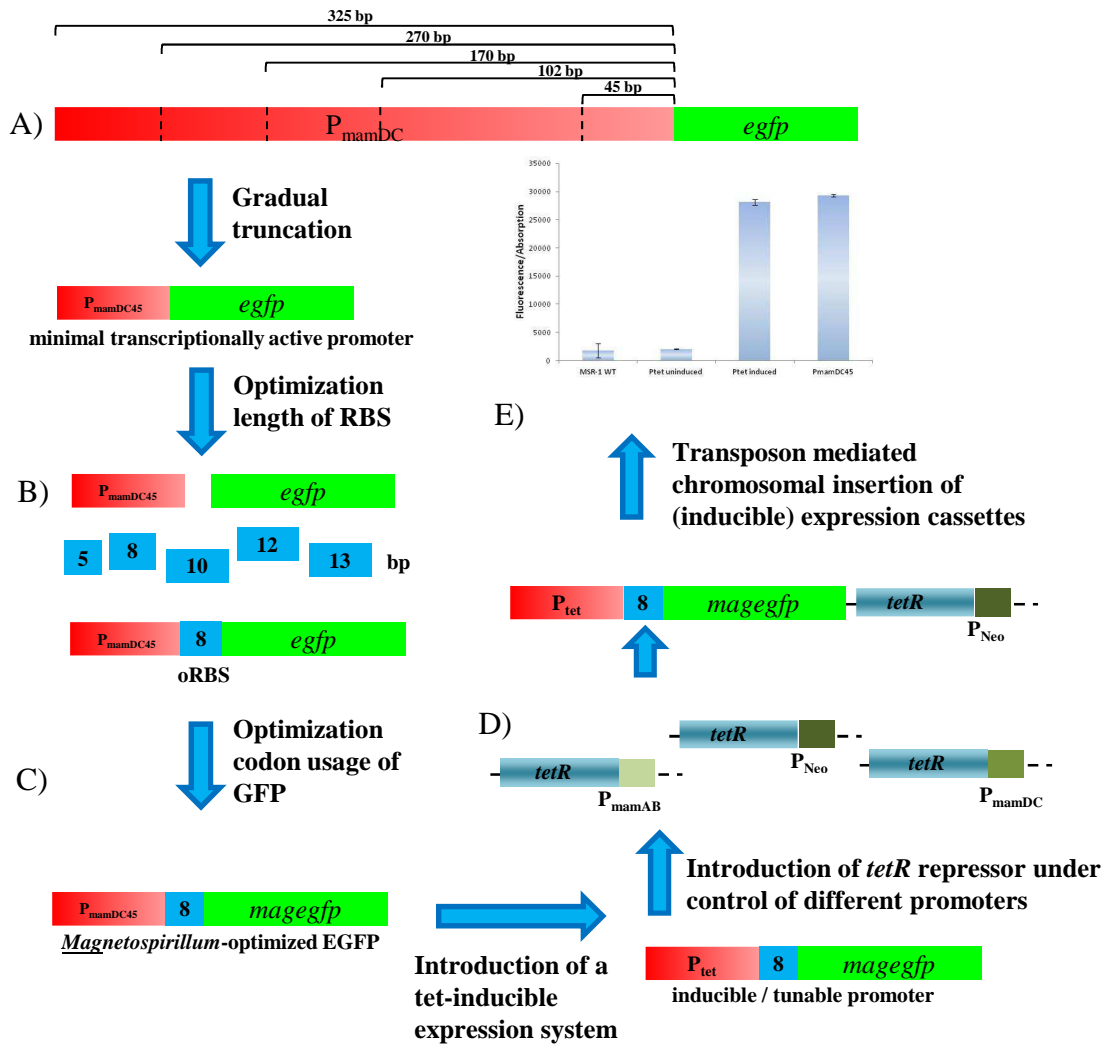


Optimization of gene expression cassette for *M. gryphiswaldense*



Suppl. Fig. S1: Optimization strategy of (inducible) expression cassette.

