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Supplementary Material

Potential of increasing yield of spring *Brassica napus* canola by using *Brassica rapa* gene pool with emphasis on yellow sarson

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Supplementary Table S1. Variance components of the inbred *Brassica napus* lines derived from *B. napus* × *B. rapa* interspecific crosses and their test hybrids for different agronomic and seed quality traits. Analysis carried out using data from (a) 10 trials with the inbred lines, and (b) three trials with the test hybrids.

(a) Inbred lines

	Days to flowering	Days to maturity	Plant height	Seed yield	Oil	Protein	Glucosinolates
Genotype	4.25**	11.82*	62.38**	223.86*	1.89***	1.31***	3.74***
Environment	0.10**	0.27***	1.40*	503.70***	0.04***	0.03***	0.08***
Genotype(Environment)	2.74	7.13*	41.59	214.99***	1.04***	0.92***	1.32***
Error	5.49	14.18	82.77	426.12	2.08***	1.83	2.63
H	59.92	61.52	59.20	50.50	63.55	57.88	72.62

(b) Test hybrids

	Days to flowering	Days to maturity	Plant height	Seed yield	Oil	Protein	Glucosinolates
Genotype	6.71	5.41	77.64	139.49**	9.51***	6.99*	8.44***
Environment	0.50**	0.11	8.40**	144.20***	0.01	0.01	1.10
Genotype(Environment)	5.23	4.36	46.21	70.21	5.34	3.63	1.10
Error	6.71	4.34	59.72	101.32	8.29	4.34	2.02
H	53.9	54.75	58.71	39.29	63.98	79.31	79.32

*, **, *** indicate significant at $P < 0.05$, < 0.01, and < 0.001, respectively; *H*, Broad-sense heritability.

Supplementary Table S2. Agronomic and seed quality traits (mean ± s.e.) of the inbred *Brassica napus* populations derived from *B. napus* A04-73NA × *B. rapa* T4-3-3-1, *B. napus* A04-73NA × *B. rapa* YS49, and (*B. napus* A04 73NA × *B. rapa* YS49) × *B. napus* A04-73NA interspecific crosses; data of the *B. napus* parent A04-73NA also included. LSmean data of 10 trials presented.

