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Novel Resources for Oilseed Rape Breeding –
Improving Harvest Index (NOVORB-HI)

by

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1. ABSTRACT

At the end of the season, the proportion of harvested product relative to the total above-ground biomass of the plant is termed the Harvest Index. In oilseed rape, this value is typically 0.2 – 0.25, which is around half that of crops such as wheat. This inefficiency in the production of seeds is thought to be largely a consequence of the architecture of the inflorescence of the plant, which impacts the properties of the canopy of the crop. The genetic control of inflorescence/canopy architecture in oilseed rape is poorly characterised and likely to be complex. We aimed to improve our understanding of this control by conducting detailed morphological analyses of the inflorescence of oilseed rape, as grown in the field, along with quantitative genetic analyses. The study exploited a pre-existing mapping population derived from a cross between an old European variety of winter habit oilseed rape (Tapidor) and a Chinese cultivar of semi-winter habit (Ningyou 7). This represents a cross between the genetic extremes available in oilseed rape (species *Brassica napus*). In addition, two new populations were developed and studied. These involved four relatively modern varieties adapted to UK conditions (Capitol x Rocket and Verona x Grizzly) and selected on the basis of exhibiting contrasting canopy architecture.

The results of our analyses showed there to be a wide range of variation for most of the inflorescence/canopy architecture traits measured. This was much greater in the population derived from the cross between European and Chinese material than in the new crosses between UK-adapted varieties. Despite the inherent environmental effects and errors associated with field data, major genetic components were identified for most of the traits. The quantitative genetic analyses showed that the basis of this genetic component is complex, typically consisting of contributions from numerous different parts of the genome (loci), each having only a small effect. We tested whether the positions of these loci coincided with the positions of genes, identified from studies in *Arabidopsis thaliana*, which were candidates for potentially being involved in control of the traits. Some of these, including: *TB-like*, *TCP* and *BLR*, ('length traits'), *GAI*, *RGL1* and *MAX2* (branch and pod angle), *BLR* (fertile branch number and pod density), *RGL1* (seed density and *GAI* (stem width), were coincident with the peaks of QTL (quantitative trait loci). These coincidences represent the bases for hypotheses to be tested in future studies.

Our study confirmed that canopy architecture in oilseed rape is under complex genetic control. We found evidence that some candidate genes arising from studies in other species may well have a role in the control of corresponding traits in oilseed rape, but for most we found no indication of involvement. Indeed, numerous loci influencing canopy architecture traits were identified that appear not to correspond to the positions of candidate genes. Our results direct focus upon specific known genes that may be involved in the control of aspects of canopy architecture that are likely to impact seed yield. In addition, they indicate that studies conducted to date in *A. thaliana*, which used mutation-based approaches, ought to be supplemented with studies exploiting natural genetic variation in order to assist the identification of the genes underlying many of the important loci that we have identified in oilseed rape.

2. SUMMARY

2.1. Introduction

Improving the productivity of oilseed rape (*Brassica napus*) as a crop within the UK has proven difficult and there has been no increase in national yield apparent during the last 20 years. Crop biomass production is high but harvest index (HI) is low (20 - 25%) resulting in low yields. Shifting dry matter partitioning from vegetative to reproductive structures at harvest will increase harvested yield with the same overall productivity. Key to achieving this is to understand the complexities of canopy architecture and its genetic control. In part this complexity arises because there are many separate traits determining canopy structure which show large $G \times E$ effects and which are frequently quantitative and under polygenic genetic control.

Using three doubled haploid (DH) populations of oilseed rape we have explored the complex nature of the canopy by dividing it into many relatively simple component traits. The genetic control of these traits has been studied through quantitative trait locus (QTL) analysis of two of these populations. Additionally, we have developed molecular markers linked to homologues of specific genes of *Arabidopsis thaliana* that are candidates for control of aspects of canopy architecture which have also been mapped in these DH populations.

Three DH populations were used: TNDH (Tapidor $\times$ Ningyou 7) and two new ones CRDH (Capitol $\times$ Rocket) and VGDH (Verona $\times$ Grizzly) from each of which 94 plants were selected for field trials. These were sown in two randomised field trials including the parents and appropriate control varieties. TNDH was sown in 2006-2007, at Barton, Cambridge and Cowlinge, Newmarket, while CRDH and VGDH were sown at Cantelupe Farm, Cambridge and Cowlinge in 2007-2008. Three plants for trait measurement and five for HI determination were harvested from each plot ca 3-4 weeks before the estimated time of harvest (swathing) while the plants were still green to minimise damage. All plots were combine harvested for yield and the seed used to estimate seed storage products. Basic descriptors of plant architecture were determined for each plant (eg height, stem width, branch numbers) while more detailed measurements were made on the terminal raceme (eg pod number) and on ten typical pods (eg pod and pedicel length and angles, seed number and weight)

(Summary Table I). Seed storage characters including oil, protein and glucosinolate content were measured by near infrared spectroscopy (NIRS) for certain trials.

One hundred and eighteen single-nucleotide polymorphism (SNP) markers previously mapped to the TNDH population (<http://brassica.bbsrc.ac.uk/IMSORB>) were screened by sequencing PCR products for polymorphisms in the CRDH and VGDH populations (HGCA APR3098 2007). Probes corresponding to the candidate genes were produced by PCR from *Arabidopsis* BACs predicted to contain the genes of interest. BAC clones containing the genes of interest were identified by the hybridisation of these probes to the JBNY and JBNB BAC libraries derived from *B. napus* cv Tapidor. For MAX3 and MAX4 an alternative data-mining approach was used to obtain sequences linked to the genes of interest using *B. rapa* BACs from the KBrH and KBrB BAC libraries and genome shotgun sequences (GSS) and expressed sequence tags (ESTs) derived from *B. oleracea*. These sequences were used to design amplicons linked to the genes of interest which were used to screen the parents for polymorphisms that could be used as molecular markers.

2.2. Results

2.2.1. Marker development and mapping

Screening of the IMSORB marker set identified 32 markers which were polymorphic in CRDH and 11 in VGDH. Of the 32 pyrosequencer marker assays previously developed on TNDH, six were transferable to CRDH and three transferable to VGDH (HGCA APR3098 2008). Eleven CAPS (cleaved amplified polymorphic sequences) assays (seven for CRDH and four for VGDH) were developed of which ten were genotyped. An additional fifteen IMSORB markers were genotyped on CRDH and four on VGDH.

Polymorphisms were identified in 42 of the sequences linked to candidate genes in the TNDH population, 27 in the VGDH population and 26 in the CR population. All new markers, polymorphic in Tapidor and Ningyou 7, including 37 of the candidate gene markers, have been integrated with the existing TNDH linkage map. Mapping was carried out in two stages in which 26 markers were added where they satisfied the requirements for a high stringency map. The 11 candidate gene and other markers

which failed to meet these requirements were subsequently 'forced' so that a 'best estimate' of their position was possible.

A total of 122 markers were used to develop a skeleton genetic linkage map for CRDH: 23 IMSORB markers and 12 candidate genes developed in this project were combined with 87 SSR markers provided by Warwick HRI. Of these, 100 markers were mapped into 18 discrete linkage groups of between two and 14 markers. Twenty-two markers remained unlinked. These groups were tentatively allocated to chromosomes using homologies with TNDH. The largest linkage groups were A3, A7 and C1 while seven were ambiguous or unidentified. Because very few markers were genotyped in the VGDH population, genetic linkage mapping was not possible.

2.2.2. Trait analysis

In these trials each population exhibited similar behaviour such that all traits showed large plasticity both within individual plots, blocks and between sites demonstrating the capacity of the canopy to respond to changes in the environment. In the case of TNDH, this included a response to phoma stem canker and, in CRDH and VGDH, responses to uneven establishment and grazing by deer, such that variation in both populations was greater at Cowlinge than Cantelupe.

Both environmental and genotype $\times$ environment interactions complicated the analysis for each population. Certain trends were, however, evident in all populations. Post-flowering traits, such as the size and angles of pods and pedicels, which develop later after the canopy has 'filled out' and were also better replicated, were more accurately determined than pre-flowering traits such as stem thickness, branch number and angles, which were subject to greater environmental errors arising from variation in plant density and grazing. In TNDH, traits such as seed weight and yield were also affected by the incidence of phoma stem canker. In spite of these factors each population showed significant variation for all traits, with values both greater and lower than that observed for their parents. The difference between the lowest and highest values ranged from 1.09 to 6.45 fold depending on the trait (Summary Table I). In general, post-flowering traits were more heritable than pre-flowering traits. The usefulness of this variation was confirmed by subsequent successful QTL analysis.

Summary Table I. Trait measurements for TNDH¹, parents and controls from the main field trials grown at Barton, Cambridge and Cowlinge, Newmarket in 2006-2007.

	TNDH				Ningyou 7		Tapidor		Controls	
	mean	min	max	sem	mean	sem	mean	sem	mean	sd
Seed traits										
Seed weight	0.72	0.40	1.08	0.010	0.67	0.107	0.68	0.047	0.85	0.230
Pod weight	0.40	0.24	0.54	0.005	0.41	0.059	0.40	0.023	0.45	0.080
Pod HI	0.64	0.56	0.71	0.002	0.62	0.020	0.63	0.015	0.65	0.034
Mean seed weight	4.47	2.93	6.61	0.044	4.95	0.283	4.62	0.141	4.50	1.066
Seed number/pod	16.3	8.1	23.9	0.22	14.0	2.45	14.8	0.88	19.8	5.25
Plant traits										
Height	141.5	110.9	167.8	0.80	129.9	5.62	130.1	3.89	152.3	16.53
Terminal length	47.5	35.6	60.9	0.37	46.2	2.94	46.3	3.45	52.4	6.71
Foot length	59.1	32.3	89.1	0.80	44.9	6.93	43.6	4.44	64.5	16.08
Pod no. on terminal	57.9	35.0	76.3	0.59	53.5	5.10	44.3	5.37	54.6	10.57
Stem width at base	1.02	0.73	1.47	0.009	1.00	0.063	1.15	0.158	0.99	0.243
Branching traits										
Fertile branch no.	6.4	4.1	10.7	0.08	6.9	0.8	6.98	0.9	5.5	1.87
Infertile branch no.	0.9	0.1	1.9	0.03	1.2	0.4	0.85	0.4	0.7	0.84
Remaining nodes	21.9	15.2	28.2	0.20	20.2	1.6	21.00	1.9	21.4	3.70
Total nodes	29.2	22.1	36.2	0.22	28.3	2.0	28.24	1.9	27.6	4.77
Node density	0.20	0.29	0.15	0.130	4.70	0.287	4.72	0.325	5.67	1.173
Branch density	0.09	0.07	0.14	0.001	0.10	0.005	0.09	0.006	0.07	0.017
Branch angle	40.0	31.1	47.8	0.26	39.2	1.5	37.36	1.9	36.8	4.57
Branch angle (top 4)	43.5	34.7	50.7	0.26	43.0	1.9	41.32	2.8	39.1	5.54
Pod traits										
Beak length	1.13	0.66	1.55	0.011	0.92	0.116	1.01	0.045	1.24	0.223
Pedicle length	2.27	1.84	2.92	0.014	2.09	0.079	1.99	0.087	2.29	0.316
Pod length	5.31	3.76	6.27	0.034	4.65	0.287	5.13	0.233	5.56	0.671
Pod width	0.40	0.34	0.45	0.001	0.42	0.018	0.38	0.011	0.42	0.033
Pedicle angle	81.8	68.5	94.7	0.36	78.9	3.1	78.4	2.63	83.8	6.14
Pod angle	164.7	156.9	172.7	0.27	161.6	1.6	162.4	2.05	165.4	4.88
Angle to rachis	66.5	49.1	81.0	0.50	60.5	4.0	60.8	2.98	69.1	7.27
Biomass measures										
Yield (t ha ⁻¹)	4.20	1.99	6.74	0.084	0.88	0.225	3.00	0.225	3.45	0.318
Harvest Index	0.27	0.18	0.40	0.003	0.26	0.118	0.28	0.118	0.27	0.166
Scored traits										
Canker	1.90	0.30	4.50	0.196	5.50	0.224	1.17	0.224	0.63	0.400
Start of flowering	32.4	23.5	40.0	3.3	14	1.70	33	1.70	37.8	2.59

¹A doubled haploid population derived from a cross between the European winter cultivar Tapidor and the Chinese cultivar Ningyou 7

Summary Table II. Correlation matrix for selected canopy architecture traits in TNDH. Mean of Barton, Cambridge and Cowlinge, Newmarket 2006-2007.

Mean seed wt.	0.41												
Seed no/pod	0.78	-0.23											
Plant height	0.39	0.08	0.38										
Pod no.	0.21	-0.02	0.25	0.36									
Fertile branches	0.01	0.07	-0.06	-0.03	-0.10								
Branch angle	0.24	0.06	0.23	0.12	0.19	-0.35							
Pedicel length	0.20	0.27	0.02	0.22	0.07	-0.03	-0.05						
Pod length	0.53	-0.04	0.60	0.31	0.22	-0.11	0.30	0.27					
Pedicel angle	0.30	0.10	0.24	0.18	0.29	-0.24	0.50	0.06	0.36				
Pod angle	0.22	-0.10	0.30	-0.01	0.14	-0.22	0.37	-0.04	0.42	-0.26			
Yield	0.33	-0.13	0.46	0.26	0.38	-0.30	0.34	-0.22	0.26	0.23	0.37		
Harvest Index	0.12	-0.04	0.13	-0.10	0.05	0.09	-0.01	-0.05	-0.01	0.15	-0.09	0.05	
Canker*	-0.12	0.11	-0.24	-0.16	-0.25	0.19	-0.24	0.27	-0.16	-0.16	-0.32	-0.69	0.02

	Seed wt. (10 pods)	Mean seed wt.	Seed number/pod	Plant height	Pod no. on terminal	Fertile branches	Branch angle	Pedicel length	Pod length	Pedicel angle	Pod angle	Yield	Harvest Index
r = positive		$P < 0.001$			$P < 0.01$			$P < 0.05$					
r = negative		$P < 0.001$			$P < 0.01$			$P < 0.05$					

* only assessed at Cowlinge

Many statistically significant associations were observed among these traits in all three populations, however, as expected where there are many quantitative and environmentally responsive traits, their biological significance was often low. Typical results are given in Summary Table II for the mean correlations from both sites for TNDH. Higher yield was strongly correlated with late flowering ($r = + 0.57$) and early maturation ($r = - 0.67$) (though canker was also associated with early flowering and low yields). HI showed no relationship with any trait, demonstrating the variability of HI and that it is derived from many traits working together, each contributing only a small proportion of the total variation. However, it was observed that many other traits showed significant relationships with yield though with smaller r^2 values. Thus, as expected, yield components, including increased seed weight per pod, more and longer pods with more seeds, and branch density, were positively correlated with yield. In contrast thicker stems and increased branching were negatively correlated with yield. Yield was also positively correlated with long horizontal pods. Branch, pedicel and pod angles were all positively associated though the more 'horizontal' pods tended to have more 'vertical' pedicels.

Interestingly, it was noted that relationships among those traits, such as foot length, terminal length and height, where autocorrelation was expected, were complex. Foot and terminal length were correlated with height ($r = +0.707$ and $+0.509$) but were not themselves linked, suggesting independent genetic control of these characters. The r^2 values calculated from these correlations were 50% and 25.9% and also indicate that, despite the large experimental and environmental variation, there is considerable unexplained genetic variation that may be exploited by breeders. Thus for example, as this terminal length is linked to pod density and yield, it should be possible to select for long terminals with many pods without increasing plant height.

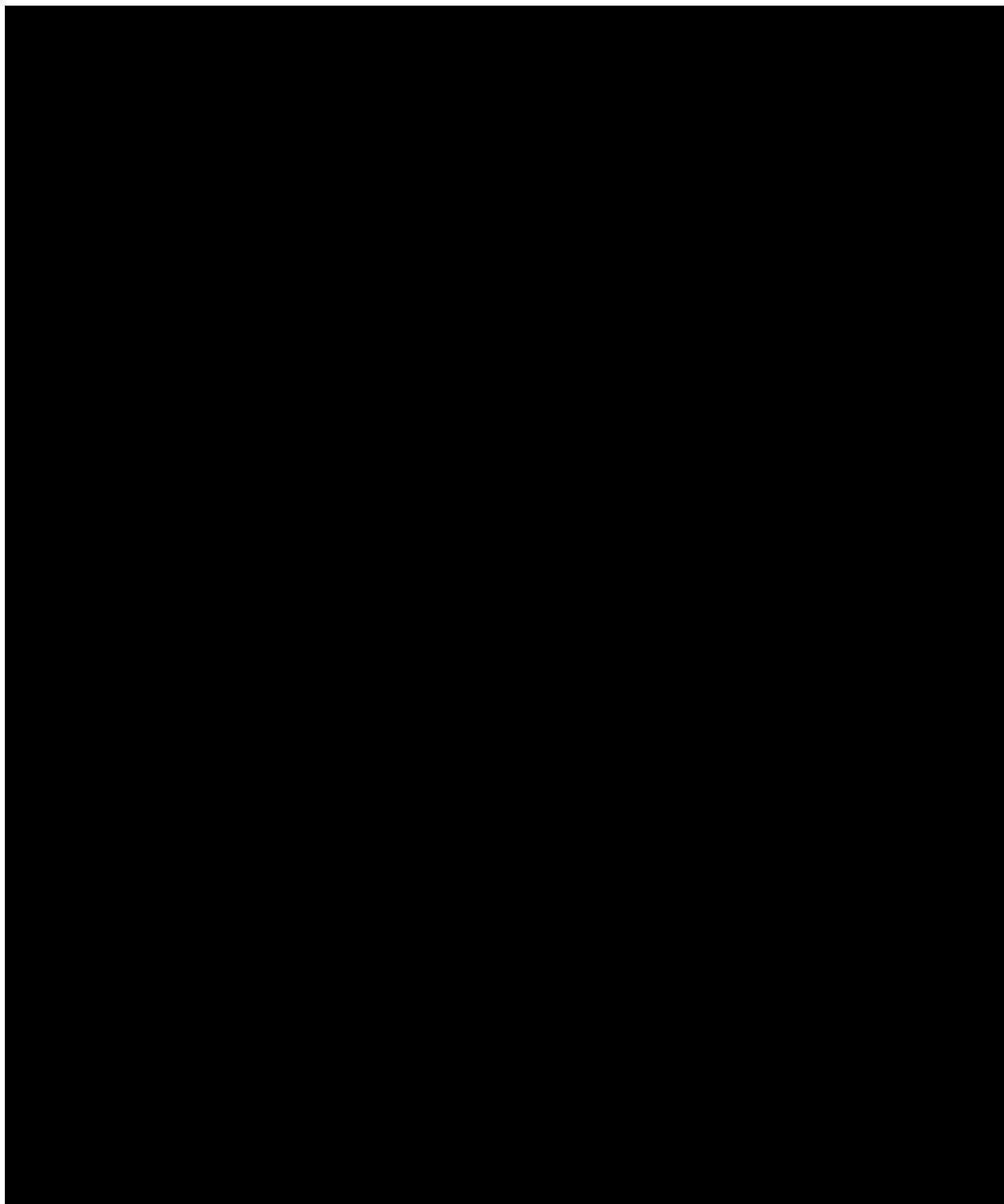
In contrast, neither CRDH nor VGDH showed any major traits association with yield except flowering time at Cowlinge where, in contrast to TNDH, they showed a significant negative correlation ($r = -0.480$) thus early flowering lines tended to have higher yields. In both populations at both sites long pods were associated with a more horizontal habit (mean $r = +0.396$ and $+0.565$ for CRDH and VGDH respectively). Both CRDH and VGDH had very similar relationships for the component measurements of height, thus height was again correlated with terminal length ($r = +0.331$ and $+0.587$ for CRDH and VGDH) and foot length ($r = +0.426$ and $+0.271$ for CRDH and

VGDH) while these two traits showed no significant correlations. There were, however, no associations of these traits with pod length as found for TNDH.

QTL discovery was carried out on TNDH and CRDH by single marker regression analysis (SM) treating sites as distinct environments. In TNDH (Summary Table III) many putative QTL ($P < 0.05$) were observed across the whole genome and were more frequent in the A than the C genome (9.3 compared to 6.3 per linkage group). More QTL were identified at Barton than Cowlinge (171 and 139 respectively). Taking average values for both sites A1, A6, A3 and C3 had most QTL (16.5, 13, 11.5 and 11 respectively) while C2 and C7 had the least (1.5 and 1 respectively). The number of QTL varied among the traits, with an average of 8, ranging from pod HI where only a single different QTL was identified at each site to pod angle to the rachis where 11 QTL were identified at Barton. While some QTL were unique to a site, others were evident at both sites. Examples of the most significant of these included QTL for yield, branch and pedicel angle on A1; yield and pod angle on A10; branch, pod and pedicel angles on A3; and seed weight, branch angle and pod length on A6. Many QTL for different traits co-locate on linkage groups indicating pleiotropy and/or multiple genes. It was noted that despite the association of phoma stem canker with yield, those QTL associated with it were not usually directly coincident with other QTL. Re-analysis of the data using canker as a covariate showed significant statistical effects but did not have major effects on the covariate adjusted values. That many traits exhibited multiple QTL confirms their polygenic nature with both increasing and decreasing effects noted to come from each parent hence the observed transgenic segregation.

Clusters of QTL for many associated traits were observed to be coincident at specific locations, thus, for example, QTL for terminal length, node number and density, stem and pod widths and branch and pedicel angle were observed between approx. 30 and 50cM on A3 at Cowlinge while QTL for pedicel and pod angles were evident between 50 and 60cM. Importantly, it was observed that many traits had QTL on many different linkage groups. This reflected the polygenic control of many canopy traits resulting from the complex physiological pathways involved in the determination of these traits, the effect of environment on their expression and also the genomic complexity of the *B. napus* genome. One important implication of this is that the contribution of each QTL to the overall expression of the trait is 'diluted' by the number of active genes, making the accurate identification of each more difficult.

Summary Table III. Significance level and peak position of QTL (cM) for selected traits in TNDH at Barton and Cowlinge 2007-2008 using single marker regression analysis.



Fewer QTL were detected in CRDH partly because it showed less trait variation but mainly because less of the genome was covered by the linkage map. At Cowlinge the most significant QTL ($P < 0.0001$) was for plant height on A7, on which one was also detected in TNDH at Barton ($P < 0.001$). QTL for pedicel length were detected on A3 at both sites ($P < 0.001$ and $P < 0.01$). QTL for mean seed weight (only analysed at Cowlinge) were present on A9, C1 and C3 ($P < 0.001$ or $P < 0.01$). QTL for node number were observed at both sites on A7 ($P < 0.05$ and $P < 0.001$ at Barton and Cowlinge respectively) and on A4/C4 at Cantelupe ($P < 0.001$) and also in TNDH at Barton on A7 ($P < 0.001$). In CRDH, QTL for pedicel angle were observed on A10 at both sites ($P < 0.0001$ and $P < 0.01$) and also in TNDH at Cowlinge ($P < 0.01$). Several of the candidate genes mapped within identified QTL at both sites, though not necessarily close to the peak of the QTL where it is likely that they are acting as simple markers and are not causally associated with the overlying QTL.

Thirty-five candidate genes were genotyped in TNDH of which 24 mapped to 13 linkage groups. All of these 24 markers showed at least one single marker QTL ($P < 0.05$ or less) of which 14 markers were either at or close to the peak of 16 QTL (Summary table IV). At Barton the most significant candidate gene markers ($P < 0.001$) included TB-like (A2) for height, terminal length and pod density (all auto-correlated traits), RGL1a (A5) for seed density, TCP (A7) for pod density and MAX2g (C4) for branch and pod angles. Similar numbers of candidate genes occurring close to the peak of QTL were also observed at Cowlinge though only TB-like on A2 for plant height was coincident with one at Barton. The most significant of these ($P < 0.0001$) was TB_like (A2) for plant height while other significant markers ($P < 0.001$) included MAX1f and MAX2g (C4) for node density.

Twelve candidate genes were genotyped in CRDH of which ten were mapped in the skeleton map. Only one, MAX2_I (mapped to A3 in CRDH), was also mapped in TNDH where it was alternatively located on C7. At Cantelupe only MAX3_m co-located with the peak of a QTL, in this case for the number of nodes and associated traits. No candidate genes co-located with QTL at Cowlinge. Only six candidate genes were genotyped in VGDH of which only two, DELLA_GRA and GAI23.6 were 'mapped' to A7 and A6 respectively. Of these only GAI23.6 had QTL ($P < 0.05$) which were identified for fertile branch and node number at Cantelupe and for foot length at Cowlinge.

Summary Table IV. Candidate genes mapped to within 2cM of peak of a QTL in TNDH at Barton and Cowlinge by single marker analysis.

Marker to Candidate gene	Linkage groupG	Position of marker (cM)																		
			Barton Cowlinge	Barton Cowlinge	Barton Cowlinge	Barton Cowlinge	Barton Cowlinge	Barton Cowlinge	Barton Cowlinge	Barton Cowlinge	Barton Cowlinge	Barton Cowlinge	Barton Cowlinge	Barton Cowlinge	Barton Cowlinge	Barton Cowlinge	Barton Cowlinge	Barton Cowlinge	Barton Cowlinge	Barton Cowlinge
JICB0055_(TB-like)	A2	71.3																		
KBrB001H24-13_(RGL2?)	A3	59.1																		
JICB0094_(MAX1g)	A5	18.6																		
JICB0153_(MAX2h)	A5	20.2																		
JICB0384_(RGL1a)	A5	##																		
KBrB086M23-6_580_(GAI)	A6	49.3																		
JICB0274_(Blrk)	A7	99.0																		
JICB0011_(TCP)	A7	##																		
JICB0335_(GAIb)	A8	22.3																		
JICB0192_(Bpf)	A9	27.2																		
JICB0272_(Blrj)	A10	53.4																		
JICB0088_(MAX1f)	C4	22.7																		
JICB0149_(MAX2g)	C4	##																		
KBrB086M23-6_575_(GAI)	C5	57.8																		
QTL significance																				

 $P < 0.05$
 $P < 0.01$
 $P < 0.001$
 $P < 0.001$

2.3. Conclusions

The two new populations developed, CRDH and VGDH, have shown significant genetic diversity in many traits and thus form important new genetic resources for further genetic studies in oilseed rape. In particular, the results of our analyses showed there to be a wide range of variation for the majority of the inflorescence/canopy architecture traits measured. This was much greater in the population derived from the cross between European and Chinese material (TNDH) than in the new crosses between UK-adapted varieties. Despite the inherent environmental effects and errors associated with field data, major genetic components were identified for most of the traits. The quantitative genetic analyses showed that the basis of this genetic component is complex, typically consisting of contributions from numerous different parts of the genome (loci), each having only a small effect. Several of these loci coincided (within 2cM) with the positions of markers for genes, identified from studies in *Arabidopsis thaliana*, which were candidates for potentially being involved in control of the traits. These included: *TB-like*, *TCP* and *Blr*, ('length traits'), *GAI*, *RGL1* and *MAX2* (branch and pod angle), *Blr* (fertile branch number and pod number), *RGL1* (seed density) and *GAI* (stem width) and represent the bases for hypotheses to be tested in future studies. However, most of the candidate genes tested in these studies showed no indication of involvement in controlling canopy traits, either because they are indeed not important in these populations or that we have been unable to resolve the data sufficiently. Indeed, numerous loci influencing canopy architecture traits were identified that appeared not to correspond to the positions of the limited number of candidate genes selected in this study. Our results directly focus upon specific known genes that may be involved in the control of aspects of canopy architecture that are likely to impact on seed yield. In addition, they indicate that studies conducted to date in *A. thaliana*, which used mutation-based approaches, should be supplemented with studies exploiting natural genetic variation in order to assist the identification of the genes underlying many of the important loci that we have identified in oilseed rape.

3. TECHNICAL DETAIL

3.1. Introduction

Improving the productivity of oilseed rape (*Brassica napus*) as a crop within the UK has proven difficult and there has been no apparent increase in yield during the last 20 years. That 'the oilseed crop is, in some ways, more like a weed than a crop' (Thompson and Hughes, 1986) is generally acknowledged to describe some of the many problems restricting the development and improvement of the crop. This is seen particularly in crop architecture, where the indeterminate nature of plant growth leads to a very inefficient canopy, and is best illustrated by its low Harvest Index (HI), which is the ratio of seed yield to above ground biomass, expressed as a percentage, and usually around 20 - 25%. One of several reasons for this is the complexity of the traits involved. This complexity arises from the interaction of many characters, including yield components, each determining part of the expression of HI and all of which frequently show considerable G × E (genotype x environment) effects. These individual characters are also frequently quantitative and under polygenic control.

The range of genetic variation available to provide new traits for breeding programmes is restricted. There are two reasons for this. Firstly, oilseed rape (OSR) originated only very recently as an amphidiploid species derived from a spontaneous cross between two diploid parents (an unknown *Brassica rapa* and an unknown *Brassica oleracea* species). The genetic variation within the oilseed rape genome is, therefore, restricted to that contributed by each of these parents plus that contributed by subsequent evolution. Secondly, we can expect there to have been a reduction in the number and range of alleles that were once present within the oilseed rape genome as a result of breeding programmes focussed on adapting the crop for the restricted range of agricultural and environmental conditions under which it is normally grown. A consequence of the lack of genetic diversity is that the crop does not have the capacity to respond to environmental or agronomic changes.

Harvest index is known to be a fundamental determinant of seed yield in a range of species including oilseed rape. It has been clearly shown that variation exists for this trait in cultivars of oilseed rape and that, by manipulating canopy architecture through the use of growth regulators, HI can be increased with a corresponding increase in

yield. The use of growth regulators is, however, unreliable, expensive and does not lead to sustainable agricultural practice. In contrast to this chemical manipulation of HI, the potential success and importance of manipulating HI genetically, through the introduction of novel alleles, has been amply demonstrated through its application within recent wheat (and other cereals) breeding programmes in which increases in yield have been brought about through raising HI from ca 0.25 to ca 0.5 in current cultivars. Similar results, expressed in terms of dry weight, in oilseed rape may be more difficult to achieve because of the high calorific content of the seed oil in relation to that of carbohydrate and protein in wheat. However, increased HI, expressed in energy terms, will still represent an important improvement in oilseed agronomy and sustainability.

This research addresses the problem of poor HI by using novel populations (new combinations of oilseed rape cultivars) and an exotic population (a wide cross between a European oilseed cultivar and a Chinese cultivar of *B. napus*) to develop a better understanding of the genetic control of canopy architecture traits that are components of harvest index. The novel populations utilise variation present within well-developed germplasm, which should be rapidly exploitable. The exotic population makes available variation from beyond conventional germplasm, which is likely to have a larger impact, but will take longer to introduce into competitive varieties. We have developed molecular markers linked to homologues of specific genes of *A. thaliana* that are candidates for control of aspects of inflorescence/canopy architecture and have placed these on the existing linkage maps for the wide population (TNDH) and on the new linkage map developed for one of the new populations (CRDH). Although the macrostructure of the oilseed rape genome shows numerous gross rearrangements compared to that of *A. thaliana*, the microstructure of large segments is well conserved, so useful alignment is feasible. For the candidate genes, alignment is ensured as the oilseed rape markers to be developed will be physically linked (within less than 150 kb) to the homologue of the candidate gene as a consequence of the markers being developed from sequences derived from BAC clones hybridising to gene-specific probes.

In addition to understanding the genetic control of canopy architecture relating to HI, our approach provides a model for the use of novel and exotic germplasm to understand the control of important traits and for the development of approaches to

identify and exploit variation no longer present in conventional breeding material. The success of attempts to improve yield in many crops has been made more difficult because of 'yield compensation' among the components of yield with no associated increase in total reproductive dry matter production or yield. In oilseed rape these traits (e.g. fertile branch number, fertile flowers, pod size and number, seed size and seed number) frequently show these negative correlations thus, for example, increasing seed size will result in fewer seeds being produced per pod. We are, however, addressing this problem by researching canopy traits that will alter the balance of dry matter production between the reproductive parts of the plant and the vegetative parts. By modifying the canopy so that it produces less unwanted and hence wasted vegetative matter and maximising the effective use of its reproductive capacity it should be possible to utilise the inherent tendency of the plant to maintain a constant biomass production and compensate for the reduced vegetative tissue and wasted reproductive matter with an increase in relative seed yield.

3.2. Material and Methods

3.2.1. Populations

Three populations have been used: TNDH, a pre-existing double haploid (DH) population which has been adopted as a Brassica reference population and which was developed from a cross between Tapidor (a European winter OSR cultivar) and Ningyou 7 (a Chinese semi-winter OSR cultivar), and two additional new DH populations which have been developed as part of the project. The parents for these populations were selected by the consortium members. F₁ hybrids from the crosses Capitol × Rocket (CRDH) and Verona × Grizzly (VGDH) were made at CPB-Twyford (now KWS UK) in winter 2004-2005 and then grown to produce the two DH populations during 2005-2006. CRDH and VGDH consisted of 244 and 251 lines respectively. These were subsequently grown by Elsoms Seeds and Nickersons in 2006-2007 for assessment and bulking of seed. A selection of the best 94 plants from each population was made by the breeders for full scale trials. Seed of all the DH lines has been distributed to consortium partners as required.

3.2.2. Field trials

Seed of 150 lines of the TNDH population was sown in 2005-2006 in small 1.5 m² plots as a single block trial without replication at Spalding (Elsoms Seeds) and Rothwell (Nickersons) to produce sufficient selfed seed, obtained by bagging several plants from each plot, for full scale field trials. This was the first TNDH field trial undertaken in the UK. In addition, preliminary assessment of the material was carried out at Spalding to help the selection of the most suitable subset of 94 lines and also develop the methodologies needed for the measurement of traits of interest. These trials were not fungicide treated. It was observed that TNDH showed great variation for flowering time and was, in general, very susceptible to stem canker (*Leptosphaeria maculans*). It was thought that earliness and canker susceptibility originated from Ningyou 7, a variety requiring minimal vernalisation and which had been bred in an environment where stem canker was not endemic and had therefore acquired no resistance. The most extreme material was removed during the selection process to optimise the population for UK conditions. Two field trials were sown in 2006-2007, at Barton, Cambridge and Cowlinge, Newmarket, in which the selected set of 94 lines were sown in two randomised blocks. Plots of the parents and control varieties selected from Castille, Escort, Fortis, Fortress and Winner were also sown. Seed was sown at normal agronomic density in plots 1.2 × 6m and 1.8 × 12m at Barton and Cowlinge respectively. Plots received normal agronomic treatments with extra fungicide treatments to minimise stem canker. Plots were left standing until maturity and plot yields were obtained by combining the plots. All lines of CRDH and VGDH were sown in small plots in 2006-2007 to provide sufficient selfed seed, as described for TNDH in 2005-2006. A 94 line subset was selected from each population. These were sown in full scale field trials at Cantelupe Farm, Cambridge and Cowlinge in 2007-2008 as described for TNDH in 2006-2007.

3.2.3. Plant sampling

Three TNDH plants per plot were collected randomly from an area of uniform establishment in the centre of each plot at Spalding and the main trials at Barton and Cowlinge. To avoid excessive damage and seed loss by sampling the dry, mature plants this occurred ca 3-4 weeks before the estimated time of harvest (*i.e.* just before the normal timing for swathing). These plants were subsequently processed in

the laboratory. A similar sample of five plants was also taken from each plot for estimating Harvest Index from the main trials only. All plots were combine harvested for yield and the seed used to estimate seed storage products. In a similar way samples of either three or five plants per plot were also collected from the CRDH and VGDH trials. This occurred about one week earlier than for TNDH with the result that less damage was done to the plants but the seed of the later maturing lines was less well developed. All plots were combined at harvest and seed retained for estimation of seed size at Cowlinge.

3.2.4. Plant processing

All harvested plants were allowed to dry naturally in a glasshouse before processing. For each plant the roots were cut off at soil level and height measured from the tip of the terminal raceme to the base. The number of branches with fertile pods, aborted branches (including those with only essentially sterile pods) and the remaining nodes were counted. The length of the terminal branch was measured and the number of pods on it also counted. A small section from the base of the stem, a few centimetres of stem encompassing each branching nodes and ten typical pods from the centre of the terminal raceme were taken and photographed for later analysis using SigmaScan Pro 5.0 (<http://www.spss.com>) to measure the adaxial angles of each branch to the stem, pedicel to raceme and pod to raceme; the length of each pod, pedicel and beak; and stem and pod widths. The ten pods were subsequently threshed as a single sample and the seed and pod valves weighed and the seed counted. A list of the traits measured is given in Table 1.

Table 1. Measured traits, details of measurement and trials on which they were measured.

Trait name	Description	Comments	Trials
Seed traits			
Seed weight (g)	Weight of seed from the ten typical pods taken from the terminal raceme	10 pods from the 3-plant harvest	a, b, c, e, g
Valve weight (g)	Weigh of the valves from the ten typical pods taken from the terminal raceme	10 pods from the 3-plant harvest	a, b, c, e, g
Pod HI	Ratio of seed weight to weight of seed + valves	10 pods from the 3-plant harvest	a, b, c, e, g
Mean seed weight (mg)	Average weight of seeds from the ten typical pods taken from the terminal raceme	10 pods from the 3-plant harvest	a, b, c, e, g
Seed number/pod	Average number of seeds per pod from the ten typical pods taken from the terminal raceme	10 pods from the 3-plant harvest	a, b, c, e, g
Seed density (seeds/cm)	Average number of seeds per pod / pod length	10 pods from the 3-plant harvest	a, b, c, e, g
Plant traits			
Height (cm)	Length of harvested plant from base to tip of terminal raceme	3-plant harvest	a, b, c, d, e, f, g
Terminal (cm)	Length of terminal raceme	3-plant harvest	a, b, c, d, e, f, g
Foot length (cm)	Length of stem from ground to lowest fertile branch	3-plant harvest	a, b, c, d, e, f, g
Pod no. on terminal	Numbers of fertile pods on terminal raceme	3-plant harvest	a, b, c, d, e, f, g
Pod density (pods/cm)	Number of pods / terminal length	3-plant harvest	a, b, c, d, e, f, g
Stem width at base (cm)	Width of stem 3-5cm from ground level	3-plant harvest	a, b, c, d, e, f, g
Branching traits			
Fertile branch no.	Number of fertile branches	3-plant harvest	a, b, c, d, e, f, g
Infertile branch no.	Number of infertile branches	3-plant harvest	a, b, c, d, e, f, g
Remaining nodes	Number of nodes not forming any branches	3-plant harvest	a, b, c, d, e, f, g
Total nodes	Total number of nodes produced	3-plant harvest	a, b, c, d, e, f, g
Node density (nodes/cm)	Average density of nodes (total nodes/height)	3-plant harvest	a, b, c, d, e, f, g
Branch density (branch/cm)	Average density of branches in 'fertile canopy' (branch number / (height-foot))	3-plant harvest	a, b, c, d, e, f, g
Branch angle (°)	Average angle of branch to main stem	SigmaScan	a, b, c, d, e, f, g
Branch angle (top 4) (°)	Average angle of top four branches to main stem	SigmaScan	a, b, c, d, e, f, g
Pod traits			
Beak length	Length of beak	SigmaScan	a, b, c, d, e, f, g
Pedicle length	Length of pedicel	SigmaScan	a, b, c, d, e, f, g
Pod length	Length of pod	SigmaScan	a, b, c, d, e, f, g
Silique length	Length of pod + beak	SigmaScan	a, b, c, d, e, f, g
Pod width	Widest cross sectional diameter of pod	SigmaScan	a, b, c, d, e, f, g
Pedicle angle (°)	Vertical angle between pedicel and raceme stalk	SigmaScan	a, b, c, d, e, f, g
Pod angle (°)	Vertical angle between pod and pedicel	SigmaScan	a, b, c, d, e, f, g
Angle to rachis (°)	Vertical angle between pod and raceme stalk	SigmaScan	a, b, c, d, e, f, g

Trait name	Description	Comments	Trials
			f, g
Biomass measures			
Yield (t ha ⁻¹)	Combined seed yield	Plot	a, b, c, d, e, f, g
Harvest Index	Ratio of seed yield to biomass	5-plant harvest	a, b, c, d, e, f, g
Biomass	Estimated as HI * yield	5-plant harvest	a, b, c, d, e, f, g
Straw	Estimated as (1-HI) * yield	5-plant harvest	a, b, c, d, e, f, g
Scored traits			
Canker	Scored: 1=resistant, 7=susceptible	Plot	a, c, e, g
Autumn vigour	Scored: 1=low, 7=high	Plot	a, c, e, g
Spring vigour	Scored: 1=low, 7=high	Plot	a, c, e, g
Appearance before flowering	Scored: 1=poor, 7=good	Plot	a, c, e, g
Appearance at harvest	Scored: 1=poor, 7=good	Plot	a, c, e, g
Lodging at maturity	Scored: 1=poor, 7=good	Plot	a, c, e, g
Start of flowering	Scored: 1=early, 7=late	Plot	a, c, e, g
End of flowering	Scored: 1=early, 7=late	Plot	a, c, e, g
Flowering period	Scored	Plot	a, c, e, g
Maturity	Scored	Plot	a, c, e, g
Height (cm)	Mean height of plot	Plot	a, c, e, g
Seed storage traits			
Oil (%) seed	Oil content of harvested seed	Plot/NIR	b, c, e, g
Glucosinolate	Glucosinolate content of harvested seed	Plot/NIR	b, c, e, g
Protein (%)	Protein content of harvested seed	Plot/NIR	b, c, e, g

3.2.5. Production of gene specific probes for colony hybridisation

Probes corresponding to the candidate genes were produced by PCR from *Arabidopsis* BACs predicted to contain the genes of interest at <http://brassica.bbsrc.ac.uk/IGF/>. The *Arabidopsis* BACs predicted to contain the genes of interest were grown up overnight in 5ml LB (10g bacto-tryptone, 5g yeast extract, 10g NaCl made up to 1 litre with ddH₂O, pH 7.5) containing 10mg/ml of kanamycin antibiotic in a 37°C shaking incubator. Cells were pelleted from 2ml of overnight BAC culture by spinning for 10min at 13000rpm in a micro-centrifuge and pouring off the supernatant. DNA was prepared using the QIAprep Spin miniprep kit (Qiagen Ltd. 2005) following the manufacturer's instructions. DNA was eluted into 50µl of sterile ddH₂O. Primers for the production of the candidate gene probes were designed from the largest exon from the *A. thaliana* gene sequences using the Primer3 program (Rozen S. and Skaletsky H. J. 2000). To produce the probe, touchdown PCR was carried out in 0.2ml tubes with a reaction volume of 100µl containing:

67.6µl	ddH ₂ O
10µl	10 x PCR buffer
3µl	MgCl ₂ (50mM)
10µl	dNTPs (2mM)
2µl	forward primer (10mM)
2µl	reverse primer (10mM)
0.4µl	Platinum Taq (5u/µl – Invitrogen)
5µl	BAC DNA (1/5 dilution of original DNA preparation, ~100ng)

PCR was carried out on a MWGAG Biotech Primus96 plus thermo-cycler on a 15 step touchdown cycle with the initial annealing temperature 1°C higher than the greatest primer T_m followed by 35 cycles with a 56°C annealing temperature. The probe was purified to remove unincorporated primer and dNTPs using the QiaQuick PCR purification kit (Qiagen Ltd. 2002) with the DNA eluted into 30µl of H₂O.

3.2.6. Identification of BAC clones containing the genes of interest

Colony hybridisation using these probes was performed as described by O' Neil and Bancroft (2000) with the JBNY (Rana *et al.* 2004) and JBNB *B. napus* genomic clone library (Cho *et al.* 2010) by the Gene Transfer Clone Identification and Distribution Service (GetCID) <http://www.getcid.co.uk/>, one with a pool of the four MAX probes and one with a pool of the BP and BLR probes, for each BAC library. To confirm the presence of the gene of interest, Southern hybridisation was conducted for individual probes on positively hybridising clones using fingerprinted clone DNA as described by Rana *et al.* (2004).

Hybridisation, selection, conformation and sequencing of the positively hybridising clones for the *AtTB1* and *TCP* candidate genes had been performed previously by Roohaida Othman. Hybridisation and conformation of the *GAI*, *RGL*, *RGA*, *DELLA* and *GRAS* probes on the JBr *B. rapa* library was performed by Llewelyn Hynes.

Genomic clones identified by Southern hybridisation were grouped into bins representing different homologues, as described by O'Neill and Bancroft (2000). Clones were end-sequenced to confirm alignment to the expected region of the *A. thaliana* genome. One clone per bin was chosen for marker development.

3.2.7. Identification of locus-specific sequences via data-mining

For MAX3 and MAX4 an alternative data-mining approach was used to obtain sequences linked to the genes of interest using *B. rapa* BACs from the KBrH and KBrB BAC libraries being end sequenced as part of the *B. rapa* genome project (<http://www.brassica-rapa.org/>) and *B. oleracea* genome shotgun sequences (GSS) (Ayele M., Haas B.J. *et al.* 2005). The BAC end sequences are publicly available and have been aligned in-silico, along with *B. oleracea* GSS to the *A. thaliana* genome on the *Arabidopsis thaliana* Insertion Database (<http://atidb.org/>). Whole BACs or both BAC ends have been anchored however, in some cases, only a single BAC end has been aligned.

Clones showing a high likelihood of containing the gene of interest, end sequences aligned in the region of the gene of interest with high probability or GSS aligned close

to or within the gene, were selected and the sequences were retrieved from the NCBI website <http://www.ncbi.nlm.nih.gov/>. As with other sequences these were treated as those retrieved from the BAC library screen.

3.2.8. Marker production

Clones confirmed to contain the candidate genes were end sequenced by the JIC genome laboratory (<http://www.jicgenomelab.co.uk/jgl/>) using the ABI Prism BigDye v3.1 terminator sequencing kit following the manufacturer's protocol (Applied Biosystems 2002) and a BLAST search was performed with the end sequences using IMSORB BLAST (<http://brassica.bbsrc.ac.uk/IMSORB/>) against known *Brassica* sequence to determine if the sequences were repetitive within *Brassica* species. Any sequence identifying greater than 10 homologues was discarded as possibly repetitive within the genome and therefore not guaranteed to amplify a region close to the gene of interest. Products from these may also be difficult to sequence due to the production of a mixed amplicon. Primers were designed for one clone for each locus with a reverse or forward end sequence meeting these criteria using the Primer3 program (Rozen S. and Skaletsky H. J. 2000). Primer design criteria were set to an optimum product size of 500bp, with primers having an optimum size of 20 bases, optimum GC percentage of 50% and optimum T_m of 60°C.

The primers were used to amplify product in all parental material using touchdown PCR. Products were run on 1.5% agarose to confirm amplification before sequencing using the BigDye v3.1 terminator cycle sequencing kit following manufacturer's instruction (Applied Biosystems 2002). Reactions were carried out in a MWGAG Biotech Primus96 plus thermo-cycler.

Sequencing reactions were cleaned up by precipitation. Two and a half microlitres of 125mM EDTA pH8.0 (Fluka Biochemika) and 30µl of 100% ethanol (EtOH) were added to a 10µl sequencing reaction to precipitate the product. The plate was sealed, vortexed gently to mix and left at room temperature for 15 minutes and no longer. This was then spun in a Qiagen plate centrifuge at 4500rpm at 4°C for 30min to pellet the product. Plates were inverted and spun onto blue towel at 300rpm for 1min to remove the EtOH. Samples were washed twice by adding 60µl of 70% EtOH and

spinning at 4500rpm at 4°C for 30min. EtOH was removed by inverting and spinning at 300rpm for 1min.

Samples were dried at room temperature in the dark (to prevent product degradation) for approximately 30min to allow the remaining EtOH to evaporate. Pellets were then re-suspended in 15µl of Hi-Di Formamide (Applied Biosystems) and denatured by heating to 96°C for 3min before sequencing.

3.2.9. Identification of sequence polymorphism

To identify polymorphisms between the parental PCR products, sequences were aligned using the computer programs NclustalW, for text alignment, (<http://srs.ebi.ac.uk/>, SRS release 7.1.3.1) and MutationSurveyor, for the alignment of trace files (<http://www.softgenetics.com/mutationSurveyor.html>). Where no polymorphism was identified, an alternative BAC end sequence was used where possible. Polymorphism data were transferred to Biogemma and genotyping carried out using an appropriate assay.

3.2.10. Statistical analysis

All data were analysed using Genstat (Payne et al, 2009). Quantitative trait locus (QTL) analysis was carried out using single marker regression analysis, also using Genstat, with a permutation test of 1000 iterations used to estimate significance values of 5%, 1% and 0.1%. In general using these permuted values gave greater significance to the regression values than indicated by the Fprobabilities calculated from standard tables, thus the results used are mostly conservative estimates of the real probabilities. QTL were identified as centred on the marker with the greatest significance and with a spread of approximately all contiguous markers significant at the 5% level.

3.3. Results

3.3.1. IGF marker development

One hundred and eighteen SNP markers previously mapped to the TNDH population (ref: IMSORB) were screened by sequencing PCR products for polymorphisms in the CRDH and VGDH populations (Table 2; HGCA 2006 report). Of 32 pyrosequencer marker assays previously developed by Biogemma or JIC on TNDH as part of the IMSORB project, six were transferable to CRDH and three were transferable to VGDH (HGCA 2008 report). For the remaining markers a variety of marker assays were used and assessed on the populations for their suitability and cost. These included specific amplification/size polymorphism, CAPS (cleaved amplified polymorphic sequences), fluorescence polarisation, pyrosequencing and primer extension. Size polymorphism and CAPs assays were cheapest and simplest but were limited in transferability between populations. The others were more transferable but also more expensive. Site-specific differences in scoring markers at Biogemma and JIC included false positive calls from the original screen, amplification problems and specificity issues (or numbers lost from each population) (Supp. Table 1).

Table 2. Summary of marker development from IMSORB markers.

	Capitol x Rocket	Verona x Grizzly
Total markers	116	116
No. sequenced	105	110
No. polymorphic	32	11
No. monomorphic	43	74
Female parent failure	1	1
Male parent failure	5	0
Female parent poor	11	9
Male parent poor	4	5
Both parents poor	11	10
Heterozygous	1	0
Polymorphism rate	27.6%	9.5%

Eleven CAPS assays (seven for CRDH and four for VGDH) were developed by Biogemma of which ten were genotyped at CPB Twyford (now KWS UK Ltd). An additional fifteen IMSORB markers were genotyped on CRDH and four on VGDH at Biogemma. Using the polarisation technique established at Biogemma, where possible at least two potential polymorphisms per locus were tested on parent lines and a small subset of each population. Markers with a good separation of alleles were then genotyped on the full population using this technique.

3.3.2. Candidate gene marker development

In the development of molecular markers for candidate genes *approx.* 450 sequenced BAC ends have been obtained at 118 loci that are physically linked to members of 13 candidate genes and 2 candidate protein motifs. 35 of these were identified *in silico* using data from the Multinational *Brassica* Genome Project (MBGP) and GSS identified from NCBI (<http://www.ncbi.nlm.nih.gov/Genbank/>) (Supp. Table 2). From the sequenced BAC ends, 161 primer pairs were used to obtain sequences linked to these 118 potential homologues of candidate genes across the six oilseed rape lines that were parents of the mapping populations. Polymorphisms were identified in 41 of the sequences linked to candidate genes in the TNDH population, 26 in the VGDH population and 24 in the CRDH population (Table 3).

Table 3. Polymorphisms of candidate genes in TNDH, CRDH and VGDH.

Gene	TNDH			CRDH			VGDH		
	No. polymorphic loci	% with primers	% of total	No. polymorphic loci	% with primers	% of total	No. polymorphic loci	% with primers	% of total
TCP	4	57.1	57.1	1	14.3	14.3	1	14.3	14.3
TB1	4	44.4	40	3	33.3	30	1	11.1	10
MAX1	4	50	40	3	37.5	30	2	25	20
MAX2	4	44.4	36.4	3	33.3	27.3	3	33.3	27.3
MAX3*	7	70	50	2	20	14.3	3	30	21.4
MAX4*	2	12.5	10	1	6.3	5	3	18.8	15
BP**	3	33.3	16.7	1	11.1	5.6	3	33.3	16.7
BLR	4	50	36.4	3	37.5	27.3	3	37.5	27.3
<i>Rapa contigs</i>									
GAI	1	50	50	1	50	50	1	50	50
RGA	2	50	50	2	50	50	3	75	50
RGL1	1	50	50	1	50	50	1	50	50
RGL2	1	100	100	0	0	100	0	0	100
RGL3	1	100	100	1	100	100	0	0	100
<i>Protein motifs</i>									
DELLA +	1	50	50	1	50	50	1	50	50
GRAS***									
DELLA***	2	66.7	66.7	1	33.3	66.7	1	33.3	66.7

* *in silico* data

**

Fourteen of these candidate gene markers were genotyped on 188 lines of the TNDH population. Preliminary mapping showed them to be distributed across ten linkage groups. Additionally, eight candidate gene markers were genotyped in CRDH and one in VGDH. As with the IMSORB markers, candidate gene markers showed limited

polymorphism in CRDH and VGDH and similar problems with transferability between laboratories were present (Supp. Table 3).

Twenty-six markers that were problematic at Biogemma, not including six that could be assayed using CAPS, were identified as possible to genotype in TNDH at JIC. Of these, seventeen were genotyped and mapped. A further five candidate gene markers based upon sequences from the *Brassica rapa* Genome Sequencing Project were developed at JIC though two of these are now predicted not to include the gene model.

3.3.3. Map development

TNDH

All markers generated have been integrated with the existing TNDH linkage map (Qui et al; web pages) using Joinmap 3.0 (Van Oijen J.W. and Voorrips R. E. , 2001). Mapping was carried out in two stages. Firstly markers were added where they satisfied the requirements for a high stringency map, in which the chi-square values for individual markers are mostly less than two. Secondly, any markers which failed to meet these requirements were 'forced' so that a 'best estimate' of their position was possible (Table 4).

CRDH

Using the set of 94 selected lines, a total of 112 markers were used to develop a skeleton genetic linkage map. Seventy-seven were SSR markers provided by Warwick HRI, 23 were IMSORB markers and 12 were candidate genes (Table 5). Eighteen discrete linkage groups were identified by Joinmap totalling 100 markers and varying in size from 14 markers to two markers with 22 markers remaining unlinked. These groups were tentatively allocated to chromosomes using homologies with TNDH. Linkage groups A3 and C1 were the largest with several groups appearing to be sub-groups of A3.

VGDH

Using the set of 94 selected lines, six candidate genes and eight IGF markers were found to be polymorphic and genotyped in VGDH (Table 6) but were not mapped.

Table 4. Candidate gene markers mapped or unmapped to TNDH population.

Candidate gene	Marker name	LG	cM
<i>RGL1</i>	KBrB010O09-1	A2	62.1
<i>TB-like</i>	JICB0055	A2	71.3
<i>RGL3*</i>	KBrB017M18-36	A2	95.1
<i>RGL2*</i>	KBrB001H24-13	A3	59.1
<i>MAX3f</i>	JICB0283	A4	79.6
<i>MAX1g</i>	JICB0094	A5	18.6
<i>MAX2h</i>	JICB0153)	A5	20.2
<i>RGL1a</i>	JICB0384	A5	113.3
<i>GAI</i>	KBrB086M23-6_580	A6	49.3
<i>DELLA+GRASa</i>	JICB0416	A7	96.6
<i>Blrk</i>	JICB0274	A7	99
<i>TCP</i>	JICB0011	A7	100.1
<i>GAIb</i>	JICB0335	A8	22.3
<i>AtTB</i>	JICB0018	A8	78.6
<i>Bpf</i>	JICB0192	A9	27.2
<i>Blrj</i>	JICB0272	A10	53.4
<i>Blrd</i>	JICB0245	A10	77.9
<i>Blrg</i>	JICB0260	C3	0
<i>Bp3</i>	JICB0220	C3	53.3
<i>MAX1f</i>	JICB0088	C4	22.7
<i>MAX2g</i>	JICB0149	C4	121.2
<i>MAX1h</i>	JICB0111	C4	124
<i>GAI</i>	KBrB086M23-6_575	C5	57.8
<i>MAX2l</i>	JICB0172	C7	91.2
<i>TCP</i>	JICB0009	U	
<i>MAX1b</i>	JICB0064	U	
<i>MAX1h</i>	JICB0101	U	
<i>MAX2a</i>	JICB0128	U	
<i>MAX2b</i>	JICB0134	U	
<i>Bpa</i>	JICB0176	U	
<i>MAX3l</i>	JICB0289	U	
<i>MAX4p</i>	JICB0313	U	
<i>RGA2</i>	JICB0373	U	
<i>DELLAb</i>	JICB0435	U	
<i>DELLAc</i>	JICB0448	U	

* now not thought to contain candidate gene motif

Table 5. List of candidate genes and IGF markers genotyped in CRDH.

IGF	New markers	Originator	Putative map positions in TNDH	
	Candidate genes		LG	cM
	AtTB1_f	BGA	C3/A3/C8	13.6
	MAX_4n	BGA	C1	101.2
	MAX_4r	BGA	C1	89.9
	MAX2_b	BGA	um	-
	MAX2_l	BGA	A3	12.8
	MAX3_m	BGA	A4/C4	10
	MAX4_p	BGA	A1	19.5
	RGA12_30	JIC	A2/A6	0
	RGA2_H24_13_150	JIC	A3	111.7
	RGA2_H24_14_300	JIC	A3	111.7
	RGL12_31_300	JIC	A2/A6	8.5
	RGL3_a	BGA	um	-
IGF0191b		KWS	um	-
IGF0504b		BGA	C1	24.8
IGF0504f		BGA	A7	87.8
IGF0568d		BGA	C3	0
IGF1059e		KWS	C1	27.1
IGF1073a		KWS	A10	6
IGF1207c		BGA	A9	0
IGF1226a		BGA	A7	42.3
IGF1226f		BGA	A7	53.1
IGF2128c		KWS	um	-
IGF3100b		BGA	A3	108.5
IGF3112a		BGA	A9/C5	0
IGF3239d		KWS	A2/A6	32.1
IGF3315b		BGA	C1	38.1
IGF3338a		BGA	C1	15.3
IGF5101b		KWS	um	-
IGF5193a		BGA	9	14.2
IGF5222b		BGA	A9	0
IGF5272c		BGA	A3	0
IGF5415a		BGA	C7	22.8
IGF5702e		KWS	C7	0
IGF5706e		BGA	A9	37
IGF5707b		KWS	C7	7.6

Table 6. List of candidate genes and IGF markers genotyped in VGDH.

IGF	New markers	Originator	Map position in TNDH	
	Candidate genes		LG	cM
	DELLA_GRA	BGA	A7	97
	GAI23.6	JIC	A6	52*
	RGA12_3	JIC	np	
	RGA12_30	JIC	np	
	RGA12_31	JIC	np	
	RGA3_M18.33_250	JIC	np	
IGF1027z		KWS	A6	34.5
IGF1075d		KWS	A6	66.2
IGF1075e		BGA	A6	66
IGF1178b		KWS	A7	35.1*
IGF1226a		BG	A7	107.7
IGF1226f		BGA	A7	99.2
IGF5101b		KWS	A10	41*
IGF5272c		BGA	A3	4.7

* low stringency

3.3.4. TNDH (2005-2007)

Trait analysis - Spalding, 2005-2006

Data for whole plant, raceme, pod and seed traits analyses from the 150 lines grown in the small scale trial at Spalding in 2006 are summarised in Table 7 (columns 1-4). This trial received no fungicide treatment and significant, high levels of stem canker were identified and scored (Jon West (R. Res)). Traits which 'developed' after initial pod development were most severely affected, thus seed weight for the ten harvested pods in the TNDH population had a mean value of 6.3g compared to 20.4g for the control varieties. The increased variation in this trait due to stem canker was observed in increased coefficients of variation (CV%) which were often twice that of the controls. Flowering time was also recorded on a weekly basis.

These data were used to help select a subset of 94 lines best suited to UK conditions for subsequent trials. The selection was made primarily on the basis of removing those lines that flowered very early and were susceptible to stem canker. These lines were reanalysed to see how representative they were of the original population in terms of their genetic composition, trait and QTL expression for canopy architecture traits (Table 7, columns 5-8). It can be seen that, in general, there was good agreement of the mean and SD between the two analyses for all the measured traits. Analysis of variance of these data (Table 8) showed that differences among lines were highly significant ($P < 0.001$) for all traits and for both sets of lines. Heritabilities were higher than expected given the effects of stem canker and flowering time, ranging from branch angle (18.1%) to mean seed weight (69.8%). It is likely that this was because the effects of stem canker were very line-specific and resulted in an increase in the among-line variation for many traits while not affecting the within-plant error determination, thus the heritabilities reflect trait expression under the influence of canker rather than the *per se* trait heritabilities. Correlations and coefficients of determination among the traits are given in Table 9 and Supp. Table 4b respectively. Traits associated with length and height tended to be strongly positively associated together (e.g. $r = 0.498$ for pod length and plant height). Pod, pedicel and branch angles were all positively correlated (e.g. $r = 0.314$ for branch (top 4) and pod angle), while terminal length and pod number often showed negative associations (e.g. $r = -0.611$ with pod number on the terminal branch and fertile branch number).

Table 7. Summary of trait variation for TNDH at Elsoms 2005-2006. All lines assessed and subset selected for further trial.

	150 line set					94 (92 set)					Control ¹		
	mean	min	max	SD	CV %	mean	min	max	SD	CV %	mean	SD	CV %
Seed traits													
Seed weight in 10 pods	6.29	0.195	18.55	3.32	52.7	6.32	0.61	18.6	3.27	51.8	10.44	2.92	28.0
Weight of valve	3.81	0.17	19.75	1.71	44.7	3.89	1.12	19.8	1.79	46.1	4.82	1.44	29.9
Pod harvest index	0.61	0.12	0.74	0.08	13.3	0.60	0.12	0.73	0.08	13.1	0.69	0.03	4.8
Mean seed weight	3.48	0.29	15.05	1.39	39.8	3.54	0.29	15.0	1.45	41	4.20	0.75	18.0
Number of seeds per pod	17.95	0.95	40.2	5.83	32.5	17.8	2	31.9	5.67	31.9	24.8	4.23	17.1
Seed density	3.32	0.19	7.30	1.17	35.2	3.24	0.62	6.99	1.14	35.1	4.65	0.89	19.1
Plant traits													
Plant height	127.9	49	195	21.4	16.7	131.8	85	182	18.1	13.7	162.3	13.3	8.2
Terminal length	43.22	1	94	10.8	24.9	44.0	5	68	8.68	19.7	45.6	5.78	12.7
Foot length	38.85	1	108	19.1	49.2	39.6	1	108	18.6	46.9	80.3	14.5	18.0
Pod number on terminal	16.02	6	35	3.53	22	16.7	9	35	3.76	22.7	16.7	2.74	16.4
Stem width at base	1.05	0.5	2.22	0.24	23.2	1.07	0.5	2.22	0.26	24.5	0.99	0.27	27.1
Branching traits													
Number of fertile branches	7.6	2	15	2.36	30.8	7.8	2	15	2.44	31.3	4.6	1.58	34.3
Number of infertile branches	1.2	0	6	1.14	97.9	1.2	0	5	1.09	91.2	1	1.33	133.0
Rest of nodes	14.2	1	27	3.88	27.3	14.7	3	27	3.98	27	18.4	4.64	25.2
Total number of nodes	23.1	10	37	3.95	17.1	23.7	11	37	4.12	17.4	24.1	4.2	17.4
Branch angle	33.9	17.7	52.3	5.3	15.5	33.9	21.8	51.6	5.1	15.1	36.1	3.3	9.1
Branch angle (top 4)	32.8	18.3	52.3	6.7	20.7	32.6	18.3	51.5	7	21.3	34.5	3.6	10.4
Pod traits													
Beak length	0.96	0.25	3.80	0.33	35	0.93	0.25	1.78	0.27	28.6	1.35	0.13	10.0
Pedicel length	2.21	1.05	3.37	0.34	15.4	2.23	1.05	3.37	0.35	15.9	2.08	0.26	12.3
Pod length	5.56	3.34	7.52	0.75	13.4	5.62	3.34	7.52	0.76	13.5	5.60	0.47	8.4
Pod width	0.35	0.19	0.51	0.05	13.6	0.35	0.19	0.47	0.05	13.6	0.39	0.03	8.5
Pedicel to rachis angle	76.1	52.5	94.4	7.5	9.8	76.8	52.5	93.3	7.5	9.8	81.1	3.2	3.9
Pod to pedicel angle	158.3	135.6	177.9	6.4	4	158.5	135.6	174.1	6.6	4.2	158.4	3.5	2.2
Scored traits													
Canker	5.43	6	1.8	0.66	12.2	5.31	6	1.8	0.74	21.9	-	-	-
Start of flowering	4.82	8	2	1.17	24.3	4.51	6	2	0.99	21.9	-	-	-

¹ Control varieties: Escort, Tequila and Winner

Table 8. Mean squares and heritabilities, TNDH at Elsoms 2005-2006.

