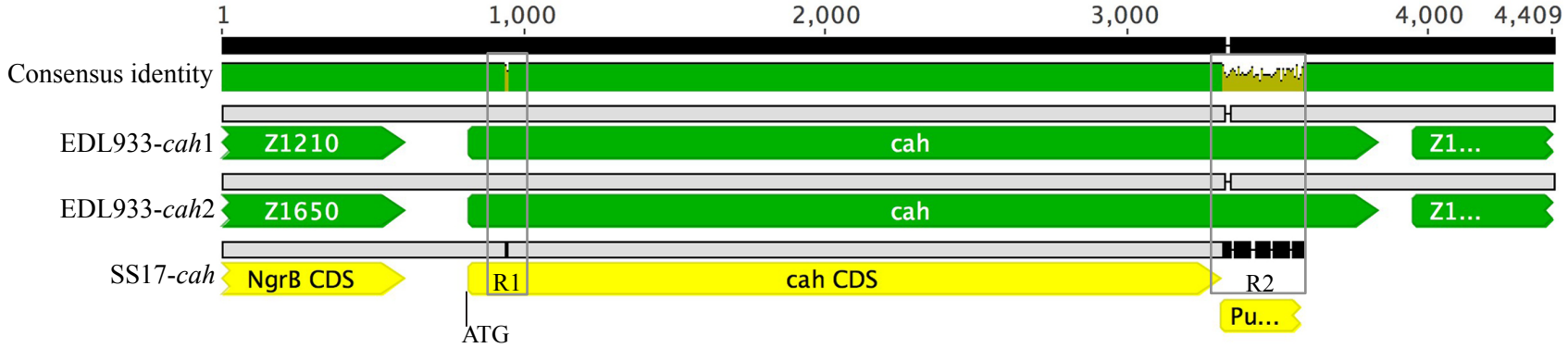
A



B

ATCACTGACCTGCCCGGGGTGGGCGAGAGCCGGGACAGGGATGCAGAGTATGAAGCCCTGTACCGTGACATTCTGCCTGAACTGGACTTGGTACTGTGGC

-35 box -10 box

TG**A**TTAAAGCCGATGACCGTGCCCTGTCTGTGGATGAGTATTTCTGGCGACACATACTGCACCGGGGACATCAGCAGGTGCTGTTTGTGGTGACGCAGGC

+1

CGACAAAACAGAGCCCTGCCATGAATGGGATATGGCAGGTATTCAGCCTTCTCCCGCACAGGAACAGAACATTCGCGAAAAAACAGATGCGGTATTCCGG

CTGTTCCGGCCCGTACATCCGGTTGTTGCCGTATCGGCCCGCACCGGCTGGGAACTGGATACGCTGGTCAGTGCGCTCATGACAGCGCTTCCCGACCATG

CCGCCAGTCCCCTGATGACCCGCCTGCAGGACGAGCTGTGCACGGAATCTGTCTGGGGGCAGGCCCGTGAACAGTTTACCGGTGCGGTGGACCGGATATT

TGACACGGTGGAGAGCGTCTGTGTTGCCTCTGTTGCACGCACAGTTCTGCGTGCCGTCCGTGACACGGTGGTCTCTGTTGCCCGCGCGGTATGGAACTGG

ATTTTCTTCTGAACAGTCTGCCAGGGGAAATGTCTGATTACATTGCGTTAACCAACTGAAAACATGATACAAACACCTCATGCCCCTCCTGTTTCTCTTG

-35 box

CGTGACTGCTCTACTGTTAATAGAATAAAACG**A**TCGATAAAACAGGTATCGATCGTTTATATCGATCGTTTATAGTGGTTAATGGCCTGCGAAAAGGCAG

-10 box +1

CTGAATCTCTTCATCATG

Figure S1. Sequence alignment of *cah* (**A**) and predicted *cah* promoters (**B**). ClustalW alignment of cloned DNA fragment containing *cah* and its up- and down stream genes. The two EDL933-*cah* DNA fragments display 100% identify, whereas the identity between cloned EDL933-*cah* and SS17-*cah* is 95.6%. The alignmet was generated in Geneious (Geneious®8.1.8, Biomatters). R1 