

Applied Microbiology and Biotechnology

Supplementary information

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

Miiku Takahashi^a, Yukino Karitani^a, Ryosuke Yamada^{a*}, Takuya Matsumoto^a, Hiroyasu Ogino^a

^aOsaka Metropolitan University, Department of Chemical Engineering, 1-1 Gakuen-cho, Naka-ku, Sakai, Osaka
599-8531, Japan

*Corresponding author: Ryosuke Yamada

Tel: +81-72-254-9504

E-mail address: ryamada@omu.ac.jp (R. Yamada)

Table S1. Green algae genes whose expression levels increased due to co-cultivation of green algae 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	8.00
CHLRE_03g204500v5	2.67	7.30
CHLRE_05g241634v5	9.19	7.14
CHLRE_07g325740v5	10.99	7.10
CHLRE_09g390838v5	13.10	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	6.40
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	5.50
CHLRE_10g442800v5	2.61	5.49
CHLRE_05g234656v5	4.70	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	6.20	4.81
CHLRE_12g546600v5	5.98	4.81
CHLRE_11g467709v5	8.02	4.72
CHLRE_07g315050v5	8.80	4.67
CHLRE_01g012700v5	19.00	4.64
CHLRE_11g467709v5	6.16	4.53
CHLRE_09g393700v5	11.76	4.47
CHLRE_03g149350v5	3.30	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	9.80	4.17
CHLRE_10g433476v5	4.19	4.17
CHLRE_10g433476v5	4.10	4.16
CHLRE_04g214600v5	2.05	4.15
CHLRE_11g467539v5	2.60	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	16.70	3.86
CHLRE_10g445000v5	3.38	3.86
CHLRE_06g257200v5	6.23	3.83
CHLRE_06g309000v5	5.66	3.80
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	3.70
CHLRE_10g445050v5	8.23	3.66
CHLRE_06g300500v5	2.88	3.64
CHLRE_01g066187v5	2.75	3.64
CHLRE_02g099950v5	23.05	3.60
CHLRE_12g552650v5	27.16	3.58
CHLRE_07g332275v5	10.34	3.58
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	3.10
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
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	9.30	2.91
CHLRE_15g635998v5	2.29	2.90
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	4.30	2.83
CHLRE_12g531000v5	10.85	2.82
CHLRE_12g507800v5	4.37	2.82
CHLRE_11g478800v5	12.01	2.81
CHLRE_12g541250v5	2.30	2.81
CHLRE_09g389504v5	5.40	2.80
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	2.70
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	2.60
CHLRE_13g586450v5	5.87	2.59
CHLRE_03g174400v5	5.05	2.59
CHLRE_16g658800v5	9.20	2.58
CHLRE_01g053000v5	11.62	2.57
CHLRE_04g222750v5	6.30	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	3.20	2.52
CHLRE_11g479600v5	3.59	2.51
CHLRE_08g374450v5	4.26	2.50
CHLRE_16g677100v5	2.70	2.50
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	2.20	2.48
CHLRE_17g700650v5	12.70	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	6.70	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	9.10	2.42
CHLRE_17g714050v5	3.85	2.42
CHLRE_02g142650v5	3.60	2.40
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	4.60	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
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	25.80	2.30
CHLRE_03g182700v5	12.69	2.30
CHLRE_09g396600v5	8.98	2.30
CHLRE_06g271376v5	8.20	2.30
CHLRE_09g402500v5	4.06	2.30
CHLRE_12g538000v5	4.03	2.30
CHLRE_09g406600v5	3.29	2.30
CHLRE_10g454150v5	2.53	2.30
CHLRE_09g405500v5	2.35	2.30
CHLRE_02g109450v5	4.60	2.27
CHLRE_16g693601v5	4.60	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	7.50	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	43.50	2.20
CHLRE_06g306000v5	2.26	2.20
CHLRE_13g605200v5	19.34	2.19
CHLRE_02g101700v5	3.95	2.18
CHLRE_09g413150v5	2.90	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
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	2.10
CHLRE_09g387208v5	4.73	2.10
CHLRE_01g034250v5	3.22	2.10
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	23.80	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	5.30	2.05
CHLRE_09g394200v5	4.76	2.05
CHLRE_14g631000v5	4.50	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	4.50	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	2.00
CHLRE_09g392951v5	3.48	2.00
CHLRE_12g525700v5	2.92	2.00
CHLRE_06g265350v5	5.12	1.99
CHLRE_15g637900v5	2.16	1.99
CHLRE_07g344550v5	7.50	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	4.00	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	7.60	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	7.20	1.91
CHLRE_08g372550v5	5.99	1.91
CHLRE_06g267650v5	5.26	1.91
CHLRE_06g276700v5	2.90	1.91
CHLRE_06g266600v5	5.88	1.90
CHLRE_17g709150v5	5.01	1.90
CHLRE_12g504650v5	3.16	1.90
CHLRE_12g552200v5	19.36	1.89
CHLRE_17g715300v5	13.09	1.89
CHLRE_01g009950v5	2.90	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
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	1.80
CHLRE_16g673057v5	5.51	1.80
CHLRE_10g458500v5	3.14	1.80
CHLRE_16g653450v5	2.92	1.80
CHLRE_13g592200v5	32.82	1.79
CHLRE_14g620850v5	20.62	1.79
CHLRE_13g588501v5	12.30	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	6.30	1.76
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	2.40	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	1.70
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	4.00	1.67
CHLRE_01g008950v5	3.97	1.67
CHLRE_06g297250v5	3.60	1.67
CHLRE_09g386756v5	2.56	1.67
CHLRE_06g273900v5	2.19	1.67
CHLRE_13g570000v5	2.14	1.67
CHLRE_02g141166v5	4.60	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
CHLRE_12g485100v5	2.91	1.61
CHLRE_17g735500v5	2.65	1.61
CHLRE_04g213450v5	2.53	1.61
CHLRE_12g554400v5	19.05	1.60
CHLRE_03g194850v5	10.79	1.60
CHLRE_17g725200v5	10.32	1.60
CHLRE_07g340450v5	8.59	1.60

