

<i>OsEPSPS</i>	AAATAAAATCCCGCCACCACGGCGCGATGGTAAAAGGGGGACGCTTCTAAACGGGGCCGG	60
<i>TaEPSPS-7A1</i>	-----	
<i>TaEPSPS-7D1</i>	-----	
<i>TaEPSPS-4A1</i>	-----	
<i>OsEPSPS</i>	GCACGGGACGATCGGCCCCGAACCCGGCCCATCTAACCGCTGTAGGCCACCGCCACCA	120
<i>TaEPSPS-7A1</i>	-----	
<i>TaEPSPS-7D1</i>	-----	
<i>TaEPSPS-4A1</i>	-----	
<i>OsEPSPS</i>	ATCCAACCTCCGTACTACGTGAAGCGCTGGATCCGCAACCCGTTAAGCAGTCCACACGACT	180
<i>TaEPSPS-7A1</i>	-----	
<i>TaEPSPS-7D1</i>	-----	
<i>TaEPSPS-4A1</i>	-----	
<i>OsEPSPS</i>	CGACTCGACTCGCGCACTCGCCGTGGTAGGTGGCAACCCTTCTTCCTCCTCTATTTCTTC	240
<i>TaEPSPS-7A1</i>	-----	
<i>TaEPSPS-7D1</i>	-----	
<i>TaEPSPS-4A1</i>	-----	
<i>OsEPSPS</i>	TTCTTCCTCCCTTCTCCGCTCACCACACCAACCGCACCAACCCCAACCCCGCGCGCGCTC	300
<i>TaEPSPS-7A1</i>	-----	
<i>TaEPSPS-7D1</i>	-----	
<i>TaEPSPS-4A1</i>	-----	
<i>OsEPSPS</i>	TCCCTCTCCCTTCCACCAACCCACCCCATCCTCCCGACCTCCACGCCGCCGGAATG	360
<i>TaEPSPS-7A1</i>	-----	
<i>TaEPSPS-7D1</i>	-----	
<i>TaEPSPS-4A1</i>	-----	
	+1	
<i>OsEPSPS</i>	GCGGCGACCATGGCGTCCAACGCCGCGGCTGCGGCGCGGTGTCCCTGGACCAGGCCGTG	420
<i>TaEPSPS-7A1</i>	-----GCAATGGCGATGGCTGCCGCGCGACCGTGGCCGCGTCCGCGTCCAGCGCG	54
<i>TaEPSPS-7D1</i>	-----	
<i>TaEPSPS-4A1</i>	-----	
	 F1.2	
<i>OsEPSPS</i>	GCGGCGTCGGCGGCGTTCTCGTCGCGGAAGCAGCTGCGGCTGCCCCGCCGCGGCGCGGGG	480
<i>TaEPSPS-7A1</i>	GTGTCGCTCGACCGCGCCGCCCGGCCACCCGCGCCGCTGCGGATGCCGGCGGCCCGG	114
<i>TaEPSPS-7D1</i>	-----	
<i>TaEPSPS-4A1</i>	-----	
<i>OsEPSPS</i>	GGGATGCGGGTGCGGGTGC GGCGCGGGGCGGCGGGAGGCGGTGGTGGCGTCCCGG	540
<i>TaEPSPS-7A1</i>	GCGGCCAC---CGCGGGCGGTGCGGCTGTGGGGGCCCCGCGGCGCGGGCGCGCGCG	171
<i>TaEPSPS-7D1</i>	-----	
<i>TaEPSPS-4A1</i>	-----	
<i>OsEPSPS</i>	TCGTCGTCGTCGGTGGCAGCGCCGGCGGCGAAGGCGGAGGAGATCGTGCTCCAGCCCATC	600
<i>TaEPSPS-7A1</i>	ACGTCCGTGGCGGCCCCCGCGCGCCCGGGCGCCGAGGAGGTCTGTGCTGCAGCCCATC	231
<i>TaEPSPS-7D1</i>	-----	
<i>TaEPSPS-4A1</i>	-----	
<i>OsEPSPS</i>	AGGGAGATCTCCGGGGCGGTTCAGCTGCCAGGGTCCAAGTCGCTCTCCAACAGGATCCTC	660
<i>TaEPSPS-7A1</i>	CGCGAGATCTCCGGCGCCGTGCAGCTGCCCGGCTCCAAGTCGCTCTCCAACCGGATCCTC	291
<i>TaEPSPS-7D1</i>	-----	
<i>TaEPSPS-4A1</i>	-----	
<i>OsEPSPS</i>	CTCCTCTCCGCCCTCTCCGAGGTGAGACGCGGATCCCTTCTTGCCTGAATTCCATTT	720
<i>TaEPSPS-7A1</i>	CTCCTCTCCGCCCTCTCCGAGGTGA-----CTCCCCCTCCTCCGCTCTTCCTTTG	343
<i>TaEPSPS-7D1</i>	-----	
<i>TaEPSPS-4A1</i>	-----	

