Table S9 Fold changes of genes involved in fermentation and amino acid catabolism for the SOK2 overexpressing strain versus control.

Systematic name	Gene name	Functional Description	SOK vs Control
YJR155w	AAD10	Putative aryl-alcohol dehydrogenase	-4.17
YNL331c	AAD14	Putative aryl-alcohol dehydrogenase	-2.33
YCR107w	AAD3	Putative aryl-alcohol dehydrogenase	-1.57
YDL243c	AAD4	Putative aryl-alcohol dehydrogenase	-1.60
YGL256w	ADH4	alcohol dehydrogenase IV	3.10
YBR145w	ADH5	alcohol dehydrogenase V	1.57
YMR170c	ALD2	aldehyde dehydrogenase 2 (NAD+)	-1.82
YMR169c	ALD3	stress inducible aldehyde dehydrogenase	-11.49
YPL061w	ALD6	aldehyde dehydrogenase, cytosolic	1.69
YGL148w	ARO2	chorismate synthase	2.31
YBR249c	ARO4	2-dehydro-3-deoxyphosphoheptonate aldolase, catalyzes the first step in aromatic amino acid biosynthesis	3.35
YGL202w	ARO8	Aromatic aminotransferase, expression is regulated by general control of amino acid biosynthesis	2.18
YHR137w	ARO9	Aromatic aminotransferase, catalyzes the first step of tryptophan, phenylalanine, and tyrosine catabolism	-2.05
YDR380w	ARO10	Phenylpyruvate decarboxylase, catalyzes the first specific step in the Ehrlich pathway	-3.02
YGR177C	ATF2	Alcohol acetyltransferase, forms volatile esters during fermentation	4.38
YCL064c	CHA1	L-serine/L-threonine deaminase, catalyzes the degradation of both L-serine and L-threonine	3.33
YDL174c	DLD1	D-lactate dehydrogenase, oxidizes D-lactate to pyruvate	-2.52
YEL071w	DLD3	D-lactate dehydrogenase	3.06
YEL066W	HPA3	D-Amino acid N-acetyltransferase, catalyzes N-acetylation of D-amino acids	2.29
YER086w	ILV1	Threonine deaminase, catalyzes the first step in isoleucine biosynthesis	1.97
YMR108w	ILV2	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis	1.50
YLR355c	ILV5	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis	1.58
YCL009c	ILV6	Regulatory subunit of acetolactate synthase	1.62
YOR108w	LEU9	2-Isopropylmalate synthase, catalyzes the first step in the leucine biosynthesis pathway	2.32
YDR081c	PDC2	pyruvate decarboxylase regulatory protein	-1.51

YLR134w	PDC5	pyruvate decarboxylase, isozyme 2	-2.21
YGR087c	PDC6	pyruvate decarboxylase 3	-5.09
YPR026w	ATH1	acid trehalase, vacuolar	-3.40
YDR001c	NTH1	neutral trehalase (alpha,alpha-trehalase)	-2.20
YBR001c	NTH2	alpha,alpha-trehalase	-3.92
YKL127w	PGM1	phosphoglucomutase, minor isoform	3.03
YMR105c	PGM2	phosphoglucomutase, major isoform	-1.85
YBR126c	TPS1	alpha,alpha-trehalose-phosphate synthase, 56 KD subunit	-1.80
YDR074w	TPS2	alpha,alpha-trehalose-phosphate synthase, 102 KD subunit	-2.45
YMR261c	TPS3	alpha,alpha-trehalose-phosphate synthase, 115 KD subunit	-1.52
YML100w	TSL1	alpha,alpha-trehalose-phosphate synthase, 123 KD subunit	-2.77
YAL054c	ACS1	acetyl-CoA synthetase	-2.20
YLR153c	ACS2	acetyl-coenzyme A synthetase	2.17
YPL028W	ERG10	Acetyl-CoA C-acetyltransferase; involved in the first step in mevalonate biosynthesis	1.77
YML126C	ERG13	3-hydroxy-3-methylglutaryl-CoA synthase, involved in the second step in mevalonate biosynthesis	2.09
YIL160C	POT1	3-ketoacyl-CoA thiolase involved in beta-oxidation of fatty acids	-4.82