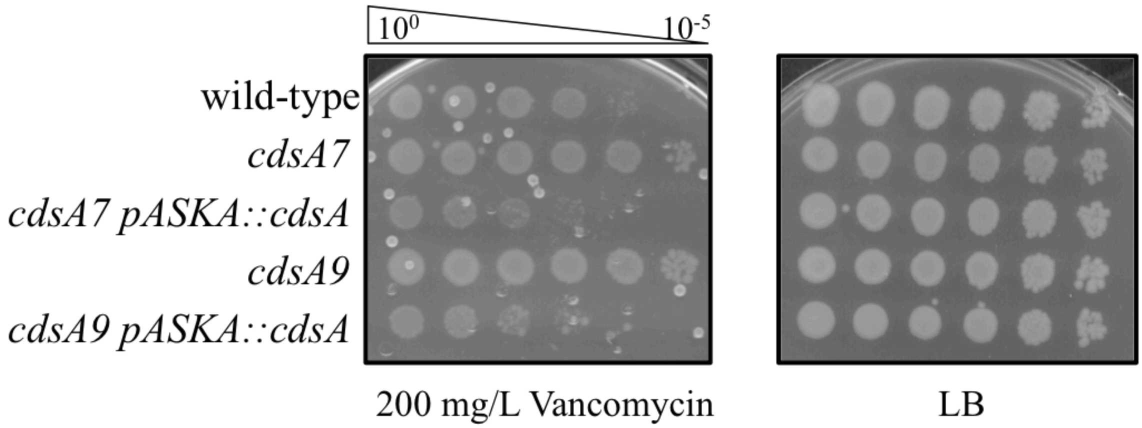


Fig. S1: *cdsA* mutants are recessive to wild-type. EOPs of strains supplemented with 200 mg/l vancomycin. IPTG was not supplemented in media to avoid overexpression of *cdsA*.

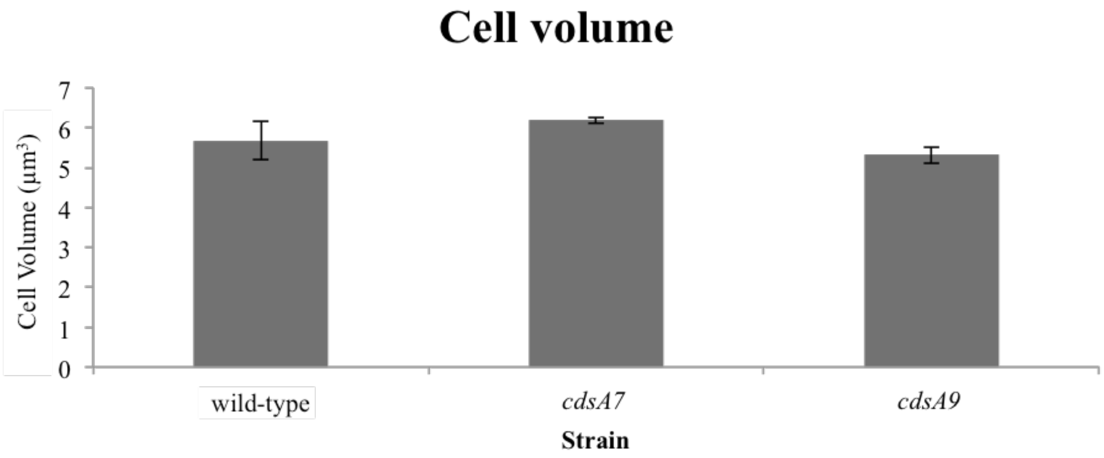


Fig. S2: *cdsA* mutant cell size does not differ from wild-type. Cell dimensions were quantified with MicrobeTracker version 0.936 (21), using MATLAB version R2013a. Error bars represent the standard error of the mean (n = 3 replicates of approximately 100 cells each). *P*-values were calculated using a Student's *t*-test. All *p*-values were > 0.05.

