 bp and average sizes of 413 bp and 392 bp in the Darmor*-bzh* and Tapidor assemblies respectively (Figure 1, Supplementary Table 6). We also identified 43,775 and 2,191 repetitive regions, where the sequence is represented more than once in the assembly, totalling 31,807,543 bp and 972,605 bp, with an average of 720 bp and 437 bp in Darmor*-bzh* and Tapidor respectively (Figure 2, Supplementary Table 7).

Genes were identified in both the collapsed and repetitive regions of the Darmor*-bzh* and Tapidor assemblies. In Darmor*-bzh*, 2,455 genes (3.1%) were located in collapsed regions and 5,703 (7.1%) were located in repetitive regions, while in Tapidor, 2,651 genes (3.8%) were located in collapsed regions and 246 (0.4%) were located in repetitive regions (Supplementary Table 8). In Tapidor, chromosome A2 and C2 carried the largest number of collapsed genes (410, 15% and 245, 9.2%) while in Darmor*-bzh*, chromosomes A3 and C3 carried the largest number of collapsed genes (212, 8.6% and 222, 9.0%). In Darmor*-bzh*, the chromosomes A3 and C3 carried the largest number of repetitive genes (588, 10.3% and 470, 8.2%) while chromosomes A1 and C1 carried the most repetitive genes in Tapidor (26, 10.5% and 28, 11.4%).

Pfam protein domains and UniProtKB/Swiss-Prot hits were identified for genes located in repetitive and collapsed regions in both assemblies. Both sets of results were compared between Darmor*-bzh* and Tapidor in order to identify any common patterns that may lead to problems in genome assemblies. The largest number of shared Pfam domains and shared Swiss-Prot hits was between genes located in repetitive regions in Darmor*-bzh* and genes located in collapsed regions in Tapidor. In repetitive genes in Darmor*-bzh*, 10% of Pfam domains overlapped with collapsed genes in Tapidor and Pfam domains collapsed in Darmor*-bzh*, while only 0.5% of genes located in collapsed and repetitive regions in Tapidor shared Pfam domains (Figure 3).

The repetitive genes in Darmor*-bzh* and collapsed genes in Tapidor contained repetitive domains such as “Myb-like DNA-binding domain” or “pentatricopeptide repeat” (PPRs) (Supplementary Table 9). A similar pattern was exhibited in shared Swiss-Prot hits where the greatest overlap in terms of Swiss-Prot hits was between the set of proteins encoded by Darmor*-bzh* genes located in collapsed regions and Tapidor genes located in repetitive regions (Supplementary Figure 3). As with the Pfam domain overlaps, 10% of Swiss-Prot hits were shared between repetitive genes in Darmor*-bzh* and collapsed genes in Tapidor. The Swiss-Prot hits contained proteins such as “Myosin-6” or “Proline-rich receptor-like protein kinase” (Supplementary Table 10).

# Discussion

*Brassica napus* canola is an important global crop and a major source of vegetable oil for human consumption. While genetic markers have been used for crop improvement for several years (Hayward et al., 2012), the application of genomics is only now leading to improved traits in the field. A major limitation of genomics based crop improvement is the lack of available reference genome assemblies. The first public *Brassica napus de novo* whole genome assembly was published in 2014, supported by a large multinational endeavour (Chalhoub et al., 2014). Since this achievement, DNA sequencing and bioinformatics technologies have advanced, and it has become increasingly accepted from studies in a wide range of crop species that a single reference is insufficient to describe the gene content of a species. To start to address this issue, we produced a second *de novo* whole genome assembly for a closely related cultivar, *B. napus* Tapidor. Tapidor and Darmor-*bzh* both share Jet Neuf as an ancestor, but Darmor-*bzh* additionally has the cultivar Bronowski in its direct ancestry (Foisset et al. 1995), while Tapidor contains Bienvenu in its ancestry (Sharpe et al. 2003).

To permit a direct comparison between the Tapidor and Darmor-*bzh* genome assemblies, we improved the published Darmor*-bzh* genome using high resolution skim genotyping by sequencing (Bayer et al. 2015) to position previously unplaced contigs within pseudomolecules. Both assemblies were then annotated using the same data and methods to prevent confounding.

The assembly of the cultivar Tapidor was smaller (635 Mbp) compared with an assembly size of 850 Mbp for Darmor*-bzh* (Table 1). By using k-mers to predict both the assembly size and the genome size, we found that the estimated genome size was similar for both Darmor*-bzh* (1,345 Mbp) and Tapidor (1,335 Mbp). In contrast, the predicted assembly size was similar to, though smaller than the actual assembly size with an estimated 808 Mbp for Darmor*-bzh* and 697 Mbp for Tapidor. The predicted genome size estimate accounts for coverage, sequencing depth and unique k-mers, while the genome assembly estimates account only for unique k-mers. The Tapidor sequence data contains fewer unique k-mers than the Darmor*-bzh* sequencing data, which suggests that the Tapidor genome is actually smaller than the Darmor*-bzh* genome. Both estimated genome sizes here are larger than the flow-cytometry based estimations for different *B. napus* (AACC) cultivars of 1,129 to 1,235 Mbp (Arumuganathan et al. 1991). While the predicted genome size difference probably reflects a real difference in genome size, the discrepancy between the assembly size of Tapidor and Darmor*-bzh* is probably due to the different sequencing technologies that were used for assembly. Tapidor was assembled with short paired end sequences, while Darmor*-bzh* was assembled using a combination of paired end, 454 and Sanger sequencing (Chalhoub et al. 2014). The consistent differences between the assembly sizes and predicted genome sizes is common for genome assemblies and reflects the challenges of assembling the most repetitive regions of the genome.