represents synonymous mutations detected in SS17-*cah* coding regions, which does not alter the amino acids in Cah. R2 reprents the large deletion shown in Figure 2. The promoters were predicted using BPROM progam at SoftBerry website. The start codon of *cah* is indicated in red box. -10 and -35 regions in a promoter are indicated in blue boxes. The predicted transcrption sites (+1) are in bold and underlined.

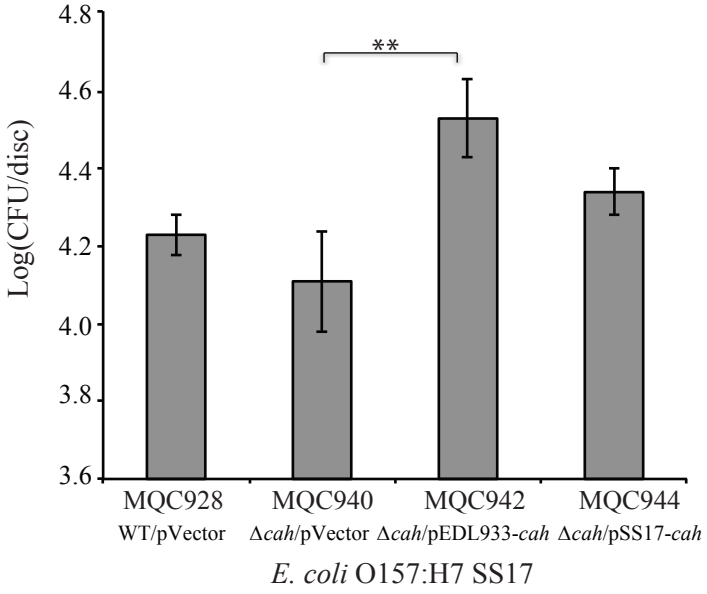


Figure S2. Contribution of Cah to attachment of *E. coli* O157:H7 to spinach leaves. Bacterial adhesion to baby spinach leaves was assessed in STEC strain SS17 wild type (WT) and *cah* deletion mutant. The population of attached SS17 cells on spinach leaves was expressed as CFUs per disc. Strain MQC928 is the SS17 WT strain transformed with the expression vector pBBR1MCS. Strain MQC940 is the SS17Δ *cah* mutant transformed with the expression vector pBBR1MCS. Strain MQC942 is the SS17Δ*cah* mutant transformed cloned EDL933-*cah*. Strain MQC944 is the SS17Δ*cah* mutant transformed with with cloned SS17-*cah*. Each bar represents the average number of attached cells and SEM from two discs of tissue per leaf and from four replicate leaves. ** indicates significant differences in the means between two strains (Tukey's Multiple Comparisons test, $P<0.001$).