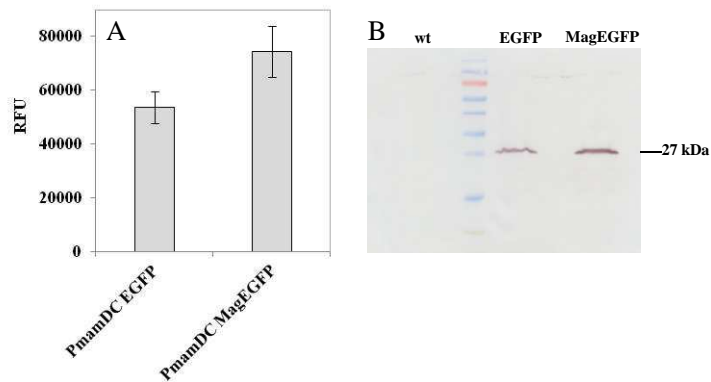
CLUSTAL 2.1 multiple sequence alignment

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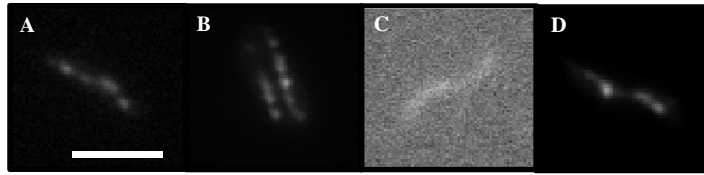
non-opt      ATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCTATCCTGGTCGAGCTGGAC 60
opt          ATGGTGTGCAAGGGCGAGGAACTGTTACCGGCGTCTGCCGATCCTGGTCGAGCTGGAC 60
*****
non-opt      GCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTAC 120
opt          GCGACGTCAACGGCCATAAGTTCAGCGTGTCCGGCGAGGGCGAAGGGCGAGCCACCTAI 120
*****
non-opt      GGCRAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCTGGCCACC 180
opt          GGCRAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCTGGCCACC 180
*****
non-opt      CTCGTGACCACCCTGACCTACGGCGTGCAGTGTTCAGCGGCTACCCCGACCACATGAAG 240
opt          CTCGTGACCACCCTGACCTACGGCGTGCAGTGTTCAGCGGCTACCCCGACCACATGAAG 240
*****
non-opt      CAGCAGACTTCTTCAAGTCCGCCATGCCGAGGCTACGTCCAGGAGCGCACCAITTC 300
opt          CAGCAGACTTCTTCAAGTCCGCCATGCCGAGGCTACGTCCAGGAGCGCACCAITTC 300
*****
non-opt      TTCRAAGGACGACGGCACTACCAAGACCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTG 360
opt          TTCRAAGGACGACGGCACTACCAAGACCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTG 360
*****
non-opt      GTGAACCGCAICGAGCTGAAGGGCAICGACTTCAAGGAGGACGGCAACATCCTGGGGCAC 420
opt          GTCAACCGCAICGAGCTGAAGGGCAICGACTTCAAGGAGGATGGCAACATCCTGGGGCAC 420
*****
non-opt      AAGCTGGAGTACAACCTACAACAGCCACAACGCTATATATCAITGGCCGACAAAGCAGAAGAAC 480
opt          AAGCTGGAAATATAACTATAACTGCGCACACGCTATATATCAITGGCCGACAAAGCAGAAGAAC 480
*****
non-opt      GGCATCAAGGTGAACCTTCAAGATCCGCCACAACATCGAGGACGGCGAGCTGCAGCTCGCC 540
opt          GGCATCAAGGTCAACTTCAAGATCCGCCATAACATCGAGGACGGCTCGGTCCAGCTGGCC 540
*****
non-opt      GACCACTACCAGCAGAACACCCCAICGGCGACGGCCCGGTGCTGCTGCCGACAAACCAAC 600
opt          GACCAITATCAGCAGAACACCCGATCGGCGACGGCCCGGTCTGCTGCCGACAAACCAI 600
*****
non-opt      TACCTGAGCACCCAGTCCGCCCTGAGCAAGACCCCAACGAGAGCCGATCACATGGTC 660
opt          TATCTGTCCACCAGTCCGCCCTGTGCAAGGACCCGAAAGGAGGCGGACCAACATGGTC 660
*****
non-opt      CTGCTGGAGTTCGTGACCGCCGCCGGATCACTCTCGGCAITGGACGAGCTGTACAAGTAA 720
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*****