CHLRE_13g582600v5	5.54	1.60
CHLRE_10g433950v5	3.94	1.60
CHLRE_01g013200v5	3.25	1.60
CHLRE_03g195950v5	2.33	1.60
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	2.60	1.54
CHLRE_03g207250v5	23.21	1.53
CHLRE_07g347400v5	7.15	1.53
CHLRE_11g467649v5	6.80	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	3.20	1.51
CHLRE_03g177600v5	2.47	1.51
CHLRE_10g434950v5	2.27	1.51
CHLRE_12g512000v5	5.55	1.50
CHLRE_09g391801v5	5.37	1.50
CHLRE_12g504550v5	4.93	1.50
CHLRE_17g709200v5	3.00	1.50
CHLRE_02g079450v5	2.08	1.49
CHLRE_06g268000v5	4.50	1.48
CHLRE_01g011600v5	3.42	1.48
CHLRE_09g392750v5	2.30	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
CHLRE_02g105100v5	27.60	1.43
CHLRE_12g505050v5	3.20	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	2.50	1.42

CHLRE_09g387500v5	2.00	1.42
CHLRE_03g145507v5	2.35	1.41
CHLRE_06g308500v5	11.26	1.40
CHLRE_08g358580v5	5.83	1.40
CHLRE_10g461050v5	2.65	1.40
CHLRE_16g680566v5	2.43	1.40
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	3.90	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	1.30
CHLRE_06g257950v5	2.61	1.30
CHLRE_02g079300v5	2.23	1.30
CHLRE_16g675958v5	2.12	1.30
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
CHLRE_16g683250v5	2.10	1.23
CHLRE_06g262900v5	2.05	1.23
CHLRE_09g396100v5	6.11	1.21
CHLRE_16g685050v5	2.24	1.20
CHLRE_16g650250v5	2.20	1.20
CHLRE_10g458450v5	2.03	1.18
CHLRE_08g379400v5	2.19	1.17

CHLRE_10g424250v5	2.09	1.17
CHLRE_08g372900v5	6.70	1.16
CHLRE_05g238311v5	4.95	1.16
CHLRE_12g499800v5	2.78	1.16
CHLRE_03g154350v5	2.50	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	1.00
CHLRE_01g042750v5	2.44	1.00
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	0.70
CHLRE_12g549550v5	5.26	0.69
CHLRE_12g516200v5	5.67	0.65
CHLRE_17g698000v5	2.06	0.63
CHLRE_12g551501v5	2.89	0.59

^aGramene (<https://www.gramene.org/>)

Table S2. Green algae genes whose expression levels decreased due to co-cultivation of green algae 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	-3.30
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	2.20	-3.15

