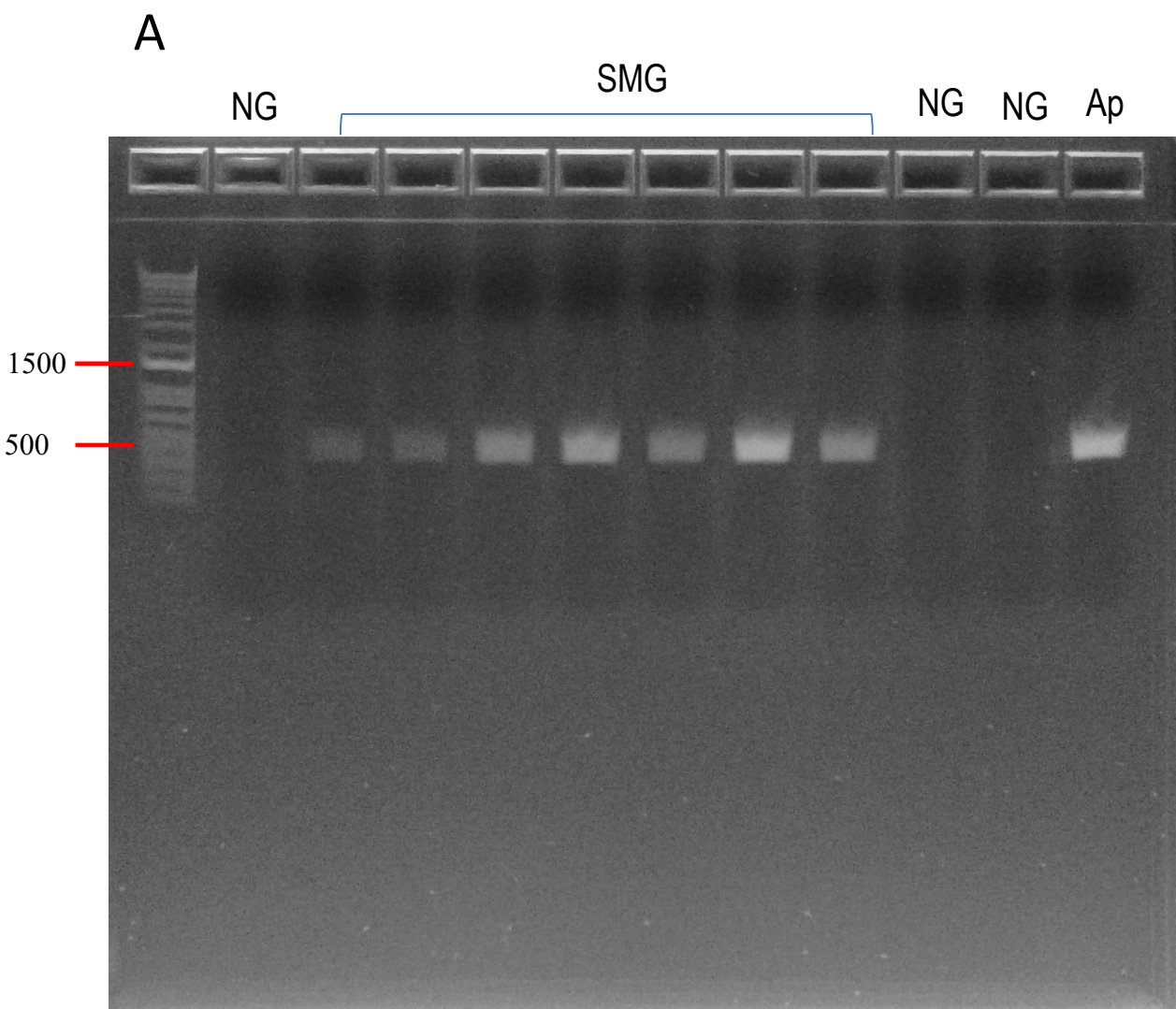


Supplementary figure captions

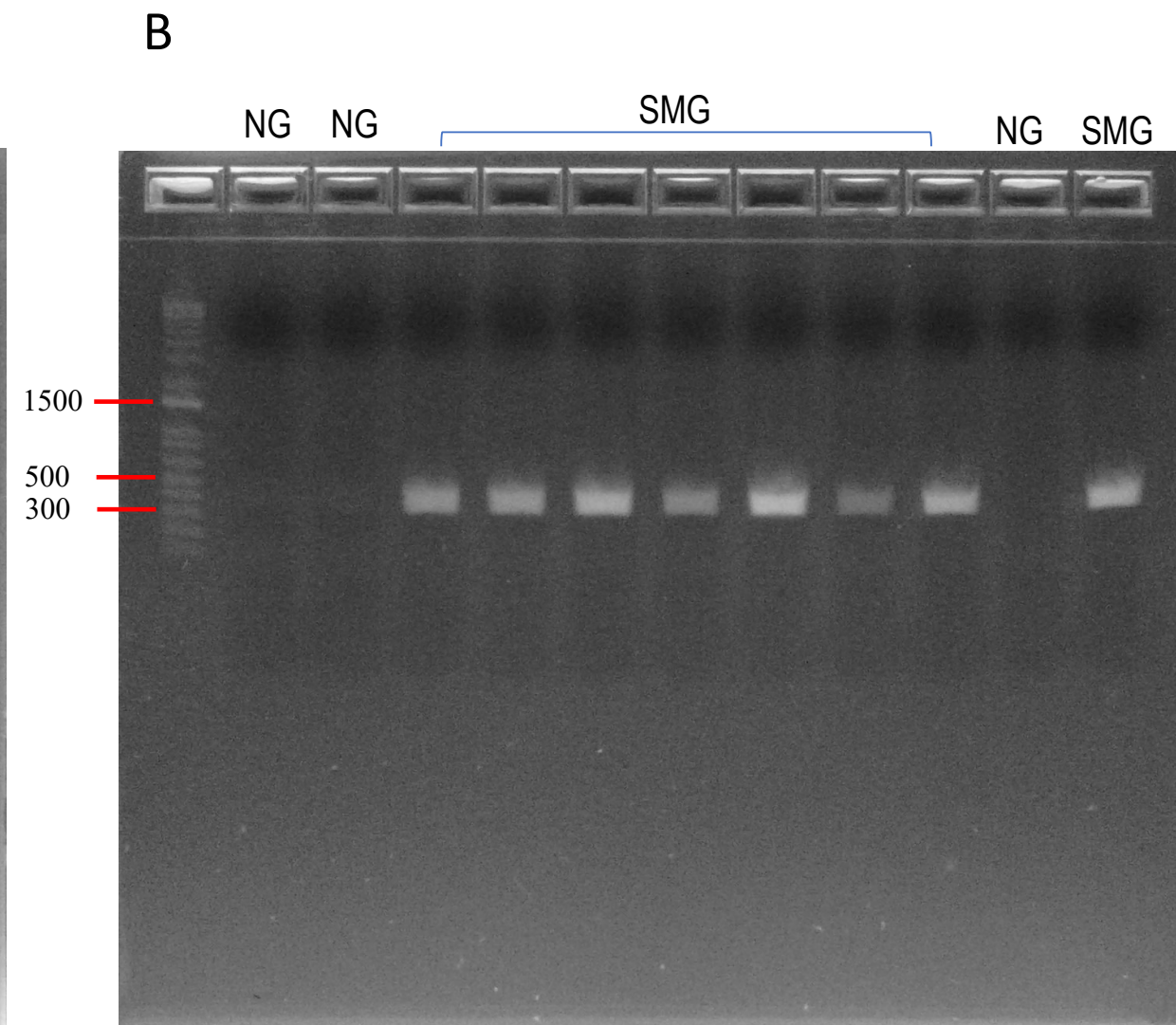
Figure S1. Representative gel images of PCR analysis when co-cultures were grown in simulated microgravity (SMG) or normal gravity (1G). Strong bands were visualized for both (A) *bla*_{OXA-500} and (B) *ISAbal* amplification in *S. aureus* isolates when co-cultured with the donor under SMG. This was in contrast to the absence of bands when grown under 1G. “Ap” indicates the positive control which is DNA extracted from *A. pittii* parental strain. The no template PCR control (NTC) and DNA extraction negative control had no bands on the gels.

Figure S2. Colony forming units of strains grown in SMG or 1G. The graph shows the counts of *S. aureus* grown on MSA after growth in SMG or 1G, either on its own or in a co-culture with *A. pittii*. There were no differences in growth regardless of single or co-culture growth or under the different growth conditions. The same analyses were performed for *A. pittii* but the data is not shown.

Figure S3. Schematic of where the designed primers (A) *bla*_{OXA-500} and (B) *ISAbal* are located in the *A. pittii* genome and the sequence of the PCR products.

