

Supplementary Material

1 Supplementary Figures

Primer ID	Forward sequence (5'-3')	Reverse sequence (5'-3')	Application
CAC	aagtttggttgaggctgtg	gagcgaactccttcttgagtga	RT-qPCR for <i>CAC</i>
CQ	gtcgctctgctaccgagataag	cttgacacacctccagaattg	RT-qPCR for <i>BhAPRR2</i>
PS CAPS	tcacttccttctggttctccacacaata	tgcagttgagttcttctgaaaccactctc	MAS test
DAPRR2	atggttgtactgccgacgatttac	tcaggagggtctggagccgttgatt	CDS of <i>BhAPRR2</i>

Supplementary Figure 1. Primers used in this study.

Primer ID	Primer X	Primer Y	Primer C	Application
PS7	gaaggtgaccaagttcatgctgtctgcattgtggttcccatc	gaaggtcggagtcaacggattgtctgcattgtggttcccatc	catccatggcatcctccaggaac	Reduce interval to 3.6 Mb
PS8	gaaggtgaccaagttcatgctggaactcccacagttctttaca	gaaggtcggagtcaacggattgaaactcccacagttctttacg	aagaaccgtcgggagttcccag	Reduce interval to 3.6 Mb
PS11	gaaggtgaccaagttcatgctgttctcgctctgtttggatcaaac	gaaggtcggagtcaacggattgttctcgtctgtttggatcaaaa	aaattacaaaacacatgagtgttacatagc	Reduce interval to 3.6 Mb and 179 Kb
PS13	gaaggtgaccaagttcatgcttaggtaaaaatgtcaacgttacagatc	gaaggtcggagtcaacggattttataggtaaaaatgtcaacgttacagatt	tcaacatgtcaagcttgcctgtggc	Reduce interval to 3.6 Mb and 179 Kb
PS13.4	gaaggtgaccaagttcatgcttctcatcttgatacctccattctag	gaaggtcggagtcaacggatttctcatcttgatacctccattctaa	cggctggaatctacaatctacaatatattg	Reduce interval to 179 Kb
PS13.6	gaaggtgaccaagttcatgcttttggggcaattagatgtttgttatg	gaaggtcggagtcaacggattgtttggtggcaattagatgtttgttatt	gtaaaaccattaatgtcatagataaacaatttca	Reduce interval to 179 Kb
PS14	gaaggtgaccaagttcatgctcaatccacgattggtaggtttaca	gaaggtcggagtcaacggatttccacgattggtaggtttacg	cggttaacgaattgaatcaaagaacaaatc	Reduce interval to 179 Kb
PS15	gaaggtgaccaagttcatgctgaagcttggtcagccatggg	gaaggtcggagtcaacggattggaagcttggtcagccatgga	ccagcgaatttccagttcttcaacc	Reduce interval to 3.6 Mb
PS16	gaaggtgaccaagttcatgctcattagataacaccaaggatgactg	gaaggtcggagtcaacggattgtcattagataacaccaaggatgacta	gtgcagtcttgatcatgacttcag	Reduce interval to 3.6 Mb and 179 Kb
PS18	gaaggtgaccaagttcatgctgtaccaaattaatcaatcacacaatga	gaaggtcggagtcaacggattctaccaaattaatcaatcacacaatgg	catatagaaataagaatataatgcattaaagctttagg	Reduce interval to 3.6 Mb and 179 Kb
PS20	gaaggtgaccaagttcatgctgaagactctaaagactgaagtccg	gaaggtcggagtcaacggattgaagactcttaagactgaagtcct	gaagttgaagtcttggaaagaatacttgtatc	Reduce interval to 3.6 Mb

