

Eukaryotic-like gephyrin and cognate membrane receptor coordinate corynebacterial cell division and polar elongation

In the format provided by the
authors and unedited

This PDF file includes:

Figures S1 to S3

Tables S2, S5 and S6

Supplementary References

Note: Tables S1, S3 and S4 are provided separately as an excel file

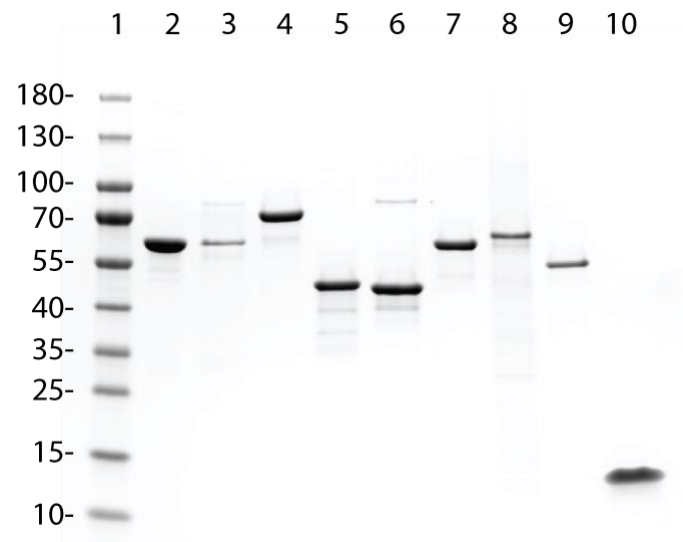
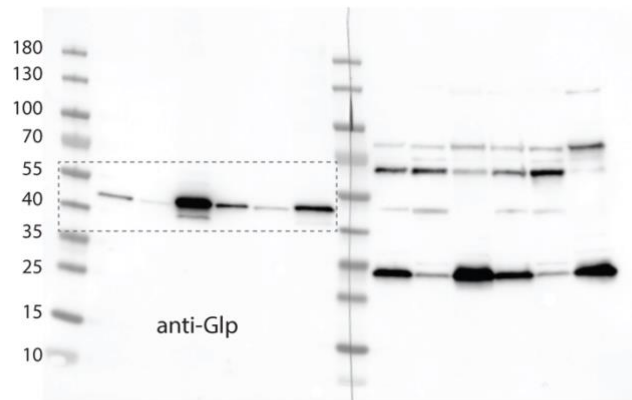
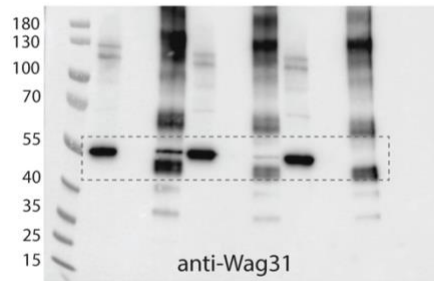


Figure S1. SDS-PAGE on a 4-20% polyacrylamide gel of all purified recombinant proteins used in this work. Lane 1: Molecular weight ladder (kDa); lane 2: His-Sumo-GLP (56.3 kDa); lane 3: His-Sumo-GLP Δ loop (55.1 kDa); lane 4: His-Sumo-FtsZ (59.2 kDa); lane 5: GLP (44.2 kDa); lane 6: GLP Δ loop (43 kDa); lane 7: FtsZ (47.2 kDa); lane 8: His-GLPR (40.7 kDa); lane 9: Wag31 (38.7 kDa); lane 10: Wag31₁₋₆₁ (7.1 kDa). Equivalent migration profiles have been obtained at least three times.

Corresponds to Figure 3c



Corresponds to Figure 4g



Corresponds to Figure 4g

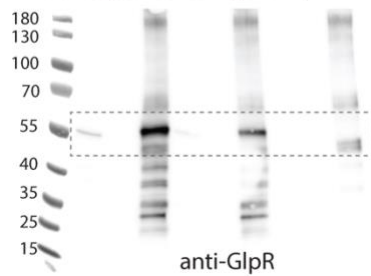


Figure S2. Full uncropped Western Blots of all cropped analyses shown in this work. The boxes correspond to the crops used in the named figures. In Figure 4g, background signals in elution fractions corresponds to the anti-GLPR rabbit antibodies used for the co-IP, which are recognized by the secondary anti-rabbit antibodies used to reveal the Western Blot. Molecular weight markers (kDa) are shown on the left of each blot.

