

**Table S1 Information of Physicochemical properties of NCED gene family members**

Gene name	Gene ID	Scaff	Scaff rename	Deduced protein		
				Size of aa	MW(kD)	pI
<i>PbNCED1</i>	XM_009356579.2	NW_008988076.1	Scaff2	613	68.37	6.63
<i>PbNCED2</i>	XM_009362625.2	NW_008988119.1	Scaff3	603	66.64	6.45
<i>PbNCED4</i>	XM_009366657.2	NW_008988157.1	Scaff5	583	65.03	5.72
<i>PbNCED5</i>	XM_009366793.1	NW_008988158.1	Scaff6	474	53.92	5.88
<i>PbNCED6</i>	XM_009366794.2	NW_008988158.1	Scaff6	508	57.54	6.40
<i>PbNCED7</i>	XM_009367200.2	NW_008988163.1	Scaff7	601	66.04	7.31
<i>PbNCED8</i>	XM_009367201.2	NW_008988163.1	Scaff7	601	66.12	7.64
<i>PbNCED9</i>	XM_009369180.2	NW_008988186.1	Scaff8	563	62.21	6.68
<i>PbNCED10</i>	XM_009369225.2	NW_008988186.1	Scaff8	615	69.13	5.61
<i>PbNCED11</i>	XM_009369487.2	NW_008988189.1	Scaff9	617	68.67	6.65
<i>PbNCED12</i>	XM_009369488.2	NW_008988189.1	Scaff9	617	68.67	6.65
<i>PbNCED13</i>	XM_009369742.2	NW_008988191.1	Scaff10	615	69.13	5.61
<i>PbNCED14</i>	XM_009374927.1	NW_008988263.1	Scaff11	616	68.38	5.99
<i>PbNCED15</i>	XM_009378252.2	NW_008988325.1	Scaff12	584	65.28	6.10
<i>PbNCED16</i>	XM_018645641.1	NW_008989098.1	Scaff13	517	58.04	5.63
<i>PbNCED17</i>	XM_018646301.1	NW_008989585.1	Scaff14	569	64.34	5.63
<i>PbNCED18</i>	XM_018647118.1	NW_008988075.1	Scaff1	555	62.63	6.16
<i>PbNCED19</i>	XM_018649309.1	NW_008988157.1	Scaff5	583	65.06	5.81

**Table S2 Secondary structure of NCED family proteins**

Gene name	Alpha helix/%	Beta turn/%	Extended strand/%	Random coil/%	Subcellular localization
<i>PbNCED1</i>	17.13	6.36	21.53	54.98	Chloroplast
<i>PbNCED2</i>	15.26	5.80	24.05	54.89	Chloroplast
<i>PbNCED3</i>	17.14	6.49	54.24	22.13	Chloroplast
<i>PbNCED4</i>	14.92	6.35	56.60	22.13	Chloroplast
<i>PbNCED5</i>	13.71	6.54	55.49	24.26	Peroxisome
<i>PbNCED6</i>	12.20	5.31	59.65	22.83	Cytoplasmic
<i>PbNCED7</i>	15.31	5.82	57.07	21.80	Chloroplast
<i>PbNCED8</i>	14.64	5.99	57.24	22.13	Chloroplast
<i>PbNCED9</i>	17.94	6.75	52.22	23.09	Cytoplasmic
<i>PbNCED10</i>	20.00	4.72	54.96	20.33	Chloroplast; Cytoplasmic
<i>PbNCED11</i>	14.91	5.02	58.67	21.39	Chloroplast
<i>PbNCED12</i>	14.91	5.02	58.67	21.39	Chloroplast
<i>PbNCED13</i>	20.00	4.72	54.96	20.33	Chloroplast; Cytoplasmic
<i>PbNCED14</i>	17.69	6.01	54.71	21.59	Chloroplast
<i>PbNCED15</i>	17.64	6.16	54.11	22.09	Chloroplast
<i>PbNCED16</i>	13.54	6.00	56.87	23.60	Mitochondria
<i>PbNCED17</i>	11.25	5.98	60.81	21.97	Cytoplasmic
<i>PbNCED18</i>	20.90	6.31	48.47	24.32	Peroxisome; Cytoplasmic
<i>PbNCED19</i>	15.27	5.66	57.29	21.78	Chloroplast

**Table S3 Analysis of duplication time of Ka/Ks values response of the homologous gene pairs for NCED gene family in pear**

Homologous gene pair	Ka	Ks	Ka/Ks	Duplication time (millions years ago)
PbNCED1 & PbNCED11	0.0394	0.2550	0.1547	84.984
PbNCED1 & PbNCED12	0.0394	0.2550	0.1547	84.984
PbNCED5 & PbNCED18	0.0337	0.1313	0.2566	43.763
PbNCED6 & PbNCED18	0.0349	0.0942	0.3707	31.402
PbNCED4 & PbNCED19	—	—	—	—

**Table S4 Effects of different treatments on concentrations of hormones in sepal and ovary of ‘*Pyrus sinkiangensis* Yu’.**

