Supplementary Tables

Table S1. gRNA-sites used in this study.

Target within *FAS2*	**Sequence encoding gRNA (20 bp)**	**Target ID (CRISPy)**
K83	CAGCTAGTTCGGATGGATCT	649518
K173	ACAATCAAAGACTTGGTCGG	623380
K1551	ATTCCACGGTACATCCACAA	623611

Table S2. PCR-primers used in this study.

F-gRNA-HR	TAGGCGTATCACGAGATCGCGTCAGCTGAAGCTTCTCTTTGAAAAGATAATGTATGATTATGC
R-gRNA-HR	ATACGAAGTTATATTAAGGGTTGTCGACCTGCAGCAGACATAAAAAACAAAAAAAGCACC
F-gRNA-K83	CAGCTAGTTCGGATGGATCTGTTTTAGAGCTAGAAATAGCAAG
R-gRNA-K83	AGATCCATCCGAACTAGCTGGATCATTTATCTTTCACTGCGGA
F-gRNA-K173	ACAATCAAAGACTTGGTCGGGTTTTAGAGCTAGAAATAGCAAG
R-gRNA-K173	CCGACCAAGTCTTTGATTGTGATCATTTATCTTTCACTGCGGA
F-gRNA-K1551	ATTCCACGGTACATCCACAAGTTTTAGAGCTAGAAATAGCAAG
R-gRNA-K1551	TTGTGGATGTACCGTGGAATGATCATTTATCTTTCACTGCGGA

Table S3. Repair-oligonucleotides used in study.[1]

F-K83-Gln	CATAGAGAAATCTTATGCTATTCGCAAGATGCCAAAGAGATTTATTATACTCCAGATCCATCCGAACTAGCTGCAAAGGA
R-K83-Gln	TCCTTTGCAGCTAGTTCGGATGGATCTGGAGTATAATAAATCTCTTTGGCATCTTGCGAATAGCATAAGATTTCTCTATG
F-K83-Arg	CATAGAGAAATCTTATGCTATTCGCGGGATGCCAAAGAGATTTATTATACTCCAGATCCATCCGAACTAGCTGCAAAGGA
R-K83-Arg	TCCTTTGCAGCTAGTTCGGATGGATCTGGAGTATAATAAATCTCTTTGGCATCCCGCGAATAGCATAAGATTTCTCTATG
F-K173-Gln	TCCATTCCAATGTCCAAGACAATCCAGGACCTAGTGGGTGGTAAATCTACAGTCCAAAAT
R-173-Gln	ATTTTGGACTGTAGATTTACCACCCACTAGGTCCTGGATTGTCTTGGACATTGGAATGGA
F-K173-Arg	TCCATTCCAATGTCCAAGACAATCCGAGACCTAGTGGGTGGTAAATCTACAGTCCAAAAT
R-K173-Arg	ATTTTGGACTGTAGATTTACCACCCACTAGGTCTCGGATTGTCTTGGACATTGGAATGGA
F-K1551-Gln	GTGTCGCTTCATTCCACGGTACATCCACTAAAGCTAATGACCAAAACGAATCTGCCACAATTAATGAAAT
R-K1551-Gln	ATTTCATTAATTGTGGCAGATTCGTTTTGGTCATTAGCTTTAGTGGATGTACCGTGGAATGAAGCGACAC
F-K1551-Arg	GTGTCGCTTCATTCCACGGTACATCCACTAAAGCTAATGACCGGAACGAATCTGCCACAATTAATGAAAT
R-K1551-Arg	ATTTCATTAATTGTGGCAGATTCGTTCCGGTCATTAGCTTTAGTGGATGTACCGTGGAATGAAGCGACAC

[1] Red color indicates where modifications are introduced to alter sites K83/K173/K1551, green color indicates where modifications are introduced to alter PAM/gRNA-site.

Table S4. Fold change difference in degree of acetylation detected in mutants (*sir2*Δ, *snf1*Δ, *gcn5*Δ, *sir2*Δ*snf1*Δ, *sir2*Δ*gcn5*Δ, *snf1*Δ*sir2*Δ) compared to the control strain.[1]

	***sir2*Δ**	***snf1*Δ**	***gcn5*Δ**	***sir2*Δ *snf1*Δ**	***sir2*Δ *gcn5*Δ**	***snf1*Δ *gcn5*Δ**
K1551(1)			1.62	-2.3	-2.92	
K1551(2)	-3.01	-3.46	0.95	-2.4		
K1551(3)	-2.44	-2.18	1.31	-1.79	-3	-2.05
K173	-3.46	-3.4	0.06	-2.78	-3.96	-3.47
K83			0.73	-1.91		

K1551(1) *ANDK(Acetyl)NESATINEM(Oxidation)M(Oxidation)K*
K1551(2) *ANDK(Acetyl)NESATINEMM(Oxidation)K*
K1551(3) *ANDK(Acetyl)NESATINEMMK*
K173 *TIK(Acetyl)DLVGGK*
K83 *EILCYSK(Acetyl)DAK*

[1] Samples were harvested in glucose-limited chemostats, with the exception of "Batch", which indicates the degree of acetylation difference between the control strain in glucose-limitation to unlimited glucose conditions (Batch). Detected peptide sequences are indicated below the table. (Kumar et al., unpublished).