

Biotechnology for Biofuels
Additional file 2:

Additional table (Table S1)

A pyruvate carbon flux tugging strategy for increasing 2,3-butanediol production and reducing ethanol subgeneration in the yeast *Saccharomyces cerevisiae*

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Table S1

List of primers.

No.	Primer	Sequence
1	PDC5_URAb_1 (dPDC5up-URA3_fw)	5'- TTTCTCTCTTTCTTATTACACTTATTTACATAATCAATCTCAAAGAGAACAACA CAATACAATAACAAGAAGAACAATTTTTTGTTCCTTTTTTTTTGA
2	PDC5_URAb_2 (dPDC5up-URA3_rv)	5'- ATTGTGTTGTTCTCTTTGAGGGGTAATAACTGATATAATT
3	PDC5_URAb_3 (dPDC5dn_fw)	5'- AATTATATCAGTTATTACCCCTCAAAGAGAACAACACAATACAATAACAAGAAGA ACAAAGCTAATTAACATAAACTCATGATTCAACGTTTGTGTATT
4	PDC5_URAb_4 (dPDC5dn_rv)	5'- CTTC AATTAGCTAAGATCATAGCTAAAGGTACAAAACCGA
5	PDC5_URAb_check_fw	5'- TGCATACTTTATGCGTTTATGCGTTTTGCGCCCCTTGGA
6	PDC5_URAb_check_rv	5'- AAAAAAAGCTTGTGAATAAAAATCTTTCGCTAAAAATCAA
7	PDC6_URAb_1 (dPDC6up-URA3_fw)	5'- CTTGTGCTATTGCAGTCCTCTTTTATATACAGTATAAATAAAAAACCCACGTAATAT AGCAAAAACATATTGCCAACAAATTTTTTGTTCCTTTTTTTTTGA
8	PDC6_URAb_2 (dPDC6up-URA3_rv)	5'- GCTATATTACGTGGGTTTTTGGGTAATAACTGATATAATT
9	PDC6_URAb_3 (dPDC6dn_fw)	5'- AATTATATCAGTTATTACCCAAAAACCCACGTAATATAGCAAAAACATATTGCCAA CAAAGCCATTAGTAGTGTACTCAAACGAATTATTGTTGCAAATA
10	PDC6_URAb_4 (dPDC6dn_rv)	5'- TTTATAAGACAAGCGCAGGGCCAAAGAAAAAATAATAATT
11	PDC6_URAb_check_fw	5'- CCCACACCAAAGGATGTTTTTTTTATATCACGTTCCCTTTT

12	PDC6_URAb_check_rv	5'- GAGATGAGCCAAAGCAGAAAAACAGGGGACGCCGCCCTTC
13	MTH1dT_URAb_1 (MTH1dTup-URA3_fw)	5'- CAAGCTCCCTACAGGCCATTCCGGAAAACACGATGAGTGGCAGTGATAATGCTT CTTTTCAAAGTTTGCCACTATCAATGTTTTTTGTTCTTTTTTTTTGA
14	MTH1dT_URAb_2 (MTH1dTup-URA3_rv)	5'- GAAAAGAAGCATTATCACTGGGGTAATAACTGATATAATT
15	MTH1dT_URAb_3 (MTH1dTdn_fw)	5'- AATTATATCAGTTATTACCCAGTGATAATGCTTCTTTTCAAAGTTTGCCACTATCA ATGTTTTCTGCCCCCTCTACTGTGCACACGCAACTAACTAATG
16	MTH1dT_URAb_4 (MTH1dTdn_rv)	5'- ACCCACCGTTATTACTTCCGGTAGTTGATTACCCCATTCG
17	MTH1dT_URAb_check_f w	5'- CAAATGACATTTTTCTTTCTTCTCAAACCTTGTAATGCG
18	MTH1dT_URAb_check_rv	5'- TAGCCTCCATGTACAGATCCGAATGGACTAACGTTGCGAT
19	PDC1_URAb_1 (dPDC1up-URA3_fw)	5'- TATTTCTTGTCATATTCCTTTCTCAATTATTATTTTCTACTCATAACCTCACGCAAAA TAACACAGTCAAATCAATCAAATTTTTTTGTTCTTTTTTTTTGA
20	PDC1_URAb_2 (dPDC1up-URA3_rv)	5'- TATTTTGC GTGAGGTTATGAGGGTAATAACTGATATAATT
21	PDC1_URAb_3 (dPDC1dn_fw)	5'- AATTATATCAGTTATTACCCTCATAACCTCACGCAAAAATAACACAGTCAAATCAAT CAAAGCGATTTAATCTCTAATTATTAGTTAAAGTTTTATAAGCA
22	PDC1_URAb_4 (dPDC1dn_rv)	5'- TGTTCCCTTAATCAAGGATACCTCTTTTTTTTTTCCTTGGTT
23	PDC1_URAb_check_fw	5'- TGGAATAATCAATCAATTGAGGATTTTATGCAAATATCGT
24	PDC1_URAb_check_rv	5'- GGCAGTTTTGAATTGAGTAACCATTATTTGTATCGAGGTG
25	InF_XmaI_ALSAo_fw	5'- TAGTGGATCCCCCGGGATGGCCGATGAAAGTACTGTGGGAAGC

