Manipulation of the precursor supply for high-level production of longifolene by metabolically engineered *Escherichia coli*

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Supplementary figure captions

Figure S1 Codon optimization of the longifolene synthase gene. wlgfs, wild-type longifolene synthase gene; olgfs, codon-optimized longifolene synthase gene. The identical codons are shown in dark blue and the optimized codons are shown in light blue. The amino acid encoded by each codon is shown as its abbreviation.

Figure S2 Time-course profiles for cell density (OD_{600}) and mevalonate production during shake-flasks culture of strain BL21/pA-mvaES. Cultures were performed in 500 ml shake flasks containing 50 ml liquid M9 mineral medium supplemented with 1 mM $MgSO_4$ and 20 g/L glucose. Error bars represent the range of three independent fermentations.

Figure S3 Schematic diagram of the expression constructs containing the genes encoding longifolene biosynthesis pathway. lgfS, longifolene synthase; ispA, *E. coli* FPP synthase; isoA, *B. trispora* FPP synthase; erg20, *S. cerevisiae* FPP synthase; mvaE, acetoacetyl-CoA synthase/HMG-CoA reductase; mvaS, HMG-CoA synthase gene; erg19, mevalonate kinase; erg8, phosphomevalonate kinase; erg12, mevalonate pyrophosphate decarboxylase; idi1, IPP isomerase.

