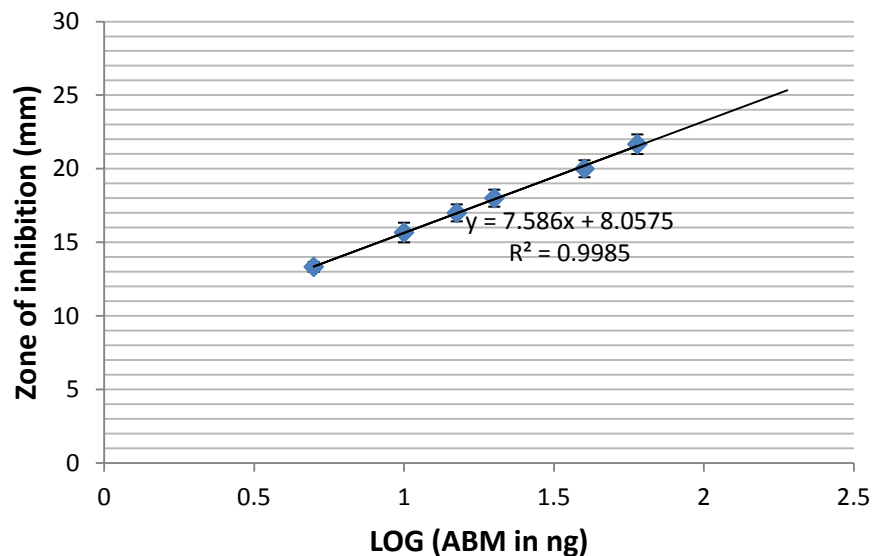
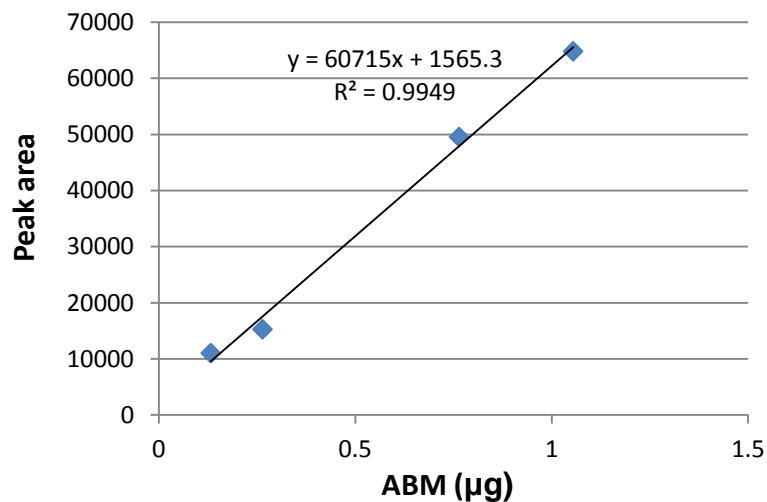


	Gene Name	Nucleotide Identity
<i>sgr6646</i>	<i>metX</i>	91%
<i>sgr6647</i>	<i>metY</i>	93%
<i>sgr2579</i>	<i>metB</i>	96%
<i>sgr3417</i>	<i>malY</i>	89%
<i>sgr5847</i>	<i>metH</i>	96%
<i>sgr1212</i>	<i>metE</i>	90%
<i>sgr6058</i>	<i>metK</i>	96%
<i>sgr4513</i>	<i>sahh</i>	97%
<i>sgr4452</i>	<i>mtcB</i>	96%
<i>sgr3660</i>	<i>mtcC</i>	93%

