(Haudry *et al*, 2013)

(Nguyen *et al*, 2019)

(Rawat *et al*, 2015)

(Cheng *et al*, 2017)

(Kliver *et al*, 2018)

(Lee *et al*, 2017)

(Song *et al*, 2021)

(Yang *et al*, 2021)

(Yang *et al.*, 2021)

(Sun *et al*, 2017)

(Perumal *et al*, 2020)

(Paritosh *et al*, 2020)

(Cai *et al*, 2020)

(Belser *et al*, 2018)

(Zhang *et al*, 2018)

(Nordberg *et al*, 2014)

(Kagale *et al*, 2014)

(Slotte *et al*, 2013)

(Slotte *et al.*, 2013)

(Gan *et al*, 2016)

(Yang *et al*, 2013)

(Haudry *et al.*, 2013)

(Zhang *et al*, 2015)

(Oh *et al*, 2014)

(Haudry *et al.*, 2013)

Belser C, Istace B, Denis E, Dubarry M, Baurens F-C, Falentin C, Genete M, Berrabah W, Chèvre A-M, Delourme R *et al* (2018) Chromosome-scale assemblies of plant genomes using nanopore long reads and optical maps. *Nature Plants* 4: 879-887

Cai X, Wu J, Liang J, Lin R, Zhang K, Cheng F, Wang X (2020) Improved Brassica oleracea JZS assembly reveals significant changing of LTR-RT dynamics in different morphotypes. *Theoretical and Applied Genetics* 133: 3187-3199

Cheng C-Y, Krishnakumar V, Chan AP, Thibaud-Nissen F, Schobel S, Town CD (2017) Araport11: a complete reannotation of the Arabidopsis thaliana reference genome. *The Plant Journal* 89: 789-804

Gan X, Hay A, Kwantes M, Haberer G, Hallab A, Ioio RD, Hofhuis H, Pieper B, Cartolano M, Neumann U *et al* (2016) The Cardamine hirsuta genome offers insight into the evolution of morphological diversity. *Nature Plants* 2: 16167

Haudry A, Platts AE, Vello E, Hoen DR, Leclercq M, Williamson RJ, Forczek E, Joly-Lopez Z, Steffen JG, Hazzouri KM *et al* (2013) An atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions. *Nat Genet* 45: 891-898

Kagale S, Koh C, Nixon J, Bollina V, Clarke WE, Tuteja R, Spillane C, Robinson SJ, Links MG, Clarke C *et al* (2014) The emerging biofuel crop Camelina sativa retains a highly undifferentiated hexaploid genome structure. *Nature Communications* 5: 3706

Kliver S, Rayko M, Komissarov A, Bakin E, Zhernakova D, Prasad K, Rushworth C, Baskar R, Smetanin D, Schmutz J *et al* (2018) Assembly of the Boechera retrofracta Genome and Evolutionary Analysis of Apomixis-Associated Genes. *Genes* 9

Lee C-R, Wang B, Mojica JP, Mandáková T, Prasad KVSK, Goicoechea JL, Perera N, Hellsten U, Hundley HN, Johnson J *et al* (2017) Young inversion with multiple linked QTLs under selection in a hybrid zone. *Nature Ecology & Evolution* 1: 0119

Nguyen T-P, Mühlich C, Mohammadin S, van den Bergh E, Platts AE, Haas FB, Rensing SA, Schranz ME (2019) Genome Improvement and Genetic Map Construction for Aethionema arabicum, the First Divergent Branch in the Brassicaceae Family. *G3 (Bethesda, Md)* 9: 3521-3530

Nordberg H, Cantor M, Dusheyko S, Hua S, Poliakov A, Shabalov I, Smirnova T, Grigoriev IV, Dubchak I (2014) The genome portal of the Department of Energy Joint Genome Institute: 2014 updates. *Nucleic Acids Res* 42: D26-31

Oh D-H, Hong H, Lee SY, Yun D-J, Bohnert HJ, Dassanayake M (2014) Genome Structures and Transcriptomes Signify Niche Adaptation for the Multiple-Ion-Tolerant Extremophyte Schrenkiella parvula. *Plant Physiology* 164: 2123-2138

Paritosh K, Pradhan AK, Pental D (2020) A highly contiguous genome assembly of Brassica nigra (BB) and revised nomenclature for the pseudochromosomes. *BMC Genomics* 21: 887

Perumal S, Koh CS, Jin L, Buchwaldt M, Higgins E, Zheng C, Sankoff D, Robinson SJ, Kagale S, Navabi Z-K *et al* (2020) High contiguity long read assembly of <em>Brassica nigra</em> allows localization of active centromeres and provides insights into the ancestral <em>Brassica</em> genome. *bioRxiv*: 2020.2002.2003.932665

Rawat V, Abdelsamad A, Pietzenuk B, Seymour DK, Koenig D, Weigel D, Pecinka A, Schneeberger K (2015) Improving the Annotation of Arabidopsis lyrata Using RNA-Seq Data. *PLOS ONE* 10: e0137391

Slotte T, Hazzouri KM, Ågren JA, Koenig D, Maumus F, Guo Y-L, Steige K, Platts AE, Escobar JS, Newman LK *et al* (2013) The Capsella rubella genome and the genomic consequences of rapid mating system evolution. *Nature Genetics* 45: 831-835

Song X, Wei Y, Xiao D, Gong K, Sun P, Ren Y, Yuan J, Wu T, Yang Q, Li X *et al* (2021) Brassica carinata genome characterization clarifies U’s triangle model of evolution and polyploidy in Brassica. *Plant Physiology* 186: 388-406

Sun F, Fan G, Hu Q, Zhou Y, Guan M, Tong C, Li J, Du D, Qi C, Jiang L *et al* (2017) The high-quality genome of Brassica napus cultivar ‘ZS11’ reveals the introgression history in semi-winter morphotype. *The Plant Journal* 92: 452-468

Yang J, Wang J, Li Z, Li X, He Z, Zhang L, Sha T, Lyu X, Chen S, Gu Y *et al* (2021) Genomic signatures of vegetable and oilseed allopolyploid Brassica juncea and genetic loci controlling the accumulation of glucosinolates. *Plant Biotechnology Journal* 19: 2619-2628

Yang R, Jarvis D, Chen H, Beilstein M, Grimwood J, Jenkins J, Shu S, Prochnik S, Xin M, Ma C *et al* (2013) The Reference Genome of the Halophytic Plant Eutrema salsugineum. *Frontiers in Plant Science* 4

Zhang L, Cai X, Wu J, Liu M, Grob S, Cheng F, Liang J, Cai C, Liu Z, Liu B *et al* (2018) Improved Brassica rapa reference genome by single-molecule sequencing and chromosome conformation capture technologies. *Horticulture Research* 5: 50

Zhang X, Yue Z, Mei S, Qiu Y, Yang X, Chen X, Cheng F, Wu Z, Sun Y, Jing Y (2015) A de novo genome of a Chinese radish cultivar. *Horticultural Plant Journal* 1: 155-164