While there appears to be a real difference in the genome size of these two homozygous individuals, we hypothesize that the different assembly methods cause the majority of observed differences between the assemblies. The CEGMA results suggest that both assemblies contain the majority of the gene content and that both assemblies are of high quality. Both assemblies contain all core eukaryotic genes (CEGs), though two CEGs were only partially present in Tapidor, which suggests that this assembly may be more fragmented. Similarly, the BUSCO results show that both assemblies carry the majority of gene content, with the Darmor*-bzh* assembly having more gene copies than Tapidor. This suggests that some gene copies have collapsed in the Tapidor assembly which have not collapsed in the Darmor*-bzh* assembly. The increased collapsing of regions in the Tapidor assembly compared to the Darmor*-bzh* assembly is probably due to the use of long read 454 and Sanger sequence data in the production of the Darmor*-bzh* assembly.

Both the genomes were annotated using the same methods and supporting data. Gene prediction is dependent on a wide range of factors and the number of predicted genes is influenced by the stringency of gene calling. To enable the most robust comparison of predicted genes between these assemblies, we applied a relatively strict gene calling approach. The number of predicted genes for Darmor*-bzh* is lower in our study than the 101,040 gene models originally predicted by Chalhoub et al. (2014), and this difference is likely due to the more stringent methods of repeat masking employed, including the removal of transposon-related and short genes.

As the Tapidor contigs were scaffolded based on the Darmor*-bzh* assembly, and both Tapidor and Darmor-*bzh* have shared ancestry, we expected to see extensive collinearity between the genome assemblies. We assessed this by comparison of genes present in collinear blocks along the pseudomolecules. We also examined whether genes which were predicted to be missing from collinear blocks were in fact missing or just remained unannotated. In Darmor*-bzh*, 11,688 genes (14.5%) and in Tapidor 10,903 genes (15.5%) were not in collinear blocks and were not identified in their expected regions, suggesting that they are either misplaced in the assembly or are non-syntenic in the genome. Extensive homeologous recombination has been observed in *B. napus* genes (Nicolas et al. 2007, Cai et al. 2014, Chalhoub et al. 2014) which should explain some of the non-syntenic regions observed here.

As differences in genome assembly and annotation may suggest differences in gene content which are not reflected in the actual genome, we investigated the number of genes predicted to be absent in each cultivar based on raw data and independent of gene assembly or annotation (Table 1). Mapping genomic sequence reads between references suggests that 73 genes are unique to Darmor*-bzh* and absent in Tapidor, while three genes are unique to Tapidor and absent in Darmor*-bzh*. Out of the 73 genes predicted to be absent 27 (37%) were expressed in Darmor-*bzh* and Ningyou-7 but not in Tapidor, with clear segregation in the Tapidor x Ningyou-7 DH population, suggesting that these genes have been truly lost in Tapidor but are present in Ningyou-7 (Supplementary Table 3). The 19 (26%) genes expressed in Darmor-*bzh* but not in Tapidor or Ningyou-7 may also be absent in Ningyou-7, or their expression may not be captured in the Darmor-*bzh* RNA-Seq libraries. Some error remains, as 2 genes (2.7%) predicted to be absent in Tapidor and present in Darmor-*bzh* appear to be expressed in Tapidor but not in Darmor-*bzh,* and 4 genes (5.5%) appear to be expressed in all cultivars. These results may be due to the more relaxed mapping parameters for the single RNASeq reads compared to the paired genomic sequence reads, leading to erroneous read mapping and false calling of gene presence in the RNASeq analysis. Genes which showed no expression in any of the cultivars assessed may be pseudogenes, misannotated or only expressed in certain conditions or tissues which were not sampled during RNA-Seq library preparation (Supplementary Table 4).

The relatively small difference in the presence of unique genes compares with 10,220 annotated Darmor*-bzh* genes which are not found in the Tapidor assembly. To test whether this difference is due to duplicate gene copies that have collapsed into single copies in the Tapidor assembly, we investigated the number and size of collapsed and repetitive regions in both assemblies (Supplementary Table 6, Supplementary Table 7, Figure 1, Figure 2). The number and the size of repetitive regions was greater in the Darmor*-bzh* assembly by a factor of 19 and 32, respectively. These numbers are in line with the above gene number differences as well as the differences of assembly size and estimated assembly size, and suggests that the longer 454 and Sanger reads used in the Darmor*-bzh* assembly lead to more repetitive regions being assembled and less collapsing of genomic regions in Darmor*-bzh*.