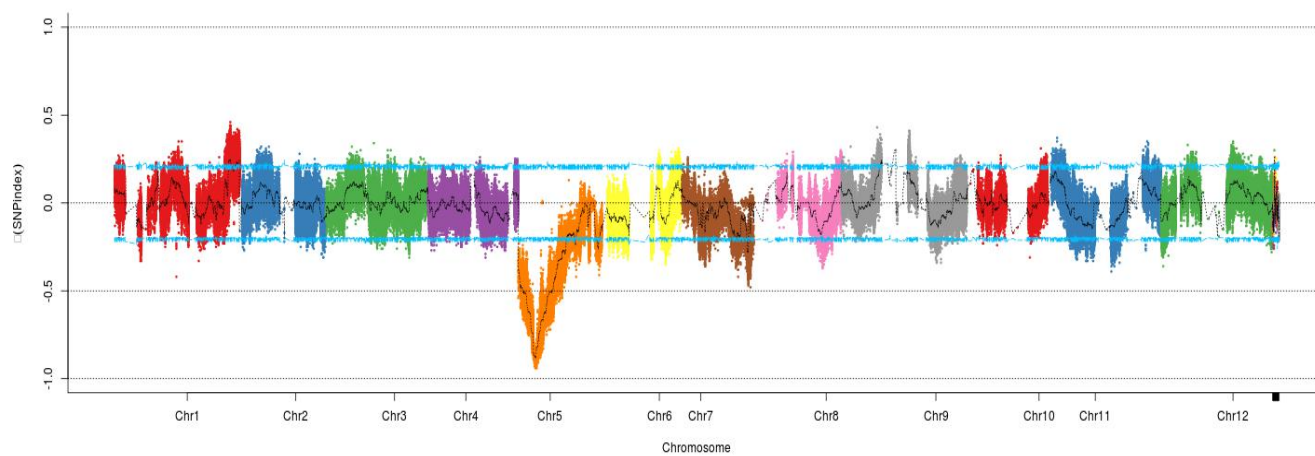
PS21	gaaggtgaccaagttcatgctccacc acaaagggctccaacat	gaaggtcggagtcaacggattcac caciaagggctccaacac	gtggattcacttcgag gtctgcc	Reduce interval to 3.6 Mb
PS25	gaaggtgaccaagttcatgctgttg tggtttgtttacacttttg	gaaggtcggagtcaacggattgtg ttgtggtttgtttacactttga	atggaaggcagggga ggtgttg	Reduce interval to 3.6 Mb
PS7	gaaggtgaccaagttcatgtaacaa ttcaaattaatccaaaactgattctt	gaaggtcggagtcaacggattcaa ttcaaattaatccaaaactgattct c	cataaggtccccttagt aactcaaaagg	Reduce interval to 3.6 Mb
PS29	gaaggtgaccaagttcatgctggcag catttggtacacataatcc	gaaggtcggagtcaacggattgg cagcatttggtacacataatcg	gaatctgtataaaaga ggggttagaccag	Reduce interval to 3.6 Mb
PS31	gaaggtgaccaagttcatgctccctat gatccccaagtatcca	gaaggtcggagtcaacggattccc tatgatccccaagtatccg	tggagcacttcgctttg taaagagg	Reduce interval to 3.6 Mb
PS33	gaaggtgaccaagttcatgctgaatta gtgaattgagtgaattgaaatgg	gaaggtcggagtcaacggattgaa ttagtgaattgagtgaattgaaatg a	gaaaaccccaaattta aacatttcatttgaat tc	Reduce interval to 3.6 Mb

Supplementary Figure 2. KASP markers used in this study.

Number	Inbred line	Phenotype	Genotype *	Number	Inbred line	Phenotype	Genotype
7	GX-71	green	A	30	KF-4-3	green	A
8	MY-1	white	B	31	Hechijiegua	green	A
9	F ₁ of GX-71×MY-1	green	H	32	7-2-1-4-2-2	green	A
10	KX-2	green	A	33	YO-13-2-2-1	green	A
11	YO-16	white	B	34	Mengshanji egua	green	A
12	F ₁ of KX-2×YO-16	green	H	35	Baidonggua	green	A
13	GK-3-4-3-2-1-3	green	A	36	YO-11-3-1	green	A
14	HX-1	green	A	37	GM-7-2-2-2	green	A
15	Rongshuijie gua	green	A	38	YMY-1-6-8-1	white	B
16	TL-1-2-2	green	A	39	YS-1-3-1-1	white	B
17	LF-1	green	A	40	YMY-1-5-0-1	white	B
18	Kx-2-3	green	A	41	YSB-1-3-1	white	B
19	HT-7-1-2-1	green	A	42	YO-16-1-2-6-1	white	B
20	GH-1-1-3	green	A	43	YMY-24-1-6-1	white	B

21	YO-2-2-1-6-1	green	A	44	YMY-2-2-1	white	B
22	GK-3-4-3	green	A	45	YSB-1-1-2	white	B
23	GF-7-1-1	green	A	46	JINGYUA N2HAO	white	B
24	YO-6-3-1-2-1	green	A	47	YMY-2-2	white	B
25	7-2-1-2	green	A	48	YO-11-1-1	white	B
26	GD-1	green	A	49	YO-24-1-3-1	white	B
27	NH-2	green	A	50	YO-2-2-3	white	B
28	GF-71	green	A	51	YS-4-5-1	white	B
29	M-1-2-1	green	A	52	YL-1-1-1	white	B

Supplementary Figure 3. MAS testing in 40 *Benincasa hispida* inbred lines and four parent lines and F₁ using PS CAPS.*A representatives genotype of male parent(green),B representatives genotype of female parent(white).H representatives Heterozygote.



