

Supplementary Table S6. Annotation of variants identified in genes having differential expression between *E. coli*(+) and *E. coli*(-).

| Gene | BT A | SNP | MAF POS | REF | AL T | +ve cows (n) | MAF NEG | -ve cows (n) | Consequence | Impact | Gene_ensembl | Existing varn |
|-----------------|---------|-----------|------------|-----|---------|--------------------|------------|--------------------|-------------------------|----------|--------------------|---------------|
| <i>EYA3</i> | 2 | 125367162 | 0.25 | G | T | 8 | 0.833 | 9 | intron_variant | MODIFIER | ENSBTAG00000043989 | rs110270588 |
| <i>RAC2</i> | 5 | 75664664 | 0.278 | G | T | 9 | 0.833 | 9 | intron_variant | MODIFIER | ENSBTAG00000011043 | rs137621320 |
| <i>GNG7</i> | 7 | 21014556 | 0.25 | G | C | 8 | 0.813 | 8 | intron_variant | MODIFIER | ENSBTAG00000007644 | rs209187815 |
| <i>ARHGAP26</i> | 7 | 54231683 | 0.833 | A | G | 9 | 0.222 | 9 | intron_variant | MODIFIER | ENSBTAG00000027151 | rs42350004 |
| <i>EBF1*</i> | 7 | 70585950 | 0.063 | G | T | 8 | 0.833 | 9 | intron_variant | MODIFIER | ENSBTAG00000037508 | |
| <i>EBF1*</i> | 7 | 70585950 | 0.875 | G | C | 8 | 0.111 | 9 | intron_variant | MODIFIER | ENSBTAG00000037508 | rs41656037 |
| <i>FAM129A</i> | 16 | 66006047 | 0.25 | A | G | 8 | 0.889 | 9 | intron_variant | MODIFIER | ENSBTAG00000014548 | rs41817426 |
| <i>WIPI1</i> | 19 | 61782120 | 0.25 | T | C | 8 | 0.889 | 9 | downstream gene variant | MODIFIER | ENSBTAG00000010637 | rs41928661 |
| <i>ARSG*</i> | 19 | 61782120 | 0.25 | T | C | 8 | 0.889 | 9 | intron_variant | MODIFIER | ENSBTAG00000039556 | rs41928661 |
| <i>ARSG*</i> | 19 | 61874326 | 0.813 | C | A | 8 | 0.167 | 9 | intron_variant | MODIFIER | ENSBTAG00000003074 | rs450146987 |
| <i>SLC16A6</i> | 19 | 61874326 | 0.813 | C | A | 8 | 0.167 | 9 | intron_variant | MODIFIER | ENSBTAG00000010637 | rs450146987 |
| <i>PFKFB4</i> | 22 | 51327126 | 0.938 | A | G | 8 | 0.222 | 9 | intron_variant | MODIFIER | ENSBTAG00000006752 | rs42013635 |
| <i>BOLA-DOA</i> | 23 | 7314809 | 0.063 | T | G | 8 | 0.889 | 9 | downstream gene variant | MODIFIER | ENSBTAG00000006490 | Not reported |
| <i>CCND3</i> | 23 | 15736092 | 1 | T | C | 8 | 0.056 | 9 | intergenic_variant | MODIFIER | Not reported | rs110778610 |