Supporting Information

Development of a genetically-encoded biosensor for reporting the methyltransferase-dependent biosynthesis of semi-synthetic macrolide antibiotics

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Supplemental Methods

Supplementary Table S1. Sequences of DNA constructs. RBS for each gene of interest is underlined. The promoter region for each gene of interest is bold italicized. Mutations are bolded and underlined.

Construct Name	**DNA Sequence**
pMLGFP	GGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGA ACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAG TCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAG GTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCC TTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAG TATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCAC CGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATC TTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCT TCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACC AATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGA TAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGA TTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCT ATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCA TCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCC ATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCAT GGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCA AGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAACACGGGATAATACCGCGCCACATAG CAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCC AGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAAC AGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATAT TATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAAAAGAGTT TGTAGAAACGCAAAAAGGCCATCCGTCAGGATGGCCTTCTGCTTAATTTGATGCCTGGCAGTTTATGGCGGGCGTCCTG CCCGCCACCCTCCGGGCCGTTGCTTCGCAACGTTCAAATCCGCTCCCGGCGGATTTGTCCTACTCAGGAGAGCGTTCACC GACAAACAACAGATAAAACGAAAGGCCCAGTCTTTCGACTGAGCCTTTCGTTTTATTTGATGCCTGGCAGTTCCCTACTC TCGCATGGGGAGACCCCACACTACCATCGGCGCTACGGCGTTTCACTTCTGAGTTCGGCATGGGGTCAGGTGGGACCA CCGCGCTACTGCCGCCAGGCAAATTCTGTTTTATCAGACCGCTTCTGCGTTCTGATTTAATCTGTATCAGGCTGAAAATCT TCTCTCATCCGCCAAAACAGCCAAGCTGGAGACCGTTTAAACTCAATGATGATGATGATGATGGTCGACGGCGCTATTC AGATCCTCTTCTGAGATGAGTTTTTGTTCGGGCCCAAGCTTATTTGTAGAGCTCATCCATGCCATGTGTAATCCCAGCAG CAGTTACAAACTCAAGAAGGACCATGTGGTCACGCTTTTCGTTGGGATCTTTCGAAAGGGCAGATTGTGTCGACAGGTA

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pSense- M9C4-E7- MphA	GGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGA ACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAG TCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAG GTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCC TTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAG TATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCAC CGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATC TTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCT TCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATCCATGGATATGAGTAAACTTGGTCTGAC AGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTC GTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCG GCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCA TCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCT ACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACAT GATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTT ATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGT ACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAACACGGGATAATACCGC GCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTG TTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGA GCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTT TTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACA AAAAGAGCATGCGTTTGTAGAAACGCAAAAAGGCCATCCGTCAGGATGGCCTTCTGCTTAATTTGATGCCTGGCAGTTT ATGGCGGGCGTCCTGCCCGCCACCCTCCGGGCCGTTGCTTCGCAACGTTCAAATCCGCTCCCGGCGGATTTGTCCTACTC

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pCOLADuet -EryG	AAGTCGAACAGAAAGTAATCGTATTGTACACGGCCGCATAATCGAAATTAATACGACTCACTATAGGGGAATTGTGAGC GGATAACAATTCCCCATCTTAGTATATTAGTTAAGTATAAGAAGGAGATATACATATGGCAGATCTCAATTGGATATCG GCCGGCCACGCGATCGCTGACGTCGGTACCCTCGAGTCTGGTAAAGAAACCGCTGCTGCGAAATTTGAACGCCAGCAC ATGGACTCGTCTACTAGCGCAGCTTAATTAACCTAGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGG CCTCTAAACGGGTCTTGAGGGGTTTTTTGCTGAAACCTCAGGCATTTGAGAAGCACACGGTCACACTGCTTCCGGTAGT CAATAAACCGGTAAACCAGCAATAGACATAAGCGGCTATTTAACGACCCTGCCCTGAACCGACGACAAGCTGACGACC GGGTCTCCGCAAGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATG TATCCGCTCATGAATTAATTCTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAAT ACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGG TATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGA GAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGC CAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAA TACGCGGTCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAAC AATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCGGGGATCGCAGTGGTGAGTAACCATG CATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTC ATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGAT AGATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAAT CGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGT TATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGCATGCTAGCGCAGAAACGTCCTA GAAGATGCCAGGAGGATACTTAGCAGAGAGACAATAAGGCCGGAGCGAAGCCGTTTTTCCATAGGCTCCGCCCCCCTG ACGAACATCACGAAATCTGACGCTCAAATCAGTGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCC TGATGGCTCCCTCTTGCGCTCTCCTGTTCCCGTCCTGCGGCGTCCGTGTTGTGGTGGAGGCTTTACCCAAATCACCACGT CCCGTTCCGTGTAGACAGTTCGCTCCAAGCTGGGCTGTGTGCAAGAACCCCCCGTTCAGCCCGACTGCTGCGCCTTATCC GGTAACTATCATCTTGAGTCCAACCCGGAAAGACACGACAAAACGCCACTGGCAGCAGCCATTGGTAACTGAGAATTA GTGGATTTAGATATCGAGAGTCTTGAAGTGGTGGCCTAACAGAGGCTACACTGAAAGGACAGTATTTGGTATCTGCGC TCCACTAAAGCCAGTTACCAGGTTAAGCAGTTCCCCAACTGACTTAACCTTCGATCAAACCGCCTCCCCAGGCGGTTTTT TCGTTTACAGAGCAGGAGATTACGACGATCGTAAAAGGATCTCAAGAAGATCCTTTACGGATTCCCGACACCATCACTC TAGATTTCAGTGCAATTTATCTCTTCAAATGTAGCACCTGAAGTCAGCCCCATACGATATAAGTTGTAATTCTCATGTTAG TCATGCCCCGCGCCCACCGGAAGGAGCTGACTGGGTTGAAGGCTCTCAAGGGCATCGGTCGAGATCCCGGTGCCTAAT GAGTGAGCTAACTTACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAA TGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCCAGGGTGGTTTTTCTTTTCACCAGTGAGACGGG CAACAGCTGATTGCCCTTCACCGCCTGGCCCTGAGAGAGTTGCAGCAAGCGGTCCACGCTGGTTTGCCCCAGCAGGCG AAAATCCTGTTTGATGGTGGTTAACGGCGGGATATAACATGAGCTGTCTTCGGTATCGTCGTATCCCACTACCGAGATG TCCGCACCAACGCGCAGCCCGGACTCGGTAATGGCGCGCATTGCGCCCAGCGCCATCTGATCGTTGGCAACCAGCATC

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pSense- M9C4-E7- MphA-EryG	TAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTC CGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCT CCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAAC CCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCT ACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAG TTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAA GCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAC GAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAG TTTTAAATCAATCTAAAGTATCCATGGATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTA TCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTA

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pSense-1	ATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTT TTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTAT AAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCC GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTC

	CAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACC CGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTA CAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGT TACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAG CAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACG AAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGT TTTAAATCAATCTAAAGTATCCATGGATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTAT CTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTAC CATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGC CGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGA GTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGG TATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCT CCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCT CTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCG GCGACCGAGTTGCTCTTGCCCGGCGTCAACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATT GGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCAC CCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAA GGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATT GTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAAAAGAGCATGCGTTTGTAGAAACGCAAAAAG GCCATCCGTCAGGATGGCCTTCTGCTTAATTTGATGCCTGGCAGTTTATGGCGGGCGTCCTGCCCGCCACCCTCCGGGC CGTTGCTTCGCAACGTTCAAATCCGCTCCCGGCGGATTTGTCCTACTCAGGAGAGCGTTCACCGACAAACAACAGATAA AACGAAAGGCCCAGTCTTTCGACTGAGCCTTTCGTTTTATTTGATGCCTGGCAGTTCCCTACTCTCGCATGGGGAGACCC CACACTACCATCGGCGCTACGGCGTTTCACTTCTGAGTTCGGCATGGGGTCAGGTGGGACCACCGCGCTACTGCCGCCA GGCAAATTCTGTTTTATCAGACCGCTTCTGCGTTCTGATTTAATCTGTATCAGGCTGAAAATCTTCTCTCATCCGCCAAAA CAGCCAAGCTGGAGACCGTTTAAACGGGCCCAAGCTTTTTGTAGAGCTCATCCATGCCATGTGTAATCCCAGCAGCAGT TACAAACTCAAGAAGGACCATGTGGTCACGCTTTTCGTTGGGATCTTTCGAAAGGACAGATTGTGTCGACAGGTAATGG TTGTCTGGTAAAAGGACAGGGCCATCGCCAATTGGAGTATTTTGTTGATAATGGTCTGCTAGTTGAACGGAACCATCTT CAACGTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTTTGTCTGCCGTGATGTATACATTGTGTGAGTTAA AGTTGTACTCGAGTTTGTGTCCAAGAATGTTTCCATCTTCTTTAAAATCAATACCCTTTAACTCGATACGATTAACAAGGG TATCACCTTCAAACTTGACTTCAGCACGCGTCTTGTAGGTCCCGTCATCTTTGAAAGATATAGTGCGTTCCTGTACATAAC CTTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATGTGATCCGGATAACGGGAAAAGCATTGAACACCATAGGT CAGAGTAGTGACAAGTGTTGGCCACGGAACAGGTAGTTTTCCAGTAGTGCAAATAAATTTAAGGGTGAGTTTTCCGTTT GTAGCATCACCTTCACCCTCTCCACGGACAGAAAATTTGTGCCCATTAACATCACCATCTAATTCAACAAGAATTGGGAC AACTCCAGTGAAAAGTTCTTCTCCTTTGCTCATACTAGTTTCCTCCTGTTAGCCCACCTAAATGTAACAGTCACGTCGGTT ATATTCAATCCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA TTAATTGCGTTGCGCTCTAGATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCCCCAACCCATACAGAAGGTG

	AACACTGATGCCCCGCCCCAAGCTCAAGTCCGATGACGAGGTACTCGAGGCCGCCACCGTAGTGCTGAAGCGTTGCGG TCCCATAGAGTTCACGCTCAGCGGAGTAGCAAAGGAGGTGGGGCTCTCCCGCGCAGCGTTAATCCAGCGCTTCACCAA CCGCGATACGCTGCTGGTGAGGATGATGGAGCGCGGCGTCGAGCAGGTGCGGCATTACCTGAATGCGATACCGATAG GCGCAGGGCCGCAAGGGCTCTGGGAATTTTTGCAGGTGCTCGTTCGGAGCATGAACACTCGCAACGACTTCTCGGTGA ACTATCTCATCTCCTGGTACGAGCTCCAGGTGCCGGAGCTACGCACGCTTGCGATCCAGCGGAACCGCGCGGTGGTGG AGGGGATCCGCAAGCGACTGCCCCCAGGTGCTCCTGCGGCAGCTGAGTTGCTCCTGCACTCGGTCATCGCTGGCGCGA CGATGCAGTGGGCCGTCGATCCGGATGGTGAGCTAGCTGATCATGTGCTGGCTCAGATCGCTGCCATCCTGTGTTTAAT GTTTCCCGAACACGACGATTTCCAACTCCTCCAGGCACATGCGTAACATAGTATCCAAAATCTAAACCCGTCAAGCCCTC AGGAGTGAATCATGACCGTAGTCACGACCGCCGATACCTCCCAACTGTACGCACTTGCAGCCCGACATGGGCTCAAGCT CCATGGCCCGCTGACTGTCAATGAGCTTGGGCTCGACTATAGGATCGTGATCGCCACCGTCGACGATGGACGTCGGTG GGTGCTGCGCATCCCGCGCCGAGCCGAGGTAAGCGCGAAGGTCGAACCAGAGGCGCGGGTGCTGGCAATGCTCAAGA ATCGCCTGCCGTTCGCGGTGCCGGACTGGCGCGTGGCCAACGCCGAGCTCGTTGCCTATCCCATGCTCGAAGACTCGAC TGCGATGGTCATCCAGCCTGGTTCGTCCACGCCCGACTGGGTCGTGCCGCAGGACTCGGAGGTCTTCGCGGAGAGCTT CGCGACCGCGCTCGCCGCCCTGCATGCCGTCCCCATTTCCGCCGCCGTGGATGCGGGGATGCTCATCCGTACACCGACG CAGGCCCGTCAGAAGGTGGCCGACGACGTTGACCGCGTCCGACGCGAGTTCGTGGTGAACGACAAGCGCCTCCACCG GTGGCAGCGCTGGCTCGACGACGATTCGTCGTGGCCAGATTTCTCCGTGGTGGTGCATGGCGATCTCTACGTGGGCCA TGTGCTCATCGACAACACGGAGCGCGTCAGCGGGATGATCGACTGGAGCGAGGCCCGCGTTGATGACCCTGCCATCGA CATGGCCGCGCACCTTATGGTCTTTGGTGAAGAGGGGCTCGCGAAGCTCCTCCTCACGTATGAAGCGGCCGGTGGCCG GGTGTGGCCGCGGCTCGCCCACCACATCGCGGAGCGCCTTGCGTTCGGGGCGGTCACCTACGCACTCTTCGCCCTCGAC TCGGGTAACGAAGAGTACCTCGCTGCGGCGAAGGCGCAGCTCGCCGCAGCGGAATGAGGTGTGCAGAGTCCCTGCGG CAGGCGACGAACACGACCGTCGTCGATTAGTACCGGAGATCCTCCACCCGAAATTCTAAGGAGGAGACCATATGAGCG TGAAGCAGAAGTCAGCGTTGCAGGACCTGGTCGACTTCGCCAAGTGGCACGTGTGGACCAGGGTGCGGCCGTCCAGC CGTGCGCGCCTGGCCTACGAGCTGTTCGCCGACGACCACGAGGCCACGACCGAGGGCGCCTACATCAACCTCGGCTAC TGGAAGCCCGGGTGCGCCGGCCTGGAGGAGGCCAACCAGGAGCTGGCGAACCAGCTCGCCGAGGCCGCGGGGATCA GCGAGGGCGACGAGGTGCTCGACGTCGGGTTCGGGCTCGGCGCGCAGGACTTCTTCTGGCTCGAGACGCGCAAGCCG GCCAGGATCGTCGGCGTCGACCTGACCCCGAGCCACGTCCGCATCGCCTCCGAGCGCGCGGAGCGCGAGAACGTGCA GGACCGCCTGCAGTTCAAGGAGGGCTCGGCGACCGACCTGCCCTTCGGCGCGGAGACCTTCGACCGCGTCACCTCCCT GGAGTCGGCCCTGCACTACGAGCCGCGGACCGACTTCTTCAAGGGCGCGTTCGAGGTGCTCAAGCCCGGAGGCGTGCT GGCCATCGGCGACATCATCCCGCTCGACCTGCGCGAGCCCGGTTCCGACGGACCGCCGAAGCTGGCGCCGCAGCGGTC GGGATCGCTGTCCGGCGGCATCCCGGTGGAGAACTGGGTGCCCCGCGAGACCTACGCCAAGCAGCTCCGCGAAGCGG GCTTCGTCGACGTCGAGGTGAAGTCGGTCCGCGACAACGTGATGGAGCCCTGGCTGGACTACTGGCTGCGCAAGCTGC AGGACGAGTCGTTCAAGAAGAGCGTGAGCAGGCTCTTCTACAGCCAGGTCAAGCGGTCGCTGACCAGCGACTCGGGC ATGAAGGGCGAGCTGCCCGCGCTCGACTTCGTGATCGCCTCAGCCCGCAAGCCCGGCGCGTAGGGATCCGAATTCGGT ACCTACGGTCGGTGGTATCGAAGTCTTGATCACTGTACACTAGAGGTAATACGGTTATCCACAGAATCAGGGG
pSense-2	ATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTT TTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTAT

	AAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCC GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTC CAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACC CGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTA CAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGT TACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAG CAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACG AAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGT TTTAAATCAATCTAAAGTATCCATGGATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTAT CTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTAC CATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGC CGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGA GTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGG TATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCT CCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCT CTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCG GCGACCGAGTTGCTCTTGCCCGGCGTCAACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATT GGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCAC CCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAA GGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATT GTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAAAAGAGCATGCGTTTGTAGAAACGCAAAAAG GCCATCCGTCAGGATGGCCTTCTGCTTAATTTGATGCCTGGCAGTTTATGGCGGGCGTCCTGCCCGCCACCCTCCGGGC CGTTGCTTCGCAACGTTCAAATCCGCTCCCGGCGGATTTGTCCTACTCAGGAGAGCGTTCACCGACAAACAACAGATAA AACGAAAGGCCCAGTCTTTCGACTGAGCCTTTCGTTTTATTTGATGCCTGGCAGTTCCCTACTCTCGCATGGGGAGACCC CACACTACCATCGGCGCTACGGCGTTTCACTTCTGAGTTCGGCATGGGGTCAGGTGGGACCACCGCGCTACTGCCGCCA GGCAAATTCTGTTTTATCAGACCGCTTCTGCGTTCTGATTTAATCTGTATCAGGCTGAAAATCTTCTCTCATCCGCCAAAA CAGCCAAGCTGGAGACCGTTTAAACGGGCCCAAGCTTTTTGTAGAGCTCATCCATGCCATGTGTAATCCCAGCAGCAGT TACAAACTCAAGAAGGACCATGTGGTCACGCTTTTCGTTGGGATCTTTCGAAAGGACAGATTGTGTCGACAGGTAATGG TTGTCTGGTAAAAGGACAGGGCCATCGCCAATTGGAGTATTTTGTTGATAATGGTCTGCTAGTTGAACGGAACCATCTT CAACGTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTTTGTCTGCCGTGATGTATACATTGTGTGAGTTAA AGTTGTACTCGAGTTTGTGTCCAAGAATGTTTCCATCTTCTTTAAAATCAATACCCTTTAACTCGATACGATTAACAAGGG TATCACCTTCAAACTTGACTTCAGCACGCGTCTTGTAGGTCCCGTCATCTTTGAAAGATATAGTGCGTTCCTGTACATAAC CTTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATGTGATCCGGATAACGGGAAAAGCATTGAACACCATAGGT CAGAGTAGTGACAAGTGTTGGCCACGGAACAGGTAGTTTTCCAGTAGTGCAAATAAATTTAAGGGTGAGTTTTCCGTTT GTAGCATCACCTTCACCCTCTCCACGGACAGAAAATTTGTGCCCATTAACATCACCATCTAATTCAACAAGAATTGGGAC AACTCCAGTGAAAAGTTCTTCTCCTTTGCTCATACTAGTTTCCTCCTGTTAGCCCACCTAAATGTAACAGTCACGTCGGTT

	ATATTCAATCCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA TTAATTGCGTTGCGCTCTAGATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCCCCAACCCATACAGAAGGTG AACACTGATGCCCCGCCCCAAGCTCAAGTCCGATGACGAGGTACTCGAGGCCGCCACCGTAGTGCTGAAGCGTTGCGG TCCCATAGAGTTCACGCTCAGCGGAGTAGCAAAGGAGGTGGGGCTCTCCCGCGCAGCGTTAATCCAGCGCTTCACCAA CCGCGATACGCTGCTGGTGAGGATGATGGAGCGCGGCGTCGAGCAGGTGCGGCATTACCTGAATGCGATACCGATAG GCGCAGGGCCGCAAGGGCTCTGGGAATTTTTGCAGGTGCTCGTTCGGAGCATGAACACTCGCAACGACTTCTCGGTGA ACTATCTCATCTCCTGGTACGAGCTCCAGGTGCCGGAGCTACGCACGCTTGCGATCCAGCGGAACCGCGCGGTGGTGG AGGGGATCCGCAAGCGACTGCCCCCAGGTGCTCCTGCGGCAGCTGAGTTGCTCCTGCACTCGGTCATCGCTGGCGCGA CGATGCAGTGGGCCGTCGATCCGGATGGTGAGCTAGCTGATCATGTGCTGGCTCAGATCGCTGCCATCCTGTGTTTAAT GTTTCCCGAACACGACGATTTCCAACTCCTCCAGGCACATGCGTAACATAGTATCCAAAATCTAAACCCGTCAAGCCCTC AGGAGTGAATCATGACCGTAGTCACGACCGCCGATACCTCCCAACTGTACGCACTTGCAGCCCGACATGGGCTCAAGCT CCATGGCCCGCTGACTGTCAATGAGCTTGGGCTCGACTATAGGATCGTGATCGCCACCGTCGACGATGGACGTCGGTG GGTGCTGCGCATCCCGCGCCGAGCCGAGGTAAGCGCGAAGGTCGAACCAGAGGCGCGGGTGCTGGCAATGCTCAAGA ATCGCCTGCCGTTCGCGGTGCCGGACTGGCGCGTGGCCAACGCCGAGCTCGTTGCCTATCCCATGCTCGAAGACTCGAC TGCGATGGTCATCCAGCCTGGTTCGTCCACGCCCGACTGGGTCGTGCCGCAGGACTCGGAGGTCTTCGCGGAGAGCTT CGCGACCGCGCTCGCCGCCCTGCATGCCGTCCCCATTTCCGCCGCCGTGGATGCGGGGATGCTCATCCGTACACCGACG CAGGCCCGTCAGAAGGTGGCCGACGACGTTGACCGCGTCCGACGCGAGTTCGTGGTGAACGACAAGCGCCTCCACCG GTGGCAGCGCTGGCTCGACGACGATTCGTCGTGGCCAGATTTCTCCGTGGTGGTGCATGGCGATCTCTACGTGGGCCA TGTGCTCATCGACAACACGGAGCGCGTCAGCGGGATGATCGACTGGAGCGAGGCCCGCGTTGATGACCCTGCCATCGA CATGGCCGCGCACCTTATGGTCTTTGGTGAAGAGGGGCTCGCGAAGCTCCTCCTCACGTATGAAGCGGCCGGTGGCCG GGTGTGGCCGCGGCTCGCCCACCACATCGCGGAGCGCCTTGCGTTCGGGGCGGTCACCTACGCACTCTTCGCCCTCGAC TCGGGTAACGAAGAGTACCTCGCTGCGGCGAAGGCGCAGCTCGCCGCAGCGGAATGAGGTGTGCAGAGTCCCTGCGG CAGGCGACGAACACGACCGTCGTCGATTAGTACCCCTCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATATACCAT GGGCAGCAGCCATCATCATCATCATCACAGCAGCGGCCTGGTGCCGCGCGGCAGCCATATGAGCGTGAAGCAGAAGTC AGCGTTGCAGGACCTGGTCGACTTCGCCAAGTGGCACGTGTGGACCAGGGTGCGGCCGTCCAGCCGTGCGCGCCTGG CCTACGAGCTGTTCGCCGACGACCACGAGGCCACGACCGAGGGCGCCTACATCAACCTCGGCTACTGGAAGCCCGGGT GCGCCGGCCTGGAGGAGGCCAACCAGGAGCTGGCGAACCAGCTCGCCGAGGCCGCGGGGATCAGCGAGGGCGACGA GGTGCTCGACGTCGGGTTCGGGCTCGGCGCGCAGGACTTCTTCTGGCTCGAGACGCGCAAGCCGGCCAGGATCGTCG GCGTCGACCTGACCCCGAGCCACGTCCGCATCGCCTCCGAGCGCGCGGAGCGCGAGAACGTGCAGGACCGCCTGCAGT TCAAGGAGGGCTCGGCGACCGACCTGCCCTTCGGCGCGGAGACCTTCGACCGCGTCACCTCCCTGGAGTCGGCCCTGC ACTACGAGCCGCGGACCGACTTCTTCAAGGGCGCGTTCGAGGTGCTCAAGCCCGGAGGCGTGCTGGCCATCGGCGACA TCATCCCGCTCGACCTGCGCGAGCCCGGTTCCGACGGACCGCCGAAGCTGGCGCCGCAGCGGTCGGGATCGCTGTCCG GCGGCATCCCGGTGGAGAACTGGGTGCCCCGCGAGACCTACGCCAAGCAGCTCCGCGAAGCGGGCTTCGTCGACGTC GAGGTGAAGTCGGTCCGCGACAACGTGATGGAGCCCTGGCTGGACTACTGGCTGCGCAAGCTGCAGGACGAGTCGTT CAAGAAGAGCGTGAGCAGGCTCTTCTACAGCCAGGTCAAGCGGTCGCTGACCAGCGACTCGGGCATGAAGGGCGAGC

	TGCCCGCGCTCGACTTCGTGATCGCCTCAGCCCGCAAGCCCGGCGCGTAGGGATCCGAATTCCATATGGAATTCGGTAC CTACGGTCGGTGGTATCGAAGTCTTGATCACTGTACACTAGAGGTAATACGGTTATCCACAGAATCAGGGG
pSense-3	ATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTT TTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTAT AAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCC GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTC CAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACC CGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTA CAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGT TACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAG CAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACG AAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGT TTTAAATCAATCTAAAGTATCCATGGATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTAT CTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTAC CATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGC CGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGA GTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGG TATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCT CCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCT CTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCG GCGACCGAGTTGCTCTTGCCCGGCGTCAACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATT GGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCAC CCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAA GGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATT GTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAAAAGAGCATGCGTTTGTAGAAACGCAAAAAG GCCATCCGTCAGGATGGCCTTCTGCTTAATTTGATGCCTGGCAGTTTATGGCGGGCGTCCTGCCCGCCACCCTCCGGGC CGTTGCTTCGCAACGTTCAAATCCGCTCCCGGCGGATTTGTCCTACTCAGGAGAGCGTTCACCGACAAACAACAGATAA AACGAAAGGCCCAGTCTTTCGACTGAGCCTTTCGTTTTATTTGATGCCTGGCAGTTCCCTACTCTCGCATGGGGAGACCC CACACTACCATCGGCGCTACGGCGTTTCACTTCTGAGTTCGGCATGGGGTCAGGTGGGACCACCGCGCTACTGCCGCCA GGCAAATTCTGTTTTATCAGACCGCTTCTGCGTTCTGATTTAATCTGTATCAGGCTGAAAATCTTCTCTCATCCGCCAAAA CAGCCAAGCTGGAGACCGTTTAAACGGGCCCAAGCTTTTTGTAGAGCTCATCCATGCCATGTGTAATCCCAGCAGCAGT TACAAACTCAAGAAGGACCATGTGGTCACGCTTTTCGTTGGGATCTTTCGAAAGGACAGATTGTGTCGACAGGTAATGG TTGTCTGGTAAAAGGACAGGGCCATCGCCAATTGGAGTATTTTGTTGATAATGGTCTGCTAGTTGAACGGAACCATCTT CAACGTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTTTGTCTGCCGTGATGTATACATTGTGTGAGTTAA AGTTGTACTCGAGTTTGTGTCCAAGAATGTTTCCATCTTCTTTAAAATCAATACCCTTTAACTCGATACGATTAACAAGGG TATCACCTTCAAACTTGACTTCAGCACGCGTCTTGTAGGTCCCGTCATCTTTGAAAGATATAGTGCGTTCCTGTACATAAC

	CTTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATGTGATCCGGATAACGGGAAAAGCATTGAACACCATAGGT CAGAGTAGTGACAAGTGTTGGCCACGGAACAGGTAGTTTTCCAGTAGTGCAAATAAATTTAAGGGTGAGTTTTCCGTTT GTAGCATCACCTTCACCCTCTCCACGGACAGAAAATTTGTGCCCATTAACATCACCATCTAATTCAACAAGAATTGGGAC AACTCCAGTGAAAAGTTCTTCTCCTTTGCTCATACTAGTTTCCTCCTGTTAGCCCACCTAAATGTAACAGTCACGTCGGTT ATATTCAATCCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA TTAATTGCGTTGCGCTCTAGATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCCCCAACCCATACAGAAGGTG AACACTGATGCCCCGCCCCAAGCTCAAGTCCGATGACGAGGTACTCGAGGCCGCCACCGTAGTGCTGAAGCGTTGCGG TCCCATAGAGTTCACGCTCAGCGGAGTAGCAAAGGAGGTGGGGCTCTCCCGCGCAGCGTTAATCCAGCGCTTCACCAA CCGCGATACGCTGCTGGTGAGGATGATGGAGCGCGGCGTCGAGCAGGTGCGGCATTACCTGAATGCGATACCGATAG GCGCAGGGCCGCAAGGGCTCTGGGAATTTTTGCAGGTGCTCGTTCGGAGCATGAACACTCGCAACGACTTCTCGGTGA ACTATCTCATCTCCTGGTACGAGCTCCAGGTGCCGGAGCTACGCACGCTTGCGATCCAGCGGAACCGCGCGGTGGTGG AGGGGATCCGCAAGCGACTGCCCCCAGGTGCTCCTGCGGCAGCTGAGTTGCTCCTGCACTCGGTCATCGCTGGCGCGA CGATGCAGTGGGCCGTCGATCCGGATGGTGAGCTAGCTGATCATGTGCTGGCTCAGATCGCTGCCATCCTGTGTTTAAT GTTTCCCGAACACGACGATTTCCAACTCCTCCAGGCACATGCGTAACATAGTATCCAAAATCTAAACCCGTCAAGCCCTC AGGAGTGAATCATGACCGTAGTCACGACCGCCGATACCTCCCAACTGTACGCACTTGCAGCCCGACATGGGCTCAAGCT CCATGGCCCGCTGACTGTCAATGAGCTTGGGCTCGACTATAGGATCGTGATCGCCACCGTCGACGATGGACGTCGGTG GGTGCTGCGCATCCCGCGCCGAGCCGAGGTAAGCGCGAAGGTCGAACCAGAGGCGCGGGTGCTGGCAATGCTCAAGA ATCGCCTGCCGTTCGCGGTGCCGGACTGGCGCGTGGCCAACGCCGAGCTCGTTGCCTATCCCATGCTCGAAGACTCGAC TGCGATGGTCATCCAGCCTGGTTCGTCCACGCCCGACTGGGTCGTGCCGCAGGACTCGGAGGTCTTCGCGGAGAGCTT CGCGACCGCGCTCGCCGCCCTGCATGCCGTCCCCATTTCCGCCGCCGTGGATGCGGGGATGCTCATCCGTACACCGACG CAGGCCCGTCAGAAGGTGGCCGACGACGTTGACCGCGTCCGACGCGAGTTCGTGGTGAACGACAAGCGCCTCCACCG GTGGCAGCGCTGGCTCGACGACGATTCGTCGTGGCCAGATTTCTCCGTGGTGGTGCATGGCGATCTCTACGTGGGCCA TGTGCTCATCGACAACACGGAGCGCGTCAGCGGGATGATCGACTGGAGCGAGGCCCGCGTTGATGACCCTGCCATCGA CATGGCCGCGCACCTTATGGTCTTTGGTGAAGAGGGGCTCGCGAAGCTCCTCCTCACGTATGAAGCGGCCGGTGGCCG GGTGTGGCCGCGGCTCGCCCACCACATCGCGGAGCGCCTTGCGTTCGGGGCGGTCACCTACGCACTCTTCGCCCTCGAC TCGGGTAACGAAGAGTACCTCGCTGCGGCGAAGGCGCAGCTCGCCGCAGCGGAATGAGGTGTGCAGAGTCCCTGCGG CAGGCGACGAACACGACCGTCGTCGATTAGTACCCGCGAAAT***TAATACGACTCACTATAGG***GGAATTGTGAGCGGATA ACAATTCCCCTCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATATACCATGGGCAGCAGCCATCATCATCATCATCA CAGCAGCGGCCTGGTGCCGCGCGGCAGCCATATGAGCGTGAAGCAGAAGTCAGCGTTGCAGGACCTGGTCGACTTCG CCAAGTGGCACGTGTGGACCAGGGTGCGGCCGTCCAGCCGTGCGCGCCTGGCCTACGAGCTGTTCGCCGACGACCACG AGGCCACGACCGAGGGCGCCTACATCAACCTCGGCTACTGGAAGCCCGGGTGCGCCGGCCTGGAGGAGGCCAACCAG GAGCTGGCGAACCAGCTCGCCGAGGCCGCGGGGATCAGCGAGGGCGACGAGGTGCTCGACGTCGGGTTCGGGCTCG GCGCGCAGGACTTCTTCTGGCTCGAGACGCGCAAGCCGGCCAGGATCGTCGGCGTCGACCTGACCCCGAGCCACGTCC GCATCGCCTCCGAGCGCGCGGAGCGCGAGAACGTGCAGGACCGCCTGCAGTTCAAGGAGGGCTCGGCGACCGACCTG CCCTTCGGCGCGGAGACCTTCGACCGCGTCACCTCCCTGGAGTCGGCCCTGCACTACGAGCCGCGGACCGACTTCTTCA AGGGCGCGTTCGAGGTGCTCAAGCCCGGAGGCGTGCTGGCCATCGGCGACATCATCCCGCTCGACCTGCGCGAGCCCG

	GTTCCGACGGACCGCCGAAGCTGGCGCCGCAGCGGTCGGGATCGCTGTCCGGCGGCATCCCGGTGGAGAACTGGGTG CCCCGCGAGACCTACGCCAAGCAGCTCCGCGAAGCGGGCTTCGTCGACGTCGAGGTGAAGTCGGTCCGCGACAACGTG ATGGAGCCCTGGCTGGACTACTGGCTGCGCAAGCTGCAGGACGAGTCGTTCAAGAAGAGCGTGAGCAGGCTCTTCTAC AGCCAGGTCAAGCGGTCGCTGACCAGCGACTCGGGCATGAAGGGCGAGCTGCCCGCGCTCGACTTCGTGATCGCCTCA GCCCGCAAGCCCGGCGCGTAGGGATCCGAATTCCATATGGAATTCGGTACCTACGGTCGGTGGTATCGAAGTCTTGATC ACTGTACACTAGAGGTAATACGGTTATCCACAGAATCAGGGG

Supplementary Table S2. Strains and plasmids used in this study.

Bacterial Strain/plasmid	Genotype/description	Reference
E. cloni® 10G	F- *mcr*A Δ(*mrr-hsd*RMS-*mcr*BC) *end*A1 *rec*A1 ϕ80d*lac*ZΔM15 Δ*lac*X74 *ara*D139 Δ(*ara*,*leu*)7697 *gal*U *gal*K *rps*L(Str^R) *nup*G λ- *ton*A	Lucigen
E. coli TOP10	F- *mcr*A Δ(*mrr-hsd*RMS-*mcr*BC) ϕ80*lac*ZΔM15 Δ*lac*X74 *rec*A1 *ara*D139 Δ(*ara-leu*)7697 *gal*U *gal*K λ- *rps*L(Str^R) *end*A1 *nup*G	Invitrogen
E. coli BL21 (DE3)	Used to express MphR for structure determination	Promega
pMLGFP	Houses the reporter module (P_{MphR}-*gfp*) and *MphR*. Amp resistance.	Gardner et al., Mol Biosyst. 2011, 7, 2554
pMLGFPK	Derivative of pMLGFP with inserted *Kpn*I restriction site to facilitate cloning mutant MphR genes. Amp resistance.	This study
pJZ12	Carries the macrolide phosphotransferase MphA. Tet resistance.	Gardner et al., Mol Biosyst. 2011, 7, 2554
pCOLADuet-EryG	Derivative of pCOLADuet containing wild-type EryG	This study
pSense-MphR-MphA	Derivative of pSense containing wild-type MphR and MphA	This study
pSense-MphA-MphR-RBScalculate	Derivative of pSense-MphA-MphR with a calculated RBS	This study
pSense-1	Derivative of pSense-MphA-MphR-RBScalculate containing EryG	This study
pSense-2	Derivative of pSense-1 containing the pET28a RBS (AAGGAG) for EryG	This study
pSense-3	Derivative of pSense-2 containing the T7 promoter driving EryG	This study
pSense-M9C4-E7-MphA-EryG	Derivative of pSense-3 containing M9C4 MphR with the E7 RBS upstream to it	This study

Supplementary Table S3. Oligonucleotides used in this study.

Entry	Primer name	Sequence
1	MphR_SSM_R122_F	TACGCACGCTTGCGATCCAGNNKAACCGCGCGGTGGTGGAGGGGAT
2	MphR_SSM_R122_R	ATCCCCTCCACCACCGCGCGGTTMNNCTGGATCGCAAGCGTGCGTA
3	MphR_SSM_N123_F	ACGCTTGCGATCCAGCGGNNKCGCGCGGTGGTGGAGGGGAT
4	MphR_SSM_N123_R	ATCCCCTCCACCACCGCGCGMNNCCGCTGGATCGCAAGCGT
5	MphR_SDM_R122I_F	TACGCACGCTTGCGATCCAGATTAACCGCGCGGTGGTGGAGGG
6	MphR_SDM_R122I_R	CCCTCCACCACCGCGCGGTTAATCTGGATCGCAAGCGTGCGTA
7	MphR_SDM_R122P_F	TACGCACGCTTGCGATCCAGCCGAACCGCGCGGTGGTGGAGGG
8	MphR_SDM_R122P_R	CCCTCCACCACCGCGCGGTTCGGCTGGATCGCAAGCGTGCGTA
9	MphR_SDM_R122N_F	TACGCACGCTTGCGATCCAGAACAACCGCGCGGTGGTGGAGGG
10	MphR_SDM_R122N_R	CCCTCCACCACCGCGCGGTTGTTCTGGATCGCAAGCGTGCGTA
11	MphR_SDM_R122K_F	TACGCACGCTTGCGATCCAGAAGAACCGCGCGGTGGTGGAGGG
12	MphR_SDM_R122K_R	CCCTCCACCACCGCGCGGTTCTTCTGGATCGCAAGCGTGCGTA
13	MphR_SDM_K132N_F	TGGAGGGGATCCGCAATCGACTGCCCCCAGGTGCTC
14	MphR_SDM_K132N_R	GAGCACCTGGGGGCAGTCGATTGCGGATCCCCTCCA
15	MphR_SDM_A151T_F	TGCTCCTGCACTCGGTCATCACTGGCGCGACGATGCAGTGG
16	MphR_SDM_A151T_R	CCACTGCATCGTCGCGCCAGTGATGACCGAGTGCAGGAGCA
17	MphR_SDM_H184Q_F	TGTTTAATGTTTCCCGAACAAGACGATTTCCAACTCCTCCA
18	MphR_SDM_H184Q_R	TGGAGGAGTTGGAAATCGTCTTGTTCGGGAAACATTAAACA
19	NCR	GATAGCGCCCCCCAACCCATACAGAAGGTGAACACTGATGC
20	NCR	GCATCAGTGTTCACCTTCTGTATGGGTTGGGGGGCGCTATC
21	K132N	TGGAGGGGATCCGCAATCGACTGCCCCCAGGTGCTC
22	K132N	GAGCACCTGGGGGCAGTCGATTGCGGATCCCCTCCA
23	A151T	TGCTCCTGCACTCGGTCATCACTGGCGCGACGATGCAGTGG
24	A151T	CCACTGCATCGTCGCGCCAGTGATGACCGAGTGCAGGAGCA
25	H184Q	TGTTTAATGTTTCCCGAACAAGACGATTTCCAACT CCTCCA
26	H184Q	TGGAGGAGTTGGAAATCGTCTTGTTCGGGAAACATTAAACA
27	R122I	TACGCACGCTTGCGATCCAGATTAACCGCGCGGTGGTGGAGGG
28	R122I	CCCTCCACCACCGCGCGGTTAATCTGGATCGCAAG CGTGCGTA
29	MphR_INS_Kpn1_F	CGTCGTCGATTAGGTACCGGTACGG
30	MphR_INS_Kpn2_R	CCGTACCGGTACCTAATCGACGACG
31	MphR_EPPCR_F	CGAGCTCTAGATGGTGCAAAACCTTTC
32	MphR_EPPCR_R	CTGCGTTATCCCCTGATTCT

