Supplementary

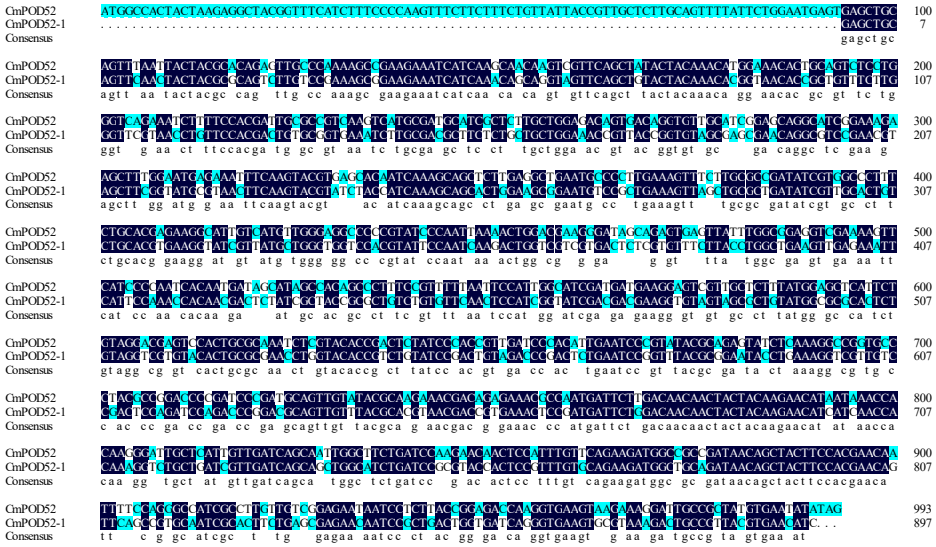


Figure S1. The sequence of *CmPOD52*. Note: CmPOD52: The coding sequence of *CmPOD52*; CmPOD52-1: The codon-optimized sequence of *CmPOD52*.

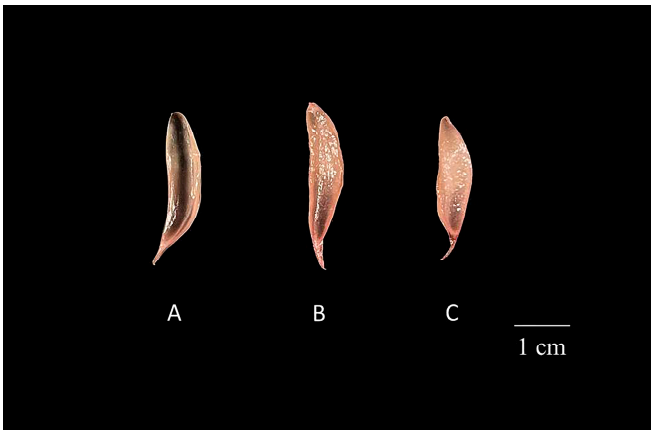


Figure S2. Comparison of juice sac granulation phenotype in 'Sanhong' pomelo and its wild-type (WT). (A): WT; (B), (C): granulated juice sacs of pomelo.

