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Co-utilization of microalgae and heterotrophic microorganisms improves wastewater treatment efficiency

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Abstract

Wastewater treatment using co-culture systems of microalgae and heterotrophic microorganisms is expected to be useful under atmospheric dilute carbon dioxide conditions. In this study, we investigated the combination of microalgae and heterotrophic microorganisms to improve the efficiency of wastewater treatment. Furthermore, to elucidate the cause of the changes in wastewater treatment efficiency in the co-culture system, changes in gene expression were revealed through transcriptome analysis. Three types of microalgae and five heterotrophic microorganisms were used in combination for wastewater treatment. The combination of *Chlamydomonas reinhardtii* NIES-2238 and *Saccharomyces cerevisiae* SH-4 showed the highest wastewater treatment efficiency. Using this combination for artificial wastewater treatment, the removal rates of TOC (Total organic carbon), $PO4^{3-}$, and NH_4^+ reached 80%, 93%, and 63%, respectively, after 18 h of treatment. Transcriptome analysis revealed that the combined wastewater treatment altered the expression of 1371 and 692 genes in *C. reinhardtii* and *S. cerevisiae*, respectively. The genes upregulated in *C. reinhardtii* included those related to molecular and ion transport. Genes upregulated in *S. cerevisiae* included those related to cell protection from various types of damage and stress. To the best of our knowledge, this is the first study to show that a combination of green algae and yeast improves the efficiency of wastewater treatment. As both the green alga *C. reinhardtii* and the yeast *S. cerevisiae* are highly safe microorganisms, the establishment of their effective combination for wastewater treatment is highly significant.

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30

31 **Keywords**

32 green algae; heterotrophic microorganisms; microalgae; wastewater treatment; yeast

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1. Introduction

Daily household and industrial activities discharge water containing carbon and nutrient compounds, such as nitrogen and phosphorus. These compounds are the main causes of eutrophication in oceans and lakes (Dodds et al., 2016; Nguyen et al., 2020). Eutrophication disrupts the balance of the water ecosystem and leads to environmental pollution; therefore, it is necessary to remove nutrient compounds to avoid eutrophication (Nguyen et al., 2020). In general wastewater treatment, the activated sludge method is used in which organic matter is decomposed by microorganisms (Gernaey et al., 2004; Mujtaba et al., 2017; Wilén et al., 2018). However, the decomposition of organic matter using the activated sludge method requires a large amount of oxygen, which means that a large amount of electricity is required for aeration. The energy for aeration accounts for 60–80% of the total energy used in wastewater treatment using the activated sludge method (Chauchuat et al., 2005). Furthermore, because the activated sludge method has low nitrogen and phosphorus removal efficiency, additional treatment is often required.

Wastewater treatment with microalgae has attracted attention as an energy-saving alternative to activated sludge treatment (Abdel-Raouf et al., 2012; Mujtaba et al., 2017; Wang et al., 2016). As microalgae perform photosynthesis, they do not require aeration and are expected to fix dilute CO_2 in the atmosphere. In addition, they are characterized by high nitrogen and phosphorus removal capacities compared to common microorganisms. In a previous study, the green alga *Chlamydomonas reinhardtii* was used for wastewater treatment in a palm oil mill with

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52 removal rates of 100% for ammonium and nitrate, 66–89% for phosphate, and 16.7–33.2% for
53 chemical oxygen demand (COD) (Mohd et al., 2024). In another report, more than 80% of the
54 phosphorus and nitrogen in wastewater were removed when wastewater was treated with the green
55 algae *Chlorella vulgaris* and *Scenedesmus sp.* (Tam et al., 1990). In addition, when wastewater was
56 treated with the cyanobacterium *Arthrospira platensis*, more than 98% of the COD, phosphorus,
57 and nitrogen were removed within 4–5 days of treatment (Hena et al., 2018).

58 One problem with photosynthetic microalgae is that their growth rate is lower than that of
59 common microorganisms in an atmosphere of dilute CO_2 (Chinnasamy et al., 2009). In microalgae
60 cultivation, high-concentration carbon dioxide aeration is performed to increase the growth ability
61 of the microalgae. Therefore, the co-cultivation of microalgae and heterotrophic microorganisms is
62 attracting attention to improve the growth of microalgae without the aeration of high-concentration
63 carbon dioxide (Naseema Rasheed et al., 2023; Ray et al., 2022). Previous studies reported that the
64 growth rate of microalgae increases under dilute CO_2 atmospheric conditions when *C. reinhardtii*
65 and *Saccharomyces cerevisiae* are co-cultured (Karitani et al., 2024a; Karitani et al., 2024b). Co-
66 cultivation of *C. reinhardtii* and *Escherichia coli* promotes microalgal growth (Yamada et al.,
67 2023). These coculture systems of microalgae and heterotrophic microorganisms are expected to
68 increase the growth rate of microalgae, even in wastewater treatment, and improve the efficiency of
69 wastewater treatment using microalgae.

70 In this study, we investigated different combinations of microalgae and heterotrophic

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71 microorganisms to improve the efficiency of wastewater treatment. Specifically, three types of
72 microalgae and five types of heterotrophic microorganisms were used in combinations for
73 wastewater treatment, and the optimal combination for wastewater treatment was determined.
74 Subsequently, wastewater containing higher concentrations of carbon, nitrogen, and phosphorus
75 was treated with the optimal combination of microorganisms, and the removal efficiency was
76 evaluated. Furthermore, to elucidate the cause of the changes in wastewater treatment efficiency
77 with the optimal combination, changes in gene expression were assessed through transcriptome
78 analysis.
79
80 **2. Results**
81 **2.1. Optimal combination of microalgae and heterotrophic microorganisms for wastewater**
82 **treatment**
83 Microalgae and heterotrophic microorganisms were combined for 1x artificial wastewater
84 treatment to determine optimal combinations. Fig. 1 shows the removal rates of TOC (Total organic
85 carbon), PO_4^{3-}, and NH_4^+ in wastewater treatment using microalgae and heterotrophic
86 microorganisms alone and in combination.
87 The TOC removal rate was 11% for *C. vulgaris* NIES-1269, which was the highest among
88 the three microalgae when treated alone (Fig. 1a). When only heterotrophic microorganisms were
89 used, *S. cerevisiae* SH-4 exhibited the highest removal rate (84 %) among the five heterotrophic

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90 microorganisms. When the three types of microalgae and *S. cerevisiae* YPH499 were used in
91 combination for wastewater treatment, the TOC removal rates remained low, whereas when the
92 three types of microalgae and *S. cerevisiae* SH-4 were used in combination, the TOC removal rates
93 were relatively high. Among the 15 microbial combinations, the combination of *C. reinhardtii*
94 NIES-2238 and *S. cerevisiae* SH-4 resulted in the highest TOC removal rate (82 %).

95 *C. vulgaris* NIES-1269 exhibited the highest PO_4^{3-} removal rate (31%) among the three
96 microalgae when the wastewater was treated with microalgae alone (Fig. 1b). When heterotrophic
97 microorganisms were used alone, *S. cerevisiae* SH-4 showed the highest removal rate (94 %) among
98 the five microorganisms. Similar to the TOC removal rate, when the three types of microalgae and
99 *S. cerevisiae* YPH499 were used in combination for wastewater treatment, the PO_4^{3-} removal rates
100 remained low, whereas when the three types of microalgae and *S. cerevisiae* SH-4 were used in
101 combination, PO_4^{3-} removal rates were relatively high. Among the 15 microbial combinations, the
102 PO_4^{3-} removal rate was the highest when *C. reinhardtii* NIES-2238 and *C. vulgaris* NIES-1269 were
103 combined with *S. cerevisiae* SH-4, with 93% and 94%, respectively.

104 *A. platensis* NIES-39 exhibited the highest NH_4^+ removal rate (34%) among the three
105 microalgae when wastewater was treated with microalgae alone (Fig. 1c). When only heterotrophic
106 microorganisms were used, *S. cerevisiae* SH-4 exhibited the highest removal rate (66 %) among the
107 five heterotrophic microorganisms. Similar to the TOC removal rate, when the three types of
108 microalgae and *S. cerevisiae* YPH499 were used in combination for wastewater treatment, the NH_4^+

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109 removal rates remained low. When the three types of microalgae and *S. cerevisiae* SH-4 were used
110 in combination, the NH_4^+ removal rates were relatively high. Among the 15 microbial
111 combinations, the highest NH_4^+ removal rate was achieved when *C. reinhardtii* NIES-2238 and *C.*
112 *vulgaris* NIES-1269 were used in combination with *S. cerevisiae* SH-4 (71% and 70 %,
113 respectively).
114
115 **2.2. Wastewater treatment by optimal combination**
116 Among 15 microbial combinations, the combination of *C. reinhardtii* NIES-2238 and *S.*
117 *cerevisiae* SH-4 was optimal for wastewater treatment (Fig. 1). With this combination, wastewater
118 treatment was conducted for 18 h using 2x artificial wastewater with increased concentrations of
119 TOC, PO_4^{3-} and NH_4^+ to evaluate the wastewater treatment performance (Fig. 2).
120 A similarly high TOC removal rate of over 80% was achieved when *S. cerevisiae* SH-4 was
121 used alone, and when *C. reinhardtii* NIES-2238 and *S. cerevisiae* SH-4 were used in combination
122 (Fig. 2a). The combination of *C. reinhardtii* NIES-2238 and *S. cerevisiae* SH-4 achieved the highest
123 PO_4^{3-} removal rate of 93% (Fig. 2b). This was 7.0 times higher than that achieved with *C.*
124 *reinhardtii* NIES-2238 alone (13%) and 1.1 times higher than that achieved with *S. cerevisiae* SH-4
125 alone (88%). The combination of *C. reinhardtii* NIES-2238 and *S. cerevisiae* SH-4 achieved the
126 highest NH_4^+ removal rate of 63%, which was 1.3 times higher than that achieved with *S. cerevisiae*
127 SH-4 alone (47%) (Fig. 2c). Therefore, the removal rate of PO_4^{3-} and NH_4^+ from 2x artificial

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wastewater was significantly increased using *C. reinhardtii* NIES-2238 and *S. cerevisiae* SH-4 in combination for wastewater treatment.

2.3. Comparison of gene expression in wastewater treatment alone and in combination

After 18 h of wastewater treatment with *C. reinhardtii* NIES-2238 or *S. cerevisiae* SH-4 alone or in combination, total RNA was extracted from each cell and subjected to transcriptome analysis. Volcano plots showing p-values and fold-changes for each gene of *C. reinhardtii* NIES-2238 and *S. cerevisiae* SH-4 obtained by transcriptome analysis are shown in Fig. 3.

In *C. reinhardtii* NIES-2238, the expression of 1371 genes, 636 with upregulated and 735 with downregulated expression, was altered by the combined wastewater treatment (Fig. 3a). In contrast, as shown in Fig. 3b, in *S. cerevisiae* SH-4, the expression of 692 genes, 305 with upregulated and 387 with downregulated expression, was altered by the combined wastewater treatment.

Gene ontology (GO) analysis was performed on the upregulated and downregulated genes in *C. reinhardtii* NIES-2238 and *S. cerevisiae* SH-4 to identify gene functions that were significantly more frequent among the differentially expressed genes (DEGs). The 20 GO terms with the highest log10 (p-value) values obtained by GO analysis are shown in Fig. 4 (for *C. reinhardtii* NIES-2238) and Fig. 5 (for *S. cerevisiae* SH-4).

The GO terms for the upregulated genes in *C. reinhardtii* NIES-2238 were mainly

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147 associated with functions related to chromatin components and nucleosomes (Fig. 4a). They were
148 also associated with functions related mainly to the transport of molecules and ions, such as
149 transporter activity and inorganic molecular body transmembrane transporter activity. Some GO
150 terms for the genes downregulated in *C. reinhardtii* NIES-2238 were related to functions of
151 thylakoids, plastids, chloroplasts, and photosynthetic membranes (Fig. 4b).

152 Some GO terms for the genes upregulated in *S. cerevisiae* SH-4 were associated with
153 functions related to membrane-bound organelles, cellular processes, and signal receptor activity
154 (Fig. 5a). Some GO terms of the genes downregulated in *S. cerevisiae* SH-4 were associated with
155 functions such as cellular processes, intracellular anatomical structure, and cellular anatomical
156 entities (Fig. 5b).

157

158 **3. Discussion**

159 The objective of this study is to clarify the optimal combination of microalgae and
160 heterotrophic microorganisms to improve the efficiency of wastewater treatment by combining
161 microalgae and heterotrophic microorganisms. When *C. reinhardtii* NIES-2238 and *S. cerevisiae*
162 SH-4 were combined for wastewater treatment, TOC decreased from 424 mg/L to 86 mg/L
163 (equivalent to approximately 1275 mg/L and 264 mg/L of COD, respectively [Dubber et al., 2010])
164 with an 80% removal rate, while total phosphorus decreased from 12 mg/L to 0.90 mg/L with a
165 93% removal rate of PO_4^{3-}, and total nitrogen decreased from 39 mg/L to 14 mg/L with a 63%

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166 removal rate of NH_4^+ in 18 h (Fig. 2). Similar to the present study, a previous study treating
167 wastewater containing similar concentrations of carbon, phosphorus, and nitrogen showed that
168 combined wastewater treatment with the microalgae *C. vulgaris* and the fungal *Aspergillus* sp. in
169 concentrated wastewater decreased COD from 1660 mg/L to 622 mg/L with a 63% removal rate,
170 total phosphorus from 52.6 mg/L to 5.35 mg/L with a 90% removal rate, and total nitrogen from
171 97.2 mg/L to 40.0 mg/L with a 59% removal rate after 24 h. (Zhou et al., 2012). In another study,
172 wastewater treatment using a combination of microalgae (*C. vulgaris*) and a fungus *(Ganoderma*
173 *lucidum*) resulted in COD, total phosphorus, and total nitrogen removal rates of 80%, 85%, and
174 74%, respectively (Guo et al., 2017). Therefore, the wastewater treatment efficiency in this study
175 using safer microorganisms was comparable to or higher than that of previous studies. Interestingly,
176 in the present study, the removal rates of TOC, PO_4^{3-}, and NH_4^+ were similar whether 1x artificial
177 wastewater or 2x artificial wastewater was used. Therefore, wastewater containing high
178 concentrations of TOC, PO_4^{3-}, and NH_4^+ could be treated efficiently. However, the composition of
179 actual urban wastewater varies greatly depending on factors, such as region and season. Future
180 studies should examine the combination of *C. reinhardtii* NIES-2238 and *S. cerevisiae* SH-4
181 established in this study, including the treatment of wastewater with various TOC, PO_4^{3-}, and NH_4^+
182 concentrations and actual wastewater containing various compounds.

183 Among the genes with increased expression in *C. reinhardtii* NIES-2238, many were
184 involved in transporting molecules and ions, such as transporter activity and inorganic molecule

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transmembrane transporter activity (Fig. 4a). These genes included those encoding proteins responsible for the uptake of phosphate (CHLRE_02g144750v5) and ammonium (CHLRE_03g159254v5) ions (Supplementary Table 1). Therefore, the combination of *C. reinhardtii* NIES-2238 and *S. cerevisiae* SH-4 may have increased the expression of these genes, contributing to increased phosphorus and nitrogen removal rates.

The GO terms of the downregulated genes in the microalga *C. reinhardtii* NIES-2238 were mainly related to thylakoids, chloroplasts, and photosynthesis (Fig. 4b). Previous studies have reported that when microalgae and heterotrophic microorganisms are co-cultured, light is shielded by heterotrophic microorganisms, and the photosynthetic activity of microalgae is suppressed (Karitani et al., 2024a; Yamada et al., 2023). In the present study, the photosynthetic activity of microalgae could have been suppressed by the co-utilization of microorganisms for wastewater treatment. However, in this study, the combination of *C. reinhardtii* NIES-2238 and *S. cerevisiae* SH-4 did not decrease the removal rate of nutrients but rather increased it. Therefore, it is likely that the light-shielding effect of the co-utilization of these microorganisms did not adversely affect the nutrient removal efficiency. However, the effect of light irradiation conditions on nutrient removal efficiency is unclear, and future optimization of light irradiation conditions for wastewater treatment combining *C. reinhardtii* NIES-2238 and *S. cerevisiae* SH-4 is required.

The GO terms associated with upregulated yeast genes in wastewater treatment in combination with the microalga *C. reinhardtii NIES-2238* were primarily linked to organelles (Fig.

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5a). Among the genes in this GO term were those related to the mitochondria, a type of organelle. The mitochondria are responsible for ATP production (Dimmer et al., 2002; Frey et al., 2000). Previous studies have reported that ATP depletion within *S. cerevisiae* causes cell damage (Schimz et al., 1979). Therefore, when the expression of mitochondrial genes is elevated, the mitochondria are more active in ATP production, and the use of this ATP may protect yeast from cell damage. In line with this, *ATP1*, which is involved in ATP synthesis, was among the upregulated genes (Supplementary Table 3). Therefore, the increased expression of these genes may have contributed to protecting yeast from cell damage and improving the efficiency of wastewater treatment. Among the yeast genes with elevated expression (*TRX1* and *GRX3*), those that protect cells from oxidative stress and damage were identified (Supplementary Table 3). In general, toxicity to microorganisms caused by oxidative stress is an issue in wastewater treatment using microorganisms (Osundeko et al., 2013). Therefore, the microorganisms used must be resistant to oxidative stress. In this study, the combination of microalgae and yeast increased the expression of genes that protect cells from various types of damage and stress, which may have contributed to improved efficiency of wastewater treatment.

