Supplemental Figure 1: SBS homology with proteins of the kaurene synthase-like family. Amino acids were aligned with the Clustal W program. Identical residues are shaded in black, similar residues are shaded in grey. Dashes are gaps introduced to maximize alignment. A black horizontal bar shows the position of the conserved catalytic site motif DDXXD. The sequences are derived from *Arabidopsis thaliana* (At), *Cucurbita maxima* (Cm), *Hordeum vulgare* (Hv), *Oryza sativa* (Os), *Nicotiana tabacum* (Nt), *Stevia rebaudiana* (Sr), *Solanum habrochaites* (Sh). KS, ent-kaurene synthase; KSL, kaurene synthase-like.
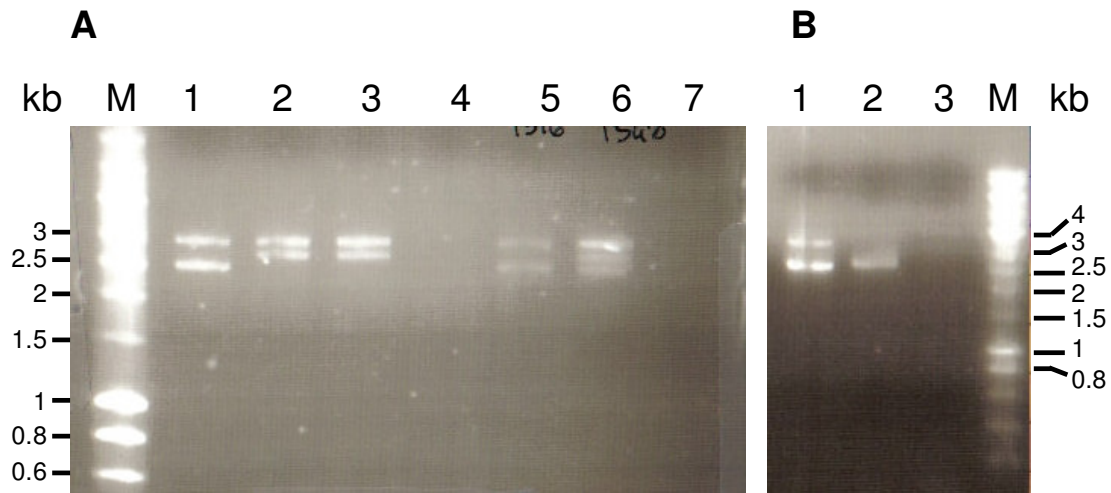