Source	150 set ¹			94 (2) set ²		
	MS			MS		
	Residual	Line	Heritability	Residual	Line	Heritability
Seed traits						
Seed weight	0.08382	0.23153	37	-	-	-
Pod weight	0.15	0.4086	36.5	0.000261	0.0005444	26.6
Pod HI	0.008402	0.015867	22.8	0.006738	0.014297	27.2
Mean seed weight	2.21	4.851	28.5	2.646	6.918	35
Seed number/pod	27.42	75.15	36.7	23.62	77.54	43.2
Plant traits						
Height	116.4	1205.4	75.7	112	781.7	66.6
Terminal length	67.59	251.9	47.6	54.77	119.8	28.4
Foot length	267.7	779.4	38.9	287.1	698.4	32.3
Pod no. on terminal	7.923	22.87	38.6	8.892	25.791	38.8
Stem width at base	0.04413	0.09025	25.8	0.04654	0.11402	32.6
Branching traits						
Fertile branch no.	4.465	10.258	30.2	4.79	10.844	29.6
Infertile branch no.	0.9273	2.062	29	0.8711	1.9482	29.2
Remaining nodes	7.918	31.109	49.4	8.131	34.09	51.6
Total nodes	9.11	29.715	43	9.147	32.935	46.4
Branch angle	17.24	49.36	38.3	16.19	47.39	39.1
Branch angle (top 4)	36.16	67.14	22.2	40.99	68.09	18.1
Pod traits						
Beak length	0.06622	0.25471	48.7	0.03589	0.15444	52.4
Pedicel length	0.05097	0.25953	57.7	0.05752	0.27958	56.3
Pod length	0.4349	1.0052	30.4	0.4557	1.1088	32.3
Pod width	0.001404	0.004774	44.4	0.00124	0.005078	50.8
Pedicel angle	28.3	121.45	52.3	25.49	119.7	55.2
Pod angle	28.07	74.61	35.6	25.45	84.5	43.6

¹ df = 159-162

² df = 87-89

Table 9. Correlation matrix for 92 set, Elsoms 2005-2006.

[illegible]

Trait analysis - Cowlinge and Barton, 2006-2007

Data from both sites for the 94 line subset of the TNDH population are summarised in Table 10, while the parents plus five control varieties are summarised in Table 11. Broadly speaking, means and variances for all traits were similar at both sites both showing large variation. The greatest range was observed in measures of biomass, in particular yield, which varied sixfold and threefold at Barton and Cowlinge respectively. Seed and plant traits directly related to yield varied more than twofold when averaged for both sites, while branching and pod traits only varied about 1.6 times. Though the trials were sprayed with fungicide to prevent stem canker, it was observed that Ningyou 7 was badly affected at both sites together with some of the TNDH lines. Sections of stems were scored for stem canker (0 = resistant, 7 = susceptible) at Cowlinge (Jon West, R. Res), where Tapidor, with a value of 1.17, was similar to those of the control varieties (0.63) in contrast to 5.5 for Ningyou 7. Tapidor out-yielded Ningyou 7 fourfold at Cowlinge and threefold at Barton, a result mirrored in the large range of yields obtained in the population 6.5- and 2.9-fold at Cowlinge and Barton respectively. It is thought that canker was the primary reason for the larger variation for seed and plant characters than for branching and pod characters, which were established before the onset of the effects of canker. The variation measured in both trials was similar. The CV% was very high for yield and measures of biomass (30% and 28.8% for Barton and Cowlinge respectively) and also high for branching traits (18.1% and 16.2%). Variation was less for seed and plant traits which averaged 13.6% and were even lower for pod traits which were the best estimated with a mean CV% of 7.9%. Thus, the effects of canker were mostly seen after the branching and pod structures are in place, when it inhibited seed filling and reduced yield by causing premature cessation of growth and stem damage. Transgressive segregation was observed for most traits and in most cases, including yield, the best TNDH lines exceeded values for the control varieties. Analysis of variance, however, showed a more complex pattern of behaviour.

Table 10. Summary of TNDH trait measurements for the main field trials grown at Barton and Cowlinge in 2006-2007.

	Barton					Cowlinge				
	mean	min	max	SD	CV %	mean	min	max	SD	CV %
Seed traits										
Seed weight	0.713	0.387	1.019	0.137	19.2	0.729	0.421	1.143	0.148	20.3
Pod weight	0.404	0.232	0.553	0.069	17.1	0.395	0.242	0.529	0.066	16.7
Pod HI	0.634	0.552	0.699	0.03	4.7	0.645	0.566	0.717	0.027	4.2
Mean seed weight	4.259	2.813	6.989	0.61	14.3	4.679	3.041	6.24	0.592	12.7
Seed number/pod	16.9	7.9	24.7	3.1	18.3	15.6	8.2	23.1	2.8	17.9
Seed density	3.115	2.112	4.592	0.481	15.4	2.987	1.995	4.168	0.432	14.5
Plant traits										
Height	141.3	106.4	165.8	10.4	7.4	141.6	115.3	169.7	11.4	8.1
Terminal length	47.2	35	59.5	5.1	10.8	47.8	36.2	62.2	5.1	10.7
Foot length	61.3	35.8	91.1	10.2	16.6	56.9	28.8	87	11.7	20.6
Pod no. on terminal	53	32.2	69.7	7.3	13.8	62.7	37.7	82.9	8.7	13.9
Pod density	1.134	0.708	1.538	0.137	12.1	1.323	0.815	1.815	0.178	13.5
Stem width at base	1	0.74	1.33	0.11	11	1.03	0.72	1.6	0.13	12.6
Branching traits										
Fertile branch no.	6.3	4	8.9	1	15.9	6.5	4.2	12.5	1.3	20
Infertile branch no.	0.5	0	1.3	0.3	60	1.2	0.2	2.5	0.5	41.7
Remaining nodes	21	15.3	25.3	2.3	11	22.7	15	31	3.1	13.7
Total nodes	27.8	22.2	32.1	2.3	8.3	30.5	21.9	40.3	3.5	11.5
Node density	0.19	0.25	0.15	1.94	1021.1	0.21	0.32	0.14	1.6	761.9
Branch density	0.08	0.06	0.13	0.01	12.5	0.09	0.07	0.15	0.01	11.1
Branch angle	38.2	28.4	45.7	3.7	9.7	41.7	33.8	49.8	3.4	8.2
Branch angle (top 4)	41.7	31	48.9	3.8	9.1	45.3	38.3	52.5	3.4	7.5
Pod traits										
Beak length	1.21	0.73	1.67	0.16	13.2	1.04	0.58	1.43	0.15	14.4
Pedicle length	2.26	1.81	2.88	0.19	8.4	2.27	1.87	2.95	0.19	8.4
Pod length	5.42	3.66	6.21	0.48	8.9	5.19	3.86	6.33	0.46	8.9
Silique length	6.64	4.39	7.53	0.59	8.9	6.23	4.68	7.74	0.54	8.7
Pod width	0.38	0.31	0.43	0.02	5.3	0.42	0.37	0.46	0.02	4.8
Pedicle angle	81.9	70.7	96.2	5	6.1	81.7	66.2	93.2	4.8	5.9
Pod angle	163.8	154.3	171.6	3.9	2.4	165.6	159.5	173.7	3.4	2.1
Angle to rachis	65.8	49.5	80.1	7.2	10.9	67.2	48.6	81.8	6.5	9.7
Biomass measures										
Yield (t ha ⁻¹)	1.86	0.55	3.55	0.62	33.3	6.53	3.43	9.93	1.51	23.1
Harvest Index	0.264	0.184	0.427	0.038	14.4	0.282	0.167	0.373	0.041	14.5
Biomass	184.1	95	540.9	68.2	37	205.1	78.9	558.9	81.8	39.9
Straw	144.9	74.2	393.2	51.2	35.3	159.1	62.4	412	60.2	37.8
Scored traits										
Canker	-	-	-	-		1.9	0.3	4.5	1	52.6
Autumn vigour	-	-	-	-		6.7	5	8	0.6	9
Spring vigour	-	-	-	-		6.9	5	8.5	0.8	11.6
Appearance before flowering	-	-	-	-		6.6	5.5	8	0.7	10.6
Appearance at harvest	-	-	-	-		4.9	1	8	1.7	34.7
Lodging at maturity	-	-	-	-		5.2	1	9	2	38.5
Start of flowering	-	-	-	-		32.4	23.5	40	4.6	14.2
End of flowering	-	-	-	-		73.4	66	82	4.3	5.9
Flowering period	-	-	-	-		41.1	34	55.5	3.5	8.5
Maturity	-	-	-	-		6.6	3.5	9	1.6	24.2
Height	-	-	-	-		150.7	130	172.5	9	6
Seed storage traits										
Oil % seed	46.4	43.1	51.3	1.6	3.4	-	-	-	-	
Glucosinolate	38.3	12.2	70.3	12.6	32.9	-	-	-	-	
Protein	23.1	21.1	25.1	0.9	3.9	-	-	-	-	

Table 11. Summary of mean and standard error or standard deviation of the Parents and Control varieties for the TNDH population grown in the main trial at Barton and Cowlinge, 2006-2007.

	Barton Ningyou 7		Tapidor		Controls		Cowlinge Ningyou 7		Tapidor		Controls	
	mean	sem	mean	sem	mean	SD	mean	sem	mean	sem	mean	SD
Seed traits												
Seed weight	0.715	0.062	0.787	0.063	0.864	0.221	0.630	0.138	0.581	0.021	0.828	0.238
Pod weight	0.392	0.042	0.482	0.026	0.454	0.078	0.422	0.072	0.319	0.020	0.444	0.083
Pod HI	0.647	0.017	0.617	0.017	0.651	0.033	0.590	0.023	0.647	0.013	0.645	0.035
Mean seed weight	4.725	0.238	5.3	0.018	4.27	0.785	5.175	0.321	3.942	0.199	4.727	1.346
Seed number / pod	15.37	1.608	14.86	1.185	20.67	4.35	12.66	3.063	14.8	0.36	18.85	6.14
Seed density	2.909	0.226	2.963	0.291	3.699	0.703	2.856	0.636	2.864	0.115	3.368	0.906
Plant traits												
Height	130	3.91	127.2	4.99	154.1	16.09	129.8	6.92	133	2.32	150.4	16.96
Terminal length	45.17	3.44	43	4.17	52.34	6.59	47.17	2.34	49.67	2.53	52.46	6.83
Foot length	53.33	4.99	36.5	4.25	68.38	15.33	36.5	8.43	50.67	4.62	60.7	16.82
Pod no. on terminal	47.17	5.94	34	5.73	54.29	10.9	59.83	4.09	54.67	4.98	54.93	10.23
Pod density	1.075	0.164	0.813	0.130	1.060	0.276	1.287	0.114	1.128	0.139	1.070	0.261
Stem width at base	0.86	0.059	1.34	0.178	0.975	0.246	1.138	0.067	0.96	0.135	1.005	0.239
Branching traits												
Fertile branch no.	6.167	0.792	8.8	1.158	5.516	1.86	7.667	0.843	5.167	0.654	5.548	1.877
Infertile branch no.	0.667	0.333	0.2	0.2	0.645	0.839	1.833	0.401	1.5	0.563	0.677	0.832
Remaining nodes	19.33	0.95	22	1.95	21.1	3.87	21	2.02	20	1.77	21.74	3.53
Total nodes	26.17	1.8	29.8	1.5	27.27	4.93	30.5	2.17	26.67	2.19	27.97	4.61
Node density	5.056	0.283	4.31	0.275	5.823	1.228	4.335	0.29	5.129	0.368	5.516	1.117
Branch density	0.089	0.006	0.097	0.006	0.072	0.018	0.101	0.004	0.081	0.006	0.070	0.016
Branch angle	38.23	1.83	35.97	1.61	36.46	4.1	40.13	1.15	38.74	2.11	37.18	5.04
Branch angle (top 4)	42.45	2.05	41.2	2.83	38.58	5.01	43.6	1.76	41.43	2.82	39.55	6.07
Pod traits												
Beak length	0.951	0.058	1.075	0.048	1.262	0.205	0.886	0.153	0.950	0.042	1.224	0.241
Pedicle length	1.943	0.072	2.1	0.119	2.275	0.339	2.228	0.086	1.877	0.029	2.307	0.293
Pod length	5.051	0.307	5.072	0.286	5.612	0.61	4.243	0.265	5.195	0.163	5.509	0.731
Silique length	6.002	0.351	6.147	0.331	6.85	0.754	5.129	0.397	6.145	0.182	6.706	0.925
Pod width	0.381	0.011	0.3876	0.014	0.417	0.034	0.452	0.022	0.372	0.005	0.419	0.033
Pedicle angle	75.38	2.85	80.52	3.16	83.55	6.02	82.46	3.31	76.31	1.97	84	6.25
Pod angle	162.18	1.04	159.4	2.62	165.1	4.91	161.1	2.01	165.4	1.23	165.6	4.84
Angle to rachis ²	57.56	3.11	59.88	3.62	68.64	7.12	63.51	4.71	61.75	2.16	69.64	7.41
Biomass measures												
Yield (t ha ⁻¹)	0.8	0.23	2.2	0.23	3.02	0.318	0.95	0.23	3.80	0.23	3.89	0.318
Harvest Index	0.24	0.118	0.27	0.118	0.25	0.166	0.27	0.118	0.29	0.118	0.29	0.166
Scored traits												
Canker	5.5	0.224	1.17	0.224	0.627	0.4	5.5	0.224	1.17	0.224	0.627	0.4

¹ Controls = Castille, Expert, Fortis, Fortress, Winner

² calculated from combined pod and pedicle angle

All data from the three plants harvested from each plot at two sites were initially analysed together using lines, sites and blocks as main effects (Supp. Table 5). This analysis showed that though there was highly significant (statistically) within line variation ($P < 0.001$) for all the measured traits this was also evident at all levels of the ANOVA thus three way interactions (line $\times$ site $\times$ block) and two way interactions (line $\times$ site, line $\times$ block and site $\times$ block) were also highly significant. Because of the high degrees of freedom available for the analysis these high levels of statistical significance were apparent even where the variance ratios were small so that, for example, a mean square of 1.32 for the number of infertile branches was significant at $P < 0.05$. A more realistic, biological assessment was attained by partitioning the variance by estimating expected mean squares (Table 12). From this it was seen that high statistical significance did not necessarily contribute greatly to the total variation. Thus the three way interactions accounted for from 4.5% (terminal branch length) to 21.1% (pod number on the terminal branch) of the overall variation, while the two-way interaction terms were, in general, found to contribute even less to the overall variation *e.g.* line $\times$ site varied from 11.7% for node number to 0.8% for mean seed weight. Residual error was high in both trials and accounted for a large proportion of the variation ranging from 71.9% for stem basal width to 23.9% for pod width. In general, those traits assessing pod characteristics were the best determined while those associated with the whole plant, including branching and plant size were least well determined. This was largely the result of the large variation between the three harvested plants resulting from variation in establishment and the presence of focal points of stem canker incidence within the population. These factors tended to affect plant traits such as numbers of branches, size of plant (height and stem thickness) but affected pod characters less because within plant competition was more uniform and less affected by these factors. Additionally these were better replicated with ten pods measured per plant. The data were also reanalysed separately for each site and the expected mean squares and heritabilities summarised in Supp. Table 6.

Table 12. Mean squares and expected mean squares from the analysis of the TNDH population grown at Barton and Cowlinge in 2006-2007.

Source of variation		Mean squares and Expected Mean Squares							EMS
		line ²	site ³	block ⁴	line.site ⁵	line.block ⁶	site.block ⁷	line.site.block ⁸	
Seed traits									
seed wt	MS	0.17454	0.0523 ^{ns}	0.09741 ^{ns}	0.0721	0.06408	0.16031 [*]	0.05954	0.0310
	EMS	24.6	0.2	0.3	3.6	1.3	0.6	16.3	53.2
pod harvest index	MS	0.00725	0.02977	0.00259 ^{ns}	0.00319	0.00269	0.00013 ^{ns}	0.00239	0.0013
	EMS	23.8	2.1	0.2	5.4	2	-0.3	14.8	52
seeds per pod	MS	77.5	512.65	42.59 ^{ns}	29.57	21.58	1.04 ^{ns}	21.39 ^{ns}	11.81
	EMS	26.8	3.8	0.3	5.8	0.1	-0.3	13.5	49.9
mean seed weight ^x	MS	0.00339	0.04844	0.00005 ^{ns}	0.00091	0.00102	0.00441	0.00087 [*]	4.29x10 ⁻⁷
	EMS	28.3	8.7	0	0.8	2.6	1.3	14.8	43.5
density of seeds in pod	MS	2.0025	4.4036	1.0906 [*]	0.6022	0.5624	0.0472 ^{ns}	0.5353	0.2723
	EMS	30.1	1.4	0.4	2	0.8	-0.3	16	49.6
Plant traits									
plant height	MS	1255.64	1.13 ^{ns}	5478.26	330.62	317.42	1980.52	239.99	80.2
	EMS	36.6	0	3.5	5.4	4.6	2.2	19.1	28.7
length of terminal branch	MS	242.15	81.25 ^{ns}	534.11	73.43	50.75 [*]	40.97 ^{ns}	45.57 ^{ns}	36.73
	EMS	29.9	0.2	1.4	7	1.3	0	4.5	55.7
length of foot	MS	1232.6	5423.4	335.3 [*]	303.4	342.1	1173.5 ^{**}	285.7	138
	EMS	32.3	3.1	0.2	0.9	3	1	15.6	43.9
pod number on terminal raceme	MS	603.32	26714.9	3762.97	202.8	183.35	19.93 ^{ns}	219.84	79.72
	EMS	23	21.4	3	-1.3	-2.7	-0.3	21.1	35.9
stem base width [*]	MS	0.11177	0.1436 ^{ns}	0.87389	0.0603 ^{ns}	0.07913	0.08246 ^{ns}	0.05698 ^{ns}	0.0471
	EMS	13.7	0.4	2.4	0.8	5.6	0.1	5	71.9
Branching traits									
number of fertile branches	MS	10.728	18.47 ^{**}	16.993 [*]	5.02	3.894 ^{**}	0.28 ^{ns}	3.021 ^{ns}	2.706
	EMS	20.4	0.8	0.7	7.9	3.5	-0.2	2.5	64.5
number of infertile branches	MS	1.487	144.39	5.9076 ^{**}	1.2559	1.5955	12.212	0.9327 [*]	0.705
	EMS	8.1	18.8	0.7	4	8.1	2.9	5.6	51.8
rest nodes	MS	55.94	778.51	154.62	36.86	27.13	54.1 [*]	19.41	11.09
	EMS	5.7	1.1	12	5.3	0.5	11.5	45.9	17.9
total number of nodes	MS	63.9	1914.3	389.75	50.28	40.23	100.16 [*]	25.51 ^{**}	16.5
	EMS	13.6	9.6	1.9	11.7	7	0.8	8.5	46.9
branch angle - top 4 only	MS	123.85	4129.95	2.6 ^{ns}	38.75	38.89	855.04	35.45	19.66
	EMS	22	15.7	0	1.2	1.2	6.3	11.3	42.3

Source of variation		Mean squares and Expected Mean Squares							EMS
		line ²	site ³	block ⁴	line.site ⁵	line.block ⁶	site.block ⁷	line.site.block ⁸	
Pod traits									
beak length	MS	0.25058	8.4218***	0.01318 ^{ns}	0.05086	0.05185	0.00001 ^{ns}	0.04031	0.0208
	EMS	31	22.5	0	2.7	2.9	-0.2	9.8	31.3
pedicel length	MS	0.39074	0.0137 ^{ns}	0.66928	0.09324	0.10659	0.07339 ^{ns}	0.08235	0.0327
	EMS	36.3	0	1.3	2.1	4.6	0	18.8	37
pod length	MS	2.0302	18.3743	1.524**	0.6896	0.5232	0.1755 ^{ns}	0.3912**	0.23
	EMS	29.5	5.9	0.5	9	4	-0.1	9.7	41.6
pod width	MS	0.00437	0.45172	0.00379**	0.00147	0.00141	0.00093 ^{ns}	0.00104	0.0005
	EMS	18.1	41	0.3	3.6	3.1	0	9.8	23.9
pedicel angle to raceme	MS	254.15	100*	53.43 ^{ns}	50.95	50.68	71.49 ^{ns}	41.96	24.21
	EMS	38.5	0.3	0.2	2.8	2.7	0.2	10.9	44.5
pod angle to pedicel	MS	135.77	695.62	23.23 ^{ns}	34.18	30.08	1.14 ^{ns}	20.98	11.95
	FMS	35.6	4	0.1	7.1	4.9	-0.2	9.7	38.7

number of replications = 3

⁴ block df = 2

⁸ line.site.block df = 69 (57-78)

¹ residual df = 637 (577-678)

⁵ line.site df = 92 (91-93)

^{*} badly affected by stem canker

² line df = 93

⁶ line.block df = 92 (88-93)

^x ÷ /1000

³ site df = 2

⁷ site.block df = 1

all significant to $P < 0.001$ except where indicated

Correlations among the traits were more apparent at Cowlinge than Barton. At Cowlinge (Table 13) yield was, as expected, strongly positively correlated with weight of siliques (*i.e.* seed and valve weight), pod number on the terminal raceme and number of seed per pod (and density within the pod though it is not known whether this resulted from closer packing and/or failure to set seed) (r values between 0.41 and 0.33; $P < 0.001$). There was no relationship, however, with seed size (mean seed weight). Yield was also correlated with branching traits such that fewer fertile branches (and infertile branches) ($r = -0.39$; $P < 0.001$) spaced at increased density in the reproductive canopy ($r = 0.43$; $P < 0.001$) were associated with increased yield. Higher yield was also related to longer, more horizontal pods. Yield was, however, very strongly correlated with incidence of stem canker ($r = -0.73$; $P < 0.001$) and maturity ($r = -0.67$; $P < 0.001$) (plants dry and 'mature' earlier where canker is present). Oil was only slightly positively related to yield. Harvest Index showed only a slight negative correlation with mean seed weight and pod valve weight. Though these correlations were statistically significant, the importance of the relationship was assessed through determining the coefficients of determination (r^2) (supp. Table 7). These showed that, apart from autocorrelations, the greatest proportion of the variation in yield could be accounted for by maturity (44.8%) and canker (53.0%) and, apart from these, the maximum variation accounted for was less than 30%. Because of the strong stem canker effect on many traits the data were re-analysed using stem canker scores as a covariate. Only plant height and pedicel length showed a high probability for the covariate effect ($P < 0.001$) though eight other traits were significant at $P < 0.05$ and a further eight at $P < 0.1$. The effect of stem canker on means and on the significance among lines was small though there were noticeable effects on the correlations among some traits (Supp. Table 8). Most correlations increased after adjustment indicating that one effect of canker was to increase variation and obscure relationships among the traits. However, several traits, notably HI, pod width, fertile branch number, seed number and density, decreased.. Further analysis of correlations on data adjusted by using stem canker as cofactor showed increased correlations with yield for most traits, but were particularly strong for plant height (increase in $r = +0.252$) and associated 'length' traits (*e.g.* terminal and foot length) including pedicel length (increase in $r = +0.179$). Correlation coefficients also increased for all measures of angles (increase in r from $= +0.051$ to $+0.179$) with respect to yield. It was noted that most pod trait correlations with seed weight, except pedicel length, were stronger than those with yield indicating their closer and simpler

Table 13. Correlation matrix, Cowlinge 2006-2007 (split in three parts to display on page). Part 1.

[illegible]

df = 92

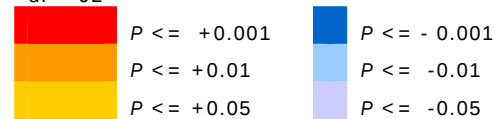


Table 13. Correlation matrix, Cowlinge 2006-2007 (split in three parts to display on page). Part 2.

Branch angle	0.295	0.295	0.071	0.173	0.256	0.136	0.096	-0.016	0.375	0.193	0.205	-0.234	-0.388	-0.151	0.04	-0.126	0.125
Branch angle (top 4)	0.263	0.274	0.066	0.218	0.168	0.06	0.133	-0.109	0.295	0.149	0.237	-0.072	-0.121	0.075	0.098	0.056	-0.012
Beak length	0.412	0.39	0.119	0.125	0.399	0.245	0.37	0.375	0.336	0.013	-0.296	-0.03	-0.234	-0.102	0.12	0.002	0.222
Pedicle length	0.292	0.135	0.278	0.188	0.157	-0.02	0.343	0.2	0.331	0.071	-0.084	0.168	-0.124	0.132	0.281	0.222	0.013
Pod length	0.563	0.531	0.198	-0.012	0.635	0.206	0.392	0.198	0.527	0.163	0.02	-0.156	-0.277	-0.071	0.137	0.002	0.217
Siliques length	0.593	0.56	0.201	0.025	0.651	0.243	0.438	0.275	0.542	0.143	-0.066	-0.14	-0.301	-0.09	0.15	0.002	0.248
Pod width	0.549	0.603	0.108	0.538	0.309	0.272	0.126	0.049	0.174	0.068	0.053	-0.109	-0.028	-0.111	-0.032	-0.054	0.103
Pedicle angle	0.391	0.351	0.192	0.199	0.293	0.142	0.215	0.136	0.313	0.332	0.261	-0.109	-0.304	-0.067	-0.092	-0.196	0.278
Pod angle	0.384	0.417	0.058	0.129	0.342	0.129	0.058	0.016	0.282	0.157	0.139	-0.306	-0.324	-0.299	0.015	-0.159	0.171
Angle to rachis	0.49	0.478	0.172	0.214	0.396	0.173	0.189	0.108	0.379	0.327	0.266	-0.241	-0.395	-0.207	-0.059	-0.228	0.294
Yield	0.363	0.348	0.089	0.011	0.414	0.354	0.192	0.275	0.337	0.361	0.143	-0.274	-0.387	-0.285	0.061	-0.139	0.186
Harvest Index	-0.096	-0.251	0.291	-0.293	0.079	0.221	-0.154	0.073	-0.051	0.004	-0.024	-0.128	0.014	-0.121	-0.076	-0.097	-0.035
Canker	-0.15	-0.163	-0.059	0.012	-0.209	-0.171	-0.029	-0.237	-0.087	-0.221	-0.031	0.307	0.268	0.326	-0.111	0.055	-0.003
Start of flowering	0.235	0.239	-0.03	-0.096	0.366	0.245	0.261	0.264	0.404	0.28	0.052	-0.289	-0.417	-0.225	0.19	-0.019	0.159
Maturity	-0.385	-0.382	-0.058	-0.081	-0.405	-0.269	-0.259	-0.412	-0.308	-0.242	0.089	0.275	0.335	0.361	-0.184	0.017	-0.148
Oil	0.019	-0.001	0.078	-0.275	0.235	0.233	-0.058	0.004	0.038	0.114	0.103	-0.301	-0.032	-0.066	-0.133	-0.145	0.091
Glucosinolate	-0.243	-0.236	-0.044	-0.103	-0.232	-0.272	-0.139	-0.23	-0.139	-0.161	0.038	0.174	0.178	0.268	-0.141	-0.009	-0.057
Protein	-0.256	-0.214	-0.11	0.081	-0.374	-0.353	-0.149	-0.335	-0.192	-0.242	0.054	0.17	0.299	0.302	-0.087	0.077	-0.132
	Seed wt.	Pod wt.	Pod HI	Mean seed wt.	Seed number/pod	Seed Density	Plant height	Terminal length	Foot length	Pod no. on terminal	Pod density	Stem width at base	Fertile branches	Infertile branches	Rest nodes	Total nodes	Node density

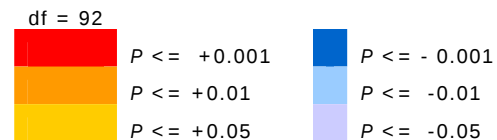
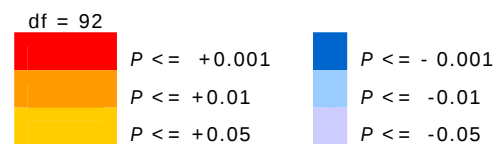


Table 13. Correlation matrix, Cowlinge 2006-2007 (split in three parts to display on page). Part 3.

Branch angle	0.211																		
Branch angle (top 4)	-0.104	0.836																	
Beak length	0.36	0.079	-0.061																
Pedicle length	0.051	-0.038	0.039	0.115															
Pod length	0.22	0.328	0.27	0.422	0.35														
Silique length	0.288	0.301	0.213	0.637	0.329	0.968													
Pod width	0.06	0.16	0.174	0.138	0.12	0.176	0.188												
Pedicle angle	0.216	0.438	0.453	0.094	0.162	0.383	0.353	0.265											
Pod angle	0.289	0.446	0.261	0.346	0.024	0.496	0.517	0.217	0.234										
Angle to rachis	0.311	0.556	0.47	0.252	0.132	0.543	0.532	0.309	0.858	0.7									
Yield	0.429	0.36	0.156	0.227	-0.231	0.285	0.306	0.11	0.181	0.482	0.387								
Harvest Index	0.001	0.011	0.017	-0.172	-0.118	-0.083	-0.112	-0.009	0.169	-0.107	0.068	0.027							
Canker	-0.384	-0.225	-0.055	-0.156	0.276	-0.137	-0.161	-0.025	-0.08	-0.368	-0.253	-0.728	0.051						
Start of flowering	0.405	0.318	0.106	0.215	-0.069	0.38	0.382	-0.034	0.057	0.378	0.241	0.569	-0.273	-0.458					
Maturity	-0.521	-0.375	-0.096	-0.407	0.028	-0.4	-0.454	-0.125	-0.096	-0.555	-0.363	-0.669	0.162	0.527	-0.668				
Oil	0.009	0.322	0.267	0.05	-0.267	0.159	0.149	0.009	0.094	0.246	0.198	0.308	0.241	-0.265	0.154	-0.261			
Glucosinolate	-0.344	-0.256	-0.041	-0.192	0.232	-0.035	-0.084	-0.064	0.026	-0.241	-0.108	-0.529	-0.074	0.477	-0.359	0.495	-0.4		
Protein	-0.443	-0.354	-0.058	-0.335	0.207	-0.202	-0.264	-0.042	0.023	-0.403	-0.196	-0.657	0.014	0.527	-0.572	0.642	-0.48	0.648	
	Branch density	Branch angle	Branch angle (top 4)	Beak length	Pedicle length	Pod length	Silique length	Pod width	Pedicle angle	Pod angle	Angle to rachis	Yield	Harvest Index	Canker	Start of flowering	Maturity	Oil	Glucosinolate	



linkage and that the data were more accurately determined than yield. Pod and branch angles were positively correlated but both were negatively correlated to branch numbers, thus plants with more branches had more erect branches and pods.

Similar trends were observed for the trial at Barton (Table 14) though several associations observed at Cowlinge, such as pedicel and pod angles to seed weight per pod, were not significant. In general, coefficients of determination were less than 30%. Maturity and canker were not assessed at Barton so it was not possible to see if these traits were as significantly correlated with yield as at Cowlinge. The low r^2 values may have resulted from the great environmental variation observed, particularly in relation to the incidence of stem canker, but may also reflect the complex interactions of the traits where simple cause/effect is not easily apparent. They also suggest that there exists variation within the TNDH population which may be exploited by the breeder. Combined correlations for both sites confirmed the similarity of the relationships among traits at both sites (supp. Table 9)

QTL analysis - Spalding, 2005-2006

Putative single marker QTL, identified by regression analysis of all 150 lines, with significance levels greater than $P < 0.05$ are summarised in Table 15. Linkage groups from the A genome (A1-A9) showed many more QTL than did those from the C genome (C1-C9). While most linkage groups showed at least one QTL several linkage groups, including A2, A3, A9 and C5, had QTL for more than one trait while there were none on C7. Many of these QTL were coincident possibly because the traits were related physiologically (e.g. seed number per pod and weight of seed per 10 pods) or were arithmetically associated and thus auto-correlated (e.g. height and terminal length). QTL identified for flowering time and stem canker were coincident with many of the canopy trait QTL indicating the likelihood of plant development and disease as important factors in their expression. Though QTL for these two traits were present and overlapping on A2 their peak positions differed. There were major QTL for flowering time on A2, A3, A5 and C5 which were coincident with traits such as numbers of nodes and fertile branches. The most significant flowering time QTL occurred at 36cM (span 0-65) on A3 where QTL were present for nearly all the other measured traits though no stem canker QTL. They were, however, not all coincident. For instance, while height also peaked at 35cM, QTL for branch angles peaked at 73 cM.

Table 14. Correlation matrix, Barton 2006-2007 (split in three parts to display on page). Part 1.

Pod wt.	0.825																	
Pod HI	0.433	-0.131																
Mean seed wt.	0.368	0.262	0.187															
Seed number/pod	0.754	0.628	0.341	-0.31														
Seed Density	0.593	0.374	0.457	-0.351	0.863													
Plant height	0.257	0.238	0.041	0.009	0.263	0.176												
Terminal length	0.131	0.127	0.047	0.026	0.13	0.091	0.49											
Foot length	0.168	0.133	0.05	-0.14	0.276	0.204	0.698	-0.016										
Pod no. on terminal	0.246	0.248	0.072	-0.054	0.3	0.216	0.4	0.562	0.124									
Pod density	0.18	0.18	0.052	-0.081	0.239	0.173	-0.019	-0.268	0.123	0.633								
Stem width at base	0.103	-0.015	0.208	0.134	0.004	0.009	0.286	0.134	0.072	0.068	-0.046							
Fertile branches	0.113	0.007	0.176	0.156	0.007	0.043	-0.015	-0.114	-0.337	0.05	0.164	0.364						
Infertile branches	0.05	0.003	0.056	0.12	-0.009	-0.033	-0.092	-0.177	-0.031	0.043	0.226	-0.037	-0.077					
Rest nodes	-0.058	-0.004	-0.048	-0.311	0.175	0.127	0.277	0.277	0.254	0.32	0.122	0.108	-0.193	-0.068				
Total nodes	-0.022	-0.025	0.043	-0.241	0.165	0.138	0.251	0.192	0.091	0.324	0.209	0.257	0.23	0.041	0.891			
Node density	0.175	0.172	-0.032	0.203	0.025	-0.01	0.521	0.186	0.424	-0.018	-0.22	-0.001	-0.185	-0.131	-0.579	-0.682		
Branch density	-0.032	0.096	-0.202	-0.035	-0.012	-0.065	0.272	0.643	0.086	0.221	-0.331	-0.168	-0.684	-0.261	0.194	-0.168	0.337	
	Seed wt.	Pod wt.	Pod HI	Mean seed wt.	Seed number/pod	Seed Density	Plant height	Terminal length	Foot length	Pod no. on terminal	Pod density	Stem width at base	Fertile branches	Infertile branches	Rest nodes	Total nodes	Node density	

Table 14. Correlation matrix, Barton 2006-2007 (split in three parts to display on page). Part 2.

Branch angle	0.177	0.226	-0.06	-0.046	0.211	0.057	0.136	0.14	0.299	0.189	0.071	-0.159	-0.31	-0.159	-0.004	-0.162	0.239
Branch angle (top 4)	0.187	0.158	0.05	0.089	0.141	0.023	0.095	0.012	0.195	0.157	0.153	0.014	0.043	-0.039	-0.164	-0.157	0.207
Beak length	0.288	0.397	-0.115	-0.126	0.417	0.18	0.197	0.158	0.173	0.17	0.056	0.019	-0.104	0.016	0.1	0.031	0.122
Pedicle length	0.109	-0.005	0.158	0.343	-0.109	-0.222	0.095	0.149	-0.005	0.07	-0.032	0.187	0.073	-0.038	-0.02	0.012	0.074
Pod length	0.499	0.588	-0.038	-0.06	0.552	0.135	0.222	0.067	0.158	0.274	0.276	0.026	0.07	0.074	0.032	0.065	0.107
Silique length	0.488	0.591	-0.063	-0.081	0.565	0.16	0.235	0.096	0.178	0.269	0.241	0.025	0.026	0.064	0.051	0.058	0.124
Pod width	0.457	0.493	0.02	0.322	0.224	0.264	-0.006	-0.092	-0.011	-0.021	0.079	-0.036	-0.088	0.13	-0.146	-0.179	0.101
Pedicle angle	0.195	0.245	-0.058	-0.009	0.187	0.031	0.14	0.046	0.212	0.248	0.223	-0.134	-0.173	-0.262	-0.118	-0.225	0.304
Pod angle	0.04	0.169	-0.182	-0.312	0.257	0.125	-0.084	-0.08	0.085	0.127	0.217	-0.151	-0.101	-0.156	0.053	-0.026	-0.031
Angle to rachis	0.156	0.261	-0.14	-0.177	0.27	0.089	0.051	-0.012	0.193	0.241	0.273	-0.176	-0.175	-0.267	-0.053	-0.17	0.194
Yield	0.296	0.335	0.024	-0.273	0.51	0.434	0.328	0.373	0.315	0.388	0.09	-0.096	-0.205	-0.243	0.35	0.198	0.057
Harvest Index	0.315	0.099	0.415	0.217	0.181	0.228	-0.052	-0.114	-0.049	0.104	0.225	0.187	0.156	0.118	-0.013	0.065	-0.13
Canker	-0.094	-0.128	0.012	0.213	-0.266	-0.188	-0.293	-0.386	-0.222	-0.275	0.043	-0.002	0.104	0.103	-0.234	-0.156	-0.069
Oil	0.242	0.157	0.206	-0.304	0.436	0.413	-0.107	-0.168	0.048	0.032	0.225	-0.166	0.031	-0.036	-0.043	-0.016	-0.07
Glucosinolate	-0.03	-0.035	0.023	0.17	-0.179	-0.191	-0.23	-0.257	-0.205	-0.119	0.098	0.107	0.207	-0.038	-0.17	-0.061	-0.107
Protein	-0.165	-0.169	-0.06	0.288	-0.384	-0.351	-0.139	-0.268	-0.125	-0.207	-0.005	0.064	0.199	0.075	-0.288	-0.19	0.096
	Seed wt.	Pod wt.	Pod HI	Mean seed wt.	Seed number/pod	Seed Density	Plant height	Terminal length	Foot length	Pod no. on terminal	Pod density	Stem width at base	Fertile branches	Infertile branches	Rest nodes	Total nodes	Node density

df = 92

	$P \leq +0.001$		$P \leq -0.001$
	$P \leq +0.01$		$P \leq -0.01$
	$P \leq +0.05$		$P \leq -0.05$

Table 14. Correlation matrix, Barton 2006-2007 (split in three parts to display on page). Part 3.

	Branch angle	Branch density	Branch angle (top 4)	Branch angle (top 4)	Beak length	Pedicle length	Pod length	Silique length	Pod width	Pedicle angle	Pod angle	Angle to rachis	Yield	Harvest Index	Canker	Oil	Glucosinolate	Protein
Branch angle	0.195																	
Branch density	-0.113	0.86																
Branch angle (top 4)	0.177	0.102	0.1															
Beak length	0.029	-0.055	0.011	0.196														
Pedicle length	-0.026	0.271	0.237	0.569	0.188													
Pod length	0.029	0.249	0.219	0.739	0.211	0.974												
Silique length	0.057	-0.211	-0.167	0.133	0.031	-0.051	-0.004											
Pod width	0.169	0.552	0.487	0.16	-0.038	0.342	0.324	-0.015										
Pedicle angle	0.045	0.277	0.204	0.39	-0.104	0.33	0.375	-0.033	0.293									
Pod angle	0.141	0.534	0.449	0.323	-0.083	0.417	0.429	-0.028	0.854	0.749								
Angle to rachis	0.319	0.318	0.131	0.353	-0.203	0.234	0.286	-0.032	0.273	0.242	0.321							
Yield	-0.216	-0.027	0.018	-0.024	0.027	0.065	0.043	0.021	0.138	-0.074	0.058	0.079						
Harvest Index	-0.23	-0.26	-0.145	-0.174	0.257	-0.177	-0.189	0.165	-0.227	-0.273	-0.307	-0.636	-0.019					
Canker	-0.158	0.209	0.181	-0.05	-0.267	0.241	0.185	-0.014	0.167	0.352	0.308	0.147	0.121	-0.138				
Oil	-0.286	-0.117	0.03	-0.165	0.29	0.006	-0.037	0.008	-0.049	-0.135	-0.108	-0.357	0.069	0.415	-0.1			
Glucosinolate	-0.245	-0.262	-0.094	-0.116	0.307	-0.138	-0.14	0.077	-0.02	-0.29	-0.171	-0.498	-0.102	0.462	-0.445	0.402		

df = 92

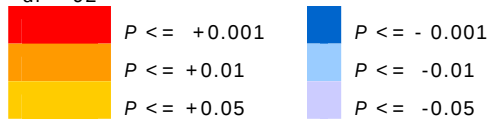
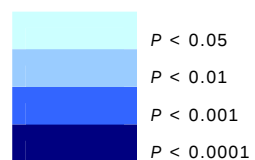


Table 15. Single marker analysis TNDH 150 lines. Spalding 2005-2006. Span of QTL is given as between marker positions above $P<0.05$ with the probability level indicated by coloured box.

Elsoms	150 set	seed wt.	valve wt.	pod harvest index	mean seed wt	seed no per pod	height	terminal length	foot length	pod no per raceme	stem width	fertile branch	infertile branch	remainder of nodes	total nodes	branch angle	top 4 branch	Beak length	pedicel length	pod length	pod width	pedicel angle	pod angle	canker	flowering time
A1	Span Peak pos.			31- 89 50.3			55- 85 77.9						26- 34 31.1							50- 85 67.6					
A2	Span Peak pos.				0-18 11.9				0-31 11.9	46- 91 75.8			31- 66 61.0	9-50 21.9	12- 31 21.9								31- 61 49.6	31- 76 65.9	59- 94 75.8
A3	Span Peak pos.	32- 37 35.6	16- 112 20.5	56- 86 72.2		30- 75 56.6	0-47 35.2	30- 47 41.4	34- 41 38.8	72- 96 75.0			57- 86 75.6	30- 63 36.9	30- 96 63.5	106- 122 106.2	106- 122 116.0	32- 98 122.0	7-44 15.5	0-75 38.8			81- 105 81.4	0-47 33.7	0-65 35.6
A4	Span Peak pos.		79- 81 80.2	114. 5		0-28 15.0				18- 28 18.9									0- 3.5 3.5				40- 66 50.0		
A5	Span Peak pos.		54- 59 59.1				69- 131 114.3	69- 95 83.0								56- 94 73.3	56- 95 73.3	21- 52 37.0							69- 95 92.4
A6	Span Peak pos.	0-12 4.5		2-77 77.1									32- 76 62.0					126- 127 126.9	58- 91 90.7		26- 72 35.8				
A7	Span Peak pos.			50- 98 61.5		0-13 0.0		0-31 7.1		82- 98 83.4		60- 82 70.1							39- 98 84.5					85- 98 98.1	

Elsoms	150 set	seed wt.	valve wt.	pod harvest index	mean seed wt	seed no per pod	height	terminal length	foot length	pod no per raceme	stem width	fertile branch	infertile branch	remainder of nodes	total nodes	branch angle	top 4 branch	Beak length	pedicel length	pod length	pod width	pedicel angle	pod angle	canker	flowering time
A8	Span Peak pos.												50- 86 81.5												
A9	Span Peak pos.	65- 76 76.1		61- 88 66.0	61- 76 76.1					38- 123 65.4				67- 102 76.1	65- 102 76.1	65- 76 74.3		35- 48 48.0	0-41 27.6	0-50 18.4				28- 83 70.9	
A10	Span Peak pos.					43- 45 44.1	25- 45 71.4	38- 59 44.1		54- 74 59.3											35- 45 38.4			35- 75 53.7	
C1	Span Peak pos.					22- 42 22.0										12- 31 23.3	0-29 12.9		23- 36 31.0						
C2	Span Peak pos.	17- 63 23.8													90- 97 97.1				90- 97 89.8				0-16 0.0		
C3	Span Peak pos.				7-22 10.3							7-25 12.6									73- 78 73.4		47- 75 62.6	97- 125 102.7	
C4	Span Peak pos.			125- 138 131.9																			100- 125 99.6	23- 56 33.8	
C5	Span Peak pos.		77- 88 76.6				13- 88 82.6		4-31 20.7						21- 34 33.5						4-21 4.4		0-57 20.7		13- 87 82.6

Elsoms	150 set	seed wt.	valve wt.	pod harvest index	mean seed wt	seed no per pod	height	terminal length	foot length	pod no per raceme	stem width	fertile branch	infertile branch	remainder of nodes	total nodes	branch angle	top 4 branch	Beak length	pedicel length	pod length	pod width	pedicel angle	pod angle	canker	flowering time
C6	Span Peak pos.			38- 54 42.3			0-74 43.4							11- 54 45.6	11- 68 53.6				0-26 24.8						0-74 53.6
C7	Span Peak pos. Fprob																								
C8	Span Peak pos.																				60- 63 64.8				
C9	Span Peak pos.						0-36 8.9					18- 66 44.8							43- 59 44.8						9-36 35.9



The subset of 94 lines selected for further full scale trials was selected to remove those lines showing particularly strong stem canker susceptibility and early flowering, so the analysis was repeated on this subset to observe if there was any distortion in QTL expression (Supp. Table 10). Most noticeably, both the number of identified QTL and their significance level were reduced for all traits. Additionally, analysis of the parental genotyping ratio indicated an increase in the presence of Tapidor alleles in the regions where there were QTL for stem canker and flowering time. However, analysis of the trait data showed that removing these lines had minimal effects on the mean and range of the canopy trait data (Table 7). It seems likely that this was a result of the reduced statistical ability to resolve QTL because of the reduction in line number, in addition to the removal of extreme lines for earliness and canker susceptibility.

QTL analysis - Cowlinge and Barton, 2006-2007

QTL discovery was carried out, as for the trial at Spalding, by single marker regression analysis and summarised for the trials at Barton and Cowlinge separately (Tables 16 and 17 respectively). These data are highly complex and examples are given here to illustrate important principles used in interpreting it. Importantly, though stem canker was observed, the strong QTL on A2 and A9 observed at Spalding, where the plots were untreated by fungicide, were not observed. A stem canker QTL was observed on A1 ($P = 0.003$) which overlapped with, though it did not necessarily peak at the same location as, QTL for other traits such as fertile branch number, pod number yield and seed storage traits. Many putative QTL were observed across the whole genome though, as at Spalding, were more frequent in the A genome. It was difficult to localise many of these QTL because of noise in the data.

Certain traits, particularly those associated with seeds, exhibited major differences between the two sites. At Barton, for instance, there were highly significant QTL on A1 and A6 ($P < 0.001$) and minor QTL on C5 and C9 for weight of seed per pod. This was in contrast to results from Cowlinge where the main QTL was on C9 ($P < 0.01$) but where there were no significant QTL on A1 and only minor ones on A6, A10 and C1. Mean seed weight had a very significant QTL at Barton on A4 ($P < 0.0001$) plus minor QTL on A5-A8, C4 and C8, while at Cowlinge only minor coincident QTL were identified on A7 and C8. In contrast to seed traits, QTL for pod traits were often coincident at both sites such that, for example, coincident QTL for the vertical angle of pods were

Table 16. Single marker analysis TNDH 94 lines. Barton 2006-2007. Span of QTL is given as between marker positions above $P < 0.05$ with the probability level indicated by coloured box.

		seed wt.	valve wt.	pod HI	mean seed wt.	seed no per pod	seed density	height	terminal length	foot length	pod no per raceme	pod density	stem width	fertile branch	infertile branch	remainder of nodes	total nodes	node density
A1	Span	46-71	46-71		27-71		37-63			22-64								
	peak pos	57.7	52.9		63.9		48.2			37.6								
A2	Span						34-77	34-93	46-71			52-72	59-66					
	peak pos						70.1	70.1	70.1			70.1	65.8					
A3	Span									83-108	86-108						56-60	
	peak pos									94.4	100.3						56	
A4	Span				0-37	11-64	11-64			39-68	50-73			56-86				
	peak pos				28.9	37.2	37.2			51.5	63.6			67.8				
A5	Span				93-116	13-116	108-116								18-40	49-63	49-63	
	peak pos				96.2	113.3	113.3								38.2	54.6	54.6	
A6	Span	34-91	17-95		49-64					62-71								
	peak pos	51.1	54.7		49.8					69.6								
A7	Span				0-55		0-13	0-61			81-104				21-25	18-55	18-55	0-61
	peak pos				26.2		12.9	21.1			100.1				21.1	26.2	26.2	27.7
A8	Span			0-8	25-51		61-65						0-63					
	peak pos			7.7	39.4		63.3						22.3					
A9	Span		84-93			56-87	56-87		101-126		115-118							40-47
	peak pos		86.9			86.9	69		117.8		117.8							47.3
A10	Span											10-15	8-30	44-65				
	peak pos											10	20.2	55.7				

		seed wt.	valve wt.	pod HI	mean seed wt.	seed no per pod	seed density	height	terminal length	foot length	pod no per raceme	pod density	stem width	fertile branch	infertile branch	remainder of nodes	total nodes	node density
C1	Span															42-63		
	peak pos															60.2		
C2	Span								17-36		44-62							
	peak pos								57.5		57.5							
C3	Span				89-149	89-149			19-30									
	peak pos				96.8	99.8			22.3									
C4	Span		121-140		109-140				40-60		42-67					60-67		
	peak pos		133.8		114.8				42.8		62.9					65.9		
C5	Span	4-7				4-7	4-7				57-63							
	peak pos	5				5	5				57.8							
C6	Span																	
	peak pos																	
C7	Span																	
	peak pos																	
C8	Span				20-33			39-66								0-16		
	peak pos				32.9			60.6								0		
C9	Span	48-81	50-88			48-88		11-88			57-74							11-60
	peak pos	60	81.1			68.9		84.9			68.9							46.2

		branch density	branch angle	branch angle (top 4)	Beak length	pedicel length	pod length	silique length	pod width	pedicel angle	pod angle	angle to rachis	yield	HI	canker	Oil %	glucosinolates	protein
A1	Span		37-60	52-61			34-71	45-68		52-64	35-38	34-39	15-32		15-38	31-71	15-32	
	peak pos		37.6	57.1			58.3	58.3		57.1	35.8	37.6	19.1		21.1	61.1	21.1	
A2	Span					52-77				64-75		60-75						
	peak pos					74.4				66.9		66.9						
A3	Span		49-64	104-132						16-74	73-75	20-45		0-21				
	peak pos		59.2	125.6						42.8	73.8	38.5		0				
A4	Span					0-24				11-21						49-68		0-40
	peak pos					3.4				14.2						63.6		19.1
A5	Span						13-29	13-29		49-55	96-114	59-58?						
	peak pos						28.5	28.5		54.6	113.3	49.1						
A6	Span		75-96		16-71	0-40	0-95	0-95	62-82	82-92		75-92	117-133					
	peak pos		82.1		54.7	18.6	44.3	46.6	63.5	82.1		82.1	117.7					
A7	Span					0-52												18-20
	peak pos					19.1												19.1
A8	Span															59-83		
	peak pos															64.5		
A9	Span		53-140	64-140	53-87	3-127	0-28	0-22		120-140		115-140	26-41					
	peak pos		81.4	81.4	56.8	19.8	11.5	11.5		138.2		120.5	33					
A10	Span				14-45						8-46	7-45	1-39		10-15			
	peak pos				33.9						33.9	29.2	11.7		11.7			
C1	Span			15-54	15-33	7-37												
	peak pos			32.5	23.3	22.1												

	branch density	branch angle	branch angle (top 4)	Beak length	pedicel length	pod length	siliques length	pod width	pedicel angle	pod angle	angle to rachis	yield	HI	canker	Oil %	glucosinolates	protein
C2	Span									0-27							
	peak pos									23.9							
C3	Span	124-141	19-41			124-126	124-126			35-132	106-125	93-100	93-126		89-149		93-137
	peak pos	125.4	38.2			125.4	125.4			113.7	113.7	96.8	111.5		131.9		130.1
C4	Span	0-48	98-134	98-140						98-127	98-140					0-67	19-67
	peak pos	19.2	99	121.2						121.2	121.2					25.4	42.8
C5	Span		57-80	63-88	31-88									0-8		73-88	73-88
	peak pos		62.2	80.1	80									0		87.5	73.2
C6	Span					0-27	11-27	17-47									
	peak pos					25.6	26.2	45.1									
C7	Span																
	peak pos																
C8	Span				65-73			48-73	10-21		10-16						
	peak pos				65.4			65.4	10.4		10.4						
C9	Span			68-88	0-51	0-88	0-88		58-81	60-88	58-85					11-60	
	peak pos			81.1	60.6	81.1	81.1		60	81.1	60					11.4	

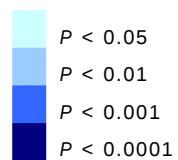


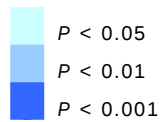
Table 17. Single marker analysis TNDH 94 lines. Cowlinge 2006-2007. Span of QTL is given as between marker positions above $P < 0.05$ with the probability level indicated by coloured box.

		seed wt.	valve wt.	pod HI	mean seed wt.	seed no per pod	seed density	height	terminal length	foot length	pod no per raceme	pod density	stem width	fertile branch	infertile branch	remainder of nodes	total nodes	node density
A1	Span		45-59							22-64	19-64		56-79	15-39				45-61
	peak pos		48.2							46	26.7		78.9	22.3				57.1
A2	Span							34-82	34-92			59-77	30-82	66-75				
	peak pos							70.1	46.1			65.8	60.9	68.9				
A3	Span				38-46				33-50			40-105	29-46	33-74		29-50	29-60	32-60
	peak pos				42.8				41.3			95.3	35.9	73.8		43.5	41.3	44.2
A4	Span		63-68			36-52	36-52							20-106				
	peak pos		63.6			63.6	37.2							67.8				
A5	Span					62-86						49-97						0-21
	peak pos					71.7						62.5						0
A6	Span	35-83	49-83			54-83								75-92			74-79	75-79
	peak pos	66.2	70.8			66.2								82.1			78.6	78.6
A7	Span				0-55				93-101					88-95				
	peak pos				49.6				99.5					93.1				
A8	Span																	
	peak pos																	
A9	Span							69-127				66-106		53-87				
	peak pos							71.7				86		68.3				
A10	Span	29-45				29-45						53-59	5-18			29-65		
	peak pos	0				33.9						53.4	10			45.7		

		seed wt.	valve wt.	pod Hl	mean seed wt.	seed no per pod	seed density	height	terminal length	foot length	pod no per raceme	pod density	stem width	fertile branch	infertile branch	remainder of nodes	total nodes	node density
C1	Span	22-30																
	peak pos	22.1																
C2	Span																	
	peak pos																	
C3	Span				113-137		99-114				22-41			0-34				
	peak pos				130.5		113.7				30.2			22.3				
C4	Span					61-68												
	peak pos					62.2												
C5	Span														79-81			
	peak pos														79.7			
C6	Span						20-54			0-46								
	peak pos						40.5			26.2								
C7	Span																	
	peak pos																	
C8	Span	39-81	39-74		32-73		51-66				0-22	0-22		10-22				
	peak pos	60.6	60.6		32.3		60.6				12.9	12.9		12.9				
C9	Span						38-51	38-51	38-49									38-51
	peak pos						45.6	11.4	17.2									38.9

		branch density	branch angle	branch angle (top 4)	Beak length	pedicel length	pod length	siliques length	pod width	pedicel angle	pod angle	angle to rachis	yield	HI	canker	Oil %	glucosinolates	protein
A1	Span		15-71	31-71	54-88				48-61	52-69		50-69	15-67		15-39	17-69	15-39	21-32
	peak pos		37.6	60.9	70.6				58.2	58.2		56.6	31.6		21.1	31.6	21.1	31.6
A2	Span					34-60							11-31					
	peak pos					46.1							23					
A3	Span		35-64		0-17				33-64	34-62	33-67	33-67						
	peak pos		35.9		10.5				42.8	60.5	61.5	60.5						
A4	Span					0-24				11-19						49-68		
	peak pos					11.8				14.2						50.8		
A5	Span												0-52					
	peak pos												0					
A6	Span		49-55	49-52	34-96		29-95	23-95	47-112		39-55							
	peak pos		51.1	51.1	54.7		54.7	54.7	66		51.1							
A7	Span					0-25			54-82				0-52			0-20		
	peak pos					18.7			65.2				17.1			17.1		
A8	Span															22-87		
	peak pos															78.6		
A9	Span	17-30	66-82								51-73						93-127	
	peak pos	27.2	81.4								53.3						120.5	
A10	Span		14-46	18-45	14-78			33-46			5-46	8-46	0-35			29-39		
	peak pos		29.2	29.2	55.7			39.1			33.9	29.2	11.7			33.9		
C1	Span			7-40	0-8		22-37	22-36			15-42	22-37						
	peak pos			36.8	6.5		34.6	23.3			29.5	22.1						

		branch density	branch angle	branch angle (top 4)	Beak length	pedicel length	pod length	siliques length	pod width	pedicel angle	pod angle	angle to rachis	yield	HI	canker	Oil %	glucosinolates	protein
C2	Span																	
	peak pos																	
C3	Span		22-41	22-41		90-114										89-149		76-106
	peak pos		23.3	38.2		99.8										131.9		95.3
C4	Span	19-48	98-126							55-67			42-51			98-140	0-68	9-68
	peak pos	22.7	99							57.4			42.8			124	22.8	60.2
C5	Span				73-84				4-8				0-8		0-8			
	peak pos				79.7				5				0		0			
C6	Span				17-26	27-59	17-46											
	peak pos				21	26.2	26.2											
C7	Span															7-43		
	peak pos															35.4		
C8	Span																	
	peak pos																	
C9	Span	11-60															38-62	
	peak pos	11.4															11.4	



found on A1, A3 and A10, the most significant of these being on A3 ($P = 0.000047$ and $P < 0.001$ at Barton and Cowlinge respectively).

As before, many coincident QTL were observed on particular linkage groups, for example QTL for terminal length, node number and density, stem and pod widths and branch and pedicel angle were observed between *approx.* 30 and 50cM on A3. QTL for the angle of the pods to the raceme and other angles also showed high levels of significance between 50 and 60cM on A3 illustrating the complexity of these data. Importantly, it was observed that many traits had QTL on many different linkage groups. This reflected the polygenic control of many canopy traits resulting from the complex physiological pathways involved in the determination of these traits, the effect of environment on their expression and also the genomic complexity of the *B. napus* genome, where up to six homologous alleles may be present for each gene. One important implication of this is that the contribution of each QTL to the overall expression of the trait is 'diluted' by the number of active genes making the accurate identification of each more difficult.

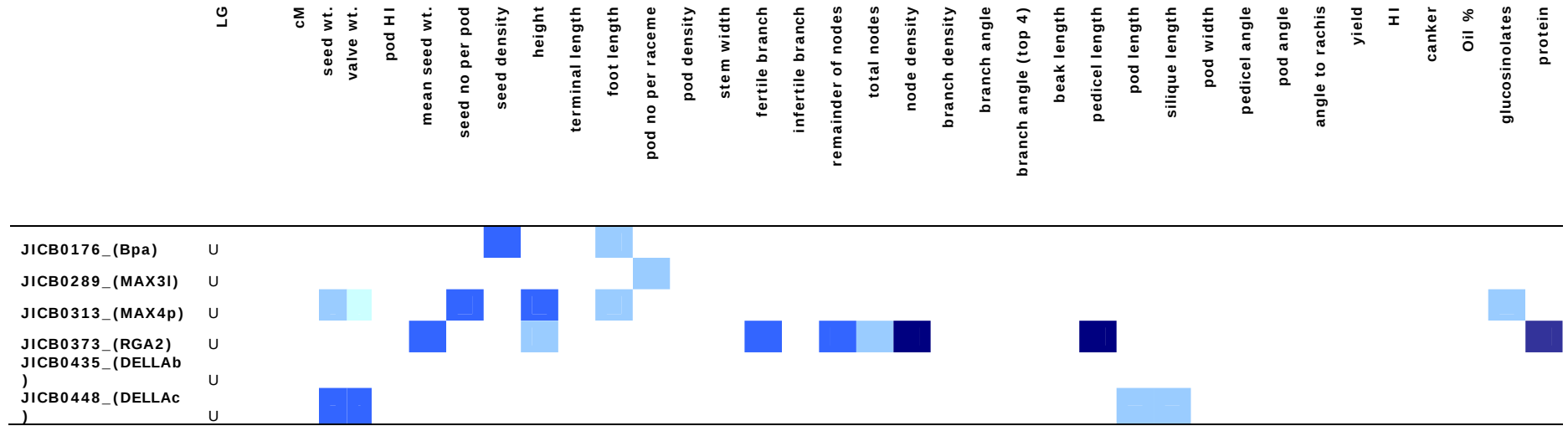
Major QTL for yield were observed at Cowlinge on A1 ($P < 0.01$) and A10 ($P < 0.001$) with minor ones on A2, C4 and C5 (though the QTL on A1 and C5 were close to a canker QTL). Similar QTL were also observed at Barton on A1 ($P < 0.05$) and A10 ($P < 0.001$) as well as new minor QTL on A6 and A9. The major yield QTL on A10 was coincident with QTL for stem width, pod and vertical angles, beak length, pod density and the fertile branch number at Barton. These QTL were also identified at Cowlinge with additional QTL for oil, pedicel and silique length, pedicel angle, seed per pod, seed weight per pod and non-branching nodes. Of these, fertile branch number, seeds per pod and seed weight per pod may be considered as yield components affecting yield directly while others such as pod angles may influence yield indirectly.

Specific associations of the candidate genes are summarised in Tables 18 and 19 for Barton and Cowlinge respectively. At both sites several of these occurred within but not close to the peak of the QTL, and where it is likely that they are acting as simple markers not causally associated with the overlying QTL. However, some were closely associated (within 2 cM) with peak QTL. Among these, at Cowlinge, several markers which had high single marker regression probability values included RGL1 for stem width and TB_like for plant height (A2), RGL2 for pedicel and pod angles (A3), MAX1g

Table 18. Single marker analysis of candidate genes in main trial of TNDH at Barton 2006-2007.

