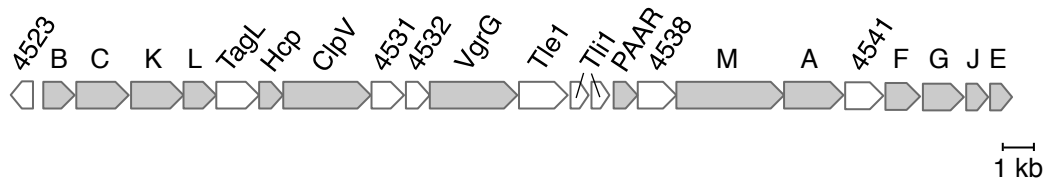


## Supplemental Fig S1

A

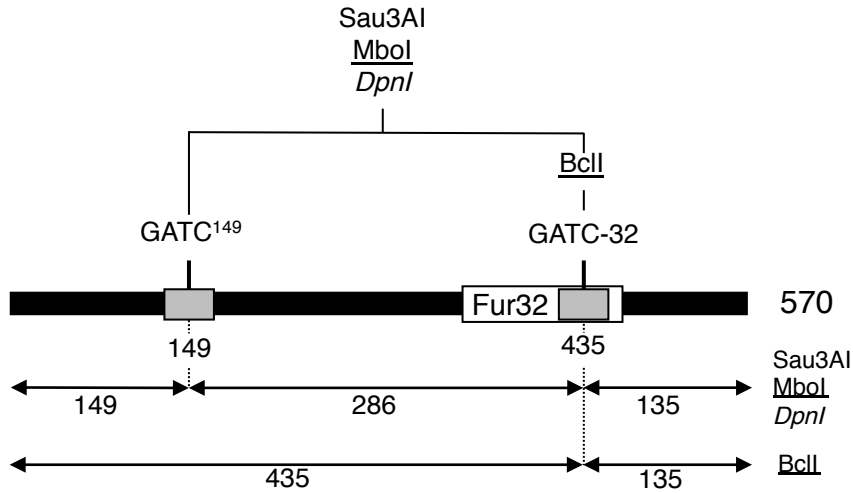


B

<i>tssB-tssC</i> TGA(N) <sub>21</sub> <b>atg</b>	<i>tssC-tssK</i> TAA(N) <sub>15</sub> <b>atg</b>	<i>tssK-tssL</i> <u>caTGA</u> at -4	<i>tssL-tagL</i> TAA(N) <sub>2</sub> <b>atg</b>
<i>tagL-hcp</i> TAA(N) <sub>5</sub> <b>atg</b>	<i>hcp-clpV</i> TAA(N) <sub>159</sub> <b>gtg</b>	<i>clpV-4531</i> <u>ttaTGA</u> cc -4	<i>4531-4532</i> <u>atggTAA</u> -7
<i>4532-vgrG</i> <u>atgaatctcacTGA</u> -14	<i>vgrG-tle1</i> gaa <b>TGA</b> ca -4	<i>tle1-tli1</i> TAA(N) <sub>19</sub> <b>atg</b>	<i>tli1b-PAAR</i> TGA(N) <sub>31</sub> <b>atg</b>
<i>PAAR-4538</i> TAA(N) <sub>3</sub> <b>atg</b>	<i>4538-tssM</i> <u>aatgaaTAA</u> a -8	<i>tssM-tssA</i> gac <b>TGA</b> tggct -1	<i>tssA-4541</i> TGA <b>atg</b>
<i>4541-tssF</i> TGA(N) <sub>7</sub> <b>atg</b>	<i>tssF-tssG</i> <u>atg(N)<sub>40</sub>TAA</u> -46	<i>tssG-tssJ</i> <u>atg(N)<sub>14</sub>TAA</u> -20	<i>tssJ-tssE</i> TAG(N) <sub>2</sub> <b>atg</b>

**SUPPLEMENTAL FIG 1** (A) Schematic organization of the EAEC *sciI* T6SS gene cluster (*EC042\_4524* to *EC042\_4545*). Genes encoding T6SS core components are indicated in grey. Accessory genes or of unknown function are represented in white. (B) Intergenic regions of the genes of the *sciI* gene cluster. Stop codons are indicated in capital letters whereas the start codons of the next genes are indicated in bold letters. The number of nucleotides (N) between stop and start codons is indicated. When the start codon locates within the preceding gene, the position of the start codon relative to the stop codon is indicated in green.

## Supplemental Fig S2



**SUPPLEMENTAL FIG 2** Schematic representation of the  $P_{4532}$  promoter region. The positions of the Fur box (Fur-32) and of the GATC sites are indicated (GATC<sup>149</sup>, distal GATC at position 149 and GATC-32). The two GATC sites are targets of the Sau3AI, MboI and *DpnI* enzymes, whereas the GATC-32 motif is part of a palindrome sequence recognized by BclI. Methylation-sensitive (MboI and BclI), -insensitive (Sau3AI) or -dependent (*DpnI*) restriction enzymes are underlined, in plain letters or in italics respectively. The size of the digestion products obtained for each enzyme (if accessible for digest) is indicated.