Supplementary Figures

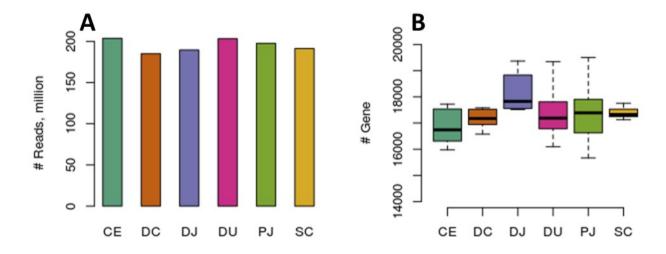
Host mechanisms involved in cattle *Escherichia coli* O157 shedding: a fundamental understanding for reducing foodborne pathogen in food animal production

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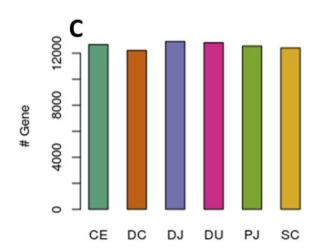


Figure S1. RNA-Sequencing results: (A) Number of reads generated for all tissue samples, ranged from 185 million to 203.7 million. (B) Number of genes detected in each sample, ranged from 16,846 ± 639 (CE) to 18,137 ± 696 (DJ). (C) Number of genes in core transcriptome of each gene, ranged from 12,216 (in DC) to 12,905 (in DJ). DU, duodenum; PJ, proximal jejunum; DJ, distal jejunum; CE, cecum; SC, spiral colon; DC, descending colon.

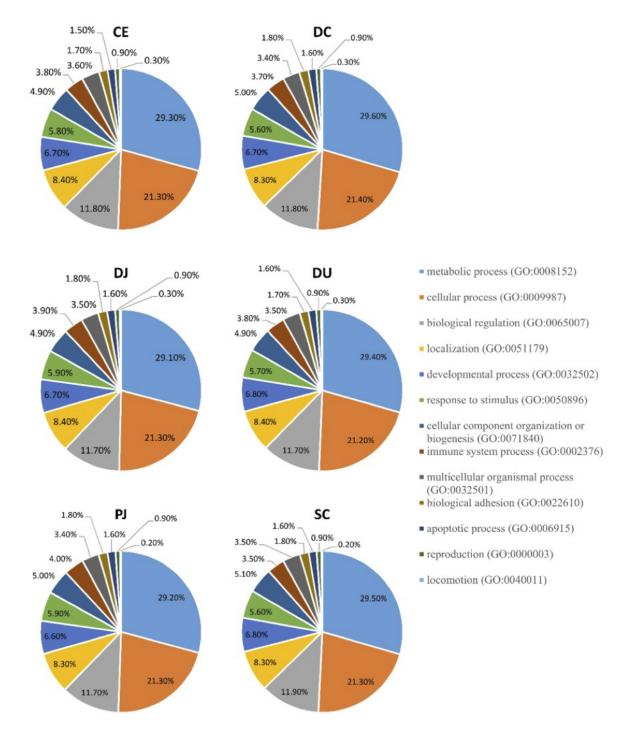


Figure S2. Top GO terms enriched for core transcriptome of each intestinal region. The pie charts indicated the percentage of "number of genes / number of GO term hits" scale. About 50% of genes are associated with two GO terms including "metabolic process", "cellular process". DU, duodenum; PJ, proximal jejunum; DJ, distal jejunum; CE, cecum; SC, spiral colon; DC, descending colon.

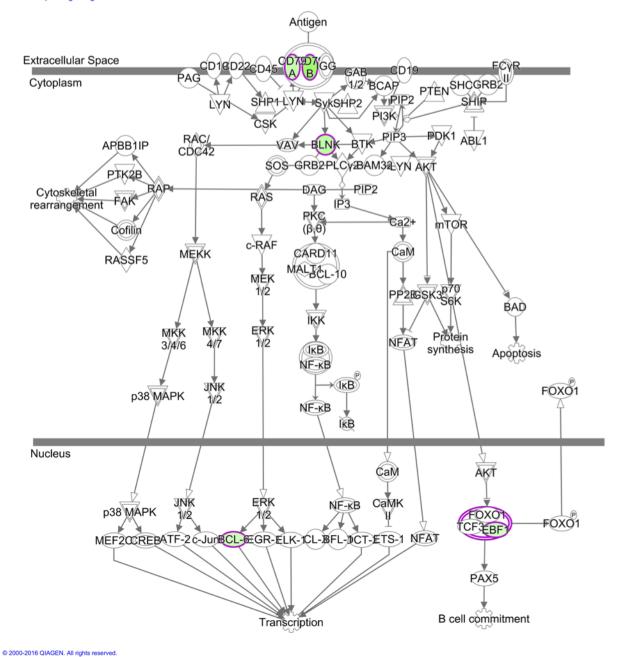


Figure S3. B-cell signalling pathway, the green coloured genes were down-regulated in the distal jejunum of super-shedders. The figure was generated using Ingenuity Pathway Analysis (IPA, QIAGEN, Redwood City, CA, United States www.qiagen.com/ingenuity). Permission was granted by QIAGEN Silicon Valley to use the copyrighted figure for publication. Figures produced from IPA are available under an open-access CC-BY license for purposes of publication.