	LG	cm	seed wt. valve wt.	pod HI	mean seed wt.	seed no per pod	seed density	height	terminal length	foot length	pod no per raceme	pod density	stem width	fertile branch	infertile branch	remainder of nodes	total nodes	node density	branch density	branch angle	branch angle (top 4)	beak length	pedicel length	pod length	siliques length	pod width	pedicel angle	pod angle	angle to rachis	yield	HI	canker	Oil %	glucosinolates	protein	
KBrB010O09-1_ (RGL1)	A2	62 ¹																																		
JICB0055_ (TB-like)	A2	71.3																																		
KBrB017M18-36_ (RGL3?)	A2	95 ¹																																		
KBrB001H24-13_ (RGL2?)	A3	59.1																																		
JICB0283_ (MAX3f)	A4	79.6																																		
JICB0094_ (MAX1g)	A5	18.6																																		
JICB0153_ (MAX2h)	A5	20.2																																		
JICB0384_ (RGL1a)	A5	113.3																																		
KBrB086M23-6_ 580_ (GAI)	A6	49.3																																		
JICB0416_ (DELLA+GRASa)	A7	96.6																																		
JICB0274_ (Blrk)	A7	99.0																																		
JICB0011_ (TCP)	A7	100.1																																		
JICB0335_ (GAIb)	A8	22.3																																		
JICB0018_ (AtTB)	A8	78.6																																		

	LG	cM	seed wt. valve wt.	pod HI	mean seed wt.	seed no per pod	seed density	height	terminal length	foot length	pod no per raceme	pod density	stem width	fertile branch	infertile branch	remainder of nodes	total nodes	node density	branch density	branch angle	branch angle (top 4)	beak length	pedicel length	pod length	silique length	pod width	pedicel angle	pod angle	angle to rachis	yield	HI	canker	Oil %	glucosinolates	protein		
JICB0192_(Bpf)	A9	27.2																																			
JICB0272_(Blrj)	A1 0	53.4																																			
JICB0245_(Blrd)	A1 0	77.9																																			
JICB0260_(Blrg)	C3	0.0																																			
JICB0220_(Bp3)	C3	53.3																																			
JICB0088_(MAX1f)	C4	22.7																																			
JICB0149_(MAX2g)	C4	121.2																																			
JICB0111_(MAX1h)	C4	124.0																																			
KBrB086M23-6_575_(GAI)	C5	57.8																																			
JICB0172_(MAX2I)	C7	91.2																																			
JICB0009_(TCP)	U																																				
JICB0064_(MAX1b)	U																																				
JICB0101_(MAX1h_E07F)	U																																				
JICB0128_(MAX2a)	U																																				
JICB0134_(MAX2b)	U																																				



1 = low stringency

 = within a QTL

P indicates at or within 2 cM of QTL peak

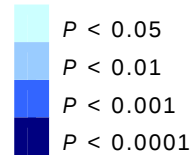
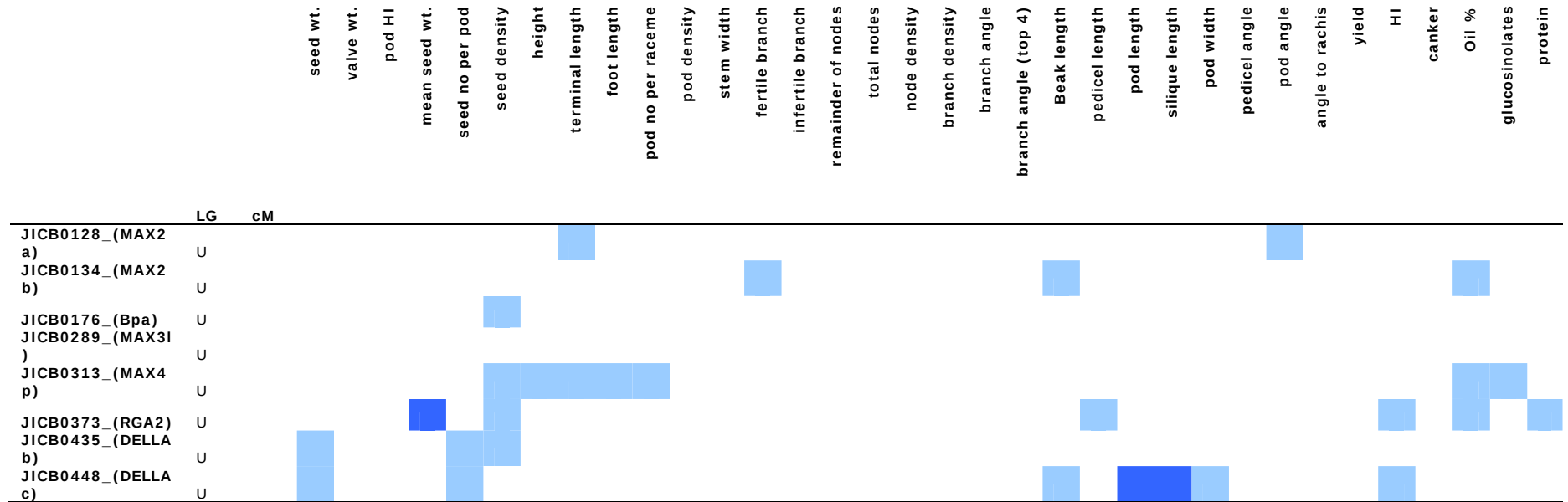


Table 19. Single marker analysis of candidate genes in TNDH in main trial at Cowlinge 2006-2007.

			seed wt.	valve wt.	pod HI	mean seed wt.	seed no per pod	seed density	height	terminal length	foot length	pod no per raceme	pod density	stem width	fertile branch	infertile branch	remainder of nodes	total nodes	node density	branch density	branch angle	branch angle (top 4)	Beak length	pedicel length	pod length	siliques length	pod width	pedicel angle	pod angle	angle to rachis	yield	HI	canker	Oil %	glucosinolates	protein	
	LG	cM																																			
KBrB010O09-1_ (RGL1)	A2	62 ¹																																			
JICB0055_ (TB-like)	A2	71.3																																			
KBrB017M18-36_ (RGL3?)	A2	95 ¹																																			
KBrB001H24-13_ (RGL2?)	A3	59.1																																			
JICB0283_ (MAX3f)	A4	79.6																																			
JICB0094_ (MAX!g)	A5	18.6																																			
JICB0153_ (MAX2h)	A5	20.2																																			
JICB0384_ (RGL1a)	A5	113.3																																			
KBrB086M23-6_580_ (GAI)	A6	49.3																																			
JICB0416_ (DELLA+GRASa)	A7	96.6																																			
JICB0274_ (Blrk)	A7	99.0																																			
JICB0011_ (TCP)	A7	100.1																																			
JICB0335_ (GAIb)	A8	22.3																																			

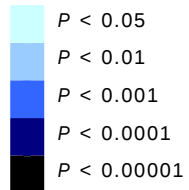
	LG	cM	seed wt.	valve wt.	pod HI	mean seed wt.	seed no per pod	seed density	height	terminal length	foot length	pod no per raceme	pod density	stem width	fertile branch	infertile branch	remainder of nodes	total nodes	node density	branch density	branch angle	branch angle (top 4)	Beak length	pedicel length	pod length	siliqua length	pod width	pedicel angle	pod angle	angle to rachis	yield	HI	canker	Oil %	glucosinolates	protein
JICB0018_(AtTB)	A8	78.6																																	p	
JICB0192_(Bpf)	A9	27.2																		p																
JICB0272_(Blrj)	A1 0	53.4											p										p													
JICB0245_(Blrd)	A1 0	77.9																																		
JICB0260_(Blrg)	C3	0.0																																		
JICB0220_(Bp3)	C3	53.3																																		
JICB0088_(MAX1f)	C4	22.7																		p															p	
JICB0149_(MAX2g)	C4	121.2																																		
JICB0111_(MAX1h)	C4	124.0																																	p	
KBrB086M23-6-575_(GAI)	C5	57.8																																		
JICB0172_(MAX2I)	C7	91.2																																		
JICB0009_(TCP)	U																																			
JICB0064_(MAX1b)	U																																			
JICB0101_(MAX1h_E07F)	U																																			



1 = low stringency

 = within a QTL

P indicates at or within 2 cM of QTL peak



and MAX2h for node density (A5), GAI for branch and pod angle (A6), Blrk and TCP for terminal length (A7), Bpf for branch density (A9), Blrj for beak length (A10) and MAX1f for branch density (C4). Candidate genes close to QTL peaks found at Barton included *TB-like* for height, terminal length, foot length and pod density (A2), *RGL2* in branch angle (A3), *RGL1a* in seed/pod, seed density and pod angle (A5), *Blrk* and *TCP* in pod density (A7), *GAIb* in stem width (A8), *Blrj* in fertile branch number (A10), *MAX2g* in branch and pod angle (C4) and *GAI* in pod number on raceme (C5).

3.3.5. CRDH (2007-2008)

Trait analysis

Analysis of CRDH at both sites showed that an average of 47.7% of the total variation was accounted for by the residual variation, varying from 26.7% for stem width to an extreme of 91.2% for pod width. Additionally, in nearly all cases, except pod width, significant line $\times$ site interactions accounted for a further 5.4% and 19% (Table 20). Despite this, highly significant variation was noted for nearly all traits between sites, with the exception of the number of non-branching nodes, and among lines, with the exception of pod width, and between sites. Heritabilities (from expected mean squares) were low for most traits, though beak length, pedicel length and height exceeded 40% suggesting that these were less affected by the environment (Table 20). In part, these differences between sites and the interactions were explained by two problems at Cowlinge. Here, the trial suffered badly from very uneven establishment which resulted in great variation in plant density which, in turn, resulted in increased variation for plant size. Additionally, in some plots, grazing by deer and pigeons destroyed up to 90% of plant apices which lead to increased numbers of side shoots. Thus plant size, as determined by basal stem width, was, on average, 34% greater and more variable at Cowlinge than at Cantelupe (1.25cm and 0.93cm and with coefficients of variation of 17.2% and 7.1% respectively, Table 21). Even more noticeable was the large variation for fertile branch number at both sites with more than double the number of fertile branches at Cowlinge than Cantelupe (means = 6.6 and 3.2 respectively; CV = 31.6% and 46.4%). Branches were angled about 5° more vertically at Cantelupe possibly due to the increased effective plant density. Pod traits were however basically similar on both sites as these were less directly affected by the problems described above. Plot yields were, on average, 13% greater at Cantelupe with a similar range of values. Yield of the parents were also

Table 20. Mean squares and expected mean squares from the analysis of the combined main traits of the CRDH population grown at Cantelupe and Cowlinge in 2007-2008.

		Mean squares and Expected Mean Squares			
		line	site	line*site	Residual
Plant traits					
Height	MS	2080.6	1194.4 [*]	691.6	280.9
	EMS	41.6	0.4	19	39
Terminal length	MS	269	993.9 [*]	224.8 ^{**}	157.9
	EMS	9.2	1.5	11.1	78.3
Foot length	MS	1760.5	65463.4	1133.4	717.6
	EMS	13.8	18.2	11	57
Pod no. on terminal	MS	654.1	73992.5	412.9	190.3
	EMS	12.8	43.4	12.3	31.5
Pod density	MS	0.4511	32.5737	0.2578	0.168
	EMS	13.1	31.9	8.3	46.7
Stem width at base	MS	0.14762	28.1355	0.15023	0.05367
	EMS	7.8	49.5	16	26.7
Branching traits					
Fertile branch no.	MS	21.661	3139.245	16.885	9.165
	EMS	8.4	44.5	10.3	36.8
Infertile branch no.	MS	-	-	-	-
	EMS	-	-	-	-
Remaining nodes	MS	1.1172 ^{**}	2.8784 ^{ns}	1.1687 ^{**}	0.7651
	EMS	6.1	0.8	13.9	79.2
Total nodes	MS	34.06	3338.958	18.971	7.256
	EMS	16.3	43.1	14.2	26.4
Node density	MS	29.641	2818.632	18.052	9.601
	EMS	13	38.7	11	37.3
Branch density	MS	129.45 [*]	765.34 ^{**}	136.36 ^{**}	94.74
	EMS	5	2	11.9	81.1
Branch angle	MS	79.9	4207.92	36.48	19.71
	EMS	20	29.6	11.1	39.3
Branch angle (top 4)	MS	98.24	10112.75	54.22	23.05
	EMS	15.3	43.8	12.7	28.2
Pod traits					
Beak length	MS	0.21172	2.4309	0.05294	0.02603
	EMS	41.6	11.5	12	35
Pedicel length	MS	0.62743	10.99243	0.11138 ^{**}	0.07574
	EMS	42.1	17.7	5.4	34.7
Pod length	MS	1.9538	171.0169	0.9591	0.4821
	EMS	16.4	40.6	10.7	32.3
Pod width	MS	0.01608 ^{ns}	0.28224	0.01466 ^{ns}	0.01429
	EMS	1.9	6.1	0.8	91.2
Pedicel angle	MS	134.83	211.92 [*]	59.09	34.88
	EMS	27.7	1	13.4	57.9
Pod angle	MS	44.97	2005.66	22.38	14.08
	EMS	17.7	24.3	9.5	48.5

all *** unless given otherwise

give df for terms

Table 21. Summary of CRDH trait measurements for the main field trials grown at Cantelupe and Cowlinge in 2007-2008.

	Cantelupe						Cowlinge					
	mean	min	max	SD	ratio max/min	CV %	mean	min	max	SD	ratio max/min	CV %
Seed traits												
Seed weight	-	-	-	-	-	-	5.76	4.689	7.002	0.41	1.49	7.1
Plant traits												
Height	139.4	113.8	163.5	11.71	1.44	8.4	137.5	77.8	183.3	18.67	2.36	13.6
Terminal length	59.26	46.17	74.5	5.72	1.61	9.7	57.25	37.5	75.67	7.22	2.02	12.6
Foot length	56.61	15	90.67	18.4	6.04	32.5	41.59	4.33	71.67	12.04	16.55	28.9
Pod no. on terminal	44.71	28.17	57.83	5.98	2.05	13.4	60.92	34.28	93.33	12.34	2.72	20.3
Pod density	1.379	0.944	2.287	0.228	2.42	16.5	1.040	0.673	2.338	0.2688	3.47	25.8
Stem width at base	0.933	0.795	1.077	0.066	1.35	7.1	1.249	0.855	2.137	0.2149	2.50	17.2
Branching traits												
Fertile branch no.	3.199	2	16.33	1.485	8.17	46.4	6.566	2	12.33	2.076	6.17	31.6
Infertile branch no.	0.545	0	1.5	0.320	*	58.8	0.638	0	2.333	0.4711	*	73.9
Remaining nodes	10.95	6.33	14.17	1.427	2.24	13.0	14.40	7.54	20.67	2.623	2.74	18.2
Total nodes	14.69	11.33	29.67	2.167	2.62	14.8	21.61	11.2	28.5	3.833	2.54	17.7
Node density	9.87	6.477	12.68	1.084	1.96	11.0	6.748	4.572	11.96	1.225	2.61	18.2
Branch density	8.07	*	21.21	5.34	*	66.2	6.334	*	15.83	3.07	*	48.5
Branch angle	35.77	29.1	41.46	2.63	1.42	7.4	39.63	32.52	48.39	3.2	1.49	8.1
Branch angle (top 4)	35.92	29.92	41.54	2.61	1.39	7.3	41.89	32.39	52.34	4.04	1.62	9.6
Pod traits												
Beak length	1.122	0.688	1.407	0.154	2.05	13.7	1.029	0.619	1.36	0.1409	2.20	13.7
Pedicle length	2.521	1.894	3.081	0.267	1.63	10.6	2.324	1.842	2.916	0.23	1.58	9.9
Pod length	5.234	4.43	6.476	0.439	1.46	8.4	4.45	3.06	6.097	0.531	1.99	11.9
Pod width	0.464	0.418	1.165	0.075	2.79	16.2	0.494	0.455	0.552	0.0194	1.21	3.9
Pedicle angle	79.45	67.46	88.47	4.01	1.31	5.0	80.53	69.99	89.41	4.05	1.28	5.0

	Cantelupe						Cowlinge					
	mean	min	max	SD	ratio max / min	CV %	mean	min	max	SD	ratio max / min	CV %
Pod angle	157.66	153.4	163.7	2.26	1.07	1.4	160.3	152.8	165.8	2.38	1.09	1.5
Biomass traits												
Yield (t ha-1)	3.9	2.805	5.21	0.528	1.86	13.5	3.439	2.41	4.655	0.507	1.93	14.7
Harvest Index	0.234	0.149	0.342	0.041	2.29	17.3	0.231	0.083	0.398	0.0458	4.80	19.9
Scored traits												
start flower ¹	-	-	-	-	-	-	50.71	42	59.5	3.44	1.42	6.8
Autumn vigour ²	-	-	-	-	-	-	4.8	3.5	6	0.5	1.7	11.1
Spring vigour ²	-	-	-	-	-	-	4.9	3	6.5	0.7	2.2	14.5
Appearance before flowering	-	-	-	-	-	-	4.8	3	6.5	0.7	2.2	15.2
Appearance at harvest	-	-	-	-	-	-	5.2	3.5	7	0.8	2	14.8
Height	-	-	-	-	-	-	144.9	117.5	167.5	11.1	1.4	7.7
End of flowering ¹	-	-	-	-	-	-	87.4	84	91.5	1.6	1.1	1.8
Flowering period (days)	-	-	-	-	-	-	36.7	28.5	44	2.9	1.5	8
Seed Storage traits												
% seed oil	-	-	-	-	-	-	49.19	46.45	51.65	1.17	1.11	2.4
0% moisture	-	-	-	-	-	-	18.047	13.9	25.15	2.156	1.81	11.9
GSL µmol/g Fwt Protein	-	-	-	-	-	-	19.191	17.5	20.95	0.726	1.20	3.8
0% moisture	-	-	-	-	-	-						

¹ after 01.03.

² 8=vigorous

greater at Cantelupe with the population showing transgressive segregation, the best lines being 15.8% higher at Cantelupe and 27% at Cowlinge than the mean of their parents. HI from both sites was similar and the overall similarity in yields despite the damage demonstrating the plasticity of the OSR canopy to compensate for variation in plant establishment. A summary of the trait data for the parental lines and control varieties at both sites is given in Table 22. Transgressive segregation was observed for all traits.

Beak length and pod length were strongly associated at each site ($r = +0.563^{***}$ and $+0.687^{***}$ where $*$ = $P < 0.05$; $**$ = $P < 0.01$ $***$ = $P < 0.001$) but showed no relationship with pedicel length (Cantelupe, Table 23 and Cowlinge, Table 24). Other traits relating to lengths, e.g. height, terminal length and foot length which exhibited a degree of autocorrelation were not correlated as highly as might be expected ($r = +0.295^{**}$, $+0.401^{***}$ at Cantelupe and $r = +0.366^{***}$, $+0.451^{***}$ at Cowlinge) indicating that there is some degree of independent control over these traits. The length of foot is highly correlated with the number of undifferentiated nodes ($r = +0.508^{***}$ and $+0.594^{***}$) but not to the expression of branch number. At Cantelupe the very strong negative correlation ($r = -0.718^{***}$) between foot length and branch density and the absence of association with fertile branch number ($r = +0.025^{ns}$) suggests that plants with a longer foot still retain similar numbers of fertile branches and thus have a more compact canopy. Pod length and pod angle were also strongly associated at both sites ($r = +0.372^{***}$ and $+0.419^{***}$ respectively) thus longer pods were more horizontal. At both sites it was observed that bigger, more vigorous plants as assessed by stem width, tended to have more horizontal branches ($+0.275^{**}$ and $+0.524^{***}$). Angles of pods and branches were not associated at either site. At Cantelupe, HI showed very significant negative correlations with beak length and pod length ($r = -0.357^{***}$ and -0.394^{***} respectively) and to a lesser extent with pod number on the terminal racemes ($r = -0.283^{**}$) though at Cowlinge HI was correlated with branch angle ($r = 0.318^{***}$) and negatively correlated with plant height ($r = -0.237^{*}$). At Cantelupe yield was correlated with height ($r = +0.325^{***}$) and beak length ($r = +0.282^{**}$) though these were not observed at Cowlinge. Flowering traits were only assessed at Cowlinge where late flowering and late maturation were associated with lower yields ($r = -0.48^{***}$ and -0.361^{***} respectively) though the duration of the flowering period was positively associated with increased yield ($r = +0.365^{***}$). Relationships of these traits were similar for HI though less significant. Long beaks and pods lengths were highly

Table 22. Trait summary for parents of CRDH and VGDH and control varieties grown at Cantelupe and Cowlinge 2007-2008.

	Cantelupe								Cowlinge								controls	
	Capitol mean	SD	Rocket mean	SD	Grizzly mean	SD	Verona mean	SD	Capitol mean	SD	Rocket mean	SD	Grizzly mean	SD	Verona mean	SD	mean	SD
Seed traits																		
Seed weight	-	-	-	-	-	-	-	-	6.114	0.102	4.558	0.032	4.974	0.113	4.262	0.013	5.393	0.209
Plant traits																		
Height	121.6	15.13	129	15.06	129.7	0.49	121	3.253	119.5	21.43	134	5.091	119.9	12.52	125.2	6.364	131.6	13.53
Terminal length	56.61	3.78	65.11	9.192	47.5	0.24	35.34	1.888	51.81	1.648	50.22	10.25	38.84	3.062	39.84	0.233	51.59	8.227
Foot length	49.325	1.65	37.33	6.838	57.67	8.01	65.33	2.828	42.54	5.063	44.29	26.4	47.5	4.95	47.33	5.657	42.05	13.29
Pod no. on terminal	47.14	3.54	49.98	12.25	40.17	7.3	35.84	0.233	54.6	19.33	49.93	15.56	66.67	13.67	60	8.952	59.94	13.8
Pod density	1.207	0.17	1.377	0.484	1.229	0.26	0.984	0.042	1.031	0.354	1.076	0.187	0.59	0.074	0.675	0.099	0.955	0.257
Stem width at base	1.0317		0.763	0.104	0.853	0.18	0.867	0.042	1.325	0.47	0.865	0.007	1.288	0.361	1.218	0.049	1.231	0.202
Branching traits																		
Fertile branch no.	2.8225	1.65	3.823	0.235	3	0	3.5	0.236	5.493	4.478	5.743	1.532	9.667	3.3	7.667	0.943	6.446	2.272
Infertile branch no.	0.4982	0.24	-0.002	0	0.833	0.24	0.333	0.471	0.583	0.354	0.5	0.707	0	0	0.667	0	0.708	0.532
Remaining nodes	12.375	2.35	9.875	0.233	11.17	1.18	12.67	0.474	13.9	4.596	16.57	3.889	16.5	3.069	16.5	1.655	14.93	2.495
Total nodes	15.7	4.24	13.7	0	15	0.95	16.5	0.24	19.98	9.433	22.82	1.648	26.17	6.364	24.83	0.707	22.06	2.752
Node density	8.0505	0.99	9.48	0.893	8.713	0.57	7.415	0.025	6.571	2.098	5.938	0.223	4.67	0.667	5.081	0.069	6.287	0.968
Branch density	5.4575	0.47	6.458	3.143	8.098	2.57	5.6	0.378	4.597	1.931	5.965	2.291	3.403	0.258	4.988	0.752	6.203	1.951
Branch angle	35.45	-	38.17	2.482	38.35	2.39	41.31	0.792	37.98	6.307	35.42	0.636	43.82	1.895	44.07	0.297	40.24	2.601
Branch angle (top 4)	36.39	-	38.21	2.425	38.35	2.39	41.53	0.481	43.41	9.058	36.89	1.442	49.92	0.679	46.99	2.079	43.24	4.609
Pod traits																		
Beak length	1.301	-	1.04	0.016	1.185	0.04	1.24	0.133	1.258	0.094	1.072	0.001	1.105	0.192	1.139	0.019	1.204	0.402
Pedicel length	2.452	-	2.801	0.141	1.994	0.11	2.044	0.108	2.329	0.258	2.261	0.057	1.841	0.04	1.867	0.032	2.286	0.351
Pod length	5.135	-	5.144	0.128	5.732	0.59	5.198	0.371	4.615	0.484	5.13	0.281	6.046	0.906	5.153	0.303	4.883	0.631
Pod width	0.4672	-	0.423	0.017	0.421	0.02	0.404	7.00E-04	0.516	0.006	0.47	0.014	0.458	0.024	0.438	0.017	0.466	0.033
Pedicel angle	80.1	-	72.59	6.498	85.72	1.95	81.83	0.368	79.48	0.382	73.03	5.544	83.13	0.877	84.48	0.453	79.79	4.164
Pod angle	158.3	-	161.5	3.111	160.2	1.2	159.4	0.849	159.1	0.071	165.2	3.536	163.7	0.424	162.8	1.344	161.9	2.489
Biomass traits																		
Yield (t ha-1)	4.545	1.75	4.45	1.499	4.303	0.95	3.95	0.54	3.62	0.294	3.714	0.125	3.682	0.233	3.943	0.403	3.751	0.528

	Cantelupe								Cowlinge									
	Capitol		Rocket		Grizzly		Verona		Capitol		Rocket		Grizzly		Verona		controls	
	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD
Harvest Index	19.21	0.15	20.35	1.009	20.93	-	18.03	-	19.85	-	20.28	1.949	24.87	1.492	27.04	-	18.45	3.946
Scored traits																		
start flower ¹	-	-	-	-	-	-	-	-	49.5	0.707	54	0	56.5	0.707	53	1.414	47.44	3.932
Autumn vigour ²	-	-	-	-	-	-	-	-	4	0	4.5	0.707	5.5	0.707	5	0	5.063	0.998
Spring vigour ²	-	-	-	-	-	-	-	-	5.5	0.707	4	0	4	0	5	0	5.625	0.619
Appearance before flowering	-	-	-	-	-	-	-	-	5.5	0.707	4	0	4	0	5	0	5.625	0.619
Appearance at harvest	-	-	-	-	-	-	-	-	6.5	0.707	5	1.414	5	1.414	5.5	0.707	5.938	0.772
Height	-	-	-	-	-	-	-	-	147.5	3.536	127.5	3.536	130	0	127.5	3.536	140.3	10.24
End of flowering ¹	-	-	-	-	-	-	-	-	88	0	86.5	0.707	86.5	2.121	85	1.414	86.06	2.048
Flowering period (days)	-	-	-	-	-	-	-	-	38.5	0.707	32.5	0.707	30	1.414	32	0	38.63	3.202
Seed Storage traits	-	-	-	-	-	-	-	-										
% seed oil 0% moisture	-	-	-	-	-	-	-	-	50.35	0.071	50.75	0.071	50.3	0.424	50.95	0.212	50.42	0.816
GSL $\mu\text{mol/g}$ Fwt	-	-	-	-	-	-	-	-	18.3	0.141	17.35	0.778	19.8	1.838	18	0.424	17.63	2.549
Protein 0% moisture	-	-	-	-	-	-	-	-	18.7	0.141	18.15	0.212	17.85	0.495	16.9	0.424	17.88	0.874

Control varieties = Castille, Expert, Fortis and Winner

Table 23. Correlation matrix for CRDH at Cantelupe.

[illegible]

$P \leq -0.001$
 $P \leq -0.01$
 $P \leq -0.05$

Table 24. Correlation matrix for CRDH at Cowlinge. Part 1 (table split to fit to page).

Height	-0.044																	
Terminal	-0.064	0.366																
Foot	0.012	0.451	0.064															
Podno	-0.142	0.455	0.534	0.33														
Poddensity	0.151	-0.215	-0.083	-0.276	-0.736													
Stemw	0.089	-0.103	0.025	-0.118	-0.033	0.031												
Fertile	-0.113	0.529	0.124	-0.038	0.56	-0.45	-0.028											
Infertile	0.164	-0.073	-0.024	0.005	0.019	-0.035	-0.068	-0.054										
Nodes	-0.003	0.411	-0.024	0.594	0.488	-0.456	-0.154	0.414	0.121									
Totnodes	-0.044	0.535	0.048	0.346	0.616	-0.538	-0.121	0.806	0.163	0.861								
Nodedensity	0.012	0.148	0.267	-0.109	-0.357	0.489	0.062	-0.514	-0.229	-0.668	-0.729							
Branchdensity	0.077	0.244	-0.108	-0.17	-0.493	0.513	0.071	-0.287	-0.067	-0.342	-0.385	0.646						
Branchang	-0.061	0.194	0.12	0.055	-0.014	-0.003	0.359	-0.028	-0.102	-0.158	-0.128	0.264	0.166					
Branch4	-0.048	0.103	0.113	0.028	-0.049	0.021	0.524	-0.114	-0.076	-0.21	-0.205	0.283	0.141	0.929				
Bkl	0.161	0.012	-0.03	-0.012	-0.022	0.046	-0.097	0.069	0.068	-0.026	0.032	-0.035	0.137	-0.22	-0.27			
Pedl	-0.139	0.078	0.142	-0.024	0.108	-0.136	-0.023	0.046	0.158	-0.03	0.025	0.082	-0.042	0.075	0.093	-0.13		
	Meanseedwt	Height	Terminal	Foot	Podno	Poddensity	Stemw	Fertile	Infertile	Nodes	Totnodes	Nodedensity	Branchdensity	Branchang	Branch4	Bkl		

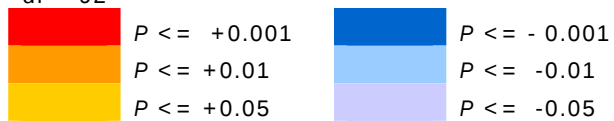
Table 24. Correlation matrix for CRDH at Cowlinge. Part 2 (table split to fit to page).

Podl	-0.037	0.055	-0.03	-0.064	0.024	-0.037	-0.045	0.121	0.085	-0.094	0.02	0.017	0.152	-0.055	-0.121	0.687
Podw	0.045	-0.157	-0.109	-0.186	-0.087	0.046	0.218	-0.032	0.122	-0.17	-0.108	0.022	0.093	0.164	0.137	0.085
Pedang	0.003	-0.007	-0.086	-0.121	0.038	-0.091	0.145	0.129	0.032	0.001	0.078	-0.1	-0.073	0.138	0.113	0.087
Podang	-0.029	0.125	-0.202	0.112	-0.08	-0.037	-0.357	0.055	-0.08	0.126	0.1	-0.044	0.156	0.021	-0.085	0.24
Yield t/ha	0.074	-0.06	-0.081	0.106	0	-0.014	0.253	-0.012	0.022	0.104	0.06	-0.155	-0.164	-0.025	0.063	0.091
HI	-0.237	0.054	0.094	0.129	0.061	-0.102	0.018	-0.12	0.014	0.074	-0.02	0.079	0.067	0.317	0.318	-0.184
Start flowering	0.018	0.14	-0.005	0.054	-0.029	0.109	-0.322	0.078	-0.012	-0.084	-0.009	0.124	0.121	-0.224	-0.317	0.421
%oil	-0.081	0.119	0.044	0.321	-0.012	-0.021	-0.094	-0.128	0.059	0.155	0.032	0.037	0.038	0.03	-0.041	0.205
GSL	0.318	0.085	-0.002	-0.185	-0.081	0.071	-0.027	0.196	-0.065	-0.01	0.093	-0.007	0.06	-0.064	-0.059	-0.109
Protein	0.194	-0.006	0.027	-0.149	0.067	-0.027	0.03	0.084	0.063	-0.097	-0.007	0	-0.088	0.009	0.089	-0.278
Autum vig.	-0.179	0.003	0.049	0.009	0.154	-0.216	-0.04	0.142	-0.142	0.094	0.12	-0.162	-0.241	-0.086	-0.077	0.027
Spring vig.	0.115	0.117	0.098	0.188	0.176	-0.187	0.261	0.104	-0.076	0.161	0.148	-0.109	-0.202	0.157	0.233	-0.077
App. B. flow	0.084	0.176	0.12	0.218	0.238	-0.246	0.251	0.167	-0.124	0.182	0.191	-0.11	-0.168	0.135	0.198	-0.036
App. at harvest	0.198	-0.047	0.097	0.061	0.005	0.016	0.208	-0.051	0.035	-0.095	-0.082	0.003	-0.098	0.044	0.118	0.134
Plant height	0.336	-0.048	0.007	0.021	-0.011	0.031	0.442	-0.029	-0.055	-0.049	-0.054	-0.015	-0.014	0.048	0.175	0.144
End flowering	0.156	0.044	-0.048	-0.084	-0.118	0.177	0.057	-0.011	-0.059	-0.103	-0.076	0.136	0.18	-0.038	-0.034	0.207
Flowering period	0.063	-0.139	-0.016	-0.111	-0.027	-0.032	0.411	-0.096	-0.019	0.04	-0.032	-0.069	-0.044	0.245	0.357	-0.386
	Meanseedwt	Height	Terminal	Foot	Podno	Poddensity	Stemw	Fertile	Infertile	Nodes	Totnodes	Nodedensity	Branchdensity	Branchang	Branch4	Bkl

Table 24. Correlation matrix for CRDH at Cowlinge. Part 3 (table split to fit to page).

[illegible]

df = 92



correlated with early flowering ($r = +0.421^{***}$ and $+0.419^{***}$) though negatively correlated with the duration of flowering ($r = -0.386^{***}$ and -0.376^{***}). In a similar way early flowering was associated with thinner stems ($r = -0.322^{**}$) and more upright branches ($r = -0.317^{**}$) while reversing this association with the duration of flowering ($r = +0.455^{***}$ and 0.357^{***}). Many combinations of traits are highly significant statistically ($P < 0.001$), a result of the high degree of freedom used, where coefficients of determination (r^2) give a better assessment of their importance in relation to the total variability of the crop. These are given in Supp. Tables 11 and 12 for Cantelupe and Cowlinge respectively.

QTL analysis

A skeleton genetic linkage map for CRDH was made using the 112 markers found to be polymorphic between the parents. These mapped together to form 18 linkage groups ranging from two to 14 markers per group and 22 unlinked markers. These groups were tentatively assigned to chromosomes based on marker order in existing mapping populations, especially TNDH. More putative QTL ($P < 0.05$) were found at Cantelupe (Table 25) than Cowlinge (Table 26) with several identified at both sites. Expanded versions giving the mean expression of these traits with respect to the parental alleles are given as supplemental tables (Supp. Tables 13 and 14). While QTL ($P < 0.01$) for yield at Cantelupe were observed on the longer linkage group for A3 there were no coincident QTL, however, on A4/C6 there were QTL associated with the number of nodes and foot length. QTL for HI were also observed at Cantelupe on the shorter linkage group for A3 ($P < 0.01$), C1 ($P < 0.001$) and C3/A3/C8 ($P < 0.01$). For both A3 and C3/A3/C8 coincident QTL were observed for pedicel length ($P < 0.01$) suggesting that they formed part of the same QTL on A3. No QTL for these traits were observed at Cowlinge. At Cantelupe the most significant QTL ($P < 0.0001$) were node number (A7), pedicel angle (A10) and beak length (uk1) with less significant QTL ($P < 0.001$) for node number (A4/C4; MAX3_m). QTL for traits controlling 'length' occurred in different combinations such that QTL for height, foot length (but not terminal length), and beak and pedicel length (but not pod length) occurred on the shorter A3 segment. Height and terminal length were coincident on A10, and in a similar way terminal length and pedicel length (C3/A3/C8), height, terminal length and foot length (uk1), foot length and beak length (uk1), height, foot length, beak length and pod length (but not terminal length or pedicel length) on A7. Though there were no QTL for yield or HI at Cowlinge a QTL for terminal length on A7 was highly significant

Table 25. Single marker analysis CRDH at Cantelupe 2007-2008.

markers	position of marker in TNDH	cM	LG																					
				height of plant	terminal length	foot length	pod number on terminal	pod density on terminal	stem width	fertile branch number	infertile branch number	node number	total node number	node density	branch density	branch angle	branch angle of top 4 branches	beak length	pedicel length	pod length	pod width	pedicel angle	pod angle	yield t/ha
SN11641_405	A1	0.0	13																					
KBrB048	A1	2.4	13																					
F07(2)		11.																						
CB10097_191	A1	0	13																					
MAX4_p	A1	19.5	13																					
CB10427_152	A3	0.0	2																					
BRAS038_108	A3	2.4	2																					
BRAS087_160	A3	2.7	2																					
SSR18_175	A3	4.2	2																					
CB10036_160	A3	6.4	2																					
OL10D03_101	A3	6.4	2																					
IGF5272c	A3	0.0	10																					
BRMS008_115	A3	6.7	10																					
		12.																						
MAX2_l	A3	8	10																					
BRMS330_241	A3	19.9	10																					
RA2E11_200	A3	42.1	10																					
CB10036_131	A3	43.3	10																					
OL11B05_109	A3	66.4	10																					
NA12E02_118	A3	66.7	10																					
CB10427_138	A3	68.1	10																					
SN11722_93	A3	94.4	10																					
NA10D03_157	A3	106.0	10																					
IGF3100b	A3	108.5	10																					
RGA2_H24_13_150	A3	111.7	10																					
RGA2_H24_14_300	A3	111.7	10																					
CB10320_253	A5	0.0	17																					
BRMS061_284	A5	29.5	17																					
BRAS063	A5	44.	17																					

_236		2											
NA12A05_157	A7	0.0	12										
OL12E03_110	A7	5.4	12										
IGF1226a	A7	42.	12										
		53.	3										
IGF1226f	A7	1	12										
BRMS036_130	A7	85.	12										
		87.	6										
IGF0504f	A7	8	12										
IGF5222b	A9	0.0	18										
IGF5706e	A9	37.	18										
IGF1207c	A9	0	19										
OL12F02_119	A9	1.1	19										
FIT0247_277	A10	0.0	15										
RA2E07_93	A10	5.8	15										
IGF1073a	A10	6.0	15										
KBrB078A03(1)	C1	0.0	11										
BRAS067_136	C1	1.0	11										
NA12H02_219	C1	1.0	11										
SN3734_288	C1	2.1	11										
IGF3338a	C1	15.	11										
		3	11										
IGF0504b	C1	24.	11										
		8	11										
IGF1059e	C1	27.	11										
		1	11										
KBrB036M22(3)	C1	30.	11										
		9	11										
IGF3315b	C1	38.	11										
		1	11										
RA2E11_205	C1	51.	11										
		0	11										
OL12F11_233	C1	52.	11										
		9	11										
MAX_4r	C1	89.	11										
		9	11										
MAX_4n	C1	101	11										
		.2	11										
IGF0568d	C3	0.0	1										
		20.	1										
CALSSR_137	C3	9	1										
SN4513_369	C3	26.	1										
		0	1										
BRAS068_115	C3	42.	1										
		0	1										
CB10299_140	C7	0.0	7										
BRMS296_142	C7	0.1	7										
BRAS019_128	C7	16.	7										
		6	7										
IGF5702e	C7	0.0	16										
		0.0	16										
IGF5707b	C7	7.6	16										

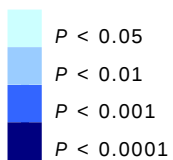
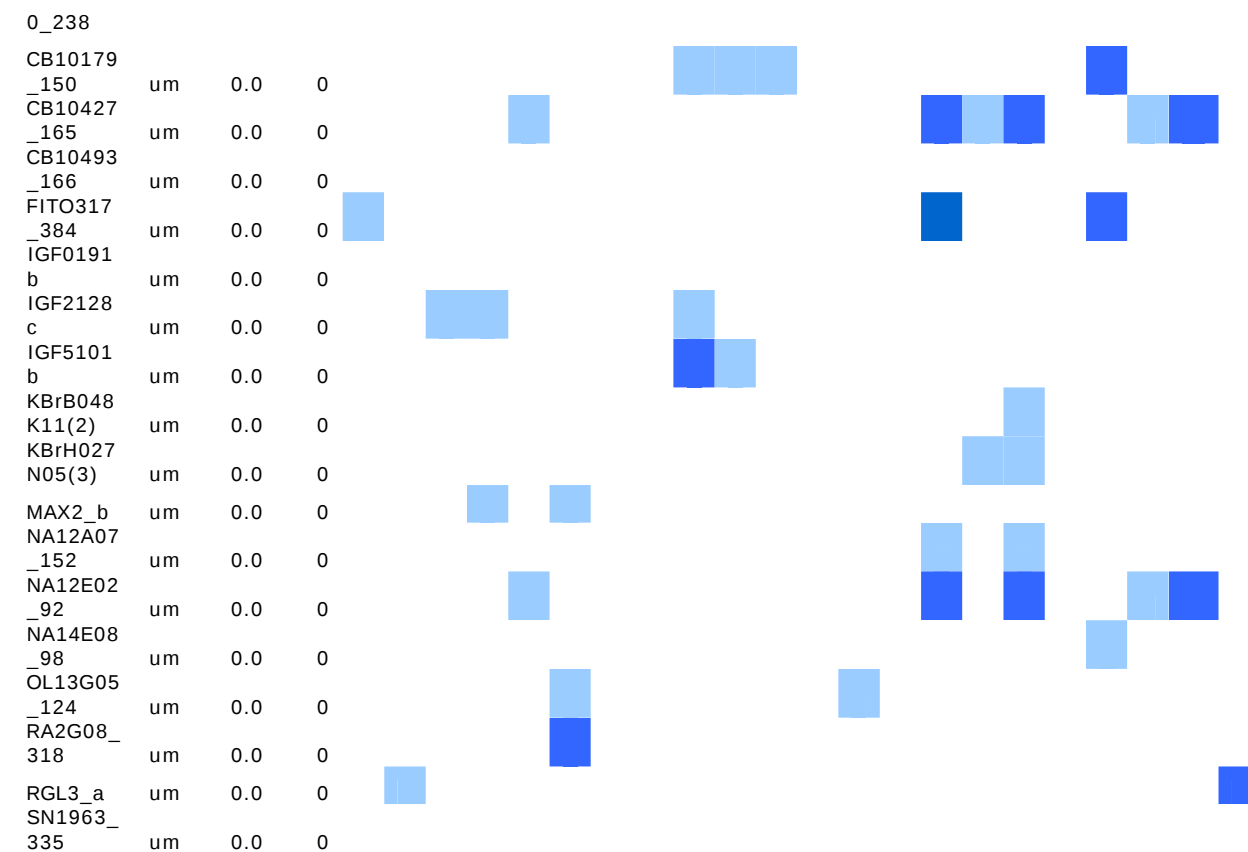


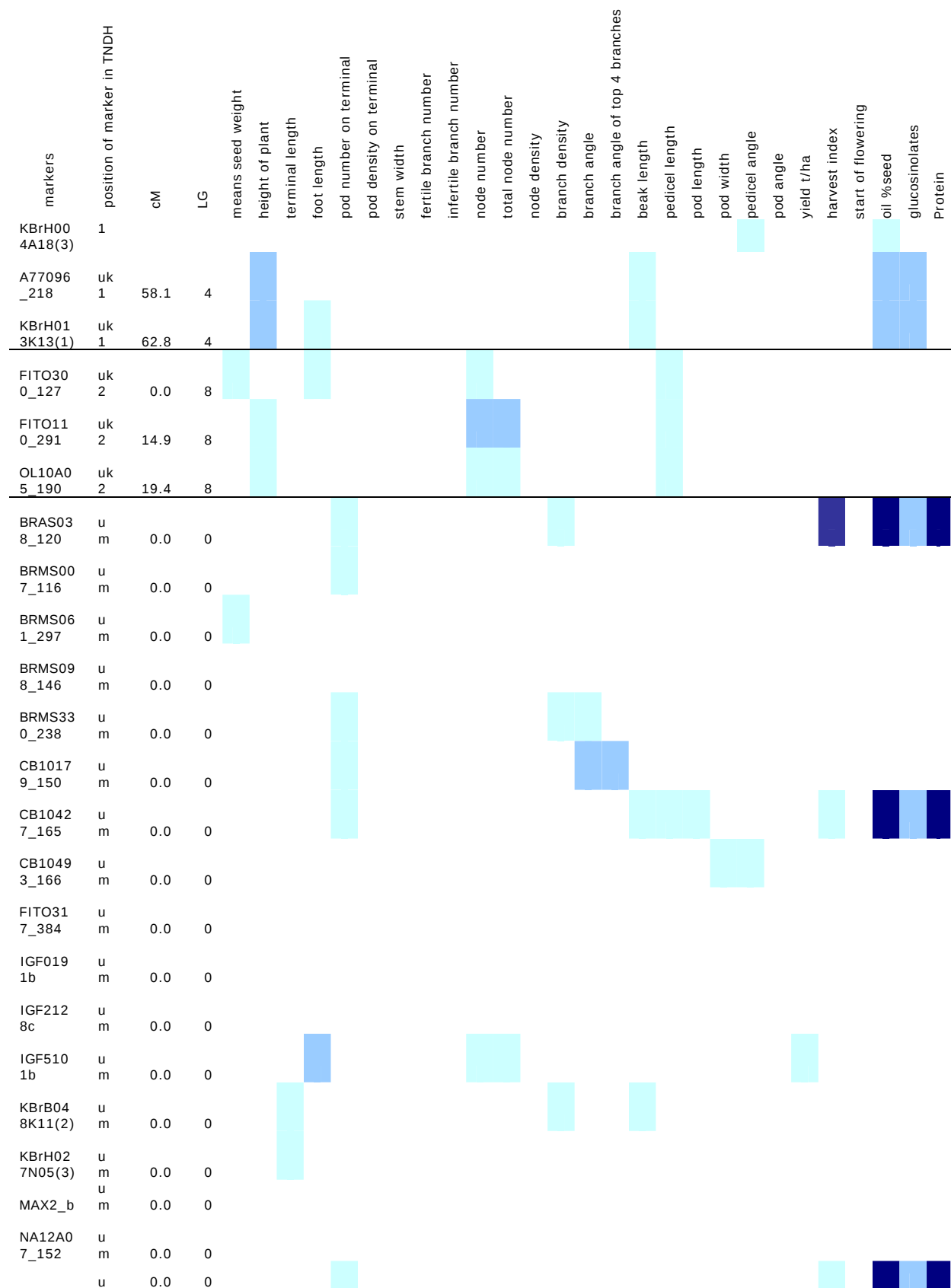
Table 26. Single marker analysis CRDH at Cowlinge 2007-2008.

markers	position of marker in TNDH	cM	LG	means seed weight	height of plant	terminal length	foot length	pod number on terminal	pod density on terminal	stem width	fertile branch number	infertile branch number	node number	total node number	node density	branch density	branch angle	branch angle of top 4 branches	beak length	pedicel length	pod length	pod width	pedicel angle	pod angle	yield t/ha	harvest index	start of flowering	oil %seed	glucosinolates	Protein
SN1164 1_405	A1	0.0	13																											
KBrB04 8F07(2)	A1	2.4	13																											
CB1009 7_191	A1	11.0	13																											
MAX4_p	A1	19.5	13																											
CB1042 7_152	A3	0.0	2																											
BRAS03 8_108	A3	2.4	2																											
BRAS08 7_160	A3	2.7	2																											
SSR18_ 175	A3	4.2	2																											
CB1003 6_160	A3	6.4	2																											
OL10D0 3_101	A3	6.4	2																											
IGF527 2c	A3	0.0	10																											
BRMS00 8_115	A3	6.7	10																											
MAX2_l	A3	12.8	10																											
BRMS33 0_241	A3	19.9	10																											
RA2E11 _200	A3	42.1	10																											
CB1003 6_131	A3	43.3	10																											
OL11B0 5_109	A3	66.4	10																											
NA12E0 2_118	A3	66.7	10																											
CB1042 7_138	A3	68.1	10																											
SN1172 2_93	A3	94.4	10																											
NA10D0 3_157	A3	106. 0	10																											
IGF310 0b	A3	108. 5	10																											

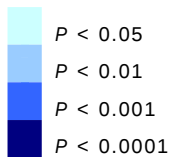
markers	position of marker in TNDH	cM	LG	means seed weight	height of plant	terminal length	foot length	pod number on terminal	pod density on terminal	stem width	fertile branch number	infertile branch number	node number	total node number	node density	branch density	branch angle	branch angle of top 4 branches	beak length	pedicel length	pod length	pod width	pedicel angle	pod angle	yield t/ha	harvest index	start of flowering	oil %seed	glucosinolates	Protein
RGA2_H 24_13_150	A3	111.7	10																											
RGA2_H 24_14_300	A3	111.7	10																											
CB1032 0_253	A5	0.0	17																											
BRMS06 1_284	A5	29.5	17																											
BRAS06 3_236	A5	44.2	17																											
NA12A0 5_157	A7	0.0	12																											
OL12E0 3_110	A7	5.4	12																											
IGF122 6a	A7	42.3	12																											
IGF122 6f	A7	53.1	12																											
BRMS03 6_130	A7	85.6	12																											
IGF050 4f	A7	87.8	12																											
IGF522 2b	A9	0.0	18																											
IGF570 6e	A9	37.0	18																											
IGF120 7c	A9	0.0	19																											
OL12F0 2_119	A9	1.1	19																											
FITO24 7_277	A1 0	0.0	15																											
RA2E07 _93	A1 0	5.8	15																											
IGF107 3a	A1 0	6.0	15																											
KBrB07 8A03(1)	C1	0.0	11																											
BRAS06 7_136	C1	1.0	11																											
NA12H0 2_219	C1	1.0	11																											

markers	position of marker in TNDH	cM	LG	means seed weight	height of plant	terminal length	foot length	pod number on terminal	pod density on terminal	stem width	fertile branch number	infertile branch number	node number	total node number	node density	branch density	branch angle	branch angle of top 4 branches	beak length	pedicel length	pod length	pod width	pedicel angle	pod angle	yield t/ha	harvest index	start of flowering	oil %seed	glucosinolates	Protein
SN3734_288	C1	2.1	11																											
IGF3338a	C1	15.3	11																											
IGF0504b	C1	24.8	11																											
IGF1059e	C1	27.1	11																											
KBrB036M22(3)	C1	30.9	11																											
IGF3315b	C1	38.1	11																											
RA2E11_205	C1	51.0	11																											
OL12F11_233	C1	52.9	11																											
MAX_4r	C1	89.9	11																											
MAX_4n	C1	101.2	11																											
IGF0568d	C3	0.0	1																											
CALSSR_137	C3	20.9	1																											
SN4513_369	C3	26.0	1																											
BRAS068_115	C3	42.0	1																											
CB10299_140	C7	0.0	7																											
BRMS296_142	C7	0.1	7																											
BRAS019_128	C7	16.6	7																											
IGF5702e	C7	0.0	16																											
IGF5707b	C7	7.6	16																											
IGF5415a	C7	22.8	16																											
BRMS008_156	A3/A4	0.0	9																											
IGF5193a	A3/A4	14.2	9																											

markers	position of marker in TNDH	cM	LG	means seed weight	height of plant	terminal length	foot length	pod number on terminal	pod density on terminal	stem width	fertile branch number	infertile branch number	node number	total node number	node density	branch density	branch angle	branch angle of top 4 branches	beak length	pedicel length	pod length	pod width	pedicel angle	pod angle	yield t/ha	harvest index	start of flowering	oil %seed	glucosinolates	Protein
BRMS26 9_313	C3 /A 3/ C8	6.4	3																											
BRAS06 5_219	C3 /A 3/ C8 C3 /A 3/ C8	10.2	3																											
AtTB1_f	C8	13.6	3																											
RGA12_ 30	A2 /A 6	0.0	5																											
RGL12_ 31_300	A2 /A 6	8.5	5																											
CB1041 6_251	A2 /A 6	31.1	5																											
IGF323 9d	A2 /A 6	32.1	5																											
FITO23 2_130	A2 /A 6	44.2	5																											
RA1F06 175	A2 /A 6	65.8	5																											
NA12E0 5_146	A4 /C 4(6)	0.0	6																											
CB1049 3_155	A4 /C 4(6)	3.2	6																											
OL10B0 1_177	A4 /C 4(6)	3.9	6																											
MAX3_ m	A4 /C 4(6)	10.0	6																											
IGF311 2a	A9 /C 5	0.0	14																											
OL12F0 2_148	A9 /C 5	35.5	14																											
NA12D1 0 150	A9 /C 5	36.6	14																											
RA1F06 _190	uk 1	0.0	4																											
CALSSR _142	uk 1	19.0	4																											
SN4513 _366	uk 1	23.5	4																											
	uk	39.4	4																											



markers	position of marker in TNDH	cM	LG	means seed weight	height of plant	terminal length	foot length	pod number on terminal	pod density on terminal	stem width	fertile branch number	infertile branch number	node number	total node number	node density	branch density	branch angle	branch angle of top 4 branches	beak length	pedicel length	pod length	pod width	pedicel angle	pod angle	yield t/ha	harvest index	start of flowering	oil %seed	glucosinolates	Protein
NA12E02_92	m																													
NA14E08_98	u m	0.0	0																											
OL13G05_124	u m	0.0	0																											
RA2G08_318	u m	0.0	0																											
RGL3_a	u m	0.0	0																											
SN1963335	u m	0.0	0																											



($P < 0.0001$) which was coincident for pedicel length (in a different region to those found at Cantelupe). QTL for mean seed weight were seen on A9, C3 ($P < 0.001$) and C1 ($P < 0.01$) while QTL ($P < 0.001$) were found for node associated traits on A9/C5.

Of the candidate genes, MAX 3_m (A4/C4) had a significant QTL ($P < 0.01$) for the number of infertile branches and number of nodes while MAX2_l ($P < 0.01$) was close to a QTL for pedicel length though unlikely to be causal. MAX_4r on C1 and MAX 4_p were only slightly significant ($P < 0.05$) for several traits. RGA2_H24_13_150 (and _300) on A3 were significant for HI ($P < 0.001$) and pod length ($P < 0.01$). AtTB1_f (C3/A3/C8) was coincident with QTL ($P < 0.05$) for branch angles, pedicel length, pod width as well as yield and HI. RGA12_30 and RGL12_31_300 were also variously coincident with QTL ($P < 0.05$) for plant height, branch angles, pod length, pod width, yield and HI.

3.3.6. VGDH (2007-2008)

Trait analysis

As with CRDH, analysis of VGDH for both sites showed that the residual variance was very high for all traits ranging from 76.4% for the number of remaining nodes to 21% for stem width (Table 27). Again, despite this large experimental error variation error, there were highly significant differences between sites and among lines for nearly all the traits measured. Site $\times$ line interactions were significant for most of these traits with the proportion of the total variation accounted for by these ranging from 0 (pod density) to 22.2% (height). The proportion of variation accounted for by differences between the sites ranged from 8.6% (terminal length) to 66.4% (pod number). With so much of the variation accounted for by these factors, trait heritabilities were very low, the highest being those traits either better determined or less affected by the environment *e.g.* the pod associated traits. The VGDH population at Cowlinge suffered similarly to CRDH from uneven establishment and deer and pigeon damage. Plant size and branching was affected similarly. Thus plant size, as determined by basal stem width, was, on average, 38% greater and more variable at Cowlinge than at Cantelupe (1.215cm and 0.88 cm) however, showing similar variation (CV=9.6% and 7.1% respectively) (Table 28). As with the CRDH population it was noticeable that there was large variation for fertile branch number at both sites with more than double the number of fertile branches at Cowlinge than Cantelupe (means = 7.6 and

Table 27. Mean squares and expected mean squares from the analysis of the combined main trials of the VGDH population grown at Cantelupe and Cowlinge in 2007-2008.

Mean squares and Expected Mean Squares					
		line	site	line*site	Residual
Plant traits					
Height	MS	606.2	14020.1	383.2	148.4
	EMS	21.7	14	22.2	42.1
Terminal length	MS	179.03	3393.6	153.18	88.18
	EMS	11.1	8.6	15.8	64.5
Foot length	MS	285.2	58574.4	336.5	173.2
	EMS	4.1	45.7	12	38.2
Pod no. on terminal	MS	284.9	105015.1	228.3	129.2
	EMS	4.6	66.4	5.9	23.1
Pod density	MS	0.3431 ^{ns}	68.858	0.2531 ^{ns}	0.2836
	EMS	1.9	46.2	0	53.9
Stem width at base	MS	0.05463	30.17774	0.04903	0.03105
	EMS	2.7	72.3	4.1	21
Branching traits					
Fertile branch no.	MS	9.341	4099.132	5.908 ^{ns}	4.997
	EMS	3.5	70.7	1.5	24.3
Infertile branch no.	MS	-	-	-	-
	EMS	-	-	-	-
Remaining nodes	MS	1.0063	20.83	0.6447 ^{ns}	0.5615
	EMS	10.1	9.8	3.8	76.4
Total nodes	MS	13.37 [*]	8953.68	16.69	10.34
	EMS	1.1	71	4.7	23.1
Node density	MS	12.591	3840.813	11.0572	7.667
	EMS	3.5	58.6	4.9	33
Branch density	MS				
	EMS	14.134	1108.409	9.717 ^{ns}	7.751
Branch angle	MS	8	29.2	4.9	58
	EMS	42.45	7332.88	39.5	16.12
Branch angle (top 4)	MS	8.1	47.8	14.4	29.7
	EMS	38.74	23108.37	43.52	19.81
		2.8	72.6	7	17.6
Pod traits					
Beak length		0.04974	2.40261	0.01223 ^{ns}	0.01193
	MS	23.5	31.6	0.4	44.5
Pedicel length	EMS	0.15701	5.2897	0.06583	0.02705
	MS	27	23.2	16.1	33.7
Pod length	EMS	1.3385	76.5268	0.3719 [*]	0.2771
	MS	23.4	35.8	4.2	36.7
Pod width	EMS	0.0011661	0.3707867	0.0010155 ^{**}	0.0006992
	MS	3.5	59.8	4.8	31.9
Pedicel angle	EMS	40	1960.35	26.26 ^{**}	18.62
	MS	11.3	21.8	8.1	58.9
Pod angle	EMS	38.85	637.37	20.82	12
		20.7	10.3	13.6	55.5

All *** unless given otherwise.

Table 28. Summary of VGDH trait measurements for the main field trials grown at Cantelupe and Cowlinge in 2007-2008.

	VG Cantelupe						VG Cowlinge					
	mean	min	max	SD	ratio max / min	CV %	mean	max	min	SD	ratio max / min	CV %
Seed traits												
meanseedwt	-	-	-	-	-	-	4.658	5.283	4.284	0.209	1.23	4.49
Plant traits												
Height	128.38	115.1	158.3	7.23	1.38	5.6	121.73	156.7	101.8	8.79	1.54	7.22
Terminal length	42.49	29	65.33	5.57	2.25	13.1	47.71	64.67	25	7.77	2.59	16.29
Foot length	61.99	46.33	77.66	6.54	1.68	10.6	57.35	76.67	42.5	7.81	1.80	13.62
Pod no. on terminal	38.45	26.84	51.25	4.85	1.91	12.6	38.86	54.83	29.17	4.91	1.88	12.64
Pod density	1.1484	0.895	1.591	0.1389	1.78	12.1	1.2063	1.507	0.865	0.116	1.74	9.62
Stem width at base	0.8789	0.6381	1.0016	0.0623	1.57	7.1	0.697	1.1634	0.5526	0.1028	2.11	14.75
Branching traits												
Fertile branch no.	3.7	1.956	5.167	0.514	2.64	13.9	7.562	11.167	3.167	1.386	3.53	18.33
Infertile branch no.	0.4681	0	1.1666	0.2656	*	56.7	0.773	2	0	0.4405	*	56.99
Remaining nodes	12.074	9.67	14.67	1.072	1.52	8.9	17.574	21.17	13.02	1.564	1.63	8.90
Total nodes	16.236	13.83	20.5	1.229	1.48	7.6	25.9	30	20.32	2.04	1.48	7.88
Node density	8.047	6.587	11.79	0.749	1.79	9.3	4.788	7.181	3.95	0.442	1.82	9.23
Branch density	6.698	4.028	11.378	1.459	2.82	21.8	4.704	8.472	3.237	0.798	2.62	16.96
Branch angle	37.91	32.04	44.01	2.46	1.37	6.5	43	50.04	36.52	2.74	1.37	6.37
Branch angle (top 4)	38.46	32.6	44.11	2.45	1.35	6.4	47.51	52.75	41.06	2.77	1.28	5.83
Pod traits												
Beak length	1.1873	1.042	1.438	0.0718	1.38	6.0	1.0946	1.312	0.949	0.0722	1.38	6.60
Pedicle length	1.9694	1.6	2.4	0.1266	1.50	6.4	1.832	2.581	1.562	0.145	1.65	7.91
Pod length	5.715	4.568	6.748	0.385	1.48	6.7	5.194	5.958	4.471	0.37	1.33	7.12
Pod width	0.4089	0.3835	0.441	0.0131	1.15	3.2	0.4452	0.4758	0.4181	0.0139	1.14	3.12

Pedicle angle	81.58	74.53	85.98	2.3	1.15	2.8	84.23	90.06	77.36	2.41	1.16	2.86
Pod angle	160.56	155.2	165.6	2.15	1.07	1.3	162.06	167.1	157.2	2.31	1.06	1.43
Biomass traits												
Yield (t ha ⁻¹)	3.725	2.85	4.67	0.432	1.64	11.6	3.935	4.633	3.114	0.306	1.49	7.78
Harvest Index	0.236	0.123	0.877	0.078	7.13	33.1	0.3108	0.3559	0.0559	0.051	6.37	16.41
Scored traits												
start flower ¹	-	-	-	-	-	-	53.6	58.5	47.5	2.15	1.23	4.01
Autumn vigour ²	-	-	-	-	-	-	5.8	7.5	4.5	0.7	1.67	11.6
Spring vigour ²	-	-	-	-	-	-	4.9	6.5	3.5	0.6	1.86	11.6
Appearance before flowering	-	-	-	-	-	-	4.9	6.5	3.5	0.6	1.86	11.6
Appearance at harvest	-	-	-	-	-	-	5.9	7.5	4.5	0.6	1.67	9.5
Height	-	-	-	-	-	-	131.3	152.5	110	6.9	1.39	5.3
End of flowering ¹	-	-	-	-	-	-	85.5	87.5	82	1.1	1.07	1.3
Flowering period (days)	-	-	-	-	-	-	31.9	38.5	27.5	1.9	1.40	5.9
Seed Storage traits												
% seed oil 0% moisture	-	-	-	-	-	-	50.38	51.4	49.55	0.44	1.04	0.87
GSL µmol/g Fwt	-	-	-	-	-	-	18.577	21.85	14.35	1.419	1.52	7.64
Protein 0% moisture	-	-	-	-	-	-	17.718	18.95	16.7	0.448	1.13	2.53

¹ after 01.03.

² 8=vigourous

3.7 respectively) though once again there was less and similar variability (CV = 30.5% and 47.1%). Again, branches were angled about 5° more vertically at Cantelupe due to the increased effective plant density (37.9° and 43.0° respectively). Pod traits were however basically similar on both sites as these were less directly affected by the problems above. In contrast to CRDH plot yields were, on average, 6% greater at Cowlinge with a similar range of values. Yields of the parents were however greater at Cantelupe with the population showing transgressive segregation, the best lines being 13.2% higher at Cantelupe and 21.7% at Cowlinge than the mean of their parents. HI measurements were not completed, though from the data obtained both sites were very variable with means of 0.24 and 0.31 respectively for Cantelupe and Cowlinge respectively. Transgressive segregation was observed for all traits.

Yield and HI at Cantelupe (Table 29) were not strongly correlated together or with any other trait. This is in contrast to Cowlinge (Table 30), where yield was correlated with HI ($r = +0.345$) and was also associated with traits reflecting rate of development such as the total number of nodes and height ($r = +0.341$ and $+0.296$ respectively). Yield was also negatively correlated with beak and pod lengths ($r = -0.289$ and -0.367 respectively), as was also observed for the CRDH population, thus short pods yielded more highly than long ones. HI was also positively correlated, as was yield, with the total number of nodes ($r = +0.358$) and negatively with density ($r = -0.423$) though yield was not. Thus yield was associated with ($r = +0.296$) with height and node number but negatively with node density. Coefficients of determinations are summarised in supplementary tables 15 and 16). Long pods were associated with horizontal pods ($r = +0.531$ and $+0.598$).

