

*PbCSE1* promotes lignification during stone cell development in  
pear (*Pyrus bretschneideri*) fruit

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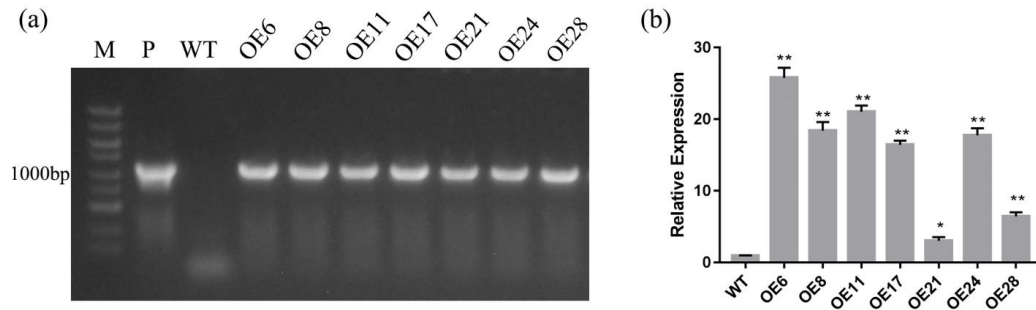
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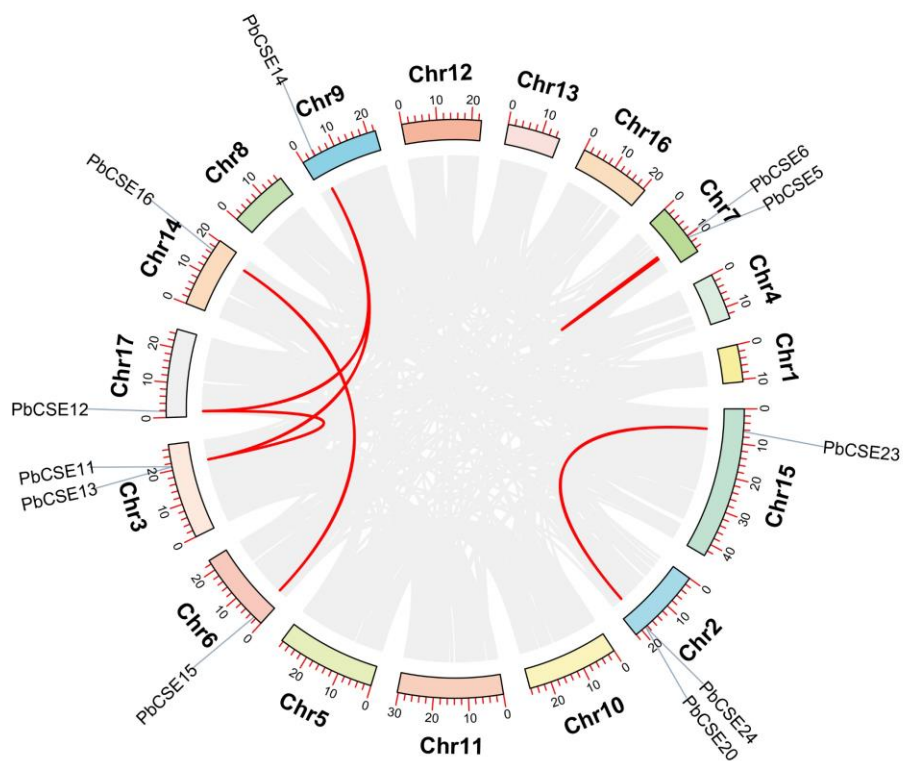
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## Supplementary data



**Figure S1.** Identification of transgenic *Arabidopsis*-positive seedlings. **(a)** T1 generation positive seeding detection of *PbcSE1*. OE = overexpression, M = marker, WT = wild type, P = positive control. This is the grouping of gels cropped from different parts of the same gel. **(b)** The relative expression of *PbcSE1* in different lines of T1 positive plants.



