

SBT Code	Subfamily	AGI Code	left primer	right primer	amplicon size (bp)	
					cDNA	gDNA
AtSBT1.1	1	At1g01900	GGAGAGGAGCTTCTTGCTGA	CATACGCGGTTCTCTGAAT	136	136
AtSBT1.2	1	At1g04110	TCAATTACCCGTCGATAGCC	TGGAGCCTTGACATTCAGT	119	119
AtSBT1.3	1	At5g51750	GCCGATATCAGCTTTGTTCC	ATGGCGAGACAGAAACCTTG	113	113
AtSBT1.4	1	At3g14067	AAAACGTGGGAAGCAATGTC	TCCAACACGCTCTTCTCCTT	118	118
AtSBT1.5	1	At3g14240	CCGGAGAAGCTATCGTTCAG	TCTCCACATTTGTGCTCCT	103	103
AtSBT1.6	1	At4g34980	GTTATAAGGACGCGCAGCAA	ACGGCCGAAGTAAACACAAG	119	119
AtSBT1.7	1	At5g67360	CTTCGGAGACGACAGGAGTC	GACGGCTTCGACGAGTCTAC	115	115
AtSBT1.8	1	At2g05920	TGGTTGGTCTGACGCTATTG	AAGACCCGCTAAACCACTGA	108	230
AtSBT1.9	1	At5g67090	CAGCGAGAAAAACGAGAAGC	TTCATCAACCCAACCTACCA	100	100
AtSBT2.1	2	At1g30600	AGCTCTTGACCCTGGTTTGA	AGAGGCTGCAAGGGAAGAGT	136	240
AtSBT2.2	2	At4g20430	GCTTTGGATCCTGGCCATAAT	TTTGTGCCGGTGTAGTTGAA	107	196
AtSBT2.3	2	At5g44530	TACCGCAACACCGCTGATA	CCGTTGATCCCACAAGAAA	125	195
AtSBT2.4	2	At1g62340	GGGCCATGTTAATCCTGCTA	ACAAGACTCCTGTCCGCTCT	136	254
AtSBT2.5	2	At2g19170	GCCACTCCTTTGATTATGG	GGGGTTGTGCATAAGAATCC	115	195
AtSBT2.6	2	At4g30020	TTTGATTATGGAAGCGGTCA	GAGCATCGATACCAGGTGTG	118	250
AtSBT3.1	3	At4g21323	TTGCAGGAATCGTAGCACTC	GCCGTATGGATCAGTTTTCA	103	186
AtSBT3.2	3	At1g32970	ATCACCTGTCGCCAAGATTC	GTTTACTCCAGGTGCTGCAA	144	464
AtSBT3.3	3	At1g32960	AAGCTTTGCATCCTGAATGG	CTGCAAAAATCTGCTCTCCA	96	184
AtSBT3.4	3	At1g32950	GGAGAACCTGTTGGGACAAA	GAGGGTGTCTATGGGAGATG	130	205
AtSBT3.5	3	At1g32940	GACAACCTGTGGGGACAAAAG	CTTGAATTGGAATCGGGAGA	136	217
AtSBT3.6	3	At4g10550	TTGGTACAAAAGTGGCAACG	GCTGCCAATATGCTCACTCC	103	184
AtSBT3.7	3	At4g10510	AGCTCTGCATCCTGATTGGT	CAGCTGGCTTCTAGGTGAC	120	198
AtSBT3.8	3	At4g10540	ATTCAATTGAGCCTGCCATC	AAATGAATCCTCGGTCTTG	100	199
AtSBT3.9	3	At4g10520	TCAAAGACGCTTTTTGGACA	GTTACACACCAGGTGCTGCTA	115	214
AtSBT3.10	3	At4g10530	AGCCATAACACTTGGGAACAA	ACTCTTGGGATTGGCAGAGA	130	343
AtSBT3.11	3	At5g11940	GCTGCGCTTAAATCAGCTCT	TCCTCCTCCGAAGTCAAATG	117	305
AtSBT3.12	3	At4g21326	TGCTGCGCTAAAATCTGCTA	TGCACCGTAGTCAAATGGAT	114	209
AtSBT3.13	3	At4g21650	TGGTCAGCCTGCAACAACCTA	ACTTATTGCCGCGAGTATGC	121	219
AtSBT3.14	3	At4g21630	TACGACCCTAAACGGTCAGC	ACTCACTGCCGCGAGTATG	133	224
AtSBT3.15	3	At4g21640	CCTGCCCCAGACAATTTCTA	GTTGTGGCCGCACTAATTCT	98	207
AtSBT3.16	3	At1g66210	TACACCTGTCTGTGTCAGGAA	CCGATGGGTCCGTTTTGTAAC	113	198
AtSBT3.17	3	At1g66220	ACACACCCTCACTGGTCTCC	TCAAATGGGTGTCAGCAAGTTT	126	449
AtSBT3.18	3	At4g26330	CAGAAGCGCTATCATGACCA	ACGGGTGTCAGTGGACTTCATC	90	171
AtSBT4.1	4	At2g39850	AAATCTGCCCTCATGACCAC	CGGGTCTCGGACTTTTGTAG	99	183
AtSBT4.2	4	At4g15040	ACGGGAACATCTATGGCTTG	GCATTTTTTCGAAGCGTTCAT	137	226
AtSBT4.3	4	At5g59190	TCCTCATGTGGCAGGTGTAG	AATTCTTGCTCGGGTTCTT	129	212
AtSBT4.4	4	At5g59100	GCCGCTATGTCAAGACTTT	GGCCAGATCCATATGCAAAC	133	219
AtSBT4.5	4	At3g46840	GCCCAAACACAATCATTCTC	AAGTTCGGTATCAACGGAGT	141	209
AtSBT4.6	4	At3g46850	AAACGTTTCACCCACTCTGG	GCCAACTCGTTAGACGGAGA	100	222
AtSBT4.7	4	At5g58820	CCCGCAAGGACTTTTTCTTA	AAGGTGAATAGGCTGCGAGA	159	236
AtSBT4.8	4	At5g58830	TCCGGAACCTCTATGGCTTG	TTCAGCCCCAGTTCAGTAG	144	236
AtSBT4.9	4	At5g58840	CCAGGCAGCTCCTAAAGTTG	GCTGGTGAATTCAAAGGTGA	132	214
AtSBT4.10	4	At5g58810	GTGTGGCTGCGTACATCAAG	TGCGTCAAGTCCAGAAGGAT	106	200
AtSBT4.11	4	At5g59130	TCCCTTCCATGATCAAAATC	TGACCTGCTCCATAAGCAAA	101	198
AtSBT4.12	4	At5g59090	GGTGGCTGCGTATGTCAAG	CATGTCCAGCTCCATAAGCA	140	221
AtSBT4.13	4	At5g59120	TGGCTGCTTATGTCAAAACG	CAAACCTGTGCGATGCGATG	120	214
AtSBT4.14	4	At4g00230	ATCCTGTCTGGCACCTCAAT	ACTCTCCGGCTTATCGGTTT	137	208
AtSBT4.15	4	At5g03620	CAATCAAATCCGCCCTTATG	CGTCTCTGTGATGTCGTA	139	220
AtSBT5.1	5	At1g20150	CTGCTCGTCTCAAATCCAGA	AAGGTGTGGCCTTTTCTCCT	132	211
AtSBT5.2	5	At1g20160	CCTCATGTTTCAGCTGTTGC	TCATAAGGTGTGGCTGTTGC	155	235
AtSBT5.3	5	At2g04160	TTGCGGGTCTTCTCAAAACT	TGTTGCCTTCATGTTGGTTG	129	353
AtSBT5.4	5	At5g59810	CATCAGTGTGCAGATGCTA	TGCGTTGTCTCCTCTCAGAC	127	205
AtSBT5.5	5	At5g45640	AATTGCCCTTCTCAAAAGCA	TTCATTGTCTCGTTGGTCA	97	217
AtSBT5.6	5	At5g45650	CAAAGCCATTATCCCAAAT	GGATCGGTTTCTTCTGTGCG	92	200
AtSBT6.1	6	At5g19660	GTTGGAGATCAGCCAAGGAA	GCAAGTACGATCCAGCGAGT	124	206
AtSBT6.2	6	At4g20850	ACTGGCGGATGCACTATACC	TCACGTCTACCCATTTTGTCA	149	341
AtACT2		At3g18780	CTCAAAGACCAGCTCTTCCATC	GCCTTTGATCTTGAGAGCTTAG	459	545