<i>OsEPSPS</i>	CTGGAGATGAGATTTTAGGGGGTTTATTAGGTGAGGTGGCTGTGTTTGTGAAATCCTAGG	780
<i>TaEPSPS-7A1</i>	GGTGATGCGAATTGGGTGCAGAGATGGGATTCTAGGGGGTTTAGCTGACGCACCCTGTCA	403
<i>TaEPSPS-7D1</i>	-----	
<i>TaEPSPS-4A1</i>	-----	
<i>OsEPSPS</i>	AATTATCTCTCAAGTCAATCTAACGATGAGATATAACTGAGGTCTGGTTTTAATCACAC	840
<i>TaEPSPS-7A1</i>	TGCTAGCT-----AGGTGCTCGCGAGATCATGGGGATTTAACTCCCCGACCATAG	454
<i>TaEPSPS-7D1</i>	-----	
<i>TaEPSPS-4A1</i>	-----	
<i>OsEPSPS</i>	ACTCATATAACCAATTTATTGAAACATTTTGGTTTGGCATAAGAAACTGCTTACGAAGGT	900
<i>TaEPSPS-7A1</i>	GTTAACGAGGGCAGGTTGTT-----TGGTAGCCAATTCATGCGTTTGCTTACCAGATC	507
<i>TaEPSPS-7D1</i>	-----	
<i>TaEPSPS-4A1</i>	-----	
<i>OsEPSPS</i>	ATGATATCCTCCTACATGTCAGGCTACTAAATTTTCACGACGGTATGATCCACTCAAAAC	960
<i>TaEPSPS-7A1</i>	ATTGTATTGTGTAGCTTGATTTGGATCAAGATATCGATGCATCAGAATGACCAGGAGAC	567
<i>TaEPSPS-7D1</i>	-----	
<i>TaEPSPS-4A1</i>	-----	
<i>OsEPSPS</i>	AAGTTTCTTAACGAGTCTGGTGAGGTCTGTTATGAAATTTGTGTAACTAAGGCAACTTT	1020
<i>TaEPSPS-7A1</i>	CCTCCTCTAATTTAGGCTACCAAATTGTCTGATGGCTCCTTTATGAAAAGTAGCATGTT	627
<i>TaEPSPS-7D1</i>	-----	
<i>TaEPSPS-4A1</i>	-----	
<i>OsEPSPS</i>	GGAGGTTTCGCACTGTACCAATGTTATGTTTGAACATTTTGCAAGCAGTGCTTTCTCCCA	1080
<i>TaEPSPS-7A1</i>	GTAATGCTGTTATGAACTCTTATTCATGTATCTGCATTTAAATGGTGCAACCTAAGGTC	687
<i>TaEPSPS-7D1</i>	-----	
<i>TaEPSPS-4A1</i>	-----	
<i>OsEPSPS</i>	AAATTATGCAATTTTGAGGCTCCTCTACATCATTATAATTCCCCAATACATTGCTCTTTA	1140
<i>TaEPSPS-7A1</i>	TATTCAC---ATTTTGTGAGACGGTGTGACCAC--AAAAGCCG---ATACTATTTTACA	738
<i>TaEPSPS-7D1</i>	---CAC---ATTCTGTGAGACGACGTCATCATGAAAAAGGCG---ATATTATTTTGA	49
<i>TaEPSPS-4A1</i>	---CAC---ATTTTGTGAGACGGCGTGGCCACTAAAAGACAG---ATATTATTTTAGA	49
<i>OsEPSPS</i>	TTCTTAATAGCTTTGATCGCGAAATTTAACATTTTAATTCTTGAGCTGTTATTTTGTAGC	1200
<i>TaEPSPS-7A1</i>	CGAGAAATC-GTTGAATTGCTATTCGTGGCATTAGTTTTTCATGAGCTATATAGGTACTAA	797
<i>TaEPSPS-7D1</i>	TGAGAAATC-CTTGAATTGCTATTTGTAGCATTTGTTTTCATGAGCTATATAGGTACTAA	108
<i>TaEPSPS-4A1</i>	TGAGAAATC-CTTGAATTGCTATTCG-ACTATT-----	80
Int1_F2-A/B		
<i>OsEPSPS</i>	ATCAGTTTATCATGAGCCATGTTTGGTACTAAATATACAATCCCTTGGGTTTATTTGTTT	1260
<i>TaEPSPS-7A1</i>	ATC----TAGGATCCTCCAGGCTTTATAT-GTTTCCACTGATCAGAAAGCAATATTGCAG	852
<i>TaEPSPS-7D1</i>	ATCAAGGTAGGATCCTTAAGGCTTTATATCGTTTCCACTGATCAGAAAACATATAGAGCAG	168
<i>TaEPSPS-4A1</i>	-----GGTAGGATCCTCCACGCTTTATATGGTTTCCACTGATCAGAAAACAATATTGCAG	135
Int1_F2-D		
<i>OsEPSPS</i>	CCAAGCATGTCAT-TAACTTATCTTAATGTGGACAAGAACTGATGCCTGCTTACATTGC	1319
<i>TaEPSPS-7A1</i>	CATGTCCTGTTCTCTTACTTATTTATAGTAAGATGAGAAATTGGAGCTGGTTTACTTCAC	912
<i>TaEPSPS-7D1</i>	CATGTCCTGTTATCTTATTTATTTATAGTAAGATGAGAAATTGGAGCTGGTTTACTTCAT	228
<i>TaEPSPS-4A1</i>	CATGTCCTGTTCTCTTGCTTATTTATAGTAAGATGAGAAATTGGAGCTGGTTTACTTCAC	195
<i>OsEPSPS</i>	TATTATTTCAAGCGGGTATTGATCCTTTGACATGTGATTGATCATTTTTTTTCTCTGGT	1379
<i>TaEPSPS-7A1</i>	TGTCATCTCCAGC-----TGATCCGTAG-----CTTGTCTCTGGT	947
<i>TaEPSPS-7D1</i>	TGTCATCTCTAGC-----TGATCCGTAG-----CTTGTCTCTGCT	263
<i>TaEPSPS-4A1</i>	TGTCATATCTAGC-----TGATCTGTAG-----CTTGTCTCTGCT	230

