

Supplementary material

Supplementary Table S1. Distribution of SSR loci in *CpTPS* genes.

subfamily	gene ID	promoter (2000bp upstream of the gene)	gene	2000bp sequence downstream of the gene	Total number of each gene	Total number of each subfamily	average of each subfamily
TPS-a	<i>CpTPS02</i>	0	9	0	9	62	3.44
	<i>CpTPS07</i>	1	0	1	2		
	<i>CpTPS08</i>	1	0	0	1		
	<i>CpTPS14</i>	0	0	0	0		
	<i>CpTPS15</i>	0	0	1	1		
	<i>CpTPS16</i>	0	0	0	0		
	<i>CpTPS20</i>	0	1	0	1		
	<i>CpTPS21</i>	0	2	0	2		
	<i>CpTPS22</i>	0	3	0	3		
	<i>CpTPS23</i>	0	27	0	27		
	<i>CpTPS24</i>	0	0	0	0		
	<i>CpTPS25</i>	0	0	2	2		
	<i>CpTPS39</i>	0	1	0	1		
	<i>CpTPS40</i>	0	0	0	0		
	<i>CpTPS44</i>	0	0	2	2		
	<i>CpTPS48</i>	0	2	0	2		
	<i>CpTPS49</i>	0	2	0	2		
	<i>CpTPS52</i>	0	0	2	2		
	<i>CpTPS01</i>	0	5	0	5		
	<i>CpTPS03</i>	1	5	0	6		
TPS-b	<i>CpTPS04</i>	0	0	0	0	67	2.79
	<i>CpTPS09</i>	0	0	0	0		
	<i>CpTPS17</i>	2	0	0	2		
	<i>CpTPS18</i>	1	0	0	1		
	<i>CpTPS19</i>	0	2	0	2		
	<i>CpTPS26</i>	1	3	0	4		
	<i>CpTPS27</i>	3	1	0	4		
	<i>CpTPS28</i>	1	0	1	2		
	<i>CpTPS29</i>	1	4	0	5		
	<i>CpTPS30</i>	1	1	0	2		
	<i>CpTPS31</i>	1	2	1	4		
	<i>CpTPS32</i>	2	0	0	2		
	<i>CpTPS33</i>	1	5	0	6		
	<i>CpTPS34</i>	1	1	1	3		
	<i>CpTPS36</i>	1	4	0	5		
	<i>CpTPS37</i>	1	0	1	2		
	<i>CpTPS38</i>	1	2	0	3		
	<i>CpTPS43</i>	0	1	1	2		
	<i>CpTPS45</i>	1	0	1	2		
	<i>CpTPS46</i>	2	0	0	2		
TPS-c	<i>CpTPS47</i>	1	1	0	2	4	4
	<i>CpTPS50</i>	1	0	0	1		
	<i>CpTPS10</i>	1	2	1	4		
TPS-e/f	<i>CpTPS05</i>	1	2	0	3	17	3.40
	<i>CpTPS06</i>	3	4	0	7		
	<i>CpTPS11</i>	0	2	1	3		
	<i>CpTPS12</i>	1	1	0	2		
TPS-g	<i>CpTPS13</i>	0	1	0	1	2	0.50
	<i>CpTPS35</i>	0	1	0	1		
	<i>CpTPS41</i>	0	0	0	0		
	<i>CpTPS42</i>	0	0	0	0		
	<i>CpTPS51</i>	0	1	0	1		
	total	32	98	16	146		
	average	0.62	1.88	0.31	2.81		