QTL analysis

Of the 14 polymorphic markers in the VGDH population six were candidate genes (Table 6). More SM QTL, with higher levels of significance, were observed at Cowlinge than at Cantelupe (Table 31 and 32 and Supplementary tables 17 and 18). The only marker which showed a significance level greater than 0.001 was unmapped RGA3_M18.33_250 for beak length ($P < 0.00732$) at Cowlinge with a probability of $P = 0.06$ at Cantelupe. Four of the markers putatively mapped to A6 and four to A7. At Cowlinge there was little evidence of QTL on A7 but, however on A6, IGF1027z was significant for foot length, pod length and pedicel angle (and also height, pod and

Table 29. Correlation matrix for VGDH at Cantelupe, 2007-2008.

	Height	Terminal length	Foot length	Pod no.	Pod density	Stemw	Fertile branches	Infertile branches	Nodes	Total nodes	Node density	Branch density	Branch angle	Branch angle - top 4	Beak length	Pedicle length	Pod length	Pod width	Pedicle angle	Pod angle	Yield t/ha	HI
Terminal length	0.651																					
Foot length	0.302	0.105																				
Pod no.	0.288	0.61	0.164																			
Pod density	0.385	0.411	0.064	0.405																		
Stemw	0.374	0.225	0.303	0.257	0.052																	
Fertile branches	0.009	0.135	-0.46	0.172	0.384	0.494																
Infertile branches	0.164	0.014	0.248	0.165	0.178	0.014	0.175															
Nodes	0.104	0.091	0.423	0.075	0.221	0.101	0.098	0.087														
Total nodes	0.05	0.134	0.125	0.176	0.396	0.118	0.468	0.068	0.898													
Node density	0.624	0.552	0.087	0.088	0.558	0.143	0.363	0.136	0.616	0.722												
Branch density	0.295	0.073	0.439	0.143	0.279	0.401	0.051	0.223	0.401	0.281	0.415											
Branch angle	0.233	0.263	0.102	0.262	0.032	0.075	0.019	0.091	0.266	0.222	0.022	0.064										
Branch angle - top 4	0.239	0.268	0.168	0.195	-0.11	0.121	0.105	0.139	0.207	0.108	0.103	0.062	0.976									
Beak length	0.183	0.103	0.239	0.189	0.119	0.035	0.065	0.052	0.121	0.146	0.215	0.128	0.007	0.041								
Pedicle length	0.064	0.113	-0.03	0.049	0.113	0.054	0.213	0.163	0.327	0.341	0.297	0.099	0.251	0.2	0.157							
Pod length	0.182	-0.28	0.128	0.163	0.052	-0.13	0.137	0.019	0.066	-0.11	0.067	0.003	0.096	0.072	0.38	0.283						
Pod width	0.485	0.234	0.192	0.031	0.277	0.432	0.037	0.119	0.071	0.102	0.39	0.263	0.036	0.003	0.36	0.153	-0.04					
Pedicle angle	0.035	0.001	0.023	0.018	0.129	0.012	0.058	0.046	0.033	0.014	0.025	0.129	0.356	0.343	0.276	0.191	0.001	0.095				
Pod angle	0.203	0.282	0.119	0.072	0.231	0.191	0.106	0.098	0.012	0.035	0.123	0.083	0.152	0.153	0.164	0.256	0.531	0.145	0.187			
Yield t/ha	0.041	0.006	0.145	0.116	0.134	0.095	0.114	0.073	0.072	0.004	0.045	0.217	0.019	0.043	0.164	0.071	0.098	0.033	0.095	0.036		
HI	0.145	0	0.046	0.034	0.047	0.143	0.204	0.056	0.097	0.022	0.107	0.166	0.029	0.055	0.115	0.072	0.018	0.109	0.104	0.178	0.188	

df = 92

$P \leq +0.001$

$P \leq +0.01$

$P \leq +0.05$

$P \leq -0.001$

$P \leq -0.01$

$P \leq -0.05$

Table 30. Correlation matrix for VGDH at Cowlinge, 2007-2008 (split in 2 to fit on page).

[illegible]

Table 31. Single marker analysis VGDH at Cowlinge, 2007-2008.

			means seed weight	height of plant	terminal length	foot length	pod number on terminal	pod density on terminal	stem width	fertile branch number	infertile branch number	node number	total node number	node density	branch density	branch angle	branch angle of top 4 branches	beak length	pedicel length	pod length	pod width	pedicel angle	pod angle	yield t/ha	harvest index	start of flowering	oil %seed	glucosinolates	Protein
position of marker in TNDH	cM	marker																											
A7	95	DELLA_GRA																											
A6	52*	GAI23.6																											
A6	34.5	IGF1027z																											
A6	66.2	IGF1075d																											
A6	66	IGF1075e																											
A7	35.1*	IGF1178b																											
A7	107.7	IGF1226a																											
A7	99.2	IGF1226f																											
A10	41	IGF5101b																											
A3	4.7	IGF5272c																											
np	-	RGA12_3																											
np	-	RGA12_30																											
np	-	RGA12_31																											
np	-	RGA3_M18.33_250																											

$P < 0.05$

$P < 0.01$

$P < 0.001$

Table 32. Single marker analysis VGDH at Cantelupe, 2007-2008.

			height of plant	terminal length	foot length	pod number on terminal	pod density on terminal	stem width	fertile branch number	infertile branch number	node number	total node number	node density	branch density	branch angle	branch angle of top 4 branches	beak length	pedicel length	pod length	pod width	pedicel angle	pod angle	yield t/ha	harvest index
position of marker in TNDH	cM	marker																						
A7	95	DELLA_GRA																						
A6	52*	GAI23.6																						
A6	34.5	IGF1027z																						
A6	66.2	IGF1075d																						
A6	66	IGF1075e																						
A7	35.1*	IGF1178b																						
A7	107.7	IGF1226a																						
A7	99.2	IGF1226f																						
A10	41	IGF5101b																						
A3	4.7	IGF5272c																						
np	-	RGA12_3																						
np	-	RGA12_30																						
np	-	RGA12_31																						
np	-	RGA3_M18.33_250																						

$P < 0.05$ $P < 0.01$

branch density at $P < 0.05$) – associated with length while IGF1075c for stem width and infertile branch number at $P < 0.01$ (and also fertile branch number and pod angle at $P < 0.05$). These markers appeared to be indicative of separate QTL. When these SM QTL were compared to those at Cantelupe, only branch and foot length were present at both sites for IGF1027z while IGF1075c was only significant at both sites for fertile branch number.

3.4. Discussion

The results described in this report show clearly that, within all three populations studied, there is considerable variation for all of the traits assessed and which, additionally, show values above and below those observed for the parental and the control varieties. This variation was greatest where the genetic distance between the parents, as indicated by polymorphism rate, was maximised. Thus the variation observed in TNDH, which was developed from European and Chinese germplasm, exceeds that of CRDH which in turn exceeds that of VGDH which were both developed from relatively modern UK-adapted cultivars. These populations are a new addition to the genetic resources available for the plant breeder. The large number of QTL observed unique to one environment indicate that traits associated with canopy architecture are extremely responsive to environmental variation. This sensitivity was also observed in the large residual errors determined and low calculated heritabilities of the traits. Much of this environmental variation came from disparities in plant establishment and consequent variation in plant density, resulting in competition between plants, and also from the effects of pests and diseases. Many QTL have been observed for each trait indicating that they are subject to complex polygenic genetic control with many potential pleiotropic and epigenetic factors complicating their expression. Because of these factors it would be expected that the proportion of the trait variation attributed to any one QTL would be low while the statistic associated with the determination of the QTL likely to be equally low. This makes the determination of these traits difficult with likely problems of false positive QTL while many real QTL are missed.

Though QTL for yield were observed, QTL for harvest index were not detected for which two possible reasons are suggested. Firstly, it was difficult to get accurate estimates of harvest index because of the problems of premature pod shatter.

Secondly, harvest index is determined by the sum effect of many independently controlled traits but the plant has the capacity to compensate for changes in one trait by a corresponding change in another. These changes are usually negatively correlated and are particularly evident among the components of yield. Thus, though much variation was seen in individual traits their individual effects may have been cancelled out in the final determination of harvest index.

The large number of QTL identified in this study may result from the presence of homologous loci of which there may be up to six as a result of the genetic composition of *B. napus* but may also result from several different genes controlling the same trait. Indications for the former may be seen where QTL are coincident on homologous regions of the genome, as suggested from studies with *Arabidopsis*, such as A6 and C6 for pod length and on A4, A7, C8 and C9 for pedicel length. Where there are no apparent homologies unique genes are indicated.

From our results therefore, and despite the inherent environmental effects and errors associated with field data, we have been able to identify major genetic components for most of the traits. Our results confirm the view that the basis of these genetic components is complex, typically consisting of contributions from many different QTL, each having only a small effect which are distributed throughout the genome. The peak position of several of these QTL were coincident, within 2cM, of the positions of markers for genes which have been identified from studies in *A. thaliana* as potential candidates for being involved in the control of the traits. Among these, for example, markers for *TB-like*, *TCP* and *Blr* were found close to the peaks of QTL for 'length' traits; *GAI*, *RGL1* and *MAX2* to branch and pod angles; *Blr* to fertile branch number and pod density; *RGL1* to seed density and *GAI* to stem width. These represent the bases for hypotheses to be tested in future studies. Despite these potential links, no QTL were observed for the majority of the candidate genes tested in these studies because, they were either not important in these populations or that we have been unable to resolve the data sufficiently. However, in this study we have only tested a limited selection of candidate genes that influence architectural traits in *A. thaliana* and it was therefore not surprising that we identified numerous QTL that did not correspond to the positions of those that we had selected.

Our results directly focus upon specific known genes that may be involved in the control of aspects of canopy architecture that are likely to impact on seed yield. In addition, they indicate that studies conducted to date in *A. thaliana*, which used mutation-based approaches, should be supplemented with studies exploiting natural genetic variation in order to assist the identification of the genes underlying many of the important loci that we have identified in oilseed rape. Repeated field trials under a greater range of environments will help to identify which of the putative QTL identified in this study are of most significance in determining trait expression.

3.5. References

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3.6. Supplementary Tables

Supplementary Table 1. Summary of marker development.

Pop.	locus	Technique	Source of problem					JIC/BGA comparison			
			Amplification problem	Monospecific sequences	Multiple sequences/uuuuu peaks	Multi-band PCR profile	No polymorphisms on gel	No PCR primers	Different sequences	Paralogous sequences	Identical sequences
CRDH	IGF0235b	Polarisation		x			x		x		
	IGF3222b	Polarisation		x			x		JIC sequence missing		
	IGF3369a	Polarisation	x								
	IGF1072c	Polarisation	x								
	IGF1578a	Polarisation		x			x		JIC sequence missing		
	IGF3165b	Polarisation			x		x		JIC sequence missing		
VGDH	IGF9014a	Polarisation		x			x				x
	IGF3112a	Polarisation		x			x				x
	IGF1072c	Polarisation		x			x				x
	IGF3134a	Polarisation				x	x				

Supplementary Table 2. Library details.

Gene	AGI code	<i>B. napus</i> library details		<i>B. rapa</i> library details	
		No. of loci	No. with primers	No. of contigs or KBrH BACs	No. with primers
TCP	At4g18930	8	6		
AtTB1	At1g53230	8	7	2	2
Bp	At4g08150	19*	9		
Blr	At5g0203	11	8		
MAX1	At2g26170	10	7		
MAX2	At2g42620	11	8		
MAX3	At2g44990			15*	10
MAX4	At4g32810			20*	16
GAI	At1g14920			2	1
RGA	At2g01570			4	1
RGL1	At1g66350			2	1
RGL2	At3g03450			1	1
RGL3	At5g17490			1	1
DELLA + GRAS				2	0
DELLA				3	1

* *in silico* data

Supplementary Table 3. Marker problems.

Pop.	locus	Technique	Source of problem						JIC/BGA comparison		
			Amplification problem	Monospecific sequences	Double sequences/double peaks	Multi-band PCR profile	No polymorphisms on gel	No PCR primers	Different sequences	Paralogous sequences	Identical sequences
TNDH	Max2_l	INDEL				x	x				
	Bellringer_d	Polarisation	x								
	Max_3b	INDEL			x		x		Double sequences		
	Max_3c	Polarisation				x	x				
	Max_3e	INDEL				x	x				
	Max_4n	INDEL		x			x		x		
	RGA_a	INDEL	x								
	RGL3_a	INDEL		x			x		JIC sequence missing		
	DELLA_b	INDEL			x		x		Double sequences		
RCDH	AtTB1_a	Polarisation		x			x				x
	MAX_2d	Polarisation		x			x				x
	MAX_2g	Polarisation		x			x			x	
	Bellringer_a	Polarisation		x			x		x		
	MAX_3l	INDEL					x		JIC sequence missing		
	MAX_4o	INDEL	x								
	GAI_b	INDEL				x	x				
	RGA_d	Polarisation		x			x		JIC sequence missing		
	DELLA_b	Polarisation & INDEL			x		x		Double sequences		
VGDH	AtTB1_f	Polarisation			x		x				x
	MAX_2a	Polarisation		x			x				x
	MAX_2b	INDEL			x		x		x		
	MAX_2d	Polarisation		x			x				x
	MAX_2l	Polarisation & INDEL		x			x		x		
	Brevipedicellus	Polarisation		x			x		JIC sequence missing		
	Bellringer_c	INDEL	x								
	Bellringer_d	Polarisation	x								
	MAX_3g	Polarisation		x			x				x
	MAX_3m	Polarisation			x		x				x
	MAX_3n	Polarisation			x		x			x	
	MAX_3o	Polarisation						x			
	MAX_4n	Polarisation			x		x		Double sequences		
	GAI_b	INDEL				x	x				
	RGA_d	Polarisation		x			x				x
	RGL3_a	INDEL		x			x		JIC sequence missing		
	DELLA_b	INDEL			x		x		Double sequences		

Supplementary Table 4. Coefficients of determination matrix for Spalding 2005-2006.

[illegible]

Supplementary Table 5. Variance ratios and Expected Mean Squares for TNDH grown at Barton and Cowlinge in 2007.

Source of variation	Residual MS 1	Variance Ratios (% expected mean squares)						
		line ²	site ³	block ⁴	line.site ⁵	line.block ⁶	site.block ⁷	line.site.block ⁸
seed wt	0.03097	5.64***	1.69	3.15	2.33***	2.07***	5.18*	
	53.2	24.6	0.2	0.3	3.6	1.3	0.6	16.3
pod harvest index	0.001289	5.62***	23.09***	2.01	2.48***	2.09***	0.1	1.85***
	52	23.8	2.1	0.2	5.4	2	-0.3	14.8
seeds per pod	11.81	6.56***	43.41***	3.61	2.5***	1.83***	0.09	1.81***
	49.9	26.8	3.8	0.3	5.8	0.1	-0.3	13.5
density of seeds in pod	0.2723	7.35***	16.17***	4*	2.21***	2.07***	0.17	1.97***
	49.6	30.1	1.4	0.4	2	0.8	-0.3	16
mean seed weight	4.29E-07	7.89***	112.87***	0.11	2.13***	2.38***	10.27***	2.02***
	43.5	28.3	8.7	0	0.8	2.6	1.3	14.8
plant height	80.2	15.66***	0.01	68.31***	4.12***	3.96***	24.7***	2.99***
	28.7	36.6	0	3.5	5.4	4.6	2.2	19.1
length of terminal branch	36.73	6.59***	2.21	14.54***	2***	1.38*	1.12	1.24
	55.7	29.9	0.2	1.4	7	1.3	0	4.5
length of foot	138	8.93***	39.29***	2.43*	2.2***	2.48***	8.5**	2.07***
	43.9	32.3	3.1	0.2	0.9	3	1	15.6
number of fertile branches	2.706	3.97***	6.83**	6.28*	1.86***	1.44**	0.1	1.12
	64.5	20.4	0.8	0.7	7.9	3.5	-0.2	2.5
number of infertile branches	0.705	2.11***	204.8***	8.38**	1.78***	2.26***	17.32***	1.32*
	51.8	8.1	18.8	0.7	4	8.1	2.9	5.6
total number of nodes	16.5	3.87***	116.03***	23.62***	3.05***	2.44***	6.07*	1.55**
	46.9	13.6	9.6	1.9	11.7	7	0.8	8.5
branch density	0.0002284	7.42***	57.08***	2.98	2.07***	1.56**	1.04	1.31
	50.5	30.5	5.1	0.3	6.4	2.1	0	5.2
pod number on terminal raceme	79.72	7.57***	335.1***	47.2***	2.54***	2.3***	0.25	2.76***
	35.9	23	21.4	3	-1.3	-2.7	-0.3	21.1

Source of variation	Residual MS ¹	Variance Ratios (% expected mean squares)						
		line ²	site ³	block ⁴	line.site ⁵	line.block ⁶	site.block ⁷	line.site.block ⁸
beak length	0.02077	12.06***	405.4***	0.63	2.45***	2.5***	0	1.94***
	31.3	31	22.5	0	2.7	2.9	-0.2	9.8
branch angle - top 4 only	19.66	6.3***	210.11***	0.13	1.97***	1.98***	43.5***	1.8***
	42.3	22	15.7	0	1.2	1.2	6.3	11.3
pedicel angle to raceme	24.21	10.5***	4.13*	2.21	2.1***	2.09***	2.95	1.73***
	44.5	38.5	0.3	0.2	2.8	2.7	0.2	10.9
pod angle to pedicel	11.95	11.36***	58.19***	1.94	2.86***	2.52***	0.1	1.76***
	38.7	35.6	4	0.1	7.1	4.9	-0.2	9.7
pod angle to raceme	42.18	11.74***	6.36**	3.49	2.63***	2.76***	1.29	1.72***
	39.5	37.6	0.4	0.2	6	6.8	-0.1	9.5
pedicel length	0.03265	11.97***	0.42	20.5***	2.86***	3.27***	2.25	2.52***
	37	36.3	0	1.3	2.1	4.6	0	18.8
pod length	0.23	8.83***	79.9***	6.63**	3***	2.28***	0.76	1.7**
	41.6	29.5	5.9	0.5	9	4	-0.1	9.7
pod width	0.0004672	9.35***	966.96***	8.11**	3.14***	3.02***	1.99	2.23***
	23.9	18.1	41	0.3	3.6	3.1	0	9.8
stem base width*	0.04713	2.37***	3.05	18.54***	1.28	1.68***	1.75	1.21
	71.9	13.7	0.4	2.4	0.8	5.6	0.1	5

number of replications = 3

¹ residual df = 637(577-678)

² line df = 93

³ site df = 2

⁴ block df = 2

⁵ line.site = 2

Supplementary Table 6. Mean squares and h² from ANOVA for blocks separately at Barton and Cowlinge for TNDH 2006-2007.

	Block	Barton								Cowlinge							
		1				2				1				2			
		Source of variation	df	ms	h ²	df	ms	h ²	df	ms	h ²	df	ms	h ²	df	mean	h ²
seed weight	line		88	0.0929***	42.6	91	0.08057***	32.9	88	0.07357***	38.9	89	0.10021***	36.1	37.6		
	Residual		167	0.02877		175	0.03258		163	0.0253		163	0.03716				
pod HI	line		88	0.003545***	41.9	91	0.004624***	42.2	88	0.0028521***	48.7	89	0.00353***	23.4	39.1		
	Residual		167	0.001122		174	0.001448		163	0.0007403		163	0.00184				
seed per pod	line		88	42.57***	45.9	91	36.4***	38.8	89	28.134***	38.5	89	36.08***	37.3	40.1		
	Residual		165	12		176	12.54		166	9.767		157	12.95				
seed density	line		72	1.0425***	43.9	90	0.851***	39.7	83	0.6317***	38.4	88	0.801***	38.7	40.2		
	Residual		133	0.311		167	0.2859		155	0.2202		155	0.2766				
mean seed weight	line		88	0.0000011***	48	91	0.000002107***	36.7	88	0.000001181***	47.2	89	0.000001537***	58.1	47.5		
	Residual		165	3.03E-07		173	7.70E-07		160	3.20E-07		157	2.98E-07				
fertile branches	line		86	4.629***	17.1	91	4.191***	20	89	6.059***	25.7	90	6.434***	32.6	23.8		
	Residual		162	2.86		179	2.393		165	2.976		169	2.625				
infertile branches	line		86	0.578ns	2.9	91	0.4627ns	0.2	89	1.398*	12.1	90	1.8934***	28.8	11		
	Residual		164	0.5305		179	0.46		165	0.9889		170	0.8559				
rest nodes	line		85	26.24***	33.8	88	20.981***	30.1	87	24.77***	28.5	90	49.11***	46.8	34.8		
	Residual		143	10.37		156	9.16		146	11.29		155	13.48				
total nodes	line		85	29.99***	21.6	88	24.55***	25	87	36.47***	28.2	90	62.78***	40.6	28.8		
	Residual		141	16.44		156	12.28		146	16.75		154	20.58				
branch angle top 4	line		72	64.88***	36.2	91	52.16***	36.3	84	49.73***	38.6	88	44.96***	31.6	35.7		
	Residual		137	23.99		175	19.23		156	17.23		169	18.83				
pedicel angle	line		72	79.18***	45.3	91	98.17***	50.5	84	98.45***	49.4	88	87.02***	45.9	47.8		
	Residual		135	22.74		171	24.2		164	25.04		165	24.58				
pod angle	line		72	54.64***	51	91	59.19***	58.4	84	44.851***	58.5	88	47.68***	42.4	52.6		
	Residual		135	13.26		171	11.36		164	8.588		165	14.85				
plant height	line		85	445.15***	58.9	88	364.92***	50.5	87	447.36***	59.5	90	557.08***	71.7	60.1		

	Block	Barton							Cowlinge						
		1			2				1			2			
		Source of variation	df	ms	h ²	df	ms	h ²	df	ms	h ²	df	ms	h ²	mean h ²
terminal length	Residual	144	84.14			155	89.83			148	82.86		159	64.75	
	line	86	112.36***	34.7		91	86.27***	24.5		89	94.89***	39.7	90	99.06***	36.2
pod number on term	Residual	160	43.35			172	43.75			170	31.86		161	27.78	
	line	86	202.56***	36.3		91	260.4***	47.4		89	328.55***	47.5	90	317.25***	44.7
foot length	Residual	158	74.85			169	70.36			171	88.53		161	84.98	
	line	86	448.9***	45.7		88	377.3***	40.2		87	551.5***	44	90	601.8***	45.8
	Residual	145	127.5			158	125.1			150	164.1		159	135.9	
beak length	line	72	0.09146***	48.7		91	0.11123***	49.2		84	0.07927***	65.9	88	0.08638***	54.3
	Residual	134	0.02375			171	0.02846			163	0.01165		165	0.01941	
pedicel length	line	72	0.15899***	54.8		91	0.13567***	49.6		84	0.1291***	50.6	88	0.16947***	53.8
	Residual	135	0.03431			171	0.03437			164	0.03172		165	0.03041	
pod length	line	72	0.854***	53.6		91	0.8765***	46.9		84	0.8018***	51.9	88	0.8463***	47.8
	Residual	135	0.1911			171	0.2404			164	0.1894		165	0.2913	
siliqua length	line	72	1.32***	54.5		91	1.3367***	50.4		84	1.0993***	54.5	88	1.2217***	49.9
	Residual	134	0.2871			171	0.3302			163	0.2396		165	0.4032	
pod width	line	73	0.0015795***	43.8		91	0.0024592***	55.5		84	0.0014605***	44.3	88	0.0018431***	48.7
	Residual	135	0.0004727			171	0.0005184			164	0.0004312		165	0.0004452	
stem base	line	70	0.0722**	22.7		89	0.06023 ^{ns}	1.6		82	0.06154***	21.7	88	0.07501*	14.1
	Residual	116	0.03837			156	0.05741			143	0.0336		162	0.05543	

Supplementary Table 7. Coefficients of determination matrix for Cowlinge 2006-2007 (Split in 3 to fit on page).

[illegible]

Branch angle (top 4)	6.9	7.5	0.4	4.8	2.8	0.4	1.8	1.2	8.7	2.2	5.6	0.5	1.5	0.6	1	0.3	0	1.1
Beak length	17	15.2	1.4	1.6	15.9	6	13.7	14.1	11.3	0	8.8	0.1	5.5	1	1.4	0	4.9	13
Pedicel length	8.5	1.8	7.7	3.5	2.5	0	11.8	4	11	0.5	0.7	2.8	1.5	1.7	7.9	4.9	0	0.3
Pod length	31.7	28.2	3.9	0	40.3	4.2	15.4	3.9	27.8	2.7	0	2.4	7.7	0.5	1.9	0	4.7	4.8
Silique length	35.2	31.4	4	0.1	42.4	5.9	19.2	7.6	29.4	2	0.4	2	9.1	0.8	2.3	0	6.2	8.3
Pod width	30.1	36.4	1.2	28.9	9.5	7.4	1.6	0.2	3	0.5	0.3	1.2	0.1	1.2	0.1	0.3	1.1	0.4
Pedicel angle	15.3	12.3	3.7	4	8.6	2	4.6	1.8	9.8	11	6.8	1.2	9.2	0.4	0.8	3.8	7.7	4.7
Pod angle	14.7	17.4	0.3	1.7	11.7	1.7	0.3	0	8	2.5	1.9	9.4	10.5	8.9	0	2.5	2.9	8.4
Angle to rachis	24	22.8	3	4.6	15.7	3	3.6	1.2	14.4	10.7	7.1	5.8	15.6	4.3	0.3	5.2	8.6	9.7
Yield	13.2	12.1	0.8	0	17.1	12.5	3.7	7.6	11.4	13	2	7.5	15	8.1	0.4	1.9	3.5	18.4
Harvest Index	0.9	6.3	8.5	8.6	0.6	4.9	2.4	0.5	0.3	0	0.1	1.6	0	1.5	0.6	0.9	0.1	0
Canker	2.3	2.7	0.3	0	4.4	2.9	0.1	5.6	0.8	4.9	0.1	9.4	7.2	10.6	1.2	0.3	0	14.7
Start of flowering	5.5	5.7	0.1	0.9	13.4	6	6.8	7	16.3	7.8	0.3	8.4	17.4	5.1	3.6	0	2.5	16.4
Maturity	14.8	14.6	0.3	0.7	16.4	7.2	6.7	17	9.5	5.9	0.8	7.6	11.2	13	3.4	0	2.2	27.1
Flowering period	0.6	0	3.3	0.3	0.3	0	3.4	2	1.1	0	1.4	1.1	0.2	2.4	0.1	0.1	2.2	1.2
Oil	0	0	0.6	7.6	5.5	5.4	0.3	0	0.1	1.3	1.1	9.1	0.1	0.4	1.8	2.1	0.8	0
Glucosinolate	5.9	5.6	0.2	1.1	5.4	7.4	1.9	5.3	1.9	2.6	0.1	3	3.2	7.2	2	0	0.3	11.8
Protein	6.6	4.6	1.2	0.7	14	12.5	2.2	11.2	3.7	5.9	0.3	2.9	8.9	9.1	0.8	0.6	1.7	19.6
	Seed wt.	Pod wt.	Pod HI	Mean seed wt.	Seed number/pod	Seed Density	Plant height	Terminal length	Foot length	Pod no. on terminal	Pod density	Stem width at base	Fertile branches	Infertile branches	Rest nodes	Total nodes	Node density	Branch density

Supplementary Table 8. Correlation matrix, adjusted for stem canker as a covariate, Cowlinge 2006-2007 (split in 3 to fit on page).

Pod wt.	0.844																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
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Branch density	-0.31	-0.267	-0.088	-0.178	-0.251	-0.143	-0.438	-0.635	-0.341	-0.289	0.237	0.203	0.69	0.364	0.047	0.338
Branch angle	0.338	0.314	0.106	0.199	0.284	0.128	0.209	0.063	0.419	0.254	0.21	-0.211	-0.387	-0.103	0.082	-0.075
Branch angle (top 4)	0.309	0.304	0.098	0.232	0.212	0.076	0.214	-0.017	0.337	0.219	0.241	-0.09	-0.154	0.077	0.139	0.082
Beak length	0.438	0.405	0.143	0.146	0.417	0.241	0.424	0.407	0.37	0.067	-0.282	-0.014	-0.237	-0.071	0.148	0.034
Pedicle length	0.326	0.177	0.296	0.188	0.211	0.021	0.322	0.251	0.348	0.118	-0.083	0.093	-0.206	0.049	0.313	0.211
Pod length	0.586	0.544	0.221	0.013	0.65	0.203	0.447	0.249	0.553	0.215	0.03	-0.15	-0.286	-0.046	0.168	0.035
Silique length	0.617	0.573	0.227	0.052	0.665	0.238	0.497	0.324	0.571	0.202	-0.053	-0.13	-0.308	-0.06	0.183	0.039
Pod width	0.522	0.59	0.101	0.534	0.295	0.266	0.105	0.031	0.159	0.051	0.051	-0.102	-0.018	-0.107	-0.04	-0.056
Pedicle angle	0.414	0.367	0.21	0.212	0.315	0.146	0.262	0.176	0.339	0.36	0.266	-0.11	-0.317	-0.056	-0.063	-0.171
Pod angle	0.434	0.432	0.104	0.169	0.366	0.107	0.221	0.107	0.352	0.237	0.149	-0.254	-0.306	-0.215	0.069	-0.085
Angle to rachis	0.526	0.492	0.206	0.241	0.42	0.162	0.305	0.182	0.429	0.383	0.269	-0.213	-0.389	-0.154	-0.008	-0.166
Yield	0.455	0.386	0.146	0.089	0.444	0.303	0.433	0.37	0.45	0.459	0.165	-0.15	-0.336	-0.106	0.128	-0.026
Biomass	0.266	0.186	0.212	0.232	0.142	0.278	0.287	0.212	0.092	0.169	0.003	0.157	0.133	-0.113	0.33	0.33
Straw	0.275	0.201	0.206	0.252	0.139	0.266	0.31	0.221	0.101	0.173	-0.001	0.158	0.141	-0.114	0.334	0.335
Canker (after covar)	0.024	-0.087	0.209	-0.142	0.114	0.277	-0.109	-0.016	-0.03	0.05	0.075	0.052	-0.042	-0.011	0.104	0.079
	Seed wt.	Pod wt.	Pod HI	Mean seed wt.	Seed number/pod	Seed Density	Plant height	Terminal length	Foot length	Pod no. on terminal	Pod density	Stem width at base	Fertile branches	Infertile branches	Rest nodes	Total nodes

Branch density	-0.57															
Branch angle	0.164	-0.264														
Branch angle (top 4)	0.022	-0.014	0.857													
Beak length	0.249	-0.394	0.121	-0.005												
Pedicle length	0.009	-0.174	0.015	0.047	0.153											
Pod length	0.244	-0.277	0.365	0.312	0.444	0.386										
Silique length	0.276	-0.344	0.343	0.263	0.652	0.369	0.969									
Pod width	0.098	-0.038	0.142	0.162	0.127	0.131	0.163	0.173								
Pedicle angle	0.295	-0.272	0.46	0.474	0.121	0.183	0.403	0.375	0.256							
Pod angle	0.223	-0.314	0.488	0.337	0.38	0.113	0.531	0.554	0.189	0.273						
Angle to rachis	0.329	-0.361	0.587	0.517	0.289	0.19	0.57	0.562	0.283	0.86	0.726					
Yield	0.28	-0.441	0.436	0.293	0.295	-0.056	0.365	0.392	0.079	0.243	0.536	0.459				
Biomass	-0.136	-0.084	0.088	0.166	0.076	0.019	-0.087	-0.053	0.064	0.104	-0.079	0.033	0.157			
Straw	-0.126	-0.092	0.082	0.166	0.089	0.034	-0.079	-0.042	0.069	0.099	-0.066	0.036	0.157	0.998		
Canker (after covar)	-0.169	0.033	0.147	0.117	-0.08	-0.183	-0.119	-0.122	0.013	0.101	-0.151	-0.007	0.118	0.457	0.401	
	Node density	Branch density	Branch angle	Branch angle (top 4)	Beak length	Pedicle length	Pod length	Silique length	Pod width	Pedicle angle	Pod angle	Angle to rachis	Yield	Biomass	Straw	

Supplementary Table 9. Coefficients of determination, adjusted for stem canker as a covariate, Cowlinge 2006-2007 (split in 3 to fit on page).

	Seed wt.	Pod wt.	Pod HI	Mean seed wt.	Seed number/pod	Seed Density	Plant height	Terminal length	Foot length	Pod no. on terminal	Pod density	Stem width at base	Fertile branches	Infertile branches	Rest nodes	Total nodes	Node density
Pod wt.	71.2																
Pod HI	28	0															
Mean seed wt.	21	31.5	0														
Seed number/pod	64.8	35	31	1.4													
Seed Density	38.7	14.5	32	3.8	74.1												
Plant height	30.7	20.7	7.6	2.9	28.4	14.1											
Terminal length	10	5.8	3.1	0.7	10.8	6.9	36.6										
Foot length	20.1	14	3.5	0.3	24.6	8.3	54.5	9.1									
Pod no. on terminal	5	2	3.4	0.2	5.7	2.5	16.7	23.5	13.9								
Pod density	0.1	0.3	0.2	0.1	0	0.3	0.6	9	2.2	46.2							
Stem width at base	0	0.1	0	0	0.1	0.1	5.9	0.9	0.4	0.7	3.1						
Fertile branches	1.3	1.1	0.1	0.1	1.6	0	1.1	4.8	20.4	6.3	0.8	15					
Infertile branches	1	1.4	0.1	0.2	0.9	1	0.5	2.2	1.7	0.5	5.1	0.4	0				
Rest nodes	7.6	1.6	6.8	0.1	6.4	4	8.4	3.8	4	3.4	0.1	14.5	0.3	0.8			
Total nodes	3.5	0.3	5.5	0	2.5	2.4	4.2	0.5	0	0.5	0.1	25	15.1	4.9	85.9		
Node density	2.6	5.5	0.7	1	2.9	0.5	19.8	9.4	20.4	2.7	0.8	7.2	15	6.9	42.9	58.4	

Branch density	9.6	7.1	0.8	3.2	6.3	2	19.2	40.3	11.6	8.4	5.6	4.1	47.6	13.2	0.2	11.4
Branch angle	11.4	9.9	1.1	4	8.1	1.6	4.4	0.4	17.6	6.5	4.4	4.5	15	1.1	0.7	0.6
Branch angle (top 4)	9.5	9.2	1	5.4	4.5	0.6	4.6	0	11.4	4.8	5.8	0.8	2.4	0.6	1.9	0.7
Beak length	19.2	16.4	2	2.1	17.4	5.8	18	16.6	13.7	0.4	8	0	5.6	0.5	2.2	0.1
Pedicle length	10.6	3.1	8.8	3.5	4.5	0	10.4	6.3	12.1	1.4	0.7	0.9	4.2	0.2	9.8	4.5
Pod length	34.3	29.6	4.9	0	42.3	4.1	20	6.2	30.6	4.6	0.1	2.3	8.2	0.2	2.8	0.1
Silique length	38.1	32.8	5.2	0.3	44.2	5.7	24.7	10.5	32.6	4.1	0.3	1.7	9.5	0.4	3.3	0.2
Pod width	27.2	34.8	1	28.5	8.7	7.1	1.1	0.1	2.5	0.3	0.3	1	0	1.1	0.2	0.3
Pedicle angle	17.1	13.5	4.4	4.5	9.9	2.1	6.9	3.1	11.5	13	7.1	1.2	10	0.3	0.4	2.9
Pod angle	18.8	18.7	1.1	2.9	13.4	1.1	4.9	1.1	12.4	5.6	2.2	6.5	9.4	4.6	0.5	0.7
Angle to rachis	27.7	24.2	4.2	5.8	17.6	2.6	9.3	3.3	18.4	14.7	7.2	4.5	15.1	2.4	0	2.8
Yield	20.7	14.9	2.1	0.8	19.7	9.2	18.7	13.7	20.3	21.1	2.7	2.3	11.3	1.1	1.6	0.1
Biomass	7.1	3.5	4.5	5.4	2	7.7	8.2	4.5	0.8	2.9	0	2.5	1.8	1.3	10.9	10.9
Straw	7.6	4	4.2	6.4	1.9	7.1	9.6	4.9	1	3	0	2.5	2	1.3	11.2	11.2
Canker (after covar)	0.1	0.8	4.4	2	1.3	7.7	1.2	0	0.1	0.3	0.6	0.3	0.2	0	1.1	0.6
	Seed wt.	Pod wt.	Pod HI	Mean seed wt.	Seed number/pod	Seed Density	Plant height	Terminal length	Foot length	Pod no. on terminal	Pod density	Stem width at base	Fertile branches	Infertile branches	Rest nodes	Total nodes

Supplementary Table 10. Correlation matrix, mean of Barton and Cowlinge, 2006-2007 (split in 3 to fit on page).

Pod wt.	0.834																
Pod HI	0.475	-0.068															
Mean seed wt.	0.409	0.416	0.085														
Seed number/pod	0.777	0.608	0.448	-0.227													
Seed Density	0.614	0.382	0.511	-0.279	0.868												
Plant height	0.387	0.331	0.143	0.079	0.379	0.275											
Terminal length	0.198	0.17	0.094	0.037	0.215	0.185	0.509										
Foot length	0.295	0.244	0.105	-0.054	0.376	0.245	0.707	0.114									
Pod no. on terminal	0.207	0.179	0.112	-0.021	0.251	0.191	0.355	0.501	0.224								
Pod density	0.068	0.058	0.046	-0.06	0.107	0.061	-0.062	-0.3	0.132	0.668							
Stem width at base	0.059	-0.001	0.097	0.084	-0.025	0.001	0.293	0.104	0.008	-0.017	-0.109						
Fertile branches	0.007	-0.05	0.112	0.073	-0.063	0.008	-0.029	-0.166	-0.385	-0.101	0.041	0.395					
Infertile branches	-0.039	-0.075	0.038	0.045	-0.074	-0.089	-0.071	-0.187	-0.084	0.035	0.217	0.056	0.002				
Rest nodes	0.098	0.051	0.101	-0.153	0.204	0.166	0.256	0.217	0.21	0.234	0.076	0.24	-0.066	-0.001			
Total nodes	0.069	0.003	0.133	-0.12	0.145	0.139	0.215	0.106	0.028	0.18	0.115	0.393	0.328	0.14	0.905		
Node density	0.151	0.191	-0.069	0.149	0.081	0.023	0.476	0.229	0.429	0.051	-0.161	-0.125	-0.276	-0.187	-0.643	-0.741	
	Seed wt.	Pod wt.	Pod HI	Mean seed wt.	Seed number/pod	Seed Density	Plant height	Terminal length	Foot length	Pod no. on terminal	Pod density	Stem width at base	Fertile branches	Infertile branches	Rest nodes	Total nodes	

Branch density	0.107	0.168	-0.083	0.059	0.096	0.038	0.286	0.622	0.165	0.224	-0.292	-0.22	-0.677	-0.35	0.062	-0.276
Branch angle	0.237	0.261	0.006	0.064	0.234	0.097	0.116	0.062	0.338	0.191	0.139	-0.197	-0.35	-0.155	0.018	-0.144
Branch angle (top 4)	0.226	0.217	0.058	0.154	0.155	0.042	0.114	-0.049	0.246	0.153	0.196	-0.029	-0.039	0.018	-0.034	-0.051
Beak length	0.352	0.394	0.002	-0.001	0.408	0.213	0.286	0.27	0.257	0.092	-0.124	-0.006	-0.17	-0.043	0.11	0.017
Pedicle length	0.202	0.065	0.219	0.268	0.024	-0.122	0.223	0.175	0.168	0.071	-0.058	0.178	-0.026	0.047	0.134	0.118
Pod length	0.532	0.561	0.081	-0.036	0.596	0.171	0.31	0.133	0.357	0.219	0.151	-0.066	-0.107	0.002	0.085	0.034
Silique length	0.543	0.576	0.07	-0.028	0.61	0.202	0.341	0.187	0.375	0.207	0.09	-0.058	-0.142	-0.013	0.101	0.03
Pod width	0.505	0.551	0.064	0.437	0.267	0.268	0.06	-0.022	0.082	0.024	0.066	-0.073	-0.058	0.01	-0.089	-0.117
Pedicle angle	0.296	0.299	0.068	0.096	0.241	0.087	0.178	0.091	0.264	0.291	0.242	-0.122	-0.24	-0.166	-0.105	-0.211
Pod angle	0.219	0.298	-0.063	-0.096	0.3	0.127	-0.013	-0.032	0.186	0.142	0.178	-0.23	-0.216	-0.229	0.034	-0.093
Angle to rachis	0.334	0.375	0.016	0.019	0.335	0.131	0.121	0.048	0.289	0.285	0.27	-0.209	-0.289	-0.237	-0.056	-0.199
Yield	0.33	0.342	0.057	-0.134	0.464	0.395	0.262	0.325	0.326	0.375	0.117	-0.187	-0.299	-0.264	0.21	0.03
Harvest Index	0.115	-0.079	0.355	-0.041	0.13	0.225	-0.103	-0.021	-0.05	0.054	0.102	0.03	0.086	-0.002	-0.045	-0.016
Canker	-0.122	-0.146	-0.024	0.114	-0.238	-0.18	-0.164	-0.314	-0.155	-0.248	0.006	0.156	0.188	0.218	-0.173	-0.051
Oil	0.132	0.079	0.143	-0.29	0.34	0.326	-0.083	-0.083	0.043	0.073	0.165	-0.235	-0.001	-0.051	-0.088	-0.081
Glucosinolate	-0.138	-0.137	-0.011	0.034	-0.206	-0.232	-0.185	-0.244	-0.172	-0.14	0.068	0.141	0.193	0.118	-0.156	-0.035
Protein	-0.211	-0.192	-0.085	0.187	-0.379	-0.352	-0.144	-0.302	-0.159	-0.225	0.025	0.117	0.25	0.191	-0.19	-0.058
	Seed wt.	Pod wt.	Pod HI	Mean seed wt.	Seed number/pod	Seed Density	Plant height	Terminal length	Foot length	Pod no. on terminal	Pod density	Stem width at base	Fertile branches	Infertile branches	Rest nodes	Total nodes

Supplementary Table 11. Coefficients of determination, mean of Barton and Cowlinge, 2006-2007 (split in 3 to fit on page).

	Seed wt.	Pod wt.	Pod HI	Mean seed wt.	Seed number/pod	Seed Density	Plant height	Terminal length	Foot length	Pod no. on terminal	Pod density	Stem width at base	Fertile branches	Infertile branches	Rest nodes	Total nodes	Node density
Pod wt.	69.6																
Pod HI	22.6	0.5															
Mean seed wt.	16.7	17.3	0.7														
Seed number/pod	60.4	37	20.1	5.2													
Seed Density	37.7	14.6	26.1	7.8	75.4												
Plant height	15	11	2	0.6	14.4	7.6											
Terminal length	3.9	2.9	0.9	0.1	4.6	3.4	25.9										
Foot length	8.7	6	1.1	0.3	14.1	6	50	1.3									
Pod no. on terminal	4.3	3.2	1.2	0	6.3	3.7	12.6	25.1	5								
Pod density	0.5	0.3	0.2	0.4	1.1	0.4	0.4	9	1.7	44.6							
Stem width at base	0.3	0	0.9	0.7	0.1	0	8.6	1.1	0	0	1.2						
Fertile branches	0	0.3	1.2	0.5	0.4	0	0.1	2.8	14.9	1	0.2	15.6					
Infertile branches	0.2	0.6	0.1	0.2	0.5	0.8	0.5	3.5	0.7	0.1	4.7	0.3	0				
Rest nodes	1	0.3	1	2.3	4.2	2.8	6.6	4.7	4.4	5.5	0.6	5.8	0.4	0			
Total nodes	0.5	0	1.8	1.4	2.1	1.9	4.6	1.1	0.1	3.2	1.3	15.4	10.8	2	81.9		
Node density	2.3	3.6	0.5	2.2	0.7	0.1	22.7	5.2	18.4	0.3	2.6	1.6	7.6	3.5	41.4	54.9	

Branch density	1.1	2.8	0.7	0.3	0.9	0.1	8.2	38.6	2.7	5	8.5	4.9	45.8	12.3	0.4	7.6
Branch angle	5.6	6.8	0	0.4	5.5	0.9	1.3	0.4	11.4	3.7	1.9	3.9	12.2	2.4	0	2.1
Branch angle (top 4)	5.1	4.7	0.3	2.4	2.4	0.2	1.3	0.2	6	2.3	3.8	0.1	0.2	0	0.1	0.3
Beak length	12.4	15.5	0	0	16.7	4.5	8.2	7.3	6.6	0.8	1.5	0	2.9	0.2	1.2	0
Pedicle length	4.1	0.4	4.8	7.2	0.1	1.5	5	3.1	2.8	0.5	0.3	3.2	0.1	0.2	1.8	1.4
Pod length	28.3	31.4	0.7	0.1	35.5	2.9	9.6	1.8	12.7	4.8	2.3	0.4	1.1	0	0.7	0.1
Siliques length	29.5	33.2	0.5	0.1	37.2	4.1	11.6	3.5	14	4.3	0.8	0.3	2	0	1	0.1
Pod width	25.5	30.3	0.4	19.1	7.1	7.2	0.4	0	0.7	0.1	0.4	0.5	0.3	0	0.8	1.4
Pedicle angle	8.8	9	0.5	0.9	5.8	0.8	3.2	0.8	6.9	8.5	5.9	1.5	5.8	2.8	1.1	4.4
Pod angle	4.8	8.9	0.4	0.9	9	1.6	0	0.1	3.4	2	3.2	5.3	4.6	5.2	0.1	0.9
Angle to rachis	11.1	14.1	0	0	11.2	1.7	1.5	0.2	8.4	8.1	7.3	4.4	8.4	5.6	0.3	4
Yield	10.9	11.7	0.3	1.8	21.5	15.6	6.8	10.6	10.7	14.1	1.4	3.5	8.9	7	4.4	0.1
Harvest Index	1.3	0.6	12.6	0.2	1.7	5.1	1.1	0	0.3	0.3	1	0.1	0.7	0	0.2	0
Canker	1.5	2.1	0.1	1.3	5.7	3.2	2.7	9.8	2.4	6.2	0	2.4	3.5	4.7	3	0.3
Oil	1.8	0.6	2	8.4	11.5	10.6	0.7	0.7	0.2	0.5	2.7	5.5	0	0.3	0.8	0.7
Glucosinolate	1.9	1.9	0	0.1	4.2	5.4	3.4	5.9	3	2	0.5	2	3.7	1.4	2.4	0.1
Protein	4.5	3.7	0.7	3.5	14.4	12.4	2.1	9.1	2.5	5.1	0.1	1.4	6.2	3.7	3.6	0.3
	Seed wt.	Pod wt.	Pod HI	Mean seed wt.	Seed number/pod	Seed Density	Plant height	Terminal length	Foot length	Pod no. on terminal	Pod density	Stem width at base	Fertile branches	Infertile branches	Rest nodes	Total nodes

Supplementary Table 12. Single marker analysis TNDH 94 (2) lines, Spalding 2005-2006.

Elsoms		seed wt	mean wt valves	pod harvest index	mean seed wt	seed no per pod	height	terminal length	foot length	pod no per raceme	stem width	fertile branch	infertile branch	remainder of nodes	total nodes	branch angle	top 4 branch	Beak length	pedicel length	pod length	pod width	pedicel angle	pod angle	canker	flowering time
A 1	Spread Peak pos. Fprob			36-59 47.8 1 2.00 E-02			56-85 84.9 1 2.00 E-03						26-38 33.6 7 3.00 E-03						26-31 26.3 4 8.00 E-03	58-78 67.5 6 2.00 E-03		55-63 59.9 4 8.00 E-03			
A 2	Spread Peak pos. Fprob								52-91 75.8 3 2.00 E-04				09-59 30.5 2.00 E-04	09-31 21.9 5.00 E-03									35-61 52.1 9 2.00 E-03	31-66 59.2 4 8.00 E-04	71-94 91.1 4 9.00 E-05
A 3	Spread Peak pos. Fprob	99-122 112. 07 2.00 E-02		58-116 112. 102 6.00 E-03		56-122 112. 07 6.00 E-03	110-122 112. 07 1.00 E-03	112-119 119. 45 3.00 E-02		74-99 95.9 8 1.00 E-02	72-83 75.7 75.7 1.00 E-02		72-93 75.5 5 2.00 E-03	37-99 95.6 5 1.00 E-02	37-96 58.3 6 1.00 E-03	106-113 106. 24 1.00 E-02		11-122 58.3 6 3.00 E-04	16-30 38.7 15.5 2.00 E-02	11-43 38.7 9 9.00 E-03		43-59 58.5 3 1.00 E-02	07-47 30.2 8 1.00 E-03	30-65 45.0 3 6.00 E-05	
A 4	Spread Peak pos. Fprob	56-86 80.2 2 6.00 E-03	79-80 79.2 7 3.00 E-02	64-119 114. 5		0-15 14.9 9 2.00 E-02	79-86 80.2 2 4.00 E-03												0-37 13.9 1 2.00 E-03	0-3.5 3.5 3.5 6.00 E-03				14-28 28.3 3 1.00 E-02	
A 5	Spread Peak pos. Fprob																					56-59 56.2 1 1.00 E-02			82-95 92.4 2 4.00 E-03
A 6	Spread			58-77									59-64			05-14		126-127							

Elsoms		seed wt	mean wt valves	pod harvest index	mean seed wt	seed no per pod	height	terminal length	foot length	pod no per raceme	stem width	fertile branch	infertile branch	remainder of nodes	total nodes	branch angle	top 4 branch	Beak length	pedicel length	pod length	pod width	pedicel angle	pod angle	canker	flowering time
92 set																									
A 7	Peak pos.		77.0	6								6.00				1.00		1.00							
	Fprob		8.00	E-03								2.78				9.28		4.56							
A 8	Spread		60-94									60-62						84-98							07-13
	Peak pos.		61.5	2								61.5						91.0							7.09
A 9	Fprob		1.00	E-02								7.00						6.00							1.00
	b											E-03						E-03							E-02
A 10	Spread	65-76	46-88	62-66				111-123		51-123		50-83			66-71	61-85	65-71	38-62	0-41	0-41					28-98
	Peak pos.	76.1	81.4	65.1				122.		65.4		63.9			66.8	74.3	65.9	38.3	18.3	27.6					51.4
A 11	Fprob	2	6	6				72		2		8			7	4	7	5	5	1					8
	b	3.00	4.00	2.00				2.00		2.00		4.00			2.00	6.00	2.00	7.00	6.00	5.00					2.00
C 1	Spread					12-42		28-32	23-42						23-29	12-29		12-42							22-40
	Peak pos.					37.2		29.3	37.2						23.2	23.2		32.3							37.2
						3		7	3						5	5		2							3

Elsoms		seed wt	mean wt valves	pod harvest index	mean seed wt	seed no per pod	height	terminal length	foot length	pod no per raceme	stem width	fertile branch	infertile branch	remainder of nodes	total nodes	branch angle	top 4 branch	Beak length	pedicel length	pod length	pod width	pedicel angle	pod angle	canker	flowering time
	92 set																								
	Fprob				1.00 E-03			1.00 E-02	3.00 E-03							2.00 E-03	7.00 E-04		7.00 E-03						9.00 E-04
C2	Spread							39-63							90-104 1.00 E+0				90-97 89.7 9				90-124 124. 07		
	Peak pos. Fprob							1.00 E-03							2.65 E-03				2.00 E-03				8.00 E-03		
C3	Spread		07-13					47-63				07-16	16-27							73-78 73.4 2					
	Peak pos. Fprob		10.3 1		2.00 E-02			62.6 3				6.61 E-03	19.6 9	3.00 E-02						7.00 E-03					
C4	Spread														49-73 57.1 8	57-73 72.5 3						01-40 33.8 2	0-26 0.58		
	Peak pos. Fprob														1.00 E-02	8.00 E-03						9.00 E-03	4.00 E-03		
C5	Spread														31-34 33.4 5							13-57 21.1 1		57-88 82.5 5	
	Peak pos. Fprob														1.00 E-02							6.00 E-03		4.00 E-03	
C6	Spread		38-47																						
	Peak pos. Fprob		43.2 8		2.00 E-02														0-54 19.4 E-04		19-54 25.5 4				
																			2.00 E-04		4.00 E-03				

Elsoms		seed wt	mean wt valves	pod harvest index	mean seed wt	seed no per pod	height	terminal length	foot length	pod no per raceme	stem width	fertile branch	infertile branch	remainder of nodes	total nodes	branch angle	top 4 branch	Beak length	pedicel length	pod length	pod width	pedicel angle	pod angle	canker	flowering time
92 set																									
C 7	Spre ad Peak pos. Fpro b																								
C 8	Spre ad Peak pos. Fpro b																			57- 73 64.8 3 8.00 E-03					
C 9	Spre ad Peak pos. Fpro b					09- 36 29.0 8 5.00 E-03			17- 59 58.7 7 1.00 E-02																18- 36 24.5 8.00 E-03

Supplementary Table 13. Coefficients of determination, CRDH Cantelupe.

[illegible]

Supplementary Table 14. Coefficients of determination, CRDH, Cowlinge (split in 3 to fit on page).

Height	0.2																		
Terminal	0.4	13.4																	
Foot	0	20.4	0.4																
Podno	2	20.7	28.5	10.9															
Poddensity	2.3	4.6	0.7	7.6	54.2														
Stemw	0.8	1.1	0.1	1.4	0.1	0.1													
Fertile	1.3	27.9	1.5	0.1	31.4	20.3	0.1												
Infertile	2.7	0.5	0.1	0	0	0.1	0.5	0.3											
Nodes	0	16.9	0.1	35.2	23.9	20.8	2.4	17.2	1.5										
Totnodes	0.2	28.6	0.2	12	38	28.9	1.5	65	2.7	74.2									
Nodedensity	0	2.2	7.1	1.2	12.8	24	0.4	26.4	5.2	44.6	53.1								
Branchdensity	0.6	6	1.2	2.9	24.3	26.3	0.5	8.2	0.4	11.7	14.8	41.8							
Branchang	0.4	3.7	1.4	0.3	0	0	12.9	0.1	1	2.5	1.6	7	2.7						
Branch4	0.2	1.1	1.3	0.1	0.2	0	27.5	1.3	0.6	4.4	4.2	8	2	86.2					
Bkl	2.6	0	0.1	0	0	0.2	1	0.5	0.5	0.1	0.1	0.1	1.9	4.9	7.3				
Pedl	1.9	0.6	2	0.1	1.2	1.8	0.1	0.2	2.5	0.1	0.1	0.7	0.2	0.6	0.9	1.7			
	Meanseedwt	Height	Terminal	Foot	Podno	Poddensity	Stemw	Fertile	Infertile	Nodes	Totnodes	Nodedensity	Branchdensity	Branchang	Branch4	Bkl			

Podl	0.1	0.3	0.1	0.4	0.1	0.1	0.2	1.5	0.7	0.9	0	0	2.3	0.3	1.5	47.2
Podw	0.2	2.5	1.2	3.4	0.8	0.2	4.8	0.1	1.5	2.9	1.2	0	0.9	2.7	1.9	0.7
Pedang	0	0	0.7	1.5	0.1	0.8	2.1	1.7	0.1	0	0.6	1	0.5	1.9	1.3	0.8
Podang	0.1	1.6	4.1	1.3	0.6	0.1	12.8	0.3	0.6	1.6	1	0.2	2.4	0	0.7	5.8
Yield t/ha	0.6	0.4	0.7	1.1	0	0	6.4	0	0	1.1	0.4	2.4	2.7	0.1	0.4	0.8
HI	5.6	0.3	0.9	1.7	0.4	1	0	1.4	0	0.6	0	0.6	0.4	10.1	10.1	3.4
Start flowering	0	2	0	0.3	0.1	1.2	10.4	0.6	0	0.7	0	1.5	1.5	5	10.1	17.7
%oil	0.7	1.4	0.2	10.3	0	0	0.9	1.6	0.4	2.4	0.1	0.1	0.1	0.1	0.2	4.2
GSL	10.1	0.7	0	3.4	0.7	0.5	0.1	3.8	0.4	0	0.9	0	0.4	0.4	0.3	1.2
Protein	3.8	0	0.1	2.2	0.5	0.1	0.1	0.7	0.4	1	0	0	0.8	0	0.8	7.8
Autum vig.	3.2	0	0.2	0	2.4	4.7	0.2	2	2	0.9	1.4	2.6	5.8	0.7	0.6	0.1
Spring vig.	1.3	1.4	1	3.5	3.1	3.5	6.8	1.1	0.6	2.6	2.2	1.2	4.1	2.5	5.4	0.6
App. B. flow	0.7	3.1	1.4	4.7	5.7	6.1	6.3	2.8	1.5	3.3	3.6	1.2	2.8	1.8	3.9	0.1
App. at harvest	3.9	0.2	0.9	0.4	0	0	4.3	0.3	0.1	0.9	0.7	0	1	0.2	1.4	1.8
Plant height	11.3	0.2	0	0	0	0.1	19.5	0.1	0.3	0.2	0.3	0	0	0.2	3.1	2.1
End flowering	2.4	0.2	0.2	0.7	1.4	3.1	0.3	0	0.3	1.1	0.6	1.8	3.2	0.1	0.1	4.3
Flowering period	0.4	1.9	0	1.2	0.1	0.1	16.9	0.9	0	0.2	0.1	0.5	0.2	0	12.8	14.9
	Meanseedwt	Height	Terminal	Foot	Podno	Poddensity	Stemw	Fertile	Infertile	Nodes	Totnodes	Nodedensity	Branchdensity	Branch	Branch	Bkl

Supplementary Table 15. Single marker analysis CRDH at Cowlinge 2007-2008.