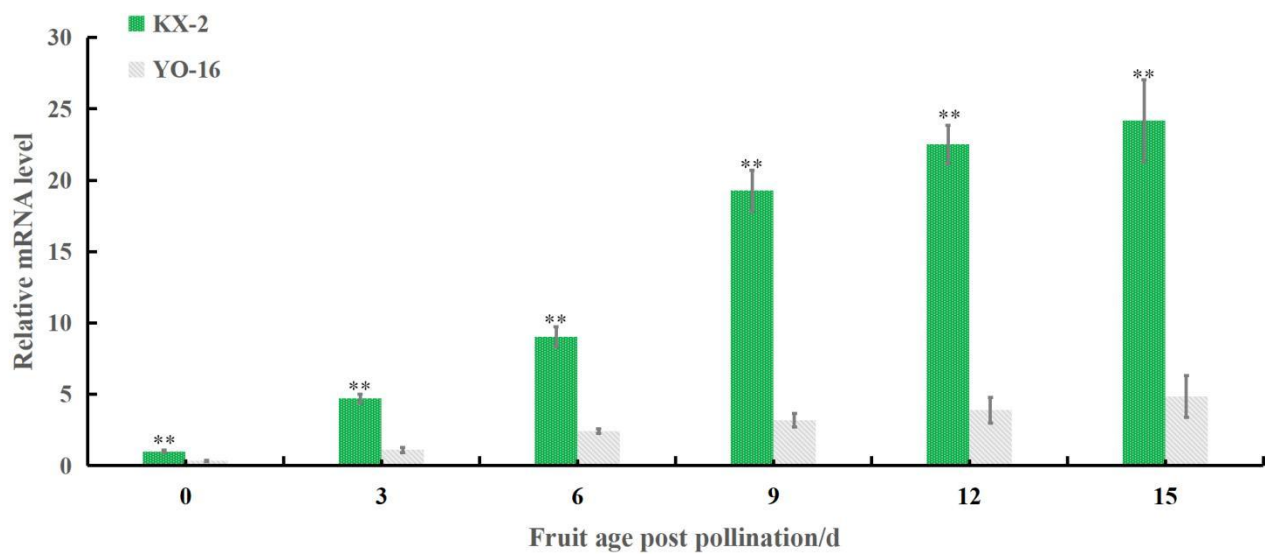
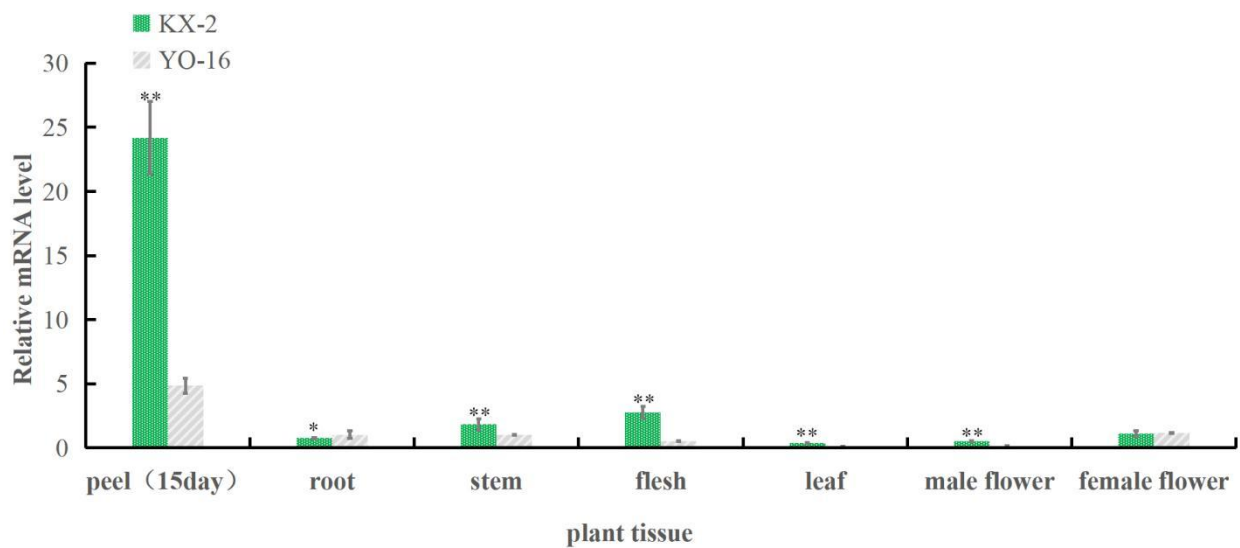
Supplementary Figure 4. Manhattan plot for mapping of wax gourd peel colour across two populations, KX-2 and YO-16.

GX-19_SEQ	ATGGTTGTGACTGCCGACGATTACAGAAGTGGAAAGACTTCCTCAAGGGCTCGAGGGTCTCTCTCTGATAGGGACAGTCGCTCTGCTACCGAGATAAGATCAAAACTTGGAGAAATG	120
GX-71_SEQ	ATGGTTGTGACTGCCGACGATTACAGAAGTGGAAAGACTTCCTCAAGGGCTCGAGGGTCTCTCTCTGATAGGGACAGTCGCTCTGCTACCGAGATAAGATCAAAACTTGGAGAAATG	120
KX-2_SEQ	ATGGTTGTGACTGCCGACGATTACAGAAGTGGAAAGACTTCCTCAAGGGCTCGAGGGTCTCTCTCTGATAGGGACAGTCGCTCTGCTACCGAGATAAGATCAAAACTTGGAGAAATG	120
MY-1_SEQ	ATGGTTGTGACTGCCGACGATTACAGAAGTGGAAAGACTTCCTCAAGGGCTCGAGGGTCTCTCTCTGATAGGGACAGTCGCTCTGCTACCGAGATAAGATCAAAACTTGGAGAAATG	120
YO-16_SEQ	ATGGTTGTGACTGCCGACGATTACAGAAGTGGAAAGACTTCCTCAAGGGCTCGAGGGTCTCTCTCTGATAGGGACAGTCGCTCTGCTACCGAGATAAGATCAAAACTTGGAGAAATG	120
Consensus	atggtttgtactgccgacgattacagaagtggaagacttcctcaagggtcgagggttctctctctgataggacagtcgctctgctacccgagataagatcaaaacttgaggaaatg	
GX-19_SEQ	GAGTAGTGTGTTTTTCTCTGCTGTGATGAGAAGGAAGCTTTGTGCGCAATTTTGAACACACCCGGGAACTTCCATGTTGCAATTTCTGGAGGTGTGTGCAAGAAATACGATGAAGATTTT	240
GX-71_SEQ	GAGTAGTGTGTTTTTCTCTGCTGTGATGAGAAGGAAGCTTTGTGCGCAATTTTGAACACACCCGGGAACTTCCATGTTGCAATTTCTGGAGGTGTGTGCAAGAAATACGATGAAGATTTT	240
KX-2_SEQ	GAGTAGTGTGTTTTTCTCTGCTGTGATGAGAAGGAAGCTTTGTGCGCAATTTTGAACACACCCGGGAACTTCCATGTTGCAATTTCTGGAGGTGTGTGCAAGAAATACGATGAAGATTTT	240
MY-1_SEQ	GAGTAGTGTGTTTTTCTCTGCTGTGATGAGAAGGAAGCTTTGTGCGCAATTTTGAACACACCCGGGAACTTCCATGTTGCAATTTCTGGAGGTGTGTGCAAGAAATACGATGAAGATTTT	240
YO-16_SEQ	GAGTAGTGTGTTTTTCTCTGCTGTGATGAGAAGGAAGCTTTGTGCGCAATTTTGAACACACCCGGGAACTTCCATGTTGCAATTTCTGGAGGTGTGTGCAAGAAATACGATGAAGATTTT	240
Consensus	gagtagtgtgtttttctctgctgtgatgagaaggaagctttgtcgccaattttgaacacacccgggaacttccatgtgtgcaattctggaggtgtgtgcaagaaattacgatgaagatgtt	
GX-19_SEQ	AAGTTACTTGGAACTTCCAAGGACTTGCCTAATAAATGACTTCAGATGTTTCATTGCTTAAGTACATGATGAAGTGCATTGCATTGGTGCAAGTTGAGTTCTTGCTGAARCCACTCTCT	360
GX-71_SEQ	AAGTTACTTGGAACTTCCAAGGACTTGCCTAATAAATGACTTCAGATGTTTCATTGCTTAAGTACATGATGAAGTGCATTGCATTGGTGCAAGTTGAGTTCTTGCTGAARCCACTCTCT	360
KX-2_SEQ	AAGTTACTTGGAACTTCCAAGGACTTGCCTAATAAATGACTTCAGATGTTTCATTGCTTAAGTACATGATGAAGTGCATTGCATTGGTGCAAGTTGAGTTCTTGCTGAARCCACTCTCT	360
MY-1_SEQ	AAGTTACTTGGAACTTCCAAGGACTTGCCTAATAAATGACTTCAGATGTTTCATTGCTTAAGTACATGATGAAGTGCATTGCATTGGTGCAAGTTGAGTTCTTGCTGAARCCACTCTCT	360
YO-16_SEQ	AAGTTACTTGGAACTTCCAAGGACTTGCCTAATAAATGACTTCAGATGTTTCATTGCTTAAGTACATGATGAAGTGCATTGCATTGGTGCAAGTTGAGTTCTTGCTGAARCCACTCTCT	360
Consensus	aagtactctgggaacttccaaggacttgcctaataaataagacttcagatgttctactgtgcttaagtactatgatgaagtgcattgcacttgggtgcagttgagttcttctgtgcaaacactctct	