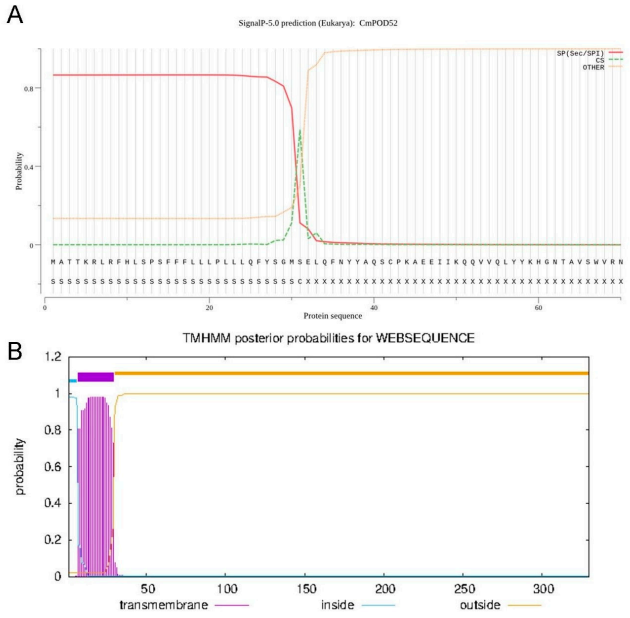
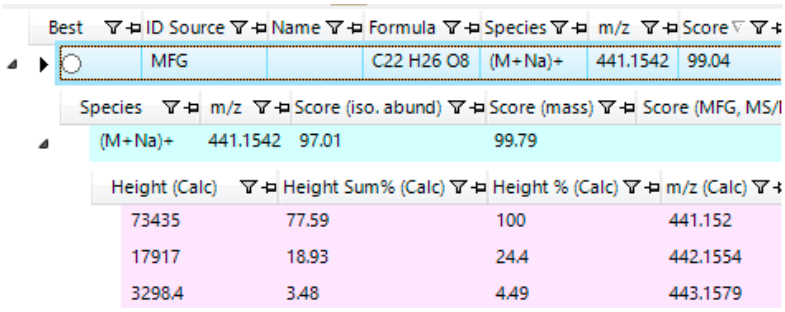


Figure S3. Prediction results of the signal peptide and transmembrane region of *CmPOD52.* (A) Signal peptide prediction results. (B) Transmembrane region prediction results.



Best	ID Source	Name	Formula	Species	m/z	Score
	MFG		C22 H26 O8	(M+Na)+	441.1542	99.04

Species	m/z	Score (iso. abund)	Score (mass)	Score (MFG, MS/I
(M+Na)+	441.1542	97.01	99.79	

Height (Calc)	Height Sum% (Calc)	Height % (Calc)	m/z (Calc)
73435	77.59	100	441.152
17917	18.93	24.4	442.1554
3298.4	3.48	4.49	443.1579

Figure S4. Predicted molecular formula of Sinapyl alcohol dimers.

Table S1. Primers used for qRT-PCR analysis in this study.

Gene Name	Primer	Primer sequences (5'-3')
CmActin	Forward	AGAACTATGAACTGCCTGATGGC
	Reverse	GCTTGGAGCAAGTGCTGTGATT
CmPOD31	Forward	CATCCACAATGCCCCCTCAT
	Reverse	AAAGCTTGCGCCTGTCAATG
CmPOD52	Forward	CTGTAGGACGAGTCCACTGC
	Reverse	TACAACTGCATCGGGATCGG
CmPOD55	Forward	CACAGGCGACAACAACTTGG
	Reverse	AGGTGCTCGGGTTGTTACTG
CmCOMT	Forward	GCCAATGCTGCTGGAGAGCTGTTC
	Reverse	ACCATCTGTTGCCGAGTTGAGCGT
CmCAD	Forward	CACCTTACACTTACACTCTC
	Reverse	CTGGAACCATCGGATAGT

CmHCT	Forward	CCATGTGTGGAGGTCTGCAT
	Reverse	AGTCGTTGTCCATCCGAACC
CmC3H	Forward	CTTACCGCAAAGCATGGGACAAC
	Reverse	ATCTGAAGGCTGGCTATTGG
Cm4CL	Forward	GCTAAGCTCCCTCATGCCAA
	Reverse	ATCTCCCCAGCTTGGTTTCG

Table S2. Primers used for gene cloning in this study.