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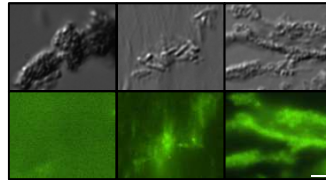
Suppl. Fig S2: Sequence alignment of non-optimized *egfp* and *Magnetospirillum*-optimized *magegfp* using CLUSTALW (version 2.1, <http://www.ebi.ac.uk/Tools/msa/clustalw2/>). Sequence similarity is 89 %, start and stop codon are overlined.



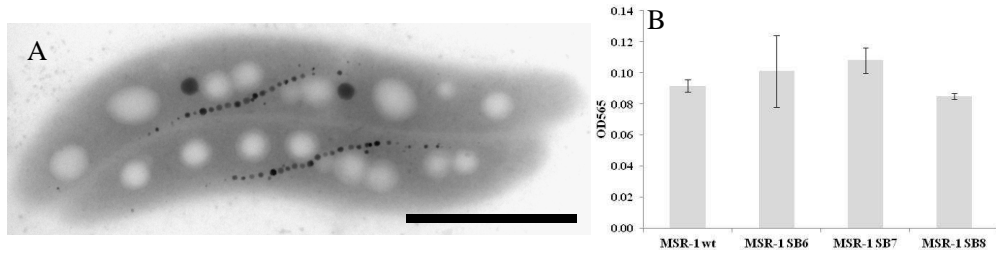
Suppl. Fig S3: (A) Fluorescence of *Magnetospirillum*-optimized (MagEGFP) versus non-optimized GFP (EGFP) expressed from the P_{mamDC45} promoter. Fluorescence was normalized to the cell density and described as relative fluorescence units (RFU). Error bars represent standard deviations, calculated from three independent experiments. (B) Western blot of whole *M. gryphiswaldense* cells expressing EGFP or MagEGFP from the control of the P_{mamDC45}. (Mag)EGFP was detected using rabbit α GFP IgG as primary, and goat anti-rabbit IgG alkaline phosphatase antibodies as secondary antibody. PageRuler™ Prestained Protein Ladder from fermentas was used as a standard.



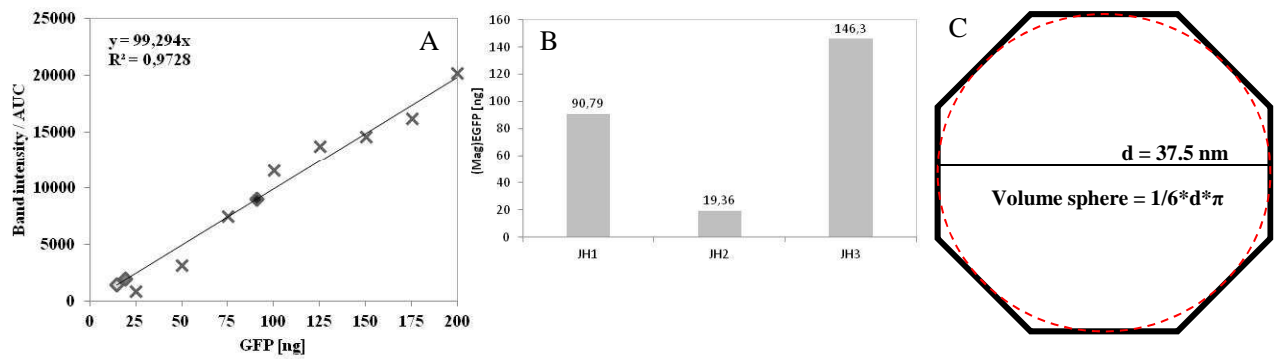
Suppl. Fig. S4: Fluorescence micrographs of *M. gryphiswaldense* ΔC strains carrying chromosomal insertions of (A) $P_{\text{mamDC45}}\text{-mamC-magegfp}$ (JH1) (B) $P_{\text{tet}}\text{-mamC-magegfp}$ (JH2) induced with 70 ng ml^{-1} Atet, (C) uninduced and (D) $P_{\text{mamDC45}}\text{-mamC-egfp-magegfp}$ (JH3) expression cassettes. White bar corresponds to 2 μm .



