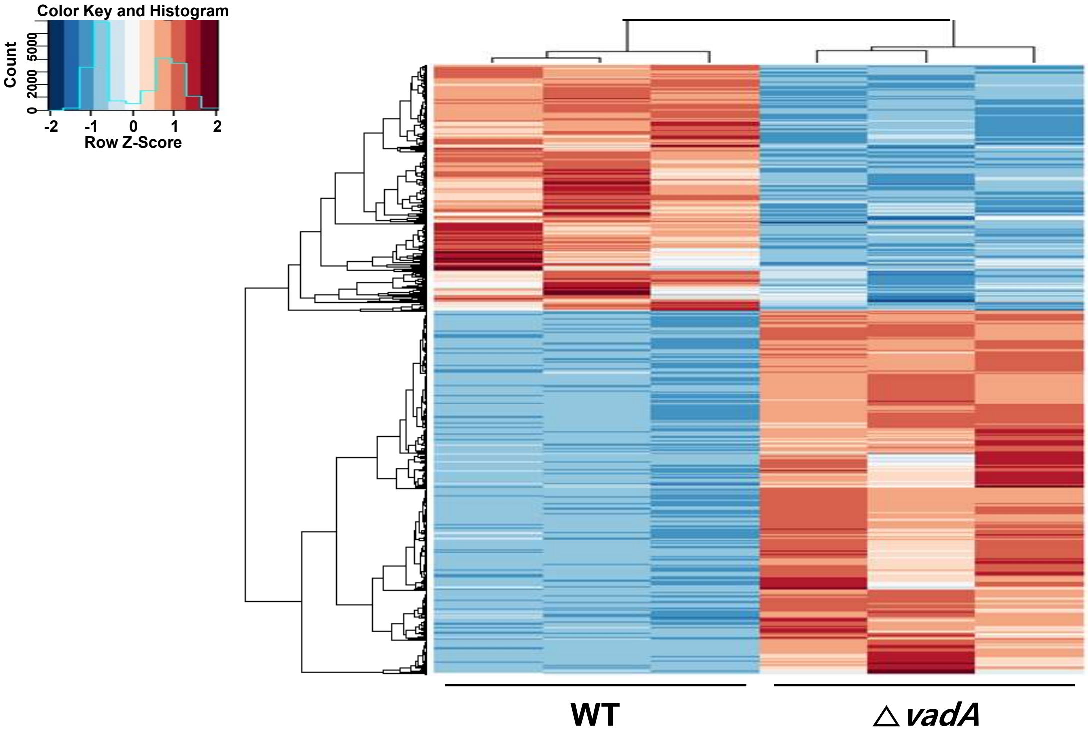
Son *et al*. Figure S1



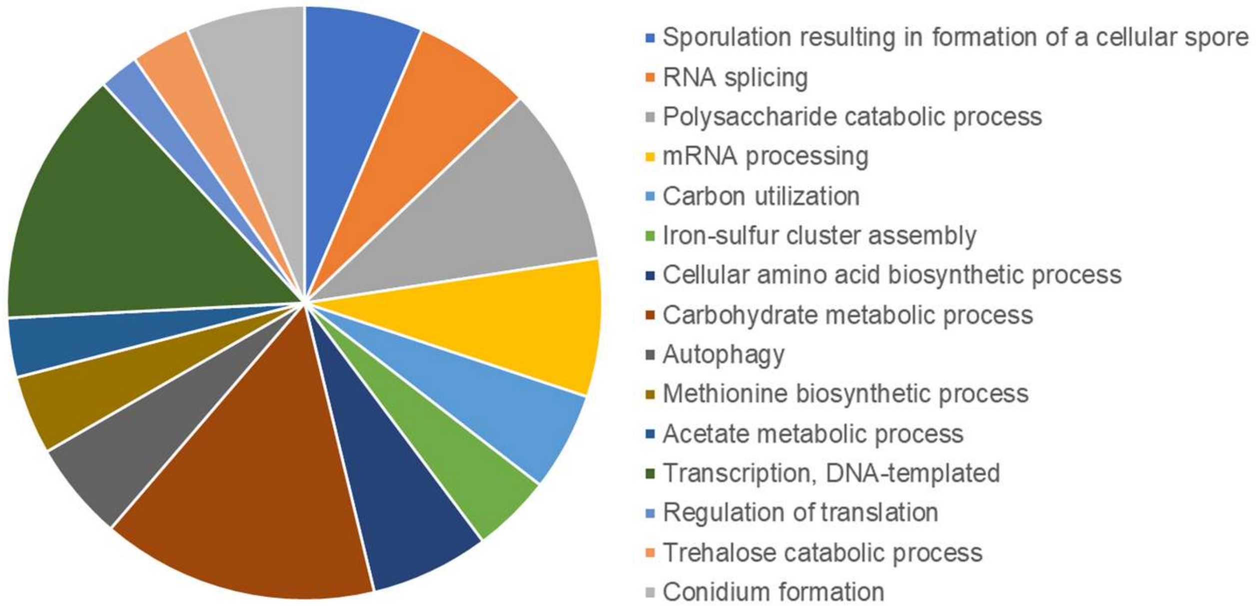
Total: 3,678 genes

(fold change > 2.0 and p-value < 0.5)

