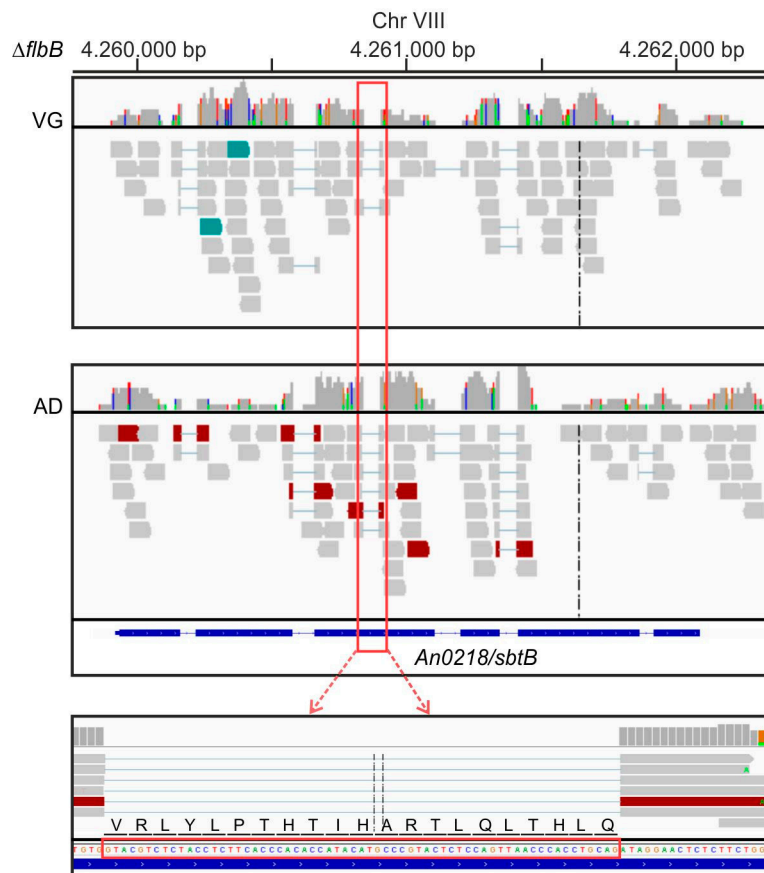
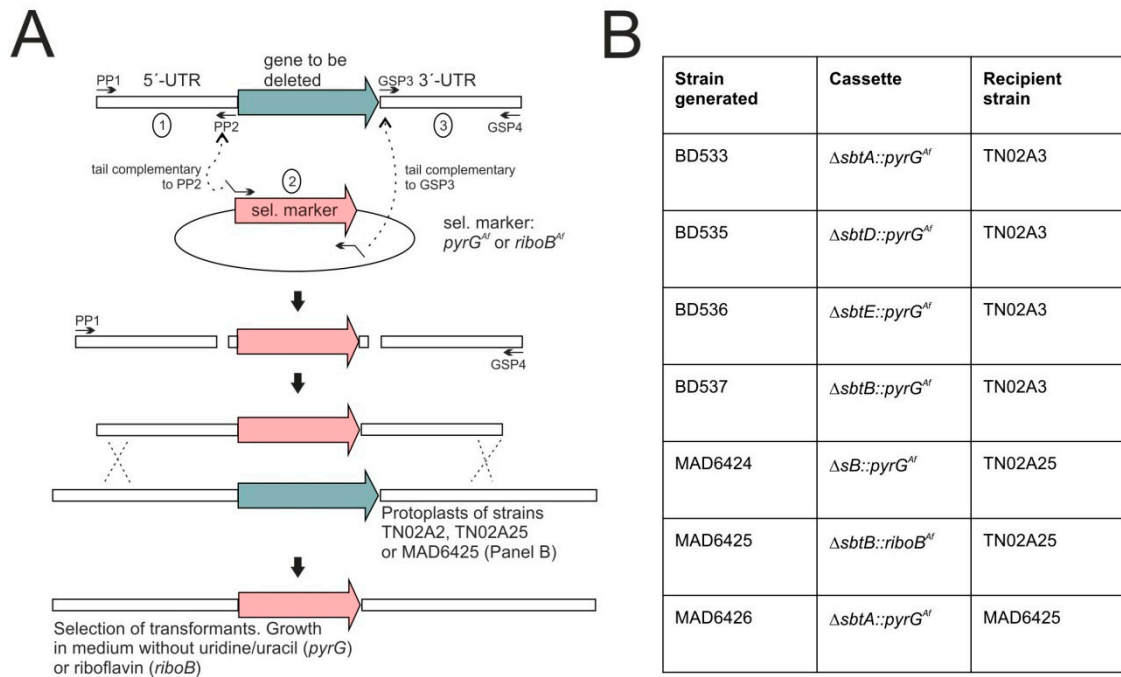


