1. (b)

**Fig. S1: Sugar consumption, ethanol production and growth profile.**  Strain SSK42 (a) and SCD00 (b). Growth profile is represented by OD.600nm.

**Fig. S2: Sugar consumption, ethanol production and growth profile of strain SCD1200 that has been evolved on xylose and glucose in sequence.** Sugars concentrations are plotted on left Y-axis while ethanol and optical density are plotted on right y-axis. Optical density represents the growth profile. Data represents the average of two biological replicates.

**Fig. S3: Metabolite production profiles of strain SCD00 and SCD78.** Solid lines represents the strain SCD78 while dotted lines represents the SCD00 strain.

|  |  |  |  |
| --- | --- | --- | --- |
| **Table S1: Differential gene expression of strain SCD00 vs SSK42** | | | |
| **Protein symbol** | **Name** | **Log2fold change** | **P values** |
| AspA | aspartate ammonia-lyase | 6.640 | 0.000070310 |
| MglB | methyl-galactoside transporter subunit | 6.205 | 0.000102261 |
| PspA | regulatory protein for phage-shock-protein operon | 5.156 | 0.000299718 |
| AraA | L-arabinose isomerase | 5.097 | 0.000552007 |
| Lon | DNA-binding ATP-dependent protease La | 4.711 | 0.000934025 |
| YcbG | hypothetical protein | 4.345 | 0.014679453 |
| GlpK | glycerol kinase | 4.116 | 0.001969458 |
| FlgH | flagellar L-ring protein precursor H | 4.046 | 0.006359024 |
| NuoB | NADH dehydrogenase subunit B | 3.992 | 0.002087669 |
| RbsD | predicted cytoplasmic sugar-binding protein | 3.988 | 0.00210928 |
| FlgM | anti-sigma factor for FliA (sigma 28) | 3.968 | 0.004532581 |
| YjiM | predicted 2-hydroxyglutaryl-CoA dehydratase | 3.922 | 0.001424113 |
| YghZ | aldo-keto reductase | 3.891 | 0.001221941 |
| YebE | hypothetical protein | 3.856 | 0.010470693 |
| ECB\_02650 | D-ribose-binding periplasmic protein | 3.832 | 0.002115122 |
| RbsB | D-ribose transporter subunit | 3.814 | 0.001968329 |
| RbsA | fused D-ribose transporter subunits of ABC superfamily: ATP-binding components | 3.722 | 0.00343718 |
| AldA | aldehyde dehydrogenase A, NAD-linked | 3.668 | 0.002972645 |
| NuoI | NADH dehydrogenase subunit I | 3.580 | 0.020995499 |
| SucC | succinyl-CoA synthetase subunit beta | 3.556 | 0.007450293 |
| YajC | preprotein translocase subunit YajC | 3.484 | 0.010946762 |
| DacB | D-alanyl-D-alanine carboxypeptidase | 3.340 | 0.025570519 |
| XylA | xylose isomerase | 3.253 | 0.005479046 |
| YdcL | predicted lipoprotein | 3.250 | 0.049735403 |
| SdhA | succinate dehydrogenase flavoprotein subunit | 3.197 | 0.003465327 |
| SdaA | L-serine deaminase I | 3.129 | 0.016945264 |
| YgiM | predicted signal transduction protein (SH3 domain) | 2.991 | 0.006964972 |
| PckA | phosphoenolpyruvate carboxykinase | 2.834 | 0.007512155 |
| NuoE | NADH dehydrogenase subunit E | 2.810 | 0.015638053 |
| XylB | xylulokinase | 2.808 | 0.010564481 |
| SucB | dihydrolipoamide acetyltransferase | 2.718 | 0.010971427 |
| SdhB | succinate dehydrogenase, FeS subunit | 2.703 | 0.010689945 |
| FumA | fumarate hydratase (fumarase A), aerobic Class I | 2.702 | 0.012591306 |
| PpsA | phosphoenolpyruvate synthase | 2.691 | 0.00914812 |
| SucD | succinyl-CoA synthetase subunit alpha | 2.650 | 0.008481498 |
| AceA | isocitrate lyase | 2.632 | 0.020727705 |