Gene Name	Primer	Primer sequences (5'-3')
Transient expression vector construction.		
CmPOD52	Forward	gagaacacgggggactctagaATGGATGGCCACTACTAA-GAGGCTACG
	Reverse	cgatcggggaaattcgagctcCTATATATTCACATAGCGG-CAATCC
Subcellular localization vector construction.		
CmPOD52	Forward	acgggggactcttgaccATGGATGGCCACTACTAAGAGGC-TACGG
	Reverse	aagttcttctcctttactagtCTATATATTCACATAGCGGCAATCC
Heterologous expression vector construction.		
CmPOD52	Forward	catggctgatatcggatccGAGCTGCAGTTTAATTACTACGCAC
	Reverse	ggtggtggtggtgctcgagCTATATATTCACATAGCGGCAATCC

Note: The lowercase part is a sequence on the carrier.

Table S3. Gradient elution programs.

Time（min）	V_A（%）	V_B（%）
10.00	40	60
15.00	10	90
20.00	10	90
20.10	70	30
25.00	70	30

V_A: H_2O; V_B: MEOH

Table S4. Analysis of the primary structure of the proteins of the *CmPODs*.

Gene ID	Sequence ID	Number of Amino Acid	Molecular Weight	Theoretical pI	Instability Index	Aliphatic Index	Grand Average of Hydropathicity	subcellular localization
CmPOD1	Cg1g001240.1	297	31873.05	8.57	46.66	77.98	-0.234	5
CmPOD2	Cg1g002980.1	329	36107.94	6.43	42.76	82.71	-0.145	7
CmPOD3	Cg1g004840.1	330	36160.2	8.82	47.21	80.76	-0.222	3

CmPOD4	Cg1g006370.1	329	36159.09	8.51	34.25	80.33	-0.219	3
CmPOD5	Cg1g008060.1	319	34627.63	9.77	28.8	89.06	-0.081	1
CmPOD6	Cg1g008440.1	326	36117.33	5.02	30.71	84.97	-0.124	3
CmPOD7	Cg1g008440.2	256	28250.16	5.12	28.41	86.09	-0.254	1
CmPOD8	Cg1g008750.1	326	35884.14	5.89	32.43	81.44	-0.108	2
CmPOD9	Cg1g009400.1	355	39618.8	8.32	38.54	81.01	-0.488	4
CmPOD10	Cg1g011660.1	249	26662.01	5.21	42.8	89.08	-0.006	1
CmPOD11	Cg1g011710.1	306	32924.14	8.1	43.46	84.87	-0.133	5
CmPOD12	Cg1g011720.1	228	24860.52	8.25	40.45	97.63	0.131	2
CmPOD13	Cg1g014690.1	464	50050.17	4.98	56.53	78.9	-0.145	7
CmPOD14	Cg1g022550.1	297	31605.4	5.84	38.18	81.78	-0.056	1
CmPOD15	Cg1g022560.1	319	34563.12	6.42	33.36	87.18	-0.062	1
CmPOD16	Cg2g001240.1	313	33415.08	4.98	25.49	80.1	-0.249	1
CmPOD17	Cg2g001370.1	350	37475.75	4.52	35.43	87	-0.072	3
CmPOD18	Cg2g001370.2	255	27120.08	4.62	31.68	81.14	-0.197	1
CmPOD19	Cg2g001380.1	351	38240.28	8.95	34.11	85.33	-0.13	7
CmPOD20	Cg2g001390.1	348	37698.57	8.41	36.86	83.02	-0.154	3
CmPOD21	Cg2g001400.1	349	38088.88	6.33	38.65	87.51	-0.137	3
CmPOD22	Cg2g001430.1	349	38006.01	8.76	40.34	84.47	-0.205	3
CmPOD23	Cg2g001440.1	350	37907.56	6.11	34.98	85.89	-0.138	7
CmPOD24	Cg2g001470.1	349	37979.66	5.51	39.58	86.68	-0.137	3
CmPOD25	Cg2g001490.1	277	29198.86	5.36	28.2	90.58	0.043	5
CmPOD26	Cg2g005940.1	297	31772.03	8.09	42.47	77.85	-0.199	1
CmPOD27	Cg2g006540.1	320	34380.86	9.31	32.94	81.44	-0.157	1
CmPOD28	Cg2g008860.1	263	27643.04	8.26	39.75	78.4	-0.143	1
CmPOD29	Cg2g009050.1	1073	116745.18	6.1	39.7	88.18	-0.167	6
CmPOD30	Cg2g010850.1	307	33131.29	4.91	40.68	80.39	-0.107	1
CmPOD31	Cg2g018020.1	325	35635.66	8.86	44.19	88.8	-0.14	3
CmPOD32	Cg2g018030.1	328	36014.36	8.69	31.16	84.48	-0.14	3
CmPOD33	Cg2g036970.1	363	40699.02	5.49	41.09	85.43	-0.356	1
CmPOD34	Cg2g042930.1	354	38902.08	9.1	47.54	87.37	-0.092	1
CmPOD35	Cg2g045100.1	335	37772.51	8.67	42.81	89.34	-0.34	7
CmPOD36	Cg3g005370.1	350	37969.6	5.63	37.04	85.54	-0.133	3
CmPOD37	Cg3g016700.1	436	47330.53	8.59	50.66	77.11	-0.357	1
CmPOD38	Cg3g016700.2	387	42005.31	8.61	51.63	72.51	-0.449	1