Gene	Accession	Sequence	Position
<i>OsEPSPS</i>		TATTAGGGCACACACAGTGGTGGACAACCTTGCTGAACAGTGAGGATGTTCACTACATGCTT	1439
<i>TaEPSPS-7A1</i>		CATTAGGGAACAACGGTGGTGGATAACCTGTTGAACAGTGAGGATGTCCACTACATGCTT	1007
<i>TaEPSPS-7D1</i>		CATTAGGGAACAACGGTGGTGGATAACCTGTTGAACAGCGAGGATGTCCACTACATGCTC	323
<i>TaEPSPS-4A1</i>		CATTAGGGAACAACGGTGGTGGATAACCTGTTGAACAGCGAGGATGTCCACTACATGCTC	290

			F2, F3
<i>OsEPSPS</i>		GAGGCCCTGAAAGCCCTCGGGCTCTCTGTGGAAGCAGATAAAAGTTGCAAAAAGAGCTGTG	1499
<i>TaEPSPS-7A1</i>		GAGGCCCTGGAAGCCCTTGGACTCTCCGTGGAAGCAGATAAAAGTTGCAAAAAGAGCTGTG	1067
<i>TaEPSPS-7D1</i>		GAGGCCCTGGAAGCCCTCGGACTCTCCGTGGAAGCAGATAAAAGTTGCAAAAAGAGCTGTG	383
<i>TaEPSPS-4A1</i>		GAGGCCCTGGAAGCCCTTGGACTCTCCGTGGAAGCAGATAAAAGTTGCAAAAAGAGCTGTG	350

