

Supplementary Information

Figure S1. Long term stability study of the MCM determining the copy number of *N. meningitidis* (a) and *S. pneumoniae* (b). The figures show the mean of the bacterial copy number with SEM during storage of the sample.

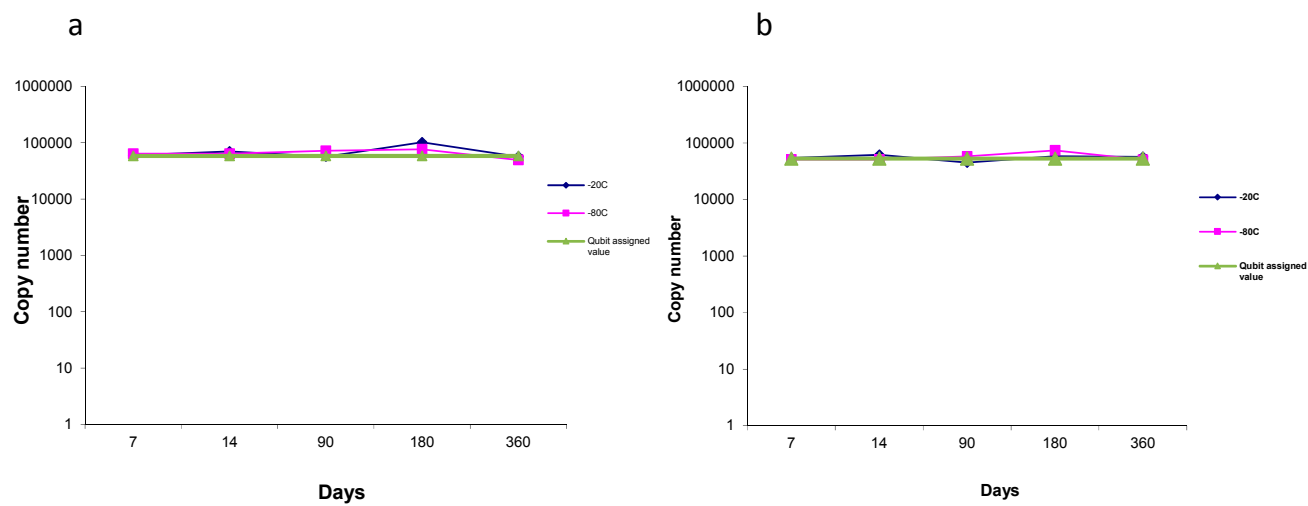


Figure S2. Gel electrophoresis on a flash gel (Lonza) showing gDNA integrity; M = Marker, MRSA = Methicillin-resistant *S. aureus*, MSSA = Methicillin-sensitive *S. aureus*, Sp n= *S. pneumoniae*, Spy = *S. pyogenes*, Sag = *S. agalactiae*, Ef = *E. faecalis*, Pa = *P. aeruginosa*, Kp = *K. pneumoniae*, Ab = *A. baumannii*, *E.coli* and *Nm* = *N. meningitides*.

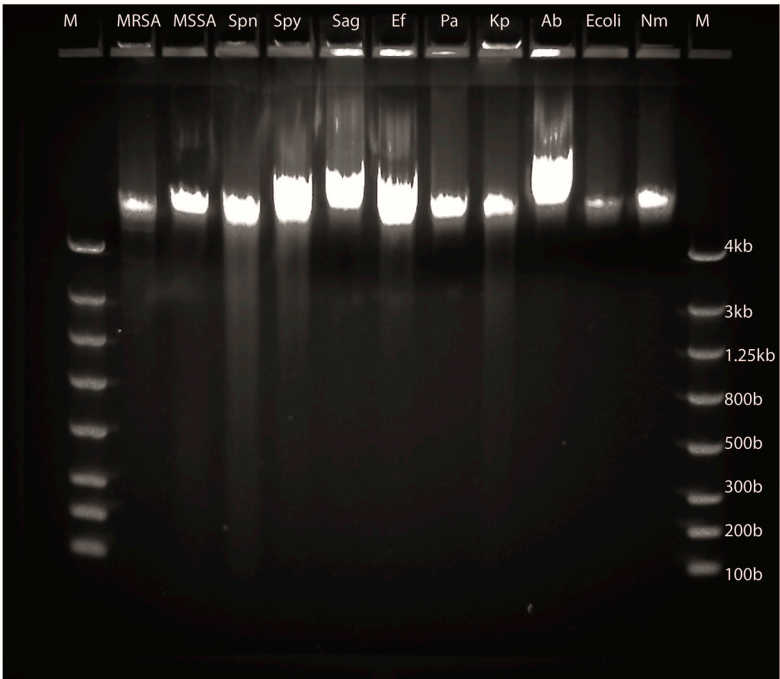


Figure S3. Variable region 1 and 2. Sequences in square indicate primer positions.