**Figure S2.** Collinear analysis of *PbCSEs*.

No.	Gene name	Gene ID	Position	Stra	Start	End	DNA/bp	CDS/bp
1	<i>PbCSE1</i>	<i>Pbr002315.3</i>	Chr17	+	417048	418317	1270	984
2	<i>PbCSE2</i>	<i>Pbr026316.1</i>	scaffold424.0	-	38552	40101	1550	909
3	<i>PbCSE3</i>	<i>Pbr026363.1</i>	scaffold424.0	+	335722	337270	1549	909
4	<i>PbCSE4</i>	<i>Pbr039057.1</i>	scaffold828.0	-	51217	52209	993	993
5	<i>PbCSE5</i>	<i>Pbr032308.1</i>	Chr7	+	10475405	10478354	960	957
6	<i>PbCSE6</i>	<i>Pbr026463.1</i>	Chr7	-	9780086	9783240	3155	960
7	<i>PbCSE7</i>	<i>Pbr003260.1</i>	Chr11	+	90243	91971	1729	915
8	<i>PbCSE8</i>	<i>Pbr042390.1</i>	Chr3	-	27244839	27246437	1599	990
9	<i>PbCSE9</i>	<i>Pbr038157.1</i>	scaffold797.0	+	161366	165308	3943	957
10	<i>PbCSE10</i>	<i>Pbr003259.1</i>	Chr11	+	78090	79811	1722	915
11	<i>PbCSE11</i>	<i>Pbr013306.1</i>	Chr3	-	21021920	21025814	3895	1284
12	<i>PbCSE12</i>	<i>Pbr034764.1</i>	Chr17	+	1718219	1722403	4185	1059
13	<i>PbCSE13</i>	<i>Pbr013307.2</i>	Chr3	+	21019023	21021277	2255	1281
14	<i>PbCSE14</i>	<i>Pbr032606.2</i>	Chr9	+	3640437	3644791	4355	930
15	<i>PbCSE15</i>	<i>Pbr028331.1</i>	Chr6	+	2620950	2625674	4725	1458
16	<i>PbCSE16</i>	<i>Pbr038811.1</i>	Chr14	+	16893331	16898472	5142	1443
17	<i>PbCSE17</i>	<i>Pbr008780.1</i>	Chr15	-	8768139	8770533	2395	1155
18	<i>PbCSE18</i>	<i>Pbr002316.1</i>	Chr17	+	418552	419030	479	387
19	<i>PbCSE19</i>	<i>Pbr000313.1</i>	Chr5	+	26316512	26317545	1034	966
20	<i>PbCSE20</i>	<i>Pbr041464.1</i>	Chr2	+	18579530	18584136	4607	1599
21	<i>PbCSE21</i>	<i>Pbr027746.2</i>	Chr2	-	16457823	16459791	1969	879
22	<i>PbCSE22</i>	<i>Pbr015620.1</i>	Chr15	+	14831830	14833767	1938	810
23	<i>PbCSE23</i>	<i>Pbr042754.1</i>	Chr15	+	6452652	6454811	2160	873
24	<i>PbCSE24</i>	<i>Pbr041469.2</i>	Chr2	+	18552536	18554396	1861	678

Table S1. Information of 24 *CSE* genes in pear.

Gene name	Primer sequences (5'-3')	Application	Note	
P1300- <i>PbCSE1F</i>	GAGAACACGGGGGACTCTAGAATGGTCATGTACTTCCAATCCC	cDNA	Used in this study	
P1300- <i>PbCSE1R</i>	GCCCTTGCTCACCATGGATCCTCAAATTCCTCCTCCAAGCC	cloning		
<i>PbCSE-1F</i>	ATGGTCATGTACTTCCAATCCC	qRT-PCR		
<i>PbCSE-1R</i>	GGACTTTGCTGGGCTTCAT			
<i>PbCSE-18F</i>	ATGGACTACGTAGAATTCCTTTG			
<i>PbCSE-18R</i>	CCCTATCCGTCGTCCCGTGT			
<i>ATC4H-F</i>	GGGAGAAATCAACGAGGACA		The genes selected for expression analysis have been previously shown to be highly expressed in stems where lignified fibers and vessels are abundant <sup>14</sup> .	