CHLRE_13g589350v5	15.79	-3.12
CHLRE_02g095650v5	3.66	-3.12
CHLRE_03g205100v5	15.79	-3.10
CHLRE_17g744647v5	8.95	-3.10
CHLRE_05g233702v5	8.00	-3.10
CHLRE_09g405100v5	8.10	-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	2.60	-3.03
CHLRE_09g391400v5	2.29	-3.01
CHLRE_10g456100v5	12.95	-2.98
CHLRE_10g440050v5	11.10	-2.98
CHLRE_02g081750v5	2.27	-2.95
CHLRE_07g342800v5	6.45	-2.94
CHLRE_09g403034v5	6.70	-2.91
CHLRE_12g547650v5	8.12	-2.90
CHLRE_06g301325v5	7.20	-2.90
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	-2.80
CHLRE_17g733250v5	3.96	-2.80
CHLRE_06g311050v5	3.42	-2.80
CHLRE_12g509600v5	3.05	-2.80
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	11.60	-2.75
CHLRE_08g358525v5	2.53	-2.75
CHLRE_07g321300v5	2.20	-2.75

CHLRE_06g301750v5	2.42	-2.74
CHLRE_10g435800v5	9.70	-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	-2.70
CHLRE_06g274700v5	5.85	-2.69
CHLRE_09g391350v5	10.99	-2.68
CHLRE_12g554929v5	5.68	-2.68
CHLRE_12g516300v5	7.40	-2.67
CHLRE_06g281350v5	3.43	-2.67
CHLRE_01g028600v5	3.40	-2.67
CHLRE_05g232800v5	5.65	-2.66
CHLRE_07g357700v5	4.10	-2.66
CHLRE_17g731650v5	3.62	-2.66
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	4.70	-2.63
CHLRE_12g548577v5	4.52	-2.62
CHLRE_09g400775v5	4.87	-2.60
CHLRE_17g700100v5	4.33	-2.60
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
CHLRE_17g712100v5	5.08	-2.54
CHLRE_09g389902v5	3.77	-2.54
CHLRE_06g289300v5	8.12	-2.53
CHLRE_12g534700v5	6.76	-2.53
CHLRE_14g624650v5	2.71	-2.53
CHLRE_02g100633v5	3.87	-2.52
CHLRE_03g203009v5	2.10	-2.52
CHLRE_11g480079v5	2.26	-2.50
CHLRE_10g430300v5	9.48	-2.49
CHLRE_12g539900v5	8.91	-2.49

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CHLRE_09g399552v5	4.23	-2.49
CHLRE_03g196950v5	2.83	-2.49
CHLRE_04g217956v5	2.16	-2.49
CHLRE_06g299200v5	2.39	-2.48
CHLRE_07g354700v5	5.52	-2.46
CHLRE_04g226900v5	3.25	-2.46
CHLRE_09g389838v5	9.20	-2.45
CHLRE_02g142967v5	3.40	-2.45
CHLRE_09g391726v5	7.23	-2.44
CHLRE_10g420600v5	11.96	-2.43
CHLRE_10g456226v5	3.37	-2.43
CHLRE_02g095100v5	2.36	-2.43
CHLRE_09g399250v5	15.12	-2.42
CHLRE_09g400590v5	4.15	-2.42
CHLRE_10g432750v5	2.74	-2.42
CHLRE_12g545900v5	9.75	-2.41
CHLRE_03g172000v5	5.49	-2.41
CHLRE_01g043450v5	2.05	-2.41
CHLRE_06g263200v5	7.57	-2.40
CHLRE_05g240225v5	6.90	-2.40
CHLRE_10g432550v5	2.21	-2.40
CHLRE_13g565350v5	13.17	-2.39
CHLRE_06g294000v5	10.71	-2.38
CHLRE_09g411800v5	4.31	-2.38
CHLRE_12g557050v5	4.15	-2.38
CHLRE_06g284250v5	5.76	-2.37
CHLRE_17g726700v5	4.25	-2.36
CHLRE_10g420600v5	11.24	-2.35
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CHLRE_06g300700v5	5.72	-2.34
CHLRE_10g456100v5	3.10	-2.34
CHLRE_05g247950v5	16.10	-2.33
CHLRE_12g555000v5	4.33	-2.33
CHLRE_10g463900v5	2.14	-2.33
CHLRE_02g091200v5	5.12	-2.32
CHLRE_10g420600v5	11.11	-2.31
CHLRE_10g433400v5	4.07	-2.31
CHLRE_16g655200v5	6.65	-2.29
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CHLRE_10g460901v5	2.54	-2.28
CHLRE_12g495959v5	15.51	-2.27
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CHLRE_11g479900v5	5.14	-2.27
CHLRE_17g731350v5	2.05	-2.27
CHLRE_03g205650v5	2.14	-2.26
CHLRE_01g048100v5	9.29	-2.25
CHLRE_10g447700v5	6.32	-2.25
CHLRE_02g107950v5	5.61	-2.25
CHLRE_02g095038v5	4.17	-2.25