| HslV | ATP-dependent protease peptidase subunit | 2.593 | 0.018465653 |
| RbsK | ribokinase | 2.589 | 0.022935044 |
| CpdB | bifunctional 2',3'-cyclic nucleotide 2'-phosphodiesterase/3'-nucleotidase periplasmic precursor protein | 2.580 | 0.01207305 |
| YegU | predicted hydrolase | 2.543 | 0.020410434 |
| Agp | glucose-1-phosphatase/inositol phosphatase | 2.478 | 0.019942638 |
| FolP | 7,8-dihydropteroate synthase | 2.463 | 0.026055579 |
| SfsA | sugar fermentation stimulation protein A | 2.414 | 0.027854813 |
| PepB | aminopeptidase B | 2.403 | 0.013116877 |
| Gst | glutathionine S-transferase | 2.377 | 0.016223205 |
| TolC | outer membrane channel precursor protein | 2.368 | 0.016596473 |
| MiaA | tRNA delta(2)-isopentenylpyrophosphate transferase | 2.327 | 0.021855534 |
| TalB | transaldolase B | 2.304 | 0.023031901 |
| YdbC | predicted oxidoreductase, NAD(P)-binding | 2.275 | 0.0332909 |
| SucA | alpha-ketoglutarate decarboxylase | 2.249 | 0.018004303 |
| GroEL | chaperonin GroEL | 2.213 | 0.021321388 |
| HybC | hydrogenase 2, large subunit | 2.191 | 0.021019659 |
| YdhH | anhydro-N-acetylmuramic acid kinase | 2.181 | 0.036058409 |
| YqiC | hypothetical protein | 2.077 | 0.042980858 |
| LysS | lysine tRNA synthetase, constitutive | 2.019 | 0.028119157 |
| HflX | predicted GTPase | -2.014 | 0.041550361 |
| RplD | 50S ribosomal protein L4 | -2.043 | 0.029300296 |
| RplP | 50S ribosomal protein L16 | -2.057 | 0.039110656 |
| LysU | lysine tRNA synthetase, inducible | -2.062 | 0.036229669 |
| YceD | hypothetical protein | -2.076 | 0.040366807 |
| GltI | glutamate and aspartate transporter subunit | -2.081 | 0.033674595 |
| YhbH | predicted ribosome-associated, sigma 54 modulation protein | -2.128 | 0.042062014 |
| Rne | fused ribonucleaseE: endoribonuclease/RNA-binding protein/RNA degradosome binding protein | -2.189 | 0.021154308 |
| RpmE | 50S ribosomal subunit protein L31 | -2.204 | 0.019350119 |
| GcvP | glycine dehydrogenase | -2.230 | 0.019921568 |
| RplR | 50S ribosomal protein L18 | -2.248 | 0.021513019 |
| YidA | predicted hydrolase | -2.253 | 0.033289114 |
| UvrA | excinuclease ABC subunit A | -2.291 | 0.023073982 |
| YjeB | predicted DNA-binding transcriptional regulator | -2.345 | 0.036785727 |
| TrpD | bifunctional indole-3-glycerol-phosphate synthase/anthranilate phosphoribosyltransferase | -2.379 | 0.022138686 |
| FruA | fused fructose-specific PTS enzymes: IIBcomponent/IIC components | -2.426 | 0.037538629 |
| SrmB | ATP-dependent RNA helicase | -2.446 | 0.034485974 |
| YjfH | 23S rRNA (Gm2251)-methyltransferase | -2.500 | 0.035648948 |
| Dld | D-lactate dehydrogenase, FAD-binding, NADH independent | -2.507 | 0.042648822 |
| YicH | hypothetical protein | -2.513 | 0.020963834 |
| YahK | predicted oxidoreductase, Zn-dependent and NAD(P)-binding | -2.517 | 0.014197307 |
| RpsP | 30S ribosomal protein S16 | -2.537 | 0.010929715 |
| AdhE | alcohol dehydrogenase | -2.580 | 0.014511012 |
| RpsF | 30S ribosomal protein S6 | -2.580 | 0.042946556 |
| RplB | 50S ribosomal protein L2 | -2.597 | 0.038186999 |
| YdgJ | predicted oxidoreductase | -2.619 | 0.04612702 |
| YiiT | stress-induced protein | -2.639 | 0.036966602 |
| GltB | glutamate synthase, large subunit | -2.712 | 0.011967592 |
| SpeA | arginine decarboxylase | -2.722 | 0.013083404 |
