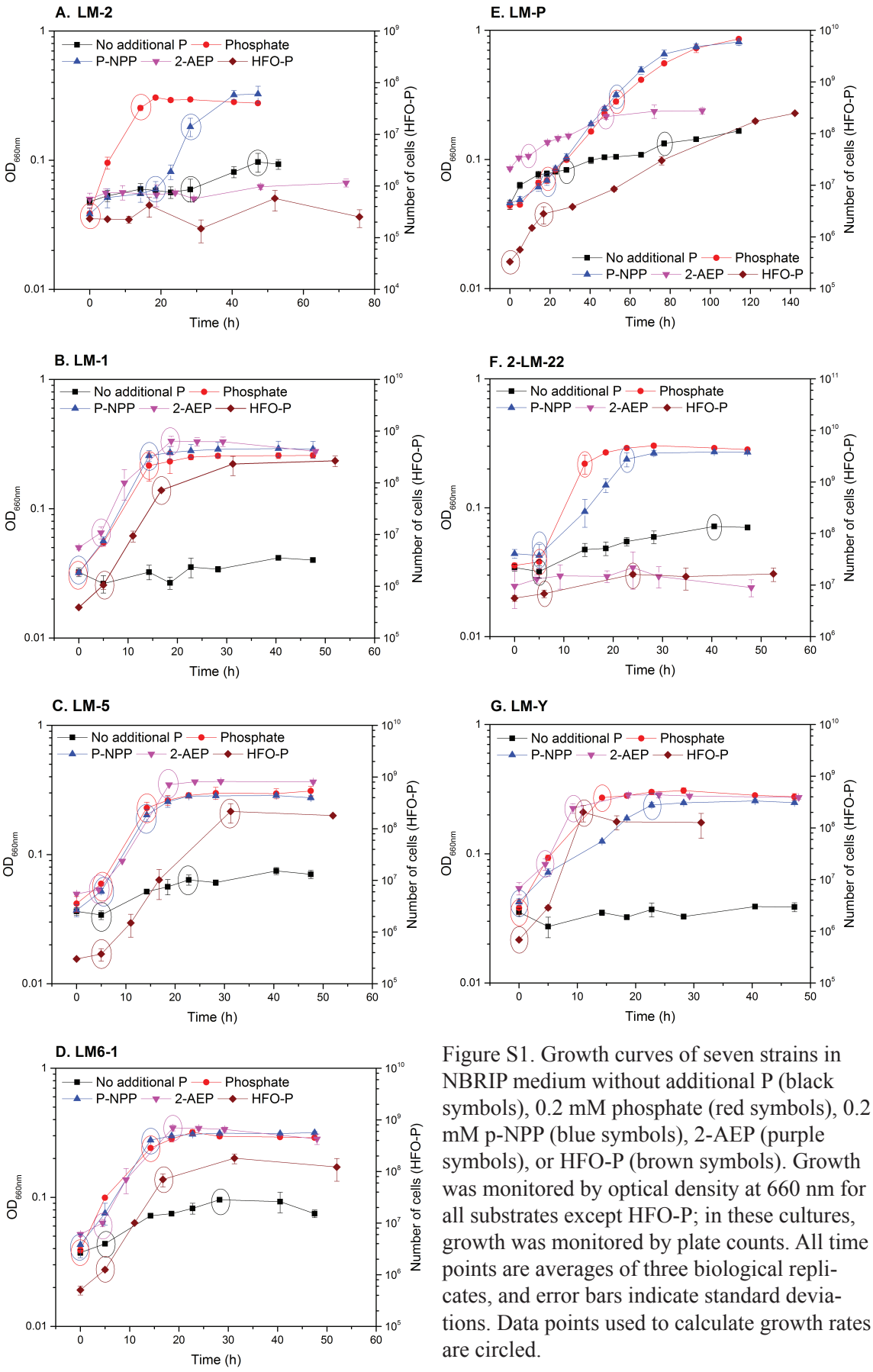

Figure S1. Growth curves of seven strains in NBRIP medium without additional P (black symbols), 0.2 mM phosphate (red symbols), 0.2 mM p-NPP (blue symbols), 2-AEP (purple symbols), or HFO-P (brown symbols). Growth was monitored by optical density at 660 nm for all substrates except HFO-P; in these cultures, growth was monitored by plate counts. All time points are averages of three biological replicates, and error bars indicate standard deviations. Data points used to calculate growth rates are circled.