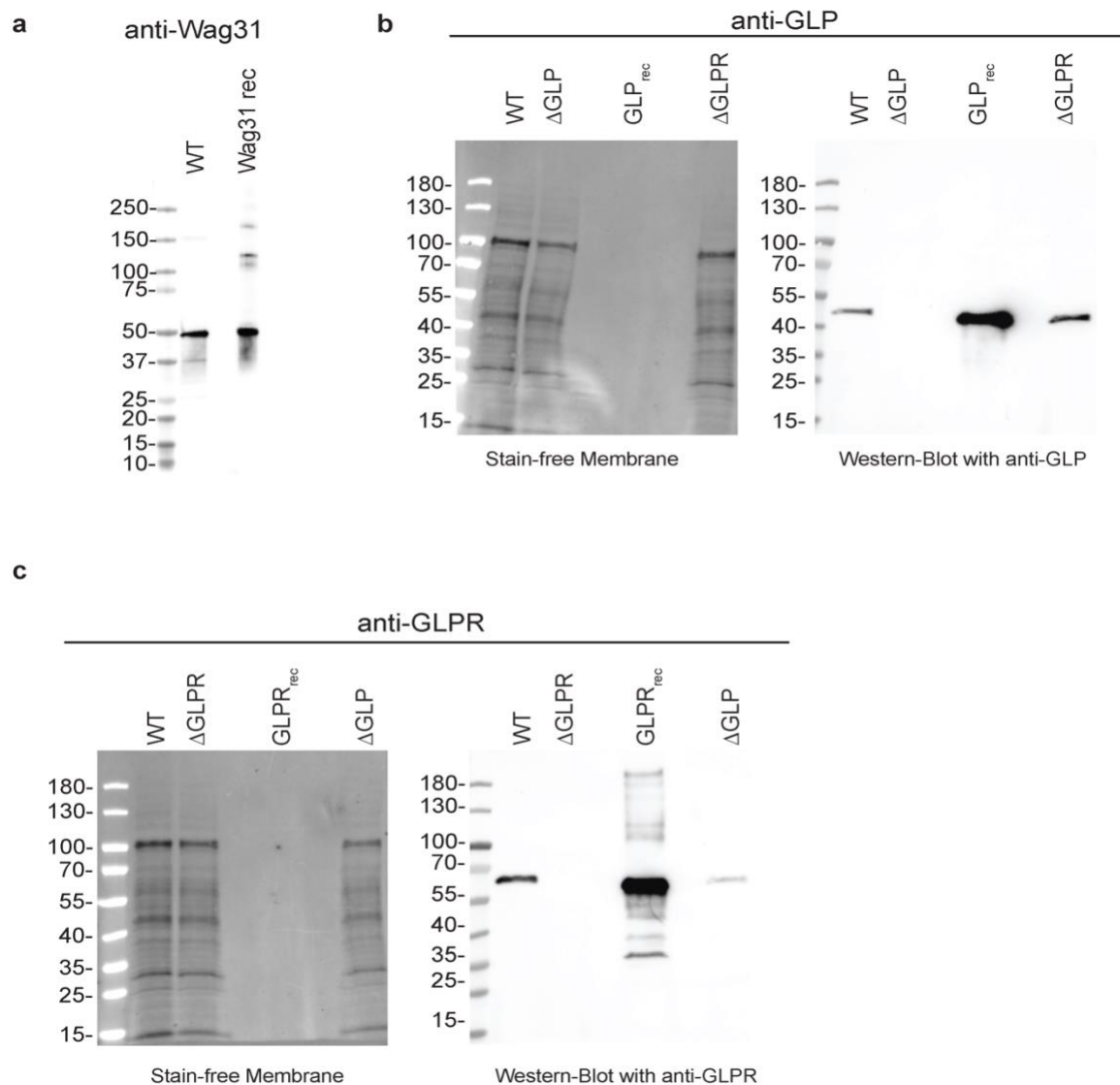


Figure S3. Antibody characterization. (a) Western blot of whole cell extracts (120 μ g) from *Cglu* strain. Wag31 levels were revealed using the α -DivIVA antibody. 10 ng of recombinant Wag31 were loaded as positive control. (b) Stain-free image and Western blot of whole cell extracts (120 μ g) from *Cglu*, *Cglu_Δglp* and *Cglu_Δglpr* strains. Cell lysates were separated on a Criterion TGX Stain-Free SDS gel, transferred onto a Nitrocellulose membrane using the Trans-Blot Turbo Transfer System, and imaged with the ChemiDoc MP imaging system. GLP levels were revealed using the α -GLP antibody. 10 ng of recombinant GLP were loaded as positive control. (c) Stain-free image and Western blot of whole cell extracts (120 μ g) from *Cglu*, *Cglu_Δglp* and *Cglu_Δglpr* strains. Cell lysates were separated on a Criterion TGX Stain-Free SDS gel, transferred onto a Nitrocellulose membrane using the Trans-Blot Turbo Transfer System, and imaged with the ChemiDoc MP imaging system. GLPR levels were revealed using the α -GLPR antibody. 10 ng of recombinant GLPR were loaded as positive control. Equivalent Blots have been obtained at least 3 times. Molecular weight markers (kDa) are shown on the left of each blot.

Table S1. Interactomic data. (a) SepF interactome, (b) differential interactome SepF_{K125E/F131A} vs SepF (or derivatives), (c) GLP interactome in wild-type *Cglu* background, (d) GLP interactome in *Cglu_Δglpr* background.

See separate Excel Table

Table S2. Crystallographic data collection and refinement statistics.

