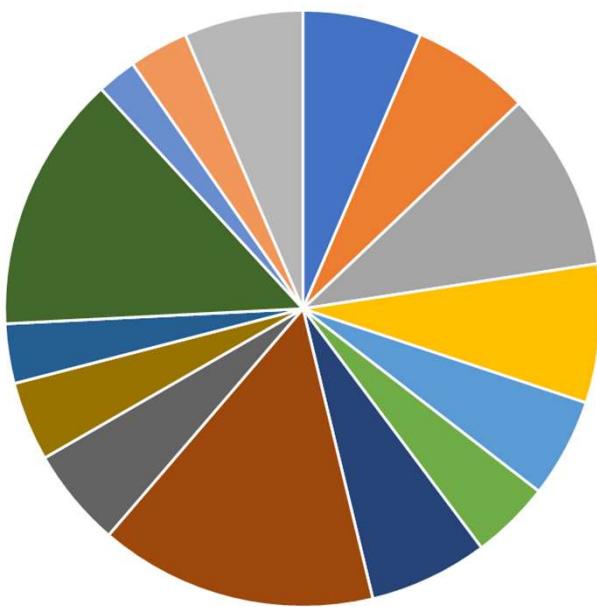


A

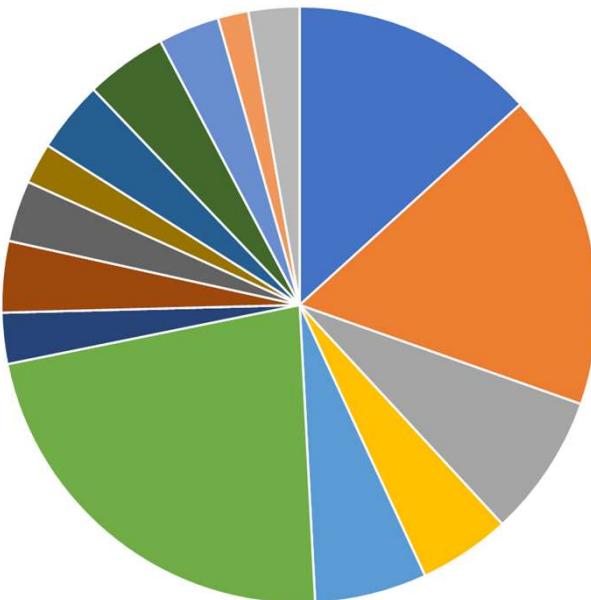
Significantly enriched categories for down-regulated genes



- Sporulation resulting in formation of a cellular spore
- RNA splicing
- Polysaccharide catabolic process
- mRNA processing
- Carbon utilization
- Iron-sulfur cluster assembly
- Cellular amino acid biosynthetic process
- Carbohydrate metabolic process
- Autophagy
- Methionine biosynthetic process
- Acetate metabolic process
- Transcription, DNA-templated
- Regulation of translation
- Trehalose catabolic process
- Conidium formation

B

Significantly enriched categories for up-regulated genes



- Polysaccharide catabolic process
- Carbohydrate metabolic process
- Cell wall organization
- Cellulose catabolic process
- Conidium formation
- Metabolic process
- Microtubule-based process
- Pectin catabolic process
- Xylan catabolic process
- Protein polymerization
- Hyphal growth
- Sterigmatocystin biosynthetic process
- Fatty acid metabolic process
- Cellular carbohydrate catabolic process
- Regulation of secondary metabolite biosynthetic process

Table S1. Oligonucleotides used in this study.

Name	Sequence (5' → 3') ^a	Purpose
OHS0044	GTAAGGATCTGTACGGCAAC	5' Actin_RT_F
OHS0045	AGATCCACATCTGTTGGAAG	3' Actin_RT_R
OHS0602	CGCATCATCCTCACAGTTC	5' <i>stcU</i> RT_F
OHS0603	TGACCGTGATCTTCTTGTGCG	3' <i>stcU</i> RT_R
OHS0604	GCTACTGTTCCAGGCGACTA	5' <i>stcE</i> RT_F
OHS0605	CACAGCTCCATCTCGGTA	3' <i>stcE</i> RT_R
OHS0797	ATGACTGGCGTCTACTCTGG	5' <i>gelA</i> _RT_F
OHS0798	GGGTTGGAGGTCTGGAGAA	3' <i>gelA</i> _RT_R
OHS1445	CCTGGTGTCCAGGACTTGAT	5' <i>gelB</i> _RT_F
OHS1446	CCGGTAATTCCCTGCCGTT	3' <i>gelB</i> _RT_R
OHS1447	ACTACCCTAACCGACCCCTCT	5' <i>afoA</i> _RT_F
OHS1448	TACATGAGTCTCGCCTCGTC	3' <i>afoA</i> _RT_R
OHS1449	GGTCATGTACTGGGCATCG	5' <i>afoB</i> _RT_F
OHS1450	GGAACAGTCTCCTCTCCGT	3' <i>afoB</i> _RT_R