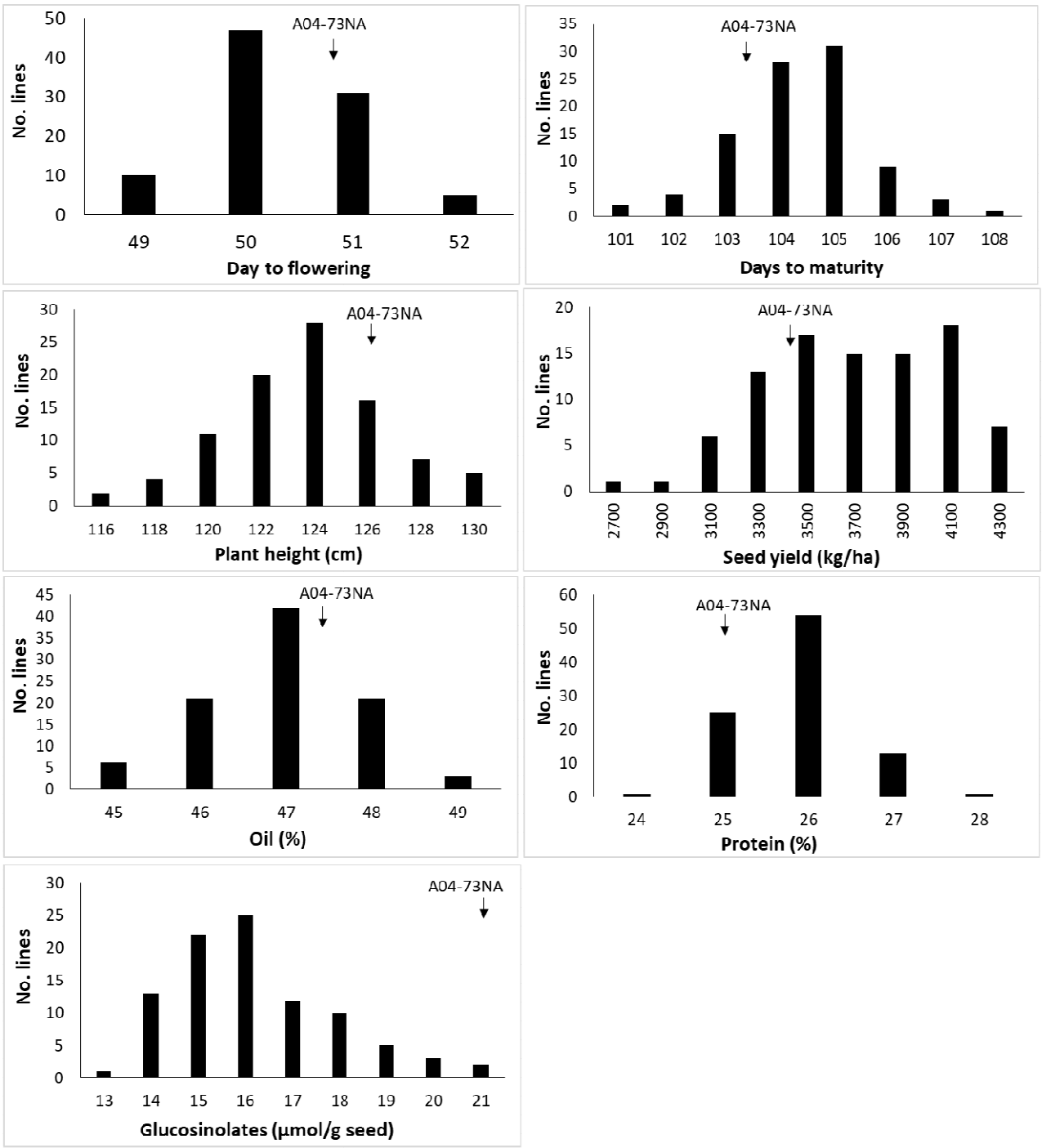
Populations[1]	Days to flowering	Days to maturity	Plant height (cm)	Seed yield (kg/ha)	Oil (%)	Protein (%)	Glucosinolates (µmol/g seed)
73 × T4	50.0 ± 0.1b	102.3 ± 0.3b	120.4 ± 0.9b	3503.4 ± 24.4a	47.5 ± 0.1a	24.4 ± 0.1b	14.7 ± 0.3d
73 × YS	50.3 ± 0.2a	103.1 ± 0.4b	119.4 ± 0.7b	3248.2 ± 31.5c	46.4 ± 0.1c	25.2 ± 0.1a	15.5 ± 0.1c
(73 × YS) × 73	49.4 ± 0.2c	101.6 ± 0.3c	116.8 ± 0.7c	3355.3 ± 30.7b	46.8 ± 0.1b	24.8 ± 0.1a	16.3 ± 0.3b
A04-73NA	50.6 ± 0.5a	103.4 ± 1.0a	126.3 ± 1.2a	3460.0 ± 56.1a	47.4 ± 0.2a	24.9 ± 0.2ab	21.4 ± 0.3a

[1] 73 × T4 = F_9 population derived from *B. napus* A04-73NA × *B. rapa* T4-3-3-1 cross. 73 × YS = F_9 population derived from *B. napus* A04-73NA × *B. rapa* YS49 cross. (73 × YS) × 73 = BC_1F_6 population derived from (*B. napus* A04 73NA × *B. rapa* YS49) × *B. napus* A04-73NA cross.
Statistical comparisons made within the group; mean values followed by the same letter indicate no significant difference (p <0.05).