Supplementary Material:



**Figure S1.** RNAseq results for *sbtB/AN0218*. Upper and lower images show mapping of reads corresponding to a  $\Delta flbB$  strain during vegetative growth (VG) or five hours after the induction of asexual development (AD) [1]. IGV (Integrative genomics viewer) software [2] was used. The lower image corresponds to an amplification of the intronic region within exon 3 not predicted by the AspGD database. The sequence of the 21 amino acid-long region that would derive from this intron is also shown.



**Figure S2.** Procedure followed for the generation of null mutants of *Aspergillus nidulans*. A) The 5'- and 3'-UTR regions of the targeted gene plus the selection marker were amplified in three independent PCR reactions. In the second PCR reaction, the selection marker (*pyrG<sup>As</sup>* or *riboB<sup>As</sup>*, *pyrG* or *riboB* genes from *A. fumigatus*) incorporated tails complementary, respectively, to the end and beginning of 5'- and 3'-UTR regions. The three fragments were fused in a fourth PCR reaction (fusion-PCR; [3]). The construct was used to transform protoplasts of recipient strains TN02A3, TN02A25 [4] or MAD6425. Selection of transformants was done based on their ability to grow on medium without uridine and uracil (*pyrG<sup>As</sup>* as selection marker) or without riboflavin (*riboB<sup>As</sup>* as selection marker). B) Table showing the strains generated in this work, the fusion-PCR constructs used to generate them and the corresponding recipient strains. See also Table S1.

**Table S1.** Strains used in this work.

Strain	Genotype	Reference
BD533	<i>pyrG89; argB2, ΔsbtA::pyrG<sup>Af</sup>; pyroA4, ΔnkuA::argB</i>	This work
BD535	<i>pyrG89; argB2; pyroA4, ΔnkuA::argB; ΔsbtD::pyrG<sup>Af</sup></i>	This work
BD536	<i>pyrG89; ΔsbtE::pyrG<sup>Af</sup>; argB2; pyroA4, ΔnkuA::argB</i>	This work
BD537	<i>pyrG89; argB2; pyroA4, ΔnkuA::argB; ΔsbtB::pyrG<sup>Af</sup></i>	This work
HHF27a	Prototrophic wild type	[5]
HHF27b	<i>ΔsltA::riboB<sup>Afum</sup></i>	[5]
MAD1685	<i>inoB2; ΔsltA::riboB<sup>Af</sup></i>	[6]
MAD1686	<i>ΔhalA::pyr4<sup>Nc</sup>; inoB2</i>	[6]
MAD2666	<i>argB2; pyroA4, ΔnkuA::argB</i>	[7]
MAD2757	<i>wA3; ΔhalA::pyr4<sup>Nc</sup>; inoB2; ΔsltA::riboB<sup>Af</sup></i>	[6]
MAD4048	<i>pyrG89, pabaA1; sltA1</i>	[8]
MAD5423	<i>inoB2; ΔnkuA::BAR?; sltA114; riboB2</i>	[8]
MAD6424	<i>pyrG89; argB2; ΔnkuA::argB, pabaB22; ΔsB::pyrG<sup>Af</sup>; riboB2</i>	This work
MAD6425	<i>pyrG89; argB2; ΔnkuA::argB, pabaB22; ΔsbtB::riboB<sup>Af</sup>, riboB2</i>	This work
MAD6426	<i>pyrG89; argB2, ΔsbtA::pyrG<sup>Af</sup>; ΔnkuA::argB, pabaB22; ΔsbtB::riboB<sup>Af</sup>, riboB2</i>	This work
TN02A3	<i>pyrG89; argB2; pyroA4, ΔnkuA::argB</i>	[4]
TN02A25	<i>pyrG89; argB2; ΔnkuA::argB, pabaB22; riboB2</i>	[4]

