

SUPPLEMENTAL MATERIAL

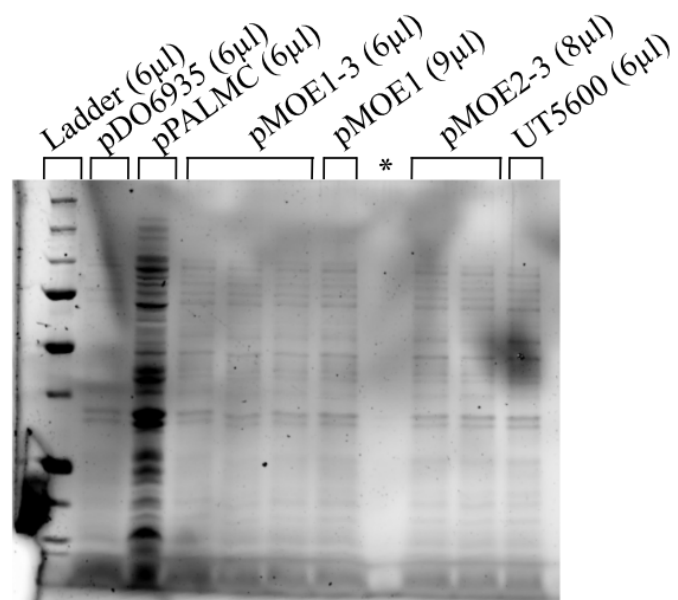


FIG. S1 SDS-PAGE gel confirms presence of resolvable proteins in all samples. 12% acrylamide SDS-PAGE gel of IPTG-induced, whole cell lysate samples and controls in Laemmli with 5% BME, run alongside Precision Plus Protein™ unstained standards. Gel was imaged using UV illumination. Asterisk indicates an empty lane. Controls include pDO6935-transformed DH5α cell lysates, pPALMC sample (obtained from team 1 epsilon), and untransformed UT5600 cell lysates. Volumes were loaded as indicated.

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FIG. S2 Sequencing results of pMOE1. Whole plasmid Nanopore sequencing (Plasmidsaurus) results of pMOE1 after extraction from transformed *E. coli* NEB 5-alpha. The obtained sequence corresponds exactly to the unmodified pENS plasmid sequence, with the exception of 12 additional base pairs corresponding to the inserted ScaI sites highlighted in red.

AAAAAAAAA C C C C C C C A G G T T C G C C T G G C G G G T T T T C A T T G G A G C T C G C T C A G A A G C T G T A G C G G T A G C C G G C T G G A A C G A C C A C G G A A T G T T G A
T C C G G T C G C C C G C G T A C T C G T A C G A A G C A T A G A G G T T G T G C C C T T G C C C A A C G C G G C G T C G A C G C C C G C C C A G T T C C A C G C G G C C T G G C G G C
C T G C G C C G C A T G G C C A A T G C C A T T G G T G C G C A C A T C G C C C G T G C T T T T G A A C T C T G C G T C C A G C C G A G C C T G G C G T A G G G T G C A C G A T G T T G C C G C
C G G C C A G G G C G A T G C G G C G G C C A A G C G C A A G C C C A G G C G G C C A G C G T G G C G G T G T T G G C G T C C A C T T G A C G C G A G G C A T T G T G G C G C G A T A G
C G T T G C C T G A C G T G C G C C A C A G A T G A C C T C G G C T G C G G T T C G G C G A A C C A G T C G T T G G G C A G C T C G A A C C G G C G C C C G C C T T C G A G C G A C C A T G C G
G C G C C G T T G T G C G G T A G T C G G C G G T A C G C G G C C G C A T C G G T G C C G G C A A T G T T G A T T G C T G A T C G T A G C G G C C A G C C C A G C C G C A G C A C G G T G T C G A G
A T A G T A G C C C C A T C G C C G A C A T A G G C G G C T A G C C G C G A C T G C A G G C C T T G A C C T T G C C G C C A C C G T C G C C G G G A T A G G T G C G G T C G C A T A G G
T G A C C C G C A A C T G C T T C T G C C C G G C G A C G T T G G T G T T C A G C A C G A A C A C G C C G T T G C C G T C C A G G G T T G C A G G G T C A G G G T C T T G T A A G A G G
T G T A G C C G A G C A G G C C G C G T A C C A G C G C C C G A C G C G C T C C A G C C A C G G T C C A G C C C G T G A C C G T G A C C G T G A C C G T G A C C G T G T G T C G T A G G C G
C G G G C T G G C G G T T G C T G A T C T G C T G G C G C T C G T G A A C G T A C G C G C C A T G G C C C G C G G C T C G G C G C G A G G C G A G C T C G C C A G G C G T T G T C C
A G C G C G T T G G A C T C G G C C A G G G C G A T G C T G G A A A G A T C C G C C G T T C A C G G C G C A T T G G C C G C C C C G A C A G G G C C T G G C C C G C G C T G C A A G C T
C C A G A C A T G C G T T T C G G A T C C T C C G C C A G G C T G T A G C G C C A C G T G C C A G G T C A A C C G C C T T G C C G A C G T T G G C C A G C C G G A A G G T G G C G T T G C C C T G
C C C C T G G G A T G C A C C A G G C C A G G C G G G C G C C C G G C T G T C G G C T C G C C T C C G G C A T T G C G C A C C A G C C G G T G C T G G C C A T C G G C G C G G C C G