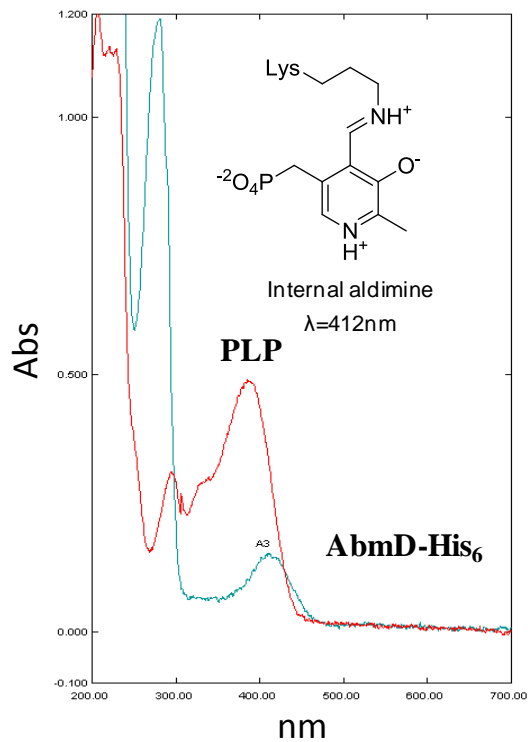
Supplemental Table S1. Comparing the key sulfur amino acid metabolic genes of ATCC 700974 with those of NBRC 13350 by BLASTN.



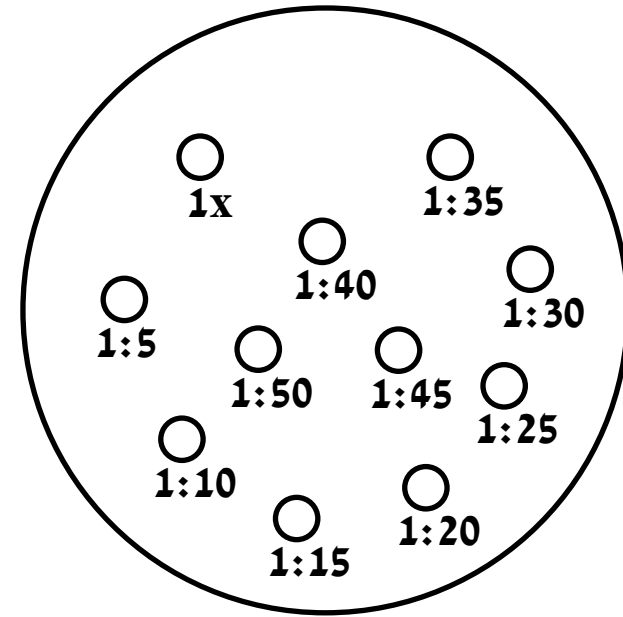
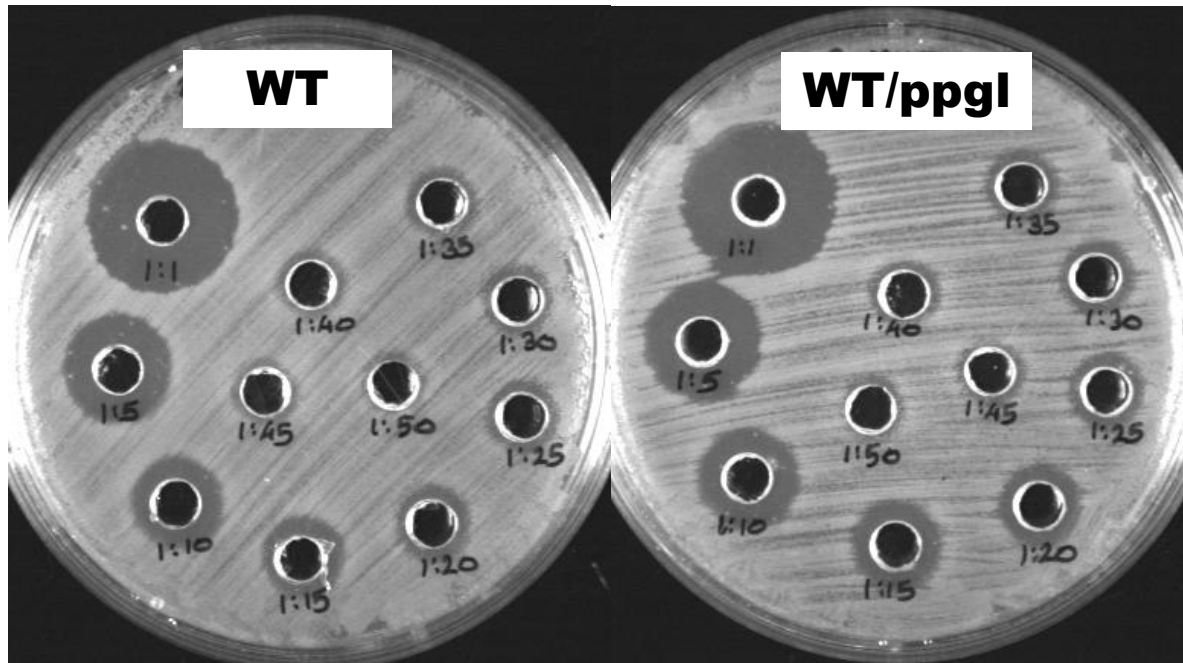
Supplemental Fig S1. A semi-log plot of the diameter of zone of inhibition vs. the amount of pure ABM used in the bioassay.