Suppl. Fig. S5: Fluorescence and DIC micrographs of isolated magnetosomes from *M. gryphiswaldense* MSR-1 ΔC (A) JH2 (induced) (B) JH1 and (C) JH3. White bar corresponds to 2 μm .



Suppl. Fig. S6: A) Transmission electron micrographs of *M. gryphiswaldense* SB6, expressing MagEGFP chromosomally from P_{mamDC45}. The black scale bar represents 200 nm. B) Optical density (OD₅₆₅) after overnight growth of strains SB6, SB7 and SB8 in comparison to wt. Error bars represent standard deviations calculated from triplicate cultures, experiment was repeated three times, data is from one representative experiment.



Suppl. Fig. S7: (A) Quantitative Western blot of GFP standard curve (marked by "x") and MM samples from strains JH1 (black square), JH2 (grey square) and JH3 (light grey square, 10x diluted). (B) Corresponding GFP protein concentrations of strains JH1, JH2 and JH3. (C) Schematic drawing of approximation of magnetosome size.

Suppl. Tab. S1: Plasmids used in this study

Plasmid name	Description	Source or reference
pJET1.2/blunt	Cloning vector; Amp ^R	Fermentas
pBBR-MCS2	Mobilizable broad-host-range vector; Km ^R	Kovach, M. E., <i>et al.</i> , 1995
pBAM1	Km ^R , Amp ^R , oriR6K, <i>tnpA</i>	Martinez-Garcia, E., <i>et al.</i> , 2011
p11AAGJZC	Amp ^R , ColE1 ori, oRBS, <i>magegfp</i>	GeneArt® (Invitrogen), life technologies, Darmstadt
pAP150	pBBR-MCS2, with P _{mamDC45} , <i>egfp</i> , terminator-fragment; Km ^R	A. Pollithy (unpublished)
pAP158	pBBR-MCS2, with P _{tet} , <i>egfp</i> , terminator-fragment, P _{mamAB} -TetR; Km ^R	A. Pollithy (unpublished)
pAP159	pBBR-MCS2, with P _{tet} , <i>egfp</i> , terminator-fragment, P _{mamDC} -TetR; Km ^R	A. Pollithy (unpublished)
pAP160	pBBR-MCS2, with P _{tet} , <i>egfp</i> , terminator-fragment, P _{Neo} -TetR; Km ^R	A. Pollithy (unpublished)
pAP161	pBBR-MCS2, with P _{mamDC325} , <i>egfp</i> , terminator-fragment; Km ^R	A. Pollithy (unpublished)
pAP162	pBBR-MCS2, with P _{mamDC102} , <i>egfp</i> , terminator-fragment; Km ^R	A. Pollithy (unpublished)
pAP163	pBBR-MCS2, with P _{mamDC170} , <i>egfp</i> , terminator-fragment; Km ^R	A. Pollithy (unpublished)
pAP164	pBBR-MCS2, with P _{mamDC270} , <i>egfp</i> , terminator-fragment; Km ^R	A. Pollithy (unpublished)
pLYJ97	pBBR-MCS2 with <i>gusA</i>	Li, Y., <i>et al.</i> , 2012
pSB1	pBBR-MCS2, with P _{mamDC45} , <i>magegfp</i> , terminator-fragment; Km ^R	this study
pSB6	pBAM1 with P _{mamDC45} , <i>magegfp</i> , Km ^R , Amp ^R	this study
pSB7	pBAM1 with P _{tet} , <i>magegfp</i> , P _{Neo} -TetR, Km ^R , Amp ^R	this study
pSB8	pBAM1 with P _{tet} , <i>gusA</i> , P _{Neo} -TetR, Km ^R , Amp ^R	this study
pJH1	pBAM1 with P _{mamDC45} , <i>mamC-magegfp</i> , Km ^R , Amp ^R	this study
pJH2	pBAM1 with P _{tet} , <i>mamC-magegfp</i> , P _{Neo} -TetR, Km ^R , Amp ^R	this study
pJH3	pBAM1 with P _{mamDC45} , <i>mamC-magegfp-egfp</i> , Km ^R , Amp ^R	this study

