Table S1 Primers used in this study

Published Name	Plasmid	Primer Sequences (5'-3')
For construction of the GenR expression plasmid		
ncgl2921e1	pZWHJ003	CGCGGATCCGATAACGTCGCCCCCACC
ncgl2921e2		CCCAAGCTTTCACCCTTTTTCGGGCACTC
ncgl2921e3	pZWHJ001	CCCAAGCTTAAAGGAGGACAACCGTGATTATGGATAACGTCGCC
ncgl2921e4		CGCGGATCCTCACCCTTTTTCGGGCACTC
laczf	pZWHJ002	CCCAAGCTTCAGCTATGACCATGATTACGG
laczr		TTGGGCGCCCTTACGCGAAATACGGGCAG
ptacr3	pZWHJ005	TGCTCTAGATATCGACTGCACGGTGCAC
ptacr4		TGCTCTAGATTCTGTTTCCTGTGTGAAATTG
For RT-PCR analysis		
prgenMF01	MFp	CATGAGGTTGCACAGTGCGATG
prgenMF02		TGGCGACGTCATTGTCACCG
prgenDF01	DFp	GCTGGAACTACTGCATCTAGC
prgenDF02		GAATATCGTCGCTGGCTCTGAC
prgenRD01	RDp	CAATCCCACTTGTGTGCCAC
prgenRD02		TATGCGGGATCTGAACAAGGC
prgenKH01	KHp	TCATTGCAGCTGTCGCCAAC
prgenKH02		AGCGCAAGTGCACCTGCTGC
For RT-qPCR analysis		
ptgenIKL01	DFM	ATGGGATATCGAGCCCGTCTAG
pgenDFM01		TGTTATCGAAGGCGAAGGCG
ptgenR06	R-Wild	TGGAAGGTAGGTGCGGGAC
ptgenR07		TTGCTGCTCCGTGACTCTGG
ptgenR03	R-mutant	TCGGGCACTCGGTAATCAGC
ptgenR10		CCCGAAAGAATTTCTAAGCTC
ptgenTX03	KH	GCCGAACTCATAACCTGCAG
pgenKH01		TGAGCCAGCAGGTTTCAAGG
pcg16S05	16S rDNA	GAGGAACACCAATGGCGAAG
pcg16S06		CGGCACAGAAGTCGTGGAAG
For construction of the promoter-cloning plasmids		
pgenDFM01	pZWHJ006 (DFMa)	CGCGGATCCACTCAACGATGTGGGTGATG
pgenDFM02		CCCAAGCTTCAGCTCTGCCTGCTCTTCTG
pgenR01	pZWHJ007 (Ra)	CGCGGATCCTCGCCATGCCAAAGAACG
pgenR02		CCCAAGCTTGCACCGGAAATGGTCAAAC
pgenKH01	pZWHJ008 (KHa)	CCCAAGCTT GCCAATGAGCACCGCAGCCAAG
pgenKH02		CGCGGATCCTGGAAGGTAGGTGCGGGAC

For S1 Nuclease protection mapping and DNase I footprinting of *genDFM*, *genR* and *genKH*

pegenDFM01 (DFM up)	DFMb	TGCTTGACGTGTTCAGTTGC
prgenRD02 (DFM down)		TATGCGGGATCTGAACAAGGC
pegenR01 (R up)	Rb	TGAGCTGCAATGCAATGTCG
pgenR01 (R down)		CGCGGATCCTCGCCATGCCAAAGAACG
pegenKH04 (KH up)	KHb	GCCAATGAGCACCGCAGCCAAG
pgenKH02 (KH down)		CGCGGATCCTGGAAGGTAGGTGCGGGAC