<i>OsEPSPS</i>		GTCGTTGGCTGTGGTGGCAAGTTTCTGTTGAGAAGGATGCGAAAGAGGAAGTGCAACTC	1559
<i>TaEPSPS-7A1</i>		GTTGTTGGCTGTGGCGGCAGGTTCCCGTTCGAAAAGGACGCCAAAGAGGAAGTAAAGCTC	1127
<i>TaEPSPS-7D1</i>		GTTGTTGGCTGTGGCGGCAGGTTCCCGTTCGAAAAGGACGCCAAAGAGGAAGTAAAGCTC	443
<i>TaEPSPS-4A1</i>		GTTGTTGGCTGTGGCGGCAGGTTCCCGTTCGAAAAGGACGCCAAAGAGGAAGTAAAGCTC	410
		** *****	
<i>OsEPSPS</i>		TTCTTGGGGAACGCTGGAAGTGAATGCGACCATTGACAGCAGCCGTGACTGCTGCTGGT	1619
<i>TaEPSPS-7A1</i>		TTCTTGGGTAATGCTGGAAGTGAATGCGGCCACTGACGGCAGCTGTAGTAGCTGCTGGT	1187
<i>TaEPSPS-7D1</i>		TTCTTGGGTAATGCTGGAAGTGAATGCGTCCATTGACGGCAGCTGTAGTAGCTGCTGGT	503
<i>TaEPSPS-4A1</i>		TTCTTGGGTAATGCTGGAAGTGAATGCGGCCATTGACGGCAGCTGTAGTTGCTGCTGGT	470

<i>OsEPSPS</i>		GGAAATGCAACGTATGTTTTTTTTTTTAAATGTTTATGAAAATATGTATGGAATTCATGGG	1679
<i>TaEPSPS-7A1</i>		GGAAATGCAACGTATGTTTTCTTTATCCTAGTGGAATAAGTATGAGATCCATGGGTATG	1247
<i>TaEPSPS-7D1</i>		GGAAATGCAACGTATGTTTTCTTTATCCTAGTTGAAATAAGTATGAGATCCATGGGTATG	563
<i>TaEPSPS-4A1</i>		GGAAATGCAACGTATGTTTTCTTTATCCTAGT-GAAATAAGTATGAGATCCATGGGTATG	529

<i>OsEPSPS</i>		GTATGTTTTATGACCTTTTTCTTTAC-----CATCAGTTATGTGCTTGATGGAG	1728
<i>TaEPSPS-7A1</i>		TTTGAGACTGATCGTTTCTTTTATT--AAAAAAAACCTTCAGTTATGTGCTTGATGGCG	1305
<i>TaEPSPS-7D1</i>		TTTGAGACTGATCGTGTCTTTTATT-AAAAAAAACCTTCAGTTATGTGCTTGATGGAG	622
<i>TaEPSPS-4A1</i>		TTTGAGACTGATCATGTCTTTTATTTAAAAAAAACCTTCAGTTATGTGCTTGATGGAG	589

<i>OsEPSPS</i>		TGCCACGAATGAGGGAGAGACCGATTGGTGACTTGTTGTGCGGTTGAAACAACTTGGTG	1788
<i>TaEPSPS-7A1</i>		TACCAAGAATGAGGGAGCGACCTATTGGTGACTTAGTTGTAGGTTTGCAACAACCTCGGCG	1365
<i>TaEPSPS-7D1</i>		TACCAAGAATGAGGGAGCGACCTATTGGTGACTTAGTTGTAGGTTTGCAACAACCTCGGCG	682
<i>TaEPSPS-4A1</i>		TACCAAGAATGAGGGAGCGACCTATTGGTGACTTGTTGTGCGGTTTGCAACAACCTCGGCG	649
		* * * *	
<i>OsEPSPS</i>		CGGATGTCGACTGTTTCTTGGCACTGAATGCCACCTGTTCTGTGTCAGGGAATTGGAG	1848
<i>TaEPSPS-7A1</i>		CAGATGTCGATTGTTTCTTGGCACAACCTGCCACCTGTCGGTATCAACGGCAAAGGAG	1425
<i>TaEPSPS-7D1</i>		CAGATGCTGATTGTTTCTTGGCACTAAGTGGCACTGTTCTGTATCAATGGCAAAGGAG	742
<i>TaEPSPS-4A1</i>		CAGATGCTGATTGTTTCTTGGCACTAAGTGGCACTGTCGGTATCAATGGCAAAGGAG	709
		* * * *	
<i>OsEPSPS</i>		GACTTCTCTGGTGGCAAGGTTAGTTACTCTAACTGCATCCTTTGTAAGTTCTGTATGCAC	1908
<i>TaEPSPS-7A1</i>		GTCTACCTGGTGGCAAGGTTAGTACTCATCAACTTGCATGTTATCTACTTT-GTGCACA	1484
<i>TaEPSPS-7D1</i>		GGTACCTGGTGGCAAGGTTAGTACTTGTGAAGTGCATGTTATGTACTTTTGTGCACA	802
<i>TaEPSPS-4A1</i>		GGTACCTGGTGGCAAGGTTAGTACTCGTGAATTGCATGTTATGTACTTTTGTGCACA	769
		* * *	
<i>OsEPSPS</i>		CTCAATTCTTTGTCAACCTTCTGCATTTATAAGGAACATTCTATGATGCAATTTCGACCTT	1968
<i>TaEPSPS-7A1</i>		C-----	1485
<i>TaEPSPS-7D1</i>		-----	
<i>TaEPSPS-4A1</i>		-----	
<i>OsEPSPS</i>		ACACTGCACAGTAACTTGAAATGTTTCATGCTTAATCAATATGCCATATTCTCTGCCAAGC	2028
<i>TaEPSPS-7A1</i>		-----TTTGTCTCTGTGCAGAGAAGT---TATTATTATGGCTAGTACGATGTAAT	1533
<i>TaEPSPS-7D1</i>		-----TTCAGTCTCTGTCAAAGAAAATAATATTATTTGGGTAGTACGATGCAAC	854
<i>TaEPSPS-4A1</i>		-----TTCAGTCTCTGTCAAAGAAAATAATATTATTTGGGTAGTACGAT-CAAT	819

