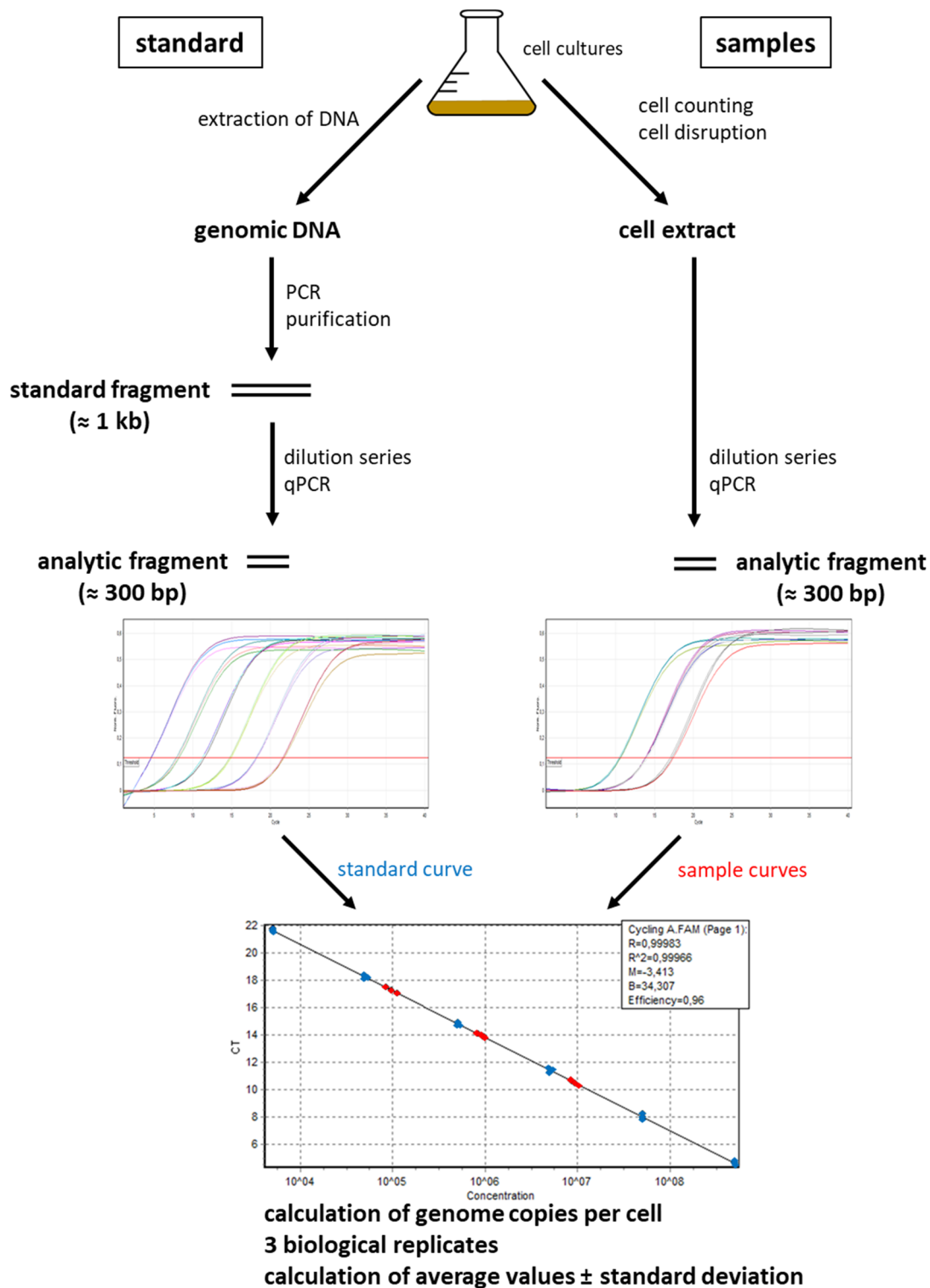