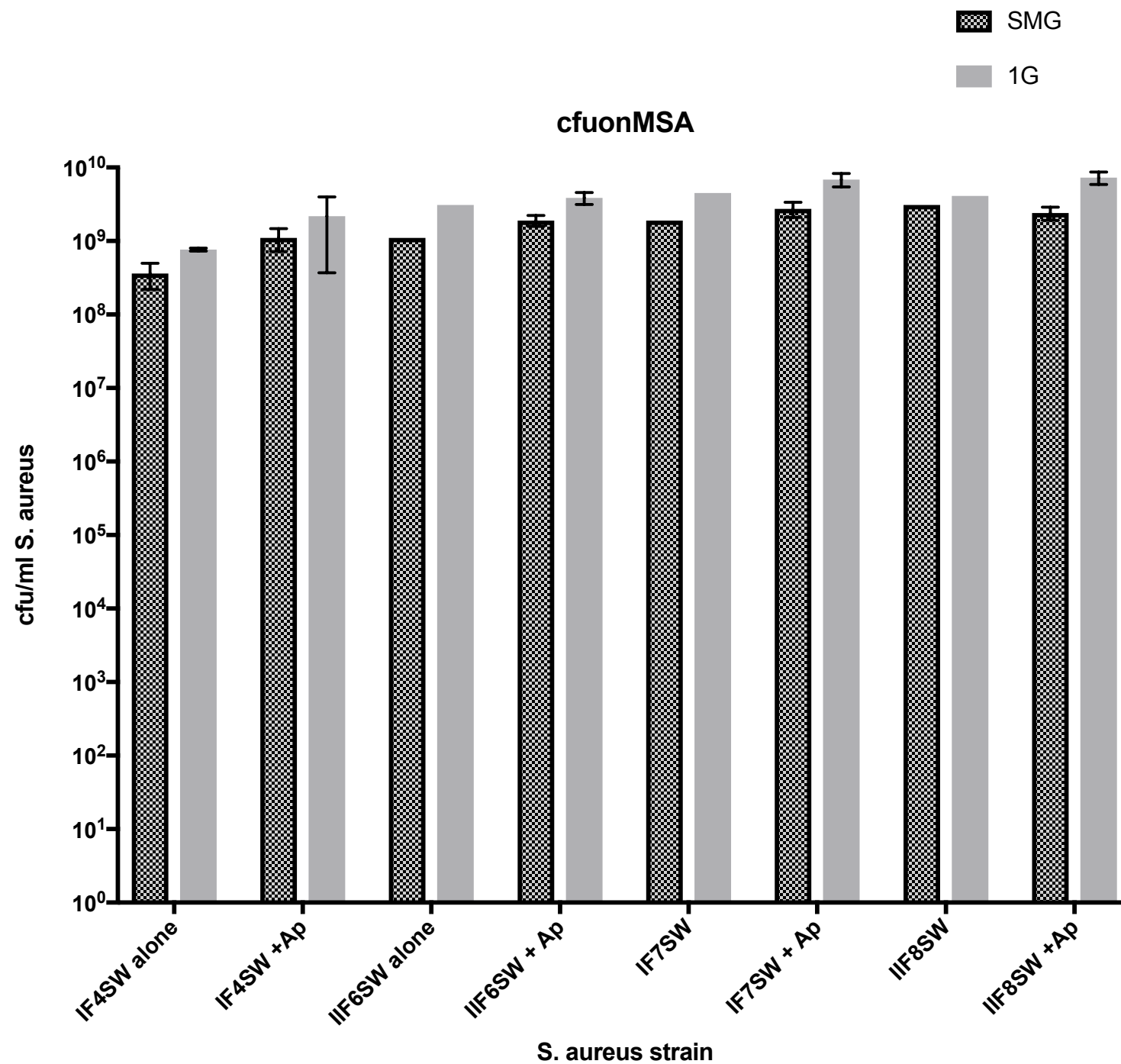


blaOXA500



Isaba1

Fig. S2



Genomic location on Acinetobacter pittii strain IIF1SW-P1

GenBank: MIZX01000006.1

Forward: 6387-6408

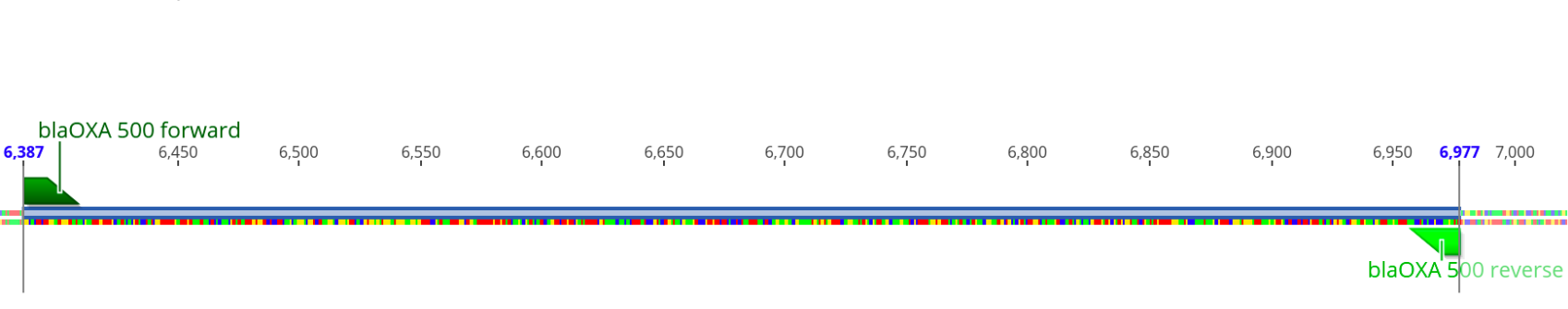
Reverse: 6958-6977

PCR product expected size: 591 bp

Sequence:

CCGAGTTGTTCCAATCCCTTATAAGCAATTTCTTTTCGAATAGAGCTAGGTATGCCTTTTTTTCATTTCTA
AATTAAGTGAGAAAGCTATAATTTCTCCTTGTGGTTGAACGACCCAGCCTGTTAACCAGCCCCTTGAGG
CTCCACATCCCATCCCCAACCACTTTTGGCATAAAATTTCCGTCCATTTTTTTCTTCTATGAACAGCATA
GATTGAACTTGTTCTTGCATATTTTTGCTAAAAGGAAGAGTTTTATGGGCTAGTTCATAAGCAAACCTGGG
CTTCTTGTTGAGGTGTAATTTTAAGTGGACCAACAAGCCAAAAATCATCTACTTTTGAACCAATATCAGC
ATTACCGAAACCAATGCGTTTTACCTCTTTAGACATAAGATCAAGGCCAATTCGTCGAGCTAGTTCCTGA
TAAACTGGAATAGCAGAAGCTTTCATCGCATCGCCTAATGTCATATCTTTTTCCCAATCGGGAAATAAAC
GCTTTTGCCCATCCCATTTAAACACTTCAGTTGGTGTGCTTTATGATGCTCAAGTCCAATCAAAGCATT
TAACATTTTAAAGGTAGAGGCGGGAACATAT

Primer Map:



Scaffold 44
GenBank: MIZX01000045.1

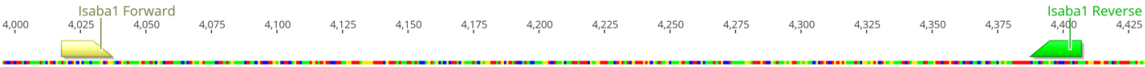
Forward: 4018-4037

