

Supplementary Figure 2. Alignment of mRNA sequences of TSP2 and sTSP2. Red and green colored letters denote the different exons of TSP2.

Alignment of: TSP2 with sTSP2. Similarity : 3045/5898 (51.63 %)

TSP2	1	AAAAGTGAGTCCCTGCCTTCCCTCTCTCCGTCTGGCTCCTCCCAGGCCTGTCTGGCAGGG	60
sTSP2	1	-----	0
TSP2	61	GCCGGGGTGCAGGAGGAGAGACGGCATCCAGTACAGAGGGGCTGGACTTGGACCCCTGC	120
sTSP2	1	-----	0
TSP2	121	AGCAGCCCTGCACAGGAGAAGCGGCATATAAAGCCGCGCTGCCCGGAGCCGCTCGGCCA	180
sTSP2	1	-----	0
TSP2	181	CGTCCACCGGAGCATCTGCACATGCAGGGCCGGTCTCTCGCTCCAGCAGAGCCTGCGCCT	240
sTSP2	1	-----	0
TSP2	241	TTCTGACTCGGTCCGGAACACTGAAACCAGTCATCACTGCATCTTTTGGCAAACCAGGA	300
sTSP2	1	-----	0
TSP2	301	GCTCAGCTGCAGGAGGCAGGATGGTCTGGAGGCTGGTCTCTGGCTCTGTGGGTGTGGC	360
sTSP2	1	-----	0
TSP2	361	CAGCACGCAAGCTGGTCACCAGGACAAAGACACGACCTTCGACCTTTTCAGTATCAGCA	420
sTSP2	1	-----	0
TSP2	421	ACATCAACCGCAAGACCATTTGGCGCCAAGCAGTTCGCGGGCCGACCCCGGCGTGCCGG	480
sTSP2	1	-----	0
TSP2	481	CTTACCGCTTCGTGCGCTTTGACTACATCCCACCGGTGAACGCAGATGACCTCAGCAAGA	540
sTSP2	1	-----	0
TSP2	541	TCACCAAGATCATGCGGCAGAAGGAGGGCTTCTTCTCACGGCCAGCTCAAGCAGGACG	600
sTSP2	1	-----	0
TSP2	601	GCAAGTCCAGGGGCACGCTGTTGGCTCTGGAGGGCCCGGTCTCTCCAGAGGCAGTTCG	660
sTSP2	1	-----	0
TSP2	661	AGATCGTCTCCAACGGCCCCGCGGACACGCTGGATCTCACCTACTGGATTGACGGCACCC	720
sTSP2	1	-----	0
TSP2	721	GGCATGTGGTCTCCCTGGAGGACGTCGGCCTGGCTGACTCGCAGTGGAAGAACGTACCG	780
sTSP2	1	-----	0
TSP2	781	TGCAGGTGGCTGGCGAGACCTACAGCTTGCACGTGGGCTGCGACCTCATAGACAGCTTCG	840
sTSP2	1	-----	0
TSP2	841	CTCTGGACGAGCCCTTCTACGAGCACCTGCAGGCGAAAAGAGCCGGATGTACGTGGCCA	900
sTSP2	1	-----	0
TSP2	901	AAGGCTCTGCCAGAGAGAGTCACTTCAGGGGTTTGCTTCAGAACGTCCACCTAGTGTTCG	960
sTSP2	1	-----	0
TSP2	961	AAACTCTGTGGAAGATATTCTAAGCAAGAAGGTTGCCAGCAAGGCCAGGAGCTGAGA	1020
sTSP2	1	-----	0
TSP2	1021	TCAACGCCATCAGTGAGAACACAGAGACGCTGCGCCTGGGTCCGCATGTACCACCGAGT	1080
sTSP2	1	-----	0
TSP2	1081	ACGTGGGCCCCAGCTCGGAGAGAGGCCGAGGTGTGCGAACGCTCGTGCAGGAGCTGG	1140
sTSP2	1	-----	0
TSP2	1141	GAAACATGGTCCAGGAGCTCTCGGGGCTCCACGTCTCGTGAACCAGCTCAGCGAGAACC	1200
sTSP2	1	-----	0
TSP2	1201	TCAAGAGAGTGTGCAATGATAACCAGTTTCTCTGGGAGCTCATTGGTGGCCCTCCTAAGA	1260
sTSP2	1	-----	0
TSP2	1261	CAAGGAACATGTCACTTGCTGGCAGGATGGCCGGTTCTTTGCGGAAAATGAAACGTGGG	1320
