

1 Supplementary Material

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Table S1. Primers used for PCR of *PpIAA* ORFs

Gene ID	Transcript name	Forward primer (5'-3')	Reverse primer (5'-3')
<i>PpIAA1</i>	<i>ppa011843m</i>	ATGGAAGGGTCAGTGAATATGAGA	TCTCATATTCACTGACCCCTCCAT
<i>PpIAA5</i>	<i>ppa011935m</i>	ATGCCAAAGAACGGTTAG	TTATTTAGGATCATTTCATAGTT
<i>PpIAA9</i>	<i>ppa006744m</i>	ATGTACCAACCGCTCTGGTG	GTTCTGTCCTGCACTTCTCCATG
<i>PpIAA11</i>	<i>ppa008953m</i>	ATGGAGGGTGTGGTAGTG	TATCGGCTGGCATCTTG
<i>PpIAA13</i>	<i>ppa010871m</i>	ATGGAGCTCAACTGGTC	ATCACTCTCTTAACCAATTG
<i>PpIAA14</i>	<i>ppa010342m</i>	ATGGGGTTGAAGAGACGGAG	GCTTCTGTCCTGCATTCTCC

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Table S2. Primers used for qRT-PCR of *PpIAA* gene family members

Gene ID	Transcript name	Forward primer (5'-3')	Reverse primer (5'-3')
<i>PpIAA1</i>	<i>ppa011843m</i>	GATCACACAGATGCCCTCC	GCTCCATCGACGCTTACTTTCA
<i>PpIAA2</i>	<i>ppa018535m</i>	CAAAGGCTACCCAGAACTCCTAA	CATCTCCAACCAGCATCCAGTCA
<i>PpIAA3</i>	<i>ppa011755m</i>	AGCTGCCAAAAGATGTGACCAA	CACATAATCCCACAACCCCTCC
<i>PpIAA5</i>	<i>ppa011935m</i>	AAAGCGAAACGAAGAACCAAG	GCTCCATCCATGCTAACCTTGAC
<i>PpIAA7</i>	<i>ppa010698m</i>	GCCAAGATGTTCAGTCCCTCACC	CATCCAATGCCATCCTTATCCTC
<i>PpIAA8</i>	<i>ppa007194m</i>	CACTGTTCTTGTCTCCGTC	ACTTTCACCTCCGAGTATCCA
<i>PpIAA9</i>	<i>ppa006744m</i>	GTATGCCACAATAGCTCGGAA	GAAGCCAAGTCTAAGGTCTG
<i>PpIAA11</i>	<i>ppa008953m</i>	TATAATGGCAGGAGCAACTAGAC	CACAGTACCAAGAAACATCCC
<i>PpIAA12</i>	<i>ppa009545m</i>	TGCTTCTCTGCTGTTGCTGT	CCCGTCTCTTGTCTCATCTTC
<i>PpIAA13</i>	<i>ppa010871m</i>	CTTCAACTGGGTCTCGCTCT	TGGTCAAAGCTCGGTTCTTGT
<i>PpIAA14</i>	<i>ppa010342m</i>	CTCTCTGATGCCCTAGCCAAA	CCAACCAGCATCCAATCTCC
<i>PpIAA15</i>	<i>ppa010303m</i>	AGCCTTAGACCAAATGTTCCC	TCCAGTCCCCATCCTTGTCTTC
<i>PpIAA16</i>	<i>ppa009254m</i>	GCTCCTCACCATCGGTAACT	CCCACAAGCATCCAATCTCC
<i>PpIAA17</i>	<i>ppa011570m</i>	TTCTCCTCTGACCATCCGTAAT	TCCTACAAGCATCCAATCCCCA
<i>PpIAA18</i>	<i>ppa007663m</i>	GTGACAGCTATGAAAACCTCTC	ACATCCCCAACAAAGCATCCT
<i>PpIAA20</i>	<i>ppa011821m</i>	CTGGCTCATCATCTTCTCCTCTC	GCCAGTTATCAGTCTCCCTCTC
<i>PpIAA26</i>	<i>ppa013361m</i>	GAAACTCTCCCTGCCATAGAT	GAGCAGAGTATATCCCCATTGCC
<i>PpIAA27</i>	<i>ppa007893m</i>	TCTCCTCTGCCCTCTCCACA	AGAGACCCAATTCCAAGTCC
<i>PpIAA27'</i>	<i>ppa009134m</i>	AGGCACAGGTTGAGGAT	TTCAGCACCATTAGGAG
<i>PpIAA29</i>	<i>ppa010683m</i>	ATTGGGTCTTCTCTGGCTCTTC	TGTGCTTCCAAACCCAAACC
<i>PpIAA30</i>	<i>ppa020369m</i>	ACAACGCCATCATCATCTTCCC	AATCCGACGATGACCCCT
<i>PpIAA32</i>	<i>ppa023002m</i>	GCAGCCTGAAACTTACCATCC	CTTGAACCTCCCTCTGCCTCT
<i>PpIAA33</i>	<i>ppa018956m</i>	GGACAAGACTCCCTGAAA	GCTACCATCCACGAACAT
<i>PpTEF-2</i>	<i>ppa001368m</i>	GTTGCCTGGTCGGTCTTGA	ATTGAACAGCAACACGCACAA