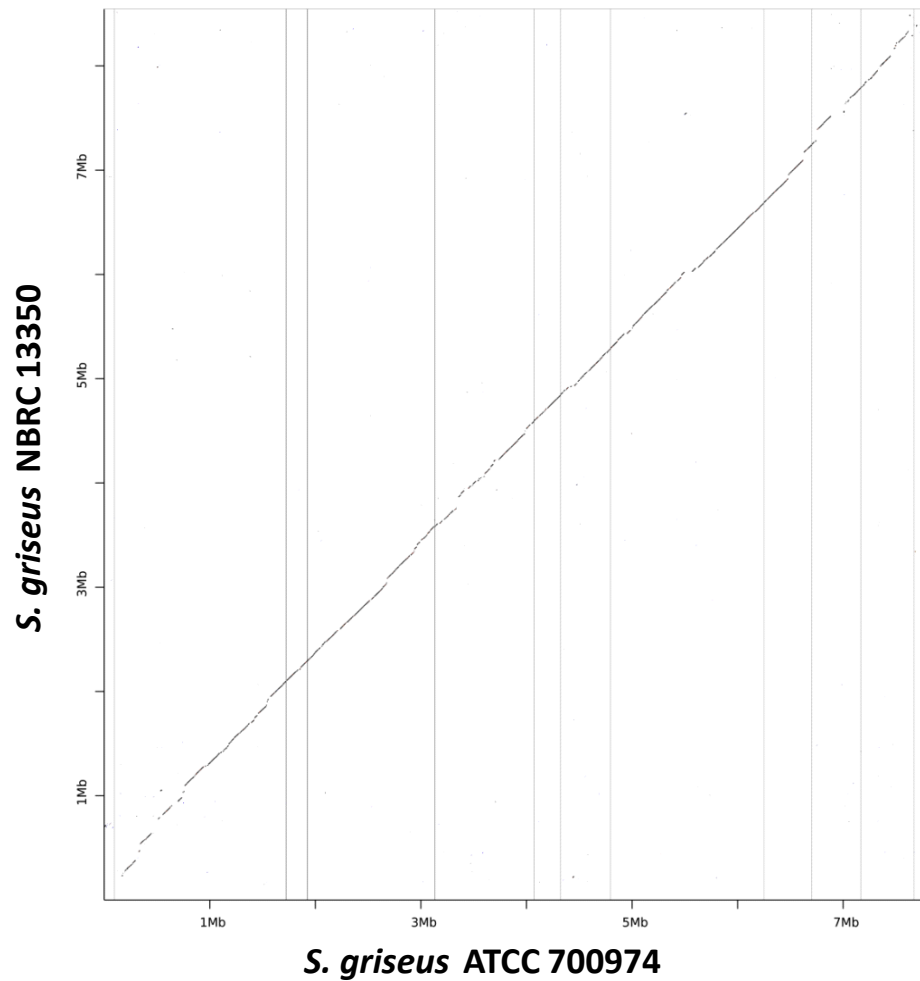
Supplemental Fig S2. HPLC quantification curve of pure ABM. The peak was detected at wavelength 425 nm.