<i>ATC4H-R</i>	CACGTGCGATTCTTCTCAA			
<i>AT4CL-1F</i>	GATGCCGTTAATGCCAAGTT			
<i>AT4CL-1R</i>	ACCGATGAGCAAAGCCTCTA			
<i>ATC3H-1F</i>	TTTCGTTGATGCGTTGCTAA			
<i>ATC3H-1R</i>	CGGTCAAGTCCAACCACTCT			
<i>ATCOMT-F</i>	TAGCCAGTGCTTCCGTTCTT			
<i>ATCOMT-R</i>	CTAGGGTCAGTCCCGTGGA			
<i>ATHCT-F</i>	TTGTCATCCCAGATTCCAT			
<i>ATHCT-R</i>	CCACAACGAAGAGAACACCA			
<i>ATF5H-1F</i>	ATGATGGGGATGTTGTCGAT			
<i>ATF5H-1R</i>	CGTCCATGATGATTGCTTTG			
<i>ATCCR-1F</i>	AGGGGCTCAAATCCTCTCTC			
<i>ATCCR-1R</i>	GCGATGGAATAAAGGCAAGA			
<i>ATCAD-6F</i>	GTCCACTGAGCCACTTTGGT			
<i>ATCAD-6R</i>	CCCAAGCATAAGCAGAGGAG			
<i>ATPAL-1F</i>	GGATTTTCCGGTATCCGATT			
<i>ATPAL-1R</i>	CACTCATCACCTCTGCGAAA			
<i>PbCAD-F</i>	CCTCCTTGTTGGTTGCTGC			The genes selected for expression analysis have been previously shown to be highly expressed in the stems where lignified fibers and vessels are abundant <sup>13</sup> .
<i>PbCAD-R</i>	CCGCCTGGGTGGTTTT			
<i>PbCCOMT-2F</i>	TACCCAAGGGAGCCTGAATC			
<i>PbCCOMT-2R</i>	AGTAGCCAGTGTAGACCCCAATC			
<i>PbC3H-1F</i>	TGATTACTGCGGGTATGGACA			
<i>PbC3H-1R</i>	AGCATTAGTGGTGTGGAGGG			
<i>PbC3H-2F</i>	GAGTCCGACCCGAAAGGT			
<i>PbC3H-2R</i>	ATAGGTGGCCCAACATAGAGG			
<i>Pb4CL-1F</i>	CTTGGACAGGGGTATGGAATG			
<i>Pb4CL-1R</i>	AGCGAAGCACCCGTATCAG			
<i>Pb4CL-2F</i>	CCTACCAATCTCATGCCGTCT			
<i>Pb4CL-2R</i>	GGTTCTGGAAGCAGTAGCTGTG			
<i>PbHCT-2F</i>	GACGCCAAAGAAGGCACTG			
<i>PbHCT-2R</i>	GGGTAGAACGGCACAAGAGC			
<i>PbHCT-4F</i>	GACCCACCTCAGACAACATT			
<i>PbHCT-4R</i>	CGTCAAGACGCTTAGTTGCTCCC			

Table S2. Sequences of the gene-specific primers used in this work.

Code	name	evalue	with	Chr	head	end	chain
			AT1G52760.1				
<i>Ro06_G16613</i>	<i>RoCSE1</i>	0		Ro06	11766242	11767225	+
<i>Ro05_G14831</i>	<i>RoCSE2</i>	1.60E-168		Ro05	8388911	8389882	-
<i>Ro03_G06463</i>	<i>RoCSE3</i>	3.21E-92		Ro03	41371272	41372237	+
<i>Ro02_G01341</i>	<i>RoCSE4</i>	2.13E-64		Ro02	7555107	7562042	+
<i>Ro07_G22034</i>	<i>RoCSE5</i>	3.01E-60		Ro07	33308609	33309595	+
<i>Ro04_G02691</i>	<i>RoCSE6</i>	4.61E-60		Ro04	4776071	4780782	-
<i>Ro03_G26661</i>	<i>RoCSE7</i>	4.83E-60		Ro03	23741694	23743524	-
<i>Ro01_G00832</i>	<i>RoCSE8</i>	1.64E-58		Ro01	2927160	2928092	+
<i>Ro04_G36219</i>	<i>RoCSE9</i>	4.07E-57		Ro04	4772872	4775565	-
<i>Ro07_G18799</i>	<i>RoCSE10</i>	1.24E-56		Ro07	34342592	34356142	+
<i>Ro05_G03655</i>	<i>RoCSE11</i>	1.29E-40		Ro05	424656	429569	-