CmPOD39	Cg3g017840.1	338	36248.44	5.87	39.33	92.63	-0.014	6
CmPOD40	Cg3g018770.1	347	38090.36	8.55	49.45	88.82	-0.158	3
CmPOD41	Cg3g023260.1	345	37461.73	6.94	38.81	93.54	-0.006	2
CmPOD42	Cg3g024510.1	317	34047.13	9.54	51.61	84.38	-0.09	1
CmPOD43	Cg4g001070.1	350	38037.88	5.25	32.17	80.03	-0.08	6
CmPOD44	Cg4g021490.1	327	36391.42	9.01	35.37	78.75	-0.239	3
CmPOD45	Cg5g004520.1	404	43374.67	9.21	56.75	67.23	-0.383	1
CmPOD46	Cg5g023710.1	345	38397.86	8.41	37.43	81.68	-0.308	2
CmPOD47	Cg5g031940.1	361	39625.21	8.88	34.87	77.01	-0.237	7
CmPOD48	Cg5g031950.1	271	29260.51	4.78	32.97	80.7	-0.311	2
CmPOD49	Cg5g036480.1	338	37000.06	6.99	32.96	83.11	-0.186	3
CmPOD50	Cg5g039000.1	338	36812.3	8.89	46.11	77.66	-0.157	3
CmPOD51	Cg5g039010.2	338	36857.17	8.42	45.38	76.75	-0.203	1
CmPOD52	Cg6g002350.1	330	36949.2	7.22	38.47	90.12	-0.165	3
CmPOD53	Cg6g010260.1	316	34482.37	8.95	37.99	87.69	-0.113	3
CmPOD54	Cg6g023390.1	327	36877.14	8.48	43.46	80.31	-0.265	3
CmPOD55	Cg7g003310.1	319	34232.59	9.28	34.96	78.93	-0.204	3
CmPOD56	Cg7g011760.1	345	37351.39	7.56	32.97	100.41	0.236	2
CmPOD57	Cg7g014170.1	330	36498.34	9.27	34.01	89.88	-0.028	1
CmPOD58	Cg7g015380.1	338	37469.78	5.85	33.44	93.2	-0.093	1
CmPOD59	Cg7g020000.1	364	40321.16	6.54	31.59	90.82	-0.016	7
CmPOD60	Cg8g001710.1	287	31731	6.67	38.54	81.6	-0.404	2
CmPOD61	Cg8g005280.1	326	35948.13	8.3	36.57	86.84	-0.127	1
CmPOD62	Cg8g013780.1	328	35188.78	9.1	30.17	95.43	0.084	1
CmPOD63	Cg9g001000.1	333	36076.67	4.43	42.89	88.77	-0.03	3
CmPOD64	Cg9g002390.1	276	30138.26	6.88	28.05	91.52	-0.032	1
CmPOD65	Cg9g002410.1	319	34782.36	7.55	34.48	87.46	-0.089	1
CmPOD66	Cg9g003710.1	323	35411.26	5.6	36.23	83.59	-0.101	3
CmPOD67	Cg9g003720.1	336	36977.12	6.4	38.78	85.89	-0.084	3
CmPOD68	Cg9g024270.1	323	34606.27	9.56	38.36	79.16	-0.192	1
CmPOD69	Cg9g024320.1	287	31269.16	7.56	35.03	83.24	-0.212	1
CmPOD70	Cg9g026080.1	320	35066.1	6.65	42.25	88.06	-0.056	1
CmPOD71	Cg9g029580.1	360	39807.86	9.29	34.66	101.33	-0.067	3