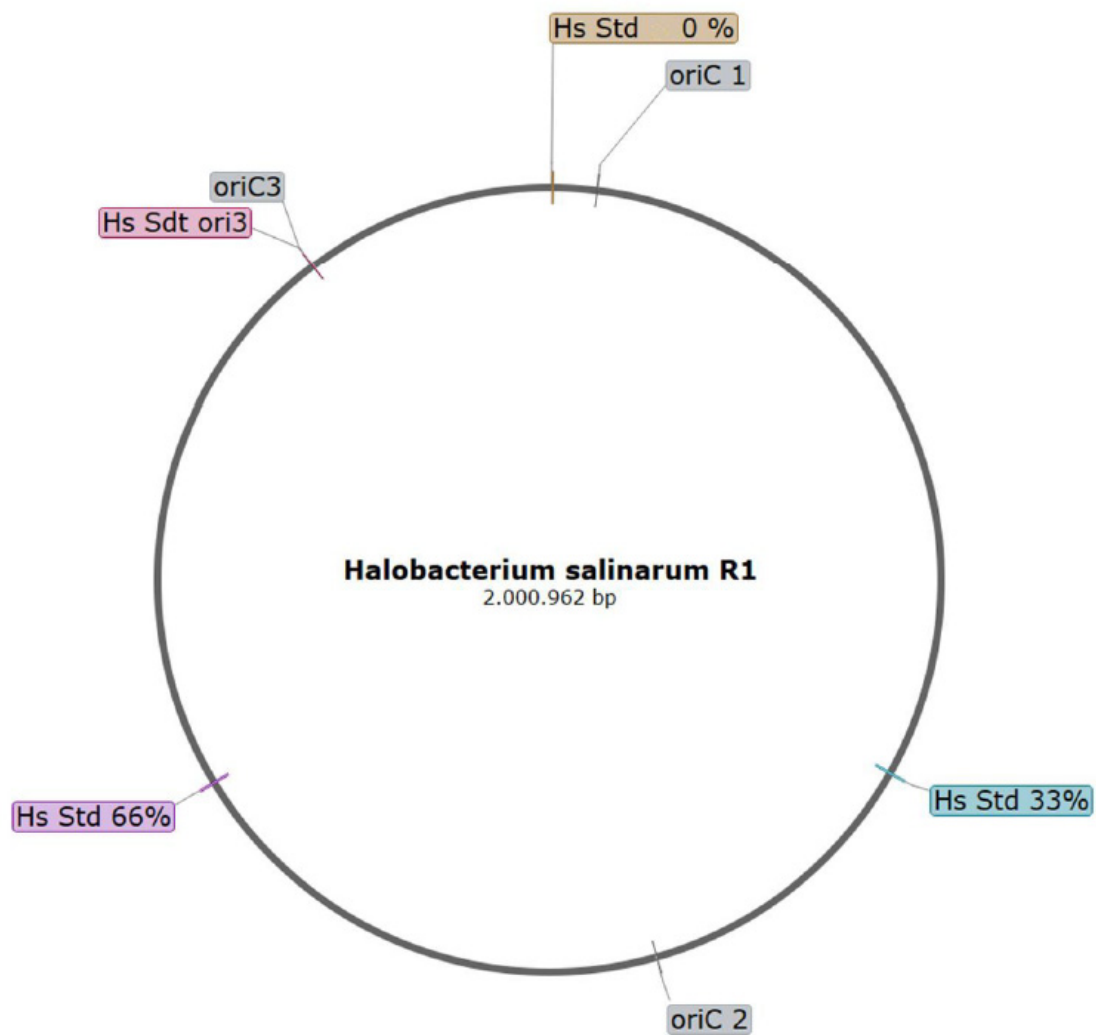




