Table S1: Primers used in this study with restriction sites shown underlined. The ribosome binding sequences (RBS) are shown as bold letters

Primer	Sequence	Purpose
*Bla*F	ACATGCATGCATGTGAATTCGACGAAAGGGCCTCGTGATACGCCT (*SphI*)	Cloning
*Bla*R	CCGCATATGACTC TTCCTTTTTCAATATTATTGAAG-3' (*NdeI*)	Cloning
AGMf	AGCATATG**TGAGGAGGATGAACGACGC**ATGTCAATTGAACAAACATT (*NdeI*)	Cloning
AGMr	ACGGATCCCTATTTAACTAATTCAGATACTGC (*BamHI*)	Cloning; RT-PCR
NAGf	GAGGATCC**TGAGGAGGATGAACGACGC**ATGACTGAGACTAGCATTAGTG (*BamHI*)	Cloning; RT-PCR
NAGr	GGAAGCTTCTACTTATGATAGGCAGCA (*HindIII*)	Cloning
UAPf	GCAAGCTT**TGAGGAGGATGAACGACGC**ATGACAGTTAAATCACAAC (*HindIII*)	Cloning
UAPr	ATGCGGCCGCTTAAATAATATCGCCATTTT (*NotI*)	Cloning
PetF	TAGGTGGTGCTCGAGTGCGGCCGCAAG(*XhoI*)	Cloning
PetR	AATGGTGCATGCAAGGAGATGGC (*SphI*)	Cloning
PucF	GGAGCATGCTTGGCGTAATCATGGTCATA (*SphI*)	Cloning
PucR	TGCTCGAGTATGGTGCACTCTCAGTACAA (*XhoI*)	Cloning
TetF	GCTTAGTACTCATGTTTGACAGCTTATCATC(ScaI)	Cloning
TetR	AATCACCGGTCCGGCTTCCATTCAGGTCGAGG(AgeI)	Cloning
NAGF1	CTATGTTGCCTAACTATAATGTCTCC	RT-PCR
NAGR1	GCACAACTTGTCATGTATATCATCA	RT-PCR
UAPF1	ATGGTAATGGTGGATTATATAAGGC	RT-PCR
UAPR1	ATCCTTGATTATCAATAACTCCACC	RT-PCR

Table S2: Plasmids used in this study.

Plasmid (size)	relevant characteristics	reference
TOPO-bluntII (3.5 kb)	Kan^R; broad range vector	Invitrogen[1]
pUC19 (2.9 kb)	Amp^R, broad range vector	Invitrogen[1]
pBBR122 (5.3 kb)	Cm^R; Kan^R; broad range vector	MoBiTec[2]
pBBR-Tet (6.4 kb)	Tet^R, Cm^R; Kan^R	this study
pUC-MCS (2.9 kb)	Amp^R; contains pET-30 MCS sequence at at *SphI* and *XhoI*	this study
pUC-bla (2.9 kb)	Amp^R ;contains *bla* promoter sequence at *SphI* and *NdeI* in PET-MCS	this study
pUC-bla-A (4.5 kb)	Amp^R; contains AGM1 sequence at *NdeI* and *BamHI* in PET-MCS	this study
pUC-bla-A-N (5.9 kb)	Amp^R ; contains NAG5 sequence at *BamHI-HindIII* in PET-MCS	this study
pUC-GlcNAc (7.3 kb)	AmpR; contains UAP1 sequence at *HindIII-NotI* in PET-MCS	this study
pBBR-GlcNAc (10.9 kb)	Kan^R; Tet^R; contains whole operon at *SphI* and *PsPOM1*	this study

1 – Carlsbad, CA
2 – Goettingen, Germany

Table S3: Mass spectrometer main working parameters for glucose and GlcNac quantitative analysis in acid hydolysates

Parameter	value
Declustering Potential (DP, V)	-30
Entrance potential (EP, V)	-10
Collison Energy (CE, V)	-11
Collison Cell exit Potential (CXP,V)	-2
Curtain Gas (CUR)	11
Collision Gas (CAD)	medium
Ion Spray Voltage (IS, V)	-2600
Temperature (℃)	350
Ion Sourse Gas 1 (GS1)	20
Polarity of anaslysis	negative
Ion transition for GlnNac, m/z	220/119
Ion transition for Glucose, m/z	179/89

Table S4: Mass spectrometer main working parameters for glucose and GlcNac analysis in enzyme hydrolysates

Parameter	value
Declustering Potential (DP, V)	-90
Entrance potential (EP, V)	-4
Curtain Gas (CUR)	10
Ion Spray Voltage (IS, V)	-4500
Temperature (℃)	200
Ion Sourse Gas 1 (GS1)	10
Polarity of anaslysis	negative
Ion for GlnNac, m/z	220
Ion for Glucose, m/z	179
Ion for Glucose-GlcNac, m/z	382
Ion for Glucose-GlcNac-Glucose, m/z	544