

Fu YB, Cheng B, Peterson GW (2013) Genetic diversity analysis of yellow mustard germplasm based on genotyping by sequencing. Genetic Resources and Crop Evolution (in press)

Supplemental online materials

Fig. S1 Workflow for the application of Roche 454 pyrosequencing in combination with genomic reduction and the DIAL pipeline to identify contigs and SNPs from 24 yellow mustard samples

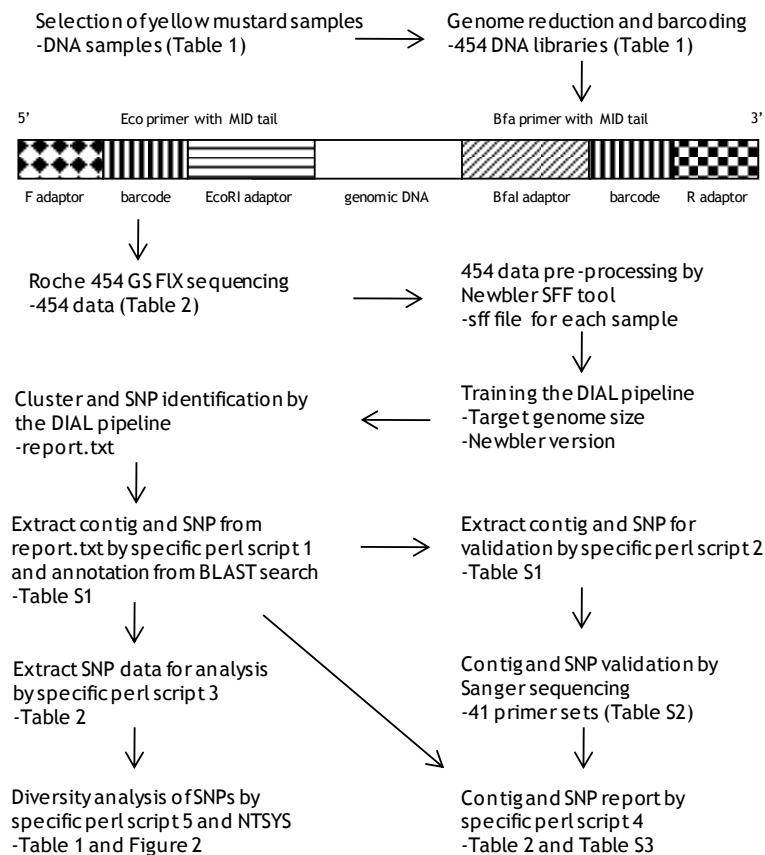


Fig. S2 BLAST hit distribution of 512 yellow mustard contigs with respect to plant species

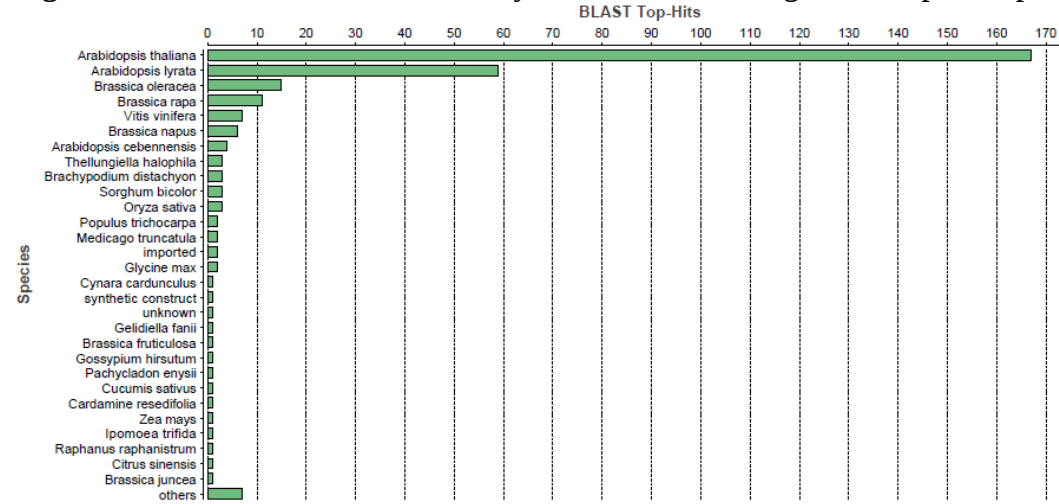


Fig. S3 The neighbor-joining tree of the 24 yellow mustard samples illustrating the negative impact of missing SNP data on the sample distance measures. The NJ tree was obtained assuming missing SNPs as 0 and available SNPs as 1. The number within the curly bracket following the sample label is the percentage of missing SNPs.

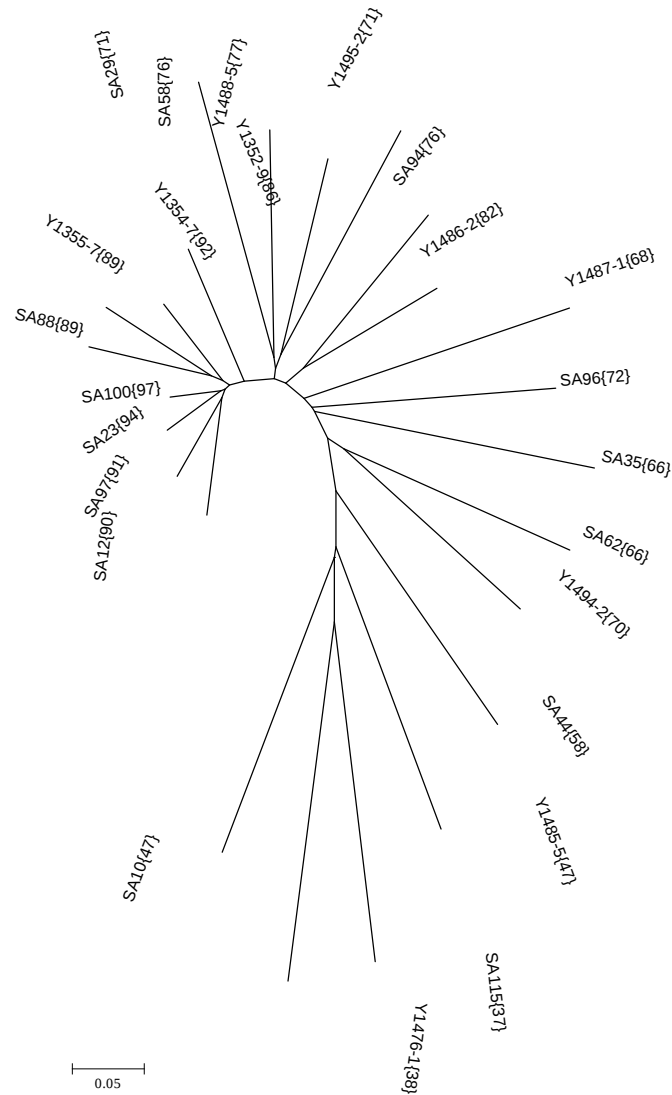


Table S1 Information on 10 assayed breeding lines

Sample	Originating germplasm	Open-pollinated plant	Inbreeding generation
Y1352-9	Andante	Y041	7
Y1476-1	Andante	Y041	5
Y1485-5	Andante	Y041	5
Y1495-2	Andante	Y041	5
Y1355-7	Andante	Y020	6
Y1487-1	Andante	Y020	7
Y1494-2	Andante	Y042	5
Y1354-7			DH
Y1486-2	Russian landrace SRS 2766		5
Y1488-5	F1 Hybrid of Sabre x SvalÖf high oil		7