L G	Homology	cM	L G	markers	means seed weight	height of plant	terminal length	foot length	pod number on terminal	pod density on terminal	stem width	fertile branch number	infertile branch number	node number	total node number	node density	branch density	branch angle	branch angle of top 4 branches
1	C3	0	1	IGF0568d	2.80E-01	9.30E-01	9.60E-01	6.10E-01	4.20E-01	8.50E-02	5.80E-01	7.50E-01	1.20E-01	2.40E-01	4.10E-01	4.30E-01	5.50E-01	2.00E-02	1.30E-01
					0.983	1.003	0.998	0.967	0.964	1.104	0.979	1.023	0.759	0.953	0.968	1.032	0.936	0.959	0.968
1	C3	20.9	1	CALSSR_137	-0.1 6.40E-03	0.393 8.20E-01	-0.09 7.20E-01	-1.391 8.90E-01	-2.231 9.40E-01	0.104 8.90E-01	-0.027 6.30E-01	0.15 6.30E-01	-0.166 4.40E-01	-0.685 8.00E-01	-0.711 9.80E-01	0.214 6.40E-01	-0.408 1.50E-01	-1.642 3.20E-01	-1.36 6.60E-01
					0.96	0.994	0.99	1.009	1.003	1.008	0.983	1.033	0.882	0.99	0.999	0.982	0.861	0.983	0.991
1	C3	26	1	SN4513_369	-0.234 4.40E-03	-0.892 8.80E-01	-0.56 5.00E-01	0.351 8.10E-01	0.183 4.80E-01	0.008 2.90E-01	-0.022 5.90E-01	0.214 5.20E-01	-0.078 4.70E-01	-0.14 6.00E-01	-0.017 9.10E-01	-0.123 9.70E-01	-0.941 6.10E-01	-0.679 2.20E-01	-0.386 4.40E-01
					0.959	1.004	0.982	0.985	0.97	1.059	0.981	1.043	0.891	0.98	0.996	1.001	0.948	0.979	0.984
1	C3	42	1	BRAS068_115	-0.241 2.00E-04	0.607 5.50E-02	-1.034 8.00E-01	-0.622 7.40E-02	-1.838 6.70E-01	0.06 2.40E-01	-0.024 7.60E-01	0.28 8.20E-01	-0.072 3.40E-01	-0.289 4.30E-01	-0.088 5.90E-01	0.01 6.20E-01	-0.336 7.30E-02	-0.835 5.40E-01	-0.659 7.20E-01
					0.948	0.948	0.993	0.899	0.982	1.065	0.989	1.015	0.865	0.971	0.98	0.981	0.836	0.99	0.993
					-0.307	-7.391	-0.381	-4.45	-1.093	0.065	-0.014	0.1	-0.093	-0.431	-0.432	-0.129	-1.137	-0.407	-0.298
2	A3	0	2	CB10427_152	3.10E-01	9.40E-02	5.50E-01	8.60E-01	9.60E-01	6.40E-01	6.30E-01	1.80E-01	2.90E-01	4.70E-01	1.70E-01	6.30E-01	2.50E-01	4.70E-02	1.50E-01
					0.979	1.065	0.979	1.014	0.997	0.965	1.024	1.123	1.228	1.038	1.069	0.975	1.163	0.955	0.961
2	A3	2.4	2	BRAS038_108	-0.119 4.00E-01	8.806 2.30E-01	-1.225 8.60E-01	0.59 9.00E-01	-0.19 7.90E-01	-0.036 6.40E-01	0.03 2.90E-01	0.793 4.60E-02	0.141 1.50E-01	0.537 6.60E-01	1.47 1.20E-01	-0.168 3.10E-01	1.008 7.20E-01	-1.79 2.00E-01	-1.628 3.50E-01
					0.983	1.046	0.994	0.99	1.015	0.966	1.052	1.182	1.319	1.023	1.079	0.948	1.05	0.971	0.974
					-0.098	6.284	-0.365	-0.414	0.922	-0.036	0.065	1.164	0.193	0.325	1.68	-0.355	0.314	-1.167	-1.077

2	A3	2.7	2	BRAS087_160	3.40E-01	5.10E-02	8.70E-01	9.90E-01	6.90E-01	6.20E-01	1.80E-01	3.90E-02	1.40E-01	5.70E-01	9.40E-02	4.90E-01	4.50E-01	1.40E-01	2.90E-01
					0.979	1.078	0.994	1.001	1.025	0.961	1.07	1.202	1.352	1.032	1.092	0.963	1.111	0.965	0.969
					-0.12	10.611	-0.356	0.051	1.523	-0.041	0.086	1.288	0.211	0.457	1.953	-0.255	0.698	-1.397	-1.281
2	A3	4.2	2	SSR18_175	3.60E-01	5.90E-01	6.20E-01	5.80E-01	8.80E-01	9.50E-01	5.70E-01	1.90E-01	4.60E-01	9.40E-01	3.90E-01	4.10E-01	4.80E-01	3.20E-02	7.20E-02
					0.98	1.022	0.981	0.952	0.991	0.995	1.029	1.128	1.168	1.004	1.046	0.955	0.897	0.948	0.948
					-0.113	3.07	-1.093	-2.017	-0.544	-0.005	0.036	0.83	0.105	0.064	0.998	-0.307	-0.659	-2.063	-2.19
2	A3	6.4	2	CB10036_160	7.10E-01	4.90E-01	9.90E-01	8.50E-01	4.80E-01	4.50E-01	4.50E-01	8.10E-02	8.10E-01	7.10E-01	2.30E-01	3.00E-01	4.50E-02	4.70E-02	1.90E-01
					0.991	1.034	1	1.02	1.051	0.93	1.046	1.194	1.066	1.024	1.077	0.933	0.669	0.944	0.955
					-0.052	4.626	0.021	0.829	3.114	-0.073	0.057	1.26	0.041	0.348	1.65	-0.457	-2.145	-2.246	-1.891
2	A3	6.4	2	OL10D03_101	2.90E-01	6.30E-01	7.40E-01	6.80E-01	6.40E-01	6.90E-01	6.90E-01	2.40E-01	5.00E-01	5.60E-01	2.70E-01	2.50E-01	1.70E-01	6.40E-02	2.70E-01
					0.975	1.022	0.986	1.041	1.032	0.965	1.023	1.126	1.172	1.036	1.067	0.929	0.782	0.95	0.964
					-0.145	3.049	-0.814	1.679	1.939	-0.037	0.029	0.818	0.107	0.513	1.439	-0.481	-1.412	-1.991	-1.519
3	C3/A3/C8	6.4	3	BRMS269_313	2.90E-01	6.30E-01	7.40E-01	6.80E-01	6.40E-01	6.90E-01	6.90E-01	2.40E-01	5.00E-01	5.60E-01	2.70E-01	2.50E-01	1.70E-01	6.40E-02	2.70E-01
					0.975	1.022	0.986	1.041	1.032	0.965	1.023	1.126	1.172	1.036	1.067	0.929	0.782	0.95	0.964
					-0.145	3.049	-0.814	1.679	1.939	-0.037	0.029	0.818	0.107	0.513	1.439	-0.481	-1.412	-1.991	-1.519
3	C3/A3/C8	10.2	3	BRAS065_219	1.50E-01	1.20E-01	4.90E-01	8.70E-01	7.20E-01	6.10E-01	1.90E-01	4.90E-03	4.80E-01	4.90E-01	3.80E-02	1.60E-01	3.30E-01	5.10E-01	8.60E-01
					0.972	1.055	0.976	0.987	1.02	1.037	1.064	1.252	1.151	1.035	1.103	0.931	0.874	0.985	0.995
					-0.162	7.533	-1.399	-0.554	1.205	0.038	0.078	1.574	0.093	0.505	2.172	-0.473	-0.824	-0.585	-0.197
3	C3/A3/C8	13.6	3	AtTB1_f	5.30E-01	2.50E-01	8.00E-01	8.80E-01	6.60E-01	2.90E-01	8.30E-01	1.90E-01	7.70E-01	9.40E-01	4.90E-01	8.20E-01	5.90E-01	2.90E-02	1.40E-01
					0.988	1.041	0.992	1.011	0.977	1.073	0.99	1.11	1.056	0.997	1.032	0.989	0.933	0.955	0.963
					-0.068	5.617	-0.468	0.468	-1.421	0.074	-0.012	0.708	0.035	-0.049	0.683	-0.071	-0.428	-1.792	-1.552
4	uk1	0	4	RA1F06_190	2.20E-01	1.50E-02	6.00E-02	3.00E-01	7.90E-01	8.40E-01	4.60E-01	8.50E-01	7.80E-01	9.20E-01	9.00E-01	7.40E-02	1.10E-01	9.10E-01	9.50E-01
					0.982	0.934	0.953	0.94	1.012	0.989	0.974	1.012	0.959	1.004	1.005	0.935	0.847	0.998	0.999
					-0.106	-9.44	-2.752	-2.614	0.704	-0.012	-0.033	0.08	-0.028	0.059	0.104	-0.455	-1.052	-0.075	-0.057
4	uk1	19	4	CALSSSR_142	6.20E-02	2.40E-01	1.90E-01	6.50E-01	5.50E-01	4.90E-01	8.20E-01	5.90E-01	8.20E-01	5.10E-01	4.50E-01	1.30E-01	1.40E-01	7.80E-01	5.10E-01
					0.97	0.964	0.963	0.971	1.029	0.959	1.009	1.041	1.041	1.029	1.032	0.939	0.853	1.005	1.015
					-0.177	-5.067	-2.192	-1.236	1.737	-0.044	0.011	0.263	0.025	0.406	0.675	-0.431	-1.043	0.208	0.615
4	uk1	23.5	4	SN4513_366	1.30E-02	2.00E-01	1.50E-01	3.60E-01	5.60E-01	6.70E-01	6.20E-01	7.30E-01	5.70E-01	9.40E-01	9.70E-01	4.10E-01	4.00E-01	9.20E-01	9.80E-01
					0.962	0.962	0.96	0.943	0.974	1.025	0.981	1.025	0.912	0.997	1.002	0.967	0.913	0.998	1

					-0.225	-5.423	-2.325	-2.482	-1.631	0.026	-0.024	0.159	-0.06	-0.046	0.035	-0.227	-0.583	-0.075	-0.019
4	uk1	39.4	4	KBrH004A18(3)	1.80E-01	7.50E-01	1.00E-01	3.40E-01	1.30E-01	3.30E-01	6.20E-01	3.50E-01	7.80E-01	7.30E-01	4.40E-01	3.30E-01	6.10E-01	6.60E-01	7.00E-01
					0.98	0.991	0.957	0.943	0.938	1.058	1.019	1.068	1.046	1.013	1.03	0.962	0.948	0.992	0.992
4	uk1	58.1	4	A77096_218	-0.118 1.60E-01	-1.245 7.90E-03	-2.52 2.20E-01	-2.476 8.30E-02	-3.934 5.50E-01	0.058 6.40E-01	0.023 4.10E-01	0.433 7.00E-01	0.029 2.10E-01	0.192 3.60E-01	0.647 3.10E-01	-0.259 6.10E-01	-0.337 1.20E-01	-0.306 7.00E-01	-0.344 7.20E-01
					0.977	0.921	0.965	0.891	0.972	1.029	0.968	0.972	0.817	0.962	0.959	0.979	0.843	1.007	1.008
					-0.133	11.448	-2.065	-4.882	-1.735	0.03	-0.04	-0.186	-0.132	-0.557	-0.897	-0.144	-1.121	0.288	0.335
4	uk1	62.8	4	KBrH013K13(1)	2.80E-01	6.50E-03	5.60E-01	2.20E-02	6.00E-01	4.60E-01	3.80E-01	7.60E-01	4.10E-01	2.00E-01	2.50E-01	6.60E-01	9.30E-02	8.70E-01	9.60E-01
					0.984	0.921	0.983	0.864	0.976	1.045	0.967	0.979	0.871	0.95	0.956	0.982	0.834	1.003	0.999
					-0.096	11.464	-0.966	-6.185	-1.486	0.046	-0.043	-0.144	-0.09	-0.747	-0.974	-0.119	-1.188	0.118	-0.051
5	A2/A6	0	5	RGA12_30	4.20E-01	2.70E-01	5.50E-01	9.00E-01	8.00E-01	6.30E-01	2.30E-01	1.90E-01	4.50E-01	2.00E-01	1.30E-01	4.20E-01	4.40E-01	6.20E-01	7.10E-01
					0.988	0.969	1.016	0.993	1.011	0.974	0.958	0.917	1.13	0.951	0.944	1.032	0.922	0.991	0.992
5	A2/A6	8.5	5	RGL12_31_300	-0.071 2.00E-01	-4.397 4.20E-01	0.921 7.80E-01	-0.312 6.20E-01	0.686 7.80E-01	-0.028 4.90E-01	-0.055 5.60E-01	-0.578 1.60E-01	0.077 2.10E-01	-0.725 6.90E-01	-1.244 3.70E-01	0.211 9.10E-01	-0.514 5.70E-01	-0.344 9.20E-01	-0.324 9.90E-01
					0.981	0.976	0.992	1.032	1.013	0.961	0.978	0.91	1.227	0.984	0.966	0.996	0.94	0.998	1
5	A2/A6	31.1	5	CB10416_251	-0.111 1.90E-01	-3.303 2.40E-01	-0.437 3.80E-01	1.302 4.00E-01	0.762 4.80E-01	-0.041 8.30E-01	-0.028 5.00E-01	-0.626 5.90E-01	0.129 6.30E-02	-0.228 9.00E-01	-0.74 8.90E-01	-0.029 5.20E-01	-0.39 8.20E-01	-0.07 3.40E-01	0.007 3.90E-01
					0.981	0.967	0.977	0.949	0.97	0.988	0.976	0.965	1.354	0.995	0.995	0.976	1.024	1.017	1.018
5	A2/A6	32.1	5	IGF3239d	-0.113 1.60E-01	-4.643 2.90E-01	-1.348 3.40E-01	-2.183 5.30E-01	-1.881 5.00E-01	-0.013 7.10E-01	-0.031 4.60E-01	-0.238 5.10E-01	0.185 7.10E-02	-0.074 9.10E-01	-0.114 8.40E-01	-0.167 5.90E-01	0.147 7.60E-01	0.656 2.70E-01	0.738 3.30E-01
					0.979	0.97	0.974	0.962	0.971	0.98	0.973	0.956	1.346	0.996	0.992	0.979	1.033	1.019	1.02
5	A2/A6	44.2	5	FITO232_130	-0.124 9.10E-02	-4.194 4.60E-01	-1.489 2.10E-01	-1.627 9.20E-01	-1.777 2.80E-01	-0.021 3.70E-01	-0.034 8.40E-02	-0.296 3.30E-01	0.181 6.50E-01	-0.063 7.70E-01	-0.166 5.20E-01	-0.142 7.30E-01	0.203 9.60E-01	0.753 6.50E-01	0.837 8.10E-01
					0.974	0.978	0.966	0.994	0.954	1.052	0.939	0.937	1.076	0.989	0.975	1.014	1.006	1.008	1.005
5	A2/A6	65.8	5	RA1F06_175	-0.149 1.30E-02	-3.007 8.30E-01	-1.962 1.90E-01	-0.264 6.50E-01	-2.904 6.20E-01	0.052 4.30E-01	-0.08 9.20E-01	-0.435 9.40E-01	0.046 7.10E-01	-0.166 9.20E-01	-0.543 1.00E+00	0.093 7.90E-01	0.037 4.80E-01	0.318 2.80E-01	0.207 3.50E-01
					0.964	1.006	0.966	0.972	0.978	1.046	1.004	1.005	1.059	0.996	1	0.99	1.078	1.019	1.02
					-0.213	0.886	-1.94	-1.178	-1.327	0.047	0.004	0.032	0.038	-0.057	0.004	-0.071	0.473	0.752	0.815

6	A4/C4(6)	0	6	NA12E05_146	2.40E-01	5.60E-01	7.90E-01	9.50E-01	3.70E-01	1.80E-01	1.80E-01	6.30E-01	2.20E-02	7.70E-01	7.40E-01	8.40E-01	7.90E-01	4.80E-02	3.20E-02
					0.982	0.983	0.993	1.004	0.962	1.077	0.953	0.968	0.698	1.011	0.988	0.992	0.972	0.967	0.957
6	A4/C4(6)	3.2	6	CB10493_155	-0.103 2.90E-01	-2.317 5.20E-01	-0.416 8.00E-01	0.175 8.40E-01	-2.33 5.00E-01	0.077 2.90E-01	-0.06 4.40E-01	-0.216 9.50E-01	-0.225 6.60E-03	0.163 4.40E-01	-0.27 8.60E-01	-0.055 3.80E-01	-0.18 5.70E-01	-1.337 6.80E-02	-1.82 5.60E-02
					0.985	0.981	0.993	0.988	0.971	1.06	0.972	0.996	0.658	1.03	1.007	0.967	0.942	0.97	0.963
6	A4/C4(6)	3.9	6	OL10B01_177	-0.087 3.90E-01	-2.578 3.80E-01	-0.398 9.60E-01	-0.52 7.50E-01	-1.769 4.10E-01	0.061 1.80E-01	-0.035 2.70E-01	-0.03 7.00E-01	-0.266 4.10E-03	0.431 6.30E-01	0.145 8.40E-01	-0.229 5.60E-01	-0.377 6.20E-01	-1.198 6.00E-02	-1.579 4.40E-02
					0.987	0.975	1.001	0.98	0.965	1.077	0.961	0.975	0.641	1.019	0.992	0.978	0.949	0.969	0.961
6	A4/C4(6)	10	6	MAX3_m	-0.075 3.40E-01	-3.506 3.20E-01	0.076 8.90E-01	-0.832 5.40E-01	-2.164 7.20E-01	0.077 3.60E-01	-0.05 6.00E-01	-0.168 8.80E-01	-0.283 8.90E-03	0.272 9.00E-01	-0.17 7.50E-01	-0.153 6.90E-01	-0.329 3.60E-01	-1.248 5.60E-02	-1.674 8.00E-02
					0.985	0.971	1.004	0.961	0.984	1.055	0.98	1.011	0.649	0.995	0.988	0.984	0.905	0.968	0.965
					-0.086	-4.013	0.212	-1.634	-0.958	0.055	-0.025	0.069	-0.273	-0.075	-0.27	-0.107	-0.635	-1.305	-1.505
7	C7	0	7	CB10299_140	5.30E-01	6.00E-01	2.30E-01	2.20E-01	2.00E-01	3.40E-01	7.90E-01	7.50E-01	5.80E-01	1.90E-01	3.10E-01	3.10E-01	6.00E-01	4.80E-02	4.10E-02
					0.991	1.015	0.969	1.078	0.947	1.053	1.009	1.022	0.917	1.052	1.038	0.962	1.055	1.034	1.042
7	C7	0.1	7	BRMS296_142	-0.055 7.00E-01	2.062 5.20E-01	-1.802 3.30E-01	3.109 1.90E-01	-3.343 2.50E-01	0.053 3.60E-01	0.012 8.10E-01	0.142 7.20E-01	-0.056 5.80E-01	0.725 1.40E-01	0.806 2.50E-01	-0.262 2.80E-01	0.339 6.30E-01	1.316 6.90E-02	1.708 4.90E-02
					0.994	1.019	0.974	1.084	0.954	1.051	1.009	1.025	0.917	1.059	1.044	0.959	1.051	1.031	1.041
7	C7	16.6	7	BRAS019_128	-0.033 2.60E-01	2.588 1.80E-01	-1.477 6.60E-01	3.36 3.60E-01	-2.892 6.70E-01	0.052 3.80E-01	0.011 8.80E-01	0.161 6.70E-01	-0.056 9.70E-01	0.825 3.80E-01	0.924 4.10E-01	-0.282 9.70E-01	0.317 6.40E-01	1.23 1.20E-01	1.678 6.10E-02
					0.983	1.039	1.012	1.058	0.982	1.05	0.994	1.029	1.006	1.035	1.032	0.998	1.049	1.027	1.038
					-0.097	5.275	0.677	2.312	-1.111	0.05	-0.007	0.187	0.004	0.49	0.675	-0.011	0.302	1.048	1.578
8	uk2	0	8	FITO300_127	3.30E-02	1.50E-01	4.90E-01	2.90E-02	2.90E-01	3.90E-01	3.50E-01	5.60E-01	7.80E-01	3.30E-02	8.40E-02	2.90E-01	1.00E+00	8.50E-01	9.80E-01
					1.032	0.961	1.018	0.877	0.956	1.048	0.967	0.962	1.045	0.923	0.938	1.041	1	1.003	1
8	uk2	14.9	8	FITO110_291	0.181 3.40E-01	-5.529 2.40E-02	1.047 7.20E-01	-5.426 5.50E-02	-2.716 1.10E-01	0.049 1.20E-01	-0.043 8.90E-02	-0.253 1.60E-01	0.028 6.70E-01	-1.156 5.50E-03	-1.375 7.00E-03	0.269 2.50E-01	0.004 8.60E-01	0.13 4.70E-01	-0.017 8.60E-01
					1.015	0.937	1.01	0.888	0.934	1.091	0.94	0.909	0.936	0.9	0.904	1.045	1.018	1.013	0.996
8	uk2	19.4	8	OL10A05_190	0.084 2.90E-01	-8.929 3.60E-02	0.554 3.40E-01	-4.89 7.10E-02	-4.199 2.60E-01	0.091 1.00E-01	-0.077 2.30E-01	-0.63 1.80E-01	-0.043 6.50E-01	-1.522 1.20E-02	-2.187 1.30E-02	0.298 2.60E-01	0.113 9.80E-01	0.497 8.80E-01	-0.153 6.90E-01
					1.016	0.942	1.026	0.895	0.953	1.093	0.958	0.915	0.931	0.909	0.912	1.044	1.002	1.003	0.992

					0.091	-8.211	1.456	-4.58	-2.935	0.093	-0.054	-0.584	-0.046	-1.369	-1.99	0.29	0.012	0.105	-0.347
9	A3/A4	0	9	BRMS008_156	9.30E-01	2.00E-01	4.90E-01	2.90E-01	6.40E-01	7.00E-01	4.50E-01	7.10E-01	6.90E-01	5.50E-01	5.90E-01	7.30E-01	5.60E-01	8.80E-01	6.00E-01
					0.999	0.964	0.982	0.938	0.98	1.021	0.973	0.976	1.063	0.978	0.98	0.987	0.943	0.998	0.99
9	A3/A4	14.2	9	IGF5193a	-0.008	-4.978	-1.046	-2.667	-1.211	0.021	-0.034	-0.162	0.039	-0.326	-0.435	-0.087	-0.375	-0.097	-0.439
					2.90E-01	1.70E-01	3.60E-01	3.10E-01	2.70E-01	6.30E-01	5.40E-02	1.30E-01	6.40E-01	6.10E-01	2.70E-01	7.90E-01	7.40E-01	4.20E-02	1.80E-02
					1.016	0.962	0.976	0.94	0.954	1.027	0.933	0.905	1.076	0.981	0.96	1.01	1.035	0.966	0.954
1					0.092	-5.351	-1.388	-2.592	-2.868	0.027	-0.086	-0.663	0.046	-0.282	-0.892	0.069	0.215	-1.363	-1.985
0	A3	0	0	IGF5272c	3.00E-01	5.00E-01	7.70E-02	9.20E-02	3.90E-01	2.70E-01	3.30E-01	4.50E-01	2.70E-01	6.70E-01	7.90E-01	8.10E-01	4.80E-03	7.40E-01	9.00E-01
					1.016	0.98	1.049	1.112	1.039	0.941	0.964	0.95	0.844	1.017	0.99	0.99	0.754	1.006	0.998
1					0.091	-2.753	2.749	4.367	2.303	-0.064	-0.045	-0.336	-0.108	0.243	-0.216	-0.064	-1.821	0.224	-0.104
0	A3	6.7	0	BRMS008_115	7.60E-02	7.70E-01	2.40E-02	1.60E-01	3.20E-01	3.60E-01	3.60E-01	4.10E-01	5.10E-01	6.80E-01	7.90E-01	8.00E-01	1.50E-02	9.90E-01	7.70E-01
					1.027	0.992	1.06	1.089	1.043	0.952	0.968	0.947	0.904	1.016	0.99	1.009	0.786	1	0.994
1					0.15	-1.155	3.345	3.518	2.533	-0.052	-0.041	-0.359	-0.065	0.225	-0.212	0.063	-1.53	0.007	-0.244
0	A3	12.8	0	MAX2_I	2.50E-02	9.50E-01	4.90E-02	1.60E-01	8.60E-01	5.20E-01	3.10E-01	6.00E-01	6.00E-01	7.90E-01	8.50E-01	9.50E-01	2.80E-02	6.60E-01	9.60E-01
					1.036	1.002	1.061	1.101	1.008	1.034	0.96	0.962	0.916	1.011	0.993	0.998	0.805	1.008	1.001
1					0.201	0.234	3.338	3.962	0.496	0.034	-0.05	-0.251	-0.056	0.16	-0.164	-0.015	-1.421	0.321	0.042
0	A3	19.9	0	BRMS330_241	1.10E-02	7.50E-01	9.10E-03	2.70E-01	3.80E-01	8.60E-01	5.90E-01	5.10E-01	7.70E-01	9.80E-01	7.00E-01	8.70E-01	1.60E-02	5.30E-01	8.50E-01
					1.038	0.991	1.07	1.069	1.037	0.991	0.981	0.958	0.957	1.001	0.986	1.006	0.785	1.011	1.004
1					0.213	-1.263	3.848	2.765	2.243	-0.01	-0.025	-0.281	-0.028	0.013	-0.309	0.041	-1.518	0.423	0.156
0	A3	42.1	0	RA2E11_200	8.70E-02	6.70E-01	1.60E-01	7.90E-01	6.20E-01	4.60E-01	8.10E-01	3.70E-01	3.10E-01	8.20E-01	8.20E-01	5.00E-01	5.90E-01	8.00E-01	7.80E-01
					1.026	1.012	1.038	1.016	1.022	1.041	0.991	0.942	1.17	1.009	0.992	1.026	1.056	0.996	0.994
1					0.148	1.675	2.148	0.669	1.3	0.042	-0.011	-0.393	0.101	0.124	-0.181	0.174	0.347	-0.175	-0.24
0	A3	43.3	0	CB10036_131	1.40E-01	6.70E-01	2.00E-01	5.60E-01	6.50E-01	4.60E-01	6.20E-01	2.20E-01	2.40E-01	5.40E-01	9.20E-01	6.20E-01	4.50E-01	8.20E-01	7.80E-01
					1.022	1.012	1.035	1.037	1.02	1.041	0.982	0.922	1.202	1.024	0.996	1.019	1.081	0.996	0.994
1					0.124	1.701	1.97	1.495	1.198	0.042	-0.022	-0.536	0.117	0.346	-0.085	0.13	0.487	-0.158	-0.24
0	A3	66.4	0	OL11B05_109	8.00E-01	5.10E-01	1.50E-01	2.80E-01	8.40E-01	4.70E-02	5.50E-01	6.20E-01	1.40E-01	6.70E-01	8.60E-01	7.50E-01	9.00E-01	1.00E-01	3.00E-01
					1.004	1.02	1.04	1.07	1.009	1.115	0.978	0.966	0.783	1.017	0.993	1.013	0.987	0.972	0.978
1					0.022	2.686	2.267	2.837	0.542	0.115	-0.028	-0.227	-0.15	0.241	-0.146	0.085	-0.084	-1.123	-0.91
0	A3	66.7	0	NA12E02_118	9.10E-01	5.20E-01	1.50E-01	3.10E-01	7.60E-01	5.40E-02	7.00E-01	7.10E-01	1.40E-01	7.20E-01	8.80E-01	7.70E-01	8.70E-01	1.20E-01	3.30E-01

					1.002	1.019	1.041	1.066	1.014	1.113	0.985	0.974	0.777	1.014	0.994	1.012	0.983	0.973	0.979
1		68.	1		0.01	2.653	2.305	2.679	0.837	0.113	-0.019	-0.172	-0.154	0.206	-0.13	0.078	-0.109	-1.091	-0.871
0	A3	1	0	CB10427_138	9.90E-01	4.00E-01	1.20E-01	3.00E-01	4.00E-01	2.30E-01	8.60E-01	8.70E-01	4.70E-02	7.20E-01	9.40E-01	8.50E-01	3.90E-01	2.00E-01	5.00E-01
					1	1.025	1.044	1.068	1.038	1.069	0.993	1.012	0.709	1.014	1.003	1.007	0.911	0.978	0.986
1		94.	1		0.001	3.443	2.493	2.781	2.278	0.07	-0.009	0.077	-0.205	0.207	0.069	0.051	-0.579	-0.894	-0.605
0	A3	4	0	SN11722_93	3.80E-01	1.60E-01	1.60E-01	4.50E-01	9.90E-01	1.00E+00	1.30E-01	9.90E-02	6.10E-01	5.20E-01	6.10E-01	6.50E-01	6.60E-01	2.00E-01	3.40E-01
					0.987	0.961	0.963	1.047	1	1	0.948	0.896	0.922	1.025	0.981	0.983	1.042	1.022	1.02
1			1		-0.075	-5.456	-2.131	1.904	-0.019	0	-0.067	-0.719	-0.052	0.357	-0.419	-0.117	0.267	0.867	0.824
0	A3	106	0	NA10D03_157	1.40E-01	6.90E-01	3.10E-01	7.40E-01	7.40E-01	5.00E-01	3.70E-01	5.80E-01	5.40E-01	2.80E-01	6.10E-01	4.40E-01	5.90E-01	4.00E-01	6.50E-01
					0.979	0.989	0.974	1.02	0.986	1.037	0.968	0.964	1.098	1.042	1.019	0.971	1.056	1.014	1.009
1		108	1		-0.124	-1.573	-1.528	0.844	-0.85	0.038	-0.04	-0.241	0.06	0.596	0.41	-0.197	0.344	0.564	0.382
0	A3	.5	0	IGF3100b	1.60E-01	6.60E-01	5.00E-01	9.50E-01	7.30E-01	6.90E-01	5.20E-01	9.40E-01	8.80E-01	2.70E-01	4.70E-01	3.30E-01	9.20E-01	6.70E-01	8.00E-01
					0.979	0.988	0.982	1.004	1.015	1.022	0.977	0.995	1.023	1.043	1.027	0.963	1.011	1.007	1.005
1		111	1		-0.121	-1.704	-1.017	0.169	0.882	0.022	-0.029	-0.035	0.015	0.602	0.577	-0.251	0.068	0.284	0.218
0	A3	.7	0	RGA2_H24_13_150	3.50E-01	3.80E-01	3.90E-01	8.40E-01	9.20E-01	6.80E-01	2.80E-01	6.10E-01	9.90E-01	4.10E-01	7.60E-01	3.50E-01	8.00E-01	9.70E-01	8.10E-01
					0.986	0.975	0.978	0.988	1.004	1.022	0.962	0.967	1.002	1.032	1.012	0.966	1.026	1.001	0.995
1		111	1		-0.08	-3.438	-1.286	-0.517	0.26	0.023	-0.048	-0.22	0.001	0.451	0.248	-0.237	0.164	0.023	-0.204
0	A3	.7	0	RGA2_H24_14_300	3.50E-01	3.80E-01	3.90E-01	8.40E-01	9.20E-01	6.80E-01	2.80E-01	6.10E-01	9.90E-01	4.10E-01	7.60E-01	3.50E-01	8.00E-01	9.70E-01	8.10E-01
					0.986	0.975	0.978	0.988	1.004	1.022	0.962	0.967	1.002	1.032	1.012	0.966	1.026	1.001	0.995
					-0.08	-3.438	-1.286	-0.517	0.26	0.023	-0.048	-0.22	0.001	0.451	0.248	-0.237	0.164	0.023	-0.204
1			1	KBrB078A03(1)	4.50E-03	6.00E-01	1.20E-01	4.00E-02	8.90E-01	3.40E-02	6.80E-01	2.10E-01	2.40E-02	1.30E-01	5.40E-01	1.00E-01	4.50E-01	2.00E-01	1.30E-01
1	C1	0	1		0.956	1.016	1.045	0.872	0.994	1.128	0.984	1.093	0.664	0.94	0.975	1.069	1.086	0.977	0.967
1			1		-0.26	2.239	2.556	-5.557	-0.382	0.128	-0.021	0.594	-0.237	-0.887	-0.537	0.456	0.53	-0.926	-1.381
1	C1	1	1	BRAS067_136	9.50E-03	5.80E-01	1.20E-01	5.70E-02	7.70E-01	2.70E-02	4.50E-01	3.00E-01	2.70E-02	1.70E-01	5.20E-01	9.30E-02	4.20E-01	1.60E-01	1.10E-01
					0.96	1.017	1.045	0.882	0.986	1.132	0.971	1.076	0.673	0.945	0.974	1.07	1.09	0.975	0.966
1			1		-0.235	2.336	2.519	-5.104	-0.828	0.132	-0.036	0.487	-0.232	-0.806	-0.557	0.46	0.556	-0.995	-1.446
1	C1	1	1	NA12H02_219	9.50E-03	5.80E-01	1.20E-01	5.70E-02	7.70E-01	2.70E-02	4.50E-01	3.00E-01	2.70E-02	1.70E-01	5.20E-01	9.30E-02	4.20E-01	1.60E-01	1.10E-01

					0.96	1.017	1.045	0.882	0.986	1.132	0.971	1.076	0.673	0.945	0.974	1.07	1.09	0.975	0.966
1			1		-0.235	2.336	2.519	-5.104	-0.828	0.132	-0.036	0.487	-0.232	-0.806	-0.557	0.46	0.556	-0.995	-1.446
1	C1	2.1	1	SN3734_288	1.40E-02	5.60E-01	1.40E-01	9.40E-02	8.60E-01	4.30E-02	4.60E-01	3.00E-01	2.40E-02	2.50E-01	6.20E-01	1.30E-01	4.60E-01	2.40E-01	1.90E-01
					0.962	1.018	1.042	0.896	0.992	1.12	0.972	1.074	0.671	0.955	0.98	1.062	1.081	0.979	0.972
1		15.	1		-0.221	2.454	2.354	-4.461	-0.487	0.12	-0.035	0.476	-0.234	-0.664	-0.43	0.41	0.503	-0.839	-1.168
1	C1	3	1	IGF3338a	3.30E-01	9.70E-01	5.40E-01	9.30E-01	3.40E-01	2.50E-01	2.60E-01	9.90E-01	3.40E-01	3.60E-01	4.50E-01	3.40E-01	8.90E-01	5.00E-01	5.50E-01
					0.981	0.998	1.021	1.008	0.949	1.065	0.944	1.001	0.807	0.955	0.964	1.04	0.985	0.985	0.985
1		24.	1		-0.109	-0.216	1.198	0.316	-3.155	0.066	-0.07	0.006	-0.128	-0.664	-0.793	0.27	-0.094	-0.597	-0.647
1	C1	8	1	IGF0504b	7.50E-02	7.70E-01	6.50E-01	5.80E-01	2.80E-01	9.40E-02	4.20E-02	5.30E-01	8.10E-02	1.20E-01	9.40E-02	3.00E-02	2.00E-01	5.30E-01	3.70E-01
					0.972	1.009	1.013	0.964	0.952	1.102	0.926	0.956	0.738	0.938	0.936	1.092	1.151	0.988	0.981
1		27.	1		-0.161	1.215	0.759	-1.504	-2.997	0.102	-0.096	-0.297	-0.189	-0.916	-1.418	0.599	0.905	-0.461	-0.816
1	C1	1	1	IGF1059e	1.10E-01	7.30E-01	9.00E-01	6.10E-01	2.20E-01	1.20E-01	6.70E-02	7.50E-01	3.30E-01	3.20E-01	3.20E-01	2.20E-01	2.60E-01	5.30E-01	3.90E-01
					0.976	1.01	1.004	0.968	0.947	1.089	0.935	0.978	0.855	0.962	0.963	1.049	1.122	0.989	0.982
1		30.	1		-0.141	1.381	0.204	-1.326	-3.278	0.09	-0.084	-0.144	-0.098	-0.559	-0.814	0.322	0.74	-0.436	-0.747
1	C1	9	1	KBrB036M22(3)	2.30E-01	4.50E-01	4.90E-01	8.00E-01	4.00E-01	2.10E-01	1.20E-01	9.40E-01	4.80E-01	2.60E-01	3.60E-01	1.10E-01	3.40E-01	6.00E-01	4.80E-01
					0.981	1.023	1.019	0.984	0.963	1.074	0.942	0.994	0.888	0.955	0.964	1.066	1.108	0.991	0.985
1		38.	1		-0.108	3.141	1.1	-0.666	-2.283	0.075	-0.074	-0.037	-0.074	-0.661	-0.787	0.436	0.652	-0.373	-0.642
1	C1	1	1	IGF3315b	1.50E-01	6.40E-01	3.60E-01	6.20E-01	4.70E-01	7.00E-01	1.50E-01	5.40E-01	8.60E-01	4.30E-01	8.80E-01	9.80E-01	2.30E-01	6.20E-01	7.70E-01
					0.977	1.014	0.973	1.034	0.968	1.019	0.944	0.958	0.973	1.031	1.006	1.001	1.127	0.991	0.994
1			1		-0.134	1.903	-1.55	1.405	-2.014	0.02	-0.072	-0.288	-0.016	0.448	0.129	0.005	0.76	-0.358	-0.269
1	C1	51	1	RA2E11_205	6.90E-01	7.70E-01	8.10E-01	9.10E-01	1.20E-01	1.30E-01	2.70E-02	3.60E-01	3.70E-01	8.90E-01	4.90E-01	6.60E-01	2.90E-01	7.50E-01	8.30E-01
					0.994	0.992	0.994	1.007	0.936	1.085	0.925	0.941	0.872	0.995	0.975	1.017	1.111	1.005	0.996
1		52.	1		-0.035	-1.134	-0.368	0.274	-4.005	0.085	-0.097	-0.398	-0.087	-0.076	-0.554	0.11	0.668	0.21	-0.175
1	C1	9	1	OL12F11_233	6.50E-01	8.90E-01	9.80E-01	6.80E-01	2.00E-01	1.60E-01	9.80E-02	5.90E-01	3.10E-01	7.00E-01	5.00E-01	5.90E-01	3.00E-01	9.20E-01	8.00E-01
					0.993	0.996	1.001	0.976	0.948	1.079	0.943	0.965	0.856	0.986	0.976	1.02	1.109	1.002	0.995
1		89.	1		-0.039	-0.514	0.037	-1.021	-3.245	0.079	-0.074	-0.234	-0.099	-0.21	-0.536	0.136	0.655	0.065	-0.214
1	C1	9	1	MAX_4r	7.20E-01	2.90E-01	9.10E-01	8.00E-01	9.90E-01	6.50E-01	4.60E-01	5.20E-01	7.80E-01	7.80E-01	6.20E-01	7.20E-01	3.80E-01	7.80E-01	8.40E-01
					1.005	0.97	0.997	0.984	0.999	1.025	0.974	0.959	1.044	0.99	0.982	0.987	0.914	1.005	1.004
					0.031	-4.134	-0.178	-0.652	-0.037	0.025	-0.033	-0.279	0.028	-0.15	-0.391	-0.091	-0.564	0.182	0.165

1		101	1		9.30E-01	7.50E-01	4.20E-01	9.40E-01	2.60E-01	9.80E-01	7.80E-01	5.80E-01	7.30E-01	6.40E-01	9.80E-01	7.40E-01	4.60E-01	8.60E-01	8.20E-01
1	C1	.2	1	MAX_4n	1.001	0.991	1.023	1.005	1.052	1.001	0.99	0.963	0.948	1.018	0.999	0.987	0.924	0.997	1.005
					0.007	-1.299	1.289	0.208	3.087	0.001	-0.013	-0.254	-0.035	0.261	-0.019	-0.087	-0.497	-0.118	0.196
1			1		7.80E-01	3.50E-02	9.10E-01	4.10E-02	5.90E-01	3.90E-01	2.20E-01	8.10E-02	3.20E-01	3.80E-02	2.60E-02	3.30E-01	9.00E-01	9.80E-02	5.50E-02
2	A7	0	2	NA12A05_157	0.996	0.942	1.003	0.883	0.978	1.047	0.958	0.891	1.171	0.924	0.921	1.038	1.013	0.972	0.962
					-0.024	-8.254	0.183	-5.152	-1.354	0.048	-0.054	-0.757	0.1	-1.139	-1.782	0.253	0.084	-1.115	-1.627
1			1		2.10E-01	4.50E-03	7.70E-01	5.00E-03	7.10E-01	3.20E-01	3.60E-01	3.20E-01	6.70E-01	2.40E-02	4.40E-02	8.50E-01	6.70E-01	3.80E-02	2.70E-02
2	A7	5.4	2	OL12E03_110	0.982	0.925	1.008	0.847	0.984	1.055	0.968	0.937	1.069	0.919	0.929	1.007	0.958	0.966	0.957
					-0.105	-10.79	0.445	-6.891	-0.953	0.055	-0.041	-0.429	0.042	-1.214	-1.587	0.049	-0.272	-1.367	-1.836
1		42.	1		3.50E-02	1.30E-04	5.60E-01	1.70E-01	9.70E-01	8.10E-01	4.40E-02	1.90E-02	6.90E-01	5.60E-02	8.30E-03	7.80E-01	3.50E-01	2.80E-02	1.20E-02
2	A7	3	2	IGF1226a	0.969	0.899	0.984	0.92	1.002	1.013	0.93	0.856	0.94	0.93	0.908	1.01	0.909	0.964	0.951
					-0.182	14.573	-0.902	-3.455	0.098	0.013	-0.09	-1.014	-0.039	-1.038	-2.076	0.07	-0.596	-1.455	-2.085
1		53.	1		2.50E-02	6.00E-05	1.90E-01	2.10E-01	5.00E-01	6.00E-01	5.30E-02	1.20E-02	2.50E-01	6.90E-02	5.50E-03	9.10E-01	2.90E-01	2.20E-01	6.70E-02
2	A7	1	2	IGF1226f	0.967	0.894	0.966	0.925	0.972	1.03	0.932	0.847	0.833	0.933	0.903	1.004	0.897	0.979	0.964
					-0.194	15.355	-1.961	-3.229	-1.762	0.031	-0.088	-1.095	-0.116	-0.994	-2.196	0.027	-0.681	-0.826	-1.555
1		85.	1		8.40E-01	2.90E-01	3.00E-01	7.30E-01	2.00E-01	8.80E-01	5.40E-01	2.90E-01	7.20E-01	8.30E-01	4.90E-01	9.60E-01	5.30E-01	3.50E-01	5.20E-01
2	A7	6	2	BRMS036_130	0.997	0.971	1.027	0.979	1.056	1.008	0.978	0.932	1.057	0.992	0.975	1.002	1.066	0.984	0.987
					-0.018	-4.099	1.547	-0.868	3.324	0.009	-0.028	-0.46	0.036	-0.115	-0.553	0.013	0.403	-0.625	-0.542
1		87.	1		9.50E-01	4.30E-01	3.00E-01	5.40E-01	3.10E-01	4.30E-01	4.20E-01	2.60E-01	8.10E-01	6.40E-01	3.60E-01	5.30E-01	2.20E-01	1.20E-01	2.70E-01
2	A7	8	2	IGF0504f	0.999	0.977	1.028	0.963	1.044	1.045	0.972	0.928	1.04	0.982	0.966	1.025	1.137	0.974	0.978
					-0.005	-3.142	1.606	-1.584	2.63	0.045	-0.036	-0.497	0.025	-0.262	-0.748	0.164	0.804	-1.045	-0.946
1			1		7.70E-02	6.90E-01	9.00E-02	4.50E-01	3.30E-01	9.50E-01	4.00E-01	9.40E-02	3.20E-01	7.80E-01	5.60E-01	8.30E-01	5.30E-01	9.50E-02	2.60E-01
3	A1	0	3	SN11641_405	1.027	0.989	0.956	1.048	0.958	1.004	0.97	0.894	1.173	1.011	0.978	1.008	1.067	0.972	0.977
					0.156	-1.589	-2.606	1.927	-2.585	0.004	-0.039	-0.744	0.101	0.156	-0.479	0.056	0.416	-1.142	-0.969
1			1		6.90E-02	7.80E-01	6.60E-02	1.10E-01	6.10E-01	6.90E-01	5.80E-01	1.40E-01	4.00E-01	3.60E-01	9.60E-01	7.90E-01	9.70E-01	2.40E-01	4.90E-01
3	A1	2.4	3	KBrB048F07(2)	1.027	0.992	0.953	1.102	0.978	0.978	0.98	0.908	1.142	1.036	0.998	0.99	1.004	0.98	0.986
					0.155	-1.12	-2.78	4	-1.331	-0.023	-0.025	-0.639	0.084	0.508	-0.039	-0.069	0.027	-0.793	-0.59
1			1		1.20E-01	8.70E-01	3.20E-01	5.10E-01	6.10E-01	4.00E-01	7.80E-01	2.30E-01	6.40E-01	9.50E-01	5.40E-01	3.00E-01	4.20E-01	1.20E-01	4.90E-01
3	A1	11	3	CB10097_191															

					1.023	1.005	0.974	1.041	0.978	1.047	0.99	0.924	1.076	0.998	0.977	1.041	1.087	0.974	0.986
1		19.	1		0.133	0.639	-1.536	1.677	-1.354	0.047	-0.013	-0.523	0.047	-0.034	-0.503	0.268	0.528	-1.039	-0.596
3	A1	5	3	MAX4_p	1.70E-01	8.80E-01	1.70E-01	8.50E-01	4.60E-01	6.60E-01	5.40E-01	8.60E-01	4.60E-01	1.00E+00	9.90E-01	8.70E-01	7.60E-01	3.30E-01	6.10E-01
					1.02	0.996	0.964	1.011	0.969	1.024	1.022	0.988	1.123	1	1	1.006	1.031	0.984	0.99
					0.117	-0.607	-2.099	0.473	-1.911	0.025	0.027	-0.077	0.074	0	0.01	0.041	0.194	-0.647	-0.423
1			1		6.10E-01	4.50E-01	1.20E-01	2.40E-01	1.60E-01	9.80E-01	9.90E-01	4.60E-01	5.70E-01	8.20E-01	8.60E-01	4.40E-01	1.70E-02	1.00E+00	8.10E-01
4	A9/C5	0	4	IGF3112a															
					1.008	1.023	1.043	1.077	1.063	1.001	0.999	1.051	0.912	0.991	1.007	1.031	0.779	1	1.005
1		35.	1		0.046	3.096	2.443	3.074	3.716	0.001	-0.001	0.326	-0.06	-0.131	0.141	0.203	-1.577	-0.004	0.206
4	A9/C5	5	4	OL12F02_148	3.30E-01	9.60E-01	1.20E-02	1.20E-02	8.20E-01	1.30E-01	7.60E-01	7.20E-01	3.00E-01	1.60E-03	1.40E-02	2.30E-03	9.70E-01	4.90E-01	2.90E-01
					0.985	0.999	1.067	0.86	1.01	1.085	0.989	0.977	0.853	0.889	0.914	1.12	1.003	0.988	0.979
1		36.	1		-0.084	-0.195	3.736	-6.231	0.596	0.085	-0.014	-0.156	-0.101	-1.69	-1.941	0.766	0.021	-0.467	-0.897
4	A9/C5	6	4	NA12D10_150	2.30E-01	6.80E-01	3.40E-02	6.50E-03	1.00E+00	1.50E-01	6.60E-01	5.90E-01	1.90E-01	4.80E-04	4.80E-03	2.20E-03	9.80E-01	3.90E-01	1.90E-01
					0.982	0.988	1.057	0.85	1	1.082	0.984	0.965	0.817	0.879	0.903	1.121	1.003	0.985	0.974
					-0.103	-1.593	3.185	-6.748	-0.013	0.082	-0.019	-0.235	-0.129	-1.861	-2.219	0.769	0.018	-0.582	-1.104
1			1		4.10E-01	5.30E-01	3.70E-01	2.90E-01	1.00E+00	9.10E-01	8.10E-01	6.40E-01	1.10E-01	3.70E-02	1.40E-01	1.90E-01	5.10E-01	2.90E-01	4.30E-01
5	A10	0	5	FITO247_277															
					0.988	0.982	1.024	0.939	1	0.994	0.991	0.969	1.279	0.925	0.947	1.05	1.069	0.982	0.984
1			1		-0.071	-2.442	1.337	-2.638	0.012	-0.007	-0.011	-0.204	0.156	-1.125	-1.168	0.331	0.421	-0.705	-0.655
5	A10	5.8	5	RA2E07_93	5.10E-01	9.00E-01	2.20E-01	3.10E-01	3.80E-01	6.10E-01	7.70E-01	9.80E-01	3.30E-01	3.40E-02	2.00E-01	1.80E-01	6.10E-01	1.10E-01	3.40E-01
					0.99	0.996	1.033	0.94	1.038	0.973	1.011	1.002	1.162	0.923	0.953	1.053	1.053	0.973	0.981
1			1		-0.056	-0.497	1.866	-2.567	2.254	-0.028	0.013	0.01	0.096	-1.152	-1.04	0.347	0.325	-1.067	-0.807
5	A10	6	5	IGF1073a	4.60E-01	8.90E-01	2.20E-01	2.80E-01	3.50E-01	5.80E-01	6.60E-01	9.10E-01	3.40E-01	3.10E-02	2.00E-01	1.80E-01	6.30E-01	1.20E-01	3.60E-01
					0.989	0.996	1.033	0.937	1.04	0.971	1.016	1.007	1.159	0.922	0.954	1.051	1.05	0.975	0.982
					-0.063	-0.549	1.844	-2.682	2.417	-0.031	0.019	0.049	0.095	-1.167	-1.018	0.338	0.307	-1.021	-0.762
1			1		4.20E-01	4.80E-01	9.10E-01	4.20E-01	8.30E-01	5.50E-01	1.50E-01	6.20E-01	8.30E-02	7.90E-01	8.90E-01	6.70E-01	2.80E-01	9.40E-02	3.30E-01
6	C7	0	6	IGF5702e															
					1.012	1.02	0.997	1.05	0.991	1.032	1.052	1.034	0.762	0.99	0.995	1.016	0.896	0.972	0.98
1			1		0.07	2.778	-0.177	2.044	-0.568	0.034	0.064	0.217	-0.169	-0.149	-0.113	0.11	-0.688	-1.112	-0.826
6	C7	7.6	6	IGF5707b	7.60E-01	7.80E-01	9.10E-01	7.70E-01	5.60E-01	2.80E-01	5.20E-01	5.80E-01	2.30E-01	4.60E-01	3.30E-01	4.10E-01	3.70E-01	4.40E-02	9.20E-02
					0.995	0.992	0.997	1.018	0.976	1.06	1.023	0.964	0.83	0.972	0.964	1.032	0.914	0.967	0.967
					-0.027	-1.091	-0.168	0.732	-1.508	0.061	0.028	-0.242	-0.117	-0.406	-0.78	0.212	-0.571	-1.331	-1.407

1		22.	1		9.80E-	6.40E-	3.40E-	8.20E-	6.70E-	6.20E-	4.70E-	4.50E-	4.00E-	4.10E-	2.80E-	8.50E-	8.80E-	4.10E-	1.30E-
6	C7	8	6	IGF5415a	01	01	01	01	01	02	01	01	01	01	01	02	01	02	01
					1	1.014	1.026	1.014	0.981	1.109	1.027	0.951	0.872	0.968	0.959	1.068	0.984	0.965	0.969
					-0.001	1.899	1.483	0.582	-1.152	0.108	0.034	-0.331	-0.086	-0.466	-0.898	0.447	-0.101	-1.398	-1.321
1			1		6.80E-	4.30E-	2.40E-	9.90E-	7.90E-	4.00E-	6.50E-	7.50E-	4.30E-	5.10E-	6.90E-	2.90E-	2.20E-	1.60E-	7.10E-
7	A5	0	7	CB10320_253	01	01	01	01	01	01	01	01	01	01	01	01	01	01	02
					1.006	1.023	1.032	1.001	0.989	1.047	1.017	1.022	0.883	0.975	0.985	1.041	0.88	0.976	0.964
					0.037	3.11	1.784	0.026	-0.691	0.048	0.021	0.141	-0.079	-0.369	-0.319	0.273	-0.801	-0.951	-1.525
1		29.	1		1.80E-	7.60E-	4.50E-	7.00E-	1.80E-	1.20E-	6.90E-	6.30E-	8.70E-	3.90E-	7.20E-	6.50E-	5.00E-	8.80E-	8.80E-
7	A5	5	7	BRMS061_284	01	01	01	01	01	01	01	01	01	01	01	01	01	01	01
					0.98	0.991	1.021	1.024	1.06	0.917	0.986	0.969	1.025	1.034	1.014	0.982	0.932	1.003	0.997
					-0.117	-1.219	1.181	0.984	3.555	-0.09	-0.018	-0.212	0.016	0.48	0.291	-0.119	-0.442	0.102	-0.125
1		44.	1		5.80E-	2.70E-	5.30E-	4.30E-	7.00E-	6.00E-	2.00E-	1.90E-	8.20E-	7.60E-	3.50E-	6.10E-	1.00E+	8.20E-	4.10E-
7	A5	2	7	BRAS063_236	02	01	01	01	01	01	01	01	01	01	01	01	00	01	01
					0.972	0.969	1.017	0.953	1.017	0.971	0.955	0.917	0.965	0.988	0.965	1.02	1	0.996	0.983
					-0.165	-4.383	0.977	-2.03	1.025	-0.031	-0.058	-0.579	-0.023	-0.172	-0.768	0.135	0.002	-0.154	-0.706
1			1		2.70E-	8.80E-	4.10E-	1.40E-	9.20E-	7.90E-	7.90E-	4.40E-	4.90E-	3.10E-	2.30E-	1.10E-	5.40E-	1.70E-	3.60E-
8	A9	0	8	IGF5222b	02	01	01	01	01	01	01	01	01	01	01	01	02	02	02
					0.967	0.995	0.978	1.095	0.995	0.985	0.99	1.055	1.116	1.04	1.046	0.941	0.82	1.041	1.043
					-0.196	-0.647	-1.281	3.741	-0.286	-0.016	-0.013	0.35	0.071	0.569	0.982	-0.413	-1.262	1.593	1.776
1			1		3.60E-	9.50E-	4.40E-	7.80E-	9.60E-	8.10E-	4.90E-	5.70E-	3.10E-	6.50E-	4.60E-	2.50E-	8.20E-	9.90E-	5.40E-
8	A9	37	8	IGF5706e	02	01	02	01	01	01	01	01	01	01	01	01	01	01	01
					0.969	0.998	0.948	1.017	1.002	1.013	1.025	1.039	1.174	1.017	1.028	0.958	1.024	1	1.012
					-0.18	-0.228	-3.033	0.695	0.135	0.014	0.031	0.25	0.101	0.25	0.594	-0.291	0.148	-0.007	0.52
1			1		8.60E-	5.30E-	2.40E-	1.90E-	3.30E-	3.90E-	8.40E-	4.90E-	2.80E-	3.60E-	9.10E-	8.90E-	2.80E-	1.50E-	1.10E-
9	A9	0	9	IGF1207c	04	01	01	01	01	01	01	01	01	01	01	01	01	01	01
					0.953	0.982	1.031	0.924	1.042	0.954	1.007	1.047	1.184	0.966	0.996	1.005	0.896	1.025	1.033
					-0.275	-2.491	1.769	-3.323	2.523	-0.048	0.009	0.304	0.108	-0.496	-0.094	0.034	-0.699	0.971	1.369
1			1		3.30E-	4.20E-	2.90E-	1.60E-	3.70E-	4.50E-	7.50E-	4.30E-	4.90E-	3.60E-	9.00E-	9.40E-	2.50E-	1.90E-	1.40E-
9	A9	1.1	9	OL12F02_119	03	01	01	01	01	01	01	01	01	01	01	01	01	01	01
					0.959	0.977	1.028	0.918	1.039	0.96	1.011	1.054	1.112	0.966	0.995	1.003	0.889	1.023	1.03
					-0.239	-3.183	1.582	-3.536	2.31	-0.043	0.014	0.344	0.068	-0.501	-0.098	0.02	-0.744	0.887	1.235
0	um	0	0	BRAS038_120	1.60E-	5.30E-	3.60E-	3.10E-	4.00E-	5.80E-	8.10E-	8.30E-	9.80E-	2.20E-	4.60E-	2.00E-	5.00E-	6.70E-	7.20E-
					01	01	01	01	02	01	01	01	01	01	01	01	02	01	01
					0.979	1.018	0.976	0.94	0.916	1.031	0.991	1.015	1.004	0.953	0.972	1.052	1.232	0.993	0.993
					-0.125	2.502	-1.423	-2.605	-5.391	0.032	-0.011	0.096	0.003	-0.696	-0.607	0.338	1.282	-0.295	-0.313
0	um	0	0	BRMS007_116	6.80E-	9.60E-	1.60E-	1.40E-	4.60E-	8.90E-	1.60E-	2.30E-	3.30E-	2.90E-	8.60E-	7.40E-	2.30E-	6.40E-	8.30E-
					01	01	01	01	02	01	01	01	01	01	01	01	01	01	01
					0.994	0.999	1.038	0.914	1.087	1.007	1.051	1.081	0.861	0.961	0.993	1.013	0.886	0.992	0.996

					-0.035	-0.205	2.14	-3.721	5.095	0.008	0.061	0.515	-0.095	-0.578	-0.143	0.085	-0.767	-0.317	-0.178
0	um	0	0	BRMS061_297	1.60E-02	8.20E-01	9.90E-01	7.10E-02	8.80E-01	2.20E-01	4.00E-01	1.30E-01	6.30E-01	5.80E-01	7.20E-01	7.10E-01	4.60E-01	1.30E-01	6.20E-02
					1.037	0.993	1	1.117	1.006	0.934	0.97	0.902	1.08	1.022	0.987	1.015	0.924	0.974	0.962
0	um	0	0	BRMS098_146	0.209	-0.934	-0.023	4.646	0.394	-0.071	-0.038	-0.677	0.05	0.317	-0.293	0.097	-0.495	-1.028	-1.611
					2.20E-01	9.30E-01	9.30E-02	5.10E-02	4.90E-01	9.00E-01	7.90E-01	6.50E-01	3.40E-01	6.40E-02	2.60E-01	1.20E-01	3.70E-01	7.00E-01	5.20E-01
					0.982	1.002	0.957	1.124	0.971	1.007	0.991	0.971	1.156	1.072	1.042	0.944	0.913	1.007	1.013
0	um	0	0	BRMS330_238	-0.103	0.321	-2.505	4.847	-1.765	0.007	-0.011	-0.196	0.093	1	0.89	-0.388	-0.575	0.26	0.539
					4.60E-01	7.30E-01	6.50E-02	8.80E-01	2.40E-02	3.30E-01	5.60E-01	3.80E-01	8.70E-01	7.30E-01	4.60E-01	5.50E-01	1.10E-02	3.30E-02	2.20E-01
					1.021	1.019	1.092	0.982	1.182	0.902	1.04	1.112	1.05	1.025	1.052	0.957	0.538	0.933	0.954
0	um	0	0	CB10179_150	0.122	2.548	5.24	-0.742	10.92	-0.103	0.05	0.726	0.032	0.36	1.116	-0.288	-3.029	-2.667	-1.939
					3.80E-01	3.50E-01	3.20E-01	6.80E-01	2.00E-02	8.20E-02	1.30E-01	2.00E-01	7.30E-01	7.70E-01	3.60E-01	7.80E-01	6.30E-01	8.80E-03	8.60E-03
					1.013	0.973	0.974	0.975	0.905	1.099	0.945	0.917	0.948	0.989	0.966	0.989	1.051	0.956	0.948
0	um	0	0	CB10427_165	0.077	-3.721	-1.533	-1.054	-6.054	0.099	-0.07	-0.566	-0.034	-0.166	-0.748	-0.072	0.319	-1.758	-2.215
					1.10E-01	8.40E-01	2.50E-01	1.90E-01	3.80E-02	5.60E-01	9.60E-01	5.60E-01	8.30E-01	3.00E-01	6.60E-01	7.70E-01	1.90E-01	9.00E-01	8.70E-01
					0.976	0.994	0.97	0.923	0.916	1.033	0.998	1.04	0.968	0.961	0.984	1.011	1.149	1.002	1.003
0	um	0	0	CB10493_166	-0.142	-0.785	-1.757	-3.345	-5.403	0.033	-0.002	0.256	-0.021	-0.58	-0.355	0.076	0.862	0.086	0.136
					7.70E-01	1.20E-01	4.50E-01	6.90E-01	5.00E-01	8.40E-01	3.60E-01	5.90E-02	2.60E-01	6.30E-01	2.30E-01	4.50E-01	7.80E-01	9.20E-01	5.70E-01
					0.996	0.956	0.98	0.975	0.971	0.989	0.967	0.882	1.197	0.981	0.956	1.03	1.031	1.002	0.988
0	um	0	0	FITO317_384	-0.025	-6.204	-1.171	-1.05	-1.787	-0.012	-0.042	-0.836	0.115	-0.27	-0.986	0.196	0.189	0.068	-0.492
					1.30E-01	4.90E-01	5.10E-01	2.30E-01	9.20E-01	9.50E-01	2.10E-01	1.90E-01	9.00E-01	4.80E-01	8.20E-01	9.30E-01	1.00E+00	7.70E-01	7.50E-01
					1.023	1.02	1.018	0.928	1.004	0.997	1.047	1.093	1.02	0.973	1.009	1.003	1	0.995	1.007
0	um	0	0	IGF0191b	0.133	2.786	1.026	-3.09	0.256	-0.004	0.057	0.583	0.013	-0.397	0.184	0.023	0	-0.2	0.275
					1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00
					*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
0	um	0	0	IGF2128c	a-b	a-b	a-b	a-b	a-b	a-b	a-b	a-b	a-b	a-b	a-b	a-b	a-b	a-b	a-b
					9.60E-01	8.60E-01	7.10E-01	7.20E-01	5.80E-01	3.30E-01	7.80E-01	7.50E-01	2.10E-01	6.10E-01	4.90E-01	3.60E-01	4.90E-01	8.70E-01	4.20E-01
					1.001	1.005	1.01	1.022	1.023	0.949	0.99	0.979	0.823	0.981	0.975	1.035	0.933	1.003	1.016
0	um	0	0	IGF5101b	0.005	0.664	0.561	0.891	1.409	-0.055	-0.013	-0.138	-0.123	-0.279	-0.556	0.231	-0.438	0.111	0.683
					1.30E-01	7.80E-02	6.20E-01	2.40E-03	6.70E-02	2.50E-01	1.10E-01	2.10E-01	5.00E-01	2.00E-02	1.80E-02	1.40E-01	1.70E-01	7.90E-01	1.90E-01

					0.978	0.952	0.987	0.837	0.926	1.064	0.945	0.922	0.901	0.917	0.918	1.057	1.148	0.995	0.974
					-0.129	-6.824	-0.743	-7.463	-4.688	0.064	-0.071	-0.538	-0.067	-1.261	-1.861	0.375	0.869	-0.179	-1.102
0	um	0	0	KBrB048K11(2)	3.00E-01	7.80E-01	4.50E-02	5.40E-01	2.20E-01	3.80E-01	8.80E-01	8.90E-01	8.90E-01	7.40E-01	9.00E-01	9.50E-01	4.10E-02	8.70E-01	9.70E-01
					1.016	1.008	0.949	0.964	0.949	1.05	0.994	0.991	0.978	1.013	1.005	0.998	1.234	1.003	1.001
					0.09	1.081	-3.026	-1.544	-3.184	0.05	-0.007	-0.061	-0.014	0.186	0.103	-0.016	1.312	0.113	0.028
0	um	0	0	KBrH027N05(3)	4.70E-01	9.80E-01	3.40E-02	6.20E-01	2.00E-01	4.30E-01	8.30E-01	3.80E-01	9.20E-01	7.00E-01	8.40E-01	8.40E-01	1.10E-01	5.00E-01	9.30E-01
					1.011	1.001	0.946	1.031	0.947	1.045	0.993	0.944	1.016	1.015	0.992	0.992	1.182	1.012	1.002
0	um	0	0	MAX2_b	0.062	0.086	-3.219	1.257	-3.34	0.045	-0.01	-0.385	0.011	0.212	-0.168	-0.052	1.042	0.456	0.074
					6.30E-01	4.20E-01	2.30E-01	4.60E-01	3.40E-01	5.40E-01	3.10E-01	9.80E-02	5.80E-01	9.10E-01	4.20E-01	8.00E-01	4.90E-01	6.90E-01	8.20E-01
					0.993	1.026	0.965	0.951	0.957	1.037	1.04	1.127	0.905	0.995	1.032	0.99	1.081	1.007	1.005
0	um	0	0	NA12A07_152	-0.043	3.563	-2.044	-2.079	-2.615	0.038	0.048	0.793	-0.061	-0.066	0.685	-0.07	0.501	0.295	0.208
					1.80E-01	6.30E-01	2.20E-01	8.30E-01	4.10E-01	2.90E-01	7.20E-01	3.90E-01	3.60E-01	7.50E-01	9.10E-01	9.10E-01	7.50E-01	9.60E-01	5.00E-01
					1.02	0.986	0.968	1.013	0.966	1.059	0.987	0.944	1.157	1.012	0.996	1.004	1.034	0.999	0.986
0	um	0	0	NA12E02_92	0.115	-1.918	-1.87	0.535	-2.105	0.06	-0.016	-0.376	0.092	0.175	-0.094	0.028	0.21	-0.038	-0.573
					1.10E-01	8.50E-01	2.80E-01	1.40E-01	3.90E-02	6.10E-01	9.30E-01	6.80E-01	8.40E-01	1.60E-01	4.40E-01	4.90E-01	1.00E-01	9.00E-01	9.20E-01
					0.976	0.994	0.971	0.912	0.915	1.029	0.997	1.028	0.968	0.946	0.971	1.028	1.19	0.998	0.998
0	um	0	0	NA14E08_98	-0.142	-0.788	-1.689	-3.848	-5.46	0.03	-0.004	0.184	-0.021	-0.799	-0.646	0.185	1.072	-0.087	-0.093
					5.90E-01	4.50E-01	2.70E-01	6.20E-01	5.80E-02	4.20E-01	1.10E-01	1.50E-01	3.30E-01	6.40E-01	5.80E-01	7.10E-01	9.70E-01	1.90E-01	9.70E-02
					1.008	0.979	0.971	1.03	0.923	1.045	0.945	0.909	0.859	1.018	0.979	0.986	0.996	0.978	0.967
0	um	0	0	OL13G05_124	0.047	-2.935	-1.673	1.243	-4.867	0.046	-0.071	-0.626	-0.096	0.258	-0.448	-0.096	-0.028	-0.866	-1.395
					3.70E-01	8.30E-01	4.20E-03	2.80E-03	3.00E-01	3.80E-01	2.10E-01	1.80E-02	2.80E-01	7.70E-04	2.60E-01	7.20E-02	2.00E-01	1.50E-01	2.60E-01
					1.014	0.994	0.927	1.207	0.956	1.05	0.955	0.855	1.194	1.14	1.044	0.933	1.145	1.025	1.023
0	um	0	0	RA2G08_318	0.078	-0.862	-4.355	7.639	-2.746	0.051	-0.057	-1.045	0.11	1.85	0.923	-0.475	0.845	0.977	0.967
					5.30E-01	8.10E-02	7.70E-01	5.30E-01	8.00E-01	6.90E-01	1.50E-01	4.60E-02	4.00E-01	5.00E-01	1.00E-01	5.80E-01	2.30E-01	1.10E-01	1.20E-01
					1.009	1.05	0.993	0.963	1.011	1.022	1.053	1.14	1.138	1.026	1.062	0.979	1.13	1.027	1.031
0	um	0	0	RGL3_a	0.053	6.729	-0.431	-1.56	0.663	0.022	0.065	0.854	0.082	0.367	1.297	-0.142	0.769	1.051	1.292
					1.00E-01	5.20E-01	6.70E-01	4.50E-01	3.40E-01	3.00E-01	6.90E-02	1.40E-01	1.50E-01	6.90E-01	2.20E-01	4.20E-01	7.50E-01	5.50E-01	8.50E-01
					0.974	1.02	0.988	1.049	1.044	0.941	1.071	1.106	1.255	1.016	1.049	0.968	0.966	0.989	1.004

					-0.149	2.719	-0.682	2.03	2.66	-0.063	0.087	0.676	0.15	0.234	1.048	-0.215	-0.218	-0.425	0.175
0	um	0	0	SN1963_335	2.20E-01	6.70E-01	3.20E-01	7.70E-01	5.70E-01	5.90E-01	9.50E-01	9.80E-01	8.90E-01	8.20E-01	8.90E-01	6.60E-01	1.70E-01	8.40E-01	7.70E-01
					1.018	1.012	1.027	0.982	1.025	1.029	1.002	1.002	1.021	0.991	0.995	1.017	1.148	0.997	0.994
					0.105	1.678	1.514	-0.747	1.487	0.03	0.003	0.012	0.014	-0.126	-0.113	0.115	0.874	-0.138	-0.243