Figure S1

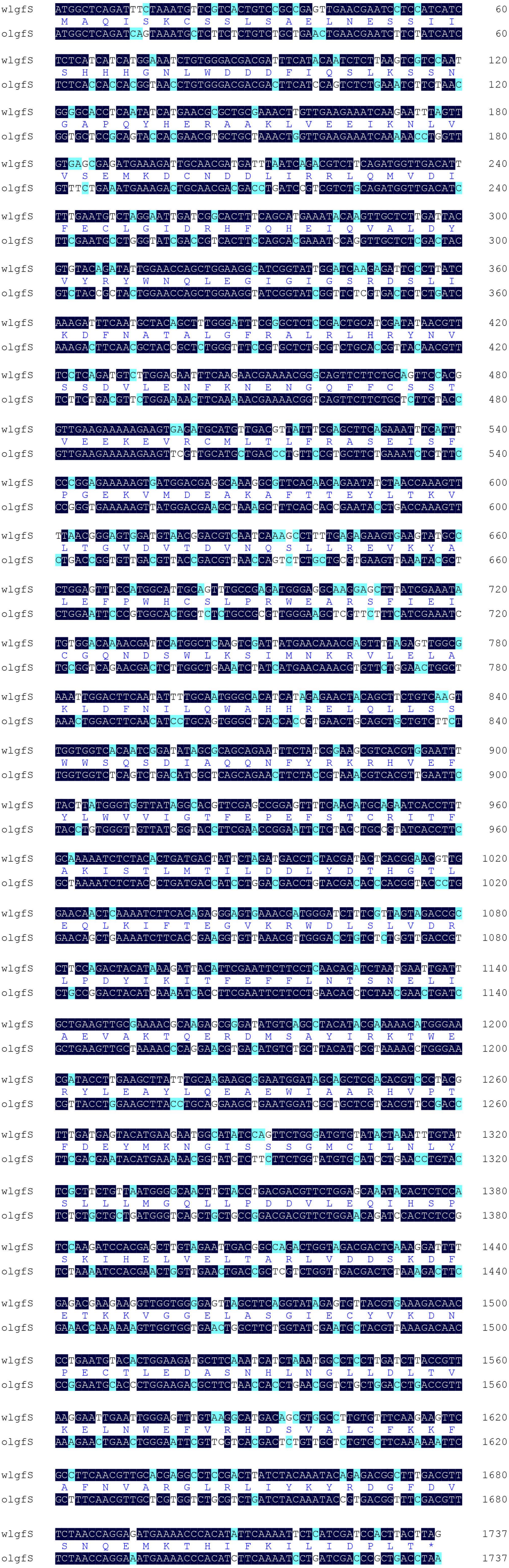


Figure S2

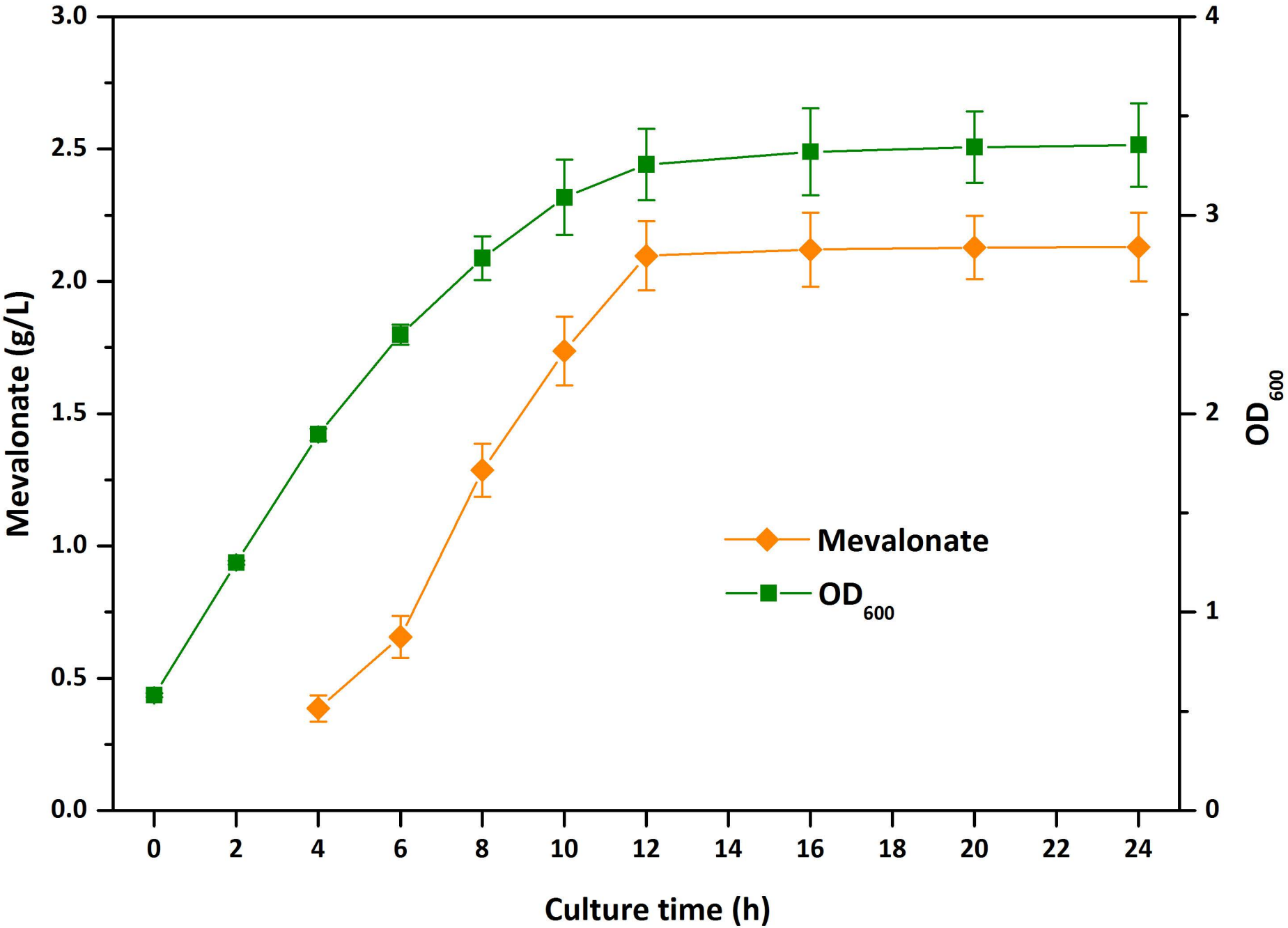
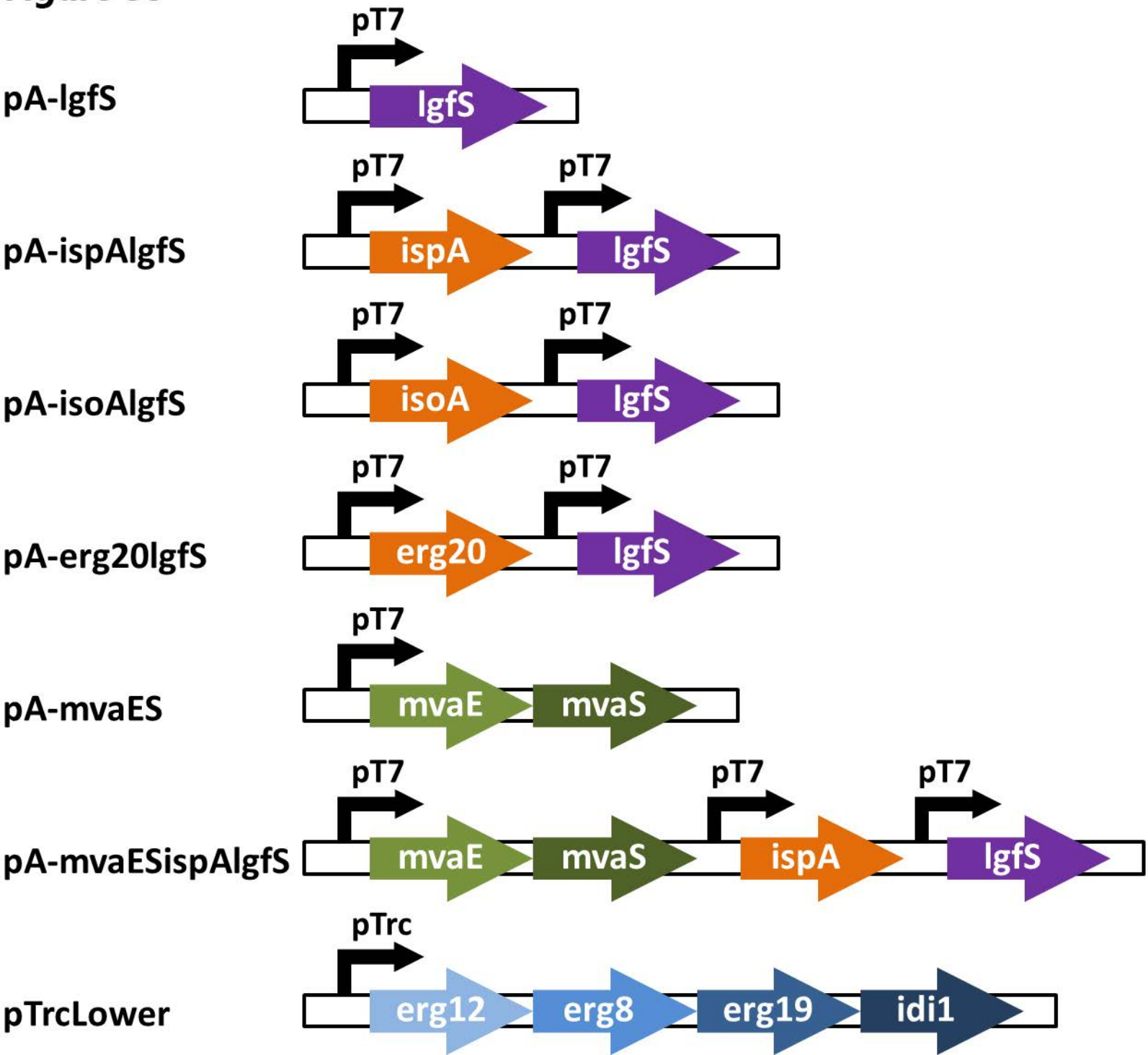

3.0
2.5
2.0
1.5
1.0
0.5
0.0
Mevalonate (g/L)
4
3
2
1
0
OD600
0
2
4
6
8
10
12
14
16
18
20
22
24
Culture time (h)
Mevalonate
OD600

Figure S3


pT7
pA-lgfS
lgfS
pT7
pT7
pA-ispAlgfS
ispA
lgfS
pT7
pT7
pA-isoAlgfS
isoA
lgfS
pT7
pT7
pA-erg20lgfS
erg20
lgfS
pT7
pA-mvaES
mvaE
mvaS
pT7
pT7
pT7
pA-mvaESispAlgfS
mvaE
mvaS
ispA
lgfS
pTrc
pTrcLower
erg12
erg8
erg19
idi1