Supplemental Figure 2. Chromosome localization of the *SBS* and *zFPS* genes on the tomato IL map. The schematic tomato chromosome 8 map is from Pan et al. (2000). Bins (grey bars) are designated by the chromosome number followed by a capital letter and indicate the unique area of introgression overlap. TA517 is a near-isogenic line carrying a small chromosome 8 introgression from *S. habrochaites* LA1777 and producing class II sesquiterpenes (Van der Hoeven et al., 2000). The black circle indicates the result of RFLP mapping with the *SBS* and *zFPS* genes.
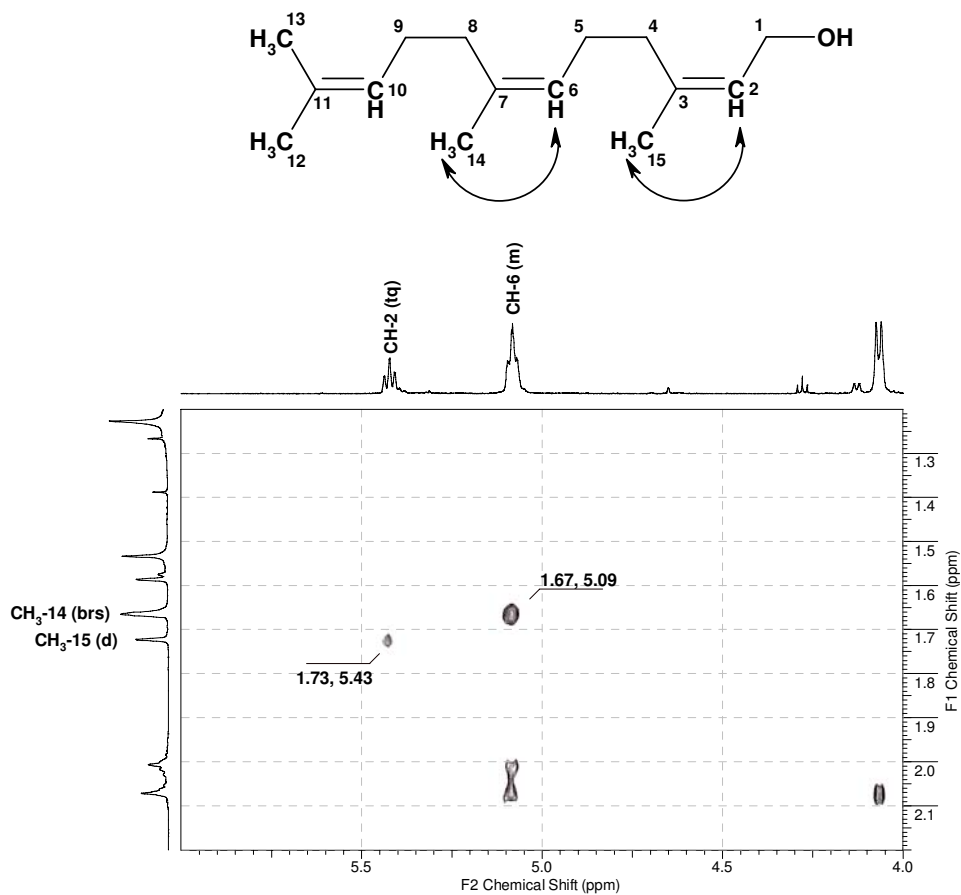
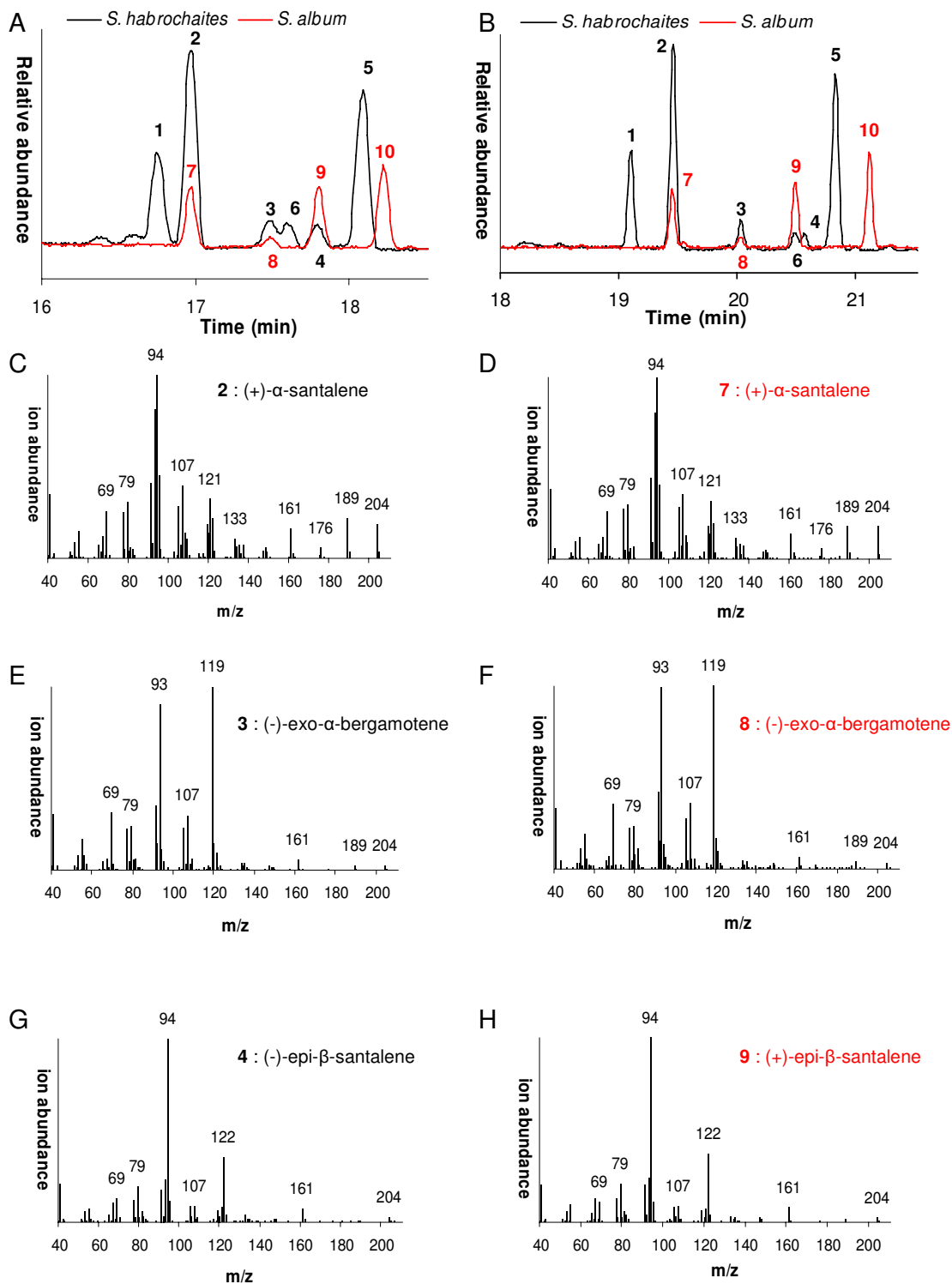**Supplemental Figure 3.** PCR polymorphism of the *SBS* and *zFPS* genes.