<i>Ro02_G00679</i>	<i>RoCSE12</i>	5.82E-30		Ro02	2895098	2897978	-
<i>Ro06_G04873</i>	<i>RoCSE13</i>	0.001		Ro06	23003354	23007264	-
<i>Ro04_G02559</i>	<i>RoCSE14</i>	0.002		Ro04	3973434	3976314	+
<i>Ro05_G13809</i>	<i>RoCSE15</i>	0.003		Ro05	13203890	13209783	+
<i>AT1G52760.1</i>	<i>ATCSE1</i>	0		Chr1	19651325	19652743	+
<i>AT1G11090.1</i>	<i>ATCSE2</i>	1.79E-90		Chr1	3702608	3703779	+
<i>AT3G62860.1</i>	<i>ATCSE3</i>	1.79E-67		Chr3	23239446	23242251	-
<i>AT2G47630.1</i>	<i>ATCSE4</i>	1.11E-64		Chr2	19534503	19537014	+
<i>AT5G14980.1</i>	<i>ATCSE5</i>	2.83E-64		Chr5	4849600	4850583	+
<i>AT3G55190.1</i>	<i>ATCSE6</i>	4.96E-63		Chr3	20458007	20459890	+
<i>AT2G39420.1</i>	<i>ATCSE7</i>	9.88E-63		Chr2	16460364	16463061	+
<i>AT3G62860.2</i>	<i>ATCSE8</i>	1.63E-61		Chr3	23239264	23242274	-
<i>AT5G16120.1</i>	<i>ATCSE9</i>	5.78E-59		Chr5	5265939	5267979	+
<i>AT5G16120.3</i>	<i>ATCSE10</i>	5.78E-59		Chr5	5265473	5267954	+
<i>AT2G47630.2</i>	<i>ATCSE11</i>	1.12E-58		Chr2	19534503	19537014	+
<i>AT5G16120.2</i>	<i>ATCSE12</i>	1.21E-58		Chr5	5265633	5267916	+
<i>AT5G16120.4</i>	<i>ATCSE13</i>	1.43E-58		Chr5	5265617	5268078	+
<i>AT2G47630.3</i>	<i>ATCSE14</i>	1.96E-58		Chr2	19535143	19537014	+
<i>AT1G77420.1</i>	<i>ATCSE15</i>	5.47E-58		Chr1	29093499	29095716	+
<i>AT2G39400.1</i>	<i>ATCSE16</i>	3.82E-57		Chr2	16452612	16454801	+
<i>AT5G19290.1</i>	<i>ATCSE17</i>	3.36E-54		Chr5	6494055	6495284	+
<i>AT3G55180.1</i>	<i>ATCSE18</i>	6.53E-52		Chr3	20454903	20456682	+
<i>AT5G11650.1</i>	<i>ATCSE19</i>	6.55E-45		Chr5	3744980	3747125	+
<i>AT1G73480.1</i>	<i>ATCSE20</i>	2.80E-42		Chr1	27628939	27632806	+
<i>AT1G18360.1</i>	<i>ATCSE21</i>	1.26E-37		Chr1	6316695	6319427	-
<i>AT2G39400.2</i>	<i>ATCSE22</i>	1.46E-32		Chr2	16452612	16454801	+
<i>AT5G11650.2</i>	<i>ATCSE23</i>	1.82E-23		Chr5	3744980	3747149	+
<i>AT2G19550.1</i>	<i>ATCSE24</i>	3.02E-07		Chr2	8464533	8465531	-
<i>AT3G47590.1</i>	<i>ATCSE25</i>	4.03E-05		Chr3	17535759	17537530	-
<i>AT5G38220.3</i>	<i>ATCSE26</i>	5.13E-05		Chr5	15268827	15271386	+

<i>AT5G38220.1</i>	<i>ATCSE27</i>	5.13E-05	Chr5	15268868	15271353	+
<i>AT1G13610.1</i>	<i>ATCSE28</i>	0.001	Chr1	4663831	4666017	-
<i>PCP011849.1</i>	<i>PCCSE1</i>	2.05E-90	scaffold00368	36096	37366	+
<i>PCP007413.1</i>	<i>PCCSE2</i>	4.92E-65	scaffold00865	23689	26167	-
<i>PCP015174.1</i>	<i>PCCSE3</i>	4.98E-63	scaffold00530	135736	136870	+