Homeologous exchanges (HEs) are frequently observed in polyploid species, and the number of genes located in repetitive and collapsed regions can be used for the detection of HE between the A and the C-genome (Chalhoub et al. 2014). Here the largest and second largest number of collapsed and repetitive genes in both assemblies is always between a chromosome and its homeologous partner chromosome in the same cultivar, such as A2 and C2 for the number of collapsed genes in Darmor-*bzh*. The pseudomolecule with the greatest size of collapsed region is C2 in Darmor-*bzh* which is also consistent with prior reports (Chalhoub et al. 2014). When comparing both cultivars, chromosome C2 shows the greatest difference, with 23 (31%) of genes not present in Tapidor in the first 10 Mbp, and 245 (9.2%) of collapsed genes in Tapidor being located on C2 in the first 10 Mbp. The number of collapsed genes suggests homeologous exchange of the first 10 Mbp between A2 and C2 with subsequent loss of the original C2 arm in Tapidor (a homeologous non-reciprocal translocation, HNRT), but that this genome structure is not present in Darmor-*bzh*. The genes in this region are enriched for the GO-term ‘floral meristem growth’ (p < 0.05), and chromosome C2 contains several breeding related QTLs such as seed yield, seed weight and heterosis (Zhao et al. 2016). This suggests that selection for agronomic traits may be responsible for the observed differences between Darmor*-bzh* and Tapidor on this chromosome.

The inability to assemble repetitive sequences can lead to the underestimation of gene content and the incorrect calling of presence/absence variation between assemblies. The annotation of genes located in repetitive and collapsed regions helps to identify which protein domains may be associated with poor assembly and subject to incorrectly called presence/absence variation. We observed an overlap in shared domains and Swiss-Prot hits between genes located in repetitive regions in Darmor*-bzh* and collapsed regions in Tapidor (Figure 3, Supplementary Figure 3). Shared domains include known repetitive domains such as WD repeats or pentatricopeptide repeats (PPRs), while shared Swiss-Prot hits included leucine-rich repeat receptor kinases, as well as somatic embryogenesis receptor kinases which contain leucine repeats (Hecht et al. 2001). This suggests that genes which have repetitive domains under-assemble using only short-read technology but at least some of these may be correctly assembled when longer sequence reads are included in the assembly process. However, the inclusion of 454 reads does not correctly assemble all repetitive genes as many collapse related Pfam and Swiss-Prot domains are located in collapsed regions in Darmor*-bzh*, indicating that there is still missing gene content in the high quality Darmor*-bzh* assembly (Figure 3). The potential collapsing of genomic regions containing important agronomic genes is important for both future genome assembly projects as well as future pangenome analysis as the capturing of all gene content which may play a role in agronomic performance is important for the application of genomics assisted breeding.

The differential assembly of genes with repetitive domains along with the presence of homeologous exchanges is likely to confound the assessment of gene presence variation between individuals and the translation of this information for the agronomic improvement of crop species. For example, there are several reports of variation in NBS LRR gene content between individuals and that this may play an important role in the resistance or susceptibility of crops to disease (Tollenaere et al. 2012, Wu et al. 2014). While the evidence suggests that there is likely to be some true variation in the presence of these genes, it is important to differentiate between true variation and assembly or annotation issues when interpreting the biological function of these genes as assembly and annotation variation can confound gene trait associations.

# Conclusions

We have *de novo* assembled and annotated a second genome for the important oilseed crop species, *B. napus* canola, and compared this with an improved and reannotated assembly of the published cultivar Darmor*-bzh* (Chalhoub et al., 2014). We demonstrate that comparison of gene content between individuals needs to account for differences in assembly and annotation to avoid misinterpretation. Between the two assemblies, only three and 73 predicted genes represent real gene loss between these closely related cultivars, 524 and 701 (0.7 to 0.8%) are due to misannotation (i.e., the gene annotation process failed to identify a gene in one assembly but predicted its presence in the other assembly), while 10,903 and 11,688 (14-15%) of the differences were due to either misplaced contigs or real gene movement. Our results suggest that researchers comparing different genome assemblies should not rely solely on the results of annotation pipelines but should also compare the assemblies and the unassembled read data to differentiate between real differences and artefacts. In particular, genes with repetitive domains may collapse leading to an underestimation of gene copy number. By accounting for these potential errors it is possible for future studies to establish an accurate pangenome for this important oilseed crop.

# Methods

## Darmor*-bzh* and Tapidor genome assemblies

All Tapidor reads were cleaned using sickle (Joshi and Fass 2011) and normalized using khmer v1.0 normalize\_by\_median.py (Brown et al. 2012, Crusoe et al. 2015). VelvetOptimiser (Gladman and Seemann 2012) was used with Velvet (Zerbino et al. 2008) to assemble contigs. Contigs greater than 1 Kbp were sorted by comparison with the Darmor*-bzh* assembly using blastn (Altschul et al. 1990) with an e-value of 1e-6. Contigs with two highest-scoring alignments within 1% were unplaced. Contigs were then sorted by using LASTZ (Harris 2007) and a custom script (LASTZSorter.py, available at <http://appliedbioinformatics.com.au/index.php/Darmor_Tapidor>). MSTMap (Wu et al. 2008) was used to calculate the genetic map using the unimputed SNPs of the DH population (distance\_function: kosambi, cut\_off\_p\_value: 0.0000001, no\_map\_size 2, missing\_threshold 0.1).

SGSautoSNP (Lorenc et al. 2012) was used with the SkimGBS pipeline (Bayer et al. 2015) to call SNPs and genotypes using either the Tapidor or Darmor*-bzh* genome as reference (Chalhoub et al. 2014). ContigPlacer was used to place unplaced contigs in the Darmor*-bzh* and Tapidor assemblies and is available at <https://github.com/philippbayer/contigPlacer>.