<i>OsEPSPS</i>	TCAAGCGAGCAATATTTGTTTGAATTTGGTACCATATTTTGTATATTTGGGCATTCCCTT	2088
<i>TaEPSPS-7A1</i>	GCAACCTTAGACCGCGCACTAAATTTTAAAGAACCAATCAACATTTAATAATTTCAATATG	1593
<i>TaEPSPS-7D1</i>	GCGACCTTACACCGTGCACTAAAGTTTAAAGAACCAATAAACATTGAATAAATTTCAATACT	914
<i>TaEPSPS-4A1</i>	GCGACCTTACACAATGCACCTAAAGTTGAAGAACCAATAAACATTGAATAATTTCAATACT	879

Int3_F1-AB, -A/B, -D

<i>OsEPSPS</i>	TTTGGTCTTGATGTCTTCTTTTGAATTAGCATTTAACTGAATTACACTCAACAGGTTAAG	2148
<i>TaEPSPS-7A1</i>	TGAGTATTGCATGATCTATGATAGCTTGGTGCTAAAGATTGAATGATTTCACAGGTTAAG	1653
<i>TaEPSPS-7D1</i>	TGAGTATTGCGTGATCAATCATAGATTGGCGCTTAACATTGAATAATTTACACAGGTTAAG	974
<i>TaEPSPS-4A1</i>	TGAGTATTGCATGATCAATCATAGATTGACACTTAATATTGAATAATTTACACAGGTTAAG	939

* *****

<i>OsEPSPS</i>	CTCTCTGGTTCCATCAGCAGTCAGTACTTGAGTGCCTTGCTGATGGCTGCTCCTTTGGCC	2208
<i>TaEPSPS-7A1</i>	CTCTCTGGTTCCATTAGCAGTCAATACCTGAGTTCCTTGCTGATGGCTGCTCCTTTGGCT	1713
<i>TaEPSPS-7D1</i>	CTCTCTGGTTCCATTAGCAGTCAATACCTGAGTTCCTTGCTGATGGCTGCTCCTTTGGCT	1034
<i>TaEPSPS-4A1</i>	CTCTCTGGTTCCATTAGCAGTCAATACCTGAGTTCCTTGCTGATGGCTGCTCCTTTGGCT	999

***** ***** ** ***** *****

<i>OsEPSPS</i>	CTTGGGGATGTGGAGATCGAAATCATTGACAACTAATCTCCATTCCCTTACGTTGAAATG	2268
<i>TaEPSPS-7A1</i>	CTTGAGGATGTGAGATTGAAATCATTGATAAACTGATCTCCGTTCCCTTATGTTGAAATG	1773
<i>TaEPSPS-7D1</i>	CTTGAGGATGTGAGATTGAAATCATTGATAAACTGATCTCCGTTCCCTTACGTTGAAATG	1094
<i>TaEPSPS-4A1</i>	CTTGAAGATGTGAGATTGAAATCATTGATAAACTGATCTCCGTTCCCTTACGTTGAAATG	1059

*** ***** ***** ***** ***** ***** ***** *****

<i>OsEPSPS</i>	ACATTGAGATTGATGGAGCGTTTTGGTGTGAAGGCAGAGCATTCTGATAGTTGGGACAGA	2328
<i>TaEPSPS-7A1</i>	ACATTGAAATTGATGGAGCATTTTGGTGTGACTGCGGAGCATTCTGATAGTTGGGACAGA	1833
<i>TaEPSPS-7D1</i>	ACATTGAAATTGATGGAGCGTTTTGGCGTGACTGCGGAGCATTCTGATAGTTGGGACAGA	1154
<i>TaEPSPS-4A1</i>	ACATTGAAATTGATGGAGCGTTTTGGCGTGACTGCGGCGCATTCTGATAGTTGGGACAGA	1119

