S2 Fig. Multiple sequence alignment of *A. flavus* **RmtA**, **RmtB**, **and RmtC**, **and phylogenetic analysis of these protein sequences and those of their putative homologs in** *A. nidulans*. (A) Sequences alignment of *A. flavus* RmtA, RmtB (EED57275.1), and RmtC (EED50528.1) using Muscle (http://www.ebi.ac.uk/Tools/msa/muscle/). Alignment was visualized with BoxShade v3.21 (http://ch.embnet.org/software/BOX_form.html). (B) Phylogenetic tree of RmtA, RmtB, and RmtC from *A. flavus* and *A. nidulans*. Accession numbers for *A. nidulans* RmtB and RmtC sequence are XP_660700.1 and XP_657738.1 respectively. The phylogenetic tree was constructed using MEGA v6.0, and it was generated with Maximum-Likelihood model with a bootstrap value of 1000.

А			
	RatA	1	
	RatB	1	STEL-STR STEL-STR STELSTR STEFSMERSMERSAFCIGQUESKRTVFITTQVVQAAHESNYDMLTAPIITTSUFHSKVLSLL
	RatA	6	RTOBADSAD12TSSADRMVCH
	RmtD RmtC	10	ETOBAGAGINISSA
	RatA RatB RatC	27 57 119	- GHARGYNTHCLITH LGMLQETREKTNFGLITHCISHODDF CGFGPLINGISGOVLMGEVARAAFCOIGYLLIFOPKLHHKOMHSZOVYTGAMAIQ
	RmtA RmtB RmtC	41 97 174	
	Rata RatB RatC	47 145 232	- EARDENTE
	RmtA RmtB RmtC	51 181 292	T
	RatA	78	
	RmtB RmtC	210 352	
	RatA	78	- EYAAXAGAXEVIGVDMSSIIE
	RmtB RmtC	235 412	NALANA KETU COLUMNATION COLUMNATI
	RmtA RmtB RmtC	99 279 472	NAROTU
	RatA	126	
	RmtD RmtC	306 532	DAEAD DYNHKT KAFEAAAD NEWE LMYTTE DE TYLEE BEGONE DE FECTORE THE CONTENT OF THE C
	RmtA RmtB RmtC	159 339 388	DVD-70X1F10XXXXYLAAHEBCEYX01
	RntA RntB RntC	192 372 648	AUTOPOTESETELTEPENOTEXIKAUTOPOTITEDETE DUTOPNINGLOITEANGERE MLCNTTCCCSINGNVREGIGUECSETPAPIUTANSISHPNRIPGOSETSIISNAM
	RmtA RmtB RmtC	234 414 708	ЪРАДИЛТКУР
	RatA RatB RatC	271 453 766	x Pet
_	RmtA RmtB RmtC	312 513 823	KUNDING
R			
			92 RmtA(A.flavus)
			└─ RmtA(A.nidulans)
			RmtB(A.flavus)
			100 RmtB(A.nidulans)
			RmtC(A.flavus)
			100 — RmtC(A.nidulans)
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		F	0.2