Son *et al*. Figure S2

A

Significantly enriched categories for down-regulated genes



B

Significantly enriched categories for up-regulated genes

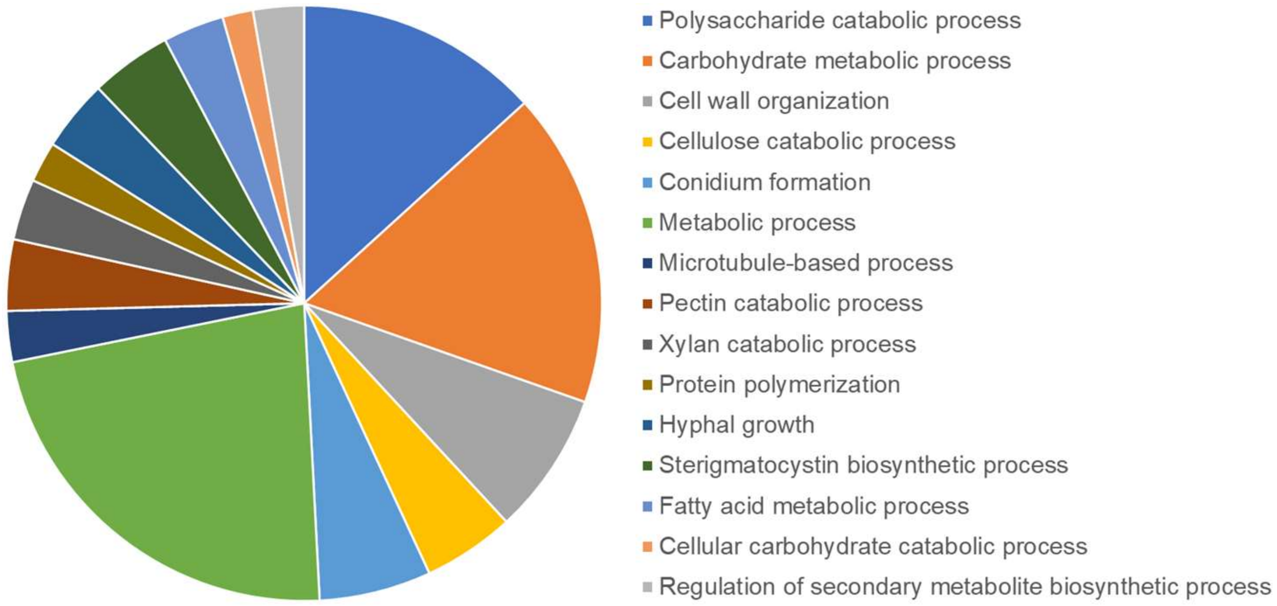


Table S1. Oligonucleotides used in this study.

Name	Sequence (5′ → 3′)[a]	Purpose
OHS0044	GTAAGGATCTGTACGGCAAC	5' Actin_RT_F
OHS0045	AGATCCACATCTGTTGGAAG	3' Actin_RT_R
OHS0602	CGCATCATCCTCACAAGTTC	5' *stcU* RT_F
OHS0603	TGACCGTGATCTTCTTGTCG	3' *stcU* RT_R
OHS0604	GCTACTGTTCCAGGCGACTA	5' *stcE* RT_F
OHS0605	CACAGCTCTCCATCTCGGTA	3' *stcE* RT_R
OHS0797	ATGACTGGCGTCTACTCTGG	5' *gelA*_RT_F
OHS0798	GGGTTGGAGGTCTTGGAGAA	3' *gelA*_RT_R
OHS1445	CCTGGTGTCCAGGACTTGAT	5' *gelB*_RT_F
OHS1446	CCGGTAATTTCCTTGCCGTT	3' *gelB*_RT_R
OHS1447	ACTACCCTAACCGACCCTCT	5' *afoA*_RT_F
OHS1448	TACATGAGTCTCGCCTCGTC	3' *afoA*_RT_R
OHS1449	GGTCATGTACTTGGGCATCG	5' *afoB*_RT_F
OHS1450	GGAACAGTCTCCTTCTCCGT	3' *afoB*_RT_R