## Genome annotation

RepeatModeler v1.0.8 and RepeatMasker v4.0.6 (http://repeatmasker.org) together with Repbase v were used to mask repeats. Gene models were produced using Tophat v2.1.0 and cufflinks v2.2.0 (Kim et al. 2013), and annotation was performed using MAKER v2.31 (Cantarel et al. 2008). RNA-Seq data for the cultivars Tapidor, Ningyou and TN DH (Higgins et al. 2012) were used together with Darmor*-bzh* RNA-Seq reads (Chalhoub et al. 2014).

CEGMA v2.5 (Parra et al. 2007) was used to annotate the *Brassica oleracea* C genome (Parkin et al. 2014) with core gene models (COGs). The annotated core genes were used as input for AUGUSTUS v3.0.2 (Keller et al. 2011). A set of ESTs from the 95k microarray (Trick et al. 2009), Brassicaceae proteins from RefSeq, and *Brassica rapa*, *Brassica oleracea* and *Brassica napus* unigenes from UniGene (NCBI Resource Coordinators 2013) were used as evidence. Predicted genes with an AED-score of 1, shorter than 100 bp, or carrying transposase-related domains were removed from subsequent analysis. Both assemblies were assessed using CEGMA v2.5 (Parra et al. 2007) and BUSCO v1.1.b1 (Simão et al 2015) with the early release plants dataset. Predicted transcripts and proteins were renamed according to the standardised *Brassica* nomenclature (Østergaard et al. 2008).

## Gene-level comparison between Darmor*-bzh* and Tapidor

MCScanX (Wang et al. 2012) was used to analyse collinearity between the Darmor*-bzh* and Tapidor genes and to assign predicted genes to blocks of at least 5 colinear genes. Custom scripts were used to parse the MCScanX output. Genes were compared with the Tapidor pseudomolecules using blastp with an e-value cutoff of 1e-10. The scripts are available at <http://appliedbioinformatics.com.au/index.php/Darmor_Tapidor> under ‘Colinearity analysis’.

Assessment of gene loss used the SGSGeneLoss pipeline v0.1 (Golicz et al. 2014). Public Darmor*-bzh* (BioProject ID: ERP005275, ERP005532) reads were aligned using bowtie2 (settings: --end-to-end, --sensitive) (Langmead et al. 2012) and extracted using samtools (Li et al. 2009). Gene expression levels of the genes predicted to be absent was measured using bowtie v1.1.2 (Langmead et al. 2009) and eXpress v1.5.1 (Roberts et al. 2012) and the same RNA-Seq data as used for the annotation. Predicted genes showing less than 5 unique fragments mapping in a library were assumed to be not expressed in that library to account for possible mismappings from expressed homeologous genes.

Genes were functionally annotated using blastp and UniProtKB Swiss-Prot. GO terms were determined from Swiss-Prot results and topGO as used to predict enriched GO-terms (Alexa et al. 2010).

To identify collapsed and repeated regions in the Tapidor and Darmor*-bzh* assemblies, reads from each cultivar were mapped to their respective genome reference assemblies using SOAPaligner v2.21 with parameters -r 0, -r 1, and -r 2 to generate three sets of alignments. Base coverage was calculated for each BAM file using BEDTools genomecov v2.21.0 (Quinlan et al. 2010). The CoReFinder pipeline (<http://appliedbioinformatics.com.au/index.php/CoReFinder>) identified collapsed and repetitive regions with a minimum block size of 50 bp. R v3.2 (R Development Core Team 2011) was used to perform the Mann-Whitney U test using the wilcox.test() function to compare the number and lengths of repetitive and collapsed regions between Darmor*-bzh* and Tapidor. Conserved domains were identified using the command-line version of InterProScan version 5.14-53.0 (Zlobnov et al. 2001) (settings: -appl Pfam).

# Data access

All raw sequence reads for the cultivar Tapidor used for assembly have been submitted to NCBI BioProject (<https://www.ncbi.nlm.nih.gov/bioproject/342383>). The Tapidor x Ningyou-7 DH data is available at <http://www.ncbi.nlm.nih.gov/bioproject/PRJNA274890>

The assemblies and annotations along with scripts and other information described in this manuscript are available at http://appliedbioinformatics.com.au/index.php/Darmor\_Tapidor

# Acknowledgments

The authors would like to acknowledge funding support from the Australian Research Council (Projects LP110100200, LP130100925, LP140100537 and DP160104497), from the UK Biotechnology and Biological Sciences Research Council (BBSRC) to GK (BB/E017797/1) and IB (BB/E017363/1) and from the National Basic Research and Development Programme of China (2006CB101600). This work was supported by resources provided by the Pawsey Supercomputing Centre with funding from the Australian Government and the Government of Western Australia, the Australian Genome Research Facility (AGRF), the Queensland Cyber Infrastructure Foundation (QCIF) and the Australian Partnership for Advanced Computing (APAC).

# Disclosure declaration

The authors declare no competing interests.

# References

Alexa, A. Rahnenfuhrer, J. (2010). topGO: enrichment analysis for gene ontology. R package version, 2(0).

Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. 1990. Basic local alignment search tool. *J Mol Biol* **215**: 403–10.

Arumuganathan, K. and Earle, E.D. 1991. Nuclear DNA Content of Some Important Plant Species. *Plant Molecular Biology Reporter* **9**(3): 211-215.

Bayer PE, Ruperao P, Mason AS, Stiller J, Chan C-KK, Hayashi S, Long Y, Meng J, Sutton T, Visendi P, Varshney RK, Batley J, Edwards D. 2015. High-resolution skim genotyping by sequencing reveals the distribution of crossovers and gene conversions in *Cicer arietinum* and *Brassica napus.* *Theor Appl Genet* **128**: 1039–47.