Alignment: Untitled

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      ....|....| ....|....| ....|....| ....|....| ....|....|
      10          20          30          40          50
Acinetobac ----- --AGAGTTTG ATCATGGCTC AGATTGAACG CTGGCGGCAG
Escherichi -----AAATT GAAGAGTTTG ATCATGGCTC AGATTGAACG CTGGCGGCAG
Klebsiella -----AATT GAAGAGTTTG ATCATGGCTC AGATTGAACG CTGGCGGCAG
Neisseria  -----TGAACA TAAGAGTTTG ATCCTGGCTC AGATTGAACG CTGGCGGCAT
Pseudomona -----GAACT GAAGAGTTTG ATCATGGCTC AGATTGAACG CTGGCGGCAG
      *****
      ....|....| ....|....| ....|....| ....|....| ....|....|
      60          70          80          90         100
Acinetobac GCTTAACACA TGCAAGTCGA GCGGGGGAAG GTAG--CTT GCTA-CTGGA
Escherichi GCCTAACACA TGCAAGTCGA ACGGTAACAG GAAKAGCTT GCTGATTTC
Klebsiella GCCTAACACA TGCAAGTCGA GCGGTAGCAC AGAG-AGCTT GCTC-TCGGG
Neisseria  GCTTTACACA TGCAAGTCGG ACGGCAGCAC AGAGAAGCTT GCTTCTCGGG
Pseudomona GCCTAACACA TGCAAGTCGA GCGGATGAAG GGAG--CTT GCTC-CTGGA
      ** * *****
      ....|....| ....|....| ....|....| ....|....| ....|....|
      110         120         130         140         150
Acinetobac C--CTAGCGG CGGACGGGTG AGTAATGCTT AGGAATCTGC CTATTAGTGG
Escherichi TGACGAGTGG CGGACGGGTG AGTAATGTCT GGGAACTGC CTGATGGAGG
Klebsiella TGACGAGCGG CGGACGGGTG AGTAATGTCT GGGAACTGC CTGATGGAGG
Neisseria  TGGCGAGTGG CGAACGGGTG AGTAACATAT CGGAACGTAC CGAGTAGTGG
Pseudomona T--TCAGCGG CGGACGGGTG AGTAATGCCT AGGAATCTGC CTGGTAGTGG
      * * * ** * *****
      ....|....| ....|....| ....|....| ....|....| ....|....|
      160         170         180         190         200
Acinetobac GGGACAACAT CTCGAAAGGG ATGCTAATAC CGCATACTGC CTACGGGAGA
Escherichi GGGATAACTA CTGGAAACGG TAGCTAATAC CGCATAACGT CGCAAGACCA
Klebsiella GGGATAACTA CTGGAAACGG TAGCTAATAC CGCATAATGT CGCAAGACCA
Neisseria  GGGATAACTG ATCGAAAGAT CAGCTAATAC CGCATACTGC TTGAGAGAGA
Pseudomona GGGATAACGT CCGGAAACGG GCGCTAATAC CGCATACTGC CTGAGGGAGA
      *****
      ....|....| ....|....| ....|....| ....|....| ....|....|
      210         220         230         240         250
Acinetobac AAGCAGGGGA TCTTCGGACC TTGCGCTAAT AGATGAGCCT AAGTCGGATT
Escherichi AAGAGGGGGA CCTTCGGGCC TCTTGCCATC GGATGTGCC AGATGGGATT
Klebsiella AAGTGGGGGA CCTTCGGGCC TCATGCCATC AGATGTGCC AGATGGGATT
Neisseria  AAGCAGGGGA CTTTCGGGCC TTGCGCTATT CGAGCGGCCG ATATCTGATT
Pseudomona AAGTGGGGGA TCTTCGGACC TCACGCTATC AGATGAGCCT AGGTCGGATT
      *****
