Supplementary Materials: Quantitative Trait Loci (QTL) Analysis of Fruit and Agronomic Traits of Tropical Pumpkin (Cucurbita moschata) in an Organic Production System

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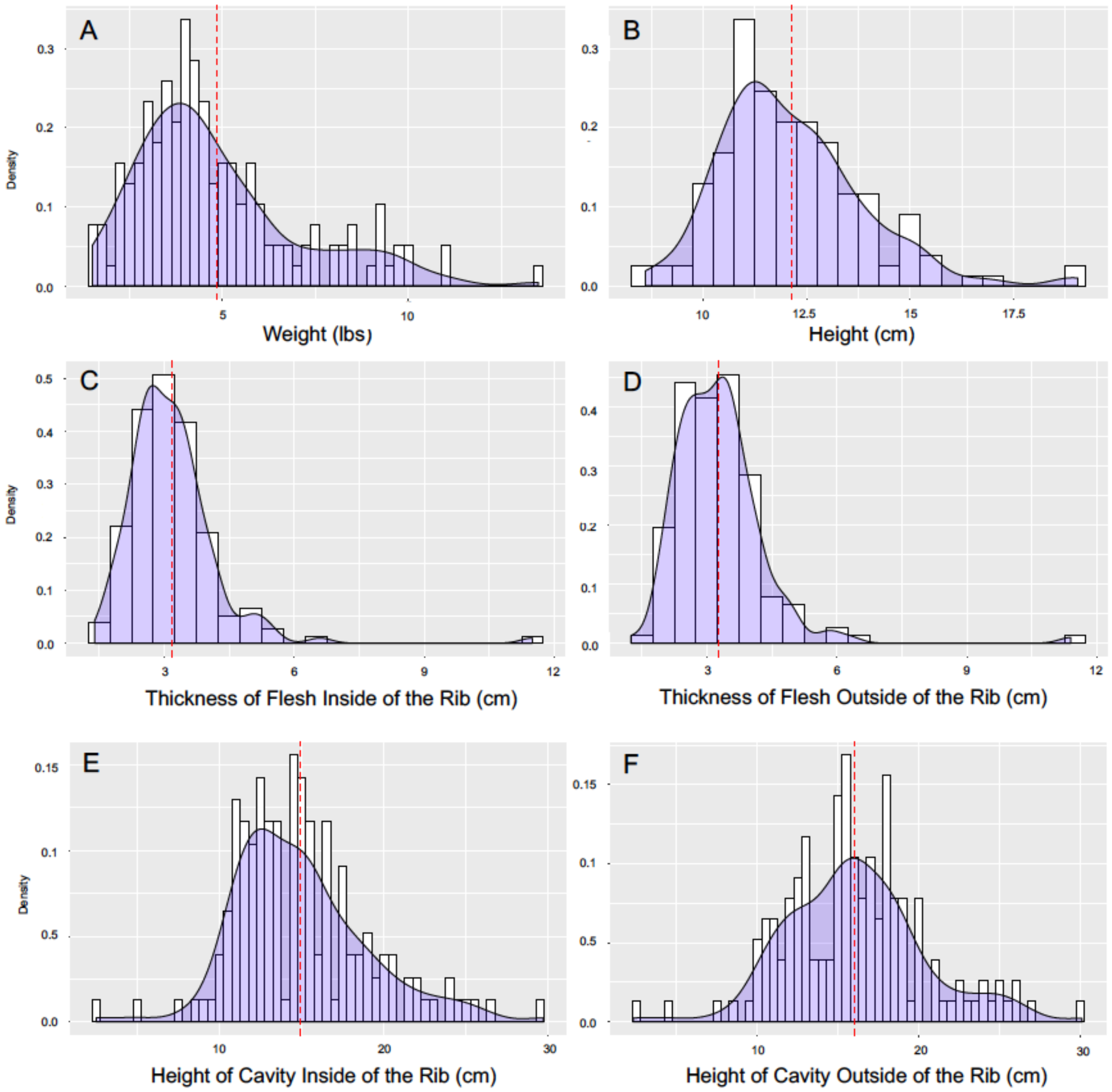

Figure S1. Phenotypic distribution of traits evaluated by the Harley-Knott (hk) regression method in R/qtl.