33	CL2056	AAAccatggGGCATCATCATCATCATCATTTGGAAAACCTATACTTTCAAGGCCCCCGCCCC AAGCTCAAG
34	CL2057	TTTgaattcCGGCCGCTACTAGTTTACGCATGTGCCTGGAGG
35	CL2062	ATGATGATGATGATGATGCCcatggtatatctccttcttaaagtt
36	CL2063	CTCCAGGCACATCGCGTAAgaattcGAGCTCCGTCGACAAGCTTGCin
37	A3_RBS_mutation_1	TAGCGCCCCCCAACCCATACGGAAGGTGAACACTGATGC
38	A3_RBS_mutation_2	GCATCAGTGTTCACCTTCCGTATGGGTTGGGGGGCGCTA
39	E7_RBS_mutation_1	GATAGCGCCCCCCAACCCATACAGATGGTGAACACTGATGC
40	E7_RBS_mutation_2	GCATCAGTGTTCACCATCTGTATGGGTTGGGGGGCGCTATC
41	H4_RBS_mutation_1	CCCAACCCATACAGAAGGCGAACACTGATGCC
42	H4_RBS_mutation_2	GGCATCAGTGTTCGCCTTCTGTATGGGTTGGG
43	EryG_PCR_NcoI	ACTCACTATAGGGGAATTGTGAGCGGATAAC
44	EryG_PCR_HindIII	GCAAGCTTGTCGACGGAGCTC
45	MphR.F	TGGCATGATAGCGCCCCCCAACCCATA
46	MphR.R	GGGTTTAGATTTTGGATACTATGTTACGCATGTGC
47	MphA.F	CATAGTATCCAAAATCTAAACCCGTCA
48	MphA.R	GGGACTCTGCACACCTCATTCCGCTGCGGCG
49	pSENSE.F	GGCGCTATCATGCCATAC
50	pSENSE.R	GGTGTGCAGAGTCCCTGC
51	CalculRBS_MCS	GGAGATCCTCCACCCGAAATTCTAaggaggaGACCATATGGAATTCGGTACCTACGGTCGG TGGTATCGAAG
52	pSense_MphAR_GA_1	ATATACATATGAGCGTGAAGCAGAAGTCAGC
53	pSense_MphAR_GA_2	ATATAGGTACCCCGGATCTCAGTGGTGGTGG
54	EryG_PCR_NdeI	ATATACATATGAGCGTGAAGCAGAAGTCAGC
55	pET28a_KpnI	ATATAGGTACCCCAATCCGGATATAGTTCCTCCTTTCAG
56	pET28a_EryG_GA_1	CGTCGTCGATTAGTACCCCTCTAGAAATAATTTTGTTTAAC
57	pET28a_EryG_GA_2	GTACCGAATTCCATATGGAATTCGGATCCCTACGC
58	pET28a_EryG_GA_3	CGTCGTCGATTAGTACCCGCGAAATTAATACGAC
59	pSense_MphAR_RBScalculated_GA_1	GCGTAGGGATCCGAATTCCATATGGAATTCGGTACCTACG
60	pSense_MphAR_RBScalculated_GA_2	AACAAAATTATTTCTAGAGGGGTACTAATCGACGACGGTC
61	pSense_MphAR_RBScalculated_GA_3	GTCGTATTAATTTCGCGGGTACTAATCGACGACGGTC

62	pMLGFPK_E7M9C4_GA_1	TGGCATGATAGCGCC
63	pMLGFPK_E7M9C4_GA_2	GTTTAGATTTTGGATACTATGTTACGCATGTGCCTGG
64	pSense_3_GA_1	CATAGTATCCAAAATCTAAACCCGTCAAG
65	pSense_3_GA_2	GGCGCTATCATGCCATACC

Supplementary Table S4. Data collection and refinement statistics.

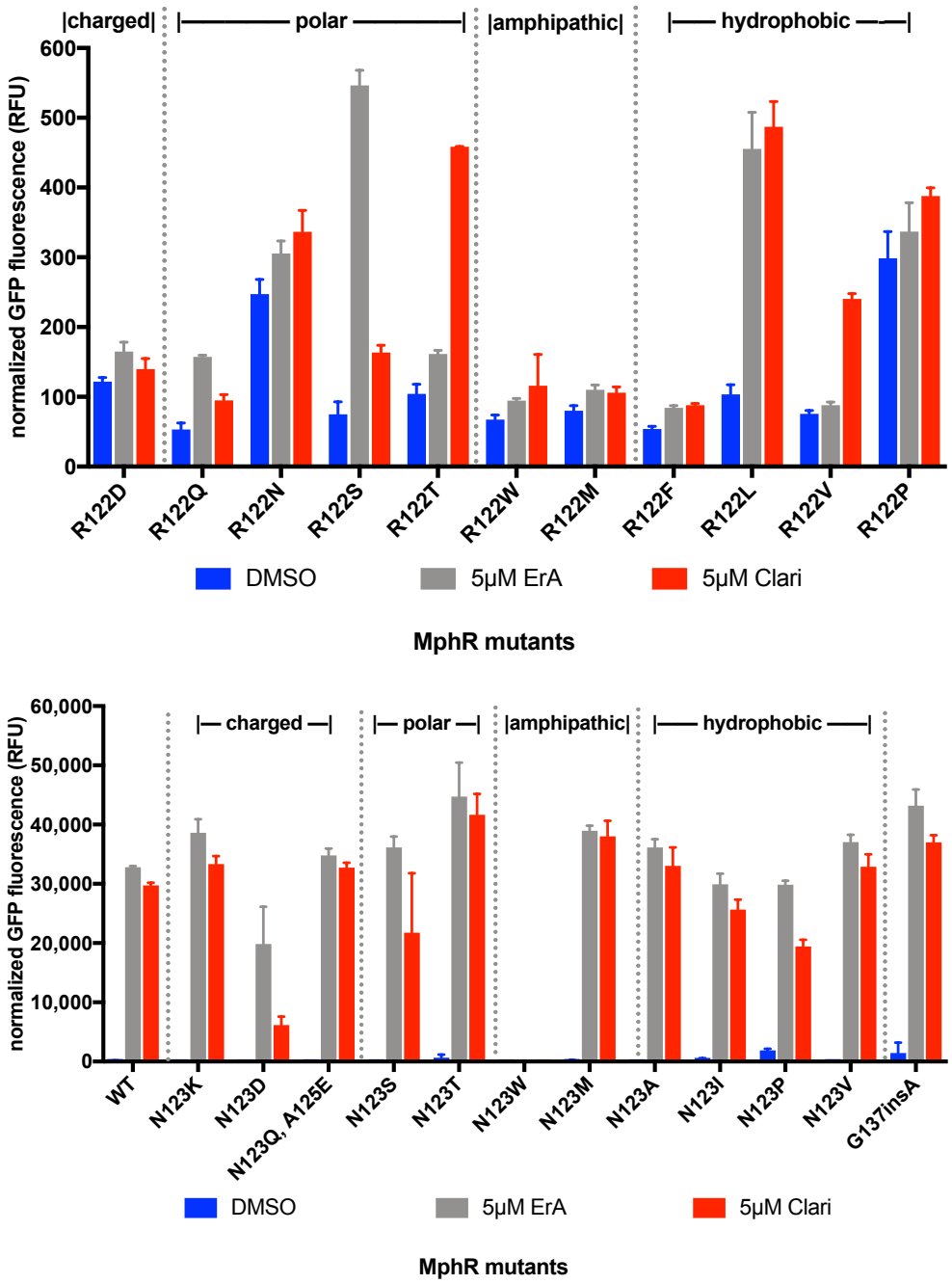
	MphR(A)-CLA
Protein Data Bank code	6U18
Data collection	
Space group	$P2_12_12_1$
Unit cell dimensions	
a, b, c (Å)	42.90, 53.16, 158.82
α, β, γ (°)	90.0, 90.0, 90.0
Resolution (Å)	2.00 (29.14 – 2.00)[a]
Completeness (%)	99.9 (100.0)[a]
Redundancy	6.1 (5.7)[a]
R_{merge}	0.048 (0.292)[a]
$\langle I \rangle / \langle \sigma(I) \rangle$	(22.8) (5.3)[a]
$CC_{1/2}$	0.999 (0.959)[a]
Refinement	
Resolution (Å)	29.14 – 2.00
No. reflections	25416
No. atoms (protein)	6038
R_{work} / R_{free}	0.202 / 0.221
Wilson <B-factor> (Å)	23.9
B_{ave} (all atoms)	33.0
RMS deviations	
Bond lengths (Å)	0.28
Bond angles (°)	0.41

[a] Values in parentheses are for highest resolution shell

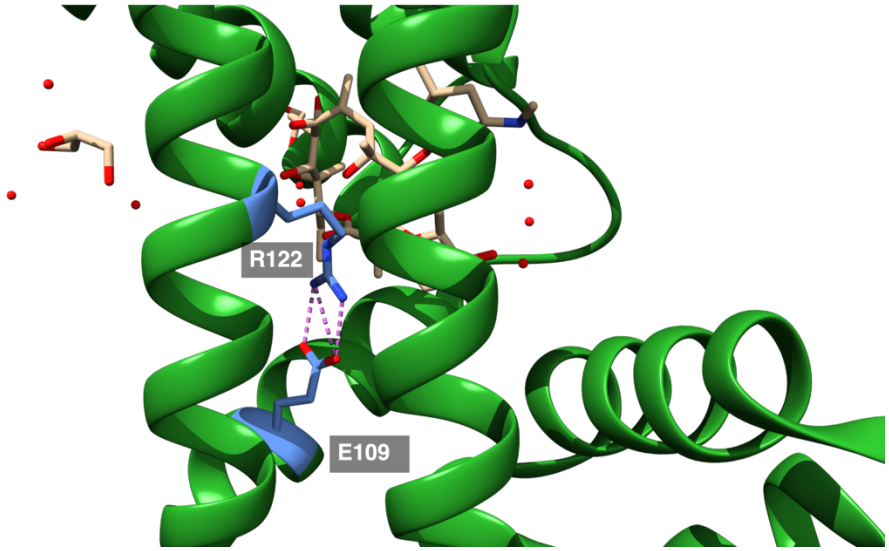
Supplementary Table S5. LC-HRMS gradient and scan parameters.