All strains carry *veA1* mutation. *BAR*, herbicide bialaphos resistance gene from *Streptomyces hygroscopicus*

**Table S2.** Oligonucleotides used in this work.

Name	Sequence (5'-3')	Objective
sbtA-PP1	GGC CAA CCA GTC CGT CG TAT CG	<i>sbtA</i> promoter
sbtA-PP2	CAT GTT GAC GCT GCG GTA GTT CGA G	<i>sbtA</i> promoter
sbtA-GSP3	TAA TCG ACA CGT AGA CGA TGC ACA TCC C	<i>sbtA</i> terminator
sbtA-GSP4	GGC AAC CCT AGC TTC GAG ATT GAC C	<i>sbtA</i> terminator
sbtA-SMP1	CTC GAA CTA CCG CAG CGT CAA CAT GAC CGG TCG CCT CAA ACA ATG CTC T	<i>pyrG<sup>Af</sup></i> SM for <i>sbtA</i> null
sbtA-GFP2	GGG ATG TGC ATC GTC TAC GTG TCG ATT AGT CTG AGA GGA GGC ACT GAT GCG	<i>pyrG<sup>Af</sup></i> SM for <i>sbtA</i> null
sbtB-PP1_MVP	TGG GTG TGA TAC TCT ATT TGC G	<i>sbtB</i> promoter
sbtB-PP2	CAT TGG GGA AGA ATC GAA CAT GGT C	<i>sbtB</i> promoter
sbtB-GSP3	TGA AAG GAG CAG ACC CTA GGC AGA GG	<i>sbtB</i> terminator
sbtB-GSP4_MVP	TCA CCT GCA ACC ACA GAG C	<i>sbtB</i> terminator
sbtB-SMP1	ACC ATG TTC GAT TCT TCC CCA ATG ACC GGT CGC CTC AAA CAA TGC TCT	<i>pyrG<sup>Af</sup></i> or <i>riboB<sup>Af</sup></i> SMs for <i>sbtB</i> nulls
sbtB-GFP2	CCT CTG CCT AGG GTC TGC TCC TTT CAG TCT GAG AGG AGG CAC TGA TGC G	<i>pyrG<sup>Af</sup></i> or <i>riboB<sup>Af</sup></i> SMs for <i>sbtB</i> nulls
sB-PP1	GGG GAG GTT GAA GTC GTC GTC GTA ATT G	<i>sB</i> promoter
sB-PP2	CAT GGT GCG TTG GTG TAA TCC AAA AAC TG	<i>sB</i> promoter
sB-GSP3	TGA TTG TGA TCT CCC TGG ATG GAG G	<i>sB</i> terminator
sB-GSP4	CAA GGC TAC GTG AAT GTC GAG TTC CGC	<i>sB</i> terminator
sB-SMP1	CTG TTT TTG GAT TAC ACC AAC GCA CCA TGA CCG GTC GCC TCA AAC AAT GCT CT	<i>pyrG<sup>Af</sup></i> SM for <i>sB</i> null