      ....|....| ....|....| ....|....| ....|....| ....|....|
      260         270         280         290         300
Acinetobac AGCTAGTTGG TGGGGTAAAG GCCTACCAAG GCGACGATCT GTAGCGGGTC
Escherichi AGCTAGTAGG TGGGGTAAAG GCTCACCTAG GCGACGATCC CTAGCTGGTC
Klebsiella AGCTAGTAGG TGGGGTAAAG GCTCACCTAG GCGACGATCC CTAGCTGGTC
Neisseria  AGCTAGTTGG TGGGGTAAAG GCCTACCAAG GCGACGATCA GTAGCGGGTC
Pseudomona AGCTAGTTGG TGGGGTAAAG GCCTACCAAG GCGACGATCC GTAACGGTC
      *****
      ....|....| ....|....| ....|....| ....|....| ....|....|
      310         320         330         340         350
Acinetobac TGAGAGGATG ATCCGCCACA CTGGGACTGA GACACGGCCC AGACTCCTAC
Escherichi TGAGAGGATG ACCAGCCACA CTGGAAGTGA GACACGGTCC AGACTCCTAC
Klebsiella TGAGAGGATG ACCAGCCACA CTGGAAGTGA GACACGGTCC AGACTCCTAC
Neisseria  TGAGAGGATG ATCCGCCACA CTGGGACTGA GACACGGCCC AGACTCCTAC
Pseudomona TGAGAGGATG ATCAGTCACA CTGGAAGTGA GACACGGTCC AGACTCCTAC
      *****
      ....|....| ....|....| ....|....| ....|....| ....|....|
      360         370         380         390         400
Acinetobac GGGAGGCAGC AGTGGGGAAT ATTGGACAAT GGGGGGAACC CTGATCCAGC
Escherichi GGGAGGCAGC AGTGGGGAAT ATTGCACAAT GGGCGCAAGC CTGATGCAGC
Klebsiella GGGAGGCAGC AGTGGGGAAT ATTGCACAAT GGGCGCAAGC CTGATGCAGC
Neisseria  GGGAGGCAGC AGTGGGGAAT TTTGGACAAT GGGCGCAAGC CTGATCCAGC
Pseudomona GGGAGGCAGC AGTGGGGAAT ATTGGACAAT GGGCGAAAGC CTGATCCAGC
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Figure S4. Phylogenetic tree of the *mis*-annotated SILVA 16S rRNA sequences shown in Table S5 with example representative taxa for their SILVA annotations and the relevant MCM species 16S rRNA sequences. 1000 bootstraps were performed and are shown next to the nodes. The tree clearly shows that the SILVA sequences from Table S5 are in fact the MCM species that hit them rather than the taxa as listed in their SILVA annotations. The green highlight shows that those sequences which the MCM *K. pneumoniae* 16S rRNA sequence aligns against are in fact *K. pneumoniae* rather than *Stenotrophomonas*, *Rhodococcus*, *Achromobacter* or *Flavobacterium* as suggested by their SILVA classifications. The red highlight shows SILVA sequence JQ315432.1.1486 branching with *Pseudomonas aeruginosa* rather than *Acinetobacter*. Finally the blue highlight demonstrates SILVA sequence CACX01001585.64.1585 is closer to *Escherichia coli* than *Strongyloides ratti* as annotated.