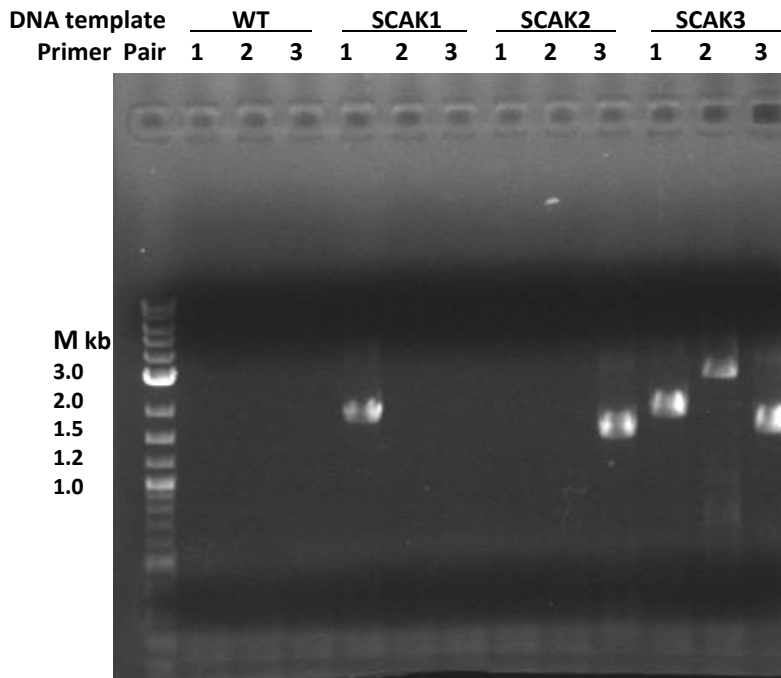
Supplemental Fig S3. UV-vis absorption spectra of pyridoxal 5'-phosphate and purified AbmD in pH 8.0, 50 mM NaH_2PO_4 buffer.



Supplemental Fig S4. Bioassay plates for determining the ABM titer of WT *S. griseus* fermented in the absence or presence of 9 mM propargylglycine (ppgl). The plate template is shown on the right. The ratio below each well is a dilution factor. The dilution was made with sterile water, and 20- μ l fermentation broth (1x) or dilute solution was loaded in each well. For example, 1:5 means the original broth was diluted five times.



Supplemental Fig S5. Comparison between *S. griseus* NBRC 13350 whole genome and ATCC 700974 draft genome.

A.

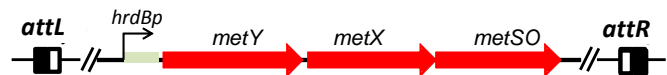
Supplemental Fig S6. PCR analysis of the construction of mutants. (A) Gel electrophoresis of the amplified fragments that are the constructed sequences of a *hrdBp* and a specific gene. Forward primer is *hrdBp*-F-BamHI (Table 2). Reverse primers are DirectSinbet-R-BglIII (1), CGS-R-HindIII (2) and *abmD*-R-NheI (3). (B) Diagram of the *attB* locus in WT and engineered strains. PCR product and the length are indicated for each strain.

B.

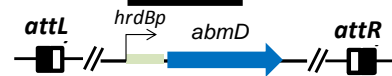
WT



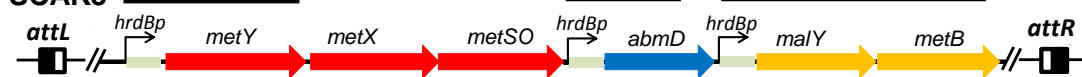
SCAK1 ~1.7 kb (1)



SCAK2 ~1.35 kb (3)



SCAK3 ~1.7 kb (1)

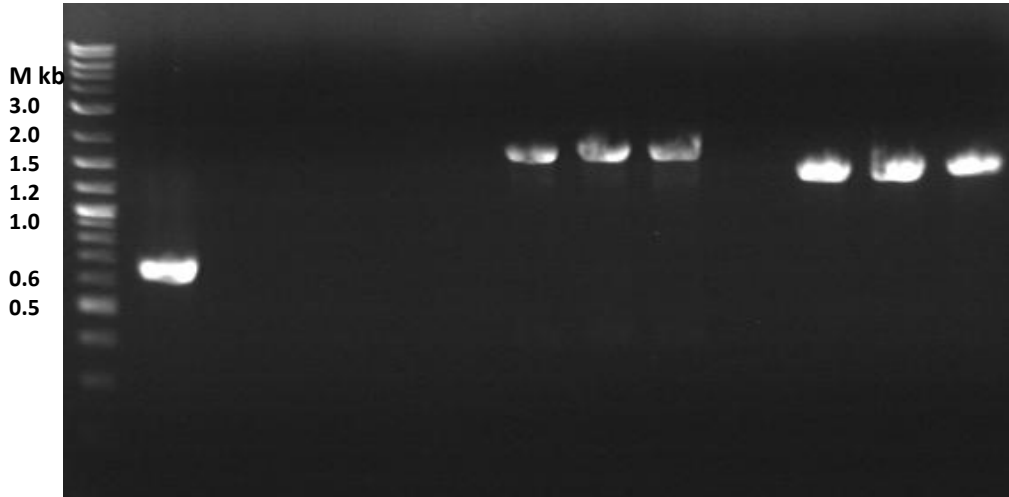


~1.35 kb (3)

~ 2.75 kb (2)

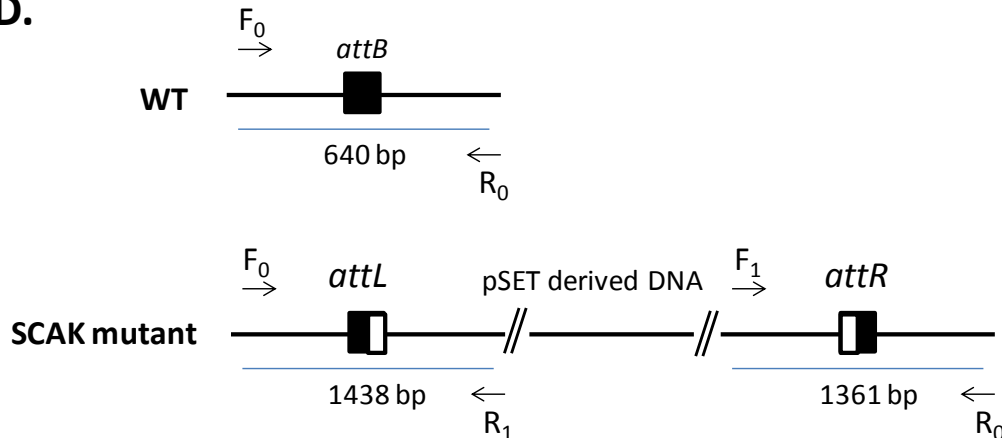
C.