Data collection	GLP Cl₄K₂Pt derivative	GLP	GLP FtsZ-CTD
Synchrotron Beamline	SOLEIL Proxima 1	SOLEIL Proxima 2A	SOLEIL Proxima 2A
Wavelength (Å)	1.0720	0.9801	0.9801
Space group	P4 ₃ 2 ₁ 2	P4 ₃ 2 ₁ 2	P4 ₃ 2 ₁ 2
Cell dimensions <i>a</i> , <i>b</i> , <i>c</i> (Å)	94.46, 94.46, 230.61	94.44, 94.44, 230.56	95.58, 95.58, 229.52
Resolution (Å)	49.2 – 2.35 (2.41 – 2.35) *	49.2 – 2.14 (2.19 – 2.14)	49.2 – 2.68 (2.81 – 2.68)
<i>R</i> _{pim}	0.018 (0.186)	0.023 (0.352)	0.050 (0.296)
<i>I</i> / <i>s(I)</i>	26.8 (3.9)	21.1 (2.2)	14.6 (2.7)
Completeness (%)	99.7 (96.8)	99.7 (96.2)	99.6 (97.1)
CC(1/2)	1.0 (0.92)	1.0 (0.777)	0.997 (0.800)
Multiplicity	26.8 (26.6)	26.4 (25.0)	9.6 (9.7)
Total observations	1197065	1551838	251139
Unique observations	44612 (3156)	58764 (4332)	30746 (3905)
Refinement			
Resolution (Å)		2.14	2.68
No. reflections			
<i>R</i> _{work} / <i>R</i> _{free} (%)		0.191 / 0.223	0.190 / 0.239
No. atoms			
Protein		5823	5959
Ligands/ions		-	-
Solvent		457	234
Average B-factors (Å ²)			
Protein		49	42
Ligand/ions		-	-
Solvent		57	50
R.m.s deviations			
Bond lengths (Å)		0.007	0.004
Bond angles (°)		0.876	0.663
Ramachandran favored (%)		98.0	98.6
Ramachandran outliers (%)		0	0.25
PDB code		8BVE	8BVF

*Values in parenthesis correspond to the highest resolution shell.

Table S3. Taxonomic sampling of Actinobacteria and protein identifiers of GLP, GLPR and MoeA paralogs. Protein identifiers correspond to the NCBI GenBank database. “NA” indicates that the protein was not identified in the corresponding genome.