<i>PCP044524.1</i>	<i>PCCSE4</i>	4.47E-62	scaffold00438	134353	137592	+
<i>PCP027588.1</i>	<i>PCCSE5</i>	4.98E-60	scaffold00158	58697	64117	-
<i>PCP033740.1</i>	<i>PCCSE6</i>	3.16E-59	scaffold00007	225900	228311	-
<i>PCP044496.1</i>	<i>PCCSE7</i>	1.64E-54	scaffold00388	47387	51504	+
<i>PCP033156.1</i>	<i>PCCSE8</i>	2.83E-53	scaffold00325	230224	233098	-
<i>PCP045179.1</i>	<i>PCCSE9</i>	3.29E-50	scaffold03738	2222	6678	+
<i>PCP037709.1</i>	<i>PCCSE10</i>	6.25E-46	scaffold138019	234	500	-
<i>PCP027928.1</i>	<i>PCCSE11</i>	1.06E-43	scaffold00498	127037	131727	-
<i>PCP006868.1</i>	<i>PCCSE12</i>	1.33E-42	scaffold00145	203696	206600	+
<i>PCP025117.1</i>	<i>PCCSE13</i>	2.29E-41	scaffold01196	66956	71990	+
<i>PCP030138.1</i>	<i>PCCSE14</i>	6.61E-36	scaffold09319	716	3220	+
<i>PCP040027.1</i>	<i>PCCSE15</i>	5.37E-35	scaffold16147	388	1648	-
<i>PCP020858.1</i>	<i>PCCSE16</i>	8.25E-14	scaffold00014	189066	193379	+
<i>PCP005039.1</i>	<i>PCCSE17</i>	8.75E-05	scaffold00004	783386	787490	+
<i>PCP004967.1</i>	<i>PCCSE18</i>	0.000642	scaffold00004	71986	74453	+
<i>PCP001353.1</i>	<i>PCCSE19</i>	0.001	scaffold02861	5956	8500	+
<i>Pbr002315.3</i>	<i>PbCSE1</i>	4.84E-109	Chr17	417048	418317	+
<i>Pbr026316.1</i>	<i>PbCSE2</i>	6.44E-65	scaffold424.0	38552	40101	-
<i>Pbr026363.1</i>	<i>PbCSE3</i>	6.44E-65	scaffold424.0	335722	337270	+
<i>Pbr039057.1</i>	<i>PbCSE4</i>	4.80E-64	scaffold828.0	51217	52209	-
<i>Pbr032308.1</i>	<i>PbCSE5</i>	5.88E-63	Chr7	10475405	10478354	+
<i>Pbr026463.1</i>	<i>PbCSE6</i>	6.61E-63	Chr7	9780086	9783240	-
<i>Pbr003260.1</i>	<i>PbCSE7</i>	9.80E-63	Chr11	90243	91971	+
<i>Pbr042390.1</i>	<i>PbCSE8</i>	2.43E-62	Chr3	27244839	27246437	-
<i>Pbr038157.1</i>	<i>PbCSE9</i>	2.76E-62	scaffold797.0	161366	165308	+
<i>Pbr003259.1</i>	<i>PbCSE10</i>	7.97E-60	Chr11	78090	79811	+
<i>Pbr013306.1</i>	<i>PbCSE11</i>	7.77E-58	Chr3	21021920	21025814	+
<i>Pbr034764.1</i>	<i>PbCSE12</i>	1.68E-54	Chr17	1718219	1722403	+
<i>Pbr013307.2</i>	<i>PbCSE13</i>	3.03E-52	Chr3	21019023	21021277	+
<i>Pbr032606.2</i>	<i>PbCSE14</i>	2.97E-50	Chr9	3640437	3644791	+
<i>Pbr028331.1</i>	<i>PbCSE15</i>	5.67E-45	Chr6	2620950	2625674	+
<i>Pbr038811.1</i>	<i>PbCSE16</i>	1.34E-43	Chr14	16893331	16898472	+
<i>Pbr008780.1</i>	<i>PbCSE17</i>	2.15E-42	Chr15	8768139	8770533	-
<i>Pbr002316.1</i>	<i>PbCSE18</i>	2.24E-40	Chr17	418552	419030	+
