

Table S1 Comparison of major metabolites quantified through GC-MS and LC-QqQ-MS between control and zinc addition based on various cell growth stages[§] (* $p < 0.05$).

Metabolites (nmol/g DCW)		Stage I (0.1 g/L biomass)			Stage II (1.5 g/L biomass)			Stage III (3.0 g/L biomass)		
		CK	Zn	Ratio (Zn/CK)	CK	Zn	Ratio (Zn/CK)	CK	Zn	Ratio (Zn/CK)
Glycolysis	G6P	7.44±2	5.19±2	0.70	0.69±0.1	1.78±0.1	2.58*	1.17±0.5	1.27±0.6	1.09
	F6P	0.87±0.2	0.59±0.1	0.68	0.26±0.1	0.64±0.0	2.46*	0.86±0.3	0.41±0.1	0.48
	FBP	1.04±0.4	0.71±0.1	0.68	0.11±0.1	0.18±0.01	1.64	0.49±0.4	0.06±0.04	0.12
	2PGA	0.59±0.4	0.30±0.3	0.51	0.073±0.1	0.2±0.3	2.74	0.11±0.1	0.062±0.1	0.56
	PEP	0.65±0.4	0.22±0.1	0.34	0.17±0.1	0.25±0.1	1.47	0.23±0.1	0.16±0.04	0.70
PP-pathway	Ru5P	0.44±0.2	0.081±0.03	0.18	0.11±0.1	0.20±0.1	1.82	0.29±0.2	0.26±0.1	0.90
	R5P	0.53±0.3	0.18±0.1	0.34	0.06±0.03	0.08±0.01	1.33	0.08±0.03	0.05±0.01	0.63

Table S1 continued

Metabolites (nmol g ⁻¹ DCW)		Stage I (0.1 g L ⁻¹ biomass)			Stage II (1.5 g L ⁻¹ biomass)			Stage III (3.0 g L ⁻¹ biomass)		
		CK	Zn	Ratio (Zn/CK)	CK	Zn	Ratio (Zn/CK)	CK	Zn	Ratio (Zn/CK)
PP-pathway	Xu5P	0.73±0.1	0.27±0.03	0.37*	0.15±0.03	0.27±0.01	1.80*	0.40±0.05	0.34±0.01	0.85
	S7P	0.50±0.2	0.23±0.1	0.46	0.073±0.05	0.14±0.1	1.92	0.16±0.1	0.35±0.1	2.19
	E4P	0.64±0.3	0.16±0.1	0.25	0.060±0.1	0.082±0.01	1.37	0.03±0.01	0.03±0.01	1.00
Amino acids	Val	264.0±29	392.65±0.0	1.49*	14.41±3	15.13±0.4	1.05	4.31±0.3	8.25±0.2	1.91*
	Gly	654.87±95	806.18±14	1.23	55.96±7	42.01±1.5	0.75	20.02±3	33.78±3	1.69*
	Ser	362.22±16	446.23±7	1.23*	22.17±2	22.73±0.6	1.03	11.69±0.4	21.00±1.1	1.80*
	Proline	310.04±14	270.88±0.0	0.87	23.04±2.6	23.69±0.5	1.03	12.56±0.9	13.71±1.1	1.09
Others	Trehalose	202.43±20	320.12±14	1.58*	33.43±2.7	26.93±1.1	0.81	292.88±65	211.98±46	0.72

Table S1 continued

Metabolites (nmol g ⁻¹ DCW)		Stage I (0.1 g L ⁻¹ biomass)			Stage II (1.5 g L ⁻¹ biomass)			Stage III (3.0 g L ⁻¹ biomass)		
		CK	Zn	Ratio (Zn/CK)	CK	Zn	Ratio (Zn/CK)	CK	Zn	Ratio (Zn/CK)
Others	Mannose	370.70±156	308.76±7	0.83	41.50±6.4	32.18±9.7	0.78	12.88±2.1	9.52±0.98	0.74
	Fructose	3913.74±32	5444.41±21	1.39*	287.94±7.5	220.17±15	0.76*	82.54±18	23.13±5.9	0.28*
	GSSG	490.71±174	303.31±103	0.62	98.14±50	160.90±54	1.64	163.94±10	242.80±7.6	1.48*
	GABA	238.35±29	337.36±43	1.42	ND	31.44±5.2		ND	16.85±0.3	
	NAD ⁺	26.13±20	12.05±9.4	0.46	4.16±2.9	6.39±4.7	1.54	3.56±2.6	3.26±2.2	0.92
	NADH	0.38±0.1	0.29±0.1	0.76	0.06±0.03	0.16±0.1	2.67	0.33±0.1	0.25±0.1	0.76
	NADP ⁺	0.61±0.1	0.12±0.03	0.20*	0.17±0.02	0.14±0.1	0.82	0.069±0.01	0.015±0.001	0.21*
	NADPH	0.11±0.1	0.01±0.01	0.09	0.01±0.002	0.01±0.002	0.94	0.01±0.001	0.001±0.001	0.26