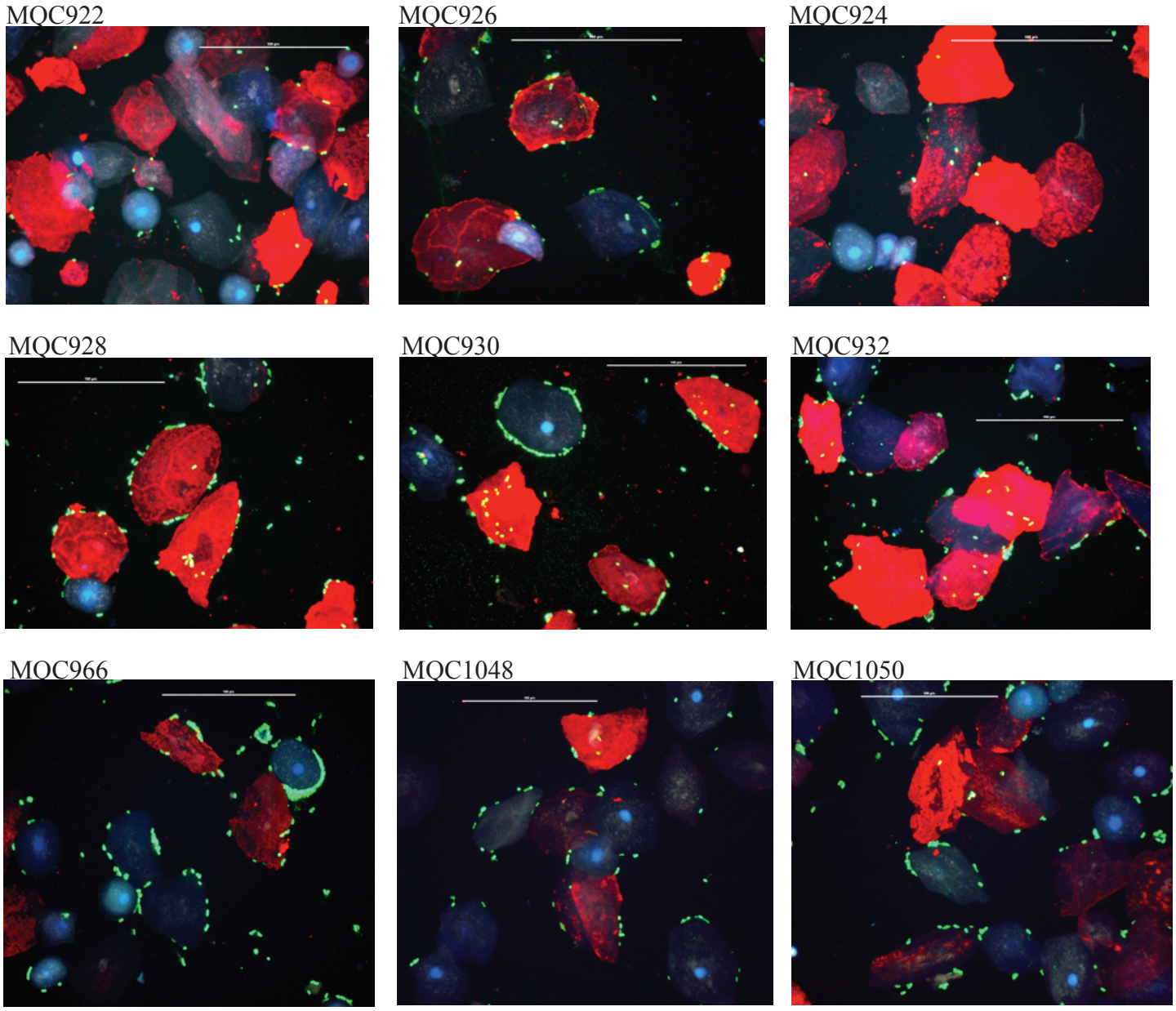


Figure S3. Adherence patterns of *E. coli* DH5α and *E. coli* O157:H7 strains SS17 and EDL933 on bovine RSE cells. Immunofluorescence stained slides are shown at 40x magnification. Bacteria are indicated by green fluorescence, RSE cells' cytokeratins are indicated by red fluorescence, and their nuclei are indicated by blue fluorescence. Strains MQC922, MQC926, and MQC924 are *E. coli* DH5a cells transformed with empty expression vector, cloned EDL933-*cah*, and cloned SS17-*cah*, respectively; whereas strain MQC928, MQC930, and MQC932 are *E. coli* O157:H7 strain SS17 carrying empty expression vector, cloned EDL933-*cah*, and cloned SS17-*cah*, respectively. Strain MQC966 is the strain EDL933 transformed with empty expression vector, strain MQC1048 is the EDL933Δ*cah* mutant transformed with empty expression vector, and strain MQC1050 is the EDL933Δ*cah* mutant transformed with cloned EDL933-*cah*.