<i>Pbr000313.1</i>	<i>PbCSE19</i>	5.59E-14	Chr5	26316512	26317545	+
<i>Pbr041464.1</i>	<i>PbCSE20</i>	0.000102	Chr2	18579530	18584136	+
<i>Pbr027746.2</i>	<i>PbCSE21</i>	0.000329	Chr2	16457823	16459791	-
<i>Pbr015620.1</i>	<i>PbCSE22</i>	0.003	Chr15	14831830	14833767	+
<i>Pbr042754.1</i>	<i>PbCSE23</i>	0.004	Chr15	6452652	6454811	+



<i>Pbr041469.2</i>	<i>PbCSE24</i>	0.006	Chr2	18552536	18554396	+
<i>FvH4_6g30610.1</i>	<i>FvCSE1</i>	0	Fvb6	23705862	23706851	+
<i>FvH4_3g04590.1</i>	<i>FvCSE2</i>	5.16E-94	Fvb3	2627189	2628148	-
<i>FvH4_2g25730.1</i>	<i>FvCSE3</i>	5.01E-71	Fvb2	20784936	20788630	-
<i>FvH4_1g06460.1</i>	<i>FvCSE4</i>	2.30E-65	Fvb1	3410244	3411131	+
<i>FvH4_3g25850.1</i>	<i>FvCSE5</i>	6.85E-63	Fvb3	18696258	18700846	+
<i>FvH4_7g20970.1</i>	<i>FvCSE6</i>	7.23E-63	Fvb7	16931877	16934612	+
<i>FvH4_7g19610.1</i>	<i>FvCSE7</i>	1.44E-61	Fvb7	16116600	16117586	+
<i>FvH4_4g27270.1</i>	<i>FvCSE8</i>	7.29E-56	Fvb4	28329851	28332764	+
<i>FvH4_4g27260.1</i>	<i>FvCSE9</i>	5.27E-52	Fvb4	28326839	28329151	+
<i>FvH4_2g35400.1</i>	<i>FvCSE10</i>	1.08E-42	Fvb2	26111866	26114552	+
<i>FvH4_5g17790.1</i>	<i>FvCSE11</i>	1.56E-40	Fvb5	10193910	10199657	+
<i>MD10G1300100</i>	<i>MDCSE1</i>	4.88E-93	Chr10	38745228	38746256	+
<i>MD03G1288300</i>	<i>MDCSE2</i>	5.14E-70	Chr03	36701304	36707923	-
<i>MD11G1309800</i>	<i>MDCSE3</i>	6.17E-70	Chr11	42315614	42319994	+
<i>MD07G1174800</i>	<i>MDCSE4</i>	2.34E-64	Chr07	25347166	25348158	+
<i>MD01G1108700</i>	<i>MDCSE5</i>	8.68E-63	Chr01	22157195	22160070	+
<i>MD01G1119700</i>	<i>MDCSE6</i>	6.48E-62	Chr01	23347436	23351576	+
<i>MD07G1188700</i>	<i>MDCSE7</i>	7.29E-61	Chr07	26945274	26948322	+
<i>MD16G1042000</i>	<i>MDCSE8</i>	3.48E-59	Chr16	2958014	2960730	+
<i>MD09G1252900</i>	<i>MDCSE9</i>	3.88E-59	Chr09	32405681	32410472	+
<i>MD16G1041900</i>	<i>MDCSE10</i>	5.16E-57	Chr16	2949505	2957478	+
<i>MD17G1244600</i>	<i>MDCSE11</i>	4.05E-55	Chr17	29299235	29304001	+
<i>MD06G1233800</i>	<i>MDCSE12</i>	6.15E-45	Chr06	36502108	36507270	+
<i>MD14G1240600</i>	<i>MDCSE13</i>	3.57E-44	Chr14	31950828	31955830	+
<i>MD15G1091700</i>	<i>MDCSE14</i>	5.46E-43	Chr15	6363670	6366529	-
<i>MD08G1112500</i>	<i>MDCSE15</i>	9.56E-43	Chr08	9940108	9943040	-
<i>MD05G1322100</i>	<i>MDCSE16</i>	4.92E-36	Chr05	44952957	44953682	+
<i>MD02G1199900</i>	<i>MDCSE17</i>	8.14E-21	Chr02	19673208	19685871	+