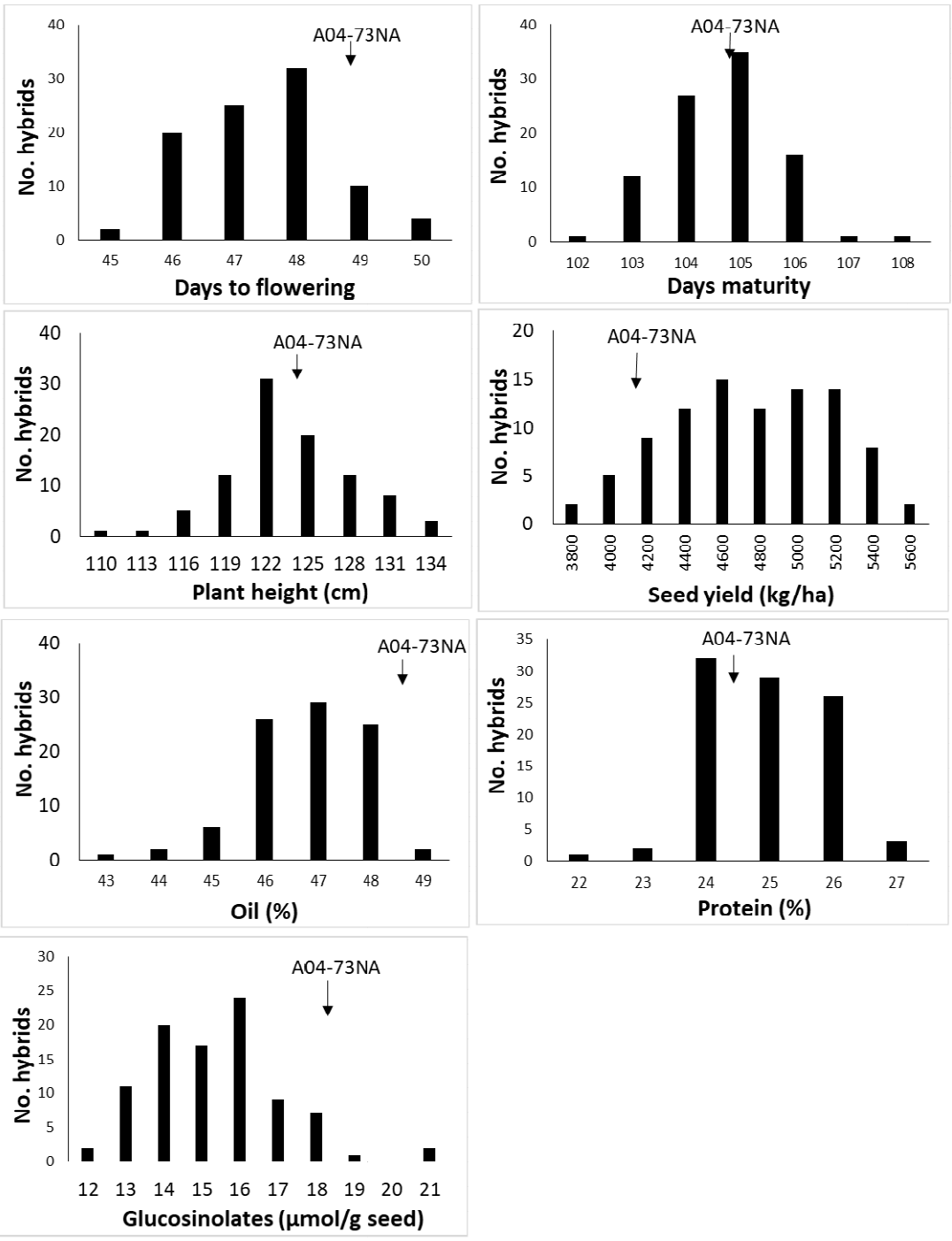
Supplementary Table S3. Agronomic and seed quality traits (mean ± s.e.) of the inbred *Brassica napus* populations (IN) derived from *B. napus* A04-73NA × *B. rapa* T4-3-3-1, *B. napus* A04-73NA × *B. rapa* YS49, and (*B. napus* A04 73NA × *B. rapa* YS49) × *B. napus* A04-73NA interspecific crosses and their test hybrids (TH), and the mid-parent heterosis (MPH) and heterosis over the *B. napus* parent A04-73NA (NPH). Data of the *B. napus* parent A04-73NA also included. LSmean data of three trials with the hybrids and their parents are presented.