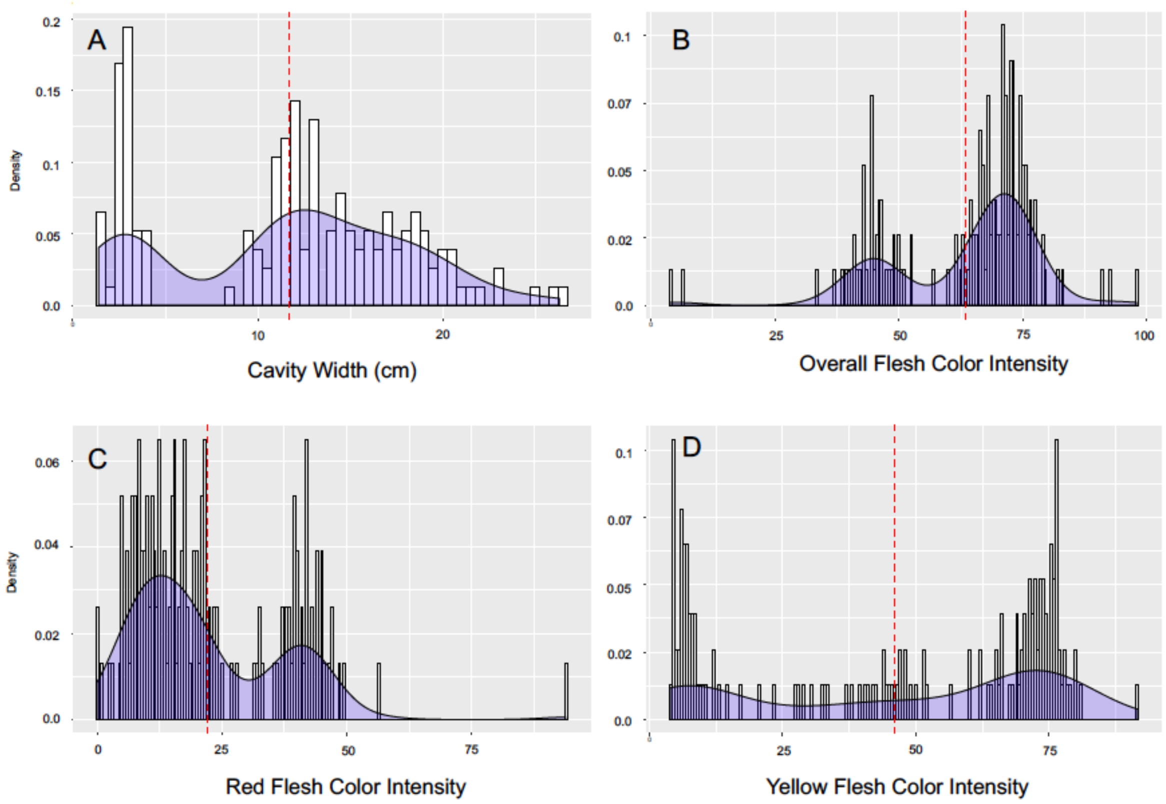

Figure S2. Phenotypic distribution of traits evaluated by 2-part, also known as bimodal, method in R/qtl.

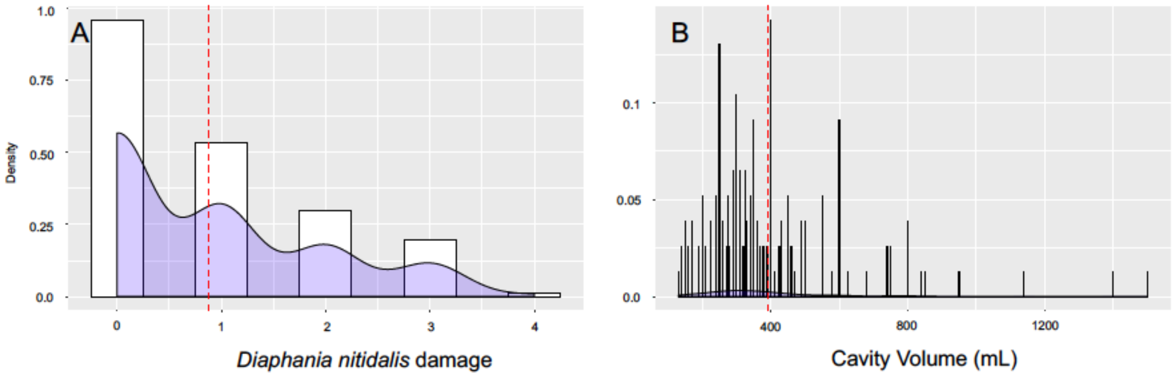

Figure S3. Phenotypic distribution of traits evaluated by non-parametric method in R/qtl.

Table S1. Sequence analysis between significant reads in this study and the pumpkin genome.

Marker	Linkage Group (cM)	Traits Associated	Direction of QTL	Percent Phenotypic Variance explained	Donor Parent	Coordinates in Genome	Annotation (if any)

				(R-squared)			
Pumpkin_282381	1 (195.1)	Flesh color intensity	Decrease in color intensity	6.8%	Taina Dorada	15:706796..706659	CmoCh05G001640.1
Pumpkin_93626	1 (194.1)	Insect damage and red color intensity	Reduction in insect damage	18.00%	Shima	1:4070770..4070940	CmoCh01G007800.1
Pumpkin_89537*	1 (21.4)	Cavity width	Increase in Cavity width	16.47%	Taina Dorada	0:20002042..20002198	-
Pumpkin_164349	9 (176.3)	Insect damage, flesh color intensity, and red color intensity	Reduction in insect damage	10.21%	Shima	15:708652..708809	CmoCh15G001520.1
Pumpkin_46427	12 (49.8)	flesh color intensity and red	Increase in color intensity	16.47%	Taina Dorada	13:8090313..8090145	CmoCh13G009130.1

		color intensity.					
Pumpkin_216447*	15 (135.0)	Insect damage	Increase in susceptibility	10.41%	Taina Dorada	18:6668762..6668914	-
Pumpkin_210956	15 (118.5)	Red color intensity	Increase in intensity	4.11%	Taina Dorada	15:3689527..3689600	CmoCh15G007520.1
Pumpkin_221779	17 (73.8)	Flesh color intensity and red color intensity.	Increase in intensity	7.57%	Taina Dorada	5:10556898…10556795	CmoCh05G013660.1

*The highest homology shown but it has multiple hits.

Table S2. Genomic comparison between *C. moshata* gene models and *Cucumis melo* genome.

***C. moshata* gene model**	***C. melo* locus**	**Comment***
CmoCh05G001640.1	MELO3C010837	Mannose-P-dolichol utilization defect 1 protein.
CmoCh01G007800.1	MELO3C001921	Kinase, putative
CmoCh15G001520.1	MELO3C008306	*CLATHRIN HEAVY CHAIN*.
CmoCh13G009130.1	MELO3C002271	Protein ApaG
CmoCh15G007520.1	MELO3C022819	F-box and Leucine Rich Repeat domains containing protein,

		putative isoform 1
CmoCh05G013660.1	MELO3C004578	Alpha/beta-Hydrolases superfamily protein

*Taken from cucurbitsgenomics.org (Zhen et al., 2018).