<i>MD13G1040700</i>	<i>MDCSE18</i>	1.06E-17	Chr13	2793374	2794551	+
<i>MD07G1114200</i>	<i>MDCSE19</i>	9.30E-09	Chr07	13683967	13684221	-
<i>MD15G1213300</i>	<i>MDCSE20</i>	0.000565	Chr15	17118247	17121661	-
<i>MD02G1086100</i>	<i>MDCSE21</i>	0.000726	Chr02	6755952	6759379	-
<i>Pm023999</i>	<i>PmCSE1</i>	0	Pm7	9815109	9816062	+
<i>Pm009952</i>	<i>PmCSE2</i>	1.17E-92	Pm3	1803044	1804012	-
<i>Pm020027</i>	<i>PmCSE3</i>	9.56E-71	Pm6	814185	817561	-
<i>Pm029072</i>	<i>PmCSE4</i>	1.60E-59	scaffold205	1234119	1236150	-
<i>Pm018723</i>	<i>PmCSE5</i>	1.37E-58	Pm5	20230879	20232937	+
<i>Pm029071</i>	<i>PmCSE6</i>	9.91E-58	scaffold205	1230266	1233383	-
<i>Pm029516</i>	<i>PmCSE7</i>	1.18E-48	scaffold266	59987	68462	+
<i>Pm016617</i>	<i>PmCSE8</i>	1.99E-45	Pm5	3188067	3193518	+
<i>Pm025280</i>	<i>PmCSE9</i>	6.99E-45	Pm7	16912167	16917837	-
<i>Pm005167</i>	<i>PmCSE10</i>	4.19E-44	Pm2	9611910	9614332	+
<i>Pm005170</i>	<i>PmCSE11</i>	8.00E-44	Pm2	9617300	9620160	+

<i>Pm018540</i>	<i>PmCSE12</i>	1.01E-31	Pm5	19077991	19078641	+
<i>Pm009567</i>	<i>PmCSE13</i>	2.78E-16	Pm2	41863844	41865065	-
<i>Prupe.5G109300.1.p</i>	<i>PrCSE1</i>	0	Pp05	11444294	11446331	-
<i>Prupe.4G040700.1.p</i>	<i>PrCSE2</i>	7.19E-93	Pp04	1914947	1915966	-
<i>Prupe.8G261500.1.p</i>	<i>PrCSE3</i>	1.74E-69	Pp08	22077044	22081224	-
<i>Prupe.1G312200.1.p</i>	<i>PrCSE4</i>	1.11E-62	Pp01	30291520	30293997	-
<i>Prupe.3G157400.1.p</i>	<i>PrCSE5</i>	1.39E-60	Pp03	17594861	17600504	+
<i>Prupe.2G213900.1.p</i>	<i>PrCSE6</i>	1.46E-59	Pp02	24528305	24529492	+
<i>Prupe.2G226400.1.p</i>	<i>PrCSE7</i>	4.01E-58	Pp02	25287132	25290401	+
<i>Prupe.1G312100.1.p</i>	<i>PrCSE8</i>	3.71E-56	Pp01	30287567	30291123	-
<i>Prupe.5G238400.1.p</i>	<i>PrCSE9</i>	2.41E-44	Pp05	18014196	18021043	+
<i>Prupe.1G446700.1.p</i>	<i>PrCSE10</i>	3.10E-44	Pp01	37773754	37776527	-
<i>Prupe.3G146300.1.p</i>	<i>PrCSE11</i>	0.000867	Pp03	16001002	16007939	-
<i>Potri.003G059200.1.p</i>	<i>PoCSE1</i>	0	Chr03	8590854	8593871	-
<i>Potri.001G175000.1.p</i>	<i>PoCSE2</i>	0	Chr01	15048240	15050382	+
<i>Potri.011G046500.1.p</i>	<i>PoCSE3</i>	3.16E-88	Chr11	3644103	3645413	-
<i>Potri.014G129000.1.p</i>	<i>PoCSE4</i>	7.99E-69	Chr14	8649670	8654120	+
<i>Potri.002G204200.1.p</i>	<i>PoCSE5</i>	1.33E-67	Chr02	16884483	16888166	+
<i>Potri.017G114800.4.p</i>	<i>PoCSE6</i>	5.13E-63	Chr17	12241178	12246057	+