| Cfa | cyclopropane fatty acyl phospholipid synthase (unsaturated-phospholipid methyltransferase) | -2.740 | 0.027494086 |
| MutS | DNA mismatch repair protein | -2.831 | 0.033083762 |
| GlnA | glutamine synthetase | -2.857 | 0.007958092 |
| YrbH | D-arabinose 5-phosphate isomerase | -2.969 | 0.035355664 |
| DppD | dipeptide transporter | -2.982 | 0.028226843 |
| NrdA | ribonucleotide-diphosphate reductase alpha subunit | -3.013 | 0.029336957 |
| ArcB | hybrid sensory histidine kinase in two-component regulatory system with ArcA | -3.025 | 0.004660799 |
| Rnr | exoribonuclease R, RNase R | -3.047 | 0.007182885 |
| FruB | fused fructose-specific PTS enzymes: IIA component/HPr component | -3.147 | 0.011020542 |
| YfiF | predicted methyltransferase | -3.302 | 0.008795573 |
| RpsO | 30S ribosomal protein S15 | -3.337 | 0.013210312 |
| ManZ | mannose-specific enzyme IID component of PTS | -3.972 | 0.001714941 |
| ArgI | ornithine carbamoyltransferase 1 | -3.973 | 0.00105122 |
| SelB | selenocysteinyl-tRNA-specific translation factor | -4.084 | 0.001429008 |
| PepA | leucyl aminopeptidase | -4.159 | 0.004511832 |

|  |  |  |  |
| --- | --- | --- | --- |
| **Table S2: Differential gene expression of strain SCD78 vs SCD00** | | | |
| **Protein symbol** | **Name** | **Log2fold change** | **P values** |
| SelB | selenocysteinyl-tRNA-specific translation factor | 5.902 | 0.000527 |
| SfcA | malate dehydrogenase, (decarboxylating, NAD-requiring) (malic enzyme) | 5.233 | 0.00062 |
| YgiF | predicted adenylate cyclase | 4.085 | 0.000444 |
| ArcB | hybrid sensory histidine kinase in two-component regulatory system with ArcA | 4.076 | 0.001506 |
| RncS | ribonuclease III | 4.050 | 0.016104 |
| MetC | cystathionine beta-lyase | 4.007 | 0.00186 |
| SspB | ClpXP protease specificity-enhancing factor | 3.723 | 0.001559 |
| CspA | major cold shock protein | 3.722 | 0.005427 |
| YgfB | hypothetical protein | 3.618 | 0.001872 |
| MgsA | methylglyoxal synthase | 3.379 | 0.002696 |
| MogA | molybdenum cofactor biosynthesis protein | 3.162 | 0.014286 |
| YdcG | glucan biosynthesis protein, periplasmic | 3.128 | 0.017582 |
| UdhA | soluble pyridine nucleotide transhydrogenase | 3.126 | 0.003489 |
| Usg | hypothetical protein | 3.117 | 0.026361 |
| FruB | fused fructose-specific PTS enzymes: IIA component/HPr component | 3.100 | 0.015079 |
| PepA | leucyl aminopeptidase | 3.082 | 0.029071 |
| AldA | aldehyde dehydrogenase A, NAD-linked | 3.071 | 0.001643 |
| YjbR | hypothetical protein | 3.047 | 0.032427 |
| LolA | outer-membrane lipoprotein carrier protein precursor | 2.942 | 0.014316 |
| YicH | hypothetical protein | 2.890 | 0.01457 |
| Rnr | exoribonuclease R, RNase R | 2.884 | 0.006658 |
| ManZ | mannose-specific enzyme IID component of PTS | 2.862 | 0.020367 |
| Nfi | endonuclease V | 2.798 | 0.016018 |
| SrmB | ATP-dependent RNA helicase | 2.710 | 0.027361 |
| YciM | hypothetical protein | 2.681 | 0.00328 |
| Ppk | polyphosphate kinase | 2.510 | 0.010843 |
| YcdW | 2-ketoacid reductase | 2.463 | 0.036535 |
| PepE | peptidase E | 2.437 | 0.039302 |
| YjiM | predicted 2-hydroxyglutaryl-CoA dehydratase | 2.411 | 0.004571 |
| FruK | phosphofructokinase | 2.392 | 0.047225 |
| YceH | hypothetical protein | 2.374 | 0.008079 |