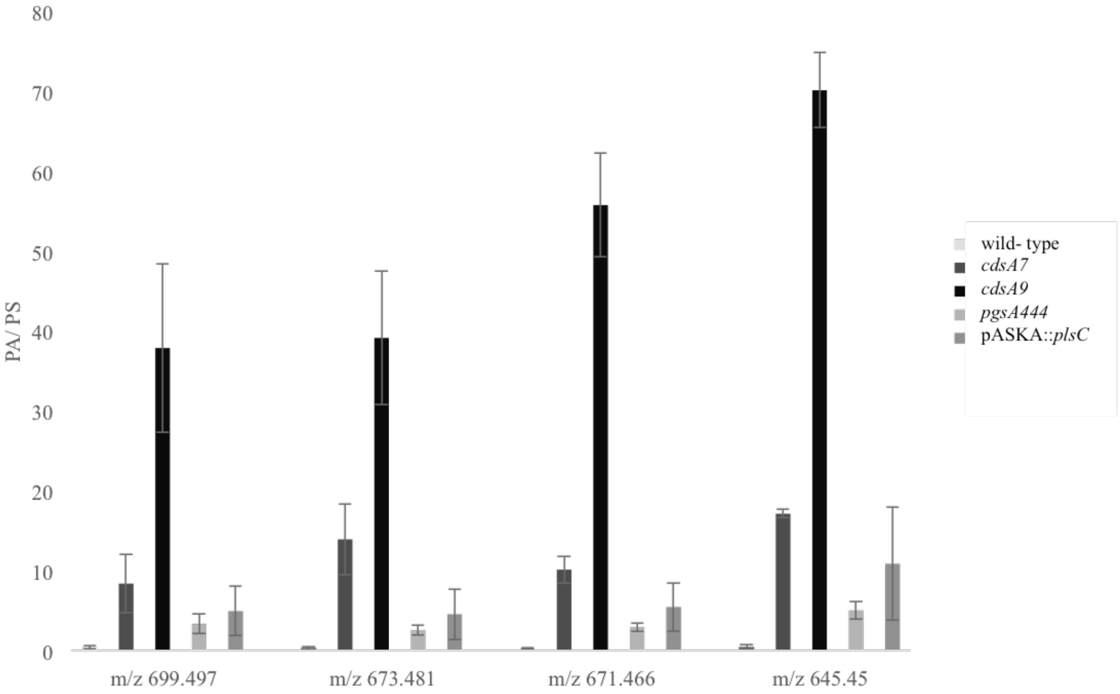
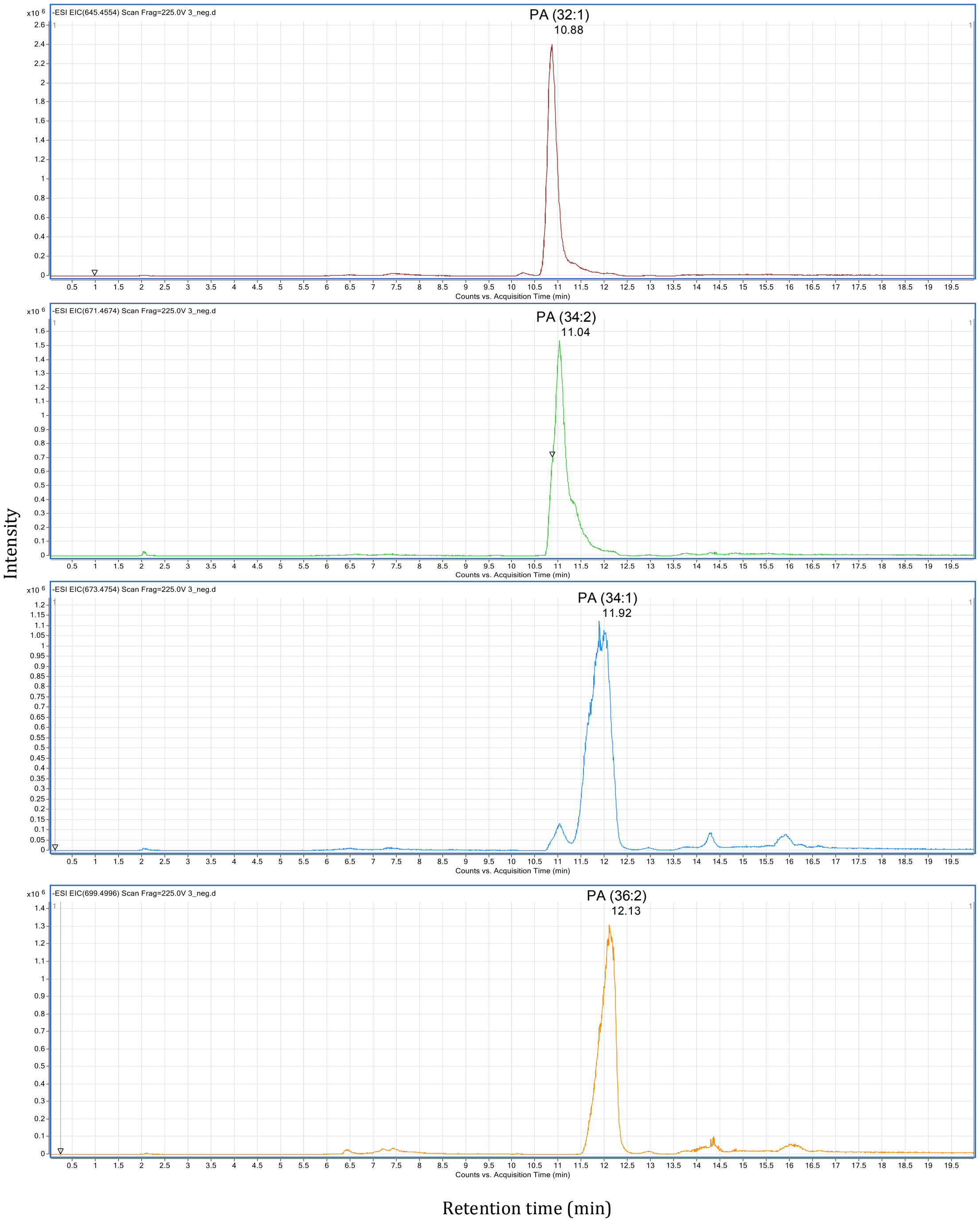