sTSP2	1	-----	0

TSP2	1321	TGGTGGACAGCTGCACCACGTGTACCTGCAAGAAATTTAAACCAATTTGCCACCAAAATCA	1380
sTSP2	1	-----	0
TSP2	1381	CCTGCCCCGCTGCAACCTGCGCCAGTCCATCCTTTGTGGAAGGCGAATGCTGCCCTTCCT	1440
sTSP2	1	-----	0
TSP2	1441	GCCTCCACTCGGTGGACGGTGAGGAGGCTGGTCTCCGTGGGCAGAGTGACCCAGTGCT	1500
sTSP2	1	-----	0
TSP2	1501	CCGTGACGTGTGGCTCTGGGACCCAGCAGAGAGGCCGGTCCTGTGACGTCACCAGCAACA	1560
sTSP2	1	-----	0
TSP2	1561	CCTGCTTGGGGCCCTCCATCCAGACACGGGCTTGCACTGTGAGCAAGTGTACACCCGCA	1620
sTSP2	1	-----	0
TSP2	1621	TCCGGCAGGACGCGCGGTGGAGCCACTGGTCACCTTGGTCTTCATGCTCTGTGACCTGTG	1680
sTSP2	1	-----	0
TSP2	1681	GAGTTGGCAATATCACACGCATCCGTCTCTGCAACTCCCCAGTGCCCCAGATGGGGGGCA	1740
sTSP2	1	-----	0
TSP2	1741	AGAAATGCAAAGGGAGTGGCCGGGAGACCAAAGCCTGCCAGGGCGCCCATGCCCAATCG	1800
sTSP2	1	-----	0
TSP2	1801	ATGGCCGCTGGAGCCCCTGGTCCCCGTGGTCGGCCTGCACGTGTCACCTGTCCCGTGGGA	1860
sTSP2	1	-----	0
TSP2	1861	TCCGGGAGCGCACCCGGGTCTGCAACAGCCCTGAGCCTCAGTACGGAGGGAAGGCCTGCG	1920
sTSP2	1	-----	0
TSP2	1921	TGGGGGATGTGCAGGAGCGTCAGATGTGCAACAAGAGGAGCTGCCCGTGGAATGGCTGTT	1980
sTSP2	1	-----	0
TSP2	1981	TATCCAACCCCTGCTTCCCGGAGCCCAGTGCAGCAGCTTCCCGATGGGTCTGGTCAT	2040
sTSP2	1	-----	0
TSP2	2041	GCGGCTCTTGCCCTGTGGGCTTCTTGGGCAATGGCACCCACTGTGAGGACCTGGACGAGT	2100
sTSP2	1	-----	0
TSP2	2101	GTGCCCTGGTCCCCGACATCTGCTTCTCCACCAGCAAGGTGCCTCGCTGTGTCAACACTC	2160
sTSP2	1	-----	0
TSP2	2161	AGCCTGGCTTCCACTGCCTGCCCTGCCCGCCCCGATACAGAGGGAACCAAGCCGTGGGG	2220
sTSP2	1	-----	0
TSP2	2221	TCGGCCTGGAAGCAGCCAAGACGAAAAGCAAAGTGTGTGAGCCCGAAAACCCATGCAAGG	2280
sTSP2	1	-----	0
TSP2	2281	ACAAGACACAACTGCCACAAGCAGCGGAGTGCATCTACCTGGGCCACTTCAGCGACC	2340
sTSP2	1	-----	0
TSP2	2341	CCATGTACAAGTGCAGTGCCAGACAGGCTACGCGGGCGACGGGTCATCTGCGGGGAGG	2400
sTSP2	1	-----	0
TSP2	2401	ACTCGGACCTGGACGGCTGGCCCAACCTCAATCTGGTCTGCGCCACCAACGCCACCTACC	2460
sTSP2	1	-----	0
TSP2	2461	ACTGCATCAAGGATAACTGCCCCCATCTGCCAAATCTGGGCAGGAAGACTTTGACAAGG	2520
sTSP2	1	-----	0
TSP2	2521	ACGGGATTGGCGATGCCGTGTGATGATGACGATGACAAATGACCGTGTGACCGATGAGAAGG	2580
sTSP2	1	-----gtgaccgatgagaagg	16
TSP2	2581	ACAACTGCCAGCTCCTCTTCAATCCCCGCCAGGCTGACTATGACAAGGATGAGGTTGGGG	2640
sTSP2	17	acaactgccagctcctcttcaatccccgccaggctgactatgacaaggatgaggttgggg	76