Population and statistic	Days to flowering	Days to maturity	Plant height (cm)	Seed yield (kg/ha)	Oil (%)	Protein (%)	Glucosinolates (µmol/g seed)
IN: 73 × T4	48.8 ± 0.2a	103.4 ± 0.4b	124.2 ± 1.3b	3316.7 ± 128.8a	47.7 ± 0.3a	24.2 ± 0.2b	15.0 ± 0.3b
IN: 73 × YS	48.3 ± 0.2a	104.1 ± 0.3b	119.7 ± 1.0b	3266.9 ± 93.2b	46.4 ± 0.3b	25.0 ± 0.2a	16.5 ± 0.5a
IN: (73 × YS) × 73	48.4 ± 0.2a	102.0 ± 0.3c	117.8 ± 0.9c	3255.3 ± 118.9b	47.0 ± 0.3a	24.6 ± 0.2a	16.8 ± 0.4a
A04-73NA	48.7 ± 0.5a	104.9 ± 0.2b	124.0 ± 1.6b	4154.0 ± 76.4c	48.5 ± 0.1c	24.4 ± 0.1b	18.2 ± 0.1a
TH: 73 × T4	47.5 ± 0.2b	104.4 ± 0.3a	124.2 ± 1.8a	4598.1 ± 122.4ab	48.1 ± 0.1a	24.3 ± 0.1b	14.5 ± 0.2c
TH: 73 × YS	47.4 ± 0.2b	104.4 ± 0.2a	121.4 ± 1.5b	4808.8 ± 134.4a	46.6 ± 0.2c	25.1 ± 0.2a	15.0 ± 0.2c
TH: (73 × YS) × 73	47.5 ± 0.2b	104.4 ± 0.3a	121.2 ± 1.8b	4558.1 ± 132.4b	47.1 ± 0.1b	25.1 ± 0.1a	16.4 ± 0.2b
A04-73NA	48.7 ± 0.5a	104.9 ± 0.2a	124.0 ± 1.6a	4154.0 ± 76.4c	48.5 ± 0.1a	24.4 ± 0.1b	18.2 ± 0.1a
MPH: 73 × T4	-2.4 ± 0.3a	-0.4 ± 0.2a	-0.2 ± 0.4a	10.7 ± 1.7b	-0.9 ± 0.2a	0.6 ± 0.3a	-9.8 ± 1.1ab
MPH: 73 × YS	-1.9 ± 0.2a	-0.7 ± 0.2a	-0.6 ± 0.5a	24.3 ± 1.7a	-1.4 ± 0.3a	0.6 ± 0.4a	-13.3 ± 1.1b
MPH: (73 × YS) × 73	-3.2 ± 0.4b	-0.5 ± 0.2a	-0.4 ± 0.5a	12.8 ± 2.3b	-1.8 ± 0.3b	-0.4 ± 0.5a	-7.4 ± 0.8a
NPH: 73 × T4	-2.4 ± 0.4a	-0.6 ± 0.2a	-0.5 ± 0.9a	11.6 ± 1.4b	-2.2 ± 0.3a	1.0 ± 0.4b	-16.1 ± 1.2b
NPH: 73 × YS	-1.9 ± 0.4a	-0.7 ± 0.2a	-2.3 ± 0.7b	20.5 ± 2.3a	-3.5 ± 0.5b	3.2 ± 0.8a	-17.4 ± 1.3b
NPH: (73 × YS) × 73	-4.2 ± 0.4b	-0.8 ± 0.2a	-1.9 ± 0.5ab	11.2 ± 1.8b	-3.9 ± 0.5b	0.7 ± 0.7b	-9.4 ± 1.3a

