

Table S1 Validation of transcriptomic results by quantitative PCR

Oligonucleotides	<i>S. cerevisiae</i> gene name	<i>Y. lipolytica</i> gene name	Ratio Met	Ratio Cys	Ratio Sul
CGGAGACATTGACCACTT_F TAGTTCCTTTCGGATAATGGCG_R	MET3	YALI0B08184g	0.04 ± 0.02	0.19 ± 0.07	0.35 ± 0.09
ACGACAAGTTCATTTCTGACCGTT_F GGTTGGGAAGAGCTCCAGAGAT_R	ARO9	YALI0C05258g	0.01 ± 0.01	0.01 ± 0.00	0.01 ± 0.00
TGTCTGAGCCCATGCAA_F GCAGAGCAGTCACAAAAGC_R	JLP1		0.01 ± 0.00	0.06 ± 0.04	0.06 ± 0.02
ACCGAGCGAGACGAGTA_F GGCCTCATCAATGTACACAGA_R	SPE3	YALI0E33143g	3.49 ± 0.02	2.98 ± 0.48	2.74 ± 0.19
CTCTCGGCGTCGGAACC_F GTTGGCTCCCAGCTTCTTGT_R	BAT1	YALI0D01265g	3.57 ± 1.27	3.37 ± 0.51	-
ACCATGATTCTTCCCATCG_F TGACAAAACCCAAAGGCG_R	SSU1	YALI0E24167g	-	-	29.79 ± 4.29
TCCAGGCCGTCTCTCCC_F GGCCAGCCATATCGAGTCGCA_R	ACT1		-	-	-

Ratio Met: high/low methionine; Ratio Cys: high /low cystine; Ratio Sul: high/low sulfate.

Values indicated are means of three experiments, with ecart-type.