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GX-71_SEQ	GAAGCAAACTCAGGAATATCTGGCAGCATGTCATTCAACAAGGCAATTTTCAATACCTTCAAGGCTGATGAAGACTCTGTAGCATCTTGTAGCAACTCCAATTAGAGAATGAAACAAAG	480
KX-2_SEQ	GAAGCAAACTCAGGAATATCTGGCAGCATGTCATTCAACAAGGCAATTTTCAATACCTTCAAGGCTGATGAAGACTCTGTAGCATCTTGTAGCAACTCCAATTAGAGAATGAAACAAAG	480
MY-1_SEQ	GAAGCAAACTCAGGAATATCTGGCAGCATGTCATTCAACAAGGCAATTTTCAATACCTTCAAGGCTGATGAAGACTCTGTAGCATCTTGTAGCAACTCCAATTAGAGAATGAAACAAAG	480
YO-16_SEQ	GAAGCAAACTCAGGAATATCTGGCAGCATGTCATTCAACAAGGCAATTTTCAATACCTTCAAGGCTGATGAAGACTCTGTAGCATCTTGTAGCAACTCCAATTAGAGAATGAAACAAAG	480
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KX-2_SEQ	AATGGAGTTTCGGAAGATATGGAAGTTCTTTCTGGATTTCAGGATATTGTGTGGGAGGAACAGAGAAGAGTGATAAGTCTCAACTGATCATGGAAGCATCTAGGCAAGGTAGCTGGGAA	600
MY-1_SEQ	AATGGAGTTTCGGAAGATATGGAAGTTCTTTCTGGATTTCAGGATATTGTGTGGGAGGAACAGAGAAGAGTGATAAGTCTCAACTGATCATGGAAGCATCTAGGCAAGGTAGCTGGGAA	598
YO-16_SEQ	AATGGAGTTTCGGAAGATATGGAAGTTCTTTCTGGATTTCAGGATATTGTGTGGGAGGAACAGAGAAGAGTGATAAGTCTCAACTGATCATGGAAGCATCTAGGCAAGGTAGCTGGGAA	598
Consensus	aatggagtttcggaagatatggaagttctttctggatttcaggatattgtgtgggaggaacagagaagagtgataagttccaactgatcatggaagcatctaggcaaggtagctgggaa	
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GX-71_SEQ	AGCGGAGATCAAAAGACTGTTCAATAGAAACAGATTGCAGGGAACAAGAGTGTTCAGTCTAAATTCGTGAAACTACTTCCACATGATTGGTTTGTGAAGACCCCATTCAGGAGGGCCAA	720
KX-2_SEQ	AGCGGAGATCAAAAGACTGTTCAATAGAAACAGATTGCAGGGAACAAGAGTGTTCAGTCTAAATTCGTGAAACTACTTCCACATGATTGGTTTGTGAAGACCCCATTCAGGAGGGCCAA	720
MY-1_SEQ	AGCGGAGATCAAAAGACTGTTCAATAGAAACAGATTGCAGGGAACAAGAGTGTTCAGTCTAAATTCGTGAAACTACTTCCACATGATTGGTTTGTGAAGACCCCATTCAGGAGGGCCAA	718
YO-16_SEQ	AGCGGAGATCAAAAGACTGTTCAATAGAAACAGATTGCAGGGAACAAGAGTGTTCAGTCTAAATTCGTGAAACTACTTCCACATGATTGGTTTGTGAAGACCCCATTCAGGAGGGCCAA	718
Consensus	agcggagatcaaaagactgttccaatagaaacagattgcagggaacaagagtttcagtcctaatttcgtgaaactacttccacatgatttgggttgtggaagaccocatccaggagggccaa	
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GX-71_SEQ	CCTCAATTATCTGACAAGATAAATCTGGTGTCAAAAGTGATCTTTAGTGTCTGAAACTCAATCCAAGGATCTGATGTGAACATTCTGCTGGACCCCAAGCGAGGAAATCAAGTG	840
KX-2_SEQ	CCTCAATTATCTGACAAGATAAATCTGGTGTCAAAAGTGATCTTTAGTGTCTGAAACTCAATCCAAGGATCTGATGTGAACATTCTGCTGGACCCCAAGCGAGGAAATCAAGTG	840
MY-1_SEQ	CCTCAATTATCTGACAAGATAAATCTGGTGTCAAAAGTGATCTTTAGTGTCTGAAACTCAATCCAAGGATCTGATGTGAACATTCTGCTGGACCCCAAGCGAGGAAATCAAGTG	838
