

Supplementary Tables and Figure

Table S1. Phenotype-based EBLUP and heritability for the RIL population.

Trait	Pryzeth	Suneson	RIL 2017	RIL 2018	Range	Heritability
SA	2.24 ±0.12	1.35 ±0.04	1.56 ±0.004	1.64 ±0.004*	1.33-1.94	0.85 ±0.017
SL	2.4 ±0.05	1.75 ±0.03	1.96 ± 0.004	1.99 ±0.003*	1.76-2.19	0.88 ±0.014
SW	1.17 ±0.04	1.00 ±0.03	1.02 ± 0.001	1.04 ±0.001*	0.95-1.14	0.79 ±0.023
PA	37.43 ±1.69	20.77 ±1.57	26.41 ± 0.105	27.2 ±0.109*	21.10-35.66	0.80 ±0.022
PL	9.97 ±0.61	7.98 ±0.51	8.14 ± 0.024	8.54 ±0.02*	6.51-9.77	0.83 ±0.019
PW	5.69 ±0.13	3.94 ±0.15	4.68 ± 0.01	4.72 ±0.012*	4.00-5.41	0.80 ±0.022
TS	1.86 ±0.15	1.09 ±0.06	1.29 ±0.004	1.38 ±0.004*	1.09-1.65	0.80±0.023
SPP	13.19 ±1.14	11.7 ±1.53	14.24 ±0.064	14.03 ±0.071*	9.77-17.95	0.72 ±0.031
TOC	33.69±0.87	37.15±1.37	35.85±0.064	35.97±0.071	30.83-40.74	0.66±0.036

SA: seed area (mm²); SL: seed length (mm); SW: seed width (mm); PA: pod area (mm²); PL: pod length (mm); PW: pod width (mm); TSW: thousand seed weight (g); SPP: seed number per pod. TOC: total oil content (%)
Means ± SE

* = P < 0.001 from *t*-Test showing year to year significance

Table S2. Pearson's correlation coefficients among seed area (SA), seed length (SL), seed width (SW), pod area (PA), pod length (PL), pod width (PW), thousand seed weight (TSW) and seed number per pod (SPP).

Trait	SA	SL	SW	PA	PL	PW	TSW	SPP
SL	0.92***							
SW	0.88***	0.65***						
PA	0.39***	0.43***	0.22**					
PL	0.34***	0.39***	0.16*	0.84***				
PW	0.35***	0.31***	0.30***	0.70***	0.31***			
TSW	0.89***	0.79***	0.82***	0.35***	0.34***	0.30***		
SPP	-0.30***	-0.24**	-0.31***	0.39***	0.31***	0.25**	-0.32**	
TOC	-0.20***	-0.32***	-0.04	-0.14***	-0.16***	-0.07	-0.18***	-0.32

*** Significance level: p<0.001

** Significance level: p<0.01

* Significance level: p<0.1

Table S3. Summary of putative candidate genes associated with seed and/or pod development (SA17.1) and oil biosynthesis (TOC9.1).

Candidate gene	Arabidopsis ortholog	Gene description	Reference
SA17.1			
Csa17g028400	At1g77850	auxin response factor 17-like	Mallory, et al. (2005)
Csa17g028440	At1g21690	replication factor C subunit 4	Qian, et al. (2018)
Csa17g028530	At1g77540	acetyltransferase -like	Song, et al. (2015)
Csa17g028640	AT1g35540	putative auxin response factor 14	Mallory, et al. (2005)
Csa17g029060	AT1g22140	zinc finger CCCH domain-containing protein 15	Wang, et al. (2008)
Csa17g029440	AT1g22500	E3 ubiquitin-protein ligase ATL15	Aoyama, et al. (2017)
Csa17g029450	AT1g22510	E3 ubiquitin-protein ligase RNF170	Aoyama, et al. (2017)
Csa17g029550	AT1g22640	transcription factor MYB3	Wan, et al. (2016)
Csa17g029620	AT1g22690	gibberellin-regulated protein 9	Roxrud, et al. (2007)
Csa17g029640	AT1g22710	sucrose transport protein SUC2	Wang, et al. (2015)
Csa17g030160	AT1g23080	auxin efflux carrier component 7	Wang, et al. (2018)
Csa17g030300	AT1g23190	probable phosphoglucomutase 1	Egli, et al. (2010)
Csa17g030320	AT1g23200	probable pectinesterase inhibitor 6	Louvet, et al. (2006)
Csa17g030330	AT1g17150	exopolygalacturonase-like	Babu, et al. (2013)
Csa17g030550	AT1g23380	homeobox protein knotted-1-like 6	Hay and Tsiantis (2010)
Csa17g030560	AT1g23380	homeobox protein knotted-1-like 6	Hay and Tsiantis (2010)
Csa17g030620	AT1g23460	probable polygalacturonase	Babu, et al. (2013)
Csa17g030630	AT1g23480	cellulose synthase like A3	Goubet, et al. (2009)
Csa17g030920	AT1g23800	aldehyde dehydrogenase family	Shin, et al. (2009)
Csa17g030930	AT1g23800	aldehyde dehydrogenase family	Shin, et al. (2009)
Csa17g030940	AT1g23820	spermidine synthase 1	Tao, et al. (2018)
TOC9.1			
Csa09g075230	AT1g71890	sucrose transport protein SUC5-like	Baud, et al. (2005)
Csa09g072620	At1g71250	GDSL lipase	Ding, et al. (2019)