See separate Excel Table

Table S4. Taxonomic sampling of Bacteria and protein identifiers of MoeA paralogs. Protein identifiers correspond to the NCBI GenBank database. “NA” indicates that the protein was not identified in the corresponding genome.

See separate Excel Table

Table S5. Plasmids and strains used in this study.

Strains	Characteristics	Reference
<i>E. coli</i>		
DH5 α	F- endA1 Φ 80dlacZ Δ M15 Δ (lacZYA-argF)U169 recA1 relA1 hsdR17(rK-mK+) deoR supE44 thi-1 gyrA96 phoA λ -; strain used for general cloning procedures	¹
CopyCutter EPI400	F- mcrA Δ (mrr-hsdRMS-mcrBC) Φ 80dlacZ Δ M15 Δ lacX74 recA1 endA1 araD139 Δ (ara, leu)7697 galU galK λ - rpsL (StrR) nupG trfA tonA pcnB4 dhfr; strain used for general cloning procedures	²
BL21(DE)	F- ompT hsdSB(rB-mB-) gal dcm (DE3); host for protein production	³
<i>C. glutamicum</i>		
ATCC 13032	Biotin-auxotrophic wild type	⁴
Δ GLP	<i>C. glutamicum</i> ATCC13032 derivative with chromosomal deletion of GLP	This work
Δ GLPR	<i>C. glutamicum</i> ATCC13032 derivative with chromosomal deletion of GLPR	This work

Plasmids for <i>C. glutamicum</i> knock out generation		Reference
<i>pK19mobsacB</i>	KanaR; plasmid for allelic exchange in <i>C. glutamicum</i> ; (pK18 oriVEc, sacB, lacZ α)	⁵
pk19- Δ GLP	KanaR; pK19mobsacB derivative for GLP chromosomal deletion	This work
pk19- Δ GLPR	KanaR; pK19mobsacB derivative for GLPR chromosomal deletion	This work

Plasmids for recombinant protein expression in <i>E. coli</i>		Reference
pET-SUMO-FtsZ	KanaR; pET derivate for <i>C. glutamicum</i> FtsZ recombinant expression containing a N-terminal His-tag followed by a SUMO protease cleavage site	⁶
pET-SUMO-GLP	KanaR; pET derivate for <i>C. glutamicum</i> GLP recombinant expression containing a N-terminal His-tag followed by a SUMO protease cleavage site	This work
pET-SUMO-GLP Δ Loop	KanaR; pET derivate for <i>C. glutamicum</i> GLP Δ Loop mutant recombinant expression containing a N-terminal His-tag followed by a SUMO protease cleavage site	This work
pET-SUMO-Wag31	KanaR; pET derivate for <i>C. glutamicum</i> Wag31 recombinant expression containing a N-terminal His-tag followed by a SUMO protease cleavage site	This work
pET-His-TEV-Wag31	KanaR; pET derivate for <i>C. glutamicum</i> Wag31 recombinant expression containing a N-terminal His-tag followed by a TEV protease cleavage site	This work
pET-His-TEV-Wag31 ₁₋₆₁	KanaR; pET derivate for <i>C. glutamicum</i> N-terminal DivIVA domain of Wag31 (1-61) recombinant expression containing a N-terminal His-tag followed by a TEV protease cleavage site	This work
pET-SUMO-GLPR _{IDR1}	KanaR; pET derivate for the recombinant expression of GLPR IDR1 domain (24-214) containing a N-terminal His-tag followed by a SUMO protease cleavage site.	This work
pET-His-GLPR	AmpR; pET derivate for the recombinant expression of GLPR containing a N-terminal His-tag followed by a TEV protease cleavage site	This work

pET-GLPR-His	KanaR; pET derivative for the recombinant expression of GLPR containing a C-terminal His-tag.	This work
--------------	---	-----------