YO-16_SEQ	CCTCAATTATCTGACAAGATAAATCTGGTGTCAAAAGTGATCTTTAGTGTCTGAAACTCAATCCAAGGATCTGATGTGAACATTCTGCTGGACCCCAAGCGAGGAAATCAAGTG	838
Consensus	cttcaattatctgacaagaataaactctgggtgtcaaaagtgtactttagtctgtgaaactccaatccaaggatctgatgtgaaccattctctgtggaccccaagcgaggaaaactaaggtg	
GX-19_SEQ	GACTGGAATCCGACAGCTACATAGAAAATTTGTCAGGCAAGTTGAACAGTTAGGCATAGATCATGCAATTCCTTCCAAAGTACTTGAGCTTATGAAAGTTGAAGGTTTGAACAGGCATAAT	960
GX-71_SEQ	GACTGGAATCCGACAGCTACATAGAAAATTTGTCAGGCAAGTTGAACAGTTAGGCATAGATCATGCAATTCCTTCCAAAGTACTTGAGCTTATGAAAGTTGAAGGTTTGAACAGGCATAAT	960
KX-2_SEQ	GACTGGAATCCGACAGCTACATAGAAAATTTGTCAGGCAAGTTGAACAGTTAGGCATAGATCATGCAATTCCTTCCAAAGTACTTGAGCTTATGAAAGTTGAAGGTTTGAACAGGCATAAT	960
MY-1_SEQ	GACTGGAATCCGACAGCTACATAGAAAATTTGTCAGGCAAGTTGAACAGTTAGGCATAGATCATGCAATTCCTTCCAAAGTACTTGAGCTTATGAAAGTTGAAGGTTTGAACAGGCATAAT	958
YO-16_SEQ	GACTGGAATCCGACAGCTACATAGAAAATTTGTCAGGCAAGTTGAACAGTTAGGCATAGATCATGCAATTCCTTCCAAAGTACTTGAGCTTATGAAAGTTGAAGGTTTGAACAGGCATAAT	958
Consensus	gacttgaatccacagctacatagaaaatttgttcaggcaggttgacagcttaggcagctatgcgaatttccttccaaagtacttgagcttctgaagttgaaagtttgacaaggtgataat	
GX-19_SEQ	GTTCGAACTCATCTCCAGAGTACAGGATGCAAAAGAAACATGTAATGCAGAGAGAGAAATCCAGGTGGTCACATTATCCAGAGATGTACAAATCAAAACCAATCACTTGAACCTATA	1080
GX-71_SEQ	GTTCGAACTCATCTCCAGAGTACAGGATGCAAAAGAAACATGTAATGCAGAGAGAGAAATCCAGGTGGTCACATTATCCAGAGATGTACAAATCAAAACCAATCACTTGAACCTATA	1080
KX-2_SEQ	GTTCGAACTCATCTCCAGAGTACAGGATGCAAAAGAAACATGTAATGCAGAGAGAGAAATCCAGGTGGTCACATTATCCAGAGATGTACAAATCAAAACCAATCACTTGAACCTATA	1080
MY-1_SEQ	GTTCGAACTCATCTCCAGAGTACAGGATGCAAAAGAAACATGTAATGCAGAGAGAGAAATCCAGGTGGTCACATTATCCAGAGATGTACAAATCAAAACCAATCACTTGAACCTATA	1078
YO-16_SEQ	GTTCGAACTCATCTCCAGAGTACAGGATGCAAAAGAAACATGTAATGCAGAGAGAGAAATCCAGGTGGTCACATTATCCAGAGATGTACAAATCAAAACCAATCACTTGAACCTATA	1078
Consensus	gttgcgaactcatctccagagtagcaggtgcaaaagaaacatgtaatgcagagagagaagaaatccaagttggtcacattatccaagatgtacaatacaaaacaaactcacttgaacactata	
GX-19_SEQ	ATGGCTATCCCTTCTTCCTATCAACCAAACTGTGGAATATCAGTGTCTGCTGTTTTCACAACTGGAGACAGACCAATGGCCATCCACCTATTGTGCCACACGTGGGGCCCACTGTTAT	1200
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KX-2_SEQ	ATGGCTATCCCTTCTTCCTATCAACCAAACTGTGGAATATCAGTGTCTGCTGTTTTCACAACTGGAGACAGACCAATGGCCATCCACCTATTGTGCCACACGTGGGGCCCACTGTTAT	1200
MY-1_SEQ	ATGGCTATCCCTTCTTCCTATCAACCAAACTGTGGAATATCAGTGTCTGCTGTTTTCACAACTGGAGACAGACCAATGGCCATCCACCTATTGTGCCACACGTGGGGCCCACTGTTAT	1198