Digital representation of subcellular localization: 1: Chloroplast; 2: Cytoplasm; 3: extracellular; 4: mitochondrial; 5: nuclear ; 6: plasma membrane; 7: vacuol

Table S5. E-values of *CmPODs* 24

Gene ID	Sequence ID	E-values	Log_{10}(E-value)	- Log_{10}(E-value)
CmPOD1	Cg1g001240.1	5.20E-77	-76.28399666	76.28399666
CmPOD2	Cg1g002980.1	3E-75	-74.52287875	74.52287875
CmPOD3	Cg1g004840.1	1.1E-76	-75.95860731	75.95860731
CmPOD4	Cg1g006370.1	2.6E-71	-70.58502665	70.58502665
CmPOD5	Cg1g008060.1	1.5E-78	-77.82390874	77.82390874
CmPOD6	Cg1g008440.1	8.4E-69	-68.07572071	68.07572071
CmPOD7	Cg1g008440.2	1.8E-56	-55.74472749	55.74472749
CmPOD8	Cg1g008750.1	6.7E-75	-74.1739252	74.1739252
CmPOD9	Cg1g009400.1	9.3E-60	-59.03151705	59.03151705
CmPOD10	Cg1g011660.1	3.6E-56	-55.4436975	55.4436975
CmPOD11	Cg1g011710.1	1.5E-79	-78.82390874	78.82390874
CmPOD12	Cg1g011720.1	8.1E-56	-55.09151498	55.09151498
CmPOD13	Cg1g014690.1	4.1E-60	-59.38721614	59.38721614
CmPOD14	Cg1g022550.1	1.3E-64	-63.88605665	63.88605665
CmPOD15	Cg1g022560.1	1.3E-75	-74.88605665	74.88605665
CmPOD16	Cg2g001240.1	1.5E-69	-68.82390874	68.82390874
CmPOD17	Cg2g001370.1	4.4E-71	-70.35654732	70.35654732
CmPOD18	Cg2g001370.2	1.2E-55	-54.92081875	54.92081875
CmPOD19	Cg2g001380.1	2.3E-72	-71.63827216	71.63827216
CmPOD20	Cg2g001390.1	7E-74	-73.15490196	73.15490196
CmPOD21	Cg2g001400.1	7.3E-71	-70.13667714	70.13667714
CmPOD22	Cg2g001430.1	5.9E-73	-72.22914799	72.22914799
CmPOD23	Cg2g001440.1	1E-70	-70	70
CmPOD24	Cg2g001470.1	6.3E-72	-71.20065945	71.20065945
CmPOD25	Cg2g001490.1	1.5E-70	-69.82390874	69.82390874
CmPOD26	Cg2g005940.1	9.3E-77	-76.03151705	76.03151705
CmPOD27	Cg2g006540.1	1E-79	-79	79
CmPOD28	Cg2g008860.1	2.2E-68	-67.65757732	67.65757732
CmPOD29	Cg2g009050.1	3.6E-57	-56.4436975	56.4436975
CmPOD30	Cg2g010850.1	9.5E-72	-71.02227639	71.02227639
CmPOD31	Cg2g018020.1	3.5E-71	-70.45593196	70.45593196
CmPOD32	Cg2g018030.1	3.4E-74	-73.46852108	73.46852108
CmPOD33	Cg2g036970.1	8.8E-72	-71.05551733	71.05551733
CmPOD34	Cg2g042930.1	1.7E-68	-67.76955108	67.76955108
CmPOD35	Cg2g045100.1	6.1E-61	-60.21467016	60.21467016
CmPOD36	Cg3g005370.1	1E-70	-70	70
CmPOD37	Cg3g016700.1	1.7E-44	-43.76955108	43.76955108
CmPOD38	Cg3g016700.2	1.3E-44	-43.88605665	43.88605665
CmPOD39	Cg3g017840.1	2.1E-63	-62.67778071	62.67778071
CmPOD40	Cg3g018770.1	2.2E-73	-72.65757732	72.65757732