The GO terms of *S. cerevisiae* SH-4, genes that were downregulated in wastewater treatment in combination with *C. reinhardtii* NIES-2238 included cell process control, binding, and cell development (Fig. 5b). These functions are associated with yeast cell growth. Previous studies have reported that in co-culture, competition for microbial growth occurs and microbial growth is

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inhibited (Karitani et al., 2024a). Therefore, *S. cerevisiae* SH-4 growth potential may have been reduced in wastewater treatment combined with *C. reinhardtii* NIES-2238 in the present study. However, in this study, the nutrient removal rate was improved by the combined wastewater treatment, indicating that *S. cerevisiae* SH-4 growth potential did not decrease or that the reduction in *S. cerevisiae* SH-4 growth potential did not have a negative effect on nutrient removal.

4. Conclusion

Three microalgae and five heterotrophic microorganisms were combined to determine the optimal combination for wastewater treatment. The results showed that the combination of *C. reinhardtii* NIES-2238 and *S. cerevisiae* SH-4 for wastewater treatment improved nitrogen and phosphorus removal efficiency. To the best of our knowledge, this is the first study to show that a combination of green algae and yeast improves the efficiency of wastewater treatment. Transcriptome analysis revealed the reason for the improved wastewater treatment performance of the combination of green algae and yeast. As both the green alga *C. reinhardtii* and the yeast *S. cerevisiae* are highly safe microorganisms, the establishment of their effective combination for wastewater treatment is highly significant. Based on the findings of this study, it is expected that the combination of *C. reinhardtii* and *S. cerevisiae* will further improve the efficiency of wastewater treatment, thereby establishing this technology as a new alternative to the activated sludge method of wastewater treatment.

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5. Material and methods

5.1. Media and artificial wastewater

The BG11Y medium (1 vol% BG11 broth for microbiology [Sigma-Aldrich Japan, Tokyo, Japan], 5 g/L yeast extract [Formedium, Norfolk, UK], 0.1 vol% trace metal mix A5 + Co [Sigma-Aldrich Japan]), SOT medium (16.8 g/L $NaHCO_3$ [Nacalai Tesque, Kyoto, Japan], 500 mg/L K_2HPO_4 [Nacalai Tesque], 2500 mg/L $NaNO_3$ [Nacalai Tesque], 1000 mg/L K_2SO_4 [Wako Pure Chemicals], 1000 mg/L NaCl [Nacalai Tesque], 200 mg/L $MgSO_4 \cdot 7H_2O$ [Nacalai Tesque], 40 mg/L $CaCl_2 \cdot 2H_2O$ [Nacalai Tesque], 10 mg/L $FeSO_4 \cdot 7H_2O$ [Wako Pure Chemicals], 80 mg/L $Na_2EDTA \cdot 2H_2O$ [Nacalai Tesque], 0. 1 vol% trace metal mix A5+Co, pH 9.0), yeast/peptone/glucose (YPD) medium (10 g/L yeast extract, 20 g/L peptone [Formedium], 20 g/L glucose [Nacalai Tesque]), and NBRC 802 medium (10 g/L Casein peptone [Nacalai Tesque], 2 g/L Yeast extract, 1 g/L $MgSO_4 \cdot 7H_2O$, pH 7.0) were used. For the solid medium, 20 g/L of agar powder [Nacalai Tesque] was added.

The 1x artificial wastewater (0.400 g/L D-(+)-Glucose, 0.200 g/L acetic acid [Nacalai Tesque], 0.078 g/L NH_4Cl [Nacalai Tesque], 0.018 g/L KH_2PO_4 [Nacalai Tesque], 0.013 g/L $MgSO_4 \cdot 7H_2O$, 0.043 g/L $CaCl_2 \cdot 2H_2O$, 0.005 g/L $FeSO_4 \cdot 7H_2O$, 0.200 g/L H_3BO_3 [Nacalai Tesque], 1 mL/L Trace metal mix A5+Co [Sigma-Aldrich Japan], pH 7.5), and 2x artificial wastewater (0.800 g/L D-(+)-Glucose, 0.400 g/L Acetic acid, 0.156 g/L NH_4Cl, 0.036 g/L KH_2PO_4, 0 .013 g/L

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261 $MgSO_4 \cdot 7H_2O$, 0.043 g/L $CaCl_2 \cdot 2H_2O$, 0.005 g/L $FeSO_4 \cdot 7H_2O$, 0.200 g/L H_3BO_3, 1 mL/L Trace
262 metal mix A5+Co, pH 7.5) were prepared as described in a previous study (Feng et al., 2011) with
263 some modifications. Both types of artificial wastewater were autoclaved at 121°C for 20 min before
264 use.
265
266 **5.2. Microorganisms and pre-culture conditions**
267 The green algae *C. reinhardtii* NIES-2238 (Mohd et al., 2024), green algae *C. vulgaris*
268 NIES-1269 (Tam et al., 1990), and the cyanobacterium *A. platensis* NIES-39 (Hena et al., 2018),
269 autotrophic microorganisms used for wastewater treatment in previous studies, were used. Yeasts *S.*
270 *cerevisiae* YPH499 (Ghasem et al., 2002), *S. cerevisiae* NBRC 1953 (Ghasem et al., 2002), and *S.*
271 *cerevisiae* SH-4 (Ghasem et al., 2002), and bacteria *Bacillus subtilis* NBRC 13719 (Guo et al.,
272 2021) and *Bacillus amyloliquefaciens* NBRC 14141 (Xie et al., 2013), heterotrophic
273 microorganisms used for wastewater treatment in previous studies, were also used.
274 BG11Y medium was used for the pre-culture of *C. reinhardtii* NIES-2238 and *C. vulgaris*
275 NIES-1269. The SOT medium was used for the pre-culture of *A. platensis* NIES-39. Microalgae
276 were pre-cultivated at 30°C, 120 rpm, 60 µmol photons/(m^2/s) for 5 days.
277 The YPD medium was used for the pre-culture of *S. cerevisiae* and NBRC 802 medium
278 was used for the pre-culture of *B. subtilis* NBRC 13719 and *B. amyloliquefaciens* NBRC 14141.
279 Heterotrophic microorganisms were pre-cultivated at 30°C and 120 rpm for 3 days.

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5.3. Treatment of wastewater with microalgae and heterotrophic microorganisms alone and in combination

Pre-cultured microorganisms were inoculated into 50 mL flasks containing 15 mL of artificial wastewater after one wash with artificial wastewater to achieve an OD_{750} of 0.1. Wastewater treatment was performed at 30°C, 120 rpm, and 60 μmol photons/(m^2/s) for 18 h.

5.4. Analysis of Wastewater

To measure TOC, wastewater was centrifuged at 10,000 × *g* for 1 min at 20°C. The supernatant was diluted with ultrapure water and measured using a total organic carbon meter (Shimadzu, Kyoto, Japan). $C_8H_5KO_4$, $NaHCO_3$, and Na_2CO_3 were used as standards.

For the determination of PO_4^{3-} concentration, the effluent was centrifuged at 10,000 × *g* for 1 min at 20°C, and the supernatant was diluted appropriately with ultrapure water. Subsequently, 2 mL of the diluted supernatant and 400 μL of potassium peroxodisulfate solution (40 g/L potassium peroxodisulfate) were mixed and heated in a pressure vessel at 126°C for 30 min. After cooling the pressure vessel to room temperature, 900 μL of the reaction solution and 60 μL of molybdenum chromogenic solution (10 g/L hexammonium heptamolybdate tetrahydrate, 400 mg bis[(+)tartrate]diantimony(III)acid dipotassium trihydrate, 133 mL/L concentrated sulfuric acid, 12 g/L ascorbic acid])were mixed. After standing at room temperature for 15 min, the PO_4^{3-}

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299 concentration was calculated by measuring Abs_{880} using a spectrophotometer (Shimadzu).

300 Potassium hydrogen phosphate was used as a standard.

301 For the measurement of NH_4^+ concentration, the effluent was centrifuged at 10,000 × *g*

302 for 1 min at 20°C, and the supernatant was diluted with ultrapure water. Subsequently, 2 mL of the

303 diluted supernatant and 1000 µL of sodium hydroxide/potassium peroxodisulfate solution (3.0 g/L

304 NaOH, 20 g/L potassium peroxodisulfate) were mixed and heated in a pressure vessel at 126°C for

305 30 min. After the pressure vessel was allowed to cool to room temperature, 900 µL of the reaction

306 solution and 60 µL of sodium hydroxide-boron solution [61.8 g/L boric acid, 8.0 g/L NaOH] were

307 mixed, and the NH_4^+ concentration was calculated by measuring Abs_{220} using a spectrophotometer.

308 Potassium nitrate was used as the standard.

309

310 **5.5. Transcriptome analysis**

311 Total RNA was extracted from *C. reinhardtii* NIES-2238 and *S. cerevisiae* SH-4 cells using

312 NucleoSpin RNA (Takara Bio, Otsu, Japan) and Quick-RNA MiniPrep Plus (Zymo Research The

313 MGIEasy RNA Directional Library Prep Set (MGI Tech, Shenzhen, China) was used to prepare a

314 complementary DNA library for NGS of the extracted RNA. RNA sequencing was performed using

315 DNBSEQ-G400 (MGI Tech).

316 The genome sequences of C. reinhardtii CC-503 and S. cerevisiae S288c were used as

317 reference sequences for read mapping using Geneious Prime version 2020.0.3 (Tomy Digital

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318 Biology, Tokyo, Japan). DEGs were defined as genes satisfying the following conditions:
319 significance probability (p-value) of <0.01 and differential expression $\log_2$ ratio of <−1.5 or >1.5.
320 RNA sequencing data were deposited in the DNA Data Bank of Japan nucleotide sequence database
321 under the accession number DRR568808–DRR568810.
322
323 **Author Contributions**
324 Miiku Takahashi: Investigation, Writing-Original Draft. Yukino Karitani: Investigation.
325 Ryosuke Yamada: Conceptualization, Writing-Original Draft, Writing-Review & Editing,
326 Supervision, Funding acquisition. Takuya Matsumoto: Supervision. Hiroyasu Ogino: Supervision
327
328 **Declaration of competing interest**
329 The authors declare no competing financial interest.
330
331 **Acknowledgements**
332 The microalgae *C. reinhardtii* NIES-2238, *C. vulgaris* NIES-1269, and *A. platensis* NIES-
333 39 were provided by NIES through the NBRP of MEXT (Japan). We thank Editage for the English
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Data Availability

The data supporting the findings of this study are available from the corresponding author upon reasonable request.

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Figure captions

Fig. 1 Removal rates of (a) TOC, (b) PO_4^{3-}, and (c) NH_4^+ from 1x artificial wastewater using microalgae and heterotrophic microorganisms alone and in combination.

Data represent the averages of two replicates, and error bars indicate standard deviation.

Fig. 2 Removal rates of (a) TOC, (b) PO_4^{3-}, and (c) NH_4^+ from 2x artificial wastewater with *Chlamydomonas reinhardtii* NIES-2238 and *Saccharomyces cerevisiae* SH-4 alone and in combination.

Data represent the average of three replicates, and error bars indicate standard deviation. Significant differences were calculated using Student's t-test (*; $0.05 < p < 0.10$, ** $p < 0.05$). n.s.; not significant.

Fig. 3 Volcano plot of genes for (a) *Chlamydomonas reinhardtii* NIES-2238 and (b) *Saccharomyces cerevisiae* SH-4.

Fig. 4 Top 20 GO terms associated with *Chlamydomonas reinhardtii* NIES-2238 genes whose expression was (a) increased and (b) decreased via co-cultivation.

Fig. 5 Top 20 GO terms of *Saccharomyces cerevisiae* SH-4 genes whose expression was (a)

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increased and (b) decreased via co-cultivation.

Fig. 1

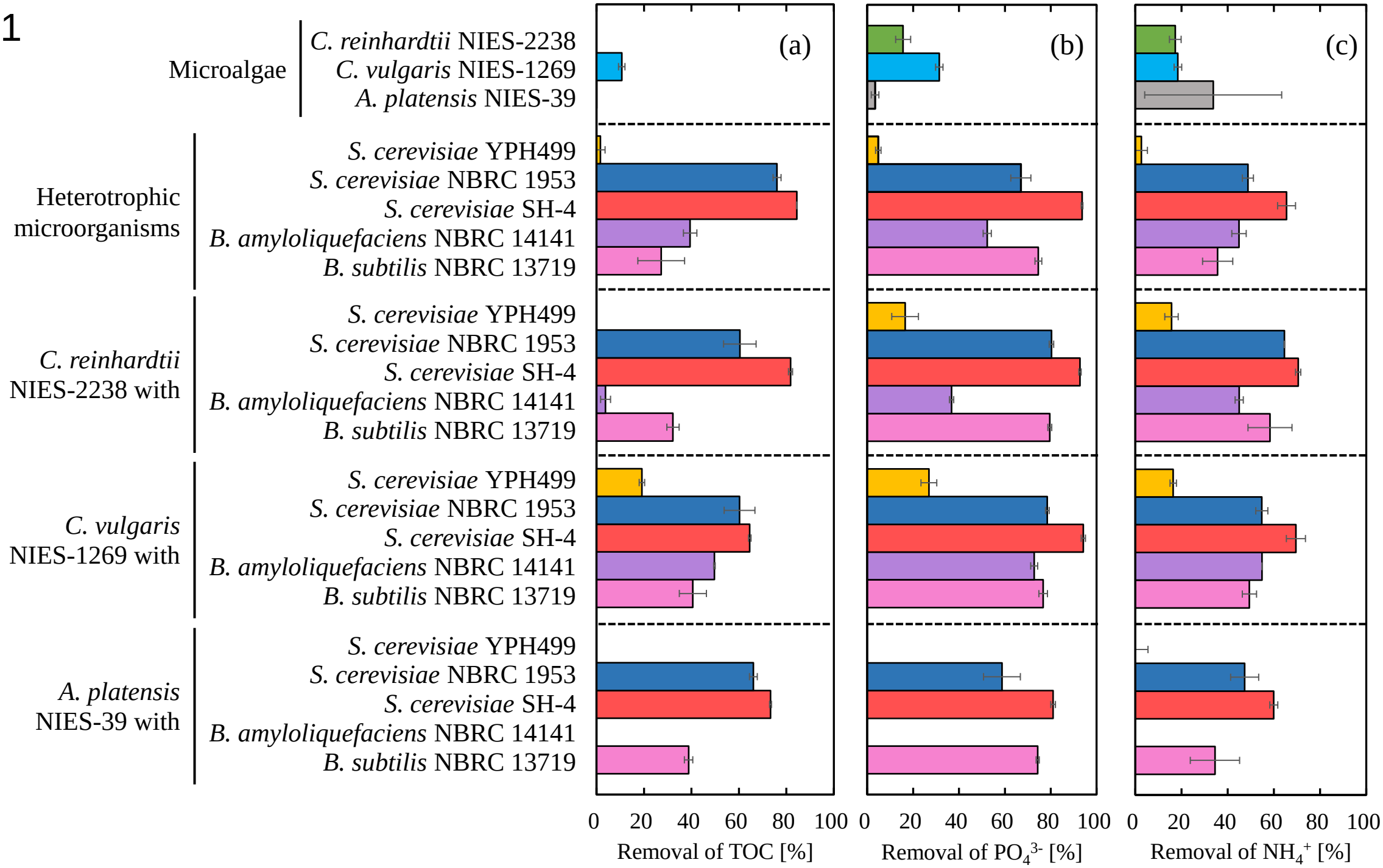

Microalgae
C. reinhardtii NIES-2238
C. vulgaris NIES-1269
A. platensis NIES-39
Heterotrophic microorganisms
S. cerevisiae YPH499
S. cerevisiae NBRC 1953
S. cerevisiae SH-4
B. amyloliquefaciens NBRC 14141
B. subtilis NBRC 13719
C. reinhardtii NIES-2238 with
S. cerevisiae YPH499
S. cerevisiae NBRC 1953
S. cerevisiae SH-4
B. amyloliquefaciens NBRC 14141
B. subtilis NBRC 13719
C. vulgaris NIES-1269 with
S. cerevisiae YPH499
S. cerevisiae NBRC 1953
S. cerevisiae SH-4
B. amyloliquefaciens NBRC 14141
B. subtilis NBRC 13719
A. platensis NIES-39 with
S. cerevisiae YPH499
S. cerevisiae NBRC 1953
S. cerevisiae SH-4
B. amyloliquefaciens NBRC 14141
B. subtilis NBRC 13719
(a)
(b)
(c)
0 20 40 60 80 100
Removal of TOC [%]
0 20 40 60 80 100
Removal of PO4 3- [%]
0 20 40 60 80 100
Removal of NH4 + [%]