Time (min)	% B
0.0	2.0
1.0	2.0
8.0	80.0
10.0	80.0
10.1	2.0
12.0	2.0

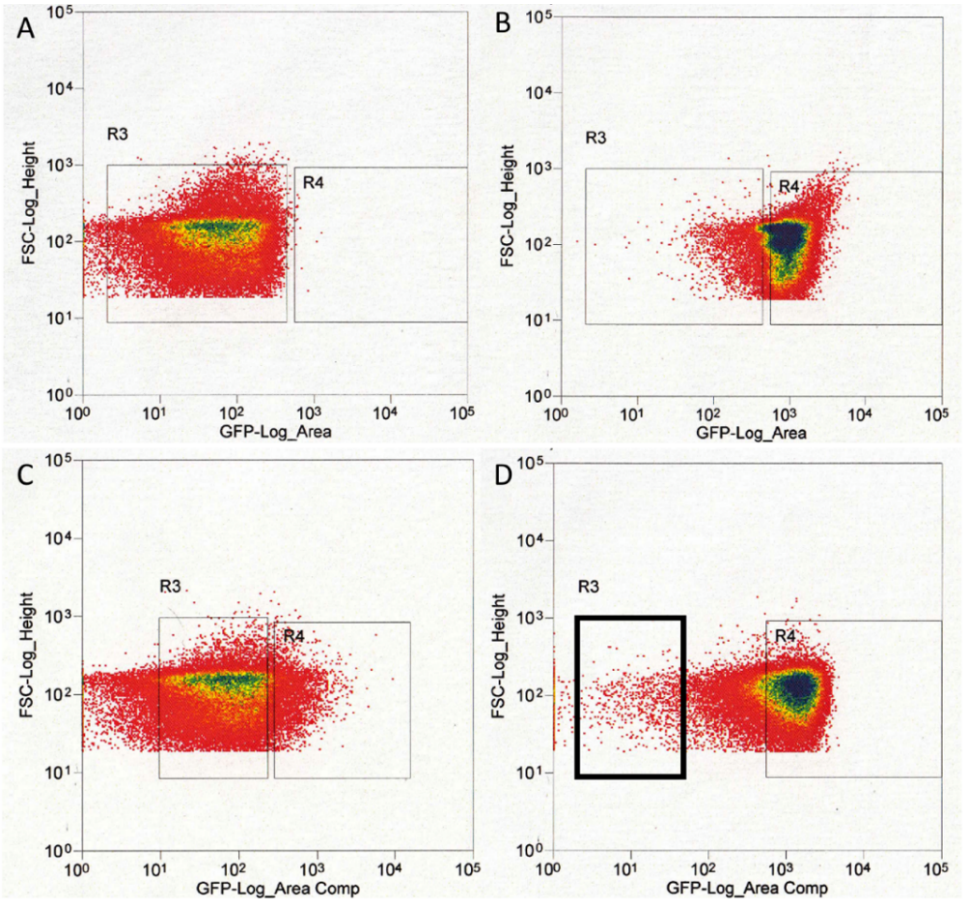
Spray voltage	3.5 kV
Capillary temperature	350 °C
Heater temp	300 °C
S Lens RF level	70 V
Sheath gas flow rate	60
Resolution	70,000
Scan Range	250-1000 m/z



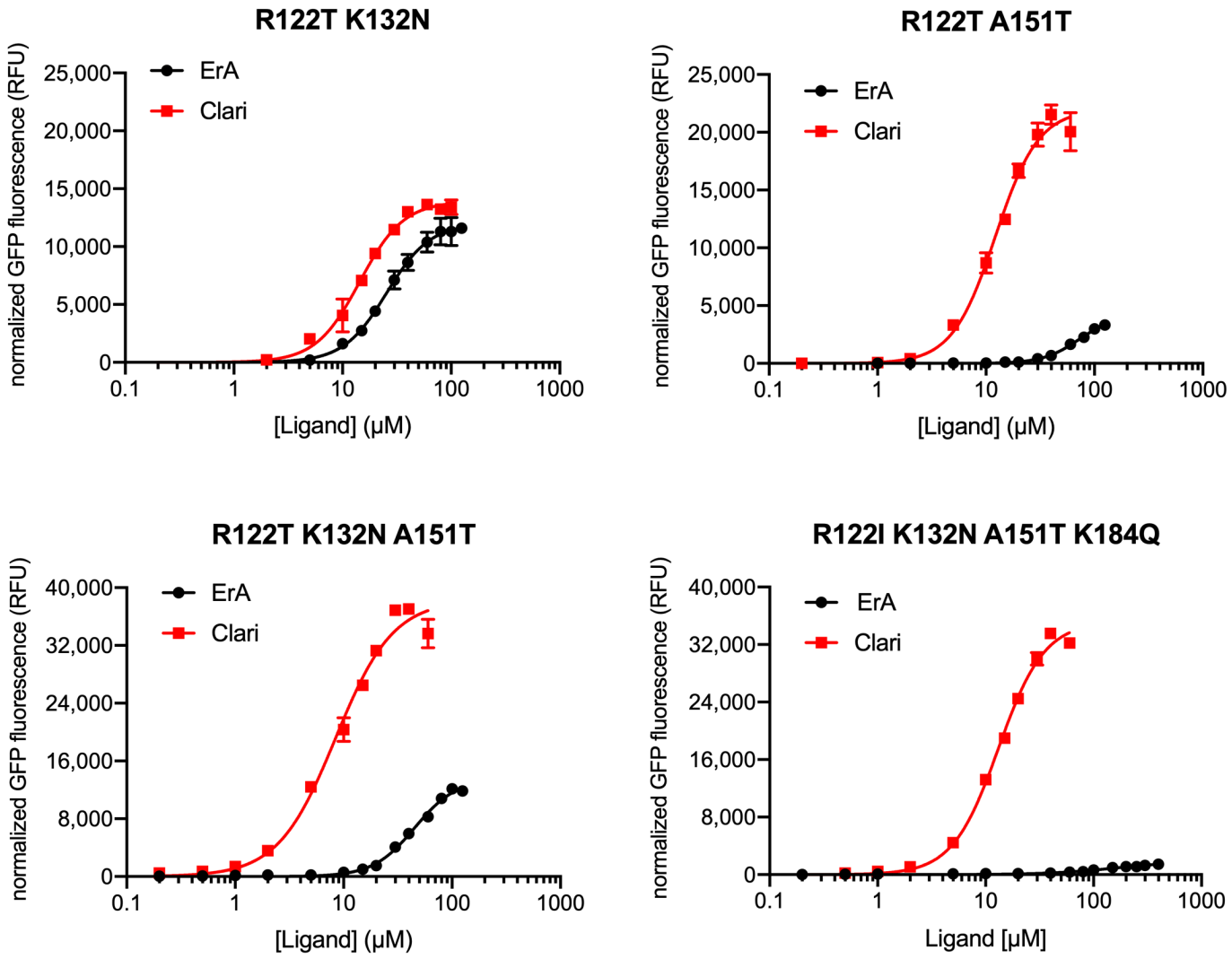
Supplementary Figure S1. Characterization of site-directed MphR biosensor variants. Activities of site-directed mutants using 5 μM ErA, 5 μM CLA, or dimethyl sulfoxide (DMSO). Error-bars represent the standard error of the mean (n = 3). Note: A125E in the N123Q/A125E variant is the result of a spurious mutation. N123Q was not tested as a single mutant.



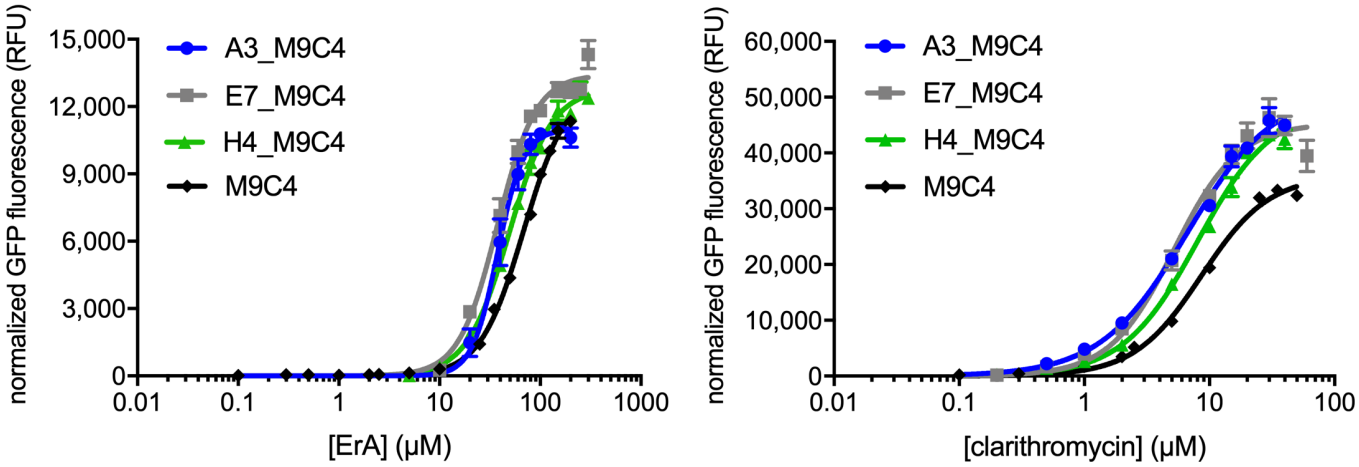
Supplementary Figure S2. The crystal structure of MphR (PDB: 3FRQ) complexed with ErA (green sticks). Locations of Arg122 and Glu109 (blue sticks) that form a salt bridge (dashed lines) are shown.