CmPOD41	Cg3g023260.1	6.1E-73	-72.21467016	72.21467016
CmPOD42	Cg3g024510.1	5.4E-75	-74.26760624	74.26760624
CmPOD43	Cg4g001070.1	6.5E-75	-74.18708664	74.18708664
CmPOD44	Cg4g021490.1	3.3E-69	-68.48148606	68.48148606
CmPOD45	Cg5g004520.1	1.7E-65	-64.76955108	64.76955108
CmPOD46	Cg5g023710.1	2.7E-59	-58.56863624	58.56863624
CmPOD47	Cg5g031940.1	2.1E-69	-68.67778071	68.67778071
CmPOD48	Cg5g031950.1	1.4E-65	-64.85387196	64.85387196
CmPOD49	Cg5g036480.1	3.8E-71	-70.4202164	70.4202164
CmPOD50	Cg5g039000.1	1.9E-73	-72.7212464	72.7212464
CmPOD51	Cg5g039010.2	3.5E-71	-70.45593196	70.45593196
CmPOD52	Cg6g002350.1	6E-57	-56.22184875	56.22184875
CmPOD53	Cg6g010260.1	9.5E-78	-77.02227639	77.02227639
CmPOD54	Cg6g023390.1	3.4E-66	-65.46852108	65.46852108
CmPOD55	Cg7g003310.1	9.2E-80	-79.03621217	79.03621217
CmPOD56	Cg7g011760.1	4.7E-66	-65.32790214	65.32790214
CmPOD57	Cg7g014170.1	7.7E-68	-67.11350927	67.11350927
CmPOD58	Cg7g015380.1	1.9E-66	-65.7212464	65.7212464
CmPOD59	Cg7g020000.1	2.2E-65	-64.65757732	64.65757732
CmPOD60	Cg8g001710.1	2.4E-49	-48.61978876	48.61978876
CmPOD61	Cg8g005280.1	5.4E-74	-73.26760624	73.26760624
CmPOD62	Cg8g013780.1	1.8E-58	-57.74472749	57.74472749
CmPOD63	Cg9g001000.1	1E-74	-74	74
CmPOD64	Cg9g002390.1	2.8E-54	-53.55284197	53.55284197
CmPOD65	Cg9g002410.1	4.1E-75	-74.38721614	74.38721614
CmPOD66	Cg9g003710.1	5.5E-71	-70.25963731	70.25963731
CmPOD67	Cg9g003720.1	6.3E-70	-69.20065945	69.20065945
CmPOD68	Cg9g024270.1	5.9E-80	-79.22914799	79.22914799
CmPOD69	Cg9g024320.1	2.9E-75	-74.537602	74.537602
CmPOD70	Cg9g026080.1	3.2E-74	-73.49485002	73.49485002
CmPOD71	Cg9g029580.1	4.5E-72	-71.34678749	71.34678749