Time (d)	Treatment	GA <sub>3</sub> (ng•g <sup>-1</sup> )		IAA (ng•g <sup>-1</sup> )		ABA (ng•g <sup>-1</sup> )	
		Sepal	Ovary	Sepal	Ovary	Sepal	Ovary
1	CK	535.98±9.94a	313.25±10.61a	762.70±9.28a	242.13±12.29a	116.68±3.70a	539.29±9.24a
	GA <sub>3</sub>	364.83±12.18b	284.44±7.78b	565.73±9.99b	226.67±10.64a	107.86±7.88a	193.07±6.48b
	PP <sub>333</sub>	532.35±11.36a	298.37±10.00ab	534.09±10.32c	196.57±6.08b	115.70±4.21a	175.40±7.07b
5	CK	505.15±11.36c	639.66±11.38a	764.90±12.36a	260.70±11.45a	189.14±5.89b	616.29±7.89b
	GA <sub>3</sub>	698.20±11.67a	574.27±11.47b	591.54±13.60c	274.40±12.68a	128.98±4.89c	415.75±8.22c
	PP <sub>333</sub>	592.34±6.91b	619.39±12.02a	634.52±12.63b	210.25±7.55b	311.99±4.17a	845.74±7.44a
9	CK	404.82±12.77a	360.43±10.02b	977.15±18.79b	223.88±7.47b	509.78±7.98b	230.99±4.98b
	GA <sub>3</sub>	302.04±11.84b	407.45±6.99a	1127.92±17.94a	280.81±11.48a	312.08±7.47c	174.47±6.24c

PP <sub>333</sub>	231.56±11.62c	239.39±10.64c	680.53±9.99c	277.03±12.29a	927.53±9.38a	552.69±6.29a
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Data are mean ± standard error. Significant differences at P < 0.05 are denoted with different letters.

Table S5 Effects of different treatments on the balance between hormones in sepal and ovary of ‘*Pyrus sinkiangensis* Yu’.

Time(d)	Treatment	GA3/ABA		IAA/ABA	
		Sepal	Ovary	Sepal	Ovary
1	CK	6.546±0.287a	0.449±0.015c	4.601±0.231a	0.581±0.01c
	GA3	5.280±0.479b	1.174±0.016b	3.393±0.139b	1.474±0.009a
	PP333	4.626±0.257a	1.121±0.011a	4.604±0.069b	1.706±0.126b
5	CK	4.046±0.062b	0.423±0.024b	2.672±0.032b	1.038±0.005b
	GA3	4.589±0.069a	0.660±0.017a	5.418±0.115a	1.381±0.002a
	PP333	2.035±0.068c	0.249±0.007c	1.899±0.048c	0.732±0.011c
9	CK	1.917±0.007b	0.969±0.011b	0.794±0.013b	1.560±0.01b
	GA3	3.615±0.029a	1.609±0.009a	0.967±0.015a	2.337±0.044a
	PP333	0.734±0.003c	0.501±0.017c	0.250±0.01c	0.433±0.016c

Data are mean ± standard error. Significant differences at P < 0.05 are denoted with different letters.

**Table S6 Additional file 1 Primer sequences for quantitative real time PCR**

Gene	Forward primer (5'-3')	Reverse primer (5'-3')
<i>PbNCED1</i>	CTACAAGACACCGCCACCTT	CAAGTTCCATTGTTGCGGCA
<i>PbNCED2</i>	CGGAGAGATGATCACGGGTG	TTTCGGACAGCACGCTTTTG
<i>PbNCED3</i>	CCTCGACGGAGCCTACATTC	ATTGGCCTGTAAAGACCCGG
<i>PbNCED4</i>	CTACAGCCCCGTGTTTCCAT	GTCAACTGCGTACCTGGGAA
<i>PbNCED5</i>	TGGGCAATGGGTCTGTCAAA	GGCCTTGGACATTTCTCCA
<i>PbNCED6</i>	CATGCATGACCCTGTACCGA	AAACAACCTTCGTCCCCCTCC
<i>PbNCED7</i>	GCTTGGTAGACAGCTCACGT	GTACTTGAGGTGCGGCTTCT
<i>PbNCED8</i>	CATGGACCCACCGGATTCAA	AGCAATACCCGAACACCTGG
<i>PbNCED10</i>	GGTGTCTGGGGAAGTTGAGG	TCCTGATCCCCAGATGGTGT
<i>PbNCED11</i>	TCAGCCAAGAACGTGACCTC	GGTCCCCTGTTTCGGTGATT
<i>PbNCED12</i>	TCAGCCAAGAACGTGACCTC	GGTCCCCTGTTTCGGTGATT
<i>PbNCED13</i>	GGTGTCTGGGGAAGTTGAGG	TCCTGATCCCCAGATGGTGT
<i>PbNCED18</i>	AGCAATGGTGGATGTCGAGG	AAGCACTCAGGAAGATGGCC
<i>PbNCED19</i>	GCGAGCTGATACATGGCTCT	GAGAGGATATCCGGCTTCGC
<i>Actin</i>	CCATCCAGGCTGTTCTCTC	GCAAGGTCCAGACGAAGG