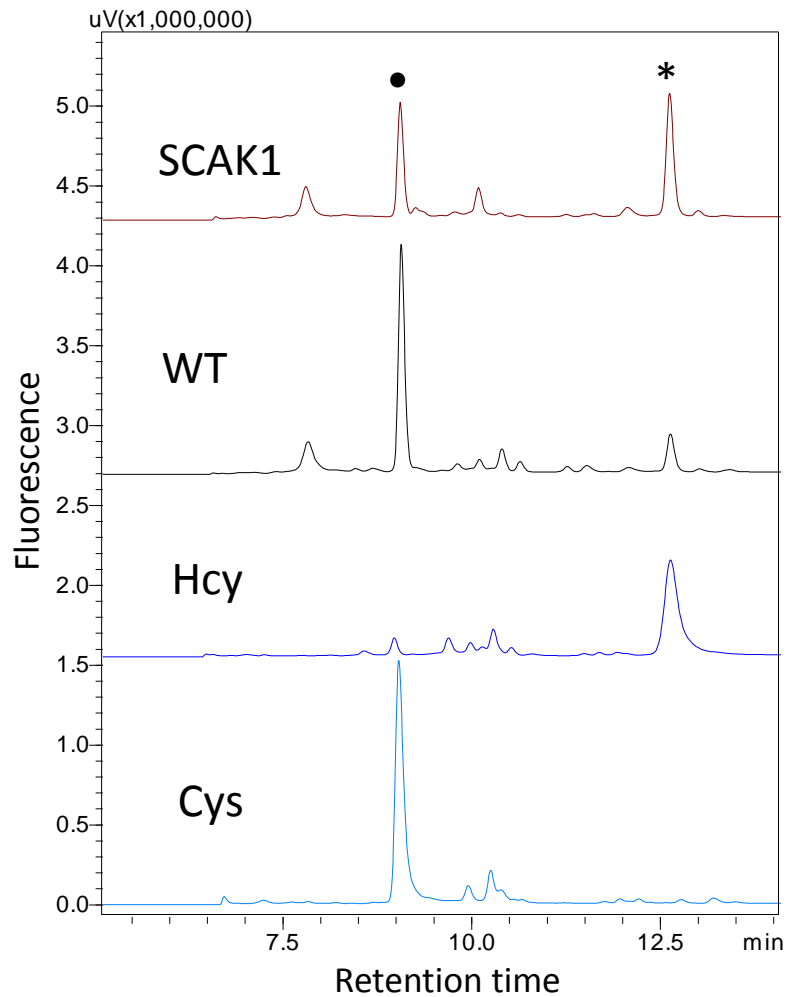
Primers	F_0/R_0			F_0/R_1			F_1/R_0				
	WT	1	2	3	WT	1	2	3	WT	1	2



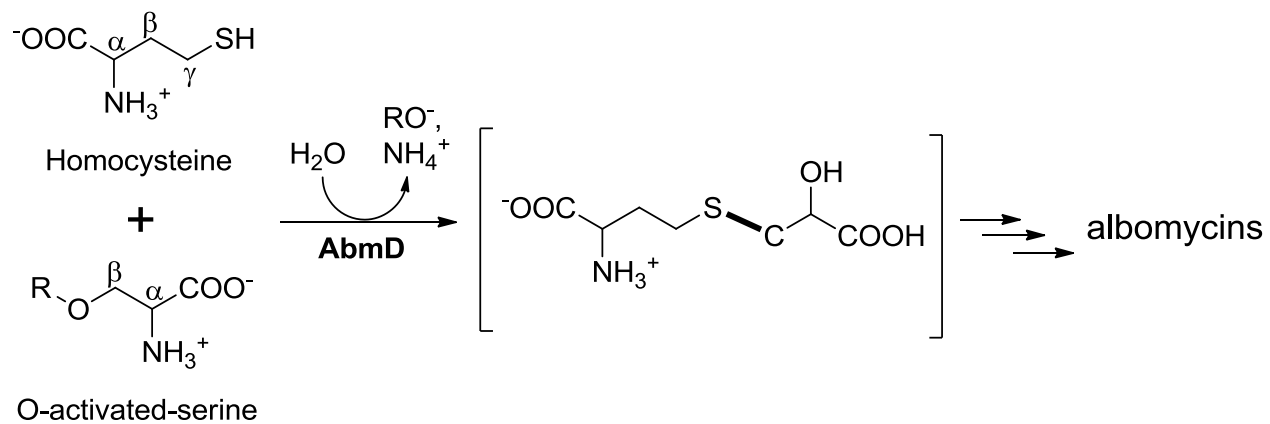
Supplemental Fig S6 (C) PCR analysis of WT and SCAK mutants with primers flanking the *attB* or *attB/P* sites. The primer sequences are: F_1 , acacgtggagcgggatcggggattgtc; R_1 , ccg-aaggattcgcataacggttgccg; F_0 , cgagttcaccggc-gatgacgcggagc; R_0 , gccctccgggaatgcgcgacg-ccttg. DNA template from strains: Wild-type (WT); SCAK1 (1); SCAK2 (2); SCAK3 (3). (D) Diagram of the amplicons.

D.





Supplemental Fig S7. HPLC – fluorescence detection of intracellular Cys (●) and Hcy (*) in WT and mutant SCAK1.



Supplemental Fig S8. Proposed AbmD reaction that forms the -C-S-C- group of ABM.