Fig. 2

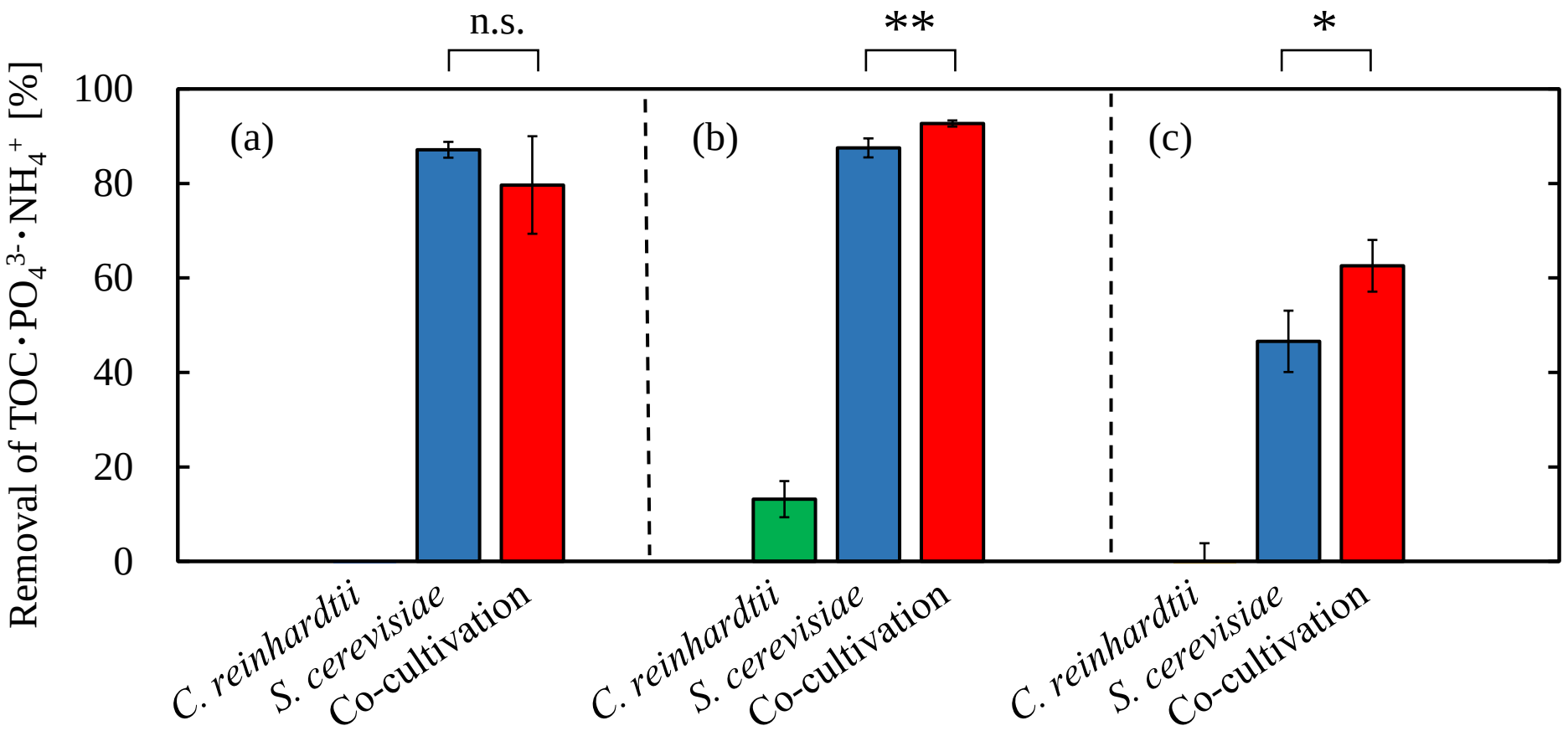
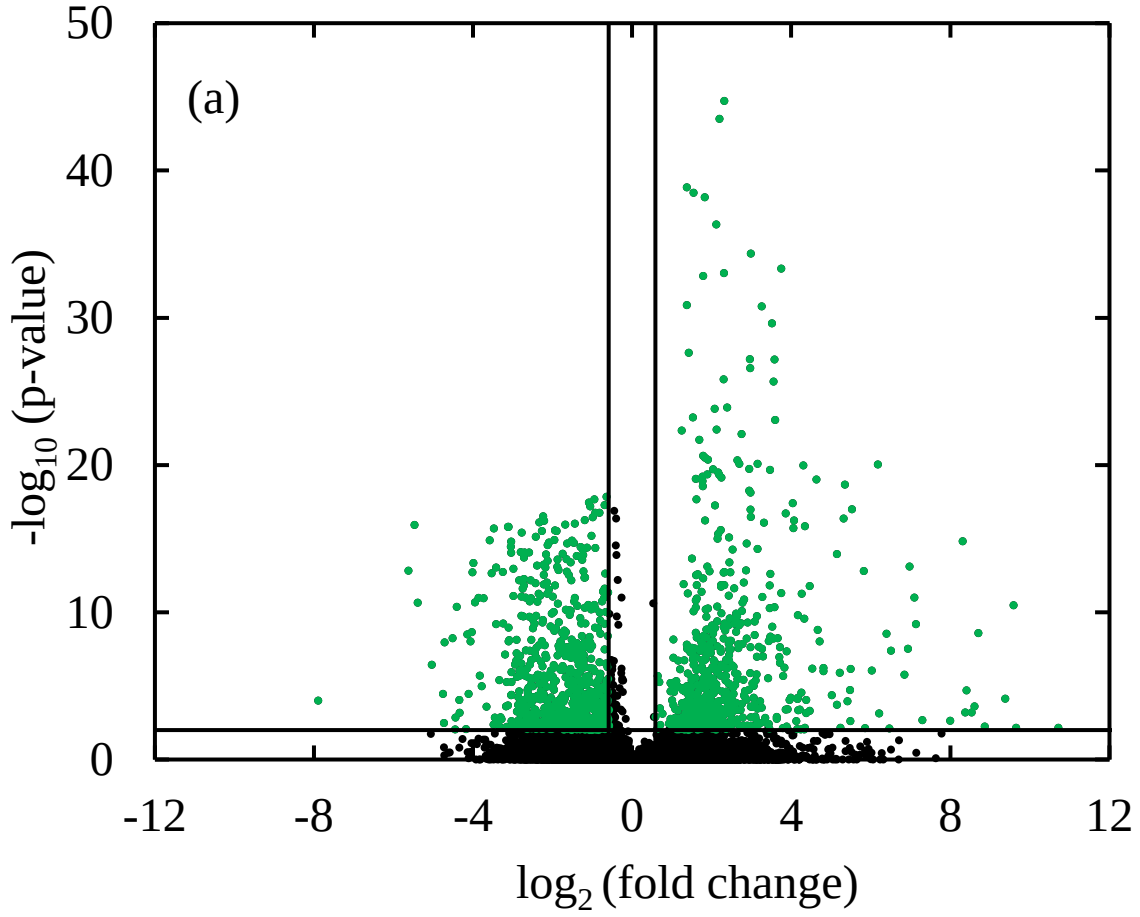

n.s.
**
*
(a)
(b)
(c)
100
80
60
40
20
0
Removal of TOC・PO_4^{3-}・NH_4^+ [%]
C. reinhardtii
S. cerevisiae
Co-cultivation
C. reinhardtii
S. cerevisiae
Co-cultivation
C. reinhardtii
S. cerevisiae
Co-cultivation

Fig. 3


(a)
50
40
30
20
10
0
-log10 (p-value)
-12
-8
-4
0
4
8
12
log2 (fold change)

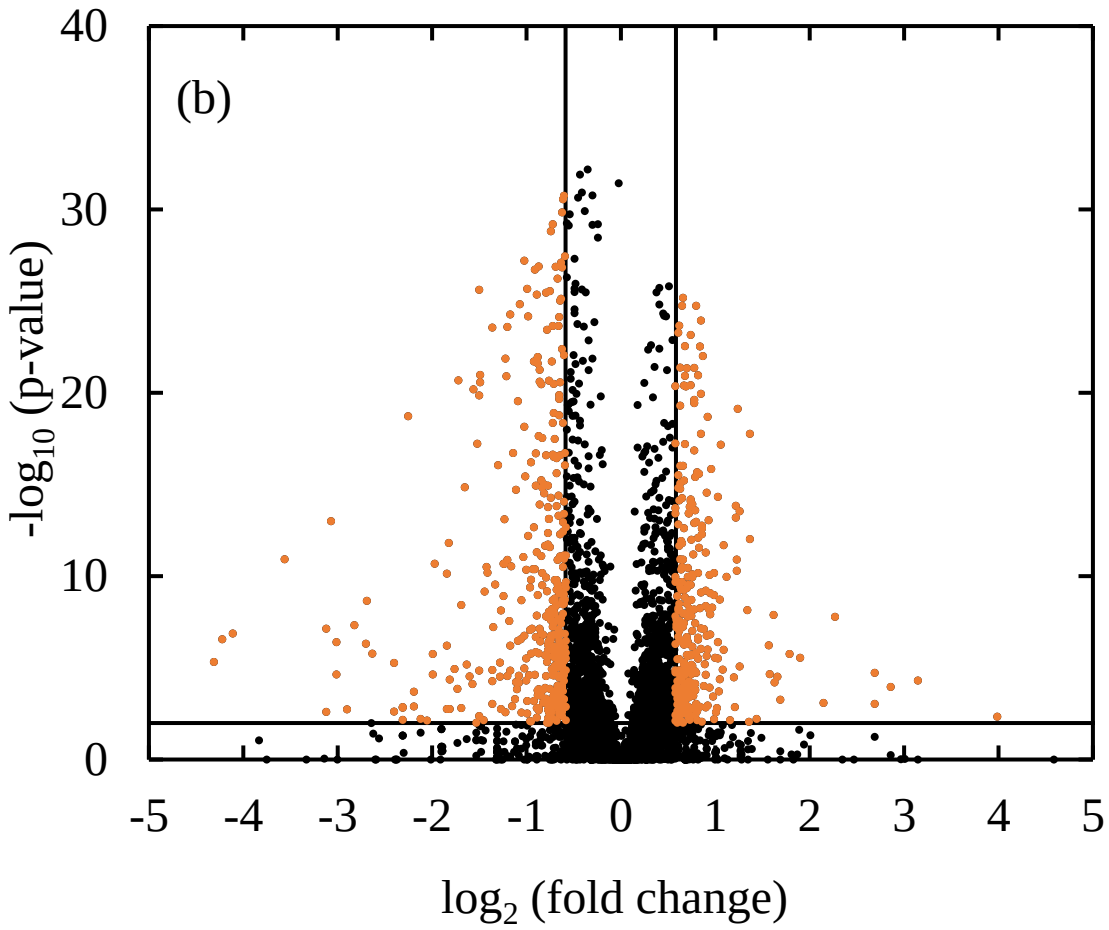
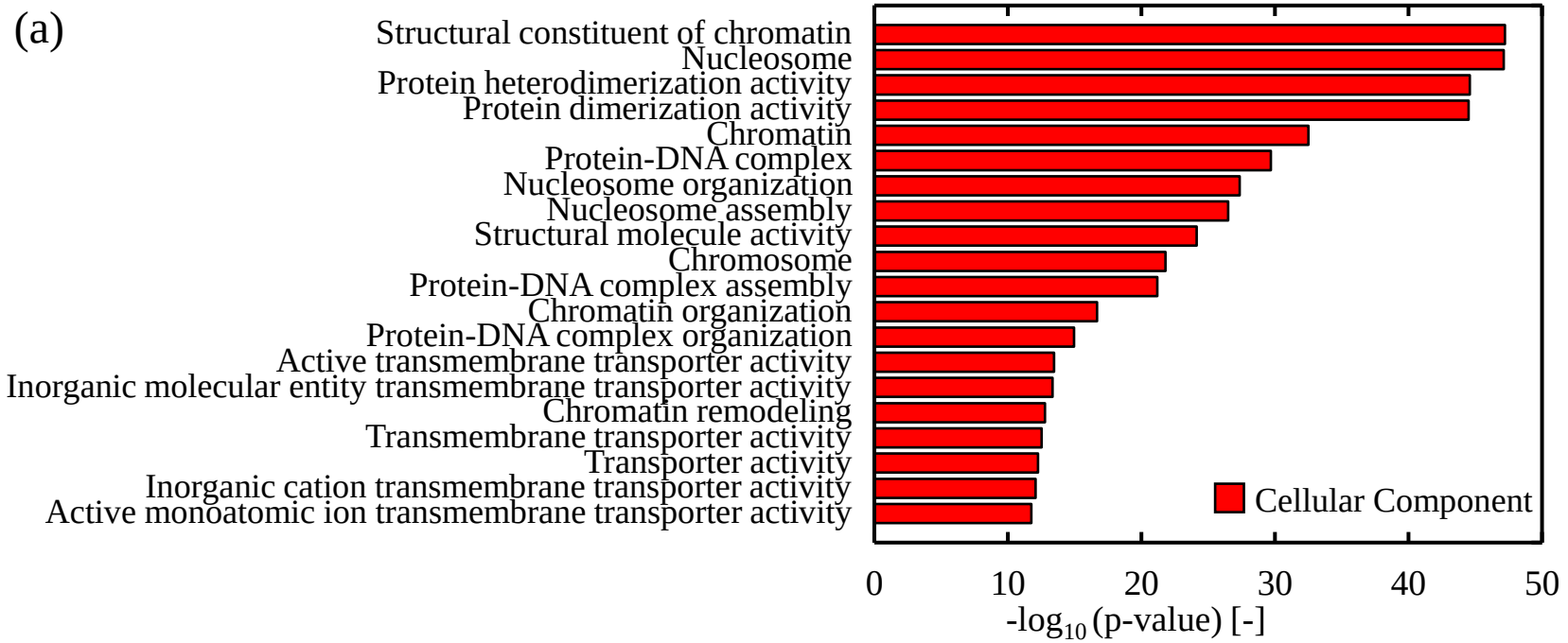

(b)
40
30
20
10
0
-log10 (p-value)
-5
-4
-3
-2
-1
0
1
2
3
4
5
log2 (fold change)

Fig. 4

(a)


Structural constituent of chromatin
Nucleosome
Protein heterodimerization activity
Protein dimerization activity
Chromatin
Protein-DNA complex
Nucleosome organization
Nucleosome assembly
Structural molecule activity
Chromosome
Protein-DNA complex assembly
Chromatin organization
Protein-DNA complex organization
Active transmembrane transporter activity
Inorganic molecular entity transmembrane transporter activity
Chromatin remodeling
Transmembrane transporter activity
Transporter activity
Inorganic cation transmembrane transporter activity
Active monoatomic ion transmembrane transporter activity
Cellular Component
0
10
20
30
40
50
-log10 (p-value) [-]

(b)

