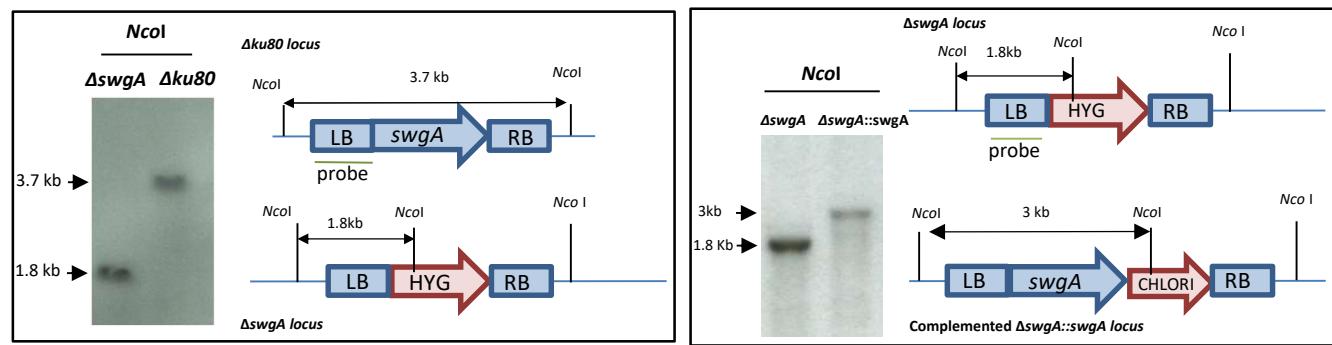


**Figure S1**



**Figure S2**

Sequence alignment of three Aspergillus species showing conserved regions and insertion/deletions. The alignment is presented in four segments, each with a different set of alignment markers (\*, -, and red bar).

Segment 1 (Amino acids 1-80):

*	20	*	40	*	60	*	80	
A.fumigatu : MVRFSLLLASAISLTATASRLKRDTLKPFQEGRFAPSNNASTSLAYDNNLLPRYYDCLPGAHLCDAGQCCDFTCCSDGS	:	80	A.fisher i : MARFSELLLALASVILNTSATSLERDTLKPFLTARFSPSGNEVSQAFENDLVPRLSCTGGGAHLCAGQCCDFTCCSDGS	:	80	A.clavatus : MARFSELLLALASVILNTSATSLERDTLKPFLTARFSPSGNEVSQAFENDLVPRLSCTGGGAHLCAGQCCLYSCCSDGS	:	80

Segment 2 (Amino acids 100-160):

-	*	100	*	120	*	140	*	160
A.fumigatu : CCGAAELCYNDVKPSKGPTYCCKIYTYKECDTRCVPMMSSECCGDGYCKWGHTCSGSYDDDDDD--VGSGGDSGDYDSTT	:	157	A.fisher i : CCPAAQLCYNDVKPSKGPTYCCEIYTYKECDTRCVPMMSSECCGNGFYCKWGHTCSGSYDDDDDDVGSGGGSKDHDSTT	:	160	A.clavatus : CCGAGELCYNDKKPSKGPTYCCAMYTEKQCDTGCVPMQSECCGNGYYCRWGRTRGGYGGTDSDDDDDHETTTERTRT	:	160