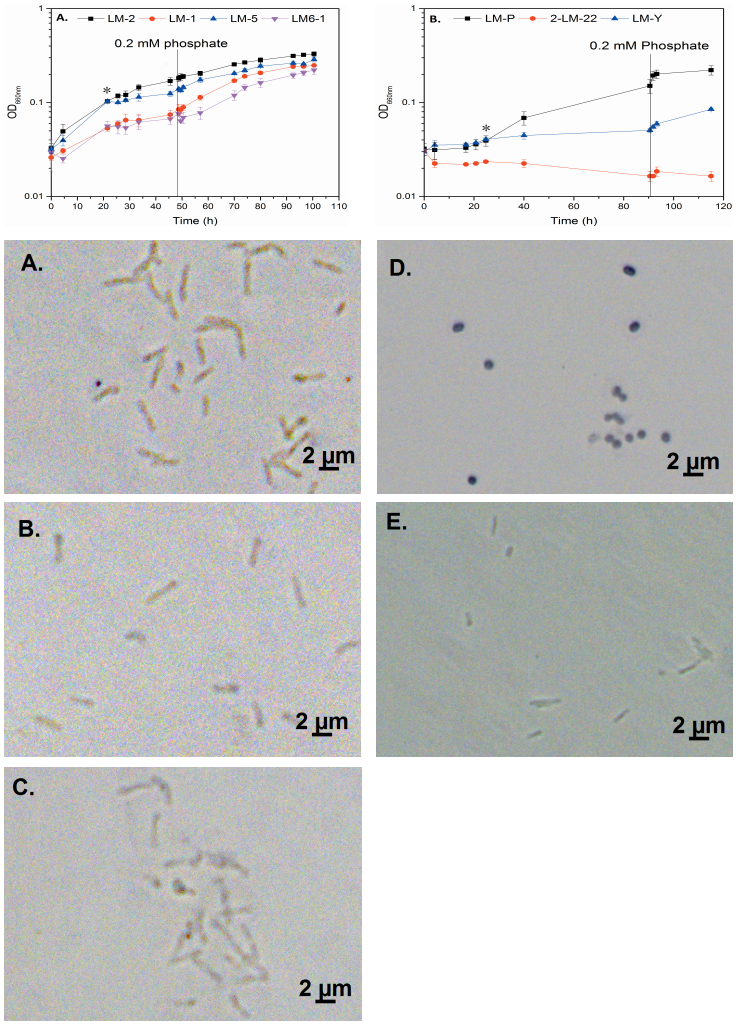

Figure S2. Neisser staining of isolates that appear not to store polyphosphate. A. LM-1. B. LM-5. C. LM-6-1. D. LM-Y. E. 2-LM-22. All cells were harvested at ~24h, where indicated on the growth curves.

	Actino.	Alphaproteobacteria				Gammaproteobacteria		
2014	LM-2	LM-1	LM-5	LM6-1	LM-P	LM6-2	LM-Y	2-LM-22
MGDG	64.3	11.0	13.8	4.7	35.2	b.d.	b.d.	6.5
DGDG	12.5	0.6	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.
GlcA-DAG	8.6	5.3	1.1	0.1	b.d.	b.d.	b.d.	0.1
DGTS	14.6	76.4	70.0	91.6	27.9	b.d.	b.d.	92.9
lyso-DGTS	b.d.	5.4	13.9	2.8	b.d.	b.d.	b.d.	0.5
OL	b.d.	0.2	b.d.	b.d.	23.0	b.d.	b.d.	b.d.
PDME	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.
PME	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.
PE	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.
PG	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.
PC	b.d.	1.1	1.2	0.8	14.0	b.d.	b.d.	b.d.
DPG	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.
%Glycolipids	85.4	16.9	15.0	4.7	35.2			6.7
%Aminolipids	14.6	82.0	83.9	94.5	50.9			93.3
%Phospholipids		1.1	1.2	0.8	14.0			