Plasmids for recombinant protein expression in <i>C. glutamicum</i>.		Reference
<i>pTGR5</i>	KanaR; <i>E. coli/C. glutamicum</i> shuttle vector for regulated gene expression of EGFP under control of tac promoter (Ptac lacI ColE1 oriVEc pGA1 oriVCg)	⁷
<i>pUMS3</i>	KanaR; <i>pTGR5</i> derivative in which <i>Ptac</i> was exchanged by <i>PgntK</i> promoter to control the expression of the EGFP protein	⁶
<i>pUMS3-PgntK</i>	KanaR; <i>pUMS3</i> derivative containing <i>PgntK</i> promoter (empty plasmid)	This work
<i>pUMS3-sepF-scarlet</i>	KanaR; <i>pUMS3</i> derivative for expression of SepF-Scarlet under control of <i>PgntK</i> promoter	⁶
<i>pUMS3-sepF_{K125/F131A}-scarlet</i>	KanaR; <i>pUMS3</i> derivative for expression of SepF _{K125E-F131A} -Scarlet mutant under control of <i>PgntK</i> promoter	⁶
<i>pUMS3-Scarlet-I</i>	KanaR; <i>pUMS3</i> derivative for expression of Scarlet-I fluorescent protein under control of <i>PgntK</i> promoter	⁶
<i>pUMS3-GLP</i>	KanaR; <i>pUMS3</i> derivative for expression of GLP under control of <i>PgntK</i> promoter	This work
<i>pUMS3-mNeon-GLP</i>	KanaR; <i>pUMS3</i> derivative for expression of mNeonGreen-GLP under control of <i>PgntK</i> promoter	This work
<i>pUMS3-mNeon-GLP_{ΔLoop}</i>	KanaR; <i>pUMS3</i> derivative for expression of mNeonGreen-GLP _{ΔLoop} under control of <i>PgntK</i> promoter	This work
<i>pUMS3-GLPR-mNeon</i>	KanaR; <i>pUMS3</i> derivative for expression of GLPR-mNeonGreen under control of <i>PgntK</i> promoter	This work
<i>pUMS3-GLPR</i>	KanaR; <i>pUMS3</i> derivative for expression of GLPR under control of <i>PgntK</i> promoter	This work
<i>pUMS3-GLPR_{ΔIDR2} (1-266)</i>	KanaR; <i>pUMS3</i> derivative for expression of GLPR with a deletion of the C-terminal IDR2 region under control of <i>PgntK</i> promoter	This work
<i>pUMS3-mNeon-MoeA1</i>	KanaR; <i>pUMS3</i> derivative for expression of mNeonGreen-MoeA1 under control of <i>PgntK</i> promoter	This work
<i>pUMS3-mNeon-MoeA3</i>	KanaR; <i>pUMS3</i> derivative for expression of mNeonGreen-MoeA3 under control of <i>PgntK</i> promoter	This work

Table S6. Oligonucleotide primers used in this study.

Oligonucleotide	Sequence 5' -->3' and properties ^a
Plasmids for <i>C. glutamicum</i> knock out generation	
pk19-ΔGLP	
OligoAS_p68	TGAGCGGATAACAATTCAC
OligoAS_p69	CAATTCCACACAACATACG
OligoAS_p207	TGTTGTGTGGAATTG CTTGACACTTTGAGCGTTCTTC
OligoAS_p208	TTACGCATCGAATAC GGACCTCCTAATCGGAAC
OligoAS_p209	CCGTATTCGATGCGTAATGCACCGTC
OligoAS_p210	AATTGTTATCCGCTCAG CAGATTCTAATGAGATAGCCTTCTGG
pk19-ΔGLPR	
OligoAS_p68	TGAGCGGATAACAATTCAC
OligoAS_p69	CAATTCCACACAACATACG
OligoAS_p216	TGTTGTGTGGAATTG ATAAGGAATTCCTCAAGCCCGT
OligoAS_p217	CTTACCCTGTGGCTA ACCTTCCCGTACGGGTGC
OligoAS_p218	GTTAGCCACAGGGTAAGGTTTCG ACTA
OligoAS_p219	AATTGTTATCCGCTCA CTGGGAAGTCATACTTCTGTCCAC
Oligonucleotides for KO screening	
OligoAS_p211	CCTATCGATGAGCACGTGAA
OligoAS_p212	ATGCTTCTCCAGCCTTAGCA
OligoAS_p220	GCACCTATTGGCAGGATTGT
OligoAS_p221	TTCCACATAACCGAGGAAC