For Primer extension and DNA sequencing ladder of *genDFM*, *genR* and *genKH*

pegenDFM01		TGCTTGACGTGTTCAGTTGC
pegenR01		TGAGCTGCAATGCAATGTCG
pegenKH04		GCCAATGAGCACCGCAGCCAAG

For EMSA

pgenDFM04	DFMan	CCCAAGCTTGCGCCCATTGTTGGAGTCC
pgenDFM09		CGCGGATCCATGGGGGGAATTTTCAGAGCTG
pgenR04	R-KHan	CCCAAGCTTGGCGACGTTATCCATAATC
pgenKH07		CCCAAGCTTGCCAATGAGCACCGCAGCCAAG
pgenDFM10	DFMan01	CGCGGATCCGATTCCACATAGCGGAATTATC
pgenDFM12		CCCAAGCTTCTGGAGTTGCGGGTGGGACTTC
pgenDFM13	DFMan01m	CGCGGATCCGCCGTTACATAGCTTGCCTATC
pgenDFM12		CCCAAGCTTCTGGAGTTGCGGGTGGGACTTC
pgenDFM11	DFMan02	CCCAAGCTTTAAGTATTCCCCTCAGGAAAC
pgenDFM01		CGCGGATCCACTCAACGATGTGGGTGATG
pgenDFM14	DFMan02m	CCCAAGCTTTAAGT GGCAACCTCAAACGGC
pgenDFM01		CGCGGATCCACTCAACGATGTGGGTGATG
pgenR04	R-KHan	CCCAAGCTTGGCGACGTTATCCATAATC
pgenKH07		CCCAAGCTTGCCAATGAGCACCGCAGCCAAG
pgenR08	R-KHan01, R-KHan01m	CCCAAGCTTGAGCCAAGTTACAATCAAAG
pgenR09		CGCGGATCCAAACCCCGGTAGACCAGCATTG
pgenKH08	R-KHan02, R-KHan02m	CGCGGATCCCACCTCGATTATGTGTTTATGAC
pgenKH10		CCCAAGCTTGGGCCGATTGGACGGTGCC

For mutated GenR binding sites

pDFMnmut01	pZWHJ009	GTTACATAGCTTGCCTATCTTGAGTCACCTTTCAAAGC
pDFMnmut02		GGCAAGCTATGTAACGGCTAAGTATTCCCCTCAGGAAACG
pDFMnmut03	pZWHJ010	CCGTTTGAGGTTGCCACTTAGATTCCACATAGCGG
pDFMnmut04		GGCAACCTCAAACGGCGGGGGTGTGACAGCTCTG
pDFMnmut04	pZWHJ011	GGCAACCTCAAACGGCGGGGGTGTGACAGCTCTG
pDFMnmut05		CCGTTTGAGGTTGCCACTTAGCCGTTACATAGCTTGC
pR-KHnmut01	pZWHJ012 and	GTTGCTATCTTTGCCGAGTGATTATGGATAACGTC
pR-KHnmut02	pZWHJ013	GGCAAAGATAGCAACGGAATCCCTTTGATTGTAACTTGG
pR-KHnmut03	pZWHJ014 and	GTTGGTGCGTTTGCCGTCATAAACACATAATCGAGG
pR-KHnmut04	pZWHJ015	GGCAAACGCACCAACGGCGGGAGGACTTGTGACAG

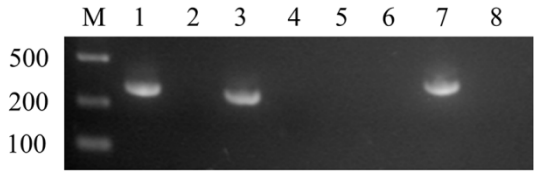

FIG S1 Transcriptional analysis of the *gen* cluster of *C. glutamcium* by RT-PCR. Lanes 1, 3, 5, and 7 show the amplified DNA fragments, here called MFp, DFp, RDp, and KHp in Fig. 1B. Lanes 2, 4, 6, and 8 show their corresponding negative controls without reverse transcriptase. No products were detected in controls and RDp amplification.

