Supplementary Figure Legends

Figure S1. Putative metabolic network of *G. xylinus*. These metabolic pathways represent a compilation of established pathways in *E. coli* and *G. xylinus*. The pathway outlined by bold arrows represents the synthetic operon proposed from genes of *C. albicans*. Additionally, a gene we have targeted for deletion (GlcNac-6-P Deacetylase, NagA) is indicated with red cross hatches. Major metabolite inputs and outputs are boxed in bold. The pathways of central carbon metabolism are shown with intermediated steps omitted for clarity. The major carbon inputs and outputs are shown in boxes.

Figure S2. Linear regression curve for known glucose (a) and for GlcNac (b) to quantify glucose and GlcNac in acid hydrolyzed BC and MBC samples by LC-MS/MS.

Figure S3. (a) Construction of recombinant pBBR-GlcNac plasmid having *C. albicans* operon with *bla* promoter. Restriction sites used for cloning are shown as bold letters. (b) Confirmation of transformants. PCR was carried out to confirm the presence of AGM1, UAP1, NAG5, tetracycline genes and bla promoter in the plasmids isolated from transformed *G. xylinus* cells. (c) AFM imaging for the morphology of GlcNac-fed engineered (+ operon) and control (- operon; plasmid only) cells.

Figure S4. Mass spectrum of cellulose samples treated with cellulase (a-b) and lysozyme (c-e). Mass spectra of MBC treated with *Tricoderma reesei* cellulase at (a) 3.6 min, and (b) 5.0 min. Mass spectra of MBC treated with chicken egg white lysozyme at (c) 2.1 min, (d) 3.5 min and (e) 4.5 min. A mixture of oligomers up to 950 Da Mw was obtained. Mass spectra of lysozyme treated undigested polymer at (f) 2.1 min, (g) 6.7 min.