<i>Potri.017G114800.1.p</i>	<i>PoCSE7</i>	1.90E-62	Chr17	12241178	12246057	+
<i>Potri.010G212200.1.p</i>	<i>PoCSE8</i>	7.32E-62	Chr10	20049814	20052628	-
<i>Potri.014G129000.3.p</i>	<i>PoCSE9</i>	3.58E-61	Chr14	8649670	8654120	+
<i>Potri.001G466700.1.p</i>	<i>PoCSE10</i>	4.96E-60	Chr01	49157554	49158555	-
<i>Potri.008G040000.1.p</i>	<i>PoCSE11</i>	2.03E-58	Chr08	2237952	2239498	+
<i>Potri.008G049000.1.p</i>	<i>PoCSE12</i>	2.87E-58	Chr08	2864262	2867016	+
<i>Potri.010G222300.1.p</i>	<i>PoCSE13</i>	4.67E-57	Chr10	20700091	20701440	-
<i>Potri.010G124000.1.p</i>	<i>PoCSE14</i>	7.03E-57	Chr10	14172963	14177362	+
<i>Potri.018G045800.1.p</i>	<i>PoCSE15</i>	3.48E-45	Chr18	3910067	3913772	+
<i>Potri.006G237200.2.p</i>	<i>PoCSE16</i>	1.21E-43	Chr06	23907564	23911467	-
<i>Potri.012G041800.7.p</i>	<i>PoCSE17</i>	3.00E-43	Chr12	3721495	3727269	-
<i>Potri.012G041800.1.p</i>	<i>PoCSE18</i>	7.11E-43	Chr12	3720119	3727203	-
<i>Potri.015G031900.4.p</i>	<i>PoCSE19</i>	4.79E-41	Chr15	2455509	2461298	+
<i>Potri.011G164300.2.p</i>	<i>PoCSE20</i>	2.82E-34	Chr11	18125120	18125483	-
<i>Potri.012G041800.2.p</i>	<i>PoCSE21</i>	2.19E-17	Chr12	3756797	3763917	-
<i>Potri.004G099700.1.p</i>	<i>PoCSE22</i>	1.29E-10	Chr04	8612851	8612982	-
<i>Potri.004G097300.1.p</i>	<i>PoCSE23</i>	0.000174	Chr04	8612851	8614187	+
<i>Pav_sc0000869.1_g590.1.mk</i>	<i>PaCSE1</i>	5.49E-170	PAV_r1.0chr5	8962318	8963124	-
<i>Pav_sc0000130.1_g1060.1.mk</i>	<i>PaCSE2</i>	5.83E-69	PAV_r1.0chr8	20259161	20263255	-
<i>Pav_sc0000554.1_g2080.1.mk</i>	<i>PaCSE3</i>	3.91E-60	PAV_r1.0chr2	19566233	19568808	+
<i>Pav_sc0000084.1_g340.1.mk</i>	<i>PaCSE4</i>	4.29E-59	PAV_r1.0chr2	18603551	18607387	+
<i>Pav_sc0001051.1_g150.1.mk</i>	<i>PaCSE5</i>	9.19E-57	PAV_r1.0chr1	24617603	24623572	-
<i>Pav_sc0002009.1_g230.1.mk</i>	<i>PaCSE6</i>	7.20E-47	PAV_r1.0chr4	2369295	2369849	-
<i>Pav_sc0000800.1_g640.1.mk</i>	<i>PaCSE7</i>	1.35E-42	PAV_r1.0chr1	32919951	32927557	-
<i>Pav_sc0001488.1_g300.1.mk</i>	<i>PaCSE8</i>	7.40E-41	PAV_r1.0chr3	9157751	9167363	-

<i>Pav_co4058231.1_g010.1.mk</i>	<i>PaCSE9</i>	2.62E-35	PAV_r1.0chr0	1.68E+08	1.68E+08	+
<i>Pav_sc0000103.1_g1170.1.mk</i>	<i>PaCSE10</i>	7.32E-13	PAV_r1.0chr5	16512290	16518121	+

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Table S3. The information about the *CSE* genes in ten species from the family evolution tree.