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CHLRE_10g424550v5	16.50	-2.23
CHLRE_07g321150v5	2.07	-2.23
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CHLRE_17g711480v5	12.53	-2.22
CHLRE_08g369451v5	11.88	-2.22
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CHLRE_17g712300v5	4.43	-2.22
CHLRE_03g144184v5	4.18	-2.22
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CHLRE_14g617450v5	16.20	-2.21
CHLRE_09g399030v5	5.30	-2.21
CHLRE_05g242750v5	3.50	-2.20
CHLRE_01g016900v5	7.75	-2.19
CHLRE_07g329650v5	5.43	-2.19
CHLRE_03g211745v5	3.42	-2.19
CHLRE_04g216826v5	13.04	-2.18
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CHLRE_07g342551v5	13.93	-2.16
CHLRE_03g158900v5	11.91	-2.16
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CHLRE_13g582250v5	3.98	-2.13
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CHLRE_11g467533v5	3.12	-2.11
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CHLRE_01g012150v5	2.92	-2.06
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CHLRE_10g463900v5	2.14	-2.06
CHLRE_08g373370v5	2.05	-2.06
CHLRE_08g367900v5	9.04	-2.05
CHLRE_07g318800v5	2.27	-2.05
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CHLRE_01g010350v5	2.37	-2.00
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CHLRE_11g467524v5	4.73	-1.96
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CHLRE_05g241648v5	2.71	-1.93
CHLRE_07g335300v5	2.53	-1.93
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CHLRE_02g095080v5	7.06	-1.87
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CHLRE_02g087700v5	10.58	-1.86
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CHLRE_07g326700v5	2.15	-1.72
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CHLRE_06g303850v5	2.46	-1.58
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CHLRE_01g006850v5	2.94	-1.24
CHLRE_03g188250v5	13.87	-1.23
CHLRE_02g085257v5	7.55	-1.23
CHLRE_02g142987v5	3.30	-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	4.20	-1.21
CHLRE_06g268600v5	3.39	-1.21
CHLRE_11g474950v5	2.49	-1.21
CHLRE_13g591150v5	12.34	-1.20
CHLRE_12g520000v5	3.52	-1.20
CHLRE_05g241647v5	16.24	-1.19
CHLRE_11g479500v5	10.30	-1.19
CHLRE_10g452050v5	7.94	-1.19
CHLRE_04g223100v5	6.24	-1.19
CHLRE_02g111450v5	2.80	-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

CHLRE_16g674700v5	2.73	-1.14
CHLRE_16g668550v5	2.10	-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	-1.10
CHLRE_16g684850v5	3.90	-1.10
CHLRE_09g387875v5	2.88	-1.10
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	2.00	-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	2.60	-1.01
CHLRE_12g545500v5	2.13	-1.01
CHLRE_13g565270v5	2.02	-1.01
CHLRE_12g528400v5	2.00	-1.01

CHLRE_08g362019v5	7.71	-1.00
CHLRE_14g623439v5	2.46	-1.00
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	2.50	-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	4.20	-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	2.90	-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	-0.90
CHLRE_11g467730v5	2.34	-0.90
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

CHLRE_11g467729v5	3.14	-0.86
CHLRE_10g452050v5	5.36	-0.85
CHLRE_16g680588v5	4.91	-0.85
CHLRE_09g416150v5	4.70	-0.84
CHLRE_10g451950v5	2.28	-0.84
CHLRE_08g359350v5	2.00	-0.84
CHLRE_16g650300v5	3.69	-0.83
CHLRE_09g386750v5	2.12	-0.83
CHLRE_16g659950v5	16.75	-0.82
CHLRE_02g141400v5	6.60	-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	-0.80
CHLRE_16g664550v5	2.94	-0.80
CHLRE_06g278178v5	2.33	-0.80
CHLRE_03g160350v5	2.15	-0.80
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	4.80	-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	3.80	-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	2.10	-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	-0.70
CHLRE_07g315150v5	3.24	-0.70
CHLRE_02g088850v5	2.39	-0.70