Brown CT, Howe A, Zhang Q, Pyrkosz AB, Brom TH. 2012. A Reference-Free Algorithm for Computational Normalization of Shotgun Sequencing Data. http://arxiv.org/abs/1203.4802

Cai G, Yang Q, Yi B, Fan C, Edwards D, Batley J, Zhou Y, Adams K, Wendel J, Otto S, et al. 2014. A Complex Recombination Pattern in the Genome of Allotetraploid *Brassica napus* as Revealed by a High-Density Genetic Map ed. H. Candela. *PLoS One* **9**: e109910.

Cantarel BL, Korf I, Robb SMC, Parra G, Ross E, Moore B, Holt C, Sánchez Alvarado A, Yandell M. 2008. MAKER: an easy-to-use annotation pipeline designed for emerging model organism genomes. *Genome Res* **18**: 188–96.

Chalhoub B, Denoeud F, Liu S, Parkin IAP, Tang H, Wang X, Chiquet J, Belcram H, Tong C, Samans B, Corréa M, Da Silva C, Just J, Falentin C, Koh CS, Le Clainche I, Bernard M, Bento P, Noel B, Labadie K, Alberti A, Charles M, Arnaud D, Guo H, Daviaud C, Alamery S, Jabbari K, Zhao M, Edger PP, Chelaifa H, Tack D, Lassalle G, Mestiri I, Schnel N, Le Paslier M-C, Fan G, Renault V, Bayer PE, Golicz AA, Manoli S, Lee T-H, Thi VHD, Chalabi S, Hu Q, Fan C, Tollenaere R, Lu Y, Battail C, Shen J, Sidebottom CHD, Wang X, Canaguier A, Chauveau A, Bérard A, Deniot G, Guan M, Liu Z, Sun F, Lim YP, Lyons E, Town CD, Bancroft I, Wang X, Meng J, Ma J, Pires JC, King GJ, Brunel D, Delourme R, Renard M, Aury J-M, Adams KL, Batley J, Snowdon RJ, Tost J, Edwards D, Zhou Y, Hua W, Sharpe AG, Paterson AH, Guan C, Wincker P. 2014. Early allopolyploid evolution in the post-Neolithic *Brassica napus* oilseed genome. *Science* **345:** 950-953.

Cheng F, Sun R, Hou X, Zheng H, Zhang F, Zhang Y, Liu B, Liang J, Zhuang M, Liu Y, Liu D, Wang X, Li P, Liu Y, Lin K, Bucher J, Zhang N, Wang Y, Wang H, Deng J, Liao Y, Wei K, Zhang X, Fu L, Hu Y, Liu J, Cai C, Zhang S, Zhang S, Li F, Zhang H, Zhang J, Guo N, Liu Z, Liu J, Sun C, Ma Y, Zhang H, Cui Y, Freeling MR, Borm T, Bonnema G, Wu J, Wang X. 2016. Subgenome parallel selection is associated with morphotype diversification and convergent crop domestication in *Brassica rapa* and *Brassica oleracea*. *Nat Genet* 1–10.

Crusoe MR, Alameldin HF, Awad S, Boucher E, Caldwell A, Cartwright R, Charbonneau A, Constantinides B, Edvenson G, Fay S, Fenton J, Fenzl T, Fish J, Garcia-Gutierrez L, Garland P, Gluck J, González I, Guermond S, Guo J, Gupta A, Herr JR, Howe A, Hyer A, Härpfer A, Irber L, Kidd R, Lin D, Lippi J, Mansour T, McA’Nulty P, McDonald E, Mizzi J, Murray KD, Nahum JR, Nanlohy K, Nederbragt AJ, Ortiz-Zuazaga H, Ory J, Pell J, Pepe-Ranney C, Russ ZN, Schwarz E, Scott C, Seaman J, Sievert S, Simpson J, Skennerton CT, Spencer J, Srinivasan R, Standage D, Stapleton JA, Steinman SR, Stein J, Taylor B, Trimble W, Wiencko HL, Wright M, Wyss B, Zhang Q, zyme en, Brown CT, Crusoe MR, Alameldin HF, Awad S, Boucher E, Caldwell A, Cartwright R, Charbonneau A, Constantinides B, Edvenson G, Fay S, Fenton J, Fenzl T, Fish J, Garcia-Gutierrez L, Garland P, Gluck J, González I, Guermond S, Guo J, Gupta A, Herr JR, Howe A, Hyer A, Härpfer A, Irber L, Kidd R, Lin D, Lippi J, Mansour T, McA’Nulty P, McDonald E, Mizzi J, Murray KD, Nahum JR, Nanlohy K, Nederbragt AJ, Ortiz-Zuazaga H, Ory J, Pell J, et al. 2015. The khmer software package: enabling efficient nucleotide sequence analysis. F1000Research 4.

Edwards D, Batley J, Snowdon RJ. 2013. Accessing complex crop genomes with next-generation sequencing. *Theoretical and Applied Genetics* **126:** 1-11

Foisset N, Delourme R, Barret P, Renard M. 1995. Molecular tagging of the dwarf BREIZH (*Bzh*) gene in *Brassica napus*. *Theor Appl Genet* **91**: 756–761.