***** ***** ***** ***** ** * *****

<i>OsEPSPS</i>	TTCTATATTAAGGGAGGGCAGAAGTACAA	2371
<i>TaEPSPS-7A1</i>	TTCTACATTAAGGGAGGACAAAAATACAA	1893
<i>TaEPSPS-7D1</i>	TTCTACATTAAGGGAGGACAAAAGTACAA	1197
<i>TaEPSPS-4A1</i>	TTCTACATCAAGGGAGGACAAAAATACAA	1162

***** ** ***** ** ** *****

<i>OsEPSPS</i>	-----	
<i>TaEPSPS-7A1</i>	AAACTTTTAATTGTTTCATTTCTTCTAATAGTGGAGTACTAATGAAAGATATCAGTTTTC	1953
<i>TaEPSPS-7D1</i>	-----GCTTTACTTCTTCTGATAGTGGAGTACAAAAGCATGATTCTAGTTTTC	1245
<i>TaEPSPS-4A1</i>	-----GCTTTACTTCTTCTGATAGTGGAGTACAAAAGCATGATTCTAATTTTC	1210

<i>OsEPSPS</i>	-----	
<i>TaEPSPS-7A1</i>	AGTTTGCC-AAATATTTACAGACGCAACCCCATTTGAATTATGGGTAAACTAGGAAATAA	2011
<i>TaEPSPS-7D1</i>	AGTCTACCCAAATATTTATAGACGCACCCCATTTGAATTATTGATAAACTAGGAAATAA	1305
<i>TaEPSPS-4A1</i>	TGTCTACCCACATATTTATAGACGCACCCCATTTGAATTATTGATAAACTAGGAAATAA	1270

<i>OsEPSPS</i>	-----	
<i>TaEPSPS-7A1</i>	ATGTTTTACTAAAATATTGACTGCTCAGTAGCTATGAAGGTGCACTGTACTATGAAACC	2071
<i>TaEPSPS-7D1</i>	ATATTGTACAAAATCTGTGCACTGCTCAGTAGCTTTCAAGGCGCACTGTACTAGGAAACC	1365
<i>TaEPSPS-4A1</i>	ATATTGTACAAAATCTGTGCACTGCTCAGTAGCTCTGAAGGCGCACTGTGCTAGGAAACC	1330

<i>OsEPSPS</i>	-----	
<i>TaEPSPS-7A1</i>	AGTGCCTACTGCCTAGGCAATCGGCCCACTGCTTACAATGAATTGTACAGTTACGTTTT	2131
<i>TaEPSPS-7D1</i>	AGTGCCTACTGCCTAGGCAATCGACCTGCTACCTACAATGCATTGCACAGTTCTGTTTT	1425
<i>TaEPSPS-4A1</i>	AGTGTCTACTGCCTAGGCAATCAACCCTTCTACCTACAATGCATTGCACAGTTCTGTTTT	1390

<i>OsEPSPS</i>	-----	
<i>TaEPSPS-7A1</i>	CTGGTACATGGACTTGATCACACCAGAAGTATAATCCATCTTAAAAATGGAATGAAAATA	2191
<i>TaEPSPS-7D1</i>	CTGG-ACATAGACTTGATCACACCAGAAGTATCATCCATCTTAAAATTGGACTGAAAATA	1484
<i>TaEPSPS-4A1</i>	CTGG-ACATATACTTGATCACACCAGAGGTATCATCCATCTTAAAATTGGACTGAAAATA	1449