26	InF_XmaI_ALSAo_rv	5'- ATTCTCTAGAC <u>CCCCGGG</u> CTACCTAATAACGATATCCAAGACAACCTG
27	NheI_alsSBs_fw	5'- AAAAGCTAGCATGACAAAAGCAACAAAAGAACAAAAATCC
28	BglII_alsSBs_rv	5'- AAAAAGATCTCTAGAGAGCTTTCGTTTTTCATGAGTTCCCC
29	NheI_alsCg_fw	5'- AATTGCTAGCGTGAATGTGGCAGCTTCTCAACAGCCCAC
30	XmaI_als1Cg_rv	5'- AAT <u>CCCCGGG</u> TATGCCTCGGTCGATTCAACGGCGGCATC
31	InF_SalI_ilvBEc_fw	5'- AAACGCTAGCGT <u>CGAC</u> ATGGCAAGTTCGGGCACAAC
32	InF_XmaI_ilvBEc_rv	5'- ATTCTCTAGAC <u>CCCCGGG</u> TATTCCCCCACCATTTCAG
33	InF_SalI_ilvGEc_fw	5'- AAACGCTAGCGT <u>CGAC</u> ATGAATGGCGCACAGTGGGT
34	InF_XmaI_ilvGEc_rv	5'- ATTCTCTAGAC <u>CCCCGGG</u> TCATGATAATTTCTCCAACA
35	InF_SalI_ilvIEc_fw	5'- AAACGCTAGCGT <u>CGAC</u> ATGGAGATGTTGTCTGGAGC
36	InF_XmaI_ilvIEc_rv	5'- ATTCTCTAGAC <u>CCCCGGG</u> TCAGGTTCTCTCCGTTTTGC
37	InF_SalI_AHAS2Gm_fw	5'- AAACGCTAGCGT <u>CGAC</u> ATGGCGGCCACAGCTTCCAGAACCAC
38	InF_XmaI_AHAS2Gm_rv	5'- ATTCTCTAGAC <u>CCCCGGG</u> TCAGTACCTCGTTCTACCGTCTCCCTC
39	SalI_AHAS3Gm_fw	5'- AATTG <u>TGCAC</u> ATGGCGGCTATAACTGCCCCAAAAGCTGCG
40	SalI_AHAS3Gm_rv	5'- AAT <u>CCCCGGG</u> TCAGTAACTTGTCTGCCATCACCCCTCAG
41	InF_SalI_ilvGHe-1_fw	5'- AAACGCTAGCGT <u>CGAC</u> ATGCATGACACCGACCGACACGACATGACC
42	InF_XmaI_ilvGHe-1_rv	5'- ATTCTCTAGAC <u>CCCCGGG</u> TCAGTCGTGACCGATGGCATCGGCCCA
43	InF_SalI_ilvGHe-2_fw	5'- AAACGCTAGCGT <u>CGAC</u> ATGACTTGTGCCAGCGACTGATCCAGCTC
44	InF_XmaI_ilvGHe-2_rv	5'- ATTCTCTAGAC <u>CCCCGGG</u> CTAAAGTGAGTCGGCCAGCCGGCGGGC
45	SalI_alsL1_fw	5'- ATACG <u>TGCAC</u> ATGTCTGAGAAACAATTTGGGGCGAACTTGGTTGTCGATAGTTTG
46	XmaI_alsL1_rv	5'- CGTAC <u>CCCCGGG</u> TCAATAAACTCTTCAGGCAATAATTTTCTGCTAATTTAATG
47	BamHI_alsLp_fw	5'- ATATGGATCCATGCCAGATAAGAAATATTACGGGGCCGAT
48	XmaI_alsLp_rv	5'- ATAT <u>CCCCGGG</u> TAAATAAACTGGTCTGGTAACATTGTCTT