CHLRE_12g483850v5	17.27	-0.69
CHLRE_01g017300v5	11.59	-0.69
CHLRE_12g494550v5	9.20	-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	2.60	-0.63
CHLRE_03g195650v5	6.28	-0.62
CHLRE_02g096150v5	4.06	-0.62
CHLRE_16g651923v5	4.03	-0.62
CHLRE_06g278213v5	3.90	-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	-0.60
CHLRE_09g412100v5	5.47	-0.60
CHLRE_04g226850v5	3.33	-0.60
CHLRE_06g250100v5	2.70	-0.59
CHLRE_17g727100v5	2.08	-0.59
CHLRE_16g683793v5	2.04	-0.59
CHLRE_03g190850v5	3.35	-0.58
CHLRE_09g395350v5	2.30	-0.58
CHLRE_07g346200v5	2.28	-0.58

^aGramene (<https://www.gramene.org/>)

Table S3. Yeast genes whose expression levels increased due to co-cultivation of green algae and yeast

Gene ^a or locus tag ^b	-Log ₁₀ (p-value)	Log ₂ (fold change)
YAR010C	5.50	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	1.90
DCG1	5.75	1.79
YNCM0019W	3.26	1.69
YOR381W-A	4.52	1.66
YNCB0006W	4.20	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	10.30	1.23
YNCK0016W	10.90	1.23
ATG41	13.19	1.22
PBA1	13.84	1.22
YNCK0005C	2.86	1.21
PCL1	4.48	1.20
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	6.40	1.03
SPL2	14.32	1.03
YNR068C	2.80	1.02
COS4	2.58	1.01
YEL068C	5.55	1.00
AIM34	2.20	0.99
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	0.90
GPI2	4.62	0.90
PIB2	8.38	0.90
TAF5	9.22	0.90
ECM3	11.29	0.90
VPS28	5.20	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	12.60	0.86
ERG28	12.61	0.86
ATF1	12.75	0.86
ZNF1	6.03	0.85
YPL229W	7.15	0.85
TVP15	9.10	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	5.50	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
SUT390	2.14	0.81

YBR196C-A	2.63	0.81
PHB1	15.67	0.81
BNA3	3.04	0.80
YMC2	4.73	0.80
AIM17	5.82	0.80
UBC7	12.97	0.80
GUT2	24.74	0.80
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	12.90	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	10.10	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	4.20	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
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	2.90	0.71
ODC2	5.10	0.71
YNL034W	5.63	0.71
TCB1	6.42	0.71
ERV15	7.80	0.71
ISC10	9.52	0.71
MFA1	9.97	0.71
MCK1	10.45	0.71
TDA10	3.56	0.70
TPS1	3.82	0.70
RMR1	5.71	0.70
VHR1	6.30	0.70
AVT1	6.68	0.70
MSC2	8.50	0.70
VPS36	9.35	0.70
YNL190W	21.34	0.70
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	3.60	0.67
AIM7	4.17	0.67

MDS3	5.17	0.67
ARO80	5.30	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	3.60	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	10.50	0.65
PCL5	11.80	0.65
ADR1	14.26	0.65
ITS2-2	24.75	0.65
RRT13	2.11	0.64
GAS3	2.70	0.64
AIM18	3.28	0.64
PMA2	3.61	0.64
SEC11	7.40	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	19.30	0.63
YCP4	21.37	0.63
YGR237C	2.12	0.62
YCR099C	2.39	0.62

YGR117C	2.40	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	8.50	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	6.70	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	0.60
PAU2	2.05	0.60
GPH1	2.66	0.60
RUF21	3.00	0.60
MDV1	3.33	0.60
MEF2	3.80	0.60
MIM2	3.91	0.60
RBL2	4.27	0.60
HOP1	5.47	0.60
YDL199C	8.91	0.60
AIM24	2.44	0.59
MTC5	3.66	0.59
YJR096W	7.20	0.59
YRA2	7.36	0.59
TFS1	7.63	0.59

^aUniProt (<https://www.uniprot.org/>)

^b*Saccharomyces* Genome Database (<https://www.yeastgenome.org/>)