L G	Homolog y	cM	L G	markers	beak length	pedicel length	pod length	pod width	pedicel angle	pod angle	yield t/ha	harvest index	start of flowering	oil %seed	glucosinolates	Protein
1	C3	0	1	IGF0568d	2.30E-01	4.20E-02	6.00E-01	4.80E-01	6.30E-01	7.10E-01	2.60E-01	7.00E-01	3.60E-01	7.90E-01	8.70E-01	3.30E-01
					1.037	0.957	1.014	0.994	1.006	0.999	1.037	1.018	1.014	0.999	1.004	1.008
					0.038	-0.101	0.061	-0.003	0.443	-0.202	0.126	0.004	0.689	-0.068	0.079	0.157
1	C3	20.9	1	CALSSR_137	9.60E-01	6.40E-02	6.40E-01	7.50E-01	2.70E-01	8.50E-01	1.50E-01	3.10E-01	7.00E-01	7.20E-01	3.00E-01	4.50E-01
					1.002	0.962	0.988	0.997	0.988	0.999	1.046	1.044	1.006	1.002	1.027	0.994
					0.002	-0.089	-0.054	-0.002	-0.961	-0.094	0.155	0.01	0.283	0.09	0.48	-0.117
1	C3	26	1	SN4513_369	9.00E-01	1.80E-02	5.90E-01	2.90E-01	4.00E-01	6.50E-01	1.30E-01	3.00E-01	7.50E-01	8.80E-01	7.60E-01	5.20E-01
					0.996	0.952	0.986	0.991	0.991	0.999	1.048	1.045	1.004	1.001	1.008	0.995
					-0.004	-0.114	-0.061	-0.004	-0.727	-0.228	0.164	0.01	0.227	0.037	0.139	-0.099
1	C3	42	1	BRAS068_115	8.30E-01	3.30E-01	4.10E-01	5.20E-01	3.70E-01	9.30E-01	4.50E-01	5.10E-02	4.10E-01	7.30E-01	3.00E-01	1.30E-01
					0.994	0.98	0.98	1.005	0.991	1	1.024	1.084	0.988	1.002	1.026	0.988
					-0.007	-0.046	-0.091	0.003	-0.762	0.041	0.08	0.018	-0.594	0.085	0.469	-0.228
2	A3	0	2	CB10427_152	4.50E-01	3.60E-02	7.10E-01	3.20E-01	5.50E-01	7.10E-01	1.80E-01	4.10E-01	4.50E-01	6.80E-01	8.00E-01	7.80E-01
					1.03	0.942	0.988	0.989	0.992	0.998	1.056	0.954	1.015	1.003	1.009	1.003
					0.031	-0.135	-0.056	-0.005	-0.685	-0.253	0.192	-0.01	0.738	0.135	0.154	0.058
2	A3	2.4	2	BRAS038_108	6.50E-01	4.50E-02	8.50E-01	3.50E-01	2.70E-01	8.00E-01	2.40E-01	2.20E-01	7.60E-01	7.90E-01	8.60E-01	8.20E-01
					1.018	0.945	0.994	0.99	0.984	1.001	1.049	0.932	1.006	1.002	1.006	1.002
					0.019	-0.13	-0.028	-0.005	-1.254	0.175	0.167	-0.016	0.302	0.088	0.11	0.046
2	A3	2.7	2	BRAS087_160	7.20E-01	4.20E-02	5.10E-01	7.10E-02	2.70E-01	5.90E-01	5.50E-02	1.40E-01	8.60E-01	5.40E-01	9.40E-01	9.80E-01
					1.015	0.94	0.976	0.979	0.983	0.998	1.085	0.913	1.004	1.004	0.997	1

					0.016	-0.142	-0.106	-0.011	-1.351	-0.385	0.288	-0.021	0.179	0.218	-0.052	0.005
2	A3	4.2	2	SSR18_175	6.60E-01	2.60E-02	4.40E-01	1.80E-01	3.90E-01	6.90E-01	1.50E-01	5.30E-01	6.40E-01	3.90E-01	6.30E-01	9.80E-01
					1.019	0.935	0.972	0.984	0.987	0.998	1.064	0.962	1.01	1.006	0.983	1
					0.019	-0.153	-0.126	-0.008	-1.051	-0.287	0.22	-0.009	0.495	0.308	-0.312	-0.007
2	A3	6.4	2	CB10036_160	8.40E-01	1.60E-02	3.90E-01	6.00E-02	5.80E-01	8.80E-01	5.80E-02	3.80E-01	9.50E-01	3.30E-01	3.40E-01	6.80E-01
					1.01	0.918	0.964	0.974	0.99	0.999	1.099	0.938	1.001	1.008	0.96	0.994
					0.01	-0.193	-0.161	-0.013	-0.806	-0.122	0.338	-0.014	0.071	0.405	-0.732	-0.106
2	A3	6.4	2	OL10D03_101	8.60E-01	4.50E-02	3.60E-01	3.30E-02	4.70E-01	8.40E-01	1.20E-01	5.70E-01	8.00E-01	1.90E-01	3.80E-01	8.40E-01
					1.008	0.934	0.963	0.972	0.988	0.999	1.078	0.962	1.006	1.011	0.964	0.997
					0.009	-0.154	-0.165	-0.014	-1.001	-0.163	0.266	-0.008	0.299	0.521	-0.644	-0.049
3	C3/A3/C8	6.4	3	BRMS269_313	8.60E-01	4.50E-02	3.60E-01	3.30E-02	4.70E-01	8.40E-01	1.20E-01	5.70E-01	8.00E-01	1.90E-01	3.80E-01	8.40E-01
					1.008	0.934	0.963	0.972	0.988	0.999	1.078	0.962	1.006	1.011	0.964	0.997
					0.009	-0.154	-0.165	-0.014	-1.001	-0.163	0.266	-0.008	0.299	0.521	-0.644	-0.049
3	C3/A3/C8	10.2	3	BRAS065_219	6.50E-01	2.40E-02	9.30E-01	1.50E-01	5.20E-01	1.00E+00	9.80E-02	5.90E-01	9.50E-01	2.40E-01	2.00E-01	5.30E-01
					1.017	0.939	0.997	0.985	0.991	1	1.068	1.03	0.999	1.008	0.958	0.993
					0.018	-0.143	-0.013	-0.008	-0.723	0.002	0.231	0.007	-0.063	0.38	-0.768	-0.127
3	C3/A3/C8	13.6	3	AtTB1_f	4.00E-01	1.00E-01	9.50E-01	5.80E-02	1.30E-01	7.90E-01	2.50E-01	8.80E-01	6.40E-01	8.30E-01	8.20E-01	3.60E-01
					1.03	0.961	0.998	0.981	0.981	0.999	1.044	0.992	1.008	1.001	1.007	1.009
					0.031	-0.091	-0.009	-0.009	-1.571	-0.169	0.151	-0.002	0.419	0.063	0.132	0.173
4	uk1	0	4	RA1F06_190	7.40E-01	5.40E-01	9.80E-01	4.60E-02	6.90E-01	6.30E-01	6.10E-01	7.40E-01	2.20E-01	3.40E-01	3.00E-01	3.80E-01
					0.99	0.987	1.001	1.017	1.004	1.002	0.984	0.986	0.983	1.005	0.974	0.993
					-0.01	-0.03	0.004	0.008	0.346	0.244	-0.055	-0.003	-0.891	0.239	-0.48	-0.136
4	uk1	19	4	CALSSSR_142	4.20E-01	3.70E-01	5.90E-01	1.40E-01	3.40E-01	4.50E-01	5.20E-01	6.90E-01	3.30E-01	7.20E-01	8.90E-01	7.80E-01
					0.975	1.021	1.015	1.013	1.011	0.997	0.979	0.982	0.985	0.998	1.004	0.998
					-0.026	0.048	0.067	0.006	0.902	-0.408	-0.074	-0.004	-0.771	-0.097	0.067	-0.047
4	uk1	23.5	4	SN4513_366	1.50E-01	9.70E-01	5.00E-01	5.90E-02	5.20E-02	8.00E-01	2.60E-01	4.40E-01	6.00E-01	1.60E-01	5.40E-01	6.60E-01
					0.957	0.999	1.018	1.017	1.022	0.999	0.964	0.966	0.992	0.993	1.016	1.004
					-0.046	-0.002	0.081	0.008	1.746	-0.129	-0.126	-0.008	-0.399	-0.368	0.292	0.072
4	uk1	39.4	4	KBrH004A18(3)	8.20E-02	4.20E-01	8.90E-01	3.20E-01	2.10E-02	5.50E-01	8.10E-01	3.40E-01	7.10E-01	1.20E-02	2.00E-01	2.10E-01
					0.95	0.983	0.996	1.009	1.026	0.998	0.992	0.959	0.995	0.987	1.035	1.01

					-0.053	-0.039	-0.016	0.004	2.057	-0.306	-0.027	-0.01	-0.278	-0.636	0.615	0.19
4	uk1	58.1	4	A77096_218	3.90E-02	6.80E-01	4.10E-01	1.30E-01	8.60E-01	5.20E-01	1.90E-01	7.60E-01	4.10E-01	1.90E-03	4.10E-03	2.10E-01
					0.939	1.009	0.977	1.014	1.002	1.002	0.958	1.015	0.987	0.983	1.084	1.011
					-0.065	0.022	-0.102	0.007	0.173	0.344	-0.149	0.003	-0.666	-0.827	1.427	0.207
4	uk1	62.8	4	KBrH013K13(1)	3.30E-02	6.90E-01	2.30E-01	1.50E-01	5.70E-01	7.90E-01	5.50E-02	8.30E-01	5.60E-01	8.00E-03	9.50E-03	4.00E-01
					0.937	0.991	0.968	1.013	1.006	1.001	0.939	1.01	0.991	0.986	1.07	1.007
					-0.067	-0.021	-0.146	0.007	0.509	0.141	-0.217	0.002	-0.456	-0.693	1.202	0.137
5	A2/A6	0	5	RGA12_30	7.90E-01	3.00E-01	3.70E-01	6.50E-01	5.20E-01	9.00E-01	6.80E-02	9.30E-02	4.60E-01	9.30E-01	6.60E-01	5.20E-01
					0.992	1.022	0.978	1.004	1.007	1	0.945	1.075	1.011	1	0.989	0.995
					-0.008	0.052	-0.102	0.002	0.559	-0.067	-0.196	0.017	0.548	0.022	-0.206	-0.101
5	A2/A6	8.5	5	RGL12_31_300	5.70E-01	2.10E-02	6.10E-01	2.60E-01	5.60E-01	9.20E-01	3.90E-01	1.30E-01	9.00E-01	9.20E-01	6.30E-01	2.70E-01
					0.983	1.051	0.987	1.009	1.006	1	0.973	1.068	1.002	1.001	0.988	0.991
					-0.017	0.115	-0.06	0.004	0.52	0.053	-0.096	0.015	0.093	0.025	-0.223	-0.168
5	A2/A6	31.1	5	CB10416_251	9.50E-01	3.80E-02	7.90E-01	3.50E-01	5.70E-02	7.90E-01	1.40E-01	1.00E-01	1.20E-01	6.10E-01	1.20E-01	5.60E-01
					1.002	1.045	0.993	1.008	1.021	1.001	0.955	1.072	1.023	1.003	0.962	0.995
					0.002	0.101	-0.03	0.004	1.633	0.132	-0.161	0.016	1.133	0.128	-0.709	-0.09
5	A2/A6	32.1	5	IGF3239d	8.20E-01	3.30E-02	6.80E-01	2.90E-01	7.10E-02	9.70E-01	1.30E-01	1.00E-01	1.50E-01	6.70E-01	9.40E-02	7.10E-01
					0.993	1.046	0.989	1.009	1.02	1	0.953	1.072	1.021	1.002	0.958	0.997
					-0.007	0.104	-0.048	0.004	1.562	0.022	-0.165	0.015	1.067	0.107	-0.771	-0.06
5	A2/A6	44.2	5	FITO232_130	8.60E-01	1.40E-01	4.60E-01	3.60E-01	3.80E-01	5.70E-01	2.00E-01	3.50E-01	3.30E-01	4.60E-01	6.80E-03	7.00E-01
					0.995	1.032	0.981	1.008	1.01	0.998	0.96	1.042	1.015	1.004	0.934	0.997
					-0.005	0.073	-0.086	0.004	0.782	-0.292	-0.141	0.009	0.728	0.189	-1.244	-0.06
5	A2/A6	65.8	5	RA1F06_175	4.70E-01	6.50E-01	6.50E-01	2.30E-01	7.10E-02	9.00E-01	1.50E-01	1.70E-02	5.60E-01	9.00E-02	2.00E-04	3.50E-01
					0.978	1.01	0.988	1.01	1.02	1	0.956	1.107	1.009	1.009	0.912	0.992
					-0.023	0.023	-0.053	0.005	1.57	-0.062	-0.157	0.024	0.428	0.418	-1.662	-0.145
6	A4/C4(6)	0	6	NA12E05_146	3.00E-01	4.40E-02	4.50E-01	2.30E-01	3.90E-01	7.10E-01	3.50E-01	7.10E-01	5.00E-01	8.80E-02	7.80E-01	1.80E-01
					1.03	0.959	1.019	1.01	1.009	1.001	1.03	0.985	0.991	1.009	1.007	0.989
					0.031	-0.097	0.083	0.005	0.737	0.187	0.1	-0.004	-0.481	0.424	0.128	-0.208
6	A4/C4(6)	3.2	6	CB10493_155	3.70E-01	1.50E-01	4.70E-01	4.10E-01	6.30E-01	6.80E-01	3.90E-01	5.50E-01	4.50E-01	6.00E-02	7.60E-01	2.50E-01
					1.027	0.971	1.019	1.007	1.005	1.001	1.027	1.024	0.989	1.009	0.992	0.991

					0.028	-0.069	0.082	0.003	0.422	0.204	0.093	0.005	-0.557	0.464	-0.139	-0.178
6	A4/C4(6)	3.9	6	OL10B01_177	4.40E-01	1.20E-01	5.00E-01	2.30E-01	9.80E-01	6.20E-01	3.90E-01	2.50E-01	3.80E-01	3.80E-02	5.00E-01	2.60E-01
					1.023	0.968	1.017	1.01	1	1.001	1.027	1.047	0.987	1.01	0.983	0.991
					0.024	-0.076	0.077	0.004	-0.021	0.24	0.092	0.01	-0.644	0.509	-0.303	-0.173
6	A4/C4(6)	10	6	MAX3_m	2.10E-01	4.20E-01	3.20E-01	1.70E-01	9.30E-01	5.90E-01	3.10E-01	7.80E-01	2.20E-01	1.60E-01	7.20E-01	2.60E-01
					1.034	0.983	1.024	1.012	0.999	1.002	1.033	1.012	0.983	1.007	0.99	0.991
					0.035	-0.04	0.104	0.006	-0.081	0.266	0.11	0.003	-0.86	0.348	-0.175	-0.177
7	C7	0	7	CB10299_140	8.20E-01	6.00E-01	3.30E-01	3.10E-01	6.90E-01	3.50E-02	5.40E-01	2.30E-01	7.90E-01	2.00E-01	9.40E-01	1.30E-01
					0.994	0.989	0.976	1.008	1.004	0.994	0.982	1.051	0.996	0.994	0.998	1.012
					-0.007	-0.026	-0.107	0.004	0.341	-1.02	-0.064	0.011	-0.186	-0.312	-0.034	0.23
7	C7	0.1	7	BRMS296_142	7.10E-01	4.60E-01	2.00E-01	3.10E-01	7.30E-01	3.90E-02	5.70E-01	2.20E-01	7.20E-01	2.00E-01	8.30E-01	9.80E-02
					0.989	0.985	0.97	1.008	1.004	0.994	0.983	1.054	0.995	0.994	1.005	1.013
					-0.011	-0.036	-0.138	0.004	0.291	-0.999	-0.059	0.012	-0.254	-0.316	0.093	0.254
7	C7	16.6	7	BRAS019_128	8.10E-01	3.00E-01	1.60E-01	6.50E-01	5.70E-01	2.20E-02	3.70E-01	3.80E-01	2.00E-01	5.00E-01	6.90E-01	4.90E-01
					0.993	0.979	0.965	1.004	1.006	0.993	1.028	1.037	0.982	0.997	0.99	1.005
					-0.006	-0.051	-0.157	0.002	0.483	-1.126	0.096	0.008	-0.917	-0.166	-0.182	0.104
8	uk2	0	8	FITO300_127	7.60E-01	3.30E-02	9.70E-01	2.60E-01	9.30E-01	4.50E-01	2.90E-01	8.00E-01	7.40E-01	5.10E-01	1.60E-01	5.00E-01
					0.991	0.957	0.999	0.991	0.999	1.002	0.968	1.01	0.995	1.003	1.036	0.995
					-0.009	-0.101	-0.003	-0.005	-0.077	0.379	-0.112	0.003	-0.234	0.161	0.638	-0.103
8	uk2	14.9	8	FITO110_291	2.10E-01	1.40E-02	7.40E-01	4.30E-01	7.20E-01	1.20E-01	1.40E-01	7.10E-01	9.00E-01	7.90E-01	7.30E-02	6.20E-01
					0.964	0.951	0.991	0.994	0.996	1.005	0.954	0.984	1.002	1.001	1.047	0.996
					-0.037	-0.117	-0.038	-0.003	-0.308	0.766	-0.161	-0.003	0.089	0.069	0.823	-0.077
8	uk2	19.4	8	OL10A05_190	2.00E-01	1.20E-02	5.80E-01	5.30E-01	5.80E-01	6.40E-02	2.00E-01	6.90E-01	8.20E-01	7.70E-01	2.60E-01	7.50E-01
					0.964	0.95	0.986	0.995	0.994	1.006	0.961	0.983	0.997	1.001	1.029	0.997
					-0.038	-0.12	-0.061	-0.003	-0.471	0.913	-0.137	-0.004	-0.162	0.073	0.516	-0.048
9	A3/A4	0	9	BRMS008_156	1.20E-01	6.90E-01	2.10E-02	7.30E-01	2.40E-01	8.10E-01	7.20E-01	9.50E-01	1.30E-01	9.50E-01	6.80E-01	5.90E-01
					0.957	1.008	0.945	0.997	0.988	0.999	1.011	1.003	0.979	1	1.01	0.996
					-0.045	0.019	-0.253	-0.001	-1	-0.122	0.038	0.001	-1.086	0.015	0.188	-0.082
9	A3/A4	14.2	9	IGF5193a	5.50E-01	6.00E-01	5.10E-02	3.80E-01	2.40E-02	9.50E-01	6.10E-01	9.10E-01	3.00E-01	8.70E-01	5.60E-01	8.60E-01
					0.983	1.011	0.953	0.993	0.977	1	1.016	0.995	0.985	1.001	1.015	1.001

					-0.018	0.025	-0.217	-0.004	-1.916	0.034	0.054	-0.001	-0.747	0.039	0.263	0.028
1 0	A3	0	1 0	IGF5272c	5.40E-01	4.60E-04	5.80E-01	5.80E-02	9.90E-01	5.00E-01	3.10E-01	4.30E-01	3.20E-01	1.30E-01	9.60E-04	6.70E-01
					0.982	1.074	0.986	1.016	1	0.998	1.032	0.967	0.986	0.992	1.087	0.997
					-0.019	0.163	-0.062	0.008	0.016	-0.344	0.11	-0.008	-0.716	-0.375	1.496	-0.067
1 0	A3	6.7	1 0	BRMS008_115	7.60E-01	1.20E-03	6.50E-01	4.50E-02	5.50E-01	8.20E-01	5.00E-01	9.70E-01	3.00E-01	2.50E-01	9.90E-06	2.00E-01
					1.009	1.067	0.989	1.016	0.994	0.999	1.021	1.001	0.985	0.994	1.111	0.99
					0.008	0.151	-0.05	0.008	-0.504	-0.113	0.072	0.001	-0.743	-0.278	1.888	-0.191
1 0	A3	12.8	1 0	MAX2_I	1.10E-01	1.10E-02	1.40E-02	4.70E-01	8.20E-01	4.00E-01	1.70E-01	8.90E-01	7.30E-02	5.90E-02	2.50E-03	7.30E-01
					0.952	1.056	0.938	1.006	1.003	0.997	1.046	0.994	0.973	0.99	1.084	1.003
					-0.05	0.126	-0.282	0.003	0.214	-0.465	0.156	-0.002	-1.406	-0.502	1.444	0.059
1 0	A3	19.9	1 0	BRMS330_241	9.30E-01	7.00E-02	1.80E-01	1.90E-01	9.80E-01	9.90E-01	2.40E-01	7.40E-01	5.60E-02	9.10E-01	7.80E-04	8.50E-02
					0.998	1.038	0.967	1.011	1	1	1.037	1.014	0.974	1.001	1.084	0.987
					-0.003	0.086	-0.148	0.005	0.017	-0.006	0.124	0.003	-1.353	0.027	1.461	-0.258
1 0	A3	42.1	1 0	RA2E11_200	4.40E-01	7.10E-01	2.80E-02	9.50E-01	7.40E-01	9.10E-01	1.70E-01	8.00E-01	1.10E-02	4.40E-02	2.40E-01	1.00E-03
					0.978	1.008	0.947	0.999	0.996	1	1.043	1.01	0.965	1.01	1.03	0.975
					-0.023	0.017	-0.242	-0.001	-0.288	0.056	0.147	0.002	-1.81	0.492	0.533	-0.49
1 0	A3	43.3	1 0	CB10036_131	8.00E-01	5.10E-01	1.30E-01	9.00E-01	9.40E-01	7.40E-01	2.40E-01	8.10E-01	3.60E-02	1.90E-02	3.90E-01	1.20E-03
					0.993	1.014	0.962	1.001	1.001	1.001	1.037	1.01	0.97	1.012	1.022	0.975
					-0.007	0.032	-0.173	0.001	0.06	0.167	0.126	0.002	-1.517	0.572	0.392	-0.486
1 0	A3	66.4	1 0	OL11B05_109	7.30E-01	1.90E-01	1.10E-01	8.70E-01	3.40E-01	4.30E-01	1.20E-01	4.30E-01	7.30E-02	1.30E-02	3.90E-01	6.60E-02
					1.01	0.972	0.96	0.999	1.011	0.997	1.051	1.035	0.974	1.013	1.022	0.985
					0.01	-0.065	-0.183	-0.001	0.848	-0.405	0.171	0.008	-1.332	0.62	0.401	-0.288
1 0	A3	66.7	1 0	NA12E02_118	7.60E-01	2.20E-01	9.90E-02	7.60E-01	3.40E-01	2.90E-01	8.80E-02	4.30E-01	5.40E-02	1.20E-02	4.50E-01	4.60E-02
					1.009	0.974	0.957	0.997	1.011	0.997	1.056	1.035	0.972	1.013	1.02	0.984
					0.009	-0.062	-0.192	-0.001	0.851	-0.543	0.189	0.008	-1.446	0.639	0.357	-0.316
1 0	A3	68.1	1 0	CB10427_138	8.50E-01	2.80E-01	1.00E-01	9.60E-01	3.00E-01	1.80E-01	1.00E-01	4.20E-01	4.00E-02	2.10E-02	5.00E-01	7.50E-02
					1.006	0.977	0.958	1	1.012	0.996	1.054	1.036	0.97	1.012	1.018	0.985
					0.006	-0.054	-0.19	0	0.925	-0.7	0.183	0.008	-1.545	0.591	0.325	-0.283
1 0	A3	94.4	1 0	SN11722_93	3.30E-01	1.30E-01	9.00E-02	2.90E-02	9.50E-01	7.00E-01	4.10E-01	1.30E-01	6.90E-01	8.80E-01	3.80E-01	4.40E-01

					0.972	1.032	0.958	1.018	1.001	0.999	0.975	1.066	0.994	1.001	0.978	1.006
					-0.029	0.074	-0.188	0.009	0.057	-0.191	-0.087	0.015	-0.285	0.038	-0.398	0.118
1 0	A3	106	1 0	NA10D03_157	6.20E-01	9.60E-01	1.40E-01	2.50E-01	6.60E-01	3.30E-01	5.40E-01	3.30E-02	3.00E-01	1.10E-01	5.30E-01	3.60E-01
					0.986	0.999	0.964	1.009	1.005	0.997	0.981	1.091	0.985	1.008	0.984	0.993
1 0	A3	108. 5	1 0	IGF3100b	-0.015	-0.002	-0.164	0.004	0.378	-0.487	-0.065	0.02	-0.75	0.387	-0.284	-0.14
					3.50E-01	9.60E-01	5.20E-02	1.60E-01	7.70E-01	3.60E-01	6.70E-01	4.80E-02	1.50E-01	1.80E-01	4.80E-01	4.30E-01
					0.973	0.999	0.953	1.012	1.003	0.997	0.987	1.085	0.98	1.007	0.982	0.994
					-0.028	-0.003	-0.215	0.006	0.251	-0.461	-0.045	0.018	-1.044	0.332	-0.319	-0.121
1 0	A3	111. 7	1 0	RGA2_H24_13_15 0	1.40E-01	9.40E-01	1.80E-02	5.00E-01	9.40E-01	1.30E-01	1.90E-01	2.80E-02	3.60E-01	1.30E-01	7.70E-01	5.90E-01
					0.959	0.998	0.943	1.006	1.001	0.995	0.961	1.094	0.987	1.007	1.007	0.996
					-0.044	-0.004	-0.259	0.003	0.066	-0.744	-0.139	0.021	-0.656	0.363	0.131	-0.082
1 0	A3	111. 7	1 0	RGA2_H24_14_30 0	1.40E-01	9.40E-01	1.80E-02	5.00E-01	9.40E-01	1.30E-01	1.90E-01	2.80E-02	3.60E-01	1.30E-01	7.70E-01	5.90E-01
					0.959	0.998	0.943	1.006	1.001	0.995	0.961	1.094	0.987	1.007	1.007	0.996
					-0.044	-0.004	-0.259	0.003	0.066	-0.744	-0.139	0.021	-0.656	0.363	0.131	-0.082
1 1	C1	0	1 1	KBrB078A03(1)	5.40E-01	4.50E-02	6.30E-01	9.20E-01	1.30E-01	8.50E-01	5.70E-01	6.40E-01	3.50E-01	4.00E-01	8.20E-04	9.90E-02
					1.019	0.956	1.013	1.001	1.017	0.999	1.019	1.021	0.986	1.005	0.914	0.986
					0.019	-0.104	0.058	0.001	1.399	-0.105	0.066	0.005	-0.736	0.223	-1.591	-0.27
1 1	C1	1	1 1	BRAS067_136	5.10E-01	3.30E-02	5.80E-01	7.60E-01	1.20E-01	8.50E-01	7.20E-01	6.30E-01	4.50E-01	4.30E-01	1.80E-03	1.60E-01
					1.02	0.954	1.015	1.003	1.017	1.001	1.012	1.022	0.989	1.004	0.92	0.988
					0.021	-0.109	0.066	0.002	1.395	0.103	0.042	0.005	-0.582	0.21	-1.477	-0.229
1 1	C1	1	1 1	NA12H02_219	5.10E-01	3.30E-02	5.80E-01	7.60E-01	1.20E-01	8.50E-01	7.20E-01	6.30E-01	4.50E-01	4.30E-01	1.80E-03	1.60E-01
					1.02	0.954	1.015	1.003	1.017	1.001	1.012	1.022	0.989	1.004	0.92	0.988
					0.021	-0.109	0.066	0.002	1.395	0.103	0.042	0.005	-0.582	0.21	-1.477	-0.229
1 1	C1	2.1	1 1	SN3734_288	5.10E-01	7.00E-02	5.90E-01	8.00E-01	2.60E-01	8.20E-01	7.40E-01	5.40E-01	4.10E-01	6.60E-01	4.90E-03	2.80E-01
					1.02	0.961	1.015	1.002	1.013	1.001	1.011	1.027	0.988	1.002	0.928	0.991
					0.02	-0.092	0.064	0.001	1.014	0.118	0.038	0.006	-0.631	0.116	-1.325	-0.174
1 1	C1	15.3	1 1	IGF3338a	1.30E-01	3.50E-01	2.10E-02	9.00E-01	2.40E-01	7.10E-01	9.10E-01	1.80E-01	2.00E-01	4.50E-01	5.30E-01	3.60E-01
					1.059	0.976	1.078	0.999	1.016	1.002	1.005	0.931	1.024	0.995	0.979	1.01

					0.059	-0.056	0.336	-0.001	1.31	0.246	0.016	-0.017	1.19	-0.236	-0.373	0.183
1			1													
1	C1	24.8	1	IGF0504b	9.80E-02	3.80E-02	3.00E-02	7.00E-01	4.60E-01	6.60E-01	2.10E-01	3.80E-01	1.10E-01	8.50E-01	2.10E-01	6.00E-01
					1.051	0.954	1.058	0.997	1.008	1.001	0.96	0.962	1.024	1.001	0.969	0.996
					0.052	-0.108	0.255	-0.002	0.681	0.234	-0.142	-0.009	1.205	0.048	-0.57	-0.086
1			1													
1	C1	27.1	1	IGF1059e	4.60E-02	3.20E-02	1.30E-02	4.10E-01	3.90E-01	4.90E-01	3.70E-01	5.80E-01	8.80E-02	9.10E-01	2.10E-01	6.80E-01
					1.059	0.956	1.064	0.993	1.009	1.002	0.972	0.977	1.025	1.001	0.968	0.997
					0.06	-0.105	0.279	-0.004	0.754	0.351	-0.097	-0.006	1.254	0.029	-0.579	-0.064
1			1													
1	C1	30.9	1	KBrB036M22(3)	2.80E-02	1.20E-01	1.40E-02	2.90E-01	9.90E-01	4.00E-01	7.40E-01	4.10E-01	2.70E-01	9.60E-01	5.50E-02	5.50E-01
					1.068	0.967	1.066	0.991	1	1.003	1.011	0.964	1.016	1	0.951	0.995
					0.068	-0.077	0.288	-0.005	-0.016	0.428	0.037	-0.009	0.817	0.013	-0.903	-0.097
1			1													
1	C1	38.1	1	IGF3315b	1.80E-01	1.50E-01	7.60E-02	2.00E-01	4.80E-01	3.60E-01	2.60E-01	6.20E-01	3.60E-01	9.40E-01	5.10E-01	8.30E-01
					1.042	0.97	1.048	0.989	1.008	1.003	0.963	1.023	1.014	1	0.982	0.998
					0.042	-0.072	0.205	-0.005	0.626	0.505	-0.128	0.005	0.724	-0.019	-0.336	-0.036
1			1													
1	C1	51	1	RA2E11_205	3.30E-01	2.40E-01	2.90E-01	8.70E-03	5.20E-01	2.90E-02	4.70E-01	7.00E-01	1.50E-01	1.70E-01	3.50E-01	2.60E-01
					1.028	0.976	1.027	0.979	1.007	1.007	0.978	0.984	1.02	1.007	0.977	0.991
					0.029	-0.056	0.117	-0.011	0.539	1.068	-0.076	-0.003	1.021	0.328	-0.42	-0.171
1			1													
1	C1	52.9	1	OL12F11_233	3.20E-01	2.30E-01	2.00E-01	7.40E-02	3.50E-01	1.80E-02	2.20E-01	6.40E-01	8.60E-02	3.10E-01	3.10E-01	4.70E-01
					1.029	0.976	1.032	0.986	1.01	1.007	0.963	0.981	1.024	1.005	0.975	0.994
					0.029	-0.057	0.141	-0.007	0.793	1.154	-0.129	-0.005	1.218	0.247	-0.452	-0.108
1			1													
1	C1	89.9	1	MAX_4r	5.40E-01	8.80E-01	9.00E-01	6.60E-01	7.80E-02	2.40E-01	1.70E-01	8.20E-01	3.30E-01	1.70E-01	4.20E-01	4.20E-01
					1.018	0.997	1.003	0.996	0.982	1.004	0.96	1.01	1.014	1.007	0.98	0.994
					0.018	-0.007	0.013	-0.001	-1.486	0.581	-0.142	0.003	0.685	0.324	-0.368	-0.123
1			1													
1	C1	101.2	1	MAX_4n	8.40E-01	4.30E-01	9.30E-01	5.90E-01	3.60E-01	5.80E-01	6.00E-01	5.30E-01	8.40E-01	6.30E-01	5.60E-01	6.10E-01
					1.006	1.017	0.998	0.995	0.99	0.998	0.984	1.027	1.003	1.002	0.985	1.004
					0.006	0.039	-0.01	-0.002	-0.824	-0.283	-0.055	0.007	0.15	0.117	-0.279	0.081
1			1													
2	A7	0	2	NA12A05_157	4.70E-01	3.70E-01	1.70E-01	4.50E-01	9.50E-01	5.00E-01	9.60E-01	8.20E-01	3.00E-01	3.80E-01	9.30E-01	7.50E-01
					0.979	0.981	0.966	1.006	0.999	1.002	1.001	1.01	0.986	1.004	0.998	0.997
					-0.022	-0.044	-0.155	0.003	-0.058	0.335	0.005	0.003	-0.74	0.216	-0.041	-0.049
1			1													
2	A7	5.4	2	OL12E03_110	3.20E-01	2.10E-01	1.30E-01	2.80E-01	7.20E-01	6.70E-01	6.30E-01	3.40E-01	2.90E-02	4.40E-01	5.20E-01	4.10E-01

					0.972	0.975	0.963	1.009	0.996	1.001	1.015	1.04	0.97	1.004	0.984	0.993
					-0.029	-0.06	-0.165	0.005	-0.306	0.211	0.051	0.009	-1.542	0.188	-0.286	-0.125
1			1													
2	A7	42.3	2	IGF1226a	5.40E-01	1.10E-02	2.40E-02	2.70E-01	7.70E-01	9.00E-02	2.20E-01	7.70E-01	5.00E-01	6.40E-01	4.00E-02	9.50E-01
					1.018	1.052	1.056	1.009	1.003	1.005	0.963	1.012	1.009	1.002	0.95	1.001
					0.018	0.117	0.242	0.005	0.246	0.846	-0.128	0.003	0.475	0.111	-0.926	0.011
1			1													
2	A7	53.1	2	IGF1226f	9.10E-01	6.10E-03	1.30E-01	1.50E-01	9.40E-01	1.10E-01	1.60E-01	1.70E-01	6.60E-01	3.90E-01	3.90E-01	6.20E-01
					1.003	1.057	1.038	1.012	1.001	1.005	0.958	1.059	1.006	1.004	0.978	0.996
					0.003	0.128	0.166	0.006	0.061	0.788	-0.149	0.013	0.311	0.207	-0.392	-0.077
1			1													
2	A7	85.6	2	BRMS036_130	9.70E-01	9.00E-02	8.80E-01	2.50E-01	3.60E-01	3.80E-01	8.30E-01	8.10E-01	4.20E-01	7.10E-01	4.90E-01	9.20E-01
					0.999	1.035	0.996	0.991	0.99	1.003	0.993	1.01	0.989	0.998	1.017	1.001
					-0.001	0.081	-0.017	-0.005	-0.771	0.436	-0.022	0.003	-0.572	-0.092	0.31	0.014
1			1													
2	A7	87.8	2	IGF0504f	9.80E-01	2.70E-01	8.30E-01	1.30E-01	2.20E-01	2.60E-01	8.40E-01	9.20E-01	3.00E-01	7.90E-01	5.70E-01	9.80E-01
					0.999	1.023	0.995	0.988	0.987	1.004	0.994	0.996	0.985	0.999	1.015	1
					0	0.054	-0.024	-0.006	-1.048	0.56	-0.021	0	-0.751	-0.065	0.262	0.003
1			1													
3	A1	0	3	SN11641_405	5.30E-01	3.40E-01	4.30E-01	7.40E-01	6.10E-02	6.20E-01	2.20E-01	7.40E-01	3.40E-01	4.80E-01	5.90E-01	2.80E-02
					1.018	1.02	1.02	0.997	0.98	0.998	0.963	1.015	1.013	0.996	1.014	1.018
					0.019	0.047	0.089	-0.001	-1.607	-0.245	-0.129	0.003	0.675	-0.174	0.248	0.338
1			1													
3	A1	2.4	3	KBrB048F07(2)	2.60E-01	6.80E-02	3.80E-01	4.70E-01	2.80E-02	6.40E-01	2.60E-01	6.30E-01	2.10E-01	8.50E-01	8.00E-01	6.50E-02
					1.033	1.038	1.022	0.994	0.977	0.999	0.966	1.021	1.018	0.999	1.006	1.015
					0.033	0.087	0.098	-0.003	-1.851	-0.233	-0.121	0.005	0.898	-0.045	0.112	0.279
1			1													
3	A1	11	3	CB10097_191	2.90E-01	3.80E-01	4.50E-01	3.60E-01	2.20E-02	6.80E-01	8.30E-02	6.30E-01	1.80E-01	7.90E-01	8.60E-01	1.10E-01
					1.031	1.018	1.019	0.992	0.976	0.999	0.948	1.02	1.019	0.999	1.005	1.012
					0.032	0.042	0.086	-0.004	-1.944	-0.206	-0.185	0.004	0.97	-0.064	0.082	0.237
1			1													
3	A1	19.5	3	MAX4_p	4.20E-02	7.80E-01	7.40E-02	4.70E-01	9.20E-02	7.40E-01	1.40E-01	7.20E-01	4.30E-02	8.50E-01	3.80E-01	4.60E-01
					1.059	1.006	1.044	0.994	0.982	1.001	0.956	1.015	1.028	1.001	0.978	1.006
					0.059	0.013	0.191	-0.003	-1.427	0.163	-0.155	0.003	1.41	0.045	-0.397	0.112
1			1													
4	A9/C5	0	4	IGF3112a	8.60E-02	5.80E-01	1.20E-01	6.80E-01	3.80E-01	2.20E-01	5.40E-02	7.60E-01	5.50E-01	9.50E-01	4.90E-01	4.50E-01
					1.052	1.011	1.038	1.004	0.99	1.004	1.062	0.987	0.992	1	1.018	0.994
					0.052	0.026	0.168	0.001	-0.78	0.629	0.206	-0.003	-0.428	-0.015	0.322	-0.12

1			1														
4	A9/C5	35.5	4	OL12F02_148	8.70E-01	5.60E-01	9.60E-01	4.50E-01	2.30E-01	4.20E-01	4.30E-01	7.10E-01	3.70E-01	3.00E-01	2.50E-01	9.20E-01	
					0.995	1.012	1.001	1.006	0.987	0.998	0.976	0.984	1.013	0.995	1.029	0.999	
					-0.005	0.028	0.005	0.003	-1.028	-0.392	-0.084	-0.003	0.641	-0.253	0.517	-0.014	
1			1														
4	A9/C5	36.6	4	NA12D10_150	9.10E-01	5.30E-01	8.90E-01	7.20E-01	3.30E-01	4.10E-01	2.40E-01	5.30E-01	1.50E-01	2.00E-01	1.60E-01	9.30E-01	
					0.997	1.013	1.003	1.003	0.99	0.998	0.965	0.974	1.02	0.994	1.035	1.001	
					-0.003	0.03	0.015	0.002	-0.827	-0.401	-0.122	-0.006	1.013	-0.306	0.618	0.013	
1			1														
5	A10	0	5	FITO247_277	8.60E-01	8.60E-01	4.30E-01	2.40E-01	3.10E-02	9.20E-01	3.70E-01	2.90E-02	6.40E-01	4.80E-01	2.50E-01	3.10E-01	
					1.005	1.004	1.02	0.99	0.978	1	0.973	0.915	1.007	0.996	1.029	1.008	
					0.005	0.008	0.086	-0.005	-1.798	-0.05	-0.094	-0.021	0.332	-0.174	0.516	0.154	
1			1														
5	A10	5.8	5	RA2E07_93	9.50E-01	8.50E-01	5.80E-01	3.30E-01	8.60E-03	4.30E-01	6.70E-01	2.50E-01	5.90E-01	5.80E-01	5.40E-01	2.70E-01	
					0.998	1.004	1.014	0.992	0.973	0.998	0.987	0.953	0.992	0.997	1.015	1.009	
					-0.002	0.009	0.061	-0.004	-2.199	-0.387	-0.045	-0.011	-0.39	-0.137	0.274	0.167	
1			1														
5	A10	6	5	IGF1073a	9.30E-01	8.00E-01	6.10E-01	2.90E-01	8.30E-03	3.40E-01	7.40E-01	2.50E-01	5.40E-01	5.90E-01	6.00E-01	3.20E-01	
					0.998	1.005	1.013	0.991	0.973	0.997	0.99	0.953	0.991	0.997	1.013	1.008	
					-0.003	0.012	0.057	-0.005	-2.188	-0.467	-0.036	-0.011	-0.443	-0.132	0.238	0.151	
1			1														
6	C7	0	6	IGF5702e	2.00E-01	2.50E-01	8.40E-01	4.40E-01	8.60E-01	3.30E-02	3.00E-01	1.20E-01	4.20E-01	1.00E-03	8.70E-02	7.20E-03	
					1.037	1.024	1.005	1.006	0.998	0.993	1.032	0.938	1.012	0.984	1.043	1.021	
					0.038	0.055	0.023	0.003	-0.155	-1.046	0.109	-0.015	0.584	-0.781	0.766	0.401	
1			1														
6	C7	7.6	6	IGF5707b	3.70E-01	3.40E-02	1.00E+00	2.90E-01	8.70E-01	1.80E-02	9.60E-01	3.00E-01	4.80E-01	3.60E-03	9.70E-02	2.20E-02	
					1.026	1.044	1	1.009	0.998	0.993	1.002	0.958	1.01	0.986	1.042	1.018	
					0.027	0.1	0.001	0.004	-0.138	-1.16	0.006	-0.01	0.508	-0.695	0.742	0.342	
1			1														
6	C7	22.8	6	IGF5415a	1.40E-01	6.00E-01	3.60E-01	9.30E-02	4.90E-01	1.80E-02	5.80E-01	2.50E-01	3.20E-01	2.40E-01	2.30E-01	1.60E-01	
					1.044	1.011	1.023	1.014	1.008	0.992	1.018	0.952	1.014	0.994	1.031	1.012	
					0.044	0.024	0.102	0.007	0.608	-1.209	0.061	-0.012	0.722	-0.286	0.56	0.221	
1			1									1.00E+00					
7	A5	0	7	CB10320_253	2.30E-01	8.00E-01	9.60E-01	5.30E-01	7.00E-01	2.70E-01	1.00E-01		6.80E-01	2.70E-01	4.10E-01	6.50E-01	
					1.035	0.995	0.999	0.995	0.996	0.997	1.05	1	1.006	0.995	1.021	1.004	
					0.036	-0.012	-0.007	-0.003	-0.323	-0.545	0.171	0	0.294	-0.268	0.367	0.069	
1			1														
7	A5	29.5	7	BRMS061_284	1.70E-01	9.70E-02	1.80E-01	5.90E-02	2.30E-01	2.30E-01	3.40E-01	2.30E-01	1.80E-01	7.70E-01	5.90E-03	9.40E-01	
					0.96	1.035	0.966	0.985	0.987	0.996	1.03	1.052	0.981	0.999	1.07	1.001	

					-0.042	0.08	-0.153	-0.008	-1.019	-0.584	0.101	0.012	-0.965	-0.071	1.22	0.011
1 7	A5	44.2	1 7	BRAS063_236	2.40E-01	4.30E-01	7.90E-01	2.10E-01	3.70E-01	9.40E-01	9.20E-01	2.30E-01	5.00E-01	8.20E-01	1.20E-02	4.50E-01
					0.966	1.017	0.993	0.99	0.99	1	1.003	1.053	0.99	1.001	1.065	0.994
					-0.036	0.039	-0.03	-0.006	-0.775	-0.036	0.011	0.012	-0.491	0.058	1.121	-0.116
1 8	A9	0	1 8	IGF5222b	6.00E-01	4.70E-01	9.40E-01	5.00E-01	1.60E-01	6.80E-01	7.00E-01	1.70E-01	7.50E-01	8.70E-01	2.90E-01	8.00E-01
					1.015	1.015	1.002	1.006	1.015	0.999	1.012	1.062	0.995	1.001	0.973	0.998
					0.015	0.035	0.008	0.002	1.228	-0.21	0.042	0.014	-0.23	0.039	-0.493	-0.039
1 8	A9	37	1 8	IGF5706e	1.20E-01	9.50E-01	3.10E-01	7.60E-01	3.00E-01	1.20E-01	6.40E-01	4.00E-02	5.60E-01	9.40E-01	2.10E-01	7.60E-01
					0.957	1.001	0.976	0.997	0.989	1.005	1.014	1.089	0.992	1	0.969	0.998
					-0.045	0.003	-0.109	-0.001	-0.881	0.766	0.049	0.019	-0.416	0.019	-0.564	-0.046
1 9	A9	0	1 9	IGF1207c	6.30E-01	9.70E-01	3.80E-01	8.40E-01	4.40E-01	2.90E-01	7.50E-01	4.10E-01	7.80E-01	7.90E-01	1.30E-01	1.20E-01
					0.986	0.999	0.978	1.002	0.992	0.997	1.01	1.036	0.996	1.001	0.962	0.988
					-0.014	-0.002	-0.099	0.001	-0.668	-0.518	0.034	0.008	-0.205	0.066	-0.697	-0.234
1 9	A9	1.1	1 9	OL12F02_119	4.70E-01	9.80E-01	3.50E-01	6.90E-01	3.10E-01	3.80E-01	8.90E-01	3.90E-01	7.10E-01	5.60E-01	1.50E-01	7.40E-02
					0.979	1	0.977	1.003	0.989	0.997	1.004	1.037	0.995	1.003	0.965	0.986
					-0.021	-0.001	-0.105	0.001	-0.857	-0.439	0.014	0.008	-0.27	0.143	-0.645	-0.271
0	um	0	0	BRAS038_120	8.50E-02	1.60E-01	8.50E-02	6.20E-01	6.20E-02	1.90E-01	2.70E-01	4.50E-03	8.30E-02		5.10E-03	9.80E-06
					0.951	0.971	0.957	0.996	1.02	0.996	0.966	0.889	1.025	0.974	1.074	1.035
					-0.052	-0.07	-0.195	-0.002	1.612	-0.665	-0.118	-0.028	1.272	-1.286	1.272	0.656
0	um	0	0	BRMS007_116	1.40E-01	6.00E-01	2.20E-01	1.50E-01	4.70E-01	9.20E-01	7.30E-01	7.90E-01	1.30E-01	7.80E-01	6.30E-01	9.30E-01
					0.959	0.989	0.97	1.012	1.008	1	0.989	1.011	0.979	1.001	0.988	1.001
					-0.043	-0.025	-0.138	0.005	0.616	-0.051	-0.037	0.003	-1.072	0.067	-0.22	0.012
0	um	0	0	BRMS061_297	5.80E-01	9.90E-01	6.60E-01	1.00E-01	6.80E-01	8.60E-01	7.20E-01	2.50E-01	1.60E-01	6.90E-01	7.50E-01	4.00E-01
					0.984	1	1.011	0.986	0.996	1.001	0.989	0.952	1.021	1.002	0.992	1.007
					-0.017	0	0.05	-0.007	-0.363	0.088	-0.038	-0.011	1.033	0.098	-0.145	0.131
0	um	0	0	BRMS098_146	4.90E-01	3.30E-01	1.40E-01	6.30E-01	2.70E-01	1.20E-01	1.60E-01	4.60E-01	2.60E-01	2.90E-01	9.00E-01	4.20E-01
					0.98	1.02	0.964	0.996	0.989	0.995	1.043	1.031	1.016	0.995	0.997	1.006
					-0.02	0.047	-0.162	-0.002	-0.92	-0.755	0.147	0.007	0.797	-0.257	-0.054	0.121
0	um	0	0	BRMS330_238	7.60E-01	4.80E-01	6.40E-01	8.90E-01	2.50E-01	8.00E-01	1.60E-01	3.10E-01	1.40E-01	7.10E-01	5.30E-01	5.80E-01

					0.984	1.028	0.978	0.998	0.977	0.999	1.083	1.08	0.961	1.003	0.971	0.992
					-0.017	0.065	-0.097	-0.001	-1.834	-0.234	0.283	0.019	-2.005	0.17	-0.53	-0.16
0	um	0	0	CB10179_150	7.70E-01	6.30E-02	8.40E-01	2.00E-01	3.10E-01	7.50E-02	7.40E-01	6.80E-01	5.20E-01	4.40E-01	1.00E+0	5.90E-01
					0.992	0.962	1.005	0.989	1.011	1.005	1.01	0.983	0.991	1.004	1	0.996
					-0.009	-0.09	0.022	-0.005	0.872	0.876	0.036	-0.004	-0.468	0.19	-0.002	-0.083
0	um	0	0	CB10427_165	3.80E-02	3.20E-02	2.60E-02	9.30E-01	6.00E-02	3.20E-01	2.50E-01	1.80E-02	2.40E-01		8.00E-03	2.40E-05
					0.942	0.956	0.946	0.999	1.02	0.997	0.964	0.907	1.017	0.976	1.069	1.033
					-0.061	-0.104	-0.25	-0.001	1.613	-0.506	-0.125	-0.023	0.862	-1.204	1.2	0.625
0	um	0	0	CB10493_166	1.80E-01	7.20E-01	2.10E-01	4.30E-02	1.90E-02	9.60E-01	7.80E-02	7.80E-01	5.30E-01	9.70E-01	9.50E-01	2.70E-01
					0.962	1.007	0.969	0.983	0.975	1	0.948	0.988	1.009	1	0.998	1.009
					-0.04	0.017	-0.139	-0.009	-2.025	0.028	-0.184	-0.003	0.446	0.009	-0.029	0.17
0	um	0	0	FITO317_384	1.30E-01	5.20E-02	6.70E-01	9.50E-01	8.60E-02	5.70E-01	5.10E-01	5.80E-01	6.60E-01	5.70E-01	8.40E-01	8.90E-01
					1.044	0.961	1.011	1.001	1.019	1.002	1.021	0.977	0.994	0.997	0.995	1.001
					0.044	-0.093	0.049	0	1.48	0.282	0.071	-0.005	-0.321	-0.143	-0.092	0.021
0	um	0	0	IGF0191b	1.00E+0	1.00E+0	1.00E+0	1.00E+0	1.00E+0	1.00E+0	1.00E+0	1.00E+0	1.00E+0	1.00E+0	1.00E+0	1.00E+0
					0	0	0	0	0	0	0	0	0	0	0	0
					*	*	*	*	*	*	*	*	*	*	*	*
					a-b	a-b	a-b	a-b	a-b	a-b	a-b	a-b	a-b	a-b	a-b	a-b
0	um	0	0	IGF2128c	5.10E-02	3.90E-01	2.30E-01	2.00E-01	2.40E-01	2.10E-01	8.20E-01	5.10E-01	1.20E-01	9.10E-01	7.70E-01	3.40E-01
					1.056	0.982	1.03	0.99	1.012	1.004	0.993	1.027	1.022	0.999	0.993	1.008
					0.056	-0.041	0.132	-0.005	0.98	0.623	-0.024	0.006	1.117	-0.028	-0.13	0.144
0	um	0	0	IGF5101b	5.10E-01	2.60E-01	6.60E-01	9.30E-01	3.30E-01	5.50E-01	2.90E-02	8.60E-01	2.80E-01	8.30E-01	5.30E-01	8.90E-01
					0.981	1.023	1.011	0.999	1.01	1.002	0.936	0.993	1.015	0.999	0.985	1.001
					-0.019	0.054	0.048	-0.001	0.823	0.297	-0.228	-0.001	0.772	-0.051	-0.28	0.021
0	um	0	0	KBrB048K11(2)	4.10E-02	5.30E-01	9.70E-01	8.30E-01	7.60E-01	3.40E-01	2.20E-01	3.90E-01	6.70E-01	8.30E-01	7.90E-01	9.70E-01
					0.943	1.013	0.999	1.002	1.003	1.003	0.963	1.037	1.006	0.999	0.993	1
					-0.06	0.03	-0.004	0.001	0.26	0.474	-0.13	0.008	0.312	-0.052	-0.12	0.005
0	um	0	0	KBrH027N05(3)	7.30E-02	2.90E-01	8.60E-01	7.90E-01	7.80E-01	3.80E-01	7.00E-01	7.20E-01	6.40E-01	8.40E-01	8.30E-01	9.20E-01
					0.95	1.022	1.004	1.002	1.003	1.003	0.988	1.015	1.007	1.001	1.005	0.999
					-0.053	0.052	0.02	0.001	0.242	0.434	-0.042	0.003	0.343	0.051	0.098	-0.016
0	um	0	0	MAX2_b	8.60E-01	5.30E-02	7.40E-01	2.30E-01	3.60E-01	3.90E-01	2.60E-01	1.80E-01	3.80E-01	6.10E-01	8.40E-01	6.90E-01

					0.994	0.959	0.991	1.011	1.011	0.997	1.039	0.938	0.988	0.997	0.995	1.003
					-0.006	-0.095	-0.041	0.005	0.852	-0.47	0.132	-0.014	-0.63	-0.13	-0.098	0.063
0	um	0	0	NA12A07_152	4.90E-01	1.60E-01	9.00E-02	5.90E-01	4.50E-01	5.90E-01	2.10E-01	2.80E-01	2.20E-01	1.20E-01	5.40E-01	3.40E-01
					0.98	0.971	0.958	0.995	1.008	1.002	0.961	0.956	1.017	1.008	1.016	0.993
					-0.021	-0.068	-0.19	-0.003	0.65	0.268	-0.136	-0.01	0.876	0.386	0.279	-0.143
0	um	0	0	NA12E02_92	7.70E-02	1.20E-01	8.30E-02	9.80E-01	5.30E-02	2.10E-01	1.30E-01	1.70E-02	1.10E-01		6.20E-03	8.60E-06
					0.95	0.968	0.957	1	1.021	0.996	0.954	0.905	1.024	0.973	1.072	1.035
					-0.053	-0.076	-0.198	0	1.683	-0.631	-0.164	-0.023	1.186	-1.348	1.25	0.662
0	um	0	0	NA14E08_98	8.00E-01	1.10E-01	8.70E-01	6.10E-01	7.60E-01	6.20E-01	4.50E-01	8.40E-01	8.00E-01	6.30E-01	9.40E-01	5.60E-01
					0.993	0.968	0.996	0.996	1.003	1.002	0.977	1.009	1.004	1.002	0.998	1.005
					-0.008	-0.076	-0.017	-0.003	0.261	0.245	-0.08	0.002	0.185	0.118	-0.032	0.088
0	um	0	0	OL13G05_124	4.20E-02	3.00E-01	1.40E-02	6.70E-03	7.60E-02	4.10E-01	9.20E-01	1.30E-01	1.30E-01	5.50E-02	1.10E-01	7.90E-01
					0.942	1.023	0.94	0.978	0.981	1.003	0.997	1.067	0.979	1.01	1.042	0.998
					-0.062	0.052	-0.278	-0.011	-1.535	0.416	-0.01	0.015	-1.087	0.483	0.74	-0.042
0	um	0	0	RA2G08_318	6.20E-01	3.40E-01	8.90E-01	4.00E-01	1.00E-02	6.80E-01	5.10E-01	1.40E-01	3.90E-01	8.00E-01	3.40E-03	9.70E-01
					0.986	1.02	0.997	0.993	0.974	1.001	0.98	1.062	0.988	0.999	0.931	1
					-0.015	0.046	-0.014	-0.003	-2.132	0.204	-0.069	0.014	-0.615	-0.063	-1.286	0.005
0	um	0	0	RGL3_a	4.40E-01	9.10E-01	3.70E-01	1.70E-01	9.60E-01	8.50E-01	7.90E-01	9.70E-02	3.50E-01	2.80E-01	9.50E-02	5.50E-01
					1.024	1.002	1.023	0.988	0.999	1.001	1.009	0.928	1.014	0.994	1.045	1.005
					0.024	0.005	0.102	-0.006	-0.044	0.099	0.03	-0.017	0.695	-0.274	0.802	0.096
0	um	0	0	SN1963_335	4.60E-02	2.60E-01	1.90E-01	6.60E-01	3.70E-01	9.80E-01	6.50E-01	3.20E-01	9.30E-01	9.70E-01	1.00E-01	6.10E-02
					0.945	0.977	0.968	0.996	1.009	1	0.986	0.959	0.999	1	1.041	1.015
					-0.058	-0.054	-0.146	-0.002	0.751	0.01	-0.047	-0.009	-0.059	-0.009	0.729	0.282

Supplementary Table 16. Single marker summary CRDH at Cantelupe including parental trait ratios and differences between parents.