<i>OsEPSPS</i>	CTTATGGGAAGAAACACCTGAAAGCTGTTGATGTCAACATGAACAAAATGCCTGATGTTG	2938
<i>TaEPSPS-7A1</i>	CATTTGGAAGGAAACACCTAAAAGCTGTTGATGTCAACATGAACAAAATGCCAGATGTCG	2758
<i>TaEPSPS-7D1</i>	CCTTTGGAAGGAAACACTTAAAGGCTGTCGATGTCAACATGAACAAAATGCCTGATGTCG	2171
<i>TaEPSPS-4A1</i>	CCTTTGGAAGGAAACACCTAAAAGCTGTTGATGTCAACATGAACAAAATGCCTGATGTCG	2136
	* * * * *	
<i>OsEPSPS</i>	CCATGACCCTTGCCGTTGTTGCACTCTTCGCTGATGGTCCAACCTGCTATCAGAGATG	2998
<i>TaEPSPS-7A1</i>	CGATGACTCTAGCCGTTGTTGCCCTGTTTGCCGATGGTCCAACCGCTATCAGAGATG	2818
<i>TaEPSPS-7D1</i>	CCATGACTCTTGCCGTTGTTGCCCTCTTTGCCGATGGTCCAACCTGCTATCAGAGATG	2231
<i>TaEPSPS-4A1</i>	CAATGACTCTTGCCGTTGTTGCCCTCTTTGCTGATGGTCCAACCTGCTATCAGAGATG	2196
	* * * * *	
	← Ex6_B-R1	
<i>OsEPSPS</i>	AACATTAAGGCCTATTATACCTGTTCTATCATACTAGCAATTACTGCTTAGCATTGTGAC	3058
<i>TaEPSPS-7A1</i>	TACGTTCTATGGCCTCCCATACCTATCATGT-----GCGTAGCGATTACTCTGTTAG	2870
<i>TaEPSPS-7D1</i>	AACTTTCTATGGCCTTCCATACCAAGCAATCTAGCACGTGCGTCGCGGTTACTCGGT-AG	2290
<i>TaEPSPS-4A1</i>	AACTTTTTATGGCCTCCCATACCTATCATGTGCGTA---GCGTAGCGATTACTCTGTTAG	2253
<i>OsEPSPS</i>	AAAACAAATAACCAAACCTTCTTCAAATAAAGGTTAGAAATATAAGAAGGGTTCGTTTTGT	3118
<i>TaEPSPS-7A1</i>	CATGAGGGAGAGGACAAAGGACTTGAATCACCCTGTTATGTGTTGCTGTTGATTTTGT	2930
<i>TaEPSPS-7D1</i>	CATCAGGGAGGGGATAAAGGACTCGAAATCACCCTGTTATGT-----	2332
<i>TaEPSPS-4A1</i>	CATCAGGGAGGGGACAAAGGACTTGAAAGCACCCTGTTATGTGTTGCTGTTGATTT-GTT	2312
<i>OsEPSPS</i>	GTGGTAAACAGTACTACTGTAGTTTTCAGCTATGAAGTTTGCTGCTGGCAATTTTCTGAAC	3178
<i>TaEPSPS-7A1</i>	TTACATGTTTTGGTCCTGACACTTGTTTGGGAATCA-----	2966
<i>TaEPSPS-7D1</i>	-----CCTGACACTTGTTTC---ATT-----	2349
<i>TaEPSPS-4A1</i>	TTACATGTTTTGGTCCTGACACTTGTTTC---ATT-----	2343
<i>OsEPSPS</i>	GGTTTCAGCTAAATTGCATGTTTGTTCATCATACTTATCCATTGTCTTCCACAGTGGCTT	3238
<i>TaEPSPS-7A1</i>	-----CTCTTCTGCAGTTGCCT	2983
<i>TaEPSPS-7D1</i>	-----CTCTTCTGCAGTTGCCT	2366
<i>TaEPSPS-4A1</i>	-----CTCTGCTGCAGTTGCCT	2360
	* * *	
<i>OsEPSPS</i>	CCTGGAGAGTAAAGGAAACCGAAAGGATGGTTGCAATTCCGACCGAGCTAACAAAGGTAA	3298
<i>TaEPSPS-7A1</i>	CCTGGAGAGTGAAGGAAACTGAAAGAATGGTCGCGATCCGGACCGAGCTGACGAAGGTAA	3043
<i>TaEPSPS-7D1</i>	CCTGGAGAGTGAAGGAAACCGAAAGAATGGTTGCGATCCGGACCGAGCTGACGAAGGTAA	2426
<i>TaEPSPS-4A1</i>	CCTGGAGAGTGAAGGAAACCGAAAGAATGGTCGCGATCCGGACCGAGCTGACGAAGGTAA	2420
	* * * * *	
<i>OsEPSPS</i>	ATTCATTAGGTCCCGTGTCTTTTCATCTTCAAGTAGTTTGTTTCATAAGTTGAATTCTCC	3358
<i>TaEPSPS-7A1</i>	TAATACACA-TGTCTCTGTTCTTATATCTCAGCCTCCTGTTGCACCCCATG-----	3094
<i>TaEPSPS-7D1</i>	TAATACACAATGTCTCTGTTCTTATATCTCAGCTTCCTG-----	2466
<i>TaEPSPS-4A1</i>	TAAACACAATGTCTCTGTTCTTATACCCAGCCTCCTGTTGCACCCCTCGGCACCTC-	2479
<i>OsEPSPS</i>	TTCAATGATGTTTAAATTCATCATCTTCTTTTTTGGTGTGTGCCAGCTGGGAGCATCGG	3418
<i>TaEPSPS-7A1</i>	-----TGCTTACCTCTCCTGTGTCTGTGCCCTATAGCTGGGAGCAACGG	3139
<i>TaEPSPS-7D1</i>	-----ATCTAACCTGTCTGTGCCCTGTGCCCTATAGCTGGGAGCAACGG	2511
<i>TaEPSPS-4A1</i>	-----ATCTGACCTGTCTTTGCA-TGTGCCCTATAGCTGGGAGCAACGG	2523
	* * * * *	
<i>OsEPSPS</i>	TTGAAGAAGGTCCTGACTACTGCATCATCACCCACCGGAGAAGCTGAACATCACGGCAA	3478
<i>TaEPSPS-7A1</i>	TGGAGGAAGGCCCGGACTACTGCATCATCACGCCGCCGAGAAGCTGAACATCACGGCGA	3199
<i>TaEPSPS-7D1</i>	TGGAGGAAGGCCCGGACTACTGCATCATCACGCCGCCAGAGAACTGAACGTACGGCGA	2571
<i>TaEPSPS-4A1</i>	TGGAGGAAGGCCCGGACTACTGCATCATCACGCCACCGGAGAAGCTGAACGTACGGCGA	2583
	* * * * *	
<i>OsEPSPS</i>	TCGACACCTACGATGATCACAGGATGGCCATGGCCTTCTCCCTCGCTGCGCCGAGG	3538
<i>TaEPSPS-7A1</i>	TCGACACCTACGATGACCACCGGATGGCGATGGCCTTCTCCCTGGCGGCCTGTGCTGAGG	3259
<i>TaEPSPS-7D1</i>	TCGATACCTACGATGACCACCGGATGGCGATGGCCTTCTCCCTGGCGGCCTGCGCCGAGG	2631
<i>TaEPSPS-4A1</i>	TCGACACCTACGACGACCACCGGATGGCGATGGCCTTCTCCCTGGCGGCCTGCGCCGAGG	2643
	* * * * *	

