## Supplementary Tables

Strains and plasmids	Description	References
M. gryphiswaldense		
strains		
MSR-1 R3/S1	Rif <sup>R</sup> Sm <sup>R</sup> , spontaneous mutant	(1)
MSR-1B	R3/S1 Spontaneous mutant,	(2)
	lacking 40,385 kb genomic	
	region	
IK-1	R3/S1 $\Delta recA$	(3)
2xGFDCop	one native and one further copy	This study
	of the <i>mamGFDC</i> operon, Km <sup>R</sup>	
2x <i>mms6</i> op	one native and one further copy	This study
	of the <i>mms6</i> operon, Km <sup>R</sup>	
2xmms6op+2xGFDC	one native and one further copy	This study
	of the mms6 and mamGFDC	
	operon, Km <sup>R</sup>	
3xmms6op	one native and two further copies	This study
	of the <i>mms6</i> operon, Km <sup>R</sup>	
4x <i>mms6</i> op/Gm	one native and three further	This study
	copies of the <i>mms6</i> operon, Km <sup>R</sup> ,	
	Gm <sup>R</sup>	

4x <i>mms6</i> op	one native and three further	This study
	copies of the <i>mms6</i> operon, Km <sup>R</sup> ,	
	Gm <sup>S</sup>	
5x <i>mms6</i> op	one native and five copies of the	This study
	<i>mms6</i> operon, Km <sup>R</sup> , Gm <sup>S</sup>	
2x <i>mamAB</i> op	one native and one further copy	This study
	of the <i>mamAB</i> operon, Km <sup>R</sup>	
3x <i>mamAB</i> op	one native and two copies of the	This study
	<i>mamAB</i> operon, Km <sup>R</sup> , Gm <sup>R</sup>	
2xABG6X	$\Delta \text{RecA}$ with one further copy of	This study
	the mamAB, mamGFDC, mms6	
	operon and mamXYZ genes	
ABG6X+feo	$\Delta \text{RecA}$ with two copies of the	This study
	mamAB, mamGFDC, mms6	
	operon and mamXYZ genes and	
	feoAB1 operon	
<i>E. coli</i> strain		
BW29427	thrB1004 pro thi rpsL hsdS	Datsenko and Wanner
	lacZDM15 RP4-	(unpublished)
	1360D(araBAD)567DdapA::[erm	
	pir]	
DH5a	1341::[erm	Invitrogen

	pir(wildtype)]trahsdR17 recA1- endA1gyrA96thi-1relA1	
DH10β	F endA1 recA1 galE15 galK16 nupG rpsL $\Delta$ lacX74 $\Phi$ 80lacZ $\Delta$ M15 araD139 $\Delta$ (ara,leu)7697 mcrA $\Delta$ (mrr- hsdRMS-mcrBC) $\lambda$	Invitrogen
S17-1λpir	RPA-2, Tc::Mu-Km::Tn7 ( مpir)	(4)
WM3064	thrB1004 pro thi rpsL hsdS lacZDM15 RP4-1360D(araBAD) 567DdapA::[erm pir]	W. Metcalf, kindly provided by J. Gescher, KIT
		Karlsruhe

## Plasmids

pJet1.2	Ap <sup>r</sup> , eco47IR, rep (pMB-1)	Fermentas
pCM157	Tet <sup>R</sup> , Cre expression vector	(5)
pBBR-MCS5	Gm <sup>r</sup> , <i>lacZa</i>	(2)
pBam-1	<i>ori</i> R6K, Km <sup>R</sup> , Ap <sup>R</sup>	(6)
pTps_AB	Km <sup>R</sup> , BSD <sup>R</sup> , mariner tps vector	(7)
	containing mamAB operon	
Gm- pTps_AB	Gm <sup>R</sup> , BSD <sup>R</sup> , mariner tps vector	This study
	containing mamAB operon	