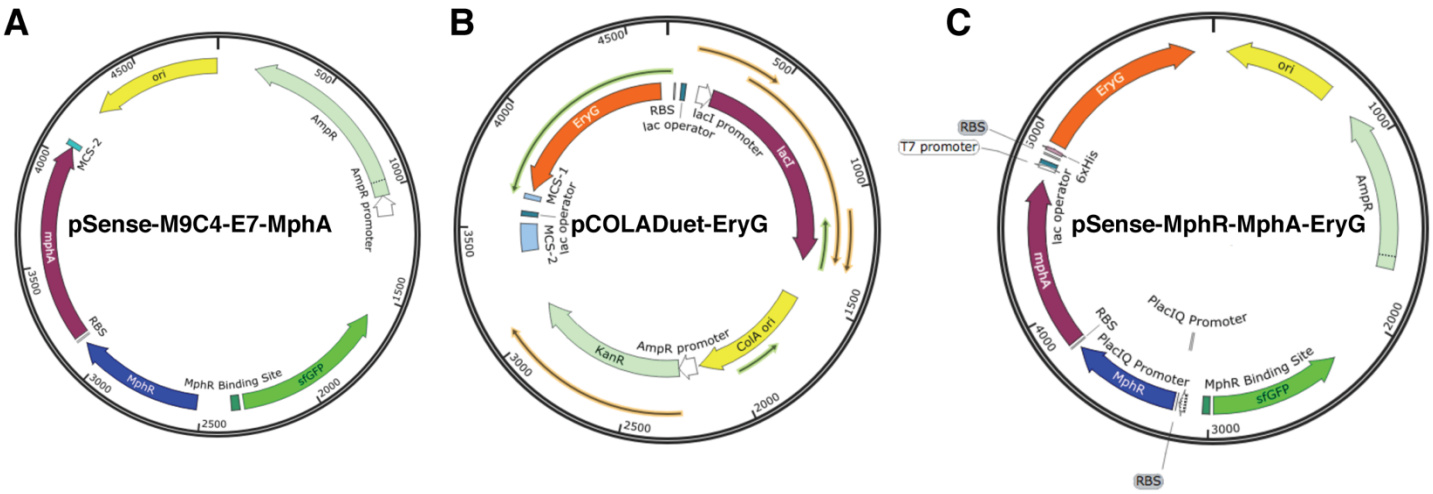
Supplementary Figure S3. FACS analysis and sorting of an error-prone PCR MphR mutant library. (A) Wild-type MphR in the absence of macrolides. (B) Wild-type MphR biosensor strain induced with addition of 5 µM ErA. (C) MphR mutant library in the absence of macrolides. (D) Induction of the MphR mutant library with addition of 5 µM ErA. The black box indicates the events corresponding to the ~5% of the library with the lowest fluorescence, corresponding to those variants that were poorly induced with ErA.



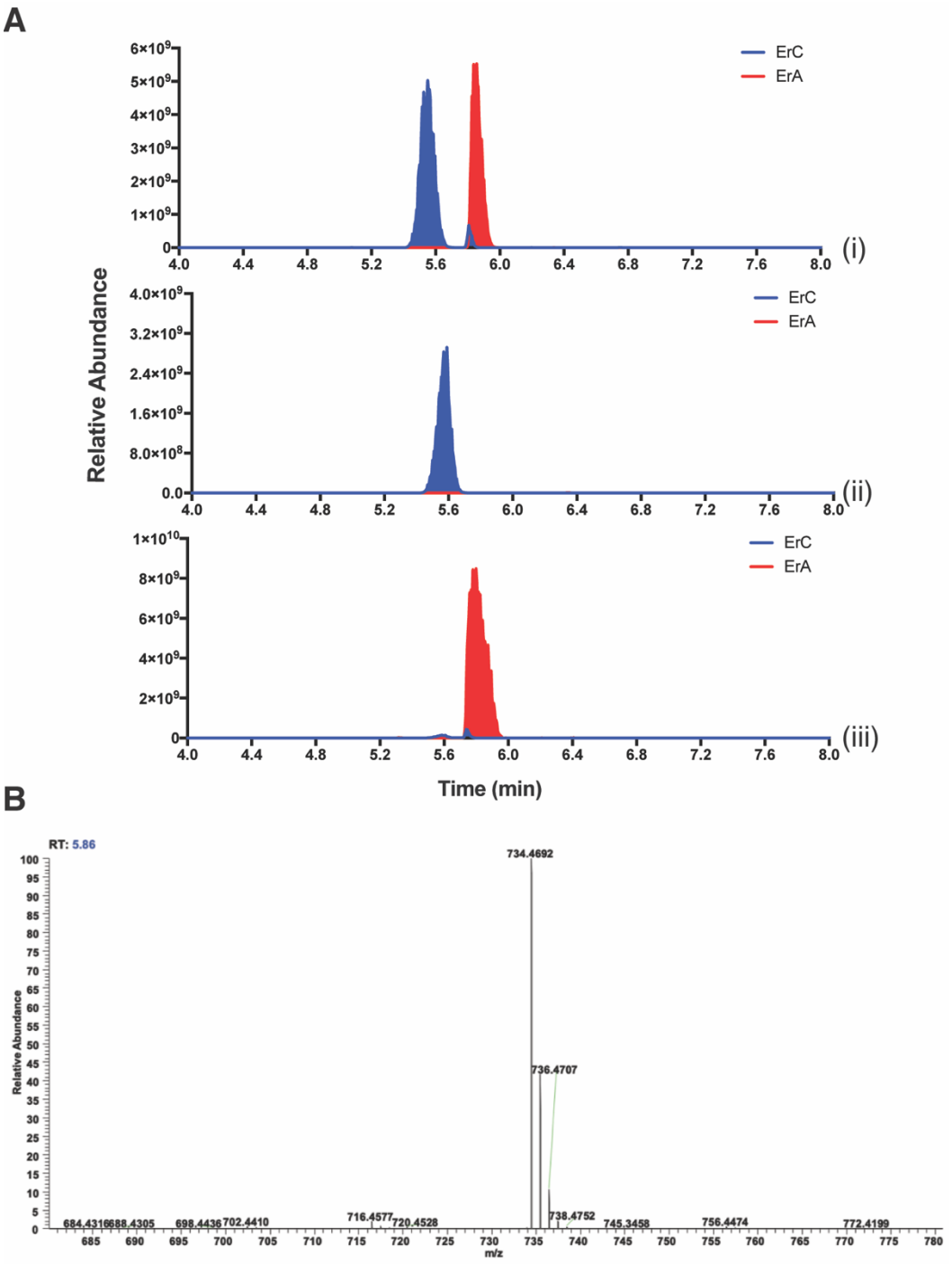
Supplementary Figure S4. Dose-response analysis of the macrolide specificity of mutants derived from M9C4. The biosensor strain is the two-plasmid system consisting of pMLGFP/pJZ12. Error-bars represent the standard error of the mean (n = 3) and are only visible when larger than the data point symbol.



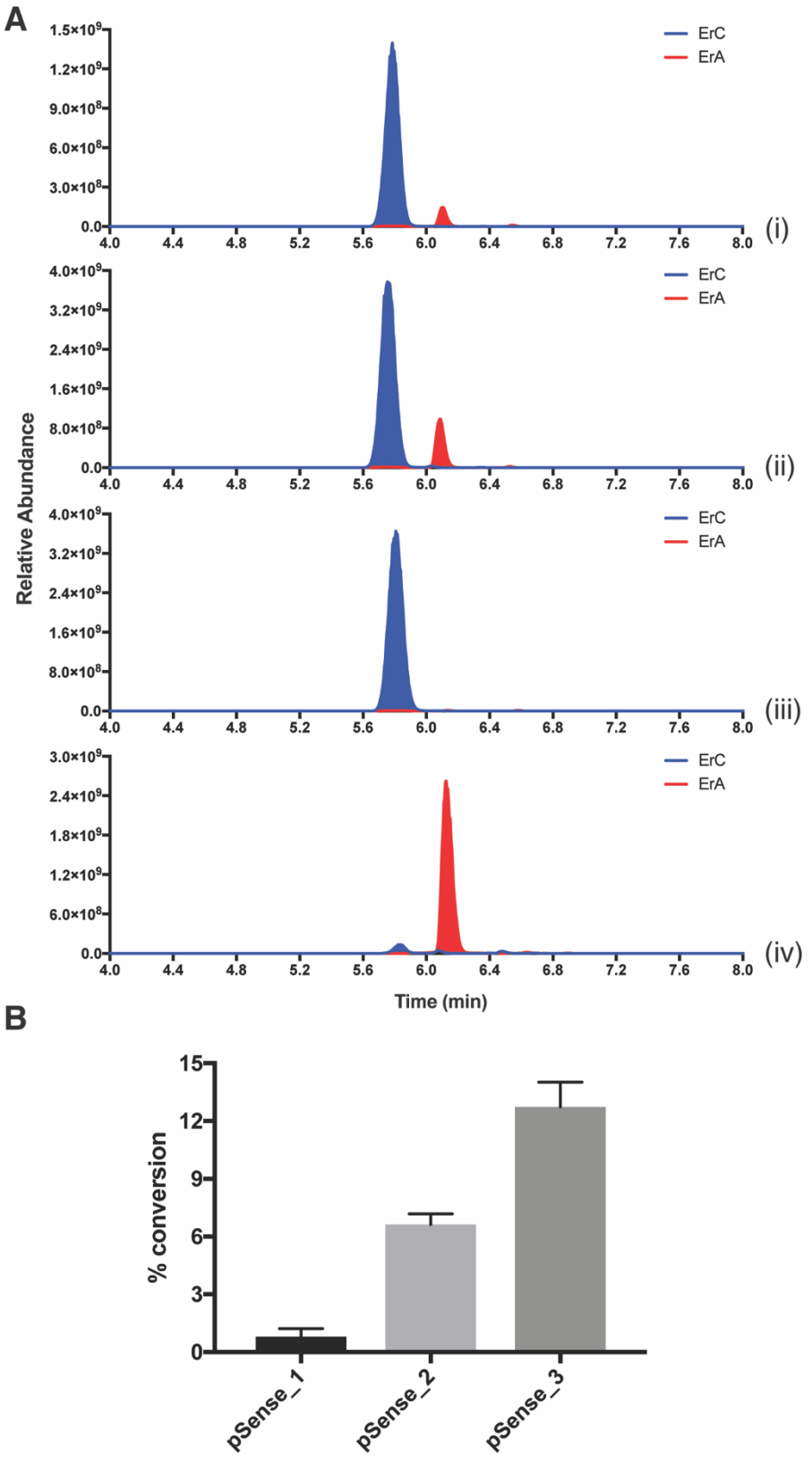
Supplementary Figure S5. Does-response analysis of RBS mutants of M9C4 MphR. The biosensor strain is the two-plasmid system consisting of pMLGFPK/pJZ12. Error-bars represent the standard error of the mean (n = 3) and are only visible when larger than the data point symbol.