F18-D, F18-AB

<i>OsEPSPS</i>	TGCCCCGTGACGATCAGGGACCCTGGTTGCACCCGCAAGACCTTCCCCAACTACTTCGACG	3598
<i>TaEPSPS-7A1</i>	TGCCAGTCACCATCAGGGACCCTGGATGCACCCGAAAGACCTTCCCCAACTACTTCGACG	3319
<i>TaEPSPS-7D1</i>	TGCCAGTCACCATCAGGGATCCGGGGTGCACCAGAAAGACCTTCCCCAATTACTTCGACG	2691
<i>TaEPSPS-4A1</i>	TGCCAGTCACCATCAGGGACCCCGGGTGCACCCGCAAGACCTTCCCCAACTACTTCGATG	2703
	***** ** * ***** ** * ***** * *****	
	← R16-D, R16-AB	
<i>OsEPSPS</i>	TTCTAAGCACTTTCGTCAGGAACTGA	3658
<i>TaEPSPS-7A1</i>	TGCTAAGCACCTTCGTCAGAAGTAG-----	3345
<i>TaEPSPS-7D1</i>	TGCTAAGCACCTTCGTCAGAAGTAGATTGGAGAATCTACGGCG-----	2735
<i>TaEPSPS-4A1</i>	TGCTAAGCACCTTCGTCAGAAGTAG-----	2729
	* ***** ***** *****	
	← R1	

Additional file 3. Nucleotide sequence alignment and primer positions. ClustalW was used to align the genomic DNA sequences of rice *EPSPS* sequence (*OsEPSPS*) [GenBank:AF413081] with *TaEPSPS-7A1* [KP411547], *TaEPSPS-7D1* [KP411548], and *TaEPSPS-4A1* [KP411549] of *T. aestivum* ‘Louise’. Asterisks indicate fully conserved nucleotides. Plus one (+1) represents the translation start codons of *TaEPSPS-7A1* and *OsEPSPS*. Exon sequences are highlighted in yellow. Labeled arrows indicate the positions of important primers.