Fig. S3: All PA species detected accumulate in the *cdsA* strains, the *pgsA444* strain, and the *plsC* overexpression strain. PA and PS were quantified by Q-TOF LC/MS. Each PA species (PA (36:2) m/z 699, PA (34:1) m/z 673, PA (34:2) m/z 671, PA (32:1) m/z 645) was normalized to sum of all PS species. The change of PA/PS is reported ± standard error from three experiments.

Reverse-Phase LC-MS EIC plot



ESI-MS $[M\text{-}H]^-$

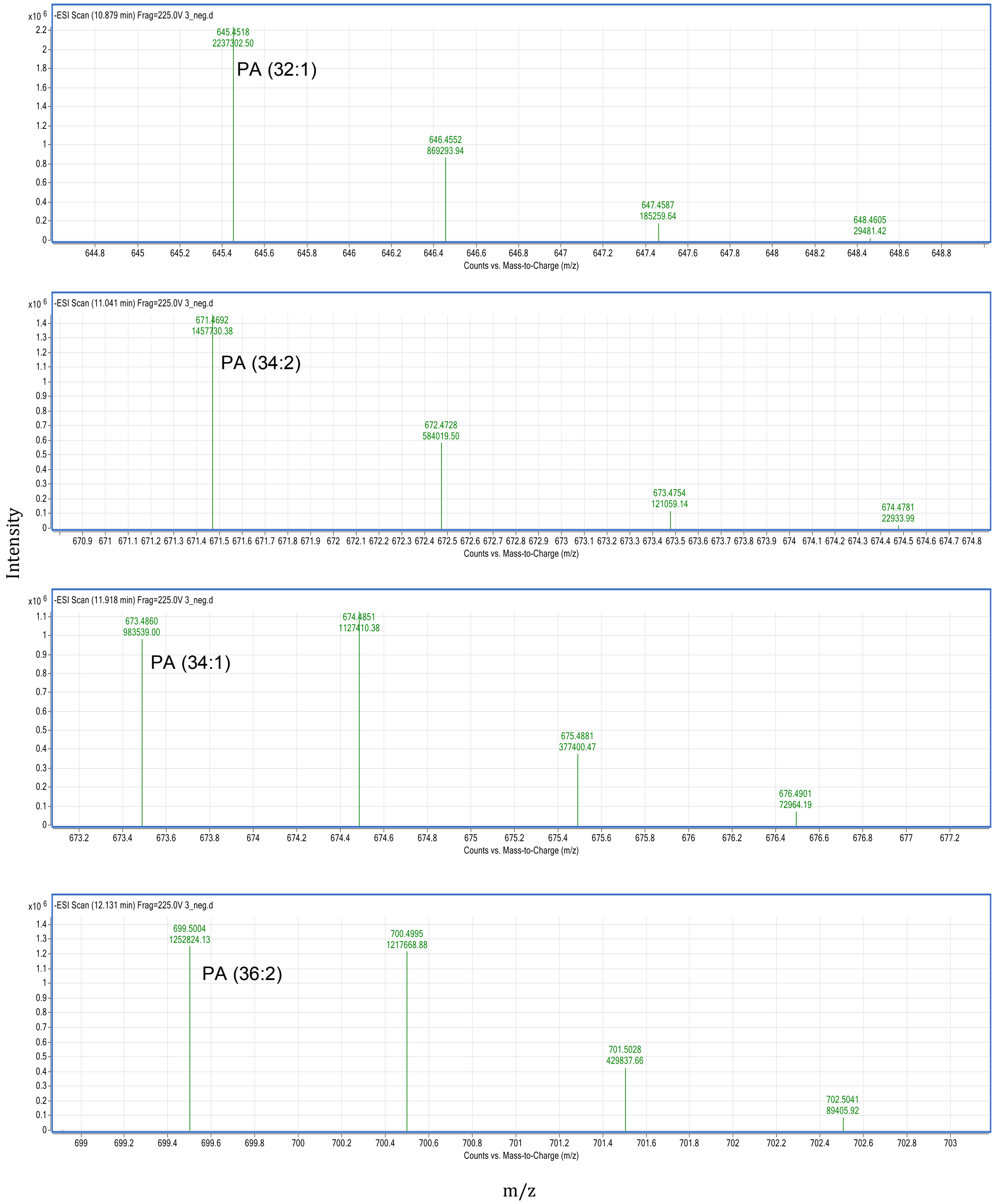


Figure S4: Retention time and ESI-MS of each PA species. PA (32:1) m/z 645, PA (34:2) m/z 671, PA (34:1) m/z 673, PA (36:2) m/z 699 accumulated in *cdsA9* strain, which was used as a representative example.

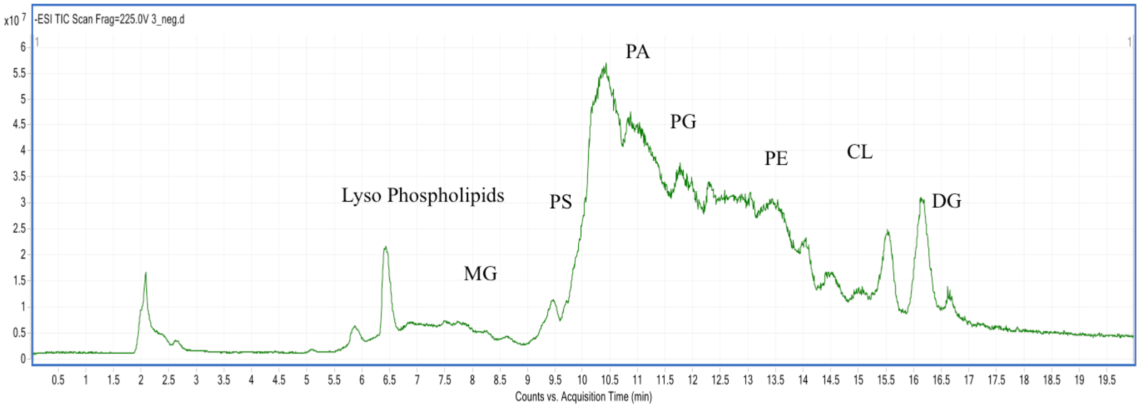
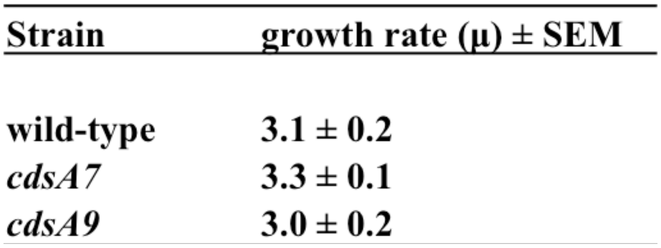


Fig. S5: ESI (Electrospray ionization)-TIC (total ion current) chromatogram from reverse-phase LC-MS analysis of phosphatidic acid (PA) and cardiolipin (CL). This chromatogram is from a *cdsA9* strain, which was used as a representative example. Monoglyceride (MG), Phosphatidylserine (PS), Phosphatidylglycerol (PG), Phosphatidylethanolamine (PE), Diglyceride (DG) are also shown on the chromatogram.



Strain	**growth rate (µ) ± SEM**
wild-type	**3.1 ± 0.2**
cdsA7	**3.3 ± 0.1**
cdsA9	**3.0 ± 0.2**

Table S1: *cdsA* mutant growth rate does not differ from wild-type. Strains were subcultured and OD_{600nm} readings were taken every 20 minutes. OD_{600nm} was plotted against time on a logarithmic scale. Linear regression analysis was used to determine a growth rate (µ) for each strain. The growth rate is reported ± standard error of the mean from three technical replicates for three biological replicates per strain.