49	NheI_alsSg-1_fw	5'- ATATGCTAGCGTGAGCCACGACCACGACGACCGGCCGCAG
50	BamHI_alsSg-1_rv	5'- ATATGGATCCCTACAGGTGCGTCGGCTCGAACATCCGCAG
51	NheI_alsSg-2_fw	5'- ATATGCTAGCATGATCAGCGTGAGCGACGCCGAGCACCGG
52	BamHI_alsSg-2_rv	5'- ATATGGATCCTCAGAGCGCCGAGTCGAGGTGCCCGAGGTG
53	NheI_alsTf_fw	5'- AATTGCTAGCATGACCGAGCAGATGACCGGAGCCCAATCG
54	XmaI_alsTf_rv	5'- AATTC CCCGGG CTATTCTTCCTCGTCGTCCCATTCAGGCGC
55	BamHI_ALS1Zm_fw	5'- AATTGGATCCATGGAGATGGAGATCCACCAGGCACTCACC
56	XmaI_ALS1Zm_rv	5'- AATTC CCCGGG TCAGTACACAGTCCTGCCATCACCATCCAG
57	InF_SalI_alsLpOp_fw	5'- AAACGCTAGCGTCGACATGCCAGACAAAAAGTATTATGGTGCCGAT
58	InF_XmaI_alsLpOp_rv	5'- ATTCTCTAGAC CCCGGG TAGTAGAATTGGTCTGGCAACATAGTTTT
59	InF_SalI_ilvBEcOp_fw	5'- AAACGCTAGCGTCGACATGGCTTCTTCTGGTACTACTTCCACCAGA
60	InF_XmaI_ilvBEcOp_rv	5'- ATTCTCTAGAC CCCGGG TCATTCACCAACCATTTTCAGTATTTGCAGC
61	InF_SalI_alsTfOp_fw	5'- AAACGCTAGCGTCGACATGACTGAACAAATGACTGGTGCCCAATCT
62	InF_XmaI_alsTfOp_rv	5'- ATTCTCTAGAC CCCGGG TCATTCTTCTTCATCATCCCATCTGGAGC
63	InF_XmaI_alsLpOp_fw	5'- AATATAAAAC CCCGGG ATGCCAGACAAAAAGTATTATGGTG
64	InF_AscI_alsLpOp_rv	5'- ATTTATTT CGGCGCGCCT TAGTAGAATTGGTCTGGCAACATAG
65	InF_SalI_aldcBsOp_fw	5'- AACAAACAAAGTCGACATGAAGAGAGAATCCAACATCCAAG
66	InF_NotI_aldcBsOp_rv	5'- TAAATTCACGCGGCCGCTCATTCTGGAGAACCTTCAGTAG
67	InF_SalI_aldcEaOp_fw	5'- AACAAACAAAGTCGACATGAACCATGCTTCTGATTGCACC
68	InF_NotI_aldcEaOp_rv	5'- TAAATTCACGCGGCCGCTTAGGATTCAACAGATCTGATGG
69	InF_SalI_aldcKpOp_fw	5'- AACAAACAAAGTCGACATGTCCGCTTTGTTGTCTGGTG
70	InF_NotI_aldcKpOp_rv	5'- TAAATTCACGCGGCCGCTTAGGATTCAACAGATCTGATG
71	InF_SalI_aldcLlOp_fw	5'- AACAAACAAAGTCGACATGACCGAAATCACCCAATTATTC

72	InF_NotI_aldcLlOp_rv	5'- TAAATTCAC <u>CGGCCGCT</u> CATTCGGCAACGTCAATATCCTTC
73	InF_AvrII_BDH1Sc_fw	5'- CTCATATACACCTAGGATGAGAGCTTTGGCATATTT
74	InF_FseI_BDH1Sc_rv	5'- ATAAGAAATTCGCG <u>GCCGGCCTT</u> ACTTCATTTACCGTGAT
75	PmeI_BDH1Sc_fw	5'- ATGCGTTTAAACATGAGAGCTTTGGCATATTTCAAGAAGGGT
76	FseI_BDH1Sc_rv	5'- ATGCG <u>GCCGGCCTT</u> ACTTCATTTACCGTGATTGTTAGGCGT

·Underlining indicates restriction enzyme sites.