TSP2	2641	ACCGCTGTGACAACTGCCCTTACGTGCACAACCCCTGCCCAGATCGACACAGACAACAATG	2700
sTSP2	77	accgctgtgacaactgcccttacgtgcacaacctgccagatcgacacagacaacaatg	136
TSP2	2701	GAGAGGGTGACGCCTGCTCCGTGGACATTGATGGGGACGATGTCCTTCAATGAACGAGACA	2760
sTSP2	137	gagagggtgacgcctgctccgtggacattgatggggacgatgtccttcaatgaacgagaca	196
TSP2	2761	ATTGTCCCTACGTCTACAACACTGACCAGAGGGACACGGATGGTGACGGTGTGGGGGATC	2820
sTSP2	197	attgtccctacgtctacaacactgaccagagggacacggatggtgacggtgtgggggatac	256
TSP2	2821	ACTGTGACAACTGCCCCCTGGTGCACAACCCCTGACCAGACCGACGTGGACAATGACCTTG	2880
sTSP2	257	actgtgacaactgccccctggtgcacaacctgaccagaccgacgtggacaatgaccttg	316

TSP2	2881	TTGGGGACCAGTGTGACAACAACGAGGACATAGATGACGACGGCCACCAGAACAACCAGG	2940
stTSP2	317	ttggggaccagtgtagacaacaacgaggacatagatgacgacggccaccagaaacaaccagg	376
TSP2	2941	ACAACTGCCCCCTACATCTCCAACGCCAACGAGGCTGACCATGACAGAGACGGCCAGGGCG	3000
stTSP2	377	acaaactgcccctacatctccaacgcccaaccaggctgacccatgacagagacggccaggcg	436
TSP2	3001	ACGCCTGTGACCCCTGATGATGACAACGATGGCGCTCCCCGATGACAGGGACAAC TGCCGGC	3060
stTSP2	437	acgcctgtgacctgatgatgacaacgatggcgccccgatgacagggacaactgccggc	496
TSP2	3061	TTGTGTTCAACCAGACACGAGGAGACTTGGACGGTGATGGACGGGGTGATATTGTAAAG	3120
stTSP2	497	ttgtgttcaaccagaccaggaggacttgacgggtgatggacggggtgatattgttaag	556
TSP2	3121	ATGATTTTGACAATGACAACATCCCAGATATTGATGATGTGTCTCTGAAAACAATGCCA	3180
stTSP2	557	atgattttgacaatgacaacatcccagatattgatgatgtgtgtcctgaaaacaatgcca	616
TSP2	3181	TCAGTGAGACAGACTTCAGGAACCTCCAGATGGTCCCCTTGGATCCCAAGGGGACACCC	3240
stTSP2	617	tcagtgagacagacttcaggaacttccagatggctccccttggatcccaagggaccaccc	676
TSP2	3241	AAATTGATCCCAACTGGGTCATTGCGCCATCAAGGCAAGGAGCTGGTTGACAGCCAACT	3300
stTSP2	677	aaattgatcccaactgggtcattcgccatcaaggcaaggagctggttcagacagccaact	736
TSP2	3301	CGGACCCCGGCATCGCTGTAGCTTTTGACGAGTTTGGGTCTGTGGACTTCAGTGGCACAT	3360
stTSP2	737	cggaccccggcacatcgctgtaggttttgacgagtttgggtcctgtggacttcagtggcacat	796
TSP2	3361	TCTACGTAAACACTGACCGGGACGACGACTATGCCGGCTTCGTCTTTGGTTACCACTCAA	3420
stTSP2	797	tctacgtaaacactgaccgggacgacgactatgccggcttcgtccttggttaccagtcaa	856
TSP2	3421	GCAGCCGCTTCTATGTGGTGATGTGGAAGCAGGTGACGCAGACCTACTGGGAGGACCAGC	3480
stTSP2	857	gcagccgcttctatgtggtgatgtggaagcaggtgacgcagacctaactgggaggaccagc	916
TSP2	3481	CCACGCGGGCCTATGGCTACTCCGGCGTGTCCCTCAAGGTGGTGAATCCACCACGGGGA	3540