Table S4. Yeast genes whose expression levels decreased due to co-cultivation of green algae 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	2.60	-3.12
TRR4	7.14	-3.12
YNCL0007W	13.00	-3.07
YNCD0024C	4.64	-3.01
YNCD0004W	6.41	-3.01
YNCI0009W	2.74	-2.90
YNCM0023C	7.32	-2.82
YNCF0009C	6.31	-2.70
YNCP0008C	8.65	-2.69
YNCN0008C	5.78	-2.63
YNCL0002C	2.61	-2.40
SUP51	5.27	-2.40
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	-1.60
YLR365W	4.12	-1.57
POG1	20.19	-1.56
YNCO0008W	2.01	-1.53
GIS4	17.22	-1.52
SUP61	2.38	-1.50

YNM0033C	4.85	-1.50
ASF1	19.85	-1.50
SNR50	25.61	-1.50
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
YNG0023C	23.56	-1.36
HXT3	7.23	-1.35
ZRG8	9.55	-1.33
BUR2	16.06	-1.30
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	20.90	-1.21
BNR1	4.55	-1.20
YNCC0005W	10.88	-1.20
YOR008C-A	23.59	-1.20
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	3.30	-1.12
YNCK0021W	4.23	-1.11
TAT2	14.71	-1.11
HTC1	3.83	-1.10
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
YNG0028W	2.57	-1.05
SNR53	8.69	-1.05
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	-1.00
AST1	5.51	-1.00
OSW1	10.34	-1.00
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	2.10	-0.96
SPT10	7.06	-0.96
DIG1	9.39	-0.96
TUP1	2.07	-0.95
HXT13	5.78	-0.95
CTH1	9.80	-0.95
AIR1	16.21	-0.95
ACK1	7.14	-0.94
CAB3	10.38	-0.93
YML037C	3.20	-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	-0.90
YGL235W	6.68	-0.90
SNR65	14.93	-0.90
YGL230C	16.69	-0.90
HSU1	2.29	-0.89
CLN3	2.81	-0.89
UPS3	7.86	-0.89
EST1	11.30	-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	21.60	-0.88
SPR3	21.95	-0.88
CMR1	2.68	-0.87
ASG7	2.81	-0.87
YOR293C-A	3.84	-0.87
TIM50	5.80	-0.87
RGS2	17.64	-0.87
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	3.10	-0.82
YRO2	3.80	-0.82
GRC3	6.81	-0.82
PMA1	14.52	-0.81
YEL023C	15.00	-0.81
BZZ1	3.91	-0.80
YHL026C	5.68	-0.80
PES4	11.66	-0.80
USV1	3.07	-0.79
DSN1	3.20	-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
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	7.60	-0.74
YMR315W-A	7.90	-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	7.90	-0.73
GAS2	8.20	-0.73
NAB2	21.70	-0.73
NEJ1	2.23	-0.72
YDL211C	3.04	-0.72
YNCD0007C	4.60	-0.72
ALY2	4.70	-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	29.20	-0.72
SRS2	3.04	-0.71
SEC6	3.49	-0.71
AAR2	3.50	-0.71
TAX4	3.71	-0.71
CBP1	4.59	-0.71
SGO1	4.80	-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	16.50	-0.71
YOR342C	18.90	-0.71
SSF1	20.49	-0.71
THR4	5.12	-0.70
YLR162W	5.55	-0.70
NDT80	7.95	-0.70
CDA1	8.77	-0.70
SKT5	9.79	-0.70
SRG1	17.48	-0.70

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	5.00	-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
SXM1	18.78	-0.65

ANY1	19.67	-0.65
CHS3	19.87	-0.65
GPI18	24.13	-0.65
TPC1	2.70	-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	27.10	-0.63
MAK10	2.37	-0.62
MRX11	2.60	-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	4.70	-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
PSR2	12.43	-0.61

RIX1	12.94	-0.61
UTP4	18.35	-0.61
PDE2	30.55	-0.61
GCG1	2.95	-0.60
YGL138C	3.29	-0.60
SED5	3.29	-0.60
DUG3	4.29	-0.60
THR1	4.61	-0.60
MRL1	4.83	-0.60
SRL4	5.37	-0.60
SCS3	5.69	-0.60
YGL149W	5.90	-0.60
YSP2	8.49	-0.60
SLD7	9.00	-0.60
PAM18	10.94	-0.60
CDC3	11.14	-0.60
FPK1	13.40	-0.60
RIA1	14.07	-0.60
DBP3	22.06	-0.60
URA7	30.74	-0.60
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

^aUniProt (<https://www.uniprot.org/>)

^bSaccharomyces Genome Database (<https://www.yeastgenome.org/>)