YO-16_SEQ	ATGGCTATCCCTTCTTCCTATCAACCAAACTGTGGAATATCAGTGTCTGCTGTTTTCACAACTGGAGACAGACCAATGGCCATCCACCTATTGTGCCACACGTGGGGCCCACTGTTAT	1198
Consensus	atggctatcccttcttccctatcaaccaaactgtggaatatcagttgtctgtgtttgtccaactggagacagaccaatggccatccacattgtgtccacacgtggggcccaactggttat	
GX-19_SEQ	AGCCATTGGCCGCAACAGGAATTCAGCCATGGAATCTTTATGCAAGGGGTGCGAGCTGATGATGGGGTTGCCCTGTGATGCTGCTTCTCACACTCCATATTTTTCATTTCCTCAGCAT	1320
GX-71_SEQ	AGCCATTGGCCGCAACAGGAATTCAGCCATGGAATCTTTATGCAAGGGGTGCGAGCTGATGATGGGGTTGCCCTGTGATGCTGCTTCTCACACTCCATATTTTTCATTTCCTCAGCAT	1320
KX-2_SEQ	AGCCATTGGCCGCAACAGGAATTCAGCCATGGAATCTTTATGCAAGGGGTGCGAGCTGATGATGGGGTTGCCCTGTGATGCTGCTTCTCACACTCCATATTTTTCATTTCCTCAGCAT	1320
MY-1_SEQ	AGCCATTGGCCGCAACAGGAATTCAGCCATGGAATCTTTATGCAAGGGGTGCGAGCTGATGATGGGGTTGCCCTGTGATGCTGCTTCTCACACTCCATATTTTTCATTTCCTCAGCAT	1318
YO-16_SEQ	AGCCATTGGCCGCAACAGGAATTCAGCCATGGAATCTTTATGCAAGGGGTGCGAGCTGATGATGGGGTTGCCCTGTGATGCTGCTTCTCACACTCCATATTTTTCATTTCCTCAGCAT	1318
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GX-19_SEQ	GCATCAGCATCACAGATATGCAACAGTAATAAGAGCTATGGCATGCTCAGAGTTTATGTGATCTTCAACCAGATGAAGAGGTGGTTGACAAGATTGTGAAGAGGCAATGAGGAAG	1440
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KX-2_SEQ	GCATCAGCATCACAGATATGCAACAGTAATAAGAGCTATGGCATGCTCAGAGTTTATGTGATCTTCAACCAGATGAAGAGGTGGTTGACAAGATTGTGAAGAGGCAATGAGGAAG	1440
MY-1_SEQ	GCATCAGCATCACAGATATGCAACAGTAATAAGAGCTATGGCATGCTCAGAGTTTATGTGATCTTCAACCAGATGAAGAGGTGGTTGACAAGATTGTGAAGAGGCAATGAGGAAG	1438
YO-16_SEQ	GCATCAGCATCACAGATATGCAACAGTAATAAGAGCTATGGCATGCTCAGAGTTTATGTGATCTTCAACCAGATGAAGAGGTGGTTGACAAGATTGTGAAGAGGCAATGAGGAAG	1438
Consensus	gcatcagcatcacagatgatgatacagtaataagagctatggcatgctcagagtttatgtgatcttcaaccagatgaagaggtggttgacaagattgtgaagaggcaatgaggag	
GX-19_SEQ	CCATGGTCACCGCTTCCATTAGGGGCTCAAACTCTCC...TACAGAAAGTGTCTCAGAGAGCTTTTAGGCAAGGAATCTCCACCGTCCCTCCTCAAAATCAAGGGCTCAGAGCTCCCTG	1556
GX-71_SEQ	CCATGGTCACCGCTTCCATTAGGGGCTCAAACTCTCC...TACAGAAAGTGTCTCAGAGAGCTTTTAGGCAAGGAATCTCCACCGTCCCTCCTCAAAATCAAGGGCTCAGAGCTCCCTG	1556
KX-2_SEQ	CCATGGTCACCGCTTCCATTAGGGGCTCAAACTCTCC...TACAGAAAGTGTCTCAGAGAGCTTTTAGGCAAGGAATCTCCACCGTCCCTCCTCAAAATCAAGGGCTCAGAGCTCCCTG	1559
MY-1_SEQ	CCATGGTCACCGCTTCCATTAGGGGCTCAAACTCTCC...TACAGAAAGTGTCTCAGAGAGCTTTTAGGCAAGGAATCTCCACCGTCCCTCCTCAAAATCAAGGGCTCAGAGCTCCCTG	1557
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Supplementary Figure 5. Full-length coding sequence of four parents.