Reverse: 4407-4388

PCR product expected size: 390 bp

Sequence:
ATGCAGCGCTTCTTTGCAGGTCAGTATTTTGATTATCGTCAAATTTCTCAGTTGATTTTCAATATGTTTT
CATTGACCAAGTGCAACTGACTTTAGATAGAACCAATTGGAAATGGGGAAAACGAAATATTAATATC
CTGATGCTCGCAATCGTTTATCGTGGAATAGCGATACCTATCCTTTGGACATTGCTTAATAAACGTGGA
AATTCAGATACGAAAGAGCGTATTGCTTTGATTCAACGCTTTATAGCCATTTTGGTAAAGACCGTATT
GTGAATGTGTTTCGCAGACAGAGAGTTTATCGGTGAGCAGTGTTTACATGGTTAATTGAACAAGACAT
CAACTTCTGCATTCTGTGTTAAAAAACTTCATTGTCACCAATCATT

Primer Map:



Scaffold 70
GenBank: MIZX01000070.1

Forward: 932-913

Reverse: 543-562

PCR product expected size: 390 bp

Sequence:
AATGATTGGTGACAATAAAGTTTTTTTAAACACGAATGCAGAAGTTGATGTCTTGTTCAATTAACCATGT
AAACCACTGCTCACCGATAAACTCTCTGTCTGCGAACACATTACAATACGGTCTTTACCAAAAATGG
AGATAAAGCGTTGAATCAAAGCAATACGCTCTTTTGTATCTGAATTTCCACGTTTATTAAGTAATGTCC
AAACGATAGGTATCGCTATTCCACGATAAACGATCGCGAGCATCAGGATATTAATATTTTCGTTTTCCCC
ATTTCCAATTGGTTCTATCTAAAGTCAGTTGCACTTTGTCTGAATGAAAATATATTGAAAATCAACTGAG
AAATTTGACGATAATCGAAATACTGACCTGCAAAGAAGCGCTGCAT

Primer Map:

