Figure 1S. Intracellular expression of LL37 causes bactericidal effect on *E. coli* TOP10 strain. *E. coli* TOP10 cells that carried pHERD30T-LL37 was treated with L-arabinose at different growth stages, OD=0.012 (■), OD=0.536 (♦) OD=1.425(×) and control (●). Arrows indicate the beginning of the addition of L-arabinose. The experiment was repeated three times with similar results.

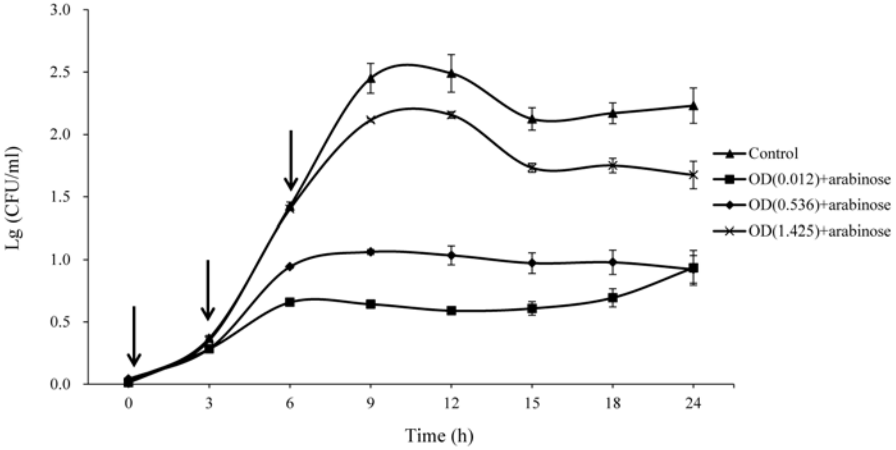

Figure S2. Cell morphology of *E.coli* after intracellular induction of LL-37 expression under aerobic growth condition. Cell membranes were stained with FM 4-64 and visualized in *E.coli* containing the empty plasmid (A), in the control cell (B) and cell after intracellular expression LL37 for 3 hours (C).

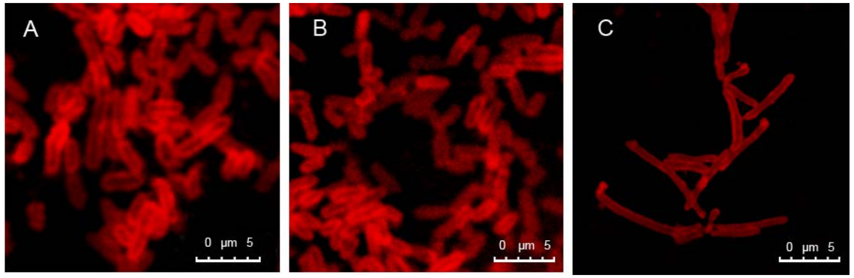

Figure S3. Comparison of genes expression data in *E. coli* TOP10 under aerobic and anaerobic conditions after intracellular expression of LL-37. The numbers of common genes are shown in the Venn diagram. Red or blue arrows indicate the up- or down-regulated genes.

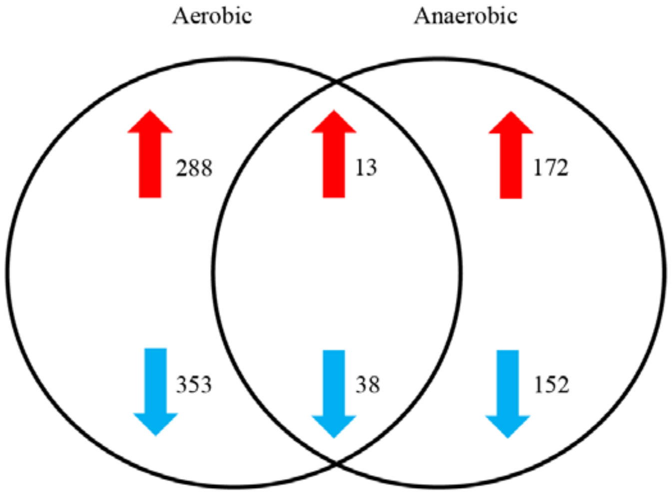

Figure S4. The morphology of *E.coli* when exogenous LL-37 were added into LB medium during bacterial growth.

