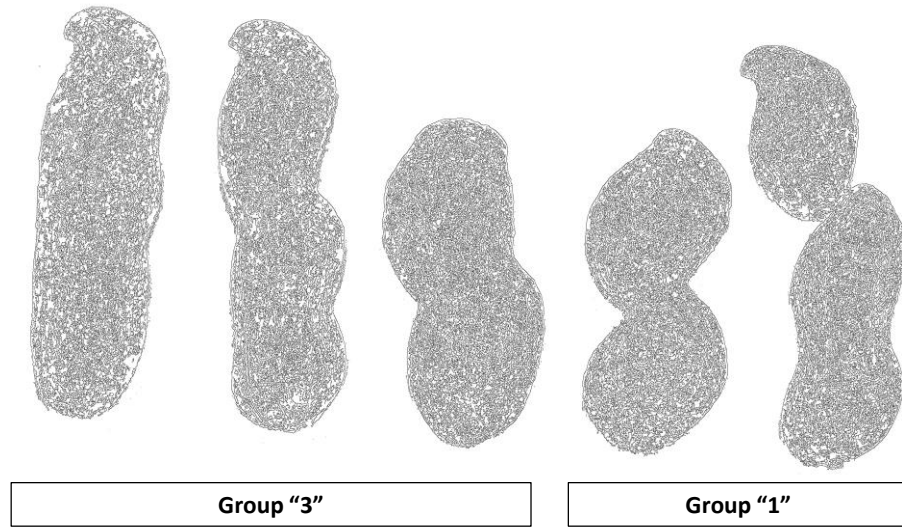
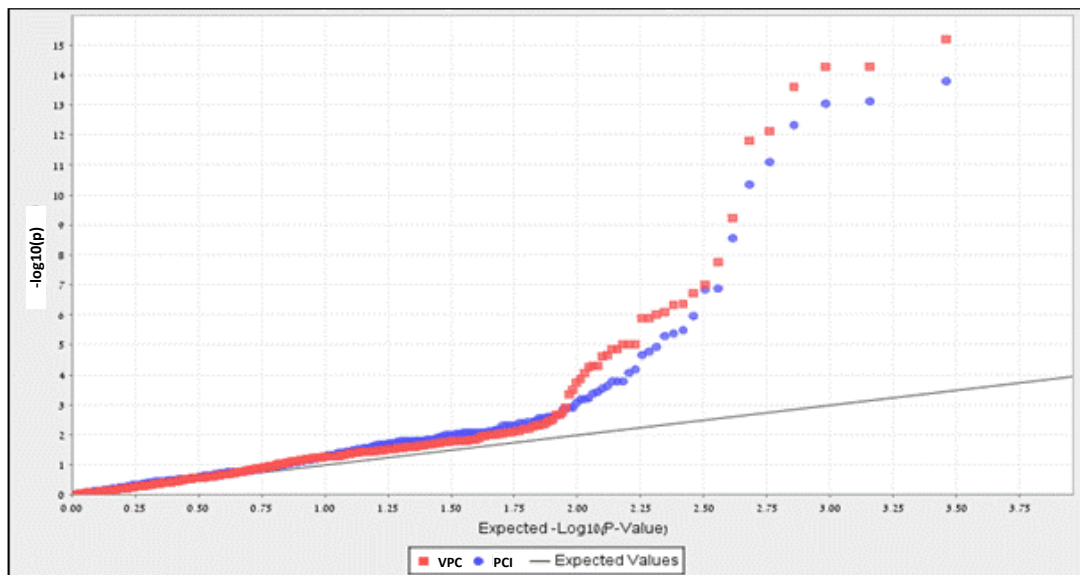


**Figure S1**



**Figure S2**



**Table S1.** Significant SNP markers associated with visual (VPC) and quantitative (PCI) assessments of the pod-constriction trait