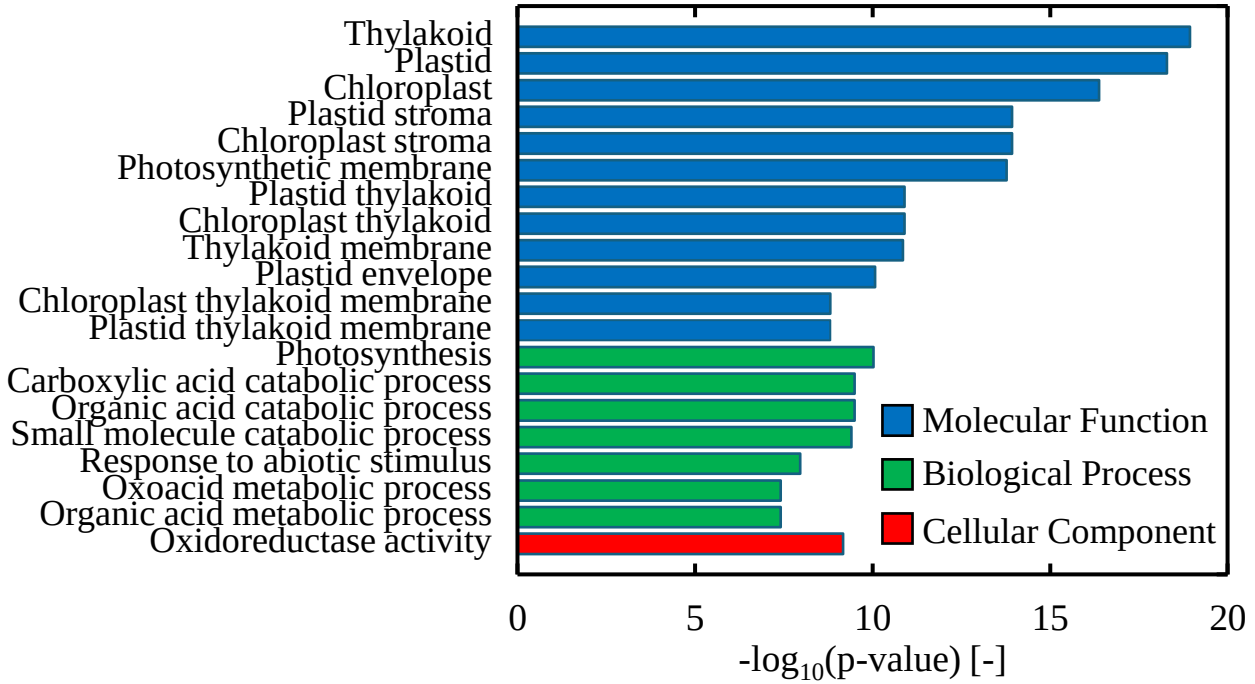
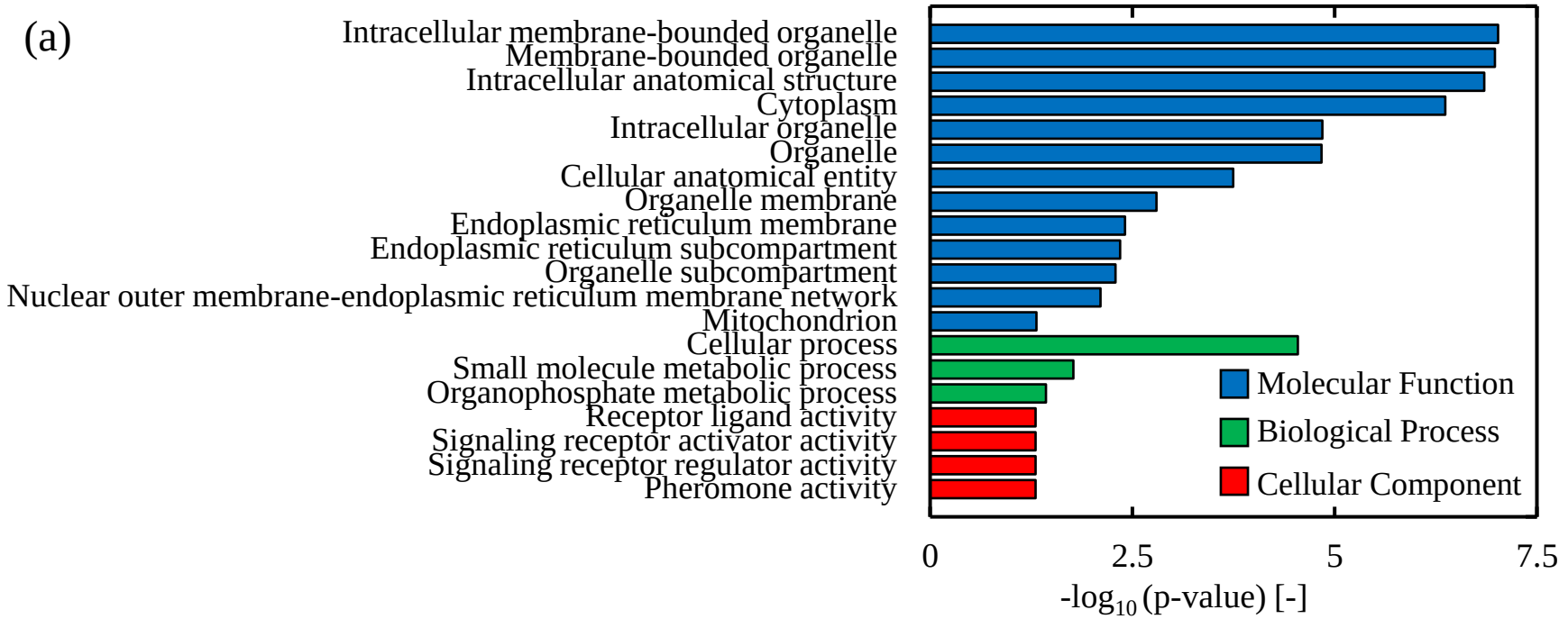
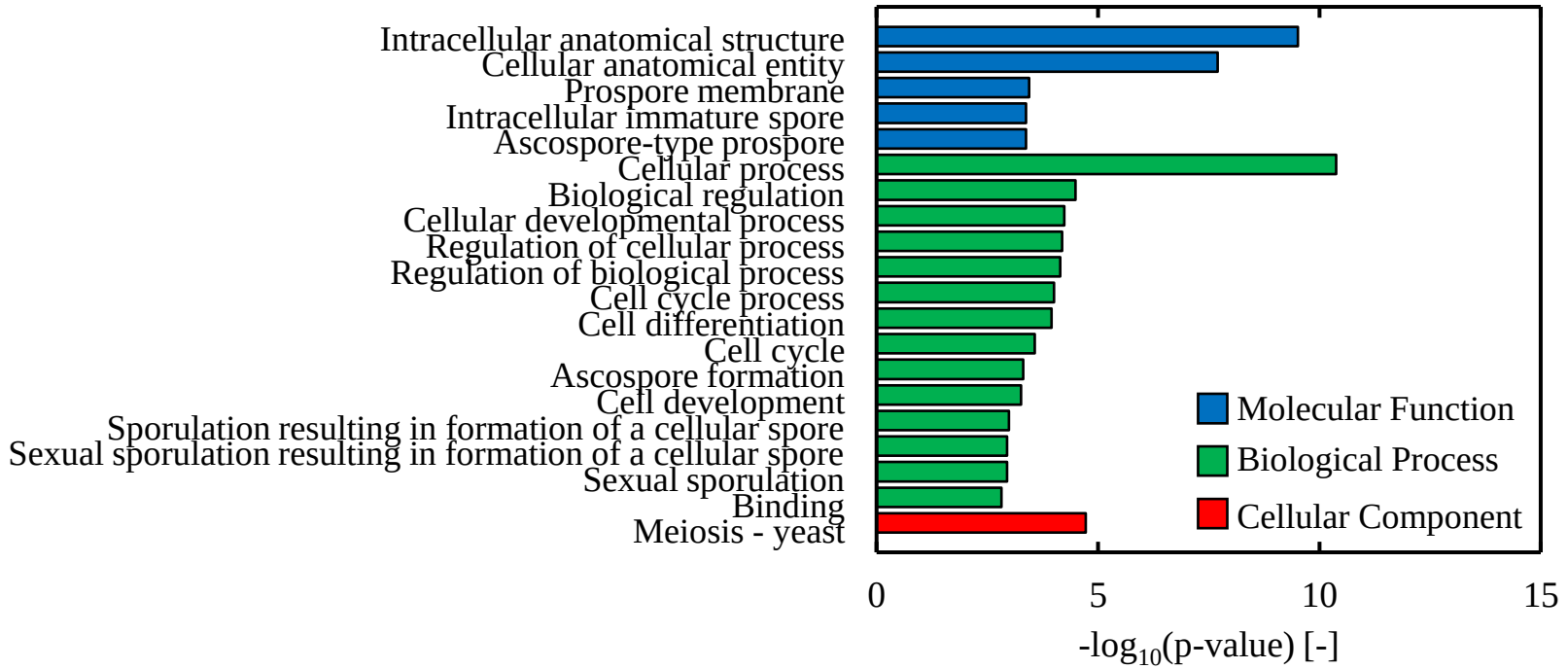

Thylakoid
Plastid
Chloroplast
Plastid stroma
Chloroplast stroma
Photosynthetic membrane
Plastid thylakoid
Chloroplast thylakoid
Thylakoid membrane
Plastid envelope
Chloroplast thylakoid membrane
Plastid thylakoid membrane
Photosynthesis
Carboxylic acid catabolic process
Organic acid catabolic process
Small molecule catabolic process
Response to abiotic stimulus
Oxoacid metabolic process
Organic acid metabolic process
Oxidoreductase activity
Molecular Function
Biological Process
Cellular Component
0
5
10
15
20
-log10(p-value) [-]

Fig. 5

(a)


Intracellular membrane-bounded organelle
Membrane-bounded organelle
Intracellular anatomical structure
Cytoplasm
Intracellular organelle
Organelle
Cellular anatomical entity
Organelle membrane
Endoplasmic reticulum membrane
Endoplasmic reticulum subcompartment
Organelle subcompartment
Nuclear outer membrane-endoplasmic reticulum membrane network
Mitochondrion
Cellular process
Small molecule metabolic process
Organophosphate metabolic process
Receptor ligand activity
Signaling receptor activator activity
Signaling receptor regulator activity
Pheromone activity
Molecular Function
Biological Process
Cellular Component
0
2.5
5
7.5
-log10 (p-value) [-]

(b)


Intracellular anatomical structure
Cellular anatomical entity
Prospore membrane
Intracellular immature spore
Ascospore-type prospore
Cellular process
Biological regulation
Cellular developmental process
Regulation of cellular process
Regulation of biological process
Cell cycle process
Cell differentiation
Cell cycle
Ascospore formation
Cell development
Sporulation resulting in formation of a cellular spore
Sexual sporulation resulting in formation of a cellular spore
Sexual sporulation
Binding
Meiosis - yeast
Molecular Function
Biological Process
Cellular Component
0
5
10
15
-log10(p-value) [-]

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Supplementary information

Co-utilization of microalgae and heterotrophic microorganisms improves wastewater treatment efficiency

Supplementary Table 1. Microalgae genes whose expression levels increased due to co-cultivation of microalgae and yeast

locus tag[a]	-Log_{10} (p-value)	Log_2 (fold change)
CHLRE_10g433200v5	2.14	10.72
CHLRE_16g691750v5	2.14	9.66
CHLRE_03g159254v5	10.46	9.59
CHLRE_10g433250v5	4.13	9.38
CHLRE_01g009400v5	2.22	8.87
CHLRE_17g708025v5	8.57	8.71
CHLRE_10g433250v5	3.61	8.61
CHLRE_02g089400v5	3.18	8.54
CHLRE_07g346950v5	4.69	8.41
CHLRE_03g206500v5	3.19	8.38
CHLRE_02g096551v5	14.82	8.31
CHLRE_10g433250v5	2.63	8
CHLRE_03g204500v5	2.67	7.3
CHLRE_05g241634v5	9.19	7.14
CHLRE_07g325740v5	10.99	7.1
CHLRE_09g390838v5	13.1	6.98
CHLRE_12g551350v5	7.51	6.94
CHLRE_06g263950v5	5.76	6.85
CHLRE_10g425100v5	7.38	6.51
CHLRE_10g433200v5	2.11	6.47
CHLRE_01g011150v5	8.54	6.4
CHLRE_10g433200v5	3.12	6.21
CHLRE_16g679150v5	20.03	6.18
CHLRE_07g346050v5	6.03	6.03
CHLRE_10g442800v5	2.13	5.86
CHLRE_01g009350v5	12.79	5.83
CHLRE_17g702900v5	16.99	5.53
CHLRE_09g410050v5	6.15	5.5
CHLRE_10g442800v5	2.61	5.49
CHLRE_05g234656v5	4.7	5.48
CHLRE_09g410050v5	3.94	5.42
CHLRE_06g252750v5	18.65	5.35
CHLRE_01g008300v5	16.35	5.32
CHLRE_09g400750v5	2.15	5.24
CHLRE_07g350100v5	5.89	5.22
CHLRE_08g362500v5	13.95	5.15
CHLRE_01g012650v5	3.71	5.15
CHLRE_16g673250v5	4.37	5.02
CHLRE_03g200750v5	6.2	4.81
CHLRE_12g546600v5	5.98	4.81

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CHLRE_11g467709v5	8.02	4.72
CHLRE_07g315050v5	8.8	4.67
CHLRE_01g012700v5	19	4.64
CHLRE_11g467709v5	6.16	4.53
CHLRE_09g393700v5	11.76	4.47
CHLRE_03g149350v5	3.3	4.47
CHLRE_03g199050v5	4.03	4.38
CHLRE_10g433476v5	3.14	4.38
CHLRE_17g735375v5	15.83	4.35
CHLRE_04g216200v5	2.15	4.35
CHLRE_10g448700v5	9.55	4.33
CHLRE_16g656750v5	2.04	4.33
CHLRE_02g093600v5	19.96	4.31
CHLRE_06g271450v5	11.25	4.27
CHLRE_07g321750v5	4.54	4.26
CHLRE_01g007400v5	2.03	4.24
CHLRE_11g467539v5	3.38	4.22
CHLRE_03g212977v5	3.34	4.18
CHLRE_03g165050v5	9.8	4.17
CHLRE_10g433476v5	4.19	4.17
CHLRE_10g433476v5	4.1	4.16
CHLRE_04g214600v5	2.05	4.15
CHLRE_11g467539v5	2.6	4.13
CHLRE_01g034850v5	16.22	4.07
CHLRE_07g347000v5	15.71	4.06
CHLRE_12g547750v5	17.39	4.04
CHLRE_02g145628v5	4.19	3.99
CHLRE_02g087900v5	4.04	3.96
CHLRE_12g525450v5	3.41	3.91
CHLRE_09g393700v5	7.33	3.89
CHLRE_04g222800v5	2.22	3.89
CHLRE_07g346900v5	2.19	3.88
CHLRE_09g414416v5	2.15	3.88
CHLRE_14g619854v5	2.13	3.87
CHLRE_16g657200v5	16.7	3.86
CHLRE_10g445000v5	3.38	3.86
CHLRE_06g257200v5	6.23	3.83
CHLRE_06g309000v5	5.66	3.8
CHLRE_03g203500v5	2.13	3.79
CHLRE_02g144750v5	33.32	3.75
CHLRE_16g674065v5	11.29	3.75
CHLRE_01g012850v5	7.62	3.72
CHLRE_17g742250v5	6.55	3.72
CHLRE_07g343050v5	6.95	3.7
CHLRE_10g445050v5	8.23	3.66
CHLRE_06g300500v5	2.88	3.64
CHLRE_01g066187v5	2.75	3.64
CHLRE_02g099950v5	23.05	3.6
CHLRE_12g552650v5	27.16	3.58
CHLRE_07g332275v5	10.34	3.58

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CHLRE_03g202100v5	25.66	3.56
CHLRE_17g700750v5	8.21	3.56
CHLRE_10g445050v5	9.02	3.53
CHLRE_16g681750v5	29.61	3.52
CHLRE_17g708750v5	12.59	3.48
CHLRE_06g271300v5	8.33	3.48
CHLRE_17g733100v5	8.24	3.48
CHLRE_01g008350v5	19.66	3.47
CHLRE_02g095137v5	11.81	3.46
CHLRE_13g587550v5	10.27	3.46
CHLRE_02g108700v5	2.08	3.45
CHLRE_07g325727v5	8.03	3.44
CHLRE_06g294200v5	2.41	3.44
CHLRE_12g524800v5	5.51	3.42
CHLRE_02g107256v5	2.48	3.38
CHLRE_17g711750v5	2.82	3.35
CHLRE_13g572600v5	16.07	3.32
CHLRE_17g730100v5	6.98	3.29
CHLRE_10g452950v5	11.04	3.28
CHLRE_10g445050v5	7.52	3.27
CHLRE_02g144500v5	30.76	3.26
CHLRE_07g342700v5	3.51	3.26
CHLRE_10g451350v5	2.47	3.23
CHLRE_10g442600v5	3.94	3.22
CHLRE_11g467644v5	7.65	3.19
CHLRE_06g307500v5	20.06	3.16
CHLRE_01g049950v5	14.29	3.16
CHLRE_02g112550v5	3.45	3.16
CHLRE_10g458850v5	2.12	3.15
CHLRE_02g112500v5	9.73	3.14
CHLRE_17g713450v5	6.96	3.14
CHLRE_14g616700v5	5.78	3.13
CHLRE_10g458850v5	2.33	3.12
CHLRE_16g663000v5	5.35	3.11
CHLRE_09g397660v5	2.75	3.11
CHLRE_16g675100v5	2.91	3.1
CHLRE_08g359450v5	9.36	3.08
CHLRE_07g339200v5	8.44	3.08
CHLRE_06g264050v5	3.77	3.08
CHLRE_03g144787v5	4.99	3.06
CHLRE_10g458850v5	4.19	3.06
CHLRE_12g549427v5	3.55	3.05
CHLRE_04g220850v5	5.08	3.04
CHLRE_17g714650v5	5.17	3.03
CHLRE_03g168200v5	34.35	2.99
CHLRE_11g468450v5	16.47	2.99
CHLRE_11g479600v5	3.58	2.99
CHLRE_10g442600v5	2.85	2.99
CHLRE_02g145950v5	2.27	2.99
CHLRE_02g145100v5	18.11	2.98

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CHLRE_04g229550v5	16.96	2.98
CHLRE_17g710300v5	7.61	2.98
CHLRE_06g266800v5	26.56	2.97
CHLRE_16g690319v5	5.87	2.97
CHLRE_12g550702v5	27.18	2.96
CHLRE_06g264000v5	19.73	2.95
CHLRE_02g095076v5	18.25	2.95
CHLRE_09g398900v5	4.72	2.94
CHLRE_01g000150v5	2.21	2.93
CHLRE_03g168100v5	9.3	2.91
CHLRE_15g635998v5	2.29	2.9
CHLRE_17g702950v5	14.66	2.88
CHLRE_06g276950v5	8.21	2.88
CHLRE_17g735450v5	4.06	2.88
CHLRE_11g467710v5	12.83	2.87
CHLRE_07g332250v5	4.65	2.84
CHLRE_17g710450v5	4.3	2.83
CHLRE_12g531000v5	10.85	2.82
CHLRE_12g507800v5	4.37	2.82
CHLRE_11g478800v5	12.01	2.81
CHLRE_12g541250v5	2.3	2.81
CHLRE_09g389504v5	5.4	2.8
CHLRE_06g274300v5	2.83	2.79
CHLRE_13g563100v5	10.65	2.78
CHLRE_10g417650v5	7.84	2.78
CHLRE_17g713500v5	10.07	2.76
CHLRE_17g696500v5	3.78	2.76
CHLRE_06g269850v5	22.09	2.75
CHLRE_17g714100v5	9.25	2.74
CHLRE_09g398900v5	3.36	2.73
CHLRE_11g467744v5	2.28	2.71
CHLRE_09g409650v5	20.06	2.7
CHLRE_17g739000v5	9.09	2.69
CHLRE_12g504600v5	7.81	2.67
CHLRE_11g467599v5	7.55	2.67
CHLRE_09g409650v5	20.31	2.65
CHLRE_09g389504v5	5.79	2.65
CHLRE_10g454150v5	5.44	2.65
CHLRE_09g397660v5	3.35	2.65
CHLRE_09g389430v5	9.73	2.64
CHLRE_12g551100v5	2.71	2.64
CHLRE_01g035700v5	2.43	2.63
CHLRE_02g095087v5	9.89	2.62
CHLRE_17g709100v5	8.67	2.62
CHLRE_05g238687v5	3.83	2.62
CHLRE_13g586700v5	9.51	2.61
CHLRE_11g467710v5	9.52	2.6
CHLRE_13g586450v5	5.87	2.59
CHLRE_03g174400v5	5.05	2.59
CHLRE_16g658800v5	9.2	2.58