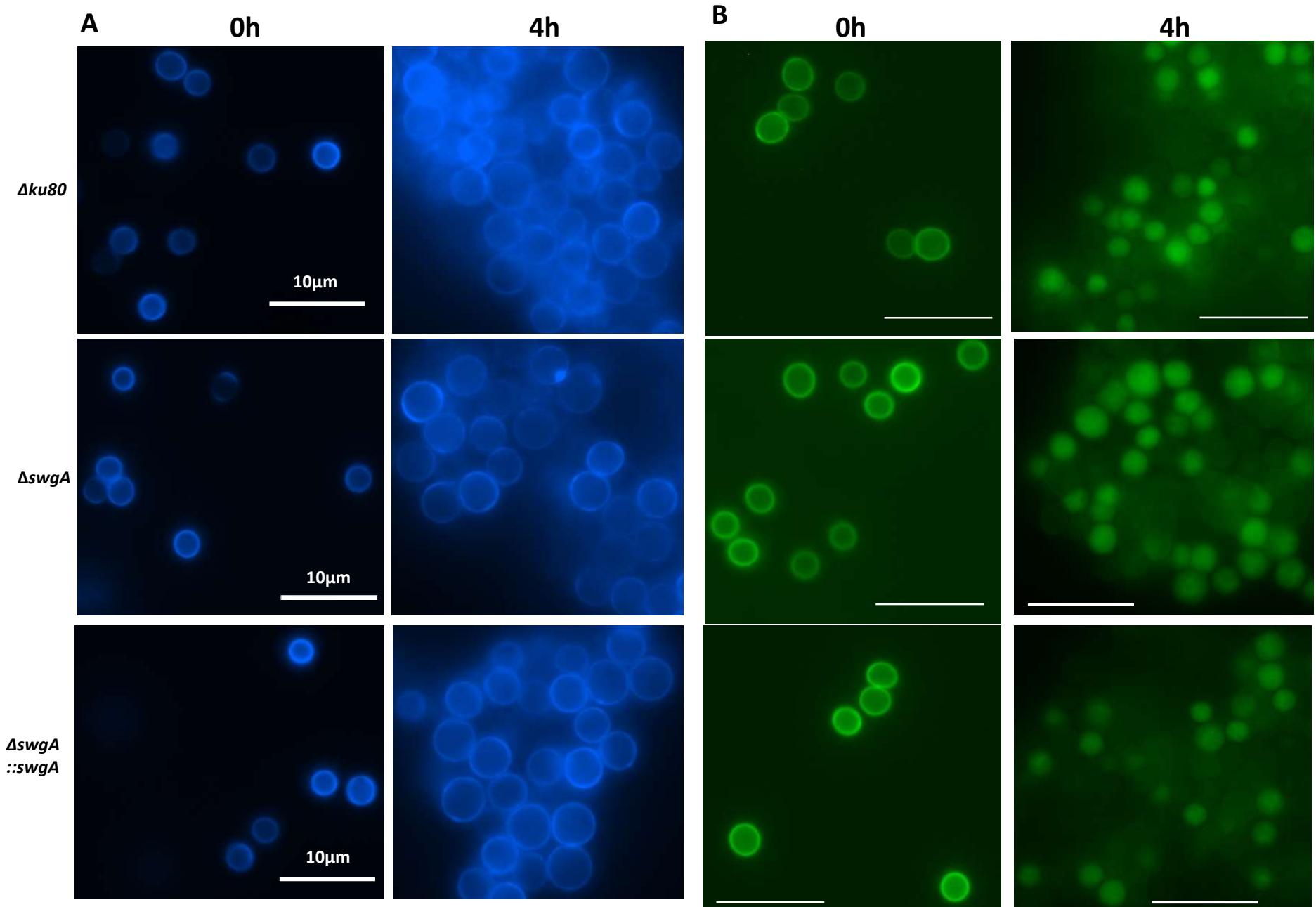
Segment 3 (Amino acids 180-240):

*	180	*	200	*	220	*	240	
A.fumigatu : SSTS YDLTTSYTSTEREVSTTSEYTTTRTEERTTTSESSTRTRATDTDAWETTE TDSSTSTSSRWTMTDFPTGLDFTP	:	237	A.fisher i : S-----MSTERKVSTTSEYTTHTKERRTT SERSTRTRSTDTLGASETTEDDSSTSTSSRRTTDFPTASDFTP	:	230	A.clavatus : YS-----PETESGS S STS TSTSRE SYTITETKSGRRSTSTDSEITTS SSSSSDAEESTS--SSRTTSTTRFTG	:	229