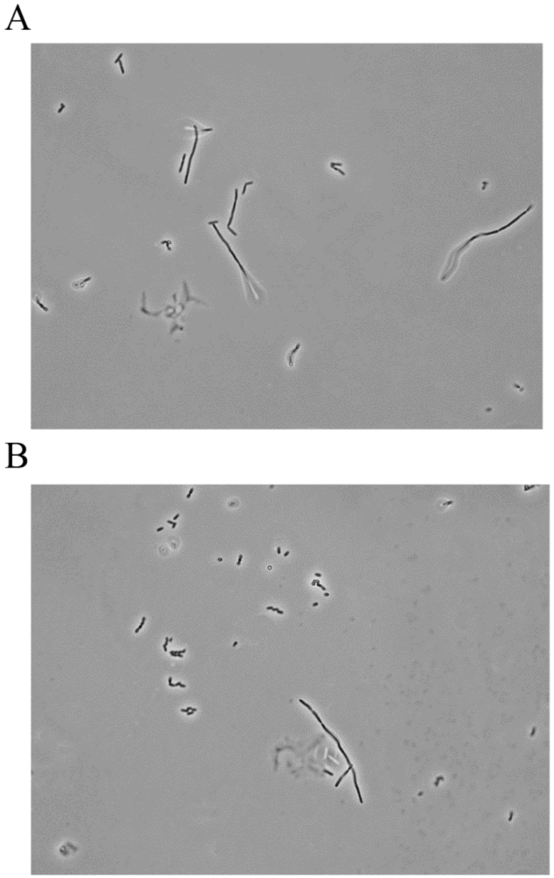

Table S1 Functional classification of the identified genes in *E. coli* based on the Clusters of Orthologous Groups of proteins (COGs) annotation at NCBI (www.ncbi.nlm.nih.gov/COG). The functional category codes are as follows: C, energy production and conversion; D, Cell cycle control, cell division, chromosome partitioning; E, amino acid transport and metabolism; F, nucleotide transport and metabolism; G, carbohydrate transport and metabolism; H, coenzyme transport and metabolism; I, lipid transport and metabolism; J, Translation, ribosomal structure and biogenesis; K, transcription; L, replication, recombination and repair; M, cell wall/membrane biogenesis; N, cell motility; O, posttranslational modification, protein turnover, chaperones; P, inorganic ion transport and metabolism; Q, secondary metabolites biosynthesis, transport and catabolism; R, general function prediction only; S, function unknown; T, signal transduction mechanisms; U, defense mechanisms; V, Intracellular trafficking, secretion, and vesicular transport –, not in COGs.

| | Aerobic | | | | Anaerobic | | | | Common genes regulated | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| COG | UP-regulated | Rate | Down- regulated | Rate | Up- regulated | Rate | Down- regulated | Rate | Up- regulated | Rate | Down- regulated | Rate | Total COG number |
| - | 70 | 0.090 | 44 | 0.056 | 37 | 0.047 | 17 | 0.022 | 2 | 0.003 | 5 | 0.006 | 779 |
| A | 0 | 0.000 | 1 | 0.500 | 0 | 0.000 | 0 | 0.000 | 0 | 0.000 | 0 | 0.000 | 2 |
| C | 15 | 0.160 | 54 | 0.189 | 8 | 0.028 | 16 | 0.056 | 0 | 0.000 | 5 | 0.018 | 285 |
| D | 1 | 0.029 | 3 | 0.086 | 0 | 0.000 | 0 | 0.000 | 0 | 0.000 | 0 | 0.000 | 35 |
| E | 26 | 0.074 | 43 | 0.123 | 10 | 0.028 | 9 | 0.026 | 0 | 0.000 | 2 | 0.006 | 351 |
| F | 4 | 0.043 | 9 | 0.096 | 3 | 0.032 | 4 | 0.043 | 0 | 0.000 | 0 | 0.000 | 94 |
| G | 17 | 0.049 | 55 | 0.157 | 16 | 0.046 | 20 | 0.057 | 1 | 0.003 | 8 | 0.023 | 350 |
| H | 5 | 0.032 | 2 | 0.013 | 3 | 0.019 | 5 | 0.032 | 0 | 0.000 | 0 | 0.000 | 157 |
| I | 3 | 0.031 | 18 | 0.186 | 5 | 0.052 | 1 | 0.010 | 0 | 0.000 | 0 | 0.000 | 97 |
| J | 8 | 0.043 | 9 | 0.049 | 5 | 0.027 | 7 | 0.038 | 0 | 0.000 | 0 | 0.000 | 184 |
| K | 40 | 0.132 | 12 | 0.040 | 20 | 0.066 | 19 | 0.063 | 0 | 0.000 | 3 | 0.010 | 302 |
| L | 35 | 0.167 | 8 | 0.038 | 9 | 0.043 | 9 | 0.043 | 0 | 0.000 | 2 | 0.010 | 209 |
| M | 11 | 0.046 | 15 | 0.063 | 7 | 0.029 | 8 | 0.033 | 1 | 0.004 | 2 | 0.008 | 239 |
| N | 19 | 0.183 | 2 | 0.019 | 5 | 0.048 | 6 | 0.058 | 0 | 0.000 | 0 | 0.000 | 104 |
| O | 28 | 0.192 | 17 | 0.116 | 5 | 0.034 | 10 | 0.068 | 1 | 0.007 | 0 | 0.000 | 146 |
| P | 30 | 0.136 | 17 | 0.077 | 6 | 0.027 | 12 | 0.054 | 0 | 0.000 | 3 | 0.014 | 221 |
| Q | 4 | 0.058 | 7 | 0.101 | 2 | 0.029 | 3 | 0.043 | 0 | 0.000 | 1 | 0.014 | 69 |
| R | 27 | 0.068 | 44 | 0.110 | 18 | 0.045 | 20 | 0.050 | 2 | 0.005 | 6 | 0.015 | 399 |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| S | 32 | 0.102 | 41 | 0.131 | 20 | 0.064 | 23 | 0.073 | 1 | 0.003 | 4 | 0.013 | 314 |
| T | 16 | 0.091 | 7 | 0.040 | 7 | 0.040 | 8 | 0.045 | 2 | 0.011 | 1 | 0.006 | 176 |
| U | 2 | 0.016 | 15 | 0.116 | 8 | 0.062 | 6 | 0.047 | 1 | 0.008 | 0 | 0.000 | 129 |
| V | 6 | 0.146 | 0 | 0.000 | 2 | 0.049 | 0 | 0.000 | 1 | 0.024 | 0 | 0.000 | 41 |