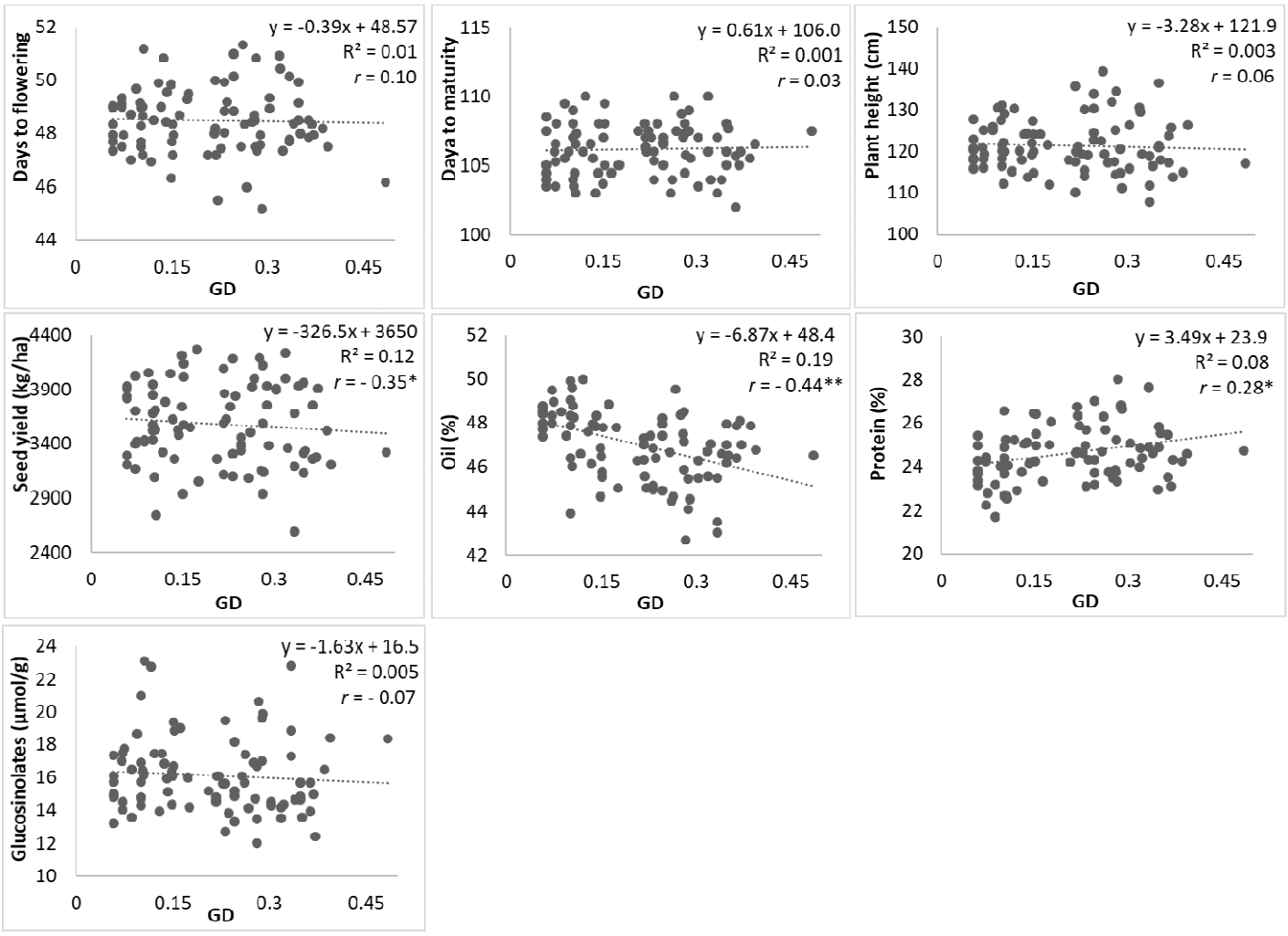
[1] 73 × T4 = F_9 population derived from *B. napus* A04-73NA × *B. rapa* T4-3-3-1 cross. 73 × YS = F_9 population derived from *B. napus* A04-73NA × *B. rapa* YS49 cross. (73 × YS) × 73 = BC_1F_6 population derived from (*B. napus* A04 73NA × *B. rapa* YS49) × *B. napus* A04-73NA cross.
Statistical comparisons made within the group; mean values followed by the same letter indicate no significant difference (p <0.05).