Trait	Probe ID	Chromosome	Position(bp)	<i>p</i> -value	$-\log_{10}(p)$	Marker $R^2$
VPC	AX177638964	17	120287958	6.2E-16	15.20	0.32
VPC	AX177640139	17	120268599	5.1E-15	14.29	0.29
VPC	AX177639436	17	120420782	5.3E-15	14.28	0.29
VPC	AX176822599	17	120699791	2.4E-14	13.61	0.28
VPC	AX177639347	17	120550537	7.6E-13	12.12	0.24
VPC	AX176808161	17	120838334	1.6E-12	11.81	0.26
VPC	AX176821561	17	121098593	5.9E-10	9.23	0.21
VPC	AX176815698	17	122055610	1.8E-08	7.76	0.18
VPC	AX176822637	17	122247802	9.6E-08	7.02	0.15
VPC	AX147256630	17	121954137	1.9E-07	6.72	0.15
VPC	AX147256649	17	122177705	4.3E-07	6.36	0.14
VPC	AX176817885	17	122260525	4.6E-07	6.34	0.14
VPC	AX177637980	17	122128386	8.0E-07	6.10	0.13
VPC	AX176806530	17	30845972	9.4E-07	6.03	0.12
VPC	AX176809651	17	114704092	1.3E-06	5.90	0.13
VPC	AX176817995	17	16412296	1.3E-06	5.89	0.13
VPC	AX176792556	8	1053912	9.7E-06	5.01	0.11
VPC	AX147256000	17	102224525	9.7E-06	5.01	0.11
VPC	AX176819626	17	106063047	9.7E-06	5.01	0.11
VPC	AX176803520	17	122476073	1.4E-05	4.86	0.11
VPC	AX177638909	17	111731434	1.4E-05	4.85	0.11
PCI	AX177638964	17	120287958	1.6E-14	13.79	0.30
PCI	AX177640139	17	120268599	7.5E-14	13.12	0.27
PCI	AX177639436	17	120420782	8.8E-14	13.05	0.27
PCI	AX176822599	17	120699791	4.6E-13	12.34	0.26
PCI	AX177639347	17	120550537	8.0E-12	11.10	0.22
PCI	AX176808161	17	120838334	4.4E-11	10.36	0.24
PCI	AX176821561	17	121098593	2.7E-09	8.57	0.20
PCI	AX176815698	17	122055610	1.3E-07	6.87	0.16
PCI	AX176822637	17	122247802	1.4E-07	6.86	0.15
PCI	AX147256630	17	121954137	1.1E-06	5.95	0.13
PCI	AX147256649	17	122177705	3.3E-06	5.49	0.12
PCI	AX177637980	17	122128386	4.1E-06	5.39	0.12
PCI	AX176817885	17	122260525	5.0E-06	5.30	0.12
PCI	AX176806530	17	30845972	1.2E-05	4.93	0.10
PCI	AX176809651	17	114704092	1.7E-05	4.78	0.11

**Table S3.** List of gene models within the B07:120287958...120699791 genomic segment.

Genome location	Gene model
Araip.B07:120285940..120287411	Predicted methyltransferase
Araip.B07:120364965..120365903	Uncharacterized protein LOC102665249 isoform X4
Araip.B07:120373162..120374726	Tetratricopeptide repeat (TPR)-like superfamily protein
Araip.B07:120394118..120406510	Myosin heavy-chain-related protein
Araip.B07:120408286..120409428	Galactose oxidase/kelch repeat superfamily protein;
Araip.B07:120465390..120466687	Heavy metal transport/detoxification superfamily
<b>Araip.B07:120468417..120472189</b>	<b>MADS-box transcription factor 1</b>
Araip.B07:120475403..120478130	Poly [ADP-ribose] polymerase 3
Araip.B07:120512267..120514427	Serine/threonine-protein phosphatase 7 long-form homolog
Araip.B07:120517039..120518963	Uncharacterized protein LOC100797259 isoform X4
Araip.B07:120537272..120546148	Uncharacterized protein LOC102661750 isoform X2 [ <i>Glycine max</i> ]
Araip.B07:120552289..120559291	Sulfate transporter 1; 3;
Araip.B07:120590131..120594404	Sulfate transporter 1; 3
Araip.B07:120595882..120599920	tRNA modification GTPase, putative
Araip.B07:120600484..120613531	Acetyl-CoA carboxylase 1