T G A C C C G C A A C T G C T T C T G C C C G G C G A C G T T G C C G C T C G C C T C C G G C A T T G C G C A C C A G C C G G T G C T G G A A T T G C A A A C C G A C C C G G C C G
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G C G T G G C C G A C T G G A G C A C T G G G T G G C C C G T G C C A G G C G G C C G T G C C A C G T A G A G A T T G C G C A G T A T C C A A A G C C C A C G T C A T A A T G A A T G C C G G
A C G A T A T C G C C G A G C C A G G C C G C C T C T C G A G G C A A C C G C A C C G G A A T G G T G G A A T G C T G G A G G A A C A C G C C A T T G C C G C T T G C C G C T T G A A G A G
T G G T G C G C A C C G C A T G T C A T T C G G C C T G G T G T G T G C G T G T T C T G T G C T T T C G T G A C C C T A A C G C G G C T G G G C G C G G C C A A G G
G A T A C T A C G G C G A T C A T G G A G C A C A T C G G C C T T C G C G A T G G C G G C G A C T G G C T G T C G A A C C T C T T T C G T T C G C G G T G G T A C C G C G C T G T T C G C C G
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T C G G C C T G A C C T G G G A C G C G G C G G C G G T A T C G G C T A C G G G C G G C G G T T C G T G A T C G C G T G T G T G G A T C T A T T A T C A G C G A G A T T T
T C T T C T C G G C C G C T T C A C C C G C A G T T C G C C A G G C T T C G G C A G C C T G C G C G G C C G C C C C G C C T G A A G G C G G C A G G C G G C C G C C A C C G C G G
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T C C A C A C A A C A T A C G A G C C G G A A G C A T A A A G T G T A A A G C C T G G G G T G C C T A A T G A G T A G A C T A A C T C A C A T T A A T T G C G T T G C G C T A C T G C C C G T T T
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A G A A C A T G T G A G C A A A A G G C C A G C A A A A G G C C A G G A A C C G T A A A A A G G C C G C G T T G C T G G C G T T T T C C A T A G G C T C C G C C C C C T G A C G A G C A T C A C
A A A A C T C G A C G C T C A A G T C A G A G G T G G C G A A A C C C G A C A G G A C T A A A A G A T A C C A G G C G T T T C C C C T G G A A G C T C C C T C G T G C G C T C T C T G T T C C G
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T T C G C T C C A A G C T G G G C T G T G T G C A G A A C C C C C G T T C A G C C C A C C C G T G C G C C T T A T C C G G T A A C T A T C G T T T G A G T C C A A C C C G G T A A G A C A C G
A C T T A T C G C C A C T G G C A G C A G C C A C T G G T A A C A G G A T T A G C A G A G C G A G G T A T G T A G G C G G T G C T A C A G A G T T C T T G A A G T G G T G G C C T A A C T A C G G C
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G A C T C C C C G T C G T G A G A T A A C T A C G A T A C G G G A G G C T T A C C A T C T G G C C C A G T G T G C A A T G A T A C C G C G A G A C C A C G C T A C C G G C T C C A G A T T
T A T C A G C A A T A A A C C A G C C A G C C G G A A G G C C G A G C G C A G A A G T G G T C C T G C A A C T T A T C C G C C T C C A T C C A G T C T A T T A A T T G T T G C C G G G A A G C T A
G A G T A A G T A G T T C C C A G T T A A T A G T T G C G C A A C G T T G T T G C A T T G C T A C A G G C A T C G T G G T G T C A C G C T C G T C G T T T G G T A T G G C T C A T T C A G C T C
C G G T T C C C A C G A T C A A G G C G A G T T A C A T G A T C C C C A T G T T G T G C A A A A A A G C G G T T A G C T C C T C G G T C C C G A T C G T T G T C A G A A G T A A G T T G G C