Gladman S, Seemann T. 2012. VelvetOptimiser (Version 2.2.4) [Software]. Available at <http://www.bioinformatics.net.au/software.velvetoptimiser.shtml>

Golicz AA, Martinez PA, Zander M, Patel DA, Van De Wouw AP, Visendi P, Fitzgerald TL, Edwards D, Batley J. 2014. Gene loss in the fungal canola pathogen *Leptosphaeria maculans. Funct Integr Genomics* **15**: 189–96.

Golicz AA, Batley J, Edwards D. 2016. Towards plant pangenomics. *Plant Biotechnol J* **14**: 1099–1105.

Golicz AA, Bayer PE, Barker GC, Edger PP, Kim H, Martinez PA, Chan CKK, Severn-Ellis A, McCombie WR, Parkin IAP, Paterson AH, Pires JC, Sharpe AG, Tang H, Teakle GR, Town CD, Batley J, Edwards D. 2016. The pangenome of an agronomically important crop plant Brassica oleracea. *Nat Commun* **7**: 13390.

Harris, R.S. 2007. Improved pairwise alignment of genomic DNA. Ph.D. Thesis, The Pennsylvania State University.

Hayward A, Mason AS, Dalton-Morgan J, Zander M, Edwards D, Batley J. 2012. SNP discovery and applications in Brassica napus*. Journal of Plant Biotechnology* **39:** 49-61

Hecht V, Vielle-Calzada JP, Hartog M V, Schmidt ED, Boutilier K, Grossniklaus U, de Vries SC. 2001. The Arabidopsis SOMATIC EMBRYOGENESIS RECEPTOR KINASE 1 gene is expressed in developing ovules and embryos and enhances embryogenic competence in culture. *Plant Physiol* **127**: 803–16.

Higgins J, Magusin A, Trick M, Fraser F, Bancroft I. 2012. Use of mRNA-seq to discriminate contributions to the transcriptome from the constituent genomes of the polyploid crop species *Brassica napus*. *BMC Genomics* **13**: 247.

Hirsch CN, Foerster JM, Johnson JM, Sekhon RS, Muttoni G, Vaillancourt B, Peñagaricano F, Lindquist E, Pedraza MA, Barry K, de Leon N, Kaeppler SM, Buell CR. 2014. Insights into the maize pan-genome and pan-transcriptome. *Plant Cell* **26**: 121–35.

Joshi NA, Fass JN. 2011. Sickle: A sliding-window, adaptive, quality-based trimming tool for FastQ files (Version 1.33) [Software]. Available at https://github.com/najoshi/sickle.

Keller O, Kollmar M, Stanke M, Waack S. 2011. A novel hybrid gene prediction method employing protein multiple sequence alignments. *Bioinformatics* **27**: 757–63.

Kim D, Pertea G, Trapnell C, Pimentel H, Kelley R, Salzberg SL. 2013. TopHat2: accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions*. Genome Biol* **14**: R36.

Langmead B, Trapnell C, Pop M, Salzberg SL. 2009. Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. *Genome Biol* **10**: R25.

Langmead B, Salzberg SL. 2012. Fast gapped-read alignment with Bowtie 2. *Nat Methods* **9**: 357–9.

Lorenc MT, Hayashi S, Stiller J, Lee H, Manoli S, Ruperao P, Visendi P, Berkman PJ, Lai K, Batley J, Edwards D. 2012. Discovery of Single Nucleotide Polymorphisms in Complex Genomes Using SGSautoSNP. *Biology (Basel)* **1**: 370–382.

Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, Marth G, Abecasis G, Durbin R. 2009. The Sequence Alignment/Map format and SAMtools. *Bioinformatics* **25**: 2078–9.

Lin K, Zhang N, Severing EI, Nijveen H, Cheng F, Visser RGF, Wang X, de Ridder D, Bonnema G. 2014. Beyond genomic variation--comparison and functional annotation of three *Brassica rapa* genomes: a turnip, a rapid cycling and a Chinese cabbage. *BMC Genomics* **15**: 250.

Liu S, Liu Y, Yang X, Tong C, Edwards D, Parkin IAP, Zhao M, Ma J, Yu J, Huang S, et al. 2014. The *Brassica oleracea* genome reveals the asymmetrical evolution of polyploid genomes. *Nat Commun* **5**: 3930.

Lysak MA, Koch MA, Pecinka A, Schubert I. 2005. Chromosome triplication found across the tribe Brassiceae. *Genome Res* **15**: 516–25.

Nagaharu U. 1935. Genome analysis in Brassica with special reference to the experimental formation of *B. napus* and peculiar mode of fertilization. *Jpn J Bot* **7**: 389–452.

NCBI Resource Coordinators. 2013. Database resources of the National Center for Biotechnology Information. *Nucleic Acids Res* **41**: D8–D20.

Nicolas SD, Le Mignon G, Eber F, Coriton O, Monod H, Clouet V, Huteau V, Lostanlen A, Delourme R, Chalhoub B, et al. 2007. Homeologous recombination plays a major role in chromosome rearrangements that occur during meiosis of *Brassica napus* haploids. *Genetics* **175**: 487–503.

Østergaard L, King GJ, Liljegren S, Roeder A, Kempin S, Gremski K, Østergaard L, Guimil S, Reyes D, Yanofsky M, et al. 2008. Standardized gene nomenclature for the *Brassica* genus. *Plant Methods* **4**: 10.