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CHLRE_01g053000v5	11.62	2.57
CHLRE_04g222750v5	6.3	2.55
CHLRE_09g396650v5	4.44	2.55
CHLRE_06g265400v5	4.87	2.54
CHLRE_02g097050v5	14.25	2.53
CHLRE_07g331450v5	3.59	2.53
CHLRE_12g506450v5	6.39	2.52
CHLRE_06g274150v5	3.99	2.52
CHLRE_01g012950v5	3.2	2.52
CHLRE_11g479600v5	3.59	2.51
CHLRE_08g374450v5	4.26	2.5
CHLRE_16g677100v5	2.7	2.5
CHLRE_14g619050v5	8.06	2.49
CHLRE_06g292900v5	3.08	2.49
CHLRE_06g283200v5	2.54	2.49
CHLRE_17g707137v5	7.46	2.48
CHLRE_17g714800v5	2.2	2.48
CHLRE_17g700650v5	12.7	2.47
CHLRE_06g278252v5	3.79	2.47
CHLRE_08g374436v5	9.58	2.46
CHLRE_10g442600v5	2.45	2.46
CHLRE_03g177350v5	13.38	2.45
CHLRE_12g554350v5	8.05	2.45
CHLRE_11g467594v5	15.08	2.44
CHLRE_11g467601v5	7.46	2.44
CHLRE_12g550450v5	7.08	2.44
CHLRE_12g489700v5	6.7	2.44
CHLRE_10g440150v5	3.34	2.44
CHLRE_08g378150v5	2.26	2.44
CHLRE_12g488000v5	11.12	2.43
CHLRE_07g349119v5	7.84	2.43
CHLRE_02g097800v5	5.15	2.43
CHLRE_07g332950v5	5.15	2.43
CHLRE_04g216550v5	4.29	2.43
CHLRE_17g714600v5	9.1	2.42
CHLRE_17g714050v5	3.85	2.42
CHLRE_02g142650v5	3.6	2.4
CHLRE_13g567700v5	23.89	2.39
CHLRE_02g089900v5	6.19	2.39
CHLRE_12g523026v5	6.68	2.38
CHLRE_12g523000v5	6.77	2.37
CHLRE_06g267950v5	4.6	2.37
CHLRE_05g243450v5	2.05	2.37
CHLRE_09g389850v5	5.66	2.36
CHLRE_09g389850v5	5.69	2.35
CHLRE_06g275800v5	5.37	2.35
CHLRE_03g155300v5	8.75	2.34
CHLRE_09g396600v5	9.23	2.33
CHLRE_17g714550v5	6.22	2.33
CHLRE_12g549000v5	4.15	2.33

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CHLRE_14g629840v5	3.06	2.33
CHLRE_10g454450v5	2.34	2.33
CHLRE_12g519750v5	44.72	2.32
CHLRE_03g156550v5	12.73	2.32
CHLRE_06g296750v5	11.84	2.32
CHLRE_03g200850v5	33.03	2.31
CHLRE_17g735876v5	2.55	2.31
CHLRE_17g723750v5	25.8	2.3
CHLRE_03g182700v5	12.69	2.3
CHLRE_09g396600v5	8.98	2.3
CHLRE_06g271376v5	8.2	2.3
CHLRE_09g402500v5	4.06	2.3
CHLRE_12g538000v5	4.03	2.3
CHLRE_09g406600v5	3.29	2.3
CHLRE_10g454150v5	2.53	2.3
CHLRE_09g405500v5	2.35	2.3
CHLRE_02g109450v5	4.6	2.27
CHLRE_16g693601v5	4.6	2.27
CHLRE_03g181450v5	2.59	2.26
CHLRE_04g217915v5	19.13	2.25
CHLRE_12g498650v5	9.92	2.25
CHLRE_12g517850v5	3.39	2.25
CHLRE_17g705500v5	2.12	2.25
CHLRE_16g663950v5	11.83	2.24
CHLRE_12g492950v5	11.72	2.24
CHLRE_17g713550v5	6.42	2.24
CHLRE_17g708450v5	2.32	2.24
CHLRE_01g008550v5	2.24	2.24
CHLRE_14g620600v5	15.58	2.23
CHLRE_02g115950v5	7.31	2.23
CHLRE_04g225200v5	3.17	2.23
CHLRE_17g720350v5	7.5	2.22
CHLRE_09g394200v5	5.69	2.22
CHLRE_08g374300v5	3.43	2.22
CHLRE_08g370401v5	3.33	2.22
CHLRE_08g374400v5	3.47	2.21
CHLRE_17g714200v5	43.5	2.2
CHLRE_06g306000v5	2.26	2.2
CHLRE_13g605200v5	19.34	2.19
CHLRE_02g101700v5	3.95	2.18
CHLRE_09g413150v5	2.9	2.18
CHLRE_11g467594v5	19.48	2.17
CHLRE_12g506200v5	15.32	2.17
CHLRE_03g149400v5	6.12	2.17
CHLRE_16g681800v5	2.38	2.17
CHLRE_12g548500v5	2.27	2.17
CHLRE_14g625600v5	2.83	2.16
CHLRE_13g589800v5	2.38	2.16
CHLRE_04g224800v5	14.98	2.15
CHLRE_12g504800v5	5.89	2.15

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CHLRE_13g584775v5	4.73	2.15
CHLRE_12g505500v5	3.91	2.15
CHLRE_06g265050v5	10.37	2.14
CHLRE_11g468600v5	9.37	2.14
CHLRE_09g416050v5	7.68	2.14
CHLRE_17g709050v5	3.71	2.14
CHLRE_17g732350v5	3.04	2.14
CHLRE_11g481600v5	2.43	2.14
CHLRE_16g650600v5	22.39	2.13
CHLRE_13g582800v5	2.41	2.13
CHLRE_07g355250v5	2.24	2.13
CHLRE_17g746997v5	36.33	2.12
CHLRE_07g348350v5	5.09	2.12
CHLRE_11g481600v5	2.25	2.12
CHLRE_10g452800v5	6.05	2.11
CHLRE_16g690506v5	3.63	2.11
CHLRE_06g260450v5	3.15	2.11
CHLRE_09g413150v5	2.72	2.11
CHLRE_12g505100v5	2.02	2.11
CHLRE_17g717900v5	6.16	2.1
CHLRE_09g387208v5	4.73	2.1
CHLRE_01g034250v5	3.22	2.1
CHLRE_17g711800v5	17.25	2.09
CHLRE_06g271800v5	8.92	2.09
CHLRE_06g290000v5	6.09	2.09
CHLRE_09g387600v5	2.31	2.09
CHLRE_07g336950v5	23.8	2.08
CHLRE_03g207900v5	6.61	2.08
CHLRE_06g265450v5	3.57	2.08
CHLRE_04g219600v5	3.36	2.08
CHLRE_09g403182v5	4.96	2.07
CHLRE_09g387949v5	6.72	2.05
CHLRE_02g076466v5	6.18	2.05
CHLRE_13g570600v5	5.3	2.05
CHLRE_09g394200v5	4.76	2.05
CHLRE_14g631000v5	4.5	2.05
CHLRE_02g113050v5	2.57	2.05
CHLRE_03g172300v5	19.69	2.04
CHLRE_10g439850v5	8.56	2.04
CHLRE_16g672602v5	8.06	2.03
CHLRE_16g667850v5	5.48	2.03
CHLRE_17g714000v5	4.96	2.03
CHLRE_06g275700v5	4.5	2.03
CHLRE_10g432250v5	2.78	2.03
CHLRE_12g537371v5	6.27	2.02
CHLRE_14g625300v5	2.88	2.02
CHLRE_10g435200v5	2.07	2.02
CHLRE_16g669150v5	9.09	2.01
CHLRE_12g506350v5	8.86	2
CHLRE_09g392951v5	3.48	2

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CHLRE_12g525700v5	2.92	2
CHLRE_06g265350v5	5.12	1.99
CHLRE_15g637900v5	2.16	1.99
CHLRE_07g344550v5	7.5	1.98
CHLRE_14g613950v5	7.23	1.98
CHLRE_06g295700v5	4.12	1.98
CHLRE_09g387467v5	3.01	1.98
CHLRE_06g282850v5	2.26	1.98
CHLRE_06g288600v5	3.81	1.97
CHLRE_13g584800v5	3.15	1.96
CHLRE_06g293950v5	12.76	1.95
CHLRE_03g159300v5	7.82	1.95
CHLRE_02g141926v5	7.44	1.95
CHLRE_06g276800v5	4.36	1.95
CHLRE_16g695850v5	4	1.95
CHLRE_06g264800v5	2.61	1.95
CHLRE_06g283400v5	5.58	1.94
CHLRE_08g370450v5	4.37	1.94
CHLRE_11g467725v5	2.68	1.94
CHLRE_07g346350v5	2.58	1.94
CHLRE_03g200000v5	4.46	1.93
CHLRE_06g274900v5	3.11	1.93
CHLRE_02g074800v5	2.64	1.93
CHLRE_06g274200v5	2.45	1.93
CHLRE_09g401960v5	2.42	1.93
CHLRE_11g468600v5	7.6	1.92
CHLRE_03g178650v5	4.11	1.92
CHLRE_09g396650v5	3.44	1.92
CHLRE_04g217944v5	2.59	1.92
CHLRE_15g639350v5	2.19	1.92
CHLRE_03g199800v5	20.36	1.91
CHLRE_09g410700v5	10.24	1.91
CHLRE_02g095073v5	8.81	1.91
CHLRE_06g264600v5	7.2	1.91
CHLRE_08g372550v5	5.99	1.91
CHLRE_06g267650v5	5.26	1.91
CHLRE_06g276700v5	2.9	1.91
CHLRE_06g266600v5	5.88	1.9
CHLRE_17g709150v5	5.01	1.9
CHLRE_12g504650v5	3.16	1.9
CHLRE_12g552200v5	19.36	1.89
CHLRE_17g715300v5	13.09	1.89
CHLRE_01g009950v5	2.9	1.89
CHLRE_09g409150v5	8.28	1.88
CHLRE_02g094450v5	5.28	1.88
CHLRE_17g711850v5	3.62	1.88
CHLRE_17g728750v5	3.08	1.88
CHLRE_12g503450v5	2.97	1.88
CHLRE_15g636550v5	2.72	1.88
CHLRE_07g347750v5	9.69	1.87

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CHLRE_08g368850v5	8.81	1.87
CHLRE_10g458450v5	7.09	1.87
CHLRE_09g401293v5	7.53	1.86
CHLRE_17g699750v5	5.73	1.86
CHLRE_17g710500v5	4.29	1.86
CHLRE_09g396065v5	3.21	1.86
CHLRE_16g659667v5	2.67	1.86
CHLRE_06g273100v5	10.19	1.85
CHLRE_12g522950v5	6.81	1.85
CHLRE_13g588150v5	4.84	1.85
CHLRE_02g098850v5	4.77	1.85
CHLRE_06g301000v5	3.03	1.85
CHLRE_02g113200v5	20.48	1.84
CHLRE_17g714450v5	16.22	1.84
CHLRE_14g618400v5	5.71	1.84
CHLRE_10g452800v5	4.94	1.84
CHLRE_14g620702v5	2.55	1.84
CHLRE_01g015500v5	38.17	1.83
CHLRE_06g260200v5	6.74	1.83
CHLRE_09g399550v5	5.38	1.83
CHLRE_10g458550v5	3.31	1.83
CHLRE_07g327900v5	3.11	1.83
CHLRE_03g164050v5	3.06	1.83
CHLRE_06g311700v5	5.49	1.82
CHLRE_12g504950v5	5.13	1.82
CHLRE_09g387208v5	4.21	1.82
CHLRE_07g353900v5	2.75	1.82
CHLRE_02g076650v5	2.36	1.82
CHLRE_06g276650v5	8.38	1.8
CHLRE_16g673057v5	5.51	1.8
CHLRE_10g458500v5	3.14	1.8
CHLRE_16g653450v5	2.92	1.8
CHLRE_13g592200v5	32.82	1.79
CHLRE_14g620850v5	20.62	1.79
CHLRE_13g588501v5	12.3	1.79
CHLRE_02g083800v5	6.02	1.79
CHLRE_05g232600v5	5.35	1.79
CHLRE_10g431350v5	3.78	1.79
CHLRE_09g394436v5	18.55	1.78
CHLRE_06g258800v5	6.71	1.78
CHLRE_11g467599v5	3.41	1.78
CHLRE_12g526800v5	19.21	1.77
CHLRE_14g611900v5	18.89	1.77
CHLRE_09g410700v5	7.88	1.77
CHLRE_02g095150v5	3.91	1.77
CHLRE_03g175600v5	3.15	1.77
CHLRE_01g050400v5	2.28	1.77
CHLRE_17g725150v5	7.72	1.76
CHLRE_09g401293v5	6.74	1.76
CHLRE_02g110650v5	6.3	1.76

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CHLRE_17g712900v5	5.16	1.76
CHLRE_01g008650v5	4.88	1.76
CHLRE_14g630883v5	2.71	1.76
CHLRE_11g467593v5	11.38	1.75
CHLRE_10g432250v5	2.23	1.75
CHLRE_08g360450v5	2.08	1.75
CHLRE_09g391801v5	7.96	1.74
CHLRE_06g290100v5	2.12	1.74
CHLRE_02g115450v5	2.95	1.73
CHLRE_10g432250v5	2.4	1.73
CHLRE_02g111300v5	7.39	1.72
CHLRE_06g265500v5	4.01	1.72
CHLRE_07g336900v5	7.39	1.71
CHLRE_09g396065v5	2.74	1.71
CHLRE_12g508900v5	3.44	1.7
CHLRE_06g285250v5	21.71	1.69
CHLRE_01g034325v5	3.37	1.69
CHLRE_12g545550v5	2.07	1.69
CHLRE_14g622200v5	4.07	1.68
CHLRE_17g718468v5	4	1.67
CHLRE_01g008950v5	3.97	1.67
CHLRE_06g297250v5	3.6	1.67
CHLRE_09g386756v5	2.56	1.67
CHLRE_06g273900v5	2.19	1.67
CHLRE_13g570000v5	2.14	1.67
CHLRE_02g141166v5	4.6	1.66
CHLRE_17g735950v5	3.59	1.66
CHLRE_06g265200v5	3.55	1.66
CHLRE_17g713400v5	3.44	1.66
CHLRE_09g395950v5	3.32	1.66
CHLRE_01g022200v5	2.31	1.66
CHLRE_09g392503v5	2.08	1.66
CHLRE_09g388850v5	12.58	1.65
CHLRE_11g467668v5	3.24	1.65
CHLRE_10g431350v5	3.02	1.65
CHLRE_17g734596v5	2.09	1.65
CHLRE_16g653150v5	2.02	1.65
CHLRE_03g148700v5	5.06	1.64
CHLRE_07g350750v5	4.28	1.64
CHLRE_01g005050v5	11.84	1.63
CHLRE_08g362450v5	10.92	1.63
CHLRE_06g268400v5	8.28	1.63
CHLRE_17g735400v5	3.91	1.63
CHLRE_03g145267v5	3.08	1.63
CHLRE_17g722300v5	17.65	1.62
CHLRE_09g416150v5	6.08	1.62
CHLRE_01g012750v5	3.08	1.62
CHLRE_03g189250v5	2.89	1.62
CHLRE_09g388850v5	12.51	1.61
CHLRE_11g467649v5	6.92	1.61

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CHLRE_12g485100v5	2.91	1.61
CHLRE_17g735500v5	2.65	1.61
CHLRE_04g213450v5	2.53	1.61
CHLRE_12g554400v5	19.05	1.6
CHLRE_03g194850v5	10.79	1.6
CHLRE_17g725200v5	10.32	1.6
CHLRE_07g340450v5	8.59	1.6
CHLRE_13g582600v5	5.54	1.6
CHLRE_10g433950v5	3.94	1.6
CHLRE_01g013200v5	3.25	1.6
CHLRE_03g195950v5	2.33	1.6
CHLRE_06g268100v5	4.39	1.59
CHLRE_13g563950v5	3.02	1.59
CHLRE_16g685000v5	7.53	1.58
CHLRE_03g150300v5	4.37	1.58
CHLRE_09g399550v5	3.39	1.58
CHLRE_03g146507v5	3.72	1.57
CHLRE_12g491050v5	6.81	1.56
CHLRE_01g004124v5	6.45	1.56
CHLRE_03g180250v5	38.47	1.55
CHLRE_16g685700v5	10.06	1.55
CHLRE_09g416050v5	6.42	1.55
CHLRE_10g444000v5	2.72	1.55
CHLRE_06g264750v5	2.15	1.55
CHLRE_13g574350v5	2.72	1.54
CHLRE_12g486950v5	2.6	1.54
CHLRE_03g207250v5	23.21	1.53
CHLRE_07g347400v5	7.15	1.53
CHLRE_11g467649v5	6.8	1.53
CHLRE_12g505600v5	2.12	1.53
CHLRE_02g077800v5	13.64	1.51
CHLRE_06g282200v5	7.58	1.51
CHLRE_17g713950v5	3.78	1.51
CHLRE_07g326650v5	3.2	1.51
CHLRE_03g177600v5	2.47	1.51
CHLRE_10g434950v5	2.27	1.51
CHLRE_12g512000v5	5.55	1.5
CHLRE_09g391801v5	5.37	1.5
CHLRE_12g504550v5	4.93	1.5
CHLRE_17g709200v5	3	1.5
CHLRE_02g079450v5	2.08	1.49
CHLRE_06g268000v5	4.5	1.48
CHLRE_01g011600v5	3.42	1.48
CHLRE_09g392750v5	2.3	1.48
CHLRE_06g311350v5	7.27	1.47
CHLRE_11g467527v5	2.47	1.47
CHLRE_01g023400v5	4.73	1.46
CHLRE_12g515850v5	4.21	1.46
CHLRE_13g579326v5	2.42	1.46
CHLRE_06g287450v5	2.91	1.45