C G C A G T G T T A C A C T C A T G G T T A T G G C A G C A C T G C A T A A T T C T T A C T G T C A T G C C A C C G T A A G A T G C T T T T C T G T A C T G G T A G T A C T C A C C A A G
T C A T T T C G A A A T A G T A T G C G G C A C C G A G T T G C C T T C G C C C G G C T A A T A C G G G A T A A T A C C G C G C A C A T A C C G C G C C A C A T A G C A G A A C T T T A A A A A G T G C T A C
A T T G G A A A A C G T T C T T C G G G C G A A A A C T C T C A A G G A T C T T A C C G C T G T T G A G A T C C A G T T C G A T G T A A C C C A C T C G T G C A C C C A A C T G A T C T T C A G C A
T C T T T A C T T T C A C C A G C G T T T C G G G T G A G C A A A A C A G G A A G G C A A A A T G C C G C A A A A A A G G G A A T A A G G G C G A C A C G G A A A T G T T G A A T A C T C A T
A C T C T T C C T T T T C A A T A T T A T T G A A G C A T T T A T C A G G G T A T T G T C T A T G A G C G G A T A C A T A T T T G A A T G T A T T T G A A A A A T A A A C A A A T A G G G G T T
C C G C G C A C A T T C C C C G A A A A G T G C C A C C T G A C G C G C C C T G T A G C G G C G C A T T A A G C G C G G C G G G T G T G G T G G T T A C G C G A C G G T G A C C G C T A C A C T T
G C C A G C C C T A G C C C G C T C C T T T C G C T T C T T C C C T T C C T T C T C G C A C G T T C G C C G G C T T T C C C C G T C A A A C G A G C T A A A T C G G G G G C T C C C T T A G G
G T T C C G A T T T A G T G C T T T A C G G C A C C T C G A C C C C A A A A A A C T T G A T T A G G G T G A T G G T T C A C G T A G T G G G C C A T C G C C C T G A T A G A C G G T T T T C G C C C T
T T G A C G T T G G A G T C C A C G T T C T T A A T A G T G G A C T T T G T T C C A A A C T G G A A C A C A C T C A A C C C T A T C T C G G T C T A T T C T T T T G A T T A T A A G G G A T T T T
G C C G A T T T C G G C C T A T T G G T A A A A A A A T G A G C T G A T T A A C A A A A T T T A A C G C G A A T T T A A C A A A A T A T T A A C G C T T A C A A T T C C A T T C G C C A T T C
A G G C T G C G C A A C T G T T G G A A G G G C G A T C G G T G C G G C C C T T C G C T A T T A C G C C A G C T G G C G A A A G G G G G A T G T G C T G C A A G G C G A T T A A G T T G G G T
A C G C C A G G G T T T C C A G T C A C G A C G T T G T A A A A C G A C G G C C A G T G A G C G C G C G T A A T A C G A C T C A T A G G G C G A A T T G G G T A C C G G C C C C C C C
T C G A G G T C A C G G T A T C G A T A A G C T T G A T A T C G A A T T C C T G C A A C G C C C C T T C G G T G G C C A G C C T G C T G T A C G G C C G A A G C C C G T G G T C G A G C
T G A T G G A A A A A A G C C C G T G T G C T C C G G C A A T G C C C G G C G C A T G G G C G C A T G G C G G C A T G G A C T T C T A A G T C C C G C C T T C C G G C C G A A A C C G
C C G G G C T T G C C G C G C G C G C C T T C C C

FIG. S3 Sequencing results of pMOE2. Whole plasmid Nanopore sequencing (Plasmidsaurus) results of pMOE2 after extraction from transformed *E. coli* NEB 5-alpha. The obtained sequence

corresponds exactly to the unmodified pENS plasmid sequence, with the exception of the planned deletion of 1002 base pairs in the *brkA* passenger domain region, 12 additional base pairs corresponding to the inserted ScaI sites highlighted in red, and 1 unintended additional base pair at the beginning of the sequence highlighted in pink.

