Supplementary materials

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gldA101     1 ATGACGAAAATCATTACCTCTCCAAGCAAGTTTATACAAGGCCCCGATGAATTGTCCAGG
gldA-syn    1 .....C........C.....C..CTC...A..C..C..G........C..G......C..

gldA101    61 CTTTCGGCGTATACGGAAAGGCTTGGCAAAAAAGCATTTATTATTGCGGATGATTTTGTC
gldA-syn   61 T.GAGT..C.....C...C..T.G.....G..G..C.....C..C..T..C..C..C..G

gldA101   121 ACCGGCCTTGTCGGCAAAACGGTTGAAGAAAGCTATGCCGGCAAAGAAACGGGGTATCAA
gldA-syn  121 ......T.G..G..T..G..T..G..G..GTC..................C..T..C..G

gldA101   181 ATGGCATTATTCGGTGGTGAGTGTTCTAAACCGGAAATCGAACGGCTTTGTGAAATGAGC
gldA-syn  181 .....C..G..T..C..C..A..CAG...G..T..G.....G..CT.G..C..G...TC.

gldA101   241 AAATCCGAGGAAGCCGATGTCGTTGTCGGAATCGGCGGCGGAAAAACATTGGATACCGCA
gldA-syn  241 ........A........C..T..G..G..C........T..C.....C..A..C..T..C

gldA101   301 AAAGCAGTCGGGTATTACAATAACATTCCGGTGATTGTCGCGCCGACCATCGCTTCCACC
gldA-syn  301 ..G..C..G..C..C..............C.....C..G..C..C..T..T.........

gldA101   361 AATGCCCCGACAAGCGCCCTGTCTGTTATTTACAAAGAGAACGGCGAGTTTGAAGAATAC
gldA-syn  361 ........C..CTC....T..AG...G..C..T..G...........A..C..G......

gldA101   421 TTGATGCTGCCGCTGAACCCGACTTTTGTCATTATGGATACGAAAGTGATTGCCTCTGCC
gldA-syn  421 ......T....TT.......T..C.....G..C.....C..T..G.....C.....C..T

gldA101   481 CCTGCCCGCCTGCTCGTTTCCGGCATGGGAGATGCGCTTGCAACGTATTTTGAAGCGCGC
gldA-syn  481 .........T.AT.G..............C..C..CT.G..C..T..C........C...

gldA101   541 GCCACTAAGCGGGCAAATAAAACGACGATGGCAGGCGGGCGTGTTACGGAAGCGGCGATC
gldA-syn  541 ..............C.....G..C..C.....T..T..C..C.....T..G..C..C...

gldA101   601 GCGCTTGCAAAACTTTGTTATGACACGCAAATTTCGGAAGGTTTAAAAGCAAAACTGGCA
gldA-syn  601 ..CT.G..C..GT.G..C..C.....C..G..CAGT..G..C..G..G..C..GT.A..C

gldA101   661 GCGGAAAAACATCTTGTTACGGAAGCAGTGGAAAAAATCATTGAAGCGAATACGTATCTG
gldA-syn  661 ..C..G.....CT.G..G..C..G..C..T..G..G.....C..G..C..C..T..CT..

gldA101   721 AGCGGAATCGGTTCTGAAAGCGGCGGCCTTGCTGCGGCACATGCGATCCATAATGGGCTT
gldA-syn  721 TC...T..T..C..C.....T......T.A..C..C..T..C..C..T..C..C..CT.G

gldA101   781 ACCGTGCTCGAAGAAACCCATCATATGTACCACGGCGAAAAAGTGGCATTCGGTACCCTC
gldA-syn  781 ......T.G..G..G.....C..C..............G..G.....T.....C..TT.G

gldA101   841 GCCCAGCTGATTTTGGAAGATGCGCCGAAAGCGGAAATTGAAGAGGTGGTCTCCTTCTGC
gldA-syn  841 ......T....C.....G.....C..C..G..C..G.....G........G........T

gldA101   901 CTGAGTGTCGGACTTCCCGTCACGCTCGGGGATTTGGGCGTGAAAGAACTGAATGAGGAA
gldA-syn  901 T..TCC..G..CT.G..T..T..CT.G..C..C...........G...T....C......

gldA101   961 AAGCTCCGAAAAGTGGCTGAACTTTCCTGTGCGGAAGGCGAAACGATTTATAACATGCCG
gldA-syn  961 ..AT.G..G..G.....C...T.G.....C..C..G........C..C..C........C

gldA101  1021 TTTGAAGTCACGCCTGACCTTGTGTACGCAGCAATCGTTACCGCTGATTCCGTCGGGCGG
gldA-syn 1021 .....G..G..C..C..TT.G........C..C..............C.....G..C..C

gldA101  1081 TATTATAAGGAAAAATGGGCATGA
gldA-syn 1081 .....C........G.....C.A.
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Figure S1 Nuleotide sequence alignment of *gldA101* and the codon-optimized *gldA101* (i.e., *gldA101-syn*, synthesized by Genewiz Inc). Conserved nucleotide sequences in *gldA101-syn* are indicated as dotted lines.