A. Genomic polymorphism of the *zFPS* gene. PCR was performed with primers 9I01 and 9I02 on genomic DNA of the following plant species and lines: 1, *Solanum lycopersicum* E6203; 2; *Solanum habrochaites* LA1777; 3, Introgression line TA517 which is homozygous for the *Sst2* allele from *S. habrochaites*; 4, *Solanum pennellii*; 5, Introgression line TA1316 which does not carry the *Sst2* locus; 6, Introgression line TA1548 which is heterozygous for the *Sst2* allele from S. habrochaites; 7, no DNA control. M, DNA molecular weight markers (Smart Ladder, Eurogentec); kb, size in kilobases.

B. Genomic polymorphism of the *SBS* gene. PCR was performed with primers genomic DNA 8D08 and 8G01 on genomic DNA of the following plant species: 1, *S. habrochaites* LA1777; 2, *S. lycopersicum* E6203; 3, no DNA control. M, DNA molecular weight markers (Smart Ladder, Eurogentec); kb, size in kilobases.

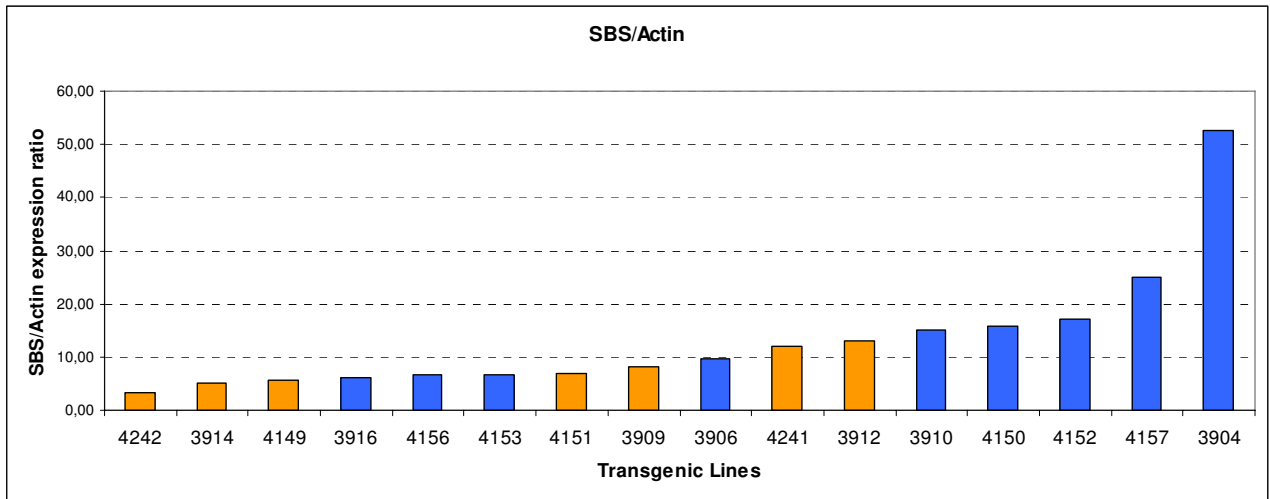The sequence of the primers is available in Supplemental Table 4 online.