Supplementary Figure S1: Schematic overview of the real-time PCR method for quantification of chromosome copy numbers per cell (taken from Fuchino et al. (see below) with modifications).

Reference:

Fuchino, K.; Wasser, D.; Soppa, J. Genome Copy Number Quantification Revealed That the Ethanologenic α -Proteobacterium *Zymomonas mobilis* Is Polyploid. *Front. Microbiol.* **2021**, *12*, 705895.



Supplementary Figure S2: Map of the main chromosome of *Halobacterium salinarum* and locations of all standard fragments. The marked chromosomal locations were utilized for amplifying four distinct standard fragments, namely Hs Std ori3, Hs Std 0%, Hs Std 33%, and Hs Std 66%. These standard fragments exhibit varying distances to different origins of replications.

Supplementary Table S1: List of primers with sequences and application.

Name	Sequence (5' -> 3')	Application
SB 005 ST 1kb	CCGTTGCGCTCGATTTTCGAC	standard fragments of <i>H. salinarum</i>
SB 006 ST 1kb	ACGGCCAGCAAGGCCATCAG	
Hs 33 SF for	GTGAGCTGGCGTTCCTGAACTCC	
Hs 33 SF rev	GCAGCGGCTTCATGTGCCGATAG	
Hs 66 SF for	CGAAGAGCTGCCCCGAGGATATCAC	
Hs 66 SF rev	ATGCGCACCGCACCGAATAC	
Hs 100 SF for	CGCAGGCGCAGGTGCAACGAATTG	
Hs 100 SF rev	ACGCCAGCCAGCGGGCTAATGTG	
qPCR SB 001 ST	CCACCCGCCAGCCAAGATCAGCGCCCGAAC	
qPCR SB 002 ST	GCAGGCACGATCACAGCAACCCGATACCAG	
Hs 33 A1 for	GAAGTCGACGGCGAGAACCTCACC	analysis fragments of <i>H. salinarum</i>
Hs 33 A1 rev	GCGTGAGCTCCTCGGCTTTCTTGG	
Hs 66 A1 for	GCTGGTCGGGTCGAACGTTG	
Hs 66 A1 rev	ATGCGCACCGCACCGAATAC	
Hs 100 A1 for	CGACGGCAGTCTGTACCGGATTCTG	
Hs 100 A1 rev	TCACGCCCTCACGGGCATCTGAAG	
oriF1	TTCGTGATCGGCCATTGGTTTC	standard fragments of <i>Z. mobilis</i>
oriR2	CAATGACCATTTTCGGCCACCTG	
oriqF3	ATTACGCAAGCAAGACCTCC	analysis fragments of <i>Z. mobilis</i>
oriqR2	ACGGACATTATCGGGATTGTCTG	
Av SF1 ori for	CCGGTGGGCACCAAGTAGTAAC	standard fragments of <i>A. vinelandii</i>
Av SF1 ori rev	CAGGCCGCTGGCAGAGAAAG	
Av SF1 ter for	GAACATGGGACAGGCGCAAAG	
Av SF1 ter rev	CCGGCATGAGGGAATGTTTGG	
Av A1 ori for	GCCTCAGGGCTGAAGCTTTCTTG	analysis fragments of <i>A. vinelandii</i>
Av A1 ori rev	GCTACGAGGACGGTAGCGAGAATC	
Av A1 ter for	TCATGCCCCGCGACAACAAAC	
Av A1 ter rev	GTACGACGGACATACTGGCAGAC	
Ec SF ori for	GCGGTGAGCAAGGTATTAAG	standard fragments of <i>E. coli</i>
Ec SF ori rev	CCGAAATAGCGGGTGTTATG	
Ec A1 ori for	CCATAATGAAGTGGCGTCCTTTTCG	analysis fragments of <i>E. coli</i>
Ec A1 ori rev	TATCGCCGTAGACAACCTCCAATCG	

Supplementary Table S2: Overview of the number of phosphate molecules that are sequestered in the genome of one cell prior to the growth in the absence of an external phosphate source, the number of phosphate molecules in the genomes of the descendants of one cell after the growth in the absence of phosphate, and the difference.

Species	No. P _i mol. in 1 Cell Prior to Starvation	No. P _i mol. in Descendants after Starvation	No. P _i mol. Missing after Starvation	Fraction P _i Missing after Starvation	Reference
<i>Z. mobilis</i>	6.25×10^7	6.08×10^7	0.17×10^7	2.7%	This study
<i>A. vinelandii</i>					
Gluc./Mann.	2.22×10^8	2.44×10^8	-0.22×10^8	-9.9%	This study
Sucrose	3.38×10^8	3.03×10^8	0.35×10^8	10.4%	This study
<i>H. salinarum</i>	1.30×10^8	1.17×10^8	0.13×10^8	10.0%	This study
<i>H. volcanii</i>	2.2×10^8	1.5×10^8	0.7×10^8	31.8%	[52]