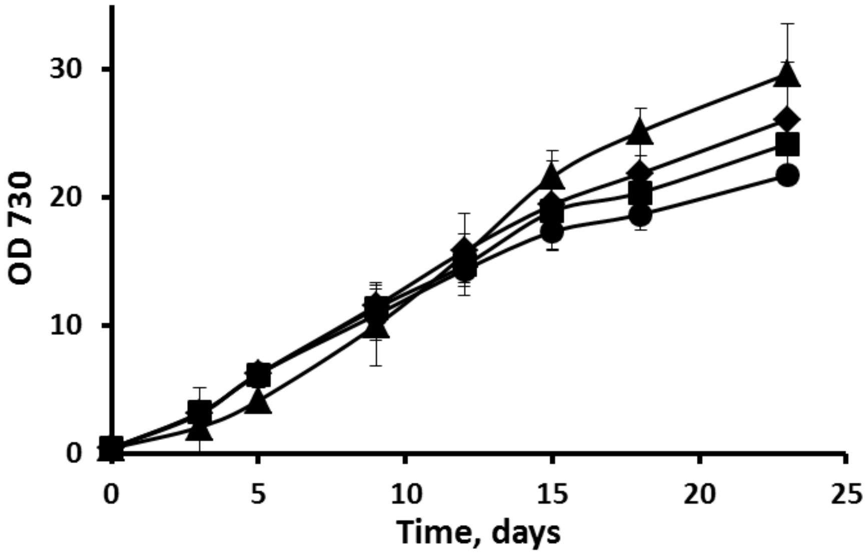
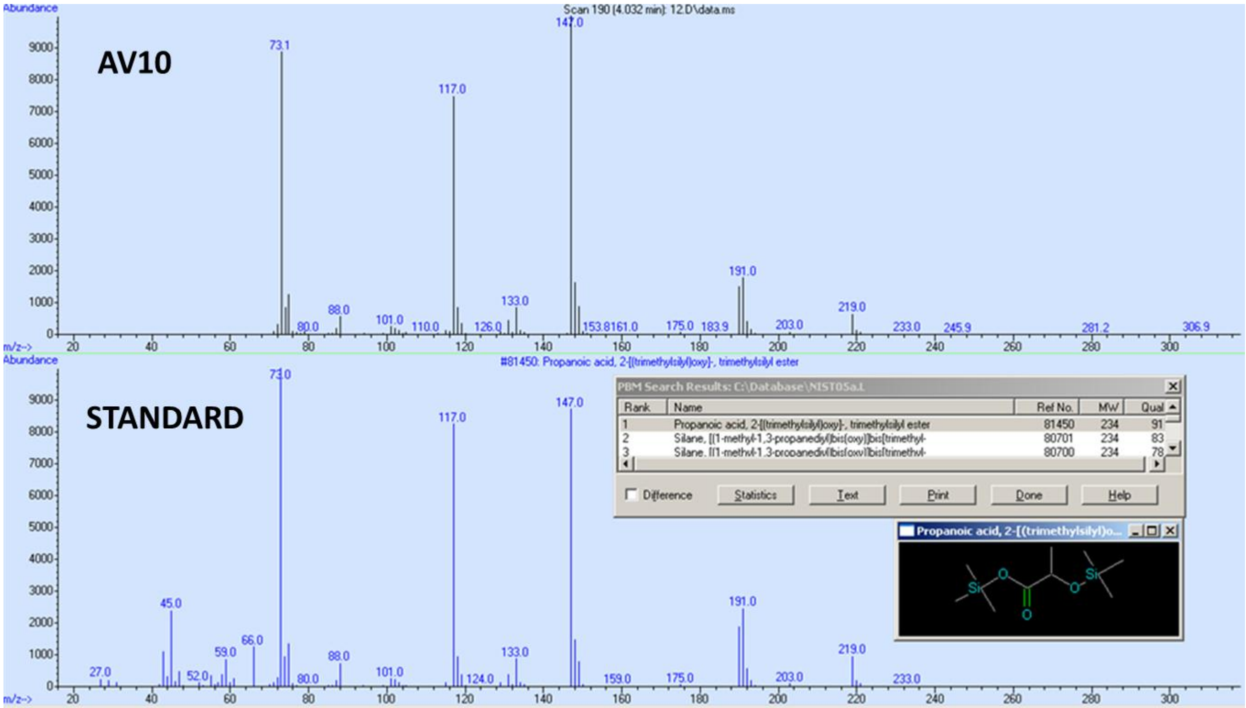


Figure S2 Autotrophic growth curve for *Synechocystis* 6803 strains shows similar growth of the engineered D-lactate producing strains as compared to the wild type strain. Diamond: Wild type. Square: AV08. Triangle: AV10. Circle: AV11.



PBM Search Results: C:\Database\NIST05a.L

Rank	Name	Ref No.	MW	Qual
1	Propanoic acid, 2-[(trimethylsilyl)oxy]-, trimethylsilyl ester	81450	234	91
2	Silane, [(1-methyl-1,3-propanediyl)bis(oxy)]bis[trimethyl-	80701	234	83
3	Silane, [(1-methyl-1,3-propanediyl)bis(oxy)]bis[trimethyl-	80700	234	78

Figure S3 Mass spectra obtained via GC-MS confirm the presence of lactate in the cell culture supernatant of AV10 strain. D/L lactate enzyme kit (R-Biopharm) was used to further confirm that the product is an optically pure D-lactate.