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AAAAAAAAACCCGCCAGGTTCCGCTGGCGGGTTTTTCATTGGAGCTCGCTCAGAAGCTGTAGCGGTAGCCGGCGTGAACGACCACGGAATGTTGAT
CCGGTCGCCC GCCGCTACTCGTACGAAGCATAGAGTTGTGCCCTTGCCCAACCGGGCGTCGACGCCCGCCAGTTCACGCGGCCGTTGGCGGCC
TGCGCCGGCATGGCCAATGCCATTGGTGGCACATCGCCCGTGCTTTGAACCTCTGCGTCCAGCCGAGCCTGGCGTAGGGCTGCACGATGTTGCCGCC
GGCCAGGGCGATGCGCGGCCGAAGCGCAAGCCAGGCGGCCAGCGTGGCGGTGTTGGCGTCCACCTTGACGCGCAGGCCATTGCTGGCGCGATAGC
GCTTGCTGACGTGCGCCACAGCATGACCTCGGCTGCGGTTCCGGCGAACAGTCTGGTGGCAGCTCGAACCGGCCCGCCCTTCGAGCGACCATGCGG
CGCCGTTGTGCGGTAGTCGGCGGTGACGCGGCCCGCATCGGTGCCGGAATGTTGATTTGCTGATCGTAGCGGCCAGCCGACGACGGTGTGAGAT
AGTAGCCGCATCGCCGACATAGCGGGCTAGCCCGGACGTGACGCCCTTGACCTTGCCGCCACCGTCGCCGGGATAGGTGCGGTCCGGCATAGGTG
TAGCCGAGCAGGCCGCCGGCTACCAGCGCCCGCCGACGCGCTCCAGCCAGGTCAGGCCGATCTCCAGCCCGTGACCGTCTGGTCTAGGCGCG
GGCGTGGCGGTTGCTGATCTGCTGGCGCTCGTGAACGTACGCGCCATGGCCCGCGGGCGTGGCGCGCAGGCCAGCTCGCCAGGCGCTTGTCCAG
CGCGTTGGACTCGCCAGGGCGATGCTGGAAGATCCGCCCGTTCACGGCGCATTGGCCGCCCGCCGACAGGGCCTGGCCCGCGCTGCAAGCTCC
AGACATGCGTCTTCGGATCTCCGCCAGGCTGTAGCGCCACGTGCCAGGTCAACCGCTTGCCGACGTTGGCCAGCCGGAAGGTGGCGTTGCCCTGCC
CTGGGTATGCACCAGGCCAGGCGGGCGCCCGGCTGCGGCTCGCCTCCGGCATTGCGCACAGCAGCGGTGCTGGCCATCGGCGGGCGGGTGC
ACCCGCAACTGGTCTTCTGCCCGGGCGACGTTGGTGTAGCACGAACACGCCCTTGCCAGGTTCCAGGGTTTCAGGGTCAAGGCTTGTAAAGAGGCC
TCAGTACTAGTACTGTCGCCGTTGTCGAACTCTCTTCTGTTGGTGGTATGATGATGCCCGCGCTCTGCGCATGCGGGCGCCGGCCACGGGCGGC
TGCGGCGCTGCGCCCGCGGGCGCCAGCCGGCCATGCCGGCAGCGCCAGAGCTGCGGCCAGCGCATGCAGGCGCCACGCGGAACGCGGGATCT
GCAAGGAAGACGGACATTGACGGAATCTATCGAGATACATGTGCCACAAAAGAGAAGTTGAACAAAACCGACCCGCTGCCGTACGACGCCGGTGAC
GCGAAGGAAAACGACTGCGTCCCGGGCGGATCAGGCACGAGCCATGCGGGGATTTGCGCAGTATCCAAAGCCCACGTCAATGAATGCCGGATGAAGT
CCGAGGCCCAAGAGCTTTCTGAATAGCCGTGCTTCTATGAGAATTGCGCACGCTCAAGGAAGACAAGAGCGGTTTGCAGGGGCTGGTGGC
CAGCCGATGCTGTCATTCCGGCTTGTGCTGGTGGCGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
CGGCGATCTATGGAGCACATCGGCCTTCGCGATGGCGGCCGACTGGCTGTCGAACCTCTTTTCGTTCCGCGTGGTGACCGCGCTGTTCCGCGTGGTCTAC
AAGCTGCTGCCAGCAAGCGCATTCCTGGCTCGACGTGATACCCGGCGGATCGTGACCGCGGCGCTGTTCTGGCCGGCAAATGGGGCATCGGCCCTG
TACCTGGGACGCGCGCGGGCGGTATCGGGCTACGGGCGCGGGTTCGCTGATCGCGCTGCTGCTGTTGATCTATTATTCAGCGCAGATTTCTTCTTCT
GGCGCGTCTTACCCGGCAGTTCGCGGAGCGCTTCGGCAGCCTGCGCGGGCGCCCGCCCTGAAGGCGGACGGCGGCCACCGCGGTGGAGCT
CCAGCTTTTGTCCCTTAGTAGGGTTAATTGCGCGCTTGGCGTAATCATGGTATAGCTGTTTCTGTGAATTTGTTATCCGCTCACAAATCCACAC
AACATACGAGCCGGAAGCATAAAGTGTAAAGCTGGGTGCTAATGAGTGAAGTCAACTACATTAATTGCGTTGCGCTCACTGCCCGCTTCCAGCTG
GGAAACCTGCTGTCAGCTGCATTAATGAATCGGCCAACGCGGGGAGAGGGGTTTGGCGATTGGGCGCTCTCCGCTTCTCGCTCACTGACTCG
CTGCGTCCGTTGCTGCTGCGGCGAGCGGTATCAGCTCACTCAAAGCGGTAATACGGTATCCACAGAATCAGGGGATAACGCGAGGAAAGAACAT
GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTGTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATC
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CAGCTACGGGATAGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTACGCTAGGTATCTCAGTCTGAGTATCTCAGTCTGAGTCTGAGTCTGCTCC
AAGCTGGGCTGTGTGACGAACCCCGTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGGTAAGACACGACTTATCG
CCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAG
AAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCCTGGTAGCGG
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AAACTCAGTTAAGGATTTTGGTATGAGATTATCAAAAAGGATCTTACCTAGATCCTTTAAATTAATAAAGTAAATTAATCAATCAATCAAGTAT
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GTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCA
ATAAACAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGT
AGTTCGCCAGTAAATAGTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACAGCTCGTCTGTTGGTATGGCTTCACTCAGCTCCGGTTC
AACGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGCGGTTAGTCTCTCCGTTCCCGATCGTTGTGCAAGTAAGTTGGCCGAGTGT
TATCACTCATGGTTATGGCAGCAGTGCATAATCTCTACTGTCAATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGGTACTCAACCAAGTCACTTGC
AGAATAGTGTATGCGGCGACCGAGTTGCTTTCGGCGCGTCAATACGGGATAATACCGGCCACATAGCAGAACTTAAAGGATTTGAAAGTAAAG
AACGTTCTTCGGGGGCAAAACTCTCAAGGATCTTACCGTGTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTACGATCTTTTAC
TTTACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGGAATAAGGGCGACCGGAAATGTTGAATACTCATACTCTTCC
TTTTCAATATATTGAAGCATTATCAGGGTATTGTCTCATGAGCGGATACATATTTGAATGATTTAGAAAAATAAACAAATAGGGGTTCCGCGCAC
ATTTCCCGAAAAAGTGCCACCTGACGCGCCCTGTAGCGGGCATTAAAGCGGGCGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGC
CTTAGCGCCGCTCCTTTCGTTCTTCCCTTCCTTTCGCCAGTTCGCCGGCTTCCCGTCAAGTCTAAATCGGGGGTCCCTTAGGGTTCGAT
TTAGTGTTCAGCGCACCTCGACCCCAAAAAAAGTATTAGGGTATGAGTTACGTTAGTGGCCATCGCCCTGATAGACGTTTTCGCCCTTTGACGTT
GGAGTCCACGTTCTTAAATAGTGGACTCTTGTTCAAAAGTGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGAATTAAGGGATTTTGGCGATTT
CGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTAACCGCAATTTAACAAAATATTAACGCTTACAATTTCCATTGCCATTAGGCTGC
GCAACTGTTGGAAAGGGCGATCGGTGCGGCCTTCTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCA
GGGTTTCCAGTACGACGTTGTAACACGACGGCCAGTGAAGCGCGCTAATACGACTACTATAGGGCGAATGGGTACCGGGCCCCCTCGAGGT
CGAAGTATCGATAAGGCTGATCAATTCCTGAGAACCGCCCTCGGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
AAACAAGCCCGTGTGCTCCGGCAATGCCCGCGCATGGGCGCATGGGCGGCATGGACTTCTAAGTCCCGCTTCCCGCGGAAACCGCCGCGC
TTGCCGCGGCGGCCTTCC
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FIG. S4 Sequencing results of pMOE3. Whole plasmid Nanopore sequencing (Plasmidsaurus) results of pMOE3 after extraction from transformed *E. coli* NEB 5-alpha. The obtained sequence corresponds exactly to the unmodified pENS plasmid sequence, with the exception of the planned deletion of 1596 base pairs in the *brkA* passenger domain region and 12 additional base pairs corresponding to the inserted *ScaI* sites highlighted in red.