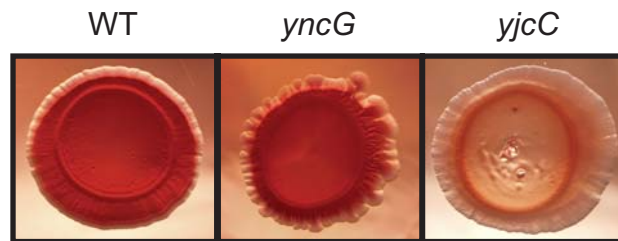


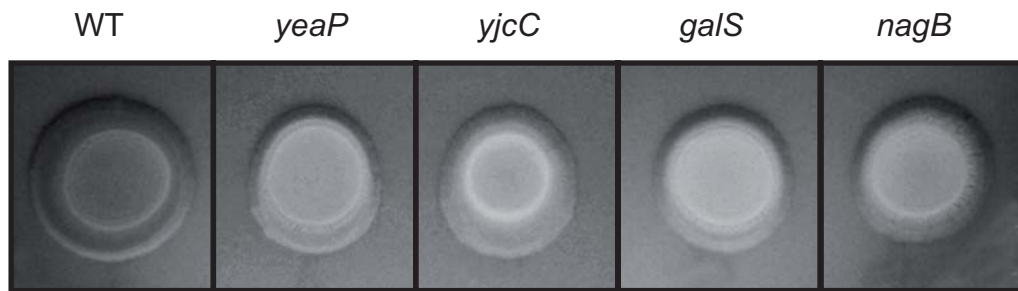
Supplementary Legends

Supplemental Figure 1: Phenotypic analysis of colonies of the indicated ASKA clones grown at 28°C on LB agar without salt supplemented with (A) Congo Red or with (B) calcofluor. These clones have altered glycogen content when compared with WT cells and over-express functions that determine the aggregative and/or social behaviour modes of the cell. In “A”, enhanced expression of *yncG* resulted in upregulation of the rdar morphotype, which is ascribed to enhanced production of extracellular matrix components such as cellulose and adhesive curli.³⁸ In addition, the *yjcC* clone of the ASKA library displayed a pdar morphotype, which is ascribed to enhanced cellulose accumulation.³⁹ In “B”, ectopic expression of *yeaP*, *yjcC*, *galS* and *nagB* resulted in high calcofluor binding ability, indicating that ectopic expression of these genes exerts a positive effect on cellulose biosynthesis.

A



B



Supplemental Figure 1

Supplemental Table 1: List of genes of the ASKA library (and functions of their products) whose enhanced expression affect glycogen content.

Gene	Function
<i>aspP</i>	ADP-sugar pyrophosphatase
<i>clpA</i>	ClpA ATP-dependent protease specificity component and chaperone
<i>cpdB</i>	2',3'-cyclic nucleotide 2'-phosphodiesterase / 3'-nucleotidase
<i>csrA</i>	carbon storage regulator; pleiotropic regulatory protein for carbon source metabolism
<i>csrD</i>	regulator of CsrB and CsrC decay
<i>cydC</i>	Component of cydDC glutathione ABC transporter
<i>cysI</i>	sulfite reductase, beta subunit, NAD(P)-binding
<i>cysP</i>	Component of the CysATWP-Sbp sulfate transporter
<i>ddg</i>	palmitoleoyl acyltransferase
<i>dos</i>	phosphodiesterase, heme-regulated
<i>erfK</i>	L,D-transpeptidase responsible covalent attachment of peptidoglycan to the outer membrane
<i>exuR</i>	transcriptional repressor of the operons involved in transport and catabolism of galacturonate and glucuronate
<i>galS</i>	transcriptional repressor of the operons involved in transport and catabolism of galactose
<i>glgA</i>	glycogen synthase
<i>glgB</i>	glycogen branching enzyme
<i>glgC</i>	glucose-1-phosphate adenylyltransferase
<i>glgP</i>	glycogen phosphorylase
<i>glgS</i>	predicted glycogen synthesis protein
<i>gltI</i>	periplasmic binding component of glutamate ABC transporter
<i>gntT</i>	high affinity gluconate transporter
<i>gor</i>	glutathione reductase
<i>gpp</i>	guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase
<i>gspD</i>	putative member of the general secretory pathway (GSP)
<i>hokA</i>	small toxic polypeptide
<i>holC</i>	DNA polymerase III, χ subunit
<i>hyuA</i>	phenylhydantoinase
<i>malP</i>	maltodextrin phosphorylase
<i>malT</i>	transcriptional activator of genes and operons involved in maltose catabolism
<i>mdtG</i>	member of major facilitator superfamily (MFS). Drug transporter
<i>methH</i>	Cobalamin-dependent homocysteine transmethylase
<i>mlc</i>	global regulator of carbohydrate metabolism
<i>nagB</i>	glucosamine-6-phosphate deaminase
<i>nagD</i>	promiscuous ribo- and deoxyribonucleoside tri-, di-, and monophosphatase
<i>napF</i>	ferredoxin-type protein
<i>pfs</i>	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase

<i>phr</i>	deoxyribodipyrimidine photolyase (photoreactivation)
<i>pnp</i>	polynucleotide phosphorylase
<i>ppdB</i>	conserved protein
<i>ppk</i>	polyphosphate kinase
<i>ppx</i>	exopolyphosphatase
<i>prfB</i>	peptide chain release factor RF2
<i>pspE</i>	thiosulfate sulfurtransferase
<i>pstC</i>	phosphate transporter subunit/membrane component of ABC superfamily
<i>ptsI</i>	PTS enzyme I
<i>ptsN</i>	phosphotransferase system enzyme IIA, regulates N metabolism
<i>putP</i>	sodium/proline symporter responsible for the uptake of proline
<i>rbsR</i>	transcriptional repressor of the rbsDACBK operon involved in ribose metabolism
<i>recQ</i>	ATP-dependent DNA helicase
<i>rpiB</i>	allose-6-phosphate isomerase / ribose-5-phosphate isomerase B
<i>rpoS</i>	alternative sigma factor σ^S
<i>rutF</i>	predicted flavin reductase implicated in pyrimidine degradation
<i>serB</i>	3-phosphoserine phosphatase
<i>smg</i>	conserved protein
<i>spoT</i>	GDP diphosphokinase / guanosine-3',5'-bis(diphosphate) 3'-diphosphatase
<i>ssuA</i>	alkanesulfonate ABC transporter
<i>talA</i>	Transaldolase
<i>tdcA</i>	transcriptional activator of the <i>tdc</i> operon involved in amino acid degradation
<i>thrB</i>	homoserine kinase
<i>tnaA</i>	L-cysteine desulfhydrase / tryptophanase
<i>ucpA</i>	predicted oxidoreductase involved in sulfate metabolism protein
<i>wzc</i>	tyrosine kinase involved in colanic acid biosynthesis
<i>xylG</i>	ATP-binding component of the xylose ABC transporter
<i>yabl</i>	conserved inner membrane protein
<i>yafV</i>	predicted C-N hydrolase family amidase, NAD(P)-binding
<i>ybcV</i>	DLP12 prophage; predicted protein
<i>ycbJ</i>	conserved protein
<i>yciN</i>	predicted protein
<i>ydcJ</i>	conserved protein
<i>yeaP</i>	diguanylate cyclase
<i>yegH</i>	putative transport protein
<i>yfaY</i>	conserved protein
<i>yfdN</i>	CPS-53 (KpLE1) prophage; predicted protein
<i>yfeD</i>	predicted DNA-binding transcriptional regulator
<i>yfjR</i>	predicted DNA-binding transcriptional regulator
<i>yhcE</i>	predicted protein, N-ter fragment (pseudogene)

<i>yifJ</i>	lipid III flippase
<i>yjcC</i>	predicted signal transduction protein (EAL domain-containing protein)
<i>yjcQ</i>	predicted multidrug efflux system component
<i>ylcG</i>	Polypeptide: DLP12 prophage; predicted protein
<i>ymgC</i>	protein involved in biofilm formation
<i>ynbD</i>	predicted phosphatase, inner membrane protein
<i>yncC</i>	predicted DNA-binding transcriptional regulator
<i>yncG</i>	predicted enzyme
<i>yoaE</i>	predicted inner membrane protein
<i>yoeB</i>	toxin of the YoeB-YefM toxin-antitoxin pair
<i>yqjA</i>	Conserved inner membrane protein