LG	Homology	cM	markers	height of plant		foot length		pod number on terminal	pod density on terminal	stem width	fertile branch number	infertile branch number	node number	total node number	node density
1	C3	0	IGF0568d	5.20E-01	2.40E-01	4.20E-01	5.20E-01	1.60E-01	4.60E-02	2.00E-01	1.50E-01	4.80E-01	1.20E-01	4.40E-01	
				0.988	1.026	0.942	0.981	1.053	0.969	0.87	0.818	0.979	0.949	1.019	
				-1.692	1.512	-3.352	-0.869	0.071	-0.03	-0.432	-0.105	-0.226	-0.753	0.188	
1	C3	20.9	CALSSR_137	7.60E-02	6.30E-01	4.20E-01	3.60E-01	3.70E-01	8.30E-02	9.80E-01	8.00E-01	6.70E-01	8.00E-01	1.80E-01	
				0.969	0.99	0.945	1.026	0.969	0.975	0.998	0.969	1.012	1.008	0.969	
				-4.393	-0.586	-3.169	1.162	-0.045	-0.024	-0.007	-0.017	0.13	0.119	-0.312	
1	C3	26	SN4513_369	1.30E-01	5.20E-01	1.90E-01	9.90E-01	8.80E-01	1.40E-01	8.10E-01	9.00E-01	8.50E-01	9.70E-01	4.60E-01	
				0.974	0.987	0.913	1	1.005	0.979	1.023	0.985	0.995	1.001	0.983	
				-3.703	-0.787	-5.138	0.011	0.007	-0.02	0.074	-0.008	-0.059	0.019	-0.17	
1	C3	42	BRAS068_115	1.50E-02	7.40E-01	2.40E-02	8.60E-01	9.40E-01	1.00E-01	6.40E-01	6.20E-01	1.70E-01	5.30E-01	5.60E-01	
				0.959	0.993	0.86	1.005	0.997	0.976	1.046	0.941	0.964	0.981	0.987	
				-5.852	-0.395	-8.565	0.228	-0.003	-0.023	0.144	-0.034	-0.407	-0.283	-0.133	
2	A3	0	CB10427_152	3.70E-02	1.00E-01	3.70E-02	9.50E-01	4.90E-01	6.40E-01	9.30E-01	1.00E+00	5.00E-01	6.90E-01	5.70E-01	
				1.049	1.044	1.196	1.002	1.033	1.009	0.988	1	1.025	1.017	1.018	
				6.84	2.613	10.766	0.105	0.045	0.009	-0.038	-0.001	0.274	0.243	0.177	
2	A3	2.4	BRAS038_108	7.10E-02	1.70E-01	1.70E-02	3.50E-01	9.90E-01	6.70E-01	2.00E-02	8.80E-01	3.60E-01	2.90E-02	8.30E-01	
				1.043	1.037	1.224	1.035	1	1.009	1.317	0.975	1.034	1.092	0.993	
				5.953	2.203	12.26	1.572	0	0.008	0.966	-0.014	0.367	1.327	-0.067	
2	A3	2.7	BRAS087_160	6.60E-02	8.70E-02	1.40E-02	6.90E-01	6.00E-01	8.70E-01	9.70E-01	8.60E-01	5.50E-01	5.30E-01	5.40E-01	

				1.047	1.05	1.251	1.015	1.026	0.997	1.002	1.031	1.024	1.02	1.02
				6.478	2.95	13.678	0.689	0.036	-0.003	0.006	0.017	0.256	0.286	0.194
2	A3	4.2	SSR18_175	2.00E-01	1.40E-01	5.20E-02	7.80E-01	3.40E-01	6.60E-01	7.00E-01	7.40E-01	9.80E-01	7.80E-01	4.30E-01
				1.032	1.043	1.195	0.989	1.049	0.991	0.945	0.943	1.001	0.987	1.027
				4.497	2.53	10.781	-0.496	0.067	-0.009	-0.175	-0.031	0.013	-0.186	0.262
2	A3	6.4	CB10036_160	8.90E-02	3.30E-02	9.40E-01	5.60E-01	9.80E-02	5.50E-01	9.80E-01	2.80E-01	9.40E-01	9.10E-01	3.60E-01
				1.05	1.073	0.991	0.973	1.097	1.015	0.997	0.787	1.004	0.994	1.036
				7	4.308	-0.519	-1.209	0.133	0.014	-0.01	-0.121	0.04	-0.083	0.355
2	A3	6.4	OL10D03_101	1.80E-01	3.80E-02	8.60E-01	9.90E-01	2.30E-01	7.60E-01	8.80E-01	2.20E-01	9.90E-01	7.90E-01	4.30E-01
				1.038	1.068	0.98	1	1.067	1.007	0.975	0.768	1.001	0.987	1.029
				5.26	3.976	-1.124	0.022	0.092	0.007	-0.078	-0.132	0.009	-0.194	0.288
3	C3/A3/C8	6.4	BRMS269_313	1.80E-01	3.80E-02	8.60E-01	9.90E-01	2.30E-01	7.60E-01	8.80E-01	2.20E-01	9.90E-01	7.90E-01	4.30E-01
				1.038	1.068	0.98	1	1.067	1.007	0.975	0.768	1.001	0.987	1.029
				5.26	3.976	-1.124	0.022	0.092	0.007	-0.078	-0.132	0.009	-0.194	0.288
3	C3/A3/C8	10.2	BRAS065_219	1.40E-01	7.00E-02	8.70E-01	4.70E-01	6.20E-01	2.70E-01	4.20E-01	4.00E-01	5.70E-01	9.50E-01	5.20E-01
				1.034	1.049	1.014	1.026	1.022	0.979	0.959	0.863	1.021	1.002	1.019
				4.762	2.857	0.809	1.17	0.03	-0.02	-0.128	-0.076	0.224	0.028	0.186
3	C3/A3/C8	13.6	AtTB1_f	4.50E-01	1.20E-01	5.80E-01	8.10E-01	2.50E-01	5.60E-01	9.40E-01	1.10E-01	9.10E-01	8.40E-01	9.10E-01
				1.016	1.039	0.953	0.992	1.045	0.989	0.991	0.768	1.004	0.992	1.003
				2.278	2.29	-2.66	-0.354	0.061	-0.01	-0.029	-0.132	0.042	-0.111	0.033
4	uk1	0	RA1F06_190	6.20E-03	1.10E-02	4.20E-02	2.00E-01	9.50E-01	5.10E-01	1.30E-01	2.10E-01	6.70E-01	5.40E-01	1.60E-02
				0.954	0.951	0.911	0.965	1.002	0.99	1.161	0.859	0.988	1.019	0.946
				-6.549	-2.999	-5.149	-1.619	0.003	-0.009	0.475	-0.082	-0.128	0.28	-0.545
4	uk1	19	CALSSR_142	4.00E-02	9.80E-01	3.40E-02	4.40E-01	4.20E-01	7.60E-01	2.70E-01	6.00E-02	6.40E-01	8.80E-01	1.30E-01
				0.961	0.999	0.856	0.977	1.031	0.995	1.13	0.788	0.986	1.005	0.962
				-5.543	-0.035	-9.047	-1.054	0.042	-0.004	0.381	-0.137	-0.156	0.076	-0.381
4	uk1	23.5	SN4513_366	3.30E-02	2.20E-01	7.60E-03	2.50E-01	5.60E-02	8.90E-01	2.50E-01	1.30E-01	5.90E-02	4.90E-01	7.00E-01
				0.961	1.027	0.829	0.967	1.074	1.002	1.13	0.825	0.947	0.977	0.991
				-5.555	1.595	-10.923	-1.506	0.097	0.002	0.382	-0.108	-0.598	-0.335	-0.094
4	uk1	39.4	KBrH004A18(3)	1.90E-01	2.00E-01	1.30E-02	9.60E-02	2.40E-02	1.10E-01	2.10E-01	2.80E-01	1.20E-01	8.40E-01	8.40E-01

				0.976	1.027	0.844	0.954	1.077	1.025	1.142	0.872	0.96	0.994	0.995
				-3.337	1.583	-9.872	-2.11	0.101	0.023	0.418	-0.076	-0.457	-0.094	-0.048
4	uk1	58.1	A77096_218	1.80E-02	9.40E-01	5.60E-03	2.10E-01	2.30E-01	3.30E-01	2.70E-01	2.70E-01	3.00E-01	9.60E-01	3.20E-01
				0.958	1.002	0.819	0.962	1.048	1.015	1.131	0.864	0.969	0.998	0.975
				-6.086	0.094	-11.751	-1.727	0.064	0.015	0.382	-0.082	-0.352	-0.029	-0.249
4	uk1	62.8	KBrH013K13(1)	3.60E-02	7.80E-01	7.10E-03	2.70E-01	1.50E-01	2.50E-01	2.80E-01	2.60E-01	1.60E-01	7.80E-01	5.60E-01
				0.961	1.006	0.826	0.967	1.056	1.018	1.127	0.869	0.959	0.99	0.985
				-5.528	0.363	-11.247	-1.516	0.075	0.017	0.373	-0.08	-0.456	-0.141	-0.146
5	A2/A6	0	RGA12_30	2.80E-02	8.40E-01	9.50E-02	7.60E-01	4.80E-01	7.80E-01	7.00E-01	4.20E-01	6.20E-01	9.80E-01	3.10E-01
				0.962	1.004	0.892	1.009	0.975	0.996	1.039	1.106	0.986	1.001	0.976
				-5.436	0.246	-6.578	0.4	-0.034	-0.003	0.121	0.055	-0.153	0.012	-0.237
5	A2/A6	8.5	RGL12_31_300	9.90E-03	3.00E-01	1.70E-01	7.90E-01	3.40E-01	4.20E-01	8.10E-01	2.60E-01	5.20E-01	9.10E-01	4.50E-01
				0.955	0.979	0.909	0.992	0.966	0.988	1.025	1.154	0.982	0.996	0.982
				-6.393	-1.271	-5.485	-0.354	-0.048	-0.012	0.079	0.078	-0.201	-0.057	-0.177
5	A2/A6	31.1	CB10416_251	2.00E-01	1.80E-01	2.10E-01	7.70E-01	1.60E-01	4.90E-01	5.00E-01	8.30E-01	4.60E-01	9.90E-01	9.90E-01
				0.977	0.973	0.918	1.009	0.953	0.99	1.07	1.028	0.98	1	1
				-3.212	-1.629	-4.873	0.382	-0.068	-0.01	0.216	0.015	-0.225	-0.005	-0.003
5	A2/A6	32.1	IGF3239d	2.10E-01	1.30E-01	2.40E-01	8.40E-01	1.60E-01	3.90E-01	5.10E-01	9.40E-01	4.60E-01	9.60E-01	1.00E+00
				0.978	0.969	0.922	1.006	0.952	0.987	1.068	1.01	0.98	0.999	1
				-3.121	-1.871	-4.651	0.262	-0.068	-0.012	0.209	0.006	-0.224	-0.021	0.002
5	A2/A6	44.2	FITO232_130	5.40E-02	2.00E-01	8.00E-02	3.20E-01	7.40E-01	9.40E-01	2.80E-01	2.00E-01	1.70E-01	7.00E-01	8.70E-01
				0.966	0.973	0.886	0.972	1.012	0.999	1.117	0.855	0.962	0.988	0.996
				-4.848	-1.607	-6.971	-1.297	0.016	-0.001	0.347	-0.088	-0.428	-0.181	-0.04
5	A2/A6	65.8	RA1F06_175	1.80E-02	3.90E-02	2.00E-01	1.80E-01	9.90E-01	9.80E-02	4.90E-01	7.80E-01	2.00E-01	6.70E-01	5.40E-01
				0.96	0.958	0.943	0.963	1	0.976	1.073	0.966	0.965	0.986	0.986
				-5.757	-2.519	-3.284	-1.705	-0.001	-0.023	0.224	-0.018	-0.394	-0.202	-0.142
6	A4/C4(6)	0	NA12E05_146	5.00E-01	7.20E-01	3.90E-02	2.90E-01	4.50E-01	1.80E-01	4.40E-01	1.50E-01	4.80E-02	4.50E-02	1.60E-01
				0.988	0.993	0.867	0.97	1.027	0.98	0.927	0.839	0.947	0.939	1.034
				-1.646	-0.433	-8.066	-1.346	0.037	-0.018	-0.243	-0.097	-0.596	-0.919	0.326
6	A4/C4(6)	3.2	CB10493_155	4.90E-01	9.80E-01	2.00E-02	6.70E-01	5.60E-01	3.50E-01	5.00E-01	7.20E-02	9.70E-03	1.70E-02	5.70E-02

				0.988	1.001	0.854	0.988	1.021	0.986	0.936	0.805	0.932	0.929	1.045
				-1.717	0.031	-8.962	-0.546	0.029	-0.013	-0.211	-0.12	-0.772	-1.087	0.437
6	A4/C4(6)	3.9	OL10B01_177	2.80E-01	9.80E-01	8.40E-03	6.50E-01	5.50E-01	3.40E-01	5.50E-01	4.00E-02	3.40E-03	9.90E-03	4.60E-02
				0.981	1	0.834	0.987	1.021	0.986	0.942	0.779	0.923	0.922	1.047
				-2.702	-0.03	-10.264	-0.562	0.029	-0.014	-0.191	-0.137	-0.872	-1.185	0.459
6	A4/C4(6)	10	MAX3_m	2.80E-01	3.90E-01	9.70E-03	5.50E-01	2.20E-01	9.30E-01	7.70E-01	2.80E-02	1.60E-04	4.00E-03	9.90E-03
				0.981	1.018	0.829	0.983	1.046	1.001	0.97	0.739	0.9	0.909	1.064
				-2.712	1.06	-10.463	-0.787	0.063	0.002	-0.099	-0.16	-1.141	-1.385	0.614
7	C7	0	CB10299_140	9.00E-01	2.50E-01	1.30E-01	8.00E-01	8.70E-01	8.30E-01	3.70E-01	9.30E-01	1.90E-01	1.40E-01	4.00E-01
				1.002	0.977	1.11	0.993	0.994	1.003	1.092	1.011	1.036	1.046	0.981
				0.302	-1.389	5.885	-0.314	-0.008	0.003	0.281	0.005	0.385	0.66	-0.19
7	C7	0.1	BRMS296_142	7.40E-01	2.90E-01	1.20E-01	8.60E-01	8.50E-01	5.50E-01	3.20E-01	8.20E-01	1.70E-01	1.30E-01	4.20E-01
				1.006	0.978	1.114	0.995	0.993	1.009	1.104	0.973	1.039	1.049	0.982
				0.825	-1.295	6.076	-0.222	-0.009	0.008	0.316	-0.015	0.412	0.701	-0.184
7	C7	16.6	BRAS019_128	4.60E-01	7.50E-01	6.50E-01	2.20E-01	3.00E-01	7.10E-01	2.00E-01	3.70E-01	6.90E-01	6.50E-01	9.40E-01
				0.987	0.993	1.032	0.966	1.037	1.005	1.134	0.898	0.989	1.014	1.002
				-1.794	-0.388	1.763	-1.55	0.05	0.005	0.399	-0.059	-0.121	0.205	0.017
8	uk2	0	FITO300_127	9.60E-01	8.60E-01	6.50E-01	9.00E-01	9.00E-01	4.20E-01	2.10E-01	9.50E-01	3.90E-01	7.60E-01	8.70E-01
				0.999	0.996	1.031	0.996	1.004	1.012	1.128	0.992	0.977	1.009	1.004
				-0.136	-0.216	1.726	-0.162	0.006	0.011	0.388	-0.004	-0.259	0.138	0.036
8	uk2	14.9	FITO110_291	4.30E-01	4.10E-01	8.40E-01	5.60E-01	6.50E-01	9.90E-01	6.40E-01	2.70E-01	6.50E-01	8.30E-01	7.30E-01
				0.986	0.983	1.014	0.984	1.016	1	1.048	1.145	0.987	1.007	0.992
				-1.985	-1.006	0.803	-0.733	0.021	0	0.149	0.074	-0.142	0.098	-0.079
8	uk2	19.4	OL10A05_190	8.50E-01	8.80E-01	6.70E-01	3.60E-01	1.70E-01	5.90E-01	4.80E-01	7.90E-01	4.00E-01	1.00E+00	8.10E-01
				0.997	0.997	1.03	0.974	1.049	1.008	1.072	1.033	0.977	1	1.006
				-0.47	-0.19	1.653	-1.174	0.067	0.007	0.223	0.018	-0.256	-0.001	0.056
9	A3/A4	0	BRMS008_156	9.90E-02	6.10E-01	1.10E-01	7.30E-01	6.90E-01	1.70E-01	5.00E-01	3.90E-01	9.90E-01	5.40E-01	1.80E-01
				0.972	0.99	0.897	0.991	1.014	0.98	1.068	1.111	1	1.019	0.97
				-4.008	-0.612	-6.159	-0.423	0.019	-0.019	0.21	0.057	-0.003	0.28	-0.302
9	A3/A4	14.2	IGF5193a	1.30E-01	2.30E-01	6.30E-02	2.80E-01	6.70E-01	3.20E-01	4.00E-01	3.70E-01	9.00E-01	5.60E-01	2.80E-01

				0.974	0.976	0.882	0.97	1.015	0.985	0.922	0.895	1.003	0.982	0.975
				-3.708	-1.453	-7.182	-1.358	0.02	-0.014	-0.262	-0.061	0.037	-0.268	-0.248
10	A3	0	IGF5272c	6.00E-01	2.70E-01	3.20E-01	7.40E-01	4.00E-01	9.20E-01	2.90E-01	9.20E-01	2.10E-01	1.30E-01	7.30E-02
				0.99	0.978	1.073	0.991	0.971	0.999	1.113	0.987	1.036	1.049	0.959
				-1.34	-1.352	3.963	-0.426	-0.041	-0.001	0.337	-0.007	0.384	0.702	-0.416
10	A3	6.7	BRMS008_115	7.60E-01	4.60E-01	1.80E-01	9.70E-01	3.50E-01	8.20E-01	2.40E-01	5.60E-01	2.70E-02	3.20E-02	5.60E-02
				1.005	0.985	1.094	0.999	0.969	1.003	1.12	0.931	1.061	1.067	0.958
				0.745	-0.882	5.086	-0.043	-0.044	0.003	0.36	-0.039	0.649	0.956	-0.429
10	A3	12.8	MAX2_I	4.20E-01	5.20E-01	6.70E-01	4.30E-01	8.50E-01	9.30E-01	6.40E-01	6.30E-01	3.60E-01	3.50E-01	2.10E-01
				0.985	0.986	1.022	0.977	0.993	1.001	1.021	0.939	1.028	1.022	0.971
				-2.156	-0.857	1.17	-1.032	-0.01	0.001	0.062	-0.034	0.296	0.308	-0.298
10	A3	19.9	BRMS330_241	9.70E-01	2.60E-01	2.00E-01	9.40E-01	3.00E-01	7.60E-01	3.00E-01	5.10E-01	1.50E-01	1.20E-01	1.60E-01
				0.999	0.978	1.09	1.002	0.965	1.005	1.106	0.923	1.04	1.048	0.969
				-0.093	-1.347	4.875	0.101	-0.049	0.004	0.322	-0.044	0.428	0.69	-0.314
10	A3	42.1	RA2E11_200	5.60E-01	8.70E-01	6.60E-01	7.40E-01	7.20E-01	9.90E-01	6.50E-01	1.60E-01	5.70E-01	3.50E-01	7.50E-01
				0.99	1.003	1.03	0.991	1.013	1	0.956	0.838	0.984	0.971	1.007
				-1.431	0.194	1.702	-0.415	0.017	0	-0.144	-0.095	-0.173	-0.428	0.072
10	A3	43.3	CB10036_131	6.90E-01	9.30E-01	6.00E-01	9.40E-01	9.90E-01	8.70E-01	6.30E-01	9.40E-02	6.20E-01	3.50E-01	7.40E-01
				0.993	0.998	1.037	0.998	1	1.002	0.953	0.814	0.986	0.971	1.008
				-0.995	-0.114	2.039	-0.093	0.001	0.002	-0.153	-0.111	-0.153	-0.434	0.079
10	A3	66.4	OL11B05_109	7.80E-01	3.10E-01	5.10E-01	5.90E-01	2.50E-01	2.80E-01	3.20E-01	1.80E-01	3.10E-01	1.20E-01	7.80E-02
				1.005	1.022	0.954	0.984	1.042	0.984	0.903	0.84	0.971	0.952	1.042
				0.708	1.27	-2.648	-0.701	0.057	-0.015	-0.322	-0.092	-0.317	-0.72	0.412
10	A3	66.7	NA12E02_118	9.00E-01	3.00E-01	5.10E-01	6.20E-01	2.60E-01	1.50E-01	2.60E-01	2.70E-01	2.80E-01	1.00E-01	7.40E-02
				1.002	1.022	0.954	0.985	1.042	0.979	0.89	0.867	0.969	0.948	1.044
				0.319	1.32	-2.667	-0.662	0.057	-0.02	-0.364	-0.077	-0.341	-0.77	0.426
10	A3	68.1	CB10427_138	9.60E-01	4.30E-01	4.90E-01	5.00E-01	2.40E-01	2.20E-01	3.00E-01	2.90E-01	4.00E-01	1.60E-01	1.80E-01
				0.999	1.017	0.951	0.98	1.043	0.981	0.898	0.869	0.976	0.955	1.033
				-0.146	1.006	-2.815	-0.895	0.059	-0.018	-0.337	-0.074	-0.268	-0.668	0.32
10	A3	94.4	SN11722_93	2.40E-02	9.10E-03	2.10E-01	4.50E-01	4.10E-01	5.60E-01	3.50E-01	6.70E-01	4.40E-01	9.10E-01	3.30E-01

				0.961	0.949	0.917	0.979	0.972	0.991	1.097	0.949	0.979	1.003	0.978
				-5.48	-3.087	-4.891	-0.964	-0.039	-0.008	0.295	-0.029	-0.231	0.05	-0.222
10	A3	106	NA10D03_157	1.80E-01	3.80E-02	3.20E-01	5.40E-01	5.40E-01	2.70E-01	3.30E-01	5.70E-01	6.30E-01	7.70E-01	3.50E-01
				0.977	0.959	0.934	0.983	0.979	0.984	1.098	0.933	0.987	1.009	0.979
				-3.287	-2.456	-3.844	-0.757	-0.029	-0.016	0.3	-0.037	-0.142	0.133	-0.21
10	A3	108.5	IGF3100b	2.20E-01	1.50E-01	2.40E-01	9.50E-01	4.70E-01	4.30E-01	3.30E-01	5.40E-01	3.90E-01	9.60E-01	5.90E-01
				0.979	0.972	0.923	1.002	0.975	0.988	1.1	0.926	0.977	1.001	0.988
				-3.024	-1.707	-4.509	0.079	-0.035	-0.011	0.306	-0.041	-0.257	0.02	-0.122
10	A3	111.7	RGA2_H24_13_150	1.10E-01	1.10E-01	2.20E-01	5.00E-01	1.90E-01	1.50E-01	4.60E-01	6.90E-01	5.60E-01	9.20E-01	3.30E-01
				0.972	0.968	0.92	1.019	0.956	0.979	1.075	0.952	0.984	1.003	0.978
				-3.888	-1.906	-4.68	0.839	-0.061	-0.02	0.231	-0.027	-0.172	0.046	-0.22
10	A3	111.7	RGA2_H24_14_300	1.10E-01	1.10E-01	2.20E-01	5.00E-01	1.90E-01	1.50E-01	4.60E-01	6.90E-01	5.60E-01	9.20E-01	3.30E-01
				0.972	0.968	0.92	1.019	0.956	0.979	1.075	0.952	0.984	1.003	0.978
				-3.888	-1.906	-4.68	0.839	-0.061	-0.02	0.231	-0.027	-0.172	0.046	-0.22
11	C1	0	KBrB078A03(1)	9.00E-01	1.50E-01	2.90E-01	6.40E-01	5.60E-02	6.90E-01	2.20E-01	3.80E-01	1.10E-01	7.60E-01	1.60E-01
				0.998	1.031	0.924	0.986	1.073	1.006	1.134	0.887	0.954	0.99	1.035
				-0.337	1.848	-4.375	-0.635	0.098	0.006	0.411	-0.064	-0.512	-0.152	0.343
11	C1	1	BRAS067_136	9.10E-01	1.70E-01	2.90E-01	6.00E-01	5.60E-02	3.80E-01	1.70E-01	2.10E-01	1.40E-01	8.50E-01	1.80E-01
				1.002	1.03	0.925	0.984	1.072	1.014	1.15	0.844	0.957	0.994	1.034
				0.313	1.773	-4.345	-0.707	0.098	0.013	0.46	-0.089	-0.473	-0.092	0.328
11	C1	1	NA12H02_219	9.10E-01	1.70E-01	2.90E-01	6.00E-01	5.60E-02	3.80E-01	1.70E-01	2.10E-01	1.40E-01	8.50E-01	1.80E-01
				1.002	1.03	0.925	0.984	1.072	1.014	1.15	0.844	0.957	0.994	1.034
				0.313	1.773	-4.345	-0.707	0.098	0.013	0.46	-0.089	-0.473	-0.092	0.328
11	C1	2.1	SN3734_288	8.00E-01	1.70E-01	3.70E-01	6.30E-01	8.90E-02	4.10E-01	2.10E-01	3.00E-01	1.70E-01	8.60E-01	1.30E-01
				1.005	1.03	0.937	0.986	1.063	1.013	1.136	0.87	0.96	0.994	1.038
				0.655	1.757	-3.658	-0.64	0.086	0.012	0.417	-0.074	-0.438	-0.083	0.367
11	C1	15.3	IGF3338a	2.80E-01	9.80E-01	7.30E-01	2.00E-01	1.70E-01	3.10E-01	6.10E-01	5.50E-01	6.90E-02	6.80E-02	2.00E-01
				0.975	1.001	0.966	0.953	1.062	0.98	0.973	1.096	0.937	0.951	1.034
				-3.483	0.039	-1.945	-2.082	0.085	-0.018	-0.083	0.053	-0.703	-0.721	0.335
11	C1	24.8	IGF0504b	2.20E-01	7.40E-01	4.40E-01	4.60E-01	5.70E-01	6.20E-01	2.60E-01	7.90E-01	1.60E-01	9.10E-02	3.00E-01

				0.977	0.993	0.944	0.978	1.021	0.992	0.885	0.966	0.959	0.944	1.026
				-3.192	-0.444	-3.281	-0.977	0.029	-0.007	-0.385	-0.019	-0.451	-0.842	0.253
11	C1	27.1	IGF1059e	4.80E-01	9.60E-01	3.50E-01	5.60E-01	5.20E-01	9.60E-01	3.90E-01	7.90E-01	1.40E-01	1.10E-01	2.30E-01
				0.987	1.001	0.936	0.984	1.023	1.001	0.918	0.967	0.959	0.951	1.028
				-1.773	0.058	-3.699	-0.74	0.031	0.001	-0.271	-0.018	-0.456	-0.734	0.278
11	C1	30.9	KBrB036M22(3)	5.40E-01	8.40E-01	3.30E-01	6.00E-01	4.30E-01	9.40E-01	5.20E-01	6.60E-01	7.60E-02	1.00E-01	1.20E-01
				0.989	1.004	0.931	0.985	1.029	1.001	0.934	0.945	0.95	0.947	1.038
				-1.598	0.261	-3.986	-0.685	0.04	0.001	-0.215	-0.031	-0.553	-0.787	0.369
11	C1	38.1	IGF3315b	2.20E-01	8.20E-01	3.80E-01	3.10E-01	4.70E-01	3.00E-01	4.70E-01	7.70E-01	2.60E-01	2.10E-01	6.30E-01
				0.977	0.995	0.935	0.969	1.028	1.016	0.923	0.962	0.968	0.959	1.012
				-3.243	-0.3	-3.815	-1.4	0.039	0.015	-0.256	-0.022	-0.357	-0.621	0.121
11	C1	51	RA2E11_205	7.70E-01	6.60E-01	4.40E-01	7.10E-01	7.50E-01	4.40E-01	3.70E-01	1.40E-01	1.70E-01	8.60E-02	1.90E-01
				0.995	1.009	0.95	1.011	1.011	1.012	0.917	0.834	0.963	0.949	1.03
				-0.719	0.518	-2.926	0.468	0.015	0.011	-0.276	-0.099	-0.409	-0.769	0.296
11	C1	52.9	OL12F11_233	6.30E-01	6.30E-01	2.10E-01	7.70E-01	7.00E-01	2.70E-01	5.20E-01	1.50E-01	4.70E-02	5.30E-02	1.60E-01
				0.992	1.01	0.92	1.008	1.013	1.016	0.939	0.839	0.948	0.943	1.032
				-1.16	0.575	-4.753	0.366	0.018	0.015	-0.201	-0.095	-0.583	-0.864	0.313
11	C1	89.9	MAX_4r	6.40E-01	7.10E-01	5.50E-01	9.10E-01	9.20E-01	2.20E-01	6.50E-01	7.90E-01	7.20E-01	9.90E-01	2.00E-01
				0.992	0.993	1.042	1.003	1.003	1.018	0.956	1.033	1.01	1	0.971
				-1.158	-0.445	2.317	0.141	0.005	0.017	-0.143	0.018	0.108	-0.003	-0.289
11	C1	101.2	MAX_4n	3.60E-01	2.10E-01	7.40E-01	5.80E-01	3.20E-01	7.30E-01	5.00E-01	8.60E-01	9.60E-01	6.70E-01	2.70E-01
				0.984	0.974	1.024	1.016	0.965	1.006	0.934	1.023	0.999	0.986	0.974
				-2.297	-1.579	1.363	0.731	-0.05	0.005	-0.22	0.013	-0.014	-0.203	-0.265
12	A7	0	NA12A05_157	8.10E-03	6.90E-01	2.90E-02	5.90E-01	4.70E-01	7.00E-01	7.30E-01	3.20E-01	5.70E-04	9.80E-03	3.40E-01
				0.955	1.008	0.862	0.985	1.026	0.994	0.967	0.888	0.912	0.924	1.023
				-6.422	0.482	-8.412	-0.683	0.035	-0.005	-0.106	-0.066	-1.01	-1.165	0.221
12	A7	5.4	OL12E03_110	4.40E-03	9.10E-01	1.10E-02	5.50E-01	3.90E-01	8.70E-01	1.20E-01	3.40E-01	8.10E-05	1.20E-01	3.80E-01
				0.953	1.002	0.845	0.984	1.03	0.998	1.16	0.891	0.903	0.954	1.02
				-6.787	0.134	-9.55	-0.737	0.041	-0.002	0.473	-0.063	-1.122	-0.696	0.196
12	A7	42.3	IGF1226a	1.20E-02	6.60E-01	3.10E-01	4.50E-01	3.10E-01	4.80E-01	2.20E-01	7.50E-02	1.50E-01	7.30E-01	3.30E-01

				0.957	0.991	0.932	1.021	0.965	0.99	1.125	0.799	0.961	0.989	0.978
				-6.162	-0.532	-3.939	0.95	-0.049	-0.01	0.381	-0.12	-0.434	-0.161	-0.224
12	A7	53.1	IGF1226f	3.30E-03	7.10E-01	2.20E-01	3.50E-01	3.60E-01	3.20E-01	2.70E-01	1.30E-01	1.20E-01	6.20E-01	2.90E-01
				0.95	1.007	0.918	1.027	0.968	0.985	1.116	0.83	0.958	0.984	0.976
				-7.208	0.442	-4.814	1.183	-0.044	-0.014	0.351	-0.102	-0.466	-0.232	-0.244
12	A7	85.6	BRMS036_130	5.20E-01	5.80E-01	5.60E-01	5.60E-02	2.50E-02	2.30E-01	1.40E-01	5.20E-01	5.20E-01	1.20E-01	3.30E-02
				0.989	0.989	1.04	1.054	0.927	1.018	1.153	1.082	1.018	1.049	0.953
				-1.583	-0.659	2.212	2.364	-0.106	0.016	0.453	0.043	0.19	0.701	-0.475
12	A7	87.8	IGF0504f	7.30E-01	5.40E-01	7.60E-01	1.80E-01	1.70E-01	8.80E-02	9.20E-02	6.50E-01	8.60E-01	2.60E-01	2.10E-01
				0.994	0.987	1.021	1.039	0.953	1.025	1.184	1.058	0.995	1.036	0.971
				-0.856	-0.753	1.198	1.695	-0.067	0.023	0.529	0.031	-0.053	0.523	-0.289
13	A1	0	SN11641_405	4.50E-01	7.50E-02	7.10E-01	3.40E-01	1.50E-02	6.80E-01	5.20E-01	5.90E-01	5.70E-02	1.00E-01	6.90E-03
				0.987	0.964	1.027	1.027	0.919	0.994	1.067	0.935	1.054	1.053	0.94
				-1.894	-2.183	1.503	1.204	-0.117	-0.006	0.206	-0.037	0.578	0.762	-0.611
13	A1	2.4	KBrB048F07(2)	7.70E-01	7.60E-02	4.60E-01	1.30E-01	2.70E-03	6.20E-01	5.50E-01	6.40E-01	6.70E-03	3.70E-02	3.40E-03
				0.995	0.965	1.052	1.043	0.903	0.993	1.061	0.945	1.076	1.067	0.936
				-0.723	-2.121	2.866	1.898	-0.141	-0.007	0.189	-0.031	0.8	0.943	-0.655
13	A1	11	CB10097_191	8.70E-01	3.10E-01	9.40E-01	3.00E-01	1.40E-01	8.10E-01	3.90E-01	3.80E-01	8.90E-02	1.20E-01	1.10E-01
				1.003	0.98	1.005	1.03	0.951	0.996	1.09	0.898	1.048	1.05	0.964
				0.411	-1.227	0.284	1.321	-0.07	-0.003	0.272	-0.059	0.51	0.71	-0.367
13	A1	19.5	MAX4_p	3.60E-01	4.00E-01	3.40E-02	2.40E-01	1.80E-01	9.20E-01	5.90E-01	6.40E-01	6.80E-02	1.10E-01	2.50E-01
				1.016	0.983	1.155	1.033	0.955	1.001	1.055	1.061	1.051	1.051	0.974
				2.269	-1.013	8.1	1.461	-0.063	0.001	0.17	0.031	0.539	0.727	-0.261
14	A9/C5	0	IGF3112a	1.70E-01	9.70E-02	7.50E-01	7.40E-01	5.70E-01	8.50E-01	1.10E-01	2.60E-01	8.00E-01	4.60E-01	4.20E-01
				1.025	1.034	0.978	1.009	1.02	1.003	1.176	0.867	0.993	1.024	1.019
				3.457	1.983	-1.265	0.42	0.028	0.003	0.517	-0.077	-0.079	0.346	0.186
14	A9/C5	35.5	OL12F02_148	3.20E-01	7.40E-01	9.40E-01	4.10E-01	4.80E-01	9.90E-01	1.70E-01	5.60E-01	8.90E-01	2.50E-01	1.40E-01
				0.983	0.993	1.005	1.023	0.976	1	1.141	1.073	1.004	1.036	0.967
				-2.421	-0.404	0.28	1.031	-0.034	0	0.42	0.039	0.042	0.517	-0.333
14	A9/C5	36.6	NA12D10_150	2.40E-01	9.90E-01	9.80E-01	3.20E-01	5.30E-01	6.10E-01	2.60E-01	4.10E-01	8.10E-01	2.70E-01	1.10E-01

				0.979	1	1.002	1.027	0.979	0.992	1.117	1.108	1.007	1.034	0.965
				-2.891	-0.023	0.085	1.204	-0.03	-0.007	0.354	0.055	0.071	0.495	-0.357
15	A10	0	FITO247_277	5.80E-01	8.20E-01	9.90E-01	9.00E-01	7.50E-01	9.50E-01	2.00E-01	3.80E-01	1.50E-01	9.30E-01	7.90E-01
				0.99	0.995	1	1.004	1.011	1.001	1.132	1.112	0.962	1.003	1.006
				-1.341	-0.271	-0.027	0.162	0.015	0.001	0.394	0.058	-0.425	0.042	0.059
15	A10	5.8	RA2E07_93	5.20E-01	9.70E-01	9.80E-01	3.00E-01	7.30E-01	4.50E-01	2.20E-01	2.50E-01	1.60E-01	9.10E-01	8.40E-01
				0.989	0.999	0.999	1.03	0.988	0.989	1.126	1.149	0.963	1.004	1.005
				-1.561	-0.051	-0.075	1.302	-0.017	-0.01	0.378	0.077	-0.415	0.053	0.046
15	A10	6	IGF1073a	4.60E-01	9.80E-01	9.90E-01	2.90E-01	7.30E-01	3.40E-01	2.50E-01	1.90E-01	1.50E-01	9.50E-01	8.30E-01
				0.987	0.999	0.999	1.03	0.988	0.986	1.116	1.173	0.962	1.002	1.005
				-1.807	-0.035	-0.052	1.324	-0.017	-0.013	0.352	0.087	-0.422	0.029	0.049
16	C7	0	IGF5702e	5.70E-01	8.40E-01	5.60E-02	1.00E-01	3.40E-01	4.20E-01	9.90E-02	1.20E-01	2.00E-01	9.90E-01	9.30E-01
				1.01	0.996	1.136	0.956	1.033	0.988	0.852	1.208	1.036	1	1.002
				1.404	-0.238	7.277	-2.02	0.045	-0.011	-0.508	0.104	0.385	-0.007	0.02
16	C7	7.6	IGF5707b	5.60E-01	6.30E-01	8.40E-01	1.60E-01	5.70E-01	1.90E-01	1.20E-01	3.80E-01	9.20E-01	4.00E-01	7.60E-01
				0.99	0.99	0.986	0.962	1.02	0.981	0.86	1.112	1.003	0.975	1.007
				-1.44	-0.577	-0.78	-1.743	0.027	-0.018	-0.479	0.058	0.029	-0.379	0.07
16	C7	22.8	IGF5415a	6.10E-01	5.90E-01	9.60E-01	3.20E-02	3.10E-01	3.60E-01	1.40E-01	7.10E-01	7.90E-01	2.20E-01	1.40E-01
				1.009	0.989	1.004	0.941	1.036	0.986	0.859	0.954	0.993	0.962	1.035
				1.29	-0.646	0.203	-2.719	0.049	-0.013	-0.481	-0.026	-0.081	-0.573	0.339
17	A5	0	CB10320_253	1.30E-01	1.10E-01	8.40E-02	2.10E-01	1.60E-01	4.90E-01	1.30E-01	7.20E-01	1.90E-01	8.40E-01	3.70E-01
				1.027	1.033	1.125	0.966	1.049	0.99	0.861	0.956	1.036	0.994	1.021
				3.726	1.907	6.695	-1.555	0.067	-0.01	-0.474	-0.024	0.392	-0.094	0.202
17	A5	29.5	BRMS061_284	5.80E-01	9.80E-01	9.90E-01	1.00E-01	5.10E-02	1.50E-01	7.00E-02	3.70E-01	9.40E-02	8.00E-01	4.40E-01
				0.99	1	0.999	1.046	0.935	0.979	0.835	0.895	1.047	0.992	0.983
				-1.374	-0.026	-0.056	2.025	-0.093	-0.02	-0.57	-0.061	0.503	-0.114	-0.173
17	A5	44.2	BRAS063_236	3.50E-01	3.40E-01	2.10E-01	4.20E-01	9.60E-01	5.10E-01	9.10E-02	6.90E-02	6.80E-01	9.70E-02	6.30E-01
				0.983	1.02	0.917	1.023	0.998	0.99	0.848	0.803	0.989	0.949	1.011
				-2.325	1.163	-4.916	1.011	-0.003	-0.009	-0.534	-0.122	-0.125	-0.764	0.111
18	A9	0	IGF5222b	2.90E-01	1.00E+00	5.70E-01	2.50E-01	3.60E-01	9.80E-01	3.20E-01	3.80E-01	3.80E-02	5.10E-02	9.00E-02

				1.019	1	0.961	1.034	0.967	1	1.108	0.892	1.06	1.064	0.961
				2.647	-0.003	-2.269	1.513	-0.045	0	0.328	-0.062	0.633	0.915	-0.394
18	A9	37	IGF5706e	3.70E-01	9.70E-01	2.80E-01	8.80E-02	2.60E-01	9.50E-01	8.40E-01	5.70E-01	1.70E-01	3.30E-01	7.00E-01
				1.016	0.999	1.078	1.049	0.962	1.001	1.02	0.933	1.038	1.031	0.991
				2.216	-0.041	4.223	2.139	-0.054	0.001	0.065	-0.038	0.405	0.448	-0.087
19	A9	0	IGF1207c	2.50E-01	9.40E-01	7.70E-02	7.50E-01	6.00E-01	9.30E-01	8.70E-02	9.10E-01	7.90E-01	3.40E-01	1.60E-01
				0.98	1.002	0.887	0.991	1.019	1.001	1.184	0.986	0.993	1.03	0.968
				-2.82	0.093	-6.824	-0.405	0.025	0.001	0.534	-0.008	-0.08	0.434	-0.322
19	A9	1.1	OL12F02_119	2.70E-01	8.70E-01	1.10E-01	8.50E-01	8.30E-01	6.80E-01	1.50E-01	8.90E-01	7.30E-01	4.50E-01	2.40E-01
				0.981	1.003	0.897	1.005	1.007	0.994	1.151	1.018	0.991	1.024	0.973
				-2.681	0.191	-6.141	0.245	0.01	-0.006	0.45	0.009	-0.104	0.342	-0.268
0	um	0	BRAS038_120	6.00E-01	1.20E-01	8.90E-01	4.30E-02	1.10E-02	5.70E-01	2.80E-01	1.20E-01	3.50E-01	2.80E-01	7.10E-01
				0.991	1.032	0.99	0.944	1.095	1.009	0.899	1.226	0.974	0.966	1.009
				-1.309	1.887	-0.554	-2.574	0.123	0.008	-0.345	0.108	-0.286	-0.504	0.086
0	um	0	BRMS007_116	5.40E-01	4.90E-01	3.90E-01	5.50E-01	6.40E-01	1.50E-01	4.40E-01	3.30E-01	1.80E-02	5.70E-02	1.10E-01
				0.989	0.986	0.943	0.984	1.016	1.021	0.927	1.125	0.938	0.943	1.037
				-1.489	-0.837	-3.327	-0.744	0.022	0.019	-0.241	0.065	-0.697	-0.857	0.363
0	um	0	BRMS061_297	3.00E-01	8.80E-01	5.50E-02	5.80E-01	8.80E-01	5.00E-02	2.70E-01	8.40E-01	5.70E-01	7.00E-01	4.70E-01
				1.019	0.997	1.14	0.984	0.995	1.029	0.894	1.025	1.016	0.988	1.017
				2.579	-0.179	7.54	-0.716	-0.007	0.027	-0.352	0.014	0.174	-0.183	0.168
0	um	0	BRMS098_146	6.90E-01	5.00E-01	2.40E-01	7.20E-01	8.30E-01	7.10E-01	1.10E-01	5.10E-01	6.80E-01	4.40E-01	7.30E-01
				0.993	0.986	1.082	0.99	0.993	0.994	0.856	1.084	1.011	0.977	1.008
				-0.962	-0.808	4.48	-0.452	-0.01	-0.005	-0.496	0.044	0.123	-0.344	0.078
0	um	0	BRMS330_238	3.10E-01	9.60E-01	8.80E-01	9.70E-01	9.90E-01	4.10E-01	7.70E-01	1.60E-01	4.30E-01	6.10E-01	7.00E-01
				1.034	1.002	0.98	0.998	1.001	1.023	1.054	0.683	1.041	1.03	0.983
				4.673	0.108	-1.144	-0.1	0.001	0.021	0.171	-0.177	0.444	0.442	-0.163
0	um	0	CB10179_150	9.90E-01	3.50E-01	2.30E-01	3.30E-01	8.30E-02	6.30E-01	4.60E-01	9.80E-01	1.30E-02	3.60E-02	2.70E-02
				1	1.019	0.919	0.973	1.062	0.993	0.929	1.003	0.934	0.937	1.052
				0.034	1.14	-4.752	-1.199	0.083	-0.006	-0.233	0.001	-0.737	-0.956	0.502
0	um	0	CB10427_165	2.90E-01	2.30E-01	7.80E-01	8.40E-02	2.30E-02	5.60E-01	4.30E-01	1.40E-01	2.50E-01	9.60E-01	9.60E-01

				0.981	1.025	0.981	0.952	1.084	1.009	1.083	1.21	0.968	1.001	0.999
				-2.622	1.473	-1.106	-2.192	0.109	0.008	0.253	0.101	-0.353	0.02	-0.013
0	um	0	CB10493_166	4.10E-01	5.90E-01	3.40E-01	5.90E-01	8.10E-01	1.90E-01	1.30E-01	8.40E-01	9.20E-01	3.70E-01	9.70E-01
				0.985	0.989	0.936	0.985	1.009	1.02	0.859	1.026	1.003	0.972	1.001
				-2.076	-0.659	-3.754	-0.691	0.012	0.018	-0.486	0.014	0.031	-0.423	0.01
0	um	0	FITO317_384	5.00E-02	7.40E-02	6.50E-01	2.80E-01	6.70E-01	7.10E-01	5.40E-01	8.60E-01	5.00E-01	9.40E-01	7.70E-01
				1.035	1.037	1.032	1.031	1.015	0.995	0.94	1.021	1.019	1.002	1.007
				4.836	2.13	1.805	1.372	0.02	-0.005	-0.196	0.011	0.207	0.035	0.068
0	um	0	IGF0191b	*	*	*	*	*	*	*	*	*	*	*
				*	*	*	*	*	*	*	*	*	*	*
				*	*	*	*	*	*	*	*	*	*	*
0	um	0	IGF2128c	6.60E-01	2.60E-01	4.80E-02	4.30E-02	2.70E-01	6.20E-01	1.70E-01	8.20E-01	4.90E-02	7.30E-01	2.50E-01
				1.008	1.023	1.141	1.057	0.963	0.993	0.876	0.973	1.054	1.011	0.974
				1.069	1.341	7.493	2.497	-0.051	-0.007	-0.422	-0.015	0.579	0.155	-0.261
0	um	0	IGF5101b	1.80E-01	4.50E-01	5.10E-01	4.40E-01	8.70E-01	8.80E-01	1.80E-01	2.30E-01	4.40E-03	1.00E-02	6.50E-02
				0.977	1.015	0.957	1.022	1.006	1.002	0.88	1.159	0.927	0.925	1.043
				-3.255	0.905	-2.507	0.974	0.008	0.002	-0.41	0.079	-0.831	-1.145	0.414
0	um	0	KBrB048K11(2)	9.90E-01	8.10E-01	6.90E-01	7.30E-01	9.00E-01	8.10E-01	2.40E-01	9.80E-01	4.00E-01	1.60E-01	2.10E-01
				1	0.995	1.028	0.99	0.996	1.004	0.891	0.996	0.977	0.958	1.03
				-0.045	-0.294	1.549	-0.44	-0.006	0.004	-0.368	-0.002	-0.251	-0.634	0.287
0	um	0	KBrH027N05(3)	4.40E-01	5.70E-01	2.90E-01	5.10E-01	8.60E-01	7.00E-01	2.10E-01	4.50E-01	8.60E-01	2.70E-01	1.60E-01
				1.014	0.988	1.076	0.981	0.994	1.006	0.886	0.913	0.995	0.966	1.033
				1.887	-0.686	4.121	-0.838	-0.009	0.005	-0.388	-0.05	-0.052	-0.503	0.319
0	um	0	MAX2_b	4.50E-01	4.00E-01	4.80E-01	2.20E-02	1.50E-01	1.90E-02	3.10E-01	4.90E-01	5.30E-01	2.30E-01	6.20E-01
				0.986	0.981	0.947	0.932	1.057	0.963	0.891	0.907	0.982	0.959	1.012
				-2.013	-1.163	-3.087	-3.112	0.077	-0.035	-0.364	-0.053	-0.203	-0.606	0.121
0	um	0	NA12A07_152	3.80E-01	6.20E-01	8.90E-01	8.20E-01	7.90E-01	3.80E-01	4.90E-01	3.90E-01	7.80E-01	7.00E-01	7.30E-01
				0.985	0.99	1.01	0.994	1.009	1.013	1.07	1.108	0.992	1.012	0.992
				-2.157	-0.607	0.54	-0.284	0.013	0.012	0.215	0.057	-0.083	0.176	-0.08
0	um	0	NA12E02_92	3.00E-01	2.30E-01	8.40E-01	8.70E-02	2.50E-02	6.80E-01	4.60E-01	8.20E-02	3.40E-01	8.70E-01	8.50E-01

0	um	0	NA14E08_98	0.982	1.026	0.986	0.952	1.083	1.006	1.078	1.247	0.973	1.005	0.995
				-2.603	1.492	-0.806	-2.203	0.109	0.005	0.236	0.118	-0.297	0.076	-0.045
				7.70E-01	8.90E-01	4.60E-01	5.80E-02	5.60E-02	7.80E-01	4.80E-01	4.70E-01	3.60E-01	3.40E-01	2.80E-01
0	um	0	OL13G05_124	1.005	0.997	0.951	0.949	1.067	1.004	0.933	1.092	0.975	0.971	1.025
				0.711	-0.164	-2.853	-2.353	0.09	0.004	-0.221	0.048	-0.272	-0.432	0.243
				3.80E-01	9.00E-01	8.50E-01	3.70E-01	3.70E-01	2.10E-02	2.50E-01	2.70E-01	5.40E-01	5.70E-01	6.40E-01
0	um	0	RA2G08_318	1.016	0.998	0.986	0.975	1.033	1.035	0.893	0.873	1.018	0.982	1.011
				2.185	-0.148	-0.775	-1.149	0.044	0.032	-0.366	-0.076	0.19	-0.265	0.109
				7.00E-02	9.70E-01	2.40E-01	3.60E-01	4.90E-01	3.50E-03	5.80E-02	8.30E-01	6.00E-01	9.90E-02	8.10E-01
0	um	0	RGL3_a	1.032	0.999	1.083	1.026	0.977	1.043	1.201	1.027	1.014	1.052	0.994
				4.374	-0.046	4.49	1.133	-0.032	0.039	0.581	0.015	0.156	0.738	-0.055
				2.20E-01	2.00E-02	8.10E-01	7.20E-02	6.50E-01	4.00E-01	1.10E-01	8.50E-01	8.20E-01	3.60E-01	5.40E-01
0	um	0	SN1963_335	1.023	1.051	1.018	1.055	0.983	1.013	1.173	1.026	0.994	1.031	1.015
				3.228	2.953	0.994	2.4	-0.023	0.012	0.526	0.014	-0.07	0.446	0.15
				8.20E-01	9.60E-01	6.00E-01	5.60E-01	5.30E-01	1.80E-01	1.70E-01	5.70E-01	5.00E-01	1.50E-01	1.10E-01
0	um	0		1.004	1.001	0.965	1.016	0.979	1.02	0.874	0.932	0.982	0.956	1.037
				0.556	0.055	-2.016	0.723	-0.03	0.018	-0.43	-0.039	-0.2	-0.653	0.363

				branch density	branch angle	branch angle of top 4 branches	beak length	pedicel length	pod length	pod width	pedicel angle	pod angle	yield t/ha	harvest index
LG	Homology	cM	markers											
1	C3	0	IGF0568d	8.90E-01	1.20E-01	4.90E-02	7.90E-01	4.50E-02	4.90E-01	2.90E-01	3.10E-01	7.50E-01	2.40E-01	2.30E-01
				1.021	0.974	0.968	1.008	0.954	0.987	0.962	0.988	0.999	0.964	0.953
				0.165	-0.921	-1.151	0.009	-0.117	-0.069	-0.018	-0.922	-0.165	-0.14	-0.011
1	C3	20.9	CALSSR_137	8.50E-01	7.80E-03	5.80E-03	5.50E-01	1.30E-01	6.30E-01	3.20E-01	3.40E-01	3.70E-01	3.50E-01	1.00E+00
				1.028	0.96	0.959	0.983	0.966	0.991	0.966	0.99	1.003	1.027	1
				0.223	-1.467	-1.516	-0.019	-0.087	-0.045	-0.016	-0.823	0.435	0.104	0
1	C3	26	SN4513_369	3.30E-01	2.60E-02	1.90E-02	2.30E-01	7.20E-02	4.20E-01	3.00E-01	6.30E-01	2.50E-01	4.80E-01	5.50E-01
				1.146	0.966	0.965	0.966	0.961	0.986	0.965	0.995	1.003	1.02	0.978
				1.109	-1.219	-1.277	-0.04	-0.101	-0.075	-0.016	-0.415	0.548	0.078	-0.005
1	C3	42	BRAS068_115	2.60E-01	3.90E-01	3.60E-01	7.60E-02	5.80E-01	2.70E-01	4.90E-01	3.20E-01	5.70E-01	5.10E-01	9.80E-01
				1.17	0.987	0.986	0.951	0.988	0.981	1.024	0.99	1.002	1.019	1.001
				1.254	-0.475	-0.499	-0.056	-0.031	-0.1	0.011	-0.828	0.27	0.073	0.001
2	A3	0	CB10427_152	9.10E-02	8.50E-02	9.10E-02	3.20E-02	2.90E-02	5.20E-01	3.70E-01	6.30E-01	9.80E-01	7.50E-01	1.20E-02
				0.7	0.965	0.966	1.084	0.936	1.015	0.959	1.007	1	0.988	0.88
				-2.538	-1.273	-1.244	0.092	-0.163	0.08	-0.019	0.556	0.015	-0.048	-0.028
2	A3	2.4	BRAS038_108	1.80E-02	6.10E-02	8.60E-02	7.70E-02	1.30E-02	5.90E-01	2.90E-01	8.90E-01	8.30E-01	2.20E-01	2.20E-03
				0.59	0.962	0.965	1.069	0.927	1.013	0.952	1.002	0.999	0.953	0.856
				-3.54	-1.383	-1.265	0.077	-0.186	0.067	-0.022	0.163	-0.135	-0.183	-0.034
2	A3	2.7	BRAS087_160	1.80E-02	1.50E-01	1.60E-01	2.60E-02	1.60E-02	5.30E-01	2.70E-01	7.20E-01	7.90E-01	3.30E-01	2.30E-03
				0.56	0.969	0.97	1.093	0.927	1.016	0.946	1.006	0.999	0.961	0.846

				-3.803	-1.099	-1.071	0.103	-0.188	0.083	-0.025	0.439	-0.184	-0.154	-0.037
2	A3	4.2	SSR18_175	3.80E-02	1.10E-01	1.00E-01	1.20E-01	1.10E-02	8.30E-01	3.00E-01	6.60E-01	9.10E-01	3.10E-01	8.90E-03
				0.609	0.965	0.964	1.066	0.921	1.006	0.949	1.007	1	0.959	0.867
				-3.296	-1.27	-1.291	0.073	-0.201	0.029	-0.024	0.53	-0.075	-0.163	-0.031
2	A3	6.4	CB10036_160	6.90E-01	2.10E-01	2.20E-01	1.90E-01	1.10E-03	9.80E-01	3.30E-01	3.30E-01	5.70E-01	4.80E-01	1.80E-03
				1.096	0.968	0.968	1.065	0.882	1.001	0.944	1.017	0.997	0.966	0.816
				0.767	-1.159	-1.136	0.072	-0.302	0.003	-0.026	1.385	-0.459	-0.133	-0.044
2	A3	6.4	OL10D03_101	7.60E-01	2.70E-01	2.70E-01	1.50E-01	3.00E-03	8.80E-01	2.80E-01	5.90E-01	8.70E-01	3.90E-01	9.90E-03
				1.069	0.973	0.973	1.067	0.898	0.996	0.941	1.009	0.999	0.961	0.854
				0.555	-0.971	-0.966	0.074	-0.262	-0.022	-0.027	0.732	-0.121	-0.155	-0.035
3	C3/A3/C8	6.4	BRMS269_313	7.60E-01	2.70E-01	2.70E-01	1.50E-01	3.00E-03	8.80E-01	2.80E-01	5.90E-01	8.70E-01	3.90E-01	9.90E-03
				1.069	0.973	0.973	1.067	0.898	0.996	0.941	1.009	0.999	0.961	0.854
				0.555	-0.971	-0.966	0.074	-0.262	-0.022	-0.027	0.732	-0.121	-0.155	-0.035
3	C3/A3/C8	10.2	BRAS065_219	8.10E-01	1.90E-01	1.50E-01	1.10E-01	6.80E-03	5.80E-01	2.40E-01	9.00E-01	3.70E-01	3.80E-01	5.30E-03
				1.045	0.974	0.971	1.061	0.923	1.013	0.947	0.998	1.004	0.968	0.872
				0.362	-0.926	-1.031	0.068	-0.198	0.068	-0.025	-0.142	0.567	-0.127	-0.031
3	C3/A3/C8	13.6	AtTB1_f	9.10E-01	1.00E-01	7.10E-02	1.30E-01	2.80E-02	9.80E-01	3.40E-01	3.70E-01	5.50E-01	1.60E-01	2.20E-02
				1.019	0.969	0.966	1.055	0.944	0.999	0.96	0.988	0.998	0.95	0.898
				0.155	-1.111	-1.226	0.061	-0.144	-0.004	-0.019	-0.93	-0.355	-0.196	-0.024
4	uk1	0	RA1F06_190	7.80E-01	6.10E-01	6.60E-01	1.60E-01	5.00E-01	9.70E-01	5.00E-01	8.70E-01	7.10E-02	6.80E-01	2.70E-02
				0.977	1.008	1.007	0.96	0.985	0.999	1.024	0.998	1.005	1.012	1.084
				-0.199	0.284	0.243	-0.045	-0.038	-0.004	0.011	-0.135	0.851	0.047	0.018
4	uk1	19	CALSSSR_142	4.00E-01	8.50E-01	6.50E-01	1.70E-01	5.40E-01	2.80E-01	6.50E-01	1.50E-01	3.40E-01	9.20E-01	1.80E-01
				1.145	0.997	0.992	0.957	1.015	1.021	1.017	1.017	1.003	0.997	1.054
				1.062	-0.114	-0.273	-0.05	0.038	0.11	0.008	1.359	0.507	-0.012	0.012
4	uk1	23.5	SN4513_366	3.10E-01	3.60E-01	2.40E-01	3.20E-02	8.80E-01	4.40E-01	6.20E-01	7.00E-02	3.70E-01	5.10E-01	6.70E-01
				1.17	0.985	0.981	0.937	0.996	1.015	1.018	1.021	1.003	0.98	1.016
				1.232	-0.543	-0.689	-0.073	-0.009	0.075	0.008	1.628	0.454	-0.079	0.004
4	uk1	39.4	KBrH004A18(3)	2.60E-01	1.80E-01	1.10E-01	1.40E-02	3.80E-01	6.40E-01	3.80E-01	9.60E-02	4.80E-01	7.60E-01	6.20E-01
				1.186	0.979	0.975	0.931	0.98	0.991	1.033	1.018	0.998	0.991	0.981

				1.315	-0.77	-0.909	-0.082	-0.051	-0.045	0.015	1.417	-0.344	-0.034	-0.004
4	uk1	58.1	A77096_218	1.30E-01	9.90E-01	9.20E-01	3.50E-04	7.10E-01	1.70E-01	3.40E-01	9.40E-01	3.20E-01	9.10E-01	7.00E-02
				1.287	1	0.998	0.898	1.009	0.975	1.038	0.999	0.997	0.997	1.075
				1.923	0.009	-0.058	-0.123	0.023	-0.135	0.017	-0.071	-0.523	-0.013	0.016
4	uk1	62.8	KBrH013K13(1)	1.30E-01	9.70E-01	9.10E-01	5.80E-05	9.50E-01	2.90E-02	4.40E-01	7.80E-01	2.70E-01	7.80E-01	8.00E-02
				1.275	1.001	1.002	0.889	1.002	0.959	1.029	0.997	0.996	0.992	1.073
				1.86	0.026	0.07	-0.135	0.004	-0.219	0.014	-0.256	-0.567	-0.032	0.016
5	A2/A6	0	RGA12_30	5.70E-01	1.20E-02	1.70E-02	2.10E-01	5.10E-01	2.80E-01	2.60E-01	8.20E-01	8.50E-02	9.70E-02	2.50E-01
				1.085	0.962	0.964	0.964	1.015	0.981	1.04	0.997	0.995	0.953	1.044
				0.651	-1.395	-1.329	-0.041	0.039	-0.102	0.018	-0.201	-0.832	-0.187	0.01
5	A2/A6	8.5	RGL12_31_300	7.00E-01	3.70E-03	2.60E-03	2.20E-01	1.50E-01	5.50E-01	1.40E-02	9.80E-01	8.20E-02	4.50E-01	2.40E-01
				1.059	0.955	0.954	0.964	1.034	0.989	1.019	1	0.995	0.979	1.046
				0.453	-1.644	-1.684	-0.042	0.083	-0.056	0.008	-0.02	-0.839	-0.085	0.01
5	A2/A6	31.1	CB10416_251	1.90E-01	7.40E-01	7.50E-01	4.60E-01	6.80E-01	1.60E-02	3.80E-01	8.20E-01	2.40E-02	5.10E-02	3.30E-01
				1.207	0.995	0.995	0.979	1.009	0.959	1.031	1.003	0.993	0.946	1.037
				1.479	-0.188	-0.18	-0.024	0.023	-0.223	0.014	0.199	-1.072	-0.218	0.009
5	A2/A6	32.1	IGF3239d	1.90E-01	6.80E-01	6.80E-01	4.90E-01	6.80E-01	4.30E-02	3.80E-01	9.80E-01	2.80E-02	4.20E-02	5.10E-01
				1.212	0.994	0.994	0.98	1.009	0.965	1.031	1	0.993	0.944	1.025
				1.508	-0.231	-0.229	-0.023	0.024	-0.189	0.014	-0.017	-1.055	-0.228	0.006
5	A2/A6	44.2	FITO232_130	2.70E-01	7.80E-01	6.30E-01	5.90E-01	7.90E-01	3.90E-02	5.00E-01	8.50E-01	2.60E-02	2.00E-01	8.00E-01
				1.178	0.996	0.992	0.984	0.994	0.964	1.024	0.998	0.993	0.963	1.01
				1.291	-0.16	-0.276	-0.018	-0.016	-0.195	0.011	-0.162	-1.08	-0.148	0.003
5	A2/A6	65.8	RA1F06_175	4.00E-01	2.90E-01	4.50E-01	5.80E-02	8.30E-01	1.70E-01	2.70E-01	5.00E-01	9.70E-01	8.20E-02	2.90E-01
				1.073	1.017	1.012	0.946	1.005	0.976	0.962	1.007	1	0.951	1.039
				0.6	0.603	0.434	-0.062	0.013	-0.124	-0.018	0.589	0.02	-0.198	0.009
6	A4/C4(6)	0	NA12E05_146	4.30E-02	4.80E-01	3.20E-01	8.00E-01	8.60E-01	7.80E-01	1.90E-01	2.70E-01	3.00E-01	4.70E-03	8.50E-01
				1.329	0.989	0.985	1.007	0.996	1.005	0.956	0.988	1.003	1.083	0.993
				2.278	-0.394	-0.552	0.008	-0.01	0.027	-0.021	-0.937	0.501	0.312	-0.001
6	A4/C4(6)	3.2	CB10493_155	4.30E-02	8.50E-01	5.60E-01	6.90E-01	6.70E-01	4.20E-01	2.40E-01	9.70E-02	8.70E-02	1.90E-02	4.00E-01
				1.332	0.997	0.991	1.012	1.01	1.015	0.96	0.983	1.005	1.069	0.97

				2.288	-0.101	-0.32	0.013	0.024	0.075	-0.019	-1.349	0.794	0.259	-0.007
6	A4/C4(6)	3.9	OL10B01_177	4.60E-02	5.00E-01	2.80E-01	8.40E-01	7.50E-01	6.50E-01	2.50E-01	2.50E-02	1.30E-01	6.00E-03	4.10E-01
				1.332	0.99	0.983	1.006	1.007	1.008	0.961	0.977	1.004	1.081	0.97
				2.289	-0.372	-0.604	0.007	0.018	0.042	-0.018	-1.85	0.706	0.304	-0.007
6	A4/C4(6)	10	MAX3_m	1.20E-01	6.50E-01	4.60E-01	6.10E-01	2.70E-01	3.90E-01	2.90E-01	1.60E-01	7.80E-01	4.40E-03	2.30E-01
				1.252	0.992	0.988	1.015	1.026	1.015	0.961	0.984	1.001	1.085	0.957
				1.809	-0.269	-0.435	0.017	0.064	0.078	-0.018	-1.253	0.142	0.32	-0.01
7	C7	0	CB10299_140	1.60E-01	8.70E-01	9.20E-01	4.30E-01	5.20E-01	5.20E-01	3.30E-01	4.10E-01	2.10E-01	5.10E-01	3.20E-01
				0.823	1.003	1.002	0.978	0.986	0.989	0.968	0.991	0.996	0.981	1.036
				-1.577	0.09	0.058	-0.025	-0.036	-0.058	-0.015	-0.692	-0.59	-0.073	0.008
7	C7	0.1	BRMS296_142	1.60E-01	7.90E-01	8.30E-01	4.10E-01	4.20E-01	4.60E-01	3.40E-01	4.20E-01	1.50E-01	4.50E-01	3.00E-01
				0.82	1.004	1.003	0.976	0.982	0.987	0.967	0.991	0.996	0.979	1.038
				-1.603	0.152	0.118	-0.027	-0.046	-0.068	-0.016	-0.69	-0.689	-0.084	0.008
7	C7	16.6	BRAS019_128	1.80E-01	8.00E-01	7.60E-01	7.10E-01	2.50E-01	1.80E-01	3.70E-01	7.10E-01	2.20E-01	6.30E-01	8.20E-01
				0.829	0.996	0.995	0.989	0.975	0.976	0.97	0.996	0.996	0.986	0.992
				-1.515	-0.14	-0.166	-0.012	-0.065	-0.126	-0.014	-0.32	-0.582	-0.055	-0.002
8	uk2	0	FITO300_127	5.70E-01	3.40E-02	1.40E-02	8.60E-01	1.30E-01	8.40E-01	3.20E-01	9.70E-01	4.00E-01	3.60E-01	6.30E-01
				0.924	1.033	1.038	0.995	0.967	0.996	1.034	1	1.003	0.974	1.017
				-0.635	1.153	1.326	-0.006	-0.084	-0.019	0.015	-0.033	0.394	-0.101	0.004
8	uk2	14.9	FITO110_291	7.60E-01	1.90E-01	1.30E-01	1.80E-01	6.60E-02	7.10E-01	3.60E-01	4.60E-01	1.60E-02	5.80E-01	1.50E-01
				0.956	1.021	1.024	0.961	0.961	0.993	1.032	0.992	1.007	0.984	1.055
				-0.352	0.734	0.855	-0.044	-0.101	-0.036	0.015	-0.637	1.149	-0.062	0.012
8	uk2	19.4	OL10A05_190	6.30E-01	1.50E-01	1.20E-01	4.70E-01	1.80E-02	6.30E-01	3.50E-01	8.40E-01	2.50E-02	6.80E-01	6.30E-01
				0.934	1.022	1.024	0.979	0.949	1.008	1.032	0.998	1.007	0.988	1.017
				-0.549	0.777	0.852	-0.024	-0.131	0.044	0.015	-0.172	1.055	-0.045	0.004
9	A3/A4	0	BRMS008_156	3.90E-01	1.30E-01	1.50E-01	9.50E-02	8.20E-01	1.90E-02	3.20E-01	9.50E-01	4.80E-01	6.80E-01	6.20E-02
				1.127	0.977	0.978	0.954	0.995	0.96	1.034	0.999	1.002	1.012	1.069
				0.961	-0.825	-0.788	-0.053	-0.013	-0.213	0.016	-0.051	0.335	0.045	0.016
9	A3/A4	14.2	IGF5193a	4.10E-01	1.70E-01	1.30E-01	7.70E-01	9.00E-01	2.20E-02	2.60E-01	4.50E-01	8.90E-01	8.90E-01	1.90E-01
				1.125	0.979	0.977	0.992	1.003	0.961	1.039	0.992	1	1.004	1.05

				0.937	-0.762	-0.827	-0.009	0.007	-0.209	0.018	-0.636	0.067	0.015	0.011
10	A3	0	IGF5272c	1.20E-01	4.90E-01	4.80E-01	6.80E-01	5.80E-03	5.40E-01	1.40E-01	3.80E-01	8.30E-01	7.30E-01	6.20E-01
				0.802	0.989	0.989	1.012	1.063	1.011	1.054	1.01	0.999	1.01	1.019
				-1.81	-0.395	-0.398	0.014	0.153	0.058	0.024	0.758	-0.106	0.039	0.004
10	A3	6.7	BRMS008_115	9.10E-02	2.80E-01	3.10E-01	5.90E-01	4.80E-03	9.80E-01	8.60E-02	5.60E-01	3.70E-01	2.10E-01	1.50E-01
				0.794	0.984	0.985	1.015	1.063	0.999	1.059	1.006	0.997	1.036	1.053
				-1.868	-0.595	-0.556	0.017	0.154	-0.003	0.027	0.483	-0.419	0.136	0.012
10	A3	12.8	MAX2_I	1.10E-01	3.30E-01	2.70E-01	8.60E-01	6.90E-02	3.90E-01	1.30E-01	2.90E-01	2.80E-01	3.60E-01	2.70E-01
				0.875	0.984	0.982	0.994	1.042	0.983	1.061	1.012	0.996	1.028	1.046
				-1.133	-0.564	-0.638	-0.006	0.102	-0.087	0.027	0.982	-0.562	0.106	0.01
10	A3	19.9	BRMS330_241	1.10E-01	5.70E-01	6.80E-01	7.20E-01	1.10E-01	6.80E-01	8.00E-02	3.40E-01	7.20E-01	4.60E-02	1.30E-01
				0.805	0.991	0.994	1.01	1.035	0.993	1.06	1.01	0.999	1.057	1.056
				-1.742	-0.308	-0.221	0.011	0.087	-0.038	0.027	0.793	-0.17	0.216	0.013
10	A3	42.1	RA2E11_200	7.60E-02	8.50E-01	8.30E-01	6.80E-01	8.10E-01	6.80E-01	8.50E-02	9.20E-02	7.40E-01	1.10E-02	2.90E-02
				0.777	1.003	1.003	1.012	1.005	0.993	1.06	1.018	0.999	1.073	1.082
				-1.983	0.107	0.119	0.013	0.013	-0.039	0.027	1.415	-0.16	0.277	0.018
10	A3	43.3	CB10036_131	8.90E-02	5.50E-01	5.50E-01	5.40E-01	7.70E-01	8.40E-01	1.00E-01	5.80E-02	9.50E-01	2.90E-02	5.00E-02
				0.783	1.009	1.009	1.018	1.007	0.996	1.058	1.02	1	1.064	1.074
				-1.929	0.337	0.334	0.02	0.017	-0.018	0.026	1.593	0.03	0.244	0.017
10	A3	66.4	OL11B05_109	6.90E-01	8.50E-01	6.70E-01	5.50E-01	5.90E-01	5.20E-01	6.20E-01	9.30E-02	7.60E-01	1.20E-02	3.70E-01
				1.059	0.997	0.993	1.018	0.988	0.988	0.982	1.018	0.999	1.075	1.034
				0.465	-0.11	-0.239	0.021	-0.031	-0.061	-0.008	1.454	-0.149	0.284	0.008
10	A3	66.7	NA12E02_118	7.10E-01	7.90E-01	6.20E-01	5.30E-01	6.70E-01	5.40E-01	6.00E-01	9.50E-02	7.90E-01	8.60E-03	3.30E-01
				1.055	0.996	0.992	1.019	0.99	0.989	0.981	1.019	0.999	1.079	1.038
				0.435	-0.154	-0.284	0.022	-0.025	-0.06	-0.008	1.468	-0.132	0.301	0.009
10	A3	68.1	CB10427_138	6.70E-01	7.80E-01	6.20E-01	5.20E-01	8.00E-01	7.20E-01	6.20E-01	1.10E-01	9.60E-01	1.10E-02	3.80E-01
				1.064	0.996	0.992	1.019	0.994	0.993	0.982	1.018	1	1.076	1.034
				0.508	-0.161	-0.284	0.022	-0.015	-0.034	-0.008	1.392	-0.023	0.29	0.008
10	A3	94.4	SN11722_93	3.80E-01	1.80E-01	2.10E-01	2.90E-01	7.70E-01	1.20E-01	2.70E-01	4.30E-01	2.90E-01	9.30E-01	8.20E-02
				1.133	1.021	1.019	0.969	1.006	0.973	1.038	1.008	0.997	0.998	1.065