Parkin IA, Koh C, Tang H, Robinson SJ, Kagale S, Clarke WE, Town CD, Nixon J, Krishnakumar V, Bidwell SL, Denoeud F, Belcram H, Links MG, Just J, Clarke C, Bender T, Huebert T, Mason AS, Pires CJ, Barker G, Moore J, Walley PG, Manoli S, Batley J, Edwards D, Nelson MN, Wang X, Paterson AH, King G, Bancroft I, Chalhoub B, Sharpe AG. 2014. Transcriptome and methylome profiling reveals relics of genome dominance in the mesopolyploid *Brassica oleracea*. *Genome Biol* **15**: R77.

Parra G., Bradnam K., Korf I. 2007. CEGMA: a pipeline to accurately annotate core genes in eukaryotic genomes. *Bioinformatics*, **23**(9), 1061-1067.

Quinlan AR, Hall IM. 2010. BEDTools: a flexible suite of utilities for comparing genomic features. *Bioinformatics* **26**: 841–2.

R Development Core Team 2011, R: A Language and Environment for Statistical Computing. Vienna, Austria : the R Foundation for Statistical Computing. ISBN: 3-900051-07-0. Available online at <http://www.R-project.org/>.

Roberts A, Pachter L. 2012. Streaming fragment assignment for real-time analysis of sequencing experiments. *Nat Methods* **10**: 71–73.

Saxena RK, Edwards D, Varshney RK. 2014. Structural variations in plant genomes. *Brief Funct Genomics* **13**: 296–307.

Schatz MC, Maron LG, Stein JC, Hernandez Wences A, Gurtowski J, Biggers E, Lee H, Kramer M, Antoniou E, Ghiban E, Wright MH, Chia J, Ware D, McCouch SR, McCombie WR. 2014. Whole genome de novo assemblies of three divergent strains of rice, *Oryza sativa*, document novel gene space of aus and indica. *Genome Biol* **15**: 506.

Sharpe AG, Lydiate DJ. 2003. Mapping the mosaic of ancestral genotypes in a cultivar of oilseed rape (*Brassica napus*) selected via pedigree breeding. *Genome* **46**: 461–8.

Simão FA, Waterhouse RM, Ioannidis P, Kriventseva E V, Zdobnov EM. 2015. BUSCO: assessing genome assembly and annotation completeness with single-copy orthologs. *Bioinformatics* **31**: 3210–2.

Thudi M, Khan AW, Kumar V, Gaur PM, Katta K, Garg V, Roorkiwal M, Samineni S, Varshney RK. 2016. Whole genome re-sequencing reveals genome-wide variations among parental lines of 16 mapping populations in chickpea (*Cicer arietinum* L.). *BMC Plant Biol* **16** Suppl 1: 10.

Tollenaere R., Hayward A., Dalton‐Morgan J., Campbell E., Lee JR., Lorenc MT., Manoli S., Stiller J., Raman R., Raman H., Edwards, D., Batley J. 2012. Identification and characterization of candidate Rlm4 blackleg resistance genes in *Brassica napus* using next‐generation sequencing. *Plant biotechnology journal,* **10**(6), 709-715.

Trick M, Cheung F, Drou N, Fraser F, Lobenhofer EK, Hurban P, Magusin A, Town CD, Bancroft I. 2009. A newly-developed community microarray resource for transcriptome profiling in *Brassica* species enables the confirmation of *Brassica*-specific expressed sequences. *BMC Plant Biol* **9**: 50.

Udall JA, Quijada PA, Osborn TC. 2005. Detection of chromosomal rearrangements derived from homologous recombination in four mapping populations of *Brassica napus* L. *Genetics* **169**: 967–79.

Wang X, Wang H, Wang J, Sun R, Wu J, Liu S, Bai Y, Mun J-H, Bancroft I, Cheng F, et al. 2011. The genome of the mesopolyploid crop species *Brassica rapa*. *Nat Genet* **43**: 1035–9.

Wang Y, Tang H, Debarry JD, Tan X, Li J, Wang X, Lee T, Jin H, Marler B, Guo H, et al. 2012. MCScanX: a toolkit for detection and evolutionary analysis of gene synteny and collinearity. *Nucleic Acids Res* **40**: e49.

Wu Y, Bhat PR, Close TJ, Lonardi S. 2008. Efficient and accurate construction of genetic linkage maps from the minimum spanning tree of a graph. ed. L. Kruglyak. *PLoS Genet* **4**: e1000212.

Wu P, Shao Z-Q, Wu X-Z, Wang Q, Wang B, Chen J-Q, Hang Y-Y, Xue J-Y. 2014. Loss/retention and evolution of NBS-encoding genes upon whole genome triplication of *Brassica rapa. Gene* **540**: 54–61.

Yang J., Liu D., Wang X., Ji C., Cheng F., Liu B., Hu Z., Chen S., Pental D., Ju Y., Yao P., Li X., Xie K., Zhang J., Wang J., Liu F., Ma W., Shopan J., Zheng H., Mackenzie SA., Zhang M.2016. The genome sequence of allopolyploid *Brassica juncea* and analysis of differential homeolog gene expression influencing selection. *Nature Genetics* 1546-1718

Yao W, Li G, Zhao H, Wang G, Lian X, Xie W. 2015. Exploring the rice dispensable genome using a metagenome-like assembly strategy. *Genome Biol* **16**: 187.

Zerbino DR, Birney E. 2008. Velvet: algorithms for de novo short read assembly using de Bruijn graphs. *Genome Res* **18**: 821–829.