vector with mamAB, mamGFDC, and mms6 operon pTps_XYZ Gm <sup>R</sup> , BSD <sup>R</sup> , mariner Tps vector (7) with mamY, mamX and mamZ Tc <sup>R</sup> , Ap <sup>R</sup> , feoAB1 operon under the control of P <sub>mamH</sub> , Tn5 vector pBam_mamGFDC pBam-1, mamGFDC operon This study pBam_mms6 1x pBam_mamGFDC, mms6 operon This study pBam_ms6 2x pBam_mamGFDC, mms6 operon This study (two mms6 operons) pBam_ms6/Gm pBam_mms6 1x, mms6 1x, mms6 1x, mis study pBam_mms6 1x pBam_ms6 1x, mis 5 1x, mis study pBam_ms6 1x, mis 5 1	pTps_ABG6	Cm <sup>R</sup> , Km <sup>R</sup> , BSD <sup>R</sup> , mariner tps	(7)	
and mms6 operon and mms6 operon and mms6 operon and mans2 and mans		vector with mamAB, mamGFDC,		
pTps_XYZGm <sup>R</sup> , BSD <sup>R</sup> , mariner Tps vector with mamY, mamX and mamZ(7)Tet-pBan_feoAB1Tc <sup>R</sup> , Ap <sup>R</sup> , feoAB1 operon under the control of PmamH, Tn5 vector(7)pBam_mamGFDCpBam-1, mamGFDC operonThis studypBam_mms6 1xpBam_1, mms6 operonThis studypBam_mms6 2xpBam_mms6 1x, mms6 operonsThis studypBam_fGFDC/fmms6pBam_mms6 1x, mms6 operonsThis studypBam_mms6 2xpBam_mms6 1x, mms6 operonsThis studypBam_mms6 2xpBam_mms6 1x, mms6 operonsThis studypBam_mms6 2xpBam_mms6 1x, mms6 operonsThis studypBam_fGFDC/GmpBam_mms6 1x, for flox66This study		and mms6 operon		
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lox71_Gmr_lox66pBam_mms6/GmpBam_mms6 1x,This studylox71_Gmr_lox66	pBam_GFDC/ <i>Gm</i>	pBam_ <i>mamGFDC</i> ,	This study	
pBam_mms6/GmpBam_mms6 1x,This studylox71_Gmr_lox66		lox71_Gm <sup>r</sup> _lox66		
lox71_Gm <sup>r</sup> _lox66	pBam_ <i>mms6</i> /Gm	pBam_ <i>mms6</i> 1x,	This study	
		lox71_Gm <sup>r</sup> _lox66		

**Supplementary Table S1**: Strains and plasmids used in this study.

Strain	Revealed insertion site/s of	Predicted name or function
	operon copies (gene name)	of the encoded protein
2xGFDCop	amb3829 homolog	Flagellar protein FlbT
2xmms6op	mgr0892	Hemolysin
		activation/secretion protein
2xmms6op+2xGFDC	mgr2596	Nitrilase/cyanide hydratase
		and apolipoprotein N-
		acyltransferase
3x <i>mms6</i> op	mgr1078	AMP fatty acid ligase
4x <i>mms6</i> op	mgr1078	AMP fatty acid ligase;
	mgr3739	TerC-like integral
		membrane protein
<i>5xmms6</i> op	mgr1078	AMP fatty acid ligase;
	mgr3739	TerC-like integral
	mgr1637	membrane protein;
		Methyl-accepting
		chemotaxis protein
2x <i>mamAB</i> op	mgr2709	molecular chaperone
		distantly related to HSP70-
		fold metalloproteases
3x <i>mamAB</i> op	mgr2709	Molecular chaperone
	mar 3006	distantly related to HSP70-
	ingi 5070	fold metalloproteases;
		NADPH-dependent
		glutamate synthase beta

		chain and related oxidoreductases
2xABG6Xop	mgr2922	Hypothetical protein;
	mgr0484	Hypothetical protein
2xABG6Xop+2xfeo	mgr2922	Hypothetical protein;
	mgr0484	Hypothetical protein;
	mgr2581	Membrane or secreted
		protein

Supplementary Table S2: Transposon insertion sites in generated

overexpression strains identified by genome sequencing.

## **Supplementary Figures**



**Figure S1.** Transmission electron micrographs of mutants 3xmms6 op and 4xmms6 op compared to IK-1. Scale bar = 1  $\mu$ m.



**Figure S2.** Transmission electron micrographs of 2*xmamAB*op, illustrating the phenotypic heterogeneity of magnetosome formation found in this mutant. (**a**) Cell with increased numbers of regular-sized magnetosomes. (**b**) Cell with increased number of magnetosomes with aberrant crystal sizes and intracellular localization.



Figure S3. Proteomic analysis of magnetosomes from 2*xmamAB*op. (a) 1D
SDS-PAGE of Coomassie blue stained proteins, which were solubilized from isolated magnetosome particles of IK-1 and 2*xmamAB*op. Bands of size of
MamM (34 kDa), MamA (24 kDa) and MamC (12 kDa) are indicated (arrows).
(b) Immnuodetection of MamM, MamA and MamC in blotted magnetosome membrane fractions from IK-1 and 2*xmamAB*op. Respective protein bands of strain IK-1 were assigned to 100%.



**Figure S4.** Magnetosome size distributions of the insertion mutant 3*xmms6*op,

2x*ABG6X*op and the parental strain IK-1.

## **Supplementary References**

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organism by transfer of bacterial magnetosome gene clusters. Nature Nanotech **9**:193-197.