Plasmids for recombinant protein expression in <i>E. coli</i>	
pET-SUMO-GLP	
OligoAS_P1	AGATCCGGCTGCTAACA AGCCCGAAAG
OligoAS_P2	GAGGCTCACCGCGAAC AGATTGGTGGC
OligoAS_p169	CGAACAGATTGGTGGC GTGCGATCAGTCGAGCAAC
OligoAS_p170	GTTAGCAGCCGATCTCT ATCGACCTGGGCAAGGAA
pET-SUMO-GLP_{ΔLoop}	
OligoMM_372	CATCAGGTCCAGGCTCGGTGTGGAGGCTTTG GGTGGTGCAACGGGCGCACCATCGCACCTATTGGCA
OligoMM_373	CAAAGCCTCCACACCGAGCCTGGACCTGATG AAACCTTTTCGACCCGCCACAGACACAAC

pET-SUMO-Wag31	
OligoMM_378	GCCACCAATCTGTTGCGGGTGAGCCTC
OligoMM_379	AGATCCGGCTGCTAACAAAGCCCGAAAGGAAG
OligoMM_403	TCACCGCGAACAGATTGGTGGCATGCCGTTGACTCCAGCTGATG
OligoMM_404	GGCTTTGTTAGCAGCCGGATCTTTACTCACCAGATGGCTTGTGTTGGTTGGTG
pET-His-TEV-Wag31₁₋₆₁	
P1_JP	ATATGTTATTACGCAACCTGCGCCTCCAG
P2_JP	TAATAACATATGGCTAGCATGACTGGTGGAC
pET-SUMO-GLPR_{IDR1}	
OligoMM_392	ATGTTGCGCCGCCAGCGCTAATTAACCTAGGCTGCTGCCAC
OligoMM_393	GCAATGGGCTTTTGGCCTCGGCCACCAATCTGTTGCGGGT
OligoMM_394	ACCGCGAACAGATTGGTGGCCGAGGCCAAAAGCCCATTGC
OligoMM_395	GTGGCAGCAGCCTAGGTTAATTAGCGCTGGCGGCGAACAT
pET-GLPR-His	
OligoMM_389	CTTTAAGAAGGAGATATACCATGTCCGGAATCCTTGTGATCG
OligoMM_390	GTGGCAGCAGCCTAGGTTAATCAGTGGTGGTGGTGGTGGT
OligoMM_388	ATCACAAGGATTCCGGACATGGTATATCTCCTTCTTAAAGTTAAACAA
OligoMM_391	ACCACCACCACCACCACTGATTAACCTAGGCTGCTGCCAC
pET-His-GLPR	
OligoPB_9	GGATCCGGCAGCTGGAGCCA
OligoPB_10	TCCCTGAAAATACAGTTTTCCGATCC
OligoMM_399	GGATCGGAAAACCTGTATTTTCAGGGAATGTCCGGAATCCTTGTGATCGGC
OligoMM_400	TGGCTCCAGCTGCCGGATCCTTAGCTCACGCGACGCTGACCCAG

Plasmids for recombinant protein expression in <i>C. glutamicum</i>.	
pUMS3-mNeon-GLP	
OligoMM_178	ATGGTCTTATCCTTTCTTTGGTGGC
OligoMM_179	AGCGGCCGCTTAAGGTAC
OligoMM_286	CAAAGAAAGGATAAGACCATATGGGTCATCACCATCATCATCACATGGTGTCCAAGGGCG AAG
OligoMM_306	TGAGCCAGATCCCTTGTACAGTTCATCCATGCCCATC
OligoMM_305	AACTGTACAAGGGATCTGGCTCAATGCGATCAGTCGAGCA
OligoMM_311	GTACCTTAAGCGGCCGCTCTATCGACCTTGGGCAAGGAAGA