| PurF | amidophosphoribosyltransferase | 2.373 | 0.009246 |
| YiiT | stress-induced protein | 2.317 | 0.012055 |
| MetH | B12-dependent methionine synthase | 2.275 | 0.008852 |
| MtlD | mannitol-1-phosphate 5-dehydrogenase | 2.230 | 0.037359 |
| YdaA | stress-induced protein | 2.207 | 0.016726 |
| Tsx | nucleoside channel, receptor of phage T6 and colicin K | 2.146 | 0.016476 |
| LplA | lipoate-protein ligase A | 2.125 | 0.015527 |
| Psd | phosphatidylserine decarboxylase | 2.121 | 0.045306 |
| UvrA | excinuclease ABC subunit A | 2.102 | 0.0154 |
| IscA | iron-sulfur cluster assembly protein | 2.070 | 0.02161 |
| HisI | bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP pyrophosphatase protein | 2.069 | 0.023958 |
| Dps | DNA protection protein | 2.054 | 0.028899 |
| RpsH | 30S ribosomal protein S8 | 2.036 | 0.016841 |
| TyrB | tyrosine aminotransferase, tyrosine-repressible, PLP-dependent | 2.034 | 0.009717 |
| DamX | Cell division protein | -2.013 | 0.011943 |
| NudG | pyrimidine (deoxy)nucleoside triphosphate pyrophosphohydrolase | -2.022 | 0.020762 |
| TrpR | Trp operon repressor | -2.037 | 0.0411 |
| BaeR | DNA-binding response regulator in two-component regulatory system with BaeS | -2.045 | 0.015964 |
| PrfC | peptide chain release factor 3 | -2.079 | 0.011169 |
| YqiC | Ubiquinone biosynthesis accessory factor | -2.092 | 0.024605 |
| YicC | hypothetical protein | -2.101 | 0.047441 |
| PepT | peptidase T | -2.122 | 0.046547 |
| YeaY | predicted lipoprotein | -2.153 | 0.032957 |
| YbaK | Cys-tRNAPro andCys-tRNACys deacylase | -2.192 | 0.005973 |
| DjlA | Dna-J like membrane chaperone protein | -2.226 | 0.017277 |
| YcfP | hypothetical protein | -2.230 | 0.022309 |
| PyrI | aspartate carbamoyltransferase regulatory subunit | -2.231 | 0.005762 |
| YdhD | glutaredoxin 4 | -2.273 | 0.037809 |
| YbiB | nonspecific DNA-binding protein | -2.275 | 0.013307 |
| YecJ | hypothetical protein | -2.298 | 0.014323 |
| YibN | predicted rhodanese-related sulfurtransferase | -2.310 | 0.016684 |
| DacB | D-alanyl-D-alanine carboxypeptidase | -2.370 | 0.014545 |
| GpsA | NAD(P)H-dependent glycerol-3-phosphate dehydrogenase | -2.402 | 0.006948 |
| YtfP | hypothetical protein | -2.451 | 0.011767 |
| YggB | mechanosensitive channel | -2.516 | 0.003646 |
| PrfA | peptide chain release factor 1 | -2.528 | 0.004231 |
| GnsB | predicted protein | -2.597 | 0.007092 |
| MurD | UDP-N-acetylmuramoyl-L-alanyl-D-glutamatesynthetase | -2.674 | 0.01774 |
| YgjD | O-sialoglycoprotein endopeptidase | -2.736 | 0.043391 |
| Lrp | DNA-binding transcriptional dual regulator, leucine-binding | -2.761 | 0.021767 |
| YhgI | predicted gluconate transport associated protein | -2.812 | 0.018464 |
| YdcL | predicted lipoprotein | -2.874 | 0.004119 |
| CydC | fused cysteine transporter subunits of ABC superfamily: membrane component/ATP-binding component | -3.069 | 0.036828 |
| YadF | carbonic anhydrase | -3.102 | 0.008802 |
| TldD | predicted peptidase | -3.169 | 0.001251 |
| YegU | predicted hydrolase | -3.213 | 0.005911 |
| Lpp | murein lipoprotein | -3.732 | 0.037601 |
| RbsB | D-ribose transporter subunit | -4.123 | 0.003029 |
| RbsK | ribokinase | -4.466 | 0.002476 |
| PspA | regulatory protein for phage-shock-protein operon | -5.515 | 0.000124 |