Supplemental Figure 4. 1H/1H NMR 2D-NOESY spectrum of Z,Z-farnesol. Peaks that support the Z,Z configuration are shown.

Supplemental Figure 5. GC-MS comparison of a leaf exudate extract from *S. habrochaites* and *Santalum album* essential oil.

(A, B) GC-MS Chromatograms of *S. habrochaites* leaf extract and *Santalum album* essential oil on non-chiral **(A)** or chiral **(B)** columns. The numbers (1 through 6) in black indicate the peaks of *S. habrochaites* and the numbers in red (7 through 10), those of *S. album*. Sesquiterpene olefinic compounds from sandalwood oil were identified on the basis of their mass spectra, matches in the NIST database, and comparison with the ISO standards description (reference ISO 3518:2002). **(C through H)**. Mass spectra of the peaks common to *S. habrochaites* and *S. album*. Peaks are as

follows: (**1**), (-)-exo-α-bergamotene; (**2**) and (**7**), (+)-α-santalene; (**3**) and (**8**), (-)-endo-α-bergamotene; (**4**), (-)-epi-β-santalene; (**5**), (+)-endo-β-bergamotene, (**6**), unknown sesquiterpene from *S. habrochaites* which is not a product of SBS activity; (**9**), (+)-epi-β-santalene; (**10**), β-santalene.

Supplemental Figure 6. Quantification of *SBS* transgene expression in tobacco. Real-time RT-PCR was done in duplex using a SBS-specific FAM probe and an Actin-specific VIC probe. The expression ratio was calculated as 2(CtActin-CtSBS), where CtActin and CtSBS represent the cycle threshold (Ct) average of triplicates of the *Actin* and *SBS* signals respectively. The expression was measured on primary transformants. The orange bars correspond to single copy T-DNA transformants and the blue bars to multicopy T-DNA transformants. The highest expressing single-copy lines were selected for volatile analysis. Line 6009 analyzed in Figure 6 is a homozygous progeny of line 3912

Supplemental Table 1: Complete ^{1}H and ^{13}C NMR assignments for Z,Z-farnesol and correlation table (CDCl$_3$).

a) Values were recorded at 500 MHz, s, singlet; brs, broad singlet, d, doublet, tq, triplet quadruplet; m, multiplet. (J in Hz). b) Values were recorded at 125 MHz.

* ^{13}C quaternary signal too weak to be assigned

Atom	δ_{1H} (ppm)[a]	NOESY	$\delta_{13C\text{-HMQC}}$ (ppm)[b]
1	4.07, d, (7.1)	4	58.8
2	5.43, tq, (7.3, 1.0)	3	124.3
3	-	-	-*
4	2.08, m	1, 15	32.1
5		6, 8	26.1
6	5.09, m	5, 14	124.7
7	-	-	-*
8	2.01, m	6, 14	31.8
9		10, 13	26.3
10	5.09, m	9, 12	124.7
11	-	-	-*
12	1.67, brs	10	25.6
13	1.59, s	9	17.5
14	1.67, brs	6, 8	23.1
15	1.73, d, (1.0)	2, 4	23.3

Supplemental Table 2. Arabidopsis genes and proteins presenting similarity to Z-IPPS. The colors indicate genes which are associated in gene clusters on the Arabidopsis genome.

Arabidopsis locus	Genbank protein ID	Protein symbol	Length (aa)	Predicted cell compartment*	Function	references
At2g17570	NP_565420	DDPS6	295	Mito	Unknown	
At2g23400	NP_179921	None	253	Other	Unknown	
At2g23410	NP_565551	ACPT/DDP!	303	Secreted	polyprenyl pyrophosphate synthase	Oh et al. (2000); Cunillera et al. (2000)
At5g58770	NP_200685	DDPS2	310	Mito	Unknown	
At5g58780	NP_568882	DDPS3	302	Secreted	Unknown	
At5g58782	NP_568883	DDPS4	289	Secreted	Unknown	
At5g58784	NP_568884	DDPS5	302	Other	Unknown	
At5g60500	NP_200858	DDPS7	271	Other	Unknown	
At5g60510	NP_200859	DDPS8	271	Other	Unknown	

*according to TargetP software

Supplemental Table 3: List of plant terpene synthases used to generate the phylogenetic tree in Figure 2. GI number: protein identification number in Genbank. Full name: includes the function and the species name in brackets. Short name is the abbreviated name appearing on Figure 2. Tps group: corresponds to the nomenclature of plant terpene synthases described by Bohlmann et al. (1998) and updated in Martin et al. (2004).