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CHLRE_02g105100v5	27.6	1.43
CHLRE_12g505050v5	3.2	1.43
CHLRE_07g347300v5	4.35	1.42
CHLRE_14g627050v5	3.87	1.42
CHLRE_02g102650v5	2.77	1.42
CHLRE_01g001400v5	2.71	1.42
CHLRE_09g395950v5	2.5	1.42
CHLRE_09g387500v5	2	1.42
CHLRE_03g145507v5	2.35	1.41
CHLRE_06g308500v5	11.26	1.4
CHLRE_08g358580v5	5.83	1.4
CHLRE_10g461050v5	2.65	1.4
CHLRE_16g680566v5	2.43	1.4
CHLRE_02g097600v5	7.52	1.39
CHLRE_09g386650v5	38.84	1.38
CHLRE_07g355850v5	30.85	1.38
CHLRE_03g200050v5	7.79	1.38
CHLRE_16g660225v5	4.96	1.38
CHLRE_02g142600v5	3.82	1.37
CHLRE_08g367550v5	3.52	1.37
CHLRE_10g459750v5	3.9	1.36
CHLRE_02g095077v5	3.72	1.35
CHLRE_06g268976v5	2.64	1.35
CHLRE_03g176250v5	2.45	1.35
CHLRE_01g004800v5	3.13	1.34
CHLRE_11g467781v5	2.64	1.34
CHLRE_12g504850v5	2.42	1.34
CHLRE_09g411900v5	2.31	1.34
CHLRE_03g176150v5	4.77	1.33
CHLRE_10g419250v5	4.61	1.32
CHLRE_11g468550v5	2.02	1.32
CHLRE_11g467567v5	6.72	1.31
CHLRE_06g278140v5	11.91	1.3
CHLRE_06g257950v5	2.61	1.3
CHLRE_02g079300v5	2.23	1.3
CHLRE_16g675958v5	2.12	1.3
CHLRE_03g177711v5	2.08	1.29
CHLRE_06g266250v5	4.83	1.27
CHLRE_13g567600v5	4.71	1.27
CHLRE_02g077550v5	3.61	1.27
CHLRE_02g077850v5	3.81	1.26
CHLRE_06g278157v5	2.85	1.26
CHLRE_03g190950v5	22.32	1.25
CHLRE_03g180750v5	2.38	1.25
CHLRE_08g358250v5	2.19	1.25
CHLRE_10g465550v5	2.11	1.25
CHLRE_01g007850v5	2.67	1.24
CHLRE_17g741000v5	2.67	1.24
CHLRE_07g319310v5	2.44	1.23
CHLRE_10g420700v5	2.34	1.23

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CHLRE_16g683250v5	2.1	1.23
CHLRE_06g262900v5	2.05	1.23
CHLRE_09g396100v5	6.11	1.21
CHLRE_16g685050v5	2.24	1.2
CHLRE_16g650250v5	2.2	1.2
CHLRE_10g458450v5	2.03	1.18
CHLRE_08g379400v5	2.19	1.17
CHLRE_10g424250v5	2.09	1.17
CHLRE_08g372900v5	6.7	1.16
CHLRE_05g238311v5	4.95	1.16
CHLRE_12g499800v5	2.78	1.16
CHLRE_03g154350v5	2.5	1.16
CHLRE_02g074511v5	3.31	1.15
CHLRE_02g141346v5	4.89	1.13
CHLRE_03g198236v5	2.03	1.13
CHLRE_16g667450v5	5.31	1.11
CHLRE_02g081050v5	2.28	1.11
CHLRE_07g330300v5	3.41	1.09
CHLRE_14g620500v5	2.54	1.09
CHLRE_02g086300v5	2.35	1.09
CHLRE_01g038250v5	5.25	1.08
CHLRE_02g114600v5	2.82	1.08
CHLRE_06g278162v5	2.53	1.07
CHLRE_02g142687v5	4.57	1.06
CHLRE_01g027000v5	8.14	1.04
CHLRE_12g521300v5	6.91	1.04
CHLRE_07g321400v5	3.68	1.04
CHLRE_01g010400v5	2.46	1.04
CHLRE_01g045550v5	2.44	1.04
CHLRE_17g718500v5	2.22	1.02
CHLRE_04g216850v5	5.03	1.01
CHLRE_07g331550v5	4.01	1.01
CHLRE_06g251000v5	2.45	1
CHLRE_01g042750v5	2.44	1
CHLRE_06g257450v5	2.35	0.98
CHLRE_14g619250v5	5.19	0.97
CHLRE_02g095140v5	4.62	0.97
CHLRE_03g159800v5	2.75	0.97
CHLRE_05g235355v5	2.42	0.93
CHLRE_02g116750v5	3.11	0.77
CHLRE_12g528450v5	2.34	0.71
CHLRE_09g397697v5	3.46	0.7
CHLRE_12g549550v5	5.26	0.69
CHLRE_12g516200v5	5.67	0.65
CHLRE_17g698000v5	2.06	0.63
CHLRE_12g551501v5	2.89	0.59

[a]Gramene (https://www.gramene.org/)

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Supplementary Table 2. Microalgae genes whose expression levels decreased due to co-cultivation of microalgae and yeast

locus tag[a]	$-Log_{10}$ (p-value)	Log_2 (fold change)
CHLRE_17g739800v5	3.98	-7.89
CHLRE_01g045426v5	12.82	-5.62
CHLRE_09g398993v5	15.91	-5.47
CHLRE_13g566000v5	10.64	-5.39
CHLRE_14g623000v5	6.42	-5.03
CHLRE_02g110263v5	4.44	-4.75
CHLRE_08g378950v5	2.48	-4.73
CHLRE_01g000550v5	7.94	-4.71
CHLRE_02g098800v5	8.22	-4.51
CHLRE_17g730350v5	2.03	-4.45
CHLRE_01g006700v5	2.83	-4.44
CHLRE_16g687300v5	10.35	-4.41
CHLRE_03g146447v5	4.03	-4.34
CHLRE_07g344186v5	3.17	-4.33
CHLRE_15g643850v5	2.06	-4.17
CHLRE_16g660700v5	8.48	-4.14
CHLRE_02g099400v5	4.44	-4.11
CHLRE_08g373436v5	8.02	-4.06
CHLRE_09g399552v5	8.65	-4.03
CHLRE_01g043250v5	12.71	-4.01
CHLRE_03g145787v5	13.34	-3.99
CHLRE_14g631600v5	10.66	-3.95
CHLRE_11g479100v5	10.96	-3.86
CHLRE_03g208304v5	5.68	-3.83
CHLRE_10g423083v5	4.97	-3.78
CHLRE_10g440050v5	10.95	-3.73
CHLRE_14g625901v5	3.58	-3.66
CHLRE_15g640426v5	14.88	-3.58
CHLRE_09g405100v5	12.63	-3.53
CHLRE_12g526650v5	2.35	-3.48
CHLRE_04g214150v5	15.68	-3.47
CHLRE_06g288850v5	2.83	-3.45
CHLRE_03g1988632v5	13.04	-3.42
CHLRE_05g240850v5	9.19	-3.42
CHLRE_02g074100v5	2.63	-3.38
CHLRE_08g377650v5	2.69	-3.35
CHLRE_12g533426v5	5.39	-3.34
CHLRE_17g706150v5	2.26	-3.34
CHLRE_02g073850v5	2.85	-3.3
CHLRE_10g464650v5	2.72	-3.28
CHLRE_06g278098v5	12.73	-3.25
CHLRE_14g610400v5	9.23	-3.24
CHLRE_11g479900v5	7.12	-3.19
CHLRE_17g713700v5	3.59	-3.17
CHLRE_12g507850v5	5.24	-3.15
CHLRE_10g464350v5	2.2	-3.15

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CHLRE_13g589350v5	15.79	-3.12
CHLRE_02g095650v5	3.66	-3.12
CHLRE_03g205100v5	15.79	-3.1
CHLRE_17g744647v5	8.95	-3.1
CHLRE_05g233702v5	8	-3.1
CHLRE_09g405100v5	8.1	-3.09
CHLRE_14g631550v5	14.45	-3.05
CHLRE_10g440050v5	14.78	-3.04
CHLRE_15g641200v5	14.04	-3.04
CHLRE_01g048150v5	4.37	-3.04
CHLRE_13g602450v5	5.93	-3.03
CHLRE_12g485550v5	5.24	-3.03
CHLRE_07g349650v5	4.39	-3.03
CHLRE_10g426000v5	2.6	-3.03
CHLRE_09g391400v5	2.29	-3.01
CHLRE_10g456100v5	12.95	-2.98
CHLRE_10g440050v5	11.1	-2.98
CHLRE_02g081750v5	2.27	-2.95
CHLRE_07g342800v5	6.45	-2.94
CHLRE_09g403034v5	6.7	-2.91
CHLRE_12g547650v5	8.12	-2.9
CHLRE_06g301325v5	7.2	-2.9
CHLRE_17g736511v5	5.59	-2.89
CHLRE_17g705450v5	3.25	-2.89
CHLRE_03g155350v5	4.24	-2.86
CHLRE_10g456226v5	3.71	-2.86
CHLRE_02g142050v5	3.67	-2.85
CHLRE_12g534550v5	2.67	-2.85
CHLRE_03g198850v5	12.17	-2.84
CHLRE_14g631250v5	4.61	-2.84
CHLRE_07g320700v5	3.68	-2.84
CHLRE_03g159700v5	3.38	-2.84
CHLRE_05g245500v5	6.04	-2.83
CHLRE_12g543902v5	2.37	-2.83
CHLRE_08g363500v5	5.68	-2.82
CHLRE_17g734805v5	3.65	-2.82
CHLRE_16g650400v5	2.31	-2.82
CHLRE_06g295450v5	7.03	-2.81
CHLRE_10g430300v5	14.07	-2.8
CHLRE_17g733250v5	3.96	-2.8
CHLRE_06g311050v5	3.42	-2.8
CHLRE_12g509600v5	3.05	-2.8
CHLRE_01g016514v5	11.06	-2.78
CHLRE_09g389245v5	9.75	-2.78
CHLRE_11g467700v5	6.52	-2.78
CHLRE_09g408300v5	15.39	-2.77
CHLRE_06g269050v5	6.06	-2.77
CHLRE_09g389838v5	11.6	-2.75
CHLRE_08g358525v5	2.53	-2.75
CHLRE_07g321300v5	2.2	-2.75

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CHLRE_06g301750v5	2.42	-2.74
CHLRE_10g435800v5	9.7	-2.73
CHLRE_09g391450v5	3.95	-2.73
CHLRE_08g361850v5	13.71	-2.72
CHLRE_10g430300v5	12.24	-2.72
CHLRE_09g391350v5	11.81	-2.72
CHLRE_03g175300v5	4.03	-2.71
CHLRE_03g210065v5	3.22	-2.71
CHLRE_17g737351v5	2.27	-2.71
CHLRE_12g534450v5	14.06	-2.7
CHLRE_06g274700v5	5.85	-2.69
CHLRE_09g391350v5	10.99	-2.68
CHLRE_12g554929v5	5.68	-2.68
CHLRE_12g516300v5	7.4	-2.67
CHLRE_06g281350v5	3.43	-2.67
CHLRE_01g028600v5	3.4	-2.67
CHLRE_05g232800v5	5.65	-2.66
CHLRE_07g357700v5	4.1	-2.66
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CHLRE_14g630775v5	3.52	-2.66
CHLRE_08g384650v5	2.81	-2.66
CHLRE_01g048900v5	2.41	-2.66
CHLRE_04g217981v5	2.41	-2.66
CHLRE_12g561000v5	2.62	-2.65
CHLRE_02g103750v5	6.16	-2.64
CHLRE_16g684750v5	2.06	-2.64
CHLRE_13g585026v5	4.7	-2.63
CHLRE_12g548577v5	4.52	-2.62
CHLRE_09g400775v5	4.87	-2.6
CHLRE_17g700100v5	4.33	-2.6
CHLRE_11g467531v5	14.06	-2.59
CHLRE_17g707600v5	2.75	-2.59
CHLRE_10g435800v5	9.69	-2.58
CHLRE_08g358544v5	5.53	-2.58
CHLRE_07g315700v5	10.73	-2.57
CHLRE_08g373352v5	7.37	-2.57
CHLRE_03g187050v5	3.06	-2.57
CHLRE_15g636050v5	6.45	-2.56
CHLRE_10g423550v5	12.17	-2.55
CHLRE_11g478100v5	10.95	-2.54
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CHLRE_11g480079v5	2.26	-2.5
CHLRE_10g430300v5	9.48	-2.49
CHLRE_12g539900v5	8.91	-2.49

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CHLRE_06g300700v5	5.72	-2.34
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CHLRE_10g447700v5	6.32	-2.25
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CHLRE_02g095038v5	4.17	-2.25

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CHLRE_07g318800v5	2.27	-2.05
CHLRE_03g200250v5	6.03	-2.04

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CHLRE_02g087700v5	10.58	-1.86
CHLRE_05g238450v5	12.86	-1.85
CHLRE_10g452100v5	7.71	-1.85

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CHLRE_08g362100v5	7.53	-1.68
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CHLRE_09g387060v5	2.97	-1.66

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CHLRE_09g396550v5	7.6	-1.51
CHLRE_01g029000v5	4.72	-1.51

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CHLRE_16g694450v5	2.2	-1.36
CHLRE_02g112100v5	2.89	-1.35
CHLRE_06g283750v5	2.57	-1.35
CHLRE_12g550400v5	6.43	-1.34
CHLRE_01g025850v5	5.9	-1.34
CHLRE_13g564100v5	4.25	-1.34
CHLRE_02g082350v5	4.11	-1.34
CHLRE_09g386753v5	4.08	-1.34
CHLRE_10g427896v5	2.76	-1.34
CHLRE_03g156050v5	2.41	-1.34
CHLRE_01g026950v5	2.29	-1.34
CHLRE_06g288700v5	7.31	-1.33
CHLRE_02g146150v5	3.21	-1.33
CHLRE_12g519150v5	2.8	-1.33
CHLRE_10g442650v5	5.35	-1.32
CHLRE_02g082852v5	3.12	-1.32
CHLRE_09g403250v5	2.08	-1.32
CHLRE_03g161550v5	5.28	-1.31
CHLRE_15g638551v5	5.28	-1.31
CHLRE_06g273700v5	4.69	-1.31
CHLRE_04g227050v5	3.64	-1.31
CHLRE_09g391726v5	3.47	-1.31
CHLRE_01g050500v5	2.86	-1.31
CHLRE_12g499350v5	2.69	-1.31
CHLRE_09g387875v5	2.21	-1.31
CHLRE_06g281700v5	2.05	-1.31
CHLRE_12g487750v5	2.03	-1.31
CHLRE_09g415950v5	9.6	-1.3
CHLRE_06g280650v5	3.64	-1.3
CHLRE_06g292050v5	2.23	-1.3
CHLRE_03g174850v5	14.43	-1.29
CHLRE_09g396550v5	6.04	-1.29
CHLRE_01g007600v5	4.07	-1.29
CHLRE_12g519300v5	3.9	-1.29
CHLRE_08g366600v5	2.12	-1.29
CHLRE_12g534100v5	9.22	-1.28
CHLRE_03g191950v5	2.84	-1.28

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CHLRE_08g385951v5	2.57	-1.28
CHLRE_06g289600v5	2.14	-1.28
CHLRE_01g015600v5	4.15	-1.27
CHLRE_06g308600v5	4.04	-1.27
CHLRE_17g696400v5	8.39	-1.26
CHLRE_02g118100v5	2.17	-1.26
CHLRE_13g562850v5	13.56	-1.25
CHLRE_12g509050v5	5.22	-1.25
CHLRE_09g392803v5	5.05	-1.25
CHLRE_10g433950v5	4.03	-1.25
CHLRE_11g467350v5	4	-1.25
CHLRE_03g150101v5	3.71	-1.25
CHLRE_12g511800v5	2.39	-1.25
CHLRE_10g462950v5	14.22	-1.24
CHLRE_12g500150v5	7.66	-1.24
CHLRE_07g315750v5	6.75	-1.24
CHLRE_01g006850v5	2.94	-1.24
CHLRE_03g188250v5	13.87	-1.23
CHLRE_02g085257v5	7.55	-1.23
CHLRE_02g142987v5	3.3	-1.23
CHLRE_14g623125v5	2.57	-1.23
CHLRE_09g395650v5	2.17	-1.23
CHLRE_12g510650v5	12.77	-1.22
CHLRE_08g362150v5	7.83	-1.22
CHLRE_10g423650v5	6.51	-1.22
CHLRE_13g579550v5	2.62	-1.22
CHLRE_17g728550v5	7.09	-1.21
CHLRE_05g236050v5	6.73	-1.21
CHLRE_16g660000v5	4.2	-1.21
CHLRE_06g268600v5	3.39	-1.21
CHLRE_11g474950v5	2.49	-1.21
CHLRE_13g591150v5	12.34	-1.2
CHLRE_12g520000v5	3.52	-1.2
CHLRE_05g241647v5	16.24	-1.19
CHLRE_11g479500v5	10.3	-1.19
CHLRE_10g452050v5	7.94	-1.19
CHLRE_04g223100v5	6.24	-1.19
CHLRE_02g111450v5	2.8	-1.19
CHLRE_03g155250v5	12.36	-1.18
CHLRE_03g189800v5	3.11	-1.18
CHLRE_09g413200v5	2.98	-1.18
CHLRE_13g606450v5	2.36	-1.18
CHLRE_12g490050v5	2.02	-1.18
CHLRE_04g224600v5	9.22	-1.17
CHLRE_12g533100v5	4.43	-1.17
CHLRE_12g501950v5	5.63	-1.16
CHLRE_09g413200v5	2.99	-1.16
CHLRE_06g294700v5	5.03	-1.15
CHLRE_01g050950v5	3.56	-1.15
CHLRE_09g411200v5	3.41	-1.14