[§]ND, not detectable.

Supplementary figures

Fig. S1. Overview of the number of unique metabolites and common metabolites at different growth stages in control and zinc-supplemented cells.

Numbers in grey and orange background means numbers of the unique metabolites detected in the control and zinc-supplemented cells at different cell growth stages, respectively, whereas numbers in green background indicate numbers of common metabolites with or without zinc addition.

Fig. S2. Effects of serine (A) and valine (B) addition on the glucose consumption of *S. cerevisiae* SPSC01 in presence of 7.5 g L⁻¹ acetic acid.

The concentrations of serine and valine used in this study were (g L⁻¹): 0, 0.2, 0.5 and 1.0, respectively. Acetic acid was added at the final concentration of 7.5 g L⁻¹ in the culture medium after autoclaving and cooling the medium to room temperature. Yeast strain of SPSC01 was activated in seed medium by overnight cultivation for two times, which was then deflocculated by 0.2 M sodium citrate, and the initial inoculum was adjusted to OD_{620nm} of 2.0. Five milliliter of the seed culture was inoculated to 250 ml flasks containing 100 ml fermentation medium and the culture was incubated at 150 rpm, 30 °C for 66 h. Samples were collected at a 12 h interval, and residual glucose concentrations were determined.

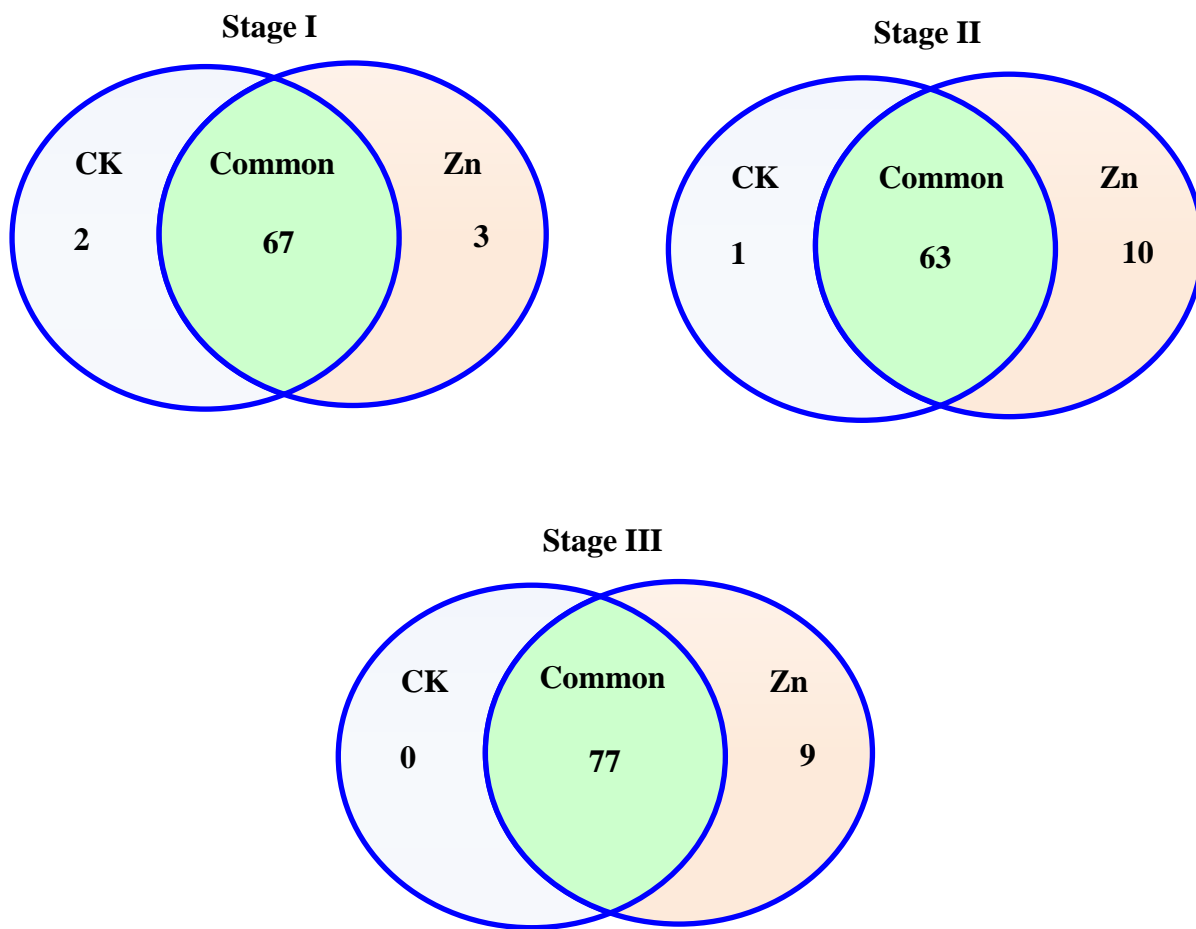


Fig. S1.

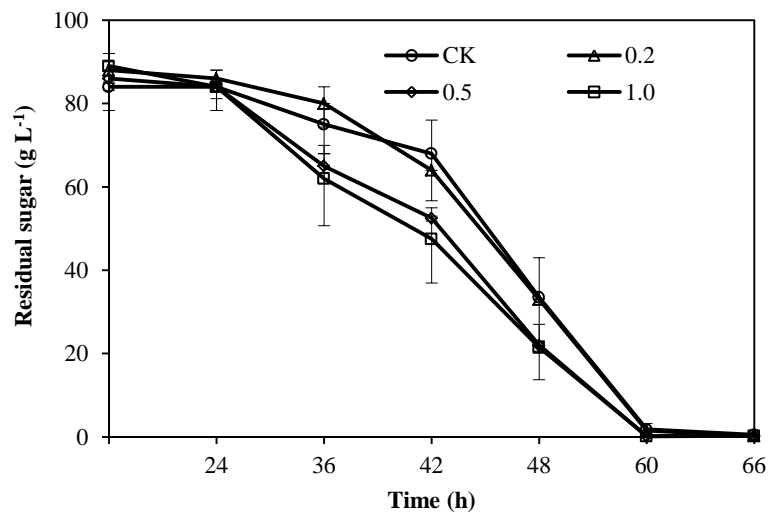


Fig. S2A

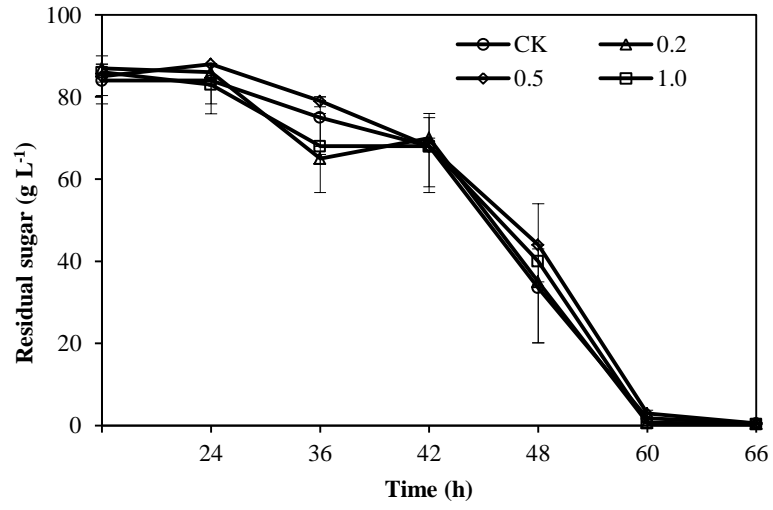


Fig. S2B