GI number	Full name [species]	Short name (on Figure 2)	Tps group
2754818	(E)-B-farnesene synthase [Mentha x piperita]	Mp (E)-B-farnesene syn	a
7381217	amorpha-4,11-diene synthase [Artemisia annua]	Aa amorphadiene syn	a
14134188	(E)-beta-farnesene synthase [Citrus junos]	Cj (E)-beta-farnesene syn	a
29468410	beta-caryophyllene/alpha-humulene synthase [Arabidopsis thaliana]	At beta-caryophyllene/alpha-humulene syn	a
28380030	Casbene synthase, chloroplast precursor [Ricinus communis]	Rc casbene syn	a
3687297	5-epi-aristolochene synthase [Capsicum annuum var. annuum]	Ca 5-epi-aristolochene syn	a
505588	5-epi-aristolochene synthase [Nicotiana tabacum]	Nt 5-epi-aristolochene syn	a
8389329	(+)-delta-cadinene synthase [Gossypium hirsutum]	Gh (+)-delta-cadinene syn	a
14279758	(-)-beta-pinene synthase [Artemisia annua]	Aa (-)-beta-pinene syn	b
21435703	(+)-limonene synthase 1 [Citrus limon]	Cl (+)-limonene syn	b
82408415	trans-alpha-bergamotene synthase [Lavandula angustifolia]	La trans-alpha-bergamotene syn	b
22900832	linalool synthase [Mentha aquatica]	Ma linalool syn	b
3309121	(+)-sabinene synthase [Salvia officinalis]	So (+)-sabinene syn	b
410230	4S-limonene synthase [Mentha spicata]	Ms 4S-limonene syn	b
9957293	myrcene/ocimene synthase [Arabidopsis thaliana]	At myrcene/ocimene syn	b
32265058	(E,E)-alpha-farnesene synthase [Malus x domestica]	Md (E,E)-alpha-farnesene syn	b
29468398	linalool synthase [Arabidopsis thaliana]	At linalool syn	b
30349142	myrcene synthase [Antirrhinum majus]	Am myrcene syn	b
15235504	ent-copalyl diphosphate synthase [Arabidopsis thaliana]	At ent-copalyl diP syn	c
2642661	copalyl pyrophosphate synthase [Stevia rebaudiana]	Sr copalyl diP syn	c
6009478	copalyl diphosphate synthase [Solanum lycopersicum]	Sl copalyl diP syn	c
1477584	abietadiene cyclase [Abies grandis]	Ag abietadiene cyclase	d
44804521	levopimaradiene/abietadiene synthase [Picea abies]	Pa levopimaradiene/abietadiene syn	d
77546864	isopimaradiene synthase [Picea abies]	Pa isopimaradiene syn	d
15865605	levopimaradiene synthase [Ginkgo biloba]	Gb levopimaradiene syn	d
2961462	gamma-humulene synthase [Abies grandis]	Ag gamma-humulene syn	d
44804575	longifolene synthase [Picea abies]	Pa longifolene syn	d
28558360	Taxadiene synthase (Taxa-4(5),11(12)-diene synthase) [Taxus brevifolia]	Tb taxadiene syn	d
3252840	E-alpha-bisabolene synthase [Abies grandis]	Ag E-alpha-bisabolene syn	d
44804486	E-alpha-bisabolene synthase [Picea abies]	Pa E-alpha-bisabolene syn	d
2411481	myrcene synthase [Abies grandis]	Ag myrcene syn	d
44804558	(-)-limonene synthase [Picea abies]	Pa (-)-limonene syn	d
2429145	(-)-4S-limonene synthase [Abies grandis]	Ag (-)-4S-limonene syn	d
2411483	pinene synthase [Abies grandis]	Ag pinene syn	d
44804535	(-)-alpha/beta-pinene synthase [Picea abies]	Pa (-)-alpha/beta-pinene syn	d
Submitted	Santalene and bergamotene synthase [Solanum habrochaites]	SBS	e
111607670	iso kaurene synthase [Oryza sativa]	Os iso kaurene synthase 1	e
50788718	Stemar-13-en synthase [Oryza sativa]	Os stemarene syn	e
73532938	stemodene synthase [Oryza sativa]	Os stemodene syn	e
111607676	ent-sandaracopimaradiene synthase [Oryza sativa]	Os ent-sandaracopimaradiene syn	e
28201163	ent-cassa-12-15-diene [Oryza sativa]	Os cassadiene syn	e
34452214	ent-kaurene synthase 1A [Oryza sativa]	Os ent-kaurene syn	e
51537819	syn-pimara-7,15-diene synthase [Oryza sativa]	Os syn-pimaradiene syn	e
3056725	ent-kaurene synthase [Arabidopsis thaliana]	At ent-kaurene syn	e
4959239	kaurene synthase [Stevia rebaudiana]	Sr ent-kaurene syn	e
62900385	Ent-kaurene synthase B [Cucurbita maxima]	Cm ent-kaurene syn	e
1491939	S-linalool synthase [Clarkia breweri]	Cb S-linalool syn	f