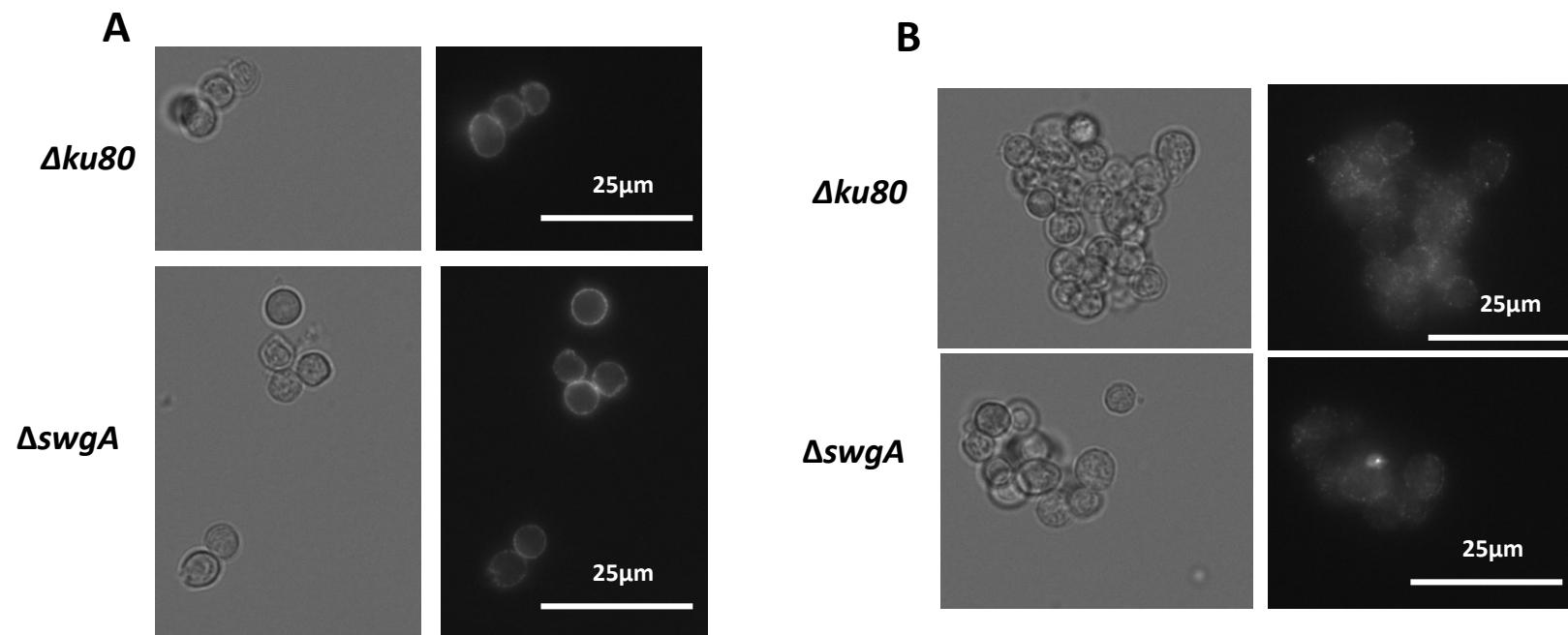
Segment 4 (Amino acids 260-280):

*	260	*	280					
A.fumigatu : AQS FVEAPVPTGPVSLSGANKNSLSSLD MGLLVIVTGAGWYLAL	:	281	A.fisher i : ARSFVVEAPAPTGT VSLSGANKNSLSSLD MGLLVIVTG TGWYFAL	:	274	A.clavatus : VATAIAAPNPHSQAGDSAASSHSTS LNTRFIVILAGI LGYI RL	:	272