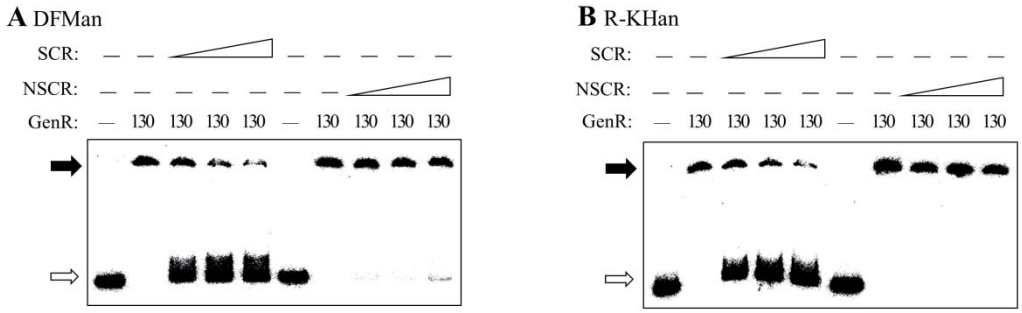

FIG S2 Electrophoretic mobility shift assays for determination of GenR binding sites upstream of *genDFM*, *genR*, and *genKH* operons. A and B. Competition assays using unlabeled specific competitor (SCR) and non-specific competitor (NSCR) DNA. Labeled probe and unlabeled competitor of 25-fold, 50-fold, and 100-fold more in amount were incubated with 130nM His_6-GenR and 300 nM 3-HBA for 30 min at 25°C. Each lane contained 0.5 ng (0.3-0.4nM) of ^{32}P-labeled DFMan and R-KHan probes. The free probes are indicated by open arrows and the retarded DNA fragments by solid arrows.

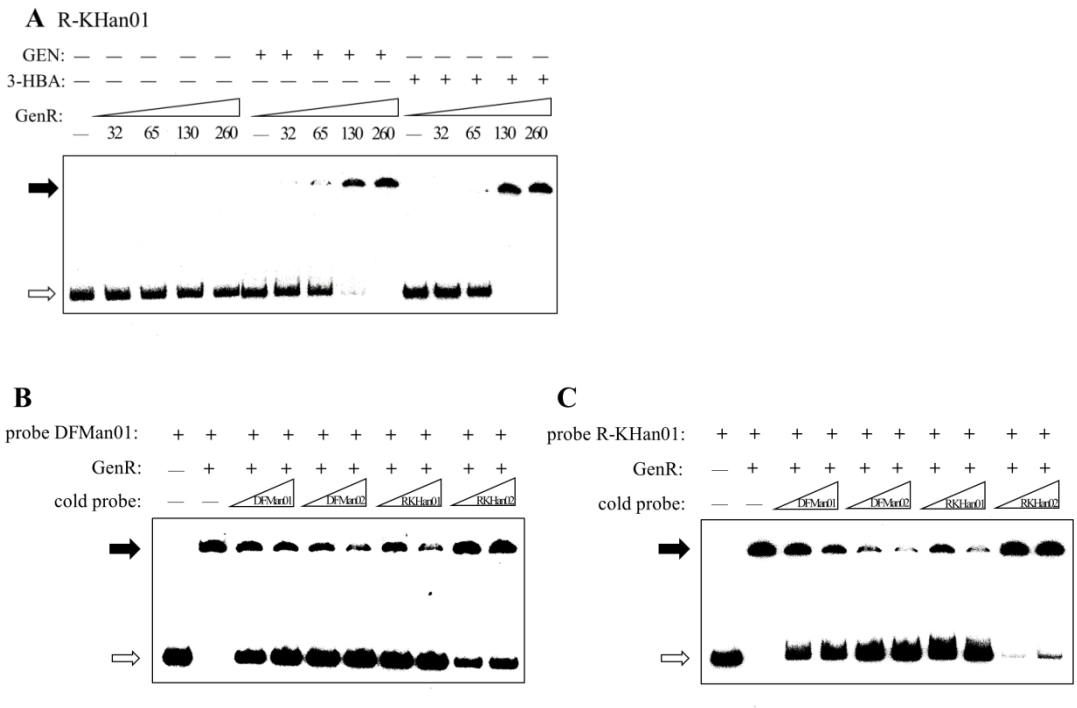

FIG S3 EMSAs for determination of GenR binding sites. A: Effects of 3-HBA and GEN on the binding affinity of GenR for the site R-KH01. The concentrations (nM) of purified His_6-GenR are indicated by numbers under parentheses, with 300 nM GEN and 3-HBA (+) or without (-). B and C: Comparison of the relative affinity of GenR to the binding sites DFMan01 and R-KHan01. Labeled probe and the unlabeled competitors were incubated with 130 nM His_6-GenR and 300 nM 3-HBA for 30 min at 25°C. The free probes are indicated by open arrows and the retarded DNA fragments are indicated by solid arrows.