References

- Aoyama, S., et al. (2017). Membrane-localized ubiquitin ligase ATL15 functions in sugar-responsive growth regulation in Arabidopsis. *Biochem Biophys Res Commun* 491: 33-39.
- Babu, Y., et al. (2013). Suspensor length determines developmental progression of the embryo in Arabidopsis. *Plant Physiol* 162: 1448-1458.
- Baud, S., et al. (2005). "The AtSUC5 sucrose transporter specifically expressed in the endosperm is involved in early seed development in Arabidopsis." *Plant J* 43(6): 824-836.
- Ding LN, Guo XJ, Li M, Fu ZL, Yan SZ, Zhu KM, et al. Improving seed germination and oil contents by regulating the GDSL transcriptional level in *Brassica napus*. *Plant Cell Rep.* 2019;38(2):243-53.
- Egli, B., et al. (2010). Loss of cytosolic phosphoglucomutase compromises gametophyte development in Arabidopsis. *Plant Physiol* 154: 1659-1671.
- Goubet, F., et al. (2009). Cell wall glucomannan in Arabidopsis is synthesised by CSLA glycosyltransferases, and influences the progression of embryogenesis. *Plant J* 60: 527-538.
- Hay, A. and M. Tsiantis (2010). KNOX genes: versatile regulators of plant development and diversity. *Development* 137: 3153-3165.
- Louvet, R., et al. (2006). Comprehensive expression profiling of the pectin methylesterase gene family during silique development in Arabidopsis thaliana. *Planta* 224: 782-791.
- Mallory, A. C., et al. (2005). MicroRNA-directed regulation of Arabidopsis AUXIN RESPONSE FACTOR17 is essential for proper development and modulates expression of early auxin response genes. *Plant Cell* 17: 1360-1375.
- Okushima, Y., et al. (2005). Functional genomic analysis of the AUXIN RESPONSE FACTOR gene family members in Arabidopsis thaliana: unique and overlapping functions of ARF7 and ARF19. *Plant Cell* 17: 444-463.
- Qian, J., et al. (2018). Arabidopsis replication factor C4 is critical for DNA replication during the mitotic cell cycle. *Plant J* 94: 288-303.
- Roxrud, I., et al. (2007). GASA4, one of the 14-member Arabidopsis GASA family of small polypeptides, regulates flowering and seed development. *Plant Cell Physiol* 48: 471-483.
- Shin, J. H., et al. (2009). Rice aldehyde dehydrogenase7 is needed for seed maturation and viability. *Plant Physiol* 149: 905-915.
- Song, X. J., et al. (2015). Rare allele of a previously unidentified histone H4 acetyltransferase enhances grain weight, yield, and plant biomass in rice. *Proc Natl Acad Sci U S A* 112: 76-81.
- Tao, Y., et al. (2018). The Spermine Synthase OsSPMS1 Regulates Seed Germination, Grain Size, and Yield. *Plant Physiol* 178: 1522-1536.
- Wang, B., et al. (2018). The RAF-like mitogen-activated protein kinase kinases RAF22 and RAF28 are required for the regulation of embryogenesis in Arabidopsis. *Plant J* 96: 734-747.
- Wang, D., et al. (2008). Genome-wide analysis of CCCH zinc finger family in Arabidopsis and rice. *BMC Genomics* 9: 44.
- Wan, L., et al. (2016). Transcriptome analysis of a new peanut seed coat mutant for the physiological regulatory mechanism involved in seed coat cracking and pigmentation. *Front Plant Sci* 7: 1491.
- Wang, L., et al. (2015). Enhanced Sucrose Loading Improves Rice Yield by Increasing Grain Size. *Plant Physiol* 169: 2848-2862

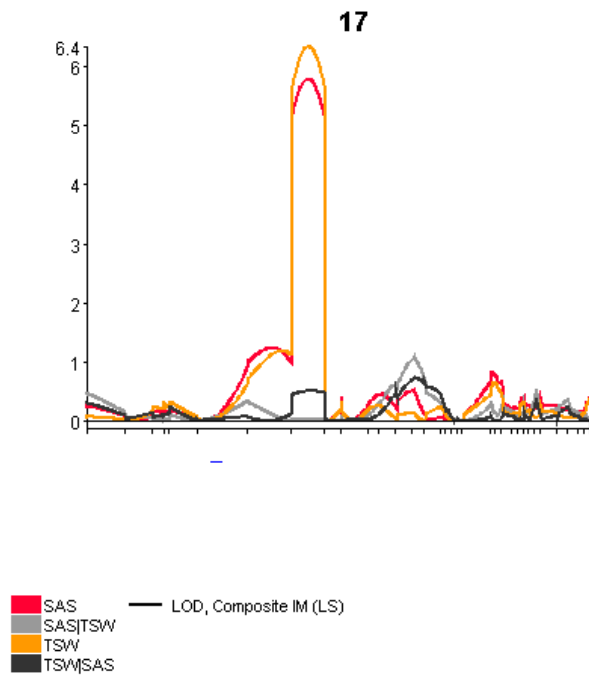


Fig. S1. Conditional analysis of seed area (SAS) and 1000-seed weight (TSW) at the major QTL region on chromosome 17. SAS/TSW, SAS Conditioned by TSW; TSW/SAS, TSW Conditioned by SAS.