pUMS3-mNeon-GLP_{ΔLoop}	
OligoMM_372	CATCAGGTCCAGGCTCGGTGTGGAGGCTTTG GGTGGTGCAACGGGGCGCACCATCGCACCTATTGGCA
OligoMM_373	CAAAGCCTCCACACCGAGCCTGGACCTGATG AAACCTTTTCGACCCGCCACAGACACAAC
pUMS3-GLPR-mNeon	
OligoMM_178	ATGGTCTTATCCTTTCTTTGGTGGC
OligoMM_353	GGAAGCGGCAGCATGGTGTCCAAGGGCGAAG
OligoMM_354	CGCCACCAAAGAAAGGATAAGACCATATG TCCGAATCCTTGTGATCGGCCTGATTGTGGTGGTGTGGCTTGTTGT
OligoMM_355	GACACCATGCTGCCGCTTCCG CTCACGCGACGCTGACCCAGGTGTGCAATGTTTCGACGTGGCTCCTCGTAG
pUMS3-GLPR	
OligoMM_374	GGACACCATGCTGCCGCTTTAGCTCACGCG ACGCTGACCCAG
OligoMM_375	CGCGTGAGCTAAAGCGGCAGCATGGTGTCCA AGGGCGAAGAG
pUMS3-GLPR_{ΔIDR2}	
OligoMM_396	GCTCTTCGCTAACGTCGAATCCG CAGGCTCCGCCGCTC
OligoMM_397	CGGATTCGACGTTAGCGAAGAGC ATTCTCCTCACGAACCTG
pUMS3-mNeon-MoeA1	
OligoMM_179	AGCGGCCGCTTAAGGTAC
OligoMM_306	TGAGCCAGATCCCTTGTACAG TTTCATCCATGCCCATC
OligoMM_358	TGTACAAGGGATCTGGCTCAATGTCTCG TTCCGGGAGCAAC
OligoMM_359	GTACCTTAAGCGGCCGCTTTAG TTGAATGGGTAAATCTTAACGATGTCGTTTTCTC
pUMS3-mNeon-MoeA3	
OligoMM_179	AGCGGCCGCTTAAGGTAC
OligoMM_306	TGAGCCAGATCCCTTGTACAG TTTCATCCATGCCCATC
OligoMM_360	GAACTGTACAAGGGATCTGGCTCAAT GGCACAGCAACGCAGCG
OligoMM_361	GTACCTTAAGCGGCCGCTTTA CATTCTCCCAGCACAAACATCAACCAGAC
pUMS3-GLP	
OligoMM_178	ATGGTCTTATCCTTTCTTTGGTGGC
OligoMM_179	AGCGGCCGCTTAAGGTAC
OligoMM_310	CCACCAAAGAAAGGATAAGACCATATG CGATCAGTCGAGCAACAGC
OligoMM_311	GTACCTTAAGCGGCCGCTCTAT CGACCTTGGGCAAGGAAGA

^aOverlaps for Gibson assembly are written in bold letters.

Supplementary References:

1. Hanahan, D. Studies on transformation of *Escherichia coli* with plasmids. *J Mol Biol* 166, 557–580 (1983).
2. D, H. *Epicentre Forum* 11, 6 (2004).
3. Studier, F. W. & Moffatt, B. A. Use of bacteriophage T7 RNA polymerase to direct selective high-level expression of cloned genes. *J Mol Biol* 189, 113–130 (1986).
4. Shimono, S. K. S. U. M. Studies on the amino acid fermentation. *J Gen Appl Microbiol* 3, (1957).
5. Schäfer, A. *et al.* Small mobilizable multi-purpose cloning vectors derived from the *Escherichia coli* plasmids pK18 and pK19: selection of defined deletions in the chromosome of *Corynebacterium glutamicum*. *Gene* 145, 69–73 (1994).
6. Sogues, A. *et al.* Essential dynamic interdependence of FtsZ and SepF for Z-ring and septum formation in *Corynebacterium glutamicum*. *Nat Commun* 11, 1641 (2020).
7. Ravasi, P., Peiru, S., Gramajo, H. & Menzella, H. G. Design and testing of a synthetic biology framework for genetic engineering of *Corynebacterium glutamicum*. *Microb Cell Fact* 11, 147–147 (2012).