Supplementary Table S2. Basic information of 33 pairs of SSR primers

Site name	Upstream primer	Downstream primer	Annealing temperature (°C)
CpTPSMS01-4	TGAAATTCTCAATATCGT AACTTC	GGGTTCAAATCCATATGTGCG	57
CpTPSMS01-5	TTGTTTGGCTTAAGATTAGGTTT	TGGACATACTTGGGCTTTCA	57
CpTPSMS02-7	TGATTTGATCCACTGTGGTTAG	TCGGCCGATAAATTTCTTCT	56
CpTPSMS03-1	ACATTGCATGTGCTTCGC	GCAATGATCTTGTACCTTG	58
CpTPSMS03-2	GGCCTTCTTCAGAGATGTGG	CGTTTTGGTTGTTGCATACG	58
CpTPSMS03-4	CCGATTTTTAAACCCCTGTTC	TCTGAGTGGAGAGGGAAGGA	58
CpTPSMS03-5	CAAATTCGGGCTCTTTAAGG	GTTTGATTGCCACTCCACCT	56
CpTPSMS03-6	TGCTTCGAACCTCAATTCAA	TTGCGTTTTTGAAGAGTGTACC	56
CpTPSMS05-1	ATTTCCTGTGGCTGTGGAG	GAAATAGACGTTTTGGAGTTG G	58
CpTPSMS05-2	TTGAACTGCCTTTTCTTTTCG	GCTTGTGTCTCCCACCATCT	59
CpTPSMS05-3	AATTGGGAATGGATGAAACAA	TTGTTGAACATCTCCATTCAA A	55
CpTPSMS06-1	CTCTCTTTCGCCCAACTCTT	GAAAGACAAGGCCTCCATCA	58
CpTPSMS06-3	TCCTCATGTATTGGCTCTGCT	TTTGGCATACCACATCAACG	59
CpTPSMS06-4	TGCATCCACCTGAATGTGTAA	TGTTGGTCAGTTAAGGGTTGG	58
CpTPSMS06-5	TTGCTCCTCAGTCCTTCTCC	TTACAAAGGGGCACACTCC	57
CpTPSMS10-2	GATTTTGTATTGACTTTTTACAA	ACGTCTTCATTAAGTATCAGC AA	58
CpTPSMS10-3	GCAGGTTGGGAATATTTGGA	TTCAATTGCAACGGGACTTT	57
CpTPSMS11-1	GTCATGGGCCGTAGGATATG	GGATGAATTCCAACCCTGAA	56
CpTPSMS11-2	GGCATACCGCCTCCTAACTT	AGGAATATCCACCGGTCACA	56
CpTPSMS12-1	TGACGGTATGCGAGTGGTTA	AAGGAAAAGAAAAATCAAAA GGT	56
CpTPSMS12-2	CCTTTCGACTCATTCGCTCT	GAGCAAGCCATGGAAGTTCT	58
CpTPSMS13	GCCCTTTCGACTCATTCATT	AGATGGTCCAATCGAGCAAG	58
CpTPSMS19-CDs	GAAATGGAGGAGCAAGGAAA	CAGATCGCCTGAGAACCATT	59
CpTPSMS19	TTTGGGACGACAACCTCCTC	GCAAATTCCTTGCATATTCTTT C	56
CpTPSMS23-6	ATGCAGTAAAACCCGTGTGCG	GCCATTGAGCTTCCTTGAAAT	57
CpTPSMS23-21	GACCTGACCCGATGTAACCT	GCTAACAAAACAGTCACCCG A	58
CpTPSMS26-4	AAATGCAATTTAAAGCCATCA	TAGCCATGATTTTCGCAGTG	59
CpTPSMS33-6	TGTGACATTTGCTTGTTCAA	CACCAAAGAAAGGTGTGCAA	59
CpTPSMS38-2	CTCTGGTGCCACCTAGGAAC	AGAGCCAAACGATGACCAAA	59
CpTPSMS43-1	TTGCCTTCATTTTCTCGTTG	GCCCTGCGTTCATGTGTATT	59
CpTPSMS47-1	CCAATCCACAACCCCATATC	ATCCCATATGTTGGGCATGT	59
CpTPSMS47-2	CGACTCGGGCTCTCAAAATA	GTGGAATCCAAGCACTCGTC	60
CpTPSMS52-1	TCAAAAGTTGTGCAACAATCAA	CATCACGACTCCATGACAGG	59

Supplementary Table S3. Percentage of variation explained by the first 3 axes

Axis	1	2	3
%	22.66	12.75	11.10
Cum %	22.66	35.41	46.51