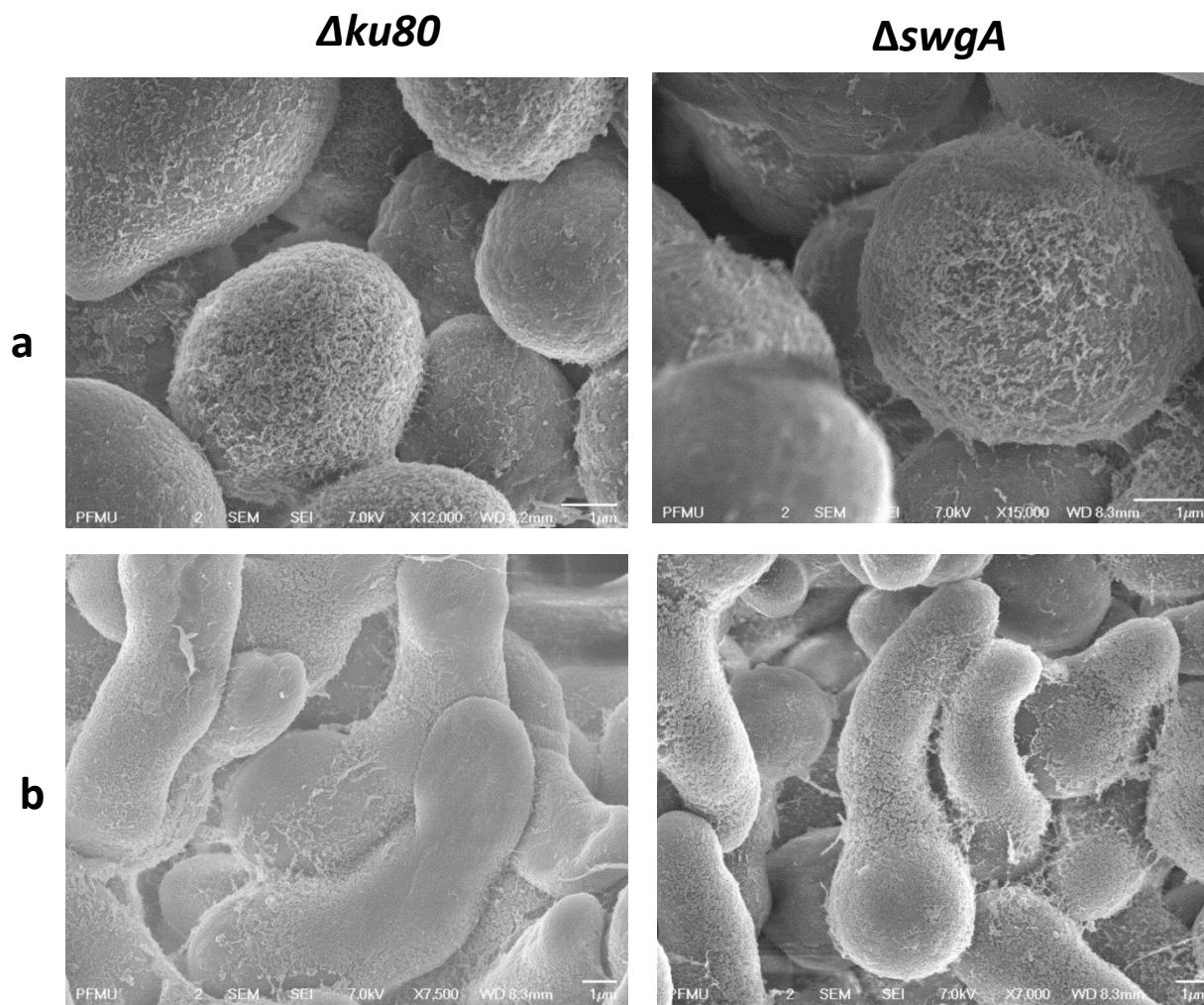
**Figure S3**



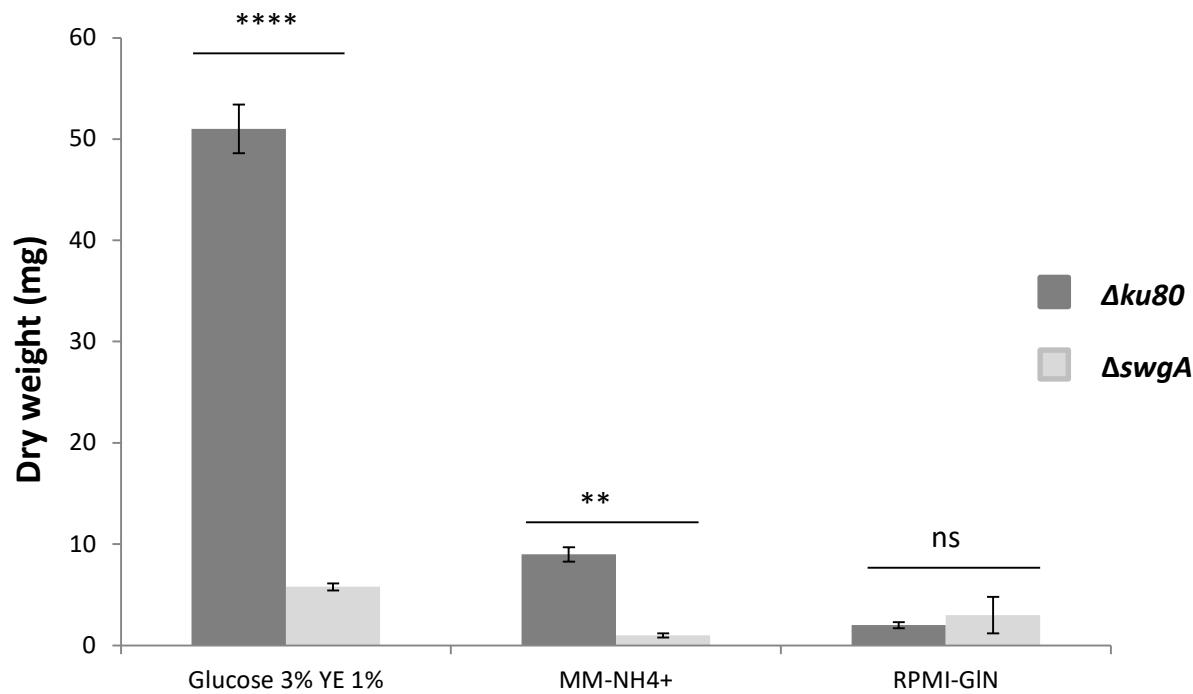
**Figure S4**



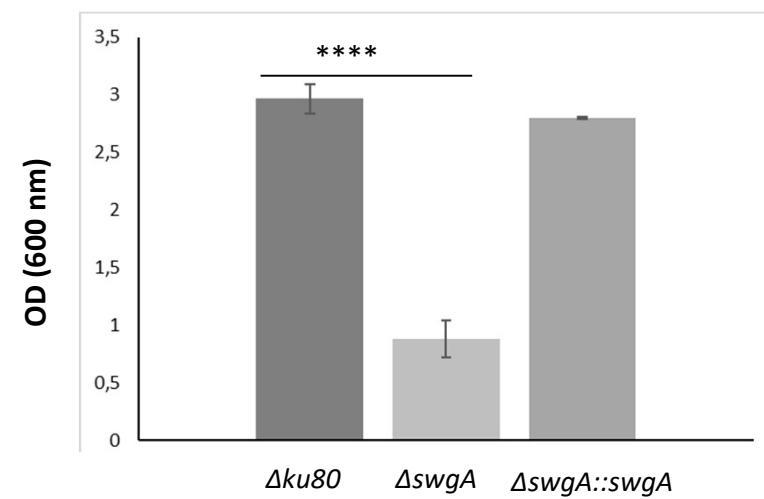
**Figure S5**



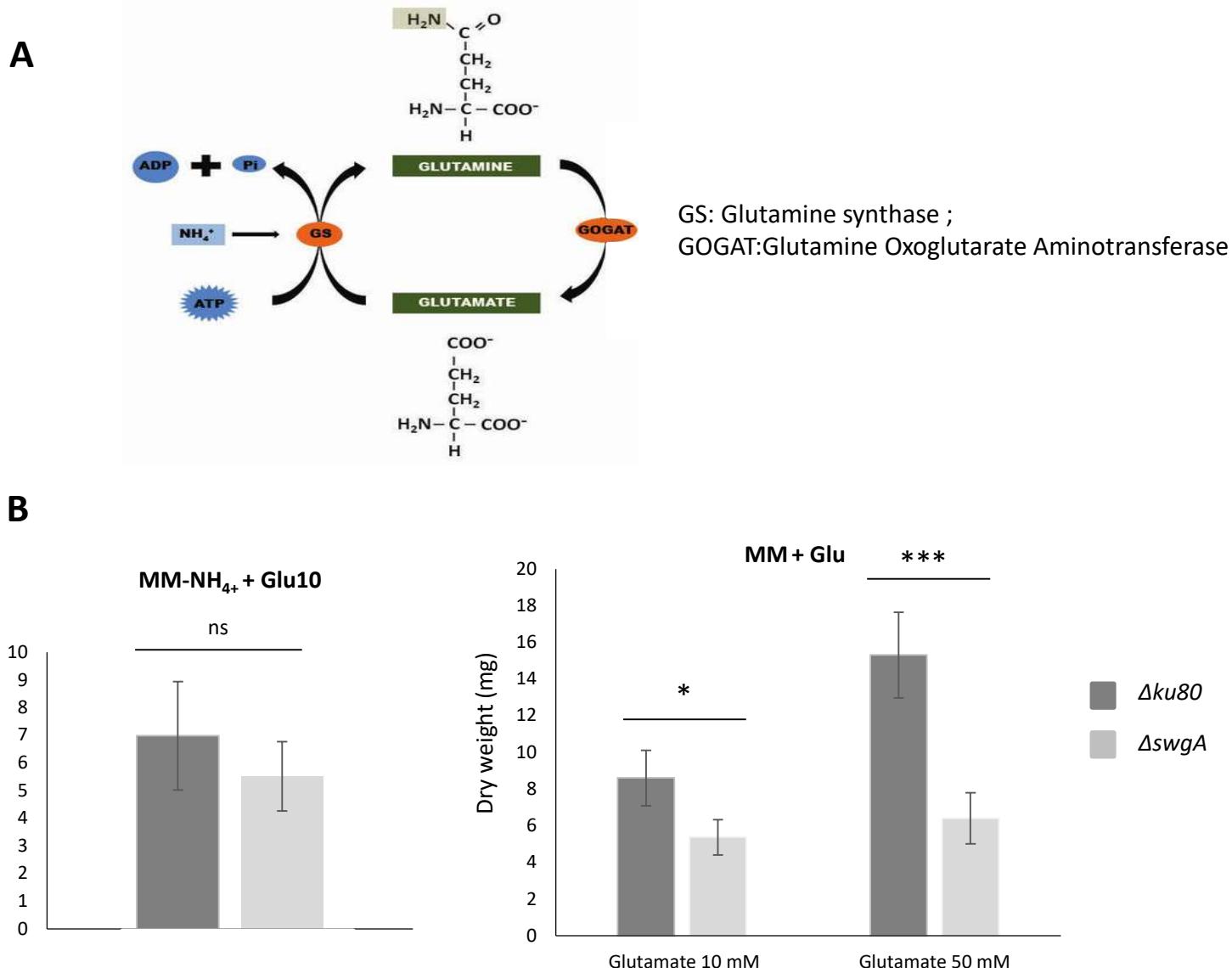
**Figure S6**



**Figure S7**



**Figure S8**



**Table S1 :** Primers used in this study

Name	Sequence
<i>swgAcompF1</i>	AATTGAGCTCGGTACT <b>GCGCAG</b> ACACACGCCGTGGTAT
<i>swgAcompR1</i>	GGACCTGAGTGATGCACCGATACAATGCGAGATA