Figure S3. Intact polar lipids in cells growh without additional phosphate (< 2.45 μM), analyzed in 2014. Values indicate percent of total lipids; "b.d." indicates below detection limit.

Abbreviations:
Glycolipids: MGDG: monoglycosyl diacylglycerol; DGDG: diglycosyl diacylglycerol; GlcA-DAG: glucuronosyl diacylglycerol.
Aminolipids: DGTS (betaine): diacylglyceryl-N,N,N-trimethylhomoserine; lyso-DGTS (betaine): monoacylglyceryl-N,N,N-trimethylhomoserine; OL: ornithine lipid.
Phospholipids: PE: phosphatidylethanolamine; PME: N-methylated PE; PDME: N-dimethylated PE; PG: phosphatidylglycerol; PC: phosphatidylcholine; DPG: diphosphatidylglycerol.

	Actino.	Alphaproteobacteria				Gammaproteobacteria		
2013	LM-2	LM-1	LM-5	LM6-1	LM-P	LM6-2	LM-Y	2-LM-22
MGDG	8.5	6.2	11.4	8.3	39.4	9.9	7.9	9.0
DGDG	1.7	1.2	1.3	1.1	0.2	0.1	1.1	1.6
GlcA-DAG	8.1	9.5	5.2	10.4	12.2	2.2	6.0	14.3
DGTS	76.5	77.1	71.9	71.3	b.d.	81.6	59.3	60.9
lyso-DGTS	3.3	4.3	6.0	7.2	b.d.	5.3	2.2	7.7
OL	2.0	1.7	4.2	1.7	48.2	0.9	9.8	5.3
PDME	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.
PME	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	0.7	b.d.
PE	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	7.2	0.5
PG	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	5.7	0.8
PC	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.
DPB	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.	b.d.
%Glycolipids	18.2	16.9	17.9	19.8	51.8	12.3	15.0	24.8
%Aminolipids	81.8	83.1	82.1	80.2	48.2	87.7	71.4	73.9
%Phospholipids							13.5	1.3

Figure S4. Intact polar lipids in cells growh without additional phosphate (< 2.45 μM), analyzed in 2013. Values indicate percent of total lipids; "b.d." indicates below detection limit. Abbreviations are as described in the legend to Figure S3.

Table S1. Lower limit of detection, retention time during normal-phase HPLC; characteristic neutral loss and product ions during MS^2 fragmentation of identified intact polar lipids (n.a.: standard not available). DGTS was used as the standard for both DGTS and lyso-DGTS.

IPL type	Detection limit (pg)	Retention time (min)	Characteristic neutral loss (Da)	Diagnostic ions (*m/z*)
MGDG	5	5.5-6.5	197 (hexose + H_2O + NH_4^+ adduct)	-
DGDG	10	12-12.8	359 (dihexose + H_2O + NH_4^+)	-
GlcA-DAG	n.a.	11-12	211 (glucuronic acid + H_2O + NH_4^+)	-
DGTS	5	7-8	236 (trimethylhomoserine)	-
OL	n.a.	12-13	Depends on side chains	N_2O_5 core structure
PDME	1	8.5-9	169 (PDME)	-
PME	1	10-11	155 (PME)	-
PE	1	11.7-12.5	141 (PE)	-
PG	5	10.3-11	189 (PG + NH_4^+)	-
PC	10	10.5-11.8	-	PC (184)
DPG	10	12.7-14	Depends on side chains	P_2O_{17} core structure