sB-GFP2	CCT CCA TCC AGG GAG ATC ACA ATC AGT CTG AGA GGA GGC ACT GAT GCG	<i>pyrG<sup>Af</sup></i> SM for <i>sB</i> null
sbtD-PP1	CTA GTC AAG ACA TAG AGC GGA GGA GCA ACC	<i>sbtD</i> promoter
sbtD-PP2	CAT CGT GGC GAG CGG CG	<i>sbtD</i> promoter
sbtD-GSP3	TGA GGT GCG GCT TTG GTC AGT C	<i>sbtD</i> terminator
sbtD-GSP4	CAA GCC CAT ACC ACC TCC TCA ACA CAT C	<i>sbtD</i> terminator
sbtD-SMP1	CGC CGC TCG CCA CGA TGA CCG GTC GCC TCA AAC AAT GCT CT	<i>pyrG<sup>Af</sup></i> SM for <i>sbtD</i> null
sbtD-GFP2	GAC TGA CCA AAG CCG CAC CTC AGT CTG AGA GGA GGC ACT GAT GCG	<i>pyrG<sup>Af</sup></i> SM for <i>sbtD</i> null
sbtE-PP1	GTA CCA AAC CGA GCT TGT CCG	<i>sbtE</i> promoter
sbtE-PP2	CAT AGC TGT CTA GGC ACG AAT AGA AGG GG	<i>sbtE</i> promoter
sbtE-GSP3	TGA GTC CTT CCC ACC ACC ACC	<i>sbtE</i> terminator
sbtE-GSP4	GCG GGC TTA AAT AGG CGT TGC TG	<i>sbtE</i> terminator
sbtE-SMP1	CCC CTT CTA TTC GTG CCT AGA CAG CTA TGA CCG GTC GCC TCA AAC AAT GCT CT	<i>pyrG<sup>Af</sup></i> SM for <i>sbtE</i> null
sbtE-GFP2	GGT GGT GGT GGG AAG GAC TCA GTC TGA GAG GAG GCA CTG ATG CG	<i>pyrG<sup>Af</sup></i> SM for <i>sbtE</i> null
sbtA-exon 1	TCG TTG CAG GAA TCC TAG GC	<i>sbtA</i> probe-Northern blot
sbtA-exon 2	CTC TGA TTT CCC ATG TTC TTC C	<i>sbtA</i> probe-Northern blot
sbtB-exon 1	AAG CGA CGT CTG TGA CGG AGC	<i>sbtB</i> probe-Northern blot
sbtB-exon 2	ACC TAG ACT CTC CAT TAC GG	<i>sbtB</i> probe-Northern blot
Pho89-exon1	CAC AAC GCA GAG TAT CAT TGG	<i>AN8956</i> probe-Northern blot
Pho89-exon2	TAA CGA GGA ACC ACA CTG G	<i>AN8956</i> probe-Northern blot
EnaA-fw 1	TCA ACG TCG GAA CAC CTC TT	<i>enaA</i> probe-Northern blot
EnaA-rev 2	TTG ACA CCG TCA CCA GTC AT	<i>enaA</i> probe-Northern blot

SM, selectable marker.