GX-19.seq_Translation	MVCTADDLQEWKDFPFGRLRVLLDRDSRSATEIRSKLEEMEYVVFSCCDEKEALSAINTPGNFHVAILEVCARNYDESFKLLGTSKDLPIIMTSDVHCLSTMMEKIALGAVEFLLKPLS	120
GX-71.seq_Translation	MVCTADDLQEWKDFPFGRLRVLLDRDSRSATEIRSKLEEMEYVVFSCCDEKEALSAINTPGNFHVAILEVCARNYDESFKLLGTSKDLPIIMTSDVHCLSTMMEKIALGAVEFLLKPLS	120
KX-2.seq_Translation	MVCTADDLQEWKDFPFGRLRVLLDRDSRSATEIRSKLEEMEYVVFSCCDEKEALSAINTPGNFHVAILEVCARNYDESFKLLGTSKDLPIIMTSDVHCLSTMMEKIALGAVEFLLKPLS	120
MY-1.seq_Translation	MVCTADDLQEWKDFPFGRLRVLLDRDSRSATEIRSKLEEMEYVVFSCCDEKEALSAINTPGNFHVAILEVCARNYDESFKLLGTSKDLPIIMTSDVHCLSTMMEKIALGAVEFLLKPLS	120
YO-16.seq_Translation	MVCTADDLQEWKDFPFGRLRVLLDRDSRSATEIRSKLEEMEYVVFSCCDEKEALSAINTPGNFHVAILEVCARNYDESFKLLGTSKDLPIIMTSDVHCLSTMMEKIALGAVEFLLKPLS	120
Consensus	mvctaddlqewkdfpfgrlrvllldrdsrsateirskleemeyvfvfscddekealsaintpgnfhvailevcarnydesfkllgtskdipiimtsdvhclstmmezialgavefllkpls	
GX-19.seq_Translation	EDKLRNIWQHVIHKAFSNTSKPDEDSVASIMQLGLENNKNGVSEDMEVLSWICDHWEEPEGSDKSLIMEASRQGSWE SGDQMNCSITDCRDKDVQSRFVETTSIDLVCEDPIQEGQ	240
GX-71.seq_Translation	EDKLRNIWQHVIHKAFSNTSKPDEDSVASIMQLGLENNKNGVSEDMEVLSWICDHWEEPEGSDKSLIMEASRQGSWE SGDQMNCSITDCRDKDVQSRFVETTSIDLVCEDPIQEGQ	240
KX-2.seq_Translation	EDKLRNIWQHVIHKAFSNTSKPDEDSVASIMQLGLENNKNGVSEDMEVLSWICDHWEEPEGSDKSLIMEASRQGSWE SGDQMNCSITDCRDKDVQSRFVETTSIDLVCEDPIQEGQ	240
MY-1.seq_Translation	EDKLRNIWQHVIHKAFSNTSKPDEDSVASIMQLGLENNKNGVSEDMEVLSWICDHWEEPEGSDKSLIMEASRQGSWE SGDQMNCSITDCRDKDVQSRFVETTSIDLVCEDPIQEGQ	183
YO-16.seq_Translation	EDKLRNIWQHVIHKAFSNTSKPDEDSVASIMQLGLENNKNGVSEDMEVLSWICDHWEEPEGSDKSLIMEASRQGSWE SGDQMNCSITDCRDKDVQSRFVETTSIDLVCEDPIQEGQ	183
Consensus	edklrniwqhvihkafntskpdedsvasimqlglennenkngvsedmevlswicdhweggsdkslimeasrqgswe sgdgqmcnsietdcrdkdvqskfvettshdlvcedpiqegq	
GX-19.seq_Translation	PQLSDRNKSGVKSDFLAENSIQGSVDVNHSAQPKARKTRVLDWNPQLHRRFVQAVEQLGIDHAIPSKVLELMKVEGLTRHNVAASHLOKRYMCKKHVMQREENPFWNSHYFERTICTNHLKPI	360
GX-71.seq_Translation	PQLSDRNKSGVKSDFLAENSIQGSVDVNHSAQPKARKTRVLDWNPQLHRRFVQAVEQLGIDHAIPSKVLELMKVEGLTRHNVAASHLOKRYMCKKHVMQREENPFWNSHYFERTICTNHLKPI	360
KX-2.seq_Translation	PQLSDRNKSGVKSDFLAENSIQGSVDVNHSAQPKARKTRVLDWNPQLHRRFVQAVEQLGIDHAIPSKVLELMKVEGLTRHNVAASHLOKRYMCKKHVMQREENPFWNSHYFERTICTNHLKPI	360
MY-1.seq_Translation		183
YO-16.seq_Translation		183
Consensus	pqlsdknksgvksdflaensiqgsdvnhsaagpkarktkvdwnpqlhrrfvgaveqlgidhaipskvlelmkvegltrhnvashlokyrmqkhhvmqreenprwshyprictiqtnhlkpi	
GX-19.seq_Translation	MAYPSSYQPNCGISVSAVPTWRQTNGHPPPIVHTWGPPGYS.HWPCQGIQFQWNSYAGVRADAWGCFVMLPSHTPYFSFPCHASASHDMCTVNSYGMFQSLCDLQPDDEEVVDRIKKEAMR	479
GX-71.seq_Translation	MAYPSSYQPNCGISVSAVPTWRQTNGHPPPIVHTWGPPGYS.HWPCQGIQFQWNSYAGVRADAWGCFVMLPSHTPYFSFPCHASASHDMCTVNSYGMFQSLCDLQPDDEEVVDRIKKEAMR	479
KX-2.seq_Translation	MAYPSSYQPNCGISVSAVPTWRQTNGHPPPIVHTWGPPGYS.HWPCQGIQFQWNSYAGVRADAWGCFVMLPSHTPYFSFPCHASASHDMCTVNSYGMFQSLCDLQPDDEEVVDRIKKEAMR	479
MY-1.seq_Translation		183
YO-16.seq_Translation		183
Consensus	maypssyqpnngisvsav ptwrqtngghppivhtwgppgys hwpq gicqwnsyagvradawgcpvmlpshtpyfsfpqhasashdm tvnksygmfpqslcdlqpdeevvdrikevamr	
GX-19.seq_Translation	KFWSPFLPLGLKSP.TESVLTLSRQGIQSTVFPQINGSRP	517
GX-71.seq_Translation	KFWSPFLPLGLKSP.TESVLTLSRQGIQSTVFPQINGSRP	517
KX-2.seq_Translation	KFWSPFLPLGLKSP.TESVLTLSRQGIQSTVFPQINGSRP	518
MY-1.seq_Translation		183
YO-16.seq_Translation		183
Consensus	kfwspflplglk p tesvltelsrqgistvfpqingsrp	

Supplementary Figure 6. Protein sequences of four parents.



Supplementary Figure 7. Expression analysis of KX-2 and YO-16 in different periods in different tissues. *: $0.01 < P < 0.05$, **: $P < 0.01$.

Species	Accession
<i>Cucumis sativus</i>	AMJ39435.1
<i>Cucumis melo</i>	XP_008465934.1
<i>Momordica charantia</i>	XP_022156603.1
<i>Cucurbita pepo</i> subsp. <i>pepo</i>	XP_023554702.1
<i>Cucurbita moschat</i>	XP_022952808.1
<i>Cucurbita maxima</i>	XP_022971967.1
<i>Citrullus lanatus</i> (Watermelon (97103) v2)	Cla97C09G175170
<i>Benincasa hispida</i>	XP_038877823.1
<i>Arabidopsis thaliana</i>	NP_567548

Supplementary Figure 8. Accession numbers of amino acid sequences downloaded from NCBI