stTSP2	917	ccacgcgggcctatggctactccggcgtgtccctcaagggtggtgaactccaccacgggga	976
TSP2	3541	CGGGCGAGCACCTGAGGAACGCGCTGTGGCACACGGGGAAACGCGCGGGGCAGGTGCGAA	3600
stTSP2	977	cgggcgagcacctgaggaacgcgctgtggcacacggggaacacgcggggcagggtgcgaa	1036
TSP2	3601	CCTTATGGCAGCACCCAGGAACATTGGCTGGAAGGACTACACGGCCTATAGGTGGCACC	3660
stTSP2	1037	ccttatggcacgacccaggaacattggctggaaggactacacggcctataggtggcacc	1096
TSP2	3661	TGACTCACAGGCCCAAGACTGGCTACATCAGAGTCTTAGTGCATGAAGGAAAAACAGGTCA	3720
stTSP2	1097	tgactcacagggcccaagactggctacatcagagtcttagtgcataagggaaaacaggtca	1156
TSP2	3721	TGGCAGACTCAGGACCTATCTATGACCAAACCTACGCTGGCGGGCGGCTGGGTCTATTTG	3780
stTSP2	1157	tggcagactcaggacctatctatgaccaaacctacgctggcgggcggtgggtctatttg	1216
TSP2	3781	TCTTCTCTCAAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGCAGAGATATTTAAA	3840
stTSP2	1217	tcttctctcaagaaatggtctatttctcagacctcaagtacgaatgcagagataatttaa	1276
TSP2	3841	CAAGATTTGCTGCATTTCCGGCAATGCCCTGTGCATGCCATGGTCCCTAGACACCTCAGT	3900
stTSP2	1277	caagatttgctgcatttccggcaatgccctgtgcatgccatggtccctagacacctcagt	1336
TSP2	3901	TCATTGTGGTCCCTTGTTGGCTTCTCTCTAGCAGCACCTCCTGTCCCTTGACCTTAACTC	3960
stTSP2	1337	ccattgtggctccttgtggcttctctctctagcagcacctcctgtcccttgaccttaactc	1396
TSP2	3961	TGATGGTTCTTTCACCTCCTGCCAGCAACCCCAAACCCAAAGTGCCCTCAGAGGATAAATAT	4020
stTSP2	1397	tgatggttcttcacctcctgccagcaaccccaaacccaagtgccttcagaggataaatat	1456
TSP2	4021	CAATGGAACCTCAGAGATGAACATCTAACCCACTAGAGGAAACCAAGTTTGGTGATATATGA	4080
stTSP2	1457	caatggaactcagagatgaacatctaaccactagaggaaaccagtttggtgatatatga	1516
TSP2	4081	GACTTTATGTGGAGTGAAAAATTGGGCATGCCATTACATTGCTTTTCTTGTTTGTTTAAA	4140
stTSP2	1517	gactttatgtggagtgaaaattgggcatagccattacattgcttttcttgttgttttaa	1576
TSP2	4141	AAGAATGACGTTTACATATAAAATGTAATTACTTATGTATTTATGTGTATATGGAGTTG	4200
stTSP2	1577	aagaatgacgtttacatataaaatgtaattacttattgtatttatgtgtatatggagttg	1636
TSP2	4201	AAGGGAATACTGTGCATAAGCCATTATGATAAAATTAAGCATGAAAAATATTGCTGAAC TA	4260
stTSP2	1637	aagggaatactgtgcataagccattatgataaattaagcatgaaaaatgttgctgaacta	1696
TSP2	4261	CTTTTGGTGCTTAAAGTTGTCACTATTCTTGAATTAGAGTTGCTCTACAATGACACACAA	4320
stTSP2	1697	cttttggtgcttaaagttgtcactattcttgaattagagttgctctacaatgacacacaa	1756
TSP2	4321	ATCCCATTAATAAATTAATAACAAGGGTCAATTCAAATTTGAAGTAATGTTTGTAGTAAG	4380
stTSP2	1757	atcccattaataaattataaacaagggtcaattcaaatttgaagtaatgttttagtaag	1816
TSP2	4381	GAGAGATTAGAAGACAACAGGCATAGCAAATGACATAAGCTACCGATTAACTAATCGGAA	4440
stTSP2	1817	gagagattagaagacaacaggcatagcaaatgacataagctaccgattaactaatcgga	1876

TSP2	4441	CATGTAAACAGTTACAAAAATAAACGAACTCTCCTCTTGTCTACAATGAAAGCCCTCA	4500
STSP2	1877	catgtaaaacagttacaaaaataaacgaactctcctcttgtcctacaatgaagccctca	1936
TSP2	4501	TGTGCAGTAGAGATGCAGTTTCATCAAAGAACAACATCCTTGCAAATGGGTGTGACGCG	4560
STSP2	1937	tgtgcagtagagatgcagtttcatcaaagacaacatccttgcaaatgggtgtgacgcg	1996
TSP2	4561	GTTCCAGATGTGGATTGGCAAAACCTCATTTAAGTAAAAGGTTAGCAGAGCAAAGTGCG	4620
STSP2	1997	gttcagatgtggatttggcaaacctcatttaagtaaaaggttagcagagcaaatgtcg	2056
TSP2	4621	GTGCTTTAGTGTCTGCTTGTGCGCTGTGGCGTCGGGGAGGCTCCTGCCTGAGCTTCCTT	4680
STSP2	2057	gtgcttttagctgctgcttgtgccgctgtggcgctggggaggtcctgcctgagcttcctt	2116
TSP2	4681	CCCCAGCTTTTGCTGCCTGAGAGGAACGAGCAGACGCACAGGCCGAAAAGGCGCATCT	4740
STSP2	2117	ccccagctttgctgcctgagaggaaccagagcagacgcacagccggaaaaggcgatct	2176
TSP2	4741	AACGCGTATCTAGGCTTTGGTAACTGCGGACAAGTTGCTTTTACCTGATTTGATGATACA	4800
STSP2	2177	aacggtatctaggtcttggttaactgcggaacagttgcttttacctgatgtgatgataca	2236
TSP2	4801	TTTCATTAAGGTTCCAGTTATAAAATATTTTGTTAATATTTATTAAGTGACTATAGAATGC	4860
STSP2	2237	tttcattaagggtccagttataaatattttgttaatatattattaagtgactatagaatgc	2296
TSP2	4861	AACTCCATTTACCAGTAACCTTATTTTAAATATGCCTAGTAACACATATGTAGTATAATTT	4920
STSP2	2297	aactccatttaccagtaacttattttaaatatgcctagtaacacatatgtagtataat	2356
TSP2	4921	CTAGAAACAAACATCTAATAAGTATATAATCCTGTGAAAATATGAGGCTTGATAATATTA	4980
STSP2	2357	ctagaacaacacatctaataagtataataatcctgtgaaaatatgaggttgataaatatta	2416
TSP2	4981	GGTTGTACAGATGAAGCATGCTAGAAGCTGTAACAGAATACATAGAGAATAATGAGGAGT	5040
STSP2	2417	ggttgtcacgatgaagcatgctagaagctgtaacagaatacatagagaataatgaggagt	2476
TSP2	5041	TTATGATGGAACCTTAAATATATAATGTTGCCAGCGATTTTAGTTCAATATTTGTTACTG	5100
STSP2	2477	ttatgatggaacctaaaatataaatgttgccagcgatttagttcaatatttgttactg	2536
TSP2	5101	TTATCTATCTGCTGTATATGGAATTCTTTTAATTCAAACGCTGAAAAGATCAGCATTTA	5160
STSP2	2537	ttatctatctgctgtataggaattccttttaattcaaacgctgaaaagaatcagcattta	2596
TSP2	5161	GTCTTGCCAGGCACACCCAATAATCAGTCATGTGTAATATGCACAAGTTTGTGTTT	5220
STSP2	2597	gtcttgccaggcacaccaataatcagtcatgtgtaaatatgcacaagttgttttgttt	2656
TSP2	5221	TTGTTTTTTTTTGTGGTTGGTTGTTTTTTTGCTTTAAGTTGCATGATCTTTCTGCAGGA	5280
STSP2	2657	ttgttttttttgttggttggttgttttttgcctttaaagttgcatgatccttctgcagga	2716
TSP2	5281	AATAGTCACTCATCCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGCTGTCTGATG	5340
STSP2	2717	aatagtcactcatcccactccacataaggggttagtaagagaagtcgtctgtctgatg	2776
TSP2	5341	ATGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAA	5400
STSP2	2777	atggatagggggcaaatcttttccccttctgttaatagtcacacatttctatgccaa	2836
TSP2	5401	ACAGGAACAATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTT	5460
STSP2	2837	acaggaaacaatccataacttagtcttaatgtacacattgcatttgataaaattaat	2896
TSP2	5461	TGTTGTTTCCTTTGAGGTTGATCGTTGTGTGTTGTTTGTGCTGCACCTTTTACTTTTTTG	5520
STSP2	2897	tgtgttttcctttgaggttgatcggtgtgtgtgtgtttgtgctgcacttttactttttg	2956
TSP2	5521	CGTGTGGAGCTGTATTCCCAGACCAACGAAGCGTTGGGATACTTCATTAAATGTAGCGA	5580
STSP2	2957	cgtgtggagctgtattcccagaccaacgaagcggtgggatacttcattaaatgtagcga	3016
TSP2	5581	CTGTCAACAGCGTGCAGGTTTTCTGTTTCTGTGTTGTGTTGGGTCACCGTACAATGGTGTG	5640
STSP2	3017	ctgtcaacagcgt-----	3029
TSP2	5641	GGAGTGACGATGATGTGAATATTTAGAATGTACCATATTTTTTGTAATTTATTTATGTTT	5700
STSP2	3030	-----	3029
TSP2	5701	TTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAAAGACTGTAA	5760
STSP2	3030	-----	3029
TSP2	5761	ATATTTATTTATGTGTTACATGGTCAAAATTTCAACACTGAAACCTGCACCTTAGCTAG	5820
STSP2	3030	-----	3029
TSP2	5821	AACCTCATTTTTAAAGATTAAACACAGGAAATAAATTGTAAAAAGGTTTCTATACATG	5880
STSP2	3030	-----	3029
TSP2	5881	AAAAAAAAAAAAAAAAA-----	5898
STSP2	3030	aaaaaaaaaaaaaaaaaaaaaaaaa	3058

Exons of TSP2 [nucleotide numbering]:

EXON1 : [321 : 372]
EXON2 : [373 : 929]
EXON3 : [930 : 1014]
EXON4 : [1015 : 1211]
EXON5 : [1212 : 1352]
EXON6 : [1353 : 1449]
EXON7 : [1450 : 1620]
EXON8 : [1621 : 1797]
EXON9 : [1798 : 1971]
EXON10 : [1972 : 2099]
EXON11 : [2100 : 2252]
EXON12 : [2253 : 2471]
EXON13 : [2472 : 2579]
EXON14 : [2580 : 2739]
EXON15 : [2740 : 2858]
EXON16 : [2859 : 3093]
EXON17 : [3094 : 3321]
EXON18 : [3322 : 3593]
EXON19 : [3594 : 3691]
EXON20 : [3692 : 3831]
EXON21 : [3832 : 3839]