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CHLRE_16g674700v5	2.73	-1.14
CHLRE_16g668550v5	2.1	-1.14
CHLRE_16g650550v5	14.38	-1.13
CHLRE_07g331650v5	5.38	-1.13
CHLRE_08g358540v5	4.24	-1.13
CHLRE_16g669650v5	3.48	-1.13
CHLRE_12g520250v5	3.39	-1.13
CHLRE_03g190050v5	2.83	-1.12
CHLRE_09g408300v5	2.43	-1.12
CHLRE_12g530000v5	2.34	-1.12
CHLRE_09g387000v5	10.48	-1.1
CHLRE_16g684850v5	3.9	-1.1
CHLRE_09g387875v5	2.88	-1.1
CHLRE_01g004900v5	5.66	-1.09
CHLRE_12g534800v5	5.41	-1.09
CHLRE_07g312300v5	4.32	-1.09
CHLRE_07g323600v5	2.52	-1.09
CHLRE_10g418450v5	17.45	-1.08
CHLRE_09g409350v5	7.61	-1.08
CHLRE_10g442650v5	3.78	-1.08
CHLRE_01g000350v5	2.05	-1.08
CHLRE_15g638400v5	8.32	-1.07
CHLRE_12g484000v5	3.64	-1.07
CHLRE_12g522250v5	2	-1.07
CHLRE_08g366700v5	5.25	-1.06
CHLRE_02g073350v5	4.19	-1.06
CHLRE_03g150550v5	2.52	-1.06
CHLRE_12g511900v5	17.19	-1.05
CHLRE_12g500750v5	7.94	-1.05
CHLRE_01g047950v5	7.49	-1.05
CHLRE_02g142146v5	6.21	-1.05
CHLRE_01g032650v5	4.63	-1.05
CHLRE_09g394325v5	3.77	-1.05
CHLRE_15g641282v5	3.89	-1.04
CHLRE_03g144484v5	2.05	-1.04
CHLRE_16g695050v5	10.18	-1.03
CHLRE_01g031100v5	6.83	-1.03
CHLRE_02g099850v5	4.32	-1.03
CHLRE_03g146167v5	3.87	-1.03
CHLRE_06g306350v5	2.58	-1.03
CHLRE_16g690655v5	2.43	-1.03
CHLRE_17g742150v5	2.16	-1.03
CHLRE_17g728200v5	2.05	-1.03
CHLRE_09g396400v5	15.19	-1.02
CHLRE_02g103100v5	2.53	-1.02
CHLRE_07g334800v5	2.27	-1.02
CHLRE_17g701700v5	2.6	-1.01
CHLRE_12g545500v5	2.13	-1.01
CHLRE_13g565270v5	2.02	-1.01
CHLRE_12g528400v5	2	-1.01

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CHLRE_08g362019v5	7.71	-1
CHLRE_14g623439v5	2.46	-1
CHLRE_08g365400v5	16.44	-0.99
CHLRE_11g479150v5	4.57	-0.99
CHLRE_02g101950v5	2.68	-0.99
CHLRE_09g399350v5	2.19	-0.99
CHLRE_12g521150v5	6.17	-0.98
CHLRE_06g304300v5	2.78	-0.98
CHLRE_17g740100v5	2.5	-0.98
CHLRE_10g438600v5	4.44	-0.97
CHLRE_02g147900v5	3.68	-0.97
CHLRE_13g573900v5	3.44	-0.97
CHLRE_14g624201v5	3.38	-0.97
CHLRE_02g095144v5	2.46	-0.97
CHLRE_11g467350v5	2.42	-0.97
CHLRE_01g015400v5	2.36	-0.97
CHLRE_12g492250v5	2.04	-0.97
CHLRE_07g355500v5	2.49	-0.96
CHLRE_07g321550v5	2.32	-0.96
CHLRE_10g452350v5	17.66	-0.95
CHLRE_13g589450v5	10.48	-0.95
CHLRE_09g415800v5	4.2	-0.95
CHLRE_03g148900v5	2.51	-0.95
CHLRE_13g603550v5	5.99	-0.94
CHLRE_06g282000v5	2.18	-0.94
CHLRE_07g332800v5	8.94	-0.93
CHLRE_12g554850v5	4.06	-0.93
CHLRE_06g253753v5	2.9	-0.93
CHLRE_02g142426v5	2.72	-0.93
CHLRE_07g352850v5	16.74	-0.92
CHLRE_10g432800v5	14.35	-0.92
CHLRE_17g716700v5	10.25	-0.92
CHLRE_10g420700v5	5.16	-0.92
CHLRE_16g686285v5	2.83	-0.92
CHLRE_10g423250v5	2.11	-0.92
CHLRE_12g519100v5	4.57	-0.91
CHLRE_02g110300v5	3.28	-0.91
CHLRE_13g575250v5	2.19	-0.91
CHLRE_17g745847v5	2.02	-0.91
CHLRE_12g543100v5	3.62	-0.9
CHLRE_11g467730v5	2.34	-0.9
CHLRE_03g179860v5	3.42	-0.89
CHLRE_03g200200v5	2.26	-0.89
CHLRE_12g505850v5	2.97	-0.88
CHLRE_12g501550v5	8.93	-0.87
CHLRE_06g310200v5	3.65	-0.87
CHLRE_05g246150v5	3.24	-0.87
CHLRE_17g746797v5	2.07	-0.87
CHLRE_16g677382v5	8.87	-0.86
CHLRE_13g571650v5	4.37	-0.86

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CHLRE_11g467729v5	3.14	-0.86
CHLRE_10g452050v5	5.36	-0.85
CHLRE_16g680588v5	4.91	-0.85
CHLRE_09g416150v5	4.7	-0.84
CHLRE_10g451950v5	2.28	-0.84
CHLRE_08g359350v5	2	-0.84
CHLRE_16g650300v5	3.69	-0.83
CHLRE_09g386750v5	2.12	-0.83
CHLRE_16g659950v5	16.75	-0.82
CHLRE_02g141400v5	6.6	-0.82
CHLRE_10g462950v5	4.41	-0.82
CHLRE_06g280050v5	3.83	-0.82
CHLRE_02g095084v5	3.48	-0.82
CHLRE_12g558000v5	9.97	-0.81
CHLRE_09g387000v5	5.59	-0.81
CHLRE_15g640750v5	2.07	-0.81
CHLRE_13g590800v5	9.44	-0.8
CHLRE_16g664550v5	2.94	-0.8
CHLRE_06g278178v5	2.33	-0.8
CHLRE_03g160350v5	2.15	-0.8
CHLRE_03g187450v5	8.53	-0.79
CHLRE_05g247851v5	5.82	-0.79
CHLRE_06g306550v5	3.68	-0.79
CHLRE_08g372950v5	3.61	-0.79
CHLRE_01g027200v5	3.61	-0.78
CHLRE_06g263150v5	2.75	-0.78
CHLRE_02g118850v5	2.56	-0.78
CHLRE_15g634650v5	2.16	-0.78
CHLRE_06g284050v5	4.8	-0.77
CHLRE_01g063997v5	3.36	-0.77
CHLRE_17g722750v5	2.11	-0.77
CHLRE_16g691440v5	2.67	-0.76
CHLRE_16g682000v5	10.72	-0.75
CHLRE_09g409350v5	3.8	-0.75
CHLRE_01g041650v5	2.14	-0.75
CHLRE_10g425900v5	3.79	-0.74
CHLRE_07g331962v5	2.62	-0.74
CHLRE_06g265800v5	11.39	-0.73
CHLRE_09g417150v5	3.71	-0.73
CHLRE_02g079200v5	2.1	-0.73
CHLRE_03g185250v5	4.95	-0.72
CHLRE_03g193950v5	4.88	-0.72
CHLRE_16g649750v5	3.38	-0.72
CHLRE_07g312900v5	2.98	-0.72
CHLRE_02g120100v5	4.24	-0.71
CHLRE_11g468950v5	3.73	-0.71
CHLRE_13g607950v5	2.17	-0.71
CHLRE_13g590750v5	10.98	-0.7
CHLRE_07g315150v5	3.24	-0.7
CHLRE_02g088850v5	2.39	-0.7

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CHLRE_12g483850v5	17.27	-0.69
CHLRE_01g017300v5	11.59	-0.69
CHLRE_12g494550v5	9.2	-0.69
CHLRE_14g611300v5	7.47	-0.69
CHLRE_12g495550v5	3.18	-0.69
CHLRE_12g510050v5	2.31	-0.69
CHLRE_16g679500v5	4.75	-0.68
CHLRE_01g018650v5	3.52	-0.68
CHLRE_16g656950v5	2.37	-0.68
CHLRE_02g143550v5	2.06	-0.68
CHLRE_10g440400v5	2.06	-0.68
CHLRE_01g062172v5	12.61	-0.67
CHLRE_12g519950v5	2.09	-0.67
CHLRE_06g300800v5	10.01	-0.66
CHLRE_01g026600v5	6.51	-0.66
CHLRE_03g206600v5	5.31	-0.65
CHLRE_12g507300v5	17.83	-0.64
CHLRE_09g394750v5	5.21	-0.64
CHLRE_13g576400v5	3.32	-0.64
CHLRE_11g480150v5	10.02	-0.63
CHLRE_14g612450v5	6.43	-0.63
CHLRE_06g275350v5	2.6	-0.63
CHLRE_03g195650v5	6.28	-0.62
CHLRE_02g096150v5	4.06	-0.62
CHLRE_16g651923v5	4.03	-0.62
CHLRE_06g278213v5	3.9	-0.62
CHLRE_10g427700v5	2.88	-0.62
CHLRE_03g160400v5	2.21	-0.62
CHLRE_12g528000v5	8.38	-0.61
CHLRE_06g285401v5	4.58	-0.61
CHLRE_15g635600v5	11.33	-0.6
CHLRE_09g412100v5	5.47	-0.6
CHLRE_04g226850v5	3.33	-0.6
CHLRE_06g250100v5	2.7	-0.59
CHLRE_17g727100v5	2.08	-0.59
CHLRE_16g683793v5	2.04	-0.59
CHLRE_03g190850v5	3.35	-0.58
CHLRE_09g395350v5	2.3	-0.58
CHLRE_07g346200v5	2.28	-0.58

[a]Gramene (https://www.gramene.org/)

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Supplementary Table 3. Yeast genes whose expression levels increased due to co-cultivation of microalgae and yeast

Gene[a] or locus tag[b]	-Log_{10} (p-value)	Log_2 (fold change)
YAR010C	5.5	6.94
YPR204W	2.33	3.99
YNCD0008W	4.31	3.15
YNCL0037W	3.96	2.86
YNCN0010C	3.03	2.69
PAU22	4.73	2.69
FIT3	7.78	2.27
YNCM0020W	3.09	2.15
MPH3	5.54	1.9
DCG1	5.75	1.79
YNCM0019W	3.26	1.69
YOR381W-A	4.52	1.66
YNCB0006W	4.2	1.63
YOL107W	7.89	1.62
YNCE0021C	4.66	1.58
HOT13	6.23	1.57
YNCJ0014C	2.21	1.44
MIT1	12.03	1.37
DUR3	17.77	1.37
YKR104W	2.05	1.36
ELP6	8.15	1.34
BSC5	5.08	1.26
KEI1	13.54	1.26
ARC18	19.12	1.24
YGR035W-A	10.3	1.23
YNCK0016W	10.9	1.23
ATG41	13.19	1.22
PBA1	13.84	1.22
YNCK0005C	2.86	1.21
PCL1	4.48	1.2
YMR247W-A	2.14	1.16
COQ9	9.97	1.12
ATP8	5.98	1.09
TKL2	11.69	1.09
GAT1	4.91	1.08
ARC19	17.17	1.06
MF(ALPHA)2	4.38	1.05
SDS22	8.73	1.05
AGA2	3.72	1.04
DIA4	5.52	1.03
ACP1	6.4	1.03
SPL2	14.32	1.03
YNR068C	2.8	1.02
COS4	2.58	1.01
YEL068C	5.55	1
AIM34	2.2	0.99

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MUD1	8.97	0.99
YLR126C	10.18	0.99
SST2	3.43	0.98
IME1	8.29	0.97
SWI1	15.84	0.96
COS6	6.83	0.95
APA1	7.93	0.95
YPR063C	9.08	0.95
LUG1	3.92	0.94
ATG33	10.07	0.94
YHM2	8.22	0.93
PUP1	13.06	0.93
OPI10	2.94	0.92
PHS1	6.01	0.92
DAL7	18.69	0.92
HAL1	5.65	0.91
DPM1	6.76	0.91
EMC10	14.55	0.91
YNCL0009C	2.85	0.9
GPI2	4.62	0.9
PIB2	8.38	0.9
TAF5	9.22	0.9
ECM3	11.29	0.9
VPS28	5.2	0.89
MOB2	4.02	0.88
MPT5	7.11	0.88
LEU4	22.01	0.87
SNX41	2.06	0.86
YLR342W-A	12.28	0.86
ILM1	12.6	0.86
ERG28	12.61	0.86
ATF1	12.75	0.86
ZNF1	6.03	0.85
YPL229W	7.15	0.85
TVP15	9.1	0.85
EAF3	17.76	0.85
YPR145C-A	19.95	0.85
APT2	23.94	0.85
BUD9	2.88	0.84
PRO3	8.25	0.84
ATP1	22.52	0.84
CIT3	11.55	0.83
YIP1	15.58	0.83
PKP2	5.5	0.82
YPR053C	5.53	0.82
VPS34	6.55	0.82
RNH203	6.65	0.82
SWC5	10.18	0.82
YFH1	12.09	0.82
ATG40	20.96	0.82

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SUT390	2.14	0.81
YBR196C-A	2.63	0.81
PHB1	15.67	0.81
BNA3	3.04	0.8
YMC2	4.73	0.8
AIM17	5.82	0.8
UBC7	12.97	0.8
GUT2	24.74	0.8
SNR6	2.42	0.79
CSM1	2.91	0.79
NNR2	3.77	0.79
ICP55	3.82	0.79
SCM4	4.13	0.79
TOS7	4.77	0.79
YFL051C	4.81	0.79
BSC6	7.44	0.79
GIS1	13.59	0.79
SNC1	15.41	0.79
PHO80	8.18	0.78
NHP6A	12.9	0.78
CAT8	16.85	0.78
PDB1	19.44	0.78
UBC9	19.62	0.78
GPD1	21.36	0.78
ECM11	2.79	0.77
MET17	3.48	0.77
TOM20	11.18	0.77
YDL012C	3.99	0.76
SEC22	4.74	0.76
YLL056C	5.11	0.76
PMT6	6.16	0.76
YMR105W-A	7.02	0.76
YNL134C	9.94	0.76
GID10	10.1	0.76
ATP5	13.92	0.76
GAB1	4.65	0.75
YMC1	5.17	0.75
RNH1	5.68	0.75
ARG7	7.83	0.75
POL30	8.71	0.75
YNR064C	11.98	0.75
TOS2	4.2	0.74
YMR181C	5.73	0.74
RFA3	9.53	0.74
TRX1	14.08	0.74
MRX18	14.19	0.74
SNU13	20.41	0.74
DMC1	23.16	0.74
YVC1	2.17	0.73
YHR173C	2.19	0.73

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BIO2	2.26	0.73
GCR1	2.42	0.73
MVP1	4.98	0.73
FRE3	8.22	0.73
AUA1	13.79	0.73
SLM2	2.27	0.72
YER181C	2.61	0.72
PBP2	3.38	0.72
MCP1	3.55	0.72
CGI121	3.64	0.72
YML054C-A	3.65	0.72
YFR012W-A	4.28	0.72
YSP3	4.87	0.72
ULP1	7.94	0.72
ORM1	13.41	0.72
YBR071W	13.44	0.72
GGA1	2.9	0.71
ODC2	5.1	0.71
YNL034W	5.63	0.71
TCB1	6.42	0.71
ERV15	7.8	0.71
ISC10	9.52	0.71
MFA1	9.97	0.71
MCK1	10.45	0.71
TDA10	3.56	0.7
TPS1	3.82	0.7
RMR1	5.71	0.7
VHR1	6.3	0.7
AVT1	6.68	0.7
MSC2	8.5	0.7
VPS36	9.35	0.7
YNL190W	21.34	0.7
YJR079W	2.58	0.69
YIP5	2.62	0.69
YNL018C	3.67	0.69
NRS1	3.97	0.69
SLC1	4.03	0.69
MET28	4.08	0.69
YPT53	20.34	0.69
PCF11	2.52	0.68
ARD1	2.95	0.68
BDH2	3.15	0.68
TES1	4.63	0.68
SUL1	7.96	0.68
GPB2	8.85	0.68
GID11	17.21	0.68
MIN6	20.93	0.68
GSF2	22.55	0.68
CIN5	2.88	0.67
YLR285C-A	3.6	0.67