<i>swgAcompF2</i>	TGGTCCATCTAGTGCTCGGTGGACGACCAGGTAGATCACGAGGCCACCTGC
<i>swgAcompR2</i>	GCCAAGCTTCATGCCCTGCGCACATGGTGTCTACCCCTGCT
<i>areA-RTF</i>	CGACCGACTCCAACCGCTGT
<i>areA-RTR</i>	GGCGGGCGACTCGATAGGAA
<i>swgA-RTF</i>	CTCCACCTCGCTAGCATACG
<i>swgA-RTR</i>	TAGACACTCCCGCTCCGTA

**Table S2:** Characteristics of the protein encoded by the AFUA\_8G01170 gene and orthologs in others species

Species	Size (amino-acids)	Signal Peptide	GPI-anchor	Gene accession number
<i>A.fumigatus</i> AF293	281	18: TAT-AS	254 SGA	AFUA_8G01170
<i>A.fumigatus</i> A1163	281	19: ATA-SR	254 SGA	AFUB_084830
<i>A.fischeri</i>	274	18: TTT-AS	246 SGA	XP_001261813.1
<i>A.clavatus</i>	272	19: TSA-TS	245 DSA	XP_001275113.1

**Table S3:** Percentage of identities between the different proteins:XP\_001275113.1-*A.clavatus*; AFUA\_8G01170-*A.fumigatus*; XP\_001261813.1-*A.fischeri*.

	<i>A.fumigatus</i>	<i>A.fischeri</i>
<i>A.clavatus</i>	43	44
<i>A.fumigatus</i>		<b>84</b>