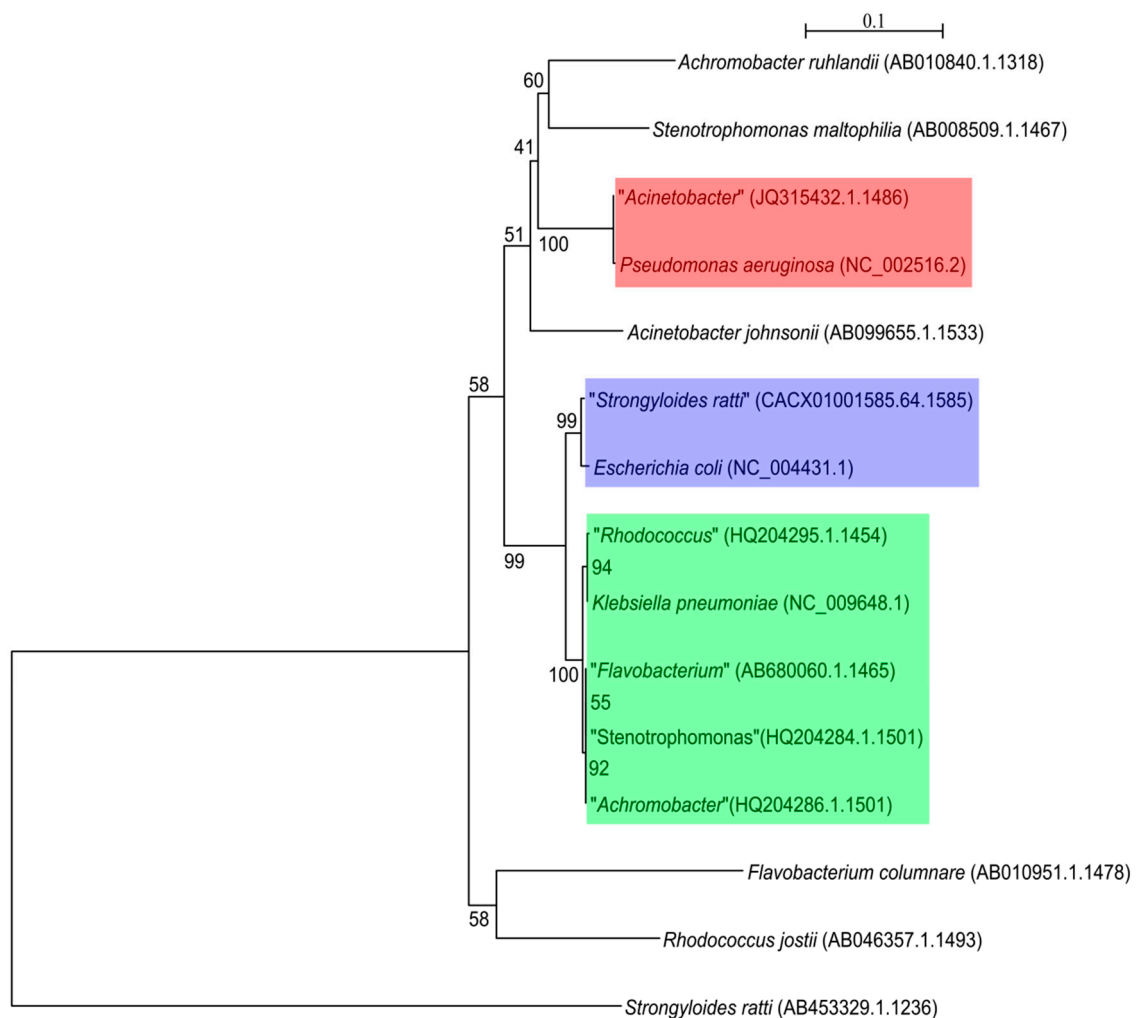


Figure S5. Amplification curves of specific target assay regarding its target bacteria and negative control (human genomic DNA). Amplification plots of specific-target assays obtained from Biomark 48.770 dPCR. Red lines indicate positive amplification and black lines correspond to no amplification. Negative control contains human genomic DNA instead of bacterial DNA. Panel 28: coA-*S. aureus*, Panel 06: coA-Human gDNA, Panel 05: uidA-*E. coli*, Panel 30: uidA-Human gDNA, Panel 13: lytA-*S. pneumoniae*, Panel 41: lytA-Human gDNA, Panel 45: ompA-*A. baumannii*, Panel 48: ompA-Human gDNA, Panel 34: Khe-*K. pneumoniae*, Panel 12: Khe-Human gDNA, Panel 37: csrR-*S. pyogenes*, Panel 18: csrR-Human gDNA, Panel 21: sip-*S. agalactiae*, Panel 24: sip-Human gDNA, Panel 08: groES-*E. faecalis*, Panel 36: groES-Human gDNA, Panel 17: regA-*P. aeruginosa*, Panel 42: regA-Human gDNA, Panel 01: ctrA-*N. meningitidis*, and Panel 29: ctrA-Human gDNA.