Supplementary Figure S6. Plasmid maps of the various MphR biosensor constructs. (A) pSense-MphR-MphA carries the minimal biosensor system components that the pSense series of plasmids were generated from. (B) pCOLADuet-EryG houses the *O*-MTase gene, EryG. (C) pSense-3 carries the EryG gene and the biosensor components in a single plasmid.



Supplementary Figure S7. Representative LC-MS chromatograms of ErA production by *E. coli* BL21(DE3) pCOLADuet-EryG. (A) Extracted ion chromatogram of (i) the *in vivo* conversion of ErC to ErA, (ii) ErC standard, and (iii) ErA standard. Calculated mass for ErA 734.4685 $[M+H]^+$ $[C_{37}H_{68}NO_{13}]^+$; observed mass for ErA standard 734.4689 (Δ, 0.54 ppm). Calculated mass for ErC 720.4529 $[M+H]^+$ $[C_{36}H_{67}NO_{13}]^+$; observed mass for ErC standard 720.4531 (Δ, 0.28 ppm). (B) The representative total ion spectra of ErA produced via *E. coli* BL21(DE3) pCOLADuet-EryG. Observed mass for ErA 734.4692 (Δ, 0.95 ppm)


A
ErC
ErA
(i)
(ii)
(iii)
(iv)
Relative Abundance
Time (min)
B
% conversion
pSense_1
pSense_2
pSense_3

Supplementary Figure S8. ErA production by *E. coli* BL21(DE3) harboring various pSense constructs to determine the requirements for optimal *in vivo* EryG activity. (A) Representative extracted ion chromatogram of (i) ErA production catalyzed by EryG from pSense-2, (ii) ErA production catalyzed by EryG from pSense-3, (iii) ErC standard, (iv) ErA standard. Calculated mass for ErA 734.4685 $[M+H]^+$ $[C_{37}H_{68}NO_{13}]^+$; observed mass for ErA standard 734.4689 (Δ, 0.54 ppm). Calculated mass for ErC 720.4529 $[M+H]^+$ $[C_{36}H_{67}NO_{13}]^+$; observed mass for ErC standard 720.4531 (Δ, 0.28 ppm). (B) Percentage conversion of ErC to ErA supported by *E. coli* BL21(DE3) harboring pSense-1 (calculated RBS upstream of EryG, wild-type MphR), pSense-2 (pET28a RBS upstream of EryG, wild-type MphR), and pSense-3 (Entry 14 in **Table 1**; T7 promoter and pET28a RBS upstream of EryG, wild-type MphR). Error-bars represent the standard error of the mean (n = 3). Representative observed mass for ErA produced by pSense-3 734.4677 (Δ, -1.1 ppm). Representative observed mass for ErC in pSense-3 sample 720.4515 (Δ, -1.9 ppm).

MPRPKLKSDDEVLEAATVVLKRCGPIEFTLSGVAKEVGLSRAALIQRFTNRDTLLVRMMERGVEQVRHYLNAIPI
GAGPQGLWEFLQVLVRSMNTRNDFSVNYLISWYELQVPELRTLAIQTNRAVVEGIRNRLPPGAPAAAELLLHSVI
TGATMQWAVDPDGELADHVLAQIAAILCLMFPEQDDFQLLQAHA

Supplementary Figure S9. Protein sequence of MphR M9C4 used for structural analysis.

SUPPLEMENTARY METHODS

Construction of M9C4 RBS variants and pCOLADuet-EryG

For construction of M9C4-A3, M9C4 -E7, and M9C4 -H4, the pMLGFPK-M9C4 plasmid was used along with the primers listed in **Supplementary Table S3** (entries 37-42). The eryG gene was sub-cloned into pET28a from pET21c-EryG (kindly provided by Dr. Blaine Pfeifer, University of Buffalo). It was then PCR amplified (using primers EryG_PCR_NcoI and EryG_PCR_HindIII, entries 43-44, **Supplementary Table S3**) and sub-cloned into pCOLADuet via the restriction sites *Nco*I and *Hin*dIII to generate pCOLADuet-EryG.

Construction of pSense_MphR_MphA (used for constructions of pSense-M9C4-MphA-EryG variants)

The pSense-2 plasmid containing *mphO* was ordered as two parts from Twist Bioscience and constructed using Gibson Assembly. MphR and MphA were PCR amplified out of pMLGFP and pJZ12, respectively using primers 45-48 (**Supplementary Table S3**). pSENSE2 was then PCR amplified using primers pSENSE.F and pSENSE.R (entries 49-50, **Supplementary Table S3**) to produce the vector fragment. The PCR products were evaluated using an agarose gel and the resulting products were extracted using an NEB Monarch Gel Extraction Kit. The three fragments were assembled via Gibson Assembly leveraging the NEBuilder Hifi DNA Assembly kit in accordance with the manufacturer's instructions. 2 μL of the Gibson Assembly were then transformed into *E. coli* Top10 competent cells and the construct was sequenced to confirm successful assembly.

Construction of pSense-M9C4-MphA-EryG variants

An RBS sequence identified via the RBS calculator was embedded into a 50 bp oligonucleotide (entry 51, **Supplementary Table S3**) that was synthesized by Integrated DNA Technologies. The RBS oligonucleotide was incorporated into pSense-MphR-MphA via Gibson Assembly using two primers (entries 52-53, **Supplementary Table S3**), furnishing pSense-MphA-MphR-RBScalculate. The sequencing data indicated 2 and 20 base pairs were randomly inserted before and after the 50-base oligonucleotide region in pSense-MphAR-RBScalculate but they are not expected to impact transcription/translation. The eryG gene was then amplified from pET28a-EryG and sub-cloned into pSense-MphA-MphR-RBScalculate via *Nde*I and *Kpn*I restriction sites to generate ‘pSense-1’ using primers 54-55 (**Supplementary Table S3**). To generate ‘pSense-2’, the calculated RBS from pSense-1 was substituted with the RBS from pET28a via Gibson Assembly using primers 56-57 and 59-60 (**Supplementary Table S3**). To generate ‘pSense-3’, the promoter in pSense-1 was substituted by the T7 promoter via Gibson Assembly using primers 57-59 and 61 (**Supplementary Table S3**). To generate ‘pSense-M9C4-E7-MphA-EryG’ (relevant to **Figure 5B-D**), wild-type MphR in pSense-3 was substituted with M9C4-E7 (amplified from pMLGFPK-E7M9C4) via Gibson Assembly using primers 62-65 (**Supplementary Table S3**).

In vivo assay of EryG activity

A 10 mL culture of BL21(DE3) containing the desired plasmids was grown in LB media supplemented with appropriate antibiotics at 37 °C with shaking at 250 rpm. The corresponding antibiotics for three-plasmid, two-plasmid and one-plasmid systems were ampicillin 67 μg/mL, tetracycline 3 μg/mL, kanamycin 33 μg/mL; ampicillin 67 μg/mL, kanamycin 33 μg/mL; and ampicillin 100 μg/mL. Cultures were grown to an OD_{600} ~0.6 at which point 50 μM ErC and 0.5 mM IPTG was added.

After incubating the cell culture at 37 °C and 250 rpm overnight, 1.5 mL of culture was withdrawn and centrifuged for 30 min at 10,000 *g*. Then, 500 µL of the supernatant was extracted three times with an equal volume of ethyl acetate and dried. The dried extract was resuspended in 200 µL of methanol for LC-HRMS analysis.

LC-HRMS analysis of ErA production

LC-HRMS analysis was performed by the NC State the Molecular Education, Technology and Research Innovation Center using a Thermo Fisher Scientific Exactive Plus mass spectrometer and Heated Electrospray Ionization (HESI). The sample was analyzed via LC-MS injection into the mass spectrometer at a flow rate of 500 µL/min. The mobile phase B was acetonitrile with 0.1% formic acid and mobile phase A was water with 0.1% formic acid. See **Supplementary Table S5** for the gradient and HESI source parameters. The mass spectrometer was operated in positive ion mode. The LC column was a Thermo Hypersil Gold 50 x 2.1 mm, 1.9 µm particle size. This assay produces ErA and ErC that can be seen as their $[M+H]^+$ ions. Calculated mass for ErA 734.4685 $[M+H]^+$ $[C_{37}H_{68}NO_{13}]^+$; representative observed mass for ErA 734.4689 (Δ, 0.54 ppm). Calculated mass for ErC 720.4529 $[M+H]^+$ $[C_{36}H_{67}NO_{13}]^+$; representative observed mass for ErC 720.4531 (Δ, 0.28 ppm). In every case, the error (Δ = [Difference/exact mass x 10^6]) was < 6 ppm.