Supplemental Table 4. List of oligonucleotide primers and probes used in this study.

Name	Sequence (5' to 3')	Dyes
7C06	GGGGACAACTTTGTATAGAAAAGTTGACGCCAGGGTTTTCCCAGTCACG	
7C07	GGGGACTGCTTTTTTGTACAAACTTGTGTGGAATTGTGAGCGGATAACAATTTCA	
7C08	GGGGACAAGTTTGTACAAAAAAGCAGGCTACGCCAGGGTTTTCCCAGTCACG	
7C09	GGGGACCACTTTGTACAAGAAAGCTGGGTTGTGGAATTGTGAGCGGATAACAATTTCA	
7D01	GGGGACAGCTTTCTTGTACAAAGTGGACGCCAGGGTTTTCCCAGTCACG	
7D02	GGGGACAACTTTGTATAATAAAGTTGTGTGGAATTGTGAGCGGATAACAATTTCA	
7E06	AGTCTAGACGTTGTAAAACGACGGCCAGTGA	
7E07	AGTCTAGAGGAAACAGCTATGACCATGATTACG	
7F05	TCCATGGTAGTTGGCTATAGAAGCACAATCA	
7I06	CTTTTAGTAAGCCGGATCCACTAGATTACGCCCCGCCCTG	
7I07	CAGGGCGGGGCGTAATCTAGTGGATCCGGCTTACTAAAAG	
8D05	TCTCGAGCATAAATTCAAATTGAGGGATTAATGA	
8D06	GCTGCTCGAGATGATTGAGTGGTTTGTAAAAGACTTCA	
8D08	CTGGTAAGCATATGATAGTTGGCTATAGAAGCACAATCA	
8G01	TTTCATCTAGAGCTTTCTTTATTTCTGA	
8H08	GAAGAACATTTTTTTGCAACAAGTGGGAAATATACAAG	
8H09	CTTGTATATTTCCCACTTGTTGCAAAAAAATGTTCTTC	
9I01	ACATATGAGTTCTTTGGTTCTTCAATGTTGGA	
9I02	ACTCGAGATATGTGTGTCCACCAAAACGTCTATG	
10D01	TCCATGGGTATGAGTTCTTTGGTTCTTCAATGTTG	
10D02	TCTCGAGTCAATATGTGTGTCCACCAAAACGT	
14F02	CGGGGTACCATGAGTTCTTTGGTTCTTCA	
14F03	CGGGGTACCTAAGCTGAGTGAGCATGAA	
14F04	CGGGGTACCATGATAGTTGGCTATAGAAGCA	
14F05	CGGGGTACCTACTTTCCCAAAACTTTCCCT	
SBS-For	TTGTCCCCGAGCCTGAATT	
SBS-Rev	CATCGACAATAGTCAGGAGCAAGA	
SBS-Pr	TCCGATGCTCGTCTCTTGTACGCG	FAM/TAMRA
Actin-For	TCATCACAATCGGTGCTGAGA	
Actin-Rev	ATTCCTACTGCTTCCATTCCAATAAAT	
Actin-Pr	TGCCCTGAGGTTCTCTTCCAGCCA	VIC/TAMRA