Table S1. Oligonucleotide primer sequences

Primer	**Gene**	**Experiment**	**Direction**	**Sequence**
SBP1-5´	*sbp1*	Cloning	forward	ATATATATCCATGGAACCAAAGAAGAAACCAGCACC
SBP1-3´	*sbp1*	Cloning	reverse	TCTCTCGGATCCTAAAGCTGCATCAAACTCAGC
SBP2-5´	*sbp2*	Cloning	forward	TCTCTCCATGGAAGCAATGAGTCTACGACCAAT
SBP2-3´	*sbp2*	Cloning	reverse	CTCTGGATCCTTGACCTAATGCTTGGCTGTT
SBP3-5´	*sbp3*	Cloning	forward	TCTCTCCATGGAAGCGGTCAAAACGAACAAAGC
SBP3-3´	*sbp3*	Cloning	reverse	TCTCTGGATCCTTCAATATTAGTTGGCATACC
SBP123kanmutup5´	*sbp123* *sbp1*	Mutant construction	forward	TATTTGCTTCTCCGATACCCA
SBP123kanmutup3´	*sbp123* *sbp1*	Mutant construction	reverse	TAGTTAGTCAGATAATTCCTTGGGTTAATA
SBP123kan5´	*sbp123* *sbp1*	Mutant construction	forward	AGGAATTATCTGACTAACTAGGAGGAATAA

SBP123kan3´	*sbp123* *sbp3*	Mutant construction	reverse	GTCTTATTCACATTATTCCCTCCAGGTACT
SBP123kanmutdn5´	*sbp123*	Mutant construction	forward	AGGGAATAATGTGAATAAGACTGCCAAAAA
SBP123kanmutdn3´	*sbp123*	Mutant construction	reverse	AAGCACAAGACAGGACCACA
SBP1kan3´	*sbp1*	Mutant construction	reverse	TGTGCCAAACCATTATTCCCTCCAGGTACT
SBP1kanmutdn5´	*sbp1*	Mutant construction	forward	GGGAATAATGGTTTGGCACACCTACTTTTG
SBP1kanmutdn3´	*sbp1*	Mutant construction	reverse	ATTGTTGGTACATTTAGTAT
SBP2kanmutup5´	*sbp2*	Mutant construction	forward	GTTTTGCTCGTGAAGTCTCAA
SBP2kanmutup3´	*sbp2*	Mutant	reverse	TAGTTAGTCACTCTTAATATGCTTAATATG

		construction		
SBP2kan5´	*sbp2*	Mutant construction	forward	ATATTAAGAGTGACTAACTAGGAGGAATAA
SBP2kan3´	*sbp2*	Mutant construction	reverse	CGGCTTAAAACATTATTCCCTCCAGGTACT
SBP2kanmutdn5´	*sbp2*	Mutant construction	forward	GGGAATAATGTTTTAAGCCGATGGTGTTTG
SBP2kanmutdn3´	*sbp2*	Mutant construction	reverse	CTTAGCCAATCATTAAAAG
SBP3kanmutup5´	*sbp3* *sbp2*	Mutant construction *sbp2* sequencing	forward	GCGGTAAATTGGCAGAAATTG
SBP3kanmutup3´	*sbp3*	Mutant construction	reverse	TAGTTAGTCAAATCTACTCCTTGATTTGGTG

SBP3kan5´	*sbp3*	Mutant construction	forward	GGAGTAGATTTGACTAACTAGGAGGAATAA
SBP3kanmutdn5´	*sbp3*	Mutant construction	forward	GGGAATAATGTGAATAAGACTGCCAAAAAG
SBP3kanmutdn3´	*sbp3*	Mutant construction	reverse	CAAAGCACAAGACAGGACCAC
P14-S2-R	*sbp2*	*sbp2* sequencing	reverse	CTAAATGTACCAACAATGGCTG

Table S2. Comparison of *sbp2* sequence (804bp/267aa) between *M. catarrhalis* strain O35E and clinical isolates

Clinical source (n)	**Total number of isolates**	**Nucleotide position**			
		97	244	615	769
AOM(2), COPD(2), NP(3) [a]	n= 7	G	G	C	G
AOM(6), COPD(8), NP(5) [b]	n=19	A	G	T	G
AOM(1), COPD(0), NP(1)	n= 2	G	A	C	G
AOM(1), COPD(0), NP(1)	n= 2	G	G	C	A
Substitution of amino acid [c]		A33T	A82T	-	A257T

[a] *sbp2* sequence of strain O35E is identical.

AOM, acute otitis media; COPD, chronic obstructive pulmonary disease; NP, nasopharynx

[b] *sbp2* sequence of strain BBH18 is identical.

[c] A, alanine; T, threonine