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Table S3 Analysis of amino acid sequence homology of PpIAA family members in peach.

PpIA A1	PpIA A2	PpIA A3	PpIA A5	PpIA A7	PpIA A8	PpIA A9	PpIA A11	PpIA A12	PpIA A13	PpIA A14	PpIA A15	PpIA A16	PpIA A17	PpIA A18	PpIA A20	PpIA A26	PpIA A27	PpIA A27'	PpIA A29	PpIA A30	PpIA A32	PpIA A33	
PpIAA1	-																						
PpIAA2	0.353	-																					
PpIAA3	0.429	0.392	-																				
PpIAA5	0.600	0.590	0.626	-																			
PpIAA7	0.503	0.514	0.573	0.610	-																		
PpIAA8	0.595	0.560	0.642	0.644	0.589	-																	
PpIAA9	0.575	0.598	0.658	0.623	0.593	0.377	-																
PpIAA11	0.728	0.720	0.752	0.768	0.746	0.769	0.765	-															
PpIAA12	0.726	0.725	0.739	0.721	0.733	0.768	0.778	0.555	-														
PpIAA13	0.785	0.784	0.792	0.789	0.777	0.808	0.816	0.792	0.785	-													
PpIAA14	0.547	0.545	0.615	0.653	0.359	0.545	0.571	0.745	0.753	0.788	-												
PpIAA15	0.643	0.634	0.673	0.659	0.603	0.676	0.671	0.784	0.775	0.806	0.590	-											
PpIAA16	0.519	0.558	0.602	0.630	0.437	0.653	0.660	0.791	0.758	0.788	0.390	0.623	-										
PpIAA17	0.559	0.596	0.583	0.613	0.503	0.569	0.555	0.716	0.688	0.763	0.550	0.581	0.521	-									
PpIAA18	0.750	0.733	0.782	0.768	0.790	0.806	0.827	0.795	0.791	0.806	0.776	0.795	0.805	0.750	-								
PpIAA20	0.774	0.747	0.763	0.756	0.779	0.777	0.750	0.679	0.722	0.749	0.781	0.749	0.790	0.744	0.772	-							
PpIAA26	0.653	0.672	0.672	0.702	0.693	0.730	0.709	0.690	0.709	0.714	0.699	0.730	0.695	0.682	0.481	0.680	-						
PpIAA27	0.569	0.555	0.643	0.667	0.633	0.564	0.564	0.756	0.797	0.822	0.598	0.676	0.684	0.594	0.809	0.770	0.739	-					
PpIAA27'	0.559	0.556	0.652	0.664	0.625	0.525	0.549	0.770	0.792	0.812	0.589	0.700	0.674	0.606	0.795	0.773	0.728	0.287	-				
PpIAA29	0.775	0.777	0.833	0.785	0.781	0.763	0.750	0.803	0.787	0.564	0.779	0.801	0.781	0.751	0.799	0.757	0.744	0.802	0.734	-			
PpIAA30	0.733	0.744	0.712	0.755	0.762	0.751	0.780	0.741	0.730	0.787	0.770	0.763	0.785	0.750	0.792	0.587	0.736	0.765	0.736	0.799	-		
PpIAA32	0.739	0.756	0.778	0.765	0.757	0.777	0.751	0.711	0.704	0.777	0.777	0.779	0.758	0.758	0.794	0.791	0.752	0.749	0.744	0.765	0.783	-	
PpIAA33	0.774	0.807	0.792	0.783	0.775	0.824	0.804	0.790	0.780	0.770	0.781	0.768	0.767	0.824	0.779	0.775	0.804	0.819	0.771	0.792	0.784	0.827	-

* Calculation model: p-distance.

The table shows the percent homology of the amino acid sequences of members of the PpIAA family in peach. Members of this family generally display 50%-80% sequence conservation in peach. The maximum similarity observed was between PpIAA3 and PpIAA29(83.3%), and the minimum similarity observed was between PpIAA27 and PpIAA27'(28%)