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AIM7	4.17	0.67
MDS3	5.17	0.67
ARO80	5.3	0.67
GRX3	6.27	0.67
YAK1	7.45	0.67
COA6	9.25	0.67
YPF1	12.62	0.67
CMI7	15.22	0.67
CAT2	20.39	0.67
MFA2	2.51	0.66
YKU80	3.6	0.66
CKI1	3.83	0.66
SNG1	3.94	0.66
SGN1	4.81	0.66
YIF1	7.24	0.66
ATG2	7.95	0.66
NCA3	10.91	0.66
SNR80	16.01	0.66
ITS2-1	25.18	0.66
SYM1	2.05	0.65
HXT8	2.66	0.65
YJL070C	2.72	0.65
DSE1	3.43	0.65
MCT1	4.48	0.65
IMG1	6.48	0.65
HMG1	9.69	0.65
DFP2	10.5	0.65
PCL5	11.8	0.65
ADR1	14.26	0.65
ITS2-2	24.75	0.65
RRT13	2.11	0.64
GAS3	2.7	0.64
AIM18	3.28	0.64
PMA2	3.61	0.64
SEC11	7.4	0.64
NGR1	9.26	0.64
WWM1	10.36	0.64
GVP36	11.91	0.64
MSS18	3.45	0.63
GPM2	4.34	0.63
MRX19	4.54	0.63
IRC24	7.17	0.63
TED1	9.42	0.63
PEX18	10.92	0.63
ORA1	14.76	0.63
LSC1	15.06	0.63
BLI1	16.01	0.63
YHR175W-A	19.3	0.63
YCP4	21.37	0.63
YGR237C	2.12	0.62

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YCR099C	2.39	0.62
YGR117C	2.4	0.62
HAP2	2.73	0.62
FRE5	2.96	0.62
CAP2	4.87	0.62
YPR1	5.48	0.62
PEX13	6.45	0.62
SNN1	7.02	0.62
PST2	7.58	0.62
RNY1	8.16	0.62
ATP16	8.5	0.62
AIM6	11.66	0.62
UGX2	14.14	0.62
AMS1	23.66	0.62
YLR410W-A	2.34	0.61
AIM11	3.04	0.61
CYB2	3.24	0.61
ANK1	3.31	0.61
MET5	3.77	0.61
ECM29	4.26	0.61
SBH1	6.7	0.61
HED1	7.54	0.61
PAT1	8.15	0.61
IZH1	8.26	0.61
BOL1	9.68	0.61
RVS167	12.83	0.61
SMT3	14.82	0.61
COI1	15.52	0.61
ATG42	23.27	0.61
YNCE0026W	2.01	0.6
PAU2	2.05	0.6
GPH1	2.66	0.6
RUF21	3	0.6
MDV1	3.33	0.6
MEF2	3.8	0.6
MIM2	3.91	0.6
RBL2	4.27	0.6
HOP1	5.47	0.6
YDL199C	8.91	0.6
AIM24	2.44	0.59
MTC5	3.66	0.59
YJR096W	7.2	0.59
YRA2	7.36	0.59
TFS1	7.63	0.59

[a]UniProt (https://www.uniprot.org/)

[b]*Saccharomyces* Genome Database (https://www.yeastgenome.org/)

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Supplementary Table 4. Yeast genes whose expression levels decreased due to co-cultivation of microalgae and yeast

Gene[a] or locus tag[b]	$-Log_{10}$ (p-value)	Log_2 (fold change)
YHR214C-E	4.85	-5.25
YNCJ0012W	5.33	-4.31
SUP53	6.56	-4.22
SUF8	6.88	-4.11
EMT1	10.93	-3.56
YNCP0017C	2.6	-3.12
TRR4	7.14	-3.12
YNCL0007W	13	-3.07
YNCD0024C	4.64	-3.01
YNCD0004W	6.41	-3.01
YNCI0009W	2.74	-2.9
YNCM0023C	7.32	-2.82
YNCF0009C	6.31	-2.7
YNCP0008C	8.65	-2.69
YNCN0008C	5.78	-2.63
YNCL0002C	2.61	-2.4
SUP51	5.27	-2.4
TRN1	2.16	-2.31
YNCG0027W	2.82	-2.31
YNCH0002C	2.86	-2.31
YOR389W	18.72	-2.25
YNCB0012W	2.89	-2.19
YNCG0037W	3.69	-2.19
YNCM0025C	2.22	-2.12
YNCG0029C	2.12	-2.05
YNCG0032W	4.64	-1.99
YIL054W	5.75	-1.99
YNCJ0008W	10.67	-1.97
YNCP0023W	2.75	-1.84
YNL067W-B	6.21	-1.84
RGD2	10.13	-1.84
YPL277C	11.82	-1.82
YNCG0042C	2.75	-1.81
SOE1	4.36	-1.81
YNCO0011W	4.93	-1.76
YNCG0011W	3.86	-1.73
tK(UUU)Q	20.67	-1.72
SUF23	2.81	-1.69
YNCP0001C	8.43	-1.69
NAT4	14.85	-1.65
SUP54	5.18	-1.63
YNCG0033W	4.53	-1.6
YLR365W	4.12	-1.57
POG1	20.19	-1.56
YNCO0008W	2.01	-1.53
GIS4	17.22	-1.52

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SUP61	2.38	-1.5
YNCM0033C	4.85	-1.5
ASF1	19.85	-1.5
SNR50	25.61	-1.5
EFM6	20.58	-1.49
AQY2	20.98	-1.49
CDC65	2.15	-1.45
ECM19	9.16	-1.44
PIG2	10.51	-1.42
tP(UGG)Q	10.19	-1.41
YNCD0017W	3.03	-1.36
YNCD0019C	4.27	-1.36
VHR2	4.89	-1.36
YNCG0023C	23.56	-1.36
HXT3	7.23	-1.35
ZRG8	9.55	-1.33
BUR2	16.06	-1.3
ZDS1	4.52	-1.28
tY(GUA)Q	5.28	-1.28
YPR064W	2.75	-1.27
YJL107C	8.13	-1.27
ATF2	8.92	-1.24
YJL027C	10.67	-1.24
ANS1	10.67	-1.23
SSK22	13.11	-1.23
SRV2	2.59	-1.22
YER158C	21.87	-1.22
SRL3	20.9	-1.21
BNR1	4.55	-1.2
YNCC0005W	10.88	-1.2
YOR008C-A	23.59	-1.2
MNL1	7.56	-1.18
tN(GUU)Q	4.85	-1.17
AQR1	6.21	-1.17
SNR71	24.27	-1.17
SNF1	10.54	-1.16
YAH1	2.92	-1.15
IRT1	16.71	-1.14
YMR082C	3.3	-1.12
YNCK0021W	4.23	-1.11
TAT2	14.71	-1.11
HTC1	3.83	-1.1
FLX1	6.48	-1.09
SNR66	19.54	-1.09
HLR1	4.19	-1.08
SRX1	4.57	-1.08
UPA1	24.83	-1.07
RDN5-1	6.56	-1.06
YNCG0028W	2.57	-1.05
SNR53	8.69	-1.05

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BUD7	11.05	-1.03
YKR041W	4.97	-1.02
YPL245W	6.76	-1.02
COM2	18.14	-1.02
ADE17	27.21	-1.02
PYC2	15.44	-1.01
YLR406C-A	4.31	-1
AST1	5.51	-1
OSW1	10.34	-1
YNCE0028C	2.51	-0.99
SIZ1	3.19	-0.99
MTD1	25.66	-0.99
FKH2	12.19	-0.98
SED1	24.16	-0.98
YPL068C	4.61	-0.97
PRY1	2.1	-0.96
SPT10	7.06	-0.96
DIG1	9.39	-0.96
TUP1	2.07	-0.95
HXT13	5.78	-0.95
CTH1	9.8	-0.95
AIR1	16.21	-0.95
ACK1	7.14	-0.94
CAB3	10.38	-0.93
YML037C	3.2	-0.92
YNCD0023C	12.66	-0.92
ENT4	21.71	-0.92
PRM10	4.63	-0.91
KNH1	10.39	-0.91
MTR4	26.72	-0.91
RAX1	5.87	-0.9
YGL235W	6.68	-0.9
SNR65	14.93	-0.9
YGL230C	16.69	-0.9
HSU1	2.29	-0.89
CLN3	2.81	-0.89
UPS3	7.86	-0.89
EST1	11.3	-0.89
GCV1	25.36	-0.89
CHA1	3.51	-0.88
YGR121W-A	3.76	-0.88
RBS1	3.77	-0.88
PDR12	8.97	-0.88
RAD7	21.6	-0.88
SPR3	21.95	-0.88
CMR1	2.68	-0.87
ASG7	2.81	-0.87
YOR293C-A	3.84	-0.87
TIM50	5.8	-0.87
RGS2	17.64	-0.87

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SPS1	26.89	-0.87
GAT3	7.14	-0.86
MAE1	13.91	-0.86
RTT10	20.61	-0.86
PCA1	21.26	-0.86
YLR255C	6.44	-0.85
SAM4	3.48	-0.84
YNL095C	6.88	-0.84
SGA1	11.09	-0.84
PRM7	15.23	-0.84
DUS3	20.46	-0.84
YLR225C	9.51	-0.83
TPK3	10.17	-0.83
LCP5	14.83	-0.83
TCD2	17.54	-0.83
PRK1	3.1	-0.82
YRO2	3.8	-0.82
GRC3	6.81	-0.82
PMA1	14.52	-0.81
YEL023C	15	-0.81
BZZ1	3.91	-0.8
YHL026C	5.68	-0.8
PES4	11.66	-0.8
USV1	3.07	-0.79
DSN1	3.2	-0.79
SPC29	3.32	-0.79
DOA1	4.56	-0.79
YPR027C	7.81	-0.79
SDS23	9.93	-0.79
UTP18	16.59	-0.79
SRP40	25.45	-0.79
SMA2	5.32	-0.78
YGR054W	7.78	-0.78
POP3	9.18	-0.78
ARN1	23.44	-0.78
YNR014W	2.25	-0.77
MSA1	2.73	-0.77
MYO4	5.62	-0.77
ART5	5.96	-0.77
RTC4	6.27	-0.77
PSK2	11.72	-0.77
CBF2	12.35	-0.77
RRT12	13.77	-0.77
SHQ1	14.93	-0.77
UBP7	2.59	-0.76
IFM1	3.18	-0.76
MRS3	6.46	-0.76
DIN7	8.06	-0.76
DEG1	13.12	-0.76
SPR28	13.12	-0.76

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SPO19	20.66	-0.76
CLB4	3.85	-0.75
LAF1	6.55	-0.75
YPK2	11.58	-0.75
BAG7	25.54	-0.75
SCM3	2.82	-0.74
YLR179C	6.54	-0.74
FRE8	6.76	-0.74
LSG1	7.6	-0.74
YMR315W-A	7.9	-0.74
GAT4	8.02	-0.74
NDE1	14.28	-0.74
GFA1	28.81	-0.74
RBH1	2.58	-0.73
PGD1	3.16	-0.73
YPR096C	3.28	-0.73
AIM4	4.93	-0.73
UBA3	7.9	-0.73
GAS2	8.2	-0.73
NAB2	21.7	-0.73
NEJ1	2.23	-0.72
YDL211C	3.04	-0.72
YNCD0007C	4.6	-0.72
ALY2	4.7	-0.72
ADD37	7.24	-0.72
tM(CAU)Q1	8.69	-0.72
OCA5	16.63	-0.72
SOK2	18.35	-0.72
BCK2	23.64	-0.72
RPL17B	29.2	-0.72
SRS2	3.04	-0.71
SEC6	3.49	-0.71
AAR2	3.5	-0.71
TAX4	3.71	-0.71
CBP1	4.59	-0.71
SGO1	4.8	-0.71
PKH3	5.66	-0.71
MCM10	5.88	-0.71
SER2	6.18	-0.71
RRG1	6.81	-0.71
PBS2	7.44	-0.71
YKL106C-A	8.07	-0.71
SNR55	16.5	-0.71
YOR342C	18.9	-0.71
SSF1	20.49	-0.71
THR4	5.12	-0.7
YLR162W	5.55	-0.7
NDT80	7.95	-0.7
CDA1	8.77	-0.7
SKT5	9.79	-0.7

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SRG1	17.48	-0.7
UME6	3.15	-0.69
RRM3	3.71	-0.69
TRF5	8.35	-0.69
RPL6B	26.88	-0.69
PAC1	2.11	-0.68
EDC1	5	-0.68
SIR3	6.06	-0.68
BUL2	6.79	-0.68
YGR273C	8.44	-0.68
NUP60	9.26	-0.68
YJR107C-A	9.78	-0.68
ATG15	13.82	-0.68
UBC11	15.62	-0.68
AQY1	16.43	-0.68
SAP155	16.54	-0.68
AFT1	2.81	-0.67
TAT1	2.92	-0.67
GAL7	3.15	-0.67
ADA2	3.92	-0.67
PET309	4.03	-0.67
SAE2	4.57	-0.67
PNS1	5.21	-0.67
UPS2	7.62	-0.67
HXT10	9.56	-0.67
GCN3	10.88	-0.67
PWP2	26.23	-0.67
MAM1	3.37	-0.66
GDE1	5.21	-0.66
SRD1	5.63	-0.66
PPR1	5.84	-0.66
DON1	5.95	-0.66
ALD5	6.05	-0.66
tS(UGA)Q2	6.16	-0.66
SOG2	7.09	-0.66
NUT2	9.35	-0.66
UTP30	13.29	-0.66
TRX3	14.39	-0.66
SPR6	23.65	-0.66
FLO8	2.46	-0.65
TBRT	2.58	-0.65
ESP1	2.81	-0.65
MSL5	3.48	-0.65
YCL021W-A	3.49	-0.65
YOL097W-A	3.92	-0.65
BIL2	4.46	-0.65
REX2	5.95	-0.65
KCH1	6.47	-0.65
SWT21	6.78	-0.65
SPS22	9.05	-0.65

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SXM1	18.78	-0.65
ANY1	19.67	-0.65
CHS3	19.87	-0.65
GPI18	24.13	-0.65
TPC1	2.7	-0.64
APC5	3.04	-0.64
SNF5	3.16	-0.64
YPL039W	3.93	-0.64
YER085C	4.58	-0.64
DUS4	6.37	-0.64
EMI2	11.08	-0.64
TMA46	12.29	-0.64
KRI1	16.59	-0.64
UTP9	20.57	-0.64
SPB1	25.03	-0.64
MED6	3.82	-0.63
ECM23	5.34	-0.63
APP1	5.86	-0.63
MIP6	6.06	-0.63
YIL067C	6.89	-0.63
FRS2	7.41	-0.63
HXT14	7.73	-0.63
PRM5	25.13	-0.63
RPL7A	27.1	-0.63
MAK10	2.37	-0.62
MRX11	2.6	-0.62
YBR182C-A	2.71	-0.62
GEM1	2.94	-0.62
YDR541C	3.16	-0.62
YML6	3.17	-0.62
YJL043W	3.28	-0.62
PXL1	3.94	-0.62
YNL143C	4.05	-0.62
UBP3	5.12	-0.62
NSE5	5.43	-0.62
DPB4	5.55	-0.62
ATP22	8.66	-0.62
PRP43	22.38	-0.62
GIP3	26.83	-0.62
RPS15	29.83	-0.62
PRP9	2.95	-0.61
PFS2	3.73	-0.61
SMK1	4.7	-0.61
MLC1	4.92	-0.61
MTO1	4.92	-0.61
ASK1	7.95	-0.61
RAP1	8.47	-0.61
SMP1	8.98	-0.61
NUP133	9.09	-0.61
PXR1	10.51	-0.61

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PSR2	12.43	-0.61
RIX1	12.94	-0.61
UTP4	18.35	-0.61
PDE2	30.55	-0.61
GCG1	2.95	-0.6
YGL138C	3.29	-0.6
SED5	3.29	-0.6
DUG3	4.29	-0.6
THR1	4.61	-0.6
MRL1	4.83	-0.6
SRL4	5.37	-0.6
SCS3	5.69	-0.6
YGL149W	5.9	-0.6
YSP2	8.49	-0.6
SLD7	9	-0.6
PAM18	10.94	-0.6
CDC3	11.14	-0.6
FPK1	13.4	-0.6
RIA1	14.07	-0.6
DBP3	22.06	-0.6
URA7	30.74	-0.6
PTP1	2.86	-0.59
EPO1	6.11	-0.59
CTS2	6.85	-0.59
PMD1	8.73	-0.59
SNF6	9.54	-0.59
PDC6	16.06	-0.59
DED81	16.72	-0.59
RIM4	27.45	-0.59

[a]UniProt (https://www.uniprot.org/)

[b]Saccharomyces Genome Database (https://www.yeastgenome.org/)