Zhao X, Li B, Zhang K, Hu K, Yi B, Wen J,Chaozhi M, Jinxiong S, Tingdong F, Tu J. 2016. Breeding signature of combining ability improvement revealed by a genomic variation map from recurrent selection population in *Brassica napus*. *Scientific Reports*, *6*.

Zdobnov EM, Apweiler R. 2001. InterProScan - an integration platform for the signature-recognition methods in InterPro. *Bioinformatics* **17**: 847–848.

# Figures

Figure 1: Comparison of the count of collapsed regions by chromosome in Darmor*-bzh* and Tapidor.

Figure 2: Comparison of the count of repetitive regions by chromosome in Darmor*-bzh* and Tapidor.

Figure 3: Number of shared Pfam domains between genes located in collapsed and repetitive regions between Darmor*-bzh* and Tapidor.

# Supplementary Figures

Supplementary Figure 1: Dotplot comparison of the Darmor-*bzh* assembly (y-axis) and the Tapidor assembly (x-axis) pseudomolecules.

Supplementary Figure 2: Comparison of ranks between 19 linkage maps from MSTMap and physical placement using the Darmor-*bzh* genome assembly as reference.

Supplementary Figure 3: Number of shared Swiss-Prot hits between genes located in collapsed and repetitive regions between Darmor-*bzh* and Tapidor.

# Tables

Table 1: Size, SNPs, predicted genes, absent genes in Darmor*-bzh* and Tapidor

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Name | Darmor*-bzh* SNPs | Darmor*-bzh* Length (Mbp) | Darmor*-bzh* SNPs / Mbp | Tapidor SNPs | Tapidor Length (Mbp) | Tapidor SNPs / Mbp | Darmor*-bzh* predicted filtered genes | Tapidor predicted filtered genes | Tapidor genes with no Darmor*-bzh* reads | Darmor*-bzh* genes with no Tapidor reads |
| chrA01 | 45,870 | 31.16 | 1,472 | 37,875 | 23.9 | 1,586 | 3,687 | 3,050 | 0 | 3 |
| chrA02 | 45,229 | 31.34 | 1,443 | 46,599 | 27.9 | 1,672 | 3,528 | 3,315 | 1 | 0 |
| chrA03 | 59,180 | 39.49 | 1,499 | 55,319 | 32.1 | 1,723 | 5,429 | 4,408 | 0 | 4 |
| chrA04 | 57,270 | 23.31 | 2,457 | 49,357 | 21 | 2,351 | 2,676 | 2,638 | 0 | 0 |
| chrA05 | 54,784 | 28.6 | 1,916 | 36,548 | 20.1 | 1,818 | 3,506 | 2,634 | 1 | 1 |
| chrA06 | 72,163 | 31.9 | 2,262 | 57,613 | 29.1 | 1,977 | 3,926 | 3,713 | 0 | 0 |
| chrA07 | 45,458 | 28.9 | 1,573 | 34,101 | 22.7 | 1,505 | 3,555 | 2,976 | 0 | 0 |
| chrA08 | 24,807 | 21.74 | 1,141 | 22,096 | 16.4 | 1,346 | 2,827 | 2,147 | 0 | 0 |
| chrA09 | 79,586 | 46.72 | 1,704 | 53,008 | 30.8 | 1,721 | 5,286 | 3,913 | 0 | 3 |
| chrA10 | 27,723 | 19.96 | 1,389 | 35,378 | 22.5 | 1,575 | 2,800 | 3,175 | 0 | 1 |
| Total A | 512,070 | 303 |  | 427,894 | 247 |  | 37,220 | 31,969 | 2 | 12 |
| chrC01 | 92,316 | 47.95 | 1,925 | 63,462 | 31.9 | 1,990 | 3,739 | 3,083 | 0 | 5 |
| chrC02 | 49,665 | 58.66 | 847 | 47,872 | 40.5 | 1,181 | 4,182 | 3,572 | 1 | 23 |
| chrC03 | 64,224 | 71.85 | 894 | 72,229 | 55.2 | 1,307 | 6,448 | 5,800 | 0 | 9 |
| chrC04 | 95,329 | 61.04 | 1,562 | 79,006 | 45.6 | 1,733 | 4,658 | 4,356 | 0 | 2 |
| chrC05 | 25,226 | 52.72 | 479 | 43,752 | 45.6 | 959 | 4,452 | 4,839 | 0 | 4 |
| chrC06 | 41,036 | 44.61 | 920 | 41,252 | 34.1 | 1,211 | 3,543 | 3,230 | 0 | 6 |
| chrC07 | 34,089 | 52.5 | 649 | 41,001 | 37.3 | 1,099 | 4,165 | 3,523 | 0 | 1 |
| chrC08 | 43,857 | 46.29 | 947 | 48,079 | 40.2 | 1,197 | 4,140 | 4,295 | 0 | 0 |
| chrC09 | 46,660 | 60.21 | 775 | 57,479 | 51 | 1,127 | 4,607 | 4,864 | 0 | 2 |
| Total C | 492,402 | 496 |  | 494,132 | 381 |  | 39,934 | 37,562 | 1 | 52 |
| Unplaced contigs | 2,513 | 51.33 | 49 | 23,380 | 8.5 | 2,752 | 3,228 | 631 | 0 | 9 |
| Total | 1,006,985 | 850 |  | 945,406 | 636 |  | 80,382 | 70,162 | 3 | 73 |