Suppl. Tab. S2: Strains used in this study

Strain	Description	Source or reference
<i>Escherichia coli</i>		
DH5 α	F ⁻ <i>supE44</i> Δ <i>lacU169</i> (Φ 80 <i>lacZDM15</i>) <i>hsdR17</i> <i>recA1</i> <i>endA1</i>	
WM3064	<i>gyrA96</i> <i>thi-1</i> <i>relA1</i> <i>thrB1004</i> <i>pro</i> <i>thi</i> <i>rpsL</i> <i>hsdS</i> <i>lacZAM15</i> RP4-1360 Δ (<i>araBAD</i>)567 Δ <i>dapA1341::[erm pir]</i>	W. Metcalf, unpublished
BW29427	DAP auxotroph derivative of <i>E. coli</i> strain B2155	K. Datsenko and B. L. Wanner, unpublished
<i>Magnetospirillum</i>		
<i>gryphiswaldense</i>		
<i>M. gryphiswaldense</i> MSR-1 R3/S1	Rif ^R , Sm ^R spontaneous mutant, lab strain	D. Schultheiss, <i>et al.</i> , 2003
<i>M. gryphiswaldense</i> Δ C	Δ <i>mamC</i>	A. Scheffel, <i>et al.</i> , 2007
<i>M. gryphiswaldense</i> (pAP150)	Km ^R , conjugated with pAP150	A. Pollithy, unpublished
<i>M. gryphiswaldense</i> (pAP160)	Km ^R , conjugated with pAP160	A. Pollithy, unpublished
<i>M. gryphiswaldense</i> (pSB1)	Km ^R , conjugated with pSB1	this study
<i>M. gryphiswaldense</i> MSR-1 SB6	Km ^R , transposon mutant with inserted <i>magegfp</i> from P _{mamDC45}	this study
<i>M. gryphiswaldense</i> MSR-1 SB7	Km ^R , transposon mutant with inserted <i>magegfp</i> from P _{tet}	this study
<i>M. gryphiswaldense</i> MSR-1 SB8	Km ^R , transposon mutant with inserted <i>gusA</i> from P _{tet}	this study
<i>M. gryphiswaldense</i> MSR-1 JH1	Km ^R , transposon mutant with inserted <i>mamC</i> - <i>magegfp</i> from P _{mamDC45}	this study
<i>M. gryphiswaldense</i> MSR-1 JH2	Km ^R , transposon mutant with inserted <i>mamC</i> - <i>magegfp</i> from P _{tet}	this study
<i>M. gryphiswaldense</i> MSR-1 JH3	Km ^R , transposon mutant with inserted <i>mamC</i> - <i>magegfp-egfp</i> from P _{mamDC45}	this study