				1.003	0.742	0.691	-0.034	0.016	-0.143	0.018	0.671	-0.509	-0.009	0.015
10	A3	106	NA10D03_157	3.10E-01	3.40E-01	3.60E-01	8.40E-01	4.10E-01	2.60E-01	3.10E-01	4.20E-01	7.90E-01	6.70E-01	5.20E-02
				1.15	1.015	1.014	0.994	0.982	0.98	1.035	1.009	0.999	1.012	1.072
				1.131	0.524	0.495	-0.006	-0.046	-0.104	0.016	0.68	-0.127	0.048	0.017
10	A3	108.5	IGF3100b	2.90E-01	4.10E-01	4.30E-01	7.50E-01	7.90E-01	2.40E-01	2.60E-01	2.30E-01	3.60E-01	5.90E-01	3.60E-02
				1.158	1.013	1.012	0.991	0.994	0.98	1.038	1.013	0.997	1.015	1.078
				1.194	0.452	0.433	-0.011	-0.015	-0.107	0.018	1.008	-0.436	0.059	0.018
10	A3	111.7	RGA2_H24_13_150	3.40E-01	6.20E-01	6.20E-01	4.30E-01	7.60E-01	5.60E-02	3.80E-01	9.20E-01	5.70E-01	8.20E-01	3.30E-03
				1.14	1.008	1.007	0.977	0.993	0.967	1.03	1.001	0.998	1.007	1.109
				1.064	0.272	0.266	-0.025	-0.017	-0.173	0.014	0.079	-0.268	0.025	0.025
10	A3	111.7	RGA2_H24_14_300	3.40E-01	6.20E-01	6.20E-01	4.30E-01	7.60E-01	5.60E-02	3.80E-01	9.20E-01	5.70E-01	8.20E-01	3.30E-03
				1.14	1.008	1.007	0.977	0.993	0.967	1.03	1.001	0.998	1.007	1.109
				1.064	0.272	0.266	-0.025	-0.017	-0.173	0.014	0.079	-0.268	0.025	0.025
11	C1	0	KBrB078A03(1)	7.60E-01	7.40E-01	6.40E-01	8.10E-01	3.20E-01	9.40E-01	4.50E-01	2.90E-01	1.30E-01	4.50E-01	5.80E-02
				1.046	0.994	0.992	0.992	0.976	1.001	0.973	1.012	1.005	0.977	0.928
				0.366	-0.2	-0.278	-0.009	-0.06	0.008	-0.012	0.957	0.778	-0.091	-0.018
11	C1	1	BRAS067_136	7.30E-01	8.30E-01	7.20E-01	7.80E-01	2.40E-01	9.80E-01	4.80E-01	2.80E-01	1.50E-01	3.70E-01	4.50E-02
				1.053	0.996	0.994	0.991	0.972	1.001	0.974	1.012	1.005	0.973	0.924
				0.42	-0.128	-0.21	-0.009	-0.07	0.003	-0.012	0.963	0.731	-0.106	-0.018
11	C1	1	NA12H02_219	7.30E-01	8.30E-01	7.20E-01	7.80E-01	2.40E-01	9.80E-01	4.80E-01	2.80E-01	1.50E-01	3.70E-01	4.50E-02
				1.053	0.996	0.994	0.991	0.972	1.001	0.974	1.012	1.005	0.973	0.924
				0.42	-0.128	-0.21	-0.009	-0.07	0.003	-0.012	0.963	0.731	-0.106	-0.018
11	C1	2.1	SN3734_288	6.90E-01	8.60E-01	7.50E-01	7.90E-01	3.80E-01	8.70E-01	5.10E-01	3.80E-01	2.30E-01	4.10E-01	3.00E-02
				1.061	0.997	0.995	0.992	0.979	1.003	0.977	1.01	1.004	0.976	0.919
				0.481	-0.1	-0.188	-0.009	-0.052	0.016	-0.011	0.776	0.597	-0.096	-0.02
11	C1	15.3	IGF3338a	9.70E-01	6.50E-01	8.20E-01	8.70E-01	8.70E-01	6.10E-01	6.10E-01	1.60E-01	3.40E-01	1.70E-01	5.30E-03
				0.993	1.009	1.005	0.994	0.995	1.012	0.975	1.02	1.004	0.951	0.87
				-0.055	0.322	0.166	-0.007	-0.011	0.064	-0.012	1.618	0.595	-0.193	-0.031
11	C1	24.8	IGF0504b	6.40E-01	1.70E-01	2.00E-01	8.90E-01	5.50E-01	5.80E-01	4.00E-01	3.90E-01	1.20E-01	2.40E-01	1.10E-02
				1.072	1.023	1.021	1.004	0.985	1.01	0.969	1.01	1.005	0.966	0.909

				0.574	0.809	0.763	0.005	-0.038	0.052	-0.015	0.787	0.774	-0.136	-0.022
11	C1	27.1	IGF1059e	5.20E-01	1.80E-01	2.30E-01	9.00E-01	4.90E-01	8.50E-01	3.80E-01	3.50E-01	3.80E-01	2.90E-01	6.80E-03
				1.095	1.021	1.019	1.004	0.984	1.003	0.97	1.01	1.003	0.97	0.904
				0.737	0.75	0.667	0.004	-0.039	0.018	-0.014	0.809	0.427	-0.119	-0.023
11	C1	30.9	KBrB036M22(3)	6.60E-01	2.70E-01	3.40E-01	2.80E-01	5.30E-01	6.30E-01	3.80E-01	5.90E-01	7.00E-01	5.30E-01	8.80E-04
				1.067	1.018	1.015	1.033	0.986	1.009	0.969	1.006	1.001	0.982	0.885
				0.527	0.634	0.551	0.037	-0.036	0.047	-0.014	0.481	0.192	-0.073	-0.028
11	C1	38.1	IGF3315b	8.90E-01	5.80E-02	9.30E-02	6.80E-01	2.40E-01	7.50E-01	3.10E-01	3.80E-01	9.40E-01	1.20E-02	4.20E-02
				1.021	1.033	1.029	0.986	0.974	1.006	0.961	1.011	1	0.929	0.921
				0.168	1.16	1.029	-0.015	-0.066	0.031	-0.018	0.847	0.039	-0.282	-0.019
11	C1	51	RA2E11_205	3.50E-01	2.20E-03	3.50E-03	5.90E-01	8.60E-01	7.50E-01	5.50E-01	9.10E-02	4.50E-01	7.70E-01	3.10E-02
				1.136	1.047	1.044	1.015	0.996	1.006	1.02	1.018	1.002	1.008	0.926
				1.031	1.632	1.55	0.017	-0.01	0.029	0.009	1.398	0.355	0.032	-0.018
11	C1	52.9	OL12F11_233	2.90E-01	3.40E-03	5.20E-03	9.80E-01	9.70E-01	8.10E-01	6.00E-01	2.60E-01	3.90E-01	9.40E-01	1.80E-02
				1.157	1.045	1.042	0.999	0.999	1.004	1.018	1.012	1.003	1.002	0.919
				1.172	1.564	1.491	-0.001	-0.002	0.022	0.008	0.938	0.406	0.007	-0.02
11	C1	89.9	MAX_4r	5.20E-01	2.90E-01	2.60E-01	7.90E-01	8.60E-01	8.80E-01	5.80E-01	7.90E-01	8.30E-01	7.10E-02	8.20E-01
				0.914	1.016	1.017	1.008	1.004	0.997	1.019	0.997	0.999	1.052	1.008
				-0.728	0.575	0.609	0.009	0.009	-0.013	0.009	-0.219	-0.103	0.198	0.002
11	C1	101.2	MAX_4n	7.20E-01	7.70E-02	9.20E-02	6.90E-01	7.50E-01	2.90E-01	7.10E-01	8.90E-01	6.40E-01	6.30E-01	8.70E-01
				0.95	1.028	1.026	0.988	1.007	0.981	1.014	1.002	0.999	1.014	1.006
				-0.416	0.981	0.928	-0.013	0.018	-0.1	0.006	0.121	-0.22	0.056	0.002
12	A7	0	NA12A05_157	9.10E-01	3.70E-01	4.50E-01	4.50E-02	4.70E-01	3.00E-03	5.10E-01	9.40E-01	3.10E-01	9.90E-01	1.90E-02
				1.016	0.986	0.988	0.944	0.984	0.95	1.023	0.999	0.997	1	1.088
				0.128	-0.497	-0.419	-0.065	-0.041	-0.269	0.011	-0.058	-0.481	-1.00E-03	0.019
12	A7	5.4	OL12E03_110	7.10E-01	4.00E-02	7.20E-02	2.40E-02	2.20E-01	5.50E-03	5.10E-01	6.30E-01	3.70E-01	5.00E-01	3.50E-02
				1.052	0.97	0.973	0.938	0.973	0.954	1.022	0.995	0.997	1.019	1.078
				0.41	-1.106	-0.971	-0.072	-0.068	-0.248	0.011	-0.4	-0.418	0.074	0.017
12	A7	42.3	IGF1226a	2.40E-01	4.90E-01	6.40E-01	5.50E-01	1.40E-01	1.50E-01	4.00E-01	4.80E-01	8.70E-01	9.00E-01	1.20E-01
				0.847	0.989	0.993	0.983	1.032	0.975	1.029	0.993	1	0.996	1.059

				-1.317	-0.379	-0.256	-0.019	0.08	-0.134	0.013	-0.596	-0.079	-0.014	0.013
12	A7	53.1	IGF1226f	1.50E-01	4.80E-02	8.10E-02	5.50E-01	2.40E-02	2.20E-01	3.50E-01	3.20E-01	4.00E-01	9.60E-01	3.30E-02
				0.816	0.97	0.974	0.983	1.051	0.979	1.033	0.99	0.997	0.999	1.08
				-1.623	-1.09	-0.958	-0.019	0.125	-0.113	0.015	-0.835	-0.403	-0.005	0.018
12	A7	85.6	BRMS036_130	1.80E-01	9.30E-01	6.90E-01	7.00E-01	7.90E-01	8.70E-01	5.60E-01	9.60E-01	6.40E-01	6.80E-01	8.00E-01
				0.832	1.001	1.006	1.011	1.006	1.003	1.02	1	0.999	0.988	1.009
				-1.49	0.048	0.216	0.012	0.015	0.016	0.009	0.038	-0.222	-0.046	0.003
12	A7	87.8	IGF0504f	4.20E-01	5.90E-01	3.80E-01	8.90E-01	9.70E-01	9.50E-01	6.00E-01	7.30E-01	7.30E-01	5.80E-01	7.40E-01
				0.894	1.009	1.014	1.004	0.999	1.001	1.019	1.004	0.999	0.984	0.988
				-0.913	0.305	0.485	0.005	-0.002	0.006	0.008	0.297	-0.168	-0.062	-0.003
13	A1	0	SN11641_405	8.30E-01	3.80E-01	3.80E-01	2.30E-01	5.80E-01	5.80E-01	3.10E-01	1.70E-01	2.10E-01	3.70E-01	4.90E-01
				0.97	0.986	0.986	1.036	1.013	1.01	0.965	0.985	0.996	0.975	1.025
				-0.244	-0.493	-0.492	0.04	0.032	0.051	-0.016	-1.173	-0.607	-0.1	0.005
13	A1	2.4	KBrB048F07(2)	7.50E-01	3.90E-01	3.90E-01	9.80E-02	2.20E-01	3.80E-01	2.70E-01	1.40E-01	2.60E-01	3.60E-01	4.30E-01
				0.956	0.987	0.987	1.049	1.028	1.016	0.963	0.984	0.997	0.975	1.029
				-0.365	-0.473	-0.473	0.054	0.069	0.081	-0.017	-1.25	-0.537	-0.101	0.007
13	A1	11	CB10097_191	8.80E-01	8.20E-01	8.20E-01	3.00E-01	6.60E-01	3.80E-01	3.30E-01	1.70E-01	3.20E-01	3.80E-01	7.90E-01
				1.022	0.996	0.997	1.03	1.01	1.016	0.967	0.985	0.997	0.976	1.01
				0.174	-0.131	-0.124	0.033	0.024	0.082	-0.016	-1.169	-0.476	-0.096	0.002
13	A1	19.5	MAX4_p	1.70E-01	6.10E-01	4.40E-01	4.40E-02	7.40E-01	4.20E-02	2.30E-01	9.50E-01	6.80E-01	1.90E-01	5.10E-01
				0.826	1.008	1.012	1.059	1.007	1.036	0.96	1.001	1.001	0.964	0.977
				-1.542	0.28	0.421	0.064	0.018	0.185	-0.018	0.058	0.199	-0.144	-0.006
14	A9/C5	0	IGF3112a	6.00E-01	2.30E-01	2.50E-01	7.90E-01	4.10E-01	6.00E-01	2.30E-01	6.20E-01	7.60E-01	6.80E-01	4.40E-02
				1.079	1.02	1.018	1.008	0.982	1.01	0.958	1.005	0.999	1.012	0.929
				0.615	0.694	0.651	0.009	-0.045	0.049	-0.02	0.433	-0.153	0.047	-0.017
14	A9/C5	35.5	OL12F02_148	4.20E-01	8.50E-01	7.60E-01	1.90E-01	1.40E-01	7.50E-01	3.10E-01	2.80E-02	3.80E-01	9.60E-01	8.20E-01
				0.895	0.997	0.995	0.963	1.033	0.994	0.966	0.977	1.003	0.999	0.992
				-0.894	-0.106	-0.165	-0.042	0.081	-0.03	-0.016	-1.831	0.417	-0.005	-0.002
14	A9/C5	36.6	NA12D10_150	3.50E-01	4.30E-01	3.60E-01	1.30E-01	8.50E-02	5.20E-01	2.80E-01	1.40E-02	4.20E-01	9.20E-01	9.00E-01
				0.88	0.988	0.986	0.958	1.039	0.989	0.964	0.975	1.002	0.997	1.005

				-1.037	-0.435	-0.497	-0.049	0.095	-0.058	-0.017	-2.045	0.383	-0.011	0.001
15	A10	0	FITO247_277	6.00E-01	6.00E-01	7.00E-01	8.00E-01	6.10E-01	4.90E-01	4.40E-01	4.30E-06	1.80E-01	4.50E-01	8.10E-02
				0.93	0.992	0.994	1.007	0.989	0.988	1.027	0.955	1.004	0.979	0.94
				-0.581	-0.283	-0.206	0.008	-0.028	-0.063	0.012	-3.62	0.622	-0.083	-0.015
15	A10	5.8	RA2E07_93	5.50E-01	7.60E-02	9.50E-02	8.60E-01	1.00E+00	7.10E-01	2.40E-01		2.10E-01	9.30E-01	1.60E-01
				0.921	0.973	0.975	1.005	1	0.993	0.961	0.949	1.004	0.997	0.95
				-0.666	-0.971	-0.912	0.006	0	-0.034	-0.018	-4.152	0.592	-0.01	-0.012
15	A10	6	IGF1073a	5.40E-01	6.80E-02	8.60E-02	8.50E-01	9.30E-01	7.30E-01	2.40E-01		2.00E-01	9.80E-01	1.70E-01
				0.918	0.973	0.974	1.005	1.002	0.994	0.961	0.949	1.004	0.999	0.952
				-0.685	-0.989	-0.929	0.006	0.005	-0.032	-0.018	-4.123	0.6	-0.003	-0.011
16	C7	0	IGF5702e	6.50E-02	4.90E-02	3.60E-02	3.20E-01	7.80E-02	3.80E-01	5.20E-01	3.60E-01	5.80E-03	8.10E-01	7.80E-01
				0.773	0.971	0.969	1.029	1.039	1.016	0.978	0.99	0.992	1.007	0.99
				-2.042	-1.068	-1.134	0.032	0.097	0.08	-0.01	-0.762	-1.276	0.026	-0.003
16	C7	7.6	IGF5707b	8.50E-01	9.20E-02	6.80E-02	8.50E-01	6.20E-03	9.80E-01	5.70E-01	1.40E-01	3.80E-03	9.30E-01	8.50E-01
				0.974	0.975	0.973	0.995	1.061	1	0.981	0.985	0.992	0.998	1.007
				-0.213	-0.917	-0.988	-0.006	0.15	0.002	-0.009	-1.212	-1.334	-0.009	0.001
16	C7	22.8	IGF5415a	5.70E-01	7.50E-01	6.10E-01	7.90E-01	1.80E-01	8.00E-01	5.10E-01	7.60E-01	1.40E-02	7.00E-01	4.80E-01
				1.086	0.995	0.992	1.008	1.03	1.005	0.977	0.997	0.993	1.011	0.974
				0.671	-0.183	-0.291	0.009	0.073	0.024	-0.01	-0.267	-1.133	0.044	-0.006
17	A5	0	CB10320_253	4.60E-01	2.10E-01	1.40E-01	7.60E-03	3.40E-01	1.30E-02	4.20E-01	6.40E-01	9.30E-01	6.40E-01	6.40E-02
				0.9	0.981	0.977	1.079	1.021	1.043	0.973	1.005	1	1.013	0.937
				-0.841	-0.685	-0.818	0.085	0.053	0.223	-0.012	0.399	0.042	0.052	-0.015
17	A5	29.5	BRMS061_284	8.80E-01	9.50E-01	8.20E-01	8.00E-01	3.70E-02	8.90E-01	3.70E-01	2.80E-01	5.40E-01	6.40E-01	3.10E-01
				1.021	0.999	0.996	1.007	1.047	1.003	0.969	0.988	1.002	1.014	1.037
				0.168	-0.036	-0.129	0.009	0.116	0.013	-0.015	-0.92	0.297	0.053	0.009
17	A5	44.2	BRAS063_236	4.10E-01	8.00E-01	9.40E-01	4.70E-01	1.20E-01	6.30E-01	3.40E-01	6.20E-01	8.40E-01	1.30E-01	2.40E-01
				1.127	1.004	1.001	0.979	1.035	0.992	1.034	0.995	1.001	1.044	1.043
				0.953	0.143	0.043	-0.025	0.087	-0.044	0.015	-0.423	0.101	0.169	0.01
18	A9	0	IGF5222b	2.50E-01	9.80E-01	9.20E-01	7.40E-01	5.60E-01	3.10E-01	4.10E-01	8.60E-01	6.60E-01	1.60E-02	3.20E-01
				1.186	1	1.002	1.01	0.987	0.982	1.03	0.998	0.999	1.07	1.037

				1.364	0.015	0.055	0.01	-0.033	-0.095	0.014	-0.152	-0.218	0.263	0.009
18	A9	37	IGF5706e	8.10E-01	7.50E-01	9.10E-01	7.60E-01	9.70E-01	4.20E-01	3.50E-01	8.70E-01	2.70E-01	5.20E-01	5.10E-01
				0.967	0.995	0.998	0.991	1.001	1.014	0.969	1.002	1.003	1.018	1.024
				-0.271	-0.173	-0.064	-0.01	0.002	0.074	-0.015	0.138	0.525	0.071	0.005
19	A9	0	IGF1207c	3.90E-01	8.00E-01	9.70E-01	5.40E-02	7.70E-02	8.10E-03	4.70E-01	3.50E-01	2.90E-01	4.70E-01	1.30E-01
				1.131	0.996	0.999	0.946	0.961	0.955	1.025	0.99	0.997	1.021	1.057
				0.985	-0.145	-0.019	-0.062	-0.1	-0.241	0.011	-0.786	-0.501	0.081	0.013
19	A9	1.1	OL12F02_119	3.80E-01	6.20E-01	7.90E-01	9.00E-02	2.40E-01	2.70E-02	4.30E-01	4.00E-01	4.30E-01	1.60E-01	1.10E-01
				1.129	0.992	0.996	0.953	0.974	0.964	1.027	0.991	0.998	1.04	1.059
				0.975	-0.272	-0.145	-0.054	-0.065	-0.192	0.013	-0.701	-0.369	0.151	0.014
0	um	0	BRAS038_120	6.10E-01	6.40E-01	7.20E-01	2.30E-02	1.10E-01	5.30E-03	6.20E-01	1.30E-01	2.50E-02	7.60E-03	4.80E-01
				0.93	0.993	0.994	0.936	0.965	0.952	1.018	1.016	0.993	0.927	0.974
				-0.587	-0.266	-0.199	-0.074	-0.092	-0.257	0.009	1.293	-1.073	-0.297	-0.006
0	um	0	BRMS007_116	4.00E-01	5.80E-02	3.90E-02	1.50E-02	8.40E-01	6.40E-02	3.30E-01	9.90E-01	6.80E-01	3.90E-01	8.60E-01
				1.123	1.029	1.032	0.933	0.996	0.968	0.967	1	1.001	0.976	0.993
				0.936	1.035	1.12	-0.077	-0.011	-0.169	-0.015	0.007	0.193	-0.096	-0.002
0	um	0	BRMS061_297	5.40E-01	4.80E-01	4.30E-01	5.10E-01	8.50E-01	3.70E-01	3.50E-01	7.40E-01	8.90E-01	9.70E-02	8.50E-02
				0.915	1.011	1.012	1.02	1.004	1.016	0.967	1.004	1	0.953	0.938
				-0.705	0.399	0.444	0.022	0.01	0.084	-0.016	0.292	-0.065	-0.187	-0.015
0	um	0	BRMS098_146	3.20E-01	4.00E-01	2.90E-01	5.60E-01	9.00E-01	1.60E-01	3.80E-01	8.90E-01	2.60E-02	9.90E-01	6.50E-01
				0.872	0.987	0.984	0.983	0.997	0.976	0.971	1.002	0.993	1	1.017
				-1.1	-0.455	-0.579	-0.019	-0.007	-0.127	-0.013	0.119	-1.03	0.002	0.004
0	um	0	BRMS330_238	7.00E-01	4.80E-01	5.20E-01	9.90E-01	8.00E-01	2.60E-01	8.50E-01	6.50E-01	3.60E-01	8.50E-01	3.60E-01
				1.101	0.98	0.981	1.001	0.989	0.963	0.988	0.991	0.995	0.99	0.938
				0.81	-0.728	-0.669	0.001	-0.026	-0.195	-0.005	-0.715	-0.822	-0.039	-0.015
0	um	0	CB10179_150	1.00E-01	5.40E-01	6.70E-01	9.30E-01	2.50E-01	5.60E-01	3.50E-01	1.20E-03	9.80E-02	3.80E-01	1.90E-01
				1.252	1.01	1.007	0.997	0.975	1.01	0.968	1.034	1.005	0.975	0.955
				1.848	0.346	0.239	-0.003	-0.064	0.053	-0.015	2.701	0.792	-0.098	-0.011
0	um	0	CB10427_165	4.90E-01	5.20E-01	6.60E-01	1.90E-03	2.60E-02	1.50E-03	6.00E-01	1.40E-01	3.20E-02	3.30E-03	5.90E-01
				0.908	0.99	0.993	0.916	0.952	0.946	1.018	1.016	0.994	0.921	0.98

				-0.787	-0.364	-0.247	-0.1	-0.126	-0.289	0.009	1.266	-1.023	-0.324	-0.005
0	um	0	CB10493_166	2.80E-01	5.70E-01	5.50E-01	4.80E-01	7.50E-01	4.20E-01	3.20E-01	3.30E-01	1.20E-01	5.00E-01	7.30E-01
				1.168	1.009	1.009	0.979	1.007	0.986	1.036	0.99	0.995	1.02	1.013
				1.24	0.322	0.335	-0.024	0.018	-0.076	0.017	-0.828	-0.764	0.078	0.003
0	um	0	FITO317_384	7.20E-01	6.40E-01	6.00E-01	2.20E-02	1.60E-01	1.20E-01	2.00E-01	4.70E-03	7.30E-01	4.40E-01	5.60E-01
				1.052	0.993	0.992	1.069	0.969	1.028	0.956	1.03	1.001	1.022	0.979
				0.409	-0.261	-0.292	0.074	-0.078	0.144	-0.021	2.357	0.162	0.087	-0.005
0	um	0	IGF0191b	*	*	*	*	*	*	*	*	*	*	*
				*	*	*	*	*	*	*	*	*	*	*
				*	*	*	*	*	*	*	*	*	*	*
0	um	0	IGF2128c	8.70E-02	7.20E-01	7.10E-01	2.60E-01	7.80E-01	1.00E+00	2.50E-01	2.20E-01	7.70E-01	6.20E-01	8.40E-01
				0.789	0.995	0.994	1.033	1.006	1	0.962	1.013	1.001	0.986	1.007
				-1.892	-0.192	-0.205	0.037	0.016	0.001	-0.018	1.011	0.138	-0.054	0.002
0	um	0	IGF5101b	5.00E-01	8.70E-01	9.40E-01	2.30E-01	4.10E-01	1.60E-01	3.20E-01	9.00E-01	6.30E-01	2.20E-01	7.80E-01
				0.912	0.997	0.999	0.966	1.018	0.976	1.034	1.001	1.001	0.966	1.01
				-0.744	-0.092	-0.043	-0.039	0.046	-0.129	0.015	0.11	0.23	-0.134	0.003
0	um	0	KBrB048K11(2)	9.00E-01	2.50E-01	3.70E-01	1.40E-01	6.50E-02	1.20E-02	5.20E-01	8.10E-02	1.30E-01	9.90E-01	3.50E-01
				1.019	1.018	1.014	0.958	1.042	1.045	0.978	1.019	1.005	1	0.967
				0.148	0.629	0.488	-0.048	0.103	0.227	-0.01	1.462	0.718	0.001	-0.008
0	um	0	KBrH027N05(3)	8.30E-01	2.10E-01	3.50E-01	2.10E-01	3.60E-02	1.20E-02	5.00E-01	1.80E-01	1.60E-01	3.10E-01	5.40E-01
				1.032	1.02	1.015	0.964	1.048	1.045	0.977	1.014	1.004	1.029	0.978
				0.251	0.698	0.519	-0.041	0.117	0.231	-0.011	1.133	0.672	0.113	-0.005
0	um	0	MAX2_b	6.70E-01	4.40E-01	4.40E-01	9.90E-01	2.60E-01	9.70E-01	3.50E-01	7.80E-01	1.30E-01	1.90E-01	4.60E-01
				1.068	0.987	0.987	1	0.974	1.001	0.964	0.997	1.005	1.039	0.97
				0.523	-0.467	-0.468	0	-0.067	0.004	-0.018	-0.265	0.789	0.15	-0.007
0	um	0	NA12A07_152	7.60E-01	5.30E-01	7.20E-01	2.50E-02	1.20E-01	3.40E-02	5.90E-01	7.30E-01	9.10E-01	7.90E-01	4.10E-01
				0.958	0.99	0.994	0.938	0.966	0.963	1.019	0.996	1	0.992	1.031
				-0.349	-0.346	-0.199	-0.072	-0.088	-0.196	0.008	-0.296	0.056	-0.03	0.007
0	um	0	NA12E02_92	5.10E-01	3.70E-01	5.00E-01	4.20E-03	8.70E-02	3.20E-03	6.00E-01	1.50E-01	3.80E-02	6.70E-03	6.00E-01
				0.91	0.986	0.989	0.921	0.962	0.949	1.018	1.016	0.994	0.926	0.981

				-0.765	-0.512	-0.382	-0.093	-0.098	-0.275	0.009	1.234	-1.004	-0.304	-0.005
0	um	0	NA14E08_98	8.30E-02	1.70E-01	2.70E-01	8.30E-01	1.10E-01	6.30E-01	3.20E-01	2.50E-02	6.30E-01	1.40E-01	6.40E-01
				1.266	1.021	1.017	0.994	0.965	1.008	0.967	1.024	1.001	0.959	0.983
				1.925	0.757	0.597	-0.007	-0.09	0.044	-0.015	1.861	0.23	-0.161	-0.004
0	um	0	OL13G05_124	2.70E-01	3.00E-02	6.60E-02	7.90E-01	9.90E-01	2.70E-01	3.40E-01	8.10E-01	4.80E-01	7.30E-01	2.10E-01
				1.175	1.035	1.029	0.992	1	1.02	1.034	1.003	0.998	1.01	1.047
				1.265	1.219	1.03	-0.009	0	0.105	0.016	0.213	-0.349	0.038	0.011
0	um	0	RA2G08_318	6.10E-01	8.80E-02	9.70E-02	7.30E-01	2.70E-01	1.10E-01	2.70E-01	7.50E-01	6.20E-01	5.90E-01	1.20E-01
				0.933	1.026	1.025	1.01	1.025	1.028	0.964	0.997	0.999	1.015	0.946
				-0.562	0.925	0.896	0.011	0.062	0.144	-0.017	-0.265	-0.233	0.059	-0.013
0	um	0	RGL3_a	4.30E-01	1.30E-01	1.60E-01	9.00E-01	6.80E-01	4.90E-01	1.70E-01	5.40E-01	3.70E-01	2.70E-01	3.50E-03
				0.887	0.976	0.977	1.004	0.991	1.013	0.951	0.993	0.997	0.967	0.893
				-0.944	-0.881	-0.824	0.005	-0.024	0.069	-0.023	-0.555	-0.455	-0.13	-0.026
0	um	0	SN1963_335	2.10E-01	2.30E-01	2.80E-01	3.00E-01	4.80E-01	2.80E-01	4.10E-01	3.60E-01	3.60E-01	7.00E-01	8.90E-01
				1.187	1.019	1.016	0.97	1.016	0.982	0.972	1.01	0.997	0.989	0.995
				1.391	0.657	0.588	-0.033	0.04	-0.098	-0.013	0.764	-0.432	-0.042	-0.001

Supplementary Table 17. Coefficients of determination, VG Cantelupe.

[illegible]

Supplementary Table 18. Coefficients of determination VGDH Cowlinge (split in 3 to fit on page).

[illegible]

Podl	2.3	6.1	2.3	10.6	0.2	0.5	1.8	0	4.4	9.5	6.6	0	0.3	1.5	2.7	2.7
Podw	13.9	3.4	4.3	0.5	0	4.4	10.6	0.1	0.9	0.1	1.1	5.5	6.5	0	0	6.6
Pedang	2.8	2.5	7.2	1.2	3.1	1.2	0.4	2.3	0.1	0	5.5	10.6	3.6	4.5	6.1	8.7
Podang	1.5	8.5	7.3	0.1	2.2	1.3	0.5	1.6	0	4.6	2.4	3.4	1.4	9.1	9.5	2.6
Yield t/ha	6.7	8.8	0.5	0.1	1.5	0.7	0.2	3.6	6	3.4	11.6	0.8	3	4.6	2.4	8.3
HI	0.3	0.8	7	3.9	6.2	0	0	0.2	5.1	14	12.8	17.9	0.1	0.6	0.3	10.7
Start flowering	0.1	20.2	6.6	0.1	0.1	5.6	2.4	4.4	3.3	9	10.4	1.4	5.6	2.2	0.7	4.1
%oil	1.2	2.4	0.2	1.2	0.1	0.9	3.3	1.3	0.1	2.4	3.3	0	0.1	0.9	1.3	0
GSL	0.4	1.1	0.2	0.1	2.4	6.7	0.4	0.4	0	0.7	8.2	5.2	0.1	1.9	3.4	2
Protein	6.6	1.2	0.1	2.4	1.2	1.9	3.2	0	1	0.1	0.7	0	0.2	2.2	4	0
Autum vig.	9.1	8.2	0.2	0.7	0.7	0.5	0.1	5.3	3.1	8.3	25.9	5.7	0.1	3.9	1.2	6.1
Spring vig.	0	16.7	0.2	4.2	0.3	1.3	0.8	1.8	5.2	10.1	12.6	0	3.1	3.2	2.2	1.3
App. B. flow	0	16.7	0.2	4.2	0.3	1.3	0.8	1.8	5.2	10.1	12.6	0	3.1	3.2	2.2	1.3
App. at harvest	2.7	18.5	0	6	0.3	0.1	1.3	5	0	3.7	12.9	0.3	0.1	0	0.4	0.7
Plant height	10.8	42.5	9.7	9.2	1.2	18.6	9.8	1.1	4	12.2	2.7	12	8.1	1.2	0.5	5
End flowering	12.7	1.4	1	2	0.6	3	0.3	8.3	8.5	1.3	20.4	9.6	0.3	6.1	0.6	12.2
Flowering period	5.4	20	12.3	1.4	0	13.4	2.1	0.6	0.2	7.8	1.3	9.5	5.8	0.1	0.3	0.1
	Meanseedwt	Height	Terminal	Foot	Podno	Poddensity	Stemw	Fertile	Infertile	Nodes	Totnodes	Nodedensity	Branchdensity	Branchang	Branch4	Bkl

Supplementary Table 19. Single marker analysis of VGDH including parental differences, Cantelupe.

position	marker	height of plant	terminal length	foot length	pod number on terminal	pod density on terminal	stem width	fertile branch number	infertile branch number	node number	total node number	node density
A3, 4.7	IGF5272c	8.20E-01	5.40E-01	8.10E-01	7.10E-01	9.70E-01	8.10E-01	4.20E-01	4.40E-01	9.80E-01	8.20E-01	6.90E-01
		1.003	1.018	0.995	1.01	0.999	0.996	0.976	1.098	0.999	0.996	1.008
		0.356	0.75	-0.331	0.395	-0.001	-0.004	-0.089	0.043	-0.007	-0.062	0.066
A6, 52 ls	GAI23.6	3.60E-01	4.70E-01	6.70E-01	5.50E-01	9.30E-01	7.70E-01	3.50E-02	7.60E-02	6.90E-02	4.20E-02	2.10E-01
		1.012	0.979	1.011	0.983	0.998	1.005	1.069	0.798	1.039	1.037	0.973
		1.474	-0.914	0.652	-0.67	-0.003	0.004	0.246	-0.109	0.462	0.591	-0.221
A6, 34.5	IGF1027z	8.40E-01	6.10E-01	9.10E-02	4.50E-01	7.60E-01	5.70E-01	4.10E-01	1.10E-01	1.20E-02	2.70E-02	6.10E-02
		1.002	0.986	1.038	0.98	0.992	0.991	1.025	0.83	1.048	1.036	0.964
		0.31	-0.596	2.317	-0.779	-0.009	-0.007	0.09	-0.088	0.561	0.567	-0.294
A6, 66.2	IGF1075d	6.50E-01	4.20E-01	7.10E-01	5.80E-02	1.30E-01	6.90E-01	6.30E-02	3.50E-01	1.50E-01	7.10E-02	6.70E-02
		0.995	0.978	0.992	0.952	1.039	0.994	1.055	0.895	1.027	1.029	0.965
		-0.693	-0.945	-0.498	-1.898	0.043	-0.006	0.198	-0.052	0.32	0.459	-0.284
A6, 66	IGF1075e	4.50E-01	4.40E-01	7.60E-01	4.00E-01	8.50E-01	8.30E-01	8.50E-03	1.20E-01	7.20E-02	1.80E-02	1.90E-02
		0.991	0.979	0.993	0.978	1.005	1.003	1.079	0.827	1.035	1.038	0.955
		-1.168	-0.919	-0.435	-0.872	0.006	0.003	0.281	-0.088	0.411	0.613	-0.37
A7, 35.1 ls	IGF1178b	7.80E-01	8.60E-01	9.90E-01	3.30E-01	4.80E-01	8.30E-01	9.50E-01	9.10E-01	8.70E-01	8.80E-01	8.80E-01
		0.997	0.995	1	0.975	1.018	0.997	1.002	0.987	0.997	0.998	1.003
		-0.419	-0.201	-0.023	-0.982	0.02	-0.003	0.006	-0.007	-0.036	-0.039	0.023
A7, 107.7	IGF1226a	4.10E-01	9.50E-01	6.40E-01	9.30E-01	5.60E-01	9.00E-01	6.40E-01	8.80E-01	6.50E-01	6.10E-01	9.30E-01

		0.99	1.002	1.011	1.002	1.015	0.998	0.987	1.018	0.992	0.992	1.002
		-1.27	0.073	0.653	0.09	0.018	-0.002	-0.051	0.008	-0.103	-0.135	0.015
A7, 99.2	IGF1226f	2.70E-01	7.10E-01	6.40E-01	6.60E-01	5.30E-01	4.80E-01	2.90E-01	7.20E-01	7.90E-01	5.00E-01	9.90E-01
		0.987	1.011	1.01	1.013	1.017	0.99	0.97	0.956	0.995	0.988	1
		-1.733	0.465	0.622	0.482	0.019	-0.009	-0.112	-0.021	-0.065	-0.189	-0.001
A7, 95.0	DELLA_GRA	2.40E-01	7.40E-01	7.60E-01	7.60E-01	3.20E-01	8.30E-01	6.20E-01	4.60E-01	2.60E-01	2.10E-01	4.90E-01
		0.985	0.99	1.007	0.991	1.028	0.997	0.985	0.906	0.978	0.978	1.015
		-1.941	-0.436	0.455	-0.345	0.032	-0.003	-0.058	-0.044	-0.271	-0.364	0.118
A10, 41 ls	IGF5101b	1.00E-01	2.80E-01	7.30E-02	7.70E-01	5.30E-02	1.60E-01	2.80E-01	8.30E-02	9.80E-01	4.10E-01	9.40E-02
		1.019	1.03	1.04	0.992	1.049	0.979	0.969	0.814	1	0.987	1.033
		2.431	1.242	2.426	-0.298	0.056	-0.018	-0.115	-0.096	-0.005	-0.211	0.259
np	RGA12_3	9.50E-01	4.40E-01	3.60E-01	6.30E-01	5.30E-01	7.40E-01	7.40E-01	1.80E-01	5.50E-01	3.30E-01	5.60E-01
		0.999	1.022	0.978	1.014	1.017	0.995	1.01	1.182	1.012	1.017	0.988
		-0.103	0.921	-1.36	0.517	0.02	-0.005	0.038	0.079	0.146	0.27	-0.1
np	RGA12_30	6.90E-01	6.70E-01	3.40E-01	7.70E-01	6.50E-01	6.10E-01	6.80E-01	1.30E-01	4.40E-01	2.30E-01	3.00E-01
		0.995	1.012	0.978	1.008	1.012	0.992	1.012	1.205	1.016	1.02	0.979
		-0.615	0.509	-1.385	0.316	0.014	-0.007	0.046	0.088	0.187	0.33	-0.173
np	RGA12_31	7.50E-01	6.60E-01	6.30E-01	6.80E-01	6.70E-01	3.60E-01	9.80E-01	2.60E-01	3.10E-01	2.40E-01	3.60E-01
		0.996	1.012	0.989	1.011	1.011	0.986	1.001	1.15	1.021	1.02	0.981
		-0.496	0.524	-0.701	0.425	0.013	-0.012	0.003	0.065	0.245	0.321	-0.152
np	RGA3_M18.33_250	3.70E-01	3.90E-02	6.70E-01	3.70E-01	1.10E-01	9.90E-01	3.00E-01	6.60E-02	4.70E-01	8.40E-01	5.50E-01
		1.011	1.058	1.01	1.025	1.043	1	0.97	0.795	1.014	0.997	1.012
		1.378	2.398	0.618	0.938	0.048	0	-0.114	-0.105	0.172	-0.054	0.098

		branch density	branch angle	branch angle of top 4 branches	beak length	pedicel length	pod length	pod width	pedicel angle	pod angle	yield t/ha	harvest index
position	marker											
A3, 4.7	IGF5272c	2.90E-01	8.60E-01	7.30E-01	6.60E-01	9.10E-01	6.00E-01	3.90E-01	9.30E-01	6.30E-01	5.40E-01	3.60E-01
		1.053	0.998	0.995	1.006	0.998	1.008	1.006	1.001	1.001	0.985	1.075
		0.342	-0.092	-0.183	0.007	-0.003	0.044	0.003	0.044	0.22	-0.059	0.017
A6, 52 ls	GAI23.6	9.30E-01	1.60E-01	3.00E-01	6.70E-01	2.00E-01	6.50E-01	2.40E-01	5.60E-01	2.00E-01	6.20E-01	6.30E-02
		0.996	0.979	0.985	0.994	0.982	0.993	0.991	1.004	0.996	0.987	0.861
		-0.029	-0.794	-0.575	-0.007	-0.035	-0.04	-0.004	0.294	-0.642	-0.048	-0.036
A6, 34.5	IGF1027z	3.90E-02	2.40E-01	3.20E-01	2.40E-01	3.60E-03	4.60E-01	5.00E-01	3.00E-01	1.90E-02	2.90E-01	1.80E-01
		0.911	0.984	0.987	0.985	0.962	0.99	0.995	0.994	0.994	0.975	0.907
		-0.628	-0.605	-0.516	-0.018	-0.076	-0.059	-0.002	-0.506	-1.047	-0.096	-0.023
A6, 66.2	IGF1075d	6.50E-01	6.40E-01	4.90E-01	8.50E-01	3.80E-01	4.50E-01	4.60E-01	7.90E-01	5.80E-01	4.40E-01	1.30E-01
		0.98	1.006	1.009	1.002	0.988	1.011	0.995	0.998	1.002	0.981	0.895
		-0.137	0.243	0.352	0.003	-0.023	0.061	-0.002	-0.13	0.246	-0.069	-0.027
A6, 66	IGF1075e	3.70E-01	4.90E-01	7.20E-01	4.40E-01	3.40E-03	9.90E-01	3.40E-01	7.80E-01	6.70E-01	8.60E-01	8.10E-01
		0.959	0.991	0.995	0.99	0.962	1	0.993	0.998	0.999	0.996	1.018
		-0.281	-0.36	-0.185	-0.012	-0.076	-0.001	-0.003	-0.139	-0.198	-0.017	0.005
A7, 35.1 ls	IGF1178b	8.40E-01	9.30E-01	9.00E-01	2.10E-01	7.30E-01	1.10E-01	4.30E-02	1.80E-02	7.00E-01	2.70E-02	4.50E-01
		0.991	0.999	0.998	0.984	1.005	0.978	0.987	1.014	0.999	1.055	1.057
		-0.062	-0.047	-0.067	-0.019	0.009	-0.127	-0.005	1.131	-0.177	0.199	0.013
A7, 107.7	IGF1226a	2.90E-01	9.70E-01	9.20E-01	5.60E-01	7.10E-01	2.50E-01	9.50E-01	1.90E-01	5.60E-01	5.70E-01	2.90E-01
		0.952	1	0.999	1.008	1.005	0.984	1	0.992	0.998	1.014	1.084

		-0.331	0.018	-0.054	0.009	0.01	-0.094	0	-0.65	-0.266	0.052	0.019
A7, 99.2	IGF1226f	1.80E-01	6.60E-01	4.70E-01	9.40E-01	8.70E-01	7.50E-01	5.00E-01	2.70E-01	8.10E-01	3.20E-01	2.00E-01
		0.936	0.994	0.99	1.001	0.998	0.995	0.995	0.993	1.001	1.027	1.109
		-0.441	-0.243	-0.405	0.001	-0.005	-0.027	-0.002	-0.566	0.11	0.098	0.025
A7, 95.0	DELLA_GRA	2.20E-01	7.60E-01	5.90E-01	8.70E-01	5.40E-01	6.60E-01	6.40E-01	8.20E-01	7.30E-01	7.20E-01	3.30E-01
		0.941	0.995	0.992	0.998	1.009	0.993	0.996	0.998	1.001	1.01	0.918
		-0.401	-0.174	-0.301	-0.002	0.017	-0.04	-0.002	-0.126	0.175	0.036	-0.02
A10, 41 ls	IGF5101b	7.80E-01	2.20E-01	1.20E-01	2.20E-02	1.40E-01	7.90E-01	7.30E-01	3.70E-02	5.60E-01	9.70E-01	5.40E-01
		1.013	0.984	0.98	1.029	0.98	1.004	0.998	0.988	0.998	1.001	1.046
		0.084	-0.63	-0.79	0.034	-0.039	0.022	-0.001	-0.989	-0.264	0.003	0.011
np	RGA12_3	3.90E-01	5.00E-02	6.10E-02	3.40E-01	6.70E-01	4.50E-01	3.30E-01	7.50E-01	2.70E-01	7.90E-01	2.50E-01
		1.042	0.973	0.975	1.013	0.994	1.011	1.007	1.002	1.003	0.993	0.911
		0.275	-1.038	-0.98	0.015	-0.011	0.061	0.003	0.15	0.508	-0.025	-0.022
np	RGA12_30	4.90E-01	7.80E-02	9.30E-02	5.00E-01	7.60E-01	6.80E-01	7.10E-01	9.70E-01	4.70E-01	6.50E-01	2.90E-01
		1.033	0.976	0.978	1.009	0.996	1.006	1.003	1	1.002	0.989	0.918
		0.22	-0.926	-0.871	0.01	-0.008	0.034	0.001	-0.017	0.344	-0.042	-0.02
np	RGA12_31	8.10E-01	1.10E-01	1.10E-01	5.90E-01	7.40E-01	8.40E-01	8.10E-01	9.70E-01	4.50E-01	7.20E-01	2.80E-01
		1.011	0.978	0.979	1.007	0.996	1.003	1.002	1	1.002	0.991	0.919
		0.075	-0.841	-0.817	0.008	-0.009	0.017	0.001	0.016	0.356	-0.033	-0.02
np	RGA3_M18.33_250	3.30E-01	4.10E-01	3.60E-01	6.00E-02	2.50E-01	2.00E-02	9.40E-01	1.10E-01	1.20E-01	9.80E-01	5.50E-01
		0.955	0.989	0.988	0.976	0.985	0.967	0.999	0.991	0.996	1.001	1.048
		-0.307	-0.433	-0.478	-0.029	-0.03	-0.191	0	-0.755	-0.722	0.003	0.011

Supplementary Table 20. Single marker analysis of VGDH and parental differences at Cowlinge, 2007-2008.

marker	position	harvest index	means seed weight	height of plant	terminal length	foot length	pod number on terminal	pod density on terminal	stem width	fertile branch number	infertile branch number	node number	total node number	node density
IGF5272c	A3, 4.7	7.40E-02	7.30E-02	3.80E-01	7.00E-01	2.40E-01	6.80E-01	8.00E-01	5.20E-01	8.40E-01	5.20E-01	8.90E-01	5.20E-01	2.30E-01
		0.921	0.983	1.014	1.01	1.042	0.985	1.032	1.012	1.003	1.011	1.005	0.981	1.035
		-0.025	-0.078	1.654	0.395	1.949	-0.117	0.025	0.214	0.087	0.051	0.022	-1.093	0.024
GAI23_6	A6, 52 ls	8.20E-01	3.10E-01	2.30E-01	7.20E-01	4.30E-02	5.90E-01	6.80E-01	5.80E-02	3.80E-01	8.80E-01	5.20E-01	5.60E-01	8.00E-01
		1.011	1.011	0.98	1.011	0.93	1.023	1.058	0.963	0.984	1.003	1.024	1.019	1.009
		0.003	0.049	-2.409	0.415	-3.546	0.173	0.042	-0.658	-0.417	0.015	0.108	1.074	0.006
IGF1027z	A6, 34.5	8.90E-01	6.00E-01	4.90E-02	8.20E-01	4.70E-03	3.00E-01	9.80E-02	1.20E-01	8.60E-01	3.10E-01	7.40E-01	4.20E-01	4.40E-01
		0.994	0.995	0.971	0.994	0.91	1.041	1.223	0.971	0.997	0.98	1.012	1.023	0.976
		-0.002	-0.024	-3.618	-0.236	-4.539	0.302	0.152	-0.509	-0.077	-0.096	0.055	1.32	-0.017
IGF1075d	A6, 66.2	8.50E-01	3.70E-02	8.50E-01	5.40E-01	9.70E-01	3.90E-01	2.00E-01	3.10E-02	1.60E-02	1.50E-02	5.00E-01	7.90E-01	5.40E-01
		0.992	1.02	1.003	1.016	1.001	0.968	0.859	0.961	0.962	1.048	1.024	1.008	1.019
		-0.003	0.091	0.337	0.619	0.067	-0.249	-0.118	-0.695	-1.008	0.221	0.111	0.437	0.013
IGF1075e	A6, 66	6.30E-01	1.10E-01	7.10E-01	5.10E-01	6.20E-01	8.90E-01	3.10E-01	2.10E-03	1.60E-02	5.60E-03	8.90E-01	1.40E-01	6.60E-01
		0.978	1.015	1.006	1.017	0.983	1.005	0.885	0.946	0.962	1.046	1.005	1.043	0.988
		-0.007	0.067	0.692	0.671	-0.798	0.038	-0.096	-0.98	-0.999	0.212	0.021	2.435	-0.009
IGF1178b	A7, 35.1 ls	9.60E-02	7.70E-01	2.40E-01	1.50E-01	3.20E-01	5.00E-01	1.90E-01	7.00E-02	4.70E-02	6.10E-01	2.60E-02	8.20E-02	5.90E-01
		1.078	0.997	1.018	0.963	1.034	1.026	1.17	1.034	1.033	0.99	1.082	0.952	1.017
		0.023	-0.012	2.169	-1.461	1.607	0.196	0.12	0.591	0.843	-0.047	0.368	-2.837	0.012
IGF1226a	A7, 107.7	8.20E-01	6.20E-01	9.90E-01	8.20E-01	2.80E-01	1.10E-01	7.10E-01	7.60E-01	2.00E-01	3.30E-01	9.30E-01	2.70E-01	1.40E-01
		0.99	1.005	1	0.994	1.037	0.944	0.957	0.994	0.98	1.016	1.003	1.032	0.959
		-0.004	0.021	0.018	-0.23	1.714	-0.437	-0.035	-0.099	-0.53	0.076	0.014	1.803	-0.029
IGF1226f	A7, 99.2	8.60E-01	5.20E-01	6.80E-01	8.20E-01	5.20E-01	5.00E-01	9.10E-01	7.80E-01	9.20E-01	7.90E-01	7.10E-01	2.40E-01	1.60E-01

DELLA_GRA	A7, 95.0	0.991	1.006	1.007	0.994	1.023	0.975	1.013	1.005	0.998	1.004	1.013	1.037	0.96
		-0.002	0.029	0.812	-0.245	1.074	-0.194	0.01	0.096	-0.045	0.021	0.059	2.072	-0.028
		9.10E-01	9.60E-01	2.90E-01	7.20E-01	5.60E-01	3.80E-01	6.80E-01	4.40E-01	3.20E-01	8.00E-01	8.20E-01	5.60E-01	4.40E-01
		1.006	1	0.983	0.99	0.978	0.966	1.058	0.985	0.983	0.996	1.008	1.018	0.976
IGF5101b	A10, 41 ls	0.002	0.002	-2.139	-0.397	-1.051	-0.264	0.042	-0.266	-0.44	-0.021	0.037	1.062	-0.017
		8.20E-02	9.70E-02	2.20E-02	1.40E-01	8.30E-01	3.40E-01	6.90E-01	9.60E-01	7.10E-01	4.60E-02	3.70E-01	8.70E-01	8.10E-02
		1.078	1.016	1.035	1.04	1.007	1.037	0.954	0.999	1.006	1.039	1.032	0.995	1.055
		0.024	0.072	4.145	1.511	0.344	0.275	-0.036	-0.015	0.157	0.182	0.148	-0.268	0.037
RGA12_3	np	1.80E-01	8.40E-01	7.30E-01	9.30E-01	7.10E-01	7.40E-02	4.20E-01	9.40E-01	3.30E-01	3.00E-01	8.30E-02	4.80E-02	1.60E-02
		1.063	0.998	0.995	0.997	1.014	0.933	1.108	1.001	0.984	1.021	1.067	0.943	1.079
		0.019	-0.009	-0.648	-0.1	0.647	-0.523	0.08	0.026	-0.423	0.101	0.307	-3.408	0.053
		1.80E-01	9.60E-01	5.50E-01	6.40E-01	8.00E-01	7.80E-02	2.20E-01	8.00E-01	4.70E-01	5.20E-01	5.40E-02	7.90E-02	1.20E-01
RGA12_30	np	1.063	1	0.991	0.987	1.009	0.934	1.169	1.005	0.988	1.013	1.074	0.949	1.052
		0.02	-0.003	-1.106	-0.5	0.438	-0.514	0.12	0.083	-0.315	0.062	0.338	-3.009	0.035
		1.80E-01	9.80E-01	2.90E-01	3.90E-01	5.10E-01	3.20E-02	2.80E-01	7.50E-01	3.40E-01	6.30E-01	1.60E-01	4.30E-02	1.60E-01
		1.063	1	0.984	0.976	1.024	0.919	1.145	1.006	0.984	1.01	1.054	0.942	1.046
RGA12_31	np	0.02	-0.001	-2.005	-0.935	1.128	-0.632	0.104	0.108	-0.424	0.045	0.245	-3.434	0.031
		8.40E-01	3.30E-02	5.70E-01	5.30E-01	5.10E-01	6.30E-01	8.50E-01	8.20E-01	6.60E-01	2.40E-01	8.40E-01	5.00E-01	7.60E-01
		0.991	1.021	1.009	1.018	1.024	0.981	0.976	0.996	0.992	1.023	1.008	1.02	0.99
		-0.003	0.096	1.071	0.678	1.122	-0.142	-0.019	-0.074	-0.197	0.111	0.037	1.162	-0.007
RGA3_M18.33_250	np	8.40E-01	3.30E-02	5.70E-01	5.30E-01	5.10E-01	6.30E-01	8.50E-01	8.20E-01	6.60E-01	2.40E-01	8.40E-01	5.00E-01	7.60E-01
		0.991	1.021	1.009	1.018	1.024	0.981	0.976	0.996	0.992	1.023	1.008	1.02	0.99
		-0.003	0.096	1.071	0.678	1.122	-0.142	-0.019	-0.074	-0.197	0.111	0.037	1.162	-0.007
		8.40E-01	3.30E-02	5.70E-01	5.30E-01	5.10E-01	6.30E-01	8.50E-01	8.20E-01	6.60E-01	2.40E-01	8.40E-01	5.00E-01	7.60E-01

Marker	position	harvest index	branch density	branch angle	branch angle of top 4 branches	beak length	pedicel length	pod length	pod width	pedicel angle	pod angle	yield t/ha	start of flowering	oil %seed	glucosinolates	Protein
IGF5272c	A3, 4.7	7.40E-02	9.70E-01	3.90E-01	3.30E-01	8.90E-01	9.00E-01	6.50E-01	5.30E-01	4.10E-01	3.70E-01	3.50E-01	8.70E-01	1.70E-02	2.90E-01	7.70E-02
		0.921	1.001	0.989	1.006	1	0.998	1.007	0.99	1.012	1.006	1.016	1.001	1.004	0.983	0.991
		-0.025	0.021	-0.504	0.492	0.066	-0.003	0.012	-0.05	0.014	0.003	0.062	0.079	0.218	-0.324	-0.169
GAI23_6	A6, 52 ls	8.20E-01	9.30E-02	3.20E-01	3.40E-01	6.60E-01	9.90E-01	6.20E-02	6.00E-01	7.90E-02	4.90E-01	9.70E-01	7.80E-01	7.80E-02	9.20E-01	1.90E-01
		1.011	0.976	0.987	0.994	1.001	1	0.967	1.009	0.974	1.005	1.001	1.003	0.997	0.998	1.008
		0.003	-1.025	-0.626	-0.523	0.224	-0.001	-0.061	0.045	-0.028	0.003	0.003	0.141	-0.175	-0.032	0.135
IGF1027z	A6, 34.5	8.90E-01	4.70E-02	1.50E-01	5.70E-01	2.00E-01	5.50E-01	2.90E-03	6.10E-01	7.30E-03	1.90E-01	1.10E-01	3.50E-01	2.40E-01	6.70E-01	1.40E-01
		0.994	0.974	0.983	1.003	0.996	1.012	0.953	0.992	0.964	1.009	0.974	1.008	0.998	1.007	1.008
		-0.002	-1.138	-0.831	0.289	-0.619	0.014	-0.089	-0.039	-0.04	0.004	-0.104	0.427	-0.108	0.126	0.138
IGF1075d	A6, 66.2	8.50E-01	4.60E-01	4.30E-01	4.10E-01	1.90E-01	6.80E-01	7.20E-01	7.00E-02	4.00E-01	3.50E-02	7.20E-01	3.80E-01	6.40E-01	1.10E-01	4.20E-01
		0.992	0.99	0.99	0.995	1.004	1.008	0.994	1.027	1.012	1.014	1.006	1.007	1.001	0.975	0.996
		-0.003	-0.419	-0.457	-0.412	0.628	0.01	-0.011	0.139	0.012	0.006	0.022	0.391	0.044	-0.465	-0.076
IGF1075e	A6, 66	6.30E-01	2.20E-01	5.60E-01	1.30E-01	2.30E-01	1.60E-01	3.50E-01	2.00E-01	6.00E-01	1.30E-02	5.10E-01	8.80E-01	8.50E-01	7.30E-02	7.20E-01
		0.978	0.984	0.993	0.991	1.004	1.028	0.987	1.019	1.007	1.016	0.989	1.001	1	0.971	0.998
		-0.007	-0.706	-0.332	-0.755	0.576	0.034	-0.025	0.1	0.008	0.007	-0.043	0.07	-0.017	-0.542	-0.035
IGF1178b	A7, 35.1 ls	9.60E-02	9.70E-01	6.20E-01	1.70E-01	4.50E-01	6.10E-01	9.90E-01	3.70E-02	3.90E-01	8.70E-01	7.70E-01	2.20E-01	7.30E-01	8.80E-01	4.70E-01
		1.078	1.001	0.994	1.008	0.998	1.01	1	0.97	0.988	0.999	0.995	1.01	0.999	0.998	1.004
		0.023	0.022	-0.289	0.695	-0.364	0.013	0	-0.16	-0.013	0	-0.019	0.558	-0.032	-0.046	0.068
IGF1226a	A7, 107.7	8.20E-01	9.80E-01	2.40E-01	9.20E-01	9.10E-01	5.10E-01	1.00E-01	4.20E-01	4.50E-01	1.30E-01	5.30E-01	2.80E-01	9.60E-01	6.70E-01	7.40E-01
		0.99	1	0.986	1.001	1	1.013	1.024	0.988	1.011	1.01	0.99	1.009	1	1.007	0.998
		-0.004	0.013	-0.682	0.052	-0.053	0.016	0.043	-0.064	0.011	0.004	-0.04	0.487	-0.004	0.128	-0.032
IGF1226f	A7, 99.2	8.60E-01	7.00E-01	6.10E-01	6.90E-01	6.00E-01	1.10E-01	8.20E-02	2.00E-01	9.40E-01	2.20E-01	3.80E-01	2.20E-01	4.60E-01	7.40E-01	1.10E-01
		0.991	1.005	0.993	1.003	0.998	1.035	1.027	0.98	1.001	1.008	0.985	1.011	1.001	1.006	0.991

DELLA_GRA	A7, 95.0	-0.002	0.235	-0.315	0.211	-0.272	0.041	0.048	-0.107	0.001	0.004	-0.058	0.567	0.071	0.109	-0.158
		9.10E-01	7.60E-01	4.30E-01	3.00E-01	6.00E-01	8.30E-01	7.70E-01	9.50E-01	2.10E-01	3.70E-01	9.40E-02	1.40E-01	3.70E-01	7.50E-01	9.80E-01
		1.006	0.995	0.989	1.006	1.002	1.005	0.995	1.001	0.982	1.006	0.972	1.013	0.998	1.006	1
IGF5101b	A10, 41 ls	0.002	-0.194	-0.508	0.542	0.274	0.006	-0.008	0.005	-0.02	0.002	-0.115	0.705	-0.09	0.107	-0.002
		8.20E-02	9.80E-01	7.90E-01	1.50E-01	4.20E-01	2.80E-02	4.70E-01	8.80E-01	1.40E-01	1.20E-01	8.30E-01	9.80E-01	2.60E-01	9.10E-02	6.70E-01
		1.078	1	0.997	0.991	0.998	1.044	1.012	1.002	1.021	1.01	1.004	1	1.002	0.974	0.998
RGA12_3	np	0.024	0.015	-0.156	-0.726	-0.389	0.052	0.022	0.011	0.022	0.005	0.013	0.012	0.103	-0.497	-0.04
		1.80E-01	3.70E-01	6.00E-01	2.80E-01	2.20E-01	5.00E-01	2.00E-01	8.80E-01	3.30E-01	5.70E-01	3.60E-01	3.40E-01	6.20E-01	5.70E-01	3.60E-02
		1.063	1.013	0.993	0.993	1.004	0.986	1.023	1.002	1.014	1.004	0.984	1.008	0.999	0.991	1.011
RGA12_30	np	0.019	0.548	-0.321	-0.55	0.602	-0.017	0.041	0.013	0.015	0.001	-0.062	0.453	-0.047	-0.175	0.201
		1.80E-01	3.20E-01	7.50E-01	2.00E-01	1.80E-01	5.40E-01	2.20E-01	8.30E-01	4.70E-01	3.30E-01	3.00E-01	2.40E-01	5.20E-01	7.50E-01	2.00E-02
		1.063	1.014	0.996	0.992	1.004	0.988	1.022	1.003	1.01	1.007	0.982	1.01	0.999	0.995	1.013
RGA12_31	np	0.02	0.598	-0.193	-0.653	0.654	-0.015	0.039	0.017	0.011	0.003	-0.07	0.553	-0.061	-0.098	0.226
		1.80E-01	2.70E-01	6.80E-01	2.30E-01	2.10E-01	2.20E-01	4.00E-01	1.00E+00	6.80E-01	7.30E-01	2.80E-01	1.80E-01	6.40E-01	7.50E-01	2.90E-02
		1.063	1.015	0.995	0.993	1.004	0.975	1.015	1	1.006	1.002	0.982	1.012	0.999	0.995	1.012
RGA3_M18.33_250	np	0.02	0.649	-0.25	-0.61	0.598	-0.031	0.027	0	0.006	0.001	-0.073	0.629	-0.044	-0.097	0.209
		8.40E-01	4.10E-01	4.50E-01	1.50E-01	7.30E-04	5.60E-01	3.90E-01	4.70E-03	3.30E-01	1.80E-01	6.60E-01	2.60E-01	7.60E-03	9.60E-01	2.70E-02
		0.991	0.989	0.99	0.991	0.99	1.012	1.015	0.958	0.986	1.009	1.007	0.99	1.005	1.001	0.988
		-0.003	-0.491	-0.456	-0.734	-1.579	0.015	0.028	-0.22	-0.015	0.004	0.029	-0.524	0.247	0.016	-0.213