**Table S3.** Orthologs of SbtA, SbtB, SB, SbtD and SbtE in filamentous fungal species, yeast and higher eukaryotes.

Species	SbtA	SbtB	SB	SbtD	SbtE
<i>Aspergillus nidulans</i>	An4904 L: 667	An0218 L: 573	An2730 L: 827	An3157 L: 755	An3665 L: 1060
<i>Aspergillus terreus</i>	ATEG_4612 L:645 Sc:988 E:0.0	ATEG_05282 L:583 Sc:869 E:0.0	ATEG_02570 L:841 Sc:1312 E:0.0	ATEG_04052 L:757 Sc:1056 E:0.0	ATEG_03129 L:1098 Sc:1473 E:0.0
<i>Aspergillus fumigatus</i>	Y699_01463 L:679 Sc:975 E:0.0	Y699_06302 L:585 Sc:853 E:0.0	Y699_06792 L:847 Sc:1299 E:0.0	Y699_01217 L:733 Sc:956 E:0.0	Y699_04898 L:1070 Sc:1464 E:0.0
<i>Aspergillus niger</i>	An02g06580 L:671 Sc:968 E:0.0	An01g01790 L:543 Sc:861 E:0.0	An15g04600 L:809 Sc:1040 E:0.0	An02g09350 L:730 Sc:985 E:0.0	An01g07860 L:1066 Sc:1498 E:0.0
<i>Penicillium italicum italicum</i>	PITC_012880 L:630 Sc:955 E:0.0	PITC_022700 L:592 Sc:805 E:0.0	PITC_019010 L:835 Sc:986 E:0.0	PITC_061370 L:772 Sc:933 E:0.0	PITC_067670 L:1057 Sc:1371 E:0.0
<i>Coccidioides immitis</i>	CIMG_13744 L:663 Sc:945 E:0.0	CIMG_02924 L:595 Sc:771 E:0.0	CIMG_04891 L:825 Sc:1072 E:0.0	CIMG_00108 L:723 Sc:845 E:0.0	CIMG_07040 L:1084 Sc:1119 E:0.0
<i>Talaromyces stipitatus</i>	<b>TSTA_032150</b> L:691 Sc:928 E:0.0	<b>TSTA_032150</b> L:691 Sc:492 E:2e-165	TSTA_019080 L:833 Sc:1081 E:0.0	TSTA_029710 L:782 Sc:846 E:0.0	TSTA_076660 L:1094 Sc:1272 E:0.0
<i>Neurospora crassa</i>	<b>NCU01480</b> L:618 Sc:774 E:0.0	<b>NCU01480</b> L:618 Sc:476 E: 4e-160	NCU03235 L:916 Sc:928 E:0.0	NCU09642 L:799 Sc:737 E:0.0	NCU02632 L:1118 Sc:900 E:0.0
<i>Fusarium oxysporum</i>	FOYG_02892 L:609 Sc:771 E:0.0	FOYG_17224 L:602 Sc:787 E:0.0	FOYG_00665 L:787 Sc:920 E:0.0	FOYG_12381 L:801 Sc:758 E:0.0	FOYG_06967 L:1082 Sc:915 E:0.0
<i>Magnaporthe oryzae</i>	<b>MGG_15203</b> L:701 Sc:770 E:0.0	<b>MGG_15203</b> L:701 Sc:465 E:1e-154	MGG_04640 L:844 Sc:940 E:0.0	MGG_09838 L:800 Sc:752 E:0.0	MGG_04433 L:1103 Sc:923 E:0.0
<i>Saccharomyces cerevisiae</i>	<b>Bor 1</b> L:576 Sc:451 E:7e-151	<b>Bor 1</b> L:576 Sc:363 E:5e-118	Sul1 L:859 Sc:526 E:1e-172	YPR003C L:754 Sc:414 E:3e-133	YGR125W L:1036 Sc:644 E:0.0
<i>Homo sapiens</i>	SCL4A1 L:911 Sc:197 E:2e-52	SCL4A3-Isoform CAE3 L:936 Sc:167 E:8.0e-43	SLC26A11 L:606 Sc:248 E:1e-70	SLC26A6-Isoform 6 L:671 Sc:169.1 E:2e-43	-----
<i>Arabidopsis thaliana</i>	At4g32510 L:675 Sc:180 E:2e-48	BOR2 L:703 Sc:170 E:3e-45	SULTR3;1 L:703 Sc:213 E:1e-58	SULTR3;3 L:631 Sc:207 E:1e-57	SULTR3;5 L:634 Sc:57.0 E:7e-08

L: Length; Sc: Score; E: E value. Yellow background indicates a common ortholog for both *sbtA* and *sbtB* in that genome.

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