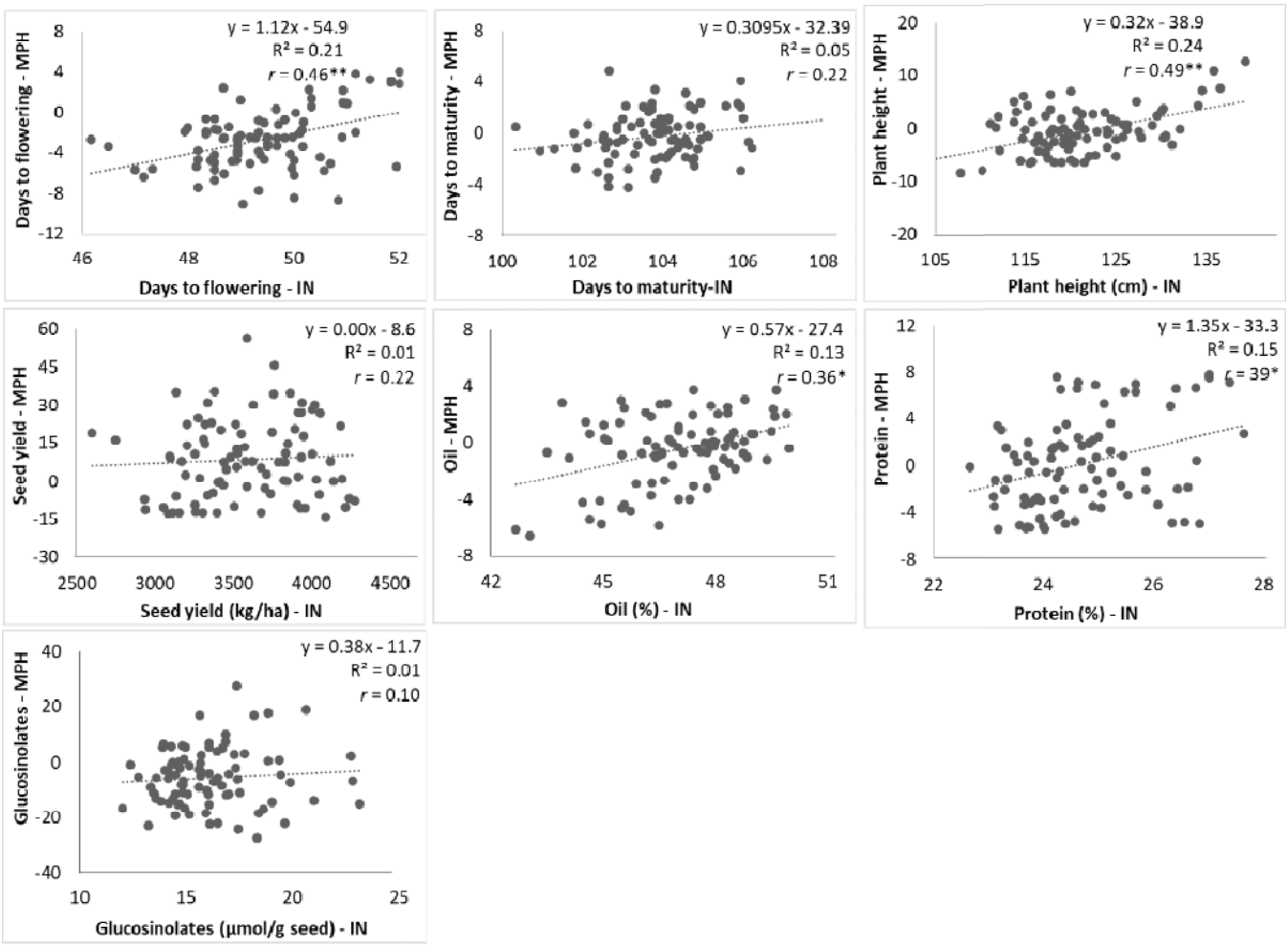
Supplementary Fig. S1. Frequenccy distribution of the inbred *Brassica napus* lines derived from *B. napus* × *B. rapa* interspecific crosses for different agronomic and seed quality traits. LSmean data of 10 field trials with the inbred lines presented. The arrows indicates the values of the *B. napus* parent A04-73NA.



Supplementary Fig. S2. Frequency distribution of the test hybrids of the inbred *Brassica napus* lines derived from *B. napus* × *B. rapa* interspecific crosses for different agronomic and seed quality traits. LSmean data of three test hybrid trials presented. The arrows indicates the values of the *B. napus* parent A04-73NA.



Supplementary Fig. S3. Relationship of the genetic distance (GD) of the inbred *Brassica napus* lines from the *B. napus* parent with different agronomic and seed quality traits. The inbred lines were derived from *B. napus* × *B. rapa* interspecific crosses. Agronomic and seed quality data of the inbred lines from three test hybrid trials. * and ** indicate significant at $p <$ 00.05 and < 0.01, respectively.



Supplementary Fig. S4. Relationship between the performance of the inbred *Brassica napus* lines and the the mid-parent heterosis for different agronomic and seed quality traits. The inbred lines were derived from *B. napus* × *B. rapa* interspecific crosses. Agronomic and seed quality data of the inbred lines and test hybrids from three test hybrid trials. * and ** indicate significant at $p <$ 0.05 and < 0.01, respectively.