Suppl. Tab. S3: Primers used in this study. Restriction sites indicated in bold

Primer name	Sequence	Restriction site
oEGFP BamHI Rev	cgaac ggatcct cacttatacagctcg	BamHI
oEGFP HindIII Fw	cgget caagctt aggagatcagcatatg	HindIII
pBam_pAP160 Fw	atc gggacccc ttccggctggctggttt	SanDI
pBam_ Tet w/o Term Rev	atc gaattc ggcggattgtcctactca	EcoRI
pBam_pAP150 Fw	atc gggacccc ggatcctcacttatacagct	SanDI
pBam_DC w/o Term Rev	gc gaattc ctcagacttttctgctttac	EcoRI
GusA BamHI Fw	gt ggatcccc gggtcattggttgcc	BamHI
GusA NdeI Rev	tt catatg ttacgtctgtagaaa	NdeI
optGFP San/Bam Fw	g gggacccc ggatcctcacttatacagctcgcc	BamHI/SandDI
optGFP linker Rev	ggaggcggaggcgggtggcggaggtggcgg aatcgat atg gtgtcgaagggcga	ClaI
mamC ov linker Fw	cgccaccgctccgct ccatgg ccaatttcttccctca	NcoI
mamC NdeI Rev	t acatag actttcaacttgccg	NdeI
optGFP2x Fw	agt ggatcct cacttatacagctcgcca	BamHI
optGFP2x Rev	ctgtgcct gcagggc gagatggtgtcgaagggcg	PstI
eGFP overl Fw	atctcgc ctgcagg cacagctgtacagctcgccatgc	PstI
mamC_RBS Rev	c gaagctt aggagatcagcatatgagctttcaact	HindIII

Suppl. Tab. S4: Insertion sites of expression cassettes in *M. gryphiswaldense* strains

Strain	Gene	Putative function
MSR-1 SB6 K7	MGR_1519	hypothetical protein
MSR-1 SB6 K8	Inter region between MGR_1092 and MGR_2997	MGR_1092 - D-alanine-D-alanine ligase MGR_2997 - acyl carrier protein
MSR-1 SB7 K1	MGR_1581	sugar kinase, ribokinase family
MSR-1 SB7 K2	MGR_1519	hypothetical protein
MSR-1 SB8	MGR_1702	transposase IS3/IS911
MSR-1 JH1	MGR_3776	insertion element ISR1 from not characterized 10 kDa protein A3
MSR-1 JH2	MGR_3148	TorC, trimethylaminoxide (TMAO)-reductase I, cytochrom C subunit
MSR-1 JH3	MGR_612	hypothetical protein

References Supplements:

1. **Kovach ME, Elzer PH, Hill DS, Robertson GT, Farris MA, Roop RM, Peterson KM.** 1995. 4 New Derivatives of the Broad-Host-Range Cloning Vector pBBR1MCS, Carrying Different Antibiotic-Resistance Cassettes. *Gene* **166**:175-176.
2. **Martinez-Garcia E, Calles B, Arevalo-Rodriguez M, de Lorenzo V.** 2011. pBAM1: an all-synthetic genetic tool for analysis and construction of complex bacterial phenotypes. *Bmc Microbiol* **11**.
3. **Li YJ, Katzmann E, Borg S, Schüler D.** 2012. The Periplasmic Nitrate Reductase Nap Is Required for Anaerobic Growth and Involved in Redox Control of Magnetite Biomineralization in *Magnetospirillum gryphiswaldense*. *J Bacteriol* **194**:4847-4856.
4. **Schultheiss D, Schüler D.** 2003. Development of a genetic system for *Magnetospirillum gryphiswaldense*. *Arch Microbiol* **179**:89-94.
5. **Scheffel A, Gärdes A, Grünberg K, Wanner G, Schüler D.** 2008. The major magnetosome proteins MamGFDC are not essential for magnetite biomineralization in *Magnetospirillum gryphiswaldense* but regulate the size of magnetosome crystals. *J Bacteriol* **190**:377-386.