

Table S4. Statistics of genetic variation for the makuwa cultivars and landraces

Variety	N	Na	Ne	I	He	uHe	%P
Cultivars	21.000	0.897	1.111	0.113	0.070	0.072	33.55%
Landraces	26.000	0.700	1.105	0.100	0.064	0.066	23.62%

N, number of individuals; Na, number of alleles; Ne, number of effective alleles; I, Information index; He, expected heterozygosity; uHe, unbiased expected heterozygosity; %P, percentage of polymorphic loci

Table S5. Results of analysis of molecular variance (AMOVA) and F-statistics within the makuwa cultivars and landraces

SV	df	SS	MS	Est. Var.	%	PhiPT
Among Pops	1	493.162	493.162	13.791	7%	0.074
Within Pops	45	7773.647	172.748	172.748	93%	
Total	46	8266.809		186.538	100%	

SV, Source of variation; df, degrees of freedom; SS, sum of squares; MS, mean square; Est. Var., Estimated variance; %, Percentage of variation.

Table S6. Pairwise distance between single nucleotide polymorphisms (SNPs).

Varieties	<i>C. melo</i> L. var. <i>makuwa</i>		<i>C. melo</i> subsp. <i>melo</i>	
	Non-matching nucleotides	Pairwise distance	Non-matching nucleotides	Pairwise distance
<i>C. melo</i> L. var. <i>makuwa</i>	0	0.00%	52	100.00%
<i>C. melo</i> subsp. <i>melo</i>	52	100.00%	0	0.00%
<i>C. melo</i> var. <i>cantalupensis</i>	50	96.15%	2	3.84%
<i>C. melo</i> subsp. <i>melo</i> 56	5	9.61%	49	94.23%
<i>C. melo</i> subsp. <i>melo</i> 54	51	98.07%	6	11.53%